Supplementary Table S2: All "Scaffold" validated proteins and peptides identified from solprotSP *S.pombe*) and from SCVMprot (*S.cerevisiae*) samples

S.pombe **- Trypsin - Whole tryptic digest**

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
1	G3P1_SCHPO	55.95%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
127	145	2	2152.02	4	1	99.2	22.7	95.00%	K.DAPMYVVGVNEEKFNPSEK.V	
324	334	2	1148.65	6.2	0	55.4	14.9	95.00%	R.VVDLVAYTAAK.D	
249	259	3	1290.69	4.5	0	28.4	19.1	93.90%	K.LAKPTNYEDIK.A	
67	86	3	2203.13	3.8	1	43.2	19.7	95.00%	K.LVIDGNAIDVHNERDPADIK.W	
163	186	2	2576.29	4.6	0	94.8	21	95.00%	K.VINDTFGIEEGLMTTVHATTATQK.T	
56	66	2	1193.6	4.2	1	61.8	20.9	95.00%	R.FDGSVEIKDGK.L	
119	139	2	2245.18	4	1	70	18.5	95.00%	R.VIISAPSKDAPMYVVGVNEEK.F	
324	336	2	1377.72	3.8	1	68.7	19.7	95.00%	R.VVDLVAYTAAKDN.-	
235	248	2	1467.82	3.7	0	76.5	14.5	95.00%	R.VPTPDVSVVDLTVK.L	
127	139	2	1449.69	3.7	0	45.1	20.7	95.00%	K.DAPMYVVGVNEEK.F	
323	334	2	1304.75	5.7	1	40.6	12.3	95.00%	R.RVVDLVAYTAAK.D	
6	13	2	819.43	6.2	0	38.4	19.9	95.00%	K.VGINGFGR.I	Deamidation (+1)
201	215	2	1343.71	4.7	0	69.9	19	95.00%	R.GASANIIPSSTGAAK.A	
87	113	2	2885.38	3.9	0	116	22.7	95.00%	K.WSTSGADYVIESTGVFTTQETASAHLK.G	
146	162	2	1818.91	4.5	0	75	21.9	95.00%	K.VISNASCTTNCLAPLAK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
2	PGK_SCHPO	74.15%	100%	28

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
359	379	2	2046.05	4.7	1	96.9	19.2	95.00%	K.TCEAGNVVIVGGGDTATVAKK.Y	Carbamidomethyl (+57)
359	378	2	1917.95	4	0	118	20.8	95.00%	K.TCEAGNVVIVGGGDTATVAK.K	Carbamidomethyl (+57)
7	15	2	986.57	5.4	0	41.1	16.6	95.00%	K.LAITDVDLK.G	
250	269	3	2127.99	3.6	1	36.8	22.8	95.00%	K.IGDSLFDEAGSKNVESMMAK.A	
273	288	2	1805.93	4.9	0	56.9	20.1	95.00%	K.NNVEVFLPVDFVTADK.F	
140	150	2	1163.6	4.3	1	57.5	19.7	95.00%	K.ADASAVEAFRK.S	
123	132	3	1145.54	4.7	0	33.9	21.1	95.00%	R.FHIEEEGSAK.V	
23	39	2	1914.96	4.6	1	38	20.8	95.00%	R.VDFNVPLDGDRITNNAR.I	
57	71	2	1591.87	2.9	0	46.2	16.1	95.00%	K.AVILMSHLGRPNGAR.V	Deamidation (+1)
23	33	2	1245.61	6.8	0	62.1	20	95.00%	R.VDFNVPLDGDR.I	
112	122	2	1211.69	4.5	0	57.3	12	95.00%	K.GGEVILLENLR.F	
330	347	2	2010.99	4.7	0	67	20	95.00%	K.TIVWNGPAGVFEFDNFAK.G	
218	230	3	1552.9	4.8	1	31.7	11.8	95.00%	K.IQLIDNLLDKVNR.L	
218	227	2	1183.69	5.5	0	39.2	15.3	95.00%	K.IQLIDNLLDK.V	
250	261	2	1237.59	4.5	0	61.5	20.1	95.00%	K.IGDSLFDEAGSK.N	
404	414	2	1040.63	5.6	0	39.4	14.9	95.00%	K.ALPGVVALSSK.-	
380	403	3	2417.21	2.5	1	72	21.2	95.00%	K.YGKEDALSHVSTGGGASLELLEGK.A	
383	403	2	2069.04	3.6	0	81.1	20.8	95.00%	K.EDALSHVSTGGGASLELLEGK.A	
75	86	3	1304.74	4.3	0	59.4	14.6	95.00%	K.YSLKPVAAELSK.L	
321	329	2	994.54	5.5	0	50.2	17.3	95.00%	K.FAEVITTSK.T	
94	105	2	1406.64	3.6	0	56.7	21.4	95.00%	K.FLDDCVGPEVEK.A	Carbamidomethyl (+57)
197	213	2	1737	3.5	0	54.1	10.4	95.00%	K.ALENPARPFLAILGGAK.V	
295	316	2	2246.01	3.8	0	60.5	23.4	95.00%	K.VGSATAEEGIPDGWMGLDCGPK.S	Carbamidomethyl (+57)
151	169	2	2020.01	5.9	0	113	21.5	95.00%	K.SLTSLGDIFVNDAFGTAHR.A	
170	181	2	1267.64	4	0	58.7	19.3	95.00%	R.AHSSMVGVDLPR.V	
150	169	3	2148.1	3.4	1	64.2	19.5	95.00%	R.KSLTSLGDIFVNDAFGTAHR.A	
123	136	3	1544.76	5.8	1	28.5	20.9	94.00%	R.FHIEEEGSAKVDGK.K	
214	227	2	1596.92	3.7	1	58.7	12.8	95.00%	K.VADKIQLIDNLLDK.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
3	ENO11_SCHPO	67.20%	100%	23

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
243	263	3	2346.17	3.2	1	32.7	20.6	95.00%	K.IGLDVASSEFYVDGKYDLDIK.A	
361	374	3	1608.73	4.7	0	47.1	22.3	95.00%	R.MSYEAGWGVMVSHR.S	
185	194	2	1204.59	5.4	0	34	20.6	95.00%	R.WGAETYHTLK.S	
346	360	2	1585.85	6	0	90.8	17.2	95.00%	K.VNQIGSVTESLNAVR.M	
311	328	2	1963.98	4.2	0	93.2	21	95.00%	K.AETDFQIVGDDLTVTNVK.R	
89	103	2	1662.85	3.3	1	74.4	19.3	95.00%	K.AADEFLLKLDGTENK.S	
288	310	3	2807.3	4.5	1	61.4	24.4	95.00%	K.KYPIVSIEDPFDQDDWSAWTHMK.A	
201	234	3	3440.71	3.8	0	65	20.1	95.00%	R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A	
289	310	3	2679.2	3	0	73.2	24.9	95.00%	K.YPIVSIEDPFDQDDWSAWTHMK.A	
65	79	2	1477.87	4	0	73.7	6.99	95.00%	K.AVGNVNNIIAPAVVK.A	
106	120	2	1560.82	4.2	0	61.3	18.8	95.00%	K.LGANAILGVSMAICR.A	Oxidation (+16)/ Carbamidomethyl (+57)
311	329	2	2120.09	4.8	1	105	19.4	95.00%	K.AETDFQIVGDDLTVTNVKR.L	
273	287	2	1812.96	4.5	0	75.4	17.8	95.00%	K.LTYQQLTDLYVELSK.K	
200	234	3	3596.81	3.8	1	68.4	20.1	95.00%	K.RYGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A	
243	257	2	1598.79	4.2	0	56.6	20.2	95.00%	K.IGLDVASSEFYVDGK.Y	
16	32	2	1837.92	4	0	84.2	20.8	95.00%	R.GNPTVEVDLTTETGIHR.A	
33	50	2	1886.97	4.8	0	105	20.2	95.00%	R.AIVPSGASTGIWEALEMR.D	
338	345	2	901.51	4.7	0	31.4	17.9	95.00%	K.CANALLLK.V	Carbamidomethyl (+57)
409	414	2	806.43	5.7	0	29.4	19.8	94.00%	K.YNELLR.I	
415	432	2	1815.87	5.1	0	83.2	21.8	95.00%	R.IEEELGSEGVYAGAHAGK.Y	
375	396	2	2201.14	2.9	0	122	19.5	95.00%	R.SGETADTFISHLTVGIGAGQLK.S	
89	96	2	905.49	4.7	0	57.4	18.1	95.00%	K.AADEFLLK.L	
80	88	2	1002.5	4.3	0	41.9	19.4	95.00%	K.ANLDVTDQK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
4	METE_SCHPO	63.48%	100%	36

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
434	449	2	1746.97	7	0	46.9	14.1	95.00%	K.LPLFPTTTIGSFPQTK.E	
461	474	2	1667.86	3.6	1	67.6	18.2	95.00%	K.GLISQEEYDAFIRK.E	
684	690	2	813.51	5.6	0	34.2	15.8	95.00%	K.LLNVLSR.Y	
393	404	2	1284.67	4.4	0	68.2	17.4	95.00%	R.AESPITNVEAVR.E	
707	716	3	1186.64	4.9	1	25.6	17	90.50%	R.VPPVSEFKER.I	
391	404	2	1511.81	4	1	42.1	18.4	95.00%	K.ARAESPITNVEAVR.E	
325	352	3	3040.6	2.2	1	77.8	15.9	95.00%	R.VQVASSSSILHIPHSLSGEDQINPEIKR.W	
325	351	3	2884.5	3.5	0	47.3	16.3	95.00%	R.VQVASSSSILHIPHSLSGEDQINPEIK.R	
261	273	2	1330.78	4	0	55.7	11.1	95.00%	K.GLPIAGVHVDVVR.A	
104	121	2	1742.9	4.6	1	66.3	19.5	95.00%	R.AATADKAAVDVPAGEMVK.W	
281	299	2	1881.08	4.8	0	87.4	8.45	95.00%	R.ALAVLGENQIISVGVVSGR.N	
147	155	2	1034.53	5.7	0	36.8	20.5	95.00%	K.ALDEFLEAK.E	
547	560	2	1596.79	3.6	0	50.8	21	95.00%	K.ESQYAQSITSKPMK.G	
461	473	2	1539.76	4.1	0	67.2	20	95.00%	K.GLISQEEYDAFIR.K	
668	679	2	1288.66	3.8	0	37	20.3	95.00%	R.LDADVVSIENSK.S	
527	546	3	2267.24	3.3	0	44.5	14.3	95.00%	R.CVRPPIIVGDVYRPAPMTVK.E	Carbamidomethyl (+57)
631	637	2	877.45	5.9	0	49	18.7	95.00%	K.WAIDAFR.L	
577	601	3	2805.42	3	1	36.5	20.1	95.00%	R.DDVHDSVQAQQIALGLRDEVLDLEK.A	
122	146	3	3061.45	2.7	1	31	23.5	95.00%	K.WFDSNYHFLRPEVSEETDFKLSSTK.A	
156	176	3	2256.33	3.9	0	51.3	4.77	95.00%	K.EAGIITRPVLVGPVTYLFIAK.A	
561	571	2	1184.7	5.1	0	40.5	13.8	95.00%	K.GMLTAPITILR.W	
622	630	2	1208.59	4.8	1	31.8	20.3	95.00%	R.RAEWDEYLK.W	
638	667	3	3497.61	3.2	0	56.4	24.9	95.00%	R.LATAAVQDDTQIHSHFCYSDFNDIFDAIQR.L	Carbamidomethyl (+57)
4	11	2	845.48	4.8	0	33.3	19.4	95.00%	K.SAVLGFPR.I	
707	714	2	901.49	4.3	0	27.7	20.9	91.90%	R.VPPVSEFK.E	
691	706	2	1818.88	3.8	0	84	21.7	95.00%	R.YTSCIGPGLFDIHSPR.V	Carbamidomethyl (+57)
499	508	2	1257.55	4.4	0	53.6	20.7	95.00%	R.NDMVQYFGER.M	
243	260	2	1982.08	3.5	0	54.1	14.3	95.00%	K.LILTTYFGSLQSNADVLK.G	
727	738	2	1466.7	4.2	0	48	22	95.00%	K.DHLWLNPDCGLK.T	Carbamidomethyl (+57)

428	449	3	2402.33	4.8	1	46	11.5	95.00%	K.QQASLKLPLFPTTTIGSFPQTK.E	
361	369	2	1017.56	4.9	0	30.5	17.4	95.00%	K.CAELAILTK.A	Carbamidomethyl (+57)
606	615	2	1199.6	4.3	0	55.1	19.7	95.00%	K.VIQCDEPALR.E	Carbamidomethyl (+57)
482	508	3	3191.51	3.7	1	53.5	23.3	95.00%	K.FQEEVGLDVLVHGEPERNDMVQYFGER.M	
85	99	2	1616.79	4.1	0	63.5	21.7	95.00%	R.LSGLSSLDTYFAMGR.G	
52	82	3	3521.71	3.5	0	48.3	22.4	95.00%	K.AQGVDIIPSNDFSLYDQIMDHSFSFNVIPPR.Y	
30	40	2	1132.6	4.2	0	58.1	17.2	95.00%	K.TSAEELLATAK.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
5	EF1A1_SCHPO	44.57%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
265	288	2	2443.35	3.1	0	42.3	13.4	95.00%	R.VETGVIKPGMIVTFAPAGVTTEVK.S	
223	245	4	2516.4	3.1	1	25	11.5	95.00%	K.GKTLLEAIDSIEPPARPTDKPLR.L	
185	214	3	3453.63	3.7	0	49.2	23.9	95.00%	K.TVPFVPVSGFQGDNMIEPTTNMPWYQGWQK.E	
135	146	2	1313.74	3.9	0	45.8	16.5	95.00%	R.EHALLAYTLGVK.Q	
165	177	2	1582.83	3.8	1	66.1	18	95.00%	R.FEEIVKETSNFIK.K	
402	421	2	2268.08	4	0	67.5	22.3	95.00%	K.MVPSKPMCVEAFTDYAPLGR.F	Carbamidomethyl (+57)
254	264	2	1024.61	4.2	0	65.4	12.6	95.00%	K.IGGIGTVPVGR.V	
6	20	2	1529.84	4.6	0	62.9	16.9	95.00%	K.GHINVVVIGHVDSGK.S	
289	311	3	2451.16	4	0	64.2	23.3	95.00%	K.SVEMHHESLDAGLPGDNVGFNVK.N	
85	100	4	1843.97	4.9	1	22.1	19.1	94.00%	K.YNVTVIDAPGHRDFIK.N	
225	245	3	2331.29	2.6	0	34.8	13.6	95.00%	K.TLLEAIDSIEPPARPTDKPLR.L	
155	164	2	1151.51	6.4	0	75.8	19.9	95.00%	K.MDTTGWSQAR.F	
85	96	2	1340.69	4.4	0	66.1	18	95.00%	K.YNVTVIDAPGHR.D	
246	253	2	974.55	4.1	0	32.1	18	95.00%	R.LPLQDVYK.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
6	KPYK_SCHPO	74.66%	100%	27

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
233	243	2	1214.66	3.9	1	28.5	18.7	93.00%	R.EVLGEEGKNIK.I	
422	433	3	1430.81	4.6	0	41.1	12.6	95.00%	K.YRPSIPIVMVTR.C	
128	138	2	1447.65	4.4	1	38.9	22.5	95.00%	K.CNDKVMYIDYK.N	Carbamidomethyl (+57)
248	271	2	2647.3	2.3	0	73.9	22.1	95.00%	K.IENQQGVNNFDSILDVTDGIMVAR.G	
57	75	3	2254	4.4	0	44.4	23.9	95.00%	R.MNFSHGSYEYHQSVIDNAR.K	
77	98	3	2294.27	3.2	1	35.9	12.8	95.00%	K.ASATNPLFPLAIALDTKGPEIR.T	
468	477	2	1186.55	5.3	0	54.8	19.9	95.00%	R.VAYGCQQAYK.M	Carbamidomethyl (+57)
361	380	2	2229.12	4.2	0	78.6	20.9	95.00%	R.VAEASIPYGSLYQEMFGLVR.R	
294	319	4	2965.41	3.9	0	47.2	24	95.00%	K.CNIAGKPVACATQMLESMTYNPRPTR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
405	417	2	1287.72	5.7	0	62	15.8	95.00%	K.AIVVLSTSGNTAR.L	
212	223	2	1368.69	4.2	0	39.8	19.2	95.00%	K.NGVDMIFASFIR.R	
381	404	2	2460.23	3.5	0	76.2	21	95.00%	R.RPLECATETTAVAAIGASIESDAK.A	Carbamidomethyl (+57)
487	497	2	1053.66	5.9	0	39.5	6.99	95.00%	K.IIVLQGAVGGK.G	
446	462	2	2050.05	3	1	46.6	20.7	95.00%	R.GVYPVIYEKEPLSDWQK.D	
224	232	3	1107.62	3.9	1	57.7	15.4	95.00%	R.RAEDVIHIR.E	
10	26	2	1880.98	3.7	0	90.9	18.9	95.00%	K.QWVAGLNSELDIPAVNR.R	
77	93	2	1741.97	3.8	0	39.2	16.3	95.00%	K.ASATNPLFPLAIALDTK.G	
225	232	2	951.52	5	0	30.1	18.5	94.70%	R.AEDVIHIR.E	
28	37	2	1088.6	5	0	46.3	16.6	95.00%	R.TSIICTIGPK.S	Carbamidomethyl (+57)
191	203	2	1429.74	3.8	1	45.1	19.2	95.00%	K.TDVDLPALSEKDK.A	
345	360	2	1743.82	5.3	0	80.9	21.8	95.00%	K.GSYPVEAVTYMAETAR.V	
272	288	2	1770.96	3.8	0	69.1	16.6	95.00%	R.GDLGIEIPASQVFVAQK.M	
76	93	2	1870.06	4.2	1	70.7	11.5	95.00%	R.KASATNPLFPLAIALDTK.G	
10	27	3	2037.08	4.1	1	30.7	16	95.00%	K.QWVAGLNSELDIPAVNRR.T	
320	344	2	2506.22	3.3	0	104	22	95.00%	R.AEVSDVGNAVLDGADLVMLSGETTK.G	Oxidation (+16)
99	127	3	3075.41	2.5	0	69.9	24.1	95.00%	R.TGLTVGGTDYPISSGHEMIFTTDDAYAEK.C	
47	56	3	1143.62	4.2	1	26	19.7	91.20%	K.LRDAGMNIVR.M	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
7	ALF_SCHPO	69.27%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
114	130	2	2061.93	2.7	0	57.4	23.9	95.00%	K.LLPWMDGMFEADEAYFK.I	
26	50	2	2496.31	4.1	0	69.4	17.6	95.00%	R.EHGFAIPAINVTSSSTAIAALEAAR.E	
207	234	4	2951.53	3.2	0	31.9	19.4	95.00%	R.ELSSVTPYFSIAAAFGNVHGVYKPGNVK.L	
113	130	2	2190.03	3.9	1	49.8	22.9	95.00%	K.KLLPWMDGMFEADEAYFK.I	
94	112	2	2098.02	4.1	0	63.5	21.7	95.00%	R.SIAPFFGVPVVMHSDHCAK.K	Carbamidomethyl (+57)
2	19	2	1823.05	3.8	0	65.3	12.3	95.00%	M.GILDIVPTGVITGDNVLK.L	
285	300	2	1825.89	3.9	0	73.6	21.4	95.00%	K.VNIDTDTQFAYVEGVR.D	
235	248	2	1564.88	4	0	58.4	13	95.00%	K.LQPALLGQHQAYVK.E	
54	71	2	1844.94	0.85	0	86	20.6	95.00%	R.SPIILQTSNGGAHFFAGK.E	Deamidation (+1)
131	149	3	2165.05	3.2	0	36.1	21.2	95.00%	K.IHGEPLFSSHMLDLSEEPK.K	
80	93	2	1399.76	5.1	0	89.1	16.8	95.00%	K.ASIAGSIAAAHYIR.S	
253	275	2	2528.21	2	0	93.7	22.4	95.00%	K.TTNDKPVFFVFHGGSGSSVNEFR.T	
345	358	2	1597.83	4.2	0	60.4	18.8	95.00%	R.VLTALEDFYTVNTL.-	
131	150	4	2293.15	3.4	1	21.8	20	93.70%	K.IHGEPLFSSHMLDLSEEPKK.E	
344	358	2	1753.93	3.7	1	52.9	17.9	95.00%	K.RVLTALEDFYTVNTL.-	
306	325	2	2236.09	3.4	1	66.1	22.3	95.00%	K.YKDYLMTPVGNPEGADKPNK.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
8	PDC2_SCHPO	57.07%	100%	26

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
204	214	2	1130.62	4.6	0	53.5	18.2	95.00%	K.ATDIAAELISK.K	
516	525	2	1047.55	4.8	0	31.2	19.7	95.00%	K.TGEELTSAIK.V	
228	237	2	949.49	5	0	30.2	19.6	94.80%	R.AAGAESAFVK.L	
532	555	2	2764.23	2.9	0	69.2	25.3	95.00%	K.EGPTLIECAIDTDDCTQELVDWGK.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
147	159	2	1436.71	3.9	0	60.9	21.1	95.00%	R.AEDAPVMIDHAIR.Q	
329	340	2	1425.76	4.3	0	95.2	18.1	95.00%	R.VYMAEFLELLAK.K	
146	159	3	1592.82	5.1	1	58.6	21.1	95.00%	K.RAEDAPVMIDHAIR.Q	
379	405	2	3015.43	1.6	0	70.1	23	95.00%	R.QIQGLVDSNTTLYAETGDSWFNGLQMK.L	
369	378	2	1157.64	5	1	28	18.4	92.30%	K.AALNRVEVMR.Q	
137	146	2	1101.64	5.4	1	51.2	15.8	95.00%	K.LTCAAVAIKR.A	Carbamidomethyl (+57)

Carbamidomethyl (+57)/ Deamidation

386	398	2	1545.76	3.9	1	63.6	21.1	95.00%	K.EKDFDVLVDHAMK.D	
169	191	2	2386.26	3.6	0	87.6	17.2	95.00%	K.SSKPQLPLIAINTTAGTASEMTR.F	
192	200	2	1078.57	4	0	35.5	18.8	95.00%	R.FAIITEETR.H	
160	191	3	3376.73	2.5	1	83.5	18.1	95.00%	K.IADYEGVDKSSKPQLPLIAINTTAGTASEMTR.F	
96	129	3	3701.97	2.4	1	70.9	15.3	95.00%	K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVKK.E	
129	148	3	2121.9	5.5	1	60.5	23.8	95.00%	K.KENCDSMVSIGGGSAHDCAK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
345	365	3	2324.09	3.1	0	49.5	23.4	95.00%	R.LGDIAFHLGCEEHTAEAALDR.I	Carbamidomethyl (+57)
375	385	3	1245.76	3.9	0	37.6	3.01	95.00%	K.IRPHLVDLGVK.E	
149	159	2	1014.58	4.8	0	36.7	18.1	95.00%	K.GIALLATNGGK.I	Deamidation (+1)
399	415	2	1851.85	4.5	0	49.6	22.1	95.00%	K.DACGATNPIQPTHDEVK.A	Carbamidomethyl (+57)
96	128	3	3573.88	3.6	0	56.5	14.9	95.00%	K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K	
130	148	2	1993.8	3.7	0	87.9	23.1	95.00%	K.ENCDSMVSIGGGSAHDCAK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
160	168	2	1008.48	5	0	40.9	20.7	95.00%	K.IADYEGVDK.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
10	THI3_SCHPO	62.72%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
119	127	2	1090.54	4.7	0	29.6	19.7	94.30%	K.IQLDDLCSK.F	Carbamidomethyl (+57)
74	95	2	2353.27	3.5	0	91.4	17.2	95.00%	R.GYPVTSFGSLLNEPFTGLITLK.G	
316	327	2	1385.71	3.6	0	53.6	20.2	95.00%	K.QEAIAEIQDEIK.Q	
128	139	2	1325.67	4.2	0	42.4	19.6	95.00%	K.FGLSPSDYTAIR.C	
316	329	2	1641.86	3.3	1	68.9	18.8	95.00%	K.QEAIAEIQDEIKQK.G	
6	27	2	2631.39	2.4	0	78.6	16	95.00%	K.ITFLTNWEATPYHLPIFLAQTR.G	
63	71	2	954.54	4.5	0	51.1	11.1	95.00%	K.AMIHTLAAK.A	
222	239	2	2030.06	3.2	1	79.8	19.3	95.00%	R.AIHSATLDMLKDPVQTYK.E	
110	118	2	968.5	4.9	0	27.7	18.5	91.90%	R.IGYVGEFGK.I	
330	339	2	992.51	5.7	0	44.3	19.3	95.00%	K.GGVFSGNSLR.Y	
285	315	3	3591.67	4.6	1	37.8	24.1	95.00%	R.LGIIPQDFEPNCTNGYLTWELDPDEKDPMGK.Q	Carbamidomethyl (+57)
189	211	3	2788.29	2.8	0	29.7	23.9	95.00%	R.LANLGCCCFCTILYIAHDEFIAK.H	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)
33	56	2	2409.27	3	0	74.8	16.7	95.00%	R.EGIEVAILEPTNPSDVTALIGSGK.V	
260	273	2	1711.79	4.7	0	88.7	21.6	95.00%	R.CFAYFSHDISNVPR.D	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
11	PMGY_SCHPO	73.46%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
122	139	2	1962.92	-0.12	1	81.3	22.8	95.00%	R.SYDIAPPNGESLKDTAER.V	Deamidation (+1)
111	120	2	1271.65	5.7	0	79.8	19.7	95.00%	K.WGAEQVQIWR.R	
70	90	2	2429.25	3.7	1	89.6	19.5	95.00%	K.TCQIILEEVGEPNLETIKSEK.L	Carbamidomethyl (+57)
95	108	2	1626.77	3.9	1	67.7	22.3	95.00%	R.YYGDLQGLNKDDAR.K	
146	157	2	1320.78	4.4	1	36.9	10.4	95.00%	K.STIVPHILKGEK.V	
23	40	2	1989.07	4.6	1	64.8	16.9	95.00%	K.LNLFTGWKDPALSETGIK.E	
2	14	2	1439.81	5.3	0	52	13.8	95.00%	M.TTEAAPNLLVLTR.H	Acetyl (+42)
70	87	2	2085.08	4.2	0	96.7	18.3	95.00%	K.TCQIILEEVGEPNLETIK.S	Carbamidomethyl (+57)
53	66	2	1615.84	4.6	1	43.1	19.1	95.00%	R.GYKFDIAFTSALQR.A	
169	184	2	1714.92	4	0	69.3	17.6	95.00%	R.ALIMDLEGLTGDQIVK.R	
169	185	2	1871.02	2.9	1	111	15.1	95.00%	R.ALIMDLEGLTGDQIVKR.E	
95	104	2	1169.58	4.8	0	46.4	19.2	95.00%	R.YYGDLQGLNK.D	
186	202	2	1854	4.1	1	68.2	16.1	95.00%	R.ELATGVPIVYHLDKDGK.Y	
1	14	2	1528.84	4.4	0	53	17.1	95.00%	-.MTTEAAPNLLVLTR.H	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
12	TPIS_SCHPO	77.51%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification

160	174	2	1615.9	4.1	0	65.3	14.3	95.00%	K.IVIAYEPVWAIGTGK.T		
175	189	2	1678.84	4.6	0	84.5	20.9	95.00%	K.TATPEQAQEVHAEIR.K		
135	145	2	1242.66	4.7	0	39.7	17.5	95.00%	R.EANETINVVVR.Q		
175	190	2	1806.93	4.5	1	52	19.4	95.00%	K.TATPEQAQEVHAEIRK.W		
71	99	4	3081.49	3.4	1	33.9	22.2	95.00%	K.NGAYTGENSAQSLIDAGITYTLTGHSERR.T		
223	249	3	2961.52	3.2	0	45.2	18.6	95.00%	K.FHDIDGFLVGGASLKPEFHNIVNVHSL.-		
206	218	2	1324.61	4.4	0	76.9	22.1	95.00%	R.VIYGGSVNGGNCK.E	Deamidation (+1)/ Carbamidomethyl (+57)	
71	98	3	2925.39	4	0	98.2	23.8	95.00%	K.NGAYTGENSAQSLIDAGITYTLTGHSER.R		
206	222	2	1841.9	2.2	1	42.9	22.3	95.00%	R.VIYGGSVNGGNCKEFLK.F	Deamidation (+1)/ Carbamidomethyl (+57)	
58	70	2	1389.73	3.4	1	50	19.4	95.00%	K.DIGVGAQNVFDKK.N		
115	134	3	2176.12	2.2	0	34.6	19.5	95.00%	K.FALEQGLTVVACIGETLAER.E	Carbamidomethyl (+57)	
32	52	2	2422.27	3.5	0	66.1	16.5	95.00%	K.LNVGDVETVIFPQNMYLITTR.Q		
146	159	2	1613.86	4.5	1	61.4	19	95.00%	R.QLNAIADKVQNWSK.I		
196	205	2	971.55	5.3	0	76.1	18.2	95.00%	K.LGASVAEGLR.V		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
13	SAHH_SCHPO	45.27%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
20	35	2	1782.93	4.3	0	65	19.5	95.00%	K.ELEIAENEMPGLIAVR.E	
216	227	2	1117.62	4.3	0	46.5	18.1	95.00%	K.VAVVAGFGDVGK.G	
119	143	3	2681.36	2.8	0	63.5	19.6	95.00%	K.SFPSGKPLNMILDDGGDLTALVHER.H	
176	187	2	1255.68	4.6	0	42.1	16.3	95.00%	K.VPAINVNDSVTK.S	
318	328	2	1281.71	3.7	0	30.2	16.5	94.80%	K.DVVNIKPQVDR.Y	
407	427	2	2266.18	3.4	0	77.1	18.6	95.00%	K.LTTLTSVQSDYLGIPVDGPYK.A	
314	328	3	1665.93	5.5	1	30.5	14.3	95.00%	K.ANAKDVVNIKPQVDR.Y	
8	18	2	1118.61	3.2	0	77.1	17.7	95.00%	K.VADISLAAFGR.K	
269	280	2	1367.66	4	0	40.1	21.4	95.00%	K.EGQIFVTTTGCR.D	Carbamidomethyl (+57)
153	167	2	1647.82	4.5	0	70.1	20.7	95.00%	R.GISEETTTGVHNLYK.M	
19	35	2	1911.02	4.5	1	76.1	16.2	95.00%	R.KELEIAENEMPGLIAVR.E	
336	344	2	1006.6	5	0	31.2	10	95.00%	R.HIILLADGR.L	
174	187	3	1496.86	5	1	47.8	13.6	95.00%	K.LKVPAINVNDSVTK.S	
103	118	2	2053.94	4.3	0	72.2	23.3	95.00%	K.GETEEEYLWCIEQQLK.S	Carbamidomethyl (+57)
240	268	3	3119.56	4.6	0	62	21.3	95.00%	R.VIVTEVDPINALQAAMDGFEVTTMEEAVK.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
14	THI2_SCHPO	44.51%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
175	187	2	1431.8	4.7	0	52.1	14.9	95.00%	K.LFNATAVEDLIVK.E	
39	55	2	1962.95	4.7	0	48.4	22	95.00%	K.AYPTYSLDESFSFAPIR.E	
309	320	2	1332.68	5.8	0	60	19.8	95.00%	K.AAQEALAIFDER.K	
2	15	2	1400.77	3.8	0	74.5	16.9	95.00%	M.APATAVVTPQTAFK.T	
244	263	3	2296.15	3.2	0	39.6	20.6	95.00%	R.LASAQLVSNLHDMRPLDMNR.A	Oxidation (+16)
175	190	3	1745.96	4.6	1	37.2	15.6	95.00%	K.LFNATAVEDLIVKEGK.D	
309	321	2	1460.77	4.2	1	58.6	18.9	95.00%	K.AAQEALAIFDERK.A	
244	270	3	3048.6	3.6	1	30.2	16.2	95.00%	R.LASAQLVSNLHDMRPLDMNRAEDLIVK.G	
295	308	2	1459.67	4	0	71.7	21.9	95.00%	R.MGPTFGGMMFSGIK.A	
131	154	2	2708.37	3.9	0	66.7	20.1	95.00%	R.KPADLFLNEIGVPYEDEGDYVVVK.H	
274	294	2	2254.05	3.3	0	79.8	23.6	95.00%	R.EVFPGMIVGGMELSEFDGANR.M	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
15	GLYD_SCHPO	52.03%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
97	123	3	2996.43	3.4	0	55	22.9	95.00%	K.WGVNVQCLSGSPANMQVYQAIMPPHGR.L	Carbamidomethyl (+57)
59	67	2	998.45	5.1	0	32.9	19.7	95.00%	K.YSEGYPGAR.Y	
303	318	3	1967.95	5.1	1	36.3	22.3	95.00%	K.QCQEPAYKEYQAQVVK.N	Carbamidomethyl (+57)
334	349	2	1669.84	3.9	0	85	19.8	95.00%	K.LAADGTDSHMVLVDVK.S	

397	405	2	1124.57	4.3	1	31	19.2	95.00%	R.GFKEQDFVR.V	
2	24	2	2616.29	3.7	1	43.7	21.5	95.00%	M.SSNDSIMLTPLKEQDPTVAEIMR.H	Acetyl (+42)
146	159	2	1649.78	3.9	0	75	21.9	95.00%	K.ISAVSTYFESMPYR.V	
183	193	2	1209.62	4.5	0	57.8	19.6	95.00%	K.ILVAGTSAYCR.L	Carbamidomethyl (+57)
453	467	2	1734.83	4.4	1	41.4	22.5	95.00%	K.EVAEWASSFPLADKW.-	
361	371	2	1254.76	4.6	0	48.8	9.03	95.00%	R.VLELINIVTNK.N	
145	159	2	1777.88	3.7	1	74.5	20.7	95.00%	K.KISAVSTYFESMPYR.V	
74	85	2	1550.75	4.7	0	96.3	22	95.00%	K.FIDQIETLCQER.A	Carbamidomethyl (+57)
86	96	2	1129.62	5.1	0	54.8	19	95.00%	R.ALAAFNLDPAK.W	
413	422	2	1075.61	4.3	0	49.9	16.1	95.00%	R.ALTFAANLQK.E	
438	452	2	1729.9	3.9	0	75.9	19.4	95.00%	K.LGEGEQYPELVQLQK.E	
46	58	2	1321.64	4.2	0	41.4	21.6	95.00%	R.AVMDALGSVMSNK.Y	
160	182	3	2686.31	2.9	0	31.8	22.3	95.00%	R.VDPNTGLIDYDMLEHDAQLFRPK.I	
406	412	2	878.45	4.3	0	35.8	18.5	95.00%	R.VVDYIDR.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
16	HSP72_SCHPO	46.68%	100%	20

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
327	340	2	1400.77	3.9	0	39.7	17.2	95.00%	K.ASVNEIVLVGGSTR.I	
125	136	2	1324.65	4.5	1	66.6	20.5	95.00%	K.MRETAEAYLGGK.V	
298	309	2	1525.74	4.2	1	30.8	21.9	95.00%	R.ARFEELCADLFR.K	Carbamidomethyl (+57)
96	110	2	1689.9	5	1	31.8	17.9	95.00%	K.DGKPVLQVEYKGETK.T	
574	593	2	2297.08	4	1	88.9	23.3	95.00%	K.ETIEWLDSNTTAAKDEFEAK.Q	
219	234	2	1647.72	4.3	0	72.5	22.8	95.00%	K.ATAGDTHLGGEDFDSR.L	
324	340	2	1742.96	4.2	1	81.9	16.6	95.00%	K.VDKASVNEIVLVGGSTR.I	
457	467	2	1182.65	4.4	0	28.3	15.8	92.70%	K.FELSGIPPAPR.G	
35	47	2	1486.7	4.2	0	60.5	21.8	95.00%	R.TTPSYVAFTDTER.L	
608	647	3	3515.61	5.3	0	39.6	24.5	95.00%	K.IYQAGGAPGGMPGAAPGAAPGAAPGAAPGGDNGPEVEEVD.-	Oxidation (+16)
347	359	2	1539.75	4.6	1	52.1	21.3	95.00%	K.LVSDFFNGKEPCK.S	Carbamidomethyl (+57)
111	124	2	1611.8	4	0	69	20.9	95.00%	K.TFTPEEISSMVLMK.M	
594	607	2	1556.83	4.2	1	73.7	18.1	95.00%	K.QKELESVANPIMAK.I	
538	548	2	1351.66	4.4	0	37.5	20.3	95.00%	K.NHLESYAYSLR.N	
137	153	2	1880.93	4	0	55	20.5	95.00%	K.VTDAVVTVPAYFNDSQR.Q	
76	86	2	1309.56	4.9	0	34.7	21	95.00%	K.FDDPEVQSDMK.H	
170	185	2	1686.9	4	0	94.1	18.3	95.00%	R.IINEPTAAAIAYGLDR.S	
422	445	3	2742.36	3.4	1	32.7	21.4	95.00%	K.KSEIFSTYSDNQPGVLIQVFEGER.A	
55	69	2	1698.82	4.2	0	74.8	20.9	95.00%	K.NQVAMNPHNTIFDAK.R	
24	34	2	1227.63	5.8	0	33.2	18.8	95.00%	R.VEIIANDQGNR.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
17	METK_SCHPO	64.40%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
76	89	2	1622.72	4.2	1	61.3	21.9	95.00%	K.SIGYDDSEKGFDYK.T	
186	206	3	2311.19	3.8	1	67.9	19.6	95.00%	R.RVDTIVVSAQHADSISTEDLR.S	
339	349	2	1256.73	4.3	0	36.5	14.1	95.00%	K.NFDLRPGVLVK.S	
253	272	2	1948.95	4	0	80.8	22.4	95.00%	K.IIVDTYGGWGAHGGGAFSGK.D	
169	185	2	1946.97	4.5	0	49.1	21.6	95.00%	K.TQVTIEYEEENGAVIPR.R	
147	155	2	931.5	4.5	0	58	19.3	95.00%	K.LNAAMSVAR.R	
20	40	3	2423.15	4	1	37.1	22.9	95.00%	K.ICDQISDAILDACLKDDPFSK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
237	251	2	1429.74	3.6	0	73.6	18.8	95.00%	R.FVVGGPQGDAGLTGR.K	
90	112	3	2612.3	3.4	0	62.4	21.3	95.00%	K.TCNVLVAIEQQSPDIAQGLHYEK.A	Carbamidomethyl (+57)
328	338	2	1257.74	4.7	1	49.3	14.3	95.00%	K.TSAELVEIIRK.N	
252	272	3	2077.05	3.9	1	61	20.1	95.00%	R.KIIVDTYGGWGAHGGGAFSGK.D	
353	378	3	3055.48	3	0	68	22.4	95.00%	K.LQTPFYLSTASYGHFTDQSKPWEQPK.E	
291	299	2	856.52	4.2	0	28.1	16.4	92.50%	K.SLVAAGLAR.R	
213	226	3	1572.93	4.6	0	37.1	9.03	95.00%	K.IIKPTVPAHLLDEK.T	
113	146	3	3640.89	4.3	1	75.5	17.5	95.00%	K.ALEELGAGDQGIMFGYATDETPEKLPLTILLAHK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
18	A1EGU1_SCHPO	51.33%	100%	20

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
457	479	2	2580.33	2.4	0	74	19.4	95.00%	K.YVISQCNNALLYPALGVACVLSR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
408	433	3	2988.58	2.9	0	71.1	16.6	95.00%	K.HVERPIIFPISNPTTLMEAKPDQIDK.W	
44	57	2	1634.91	4.4	0	89.1	14.8	95.00%	R.LPPIVETLQQQVDR.C	
113	137	3	3123.44	2.7	1	30.8	24	95.00%	K.QFSDIYRYPEGCYLDIDHNDLSYIK.Q	Carbamidomethyl (+57)
439	452	2	1418.83	4.1	0	43.8	7.78	95.00%	K.ALIATGSPLPPLNR.N	
24	35	2	1469.69	4.8	1	46.8	21.1	95.00%	R.YNKDTAFTPEER.Q	
408	438	5	3561.84	2.8	1	46.8	17.9	95.00%	K.HVERPIIFPISNPTTLMEAKPDQIDKWSDGK.A	
490	500	2	1070.58	4.5	0	54.7	17.2	95.00%	K.AASDALATVPR.S	
15	23	2	955.55	4.9	0	32.8	14.9	95.00%	K.GVTLLNSPR.Y	
456	479	3	2708.42	2.3	1	27.2	16.9	92.70%	K.KYVISQCNNALLYPALGVACVLSR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
362	396	4	3654.89	2.7	1	43.8	18.4	95.00%	K.DSDFKEVPSGDINLESAIALVKPTILLGCSGQPGK.F	Carbamidomethyl (+57)
258	292	4	3747.95	3.3	0	51.5	18.3	95.00%	R.ILDHYRPDIACFNDDIQGTGAVALAAIIGALHVTK.S	Carbamidomethyl (+57)
501	517	2	1828.94	4.1	0	33.1	20.3	95.00%	R.SLFAADEALLPDLNNAR.E	
220	234	2	1781.9	4.6	1	73.9	20	95.00%	R.VRGEQYDSFLDNVIK.A	
367	396	3	3062.64	3.1	0	30.5	14.5	95.00%	K.EVPSGDINLESAIALVKPTILLGCSGQPGK.F	Carbamidomethyl (+57)
530	547	2	1889.91	4.6	1	62.5	20.7	95.00%	K.QAVSEGMSTVDLPKDDAK.L	
548	555	2	1085.63	3.7	1	31.8	16.6	95.00%	K.LKEWIIER.E	
332	339	2	964.49	5	0	34.3	17.3	95.00%	R.GNLFMIDR.C	
178	191	2	1553.75	3.5	0	59.3	21.6	95.00%	K.GHLMTLCAGLDPNR.F	Carbamidomethyl (+57)
222	234	2	1526.73	2.5	0	68.3	22.7	95.00%	R.GEQYDSFLDNVIK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
19	HSP90_SCHPO	39.63%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
522	533	2	1405.62	4.2	0	49.6	22.3	95.00%	K.DGLELEETDEEK.A	
395	410	2	2001.89	4	1	89.8	23.2	95.00%	R.CLDMFNEIAEDKENFK.T	Carbamidomethyl (+57)
465	474	2	1170.6	4.5	0	29.7	18.6	94.30%	K.NIYFITGESK.Q	
567	587	2	2339.12	5.7	0	92.3	22.7	95.00%	K.IVGSPCLLTTGQYGWSANMER.I	Carbamidomethyl (+57)
440	458	2	2199.07	3.1	0	92.7	22.6	95.00%	R.YNSLNSPDDLISLEDYITK.M	
596	606	2	1234.5	4.9	0	67.2	20.3	95.00%	R.DTSMSAYMSSR.K	
176	189	2	1812.9	4.3	1	47.4	20.5	95.00%	R.LFMKEDQLQYLEEK.T	
362	375	2	1512.78	3.1	0	77.4	18.8	95.00%	K.GVVDSEDLPLNLSR.E	
198	212	2	1787.96	4.4	0	31.7	18.1	95.00%	K.HSEFISYPIQLVVTR.E	
522	536	2	1703.79	4.7	1	72.4	22.3	95.00%	K.DGLELEETDEEKAAR.E	
290	302	2	1526.74	4	0	75.7	22.1	95.00%	K.SLTNDWEDHLAVK.H	
48	66	2	2217.11	3	1	57.3	21.5	95.00%	R.YQSLSDPHALDAEKDLFIR.I	
490	509	3	2370.22	2.7	1	37.5	19	95.00%	K.KFDVLFMVDPIDEYAVTQLK.E	
275	289	2	1790.84	4	1	67.8	23.1	95.00%	R.NPSEVTKEEYASFYK.S	
475	487	2	1548.8	4.5	0	76.3	19.2	95.00%	K.QAVENSPFLEIFR.A	
88	99	2	1282.73	5.3	0	55.5	13.6	95.00%	K.NDLINNLGVIAK.S	
34	45	2	1274.64	4	0	41.6	20	95.00%	R.ELISNASDALDK.I	
255	267	2	1520.76	4.6	1	46.2	21.2	95.00%	K.VKETTTETEELNK.T	
321	330	2	1176.6	4.2	1	27.8	19.7	91.90%	R.RAPMDLFEAK.R	
422	436	2	1574.86	4	0	34.5	16.3	95.00%	K.LGIHEDAANRPALAK.L	
34	47	2	1543.83	3.9	1	76.1	17.6	95.00%	R.ELISNASDALDKIR.Y	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
20	ILV5_SCHPO	43.07%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
84	104	2	2141.07	4.6	0	90.4	21	95.00%	K.NDTLAIIGYGSQGHGQGLNAR.D	
330	337	2	914.47	6	0	41.2	16.6	95.00%	R.GAIDWTPR.F	
314	328	2	1725.76	3.8	0	69	23.5	95.00%	K.YGLDYMFAACSTTAR.R	Carbamidomethyl (+57)

145	163	2	2074.05	4.2	0	75.2	20.4	95.00%	K.GSIIMNLLSDAAQTETWPK.I	
345	361	2	1975.97	4.3	1	90.3	21.1	95.00%	K.VLNELYDNVENGNEAKR.S	
57	70	3	1680.8	5.1	1	41.7	22.1	95.00%	R.VMDFAGTKENVWER.S	
373	383	2	1435.73	4.6	1	44.1	20.8	95.00%	R.ELYDKELEEIR.N	
123	133	2	1198.6	4.3	0	28.6	18.9	93.10%	K.QAIEDGWVPGK.T	
144	163	2	2202.15	4.4	1	56.2	18.8	95.00%	K.KGSIIMNLLSDAAQTETWPK.I	
362	372	2	1312.61	4.6	0	61.6	20.8	95.00%	R.SLEYNSAPNYR.E	
289	313	2	2687.32	3.5	0	76.3	22.4	95.00%	R.GHSPAEAFNETVEEATQSLYPLIGK.Y	
78	104	3	2906.47	2.4	1	96.6	20.3	95.00%	K.LVDYFKNDTLAIIGYGSQGHGQGLNAR.D	
190	204	2	1639.97	3.6	1	26.8	6.99	90.40%	K.IHPPKDVDVILVAPK.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
21	6PGD_SCHPO	57.72%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
188	209	3	2659.19	3.5	0	32.6	24.7	95.00%	K.MVHNGIEYGDMQLICETYDIMK.R	Carbamidomethyl (+57)
156	166	3	1228.76	4.8	0	32.1	7.78	95.00%	R.IKPIFQTLAAK.A	
98	115	3	1971.95	5.1	1	35.5	21.6	95.00%	K.GDIIVDGGNSHYPDTTRR.C	
54	67	2	1501.78	4.1	0	57.5	19.9	95.00%	K.SIVGAHSLEEFVSK.L	
98	114	2	1815.85	4.4	0	91.7	22.1	95.00%	K.GDIIVDGGNSHYPDTTR.R	
377	403	3	3164.56	3	1	45.4	21.6	95.00%	K.DITEAFREDPNLESILFHPFFTNGVEK.A	
29	37	2	1175.49	3.9	0	36.7	20.6	95.00%	K.GFTVCCYNR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
122	139	3	1718.9	4.5	1	31	18.8	95.00%	K.KGILFVGSGVSGGEEGAR.Y	
38	51	2	1579.79	4.7	1	35.6	21.1	95.00%	R.TTSRVDEFLANEAK.G	
42	51	2	1134.56	4.5	0	47.7	19.4	95.00%	R.VDEFLANEAK.G	
123	139	2	1590.81	3.9	0	62.7	19.5	95.00%	K.GILFVGSGVSGGEEGAR.Y	
80	114	4	3722.93	3.7	1	47.4	17.6	95.00%	K.AGKPVDYLIEGLAPLLEKGDIIVDGGNSHYPDTTR.R	
211	225	2	1669.74	4.6	0	69.2	22	95.00%	R.GLGMSCDEIADVFEK.W	Carbamidomethyl (+57)
140	155	2	1669.81	4.7	0	28.8	20.9	93.30%	R.YGPSLMPGGNPAAWPR.I	
269	291	2	2504.28	3.2	0	92.8	20.1	95.00%	K.WTAQNALEMGTPVSLITEAVFAR.C	
320	333	2	1592.8	4.1	0	67.9	21	95.00%	K.QLIDDLEDALYASK.I	
437	449	2	1379.79	4.1	0	52	11.5	95.00%	R.SAVLPANLLQAQR.D	
80	97	2	1925.1	4.4	0	58.2	10.8	95.00%	K.AGKPVDYLIEGLAPLLEK.G	
410	436	3	2839.48	3.6	1	74.2	18.1	95.00%	R.RVVAQAAMLGIPVPATSTGLSFYDGYR.S	
188	210	4	2815.29	3.7	1	24.9	23.8	95.00%	K.MVHNGIEYGDMQLICETYDIMKR.G	Carbamidomethyl (+57)
5	28	2	2457.3	3	0	76	16	95.00%	K.EVADFGLIGLAVMGQNLILNGADK.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
22	K6PF_SCHPO	34.82%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
364	380	3	1831.88	4.2	0	50.7	22	95.00%	R.ICEAVDSISSTAISHSR.A	Carbamidomethyl (+57)
822	839	4	2058.08	3.2	1	52.7	17.2	95.00%	K.VYTTEVIGNIISEEAHKR.F	
419	431	2	1592.73	4.2	0	27.5	21.9	91.50%	K.WQDELCNSLSSVR.K	Carbamidomethyl (+57)
586	603	3	1720.91	4.2	0	35.8	18.5	95.00%	R.VAIIHVGAPAGGMNSATR.A	
534	545	2	1352.74	4.9	1	31.9	16.7	95.00%	K.LTHEVADAIEKK.Q	
880	896	2	1696.88	4.3	0	74.6	19	95.00%	R.ANDLGNDPSSAVVIGIR.G	
927	938	2	1323.7	4.7	0	53.3	17.6	95.00%	R.DMHNLVNILAGK.T	
77	94	2	1954.97	4.6	0	62	21.3	95.00%	R.LVPGELSLSPAAEDSEWR.G	
50	74	4	2845.32	3.6	1	31.6	23.5	95.00%	R.VCNESLREDWMHVAGNNSAESVTIK.F	Carbamidomethyl (+57)
613	628	3	1700.87	4.5	0	49.7	19.8	95.00%	R.GHTPLAIDNGFSGFLR.H	
283	308	2	2620.33	3.9	0	86.3	20.2	95.00%	K.NLISAGIDSIIVCGGDGSLTGADIFR.S	Carbamidomethyl (+57)
160	183	3	2416.24	3.9	1	44	19.6	95.00%	K.SEESGAASNLESGLATPVVETLKK.A	
798	806	2	934.49	4	0	31.5	19	95.00%	K.ATFALEAGR.N	
438	460	2	2448.28	3.4	0	60.2	17.1	95.00%	K.SIVIVAEGAIDSELNHISPEDIK.N	
254	267	2	1400.75	3.4	0	49.7	18.2	95.00%	R.GWLAEGGTLIGTAR.C	
844	861	2	1860.9	4.7	0	42.3	22	95.00%	R.TAVPGHVQQGGNPTPMDR.A	
2	31	3	3467.56	3.4	0	72.4	24.8	95.00%	M.SGETVHGISCYSVVANTEDTYNQTLDFYQK.L	Acetyl (+42)/ Carbamidomethyl (+57)

197	214	2	1760.86	4.1	0	84.8	21.2	95.00%	K.IAVMTSGGDSPGMNAVVR.A	
822	838	2	1901.98	4.1	0	50.4	20	95.00%	K.VYTTEVIGNIISEEAHK.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
23	EF3_SCHPO	33.72%	100%	20

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
333	350	2	1970.01	4.8	0	86.5	19.9	95.00%	K.IPEVSTAANPEVCLETLK.A	Carbamidomethyl (+57)
739	765	4	3135.58	3.6	1	29.1	20.4	95.00%	R.IAYVAQAAFTHLGHHPDKTPSEYIQWR.F	
596	621	4	2935.49	3.5	0	34.9	19.8	95.00%	K.DVSSIIVSHDSGFLDHVVQAIIHYER.F	
531	554	3	2606.31	3	1	37.5	21	95.00%	K.ALKENSFTDELINMPIGSLSGGWK.M	
75	103	3	2944.6	3.2	0	47.9	13	95.00%	K.GLEAVANHGSVAADVEPYLVELLPAVIAK.V	
20	34	2	1599.73	5	0	78.4	22.5	95.00%	K.HLTVCDAAEEADAAK.A	Carbamidomethyl (+57)
202	213	2	1359.69	4.1	0	43.2	20.2	95.00%	K.VCTLIANADIDR.F	Carbamidomethyl (+57)
859	870	2	1330.7	4.7	1	35.3	19.2	95.00%	K.MVAEVDRAEALK.S	
35	59	2	2604.32	3.9	0	66.4	20.5	95.00%	K.ALASFVNGPIEEQDAPSQVFSAISK.Q	
351	367	2	1809.03	4.2	1	72.9	12.3	95.00%	K.AVLGEIKVPTNEEVIAK.Y	
961	994	3	3666.67	2.8	0	62.6	24.5	95.00%	R.EFTEGLTEEVWAVNNGHMTPSGHNWVSGQGSGPR.I	
281	294	2	1550.88	4.1	0	60.5	14.1	95.00%	K.LVEDPQVVAPFLPK.L	
479	493	2	1636.88	3.9	0	73.9	17.4	95.00%	R.AIVNGQVEGFPTHLR.T	
419	447	3	3168.34	2.9	0	77.1	25.7	95.00%	K.IPGGASHAEEEEEGEDLCNCEFSLAYGAK.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
133	147	2	1550.87	3.9	0	70.6	14.1	95.00%	K.AIVPSVLESIHTTGK.W	
766	777	2	1368.59	4	0	45.5	21.6	95.00%	R.FQSGEDLEAMDK.A	
881	900	3	2293.11	2.6	0	44.8	22.5	95.00%	K.EIEEHCSLLGLDAELVSHSR.I	Carbamidomethyl (+57)
358	367	2	1098.6	4.8	0	47.3	16.7	95.00%	K.VPTNEEVIAK.Y	
880	900	3	2421.2	2	1	49.3	21.7	95.00%	R.KEIEEHCSLLGLDAELVSHSR.I	Carbamidomethyl (+57)
325	350	3	2738.42	3.2	1	45.8	17.7	95.00%	R.VGNVVDGKIPEVSTAANPEVCLETLK.A	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
24	EF2_SCHPO	33.25%	100%	20

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
565	578	2	1451.69	4.3	0	44.5	22.1	95.00%	R.ESVSEPSSMTALSK.S	
353	370	2	2024.89	3.6	0	81.7	23.5	95.00%	R.AETLYEGPMDDECAVGIR.N	Carbamidomethyl (+57)
770	785	2	1798.9	4	0	39.1	20.4	95.00%	K.AYLPVNESFGFTGELR.Q	
371	384	2	1594.76	4.1	0	55	21.2	95.00%	R.NCDANAPLMIYVSK.M	Carbamidomethyl (+57)
327	346	2	2192.18	2.4	0	55.9	15.8	95.00%	K.FLPAADALMEMIVLHLPSPK.T	
442	465	2	2595.37	4.3	0	74.7	16.4	95.00%	R.IEPIEDCPAGNIIGLVGVDQFLVK.S	Carbamidomethyl (+57)
272	283	2	1498.77	4.2	0	53.9	19.5	95.00%	R.AFNMFILDPIYR.I	
466	479	2	1474.71	3.7	0	72.8	21.7	95.00%	K.SGTLTTSEVAHNMK.V	
632	651	3	2235.11	2.7	1	41.5	21	95.00%	R.KIWCFGPDTTGANVVVDQTK.A	Carbamidomethyl (+57)
633	651	2	2107.01	3.2	0	108	21.5	95.00%	K.IWCFGPDTTGANVVVDQTK.A	Carbamidomethyl (+57)
284	292	2	1051.52	4.5	0	27.5	19.2	91.60%	R.IFDAVMNSR.K	
293	302	2	1178.66	4.6	1	62.3	13.8	95.00%	R.KDEVFTLLSK.L	
244	253	2	1266.61	5.9	0	30	20.3	94.60%	R.LWGENYFNPK.T	
151	162	3	1392.86	5.8	1	25.2	4.77	90.00%	R.IRPVVVVNKVDR.A	
544	555	2	1334.69	3.5	0	47.4	19.5	95.00%	K.DLQEDHAGIPLK.I	
652	672	2	2252.19	3.3	1	46.7	16.6	95.00%	K.AVAYLNEIKDSVVAAFAWASK.E	
303	317	3	1726.94	3.8	1	43.5	16.3	95.00%	K.LEVTIKPDEKELEGK.A	
326	346	3	2320.28	3.2	1	27.9	13.4	93.40%	R.KFLPAADALMEMIVLHLPSPK.T	
586	609	3	2657.29	3.5	0	32.6	22.9	95.00%	R.IFMTAEPMSEELSVAIETGHVNPR.D	
618	631	2	1624.73	4.2	0	45	21.9	95.00%	R.IMADEFGWDVTDAR.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
25	HSP75_SCHPO	34.26%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
162	173	2	1168.66	5	0	34.3	14.6	95.00%	K.DAGAIAGLNVLR.I	
501	517	3	1779.92	5.5	0	60.6	19.1	95.00%	R.SAHIEITNSVGHLSSTK.I	
331	344	2	1437.76	3.8	0	34.4	18.1	95.00%	K.ADVHDIVLVGGSTR.I	

115	128	2	1565.81	1.4	0	60	18.7	95.00%	K.QFTAQEISAMVLTK.M		
39	51	2	1484.72	4.2	0	50.9	21.3	95.00%	R.TTPSFVAFTETER.L		
430	450	2	2374.16	5.6	0	61.9	21.8	95.00%	R.TFTTVADNQTTVTFPVYQGER.V		
96	113	2	1987.03	4.2	0	58.5	18.1	95.00%	K.VIDNNGIPTIEVNYLGEK.K		
451	472	2	2468.2	5.8	0	62.2	22.7	95.00%	R.VNCAENEPLGEFQLTGIPPMPR.G	Carbamidomethyl (+57)	
144	157	2	1552.8	4.6	0	33.7	19.3	95.00%	K.AVITVPAYFSDSQR.A		
543	564	2	2513.21	3.3	0	64.4	22.5	95.00%	K.SQLESYISNIETTISEPNVMMK.L		
174	190	2	1729.93	3.9	0	82.9	16.7	95.00%	R.IINEPTAAAIAYGLDAK.S		
114	128	2	1693.91	3.7	1	42.8	16.6	95.00%	K.KQFTAQEISAMVLTK.M		
571	595	3	2864.36	3.4	1	74	23	95.00%	K.SKIEAQLAECMSQLELEDTNTDALR.K	Carbamidomethyl (+57)	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
26	ACT_SCHPO	54.93%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
85	95	3	1514.75	5.5	0	36	20.2	95.00%	K.IWHHTFYNELR.V	
292	312	2	2216.04	5	0	63.1	22.8	95.00%	K.DLYGNVVMSGGTTMYPGIADR.M	
96	113	2	2014.03	3.9	0	59.4	19.9	95.00%	R.VAPEEHPCLLTEAPLNPK.S	Carbamidomethyl (+57)
69	84	2	1958.89	3.6	0	64.1	23.5	95.00%	K.YPIEHGIVNNWDDMEK.I	
197	206	2	1131.53	5.1	0	41.4	21.2	95.00%	R.GYTFSTTAER.E	
216	238	2	2629.27	3.5	0	106	22.5	95.00%	K.LCYVALDFEQELQTAAQSSSLEK.S	Carbamidomethyl (+57)
257	284	3	2971.48	3	0	43.9	21.3	95.00%	R.APEALFQPSALGLENAGIHEATYNSIMK.C	
1	18	2	2007.9	4	0	79.9	22.9	95.00%	-.MEEEIAALVIDNGSGMCK.A	Acetyl (+42)/ Carbamidomethyl (+57)
255	284	3	3274.66	3.2	1	82.1	19.4	95.00%	R.FRAPEALFQPSALGLENAGIHEATYNSIMK.C	
239	254	2	1789.89	5.1	0	75.2	21.2	95.00%	K.SYELPDGQVITIGNER.F	
148	177	3	3182.62	3.4	0	67.2	18.1	95.00%	R.TTGIVLDSGDGVTHTVPIYEGYALPHAIMR.L	
360	372	2	1511.7	3.8	0	34.6	21.6	95.00%	K.QEYDESGPGIVYR.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
27	TSA1_SCHPO	63.02%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
125	132	2	901.53	4.7	0	35.7	17.6	95.00%	R.GLFLIDPK.G	
89	107	2	1915.06	3.5	1	58	15.8	95.00%	R.KEGGLGGINIPLLADPSHK.V	
66	88	2	2576.29	0.89	0	97.3	20.9	95.00%	R.NAQVILTSTDSEYSHLAFINTPR.K	
111	124	2	1523.77	4.1	0	79.7	20.6	95.00%	R.DYGVLIEDAGVAFR.G	
2	26	3	2657.41	2.2	1	56.7	15.3	95.00%	M.SLQIGKPAPDFKGTAVVNGAFEEIK.L	Acetyl (+42)
2	13	2	1341.74	4.1	0	36.9	17.2	95.00%	M.SLQIGKPAPDFK.G	Acetyl (+42)
137	147	2	1224.69	4.4	0	43.5	14.6	95.00%	R.QITINDLPVGR.S	
155	175	3	2525.19	3.9	0	36.8	23.3	95.00%	R.LLDAFQFVEEHGEVCPANWHK.G	Carbamidomethyl (+57)
14	26	2	1333.69	3.6	0	40.1	19.3	95.00%	K.GTAVVNGAFEEIK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
28	TKT_SCHPO	42.92%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
364	394	3	3276.78	4.5	1	70.7	13.2	95.00%	R.KLSEIVLDALCPVLPELVGGSADLTPSNLTR.W	Carbamidomethyl (+57)
325	336	2	1449.68	6.5	0	28.4	20.6	92.90%	K.QSYPDLSNQLER.I	Deamidation (+1)
2	18	2	1869.94	4.3	0	66.2	20.8	95.00%	M.TSSSYTDIDTLAINTIR.T	
238	252	2	1719.86	5	0	57.2	21.4	95.00%	R.EAMSCTDKPTLINLK.T	Carbamidomethyl (+57)
395	407	2	1418.65	3.9	0	52.7	20.8	95.00%	R.WEGAADFQPPSSK.L	
182	193	2	1385.74	4.7	0	41.9	18.7	95.00%	K.LSNLIAVWDNNK.I	
532	547	2	1810.95	4.2	0	72.5	18.4	95.00%	R.QNLPQLENSTIENALK.G	
589	606	2	2252.07	4.5	0	58.5	22.9	95.00%	R.VVSLPCWEVFEQQPESYR.L	Carbamidomethyl (+57)
466	494	4	3206.59	2.8	0	35.7	20.9	95.00%	R.VIYVATHDSIGLGEDGPTHQPIETFAHFR.A	
253	281	3	3132.54	2.9	0	59.8	21.5	95.00%	K.TTIGYGSELQGTHSVHGSPLKPEDCVHVK.K	Carbamidomethyl (+57)
495	531	3	4013.9	2.8	0	63.2	23.6	95.00%	R.AMPNINCWRPADGNETSAAYYSALTSDSTPSILALTR.Q	Carbamidomethyl (+57)
291	303	2	1603.8	4	0	26.8	20.5	90.30%	K.TFQVPPEVYAYYK.E	
306	318	2	1423.73	4.8	1	73.3	19.6	95.00%	R.VAIASSAEEEYKK.M	
630	648	3	2046.93	3.6	0	34	23.4	95.00%	R.YVHEAFGMHTFGDSGPAPK.L	

30	49	3	1972.02	3.9	0	31.5	19.1	95.00%	K.SGHPGAPMGLAPAAHVLFSR.I		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
29	HXK2_SCHPO	38.68%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
12	24	2	1581.77	4.1	0	62.3	21.4	95.00%	K.LVNDFEYPTESLR.E	
11	24	2	1709.87	4.5	1	44.2	20.2	95.00%	K.KLVNDFEYPTESLR.E	
392	413	3	2499.23	3.2	1	59.6	22.1	95.00%	K.KSDVGVDGSLVEHYPHFVDMLR.E	
103	122	3	2360.22	3.5	0	42.1	19.7	95.00%	R.NESVKPIIDFMSDHVELFIK.E	
374	388	2	1564.83	4.1	0	56.1	17.6	95.00%	R.MSAVPIASLYLSTGR.A	
1	11	2	1334.67	4.1	1	29.9	20.6	94.50%	-.MEANFQQAVKK.L	Acetyl (+42)
163	183	3	2351.23	3.9	1	39.5	18.6	95.00%	K.GLNIPEAINKDFAQFLTEGFK.A	
266	279	2	1598.78	3.9	0	49.6	21.3	95.00%	R.YDLLLDHDTPNAGR.Q	
434	449	2	1529.79	4.8	0	96.2	19.9	95.00%	K.DGSGIGAALCALQAVK.E	Carbamidomethyl (+57)
76	86	2	1287.67	3.9	0	30.3	19.9	94.90%	R.VCWIQLLGDGK.Y	Carbamidomethyl (+57)
76	90	3	1838.91	4.7	1	25.3	21.6	90.00%	R.VCWIQLLGDGKYEMK.H	Carbamidomethyl (+57)
25	34	2	1234.62	4.3	1	29.8	19.8	94.40%	R.EAVKEFDELR.Q	
351	369	3	2219.08	3.8	1	61.5	22.1	95.00%	R.FRSDEEALYLWDAAHAIGR.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
30	PUR9_SCHPO	31.45%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
76	91	2	1843.91	3.7	1	36	21.7	95.00%	R.DIPSDEKDLVEQSIEK.I	
138	153	2	1755.86	4.1	0	89.5	20.6	95.00%	R.VTILSDPADYATFTDK.F	
551	565	2	1519.75	4.1	0	63.8	21.2	95.00%	K.YVAAPGGSVMDQAVR.D	
39	60	2	2231.08	4.2	0	97.7	22.5	95.00%	R.ESGMEVADVSSITNAPEILGGR.V	
248	259	2	1216.65	4.7	0	30.2	19.1	94.80%	R.ENIGIPAAASFK.H	
480	498	2	2018	3.8	0	84.7	21.5	95.00%	K.SNAIDLYVLDAVPAEGSER.E	
260	278	3	1874.03	3.8	1	46.3	13.4	95.00%	K.HVSPAGAAVGLPLSDVEKK.V	
526	543	2	2131.98	3.7	0	65.5	24.5	95.00%	K.DVVCASDAFFPFPDNIYR.L	Carbamidomethyl (+57)
223	244	2	2446.25	3.4	0	45.9	20.7	95.00%	K.VLCGSPGYINLMDALNSWPLVK.E	Carbamidomethyl (+57)
566	581	2	1881.9	4.3	0	55.8	22.3	95.00%	R.DTANEFNMVFSEIPLR.L	
354	362	2	1152.54	4.8	0	28.8	21.3	93.30%	K.YCVLQMDPK.Y	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
31	IPYR_SCHPO	68.86%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
240	280	3	4115.08	2.7	0	89.4	18.3	95.00%	K.SDFSLVNVSVTGSVANDPSVSSTIPPAQELAPAPVDPSVHK.W	
186	192	2	922.44	6	0	35.4	19	95.00%	R.ATNEWFR.I	
141	156	2	1774.89	4.3	0	77	20.8	95.00%	K.VLGVMALLDEGETDWK.V	
24	42	2	2112.04	4.6	0	50.5	21	95.00%	K.NGTPISSWHDIPLYANAEK.T	
114	130	2	1830.85	4	1	98.5	22.2	95.00%	K.AKGDSDPLDVCEIGEAR.G	Carbamidomethyl (+57)
170	178	2	1101.53	3.9	0	49.3	18.2	95.00%	K.LNDIEDVER.H	
43	53	2	1283.73	4	0	66.7	15.3	95.00%	K.TILNMVVEIPR.W	
193	212	3	2286.11	3.7	1	30.4	22	95.00%	R.IYKIPDGKPENSFAFSGECK.N	Carbamidomethyl (+57)
84	113	4	3616.64	3.2	0	34.2	24.9	95.00%	R.NCFPHHGYIWNYGAFPQTYEDPNVVHPETK.A	Carbamidomethyl (+57)
157	169	2	1391.81	4.1	0	37.4	10.8	95.00%	K.VIVIDVNDPLAPK.L	
8	23	2	1839.93	4.1	0	74	20.2	95.00%	R.EVGALNTLDYQVYVEK.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
32	HSP60_SCHPO	29.90%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
137	148	2	1316.6	4	0	27.4	21.8	91.30%	R.NVAAGCNPMDLR.R	Carbamidomethyl (+57)
244	256	2	1529.84	4	0	44.5	16.2	95.00%	K.VEFENPLILLSEK.K	
382	396	2	1722.82	4	1	31.1	21.5	95.00%	R.GVMADPNLTEYEKEK.L	
258	275	2	1937.07	4.4	0	74.7	14.3	95.00%	K.VSAVQDILPSLELAAQQR.R	
229	240	2	1401.72	4.3	0	35	18.8	95.00%	R.GYISPYFITDVK.S	
45	56	2	1215.69	4.9	0	52.6	15.2	95.00%	R.ASLLTGVDTLAR.A	

257	275	3	2065.16	4	1	35.3	11.8	95.00%	K.KVSAVQDILPSLELAAQQR.R	
112	128	2	1705.86	4.1	0	84.3	20.9	95.00%	K.TNEVAGDGTTTATVLTR.A	
437	453	2	1588.85	4.6	0	29.9	18	94.50%	K.AAVSEGVLPGAGTSFVK.A	
241	256	2	1873.03	4.6	1	56.5	15.1	95.00%	K.SQKVEFENPLILLSEK.K	
168	195	3	2912.47	2.9	0	40.6	20.5	95.00%	R.DITTSEEISQVATISANGDTHIGELLAK.A	
68	79	2	1313.7	4.3	0	39.3	17.2	95.00%	R.NVLIDQPFGSPK.I	
520	533	2	1570.87	4.4	0	87.2	16.1	95.00%	R.FVDLNEIGVLDPLK.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
33	G6PI_SCHPO	37.27%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
79	101	3	2602.25	2.9	1	38.9	23.1	95.00%	K.EANVEGLRDALFAGEHINFTEDR.A	
217	228	2	1343.61	5.2	0	37.3	20.7	95.00%	K.TFTTAETCTNAK.S	Carbamidomethyl (+57)
464	477	2	1502.83	4	0	36.9	16.4	95.00%	K.TFVGNRPSNSIIAK.K	
63	75	2	1499.85	3.9	0	37.5	14.6	95.00%	K.NLITEETVELLVK.L	
446	463	3	1916.99	4.1	1	36.8	18.7	95.00%	K.TPAEVKAEGTPDEIVPHK.T	
118	128	2	1170.59	4.1	0	35.5	19	95.00%	K.VNGQDVMPGVR.K	
429	445	2	1870.94	4.8	0	69.7	20.9	95.00%	R.MLFSNFAAQTEALMLGK.T	
110	128	3	2084.06	4.5	1	31.6	19	95.00%	R.NVSEKPMKVNGQDVMPGVR.K	
372	382	2	1171.52	5.1	0	67.7	20	95.00%	R.SGDMVNYTTGK.I	
2	24	2	2548.27	3.8	0	60.7	20.5	95.00%	M.SFSLASTLPAWQAVQTHYESVGK.H	Acetyl (+42)
204	216	2	1493.75	4.3	0	51.5	20.6	95.00%	K.CDPETTLFLIASK.T	Carbamidomethyl (+57)
521	547	3	2955.5	3	1	45.6	19.8	95.00%	K.NVLAQLETKGDVENHDSSTNGLINLFK.N	
353	367	2	1711.83	4.2	0	71.8	21.5	95.00%	R.FPAYLQQLSMESNGK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
34	FAS2_SCHPO	11.89%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
1569	1579	2	1292.61	5	0	41.1	20.8	95.00%	R.NADNIDEYLAR.F	
114	146	3	3020.56	3.1	0	35.9	18.6	95.00%	K.VETAAAAAPAATPAPAPAQTSAPAAALPDEPPK.A	
517	527	2	1319.7	5.4	1	32	19	95.00%	R.KLTHYVTEMAK.G	
28	44	2	1939.01	4.4	0	67.5	18.6	95.00%	R.WIETQDVILSPPVSAER.I	
568	601	4	3840.07	4	1	20.4	16.2	91.10%	K.QLYGQVLHALSLPLPSSNDEQTPVKETIPFLHIR.K	
88	113	2	2859.27	2.2	0	60.1	25	95.00%	R.EIYYNFEDEVADEPAEAPASTSSTPK.V	
488	502	3	1650.8	4.5	0	35.5	21	95.00%	K.NVNHPTAPSTTIDER.G	
914	937	3	2504.19	3.1	0	37.5	23.5	95.00%	R.AVAAETAFDHSITNGPDSEAVFQK.T	
397	406	2	1310.58	5.6	0	36.9	21.2	95.00%	R.VYDSDWNWAR.Q	
1393	1401	2	994.61	4.5	0	27.6	8.45	91.70%	K.TPLPIVDLK.F	
1785	1813	3	2858.51	3.7	1	33.9	16.9	95.00%	K.GAAAPLKDIEIISSESGAPEVVLHGEAAK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
35	GPD1_SCHPO	44.68%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
109	124	3	1938.09	3.2	1	27.6	8.45	93.20%	R.RADILVFVVPHQFIER.V	
203	232	3	3092.63	2.8	0	70.4	16.9	95.00%	R.EQIAAVFDRPYFSVVSVDDVAGVALGGALK.N	
87	104	2	2008.06	5	0	48.8	17.6	95.00%	K.YLPGIECPPNVIAVPDVR.E	Carbamidomethyl (+57)
277	296	2	2153	2.6	0	93.7	23.3	95.00%	R.TMVEQSCGIADLVTSCLGGR.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
73	86	3	1656.86	5.1	1	38.6	19.4	95.00%	R.KLTEVFNEAHENVK.Y	
74	86	2	1528.76	4.4	0	69.8	20.9	95.00%	K.LTEVFNEAHENVK.Y	
2	20	2	1989	3.8	0	99.4	20.5	95.00%	M.SGYGQQGVSAANIDSIRPK.K	Acetyl (+42)
183	202	2	2362.1	3.9	0	116	23.4	95.00%	R.EQFCETTIGFNPPNEVDIPR.E	Carbamidomethyl (+57)
125	144	3	2172.13	4	0	27	19	92.40%	R.VCDQMVGLIRPGAVGISCIK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
317	331	2	1484.83	3.6	0	57.3	15.2	95.00%	K.ELLGGQLLQGAATSK.D	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
36	C1TC_SCHPO	14.51%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
689	707	3	1923.15	3.9	0	37.5	6.02	95.00%	R.TSGLKPDAIVIVATVQALK.L	
57	84	3	3131.52	3.1	0	32.8	21.6	95.00%	R.AANEAGISCEHVNFPEDITEYDLLLAIK.G	Carbamidomethyl (+57)
349	356	2	983.58	5.3	0	46.2	13.6	95.00%	K.VNLEILQR.L	
835	849	2	1592.78	4.3	0	53.3	22.1	95.00%	K.EMYGADGIELSPLAK.E	
2	12	2	1184.68	4.9	0	55.8	16.3	95.00%	M.ALLLEGTSLAR.K	Acetyl (+42)
457	471	3	1809.86	4.5	1	30.8	22.5	95.00%	R.MFHENTQSDAALYKR.L	
536	546	2	1228.67	4.9	1	27.4	18	91.40%	R.KITIGENPTEK.G	
324	336	2	1299.71	5.1	0	59.2	18.2	95.00%	K.NIGDLASEIGIAK.S	
381	396	2	1629.9	3.4	0	106	15.7	95.00%	K.STLTAGLVQALSNLDK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
37	SERA_SCHPO	34.98%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
422	452	3	3379.61	2.3	1	84.6	23	95.00%	K.SQFSDSRGDIAYLVADISDCTPGSLEALHQK.L	Carbamidomethyl (+57)
58	83	3	2976.59	2.3	1	36.5	15.8	95.00%	K.ILLLENVNQSALSNLKDEGYQVEFLK.T	
410	421	2	1468.77	4	0	31.9	18.5	95.00%	R.QVNELFIDHNIK.S	
302	319	2	1728.88	4.5	0	48	19.6	95.00%	K.IAGAAIDVYPSEPAGNGK.D	
248	262	2	1596.82	4.1	0	50.8	19.1	95.00%	R.ADFVSLHVPASPETK.N	
142	154	2	1394.7	4.8	0	57.8	19.8	95.00%	R.GIAVFNSPYANSR.S	
367	385	2	2078.05	3.9	0	76.6	20	95.00%	R.YINEGNSIGAVNFPEVSLR.S	
47	57	3	1247.68	3.8	0	25.6	16.7	90.60%	R.TLKPFASEDIK.I	
320	337	3	2166.02	4.5	1	39.8	22.8	95.00%	K.DKFVDSLNSWTSELTHCK.N	Carbamidomethyl (+57)
302	321	3	1972.98	2.5	1	34.2	21	95.00%	K.IAGAAIDVYPSEPAGNGKDK.F	Deamidation (+1)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
38	LYS9_SCHPO	39.11%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
177	183	2	740.49	4.7	0	33.1	8.45	95.00%	R.GVLLALR.N	
290	301	2	1276.66	4.3	1	31	18.5	95.00%	K.AESSSEADLIKK.I	
38	49	2	1259.66	4.1	0	41.7	19.4	95.00%	K.AEAFINGIPNSK.A	
149	170	2	2385.11	5.2	0	60.2	23.8	95.00%	K.SFLSYCGGLPAPEDSNNPLGYK.F	Carbamidomethyl (+57)
379	396	2	1989.93	4.3	0	76.6	22.4	95.00%	R.TCTLLDYGVPNGYTSMAK.L	Carbamidomethyl (+57)
397	426	3	3075.62	3.2	0	38.4	14.6	95.00%	K.LVGVPCGVATQQILDGVINTPGVLAPNDMK.L	Carbamidomethyl (+57)
64	85	3	2488.28	3.3	0	39.1	18.6	95.00%	K.AVSEHDLTISLIPYTYHATVMK.A	
2	22	3	2269.25	3.1	0	39	14	95.00%	M.PSILLLGSGFVAHPTLEYLSR.R	
114	135	3	2372.16	2.8	0	47.3	22	95.00%	K.AGSICMNEIGVDPGIDHLYAIK.T	Carbamidomethyl (+57)
104	113	2	1103.56	4	0	29.1	18.8	93.60%	K.MAELEEAAIK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
39	PDX1_SCHPO	34.80%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
35	49	2	1547.75	3.7	0	51.8	21.5	95.00%	R.IAEAAGACAVMALER.V	Carbamidomethyl (+57)/ Oxidation (+16)
265	280	2	1628.86	4	0	87.2	17.8	95.00%	K.ILAEVSENLGAAMVGR.S	
71	83	2	1355.75	4.3	0	66.7	17.3	95.00%	K.EIQAAVSIPVMAK.V	
150	164	2	1487.76	3.9	1	69.3	19.5	95.00%	R.TKGEAGTGDVVEAVR.H	
121	132	3	1383.7	4.4	1	31	20.7	95.00%	K.SKFTVPFVCGSR.N	Carbamidomethyl (+57)
21	34	2	1457.74	4	0	89.6	20	95.00%	K.GGVIMDVVNAEQAR.I	
140	149	2	1102.6	4.8	1	28.6	18.1	93.10%	R.RISEGAAMIR.T	
13	20	2	830.47	4.2	0	38.8	16.8	95.00%	K.AGLAQMLK.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
40	THIL_SCHPO	32.15%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
360	371	2	1405.81	4.5	0	73.2	13.8	95.00%	R.IICTLAYILAQK.D	Carbamidomethyl (+57)
340	359	3	1865.93	4.8	0	31	21.5	95.00%	R.VNINGGGVAMGHPLGSSGSR.I	
291	301	2	1160.65	4.8	0	33.2	16.6	95.00%	R.FTTSPSLAIPK.A	

14	30	2	1654.81	3.8	0	74.4	20.7	95.00%	R.TPMGSFGGSFASLPATK.L	
43	69	3	2869.45	3.7	0	43	19.9	95.00%	R.VNIKPSDVDEVFMGNVVSANLGQNPAR.Q	
278	290	2	1440.71	4.1	0	44.3	20.3	95.00%	K.IIGWGEAAQDPER.F	
148	174	3	2905.26	3	0	42.8	24.7	95.00%	R.DGLSDAYDGLPMGNAAELCAEEHSIDR.A	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
41	HSP7M_SCHPO	22.40%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
637	647	2	1313.76	3.4	1	27.8	14.3	92.00%	K.KIDEIQQLSLK.V	
366	388	3	2471.31	2.4	1	25.8	17.4	90.80%	R.ALKDANLQTSEINEVILVGGMTR.M	
622	635	2	1464.65	3.4	0	88.6	21.9	95.00%	K.VNAGDEGITSEDMK.K	
204	215	2	1124.67	4.6	0	48.3	12.8	95.00%	K.AAGAIAGLNVLR.V	
322	337	2	1645.86	3.4	0	41.2	17.9	95.00%	K.TDISLPFITADATGPK.H	
105	118	2	1578.81	4.5	0	81.4	20.5	95.00%	R.QAVINPENTFFATK.R	
185	199	2	1679.83	4.3	0	62.1	21.5	95.00%	K.NAVVTVPAYFNDSQR.Q	
622	636	2	1592.74	5	1	80.4	21.1	95.00%	K.VNAGDEGITSEDMKK.K	
496	510	2	1538.89	4.2	0	77.2	12.3	95.00%	K.LIGNFQLTGIAPAPK.G	
157	170	2	1496.8	5.1	0	59.3	18.4	95.00%	K.TYSPSQIGGFILSK.M	
216	231	2	1630.86	3.8	0	78.5	19.2	95.00%	R.VVNEPTAAALAYGLDK.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
42	CYPH_SCHPO	63.58%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
2	17	2	1835.87	3.9	0	50	21.7	95.00%	M.SNCFFDVIANGQPLGR.I	Acetyl (+42)/ Carbamidomethyl (+57)
124	139	3	1772.92	4.1	1	60.2	18.9	95.00%	K.HVVFGEVTEGMDVVKK.V	
54	67	2	1607.82	4.3	0	67.2	19.9	95.00%	R.VIPQFMLQGGDFTR.G	
75	89	2	1756.87	4.2	1	61.3	21.1	95.00%	K.SIYGEKFPDENFALK.H	
124	138	2	1644.83	4.4	0	86.7	20.3	95.00%	K.HVVFGEVTEGMDVVK.K	
90	123	3	3611.83	4	0	56	19.7	95.00%	K.HNKPGLLSMANAGPNTNGSQFFITTVVTPWLDGK.H	
22	29	2	931.51	4	0	29.7	18.7	94.30%	K.LFDDVVPK.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
43	GBLP_SCHPO	35.99%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
156	172	2	1893.9	4.3	0	71.3	22.2	95.00%	R.FSPNPDNLTFVSAGWDK.A	
48	57	2	1135.53	4.7	0	43.2	19.5	95.00%	R.DDVNYGVAQR.R	
186	212	3	2736.26	2.6	0	43.2	24.2	95.00%	R.TSHYGHTGYVSAVTISPDGSLCASGGR.D	Carbamidomethyl (+57)
9	36	3	2894.45	2.9	0	38.1	20.9	95.00%	R.ATLEGHSGWVTSLSTAPENPDILLSGSR.D	
234	245	2	1314.71	3.1	0	32.5	18.2	95.00%	K.ANINALVFSPNR.Y	
176	185	2	1264.65	5.4	0	30.1	20.1	94.70%	K.VWDLETFSLR.T	
39	47	2	1112.68	5.9	0	27.8	11.8	92.00%	K.SIILWNLVR.D	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
44	PPA1_SCHPO	13.69%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
73	92	2	2047	4	0	99.4	21.8	95.00%	R.NPTGGNAAFDAVGIANFQQR.L	
366	387	2	2501.19	3.5	0	42.6	23.5	95.00%	K.ASEFVPFAGNLITELFQCEDSK.Y	Carbamidomethyl (+57)
40	59	3	2404.13	2.5	0	63.3	23	95.00%	R.SPYHKPYFYGPSIDFPTTCK.I	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
45	IF4A_SCHPO	28.32%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
58	69	2	1173.61	5	0	69	20.1	95.00%	R.DVLAQAQSGTGK.T	
49	69	3	2154.15	3.1	1	31.7	15.4	95.00%	R.AIMPILGERDVLAQAQSGTGK.T	
155	176	3	2506.23	3.9	1	41.3	21.9	95.00%	R.RALPTDAVQMFVLDEADEMLSR.G	
2	32	3	3667.76	4	0	58	23.7	95.00%	M.VDQLEDSVIETNYDEVIDTFDDMNLKPELLR.G	
372	392	2	2549.19	2.9	0	26.7	23.3	90.20%	R.EIEQFYNTHIEEMPMNIADLI.-	

33	48	2	1854.94	3.8	0	30.4	20.6	94.90%	R.GIYAYGFERPSAIQQR.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
46	PUT2_SCHPO	30.84%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
406	422	2	1852.92	4.3	0	57.5	20.7	95.00%	K.ADDSEGFFVEPTVLLSK.N	
362	384	3	2428.26	3.2	0	27	18.4	92.40%	K.VGAPLTDFANFVGPVIHQASFNK.L	
254	274	3	2393.15	4.4	0	52.3	22.3	95.00%	K.VCFNHPEFAGLHFTGSTAVFR.S	Carbamidomethyl (+57)
233	253	2	2068.09	4.4	0	68.9	18.1	95.00%	R.EAGLPAGALQFIPGDAVEVSK.V	
495	509	2	1504.71	3.5	0	49.3	21.3	95.00%	K.CTGAVVGEQPFGGAR.A	Carbamidomethyl (+57)
388	405	2	1773.91	3.9	0	102	19.3	95.00%	K.VLESAASDSEIEVLAGGK.A	
82	92	2	1222.64	4.6	0	32.1	18.5	95.00%	K.HVEDAIEAALR.G	
275	288	2	1444.74	4.6	0	37.7	20.9	95.00%	R.SLWGTIGENVANGK.Y	
531	548	2	2036.98	5	1	47.4	22.2	95.00%	R.SIKDTFAYADSVLYPSNF.-	
484	494	2	1225.58	4.6	0	28	20.9	92.30%	R.NAAGNFYINDK.C	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
47	DHAS_SCHPO	29.69%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
112	132	3	2341.31	2.7	1	53.3	8.45	95.00%	R.REPTVPLVVPTVNTDHLDVIK.Y	
143	161	2	2003.03	3.7	0	71.4	19.8	95.00%	R.GCIITNSNCSTAAVVVPLK.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
304	318	3	1662.81	4.5	1	31.3	21	95.00%	R.LDRNNENGYAVSVGR.I	
31	39	2	856.52	4.9	0	28.2	16.4	92.50%	K.IAVLGASAR.S	
287	303	3	2003.98	4.2	0	33.9	22	95.00%	K.QAIYVFDDSTPDRPQPR.L	
267	278	2	1375.7	3.8	0	37.2	19.8	95.00%	R.EVLANYVSEPQK.L	
6	18	2	1227.7	3.7	0	35.6	16.3	95.00%	K.VGILGATGTVGQR.F	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
48	EF1B_SCHPO	40.65%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
14	22	2	1104.59	4.8	0	36.2	17.3	95.00%	K.QLNDFLLDK.S	
153	165	2	1432.74	3.9	0	44.3	19.6	95.00%	R.SIQMDGLVWGLSK.L	
2	13	2	1209.59	3.7	0	57.4	20.8	95.00%	M.GFSDLTSDAGLK.Q	
59	73	2	1561.84	4.2	0	60.9	18	95.00%	K.QIATYDLATLPGTAK.E	
129	149	2	2459.19	2.9	0	66.3	22.6	95.00%	K.SLVTLDVKPWDDETPMDELEK.A	
23	39	2	1885.92	3.6	0	50.9	21.6	95.00%	K.SFIEGYEPSQADAVVFK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
49	RL4A_SCHPO	29.75%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
122	140	2	1845.04	4.3	0	48.1	11.1	95.00%	R.YAISSAVAASGVPSLLLAR.G	
14	29	2	1695.88	4.2	0	38.3	18.9	95.00%	K.DGSVSSETIALPFVFK.A	
144	163	2	2254.18	3.5	0	34.1	17.9	95.00%	R.IEEIPEVPLVVDDAVQSFQK.T	
276	291	2	1864.94	4.5	0	39	21.5	95.00%	K.NYFLPENIISNADVTR.L	
235	248	3	1457.85	4.2	0	28.5	12.3	94.00%	R.LNLLQLAPGGHLGR.F	
292	303	2	1357.75	4	0	43.8	16.6	95.00%	R.LINSDEIQSIVK.A	
87	97	2	1197.51	4.4	0	32.6	20.8	95.00%	R.SGQAAFGNMCR.S	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
50	STI1_SCHPO	15.74%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
146	164	2	1935.97	6.4	0	78.1	21.4	95.00%	K.LASNPETASLLADSAFMAK.L	
168	183	2	1781.88	4.3	0	66.6	21.3	95.00%	K.IQQNPGSIMAELNDPR.M	
20	34	2	1711.85	3.9	0	70.3	21.1	95.00%	K.TAIDYFTQAIGLDER.N	
371	377	2	800.44	3.8	0	29.8	20.5	94.40%	R.TPDILSR.L	
76	90	3	1463.79	4.4	1	44.6	17.8	95.00%	R.KGAALHGLGDLDAAR.S	
112	132	2	2007.97	4.2	0	89.9	22.5	95.00%	K.SVEAAQTQAASGAGGFNPFAK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
51	CARB_SCHPO	7.67%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
418	433	2	1784.89	3.2	0	42	20.3	95.00%	K.TTTANFEPSLDYVVTK.I	
575	584	2	1057.58	4.7	0	32.1	18.9	95.00%	K.LVGASELDVR.A	
249	273	3	2529.22	2.7	1	48.7	21.8	95.00%	R.SAYSLGGLGSGFANNKEELQSMAAK.S	
932	943	2	1304.72	5.6	0	35.2	17.4	95.00%	K.TLGVNFIDVATR.S	
773	798	3	2736.49	2.9	0	51	14.1	95.00%	K.FANAVGYPVLVRPSYVLSGAAMSVIR.D	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
52	HXK1_SCHPO	13.64%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
447	469	2	2153.17	3.4	0	105	15.3	95.00%	K.VVTIPAEDGSGVGAALVSALEAK.G	
283	303	3	2438.2	3.1	1	37.7	21.7	95.00%	R.TKYDVAIDEESPRPGLQTYEK.M	
26	47	3	2676.35	2.8	0	37.5	20.7	95.00%	K.TLQDHLDELEEQFTIPTELLHR.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
53	OAT_SCHPO	29.91%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
154	167	2	1493.69	4.9	0	59.2	21.2	95.00%	R.TMGIISMSTDPDAR.D	
135	153	3	2184.11	3	1	28.6	20.5	94.10%	K.KIPTDEAIILSCVDNFHGR.T	Carbamidomethyl (+57)
276	291	2	1561.85	4	0	53	16.6	95.00%	K.AISGGVYPVSAVLSSR.E	
238	254	2	1838.97	4.4	0	78.8	17.9	95.00%	K.AHNVLFIADEVQTGVAR.T	
258	275	3	2051.1	4.3	0	30.2	16.6	95.00%	K.MLCIEHSNVKPDVVILGK.A	Carbamidomethyl (+57)
70	80	2	1268.71	4.2	0	28.4	13.4	92.80%	K.IIEALVEQAQR.V	
2	37	4	4216	4.3	0	58.2	24	95.00%	M.SAESLLHNTFSTEQIEVLENEYAAHNYHPLPVCFSK.A	Acetyl (+42)/ Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
54	RS18_SCHPO	28.95%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
56	66	2	1246.61	4	0	41.5	20.1	95.00%	R.AGELTTEELER.I	
67	78	2	1386.79	4	0	45.2	14.6	95.00%	R.IVTIIQNPSQFK.I	
2	14	2	1578.86	4.3	0	26.6	16.9	90.00%	M.SLVVPDNFQHILR.L	Acetyl (+42)
79	86	2	1031.56	6	0	52.6	18.1	95.00%	K.IPSWFLNR.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
55	FAS1_SCHPO	6.75%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
1117	1130	2	1421.7	4.7	0	59.8	21.1	95.00%	K.SLESVSVTEEAGSK.V	
2	12	2	1294.67	5.2	0	53.5	19.4	95.00%	M.VEAEQVHQSLR.S	
1778	1806	3	3141.54	1.9	0	40.3	21.4	95.00%	K.DSTSFSFTHPSGLLSATQFTQPALTLMEK.S	
1422	1447	3	2983.4	3.2	0	29.8	24.2	95.00%	R.GTFTDFENTFEHTQETPMQLTLATPK.D	
966	984	2	2177.07	4.2	0	92.2	21.8	95.00%	K.TTLIENFEDLNDPYPVAAR.F	
1870	1881	2	1266.57	5.2	0	37.8	21.4	95.00%	R.SDYGMVAANPSR.V	
210	224	3	1723.91	5.4	0	36.5	18	95.00%	K.GLNVLDWLAGERPER.D	
781	794	2	1545.81	3.9	0	42.1	19.1	95.00%	K.LPPMPFDGILFGSR.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
56	CYSD_SCHPO	41.49%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
47	59	2	1541.79	3.6	0	30.2	18.7	94.80%	R.LFGLQEPGYIYSR.M	
72	100	3	2787.49	3.3	0	49.9	16.5	95.00%	R.IAALEHGAAAIATSSGTSALFMALTTLAK.A	
366	377	2	1185.64	4.4	0	34.5	17	95.00%	K.LASQLANVGDAK.T	
170	210	4	4156.13	4.3	0	53.9	18.5	95.00%	R.IAEVAHAAGVPLMVDNTFGGGGYLVRPIDHGADIVTHSATK.W	
132	150	2	2074.95	4.2	0	127	22.5	95.00%	K.FVNGDDPNDLAAQIDENTK.A	
378	403	3	2798.48	2.5	0	42.6	17	95.00%	K.TLVIAPAYTTHLQLTDEEQISAGVTK.D	

2	26	3	2735.29	3.8	0	45.2	23.7	95.00%	M.PVESEHFETLQLHAGQEPDAATSSR.A	
27	39	2	1486.79	4	0	44	18.1	95.00%	R.AVPIYATTSYVFR.D	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
57	MET3_SCHPO	25.10%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
427	440	2	1651.86	4	0	77.5	18.4	95.00%	R.LDAISVFYAQELQR.A	
350	359	2	1102.6	3.9	0	29.9	17.4	94.50%	R.TLNISGTELR.R	
69	92	2	2586.35	1.6	0	44	17.9	95.00%	R.LSTGEVFPIPITLDLNESQADSLK.A	
59	68	2	1233.64	5.6	0	40.5	19.2	95.00%	K.DYLNVVENLR.L	
254	262	2	1012.62	5.1	0	33.5	11.5	95.00%	K.LSLLPLAMR.M	
364	382	2	2159.15	2.7	0	56.8	17.1	95.00%	R.VGANIPEWFSYPEVVAILR.Q	
13	29	2	1924	2.8	1	48.1	19.1	95.00%	R.DAPLREQLEQEATSLPK.I	
217	236	4	2231.2	3.6	0	31	14.8	95.00%	R.VLIHPVVGMTKPGDIDHFTR.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
58	HOSM_SCHPO	27.51%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
2	31	3	3218.5	4.8	0	47.5	23.9	95.00%	M.SVSEANGTETIKPPMNGNPYGPNPSDFLSR.V	Acetyl (+42)/ Deamidation (+1)
360	375	4	1793.95	4.6	1	20.5	17.7	91.30%	K.SRAEQLNLHLTDAQAK.E	
192	204	2	1315.66	4	0	40.8	20.8	95.00%	R.VGIADTVGCATPR.Q	Carbamidomethyl (+57)
64	85	2	2410.17	3.4	0	116	22.5	95.00%	K.ALDNFGVDYIELTSPVASEQSR.Q	
172	182	2	1264.7	4.6	0	43.4	14.8	95.00%	R.SDLVDLLSLYK.A	
401	411	2	1290.55	4.4	0	41	21.8	95.00%	R.EYHADLSDADR.I	
32	43	2	1391.75	4.9	0	68.1	17.2	95.00%	R.VNNFSIIESTLR.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
59	IF5A1_SCHPO	36.94%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
2	29	3	3107.41	2.7	1	84.1	24.4	95.00%	M.AEEEHVDFEGGEAGASLTFPMQCSALRK.N	Acetyl (+42)/ Carbamidomethyl (+57)
2	28	3	2979.31	4	0	77.3	24.9	95.00%	M.AEEEHVDFEGGEAGASLTFPMQCSALR.K	Acetyl (+42)/ Carbamidomethyl (+57)
70	87	3	2075.97	4.1	1	55.3	23	95.00%	R.KYEDMSPSTHNMDVPVVK.R	
58	69	2	1352.76	4.3	0	43.7	13.6	95.00%	K.VHIVALDIFNGR.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
60	ILV3_SCHPO	12.21%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
49	68	2	2142.97	5.2	0	90.3	23.2	95.00%	K.SQGASQAMLYATGLNEEDMK.K	
402	417	4	1843.09	3.6	1	32.1	4.77	95.00%	K.IIRPLSNPIKTEGHLR.V	
40	48	2	994.5	5.2	0	30.6	20.8	95.00%	K.YSETITGPK.S	
185	212	3	3007.42	3.5	0	69.2	23.8	95.00%	R.AGHSPCQNNAPIDIVSAFQSYGEFITGK.I	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
61	CDC48_SCHPO	10.06%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
550	563	2	1522.75	3.6	0	43.8	20.4	95.00%	K.AIANECSANFISVK.G	Carbamidomethyl (+57)
359	379	3	2280.22	4.2	1	31.5	16.3	95.00%	R.SNVVVMAATNRPNSIDPALRR.F	
316	332	2	1841.99	4.4	0	39.8	17	95.00%	K.NSPAIIFIDEIDSIAPK.R	
774	786	3	1606.83	4.7	1	28.9	19.3	94.30%	R.RYEAYAHQLLTSR.G	
588	604	2	1817.93	4.3	0	57.6	21.3	95.00%	R.AAAPCVVFLDELDSIAK.A	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
62	ADH_SCHPO	29.71%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
236	253	2	1681.87	4.1	0	56	18.4	95.00%	K.AATNGGAHGTLVLSTSPK.S	Deamidation (+1)
254	278	3	2513.21	3.1	0	41.5	22.5	95.00%	K.SYEQAAGFARPGSTMVTVSMPAGAK.L	

170	194	3	2506.29	3.6	0	33.6	19.1	95.00%	K.VGPGEWICIPGAGGGLGHLAVQYAK.A	Carbamidomethyl (+57)
42	62	3	2378.15	2.1	0	31.5	22.4	95.00%	K.YTGVCHTDLHALQGDWPLPAK.M	Carbamidomethyl (+57)
200	214	2	1571.85	4.1	1	59.6	18.3	95.00%	R.VVAIDTGDDKAELVK.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
63	UGPA1_SCHPO	16.60%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
299	314	3	1876.02	4.4	0	30	15.7	95.00%	R.LLEIAQVPPQHVEEFK.S	
74	104	3	3417.67	3.9	0	69	22.2	95.00%	R.GSEINWDLVESPKPEQVVEYDTITEAGGLSR.D	
185	194	2	1205.65	4.7	0	32.1	18.1	95.00%	K.IDILTFNQSR.Y	
115	129	2	1460.72	4.2	0	48.3	21.3	95.00%	K.LNGGLGTTMGCVGPK.S	Carbamidomethyl (+57)
287	298	2	1278.63	4.4	0	55.1	20.1	95.00%	K.GGTLIDYDGNVR.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
64	YL8C_SCHPO	41.58%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
217	232	2	1745.96	4.4	0	53	15.6	95.00%	K.GTALQYITSNILPEVK.N	
275	288	2	1456.72	4.1	0	65.8	21.4	95.00%	R.VGNEEGAVGEVLER.I	
7	33	4	3045.57	3.9	1	29.7	17.6	95.00%	K.TNNLPTLDTLQMVISDVDGTLLDKHHR.F	
173	186	2	1645.79	3.6	1	65.2	22.2	95.00%	K.MAVCEDPDKLDVVR.D	Carbamidomethyl (+57)
47	60	2	1575.87	4.2	1	37.4	14.9	95.00%	R.EKYPNFPIVLATGK.Q	
93	112	3	2269.21	3.4	0	35.2	16.2	95.00%	K.IVYADHLKPEVVMEVVEATK.G	
70	90	3	2326.19	3.3	0	38.3	20.5	95.00%	R.IPLDLDAFPAAHVNGCVLYNK.G	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
65	VIPI_SCHPO	52.53%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
69	94	2	2433.11	4.4	0	121	24.1	95.00%	K.IQITSEDGGAASTTDQGGAGGDQAAR.Q	
55	68	2	1496.86	4.3	0	41.7	13.6	95.00%	K.TALLLQDALLGQNK.I	
199	218	3	2268.13	4	1	49.3	21.5	95.00%	K.VQNAYEDGKNQLLGIHNEAR.R	
101	110	2	1087.63	5.8	0	34.3	14.8	95.00%	R.SAIISELLSR.G	
225	254	3	2955.41	4.7	1	54.3	23.5	95.00%	K.NQAEGTASPASSTPTAPAEKEPTAPTTESK.T	
111	121	2	1260.64	3.7	0	31.8	19.2	95.00%	R.GYHLSDVTLEK.S	
122	134	2	1410.71	4.2	0	61.1	20.2	95.00%	K.SIQLDQSYGVSSK.F	
137	147	2	1100.62	4.3	0	27.7	18.3	91.90%	K.GILESALSGVR.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
66	YHY6_SCHPO	14.66%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
678	698	2	2257.13	4.5	0	51.2	21.5	95.00%	K.SLCIPLEQPSGEDAIIEGTTK.C	Carbamidomethyl (+57)
161	188	4	2736.49	3.7	1	29.1	14.3	95.00%	K.SVGVNPIIVDFSAPGSATAPSKPAAQKK.K	
161	187	3	2608.39	2.9	0	26.8	16.6	92.20%	K.SVGVNPIIVDFSAPGSATAPSKPAAQK.K	
298	323	3	2901.42	3	0	27.8	22	93.40%	R.AGTSELDEPIAIRPTSETVMYPYYAK.W	
660	677	3	1900.86	4.5	1	43.4	23.2	95.00%	R.QVNGDEPEDEKAPSMGAK.S	
387	398	2	1343.81	4.3	0	30.5	8.45	95.00%	R.IYTDLLAVPVIK.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
67	ECM17_SCHPO	10.86%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
66	90	4	2646.3	3.4	0	21.2	22.4	92.70%	K.SHADPFAHIADAILAEEEVASTQPK.Q	
314	325	2	1337.8	4.6	0	39.3	9.03	95.00%	R.LTVLEPITSLPR.K	
611	636	3	2801.42	3.9	0	43.3	19.6	95.00%	K.GPSVVLAYLPYHSADDDAITVLQETK.K	
369	404	4	3916.93	3.7	0	27.1	21.2	95.00%	R.DNLSGALKPSLVCDFTDGVSQVFVPTPPSIEEAYHK.L	Carbamidomethyl (+57)
173	207	4	3899.95	3.7	1	48	20.3	95.00%	K.LNTGVLHFYSPVYDTTAALENIETLPSKEDAQHAR.V	
801	810	2	1058.57	5.4	0	27.5	19.1	91.50%	K.GADLNLSELK.Y	
759	774	2	1850.85	3.7	0	75.5	21.9	95.00%	K.IMAMDDFPIEELGNEK.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
68	RL8_SCHPO	22.01%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
24	32	2	1084.62	4.7	0	29.3	17.1	93.90%	K.NPLFVSRPR.S	
109	120	2	1171.61	4.7	0	55.2	18.9	95.00%	R.LVAEAEAVANGK.S	Deamidation (+1)
134	146	2	1425.8	4.3	0	45.6	11.8	95.00%	K.YGLNHVVALIEAK.K	
33	43	2	1188.62	4.1	0	26.8	19.9	90.30%	R.SFGIGQDIQPK.R	
81	92	2	1364.74	3.7	1	46.2	17.9	95.00%	K.TLDKNTATQVFK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
69	NACA_SCHPO	54.91%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
65	75	2	1164.62	5.8	0	59.3	18.1	95.00%	K.SSNNAYIVLGK.V	
94	118	3	2590.2	4.9	1	37.2	24.3	95.00%	K.QATETKEEAAITEESGDAQPADTAK.I	
119	137	3	2123	4.4	1	54.2	23.1	95.00%	K.IEESFEQEKAVDETGVDAK.D	
11	26	2	1637.87	4.6	0	55.2	16.5	95.00%	K.ISELPAGSTTVVHAEK.A	
52	64	2	1540.93	4.4	0	50.2	4.77	95.00%	K.NILLIINEPIVYK.S	
76	86	2	1189.58	4.9	0	47.2	21.1	95.00%	K.VTVEDMAAQAR.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
70	HSP7F_SCHPO	21.53%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
174	189	2	1665.85	4	0	78.4	19.9	95.00%	R.LMNDNAAAALTYGITK.T	
539	558	3	2226.18	2.9	1	45	17.4	95.00%	K.VADLSVSVQEDRLPTEVLEK.Y	
581	591	2	1385.65	4	0	31.1	22.1	95.00%	K.NALEEYIYDTR.A	
694	720	3	3003.37	3.5	1	48	24.6	95.00%	R.APPPPPAEEVAPENEEVETMEIDEQKE.-	
38	48	2	1194.59	3.8	0	34	20	95.00%	R.STPSLVSYGER.S	
96	106	2	1134.6	4	0	31.7	19.8	95.00%	K.LTEVDGFVGAK.V	
78	95	3	2084	3.6	1	28.9	22.1	94.40%	R.TYDDPEIKDIESNFISAK.L	
5	16	2	1249.64	6.5	0	29.4	19.2	94.00%	R.TNVVGIDFGNSK.T	
159	173	2	1534.89	4	0	42.9	9.54	95.00%	R.ALLEAANIAGLNPLR.L	
617	630	2	1684.72	4	0	75.9	21.4	95.00%	K.AEDWLYEEGEDTTK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
71	ACON_SCHPO	8.87%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
532	549	2	1853.89	4.6	0	68.9	22	95.00%	K.GYDPGSNTYVAPSSVNVK.D	
392	402	2	1203.6	5.2	0	35.2	20.2	95.00%	R.AASICQQAIDK.G	Carbamidomethyl (+57)
65	80	3	1895.95	4.5	0	26.2	21.9	91.40%	K.ILYGHLDDPVNQDIER.G	
652	666	2	1665.78	3.4	0	67.3	22.2	95.00%	R.WVTLGEQNFGEGSSR.E	
462	470	2	1052.53	5	0	36.5	19.9	95.00%	K.NSIVTSYNR.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
72	YF19_SCHPO	12.33%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
181	194	2	1439.82	3.6	0	42.9	12.6	95.00%	K.IAPAVACGNTIILK.T	Carbamidomethyl (+57)
122	132	2	1208.53	4.1	0	34.4	20.3	95.00%	R.GDVQAAADCFR.Y	Carbamidomethyl (+57)
195	208	2	1516.82	4.7	0	34.9	17.7	95.00%	K.TAELTPLSALCLTK.F	Carbamidomethyl (+57)
5	17	2	1406.78	4.6	0	33	15.2	95.00%	K.LVDHVEITVPTGK.T	
71	80	2	1161.56	3.7	0	28.3	20.5	92.70%	R.AAFQTDAPWR.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
73	LEUC_SCHPO	14.78%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
633	649	2	2002.01	4.5	0	59.4	21	95.00%	R.VIIAPSFADIFFNNCFK.N	Carbamidomethyl (+57)
59	77	4	2123.12	3.9	1	27	17.6	95.00%	R.HPELALATVDHNIPTDPRK.D	
540	563	3	2538.39	3.4	1	28.2	14	93.70%	K.FTVVEGIAAPLPMANVDTDKIIPK.Q	
603	619	3	1826.86	5.3	0	37.3	23	95.00%	R.HATVLVAHDNFGCGSSR.E	Carbamidomethyl (+57)
477	493	2	1810.88	4.1	0	36.5	21.2	95.00%	R.EFFGDVSNGSPSIITNK.N	

650	667	2	2027	4	0	40.9	21.4	95.00%	K.NGMLPIPTPIEQVNDMMK.A		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
74	GCST_SCHPO	15.25%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
165	180	2	1623.93	4	0	75.8	11.1	95.00%	R.ALIAIQGPETASVVQK.L	
81	97	2	1779.9	3.9	0	64.1	20.8	95.00%	R.GENATAYLESITPSSLK.E	
319	344	3	2566.25	4.5	0	41.9	22.7	95.00%	R.HGSAVEVDGVEVGQVTSGCPSPTLGK.N	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
75	RS6B_SCHPO	33.89%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
99	115	2	1739.01	3.8	0	65.7	10.8	95.00%	R.GCIVGQDLAVLALAIVK.Q	Carbamidomethyl (+57)
59	72	3	1625.86	4.7	0	32.2	18.6	95.00%	K.QGFPMFQGVLLPHR.V	
32	51	2	2112.99	4.1	0	51.8	22.7	95.00%	R.MGQEVPGDSVGPEFAGYVFK.I	
116	131	2	1695.88	3.9	0	43.6	18.9	95.00%	K.QGEQDIPGLTDVTVPK.R	
204	217	2	1606.78	4.3	1	54.8	21.1	95.00%	K.NREEAAEFAQLMAK.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
76	GLNA_SCHPO	31.20%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
153	170	2	1809.83	4.4	0	40.7	22.5	95.00%	K.GGFPGPQGPFYCGVGTGR.V	Carbamidomethyl (+57)
60	91	3	3497.64	3.1	0	54.8	24	95.00%	R.VWNFDGSSTGQAPGNNSDTLLKPVAMYNDPFR.R	
301	316	3	1794.86	4.7	1	31.7	22	95.00%	R.HETGSIDKFTYGVADR.G	
237	260	4	2635.31	3.2	0	28.9	21.9	95.00%	K.ISFHPKPILGDWNGAGCHTNVSTK.D	Carbamidomethyl (+57)
338	359	3	2476.24	4.1	0	26.8	20.8	92.20%	R.RPASSIDPYLVTGIITETMFEH.-	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
77	O59743_SCHPO	38.02%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
108	136	3	3442.66	3	0	31.8	22	95.00%	K.LKPVPTSWEQALQDNKPEEYYHLSAPDCK.S	Carbamidomethyl (+57)
210	225	2	1690.88	3.5	0	52.7	20	95.00%	R.SIQDVPFTSATVDIAK.K	
1	11	2	1319.72	4	1	28	18.3	92.30%	-.MDPYTVAIIKK.L	Acetyl (+42)
75	97	3	2588.33	2.8	0	31.8	18.3	95.00%	K.EALDLFLGAYNVITPELAHFEAR.C	
11	24	2	1515.82	4.5	1	53.1	18.5	95.00%	K.KLGIEEQVETAATK.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
78	GCSP_SCHPO	14.06%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
953	965	2	1458.76	1.1	0	43.1	19	95.00%	K.DNNLLVNAPHPQK.D	
657	684	3	2835.49	3.7	0	27.8	17.1	93.40%	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C	Carbamidomethyl (+57)
379	412	3	3679.8	2.3	0	51.4	21.6	95.00%	K.ATSNICTAQALLANMSAFYAIYHGPNGLQEIANR.I	Carbamidomethyl (+57)
577	604	3	3166.6	3.7	0	40.5	19.6	95.00%	K.LNAVTEMMPITNPLFANIHPYVPEEQAK.G	
87	126	3	4380.08	3.8	1	62.7	23.4	95.00%	R.TPESQLMAFGSVNPNEKNPPVNYSESEFTTLANNVANQNK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
79	SPI1_SCHPO	12.50%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
110	122	2	1514.77	4.6	0	58.5	20.5	95.00%	R.VCENIPIVLCGNK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
152	165	3	1783.91	4.6	0	29.2	20.3	94.60%	K.SNYNFEKPFLWLAR.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
80	AROG_SCHPO	11.02%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
199	226	3	2704.36	2.1	0	47.7	21	95.00%	K.NGTDGTVGVAIDAIGATAHPHTMLGVTK.Q	Deamidation (+1)
186	198	2	1364.74	4.4	0	39.9	17.9	95.00%	R.ELASALSFPVGFK.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
81	RS7_SCHPO	30.26%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
119	140	3	2393.33	3.6	0	40.9	9.54	95.00%	R.TLTAVHNAILEDIVFPTEIIGK.R	
59	70	2	1322.84	4	0	46.5	4.77	95.00%	K.AIVVFVPQPLLK.A	
119	141	4	2549.43	2.7	1	41	10	95.00%	R.TLTAVHNAILEDIVFPTEIIGKR.T	
11	34	2	2657.25	4.3	0	84.1	24.3	95.00%	R.SSSQPTETDLLVAQCLYDLESSSK.D	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
82	VATA_SCHPO	17.29%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
89	114	4	2751.53	2.9	0	22.2	9.54	94.20%	R.TGKPLSVELGPGLAETIYDGIQRPLK.Q	
373	389	2	1752.85	8	0	36.9	21.2	95.00%	R.LAEMPADSGYPAYLGAK.L	
317	331	2	1544.81	4.6	0	49.4	19.6	95.00%	R.TTLVANTSNMPVAAR.E	
182	198	2	1838.88	4.6	0	73	22.6	95.00%	R.GTVTYIAEAGSYHVDEK.L	
221	240	3	2105.14	4.1	0	35.3	16.3	95.00%	R.AARPVADNLTANQPLLTGQR.V	
465	476	2	1580.77	4.7	0	39.5	22.2	95.00%	K.YINALQPWYEER.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
83	RS0B_SCHPO	28.92%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
2	31	3	3162.63	3.2	1	83.6	19.1	95.00%	M.AESIARPSVLNATDDDIKNLLAADSHIGSK.N	Acetyl (+42)
67	88	4	2453.26	4	0	67.3	18.3	95.00%	R.VIATIENPADVCVISSRPYGHR.A	Carbamidomethyl (+57)
139	169	3	3390.76	4.3	0	25.4	16.9	90.20%	K.EASFVNIPVIALCDTDSILNHVDVAIPINNK.G	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
84	THI4_SCHPO	20.66%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
373	385	2	1353.71	4.1	0	37.5	17.6	95.00%	R.GVDSISQHTLAAR.I	
121	140	2	2014.96	4.4	0	70	22.9	95.00%	K.AAADGADYVGIGSIYETNTK.D	

Carbamidomethyl (+57)/ Deamidation

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
87	LYS12_SCHPO	14.64%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
197	208	2	1324.65	5.3	0	41.8	20.9	95.00%	K.SNVMSVTDGLFR.E	
298	307	2	1044.58	4.6	0	32.2	18.6	95.00%	R.GIANPVATFR.S	
127	138	2	1568.72	4	1	44	21.5	95.00%	R.ENTECLYVKEER.M	Carbamidomethyl (+57)
67	85	3	2071.06	4.3	1	52.5	19.9	95.00%	R.LKTECNAALFGAVQSPTHK.V	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
88	RL1B_SCHPO	16.67%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
54	75	3	2486.26	2.6	0	38.3	20	95.00%	K.LPNVPRPNMAICILGDAHDLDR.A	Carbamidomethyl (+57)
78	91	3	1486.72	4.2	1	36.5	22.1	95.00%	K.HGGVDAMSVDDLKK.L	Oxidation (+16)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
89	RL10A_SCHPO	26.24%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
129	139	2	1228.7	4.7	0	40	15.3	95.00%	R.VNIGQILMSVR.T	
41	69	3	3260.58	4	0	68.1	22.7	95.00%	R.AGVDEFPLCIHLVSNEYEQITSEALEAAR.I	Carbamidomethyl (+57)
117	128	3	1265.71	4.6	0	30	14.9	95.00%	R.HAFGKPNGLVAR.V	
33	38	2	719.4	4.8	0	27.1	15.3	90.90%	R.IFDLGR.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
90	BCA1_SCHPO	22.63%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
315	331	2	1670.97	4.2	0	59.5	10.8	95.00%	R.LLEVFGAGTAALVSPVK.A	
37	49	3	1581.74	4.5	0	25.4	22	90.20%	K.FGENFTDHMLIMK.W	
262	278	2	1795	4.2	0	43.3	14.1	95.00%	K.EIITAPLDGMILPGVTR.D	
337	359	2	2462.16	4.4	0	42.7	23.4	95.00%	K.GTEYEIPMPEGQEAGPITSEISK.W	
115	130	2	1769.96	3.9	0	43.7	15.9	95.00%	R.ISLPSFDPAELAEIIR.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
91	TAL1_SCHPO	16.15%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
27	44	3	1917.03	4	0	42	17.3	95.00%	K.YKPQDATTNPSLILAASK.K	
9	26	2	1795.89	4.5	0	86.8	21.1	95.00%	K.ATGTVVVSDTGDFESIAK.Y	
45	60	2	1721.91	3.6	0	82.8	18.2	95.00%	K.KPQYAALVDAAVDYAK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
92	RL13_SCHPO	43.75%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
172	183	2	1398.66	5.4	0	54	21.8	95.00%	K.NFNAFSTLSNER.A	
46	64	4	2080.27	3.1	0	20	0	90.20%	K.IAPRPVEAIRPAVKPPTIR.Y	
118	128	3	1326.79	4.7	0	51.2	11.8	95.00%	K.VYLAHLIVFPR.K	
135	171	3	3809.92	4.7	1	60.8	19.4	95.00%	K.KGDATDVSGAEQTDVAAVLPITQEAVEEAKPITEEAK.N	
89	100	2	1263.7	3.9	0	28.9	16.9	93.40%	R.VASTIGIPVDHR.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
93	PYC_SCHPO	5.74%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
1109	1129	3	2088.05	4.4	0	38.2	20.3	95.00%	R.ADPGNPGHVAAPMSGTIVEIR.V	
839	848	2	1297.58	4.8	0	38.2	20.6	95.00%	R.EIDSYWAQMR.L	
829	838	2	1275.63	4.5	0	27.7	20.4	91.80%	K.QLEFDNNQLR.E	
917	929	2	1447.76	4.7	0	42.2	19.5	95.00%	K.VVGDLAQFMVQNK.L	
302	315	2	1628.75	2	0	37.3	21.8	95.00%	K.YCNAGTAEFLLDQK.G	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
94	RAD24_SCHPO	35.56%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
228	267	3	4032.79	4.4	0	129	24.9	95.00%	R.DNLTLWTSDAEYSAAAAGGNTEGAQENAPSNAPEGEAEPK.A	
156	172	2	1746.93	4.5	0	64.4	17.9	95.00%	K.AASEIATAELAPTHPIR.L	
109	120	2	1236.65	4.7	0	29.1	18.5	93.70%	K.HLIPNAASAESK.V	
31	44	2	1562.75	4.1	0	82.9	21.7	95.00%	K.SVASTDQELTVEER.N	
2	14	2	1481.74	4.3	1	46.8	20.5	95.00%	M.STTSREDAVYLAK.L	Acetyl (+42)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
95	EF1G_SCHPO	15.65%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
207	216	2	1182.71	4	0	27.1	13.2	91.00%	K.FIDQPLPIIK.A	
128	139	2	1303.72	4.6	0	40.7	16.9	95.00%	K.EAETAIALIFAR.F	
299	324	3	3077.5	2.7	1	48	23	95.00%	K.VDYSYPEDLKQPVFMTNNLIGGFFQR.L	
385	400	2	1902.94	4.6	0	52.4	22	95.00%	K.AFIEDAWAWDKPIEGR.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
96	RS2_SCHPO	17.39%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
186	200	2	1799.86	4.8	0	102	22.5	95.00%	R.FLQLAGIEDCYTQSR.G	Carbamidomethyl (+57)
51	63	2	1566.86	4.2	0	34.6	15.3	95.00%	K.SIEEIYLYSLPIK.E	
141	156	3	1696.87	4.8	0	37.6	20.2	95.00%	R.GYWGTALGDPHTVPVK.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
97	RS14_SCHPO	32.37%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
117	129	2	1442.73	3.7	0	46.5	20.8	95.00%	R.IEDVTPIPTDSTR.R	
52	72	3	2181.01	3.8	1	31.5	23.2	95.00%	K.TDRDESSPYAAMLAAQDAAAK.C	
95	105	2	1037.57	5.3	0	47.1	16.8	95.00%	K.TPGPGAQAALR.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
98	SERC_SCHPO	22.88%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
376	385	2	1147.65	4.7	0	32.8	13	95.00%	R.LIDLLESFAK.A	
216	228	2	1299.74	5	0	37	13.4	95.00%	K.NAGPAGITVVFVR.D	
153	184	3	3668.68	3.6	0	33.5	25.4	95.00%	K.FTPDGETSLVYYCDNETVHGVEFNEPPTNIPK.G	Carbamidomethyl (+57)
330	352	5	2716.42	3.7	1	22	17.8	95.00%	R.IEPQELESEFLAEAEKHHLVQLK.G	
189	199	2	1282.6	4.3	0	67	21.1	95.00%	R.VCDVSSNFISR.K	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
99	PUR8_SCHPO	20.54%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
450	470	3	2305.17	3.6	1	27.1	21.1	92.60%	R.APEQTESFVNKDVSQALAPFK.S	
226	242	2	1930.91	3.5	0	32.6	22.6	95.00%	K.LSGFDNVYPVTGQTYDR.K	
268	292	3	2694.37	3.3	1	34.7	20	95.00%	R.LLANLKEVEEPFEAGQIGSSAMAYK.R	
243	261	3	2023.12	4.2	1	51.4	14.5	95.00%	R.KIDIDVLQPLASFGATAHK.I	
372	388	2	1909.94	4.9	0	55.7	21.5	95.00%	R.AELPFMATENIIMAMTK.H	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
100	RL23_SCHPO	25.18%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
15	34	2	2090	3.5	0	65.5	21.7	95.00%	R.MTLGLPVQAIMNCADNSGAK.N	Carbamidomethyl (+57)
51	65	2	1531.78	3.4	0	55.2	20.2	95.00%	R.LPAASCGDMVLATVK.K	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
101	RS3B_SCHPO	11.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
200	213	2	1513.87	4.8	0	38.9	12	95.00%	R.ATGSIFPLQNVLVR.K	
228	241	2	1524.79	4.4	0	71.2	18.6	95.00%	K.LLELHGESQDVGTK.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
102	RS22_SCHPO	27.69%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
98	108	2	1171.7	4.9	0	29.1	11.8	93.70%	R.QVGVIVLTTSR.G	
4	19	2	1814.9	4.5	0	77.6	20.6	95.00%	R.QSVLADCLNNIVNAER.R	Carbamidomethyl (+57)
89	97	2	1111.62	5.6	0	31.9	14.5	95.00%	K.WVNQLLPSR.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
103	RL6_SCHPO	22.05%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
70	87	2	1959.1	3.1	0	33.6	12.3	95.00%	R.VVVLSQLEDTLVVTGPYK.V	
50	64	2	1497.84	5	0	33.1	15.9	95.00%	R.ASLAPGTVCILLAGR.F	Carbamidomethyl (+57)
109	118	2	1031.56	5.5	0	31.2	19.4	95.00%	K.IDVSGVSVEK.F	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
104	PYR1_SCHPO	5.35%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
1135	1145	2	1229.6	4.3	0	46.2	20.1	95.00%	R.MLDDIGVDQPK.W	
1771	1784	2	1494.85	4.1	0	35.2	11.8	95.00%	R.EAIPLLLTAVNEGR.L	
457	466	2	1084.56	6.1	0	38.9	17.6	95.00%	K.LPGGTIEENR.S	
1880	1906	3	2689.36	3.3	0	28.6	20.6	94.10%	K.VSALMSPGLPHAAPSLAEAFGQAPENK.A	
1758	1770	2	1371.7	4.4	0	56.2	20	95.00%	K.FVGNTAFTGFGVR.E	
25	54	4	3287.5	4.2	1	31.3	24.4	95.00%	R.THGPKPSENDPKEPTCSPSPAFYSVNGEMK.D	Carbamidomethyl (+57)
1804	1818	3	1724.81	5.5	0	27.4	21.4	93.00%	R.LHDQDDSGVQLEVDR.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
105	RS4B_SCHPO	7.25%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
222	233	2	1232.68	5.6	0	42.4	18.1	95.00%	R.LSNVFVIGEAGK.S	
246	252	2	846.45	4.8	0	45.4	19.8	95.00%	K.LSITEER.D	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
106	GLT1_SCHPO	6.06%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
1442	1464	3	2335.04	4.9	0	32.4	23.9	95.00%	R.NSGAIAVVEGVGDHGCEYMTGGR.V	Carbamidomethyl (+57)
1897	1918	3	2189.08	3.9	1	55	21.7	95.00%	K.GKDVIVIGGGDTGNDCLGTSVR.H	Carbamidomethyl (+57)
672	685	2	1555.69	5.3	0	68	21.8	95.00%	R.ICSEADTAVNEGYK.A	Carbamidomethyl (+57)
624	638	2	1701.91	4.2	0	45.5	18.3	95.00%	R.MPTPILTVEEFNALK.N	
1690	1707	2	2063.08	4.1	0	61.9	18.4	95.00%	K.EALTQLLLTNNFPEFTGR.V	
1022	1038	3	1639.81	4.9	0	25.7	21.3	90.70%	K.MAQGAKPGEGGELPGNK.V	
1758	1776	2	1792.99	3.3	0	78.8	15.6	95.00%	R.VAIIGSGPAGLAAADQLNR.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
107	PURA_SCHPO	14.29%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
206	224	3	2169.16	3.6	0	37.8	15.7	95.00%	R.LKPFVIDAVAFMYEALQSK.K	
268	276	2	899.55	4.9	0	44.5	17.6	95.00%	R.IANSIGVVK.A	
282	304	3	2420.22	4.2	0	27.4	20.8	92.90%	R.VGAGPFPTEQLNEIGDHLQSVGR.E	
126	136	2	1129.57	4.6	0	38.6	19	95.00%	R.ADALNEAELGK.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
108	RL3A_SCHPO	11.08%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
207	222	2	1837.9	4.3	0	73.9	21.7	95.00%	K.STFEQNEMIDVIGVTR.G	
11	19	2	982.54	4.3	0	27.2	16.4	91.10%	R.HGSLGFLPR.K	
249	266	3	2035.03	4.4	0	29.3	20.6	94.70%	K.VACIGAWHPANVQWTVAR.A	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
109	PMP20_SCHPO	42.95%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
30	55	2	2747.41	3.6	0	38	19.5	95.00%	K.FIIVGVPGAFTPPCSSQVPGYIANEK.Q	Carbamidomethyl (+57)
11	29	3	2215.13	4.2	0	34.9	19.5	95.00%	K.VTLWENKPEEVVEFPSQGK.F	
135	156	2	2379.21	3.2	1	61.1	19.3	95.00%	K.VFIENEVTDVDISSADKVLSSL.-	
135	151	2	1879.91	3.7	0	64.2	22.4	95.00%	K.VFIENEVTDVDISSADK.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
110	TRX1_SCHPO	53.40%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
55	79	3	2736.35	2.8	0	37.8	21.9	95.00%	K.VDVDQLSEIAAEAGVHAMPSFFLYK.N	
40	54	2	1796.83	4.6	0	68.4	22.1	95.00%	K.FEQFSNTYSDATFIK.V	
80	94	2	1568.81	4.2	1	68.2	18.2	95.00%	K.NGEKIEEIVGANPAK.L	Deamidation (+1)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
111	SYKC_SCHPO	12.86%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
15	28	2	1454.8	4	0	41.2	16.1	95.00%	K.ALVLDPVTGEQVSK.T	
570	591	3	2490.33	2.8	1	30.8	16.1	95.00%	R.EVLLFPHMKPEVQAAEPTVVKE.-	
498	513	2	1999.9	4.4	0	72.7	23.2	95.00%	K.EICNAYTELNDIFDQR.A	Carbamidomethyl (+57)
153	176	4	2810.33	3.8	1	33.2	23.7	95.00%	K.KLQVMCQAQDADTVDFAAQHEHLR.R	Carbamidomethyl (+57)
154	176	4	2682.24	3.7	0	34.1	23.9	95.00%	K.LQVMCQAQDADTVDFAAQHEHLR.R	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
112	THI22_SCHPO	14.16%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
2	31	3	3486.71	3.2	1	43.1	22.2	95.00%	M.PYNPLYESLSNQFDPSRIETVLDPMGYTIK.R	
423	435	2	1516.6	5.3	0	56.7	20.3	95.00%	K.SCEESPACTAYSR.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
181	197	2	1890.88	4.9	0	111	21.7	95.00%	K.NQGLDISNINSVSDMER.C	
134	151	2	1829.99	4.1	0	72.6	16.9	95.00%	K.LVVDPVMVATSGDSLVTK.D	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
113	RS23_SCHPO	28.67%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
81	107	3	3006.43	2.2	0	44.3	23.1	95.00%	K.VTAFVPHDGCLNFVDENDEVLLSGFGR.K	Carbamidomethyl (+57)
80	107	3	3134.53	3.7	1	49.3	22.2	95.00%	K.KVTAFVPHDGCLNFVDENDEVLLSGFGR.K	Carbamidomethyl (+57)
125	137	2	1326.74	4.4	0	55.5	15.6	95.00%	K.VAGVGLSALFHEK.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
114	RS8A_SCHPO	21.00%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
60	74	2	1568.72	4.4	0	94.1	21.4	95.00%	R.LDSGNFSWGSEGVSK.K	
165	178	2	1475.79	4.1	0	33.2	17.2	95.00%	R.LYAVVSSRPGQSGR.C	
152	164	2	1363.68	4.8	0	51.3	20.4	95.00%	K.VDSALETQFAAGR.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
115	SODC_SCHPO	53.90%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
81	97	2	1765.87	4	0	72.3	21.3	95.00%	R.HVGDLGNLESDAQGNIK.T	
117	137	3	2198.12	3.9	1	49.5	20.5	95.00%	R.TIVIHAGEDDLGKGTSEESLK.T	
45	70	3	2825.25	4.3	0	41.5	25.2	95.00%	R.GFHIHQFGDNTNGCTSAGPHFNPEGK.T	Carbamidomethyl (+57)
98	116	2	1984.04	4.4	0	72.6	18.2	95.00%	K.TTFSDSVISLFGANSIIGR.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
116	YA03_SCHPO	33.79%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification

181	194	2	1560.83	4.5	0	43.8	18.4	95.00%	K.AADIDFLPPQLSFK.N	
14	47	4	3763.78	4.5	1	35.9	23.5	95.00%	R.HGQAQHNVGPDEDHNIRDPVLTSEGIEQCEALAK.E	Carbamidomethyl (+57)
147	172	3	2896.59	3.1	1	53.2	13	95.00%	R.SKEALEYLAALPQQQIAVITHSAFIR.F	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
117	LEU1_SCHPO	16.95%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
82	99	2	1998.98	4.3	0	62	21.5	95.00%	K.EIEVGFPSASQTDFAFVR.H	
464	479	2	1742.82	4.9	0	69.1	22.1	95.00%	R.FSVNDYTLSSNGPQSK.C	
341	362	3	2346.15	2.9	0	44.7	21.7	95.00%	R.HPYAGNLVFTAFSGSHQDAISK.G	
137	151	3	1761.87	4	0	33.2	22	95.00%	K.NATVHLYNACSPLFR.E	Carbamidomethyl (+57)
268	295	3	2788.37	3.6	1	73.8	22	95.00%	R.GTAVAAAELGQLAGGDRIEGCLFGNGER.T	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
118	HMCS_SCHPO	15.88%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
264	282	2	2060.02	4.4	0	63.4	21.5	95.00%	R.LLYTDSAAEPSNPELEGVR.E	
155	183	3	2859.53	3.9	0	40.5	15.4	95.00%	K.GNARPTGGAGCVALLVGPNAPIVFEPGLR.G	Carbamidomethyl (+57)
382	392	3	1300.68	5.1	1	26	18.3	91.10%	K.KTNLVNDLDNR.H	
217	228	2	1325.64	3.7	0	38.4	21.1	95.00%	K.ALDGAYANYNVR.D	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
119	DHE4_SCHPO	20.40%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
417	439	2	2411.16	5.2	0	85.7	22.8	95.00%	K.YCDSGSNNIPSLVDGANIAGFLK.V	Carbamidomethyl (+57)
356	367	2	1231.57	4.5	0	27.7	19.9	91.80%	R.ASGEGCWLAPGK.A	Carbamidomethyl (+57)
399	416	2	1950.98	4.6	0	78.4	20.4	95.00%	K.LAGIMQNIFEQSTDVASK.Y	
334	353	2	2102.96	4.2	0	111	23.2	95.00%	R.YVAEGSNMGSSAEAVEVFEK.S	
25	34	3	1266.71	4.3	1	33.7	14.8	95.00%	K.LFEVHPELKR.V	
93	101	2	1127.61	5.6	0	29.2	18.4	93.80%	K.FLGFEQIFK.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
120	IMDH_SCHPO	15.27%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
169	187	3	2214.08	4.5	1	37	22.2	95.00%	R.DVQFHKDTNTPVTEVMTPR.E	
2	15	2	1636.88	4	0	27	16.9	90.70%	M.SAFKPYTEALEVLK.K	Acetyl (+42)
303	313	2	1155.67	4.5	0	51.3	16	95.00%	K.IDVIAGNVVTR.E	
214	234	3	2311.28	3.6	1	29.3	11.8	94.70%	K.LPVVDKDDNLVALLSLTDLMK.N	
419	433	2	1421.67	3.9	0	52.2	21.8	95.00%	R.GMGSIAAMEGTGVNK.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
121	YHEF_SCHPO	9.36%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
54	71	3	2044.04	4.6	1	35.8	20.1	95.00%	K.SFIGLDALTESKGEFFQR.M	
54	65	2	1279.67	5.1	0	47	19.4	95.00%	K.SFIGLDALTESK.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
122	YDG7_SCHPO	26.48%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
53	77	3	2611.26	3.8	1	72.1	22.6	95.00%	R.HIDAAAIYGNEDEVGDGIKESGVPR.K	
302	321	2	2199.03	4.6	1	98.3	23.5	95.00%	R.FNQATFSNEPVFAGLEDGRT.-	
282	299	3	2106.08	4.5	1	37.8	19.1	95.00%	K.YIPLTKEDMDEINSIGIR.A	
183	204	3	2603.37	3.4	0	27.8	17.1	93.30%	K.VKPAVHQMELHPFLPQTEFVEK.H	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
123	YCO6_SCHPO	10.69%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
37	56	2	2127.01	3.9	0	105	22.1	95.00%	K.APQVNTIDEGDENLEAIDGK.L	

15	36	3	2140.01	5.3	0	26.3	22.6	91.60%	K.MSAAPTPHNTPSGTSAPNFGAK.A		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
124	ARGD_SCHPO	14.97%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
311	332	3	2276.09	4.8	0	39.5	22.1	95.00%	K.IAAEIHPGEHGSTFGGNPVACR.V	Carbamidomethyl (+57)
283	310	3	2746.56	2.7	0	43.2	6.02	95.00%	K.DVASPDIITVAKPLANGLPIGATIVSSK.I	
139	154	2	1784.85	4.1	0	92.8	22.4	95.00%	K.IFFANCGTEANETALK.F	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
125	VATB_SCHPO	8.55%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
415	427	2	1417.68	4.9	0	78	20.4	95.00%	K.SVVGEEALSQEDR.L	
439	449	2	1284.62	4.2	0	36.9	20.1	95.00%	K.TFISQGAYENR.T	
485	503	2	2015.89	5.3	1	57.2	23.3	95.00%	R.SSAYTESSKDVIDNTPESS.-	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
126	ACL1_SCHPO	6.99%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
369	381	2	1420.73	4.5	0	44	19.6	95.00%	R.GSELTYNNVPISK.V	
313	326	2	1570.9	3.9	0	58.3	12.6	95.00%	K.LPALLQEVYEGLVK.K	
156	170	2	1506.72	3.3	0	45.7	22	95.00%	K.IGNTGGMMDNIVASK.L	
313	327	3	1699	4	1	30.3	7.78	95.00%	K.LPALLQEVYEGLVKK.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
127	RL27A_SCHPO	32.35%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
23	34	2	1269.74	4.4	0	65.4	14.3	95.00%	K.VVILQAIDQGSK.S	
35	48	3	1461.76	5.9	0	42.8	19.2	95.00%	K.SHPFGHAVVAGVER.Y	
35	52	4	1963.05	4.3	1	23.2	16.3	95.00%	K.SHPFGHAVVAGVERYPLK.V	
94	107	2	1575.83	3.5	1	46.7	19.6	95.00%	K.GLITADTFKEPTQR.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
128	RS17A_SCHPO	16.03%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
24	33	2	1234.67	4.6	1	36.3	16.9	95.00%	R.LTLDFQTNKR.I	
34	44	2	1156.68	4.8	0	51	15.1	95.00%	R.IVDEVAIIASK.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
129	RL2_SCHPO	15.02%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
92	118	3	2780.44	3.2	0	52	18.8	95.00%	K.NAALTVGNVLPVGEMPEGTIISNVEEK.A	
163	173	2	940.55	4.3	0	54.6	11.5	95.00%	R.GVVGIVAGGGR.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
130	PMM_SCHPO	18.29%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
29	43	2	1728.92	4.2	0	56.6	17	95.00%	R.LSVSPEMLETLQNLR.K	
236	253	4	1938.02	4.7	1	21.7	18.9	93.40%	R.TIGHSVTNPDDTIAELKK.I	
45	58	2	1347.75	4.4	0	41.6	16.1	95.00%	K.VVAIGFVGGSDLSK.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
131	YHZ8_SCHPO	31.31%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
75	103	3	3217.69	3	0	57.2	15.9	95.00%	K.TSNPFLAFANYLTSTHAPLAEPLQLLNFK.V	
144	164	3	2285.2	4.3	0	37.3	18.3	95.00%	K.ADTSLIIHSLDDPSLYAVVTR.Y	
2	13	2	1361.7	3.8	0	57.2	19.8	95.00%	M.SFPASTHVYIAK.I	Acetyl (+42)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
132	SYLC_SCHPO	2.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
382	398	3	1730.98	4.6	0	32.6	12.8	95.00%	K.GQDLIGALVNAPLSVHK.Q	
226	241	2	1922.92	5.8	0	66.1	22.7	95.00%	R.SFITTDVNPYYDSFVR.W	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
133	SYTC_SCHPO	6.40%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
248	258	2	1187.55	4.2	0	47.1	21.4	95.00%	K.NSSSYFLGDAK.N	
8	26	3	2136.14	4.2	0	27.4	16.9	92.90%	K.GVQASLDNLSLEIPFIQHR.L	
160	174	2	1703.8	4.7	0	71.1	21.9	95.00%	R.VITNDDYSSIESYAK.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
134	SYDC_SCHPO	15.86%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
281	294	2	1356.6	4.8	0	27.5	20.5	91.60%	K.MSGASSEGGSNVFK.I	
522	554	3	3334.69	3.2	0	85.5	19.4	95.00%	K.ALGVSPDVGLQQYIDAFAIGCPPHAGGGIGLER.V	Carbamidomethyl (+57)
200	210	2	1229.65	4.9	0	29.1	18.9	93.70%	K.NLPFLVEDAGR.S	
490	499	2	1300.55	3.9	0	26.9	20.3	90.60%	R.YSNSYDFFMK.G	
429	452	3	3017.19	2.2	0	39.2	24.1	95.00%	K.VPEDEEFHYCEDPEFDDFSTPEER.A	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
135	SYRC_SCHPO	11.65%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
163	180	2	1987.02	4.1	0	33.9	18.6	95.00%	R.STIIGSFLANLHESQGWK.V	
225	238	2	1588.76	3.6	1	45.2	22.3	95.00%	K.VNADATEEDEKIQK.D	
11	24	2	1544.86	4.5	0	46.7	15.4	95.00%	K.SLSTLGLQDLPVFR.E	
452	467	2	1759.87	3.7	0	55	20.8	95.00%	K.YAQVENPEEVADIVGK.T	
480	489	2	1284.6	5.9	0	39.4	20.2	95.00%	R.INNYAFDWSR.M	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
136	SYG_SCHPO	8.74%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
187	198	2	1297.63	5.4	0	37	20.6	95.00%	R.NPATNGELETPR.Q	
216	232	3	1983.01	5	0	28	19.4	93.50%	K.GYLRPETAQGQFLNFSR.L	
492	506	2	1649.85	4.8	0	35.7	20.2	95.00%	R.TYTPNVIEPSFGLGR.I	
526	538	2	1298.77	3.9	0	28.2	12	92.60%	R.GVLSFPASIAPIK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
137	RL12_SCHPO	28.48%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
68	83	2	1538.91	3.4	0	50.5	10.8	95.00%	R.QAAVSVVPSASALVIK.A	
17	31	2	1312.7	3.6	0	46	15.8	95.00%	R.AVGGEVAGGSTLAPK.I	
131	146	2	1652.81	4	0	45.9	20.5	95.00%	K.EILGTAFSVGCTVDGK.N	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
138	MPG1_SCHPO	11.02%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
270	287	2	1776	4.2	0	35.2	14	95.00%	K.IGPNVVIGPNVTIGDGVR.L	
138	159	4	2530.28	3.4	1	22.1	20.3	94.00%	K.VEEPSKYGVVVHYPNSESLIER.F	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
139	AATR1_SCHPO	12.03%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
275	288	2	1577.78	4.4	0	46.4	21.4	95.00%	K.ELIPSFLSMDVDGR.V	
305	317	2	1562.83	3.7	0	52.6	18.5	95.00%	R.VGWFTAQPLFIER.G	
38	54	2	1856.03	4.5	0	36.8	14.8	95.00%	K.IISLAGGLPNPEYFPIR.E	

7	19	3	1436.71	5.4	0	43.2	21.1	95.00%	K.DLSHHLSVESASR.K		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
140	COFI_SCHPO	28.47%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
81	94	2	1584.9	4.1	0	54.1	14.9	95.00%	K.IIFISWSPDVAPIK.S	
32	43	2	1405.72	4.4	1	32.5	19.9	95.00%	K.MNDTKTEIVVEK.K	
8	20	2	1548.76	4.6	0	71.2	22.1	95.00%	K.VSPECLEAFQELK.L	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
141	RS10A_SCHPO	25.69%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
10	24	3	1580.91	4.1	0	31.3	10.8	95.00%	K.AIHQALFSQGVLVAK.K	
26	31	2	732.38	5.5	0	30.1	18.1	94.70%	K.DFNLPK.H	
78	93	4	1859.01	4	1	23	16.1	95.00%	R.EYLHLPAEVVPATHKR.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
142	NACB_SCHPO	41.06%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
73	90	3	1884.97	4	0	45.6	20.6	95.00%	R.APTVHSSLPNETTAIYGK.A	
130	151	2	2376.03	2.8	1	68.7	23.6	95.00%	K.GADAQADDGEIPDLVEKFDEQD.-	
95	116	2	2320.31	3	0	52.8	10	95.00%	K.TLSEILPGILNNLGPESLTALR.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
143	ADK_SCHPO	25.88%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
32	64	3	3506.56	4	1	78.5	24.6	95.00%	K.SNDAVLASESQMGIYKEPCVSYSAGGAAQNSCR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
126	138	2	1424.68	5.2	0	51	20.8	95.00%	R.SLCTNLGAANNYK.L	Carbamidomethyl (+57)
253	267	2	1483.87	4.5	0	69.4	13.2	95.00%	R.VVVITQGADATIVAK.D	
86	96	2	1295.61	3.7	0	43.7	20.5	95.00%	K.FADMLLESNEK.A	
230	245	2	1688.89	3.8	0	56.9	18.8	95.00%	K.STDVQEIALALSSVEK.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
144	RL36A_SCHPO	24.24%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
83	96	2	1545.84	4.6	1	75.1	16.9	95.00%	K.GKIEELTSVIQSSR.L	
85	96	2	1360.73	3.8	0	56.4	18.8	95.00%	K.IEELTSVIQSSR.L	
2	11	2	966.59	4.6	0	38.2	11.8	95.00%	M.APGLVVGLNK.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
145	PGM_SCHPO	6.86%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
350	358	2	1160.54	5.2	0	29	20.4	93.50%	K.FFCNLFDAK.R	Carbamidomethyl (+57)
423	435	2	1529.66	4.3	0	62.5	21.6	95.00%	R.YDYEELENEAAGK.V	
127	142	2	1631.79	4.4	0	81.8	21.3	95.00%	K.YNLGNGGPAPESVTEK.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
146	DYR_SCHPO	9.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
164	183	3	2062.15	3.7	0	25.4	11.5	90.30%	K.LTTPSLHIAGTSDTLVPLAR.S	
191	212	3	2537.31	3.6	0	37.3	19.1	95.00%	R.CENAHVLLHPGQHIVPQQAVYK.T	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
147	ACL2_SCHPO	11.99%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
382	389	2	947.52	4.5	0	26.9	19	90.60%	K.TVLDLMTR.G	
255	266	2	1367.61	3.7	0	48.5	21.5	95.00%	K.LDQTAEFECGAK.W	Carbamidomethyl (+57)

326	334	2	985.56	4.7	0	36	17.9	95.00%	K.LTILNAEGR.V	
32	61	3	3211.76	3.3	0	47.1	12.6	95.00%	K.TVSATPAVQLAQIQFPLPTLVIPAESTTYR.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
148	THRC_SCHPO	18.87%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
265	282	2	1945.01	4.9	0	46.3	19.2	95.00%	R.FIVPTGNFGDILAGYYAK.R	
437	454	3	2061.03	4.7	1	31.2	20.5	95.00%	K.TKDQDITYICLSTAHPAK.F	Carbamidomethyl (+57)
313	327	2	1443.73	4.4	0	39.8	20.6	95.00%	K.ADSTQVSPSGPISAK.E	
182	215	3	3829.81	3.8	0	34.2	23.4	95.00%	R.VSPIQEAQMTTVTDPNVHCITVNGVFDDCQDLVK.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
399	410	2	1331.7	3.6	1	37.5	19.6	95.00%	R.VSNDETIDAIKK.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
149	SLBR2_SCHPO	20.80%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
134	143	2	1115.56	4.3	0	27.1	19.1	90.90%	R.NIESSVQPSR.E	
166	192	3	3060.53	3.6	1	43.6	21.2	95.00%	R.LVTMEQELVREEAACLVAEAQLSNTTR.E	Carbamidomethyl (+57)
222	248	3	2999.47	2.8	0	39.6	22.7	95.00%	R.HLLNLIDDTPVTPGEARPAYDGYETSR.Q	
149	157	2	1075.63	4.5	0	33	14.8	95.00%	K.LLDQIYALK.H	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
150	CH10_SCHPO	22.12%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
73	84	2	1230.7	4	0	31.7	14.3	95.00%	R.VLLPAYGGSNIK.V	
62	72	2	1111.6	4.5	0	30.9	15.6	95.00%	K.LAQPSVAVGDR.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
151	TBB_SCHPO	13.84%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
104	121	3	1913.96	4.4	0	33.4	21.5	95.00%	K.GHYTEGAELADAVLDVVR.R	
123	154	3	3205.55	2.6	0	82.9	22.7	95.00%	R.EAEACDALQGFQLTHSLGGGTGSGMGTLLLSK.I	Carbamidomethyl (+57)
163	174	2	1249.62	3.9	0	41.3	19.3	95.00%	R.MMATFSVAPAPK.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
152	P25_SCHPO	17.82%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
36	52	2	1976.06	4.7	0	48.2	17.1	95.00%	K.AVIYQFPETLSPEILEK.M	
2	20	2	2064.09	2.1	0	77.6	17.6	95.00%	M.STANTVAIVIYSTYGHVVK.L	Acetyl (+42)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
153	PABP_SCHPO	8.42%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
258	266	2	1068.57	4.8	0	26.6	15.2	90.00%	K.ANFTNVYIK.N	
447	456	2	1142.61	4.9	0	33.9	17.8	95.00%	R.SQLEAQIQAR.N	
536	571	3	3524.72	4.6	0	28.7	22.3	94.20%	R.GPVPAQGRPMMMPGSVPSAGPAEAEAVPAVPGMPER.F	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
154	RS11_SCHPO	26.97%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
55	64	2	1161.6	4.7	0	33.4	19	95.00%	K.CPFVGQVSIR.G	Carbamidomethyl (+57)
41	54	2	1582.79	3.9	1	77.4	20.3	95.00%	K.TPAEAIYGEYVDKK.C	
114	130	2	1870.97	4.9	0	41.5	19.6	95.00%	R.INEGDVVTVGQCRPLSK.T	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
155	RL31_SCHPO	21.24%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
91	105	2	1650.87	4.2	0	39.3	18	95.00%	K.ALYTYVQAVDVANPK.M	

7	15	2	986.56	5	0	39.5	18.2	95.00%	K.SAINQVVTR.D		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
156	DHOM_SCHPO	20.21%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
57	67	2	1391.68	4.7	0	33.1	20.2	95.00%	K.DYQPINLSEWK.N	
125	138	2	1568.79	4.5	0	56.7	19.6	95.00%	K.AFSASNDVYQNIIK.A	
28	56	3	3047.4	3	0	33.8	24.6	95.00%	K.GFNENASTNGTTSFNVVAISSMEGHYVSK.D	
89	110	2	2284.21	4.5	0	95.1	18.6	95.00%	K.SPLPAILVDNTASEAIAQSYPK.F	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
157	RAD25_SCHPO	17.41%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
63	74	2	1417.75	4.9	1	43.2	18.6	95.00%	R.IISSIEQKEESR.G	
227	261	3	3783.73	4.6	1	57.2	25.2	95.00%	R.DNLTLWTSDAEYNQSAKEEAPAAAAASENEHPEPK.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
158	RL14_SCHPO	11.94%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
103	110	2	993.46	6	0	29.1	20.1	93.70%	R.SQLNDFDR.F	
87	94	2	905.44	5.7	0	30.4	19.5	95.00%	K.WASSAWAK.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
159	RS13_SCHPO	23.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
10	20	2	1132.63	4.4	0	38.6	17.4	95.00%	K.GIASSALPYVR.S	
44	55	2	1244.66	3.8	0	40.8	18.6	95.00%	K.GMSPSQIGVTLR.D	
28	39	2	1286.68	5	0	56.1	18.9	95.00%	K.ADADSVVEQILK.F	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
160	SCE3_SCHPO	21.65%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
250	271	3	2195.06	2.9	0	28.5	22.9	94.00%	R.SSSNVNTEATPSATTTTSSKPK.R	
46	66	2	2113.97	4.9	0	94.2	23.1	95.00%	R.ATPSSADAGYNAPSSTFESVR.S	
272	289	3	1956.03	4.3	1	43	18.7	95.00%	K.RDPFGGAKPVDNTSVLQR.V	
359	381	2	2403.05	5.1	0	111	24.3	95.00%	K.TPATEDAPATNAGEAEEEEGWTK.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
161	ACAC_SCHPO	1.49%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
1972	1994	3	2667.36	3.2	0	27.8	20	93.30%	K.TAQAINDFNHGEQLPLFILANWR.G	
197	207	2	1131.63	6.1	0	34.7	14.9	95.00%	K.ISSTIVAQSAR.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
162	PDI1_SCHPO	8.33%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
398	412	2	1637.79	4.8	0	66.2	22.3	95.00%	K.LAEEYSDDSNVVVAK.I	
125	136	3	1350.87	5.1	1	30.4	3.01	95.00%	R.KQLLPTVKPISK.D	
188	201	2	1436.77	4.3	0	45.1	17	95.00%	K.SLGSNFPGIVAFTK.D	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
163	YDMC_SCHPO	9.19%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
370	385	2	1877	4	0	39.4	17.6	95.00%	K.LTSLMESIFPEQTIIR.S	
488	513	3	3117.34	3.1	1	64.3	25.4	95.00%	K.VEPEPIDEEEAFSDDEEEEPEEIKER.I	
82	91	2	1136.53	5	0	33.4	19.7	95.00%	R.NADNSVTNFR.D	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
164	YBS7_SCHPO	12.20%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
442	471	4	3134.5	-0.033	1	26.4	23.4	95.00%	K.EQPPNKAEPAVPTEASSTKPSEAAEESTPR.F	
128	146	2	1760.86	5.1	0	31.6	21.2	95.00%	R.TSGSSTGLSNAPPSANVSK.A	
164	189	3	2841.41	3.2	0	29.4	21.2	94.70%	R.ATPEVCVPLNPDTGSVPLIHPEQTDR.G	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
165	RS12A_SCHPO	46.90%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
99	111	2	1486.76	2.4	0	27.9	18.9	92.10%	K.VLGEWAGLCVLDR.D	Carbamidomethyl (+57)
79	93	2	1671.88	4.1	0	73.8	18.4	95.00%	K.LVEALCAESETPLIK.V	Carbamidomethyl (+57)
61	78	3	2208.97	4.2	0	36.3	23.9	95.00%	R.QAHLCVLCESCDQEAYVK.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)
117	138	3	2356.11	4.1	1	43.9	23.3	95.00%	R.KVVGCSCVAVTDYGEDSAALQK.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
166	SYEC_SCHPO	6.15%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
66	77	2	1393.77	4.3	0	31.9	15.3	95.00%	K.LALQTFSQVYPK.L	
190	206	2	1731.84	3.9	0	51.4	21.6	95.00%	K.SSGPNYEIGLPDAIDGK.V	
295	309	2	1657.7	4.5	0	93.6	22.1	95.00%	K.SGQAYADDTDVETMR.H	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
167	RANG_SCHPO	25.12%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
88	98	2	1353.6	4	0	43.5	21.4	95.00%	K.TNEEEETVEFK.M	
188	198	2	1253.61	5.8	0	35.7	20.6	95.00%	R.FANSENANLFK.E	
49	80	3	3379.58	3.1	1	28.6	23.5	94.10%	K.SGASTNDEKKPAEGDEDAEPASPEVHFEPIVK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
168	O13797_SCHPO	14.83%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
197	214	2	1831.84	5.2	0	74	22.4	95.00%	K.QLNQPSDSSATSGADQAR.T	
124	152	4	3210.53	3.2	0	60.9	22.6	95.00%	R.AAAYNQLGQFENAVEDALTCLSLDPHHAR.A	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
169	YET4_SCHPO	6.80%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
190	216	3	2686.32	5.5	0	58	22	95.00%	R.NDEQLGNSPASITSKPATTSAAQPSSK.V	
487	503	3	1712.87	4.4	0	27.8	20.2	93.30%	R.KPSSTGQEPTTPSTPAK.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
170	ACBP_SCHPO	54.02%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
33	50	3	1912	4.1	0	25.6	18.7	90.50%	K.QATVGDNNTEKPGLLDLK.G	
2	13	2	1294.61	4.4	0	38.3	20.5	95.00%	M.SSTFEQAAADVK.E	Acetyl (+42)
65	81	2	1929.93	3.7	1	95	22.3	95.00%	K.SKEDAASEYISFVDELK.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
171	Q9P7B4_SCHPO	15.83%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
234	256	3	2522.27	2.7	0	34.8	20.1	95.00%	R.ENVVIADTLVFPSHQGGANHVYR.K	
233	256	4	2678.38	4.3	1	40.7	19.5	95.00%	R.RENVVIADTLVFPSHQGGANHVYR.K	
183	199	2	1918.98	6.8	0	60.8	19	95.00%	R.IMEVDPGLVETEFSVVR.F	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
172	RS5B_SCHPO	13.79%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
167	181	2	1646.83	4.1	0	68	20.6	95.00%	K.SISECLAEEIINAAK.G	Carbamidomethyl (+57)	
20	32	3	1552.84	4.7	1	30.8	15.8	95.00%	K.LFNKFPFEGVEVK.D		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
173	RL18A_SCHPO	12.30%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
81	93	2	1390.7	3.8	0	57.3	20.7	95.00%	K.TTVVVGTVTDDER.M		
56	65	3	1111.64	5.1	0	26.6	14.5	92.00%	K.TNRPPISISK.I		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
174	YFHH_SCHPO	5.21%	100%	3							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
504	529	4	3037.42	4.5	1	22.9	24.2	95.00%	K.EEERPLPSEPSQNQPAEYRDTPDTPR.N		
307	340	4	3584.77	4.2	1	20.1	21.7	90.60%	R.VAKDDDPFVVSNTANSDEPASSSKPAKPLTDLNR.A		
711	734	3	2663.22	4.7	1	32.8	24	95.00%	R.ISEVTEDSIDEDKQNEVDPSTSAR.A		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
175	LYS1_SCHPO	13.86%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
274	306	3	3758.77	3.3	0	76.7	23.6	95.00%	R.VVCDVSCDTTNPNNPIPIYNVNTTFDHPTVEVK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	
329	346	2	1904.02	3.7	0	28.9	16.5	93.50%	R.ESSEAFSEALIPSLLALK.D		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
176	Q1L854_SCHPO	21.25%	100%	3							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
143	178	3	3637.66	4	0	78.1	24.9	95.00%	R.GWGDLVNSAANPDVAENEGNTPSGAQTPAAEEENVK.T		
10	28	2	2077.07	4.4	1	50.2	19	95.00%	K.NLFDLLGEETPAATTTEKK.T		
10	27	2	1948.97	3.6	0	75.2	22.1	95.00%	K.NLFDLLGEETPAATTTEK.K		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
177	APE1_SCHPO	3.40%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
253	269	2	1912.97	5	0	42.1	20.3	95.00%	K.TLDFFSGVFGEPYPLPK.C		
137	149	2	1467.71	4.6	0	42.2	20.7	95.00%	K.YLATTQMEPTSAR.R		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
178	FIMB_SCHPO	4.89%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
508	524	2	1796.81	3.5	0	38.6	22.2	95.00%	K.TLSDSDMVAWANSMAAK.G		
158	170	2	1485.74	3.7	0	44.6	21.6	95.00%	K.LINDSVPDTIDER.V		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
179	SODM_SCHPO	20.18%	100%	3							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
162	173	2	1303.7	4.2	0	48.8	18.2	95.00%	R.ITTTANQDTIVK.S		
26	48	2	2502.32	2.9	0	32.8	16.7	95.00%	K.ATLPPLPYAYNALEPALSETIMK.L		
127	135	2	1108.52	5	0	34	20	95.00%	K.WGSLEDFQK.E		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
180	RL11_SCHPO	14.37%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
154	164	2	1349.67	4.1	0	39.8	20	95.00%	K.INAEDTINWFK.Q		
36	49	2	1531.83	4.2	0	63.5	17.9	95.00%	K.VLEQLSGQTPVFSK.A		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
181	YEI3_SCHPO	8.67%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
329	342	2	1482.75	2.8	0	41.2	20.3	95.00%	K.APQAAGVIHTDFEK.A	
43	62	2	2148.05	4.6	0	58.6	22.1	95.00%	K.SVLGNPANYPYATIDPEEAK.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
182	KAPS_SCHPO	22.77%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
157	188	3	3532.7	3.1	0	32.4	22.2	95.00%	K.EFTGISAPYEAPISPEIVVSSHTQSIEECVEK.I	Carbamidomethyl (+57)
39	52	2	1664.86	3.8	0	65.6	19.8	95.00%	K.STIACALEQYLLQR.G	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
183	IDHP_SCHPO	6.94%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
312	324	2	1431.68	4.4	0	73.7	21.4	95.00%	R.TFESEAAHGTVQR.H	
392	407	2	1800.87	4.4	0	48.7	21.9	95.00%	K.SPNGYVDTFEFLDAVK.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
184	ARO1_SCHPO	3.43%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
677	703	3	2950.41	2.7	0	45.4	22.6	95.00%	R.FACDVLRPMGCTVEQTATSTTVQGPPK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
1232	1247	2	1833.96	4.6	0	44.8	19.2	95.00%	R.ITNSMDIPLILFNMGR.F	
162	172	2	1299.72	4.7	0	45.2	18	95.00%	K.NLVGAFWQPLR.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
185	RL25A_SCHPO	19.86%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
125	137	2	1329.66	4	0	94.2	20.8	95.00%	K.LSADADALDVANR.I	
74	88	4	1806.97	3	1	20.6	17.7	91.70%	K.KIEDDNTLVFHVHLK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
186	FUMH_SCHPO	7.88%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
131	142	2	1157.67	3.6	0	43.3	16.1	95.00%	R.AIEILGGTLGSK.K	
392	417	3	2921.34	2.7	0	27.9	24	93.50%	R.LLGDACESFTDHCVVGIEPNYEGIAR.H	Carbamidomethyl (+57)/ Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
187	TBA1_SCHPO	10.33%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
65	79	2	1758.92	3.8	0	35	18.8	95.00%	R.SIYVDLEPNVIDQVR.T	
281	304	3	2899.3	3.7	0	55.7	25	95.00%	K.AFHESNSVQEITNQCFEPYNQMVK.C	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
188	RS3_SCHPO	18.88%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
30	42	2	1513.64	4.2	0	70.9	21	95.00%	R.ELSEEGYSGCEVR.V	Carbamidomethyl (+57)
154	175	3	2381.12	3.5	0	33.1	23.6	95.00%	K.FADGFMIHSGQPAVDFIDSATR.H	
97	108	2	1362.64	3.8	0	61	20.8	95.00%	R.GLCAVAQCESLR.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
189	SPEE_SCHPO	15.77%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
105	126	3	2641.27	3.1	1	46.8	23.4	95.00%	R.EVVKHECVEEAILCDIDEDVIK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
2	12	2	1291.72	4.1	0	43.5	16.1	95.00%	M.SVQELSHPLIK.D	Acetyl (+42)

18	31	2	1631.79	4.6	0	31.2	21.2	95.00%	R.EINNMWPGQAMTLK.V		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
190	G3P2_SCHPO	35.82%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
146	162	2	1818.91	4.5	0	75	21.9	95.00%	K.VISNASCTTNCLAPLAK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
87	105	2	2031.99	4.2	0	101	22	95.00%	K.WSASGAEYVIESTGVFTTK.E	
6	13	2	819.43	6.2	0	38.4	19.9	95.00%	K.VGINGFGR.I	Deamidation (+1)
249	259	3	1290.69	4.5	0	28.4	19.1	93.90%	K.LAKPTNYEDIK.A	
235	248	2	1467.82	3.7	0	76.5	14.5	95.00%	R.VPTPDVSVVDLTVK.L	
163	186	2	2576.29	4.6	0	94.8	21	95.00%	K.VINDTFGIEEGLMTTVHATTATQK.T	
324	335	2	1279.67	5	1	52.3	19.4	95.00%	R.VVDLVAYTASKD.-	
201	215	2	1343.71	4.7	0	69.9	19	95.00%	R.GASANIIPSSTGAAK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
191	RLA0_SCHPO	15.06%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
133	144	2	1308.71	5.2	0	29.1	15.8	93.70%	K.TSFFQALGIPTK.I	
98	132	3	3513.88	2.7	0	45.6	15.3	95.00%	R.ETIIANVIAAPARPNAIAPLDVFVPAGNTGMEPGK.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
192	RL19B_SCHPO	20.73%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
118	128	3	1386.74	5	0	32.3	18.6	95.00%	K.HLYHTLYLEAK.G	
22	38	2	1960.9	4.1	0	66.6	22.7	95.00%	K.VWMDPNEISEISNANSR.Q	
182	193	2	1422.69	3.6	1	31.8	20.7	95.00%	R.EQIYTAAEKIEE.-	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
193	RS15A_SCHPO	20.92%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
90	108	2	2033.08	3.1	0	80.9	17.2	95.00%	R.NMIILPEMVGSVVGIYNGK.L	
73	85	2	1396.76	4.6	0	40.4	17.5	95.00%	K.TEAPLNEKPATVK.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
194	PUR4_SCHPO	3.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
298	334	4	3616.77	4.4	1	38.1	22	95.00%	K.VETHNHPTAVSPFPGAATGSGGEIRDEGAVGQGSLSK.A	
412	425	3	1426.76	5.3	0	35.9	18.9	95.00%	R.GYHKPIMAAGGIGR.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
195	SYFA_SCHPO	4.81%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
2	14	2	1558.9	4.5	1	64.1	7.78	95.00%	M.SKLEALQVFLLEK.L	Acetyl (+42)
128	138	2	1219.56	4.9	0	33.3	21.4	95.00%	K.NTDSITDETPK.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
196	AROC_SCHPO	11.14%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
328	340	2	1331.68	5.2	0	55.6	19.5	95.00%	K.SPATIGVEQSTSR.Y	
161	191	3	3385.69	2.7	0	61.9	21.1	95.00%	K.IAIPLHETASSAILDPEDDTFESPITAEYLK.F	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
197	CYSK1_SCHPO	9.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
10	23	2	1341.78	3.9	0	59.1	14	95.00%	K.VPGIVSGFIGAIGR.T	
180	200	2	2019.93	5.1	0	71.4	24.1	95.00%	K.GTVDGFTCSTGTGGTFAGVTK.Y	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
198	P5CR_SCHPO	15.25%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
70	98	3	3111.57	2.6	0	41.3	20.4	95.00%	K.ENAEMAAISNVLLLSCKPQAAEDVLNSPK.M	Carbamidomethyl (+57)
116	129	2	1566.76	5	0	85.9	21.2	95.00%	K.TISSLQSMLDESTR.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
199	CISY_SCHPO	9.30%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
371	388	3	2156.12	3.5	1	38.1	19.6	95.00%	R.EFALEHLPKDPMFQLVSR.L	
167	192	4	2838.39	2.4	0	38.1	21.5	95.00%	R.CPPTLHPMAQFSLAVTALEHDSAFAK.A	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
200	ODP2_SCHPO	10.56%	99%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
215	238	4	2577.46	3.9	1	20.4	9.54	91.30%	R.IIKVDIENFKPVVAPKPSNEAAAK.A	
49	75	3	2873.43	2.8	0	41.8	21.9	95.00%	K.NYPAHTVINMPALSPTMTTGNIGAFQK.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
201	RL33B_SCHPO	26.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
20	32	4	1401.82	4.5	1	28.1	11.1	95.00%	R.SKHVIHPGTSIVK.I	
33	48	3	1872.86	4.3	1	30.1	22.6	95.00%	K.IEGCDSKEEAQFYLGK.R	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
202	ATPB_SCHPO	7.43%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
160	185	3	2859.39	2.5	0	29.4	22.6	94.80%	K.YSPIHADAPSFEEQSTTPEILETGIK.V	
210	222	2	1501.86	4.8	0	34.9	13.2	95.00%	K.TVFIQELINNIAK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
203	RS21_SCHPO	48.28%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
51	60	2	1113.59	4.5	0	33.8	17.6	95.00%	K.TTYAISGFVR.S	
1	16	2	1902.96	5.9	1	43.5	20.6	95.00%	-.MENEAGQLVDLYVPRK.C	Acetyl (+42)
72	87	2	1864.94	4.3	0	65.3	21.5	95.00%	R.LTTQDGLLEGVWSYQR.-	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
204	RL24A_SCHPO	20.81%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
1	12	2	1357.64	4.1	1	34.6	21	95.00%	-.MKVEVCSFSGSK.V	Carbamidomethyl (+57)
81	91	2	1097.65	4.7	0	29.4	14.6	94.00%	R.GIVGANLDVIK.E	
36	43	2	978.52	4.9	0	29.5	19.8	94.10%	K.SESLFLQR.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
205	6PGL_SCHPO	8.95%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
46	55	2	1083.61	5.4	0	52.4	15.7	95.00%	K.VLAEGLAQQR.G	
209	221	2	1488.81	4	0	42.1	15.8	95.00%	K.DILPIVIEDFTSK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
206	UBC4_SCHPO	25.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
91	101	2	1244.65	4.6	0	28.4	19.7	92.90%	R.DQWSPALTISK.V	
102	128	3	3017.59	3.1	0	65.3	15.6	95.00%	K.VLLSICSLLTDPNPDDPLVPEIAHVYK.T	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
207	RS24A_SCHPO	20.15%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
21	32	3	1363.77	4	1	39.5	15.7	95.00%	R.KQMVVDILHPGK.A	
69	83	2	1672.81	4.3	0	28.6	22.3	93.10%	R.TTGFALIYDDVEAMK.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
208	SYYC_SCHPO	10.22%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
368	395	3	2695.3	3.6	1	45.5	22	95.00%	K.KAGTTNASIAAESGAAPATESQTAESFK.K	
2	14	2	1605.83	4.1	1	47.4	18.6	95.00%	M.SLTPDEKYELITR.N	Acetyl (+42)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
209	CAN_SCHPO	18.03%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
84	101	3	2033.14	2.7	0	42.8	13.2	95.00%	R.VPETTILNLLPGEVFVHR.N	
9	34	4	2766.34	3.9	1	21.8	22.9	93.50%	R.IEEIDHQDEIIDREASTASPVSGAGK.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
210	CBPY_SCHPO	3.69%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
774	801	3	3239.34	0.62	1	55.1	25.6	95.00%	K.MACESPYGPIMSQEECDRITGAYDTCAK.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)
833	841	2	1063.57	5.5	0	55.3	18.6	95.00%	K.TGLNIYDIR.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
211	YB45_SCHPO	11.74%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
191	207	3	1910.83	3.6	1	52	22.7	95.00%	R.NDSNKEAMGGDTHNFFK.E	
224	235	2	1300.72	4.5	0	38.3	15.6	95.00%	K.ALSFLALNNNPK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
212	RL7B_SCHPO	14.00%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
2	21	2	2002.11	4.4	0	37	14.5	95.00%	M.VASSTVPSVASIFAPESLLK.K	
168	182	2	1523.86	4.4	0	56.2	12	95.00%	R.IPLSDNAIIEAALGK.Y	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
213	PPID_SCHPO	10.96%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
214	226	2	1432.74	4.4	0	72	19.4	95.00%	K.QFAQQNLDTAVAK.W	
144	169	3	2959.43	3.1	1	32.1	22.9	95.00%	R.TIENLETKNDDPVVPVVIEECGTCTK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
214	MUG64_SCHPO	11.19%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
224	238	3	1767.86	4.9	0	44.3	22.3	95.00%	K.LDVESAKPENLEHCK.S	Carbamidomethyl (+57)
108	125	2	1851.02	3.8	0	41.3	14	95.00%	R.NLGNLTPLEQTPLASVGK.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
215	RL35_SCHPO	19.67%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
11	24	2	1684.85	4.2	0	72	19.9	95.00%	K.QSQENLAEQLQELR.Q	
56	65	2	1157.65	4.3	0	33.6	16.8	95.00%	R.ILTVINESNR.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
216	SYQ_SCHPO	3.95%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification

757	773	3	1760.83	5.2	1	28.1	22.6	93.60%	K.TDSSAGVDKAENPESVR.F	
52	66	2	1574.91	4.6	0	39.6	9.03	95.00%	R.TIGNLLFTLANASLK.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
217	YBN4_SCHPO	12.62%	100%	2						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
182	203	4	2693.39	2.2	0	23.4	18.3	95.00%	K.VKPTIHQMELHPYLPQTEYLEK.H	
52	70	4	2151.08	3	1	29.4	21.1	95.00%	R.HIDTAHIYGNEKEIGEGIR.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
218	PUR7_SCHPO	13.71%	99%	2						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
159	174	3	1746.79	5.6	0	25.2	22.3	90.00%	K.AAEGHDENIHPDEVSK.I	
258	282	3	2764.43	3.8	0	38.4	17.9	95.00%	R.NWLTANNLANKPNVSLPEDVVEATR.R	

Supplementary Table S2: All "Scaffold" validated proteins and peptides identified from solprotSP (*S.pombe*) and from SCVMprot (*S.cerevisiae*) samples

***S.pombe* - Glu-C digest of large tryptic peptides (replicate A)**

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
1	G3P1_SCHPO	51.79%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
249	259	3	1290.69	4.5	1	28.4	19.9	95.00%	K.LAKPTNYEDIK.A		K.LAKPTNYEDIK.A
67	79	2	1407.7	3.2	0	89	21.9	95.00%	K.LVIDGNAIDVHNE.R		K.LVIDGNAIDVHNER.D
235	248	2	1467.82	3.7	0	76.5	15.2	95.00%	R.VPTPDVSVVDLTVK.L		R.VPTPDVSVVDLTVK.L
87	97	2	1226.55	3.2	0	36.3	23.2	95.00%	K.WSTSGADYVIE.S		K.WSTSGADYVIESTGVFTTQETAS AHLK.G
323	334	2	1304.75	5.7	1	40.6	12.8	95.00%	R.RVVDLVAYTAAK.D		R.RVVDLVAYTAAK.D
98	106	2	968.45	4	0	40	22.6	95.00%	E.STGVFTTQE.T		K.WSTSGADYVIESTGVFTTQETAS AHLK.G
173	186	2	1458.75	3.1	0	81.7	18.8	95.00%	E.GLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK. T
146	162	2	1818.91	4.5	0	75	21.7	95.00%	K.VISNASCTTNCLAPLAK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.VISNASCTTNCLAPLAK.V
324	334	2	1148.65	6.2	0	55.4	16.6	95.00%	R.VVDLVAYTAAK.D		R.VVDLVAYTAAK.D
49	61	2	1468.63	4.1	1	50.5	23.2	95.00%	K.YDSTHGRFDGSVE.I		K.YDSTHGRFDGSVEIK.D
27	41	2	1685.89	3.5	0	48.5	18.6	95.00%	K.TIQVVAINDPFIDLE.Y		K.TIQVVAINDPFIDLEYMAYMFK.Y
324	336	2	1377.72	3.8	1	68.7	20	95.00%	R.VVDLVAYTAAKDN.-		R.VVDLVAYTAAKDN.-
172	186	2	1587.8	3.6	1	49.5	21.6	95.00%	E.EGLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK. T
6	13	2	819.43	6.2	0	38.4	19.6	95.00%	K.VGINGFGR.I	Deamidation (+1)	K.VGINGFGR.I
201	215	2	1343.71	4.7	0	69.9	19.5	95.00%	R.GASANIIPSSTGAAK.A		R.GASANIIPSSTGAAK.A
119	137	2	2004.03	2.8	1	51.7	20.1	95.00%	R.VIISAPSKDAPMYVVGVNE.E	Oxidation (+16)	R.VIISAPSKDAPMYVVGVNEEK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
2	PGK_SCHPO	60.14%	100%	27

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
383	398	2	1528.7	2.3	1	32.3	23.3	95.00%	K.EDALSHVSTGGGASLE.L		K.EDALSHVSTGGGASLELLEGK.A
359	378	2	1917.95	4	1	118	21	95.00%	K.TCEAGNVVIVGGGDTATVAK.K	Carbamidomethyl (+57)	K.TCEAGNVVIVGGGDTATVAK.K
7	15	2	986.57	5.4	0	41.1	17.3	95.00%	K.LAITDVDLK.G		K.LAITDVDLK.G
302	316	2	1630.72	2.5	1	60	23.2	95.00%	E.EGIPDGWMGLDCGPK.S	Carbamidomethyl (+57)	K.VGSATAEEGIPDGWMGLDCGPK. S
273	288	2	1805.93	4.9	1	56.9	20.3	95.00%	K.NNVEVFLPVDFVTADK.F		K.NNVEVFLPVDFVTADK.F
200	213	2	1423.83	2.4	0	38.6	11.8	95.00%	E.NPARPFLAILGGAK.V		K.ALENPARPFLAILGGAK.V
362	379	2	1655.93	3.4	1	45.1	15.3	95.00%	E.AGNVVIVGGGDTATVAKK.Y		K.TCEAGNVVIVGGGDTATVAKK.Y
384	398	2	1399.66	2.7	0	56.3	23.2	95.00%	E.DALSHVSTGGGASLE.L		K.EDALSHVSTGGGASLELLEGK.A
23	39	2	1914.96	3.6	1	46.4	21.4	95.00%	R.VDFNVPLDGDRITNNAR.I		R.VDFNVPLDGDRITNNAR.I
57	71	2	1591.87	2.9	0	46.2	17.5	95.00%	K.AVILMSHLGRPNGAR.V	Deamidation (+1)	K.AVILMSHLGRPNGAR.V
23	33	2	1245.61	6.8	0	62.1	21.6	95.00%	R.VDFNVPLDGDR.I		R.VDFNVPLDGDR.I
40	48	2	910.59	3.6	0	25.3	6.99	91.10%	R.IVGALPTIK.Y		R.IVGALPTIK.Y
330	347	2	2010.99	4.7	1	67	21.3	95.00%	K.TIVWNGPAGVFEFDNFAK.G		K.TIVWNGPAGVFEFDNFAK.G
303	316	2	1501.67	2.3	0	58.3	22.9	95.00%	E.GIPDGWMGLDCGPK.S	Carbamidomethyl (+57)	K.VGSATAEEGIPDGWMGLDCGPK. S
250	261	2	1237.59	4.5	1	61.5	22	95.00%	K.IGDSLFDEAGSK.N		K.IGDSLFDEAGSK.N
218	227	2	1183.69	5.5	0	39.2	16	95.00%	K.IQLIDNLLDK.V		K.IQLIDNLLDK.V
218	230	3	1552.9	4.8	1	31.7	11.8	95.00%	K.IQLIDNLLDKVNR.L		K.IQLIDNLLDKVNR.L
404	414	2	1040.63	5.6	0	39.4	16.1	95.00%	K.ALPGVVALSSK.-		K.ALPGVVALSSK.-
277	291	2	1739.92	3.1	1	53.1	18.8	95.00%	E.VFLPVDFVTADKFDK.D		K.NNVEVFLPVDFVTADKFDK.D
321	329	2	994.54	5.5	1	50.2	18.6	95.00%	K.FAEVITTSK.T		K.FAEVITTSK.T

75	86	3	1304.74	4.3	1	59.4	15.2	95.00%	K.YSLKPVAAELSK.L		K.YSLKPVAAELSK.L
197	213	2	1737	3.6	1	57	10.8	95.00%	K.ALENPARPFLAILGGAK.V		K.ALENPARPFLAILGGAK.V
151	169	2	2020.01	5.9	0	113	21	95.00%	K.SLTSLGDIFVNDAFGTAHR.A		K.SLTSLGDIFVNDAFGTAHR.A
362	378	2	1527.83	3.7	0	84.8	16.1	95.00%	E.AGNVVIVGGGDTATVAK.K		K.TCEAGNVVIVGGGDTATVAK.K
170	181	2	1267.64	4	0	58.7	21.1	95.00%	R.AHSSMVGVDLPR.V		R.AHSSMVGVDLPR.V
150	169	3	2148.1	3.4	1	64.2	19.6	95.00%	R.KSLTSLGDIFVNDAFGTAHR.A		R.KSLTSLGDIFVNDAFGTAHR.A
214	227	2	1596.92	3.7	1	58.7	12	95.00%	K.VADKIQLIDNLLDK.V		K.VADKIQLIDNLLDK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
3	ENO11_SCHPO	59.00%	100%	28

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
80	92	2	1388.65	3.9	1	37.8	23.1	95.00%	K.ANLDVTDQKAADE.F		K.ANLDVTDQKAADEFLLK.L
258	263	2	765.39	4.7	0	25.9	21.6	92.10%	K.YDLDIK.A		K.YDLDIK.A
212	230	2	1978.03	3.5	1	46.4	19.1	95.00%	E.GGIAPDLQTPQEALDLIVE.A		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
361	374	3	1608.73	4.7	1	47.1	23.9	95.00%	R.MSYEAGWGVMVSHR.S		R.MSYEAGWGVMVSHR.S
185	194	2	1204.59	5.4	1	34	22.3	95.00%	R.WGAETYHTLK.S		R.WGAETYHTLK.S
346	360	2	1585.85	6	1	90.8	17.3	95.00%	K.VNQIGSVTESLNAVR.M		K.VNQIGSVTESLNAVR.M
346	354	2	945.48	3.7	0	31.4	21.3	95.00%	K.VNQIGSVTE.S		K.VNQIGSVTESLNAVR.M
423	432	2	929.48	5.2	0	41.8	23	95.00%	E.GVYAGAHAGK.Y		R.IEEELGSEGVYAGAHAGK.Y
201	223	2	2261.02	3	1	63.8	23.4	95.00%	R.YGSSAGNVGDEGGIAPDLQTPQE.A		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
365	374	2	1098.54	2.5	0	69.5	21.2	95.00%	E.AGWGVMVSHR.S		R.MSYEAGWGVMVSHR.S
311	328	2	1963.98	4.2	1	93.2	21.3	95.00%	K.AETDFQIVGDDLTVTNVK.R		K.AETDFQIVGDDLTVTNVK.R
313	329	2	1920	1.8	1	77.7	19.1	95.00%	E.TDFQIVGDDLTVTNVKR.L		K.AETDFQIVGDDLTVTNVKR.L
289	310	3	2679.2	3	1	73.2	24	95.00%	K.YPIVSIEDPFDQDDWSAWTHMK.A		K.YPIVSIEDPFDQDDWSAWTHMK.A
65	79	2	1477.87	4	0	73.7	6.99	95.00%	K.AVGNVNNIIAPAVVK.A		K.AVGNVNNIIAPAVVK.A
313	328	2	1763.9	2.6	0	55.8	21.3	95.00%	E.TDFQIVGDDLTVTNVK.R		K.AETDFQIVGDDLTVTNVK.R
106	120	2	1560.82	4.2	0	61.3	19.9	95.00%	K.LGANAILGVSMAICR.A	Oxidation (+16)/ Carbamidomethyl (+57)	K.LGANAILGVSMAICR.A
378	396	2	1928.04	3.2	0	62.1	15.7	95.00%	E.TADTFISHLTVGIGAGQLK.S		R.SGETADTFISHLTVGIGAGQLK.S
169	184	2	1769.85	2.9	1	43.2	22.2	95.00%	E.FMILPTGAPSFSEAMR.W	Oxidation (+16)	K.GPYVLPVPSFNVLNGGSHAGGDLAFQEFMILPTGAPSFSEAMR.W
419	432	2	1315.66	3.1	1	50.8	22.2	95.00%	E.LGSEGVYAGAHAGK.Y		R.IEEELGSEGVYAGAHAGK.Y
212	223	2	1224.6	3.2	0	46	21.8	95.00%	E.GGIAPDLQTPQE.A		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
273	287	2	1812.96	4.5	1	75.4	17.7	95.00%	K.LTYQQLTDLYVELSK.K		K.LTYQQLTDLYVELSK.K
243	257	2	1598.79	4.2	1	56.6	21.4	95.00%	K.IGLDVASSEFYVDGK.Y		K.IGLDVASSEFYVDGK.Y
338	345	2	901.51	4.7	0	31.4	19.4	95.00%	K.CANALLLK.V	Carbamidomethyl (+57)	K.CANALLLK.V
409	414	2	806.43	5.7	1	29.4	21.4	95.00%	K.YNELLR.I		K.YNELLR.I
375	396	2	2201.14	2.9	1	122	18.6	95.00%	R.SGETADTFISHLTVGIGAGQLK.S		R.SGETADTFISHLTVGIGAGQLK.S
89	96	2	905.49	4.7	1	57.4	20.4	95.00%	K.AADEFLLK.L		K.AADEFLLK.L
80	88	2	1002.5	4.3	0	41.9	20.3	95.00%	K.ANLDVTDQK.A		K.ANLDVTDQK.A
201	211	2	1054.43	4.8	0	38.8	22.5	95.00%	R.YGSSAGNVGDE.G		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
4	METE_SCHPO	53.40%	100%	31

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
325	349	2	2643.33	4.3	1	28.2	19.7	94.90%	R.VQVASSSSILHIPHSLSGEDQINPE.I		R.VQVASSSSILHIPHSLSGEDQINPEIK.R
104	118	2	1384.69	3.7	1	54.5	21.6	95.00%	R.AATADKAAVDVPAGE.M		R.AATADKAAVDVPAGEMVK.W
638	667	3	3497.61	3.2	0	56.4	22.9	95.00%	R.LATAAVQDDTQIHSHFCYSDFNDIFDAIQR.L	Carbamidomethyl (+57)	R.LATAAVQDDTQIHSHFCYSDFNDIFDAIQR.L

577	595	2	2108.02	3.6	1	78.2	21.4	95.00%	R.DDVHDSVQAQQIALGLRDE.V		R.DDVHDSVQAQQIALGLRDEVLDLEK.A
561	571	2	1184.7	5.1	0	40.5	15.3	95.00%	K.GMLTAPITILR.W		K.GMLTAPITILR.W
434	449	2	1746.96	4.2	0	74.9	14.6	95.00%	K.LPLFPTTTIGSFPQTK.E		K.LPLFPTTTIGSFPQTK.E
486	498	2	1418.76	2.9	1	38.5	19.7	95.00%	E.VGLDVLVHGEPER.N		K.FQEEVGLDVLVHGEPER.N
4	11	2	845.48	4.8	0	33.3	20.1	95.00%	K.SAVLGFPR.I		K.SAVLGFPR.I
707	714	2	901.49	4.3	1	27.7	21.4	94.40%	R.VPPVSEFK.E		R.VPPVSEFK.E
684	690	2	813.51	5.6	0	34.2	17.2	95.00%	K.LLNVLSR.Y		K.LLNVLSR.Y
691	706	2	1818.88	3.8	0	84	22.1	95.00%	R.YTSCIGPGLFDIHSPR.V	Carbamidomethyl (+57)	R.YTSCIGPGLFDIHSPR.V
499	508	2	1257.55	4.4	1	53.6	23.2	95.00%	R.NDMVQYFGER.M		R.NDMVQYFGER.M
243	260	2	1982.08	3.5	0	54.1	14.5	95.00%	K.LILTTYFGSLQSNADVLK.G		K.LILTTYFGSLQSNADVLK.G
727	738	2	1466.7	4.2	0	48	23	95.00%	K.DHLWLNPDCGLK.T	Carbamidomethyl (+57)	K.DHLWLNPDCGLK.T
428	449	3	2402.33	4.8	1	46	11.1	95.00%	K.QQASLKLPLFPTTTIGSFPQTK.E		K.QQASLKLPLFPTTTIGSFPQTK.E
157	176	3	2127.29	3	0	32.3	4.77	95.00%	E.AGIITRPVLVGPVTYLFIAK.A		K.EAGIITRPVLVGPVTYLFIAK.A
261	273	2	1330.78	4	0	55.7	11.8	95.00%	K.GLPIAGVHVDVVR.A		K.GLPIAGVHVDVVR.A
468	474	2	911.49	2.9	1	26.8	18.1	93.30%	E.YDAFIRK.E		K.GLISQEEYDAFIRK.E
122	133	2	1609.74	3.4	0	32	24	95.00%	K.WFDSNYHFLRPE.V		K.WFDSNYHFLRPEVSEETDFK.L
281	299	2	1881.08	4.8	1	87.4	10	95.00%	R.ALAVLGENQIISVGVVSGR.N		R.ALAVLGENQIISVGVVSGR.N
723	738	3	1927.98	4	1	24.5	19	95.00%	K.HVPKDHLWLNPDCGLK.T	Carbamidomethyl (+57)	K.HVPKDHLWLNPDCGLK.T
288	299	2	1227.7	3.2	0	41.8	17.2	95.00%	E.NQIISVGVVSGR.N		R.ALAVLGENQIISVGVVSGR.N
361	369	2	1017.56	4.9	1	30.5	18.3	95.00%	K.CAELAILTK.A	Carbamidomethyl (+57)	K.CAELAILTK.A
547	560	2	1596.79	3.6	1	50.8	22	95.00%	K.ESQYAQSITSKPMK.G		K.ESQYAQSITSKPMK.G
606	615	2	1199.6	4.3	0	55.1	21.4	95.00%	K.VIQCDEPALR.E	Carbamidomethyl (+57)	K.VIQCDEPALR.E
668	679	2	1288.66	3.8	1	37	20.8	95.00%	R.LDADVVSIENSK.S		R.LDADVVSIENSK.S
527	546	3	2267.24	3.3	0	44.5	14.1	95.00%	R.CVRPPIIVGDVYRPAPMTVK.E	Carbamidomethyl (+57)	R.CVRPPIIVGDVYRPAPMTVK.E
631	637	2	877.45	5.9	0	49	21.3	95.00%	K.WAIDAFR.L		K.WAIDAFR.L
85	99	2	1632.79	2.6	0	67	21.9	95.00%	R.LSGLSSLDTYFAMGR.G	Oxidation (+16)	R.LSGLSSLDTYFAMGR.G
156	176	2	2256.33	3.8	1	54.3	6.99	95.00%	K.EAGIITRPVLVGPVTYLFIAK.A		K.EAGIITRPVLVGPVTYLFIAK.A
52	82	3	3521.71	3.5	0	48.3	19.9	95.00%	K.AQGVDIIPSNDFSLYDQIMDHSFSFNVIPPR.Y		K.AQGVDIIPSNDFSLYDQIMDHSFSFNVIPPR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
5	EF1A1_SCHPO	41.09%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
267	286	2	2004.07	2.5	0	35.2	17.1	95.00%	E.TGVIKPGMIVTFAPAGVTTE.V	Oxidation (+16)	R.VETGVIKPGMIVTFAPAGVTTEVK.S
136	146	2	1184.7	2.9	0	41.4	15.9	95.00%	E.HALLAYTLGVK.Q		R.EHALLAYTLGVK.Q
402	421	2	2268.08	4	1	67.5	22	95.00%	K.MVPSKPMCVEAFTDYAPLGR.F	Carbamidomethyl (+57)	K.MVPSKPMCVEAFTDYAPLGR.F
296	311	2	1601.81	2.2	0	58.3	20.6	95.00%	E.SLDAGLPGDNVGFNVK.N		K.SVEMHHESLDAGLPGDNVGFNVK.N
147	154	2	883.55	5.8	0	26.4	16.3	92.70%	K.QLIVAVNK.M		K.QLIVAVNK.M
254	264	2	1024.61	4.2	0	65.4	12.8	95.00%	K.IGGIGTVPVGR.V		K.IGGIGTVPVGR.V
6	20	2	1529.84	4.6	0	62.9	16.7	95.00%	K.GHINVVVIGHVDSGK.S		K.GHINVVVIGHVDSGK.S
185	214	3	3453.63	3.7	0	49.2	21.7	95.00%	K.TVPFVPVSGFQGDNMIEPTTNMPWYQGWQK.E		K.TVPFVPVSGFQGDNMIEPTTNMPWYQGWQK.E
85	100	2	1843.97	4.5	1	36.7	19.5	95.00%	K.YNVTVIDAPGHRDFIK.N		K.YNVTVIDAPGHRDFIK.N
265	286	2	2216.18	3.1	1	52.8	16.1	95.00%	R.VETGVIKPGMIVTFAPAGVTTE.V		R.VETGVIKPGMIVTFAPAGVTTEVK.S
225	245	3	2331.29	2.6	1	34.8	13.2	95.00%	K.TLLEAIDSIEPPARPTDKPLR.L		K.TLLEAIDSIEPPARPTDKPLR.L
155	164	2	1151.51	6.4	0	75.8	21.9	95.00%	K.MDTTGWSQAR.F		K.MDTTGWSQAR.F
85	96	2	1340.69	4.4	0	66.1	19.8	95.00%	K.YNVTVIDAPGHR.D		K.YNVTVIDAPGHR.D
246	253	2	974.55	4.1	0	32.1	18.8	95.00%	R.LPLQDVYK.I		R.LPLQDVYK.I
135	146	2	1313.74	2.7	1	48.3	17.6	95.00%	R.EHALLAYTLGVK.Q		R.EHALLAYTLGVK.Q
402	411	2	1176.54	3.1	0	27.7	21.7	94.40%	K.MVPSKPMCVE.A	Carbamidomethyl (+57)	K.MVPSKPMCVEAFTDYAPLGR.F
412	421	2	1109.55	3.4	0	34.2	21.3	95.00%	E.AFTDYAPLGR.F		K.MVPSKPMCVEAFTDYAPLGR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
6	KPYK_SCHPO	55.21%	100%	26

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
191	201	2	1186.61	4.4	1	25.5	20.9	91.40%	K.TDVDLPALSEK.D		K.TDVDLPALSEK.D
487	497	2	1053.66	5.9	0	39.5	10.4	95.00%	K.IIVLQGAVGGK.G		K.IIVLQGAVGGK.G
454	462	2	1129.58	2.7	1	32.2	19.7	95.00%	E.KEPLSDWQK.D		R.GVYPVIYEKEPLSDWQK.D
57	65	2	1070.42	2.6	0	26.8	21.5	93.30%	R.MNFSHGSYE.Y		R.MNFSHGSYEYHQSVIDNAR.K
116	127	2	1403.63	3.1	1	42	23.4	95.00%	E.MIFTTDDAYAEK.C		R.TGLTVGGTDYPISSGHEMIFTTDDAYAEK.C
422	433	3	1430.81	3.1	0	41.7	13.6	95.00%	K.YRPSIPIVMVTR.C		K.YRPSIPIVMVTR.C
10	26	2	1880.98	3.7	1	90.9	18.7	95.00%	K.QWVAGLNSELDIPAVNR.R		K.QWVAGLNSELDIPAVNR.R
66	75	2	1201.59	3.9	0	43.3	21.7	95.00%	E.YHQSVIDNAR.K		R.MNFSHGSYEYHQSVIDNAR.K
278	288	2	1186.67	2.9	0	60.6	17.2	95.00%	E.IPASQVFVAQK.M		R.GDLGIEIPASQVFVAQK.M
128	138	2	1447.65	4.4	1	38.9	23.7	95.00%	K.CNDKVMYIDYK.N	Carbamidomethyl (+57)	K.CNDKVMYIDYK.N
248	271	2	2647.3	2.3	1	73.9	20.2	95.00%	K.IENQQGVNNFDSILDVTDGIMVAR.G		K.IENQQGVNNFDSILDVTDGIMVAR.G
77	93	2	1741.97	3.8	0	39.2	16.6	95.00%	K.ASATNPLFPLAIALDTK.G		K.ASATNPLFPLAIALDTK.G
225	232	2	951.52	5	1	30.1	20.1	95.00%	R.AEDVIHIR.E		R.AEDVIHIR.E
77	96	2	2025.09	3.4	1	53.2	16.5	95.00%	K.ASATNPLFPLAIALDTKGPE.I		K.ASATNPLFPLAIALDTKGPEIR.T
57	75	3	2254	4.4	1	44.4	24.3	95.00%	R.MNFSHGSYEYHQSVIDNAR.K		R.MNFSHGSYEYHQSVIDNAR.K
28	37	2	1088.6	5	0	46.3	18.4	95.00%	R.TSIICTIGPK.S	Carbamidomethyl (+57)	R.TSIICTIGPK.S
364	374	2	1226.59	3.5	0	35.6	21.9	95.00%	E.ASIPYGSLYQE.M		R.VAEASIPYGSLYQEMFGLVR.R
468	477	2	1186.55	5.3	0	54.8	21.9	95.00%	R.VAYGCQQAYK.M	Carbamidomethyl (+57)	R.VAYGCQQAYK.M
272	288	2	1770.96	3.8	1	69.1	16.3	95.00%	R.GDLGIEIPASQVFVAQK.M		R.GDLGIEIPASQVFVAQK.M
294	319	4	2965.41	3.1	1	47.6	22.6	95.00%	K.CNIAGKPVACATQMLESMTYNPRPTR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CNIAGKPVACATQMLESMTYNPRPTR.A
405	417	2	1287.72	5.7	0	62	16.5	95.00%	K.AIVVLSTSGNTAR.L		K.AIVVLSTSGNTAR.L
76	93	2	1870.06	4.2	1	70.7	11.1	95.00%	R.KASATNPLFPLAIALDTK.G		R.KASATNPLFPLAIALDTK.G
212	223	2	1368.69	4.2	0	39.8	20.4	95.00%	K.NGVDMIFASFIR.R		K.NGVDMIFASFIR.R
294	309	2	1761.83	2.5	0	70.6	22.8	95.00%	K.CNIAGKPVACATQMLE.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CNIAGKPVACATQMLESMTYNPRPTR.A
99	115	2	1689.79	3.7	0	65.3	23	95.00%	R.TGLTVGGTDYPISSGHE.M		R.TGLTVGGTDYPISSGHEMIFTTDDAYAEK.C
47	56	3	1143.62	4.2	1	26	20.4	95.00%	K.LRDAGMNIVR.M		K.LRDAGMNIVR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
7	ALF_SCHPO	67.60%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
285	297	2	1513.7	4	0	29.4	23	95.00%	K.VNIDTDTQFAYVE.G		K.VNIDTDTQFAYVEGVR.D
207	234	3	2951.53	3.4	1	34.8	18.6	95.00%	R.ELSSVTPYFSIAAAFGNVHGVYKPGNVK.L		R.ELSSVTPYFSIAAAFGNVHGVYKPGNVK.L
253	275	2	2528.21	2	1	93.7	21.5	95.00%	K.TTNDKPVFFVFHGGSGSSVNEFR.T		K.TTNDKPVFFVFHGGSGSSVNEFR.T
94	112	2	2098.02	3.1	0	68.5	21.5	95.00%	R.SIAPFFGVPVVMHSDHCAK.K	Carbamidomethyl (+57)	R.SIAPFFGVPVVMHSDHCAK.K
2	19	2	1823.05	3.8	0	65.3	10.8	95.00%	M.GILDIVPTGVITGDNVLK.L		-.MGILDIVPTGVITGDNVLK.L
345	358	2	1597.83	4.2	1	60.4	19.5	95.00%	R.VLTALEDFYTVNTL.-		R.VLTALEDFYTVNTL.-
194	206	2	1696.81	2.9	1	60.3	22.1	95.00%	E.LYTQPEDIWDVYR.E		K.IWIEMEIGITGGEEDGVDNSHVSHTELYTQPEDIWDVYR.E
26	47	2	2198.13	3.4	1	36.8	18.6	95.00%	R.EHGFAIPAINVTSSSTAIAALE.A		R.EHGFAIPAINVTSSSTAIAALEAAR.E
285	300	2	1825.89	3.9	1	73.6	22	95.00%	K.VNIDTDTQFAYVEGVR.D		K.VNIDTDTQFAYVEGVR.D
306	318	2	1525.72	3.1	1	49.8	23.2	95.00%	K.YKDYLMTPVGNPE.G		K.YKDYLMTPVGNPEGADKPNK.K
113	123	2	1365.65	3.4	1	59.1	22.7	95.00%	K.KLLPWMDGMFE.A		K.KLLPWMDGMFEADEAYFK.I
253	273	2	2225.05	3.8	0	53.3	22.6	95.00%	K.TTNDKPVFFVFHGGSGSSVNE.F		K.TTNDKPVFFVFHGGSGSSVNEFR.T
114	123	2	1237.56	3.3	0	38.1	22.4	95.00%	K.LLPWMDGMFE.A		K.LLPWMDGMFEADEAYFK.I
235	248	2	1564.88	3.1	0	64.8	12	95.00%	K.LQPALLGQHQAYVK.E		K.LQPALLGQHQAYVK.E

54	71	2	1843.96	2.8	0	92.8	19.3	95.00%	R.SPIILQTSNGGAHFFAGK.E		R.SPIILQTSNGGAHFFAGK.E
94	113	5	2226.12	3.2	1	16.5	20	94.60%	R.SIAPFFGVPVVMHSDHCAKK.L	Carbamidomethyl (+57)	R.SIAPFFGVPVVMHSDHCAKK.L
131	149	3	2165.05	3.2	1	36.1	21.9	95.00%	K.IHGEPLFSSHMLDLSEEPK.K		K.IHGEPLFSSHMLDLSEEPK.K
80	93	2	1399.76	5.1	0	89.1	17.2	95.00%	K.ASIAGSIAAAHYIR.S		K.ASIAGSIAAAHYIR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
8	PDC2_SCHPO	39.23%	100%	24

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
379	393	2	1650.81	2.8	0	28.3	22.1	95.00%	R.QIQGLVDSNTTLYAE.T		R.QIQGLVDSNTTLYAETGDSWFNGLQMK.L
204	214	2	1130.62	4.6	1	53.5	18.8	95.00%	K.ATDIAAELISK.K		K.ATDIAAELISK.K
440	461	2	2409.21	3.3	1	90.9	18.9	95.00%	R.TIVMVGDGSFQLTGQEISQMIR.H		R.TIVMVGDGSFQLTGQEISQMIR.H
238	253	2	1690.85	4.5	1	52.2	21.1	95.00%	K.LAEALNCAAFIMPAAK.G	Deamidation (+1)/ Carbamidomethyl (+57)	K.LAEALNCAAFIMPAAK.G
228	237	2	949.49	5	1	30.2	21.6	95.00%	R.AAGAESAFVK.L		R.AAGAESAFVK.L
440	455	2	1696.8	2.7	0	31.5	22.6	95.00%	R.TIVMVGDGSFQLTGQE.I	Oxidation (+16)	R.TIVMVGDGSFQLTGQEISQMIR.H
7	18	2	1326.66	3	0	60.8	20.4	95.00%	E.STMTVGTYLAQR.L		K.DAESTMTVGTYLAQR.L
304	328	2	2694.37	3	0	65.1	17.9	95.00%	R.AAPNPNILLNSDYTSVSIPGYVFSR.V		R.AAPNPNILLNSDYTSVSIPGYVFSR.V
147	159	2	1436.71	3	1	68.9	21.9	95.00%	R.AEDAPVMIDHAIR.Q		R.AEDAPVMIDHAIR.Q
241	253	2	1376.7	2.8	0	74.3	21.4	95.00%	E.ALNCAAFIMPAAK.G	Carbamidomethyl (+57)	K.LAEALNCAAFIMPAAK.G
379	405	2	3015.43	1.6	1	70.1	22.1	95.00%	R.QIQGLVDSNTTLYAETGDSWFNGLQMK.L		R.QIQGLVDSNTTLYAETGDSWFNGLQMK.L
44	50	2	827.37	2	0	26.4	20.6	92.80%	E.YYPGLSE.I		R.LLDFLEYYPGLSEIGCCNELNCAFAAEGYAR.S
137	146	2	1101.64	5.4	1	51.2	16.4	95.00%	K.LTCAAVAIKR.A	Carbamidomethyl (+57)	K.LTCAAVAIKR.A
394	405	2	1383.62	3.2	0	39.7	23	95.00%	E.TGDSWFNGLQMK.L	Deamidation (+1)	R.QIQGLVDSNTTLYAETGDSWFNGLQMK.L
19	25	2	770.49	4.3	1	34.4	14.8	95.00%	R.LVEIGIK.N		R.LVEIGIK.N
462	474	3	1575.97	4.8	1	29.2	3.01	95.00%	R.HKLPVLIFLLNNR.G		R.HKLPVLIFLLNNR.G
149	159	2	1236.63	2.1	0	25.8	21	91.90%	E.DAPVMIDHAIR.Q		R.AEDAPVMIDHAIR.Q
26	37	2	1429.72	4.2	0	38.3	21.1	95.00%	K.NHFVVPGDYNLR.L		K.NHFVVPGDYNLR.L
464	474	2	1310.81	4.6	0	66.2	7.78	95.00%	K.LPVLIFLLNNR.G		K.LPVLIFLLNNR.G
136	145	2	1073.63	3.9	1	39.6	13	95.00%	K.KLTCAAVAIK.R	Carbamidomethyl (+57)	K.KLTCAAVAIK.R
4	18	2	1641.77	4.2	1	65.2	23.5	95.00%	K.DAESTMTVGTYLAQR.L		K.DAESTMTVGTYLAQR.L
172	194	3	2388.19	3.8	0	22.6	20.1	92.80%	E.IPTNMANQPCPVPGPISAVISPE.I	Carbamidomethyl (+57)	R.QAILQHKPVYIEIPTNMANQPCPVPGPISAVISPEISDK.E
539	549	2	1326.48	3.9	0	57.1	20.9	95.00%	E.CAIDTDDCTQE.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.EGPTLIECAIDTDDCTQELVDWGK.A
216	225	3	1064.66	3.8	1	29.3	11.8	95.00%	K.EKPILLAGPK.L		K.EKPILLAGPK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
9	ADH4_SCHPO	42.18%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
375	385	3	1245.76	3.9	0	37.6	6.02	95.00%	K.IRPHLVDLGVK.E		K.IRPHLVDLGVK.E
210	221	2	1351.65	4.6	0	56.3	22.8	95.00%	K.HTMPILSVNDPE.T		K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
76	87	2	1282.76	5.2	0	44.2	13.6	95.00%	K.NTLIVTDPGIIK.V		K.NTLIVTDPGIIK.V
245	261	2	1750.86	4.2	0	42.9	22	95.00%	E.AYVSTAANPITDACAVK.C	Carbamidomethyl (+57)	K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
366	374	2	1027.63	6.6	1	37.3	13	95.00%	R.ISQLVLEVK.I		R.ISQLVLEVK.I
149	159	2	1014.58	4.8	0	36.7	19.4	95.00%	K.GIALLATNGGK.I	Deamidation (+1)	K.GIALLATNGGK.I
169	188	2	1998.07	2.9	0	46	16.6	95.00%	K.SSKPQLPLIAINTTAGTASE.M		K.SSKPQLPLIAINTTAGTASEMTR.F
399	413	2	1624.69	3.8	0	40.4	23.4	95.00%	K.DACGATNPIQPTHDE.V	Carbamidomethyl (+57)	K.DACGATNPIQPTHDEVK.A

345	356	2	1359.62	3.2	1	60	23.3	95.00%	R.LGDIAFHLGCEE.H	Carbamidomethyl (+57)	R.LGDIAFHLGCEEHTAEAALDR.I
101	125	3	2678.34	3.6	0	43.3	20.5	95.00%	E.QSITVHLYDGVQPNPTVGNVNQGLE.I		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K
399	415	2	1851.85	4.5	1	49.6	23.2	95.00%	K.DACGATNPIQPTHDEVK.A	Carbamidomethyl (+57)	K.DACGATNPIQPTHDEVK.A
100	125	3	2807.38	2.9	1	28.8	21	95.00%	E.EQSITVHLYDGVQPNPTVGNVNQGLE.I		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K
169	191	2	2386.26	3.6	1	87.6	17.2	95.00%	K.SSKPQLPLIAINTTAGTASEMTR.F		K.SSKPQLPLIAINTTAGTASEMTR.F
130	148	2	1993.8	3.7	1	87.9	23.9	95.00%	K.ENCDSMVSIGGGSAHDCAK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.ENCDSMVSIGGGSAHDCAK.G
160	168	2	1008.48	5	1	40.9	22.5	95.00%	K.IADYEGVDK.S		K.IADYEGVDK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
10	THI3_SCHPO	48.55%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	127	2	1090.54	4.7	0	29.6	21.8	95.00%	K.IQLDDLCSK.F	Carbamidomethyl (+57)	K.IQLDDLCSK.F
74	95	2	2353.27	3.5	0	91.4	15.3	95.00%	R.GYPVTSFGSLLNEPFTGLITLK.G		R.GYPVTSFGSLLNEPFTGLITLK.G
128	139	2	1325.67	4.2	0	42.4	20.9	95.00%	K.FGLSPSDYTAIR.C		K.FGLSPSDYTAIR.C
6	13	2	1022.51	4.4	0	32.8	22	95.00%	K.ITFLTNWE.A		K.ITFLTNWEATPYHLPIFLAQTR.G
37	56	2	1981.08	3.4	0	80.5	14.3	95.00%	E.VAILEPTNPSDVTALIGSGK.V		R.EGIEVAILEPTNPSDVTALIGSGK.V
6	27	2	2631.39	2.4	1	78.6	15.8	95.00%	K.ITFLTNWEATPYHLPIFLAQTR.G		K.ITFLTNWEATPYHLPIFLAQTR.G
63	71	2	954.54	4.5	0	51.1	14.8	95.00%	K.AMIHTLAAK.A		K.AMIHTLAAK.A
222	239	2	2030.06	3.2	1	79.8	19.1	95.00%	R.AIHSATLDMLKDPVQTYK.E		R.AIHSATLDMLKDPVQTYK.E
110	118	2	968.5	4.9	1	27.7	19.8	94.40%	R.IGYVGEFGK.I		R.IGYVGEFGK.I
14	27	3	1626.89	3.1	0	61.7	16.4	95.00%	E.ATPYHLPIFLAQTR.G		K.ITFLTNWEATPYHLPIFLAQTR.G
330	339	2	992.51	5.7	0	44.3	21.9	95.00%	K.GGVFSGNSLR.Y		K.GGVFSGNSLR.Y
189	211	3	2788.29	2.8	1	29.7	23.2	95.00%	R.LANLGCCCFCTILYIAHDEFIAK.H	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.LANLGCCCFCTILYIAHDEFIAK.H
260	273	2	1711.79	4.7	0	88.7	22.9	95.00%	R.CFAYFSHDISNVPR.D	Carbamidomethyl (+57)	R.CFAYFSHDISNVPR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
11	PMGY_SCHPO	51.18%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
176	185	2	1085.62	2.8	1	45.5	17.3	95.00%	E.GLTGDQIVKR.E		R.ALIMDLEGLTGDQIVKR.E
169	184	2	1714.92	4	1	69.3	17.2	95.00%	R.ALIMDLEGLTGDQIVK.R		R.ALIMDLEGLTGDQIVK.R
111	120	2	1271.65	5.7	1	79.8	21.1	95.00%	K.WGAEQVQIWR.R		K.WGAEQVQIWR.R
23	36	2	1589.81	2.9	1	46.9	20.2	95.00%	K.LNLFTGWKDPALSE.T		K.LNLFTGWKDPALSETGIK.E
95	108	2	1626.77	3.9	1	67.7	23.3	95.00%	R.YYGDLQGLNKDDAR.K		R.YYGDLQGLNKDDAR.K
186	199	2	1553.85	3.4	1	32.7	16	95.00%	R.ELATGVPIVYHLDK.D		R.ELATGVPIVYHLDK.D
2	14	2	1439.81	5.3	1	52	15.3	95.00%	M.TTEAAPNLLVLTR.H	Acetyl (+42)	-.MTTEAAPNLLVLTR.H
158	168	2	1149.67	4.5	0	26.5	13.2	93.00%	K.VLIAAHGNSLR.A		K.VLIAAHGNSLR.A
95	104	2	1169.58	4.8	0	46.4	20.6	95.00%	R.YYGDLQGLNK.D		R.YYGDLQGLNK.D
1	14	2	1528.84	4.4	1	53	16.6	95.00%	-.MTTEAAPNLLVLTR.H		-.MTTEAAPNLLVLTR.H
53	66	2	1615.84	4.6	1	43.1	19.7	95.00%	R.GYKFDIAFTSALQR.A		R.GYKFDIAFTSALQR.A
5	14	2	1066.65	3.8	0	62.1	4.77	95.00%	E.AAPNLLVLTR.H		-.MTTEAAPNLLVLTR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
12	TPIS_SCHPO	54.22%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
223	239	2	1800.91	2.9	0	73.8	21	95.00%	K.FHDIDGFLVGGASLKPE.F		K.FHDIDGFLVGGASLKPEFHNIVNVHSL.-
160	174	2	1615.9	3.1	0	70.7	14.8	95.00%	K.IVIAYEPVWAIGTGK.T		K.IVIAYEPVWAIGTGK.T
58	70	2	1389.73	3.4	1	50	19.8	95.00%	K.DIGVGAQNVFDKK.N		K.DIGVGAQNVFDKK.N
78	98	2	2233.11	3.5	1	107	21.5	95.00%	E.NSAQSLIDAGITYTLTGHSER.R		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R

32	52	2	2422.27	3.5	1	66.1	17.3	95.00%	K.LNVGDVETVIFPQNMYLITTR.Q		K.LNVGDVETVIFPQNMYLITTR.Q
206	219	2	1453.66	3.6	1	72.3	23.2	95.00%	R.VIYGGSVNGGNCKE.F	Deamidation (+1)/ Carbamidomethyl (+57)	R.VIYGGSVNGGNCKEFLK.F
39	52	2	1695.91	3	0	58.1	17.8	95.00%	E.TVIFPQNMYLITTR.Q		K.LNVGDVETVIFPQNMYLITTR.Q
146	159	2	1613.86	4.5	1	61.4	19.4	95.00%	R.QLNAIADKVQNWSK.I		R.QLNAIADKVQNWSK.I
196	205	2	971.55	5.3	1	76.1	19.1	95.00%	K.LGASVAEGLR.V		K.LGASVAEGLR.V
223	249	3	2961.52	3.2	1	45.2	17.9	95.00%	K.FHDIDGFLVGGASLKPEFHNIVNVHSL.-		K.FHDIDGFLVGGASLKPEFHNIVNVHSL.-
206	218	2	1324.61	4.4	0	76.9	22.9	95.00%	R.VIYGGSVNGGNCK.E	Deamidation (+1)/ Carbamidomethyl (+57)	R.VIYGGSVNGGNCK.E
78	97	2	2077	3.3	0	111	22	95.00%	E.NSAQSLIDAGITYTLTGHSE.R		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
13	SAHH_SCHPO	36.03%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
407	427	2	2266.18	3.4	0	77.1	18.3	95.00%	K.LTTLTSVQSDYLGIPVDGPYK.A		K.LTTLTSVQSDYLGIPVDGPYK.A
314	328	3	1665.93	5.5	1	30.5	14.8	95.00%	K.ANAKDVVNIKPQVDR.Y		K.ANAKDVVNIKPQVDR.Y
26	35	2	1114.58	2.9	1	29.9	19.8	95.00%	E.NEMPGLIAVR.E	Oxidation (+16)	K.ELEIAENEMPGLIAVR.E
8	18	2	1118.61	3.2	0	77.1	18.3	95.00%	K.VADISLAAFGR.K		K.VADISLAAFGR.K
216	227	2	1117.62	4.3	0	46.5	18.3	95.00%	K.VAVVAGFGDVGK.G		K.VAVVAGFGDVGK.G
269	280	2	1367.66	4	1	40.1	22.3	95.00%	K.EGQIFVTTTGCR.D	Carbamidomethyl (+57)	K.EGQIFVTTTGCR.D
119	143	3	2681.36	3.4	1	72.3	18.9	95.00%	K.SFPSGKPLNMILDDGGDLTALVHER.H		K.SFPSGKPLNMILDDGGDLTALVHER.H
176	187	2	1255.68	4.6	0	42.1	17.6	95.00%	K.VPAINVNDSVTK.S		K.VPAINVNDSVTK.S
336	344	2	1006.6	5	0	31.2	13	95.00%	R.HIILLADGR.L		R.HIILLADGR.L
174	187	2	1496.86	2.5	1	50.3	14.6	95.00%	K.LKVPAINVNDSVTK.S		K.LKVPAINVNDSVTK.S
318	328	2	1281.71	3.7	0	30.2	18	95.00%	K.DVVNIKPQVDR.Y		K.DVVNIKPQVDR.Y
318	330	2	1573.82	3.1	1	58.5	19.7	95.00%	K.DVVNIKPQVDRYE.L		K.DVVNIKPQVDRYELK.N
28	35	2	855.5	2.7	0	37.9	15.6	95.00%	E.MPGLIAVR.E		K.ELEIAENEMPGLIAVR.E
270	280	2	1238.61	3.2	0	61.6	22	95.00%	E.GQIFVTTTGCR.D	Carbamidomethyl (+57)	K.EGQIFVTTTGCR.D
245	259	2	1589.75	3.4	0	82.1	23.2	95.00%	E.VDPINALQAAMDGFE.V		R.VIVTEVDPINALQAAMDGFEVTTMEEAVK.E
158	167	2	1132.59	3.6	0	31.9	19.9	95.00%	E.TTTGVHNLYK.M		R.GISEETTTGVHNLYK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
14	THI2_SCHPO	29.27%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
175	187	2	1431.8	4.7	1	52.1	14.8	95.00%	K.LFNATAVEDLIVK.E		K.LFNATAVEDLIVK.E
2	15	2	1400.77	3.8	0	74.5	17.5	95.00%	M.APATAVVTPQTAFK.T		-.MAPATAVVTPQTAFK.T
286	294	2	1007.47	3.3	1	26.3	21.2	92.60%	E.LSEFDGANR.M		R.EVFPGMIVGGMELSEFDGANR.M
244	263	3	2296.15	3.2	0	39.6	20.3	95.00%	R.LASAQLVSNLHDMRPLDMNR.A	Oxidation (+16)	R.LASAQLVSNLHDMRPLDMNR.A
39	55	2	1962.95	4.7	1	48.4	22.6	95.00%	K.AYPTYSLDESFSFAPIR.E		K.AYPTYSLDESFSFAPIR.E
295	308	2	1459.67	4	0	71.7	22.5	95.00%	R.MGPTFGGMMFSGIK.A		R.MGPTFGGMMFSGIK.A
48	55	2	923.49	3	0	25.9	20.8	92.10%	E.SFSFAPIR.E		K.AYPTYSLDESFSFAPIR.E
131	139	2	1045.55	3.3	0	30.9	20.7	95.00%	R.KPADLFLNE.I		R.KPADLFLNEIGVPYEDEGDYVVVK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
15	GLYD_SCHPO	42.83%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
146	159	2	1649.78	3.9	1	75	22.8	95.00%	K.ISAVSTYFESMPYR.V		K.ISAVSTYFESMPYR.V
233	243	2	1234.62	3.7	0	25.4	20.5	91.20%	E.YADVVTTTTHK.S		R.QIADSVNAYLVVDMAHISGLVSAGVIPSPFEYADVVTTTTHK.S
183	193	2	1209.62	4.5	0	57.8	20.3	95.00%	K.ILVAGTSAYCR.L	Carbamidomethyl (+57)	K.ILVAGTSAYCR.L
361	371	2	1254.76	3	1	58.6	9.54	95.00%	R.VLELINIVTNK.N		R.VLELINIVTNK.N
160	173	2	1593.73	2.8	0	29.6	22.6	95.00%	R.VDPNTGLIDYDMLE.H		R.VDPNTGLIDYDMLEHDAQLFRPK.I

97	123	3	2996.43	3.4	0	55	21.4	95.00%	K.WGVNVQCLSGSPANMQVYQAIMPPHGR.L	Carbamidomethyl (+57)	K.WGVNVQCLSGSPANMQVYQAIMPPHGR.L
86	96	2	1129.62	5.1	0	54.8	20	95.00%	R.ALAAFNLDPAK.W		R.ALAAFNLDPAK.W
59	67	2	998.45	5.1	1	32.9	22	95.00%	K.YSEGYPGAR.Y		K.YSEGYPGAR.Y
277	302	3	2725.45	2.8	0	25.2	15.9	95.00%	K.INFSVFPGHQGGPHNHTITALAVALK.Q		K.INFSVFPGHQGGPHNHTITALAVALK.Q
413	422	2	1075.61	4.3	0	49.9	17.6	95.00%	R.ALTFAANLQK.E		R.ALTFAANLQK.E
46	58	2	1321.64	4.2	0	41.4	22.8	95.00%	R.AVMDALGSVMSNK.Y		R.AVMDALGSVMSNK.Y
160	182	3	2686.31	2.9	1	31.8	21.6	95.00%	R.VDPNTGLIDYDMLEHDAQLFRPK.I		R.VDPNTGLIDYDMLEHDAQLFRPK.I
334	349	2	1669.84	3.9	0	85	21.1	95.00%	K.LAADGTDSHMVLVDVK.S		K.LAADGTDSHMVLVDVK.S
457	467	2	1306.64	3	1	32.7	22.6	95.00%	E.WASSFPLADKW.-		K.EVAEWASSFPLADKW.-
406	412	2	878.45	4.3	0	35.8	21.5	95.00%	R.VVDYIDR.A		R.VVDYIDR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
16	HSP72_SCHPO	34.16%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
327	340	2	1400.77	3.9	1	39.7	17.7	95.00%	K.ASVNEIVLVGGSTR.I		K.ASVNEIVLVGGSTR.I
4	25	3	2425.14	4.3	1	39	22.7	95.00%	K.SIGIDLGTTYSCVGHFSNNRVE.I	Carbamidomethyl (+57)	K.SIGIDLGTTYSCVGHFSNNRVEIIANDQGNR.T
538	548	2	1351.66	4.4	1	37.5	21.6	95.00%	K.NHLESYAYSLR.N		K.NHLESYAYSLR.N
137	153	2	1880.93	3.1	0	71.2	20.6	95.00%	K.VTDAVVTVPAYFNDSQR.Q		K.VTDAVVTVPAYFNDSQR.Q
76	86	2	1309.56	4.9	1	34.7	23.1	95.00%	K.FDDPEVQSDMK.H		K.FDDPEVQSDMK.H
403	413	2	1086.61	3.2	0	31.7	17.4	95.00%	E.TAGGVMTPLIK.R		K.TQDLLLLDVAPLSMGIETAGGVMTPLIK.R
170	185	2	1686.9	4	0	94.1	18.7	95.00%	R.IINEPTAAAIAYGLDR.S		R.IINEPTAAAIAYGLDR.S
578	589	2	1349.61	2.9	1	55.6	23.3	95.00%	E.WLDSNTTAAKDE.F		K.ETIEWLDSNTTAAKDEFEAK.Q
219	234	2	1647.72	4.3	1	72.5	23.9	95.00%	K.ATAGDTHLGGEDFDSR.L		K.ATAGDTHLGGEDFDSR.L
55	69	2	1698.82	4.2	0	74.8	22	95.00%	K.NQVAMNPHNTIFDAK.R		K.NQVAMNPHNTIFDAK.R
457	467	2	1182.65	4.4	1	28.3	16.8	95.00%	K.FELSGIPPAPR.G		K.FELSGIPPAPR.G
235	244	2	1273.69	4.3	1	25.1	19.4	90.70%	R.LVNHFIQEFK.R		R.LVNHFIQEFK.R
35	47	2	1486.7	4.2	1	60.5	22.9	95.00%	R.TTPSYVAFTDTER.L		R.TTPSYVAFTDTER.L
366	385	2	1920.98	2.9	1	86.4	20.3	95.00%	E.AVAYGAAVQAAVLTGDTSEK.T		K.SINPDEAVAYGAAVQAAVLTGDTSEK.T
24	34	2	1227.63	5.8	1	33.2	20.7	95.00%	R.VEIIANDQGNR.T		R.VEIIANDQGNR.T
347	359	2	1539.75	4.6	1	52.1	22.7	95.00%	K.LVSDFFNGKEPCK.S	Carbamidomethyl (+57)	K.LVSDFFNGKEPCK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
17	METK_SCHPO	51.57%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
147	155	2	931.5	4.5	0	58	22	95.00%	K.LNAAMSVAR.R		K.LNAAMSVAR.R
20	40	3	2423.15	4	1	37.1	22.2	95.00%	K.ICDQISDAILDACLKDDPFSK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.ICDQISDAILDACLKDDPFSK.V
137	146	2	1117.73	2.6	0	31.1	3.01	95.00%	K.LPLTILLAHK.L		K.LPLTILLAHK.L
99	112	2	1612.79	3.3	1	57.6	22.1	95.00%	E.QQSPDIAQGLHYEK.A		K.TCNVLVAIEQQSPDIAQGLHYEK.A
2	10	2	1042.5	4.1	0	34.7	21.9	95.00%	M.AQTFLFTSE.S		-.MAQTFLFTSESVGEGHPDK.I
186	203	2	1926.97	2	1	38.1	20.9	95.00%	R.RVDTIVVSAQHADSISTE.D		R.RVDTIVVSAQHADSISTEDLR.S
237	251	2	1429.74	3.6	0	73.6	19.7	95.00%	R.FVVGGPQGDAGLTGR.K		R.FVVGGPQGDAGLTGR.K
339	349	2	1256.73	2.8	0	38.1	15.7	95.00%	K.NFDLRPGVLVK.S		K.NFDLRPGVLVK.S
117	135	2	1970.86	2.9	1	60.2	23.5	95.00%	E.LGAGDQGIMFGYATDETPE.K		K.ALEELGAGDQGIMFGYATDETPEK.L
252	272	3	2077.05	3.9	1	61	20.4	95.00%	R.KIIVDTYGGWGAHGGGAFSGK.D		R.KIIVDTYGGWGAHGGGAFSGK.D
353	378	3	3055.48	3	1	68	20.7	95.00%	K.LQTPFYLSTASYGHFTDQSKPWEQPK.E		K.LQTPFYLSTASYGHFTDQSKPWEQPK.E
291	299	2	856.52	4.2	0	28.1	16.9	94.90%	K.SLVAAGLAR.R		K.SLVAAGLAR.R
213	226	2	1572.93	3.2	1	48.7	7.78	95.00%	K.IIKPTVPAHLLDEK.T		K.IIKPTVPAHLLDEK.T
253	272	2	1948.95	4	0	80.8	22.5	95.00%	K.IIVDTYGGWGAHGGGAFSGK.D		K.IIVDTYGGWGAHGGGAFSGK.D

136	146	3	1245.82	2.2	1	43.7	6.02	95.00%	E.KLPLTILLAHK.L			K.ALEELGAGDQGIMFGYATDETPE KLPLTILLAHK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
18	A1EGU1_SCHPO	40.88%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
457	479	2	2580.33	2.4	0	74	18.6	95.00%	K.YVISQCNNALLYPALGVACVLSR. C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.YVISQCNNALLYPALGVACVLSR. C
258	292	4	3747.95	3.3	0	51.5	16.8	95.00%	R.ILDHYRPDIACFNDDIQGTGAVAL AAIIGALHVTK.S	Carbamidomethyl (+57)	R.ILDHYRPDIACFNDDIQGTGAVAL AAIIGALHVTK.S
44	57	2	1634.91	4.4	1	89.1	15.7	95.00%	R.LPPIVETLQQQVDR.C		R.LPPIVETLQQQVDR.C
535	547	2	1375.67	2.6	1	35.4	21.8	95.00%	E.GMSTVDLPKDDAK.L		K.QAVSEGMSTVDLPKDDAK.L
377	396	2	2009.14	2.3	0	36.2	10.4	95.00%	E.SAIALVKPTILLGCSGQPGK.F	Carbamidomethyl (+57)	K.EVPSGDINLESAIALVKPTILLGCS GQPGK.F
408	425	2	2093.1	2.5	1	38.9	17.6	95.00%	K.HVERPIIFPISNPTTLME.A		K.HVERPIIFPISNPTTLMEAKPDQID K.W
501	517	2	1828.94	4.1	1	33.1	21	95.00%	R.SLFAADEALLPDLNNAR.E		R.SLFAADEALLPDLNNAR.E
123	137	2	1824.84	3.4	0	67	23.2	95.00%	E.GCYLDIDHNDLSYIK.Q	Carbamidomethyl (+57)	R.YPEGCYLDIDHNDLSYIK.Q
439	452	2	1418.83	2	0	45	10.8	95.00%	K.ALIATGSPLPPLNR.N		K.ALIATGSPLPPLNR.N
508	517	2	1095.61	3.2	0	27	17.1	93.60%	E.ALLPDLNNAR.E		R.SLFAADEALLPDLNNAR.E
490	500	2	1070.58	4.5	0	54.7	19	95.00%	K.AASDALATVPR.S		K.AASDALATVPR.S
15	23	2	955.55	4.9	0	32.8	17.4	95.00%	K.GVTLLNSPR.Y		K.GVTLLNSPR.Y
332	339	2	964.49	5	0	34.3	20	95.00%	R.GNLFMIDR.C		R.GNLFMIDR.C
456	479	3	2708.42	3.5	1	44.6	16.7	95.00%	K.KYVISQCNNALLYPALGVACVLSR .C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.KYVISQCNNALLYPALGVACVLSR .C
222	234	2	1526.73	2.5	1	68.3	23.2	95.00%	R.GEQYDSFLDNVIK.A		R.GEQYDSFLDNVIK.A
178	191	2	1553.75	3.5	0	59.3	22.2	95.00%	K.GHLMTLCAGLDPNR.F	Carbamidomethyl (+57)	K.GHLMTLCAGLDPNR.F
243	248	2	762.37	2.1	0	30.1	22.4	95.00%	E.AFIHFE.D		R.EVFPEAFIHFEDFGLANAK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
19	HSP90_SCHPO	27.27%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
516	525	2	1100.61	3.2	1	26.9	19.5	93.50%	K.LVNITKDGLE.L		K.LVNITKDGLELEETDEEK.A
48	60	2	1444.65	3.4	0	33.8	22	95.00%	R.YQSLSDPHALDAE.K		R.YQSLSDPHALDAEK.D
465	474	2	1170.6	4.5	1	29.7	20.8	95.00%	K.NIYFITGESK.Q		K.NIYFITGESK.Q
645	663	2	2011.99	3.1	0	78.4	21.4	95.00%	E.TALLSSGFTLDDPSAYAQR.I		K.DLATILYETALLSSGFTLDDPSAY AQR.I
567	587	2	2339.12	5.7	1	92.3	22.7	95.00%	K.IVGSPCLLTTGQYGWSANMER.I	Carbamidomethyl (+57)	K.IVGSPCLLTTGQYGWSANMER.I
440	458	2	2199.07	3.1	1	92.7	21.6	95.00%	R.YNSLNSPDDLISLEDYITK.M		R.YNSLNSPDDLISLEDYITK.M
596	606	2	1234.5	4.9	0	67.2	22.3	95.00%	R.DTSMSAYMSSR.K		R.DTSMSAYMSSR.K
88	99	2	1282.73	5.3	0	55.5	15.1	95.00%	K.NDLINNLGVIAK.S		K.NDLINNLGVIAK.S
34	45	2	1274.64	4	1	41.6	21.2	95.00%	R.ELISNASDALDK.I		R.ELISNASDALDK.I
362	375	2	1512.78	3.1	1	77.4	19.7	95.00%	K.GVVDSEDLPLNLSR.E		K.GVVDSEDLPLNLSR.E
80	99	2	2086.12	2.8	1	54.8	16.2	95.00%	R.DTGIGMTKNDLINNLGVIAK.S		R.DTGIGMTKNDLINNLGVIAK.S
198	212	2	1787.96	4.4	1	31.7	17.7	95.00%	K.HSEFISYPIQLVVTR.E		K.HSEFISYPIQLVVTR.E
440	453	2	1578.75	2.3	0	41.2	22.6	95.00%	R.YNSLNSPDDLISLE.D		R.YNSLNSPDDLISLEDYITK.M
422	436	2	1574.86	4	1	34.5	17.6	95.00%	K.LGIHEDAANRPALAK.L		K.LGIHEDAANRPALAK.L
290	302	2	1526.74	4	1	75.7	22.4	95.00%	K.SLTNDWEDHLAVK.H		K.SLTNDWEDHLAVK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
20	ILV5_SCHPO	31.68%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
144	159	2	1689.87	3.4	1	31.9	20.2	95.00%	K.KGSIIMNLLSDAAQTE.T		K.KGSIIMNLLSDAAQTETWPK.I
84	104	2	2141.07	4.6	0	90.4	21.2	95.00%	K.NDTLAIIGYGSQGHGQGLNAR.D		K.NDTLAIIGYGSQGHGQGLNAR.D
330	337	2	914.47	6	0	41.2	19.8	95.00%	R.GAIDWTPR.F		R.GAIDWTPR.F
314	328	2	1725.76	3.8	0	69	24.5	95.00%	K.YGLDYMFAACSTTAR.R	Carbamidomethyl (+57)	K.YGLDYMFAACSTTAR.R
145	163	2	2074.05	4.2	1	75.2	20.1	95.00%	K.GSIIMNLLSDAAQTETWPK.I		K.GSIIMNLLSDAAQTETWPK.I

362	372	2	1312.61	4.6	1	61.6	22.7	95.00%	R.SLEYNSAPNYR.E		R.SLEYNSAPNYR.E
123	133	2	1198.6	4.3	1	28.6	20.9	95.00%	K.QAIEDGWVPGK.T		K.QAIEDGWVPGK.T
303	313	2	1189.68	3.5	0	34.7	17.2	95.00%	E.ATQSLYPLIGK.Y		R.GHSPAEAFNETVEEATQSLYPLIGK.Y
78	104	3	2906.47	2.4	1	96.6	19.4	95.00%	K.LVDYFKNDTLAIIGYGSQGHGQGLNAR.D		K.LVDYFKNDTLAIIGYGSQGHGQGLNAR.D
349	358	2	1166.48	4	1	29.5	22.3	95.00%	E.LYDNVENGNE.A	Deamidation (+1)	K.VLNELYDNVENGNEAK.R
190	204	2	1639.97	3.6	1	26.8	9.54	93.30%	K.IHPPKDVDVILVAPK.G		K.IHPPKDVDVILVAPK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
21	6PGD_SCHPO	39.02%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
54	63	2	1040.52	3.8	1	32	19.4	95.00%	K.SIVGAHSLEE.F		K.SIVGAHSLEEFVSK.L
156	166	3	1228.76	2.4	0	36	6.99	95.00%	R.IKPIFQTLAAK.A		R.IKPIFQTLAAK.A
140	155	2	1669.81	2.7	0	29.5	22.6	95.00%	R.YGPSLMPGGNPAAWPR.I		R.YGPSLMPGGNPAAWPR.I
97	114	3	1943.94	3.2	1	53.6	22.3	95.00%	E.KGDIIVDGGNSHYPDTTR.R		K.AGKPVDYLIEGLAPLLEKGDIIVDGGNSHYPDTTR.R
467	492	3	2753.31	3.6	1	22.6	22.1	92.80%	K.SLPADKDIHINWTGHGGNISATTYDA.-		K.SLPADKDIHINWTGHGGNISATTYDA.-
98	115	3	1971.95	5.1	1	35.5	21.5	95.00%	K.GDIIVDGGNSHYPDTTRR.C		K.GDIIVDGGNSHYPDTTRR.C
320	333	2	1592.8	4.1	1	67.9	20.8	95.00%	K.QLIDDLEDALYASK.I		K.QLIDDLEDALYASK.I
437	449	2	1379.79	4.1	0	52	11.8	95.00%	R.SAVLPANLLQAQR.D		R.SAVLPANLLQAQR.D
410	436	3	2839.48	3.6	1	74.2	17.1	95.00%	R.RVVAQAAMLGIPVPATSTGLSFYDGYR.S		R.RVVAQAAMLGIPVPATSTGLSFYDGYR.S
390	403	2	1635.84	3.2	1	32.5	20.1	95.00%	E.SILFHPFFTNGVEK.A	Deamidation (+1)	R.EDPNLESILFHPFFTNGVEK.A
98	114	2	1815.85	4.4	0	91.7	23.4	95.00%	K.GDIIVDGGNSHYPDTTR.R		K.GDIIVDGGNSHYPDTTR.R
450	458	2	1112.51	4.7	0	24.9	22.6	90.40%	R.DYFGAHTFR.V		R.DYFGAHTFR.V
29	37	2	1175.49	3.9	0	36.7	23.2	95.00%	K.GFTVCCYNR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GFTVCCYNR.T
5	28	2	2457.3	3	1	76	15.9	95.00%	K.EVADFGLIGLAVMGQNLILNGADK.G		K.EVADFGLIGLAVMGQNLILNGADK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
22	K6PF_SCHPO	21.76%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
364	380	3	1831.88	4.2	1	50.7	23.4	95.00%	R.ICEAVDSISSTAISHSR.A	Carbamidomethyl (+57)	R.ICEAVDSISSTAISHSR.A
613	628	3	1700.87	4.5	0	49.7	20.4	95.00%	R.GHTPLAIDNGFSGFLR.H		R.GHTPLAIDNGFSGFLR.H
419	431	2	1592.73	4.2	1	27.5	22.7	94.20%	K.WQDELCNSLSSVR.K	Carbamidomethyl (+57)	K.WQDELCNSLSSVR.K
283	308	2	2620.33	3.9	0	86.3	18.8	95.00%	K.NLISAGIDSIIVCGGDGSLTGADIFR.S	Carbamidomethyl (+57)	K.NLISAGIDSIIVCGGDGSLTGADIFR.S
586	603	3	1720.91	2.8	0	57	18.3	95.00%	R.VAIIHVGAPAGGMNSATR.A		R.VAIIHVGAPAGGMNSATR.A
20	31	2	1534.7	3.8	0	26.5	24	93.00%	E.DTYNQTLDFYQK.L		-.MSGETVHGISCYSVVANTEDTYNQTLDFYQK.L
798	806	2	934.49	4	1	31.5	20	95.00%	K.ATFALEAGR.N		K.ATFALEAGR.N
880	896	2	1696.88	4.3	0	74.6	19.5	95.00%	R.ANDLGNDPSSAVVIGIR.G		R.ANDLGNDPSSAVVIGIR.G
254	267	2	1400.75	3.4	1	49.7	19.4	95.00%	R.GWLAEGGTLIGTAR.C		R.GWLAEGGTLIGTAR.C
844	861	2	1860.9	4.7	0	42.3	22.3	95.00%	R.TAVPGHVQQGGNPTPMDR.A		R.TAVPGHVQQGGNPTPMDR.A
5	19	2	1635.76	3	0	40.4	23.6	95.00%	E.TVHGISCYSVVANTE.D	Carbamidomethyl (+57)	-.MSGETVHGISCYSVVANTEDTYNQTLDFYQK.L
927	938	2	1323.7	4.7	0	53.3	19	95.00%	R.DMHNLVNILAGK.T		R.DMHNLVNILAGK.T
197	214	2	1760.86	4.1	0	84.8	21.8	95.00%	K.IAVMTSGGDSPGMNAVVR.A		K.IAVMTSGGDSPGMNAVVR.A
367	380	2	1429.72	4.2	0	70.7	20.8	95.00%	E.AVDSISSTAISHSR.A		R.ICEAVDSISSTAISHSR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
23	EF3_SCHPO	13.18%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

35	46	2	1245.63	3.4	1	40.3	21.4	95.00%	K.ALASFVNGPIEE.Q		K.ALASFVNGPIEEQDAPSQVFSAISK.Q
596	621	4	2935.49	3.5	1	34.9	19.3	95.00%	K.DVSSIIVSHDSGFLDHVVQAIIHYER.F		K.DVSSIIVSHDSGFLDHVVQAIIHYER.F
47	59	2	1376.7	3.3	0	67.4	21	95.00%	E.QDAPSQVFSAISK.Q		K.ALASFVNGPIEEQDAPSQVFSAISK.Q
281	294	2	1550.88	4.1	1	60.5	14.5	95.00%	K.LVEDPQVVAPFLPK.L		K.LVEDPQVVAPFLPK.L
757	765	2	1178.58	7.8	1	24.9	21.5	90.20%	K.TPSEYIQWR.F		K.TPSEYIQWR.F
479	493	2	1636.88	3.9	1	73.9	18	95.00%	R.AIVNGQVEGFPTHLR.T		R.AIVNGQVEGFPTHLR.T
133	147	2	1550.87	3.9	1	70.6	14.1	95.00%	K.AIVPSVLESIHTTGK.W		K.AIVPSVLESIHTTGK.W
541	554	2	1471.79	2.9	0	36.9	19.1	95.00%	E.LINMPIGSLSGGWK.M		K.ENSFTDELINMPIGSLSGGWK.M
202	213	2	1359.69	4.1	0	43.2	21	95.00%	K.VCTLIANADIDR.F	Carbamidomethyl (+57)	K.VCTLIANADIDR.F
440	447	2	855.45	3	0	29.8	18.5	95.00%	E.FSLAYGAK.I		K.IPGGASHAEEEEEGEDLCNCEFSLAYGAK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
24	EF2_SCHPO	20.78%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
272	283	2	1498.77	4.2	0	53.9	20.5	95.00%	R.AFNMFILDPIYR.I		R.AFNMFILDPIYR.I
466	479	2	1474.71	3.7	1	72.8	21.9	95.00%	K.SGTLTTSEVAHNMK.V		K.SGTLTTSEVAHNMK.V
565	578	2	1451.69	4.3	1	44.5	23.4	95.00%	R.ESVSEPSSMTALSK.S		R.ESVSEPSSMTALSK.S
623	631	2	1065.49	2.6	0	26.3	21.2	92.60%	E.FGWDVTDAR.K		R.IMADEFGWDVTDAR.K
632	651	3	2235.11	2.7	1	41.5	21.9	95.00%	R.KIWCFGPDTTGANVVVDQTK.A	Carbamidomethyl (+57)	R.KIWCFGPDTTGANVVVDQTK.A
633	651	2	2107.01	3.2	0	108	22.2	95.00%	K.IWCFGPDTTGANVVVDQTK.A	Carbamidomethyl (+57)	K.IWCFGPDTTGANVVVDQTK.A
284	292	2	1051.52	4.5	0	27.5	21.3	94.20%	R.IFDAVMNSR.K		R.IFDAVMNSR.K
244	253	2	1266.61	5.9	1	30	21.9	95.00%	R.LWGENYFNPK.T		R.LWGENYFNPK.T
151	162	3	1392.86	5.8	1	25.2	6.99	95.00%	R.IRPVVVVNKVDR.A		R.IRPVVVVNKVDR.A
544	555	2	1334.69	3.5	1	47.4	20.9	95.00%	K.DLQEDHAGIPLK.I		K.DLQEDHAGIPLK.I
371	384	2	1594.76	4.1	0	55	22.5	95.00%	R.NCDANAPLMIYVSK.M	Carbamidomethyl (+57)	R.NCDANAPLMIYVSK.M
327	346	2	2192.18	2.4	1	55.9	15.8	95.00%	K.FLPAADALMEMIVLHLPSPK.T		K.FLPAADALMEMIVLHLPSPK.T
442	465	2	2595.37	4.3	1	74.7	16	95.00%	R.IEPIEDCPAGNIIGLVGVDQFLVK.S	Carbamidomethyl (+57)	R.IEPIEDCPAGNIIGLVGVDQFLVK.S
618	631	2	1624.73	4.2	1	45	23.4	95.00%	R.IMADEFGWDVTDAR.K		R.IMADEFGWDVTDAR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
25	HSP75_SCHPO	31.97%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	173	2	1168.66	5	0	34.3	15.6	95.00%	K.DAGAIAGLNVLR.I		K.DAGAIAGLNVLR.I
501	517	3	1779.92	5.5	1	60.6	19	95.00%	R.SAHIEITNSVGHLSSTK.I		R.SAHIEITNSVGHLSSTK.I
121	128	2	861.5	2.3	0	24.8	18.4	90.10%	E.ISAMVLTK.M		K.QFTAQEISAMVLTK.M
554	564	2	1265.6	3	0	32.1	22.5	95.00%	E.TTISEPNVMMK.L	Oxidation (+16)	K.SQLESYISNIETTISEPNVMMK.L
253	260	2	929.45	5.3	0	25	20.3	90.60%	K.IDISDDPR.A		K.IDISDDPR.A
144	157	2	1552.8	4.6	0	33.7	20.1	95.00%	K.AVITVPAYFSDSQR.A		K.AVITVPAYFSDSQR.A
331	344	2	1437.76	3.8	0	34.4	18.7	95.00%	K.ADVHDIVLVGGSTR.I		K.ADVHDIVLVGGSTR.I
586	595	2	1146.56	4.2	1	54.6	21.8	95.00%	E.LEDTNTDALR.K		K.IEAQLAECMSQLELEDTNTDALR.K
115	128	2	1565.81	1.4	1	60	19.8	95.00%	K.QFTAQEISAMVLTK.M		K.QFTAQEISAMVLTK.M
506	517	2	1242.66	5.5	0	25.8	18.6	91.90%	E.ITNSVGHLSSTK.I		R.SAHIEITNSVGHLSSTK.I
174	190	2	1729.93	3.9	0	82.9	16.8	95.00%	R.IINEPTAAAIAYGLDAK.S		R.IINEPTAAAIAYGLDAK.S
221	241	2	2143.01	2.9	1	49.5	23.2	95.00%	E.VLATAGDTHLGGEDFDNALVE.H		K.IQGGVFEVLATAGDTHLGGEDFDNALVEHFIQEFK.R
410	419	2	1103.56	4.7	0	36.5	20.9	95.00%	E.GNVFGVVCPR.N	Carbamidomethyl (+57)	K.TQDLLLLDVVPLSLGVAMEGNVFGVVCPR.N
286	301	2	1697.82	2.9	0	49.4	22.4	95.00%	E.VDSLSNGIDFSSSITR.A	Deamidation (+1)	R.ALSSVTQTTVEVDSLSNGIDFSSSITR.A
462	472	2	1255.68	2.8	0	26	19.5	92.20%	E.FQLTGIPPMPR.G		R.VNCAENEPLGEFQLTGIPPMPR.G

430	450	2	2374.16	5.6	1	61.9	21.3	95.00%	R.TFTTVADNQTTVTFPVYQGER.V		R.TFTTVADNQTTVTFPVYQGER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
26	ACT_SCHPO	29.07%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
148	167	2	2073.03	3.1	0	61.7	21.2	95.00%	R.TTGIVLDSGDGVTHTVPIYE.G		R.TTGIVLDSGDGVTHTVPIYEGYALPHAIMR.L
260	270	2	1144.62	2.9	0	39	20.9	95.00%	E.ALFQPSALGLE.N		R.APEALFQPSALGLENAGIHEATYNSIMK.C
85	95	3	1514.75	5.5	1	36	21	95.00%	K.IWHHTFYNELR.V		K.IWHHTFYNELR.V
292	312	2	2216.04	5	0	63.1	23.1	95.00%	K.DLYGNVVMSGGTTMYPGIADR.M		K.DLYGNVVMSGGTTMYPGIADR.M
227	238	2	1261.66	4	1	71.6	20.2	95.00%	E.LQTAAQSSSLEK.S		K.LCYVALDFEQELQTAAQSSSLEK.S
197	206	2	1131.53	5.1	1	41.4	22.8	95.00%	R.GYTFSTTAER.E		R.GYTFSTTAER.E
148	177	3	3182.62	3.4	1	67.2	18.3	95.00%	R.TTGIVLDSGDGVTHTVPIYEGYALPHAIMR.L		R.TTGIVLDSGDGVTHTVPIYEGYALPHAIMR.L
5	18	2	1447.72	3	0	55.2	21.7	95.00%	E.IAALVIDNGSGMCK.A	Carbamidomethyl (+57)	-.MEEEIAALVIDNGSGMCK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
27	TSA1_SCHPO	44.79%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	147	2	1224.69	4.4	0	43.5	15.8	95.00%	R.QITINDLPVGR.S		R.QITINDLPVGR.S
90	107	2	1786.96	3.4	1	35.1	17.5	95.00%	K.EGGLGGINIPLLADPSHK.V		K.EGGLGGINIPLLADPSHK.V
125	132	2	901.53	4.7	0	35.7	18.9	95.00%	R.GLFLIDPK.G		R.GLFLIDPK.G
66	88	2	2576.29	0.89	1	97.3	19.9	95.00%	R.NAQVILTSTDSEYSHLAFINTPR.K		R.NAQVILTSTDSEYSHLAFINTPR.K
111	124	2	1523.77	4.1	1	79.7	21	95.00%	R.DYGVLIEDAGVAFR.G		R.DYGVLIEDAGVAFR.G
91	107	2	1657.92	2.2	0	61	16.2	95.00%	E.GGLGGINIPLLADPSHK.V		K.EGGLGGINIPLLADPSHK.V
78	88	2	1317.69	2.6	0	45.9	20.6	95.00%	E.YSHLAFINTPR.K		R.NAQVILTSTDSEYSHLAFINTPR.K
2	13	2	1341.74	4.1	0	36.9	17.6	95.00%	M.SLQIGKPAPDFK.G	Acetyl (+42)	-.MSLQIGKPAPDFK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
28	TKT_SCHPO	31.97%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
325	336	2	1449.68	6.5	1	28.4	22.7	95.00%	K.QSYPDLSNQLER.I	Deamidation (+1)	K.QSYPDLSNQLER.I
2	18	2	1869.94	2.3	0	79.4	21.6	95.00%	M.TSSSYTDIDTLAINTIR.T		-.MTSSSYTDIDTLAINTIR.T
238	252	2	1719.86	5	1	57.2	21.5	95.00%	R.EAMSCTDKPTLINLK.T	Carbamidomethyl (+57)	R.EAMSCTDKPTLINLK.T
395	407	2	1418.65	3.9	1	52.7	22.6	95.00%	R.WEGAADFQPPSSK.L		R.WEGAADFQPPSSK.L
653	663	2	1249.63	3.9	0	24.8	20.3	90.10%	K.FHFTTSGVAQR.A		K.FHFTTSGVAQR.A
261	275	2	1585.83	3.6	0	29.8	20.4	95.00%	E.LQGTHSVHGSPLKPE.D		K.TTIGYGSELQGTHSVHGSPLKPEDCVHVK.K
380	394	2	1499.8	3.5	0	49	17.9	95.00%	E.LVGGSADLTPSNLTR.W		K.LSEIVLDALCPVLPELVGGSADLTPSNLTR.W
510	531	2	2288.16	3.4	0	95.6	19.5	95.00%	E.TSAAYYSALTSDSTPSILALTR.Q		R.AMPNINCWRPADGNETSAAYYSALTSDSTPSILALTR.Q
182	193	2	1385.74	4.7	0	41.9	20.1	95.00%	K.LSNLIAVWDNNK.I		K.LSNLIAVWDNNK.I
118	137	2	1736.98	2.8	0	31	12	95.00%	E.TGAGPLGQGIASAVGLAIGK.A		K.TPGHPETHNPDLNIETGAGPLGQGIASAVGLAIGK.A
630	648	3	2046.93	3.6	1	34	23.7	95.00%	R.YVHEAFGMHTFGDSGPAPK.L		R.YVHEAFGMHTFGDSGPAPK.L
495	509	2	1743.75	2.9	0	37.8	23.4	95.00%	R.AMPNINCWRPADGNE.T	Carbamidomethyl (+57)	R.AMPNINCWRPADGNETSAAYYSALTSDSTPSILALTR.Q
495	531	3	4013.9	2.8	1	63.2	20.6	95.00%	R.AMPNINCWRPADGNETSAAYYSALTSDSTPSILALTR.Q	Carbamidomethyl (+57)	R.AMPNINCWRPADGNETSAAYYSALTSDSTPSILALTR.Q
291	303	2	1603.8	4	1	26.8	21.3	93.30%	K.TFQVPPEVYAYYK.E		K.TFQVPPEVYAYYK.E
30	49	3	1972.02	2.8	0	49.5	19.8	95.00%	K.SGHPGAPMGLAPAAHVLFSR.I		K.SGHPGAPMGLAPAAHVLFSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
29	HXK2_SCHPO	33.41%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
434	449	2	1529.79	4.8	0	96.2	20	95.00%	K.DGSGIGAALCALQAVK.E	Carbamidomethyl (+57)	K.DGSGIGAALCALQAVK.E
193	205	2	1357.76	2.6	0	64.9	16.9	95.00%	E.AVINDTVGTLVTR.A		R.IEAVINDTVGTLVTR.A
392	403	2	1203.6	2.8	1	28.1	21.8	94.80%	K.KSDVGVDGSLVE.H		K.KSDVGVDGSLVEHYPHFVDMLR.E
61	75	2	1595.8	3.2	0	56.5	21.3	95.00%	E.TGDFLALDFGGTNLR.V		K.NGEVLAMAPAFISTLPTGAETGDFLALDFGGTNLR.V
76	86	2	1287.67	3.9	0	30.3	20.6	95.00%	R.VCWIQLLGDGK.Y	Carbamidomethyl (+57)	R.VCWIQLLGDGK.Y
286	296	2	1240.63	5.9	1	25.6	20.1	91.50%	R.VGGMYLGELFR.R		R.VGGMYLGELFR.R
374	388	2	1564.83	4.1	0	56.1	19.1	95.00%	R.MSAVPIASLYLSTGR.A		R.MSAVPIASLYLSTGR.A
103	118	3	1858.88	2.7	1	29.3	23.2	95.00%	R.NESVKPIIDFMSDHVE.L		R.NESVKPIIDFMSDHVELFIK.E
76	88	2	1579.77	2.1	1	31.3	21.8	95.00%	R.VCWIQLLGDGKYE.M	Carbamidomethyl (+57)	R.VCWIQLLGDGKYEMK.H
44	60	2	1687.89	2.8	0	65.4	19.1	95.00%	E.VLAMAPAFISTLPTGAE.T		K.NGEVLAMAPAFISTLPTGAETGDFLALDFGGTNLR.V
404	413	3	1313.64	2.8	0	33.2	22.9	95.00%	E.HYPHFVDMLR.E		K.SDVGVDGSLVEHYPHFVDMLR.E
266	279	2	1598.78	3.9	0	49.6	22.1	95.00%	R.YDLLLDHDTPNAGR.Q		R.YDLLLDHDTPNAGR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
30	PUR9_SCHPO	28.21%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
44	55	2	1201.59	3.6	0	62.4	22	95.00%	E.VADVSSITNAPE.I		R.ESGMEVADVSSITNAPEILGGR.V
138	153	2	1755.86	4.1	0	89.5	20.3	95.00%	R.VTILSDPADYATFTDK.F		R.VTILSDPADYATFTDK.F
571	581	2	1351.7	3.4	1	34.2	21	95.00%	E.FNMVFSEIPLR.L		R.DTANEFNMVFSEIPLR.L
551	565	2	1519.75	4.1	0	63.8	21.9	95.00%	K.YVAAPGGSVMDQAVR.D		K.YVAAPGGSVMDQAVR.D
526	543	2	2131.98	3.7	0	65.5	24.4	95.00%	K.DVVCASDAFFPFPDNIYR.L	Carbamidomethyl (+57)	K.DVVCASDAFFPFPDNIYR.L
223	244	2	2446.25	3.4	0	45.9	19	95.00%	K.VLCGSPGYINLMDALNSWPLVK.E	Carbamidomethyl (+57)	K.VLCGSPGYINLMDALNSWPLVK.E
354	362	2	1152.54	4.8	0	28.8	23.5	95.00%	K.YCVLQMDPK.Y	Carbamidomethyl (+57)	K.YCVLQMDPK.Y
201	215	2	1646.72	3	0	33.1	22.8	95.00%	R.YGANPHQSPAQAFME.Q		R.YGANPHQSPAQAFMEQGPLPFK.V
248	259	2	1216.65	4.7	1	30.2	19.1	95.00%	R.ENIGIPAAASFK.H		R.ENIGIPAAASFK.H
260	277	2	1745.93	1.5	1	47.8	17.6	95.00%	K.HVSPAGAAVGLPLSDVEK.K		K.HVSPAGAAVGLPLSDVEK.K
120	129	2	1055.64	2.9	0	90.7	15.3	95.00%	E.IDIGGVTLLR.A		R.ETIAKPNVTIPEAVEEIDIGGVTLLR.A
201	222	3	2414.16	4	1	23.8	21.7	94.40%	R.YGANPHQSPAQAFMEQGPLPFK.V		R.YGANPHQSPAQAFMEQGPLPFK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
31	IPYR_SCHPO	39.10%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
240	280	3	4115.08	2.7	1	89.4	17.6	95.00%	K.SDFSLVNVSVTGSVANDPSVSSTIPPAQELAPAPVDPSVHK.W		K.SDFSLVNVSVTGSVANDPSVSSTIPPAQELAPAPVDPSVHK.W
114	125	2	1304.56	3.3	1	43	23.7	95.00%	K.AKGDSDPLDVCE.I	Carbamidomethyl (+57)	K.AKGDSDPLDVCEIGEAR.G
186	192	2	922.44	6	1	35.4	21.7	95.00%	R.ATNEWFR.I		R.ATNEWFR.I
157	169	2	1391.81	4.1	0	37.4	11.8	95.00%	K.VIVIDVNDPLAPK.L		K.VIVIDVNDPLAPK.L
24	42	2	2113.02	2.7	1	69.7	22.6	95.00%	K.NGTPISSWHDIPLYANAEK.T	Deamidation (+1)	K.NGTPISSWHDIPLYANAEK.T
43	53	2	1283.73	4	1	66.7	15.9	95.00%	K.TILNMVVEIPR.W		K.TILNMVVEIPR.W
193	202	2	1158.63	2.7	1	25.9	19.9	92.10%	R.IYKIPDGKPE.N		R.IYKIPDGKPENSFAFSGECK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
32	HSP60_SCHPO	25.43%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
112	128	2	1705.86	4.1	1	84.3	21.2	95.00%	K.TNEVAGDGTTTATVLTR.A		K.TNEVAGDGTTTATVLTR.A
137	148	2	1316.6	4	0	27.4	23.3	94.00%	R.NVAAGCNPMDLR.R	Carbamidomethyl (+57)	R.NVAAGCNPMDLR.R
437	453	2	1588.85	4.6	1	29.9	18.9	95.00%	K.AAVSEGVLPGAGTSFVK.A		K.AAVSEGVLPGAGTSFVK.A

343	359	3	1806.88	5.1	1	21.9	22.4	91.70%	K.AQPHHLGSCGSVTVTKE.D	Carbamidomethyl (+57)	K.AQPHHLGSCGSVTVTKEDTIIMK.G
68	79	2	1313.7	4.3	0	39.3	19.4	95.00%	R.NVLIDQPFGSPK.I		R.NVLIDQPFGSPK.I
520	533	2	1570.87	4.4	1	87.2	15.3	95.00%	R.FVDLNEIGVLDPLK.V		R.FVDLNEIGVLDPLK.V
258	275	2	1937.07	4.4	1	74.7	14.9	95.00%	K.VSAVQDILPSLELAAQQR.R		K.VSAVQDILPSLELAAQQR.R
229	240	2	1401.72	4.3	0	35	20.5	95.00%	R.GYISPYFITDVK.S		R.GYISPYFITDVK.S
45	56	2	1215.69	4.9	0	52.6	16.8	95.00%	R.ASLLTGVDTLAR.A		R.ASLLTGVDTLAR.A
175	191	2	1712.83	2.8	0	49.5	22.8	95.00%	E.ISQVATISANGDTHIGE.L	Deamidation (+1)	R.DITTSEEISQVATISANGDTHIGELLAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
33	G6PI_SCHPO	27.45%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
52	62	2	1266.62	3	1	25.9	21.8	92.00%	E.EDGPILFDFSK.N		K.EEDGPILFDFSK.N
217	228	2	1343.61	5.2	1	37.3	22.6	95.00%	K.TFTTAETCTNAK.S	Carbamidomethyl (+57)	K.TFTTAETCTNAK.S
372	382	2	1171.52	5.1	0	67.7	22.5	95.00%	R.SGDMVNYTTGK.I		R.SGDMVNYTTGK.I
464	477	2	1502.83	4	0	36.9	16.4	95.00%	K.TFVGNRPSNSIIAK.K		K.TFVGNRPSNSIIAK.K
42	51	2	1189.57	3.2	1	48.2	22.4	95.00%	K.FSFTFNGLKE.E	Deamidation (+1)	K.FSFTFNGLKEEDGPILFDFSK.N
534	547	2	1559.76	2.4	0	43.7	22.4	95.00%	E.NHDSSTNGLINLFK.N	Deamidation (+1)	K.GDVENHDSSTNGLINLFK.N
2	24	2	2548.27	3.8	1	60.7	19.4	95.00%	M.SFSLASTLPAWQAVQTHYESVGK.H	Acetyl (+42)	-.MSFSLASTLPAWQAVQTHYESVGK.H
118	128	2	1170.59	4.1	0	35.5	21.3	95.00%	K.VNGQDVMPGVR.K		K.VNGQDVMPGVR.K
204	216	2	1493.75	4.3	1	51.5	21.7	95.00%	K.CDPETTLFLIASK.T	Carbamidomethyl (+57)	K.CDPETTLFLIASK.T
429	445	2	1870.94	4.8	1	69.7	21.1	95.00%	R.MLFSNFAAQTEALMLGK.T		R.MLFSNFAAQTEALMLGK.T
353	367	2	1711.83	4.2	1	71.8	22.6	95.00%	R.FPAYLQQLSMESNGK.A		R.FPAYLQQLSMESNGK.A
2	20	2	2177.05	3.9	0	45.3	22.4	95.00%	M.SFSLASTLPAWQAVQTHYE.S	Acetyl (+42)	-.MSFSLASTLPAWQAVQTHYESVGK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
34	FAS2_SCHPO	6.68%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1569	1579	2	1292.61	5	1	41.1	22.5	95.00%	R.NADNIDEYLAR.F		R.NADNIDEYLAR.F
488	502	3	1650.8	4.5	1	35.5	22.1	95.00%	K.NVNHPTAPSTTIDER.G		K.NVNHPTAPSTTIDER.G
31	44	2	1510.8	2.6	1	26.7	18.9	93.20%	E.TQDVILSPPVSAER.I		R.WIETQDVILSPPVSAER.I
381	394	2	1509.83	2.5	0	63	16.9	95.00%	E.FYASGIAPIFSPLK.A		R.AQLDLWNEEHGEFYASGIAPIFSPLK.A
114	146	3	3020.56	3.1	1	35.9	17.8	95.00%	K.VETAAAAAPAATPAPAPAQTSAPAAALPDEPPK.A		K.VETAAAAAPAATPAPAPAQTSAPAAALPDEPPK.A
397	406	2	1310.58	5.6	0	36.9	23	95.00%	R.VYDSDWNWAR.Q		R.VYDSDWNWAR.Q
1393	1401	2	994.61	4.5	0	27.6	9.54	94.30%	K.TPLPIVDLK.F		K.TPLPIVDLK.F
97	113	2	1656.79	4.6	1	38.3	23.2	95.00%	E.VADEPAEAPASTSSTPK.V		R.EIYYNFEDEVADEPAEAPASTSSTPK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
35	GPD1_SCHPO	35.58%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
281	296	2	1692.8	2.5	0	45.4	22.6	95.00%	E.QSCGIADLVTSCLGGR.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.TMVEQSCGIADLVTSCLGGR.N
203	232	3	3092.63	2.8	1	70.4	16.2	95.00%	R.EQIAAVFDRPYFSVVSVDDVAGVALGGALK.N		R.EQIAAVFDRPYFSVVSVDDVAGVALGGALK.N
2	20	2	1989	3.8	0	99.4	21.1	95.00%	M.SGYGQQGVSAANIDSIRPK.K	Acetyl (+42)	-.MSGYGQQGVSAANIDSIRPK.K
87	104	2	2008.06	5	1	48.8	17.9	95.00%	K.YLPGIECPPNVIAVPDVR.E	Carbamidomethyl (+57)	K.YLPGIECPPNVIAVPDVR.E
277	296	2	2153	2.6	1	93.7	23.3	95.00%	R.TMVEQSCGIADLVTSCLGGR.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.TMVEQSCGIADLVTSCLGGR.N
188	202	2	1668.85	2.3	1	39.2	20.3	95.00%	E.TTIGFNPPNEVDIPR.E		R.EQFCETTIGFNPPNEVDIPR.E
125	144	2	2172.13	3.4	0	59.8	19.2	95.00%	R.VCDQMVGLIRPGAVGISCIK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VCDQMVGLIRPGAVGISCIK.G

317	331	2	1484.82	2.8	1	79.3	16.7	95.00%	K.ELLGGQLLQGAATSK.D		K.ELLGGQLLQGAATSK.D
318	331	2	1355.78	2.7	0	81	15.1	95.00%	E.LLGGQLLQGAATSK.D		K.ELLGGQLLQGAATSK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
36	C1TC_SCHPO	10.89%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
689	707	3	1923.15	3.9	0	37.5	6.99	95.00%	R.TSGLKPDAIVIVATVQALK.L		R.TSGLKPDAIVIVATVQALK.L
204	219	3	1649.96	3.8	0	23.7	10.8	94.30%	R.TADIVVAAIGIPHFVK.A		R.TADIVVAAIGIPHFVK.A
2	12	2	1184.68	4.9	1	55.8	15.9	95.00%	M.ALLLEGTSLAR.K	Acetyl (+42)	-.MALLLEGTSLAR.K
324	336	2	1299.71	5.1	1	59.2	18.9	95.00%	K.NIGDLASEIGIAK.S		K.NIGDLASEIGIAK.S
381	396	2	1629.9	3.4	0	106	16.1	95.00%	K.STLTAGLVQALSNLDK.L		K.STLTAGLVQALSNLDK.L
77	84	2	947.57	2.8	0	40.6	14.5	95.00%	E.YDLLLAIK.G		R.AANEAGISCEHVNFPEDITEYDLLLAIK.G
817	827	2	1354.72	3.1	1	32.7	18.9	95.00%	R.LLYDVHEPIEK.K		R.LLYDVHEPIEK.K
349	356	2	983.58	5.3	1	46.2	14.6	95.00%	K.VNLEILQR.L		K.VNLEILQR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
37	SERA_SCHPO	23.18%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
275	284	2	1108.56	4.3	1	25.6	21.2	91.50%	K.EGSYLINASR.G		K.EGSYLINASR.G
338	351	2	1479.76	3	1	34.9	21.1	95.00%	K.NIILTPHIGGSTEE.A		K.NIILTPHIGGSTEEAQYNIGIEVSEALTR.Y
410	421	2	1468.77	4	1	31.9	19.6	95.00%	R.QVNELFIDHNIK.S		R.QVNELFIDHNIK.S
302	319	2	1728.88	4.5	0	48	20.8	95.00%	K.IAGAAIDVYPSEPAGNGK.D		K.IAGAAIDVYPSEPAGNGK.D
47	57	3	1247.68	3.8	1	25.6	17.9	95.00%	R.TLKPFASEDIK.I		R.TLKPFASEDIK.I
63	75	2	1430.7	2.9	1	64.2	21	95.00%	E.NVNQSALSNLKDE.G		K.ILLLENVNQSALSNLKDEGYQVEFLK.T
248	262	2	1596.82	4.1	1	50.8	20	95.00%	R.ADFVSLHVPASPETK.N		R.ADFVSLHVPASPETK.N
142	154	2	1394.7	4.8	0	57.8	20.3	95.00%	R.GIAVFNSPYANSR.S		R.GIAVFNSPYANSR.S
302	321	3	1972.98	1.9	1	36.9	21.5	95.00%	K.IAGAAIDVYPSEPAGNGKDK.F	Deamidation (+1)	K.IAGAAIDVYPSEPAGNGKDK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
38	LYS9_SCHPO	37.11%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
177	183	2	740.49	4.7	0	33.1	9.03	95.00%	R.GVLLALR.N		R.GVLLALR.N
122	135	2	1509.82	2.6	0	41.8	16.9	95.00%	E.IGVDPGIDHLYAIK.T		K.AGSICMNEIGVDPGIDHLYAIK.T
38	49	2	1259.66	4.1	1	41.7	19.9	95.00%	K.AEAFINGIPNSK.A		K.AEAFINGIPNSK.A
149	170	2	2385.11	5.2	1	60.2	22.9	95.00%	K.SFLSYCGGLPAPEDSNNPLGYK.F	Carbamidomethyl (+57)	K.SFLSYCGGLPAPEDSNNPLGYK.F
2	22	3	2269.25	3.1	1	39	13	95.00%	M.PSILLLGSGFVAHPTLEYLSR.R		-.MPSILLLGSGFVAHPTLEYLSR.R
379	396	2	1989.93	4.3	0	76.6	23	95.00%	R.TCTLLDYGVPNGYTSMAK.L	Carbamidomethyl (+57)	R.TCTLLDYGVPNGYTSMAK.L
114	135	3	2372.16	2.8	1	47.3	21.4	95.00%	K.AGSICMNEIGVDPGIDHLYAIK.T	Carbamidomethyl (+57)	K.AGSICMNEIGVDPGIDHLYAIK.T
336	348	2	1431.66	2.5	1	32.6	23.7	95.00%	R.GNPLDTLCATLEE.L	Carbamidomethyl (+57)	R.GNPLDTLCATLEELMQYEEGER.D
397	426	3	3075.62	3.2	0	48.5	14.3	95.00%	K.LVGVPCGVATQQILDGVINTPGVLAPNDMK.L	Carbamidomethyl (+57)	K.LVGVPCGVATQQILDGVINTPGVLAPNDMK.L
64	85	3	2488.28	3.3	1	39.1	17.6	95.00%	K.AVSEHDLTISLIPYTYHATVMK.A		K.AVSEHDLTISLIPYTYHATVMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
39	PDX1_SCHPO	19.93%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
71	83	2	1355.75	4.3	1	66.7	17.6	95.00%	K.EIQAAVSIPVMAK.V		K.EIQAAVSIPVMAK.V
38	49	2	1218.59	2.7	1	71.4	21.5	95.00%	E.AAGACAVMALER.V	Carbamidomethyl (+57)	R.IAEAAGACAVMALER.V
21	34	2	1457.74	4	1	89.6	20.6	95.00%	K.GGVIMDVVNAEQAR.I		K.GGVIMDVVNAEQAR.I
121	132	3	1383.7	4.4	1	31	21	95.00%	K.SKFTVPFVCGSR.N	Carbamidomethyl (+57)	K.SKFTVPFVCGSR.N
13	20	2	830.47	4.2	0	38.8	20.1	95.00%	K.AGLAQMLK.G		K.AGLAQMLK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
40	THIL_SCHPO	29.87%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
111	129	2	1953.96	4.4	1	43.8	21.7	95.00%	E.IVVAGGTESMSNAPYYAPK.N		K.ATILGAQTIMTGNAEIVVAGGTESMSNAPYYAPK.N
291	301	2	1160.65	4.8	0	33.2	18	95.00%	R.FTTSPSLAIPK.A		R.FTTSPSLAIPK.A
321	331	2	1105.62	3.4	0	42.8	17.9	95.00%	E.AFSVVAVANTK.I		K.HAGIEASQVDYYEINEAFSVVAVANTK.I
53	69	2	1772.9	3	0	65	20.1	95.00%	E.VFMGNVVSANLGQNPAR.Q		R.VNIKPSDVDEVFMGNVVSANLGQNPAR.Q
14	30	2	1654.81	3.8	0	74.4	21.9	95.00%	R.TPMGSFGGSFASLPATK.L		R.TPMGSFGGSFASLPATK.L
339	359	3	2023.01	2.6	1	26.5	21.1	95.00%	E.RVNINGGGVAMGHPLGSSGSR.I	Deamidation (+1)	K.ILGLDPERVNINGGGVAMGHPLGSSGSR.I
43	52	2	1114.55	3.3	0	32.7	21.1	95.00%	R.VNIKPSDVDE.V		R.VNIKPSDVDEVFMGNVVSANLGQNPAR.Q
43	69	3	2869.45	3.7	1	43	17.9	95.00%	R.VNIKPSDVDEVFMGNVVSANLGQNPAR.Q		R.VNIKPSDVDEVFMGNVVSANLGQNPAR.Q
360	371	2	1405.81	4.5	0	73.2	14.5	95.00%	R.IICTLAYILAQK.D	Carbamidomethyl (+57)	R.IICTLAYILAQK.D
340	359	2	1866.91	2.4	0	37.1	22.1	95.00%	R.VNINGGGVAMGHPLGSSGSR.I	Deamidation (+1)	R.VNINGGGVAMGHPLGSSGSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
41	HSP7M_SCHPO	19.58%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
216	232	2	1758.96	3.8	1	44.6	17.4	95.00%	R.VVNEPTAAALAYGLDKK.N		R.VVNEPTAAALAYGLDKK.N
366	376	2	1188.6	4.3	1	42.7	21	95.00%	R.ALKDANLQTSE.I		R.ALKDANLQTSEINEVILVGGMTR.M
204	215	2	1124.67	4.6	0	48.3	12.8	95.00%	K.AAGAIAGLNVLR.V		K.AAGAIAGLNVLR.V
322	337	2	1645.86	3.4	0	41.2	19.7	95.00%	K.TDISLPFITADATGPK.H		K.TDISLPFITADATGPK.H
465	480	2	1637.8	4	1	81.9	22.4	95.00%	R.KSQVFSTAADGQTAVE.I		R.KSQVFSTAADGQTAVEIR.V
105	118	2	1578.81	4.5	1	81.4	20.7	95.00%	R.QAVINPENTFFATK.R		R.QAVINPENTFFATK.R
185	199	2	1679.83	4.3	0	62.1	21.8	95.00%	K.NAVVTVPAYFNDSQR.Q		K.NAVVTVPAYFNDSQR.Q
496	510	2	1538.89	4.2	0	77.2	14	95.00%	K.LIGNFQLTGIAPAPK.G		K.LIGNFQLTGIAPAPK.G
157	170	2	1496.8	5.1	0	59.3	19.2	95.00%	K.TYSPSQIGGFILSK.M		K.TYSPSQIGGFILSK.M
155	170	2	1681.91	2.3	1	27	17.9	93.60%	R.GKTYSPSQIGGFILSK.M		R.GKTYSPSQIGGFILSK.M
216	231	2	1630.86	3.8	0	78.5	19.3	95.00%	R.VVNEPTAAALAYGLDK.K		R.VVNEPTAAALAYGLDK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
42	CYPH_SCHPO	44.44%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
90	123	3	3611.83	4	0	56	18.1	95.00%	K.HNKPGLLSMANAGPNTNGSQFFITTVVTPWLDGK.H		K.HNKPGLLSMANAGPNTNGSQFFITTVVTPWLDGK.H
2	17	2	1835.87	1.8	0	68.1	22.2	95.00%	M.SNCFFDVIANGQPLGR.I	Acetyl (+42)/ Carbamidomethyl (+57)	-.MSNCFFDVIANGQPLGR.I
22	29	2	931.51	4	0	29.7	20.8	95.00%	K.LFDDVVPK.T		K.LFDDVVPK.T
54	67	2	1607.82	4.3	0	67.2	20.3	95.00%	R.VIPQFMLQGGDFTR.G		R.VIPQFMLQGGDFTR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
43	GBLP_SCHPO	37.90%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
156	172	2	1893.9	4.3	0	71.3	22.2	95.00%	R.FSPNPDNLTFVSAGWDK.A		R.FSPNPDNLTFVSAGWDK.A
13	36	3	2480.24	2.7	1	59.3	20.5	95.00%	E.GHSGWVTSLSTAPENPDILLSGSR.D		R.ATLEGHSGWVTSLSTAPENPDILLSGSR.D
48	57	2	1135.53	4.7	0	43.2	22.3	95.00%	R.DDVNYGVAQR.R		R.DDVNYGVAQR.R
186	212	3	2736.27	3.5	0	59.8	23.3	95.00%	R.TSHYGHTGYVSAVTISPDGSLCASGGR.D	Carbamidomethyl (+57)	R.TSHYGHTGYVSAVTISPDGSLCASGGR.D
234	245	2	1314.71	3.1	0	32.5	18.9	95.00%	K.ANINALVFSPNR.Y		K.ANINALVFSPNR.Y
176	185	2	1264.65	5.4	1	30.1	21.5	95.00%	K.VWDLETFSLR.T		K.VWDLETFSLR.T
39	47	2	1112.68	5.9	0	27.8	12.6	94.50%	K.SIILWNLVR.D		K.SIILWNLVR.D
270	279	2	1033.58	3.6	0	29.4	17.1	95.00%	E.LTVDFVGVGK.K		K.VDELTVDFVGVGK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
44	PPA1_SCHPO	21.85%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
418	427	2	1194.64	3.8	0	46.9	18.5	95.00%	E.LYAYLNSPVR.V		R.HLVNEEVFPLSDCGFGPSNTSDGMCELYAYLNSPVR.V
40	59	3	2404.13	2.5	0	63.3	22.2	95.00%	R.SPYHKPYFYGPSIDFPTTCK.I	Carbamidomethyl (+57)	R.SPYHKPYFYGPSIDFPTTCK.I
260	270	2	1372.64	2.3	1	40.2	23.8	95.00%	E.IALQDYSEFCK.L	Carbamidomethyl (+57)	R.LNPYFSNYNLTNDDILNLYGICSYEIALQDYSEFCK.L
73	92	2	2046.99	2	0	108	21.9	95.00%	R.NPTGGNAAFDAVGIANFQQR.L		R.NPTGGNAAFDAVGIANFQQR.L
369	379	2	1206.63	3.4	0	27.1	20.7	93.70%	E.FVPFAGNLITE.L		K.ASEFVPFAGNLITELFQCEDSK.Y
339	365	3	3034.42	2.6	1	24.5	22.6	95.00%	E.TALGFFTDNTPENPLPTSYQVHSHSMK.A	Oxidation (+16)	R.SVENNTQQVFFAFTHDANIIPVETALGFFTDNTPENPLPTSYQVHSHSMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
45	IF4A_SCHPO	21.94%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
156	169	2	1547.76	3.3	0	59.3	22.1	95.00%	R.ALPTDAVQMFVLDE.A		R.ALPTDAVQMFVLDEADEMLSR.G
58	69	2	1173.61	5	0	69	21.1	95.00%	R.DVLAQAQSGTGK.T		R.DVLAQAQSGTGK.T
33	48	2	1854.94	3.8	1	30.4	21.1	95.00%	R.GIYAYGFERPSAIQQR.A		R.GIYAYGFERPSAIQQR.A
156	172	2	1862.87	2.2	1	55.9	22.9	95.00%	R.ALPTDAVQMFVLDEADE.M		R.ALPTDAVQMFVLDEADEMLSR.G
12	29	2	2157.95	2.7	1	63.5	24.2	95.00%	E.TNYDEVIDTFDDMNLKPE.L		-.MVDQLEDSVIETNYDEVIDTFDDMNLKPELLR.G
255	268	2	1608.84	3.6	0	47.4	19.2	95.00%	E.TVTVTQAVIFCNTR.R	Carbamidomethyl (+57)	K.LDTLCDLYETVTVTQAVIFCNTR.R
17	29	2	1535.72	3.5	0	56.7	22.9	95.00%	E.VIDTFDDMNLKPE.L		-.MVDQLEDSVIETNYDEVIDTFDDMNLKPELLR.G
384	392	2	1016.51	3.3	0	30.6	21.9	95.00%	E.MPMNIADLI.-		R.EIEQFYNTHIEEMPMNIADLI.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
46	PUT2_SCHPO	21.72%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
406	422	2	1852.92	4.3	1	57.5	21.4	95.00%	K.ADDSEGFFVEPTVLLSK.N		K.ADDSEGFFVEPTVLLSK.N
411	422	2	1335.75	2.7	0	47.3	15.3	95.00%	E.GFFVEPTVLLSK.N		K.ADDSEGFFVEPTVLLSK.N
362	384	3	2428.26	3.2	0	27	17.2	95.00%	K.VGAPLTDFANFVGPVIHQASFNK.L		K.VGAPLTDFANFVGPVIHQASFNK.L
254	274	3	2393.15	4.4	1	52.3	22	95.00%	K.VCFNHPEFAGLHFTGSTAVFR.S	Carbamidomethyl (+57)	K.VCFNHPEFAGLHFTGSTAVFR.S
275	288	2	1444.74	4.6	1	37.7	21	95.00%	R.SLWGTIGENVANGK.Y		R.SLWGTIGENVANGK.Y
495	509	2	1504.71	3.5	1	49.3	22	95.00%	K.CTGAVVGEQPFGGAR.A	Carbamidomethyl (+57)	K.CTGAVVGEQPFGGAR.A
531	548	2	2036.98	5	1	47.4	22	95.00%	R.SIKDTFAYADSVLYPSNF.-		R.SIKDTFAYADSVLYPSNF.-
484	494	2	1225.58	4.6	0	28	22.7	94.70%	R.NAAGNFYINDK.C		R.NAAGNFYINDK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
47	DHAS_SCHPO	32.21%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
19	28	2	1170.6	2.9	0	33.9	20.8	95.00%	R.FITLLSDHPE.F		R.FITLLSDHPEFK.I
229	240	2	1375.66	3.5	0	63.8	22.4	95.00%	E.LTDNVVSAQCNR.V	Carbamidomethyl (+57)	K.ILGSVNSTISGYELTDNVVSAQCNR.V
112	132	3	2341.31	2.7	1	53.3	9.54	95.00%	R.REPTVPLVVPTVNTDHLDVIK.Y		R.REPTVPLVVPTVNTDHLDVIK.Y
31	39	2	856.52	4.9	0	28.2	16.9	94.90%	K.IAVLGASAR.S		K.IAVLGASAR.S
287	303	3	2003.98	4.2	0	33.9	22.1	95.00%	K.QAIYVFDDSTPDRPQPR.L		K.QAIYVFDDSTPDRPQPR.L
19	30	3	1445.76	4.9	1	23.3	20.3	93.80%	R.FITLLSDHPEFK.I		R.FITLLSDHPEFK.I

143	161	2	2003.02	2.7	0	76.2	20.5	95.00%	R.GCIITNSNCSTAAVVVPLK.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GCIITNSNCSTAAVVVPLK.A
267	278	2	1375.7	3.8	1	37.2	21.1	95.00%	R.EVLANYVSEPQK.L		R.EVLANYVSEPQK.L
6	18	2	1227.7	3.7	0	35.6	17.2	95.00%	K.VGILGATGTVGQR.F		K.VGILGATGTVGQR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
48	EF1B_SCHPO	39.25%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
14	26	2	1580.81	2.4	1	32.6	20.5	95.00%	K.QLNDFLLDKSFIE.G		K.QLNDFLLDKSFIEGYEPSQADAVVFK.A
14	22	2	1104.59	4.8	0	36.2	19.8	95.00%	K.QLNDFLLDK.S		K.QLNDFLLDK.S
59	73	2	1561.84	4.2	0	60.9	18.5	95.00%	K.QIATYDLATLPGTAK.E		K.QIATYDLATLPGTAK.E
153	165	2	1432.74	3.9	0	44.3	20.2	95.00%	R.SIQMDGLVWGLSK.L		R.SIQMDGLVWGLSK.L
129	146	2	2088.97	4.2	1	29	23.4	95.00%	K.SLVTLDVKPWDDETPMDE.L		K.SLVTLDVKPWDDETPMDELEK.A
2	13	2	1209.59	3.7	0	57.4	22.5	95.00%	M.GFSDLTSDAGLK.Q		-.MGFSDLTSDAGLK.Q
23	39	2	1885.92	3.6	1	50.9	22.2	95.00%	K.SFIEGYEPSQADAVVFK.A		K.SFIEGYEPSQADAVVFK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
49	RL4A_SCHPO	32.23%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
122	140	2	1845.04	4.3	0	48.1	11.1	95.00%	R.YAISSAVAASGVPSLLLAR.G		R.YAISSAVAASGVPSLLLAR.G
147	163	2	1883.01	3.6	1	67.8	17.4	95.00%	E.IPEVPLVVDDAVQSFQK.T		R.IEEIPEVPLVVDDAVQSFQK.T
2	13	2	1304.71	4.5	0	25.5	17.9	91.40%	M.AAARPTVSIYSK.D	Acetyl (+42)	-.MAAARPTVSIYSK.D
235	248	3	1457.85	2.1	0	35.8	13	95.00%	R.LNLLQLAPGGHLGR.F		R.LNLLQLAPGGHLGR.F
282	291	2	1101.58	3.6	0	48.1	19.9	95.00%	E.NIISNADVTR.L		K.NYFLPENIISNADVTR.L
292	303	2	1357.75	4	1	43.8	18.1	95.00%	R.LINSDEIQSIVK.A		R.LINSDEIQSIVK.A
14	29	2	1695.88	4.2	1	38.3	19.4	95.00%	K.DGSVSSETIALPFVFK.A		K.DGSVSSETIALPFVFK.A
276	291	2	1864.94	4.5	1	39	21.7	95.00%	K.NYFLPENIISNADVTR.L		K.NYFLPENIISNADVTR.L
87	97	2	1197.51	4.4	0	32.6	22.8	95.00%	R.SGQAAFGNMCR.S	Carbamidomethyl (+57)	R.SGQAAFGNMCR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
50	STI1_SCHPO	26.23%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
214	229	2	1577.73	4.1	0	46.3	23.5	95.00%	E.FAPSSSTPSADSAKPE.T		K.EEFAPSSSTPSADSAKPETTNPPPQPQASEPMEEDK.T
543	560	2	1893.06	2.4	0	49.1	13.2	95.00%	E.VLGILQDPAMQAILGQAR.E		K.DPEVLGILQDPAMQAILGQAR.E
115	132	2	1692.83	3.3	0	65.4	22.8	95.00%	E.AAQTQAASGAGGFNPFAK.L		K.SVEAAQTQAASGAGGFNPFAK.L
146	164	2	1935.97	6.4	1	78.1	21.2	95.00%	K.LASNPETASLLADSAFMAK.L		K.LASNPETASLLADSAFMAK.L
76	90	3	1463.79	4.4	1	44.6	18.6	95.00%	R.KGAALHGLGDLDAAR.S		R.KGAALHGLGDLDAAR.S
112	132	2	2007.97	4.2	1	89.9	22.1	95.00%	K.SVEAAQTQAASGAGGFNPFAK.L		K.SVEAAQTQAASGAGGFNPFAK.L
168	183	2	1781.88	4.3	1	66.6	21.6	95.00%	K.IQQNPGSIMAELNDPR.M		K.IQQNPGSIMAELNDPR.M
20	34	2	1711.85	3.9	1	70.3	21.7	95.00%	K.TAIDYFTQAIGLDER.N		K.TAIDYFTQAIGLDER.N
230	245	2	1767.77	4	1	31.4	23.8	95.00%	E.TTNPPPQPQASEPMEE.D	Oxidation (+16)	K.EEFAPSSSTPSADSAKPETTNPPPQPQASEPMEEDK.T
371	377	2	800.44	3.8	0	29.8	21.2	95.00%	R.TPDILSR.L		R.TPDILSR.L
311	322	2	1466.61	3.4	1	31.7	23.5	95.00%	E.ADQLDDCIKTCE.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.DITYLNNLAAAYFEADQLDDCIKTCEDAIEQGR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
51	CARB_SCHPO	10.17%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
730	744	2	1630.79	2.3	1	54.5	21.8	95.00%	K.VLGTDPLMIDSAEDR.H		K.VLGTDPLMIDSAEDR.H
968	975	2	1019.52	4.9	0	24.9	20	90.40%	K.VPQFSWTR.L		K.VPQFSWTR.L
932	943	2	1304.72	5.6	0	35.2	17.9	95.00%	K.TLGVNFIDVATR.S		K.TLGVNFIDVATR.S

1016	1031	2	1630.91	2.7	0	72.1	15.9	95.00%	K.IPLPGQGILLGGDRPE.L		K.IPLPGQGILLGGDRPELAGIAADLSK.L
773	798	3	2736.49	2.9	0	51	14.1	95.00%	K.FANAVGYPVLVRPSYVLSGAAMSVIR.D		K.FANAVGYPVLVRPSYVLSGAAMSVIR.D
418	433	2	1784.89	3.1	0	51.8	20.9	95.00%	K.TTTANFEPSLDYVVTK.I		K.TTTANFEPSLDYVVTK.I
575	584	2	1057.58	4.7	1	32.1	19.7	95.00%	K.LVGASELDVR.A		K.LVGASELDVR.A
809	823	2	1533.82	2.7	0	36.2	18.8	95.00%	E.NASAVSPDHPVVITK.F		K.LENASAVSPDHPVVITK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
52	HXK1_SCHPO	18.60%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
231	246	2	1800.86	2.7	1	38.4	22.2	95.00%	E.IGVIFGTGCNACYIEK.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.LNAILSDTTGTLVASNYASPGTEIGVIFGTGCNACYIEK.F
447	467	2	1954.03	3.2	1	26.4	17.5	92.80%	K.VVTIPAEDGSGVGAALVSALE.A		K.VVTIPAEDGSGVGAALVSALEAK.G
304	315	2	1380.7	5.1	0	25.3	21	91.00%	K.MIAGCYLGDILR.R	Carbamidomethyl (+57)	K.MIAGCYLGDILR.R
2	12	3	1409.65	4.4	0	25.1	22.2	95.00%	M.SLHDAYHWPSR.T	Acetyl (+42)	-.MSLHDAYHWPSR.T
406	426	3	2369.2	3.6	1	22.8	20.3	93.20%	R.KMNKPSMIVGTDGSVYNLYPR.F		R.KMNKPSMIVGTDGSVYNLYPR.F
352	360	2	1076.47	4.3	1	33.8	23.2	95.00%	E.VDPFENLDE.T		R.DPLAMDTSVLSAIEVDPFENLDETQTLFEETYGLK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
53	OAT_SCHPO	23.06%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
5	14	2	1147.56	4.4	0	28.1	21.4	94.80%	E.SLLHNTFSTE.Q		-.MSAESLLHNTFSTEQIEVLENEYAAHNYHPLPVCFSK.A
386	398	3	1374.82	4.6	0	23.2	11.8	93.70%	R.GVLAKPTHGNIIR.F		R.GVLAKPTHGNIIR.F
154	167	2	1493.69	4.9	0	59.2	23.2	95.00%	R.TMGIISMSTDPDAR.D		R.TMGIISMSTDPDAR.D
141	153	2	1500.75	2.5	0	39.5	21	95.00%	E.AIILSCVDNFHGR.T	Carbamidomethyl (+57)	K.IPTDEAIILSCVDNFHGR.T
276	291	2	1561.85	4	0	53	16.7	95.00%	K.AISGGVYPVSAVLSSR.E		K.AISGGVYPVSAVLSSR.E
238	254	2	1838.97	4.4	1	78.8	18.6	95.00%	K.AHNVLFIADEVQTGVAR.T		K.AHNVLFIADEVQTGVAR.T
258	275	3	2051.1	4.3	1	30.2	15.9	95.00%	K.MLCIEHSNVKPDVVILGK.A	Carbamidomethyl (+57)	K.MLCIEHSNVKPDVVILGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
54	RS18_SCHPO	29.61%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	78	2	1386.79	4	0	45.2	15.7	95.00%	R.IVTIIQNPSQFK.I		R.IVTIIQNPSQFK.I
2	14	2	1578.86	2.7	0	45.7	16	95.00%	M.SLVVPDNFQHILR.L	Acetyl (+42)	-.MSLVVPDNFQHILR.L
79	86	2	1031.56	6	0	52.6	18.7	95.00%	K.IPSWFLNR.Q		K.IPSWFLNR.Q
95	106	2	1334.69	4.9	0	24.9	20.3	90.30%	K.SFQLLANNVDSK.L		K.SFQLLANNVDSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
55	FAS1_SCHPO	5.64%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1870	1881	2	1266.57	5.2	0	37.8	23	95.00%	R.SDYGMVAANPSR.V		R.SDYGMVAANPSR.V
712	726	2	1655.89	4	0	26.1	18.5	92.30%	K.ANPTFPIVLQWTGGR.A		K.ANPTFPIVLQWTGGR.A
971	984	2	1619.76	3.1	1	58.9	23	95.00%	E.NFEDLNDPYPVAAR.F		K.TTLIENFEDLNDPYPVAAR.F
1676	1692	2	1824.86	3.8	1	47.7	23.4	95.00%	E.VEQPVSAYVFTGQGSQE.Q		K.VEVLNQETSEPVLVGTAEVEQPVSAYVFTGQGSQEQGMGMDLYASSPVAR.K
824	839	2	1635.84	2.4	1	38.1	19.6	95.00%	E.KTYDGPTGGIVTVLSE.L		K.GVDDSEWEKTYDGPTGGIVTVLSELGEPIHK.L
1778	1806	3	3141.54	1.9	1	40.3	20.5	95.00%	K.DSTSFSFTHPSGLLSATQFTQPALTLMEK.S		K.DSTSFSFTHPSGLLSATQFTQPALTLMEK.S
781	794	2	1545.81	3.9	0	42.1	20	95.00%	K.LPPMPFDGILFGSR.L		K.LPPMPFDGILFGSR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
56	CYSD_SCHPO	41.03%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
47	59	2	1541.79	2.3	0	43.9	19.4	95.00%	R.LFGLQEPGYIYSR.M		R.LFGLQEPGYIYSR.M
27	39	2	1486.79	4	0	44	18.3	95.00%	R.AVPIYATTSYVFR.D		R.AVPIYATTSYVFR.D
378	395	2	2014.03	2.6	1	25	19.9	90.50%	K.TLVIAPAYTTHLQLTDEE.Q		K.TLVIAPAYTTHLQLTDEEQISAGVTK.D
72	100	3	2787.49	3.3	1	49.9	14.9	95.00%	R.IAALEHGAAAIATSSGTSALFMALTTLAK.A		R.IAALEHGAAAIATSSGTSALFMALTTLAK.A
156	169	2	1637.76	2.5	1	70.6	23.4	95.00%	E.SIGNPMYNVPDFER.I		K.AVYVESIGNPMYNVPDFER.I
10	26	2	1780.88	3.5	0	82.5	22	95.00%	E.TLQLHAGQEPDAATSSR.A		-.MPVESEHFETLQLHAGQEPDAATSSR.A
366	377	2	1185.64	4.4	0	34.5	17.8	95.00%	K.LASQLANVGDAK.T		K.LASQLANVGDAK.T
170	210	4	4156.13	4.3	1	53.9	16.1	95.00%	R.IAEVAHAAGVPLMVDNTFGGGGYLVRPIDHGADIVTHSATK.W		R.IAEVAHAAGVPLMVDNTFGGGGYLVRPIDHGADIVTHSATK.W
132	150	2	2074.95	4.2	1	127	23.3	95.00%	K.FVNGDDPNDLAAQIDENTK.A		K.FVNGDDPNDLAAQIDENTK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
57	MET3_SCHPO	16.33%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
427	440	2	1651.86	4	1	77.5	19.6	95.00%	R.LDAISVFYAQELQR.A		R.LDAISVFYAQELQR.A
42	58	2	1850.93	3.2	0	59.1	20.7	95.00%	E.LILNGGFSPLDGFMNQK.D	Deamidation (+1)	R.QFCDVELILNGGFSPLDGFMNQK.D
350	359	2	1102.6	3.9	1	29.9	19.2	95.00%	R.TLNISGTELR.R		R.TLNISGTELR.R
59	68	2	1233.64	5.6	1	40.5	20.6	95.00%	K.DYLNVVENLR.L		K.DYLNVVENLR.L
254	262	2	1012.62	5.1	0	33.5	12.6	95.00%	K.LSLLPLAMR.M		K.LSLLPLAMR.M
217	236	4	2231.2	3.6	0	31	13.4	95.00%	R.VLIHPVVGMTKPGDIDHFTR.V		R.VLIHPVVGMTKPGDIDHFTR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
58	HOSM_SCHPO	16.27%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	204	2	1315.66	4	0	40.8	22	95.00%	R.VGIADTVGCATPR.Q	Carbamidomethyl (+57)	R.VGIADTVGCATPR.Q
11	31	3	2302.11	3.4	0	46.5	21.5	95.00%	E.TIKPPMNGNPYGPNPSDFLSR.V	Deamidation (+1)	-.MSVSEANGTETIKPPMNGNPYGPNPSDFLSR.V
172	182	2	1264.7	3	0	47.7	17.2	95.00%	R.SDLVDLLSLYK.A		R.SDLVDLLSLYK.A
401	411	2	1290.55	4.4	1	41	23	95.00%	R.EYHADLSDADR.I		R.EYHADLSDADR.I
32	43	2	1391.75	4.9	1	68.1	19	95.00%	R.VNNFSIIESTLR.E		R.VNNFSIIESTLR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
59	IF5A1_SCHPO	29.30%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
14	28	2	1608.78	3.3	0	46.7	22.3	95.00%	E.AGASLTFPMQCSALR.K	Carbamidomethyl (+57)	-.MAEEEHVDFEGGEAGASLTFPMQCSALR.K
11	28	2	1851.87	3	1	51.6	22.8	95.00%	E.GGEAGASLTFPMQCSALR.K	Carbamidomethyl (+57)	-.MAEEEHVDFEGGEAGASLTFPMQCSALR.K
73	87	2	1655.77	2.8	0	40.9	23	95.00%	E.DMSPSTHNMDVPVVK.R		K.YEDMSPSTHNMDVPVVK.R
14	29	3	1752.87	3.1	1	23.8	21.9	94.40%	E.AGASLTFPMQCSALRK.N	Oxidation (+16)/ Carbamidomethyl (+57)	-.MAEEEHVDFEGGEAGASLTFPMQCSALRK.N
58	69	2	1352.76	3.3	0	46.7	15.7	95.00%	K.VHIVALDIFNGR.K		K.VHIVALDIFNGR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
60	ILV3_SCHPO	14.72%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

247	265	2	1882.89	3.6	1	62.3	23	95.00%	E.AMGMTLPGSSSYLAGSPEK.F			R.HACPGGGACGGMYTANTMASCAEAMGMTLPGSSSYLAGSPEK.F
185	207	3	2461.11	3.4	0	40.2	23.3	95.00%	R.AGHSPCQNNAPIDIVSAFQSYGE.F	Carbamidomethyl (+57)		R.AGHSPCQNNAPIDIVSAFQSYGEFITGK.I
372	384	2	1273.69	2.8	0	47	19.5	95.00%	E.GLIDGSNITVTGK.T			K.YLHAEGLIDGSNITVTGK.T
40	48	2	994.5	5.2	1	30.6	22.5	95.00%	K.YSETITGPK.S			K.YSETITGPK.S
141	159	2	2167.97	3	0	62.2	23.8	95.00%	E.TVMQGQWYDANVSIPGCDK.N	Carbamidomethyl (+57)		R.EIIADSIETVMQGQWYDANVSIPGCDK.N
185	212	3	3007.42	3.5	1	69.2	22.3	95.00%	R.AGHSPCQNNAPIDIVSAFQSYGEFITGK.I	Carbamidomethyl (+57)		R.AGHSPCQNNAPIDIVSAFQSYGEFITGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
61	CDC48_SCHPO	16.44%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
221	230	2	1110.48	4.2	0	30.3	22.1	95.00%	E.VGYDDIGGCR.R	Carbamidomethyl (+57)	R.EDEESSLAEVGYDDIGGCR.R
550	563	2	1522.75	3.6	1	43.8	21.2	95.00%	K.AIANECSANFISVK.G	Carbamidomethyl (+57)	K.AIANECSANFISVK.G
588	604	2	1817.93	4.3	1	57.6	20.9	95.00%	R.AAAPCVVFLDELDSIAK.A	Carbamidomethyl (+57)	R.AAAPCVVFLDELDSIAK.A
116	129	2	1553.82	2.5	0	38.2	18.2	95.00%	R.LGDIVTINPCPDIK.Y	Carbamidomethyl (+57)	R.LGDIVTINPCPDIK.Y
423	437	2	1594.7	3.7	0	31.4	23.5	95.00%	E.THGYVGSDLASLCSE.A	Carbamidomethyl (+57)	K.LADDVDLEQIAAETHGYVGSDLASLCSEAAMQQIR.E
359	379	3	2280.22	4.2	1	31.5	16.8	95.00%	R.SNVVVMAATNRPNSIDPALRR.F		R.SNVVVMAATNRPNSIDPALRR.F
316	332	2	1841.99	4.4	1	39.8	17.9	95.00%	K.NSPAIIFIDEIDSIAPK.R		K.NSPAIIFIDEIDSIAPK.R
461	473	2	1465.73	2.2	0	47.5	22.3	95.00%	E.VLDSLGVTMDNFR.F		K.MDMIDLDEDEIDAEVLDSLGVTMDNFR.F
344	356	2	1433.77	3.6	0	48.2	18.8	95.00%	R.VVSQLLTLMDGMK.A		R.VVSQLLTLMDGMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
62	ADH_SCHPO	28.86%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
236	253	2	1681.87	4.1	0	56	18.8	95.00%	K.AATNGGAHGTLVLSTSPK.S	Deamidation (+1)	K.AATNGGAHGTLVLSTSPK.S
254	278	3	2513.21	3.1	1	41.5	21.5	95.00%	K.SYEQAAGFARPGSTMVTVSMPAGAK.L		K.SYEQAAGFARPGSTMVTVSMPAGAK.L
170	194	3	2506.29	3.6	1	33.6	17.2	95.00%	K.VGPGEWICIPGAGGGLGHLAVQYAK.A	Carbamidomethyl (+57)	K.VGPGEWICIPGAGGGLGHLAVQYAK.A
42	62	3	2378.15	2.1	0	31.5	22.1	95.00%	K.YTGVCHTDLHALQGDWPLPAK.M	Carbamidomethyl (+57)	K.YTGVCHTDLHALQGDWPLPAK.M
200	211	2	1231.6	3.6	1	29.6	21.9	95.00%	R.VVAIDTGDDKAE.L		R.VVAIDTGDDKAELVK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
63	UGPA1_SCHPO	22.13%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
494	506	2	1495.75	3	1	57.7	21.5	95.00%	E.NCVITGNLNILEH.-	Carbamidomethyl (+57)	R.IDIPNGSVLENCVITGNLNILEH.-
1	10	2	1166.63	4.6	0	24.9	18.5	90.20%	-.MDLAPRPLGR.Q	Acetyl (+42)	-.MDLAPRPLGR.Q
201	216	2	1706.84	3.7	1	36.1	21.9	95.00%	K.ETLLPVPHTADSAIDE.W		K.ETLLPVPHTADSAIDEWYPPGHGDVFEALTNSGIIDTLIAQGK.E
15	34	2	2047.96	2.6	0	124	23.2	95.00%	K.SQSAFAFDNTATSIAASTMK.N		K.SQSAFAFDNTATSIAASTMK.N
202	216	2	1577.8	4.1	0	26.5	21.6	93.00%	E.TLLPVPHTADSAIDE.W		K.ETLLPVPHTADSAIDEWYPPGHGDVFEALTNSGIIDTLIAQGK.E
185	194	2	1205.65	4.7	0	32.1	19.1	95.00%	K.IDILTFNQSR.Y		K.IDILTFNQSR.Y
228	243	2	1613.9	2.9	0	44.7	15.3	95.00%	E.ALTNSGIIDTLIAQGK.E		K.ETLLPVPHTADSAIDEWYPPGHGDVFEALTNSGIIDTLIAQGK.E
115	129	2	1460.72	4.2	0	48.3	21.8	95.00%	K.LNGGLGTTMGCVGPK.S	Carbamidomethyl (+57)	K.LNGGLGTTMGCVGPK.S
287	298	2	1278.63	4.4	0	55.1	21.4	95.00%	K.GGTLIDYDGNVR.L		K.GGTLIDYDGNVR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
64	YL8C_SCHPO	21.12%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

217	232	2	1745.96	4.4	1	53	15.1	95.00%	K.GTALQYITSNILPEVK.N		K.GTALQYITSNILPEVK.N
7	33	4	3045.57	3.9	1	29.7	16.9	95.00%	K.TNNLPTLDTLQMVISDVDGTLLDK HHR.F		K.TNNLPTLDTLQMVISDVDGTLLDK HHR.F
70	90	3	2326.19	3.3	0	38.3	19.8	95.00%	R.IPLDLDAFPAAHVNGCVLYNK.G	Carbamidomethyl (+57)	R.IPLDLDAFPAAHVNGCVLYNK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
65	VIPI_SCHPO	33.07%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
69	94	2	2433.11	4.4	1	121	23.3	95.00%	K.IQITSEDGGAASTTDQGGAGGDQ AAR.Q		K.IQITSEDGGAASTTDQGGAGGDQ AAR.Q
55	68	2	1496.86	2.9	0	67.1	14.6	95.00%	K.TALLLQDALLGQNK.I		K.TALLLQDALLGQNK.I
101	110	2	1087.63	5.8	1	34.3	15.9	95.00%	R.SAIISELLSR.G		R.SAIISELLSR.G
122	134	2	1410.71	4.2	0	61.1	21.2	95.00%	K.SIQLDQSYGVSSK.F		K.SIQLDQSYGVSSK.F
111	121	2	1260.64	3.7	1	31.8	20.5	95.00%	R.GYHLSDVTLEK.S		R.GYHLSDVTLEK.S
137	147	2	1100.62	4.3	1	27.7	18.4	94.50%	K.GILESALSGVR.S		K.GILESALSGVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
66	YHY6_SCHPO	9.08%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
161	187	3	2608.39	2.9	0	26.8	15.6	95.00%	K.SVGVNPIIVDFSAPGSATAPSKPA AQK.K		K.SVGVNPIIVDFSAPGSATAPSKPA AQK.K
303	314	2	1339.7	3	0	41.7	20.3	95.00%	E.LDEPIAIRPTSE.T		R.AGTSELDEPIAIRPTSETVMYPYY AK.W
161	188	4	2736.49	3.7	1	29.1	14	95.00%	K.SVGVNPIIVDFSAPGSATAPSKPA AQKK.K		K.SVGVNPIIVDFSAPGSATAPSKPA AQKK.K
60	72	2	1352.8	3.7	0	34.1	10.8	95.00%	K.SQTVVPIILAALE.T		K.SQTVVPIILAALETTSTPSGIAAK.A
387	398	2	1343.81	4.3	0	30.5	9.03	95.00%	R.IYTDLLAVPVIK.G		R.IYTDLLAVPVIK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
67	ECM17_SCHPO	6.79%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
314	325	2	1337.8	4.6	0	39.3	10	95.00%	R.LTVLEPITSLPR.K		R.LTVLEPITSLPR.K
1449	1466	2	1680.8	3.1	1	72.5	22.7	95.00%	R.AGIITAVENGGANGAVHE.G	Deamidation (+1)/ Deamidation (+1)	R.AGIITAVENGGANGAVHEGVSPE AF.-
886	900	3	1738.9	3.1	1	29.5	18.7	95.00%	E.IDIDEPKPITNEDIK.Q		K.ALGLDNVEIDIDEPKPITNEDIK.Q
801	810	2	1058.57	5.4	1	27.5	20.2	94.20%	K.GADLNLSELK.Y		K.GADLNLSELK.Y
722	740	2	1801.92	3.1	0	34.4	20	95.00%	E.GLSGPPLTILFASDGGTAE.N		K.LIEGLSGPPLTILFASDGGTAENV AK.R
611	636	3	2801.42	3.9	1	43.3	19	95.00%	K.GPSVVLAYLPYHSADDDAITVLQE TK.K		K.GPSVVLAYLPYHSADDDAITVLQE TK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
68	RL8_SCHPO	30.12%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
211	225	2	1491.8	2.7	0	37.5	19	95.00%	E.LASIVSAVDANFSAK.Y		K.NELASIVSAVDANFSAK.Y
24	32	2	1084.62	4.7	0	29.3	18.1	95.00%	K.NPLFVSRPR.S		K.NPLFVSRPR.S
33	43	2	1188.62	4.1	0	26.8	20.2	93.30%	R.SFGIGQDIQPK.R		R.SFGIGQDIQPK.R
81	92	2	1364.74	3.7	1	46.2	20	95.00%	K.TLDKNTATQVFK.L		K.TLDKNTATQVFK.L
134	146	2	1425.8	4.3	1	45.6	14.9	95.00%	K.YGLNHVVALIEAK.K		K.YGLNHVVALIEAK.K
69	80	3	1338.81	2.2	1	23.5	10.8	94.10%	R.LKVPPAIAQFQK.T		R.LKVPPAIAQFQK.T
52	57	2	862.44	5.9	1	26.5	20.6	93.00%	K.WPEYIR.L		K.WPEYIR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
69	NACA_SCHPO	38.73%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	75	2	1164.62	5.8	0	59.3	19.3	95.00%	K.SSNNAYIVLGK.V		K.SSNNAYIVLGK.V

52	64	2	1540.93	4.4	0	50.2	7.78	95.00%	K.NILLIINEPIVYK.S		K.NILLIINEPIVYK.S
14	26	2	1308.71	4.4	1	36.6	17.5	95.00%	E.LPAGSTTVVHAEK.A		K.ISELPAGSTTVVHAEK.A
141	150	2	1087.58	3.8	0	30.7	19.9	95.00%	E.LVMAQANVSR.A		K.DIELVMAQANVSR.A
132	140	2	946.46	4.1	1	27.5	22.1	94.20%	E.TGVDAKDIE.L		K.AVDETGVDAKDIELVMAQANVSR.A
76	86	2	1189.58	4.9	1	47.2	22.4	95.00%	K.VTVEDMAAQAR.A		K.VTVEDMAAQAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
70	HSP7F_SCHPO	9.03%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
174	189	2	1665.85	4	0	78.4	20.6	95.00%	R.LMNDNAAAALTYGITK.T		R.LMNDNAAAALTYGITK.T
5	16	2	1249.64	6.5	0	29.4	20.5	95.00%	R.TNVVGIDFGNSK.T		R.TNVVGIDFGNSK.T
38	48	2	1194.59	3.8	1	34	22.2	95.00%	R.STPSLVSYGER.S		R.STPSLVSYGER.S
159	173	2	1534.89	4	1	42.9	10	95.00%	R.ALLEAANIAGLNPLR.L		R.ALLEAANIAGLNPLR.L
96	106	2	1134.6	4	1	31.7	21.5	95.00%	K.LTEVDGFVGAK.V		K.LTEVDGFVGAK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
71	ACON_SCHPO	11.57%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
435	452	2	1870.92	3.4	0	66.7	21.7	95.00%	K.AGGIVLANACGPCIGQWK.R	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.AGGIVLANACGPCIGQWK.R
532	549	2	1853.89	4.6	0	68.9	22	95.00%	K.GYDPGSNTYVAPSSVNVK.D		K.GYDPGSNTYVAPSSVNVK.D
392	402	2	1203.6	5.2	0	35.2	21.6	95.00%	R.AASICQQAIDK.G	Carbamidomethyl (+57)	R.AASICQQAIDK.G
65	80	2	1895.94	2.6	1	48.9	21.5	95.00%	K.ILYGHLDDPVNQDIER.G		K.ILYGHLDDPVNQDIER.G
462	470	2	1052.53	5	0	36.5	21.1	95.00%	K.NSIVTSYNR.N		K.NSIVTSYNR.N
603	620	2	1957.94	4.4	0	34.8	22.6	95.00%	R.GHLQNISNNYMIGAINAE.N		R.GHLQNISNNYMIGAINAENGEANK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
72	YF19_SCHPO	22.07%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
122	132	2	1208.53	4.1	0	34.4	22.5	95.00%	R.GDVQAAADCFR.Y	Carbamidomethyl (+57)	R.GDVQAAADCFR.Y
195	208	2	1516.82	4.7	1	34.9	18	95.00%	K.TAELTPLSALCLTK.F	Carbamidomethyl (+57)	K.TAELTPLSALCLTK.F
333	349	2	1794.85	1.9	1	47.6	23	95.00%	K.VGDPFAEDTFQGAQVSK.Q		K.VGDPFAEDTFQGAQVSK.Q
5	17	2	1406.78	4.6	1	33	15.7	95.00%	K.LVDHVEITVPTGK.T		K.LVDHVEITVPTGK.T
422	443	3	2229.12	4.1	0	21.2	20.4	90.20%	R.GNNSTYGLAAGVHTNNITNAIK.V		R.GNNSTYGLAAGVHTNNITNAIK.V
94	103	2	1203.55	3.1	1	25.8	22.6	92.00%	R.LADCIEQNLE.Y	Carbamidomethyl (+57)	R.LADCIEQNLEYLASIETLDNGK.S
71	80	2	1161.56	3.7	0	28.3	22.2	95.00%	R.AAFQTDAPWR.K		R.AAFQTDAPWR.K
181	194	2	1439.82	3.6	0	42.9	14.8	95.00%	K.IAPAVACGNTIILK.T	Carbamidomethyl (+57)	K.IAPAVACGNTIILK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
73	LEUC_SCHPO	11.61%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
633	649	2	2002.01	4.5	0	59.4	21.4	95.00%	R.VIIAPSFADIFFNNCFK.N	Carbamidomethyl (+57)	R.VIIAPSFADIFFNNCFK.N
603	619	3	1826.86	5.3	0	37.3	22.5	95.00%	R.HATVLVAHDNFGCGSSR.E	Carbamidomethyl (+57)	R.HATVLVAHDNFGCGSSR.E
477	493	2	1810.88	4.1	1	36.5	21.8	95.00%	R.EFFGDVSNGSPSIITNK.N		R.EFFGDVSNGSPSIITNK.N
650	667	2	2027	4	1	40.9	20.6	95.00%	K.NGMLPIPTPIEQVNDMMK.A		K.NGMLPIPTPIEQVNDMMK.A
545	563	2	1963.09	3	1	46.8	12.3	95.00%	E.GIAAPLPMANVDTDKIIPK.Q		K.FTVVEGIAAPLPMANVDTDKIIPK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
74	GCST_SCHPO	18.86%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
34	51	2	1940.98	3.3	1	26.8	20.1	93.40%	K.EGATIVPFAGFSMPVQYK.G		K.EGATIVPFAGFSMPVQYK.G
165	180	2	1623.93	4	1	75.8	12.8	95.00%	R.ALIAIQGPETASVVQK.L		R.ALIAIQGPETASVVQK.L
273	281	2	959.55	2.8	0	26.9	18	93.50%	E.GSLSWIIGK.R		R.LEAGMCLYGSDIDDTTSPVEGSLSWIIGK.R

330	344	2	1486.75	3.2	0	51	20.3	95.00%	E.VGQVTSGCPSPTLGK.N	Carbamidomethyl (+57)	R.HGSAVEVDGVEVGQVTSGCPSPTLGK.N
113	127	2	1603.8	4	1	47.9	21.4	95.00%	E.TGGIIDDTIISKQDE.N		K.ELKPFHSTLSAFTNETGGIIDDTIISKQDENTYYIVTNAACSEK.D
113	124	2	1231.67	2.3	0	27	19.1	93.60%	E.TGGIIDDTIISK.Q		K.ELKPFHSTLSAFTNETGGIIDDTIISK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
75	RS6B_SCHPO	22.59%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
211	217	2	807.43	3.6	0	26	17.6	92.10%	E.FAQLMAK.R		R.EEAAEFAQLMAK.R
99	115	2	1739.01	3.8	0	65.7	12.3	95.00%	R.GCIVGQDLAVLALAIVK.Q	Carbamidomethyl (+57)	R.GCIVGQDLAVLALAIVK.Q
116	131	2	1695.88	3.9	1	43.6	19.3	95.00%	K.QGEQDIPGLTDVTVPK.R		K.QGEQDIPGLTDVTVPK.R
59	72	3	1625.86	4.7	0	32.2	19.7	95.00%	K.QGFPMFQGVLLPHR.V		K.QGFPMFQGVLLPHR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
76	GLNA_SCHPO	28.69%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
60	91	3	3497.64	3.1	0	54.8	22	95.00%	R.VWNFDGSSTGQAPGNNSDTLLKPVAMYNDPFR.R		R.VWNFDGSSTGQAPGNNSDTLLKPVAMYNDPFR.R
338	354	2	1830.98	3.3	0	65.1	17.2	95.00%	R.RPASSIDPYLVTGIITE.T		R.RPASSIDPYLVTGIITETMFEH.-
153	170	2	1809.83	4.4	0	40.7	23.2	95.00%	K.GGFPGPQGPFYCGVGTGR.V	Carbamidomethyl (+57)	K.GGFPGPQGPFYCGVGTGR.V
237	260	4	2635.31	3.2	0	28.9	20.3	95.00%	K.ISFHPKPILGDWNGAGCHTNVSTK.D	Carbamidomethyl (+57)	K.ISFHPKPILGDWNGAGCHTNVSTK.D
285	296	2	1386.66	2.2	0	37.5	22.1	95.00%	E.HIAVYGDDNDLR.L		K.EHIAVYGDDNDLR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
77	O59743_SCHPO	15.29%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
127	136	2	1252.56	2.7	0	38.5	23.1	95.00%	E.YYHLSAPDCK.S	Carbamidomethyl (+57)	K.LKPVPTSWEQALQDNKPEEYYHLSAPDCK.S
210	225	2	1690.88	3.5	0	52.7	20.2	95.00%	R.SIQDVPFTSATVDIAK.K		R.SIQDVPFTSATVDIAK.K
1	11	2	1319.72	4	1	28	19.1	94.70%	-.MDPYTVAIIKK.L	Acetyl (+42)	-.MDPYTVAIIKK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
78	GCSP_SCHPO	13.86%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
953	965	2	1458.76	1.1	0	43.1	19.1	95.00%	K.DNNLLVNAPHPQK.D		K.DNNLLVNAPHPQK.D
657	684	3	2835.49	3.7	0	27.8	14.9	95.00%	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C	Carbamidomethyl (+57)	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C
114	126	2	1433.73	3.5	0	49.6	21	95.00%	E.FTTLANNVANQNK.L		K.NPPVNYSESEFTTLANNVANQNK.L
379	412	3	3679.8	2.3	1	51.4	19.4	95.00%	K.ATSNICTAQALLANMSAFYAIYHGPNGLQEIANR.I	Carbamidomethyl (+57)	K.ATSNICTAQALLANMSAFYAIYHGPNGLQEIANR.I
1000	1017	2	2072.93	3.3	1	37.5	23.4	95.00%	R.LDDAYGDKNLFCTCSPVV.-	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.LDDAYGDKNLFCTCSPVV.-
583	600	2	2083.03	3	0	47.9	20.1	95.00%	E.MMPITNPLFANIHPYVPE.E		K.LNAVTEMMPITNPLFANIHPYVPEEQAK.G
560	576	2	1831.87	2.2	0	47.9	23.7	95.00%	K.DLSLAHAMTPLGSCTMK.L	Carbamidomethyl (+57)	K.DLSLAHAMTPLGSCTMK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
79	SPI1_SCHPO	23.15%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
203	216	2	1442.63	4.3	1	44	23.2	95.00%	E.AAAMPLPDEDDADL.-		K.LVGNPNLEFVASPALAPPEVQVDQQLLAQYQQEMNEAAAMPLPDEDDADL.-
110	122	2	1514.77	4.6	1	58.5	21	95.00%	R.VCENIPIVLCGNK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VCENIPIVLCGNK.V
152	165	3	1783.91	4.6	1	29.2	20.2	95.00%	K.SNYNFEKPFLWLAR.K		K.SNYNFEKPFLWLAR.K

166	174	2	982.55	4	1	55.1	16.7	95.00%	R.KLVGNPNLE.F		R.KLVGNPNLEFVASPALAPPEVQVDQQLLAQYQQEMNEAAAMPLPDEDDADL.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
80	AROG_SCHPO	24.73%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
199	226	3	2704.36	2.1	0	47.7	19.4	95.00%	K.NGTDGTVGVAIDAIGATAHPHTMLGVTK.Q	Deamidation (+1)	K.NGTDGTVGVAIDAIGATAHPHTMLGVTK.Q
350	363	2	1528.76	3.6	1	43.4	21.8	95.00%	E.QTAPMLDDLAEAVR.A		K.YGVSITDACVSWEQTAPMLDDLAEAVR.A
187	198	2	1235.69	2.7	0	40.8	16	95.00%	E.LASALSFPVGFK.N		R.ELASALSFPVGFK.N
118	133	2	1672.85	3.8	0	36.7	20.3	95.00%	K.GLVNDPNLDGSFAINK.G		K.GLVNDPNLDGSFAINK.G
22	42	2	2235.22	3.7	1	35.3	13.6	95.00%	R.VLGYNPLVPAALVQQEIPVSE.T		R.VLGYNPLVPAALVQQEIPVSETSR.K
186	198	2	1364.74	2.5	1	40.5	19.4	95.00%	R.ELASALSFPVGFK.N		R.ELASALSFPVGFK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
81	VATA_SCHPO	14.38%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
150	165	2	1620.75	3.5	0	34.3	23.2	95.00%	R.IGDHVSGGDVFGSVFE.N		R.IGDHVSGGDVFGSVFENSLFNDHK.I
128	136	2	1002.51	5	1	25.2	21.1	90.90%	R.GINTESLNR.E		R.GINTESLNR.E
77	88	2	1228.65	3.3	0	27.1	20.1	93.70%	E.TSGLTVGDPVQR.T		K.CTIQVYEETSGLTVGDPVQR.T
373	389	2	1752.85	8	1	36.9	21.8	95.00%	R.LAEMPADSGYPAYLGAK.L		R.LAEMPADSGYPAYLGAK.L
317	331	2	1544.81	4.6	0	49.4	19.5	95.00%	R.TTLVANTSNMPVAAR.E		R.TTLVANTSNMPVAAR.E
221	240	3	2105.14	4.1	0	35.3	16.8	95.00%	R.AARPVADNLTANQPLLTGQR.V		R.AARPVADNLTANQPLLTGQR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
82	RS0B_SCHPO	32.75%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	88	4	2453.26	4	1	67.3	19.5	95.00%	R.VIATIENPADVCVISSRPYGHR.A	Carbamidomethyl (+57)	R.VIATIENPADVCVISSRPYGHR.A
4	31	3	2920.53	2.8	1	73.7	15.4	95.00%	E.SIARPSVLNATDDDIKNLLAADSHIGSK.N		-.MAESIARPSVLNATDDDIKNLLAADSHIGSK.N
231	241	2	1043.53	3.3	0	26.8	20.5	93.40%	E.AQLAAQTAAAE.F		K.AAAAAAAEEEAQLAAQTAAAEFEVTDSAAGTVDPTILDNATAGQVGQTTWEGDAEWNITGAAPSEWA.-
139	169	3	3390.76	4.3	1	25.4	14.6	95.00%	K.EASFVNIPVIALCDTDSILNHVDVAIPINNK.G	Carbamidomethyl (+57)	K.EASFVNIPVIALCDTDSILNHVDVAIPINNK.G
231	243	2	1319.64	5.7	1	70.6	21.7	95.00%	E.AQLAAQTAAAEFE.V		K.AAAAAAAEEEAQLAAQTAAAEFEVTDSAAGTVDPTILDNATAGQVGQTTWEGDAEWNITGAAPSEWA.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
83	THI4_SCHPO	17.57%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
310	338	3	3045.65	3.6	0	44.4	12.8	95.00%	K.TYIHAAQVNNDLARPVILDPVAVGATTAR.S		K.TYIHAAQVNNDLARPVILDPVAVGATTAR.S
373	385	2	1353.71	4.1	0	37.5	19.4	95.00%	R.GVDSISQHTLAAR.I		R.GVDSISQHTLAAR.I
121	140	2	2014.96	4.4	1	70	23	95.00%	K.AAADGADYVGIGSIYETNTK.D		K.AAADGADYVGIGSIYETNTK.D
249	265	4	1917.09	3.2	1	33.8	11.8	95.00%	K.LKDFTPLIHHLTNAVAK.N		K.LKDFTPLIHHLTNAVAK.N
237	248	2	1322.76	4.7	0	31.5	13	95.00%	K.DLLNQIPAALQK.L		K.DLLNQIPAALQK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
84	MMF1_SCHPO	35.80%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
59	75	2	1747.86	2.8	0	34.8	21.7	95.00%	K.ANGVIYCSGQIPVANGK.V	Carbamidomethyl (+57)/ Deamidation (+1)	K.ANGVIYCSGQIPVANGK.V
109	124	2	1781.87	4.4	0	46.5	22.1	95.00%	K.VNIFLADMDDFAAVNK.V		K.VNIFLADMDDFAAVNK.V
125	137	2	1483.81	3.9	1	42.4	16.6	95.00%	K.VYTEVLPDPKPAR.S		K.VYTEVLPDPKPAR.S
47	58	2	1247.66	5.3	0	27.4	19.2	94.10%	K.LSSAGPYNQAIK.A		K.LSSAGPYNQAIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
85	TRP_SCHPO	14.49%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
382	393	2	1355.77	4.5	0	47.2	17	95.00%	K.INNCIGQILLAK.R	Carbamidomethyl (+57)	K.INNCIGQILLAK.R
275	296	2	2168.08	2.9	0	54.9	21.1	95.00%	K.QFQSGGSVATAPPAAVVEPINE.M		K.QFQSGGSVATAPPAAVVEPINEMYLPQK.Y
400	419	3	1938.01	4.3	1	37.5	18.9	95.00%	R.IIAETGAGQHGVATAICAAK.F	Carbamidomethyl (+57)	R.IIAETGAGQHGVATAICAAK.F
275	302	3	2928.48	4.6	1	34.9	19.2	95.00%	K.QFQSGGSVATAPPAAVVEPINEMYLPQK.Y		K.QFQSGGSVATAPPAAVVEPINEMYLPQK.Y
445	461	2	1739.99	4	1	48.6	13.4	95.00%	R.LLGAEVVPVTSGTQTLR.D		R.LLGAEVVPVTSGTQTLR.D
91	114	2	2617.33	5.8	0	82.3	19.1	95.00%	R.DAGVTIPIILMGYYNPIFSYGDAK.T		R.DAGVTIPIILMGYYNPIFSYGDAK.T
450	461	2	1256.71	3.3	0	35.7	16.8	95.00%	E.VVPVTSGTQTLR.D		R.LLGAEVVPVTSGTQTLR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
86	LYS12_SCHPO	16.30%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
197	208	2	1324.65	5.3	0	41.8	22.1	95.00%	K.SNVMSVTDGLFR.E		K.SNVMSVTDGLFR.E
298	307	2	1044.58	4.6	0	32.2	19.6	95.00%	R.GIANPVATFR.S		R.GIANPVATFR.S
213	228	2	1744.79	1.9	0	31.5	24.1	95.00%	R.HAQSLDPSYASINVDE.Q		R.HAQSLDPSYASINVDEQIVDSMVYR.L
188	196	3	1047.69	4.7	0	25.1	3.01	95.00%	K.KPLVTIIHK.S		K.KPLVTIIHK.S
86	97	2	1231.7	4.7	0	25.9	15.2	92.10%	K.VAGYSSPIVALR.K		K.VAGYSSPIVALR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
87	RL1B_SCHPO	24.54%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
54	75	3	2486.26	2.6	0	38.3	19.8	95.00%	K.LPNVPRPNMAICILGDAHDLDR.A	Carbamidomethyl (+57)	K.LPNVPRPNMAICILGDAHDLDR.A
78	91	3	1486.71	4	1	36.7	22.9	95.00%	K.HGGVDAMSVDDLKK.L	Oxidation (+16)	K.HGGVDAMSVDDLKK.L
130	146	3	1787.89	3.1	1	22.6	21	92.80%	K.AGKFPSPVSHADDLYGK.I		K.AGKFPSPVSHADDLYGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
88	RL10A_SCHPO	20.36%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	128	3	1265.71	4.6	0	30	16	95.00%	R.HAFGKPNGLVAR.V		R.HAFGKPNGLVAR.V
41	56	2	1798.86	3.2	1	42.4	22.2	95.00%	R.AGVDEFPLCIHLVSNE.Y	Carbamidomethyl (+57)	R.AGVDEFPLCIHLVSNEYEQITSEALEAAR.I
129	139	2	1228.7	4.7	0	40	16.9	95.00%	R.VNIGQILMSVR.T		R.VNIGQILMSVR.T
33	38	2	719.4	4.8	0	27.1	17.3	93.70%	R.IFDLGR.K		R.IFDLGR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
89	BCA1_SCHPO	17.11%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
315	331	2	1670.97	4.2	1	59.5	11.5	95.00%	R.LLEVFGAGTAALVSPVK.A		R.LLEVFGAGTAALVSPVK.A
37	49	3	1581.74	4.5	1	25.4	22.9	95.00%	K.FGENFTDHMLIMK.W		K.FGENFTDHMLIMK.W
318	331	2	1315.75	2.9	0	57.6	15.8	95.00%	E.VFGAGTAALVSPVK.A		R.LLEVFGAGTAALVSPVK.A
262	278	2	1795	4.2	1	43.3	14	95.00%	K.EIITAPLDGMILPGVTR.D		K.EIITAPLDGMILPGVTR.D
2	19	4	1916	3.8	0	19.2	19.5	95.00%	M.VQTAALHGPKPMDSSHIK.V		-.MVQTAALHGPKPMDSSHIK.V
263	278	2	1665.95	2.7	0	68.9	11.8	95.00%	E.IITAPLDGMILPGVTR.D		K.EIITAPLDGMILPGVTR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
90	RL15A_SCHPO	19.90%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
115	128	2	1699.83	4.1	0	73.6	21.7	95.00%	R.VLNSYWVNQDATYK.F		R.VLNSYWVNQDATYK.F
78	93	3	1761.94	4.8	0	23.7	19.4	94.30%	K.GQTYGKPVHQGVNHLK.Y		K.GQTYGKPVHQGVNHLK.Y
148	157	3	1218.69	4.4	0	24.4	16	95.00%	R.INWIVNPVHK.H		R.INWIVNPVHK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
91	TAL1_SCHPO	16.15%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
27	44	2	1917.03	3.2	0	71.3	17.3	95.00%	K.YKPQDATTNPSLILAASK.K		K.YKPQDATTNPSLILAASK.K
9	26	2	1795.89	4.5	1	86.8	21.4	95.00%	K.ATGTVVVSDTGDFESIAK.Y		K.ATGTVVVSDTGDFESIAK.Y
45	60	2	1721.91	3.6	0	82.8	18.1	95.00%	K.KPQYAALVDAAVDYAK.A		K.KPQYAALVDAAVDYAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
92	RL13_SCHPO	25.96%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
172	183	2	1398.66	5.4	1	54	22.9	95.00%	K.NFNAFSTLSNER.A		K.NFNAFSTLSNER.A
118	128	3	1326.79	4.7	0	51.2	12.3	95.00%	K.VYLAHLIVFPR.K		K.VYLAHLIVFPR.K
46	64	4	2080.27	3.1	1	20	0	95.00%	K.IAPRPVEAIRPAVKPPTIR.Y		K.IAPRPVEAIRPAVKPPTIR.Y
89	100	2	1263.7	3.9	0	28.9	18.6	95.00%	R.VASTIGIPVDHR.R		R.VASTIGIPVDHR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
93	PYC_SCHPO	5.74%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
829	838	2	1275.63	4.5	1	27.7	21.6	94.40%	K.QLEFDNNQLR.E		K.QLEFDNNQLR.E
1109	1129	3	2088.05	4.4	1	38.2	20.4	95.00%	R.ADPGNPGHVAAPMSGTIVEIR.V		R.ADPGNPGHVAAPMSGTIVEIR.V
917	929	2	1447.76	4.7	0	42.2	19.7	95.00%	K.VVGDLAQFMVQNK.L		K.VVGDLAQFMVQNK.L
302	315	2	1628.75	2	1	37.3	23.4	95.00%	K.YCNAGTAEFLLDQK.G	Carbamidomethyl (+57)	K.YCNAGTAEFLLDQK.G
839	848	2	1297.58	4.8	1	38.2	22.4	95.00%	R.EIDSYWAQMR.L		R.EIDSYWAQMR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
94	RAD24_SCHPO	9.63%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
109	120	2	1236.65	4.7	1	29.1	19.1	95.00%	K.HLIPNAASAESK.V		K.HLIPNAASAESK.V
95	108	2	1659.88	3.1	1	61.2	18.8	95.00%	E.LDTICQDILTVLEK.H	Carbamidomethyl (+57)	K.IEQELDTICQDILTVLEK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
95	EF1G_SCHPO	16.14%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
93	115	3	2635.37	2.6	1	24.6	16.4	95.00%	K.VLQYCSFTNSELPGAFRPIIAPR.V	Carbamidomethyl (+57)	K.VLQYCSFTNSELPGAFRPIIAPR.V
207	216	2	1182.71	4	0	27.1	14.1	93.80%	K.FIDQPLPIIK.A		K.FIDQPLPIIK.A
355	375	3	2372.08	3.3	0	25.1	23.6	95.00%	K.GHDYVPAFDVAPDWGSYTFTK.L		K.GHDYVPAFDVAPDWGSYTFTK.L
116	127	2	1294.63	4.3	1	26.2	21.5	92.50%	R.VFGAPYDEQAAK.E		R.VFGAPYDEQAAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
96	RS2_SCHPO	28.85%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
242	251	2	1210.6	3.9	1	46	22	95.00%	E.YADILMQTEK.K		K.AAFAAASLTYGILTPNLWAERPF GQTPIEEYADILMQTEK.K
64	74	2	1441.73	5.7	1	25.1	20.7	90.60%	K.EYQIVDYFLPR.L		K.EYQIVDYFLPR.L
55	64	2	1237.7	2.3	1	43.5	16	95.00%	E.IYLYSLPIKE.Y		K.SIEEIYLYSLPIKEYQIVDYFLPR.L
174	185	3	1138.69	4.8	1	25.2	10	95.00%	R.GAGLVAAPVTKR.F		R.GAGLVAAPVTKR.F
186	200	2	1799.86	4.8	1	102	22.5	95.00%	R.FLQLAGIEDCYTQSR.G	Carbamidomethyl (+57)	R.FLQLAGIEDCYTQSR.G
141	156	3	1696.87	4.8	0	37.6	20.5	95.00%	R.GYWGTALGDPHTVPVK.V		R.GYWGTALGDPHTVPVK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
97	RS14_SCHPO	35.25%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
76	84	2	950.59	2.9	0	30.3	6.99	95.00%	E.VGITALHIK.I		K.EVGITALHIK.I
117	129	2	1442.73	3.7	1	46.5	21.3	95.00%	R.IEDVTPIPTDSTR.R		R.IEDVTPIPTDSTR.R
57	72	2	1564.76	2.6	0	67.8	22.9	95.00%	E.SSPYAAMLAAQDAAAK.C		R.DESSPYAAMLAAQDAAAK.C
95	105	2	1037.57	5.3	0	47.1	18.2	95.00%	K.TPGPGAQAALR.A		K.TPGPGAQAALR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
98	TCTP_SCHPO	21.43%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
6	21	2	1737.84	4.2	1	86.5	23.1	95.00%	K.DVISGDELVSDAYDLK.E		K.DVISGDELVSDAYDLK.E
13	22	2	1151.57	3.2	1	31.4	22.1	95.00%	E.LVSDAYDLKE.V		K.DVISGDELVSDAYDLKEVDDIVYEADCQMVTVK.Q
30	38	2	1050.49	3.7	0	25.6	21.8	91.60%	E.ADCQMVTVK.Q	Carbamidomethyl (+57)	K.EVDDIVYEADCQMVTVK.Q
64	73	2	1211.63	3.5	0	55.3	20.2	95.00%	E.TVNNLVYSFR.L		K.QGGDVDIGANPSAEDAEENAEEGTETVNNLVYSFR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
99	SERC_SCHPO	12.85%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
175	184	2	1155.6	3.2	0	29	20.3	95.00%	E.FNEPPTNIPK.G		K.FTPDGETSLVYYCDNETVHGVEFNEPPTNIPK.G
376	385	2	1147.65	4.7	1	32.8	14.5	95.00%	R.LIDLLESFAK.A		R.LIDLLESFAK.A
216	228	2	1299.74	5	0	37	14.9	95.00%	K.NAGPAGITVVFVR.D		K.NAGPAGITVVFVR.D
189	199	2	1282.6	4.3	0	67	22.5	95.00%	R.VCDVSSNFISR.K	Carbamidomethyl (+57)	R.VCDVSSNFISR.K
324	329	2	766.38	5.3	0	26.2	20	92.50%	R.MNVTFR.I		R.MNVTFR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
100	PUR8_SCHPO	10.17%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
226	242	2	1930.91	3.5	0	32.6	23.4	95.00%	K.LSGFDNVYPVTGQTYDR.K		K.LSGFDNVYPVTGQTYDR.K
437	449	2	1392.73	3.3	0	33.6	20.1	95.00%	E.LDSLLDASTFVGR.A		K.NTPYFAPIYDELDSLLDASTFVGR.A
243	261	3	2023.12	3.6	1	64	14.3	95.00%	R.KIDIDVLQPLASFGATAHK.I		R.KIDIDVLQPLASFGATAHK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
101	RL23_SCHPO	25.18%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
15	34	2	2106	3	0	87.4	22.3	95.00%	R.MTLGLPVQAIMNCADNSGAK.N	Oxidation (+16)/ Carbamidomethyl (+57)	R.MTLGLPVQAIMNCADNSGAK.N
51	65	2	1531.78	3.4	0	55.2	20.6	95.00%	R.LPAASCGDMVLATVK.K	Carbamidomethyl (+57)	R.LPAASCGDMVLATVK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
102	RS22_SCHPO	27.69%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
98	108	2	1171.7	4.9	0	29.1	13.2	95.00%	R.QVGVIVLTTSR.G		R.QVGVIVLTTSR.G
4	19	2	1814.9	4.5	1	77.6	21.1	95.00%	R.QSVLADCLNNIVNAER.R	Carbamidomethyl (+57)	R.QSVLADCLNNIVNAER.R
89	97	2	1111.62	5.6	0	31.9	15.9	95.00%	K.WVNQLLPSR.Q		K.WVNQLLPSR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
103	RL6_SCHPO	22.05%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	64	2	1497.84	5	0	33.1	16.2	95.00%	R.ASLAPGTVCILLAGR.F	Carbamidomethyl (+57)	R.ASLAPGTVCILLAGR.F
78	87	2	1091.59	3.1	0	31.5	20	95.00%	E.DTLVVTGPYK.V		R.VVVLSQLEDTLVVTGPYK.V
70	87	2	1959.1	3.1	1	33.6	14.3	95.00%	R.VVVLSQLEDTLVVTGPYK.V		R.VVVLSQLEDTLVVTGPYK.V
109	118	2	1031.56	5.5	1	31.2	19.9	95.00%	K.IDVSGVSVEK.F		K.IDVSGVSVEK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
104	PYR1_SCHPO	2.27%	100%	4									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
1135	1145	2	1229.6	4.3	0	46.2	22.2	95.00%	R.MLDDIGVDQPK.W		R.MLDDIGVDQPK.W		
234	245	2	1342.75	3.5	1	25.3	17.6	91.10%	E.NLTSQVSIKEPK.L		K.NPNTENLTSQVSIKEPK.L		
1758	1770	2	1371.7	4.4	0	56.2	21.2	95.00%	K.FVGNTAFTGFGVR.E		K.FVGNTAFTGFGVR.E		
1804	1818	3	1724.81	5.5	1	27.4	22.6	95.00%	R.LHDQDDSGVQLEVDR.S		R.LHDQDDSGVQLEVDR.S		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
105	RS4B_SCHPO	8.40%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
222	233	2	1232.68	5.6	1	42.4	17.6	95.00%	R.LSNVFVIGEAGK.S		R.LSNVFVIGEAGK.S		
40	49	2	1258.72	4.1	1	26.3	16.8	92.60%	R.ECLPLIVFLR.N	Carbamidomethyl (+57)	R.ECLPLIVFLR.N		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
106	GLT1_SCHPO	2.79%	100%	3									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
108	125	2	1904.82	2.6	0	33.6	24.4	95.00%	R.DGDGAGVMTGMPYTFMQK.E		R.DGDGAGVMTGMPYTFMQK.E		
1897	1918	3	2189.08	3.9	1	55	21.2	95.00%	K.GKDVIVIGGGDTGNDCLGTSVR.H	Carbamidomethyl (+57)	K.GKDVIVIGGGDTGNDCLGTSVR.H		
1758	1776	2	1792.99	3.2	0	90.9	15.7	95.00%	R.VAIIGSGPAGLAAADQLNR.A		R.VAIIGSGPAGLAAADQLNR.A		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
107	PURA_SCHPO	12.67%	100%	4									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
295	304	2	1080.57	3.4	0	33.6	18.6	95.00%	E.IGDHLQSVGR.E		R.VGAGPFPTEQLNEIGDHLQSVGR.E		
206	224	3	2169.16	3.6	1	37.8	15.7	95.00%	R.LKPFVIDAVAFMYEALQSK.K		R.LKPFVIDAVAFMYEALQSK.K		
268	276	2	899.55	4.9	0	44.5	17.2	95.00%	R.IANSIGVVK.A		R.IANSIGVVK.A		
413	429	2	1758.94	4.4	1	27	18	93.60%	K.FVGVPITFIGVGPGRDE.M		K.FVGVPITFIGVGPGRDEMLVK.E		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
108	RL3A_SCHPO	14.43%	100%	4									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
11	19	2	982.54	4.3	0	27.2	18.1	93.80%	R.HGSLGFLPR.K		R.HGSLGFLPR.K		
181	193	2	1315.67	3.6	1	48.3	21.3	95.00%	E.IQVNGGSVADKVE.W	Deamidation (+1)	K.AHLMEIQVNGGSVADKVEWAR.E		
319	334	3	1715.87	2.7	1	35.2	21.1	95.00%	E.NDFVMLNGATPGPVKR.V	Deamidation (+1)	R.YGVVENDFVMLNGATPGPVKR.V		
249	266	3	2035.03	4.4	0	29.3	21	95.00%	K.VACIGAWHPANVQWTVAR.A	Carbamidomethyl (+57)	K.VACIGAWHPANVQWTVAR.A		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
109	PMP20_SCHPO	26.92%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
30	55	2	2747.41	3.6	1	41.6	18.9	95.00%	K.FIIVGVPGAFTPPCSSQVPGYIANEK.Q	Carbamidomethyl (+57)	K.FIIVGVPGAFTPPCSSQVPGYIANEK.Q		
141	156	2	1647.86	3.8	1	49.9	20.2	95.00%	E.VTDVDISSADKVLSSL.-		K.VFIENEVTDVDISSADKVLSSL.-		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
110	TRX1_SCHPO	27.18%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
67	79	2	1466.74	3.4	0	31.2	21.1	95.00%	E.AGVHAMPSFFLYK.N		K.VDVDQLSEIAAEAGVHAMPSFFLYK.N		
40	54	2	1796.83	4.6	1	68.4	23.3	95.00%	K.FEQFSNTYSDATFIK.V		K.FEQFSNTYSDATFIK.V		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
111	SYKC_SCHPO	8.12%	100%	3									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
581	591	2	1169.63	3.6	1	63.8	18.8	95.00%	E.VQAAEPTVVKE.-		R.EVLLFPHMKPEVQAAEPTVVKE.-		

15	28	2	1454.8	4	1	41.2	16.8	95.00%	K.ALVLDPVTGEQVSK.T		K.ALVLDPVTGEQVSK.T
154	176	4	2682.24	3.7	1	34.1	23.3	95.00%	K.LQVMCQAQDADTVDFAAQHEHLR.R	Carbamidomethyl (+57)	K.LQVMCQAQDADTVDFAAQHEHLR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
112	THI22_SCHPO	8.17%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
134	151	2	1829.99	3.2	0	88.2	17.1	95.00%	K.LVVDPVMVATSGDSLVTK.D		K.LVVDPVMVATSGDSLVTK.D
9	18	2	1149.55	3.8	0	29.1	21.9	95.00%	E.SLSNQFDPSR.I		-.MPYNPLYESLSNQFDPSR.I
181	197	2	1890.88	4.9	1	111	22.6	95.00%	K.NQGLDISNINSVSDMER.C		K.NQGLDISNINSVSDMER.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
113	RS23_SCHPO	20.28%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	137	2	1326.74	4.4	1	55.5	17.4	95.00%	K.VAGVGLSALFHEK.K		K.VAGVGLSALFHEK.K
81	96	2	1818.83	2.4	0	35.2	23.7	95.00%	K.VTAFVPHDGCLNFVDE.N	Carbamidomethyl (+57)	K.VTAFVPHDGCLNFVDENDEVLLSGFGR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
114	RS8A_SCHPO	35.50%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
60	74	2	1568.72	4.4	1	94.1	23.2	95.00%	R.LDSGNFSWGSEGVSK.K		R.LDSGNFSWGSEGVSK.K
165	178	2	1475.79	4.1	0	33.2	18.5	95.00%	R.LYAVVSSRPGQSGR.C		R.LYAVVSSRPGQSGR.C
152	164	2	1363.68	4.8	1	51.3	21.6	95.00%	K.VDSALETQFAAGR.L		K.VDSALETQFAAGR.L
78	92	2	1751.94	4.6	1	25.6	16.8	91.60%	R.IIQVAYHPSNNELVR.T		R.IIQVAYHPSNNELVR.T
111	124	3	1682.82	4.5	1	23.1	22	93.50%	R.VWYETHYGILMGSK.G		R.VWYETHYGILMGSK.G
78	89	2	1383.68	3.9	0	32.6	21.7	95.00%	R.IIQVAYHPSNNE.L		R.IIQVAYHPSNNELVR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
115	SODC_SCHPO	40.26%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
98	116	2	1984.04	4.4	0	72.6	18.1	95.00%	K.TTFSDSVISLFGANSIIGR.T		K.TTFSDSVISLFGANSIIGR.T
81	97	2	1765.87	4	1	72.3	21.9	95.00%	R.HVGDLGNLESDAQGNIK.T		R.HVGDLGNLESDAQGNIK.T
45	70	3	2825.25	4.3	1	41.5	23.6	95.00%	R.GFHIHQFGDNTNGCTSAGPHFNPEGK.T	Carbamidomethyl (+57)	R.GFHIHQFGDNTNGCTSAGPHFNPEGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
116	YA03_SCHPO	18.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
82	97	2	1778.89	2.6	1	39.5	21.3	95.00%	E.GGPDKVPVYISPFFQE.V		K.YLAEGGPDKVPVYISPFFQEVGHLPCDIGLELDK.L
181	194	2	1560.83	4.5	0	43.8	19.8	95.00%	K.AADIDFLPPQLSFK.N		K.AADIDFLPPQLSFK.N
98	108	2	1208.59	2.8	0	33.8	22.4	95.00%	E.VGHLPCDIGLE.L	Carbamidomethyl (+57)	K.VPVYISPFFQEVGHLPCDIGLELDK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
117	LEU1_SCHPO	9.08%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
464	479	2	1742.82	4.9	0	69.1	22.8	95.00%	R.FSVNDYTLSSNGPQSK.C		R.FSVNDYTLSSNGPQSK.C
341	362	3	2346.15	2.9	0	44.7	21.6	95.00%	R.HPYAGNLVFTAFSGSHQDAISK.G		R.HPYAGNLVFTAFSGSHQDAISK.G
137	151	3	1761.87	4	0	33.2	22.6	95.00%	K.NATVHLYNACSPLFR.E	Carbamidomethyl (+57)	K.NATVHLYNACSPLFR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
118	HMCS_SCHPO	14.77%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
264	277	2	1505.69	2.5	0	25.3	23	91.10%	R.LLYTDSAAEPSNPE.L		R.LLYTDSAAEPSNPELEGVR.E
155	183	3	2859.53	3.9	0	40.5	14.9	95.00%	K.GNARPTGGAGCVALLVGPNAPIVFEPGLR.G	Carbamidomethyl (+57)	K.GNARPTGGAGCVALLVGPNAPIVFEPGLR.G

382	392	3	1300.68	5.1	1	26	20	95.00%	K.KTNLVNDLDNR.H			K.KTNLVNDLDNR.H
217	228	2	1325.64	3.7	0	38.4	22.9	95.00%	K.ALDGAYANYNVR.D			K.ALDGAYANYNVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
119	DHE4_SCHPO	16.19%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
417	439	2	2411.16	5.2	0	85.7	21.5	95.00%	K.YCDSGSNNIPSLVDGANIAGFLK.V	Carbamidomethyl (+57)	K.YCDSGSNNIPSLVDGANIAGFLK.V
356	367	2	1231.57	4.5	1	27.7	22.1	94.40%	R.ASGEGCWLAPGK.A	Carbamidomethyl (+57)	R.ASGEGCWLAPGK.A
93	101	2	1127.61	5.6	1	29.2	19.5	95.00%	K.FLGFEQIFK.N		K.FLGFEQIFK.N
399	416	2	1950.98	4.6	1	78.4	20.5	95.00%	K.LAGIMQNIFEQSTDVASK.Y		K.LAGIMQNIFEQSTDVASK.Y
195	205	2	1218.63	3	0	35.1	20.2	95.00%	E.ATGYGVVYYVK.H		K.HMLTGGSNIRPEATGYGVVYYVK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
120	IMDH_SCHPO	8.97%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
303	313	2	1155.67	4.5	0	51.3	15.6	95.00%	K.IDVIAGNVVTR.E		K.IDVIAGNVVTR.E
214	234	3	2311.28	3.6	1	29.3	12	95.00%	K.LPVVDKDDNLVALLSLTDLMK.N		K.LPVVDKDDNLVALLSLTDLMK.N
419	433	2	1421.67	3.9	1	52.2	23.3	95.00%	R.GMGSIAAMEGTGVNK.N		R.GMGSIAAMEGTGVNK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
121	YHEF_SCHPO	6.40%	100%	1

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
54	65	2	1279.67	5.1	1	47	20.3	95.00%	K.SFIGLDALTESK.G		K.SFIGLDALTESKGEFFQR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
122	YCO6_SCHPO	11.45%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
15	36	3	2140.01	5.3	0	26.3	22.5	95.00%	K.MSAAPTPHNTPSGTSAPNFGAK.A		K.MSAAPTPHNTPSGTSAPNFGAK.A
57	66	2	1068.58	2.4	0	34	16.5	95.00%	K.LGSLLHLTSE.G		K.LGSLLHLTSEGVSELPEAVQR.R
233	245	2	1434.65	4.5	0	37.9	22.7	95.00%	E.SGPSNVFLYDHAE.G		K.TYYYMEESGPSNVFLYDHAEGDK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
123	VATB_SCHPO	12.72%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
439	449	2	1284.62	4.2	1	36.9	21.6	95.00%	K.TFISQGAYENR.T		K.TFISQGAYENR.T
146	162	2	1774.93	2.5	0	62.7	19.7	95.00%	E.MIQTGISSIDGLNSIAR.G		R.IYPEEMIQTGISSIDGLNSIAR.G
108	125	2	1840.96	3	1	26	19.6	92.10%	R.VFNGSGLPIDKGPNLLAE.D	Deamidation (+1)	R.VFNGSGLPIDKGPNLLAEDYLDINGSPINPYAR.I
42	59	3	2083.09	4.5	1	23.6	18.3	94.20%	R.RPQYNEIVNLNLPDGSVR.S		R.RPQYNEIVNLNLPDGSVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
124	ACL1_SCHPO	9.59%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
369	381	2	1420.73	4.5	1	44	20.7	95.00%	R.GSELTYNNVPISK.V		R.GSELTYNNVPISK.V
171	182	3	1338.74	4.8	0	23.6	16.8	94.20%	K.LYRPGSVAYVSK.S		K.LYRPGSVAYVSK.S
156	170	2	1506.72	3.3	0	45.7	23.3	95.00%	K.IGNTGGMMDNIVASK.L		K.IGNTGGMMDNIVASK.L
137	155	2	1926.08	3.9	0	66.3	9.03	95.00%	K.NVVIIGPATVGGIKPGCFK.I	Carbamidomethyl (+57)	K.NVVIIGPATVGGIKPGCFK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
125	ASNS_SCHPO	3.23%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
516	523	2	1035.55	6.3	1	30	18.5	95.00%	K.LFDEIFPR.Q		K.LFDEIFPR.Q
399	408	2	1120.54	4.9	1	26.3	20.4	92.60%	K.STMAWGLEAR.V		K.STMAWGLEAR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
126	RL27A_SCHPO	29.41%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	48	3	1461.76	5.9	1	42.8	19.7	95.00%	K.SHPFGHAVVAGVER.Y		K.SHPFGHAVVAGVER.Y
23	34	2	1269.74	4.4	0	65.4	14.1	95.00%	K.VVILQAIDQGSK.S		K.VVILQAIDQGSK.S
94	107	2	1575.83	3.5	1	46.7	20.2	95.00%	K.GLITADTFKEPTQR.S		K.GLITADTFKEPTQR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
127	RS17A_SCHPO	23.66%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	59	3	1133.6	4.6	0	24.5	19.6	95.00%	K.IAGYTTHLMK.R		K.IAGYTTHLMK.R
34	44	2	1156.68	4.8	1	51	15.2	95.00%	R.IVDEVAIIASK.R		R.IVDEVAIIASK.R
24	33	2	1234.67	4.6	1	36.3	17.9	95.00%	R.LTLDFQTNKR.I		R.LTLDFQTNKR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
128	RL2_SCHPO	17.79%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
92	108	2	1709.87	2.7	1	42.8	20.5	95.00%	K.NAALTVGNVLPVGEMPE.G		K.NAALTVGNVLPVGEMPEGTIISNVEEK.A
128	144	2	1759.88	3	0	62	21.3	95.00%	R.SSGNYVIIVGHDVDTGK.T		R.SSGNYVIIVGHDVDTGK.T
163	173	2	940.55	4.3	0	54.6	11.8	95.00%	R.GVVGIVAGGGR.I		R.GVVGIVAGGGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
129	PMM_SCHPO	15.56%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
210	220	2	1282.6	4.5	0	35.6	22.7	95.00%	E.GFDTIHFFGDK.T		K.EGFDTIHFFGDK.T
45	58	2	1347.75	4.4	0	41.6	17.1	95.00%	K.VVAIGFVGGSDLSK.Q		K.VVAIGFVGGSDLSK.Q
236	250	2	1568.74	2.4	0	30.1	22.9	95.00%	R.TIGHSVTNPDDTIAE.L		R.TIGHSVTNPDDTIAELK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
130	YHZ8_SCHPO	39.39%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
104	119	2	1691.85	3.4	1	30.2	21.6	95.00%	K.VVDGHLDKDNLGPDAK.D		K.VVDGHLDKDNLGPDAK.D
75	103	3	3217.69	3	0	57.2	16.4	95.00%	K.TSNPFLAFANYLTSTHAPLAEPLQLLNFK.V		K.TSNPFLAFANYLTSTHAPLAEPLQLLNFK.V
144	164	3	2285.2	2.9	0	37.9	18.5	95.00%	K.ADTSLIIHSLDDPSLYAVVTR.Y		K.ADTSLIIHSLDDPSLYAVVTR.Y
2	13	2	1361.7	3.8	0	57.2	20.6	95.00%	M.SFPASTHVYIAK.I	Acetyl (+42)	-.MSFPASTHVYIAK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
131	SYLC_SCHPO	4.68%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
843	852	2	1272.56	5	0	24.8	23.4	90.20%	K.SCFYDLQNAR.D	Carbamidomethyl (+57)	K.SCFYDLQNAR.D
382	398	2	1730.97	1.8	0	62.5	12.8	95.00%	K.GQDLIGALVNAPLSVHK.Q		K.GQDLIGALVNAPLSVHK.Q
226	241	2	1922.92	5.8	0	66.1	23.3	95.00%	R.SFITTDVNPYYDSFVR.W		R.SFITTDVNPYYDSFVR.W
779	787	2	927.55	2.2	0	40.6	16	95.00%	E.ALANSAILR.L		R.LALADAGDTVDDANFEEALANSAILR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
132	SYTC_SCHPO	6.40%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
160	174	2	1703.8	4.7	1	71.1	23	95.00%	R.VITNDDYSSIESYAK.Q		R.VITNDDYSSIESYAK.Q
248	258	2	1187.55	4.2	0	47.1	22.3	95.00%	K.NSSSYFLGDAK.N		K.NSSSYFLGDAK.N
8	26	3	2136.14	4.2	1	27.4	16.1	95.00%	K.GVQASLDNLSLEIPFIQHR.L		K.GVQASLDNLSLEIPFIQHR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
133	SYDC_SCHPO	11.72%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
281	294	2	1356.6	4.8	1	27.5	22.6	94.20%	K.MSGASSEGGSNVFK.I		K.MSGASSEGGSNVFK.I

522	554	3	3334.69	3.2	1	85.5	18.1	95.00%	K.ALGVSPDVGLQQYIDAFAIGCPPHAGGGIGLER.V	Carbamidomethyl (+57)	K.ALGVSPDVGLQQYIDAFAIGCPPHAGGGIGLER.V
200	210	2	1229.65	4.9	1	29.1	19.6	95.00%	K.NLPFLVEDAGR.S		K.NLPFLVEDAGR.S
490	499	2	1300.55	3.9	0	26.9	22.9	93.50%	R.YSNSYDFFMK.G		R.YSNSYDFFMK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
134	SYRC_SCHPO	6.80%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
163	180	2	1987.02	4.1	1	33.9	19.1	95.00%	R.STIIGSFLANLHESQGWK.V		R.STIIGSFLANLHESQGWK.V
480	489	2	1284.6	5.9	0	39.4	22.3	95.00%	R.INNYAFDWSR.M		R.INNYAFDWSR.M
11	24	2	1544.86	3	0	47.1	16.2	95.00%	K.SLSTLGLQDLPVFR.E		K.SLSTLGLQDLPVFR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
135	SYG_SCHPO	6.90%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
216	232	3	1983.01	5	1	28	18.4	95.00%	K.GYLRPETAQGQFLNFSR.L		K.GYLRPETAQGQFLNFSR.L
492	506	2	1649.85	4.8	0	35.7	20.3	95.00%	R.TYTPNVIEPSFGLGR.I		R.TYTPNVIEPSFGLGR.I
526	538	2	1298.77	3.9	0	28.2	13.4	94.90%	R.GVLSFPASIAPIK.A		R.GVLSFPASIAPIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
136	RL12_SCHPO	36.97%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
68	83	2	1538.91	3.4	0	50.5	11.8	95.00%	R.QAAVSVVPSASALVIK.A		R.QAAVSVVPSASALVIK.A
95	108	2	1483.7	3.4	1	34.8	22.6	95.00%	K.DKNVAHSGNVSLDE.I		K.DKNVAHSGNVSLDEIIEVAR.T
17	31	2	1312.7	3.6	1	46	16.6	95.00%	R.AVGGEVAGGSTLAPK.I		R.AVGGEVAGGSTLAPK.I
131	146	2	1652.81	4	1	45.9	21	95.00%	K.EILGTAFSVGCTVDGK.N	Carbamidomethyl (+57)	K.EILGTAFSVGCTVDGK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
137	MPG1_SCHPO	11.29%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
270	287	2	1776	4.2	0	35.2	14	95.00%	K.IGPNVVIGPNVTIGDGVR.L		K.IGPNVVIGPNVTIGDGVR.L
244	266	2	2263.29	3.7	0	84	9.54	95.00%	E.ILAPASSNIIGNVLIDPSATIGK.N		K.HKPEILAPASSNIIGNVLIDPSATIGK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
138	AATR1_SCHPO	15.19%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
305	317	2	1562.83	3.7	1	52.6	19.5	95.00%	R.VGWFTAQPLFIER.G		R.VGWFTAQPLFIER.G
424	438	2	1702.83	3.8	0	41.2	22.1	95.00%	E.GVNLACGNWFVVDPR.V	Carbamidomethyl (+57)	K.IHAEAVEEGVNLACGNWFVVDPR.V
275	288	2	1577.78	4.4	1	46.4	22	95.00%	K.ELIPSFLSMDVDGR.V		K.ELIPSFLSMDVDGR.V
38	54	2	1856.03	4.5	1	36.8	13.8	95.00%	K.IISLAGGLPNPEYFPIR.E		K.IISLAGGLPNPEYFPIR.E
7	19	3	1436.71	5.4	1	43.2	22.2	95.00%	K.DLSHHLSVESASR.K		K.DLSHHLSVESASR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
139	DAK1_SCHPO	10.00%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
45	66	3	2123.05	5.3	0	21	20.3	90.00%	K.NVSVISGGGAGHEPTHSSFVGK.G		K.NVSVISGGGAGHEPTHSSFVGK.G
503	526	3	2700.3	3.7	1	23.8	21.5	94.40%	K.YTPARPGDSTMCDALVPFVETFVK.T	Carbamidomethyl (+57)	K.YTPARPGDSTMCDALVPFVETFVK.T
388	399	2	1358.73	4.4	1	25.9	19.2	92.10%	R.QAIVNSMENLIK.A		R.QAIVNSMENLIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
140	COFI_SCHPO	22.63%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
108	124	2	1827.87	4	1	29	22.6	95.00%	R.RAFTGIGTDIQATDFSE.V		R.RAFTGIGTDIQATDFSEVAYETVLEK.V

109	124	2	1671.77	3.1	0	75.6	23	95.00%	R.AFTGIGTDIQATDFSE.V		R.AFTGIGTDIQATDFSEVAYETVLE K.V
81	94	2	1584.9	4.1	0	54.1	15.7	95.00%	K.IIFISWSPDVAPIK.S		K.IIFISWSPDVAPIK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
141	RS10A_SCHPO	23.61%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	44	3	1428.82	4.9	1	23.6	16	94.20%	K.HPEVGVPNLQVIK.A		K.HPEVGVPNLQVIK.A
10	24	2	1580.91	2.1	0	66.9	12.6	95.00%	K.AIHQALFSQGVLVAK.K		K.AIHQALFSQGVLVAK.K
26	31	2	732.38	5.5	0	30.1	20.4	95.00%	K.DFNLPK.H		K.DFNLPK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
142	NACB_SCHPO	23.84%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
47	58	2	1357.71	3.2	1	25	19.6	90.50%	K.KLNMQNLAGIQE.V		K.KLNMQNLAGIQEVNMFK.E
59	64	2	766.37	3.5	1	32.9	20.1	95.00%	E.VNMFKE.D		K.LNMQNLAGIQEVNMFKEDGGVIN FR.A
73	90	3	1884.97	4	1	45.6	21.1	95.00%	R.APTVHSSLPNETTAIYGK.A		R.APTVHSSLPNETTAIYGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
143	ADK_SCHPO	15.29%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
253	267	2	1483.87	4.5	0	69.4	13.6	95.00%	R.VVVITQGADATIVAK.D		R.VVVITQGADATIVAK.D
126	138	2	1424.68	5.2	0	51	21.6	95.00%	R.SLCTNLGAANNYK.L	Carbamidomethyl (+57)	R.SLCTNLGAANNYK.L
41	64	3	2620.15	3	1	65.7	24	95.00%	E.SQMGIYKEPCVSYSAGGAAQNS CR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.SNDAVLASESQMGIYKEPCVSYS AGGAAQNSCR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
144	RL36A_SCHPO	19.19%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	11	2	966.59	4.6	0	38.2	12.6	95.00%	M.APGLVVGLNK.G		-.MAPGLVVGLNK.G
88	96	2	989.55	4.1	0	28.6	17	95.00%	E.LTSVIQSSR.L		K.IEELTSVIQSSR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
145	PGM_SCHPO	4.33%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	49	2	1634.8	3.7	0	42.5	21.8	95.00%	E.NFVQATMDVVEPSAK.G		K.VTVFEQPNYVENFVQATMDVVE PSAK.G
350	358	2	1160.54	5.2	0	29	23	95.00%	K.FFCNLFDAK.R	Carbamidomethyl (+57)	K.FFCNLFDAK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
146	DYR_SCHPO	9.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
164	183	3	2062.15	3.7	0	25.4	12.3	95.00%	K.LTTPSLHIAGTSDTLVPLAR.S		K.LTTPSLHIAGTSDTLVPLAR.S
191	212	3	2537.31	3.6	1	37.3	18.9	95.00%	R.CENAHVLLHPGQHIVPQQAVYK. T	Carbamidomethyl (+57)	R.CENAHVLLHPGQHIVPQQAVYK. T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
147	ACL2_SCHPO	13.01%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
193	209	2	1822.94	2.8	1	44.5	20.5	95.00%	R.ATIASTLLSDIPVEQHE.S		R.ATIASTLLSDIPVEQHESLVDFIIR. L
326	334	2	985.56	4.7	1	36	18.4	95.00%	K.LTILNAEGR.V		K.LTILNAEGR.V
382	389	2	947.52	4.5	0	26.9	20.6	93.50%	K.TVLDLMTR.G		K.TVLDLMTR.G
32	61	3	3211.76	3.3	1	47.1	13.8	95.00%	K.TVSATPAVQLAQIQFPLPTLVIPAE STTYR.E		K.TVSATPAVQLAQIQFPLPTLVIPAE STTYR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
148	THRC_SCHPO	16.54%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
265	282	2	1945.01	4.9	0	46.3	19.8	95.00%	R.FIVPTGNFGDILAGYYAK.R		R.FIVPTGNFGDILAGYYAK.R
437	454	3	2061.03	4.7	1	31.2	20.3	95.00%	K.TKDQDITYICLSTAHPAK.F	Carbamidomethyl (+57)	K.TKDQDITYICLSTAHPAK.F
313	327	2	1443.73	4.4	0	39.8	21.5	95.00%	K.ADSTQVSPSGPISAK.E		K.ADSTQVSPSGPISAK.E
182	215	3	3829.81	3.8	1	34.2	21.6	95.00%	R.VSPIQEAQMTTVTDPNVHCITVNGVFDDCQDLVK.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VSPIQEAQMTTVTDPNVHCITVNGVFDDCQDLVK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
149	ODPB_SCHPO	19.67%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
331	360	3	3021.51	4	1	35.4	18.5	95.00%	R.VSMADVPMPYSHPVEAASVPNADVVVAAAK.K		R.VSMADVPMPYSHPVEAASVPNADVVVAAAK.K
194	206	2	1391.78	2.9	1	28.6	14.8	95.00%	K.AAIRDPNPVVVLE.N		K.AAIRDPNPVVVLENEILYGK.T
318	330	2	1496.68	3.9	1	35.9	22.7	95.00%	E.SDAFDYLDAPVER.V		R.IVTVDQAYSQHGIGSEIAAQIMESDAFDYLDAPVER.V
295	310	2	1702.82	2.8	0	44.9	22.3	95.00%	R.IVTVDQAYSQHGIGSE.I		R.IVTVDQAYSQHGIGSEIAAQIMESDAFDYLDAPVER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
150	SLBR2_SCHPO	12.25%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
134	143	2	1115.56	4.3	1	27.1	21.4	93.70%	R.NIESSVQPSR.E		R.NIESSVQPSR.E
222	245	3	2655.29	2.9	1	27.6	21	95.00%	R.HLLNLIDDTPVTPGEARPAYDGYE.T		R.HLLNLIDDTPVTPGEARPAYDGYETSR.Q
149	157	2	1075.63	4.5	0	33	16.5	95.00%	K.LLDQIYALK.H		K.LLDQIYALK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
151	SYIC_SCHPO	2.26%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
358	367	2	1140.59	4	0	38.6	20	95.00%	E.ITDFAGQYVK.D		K.LYSADYVEEGSGTGIVHQAPAFGEADYDAAWAAGIIDADHQPPCPVDEQGLLTSEITDFAGQYVK.D
1050	1063	2	1559.87	3.5	0	61	14	95.00%	E.QDVQGATFLLSLLR.-		K.ETGADESNIIASEEQDVQGATFLLSLLR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
152	CH10_SCHPO	28.85%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	84	2	1230.7	4	0	31.7	16.1	95.00%	R.VLLPAYGGSNIK.V		R.VLLPAYGGSNIK.V
62	72	2	1111.6	4.5	0	30.9	17.7	95.00%	K.LAQPSVAVGDR.V		K.LAQPSVAVGDR.V
98	104	2	798.52	2.2	1	36.2	11.1	95.00%	E.LLAIIKE.-		R.DHELLAIIKE.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
153	TBB_SCHPO	9.15%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
126	154	3	2876.43	3.4	0	57.5	20	95.00%	E.ACDALQGFQLTHSLGGGTGSGMGTLLLSK.I	Carbamidomethyl (+57)	R.EAEACDALQGFQLTHSLGGGTGSGMGTLLLSK.I
163	174	2	1249.62	3.9	0	41.3	20.6	95.00%	R.MMATFSVAPAPK.S		R.MMATFSVAPAPK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
154	DLDH_SCHPO	8.81%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
113	128	2	1663.83	1.7	0	25	21.6	90.50%	R.GIDVSGVSVNLSQMMK.A		R.GIDVSGVSVNLSQMMK.A
155	168	2	1448.76	3.8	0	31.8	19.6	95.00%	K.GTGSFIDPQTLSVK.G		K.GTGSFIDPQTLSVK.G
248	262	2	1516.77	3.5	0	38.5	20.6	95.00%	E.FLPAVGGPMDADISK.A		R.LGAEVTVVEFLPAVGGPMDADISK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
155	PABP_SCHPO	4.75%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
258	266	2	1068.57	4.8	0	26.6	18.4	93.10%	K.ANFTNVYIK.N		K.ANFTNVYIK.N
447	456	2	1142.61	4.9	1	33.9	19.3	95.00%	R.SQLEAQIQAR.N		R.SQLEAQIQAR.N
99	110	2	1272.72	3.9	0	40.5	14.9	95.00%	E.LFNSIGPVASIR.V		K.AEEPEAAAEPSESTSTPTNASSV ATPSGTAPTSASLYVGELDPSVTEA MLFELFNSIGPVASIR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
156	RS11_SCHPO	17.76%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	64	2	1161.6	4.7	0	33.4	20.9	95.00%	K.CPFVGQVSIR.G	Carbamidomethyl (+57)	K.CPFVGQVSIR.G
114	130	2	1870.97	4.9	1	41.5	19.8	95.00%	R.INEGDVVTVGQCRPLSK.T	Carbamidomethyl (+57)	R.INEGDVVTVGQCRPLSK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
157	Q76N21_SCHPO	25.85%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	140	3	2329.12	1.8	1	32.2	22.3	95.00%	K.GASDGGLFIPHSPNRFPGFDIE.T		K.YEGVTEPEGEFELTEAIEDGPRP FFK.V
13	22	2	1195.61	4.9	0	30.3	22	95.00%	R.FVTCQIVSSR.V	Carbamidomethyl (+57)	K.SSPYFSRYQTKYRR.R
67	74	2	893.45	4.3	1	35.3	22.1	95.00%	K.VGLADKYE.G		R.FVTCQIVSSRVNGDYVLAHAHSS ELPR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
158	RL31_SCHPO	21.24%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
91	105	2	1650.87	4.2	0	39.3	18.8	95.00%	K.ALYTYVQAVDVANPK.M		K.ALYTYVQAVDVANPK.M
7	15	2	986.56	5	0	39.5	18.5	95.00%	K.SAINQVVTR.D		K.SAINQVVTR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
159	DHOM_SCHPO	15.43%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	138	2	1568.79	4.5	0	56.7	21	95.00%	K.AFSASNDVYQNIIK.A		K.AFSASNDVYQNIIK.A
268	278	2	1208.58	2.9	0	35.8	22.3	95.00%	E.FLAGLPNFDSE.F		K.SAVNAEEFLAGLPNFDSEFASMR .E
57	67	2	1391.68	4.7	1	33.1	21.7	95.00%	K.DYQPINLSEWK.N		K.DYQPINLSEWK.N
89	110	2	2284.21	4.5	1	95.1	18.1	95.00%	K.SPLPAILVDNTASEAIAQSYPK.F		K.SPLPAILVDNTASEAIAQSYPK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
160	RL14_SCHPO	11.94%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
103	110	2	993.46	6	0	29.1	22	95.00%	R.SQLNDFDR.F		R.SQLNDFDR.F
87	94	2	905.44	5.7	0	30.4	21.3	95.00%	K.WASSAWAK.K		K.WASSAWAK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
161	RS13_SCHPO	23.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
44	55	2	1244.66	3.8	0	40.8	19.9	95.00%	K.GMSPSQIGVTLR.D		K.GMSPSQIGVTLR.D
28	39	2	1286.68	5	1	56.1	20	95.00%	K.ADADSVVEQILK.F		K.ADADSVVEQILK.F
10	20	2	1132.63	4.4	0	38.6	18.1	95.00%	K.GIASSALPYVR.S		K.GIASSALPYVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
162	SCE3_SCHPO	15.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
46	66	2	2113.97	4.9	1	94.2	23.1	95.00%	R.ATPSSADAGYNAPSSTFESVR.S		R.ATPSSADAGYNAPSSTFESVR.S
272	289	3	1956.03	4.3	1	43	18.8	95.00%	K.RDPFGGAKPVDNTSVLQR.V		K.RDPFGGAKPVDNTSVLQR.V
250	271	3	2195.06	2.9	1	28.5	22.3	95.00%	R.SSSNVNTEATPSATTTTSSKPK.R		R.SSSNVNTEATPSATTTTSSKPK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
163	ACAC_SCHPO	2.81%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1972	1994	3	2667.36	3.2	1	27.8	18.3	95.00%	K.TAQAINDFNHGEQLPLFILANWR.G		K.TAQAINDFNHGEQLPLFILANWR.G
1856	1873	2	2026.93	2	1	28.7	23.4	95.00%	R.NNPVPISPSSDTWDRDVE.F		R.NNPVPISPSSDTWDRDVEFYPSQNGYDPR.W
1960	1971	2	1366.67	3.4	0	29.7	22.2	95.00%	E.AGQVWYPNSAFK.T		R.TIENTVPADPANPDSTEQVLMEAGQVWYPNSAFK.T
197	207	2	1131.63	6.1	0	34.7	15.8	95.00%	K.ISSTIVAQSAR.V		K.ISSTIVAQSAR.V
1972	1983	2	1315.58	1.4	0	30.2	23.1	95.00%	K.TAQAINDFNHGE.Q		K.TAQAINDFNHGEQLPLFILANWR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
164	PDI1_SCHPO	5.28%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	136	3	1350.87	5.1	1	30.4	0	95.00%	R.KQLLPTVKPISK.D		R.KQLLPTVKPISK.D
188	201	2	1436.77	4.3	0	45.1	17.4	95.00%	K.SLGSNFPGIVAFTK.D		K.SLGSNFPGIVAFTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
165	YDMC_SCHPO	3.89%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
82	91	2	1136.53	5	0	33.4	22.5	95.00%	R.NADNSVTNFR.D		R.NADNSVTNFR.D
358	369	2	1126.64	4.1	0	39.8	16.9	95.00%	E.VILAGGASNTPK.L		K.ANMEPFDISEVILAGGASNTPK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
166	YBS7_SCHPO	6.02%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
128	146	2	1760.86	5.1	0	31.6	21.8	95.00%	R.TSGSSTGLSNAPPSANVSK.A		R.TSGSSTGLSNAPPSANVSK.A
168	185	2	1942.99	3	0	34	19.3	95.00%	E.VCVPLNPDTGSVPLIHPE.Q	Carbamidomethyl (+57)	R.ATPEVCVPLNPDTGSVPLIHPEQTDR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
167	RS12A_SCHPO	8.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	111	2	1486.76	2.4	1	27.9	19.4	94.60%	K.VLGEWAGLCVLDR.D	Carbamidomethyl (+57)	K.VLGEWAGLCVLDR.D
103	111	2	1088.55	2	0	27	20.7	93.60%	E.WAGLCVLDR.D	Carbamidomethyl (+57)	K.VLGEWAGLCVLDR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
168	SYEC_SCHPO	6.15%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
190	206	2	1731.84	3.9	1	51.4	22.7	95.00%	K.SSGPNYEIGLPDAIDGK.V		K.SSGPNYEIGLPDAIDGK.V
295	309	2	1657.7	4.5	1	93.6	23.7	95.00%	K.SGQAYADDTDVETMR.H		K.SGQAYADDTDVETMR.H
66	77	2	1393.77	4.3	0	31.9	15.7	95.00%	K.LALQTFSQVYPK.L		K.LALQTFSQVYPK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
169	ASSY_SCHPO	6.34%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
320	332	2	1601.77	4.2	0	39.6	23	95.00%	K.ILYNGQFFSPCTR.M	Carbamidomethyl (+57)	K.ILYNGQFFSPCTR.M
193	205	2	1354.68	2.9	1	47.8	20.5	95.00%	E.AGILEDPSMTPPK.D		K.KPWSMDENIVHCSYEAGILEDPSMTPPK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
170	O13797_SCHPO	9.15%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
197	214	2	1831.84	5.2	0	74	23.7	95.00%	K.QLNQPSDSSATSGADQAR.T		K.QLNQPSDSSATSGADQAR.T
33	43	2	1265.61	2.9	0	26.8	22.1	93.40%	E.VAAQCIQDSFK.I	Carbamidomethyl (+57)	K.ESLEVAAQCIQDSFK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
171	YET4_SCHPO	6.80%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
190	216	3	2686.32	5.5	1	58	21.4	95.00%	R.NDEQLGNSPASITSKPATTSAAQPSSK.V		R.NDEQLGNSPASITSKPATTSAAQPSSK.V
487	503	3	1712.87	4.4	0	27.8	21	95.00%	R.KPSSTGQEPTTPSTPAK.S		R.KPSSTGQEPTTPSTPAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
172	ACBP_SCHPO	34.48%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	13	2	1294.61	4.4	1	38.3	22.7	95.00%	M.SSTFEQAAADVK.E	Acetyl (+42)	-.MSSTFEQAAADVK.E
33	50	2	1912	3.1	1	45.8	18.4	95.00%	K.QATVGDNNTEKPGLLDLK.G		K.QATVGDNNTEKPGLLDLK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
173	Q9P7B4_SCHPO	16.22%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
234	256	3	2522.27	2.7	1	34.8	19.4	95.00%	R.ENVVIADTLVFPSHQGGANHVYR.K		R.ENVVIADTLVFPSHQGGANHVYR.K
163	173	2	1163.64	5.6	0	26.5	17.4	92.90%	K.SALAQFTSALR.K		K.SALAQFTSALR.K
225	232	2	931.59	3.7	0	25	4.77	90.50%	E.VILFALTR.R		K.NSEPLTPEDIAEVILFALTR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
174	RL18A_SCHPO	12.30%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
81	93	2	1390.7	3.8	1	57.3	21.7	95.00%	K.TTVVVGTVTDDER.M		K.TTVVVGTVTDDER.M
56	65	3	1111.64	5.1	0	26.6	15.8	95.00%	K.TNRPPISISK.I		K.TNRPPISISK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
175	LYS1_SCHPO	8.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
274	304	3	3531.61	3.6	0	37.5	22.8	95.00%	R.VVCDVSCDTTNPNNPIPIYNVNTTFDHPTVE.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VVCDVSCDTTNPNNPIPIYNVNTTFDHPTVEVK.G
274	306	3	3758.77	3.3	1	76.7	21.5	95.00%	R.VVCDVSCDTTNPNNPIPIYNVNTTFDHPTVEVK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VVCDVSCDTTNPNNPIPIYNVNTTFDHPTVEVK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
176	APE1_SCHPO	4.65%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
253	269	2	1912.97	5	0	42.1	19.8	95.00%	K.TLDFFSGVFGEPYPLPK.C		K.TLDFFSGVFGEPYPLPK.C
137	149	2	1467.71	4.6	0	42.2	22.1	95.00%	K.YLATTQMEPTSAR.R		K.YLATTQMEPTSAR.R
487	497	2	1220.6	4.6	1	31.6	21.3	95.00%	R.FLSTGDVKPEE.D		R.FLSTGDVKPEEDTVIYWAPLK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
177	FIMB_SCHPO	4.89%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
508	524	2	1796.81	3.5	0	38.6	23.3	95.00%	K.TLSDSDMVAWANSMAAK.G		K.TLSDSDMVAWANSMAAK.G
158	170	2	1485.74	3.7	1	44.6	23	95.00%	K.LINDSVPDTIDER.V		K.LINDSVPDTIDER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
178	SODM_SCHPO	20.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	173	2	1303.7	4.2	0	48.8	19.3	95.00%	R.ITTTANQDTIVK.S		R.ITTTANQDTIVK.S
26	48	2	2502.32	2.9	1	32.8	15.8	95.00%	K.ATLPPLPYAYNALEPALSETIMK.L		K.ATLPPLPYAYNALEPALSETIMK.L
127	135	2	1108.52	5	1	34	22.6	95.00%	K.WGSLEDFQK.E		K.WGSLEDFQK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
179	RL11_SCHPO	14.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
36	49	2	1531.83	4.2	1	63.5	17.2	95.00%	K.VLEQLSGQTPVFSK.A		K.VLEQLSGQTPVFSK.A
154	164	2	1349.67	4.1	1	39.8	21	95.00%	K.INAEDTINWFK.Q		K.INAEDTINWFK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
180	YEI3_SCHPO	12.24%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
81	97	3	1834.04	4	1	21.8	10.4	91.40%	K.SRVPAFLTVFDIAGLTK.G		K.SRVPAFLTVFDIAGLTK.G
98	114	2	1641.86	2.2	0	46.7	19.2	95.00%	K.GASTGVGLGNAFLSHVR.A		K.GASTGVGLGNAFLSHVR.A
329	342	2	1482.75	2.8	1	41.2	21	95.00%	K.APQAAGVIHTDFEK.A		K.APQAAGVIHTDFEK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
181	RHP23_SCHPO	7.61%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
211	225	2	1515.76	4.1	0	27.1	21.5	93.70%	E.ALAPTSTGQPANLFE.Q		R.EESAAALAAQQQQSEALAPTSTGQPANLFEQAALSENENQEQPSNTVGDDPLGFLR.S
198	210	2	1301.63	4.4	0	73.2	21.9	95.00%	E.SAAALAAQQQQSE.A		R.EESAAALAAQQQQSEALAPTSTGQPANLFEQAALSENENQEQPSNTVGDDPLGFLR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
182	RL28A_SCHPO	11.49%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
94	110	2	1787.95	3.9	1	37.3	18.9	95.00%	K.NTEVAPVINVLQSGYGK.V		K.NTEVAPVINVLQSGYGK.V
97	110	2	1443.81	3	0	36.2	14.8	95.00%	E.VAPVINVLQSGYGK.V		K.NTEVAPVINVLQSGYGK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
183	CARA_SCHPO	10.84%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
324	358	4	3743.79	2.8	1	17.6	21	93.10%	R.GHNIPALDIASGNCHITSQNHGYAVDASTLPAEWK.A	Carbamidomethyl (+57)	R.GHNIPALDIASGNCHITSQNHGYAVDASTLPAEWK.A
203	212	2	1101.62	3.9	0	39	17.2	95.00%	E.VNLVSQVSTR.E		K.ISIGEEYDANDDEAFINPEEVNLVSQVSTR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
184	ARO1_SCHPO	4.77%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
677	703	3	2950.41	2.7	1	45.4	21.4	95.00%	R.FACDVLRPMGCTVEQTATSTTVQGPPK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.FACDVLRPMGCTVEQTATSTTVQGPPK.G
162	172	2	1299.72	4.7	0	45.2	18.9	95.00%	K.NLVGAFWQPLR.V		K.NLVGAFWQPLR.V
1232	1247	2	1833.96	4.6	0	44.8	18.7	95.00%	R.ITNSMDIPLILFNMGR.F		R.ITNSMDIPLILFNMGR.F
640	660	2	2079.08	2.7	1	62.5	18.1	95.00%	E.IESDASSATYPLAIAAITGTK.C		K.YQNPPHYEIESDASSATYPLAIAAITGTK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
185	RLA5_SCHPO	30.28%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
38	48	2	1273.71	3.8	0	42	18	95.00%	E.VEPIWATIFAK.A		K.AGNVEVEPIWATIFAK.A
99	109	2	1247.47	4.3	1	47.1	22.1	95.00%	E.SDEDMGFGLFD.-	Oxidation (+16)	K.EEEESDEDMGFGLFD.-
22	32	2	1217.73	2.9	1	43.8	12.8	95.00%	E.ITSDKLLSLTK.A		-.MSASELATSYAALILADEGIEITSDKLLSLTK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
186	FUMH_SCHPO	8.71%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
326	341	2	1622.87	1.8	0	30.1	16.7	95.00%	E.LILPANEPGSSIMPGK.V		R.CGLGELILPANEPGSSIMPGK.V
131	142	2	1157.67	3.6	1	43.3	16.5	95.00%	R.AIEILGGTLGSK.K		R.AIEILGGTLGSK.K

218	231	2	1574.78	3.4	1	32.5	20.9	95.00%	E.FSGYVTQVGYGIER.I		R.THMQDATPLSLGQEFSGYVTQVGYGIER.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
187	TBA1_SCHPO	8.13%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
291	304	2	1770.81	1.8	0	40.7	22.8	95.00%	E.ITNQCFEPYNQMVK.C	Carbamidomethyl (+57)	K.AFHESNSVQEITNQCFEPYNQMVK.C
65	79	2	1758.92	3.8	0	35	18.9	95.00%	R.SIYVDLEPNVIDQVR.T		K.FVPRSIYVDLEPNVIDQVR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
188	RS3_SCHPO	13.65%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
154	175	3	2381.12	2	0	41.6	22.8	95.00%	K.FADGFMIHSGQPAVDFIDSATR.H		K.FADGFMIHSGQPAVDFIDSATR.H
97	108	2	1362.64	3.8	1	61	22.9	95.00%	R.GLCAVAQCESLR.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GLCAVAQCESLR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
189	DED1_SCHPO	3.14%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
37	51	2	1398.63	4.5	0	32.2	23.3	95.00%	R.DKPSAGAAPAVGDDE.S		R.DKPSAGAAPAVGDDESVSSR.G
37	56	3	1914.9	5	1	49.2	23.3	95.00%	R.DKPSAGAAPAVGDDESVSSR.G		R.DKPSAGAAPAVGDDESVSSR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
190	SPEE_SCHPO	8.39%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	12	2	1291.72	4.1	1	43.5	17.3	95.00%	M.SVQELSHPLIK.D	Acetyl (+42)	-.MSVQELSHPLIK.D
18	31	2	1631.79	4.6	1	31.2	22.1	95.00%	R.EINNMWPGQAMTLK.V		R.EINNMWPGQAMTLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
191	SYSC_SCHPO	6.89%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
234	250	2	1864.89	3.6	1	69.5	22.4	95.00%	R.YLIATSEQPISAYHSGE.W		R.YLIATSEQPISAYHSGEWFEKPSEQLPLK.Y
358	371	2	1717.71	4.8	1	59.1	24.2	95.00%	K.ELVSCSNCTDYQSR.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.ELVSCSNCTDYQSR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
192	G3P2_SCHPO	27.46%	99%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
249	259	3	1290.69	4.5	1	28.4	19.9	95.00%	K.LAKPTNYEDIK.A		K.LAKPTNYEDIK.A
235	248	2	1467.82	3.7	0	76.5	15.2	95.00%	R.VPTPDVSVVDLTVK.L		R.VPTPDVSVVDLTVK.L
173	186	2	1458.75	3.1	0	81.7	18.8	95.00%	E.GLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK.T
146	162	2	1818.91	4.5	0	75	21.7	95.00%	K.VISNASCTTNCLAPLAK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.VISNASCTTNCLAPLAK.V
324	335	2	1279.67	5	1	52.3	20.3	95.00%	R.VVDLVAYTASKD.-		R.VVDLVAYTASKD.-
172	186	2	1587.8	3.6	1	49.5	21.6	95.00%	E.EGLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK.T
6	13	2	819.43	6.2	0	38.4	19.6	95.00%	K.VGINGFGR.I	Deamidation (+1)	K.VGINGFGR.I
201	215	2	1343.71	4.7	0	69.9	19.5	95.00%	R.GASANIIPSSTGAAK.A		R.GASANIIPSSTGAAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
193	PPA2_SCHPO	5.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
138	143	2	719.4	4.8	0	27.1	17.3	93.70%	E.LFDLGR.Q		R.IELFDLGR.Q

152	167	2	1869.88	2.4	1	82.4	23.2	95.00%	E.LFDTDVYDINTAAQER.V		R.YYELFDTDVYDINTAAQER.V
136	143	2	961.53	5.4	1	31.9	19.8	95.00%	R.IELFDLGR.Q		R.IELFDLGR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
194	LYS4_SCHPO	4.30%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
149	159	2	1179.57	4.4	0	26	21.8	92.20%	K.GQGIDFYPAGR.G		K.GQGIDFYPAGR.G
470	489	2	1872.04	4.8	1	47.2	14.6	95.00%	R.EALAYLASPAVVAASAIAGK.I		R.EALAYLASPAVVAASAIAGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
195	RLA0_SCHPO	18.59%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
133	144	2	1308.71	5.2	0	29.1	16.9	95.00%	K.TSFFQALGIPTK.I		K.TSFFQALGIPTK.I
98	132	3	3513.88	2.7	1	45.6	16.4	95.00%	R.ETIIANVIAAPARPNAIAPLDVFVPAGNTGMEPGK.T		R.ETIIANVIAAPARPNAIAPLDVFVPAGNTGMEPGK.T
302	312	2	1247.47	4.3	1	47.1	22.1	95.00%	E.SDEDMGFGLFD.-	Oxidation (+16)	K.AFLADPSAFVVAAAPAAAAGGEAEAPAAEAAAEEEEESDEDMGFGLFD.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
196	SYFA_SCHPO	4.61%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
128	138	2	1219.56	4.9	1	33.3	22.7	95.00%	K.NTDSITDETPK.V		K.NTDSITDETPK.V
280	291	2	1267.63	3.3	1	30.8	21.2	95.00%	K.VPASTDKLPDPE.Y		K.VPASTDKLPDPEYVAR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
197	YBP8_SCHPO	4.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
141	157	2	1818.9	2.4	0	70.9	21.7	95.00%	E.AEPSDVNAVDYIIQSAK.D		R.DVEYPEHIDSYLLNAEAEPSDVNAVDYIIQSAK.D
170	182	2	1403.67	5.3	0	28.2	23	95.00%	E.LSTADDVDDVLLE.S		K.LEAEIEELSTADDVDDVLLESK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
198	CYSK1_SCHPO	9.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
10	23	2	1341.78	3.9	0	59.1	14.9	95.00%	K.VPGIVSGFIGAIGR.T		K.VPGIVSGFIGAIGR.T
180	200	2	2019.93	5.1	0	71.4	24.1	95.00%	K.GTVDGFTCSTGTGGTFAGVTK.Y	Carbamidomethyl (+57)	K.GTVDGFTCSTGTGGTFAGVTK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
199	CATA_SCHPO	5.66%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
431	439	2	1061.57	5.6	0	35.4	19.5	95.00%	R.AFWQNVLGK.K		R.AFWQNVLGK.K
421	430	2	1218.59	2.4	1	47.6	22	95.00%	E.ITDVDFEQPR.A		K.WVGQVTYHMDEITDVDFEQPR.A
331	340	2	1082.61	4.6	0	27.8	15.3	94.50%	E.VSADPVLQVR.T		R.FTLNQNPTNFFADIEQAGFSPSHMVPGIEVSADPVLQVR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
200	PNPP_SCHPO	13.42%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
196	213	2	1882.01	3.5	0	46.6	17.3	95.00%	K.FLPGSGAISYPLIFSTGR.Q		K.FLPGSGAISYPLIFSTGR.Q
145	166	3	2359.15	3.2	0	61.7	21.7	95.00%	K.IGPDPSVGAVLCGMDMHVTYLK.Y	Carbamidomethyl (+57)	K.IGPDPSVGAVLCGMDMHVTYLK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
201	PRS6A_SCHPO	7.31%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

250	265	2	1657.89	4.1	0	43	18.1	95.00%	K.LAAPQLVQMFIGDGAK.L		K.LAAPQLVQMFIGDGAK.L
7	22	2	1661.71	0.00091	0	41.8	23.9	95.00%	E.LDALDQSQQGGSSNNE.G		- .MSTLEELDALDQSQQGGSSNNEG LDGIEQEILAAGIDELNSR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
202	PUR2_SCHPO	7.87%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
224	248	3	2494.13	2.3	1	33.2	23	95.00%	R.AFDGDKGPNTGGMGCYAPTPVASPK.L	Carbamidomethyl (+57)	R.AFDGDKGPNTGGMGCYAPTPVASPK.L
483	501	2	1913.96	3.5	0	25	21.2	90.50%	K.QAGWNDPLLVSATDGVGSK.L		K.QAGWNDPLLVSATDGVGSK.L
31	48	2	1678.78	1.8	1	54.6	23	95.00%	K.VYVAPGNGGTASNGAESK.M	Deamidation (+1)	K.VYVAPGNGGTASNGAESK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
203	EIF3E_SCHPO	6.39%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
267	284	3	2029.08	4.4	0	22.1	17.6	92.00%	R.YLTVAVVTNQNNANQKPR.N		R.YLTVAVVTNQNNANQKPR.N
418	431	2	1463.71	4.5	0	63.8	22	95.00%	E.STSTNVVADDLITE.A		R.NNPSVAAASNVAADQSTEDESIESTSTNVVADDLITEAETATEAEEPEPEVQFGFK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
204	P5CR_SCHPO	13.83%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
116	129	2	1566.76	5	1	85.9	21.4	95.00%	K.TISSLQSMLDESTR.V		K.TISSLQSMLDESTR.V
74	98	3	2668.4	3.2	1	47.5	17	95.00%	E.MAAISNVLLLSCKPQAAEDVLNSPK.M	Carbamidomethyl (+57)	K.ENAEMAAISNVLLLSCKPQAAEDVLNSPK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
205	CISY_SCHPO	7.82%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
91	101	2	1155.59	3.7	1	28	19.6	94.70%	E.GSVLDPNEGIR.F		R.SLIWEGSVLDPNEGIR.F
167	192	4	2838.39	2.4	1	38.1	20.5	95.00%	R.CPPTLHPMAQFSLAVTALEHDSAFAK.A	Carbamidomethyl (+57)	R.CPPTLHPMAQFSLAVTALEHDSAFAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
206	Q9USR1_SCHPO	9.31%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
231	241	2	1294.69	3.1	0	37.9	19.4	95.00%	E.QDDQPTIIPLR.F		K.LYINQPNNLSFEDAESFTPTQVIEDIVYEQDDQPTIIPLR.F
109	124	2	1403.73	4.8	0	51.6	19.6	95.00%	K.ATGTGALASSSSAPVK.G		K.ATGTGALASSSSAPVK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
207	RS0A_SCHPO	9.93%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
16	30	3	1666.89	3.3	1	33.3	16.4	95.00%	E.DIKQLLAANCHIGSK.N	Carbamidomethyl (+57)	- .MAQVGRPNILNATDEDIKQLLAANCHIGSK.N
2	15	2	1538.77	2.7	0	40	21.4	95.00%	M.AQVGRPNILNATDE.D	Acetyl (+42)	-.MAQVGRPNILNATDEDIK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
208	RS21_SCHPO	29.89%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
51	60	2	1113.59	4.5	0	33.8	19.7	95.00%	K.TTYAISGFVR.S		K.TTYAISGFVR.S
72	87	2	1864.94	4.3	1	65.3	21.7	95.00%	R.LTTQDGLLEGVWSYQR.-		R.LTTQDGLLEGVWSYQR.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
209	RL24A_SCHPO	12.75%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

81	91	2	1097.65	4.7	0	29.4	14.3	95.00%	R.GIVGANLDVIK.E		R.GIVGANLDVIK.E
36	43	2	978.52	4.9	1	29.5	21.1	95.00%	K.SESLFLQR.K		K.SESLFLQR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
210	6PGL_SCHPO	8.95%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
46	55	2	1083.61	5.4	1	52.4	17.6	95.00%	K.VLAEGLAQQR.G		K.VLAEGLAQQR.G
209	221	2	1488.81	4	1	42.1	16.7	95.00%	K.DILPIVIEDFTSK.L		K.DILPIVIEDFTSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
211	UBC4_SCHPO	25.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
102	128	3	3017.59	3.1	1	65.3	15.2	95.00%	K.VLLSICSLLTDPNPDDPLVPEIAHVYK.T	Carbamidomethyl (+57)	K.VLLSICSLLTDPNPDDPLVPEIAHVYK.T
91	101	2	1244.65	4.6	0	28.4	20.3	95.00%	R.DQWSPALTISK.V		R.DQWSPALTISK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
212	RS24A_SCHPO	20.15%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
21	32	3	1363.77	4	1	39.5	16.1	95.00%	R.KQMVVDILHPGK.A		R.KQMVVDILHPGK.A
69	83	2	1672.81	4.3	1	28.6	22.9	95.00%	R.TTGFALIYDDVEAMK.K		R.TTGFALIYDDVEAMK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
213	RL7B_SCHPO	14.00%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	21	2	2002.11	4.4	1	37	14.6	95.00%	M.VASSTVPSVASIFAPESLLK.K		-.MVASSTVPSVASIFAPESLLK.K
168	182	2	1523.86	4.4	1	56.2	14.5	95.00%	R.IPLSDNAIIEAALGK.Y		R.IPLSDNAIIEAALGK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
214	ARPC1_SCHPO	5.84%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	23	4	2564.32	3.3	1	37.1	17.8	95.00%	M.ATSQVLHILPKPSYEHAFNSQR.T	Acetyl (+42)	-.MATSQVLHILPKPSYEHAFNSQR.T
2	16	2	1723.92	3.1	0	43.5	18.6	95.00%	M.ATSQVLHILPKPSYE.H	Acetyl (+42)	-.MATSQVLHILPKPSYEHAFNSQR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
215	YNY8_SCHPO	7.44%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
221	230	2	1165.62	3.6	0	36.7	19.9	95.00%	E.LYATFLDPAR.V		R.VSAVVNTADISENYTFDAPANELYATFLDPAR.V
2	16	2	1783.84	4.8	0	36.8	22.9	95.00%	M.SATSINPNNWHWTSK.D	Acetyl (+42)	-.MSATSINPNNWHWTSK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
216	ARG56_SCHPO	6.33%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
487	524	4	4077.04	3.3	0	36.4	15.9	95.00%	K.FIQSDKPFADAIIQTQSTKPPTASSTTNNPSSSQINQK.R		K.FIQSDKPFADAIIQTQSTKPPTASSTTNNPSSSQINQK.R
861	878	2	1923.87	3	0	53.5	23.6	95.00%	K.GAATQALQNLNLSCGYDE.Y	Carbamidomethyl (+57)	K.GAATQALQNLNLSCGYDEYAGIHLD.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
217	EIF3G_SCHPO	13.48%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
14	32	2	2024.94	3.1	0	32.8	23	95.00%	E.DYGTGLPSIQTFDNPDGTK.T		K.SLDWADDEDYGTGLPSIQTFDNPDGTK.T
147	165	2	1935	2.6	0	32.2	19.6	95.00%	K.SIIGPVDEPPLDASPVSSR.A		K.SIIGPVDEPPLDASPVSSR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
218	PPID_SCHPO	5.90%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
214	226	2	1432.74	4.4	0	72	20.3	95.00%	K.QFAQQNLDTAVAK.W		K.QFAQQNLDTAVAK.W
23	30	2	931.51	4.1	0	29.7	20.8	95.00%	E.LFDNVVPK.T	Deamidation (+1)	K.IQPTIYFELFDNVVPK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
219	GUAA_SCHPO	10.76%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
170	203	4	3715.11	3.7	1	22.3	15.2	95.00%	K.NSPFAVIAHVTKPIIGLQFHPEVTHTPLGLQLIK.N		K.NSPFAVIAHVTKPIIGLQFHPEVTHTPLGLQLIK.N
231	254	4	2311.19	3.1	1	17.8	18.6	93.60%	R.KMIGPSDHVIGAVSGGVDSTVASK.V		R.KMIGPSDHVIGAVSGGVDSTVASK.V

Supplementary Table S2: All "Scaffold" validated proteins and peptides identified from solprotSP (*S.pombe*) and from SCVMprot (*S.cerevisiae*) samples

S.pombe **- Glu-C digest of large tryptic peptides (replicate B)**

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
1	G3P1_SCHPO	53.27%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
249	259	3	1290.69	4.5	1	28.4	19.9	95.00%	K.LAKPTNYEDIK.A		K.LAKPTNYEDIK.A
67	79	2	1407.71	3.9	0	89.4	22	95.00%	K.LVIDGNAIDVHNE.R		K.LVIDGNAIDVHNER.D
235	248	2	1467.82	3.7	0	76.5	15.2	95.00%	R.VPTPDVSVVDLTVK.L		R.VPTPDVSVVDLTVK.L
323	334	2	1304.75	3.7	1	45.3	13.4	95.00%	R.RVVDLVAYTAAK.D		R.RVVDLVAYTAAK.D
98	106	2	968.45	4.8	0	30.2	22.7	95.00%	E.STGVFTTQE.T		K.WSTSGADYVIESTGVFTTQETASAHLK.G
173	186	2	1458.75	2.9	0	84.3	18.9	95.00%	E.GLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK.T
146	162	2	1818.91	4.5	0	75	21.7	95.00%	K.VISNASCTTNCLAPLAK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.VISNASCTTNCLAPLAK.V
324	334	2	1148.65	6.2	0	55.4	16.6	95.00%	R.VVDLVAYTAAK.D		R.VVDLVAYTAAK.D
49	61	2	1468.63	3.7	1	43	23.1	95.00%	K.YDSTHGRFDGSVE.I		K.YDSTHGRFDGSVEIK.D
27	41	2	1685.89	3	0	42.1	18.3	95.00%	K.TIQVVAINDPFIDLE.Y		K.TIQVVAINDPFIDLEYMAYMFK.Y
163	172	2	1135.54	2.8	1	34.2	21.9	95.00%	K.VINDTFGIEE.G		K.VINDTFGIEEGLMTTVHATTATQK.T
324	336	2	1377.72	3.8	1	68.7	20	95.00%	R.VVDLVAYTAAKDN.-		R.VVDLVAYTAAKDN.-
172	186	2	1587.8	2.8	1	36.4	21.5	95.00%	E.EGLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK.T
98	113	2	1676.84	2.5	1	36.2	20.7	95.00%	E.STGVFTTQETASAHLK.G		K.WSTSGADYVIESTGVFTTQETASAHLK.G
6	13	2	819.43	6.2	0	38.4	19.6	95.00%	K.VGINGFGR.I	Deamidation (+1)	K.VGINGFGR.I
201	215	2	1343.71	4.7	0	69.9	19.5	95.00%	R.GASANIIPSSTGAAK.A		R.GASANIIPSSTGAAK.A
119	137	2	1988.04	3.3	1	43	18.2	95.00%	R.VIISAPSKDAPMYVVGVNE.E		R.VIISAPSKDAPMYVVGVNEEK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
2	PGK_SCHPO	60.14%	100%	28

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
383	398	2	1528.71	3.3	1	32.2	23.4	95.00%	K.EDALSHVSTGGGASLE.L		K.EDALSHVSTGGGASLELLEGK.A
359	378	2	1917.95	4	1	118	21	95.00%	K.TCEAGNVVIVGGGDTATVAK.K	Carbamidomethyl (+57)	K.TCEAGNVVIVGGGDTATVAK.K
7	15	2	986.57	5.4	0	41.1	17.3	95.00%	K.LAITDVDLK.G		K.LAITDVDLK.G
302	316	2	1646.71	2.2	1	64.3	23.2	95.00%	E.EGIPDGWMGLDCGPK.S	Oxidation (+16)/ Carbamidomethyl (+57)	K.VGSATAEEGIPDGWMGLDCGPK.S
273	288	2	1805.93	4.9	1	56.9	20.3	95.00%	K.NNVEVFLPVDFVTADK.F		K.NNVEVFLPVDFVTADK.F
200	213	2	1423.83	2.4	0	38.1	11.8	95.00%	E.NPARPFLAILGGAK.V		K.ALENPARPFLAILGGAK.V
362	379	2	1655.93	3.5	1	54.9	15.3	95.00%	E.AGNVVIVGGGDTATVAKK.Y		K.TCEAGNVVIVGGGDTATVAKK.Y
384	398	2	1399.66	3	0	51.9	23.2	95.00%	E.DALSHVSTGGGASLE.L		K.EDALSHVSTGGGASLELLEGK.A
23	39	2	1914.96	4.6	1	38	21.3	95.00%	R.VDFNVPLDGDRITNNAR.I		R.VDFNVPLDGDRITNNAR.I
57	71	2	1591.87	2.9	0	46.2	17.5	95.00%	K.AVILMSHLGRPNGAR.V	Deamidation (+1)	K.AVILMSHLGRPNGAR.V
23	33	2	1245.61	6.8	0	62.1	21.6	95.00%	R.VDFNVPLDGDR.I		R.VDFNVPLDGDR.I
40	48	2	910.59	3.6	0	25.3	6.99	90.80%	R.IVGALPTIK.Y		R.IVGALPTIK.Y
330	347	2	2010.99	4.7	1	67	21.3	95.00%	K.TIVWNGPAGVFEFDNFAK.G		K.TIVWNGPAGVFEFDNFAK.G
303	316	2	1501.67	2.7	0	39.1	23.2	95.00%	E.GIPDGWMGLDCGPK.S	Carbamidomethyl (+57)	K.VGSATAEEGIPDGWMGLDCGPK.S
250	261	2	1237.59	4.5	1	61.5	22	95.00%	K.IGDSLFDEAGSK.N		K.IGDSLFDEAGSK.N
218	227	2	1183.69	5.5	0	39.2	16	95.00%	K.IQLIDNLLDK.V		K.IQLIDNLLDK.V
218	230	2	1552.9	3.8	1	40.5	11.8	95.00%	K.IQLIDNLLDKVNR.L		K.IQLIDNLLDKVNR.L
404	414	2	1040.63	5.6	0	39.4	16.1	95.00%	K.ALPGVVALSSK.-		K.ALPGVVALSSK.-

277	291	2	1739.92	2.5	1	46.9	18.8	95.00%	E.VFLPVDFVTADKFDK.D		K.NNVEVFLPVDFVTADKFDK.D
330	341	2	1288.65	2.8	0	31.5	20.4	95.00%	K.TIVWNGPAGVFE.F		K.TIVWNGPAGVFEFDNFAK.G
321	329	2	994.54	5.5	1	50.2	18.6	95.00%	K.FAEVITTSK.T		K.FAEVITTSK.T
75	86	3	1304.74	4.3	1	59.4	15.2	95.00%	K.YSLKPVAAELSK.L		K.YSLKPVAAELSK.L
197	213	2	1737	3.5	1	61.6	10.8	95.00%	K.ALENPARPFLAILGGAK.V		K.ALENPARPFLAILGGAK.V
151	169	2	2020.01	5.9	0	113	21	95.00%	K.SLTSLGDIFVNDAFGTAHR.A		K.SLTSLGDIFVNDAFGTAHR.A
362	378	2	1527.83	2.9	0	72.1	16.6	95.00%	E.AGNVVIVGGGDTATVAK.K		K.TCEAGNVVIVGGGDTATVAK.K
170	181	2	1267.64	4	0	58.7	21.1	95.00%	R.AHSSMVGVDLPR.V		R.AHSSMVGVDLPR.V
150	169	3	2148.1	3.4	1	64.2	19.6	95.00%	R.KSLTSLGDIFVNDAFGTAHR.A		R.KSLTSLGDIFVNDAFGTAHR.A
214	227	2	1596.92	3.7	1	58.7	12	95.00%	K.VADKIQLIDNLLDK.V		K.VADKIQLIDNLLDK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
3	ENO11_SCHPO	59.00%	100%	29

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
258	263	2	765.39	4.7	0	25.9	21.6	91.90%	K.YDLDIK.A		K.YDLDIK.A
212	230	2	1978.03	3.8	1	26.7	19.1	93.00%	E.GGIAPDLQTPQEALDLIVE.A		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
361	374	3	1608.73	4.7	1	47.1	23.9	95.00%	R.MSYEAGWGVMVSHR.S		R.MSYEAGWGVMVSHR.S
185	194	2	1204.59	5.4	1	34	22.3	95.00%	R.WGAETYHTLK.S		R.WGAETYHTLK.S
346	360	2	1585.85	6	1	90.8	17.3	95.00%	K.VNQIGSVTESLNAVR.M		K.VNQIGSVTESLNAVR.M
346	354	2	945.48	4.5	0	30.4	21	95.00%	K.VNQIGSVTE.S		K.VNQIGSVTESLNAVR.M
423	432	2	929.48	4	0	46.6	22.9	95.00%	E.GVYAGAHAGK.Y		R.IEEELGSEGVYAGAHAGK.Y
201	223	2	2261.02	4.7	1	58.1	23.3	95.00%	R.YGSSAGNVGDEGGIAPDLQTPQE.A		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
365	374	2	1098.54	2.7	0	84.8	21.3	95.00%	E.AGWGVMVSHR.S		R.MSYEAGWGVMVSHR.S
311	328	2	1963.98	4.2	1	93.2	21.3	95.00%	K.AETDFQIVGDDLTVTNVK.R		K.AETDFQIVGDDLTVTNVK.R
313	329	2	1920	2.6	1	73.9	19.1	95.00%	E.TDFQIVGDDLTVTNVKR.L		K.AETDFQIVGDDLTVTNVKR.L
289	310	3	2679.2	3	1	73.2	24	95.00%	K.YPIVSIEDPFDQDDWSAWTHMK.A		K.YPIVSIEDPFDQDDWSAWTHMK.A
65	79	2	1477.87	4	0	73.7	6.99	95.00%	K.AVGNVNNIIAPAVVK.A		K.AVGNVNNIIAPAVVK.A
106	120	2	1560.82	4.2	0	61.3	19.9	95.00%	K.LGANAILGVSMAICR.A	Oxidation (+16)/ Carbamidomethyl (+57)	K.LGANAILGVSMAICR.A
313	328	2	1763.9	2.8	0	54.8	21.3	95.00%	E.TDFQIVGDDLTVTNVK.R		K.AETDFQIVGDDLTVTNVK.R
378	396	2	1928.04	2.5	0	68.1	15.4	95.00%	E.TADTFISHLTVGIGAGQLK.S		R.SGETADTFISHLTVGIGAGQLK.S
169	184	2	1769.85	3.5	1	50.8	22.4	95.00%	E.FMILPTGAPSFSEAMR.W	Oxidation (+16)	K.GPYVLPVPSFNVLNGGSHAGGDLAFQEFMILPTGAPSFSEAMR.W
169	181	2	1395.68	4.6	0	52.4	22.5	95.00%	E.FMILPTGAPSFSE.A		K.GPYVLPVPSFNVLNGGSHAGGDLAFQEFMILPTGAPSFSEAMR.W
419	432	2	1315.66	3.9	1	49	22.1	95.00%	E.LGSEGVYAGAHAGK.Y		R.IEEELGSEGVYAGAHAGK.Y
212	223	2	1224.6	3.3	0	35	21.8	95.00%	E.GGIAPDLQTPQE.A		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
273	287	2	1812.96	4.5	1	75.4	17.7	95.00%	K.LTYQQLTDLYVELSK.K		K.LTYQQLTDLYVELSK.K
243	257	2	1598.79	4.2	1	56.6	21.4	95.00%	K.IGLDVASSEFYVDGK.Y		K.IGLDVASSEFYVDGK.Y
252	263	2	1474.74	4.9	1	31.7	20.3	95.00%	E.FYVDGKYDLDIK.A		K.IGLDVASSEFYVDGKYDLDIK.A
338	345	2	901.51	4.7	0	31.4	19.4	95.00%	K.CANALLLK.V	Carbamidomethyl (+57)	K.CANALLLK.V
409	414	2	806.43	5.7	1	29.4	21.4	95.00%	K.YNELLR.I		K.YNELLR.I
375	396	2	2201.14	2.9	1	122	18.6	95.00%	R.SGETADTFISHLTVGIGAGQLK.S		R.SGETADTFISHLTVGIGAGQLK.S
89	96	2	905.49	4.7	1	57.4	20.4	95.00%	K.AADEFLLK.L		K.AADEFLLK.L
80	88	2	1002.5	4.3	0	41.9	20.3	95.00%	K.ANLDVTDQK.A		K.ANLDVTDQK.A
201	211	2	1054.43	4.6	0	26.4	22.5	92.60%	R.YGSSAGNVGDE.G		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
4	METE_SCHPO	51.70%	100%	31

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

325	349	2	2643.32	3.5	1	31.5	20	95.00%	R.VQVASSSSILHIPHSLSGEDQINPE.I		R.VQVASSSSILHIPHSLSGEDQINPEIK.R
104	118	2	1384.69	3.4	1	50.4	21.6	95.00%	R.AATADKAAVDVPAGE.M		R.AATADKAAVDVPAGEMVK.W
638	667	3	3497.61	3.2	0	56.4	22.9	95.00%	R.LATAAVQDDTQIHSHFCYSDFNDIFDAIQR.L	Carbamidomethyl (+57)	R.LATAAVQDDTQIHSHFCYSDFNDIFDAIQR.L
577	595	2	2108.02	2.7	1	68.8	21.5	95.00%	R.DDVHDSVQAQQIALGLRDE.V		R.DDVHDSVQAQQIALGLRDEVLDLEK.A
561	571	2	1184.7	5.1	0	40.5	15.3	95.00%	K.GMLTAPITILR.W		K.GMLTAPITILR.W
434	449	2	1746.96	2.8	0	73.3	14.6	95.00%	K.LPLFPTTTIGSFPQTK.E		K.LPLFPTTTIGSFPQTK.E
4	11	2	845.48	4.8	0	33.3	20.1	95.00%	K.SAVLGFPR.I		K.SAVLGFPR.I
707	714	2	901.49	4.3	1	27.7	21.4	94.30%	R.VPPVSEFK.E		R.VPPVSEFK.E
684	690	2	813.51	5.6	0	34.2	17.2	95.00%	K.LLNVLSR.Y		K.LLNVLSR.Y
691	706	2	1818.88	3.8	0	84	22.1	95.00%	R.YTSCIGPGLFDIHSPR.V	Carbamidomethyl (+57)	R.YTSCIGPGLFDIHSPR.V
499	508	2	1257.55	4.4	1	53.6	23.2	95.00%	R.NDMVQYFGER.M		R.NDMVQYFGER.M
243	260	2	1982.08	3.5	0	54.1	14.5	95.00%	K.LILTTYFGSLQSNADVLK.G		K.LILTTYFGSLQSNADVLK.G
727	738	2	1466.7	4.2	0	48	23	95.00%	K.DHLWLNPDCGLK.T	Carbamidomethyl (+57)	K.DHLWLNPDCGLK.T
468	473	2	783.39	2.4	0	25.4	18.7	91.00%	E.YDAFIR.K		K.GLISQEEYDAFIR.K
428	449	3	2402.33	3.5	1	49	10.8	95.00%	K.QQASLKLPLFPTTTIGSFPQTK.E		K.QQASLKLPLFPTTTIGSFPQTK.E
157	176	3	2127.29	3.3	0	20.7	6.02	90.10%	E.AGIITRPVLVGPVTYLFIAK.A		K.EAGIITRPVLVGPVTYLFIAK.A
261	273	2	1330.78	4	0	55.7	11.8	95.00%	K.GLPIAGVHVDVVR.A		K.GLPIAGVHVDVVR.A
468	474	2	911.49	4	1	33.5	18.1	95.00%	E.YDAFIRK.E		K.GLISQEEYDAFIRK.E
122	133	2	1609.74	3.1	0	32.2	24	95.00%	K.WFDSNYHFLRPE.V		K.WFDSNYHFLRPEVSEETDFK.L
281	299	2	1881.08	4.8	1	87.4	10	95.00%	R.ALAVLGENQIISVGVVSGR.N		R.ALAVLGENQIISVGVVSGR.N
723	738	3	1927.98	4	1	24.5	19	95.00%	K.HVPKDHLWLNPDCGLK.T	Carbamidomethyl (+57)	K.HVPKDHLWLNPDCGLK.T
288	299	2	1227.7	2.7	0	55.4	17.2	95.00%	E.NQIISVGVVSGR.N		R.ALAVLGENQIISVGVVSGR.N
361	369	2	1017.56	4.9	1	30.5	18.3	95.00%	K.CAELAILTK.A	Carbamidomethyl (+57)	K.CAELAILTK.A
547	560	2	1596.79	3.6	1	50.8	22	95.00%	K.ESQYAQSITSKPMK.G		K.ESQYAQSITSKPMK.G
606	615	2	1199.6	4.3	0	55.1	21.4	95.00%	K.VIQCDEPALR.E	Carbamidomethyl (+57)	K.VIQCDEPALR.E
668	679	2	1288.66	3.8	1	37	20.8	95.00%	R.LDADVVSIENSK.S		R.LDADVVSIENSK.S
527	546	3	2267.24	3.3	0	44.5	14.1	95.00%	R.CVRPPIIVGDVYRPAPMTVK.E	Carbamidomethyl (+57)	R.CVRPPIIVGDVYRPAPMTVK.E
631	637	2	877.45	5.9	0	49	21.3	95.00%	K.WAIDAFR.L		K.WAIDAFR.L
85	99	2	1616.79	4.1	0	63.5	22.1	95.00%	R.LSGLSSLDTYFAMGR.G		R.LSGLSSLDTYFAMGR.G
156	176	3	2256.33	3.9	1	51.3	6.99	95.00%	K.EAGIITRPVLVGPVTYLFIAK.A		K.EAGIITRPVLVGPVTYLFIAK.A
52	82	3	3521.71	3.5	0	48.3	19.9	95.00%	K.AQGVDIIPSNDFSLYDQIMDHSFSFNVIPPR.Y		K.AQGVDIIPSNDFSLYDQIMDHSFSFNVIPPR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
5	KPYK_SCHPO	60.90%	100%	27							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
191	201	2	1186.61	4.4	1	25.5	20.9	91.20%	K.TDVDLPALSEK.D		K.TDVDLPALSEK.D
454	462	2	1129.58	3.1	1	46.7	20	95.00%	E.KEPLSDWQK.D		R.GVYPVIYEKEPLSDWQK.D
487	497	2	1053.66	5.9	0	39.5	10.4	95.00%	K.IIVLQGAVGGK.G		K.IIVLQGAVGGK.G
116	127	2	1403.63	3.3	1	39.2	23.4	95.00%	E.MIFTTDDAYAEK.C		R.TGLTVGGTDYPISSGHEMIFTTDDAYAEK.C
422	433	3	1430.81	4	0	44.4	13.4	95.00%	K.YRPSIPIVMVTR.C		K.YRPSIPIVMVTR.C
10	26	2	1880.98	3.7	1	90.9	18.7	95.00%	K.QWVAGLNSELDIPAVNR.R		K.QWVAGLNSELDIPAVNR.R
66	75	2	1201.59	4.2	0	35.6	21.6	95.00%	E.YHQSVIDNAR.K		R.MNFSHGSYEYHQSVIDNAR.K
278	288	2	1186.67	2.9	0	27.1	17.2	93.50%	E.IPASQVFVAQK.M		R.GDLGIEIPASQVFVAQK.M
128	138	2	1447.65	4.4	1	38.9	23.7	95.00%	K.CNDKVMYIDYK.N	Carbamidomethyl (+57)	K.CNDKVMYIDYK.N
345	357	2	1415.63	3.1	1	41.3	23.5	95.00%	K.GSYPVEAVTYMAE.T		K.GSYPVEAVTYMAETAR.V
248	271	2	2647.3	2.3	1	73.9	20.2	95.00%	K.IENQQGVNNFDSILDVTDGIMVAR.G		K.IENQQGVNNFDSILDVTDGIMVAR.G
77	93	2	1741.97	3.8	0	39.2	16.6	95.00%	K.ASATNPLFPLAIALDTK.G		K.ASATNPLFPLAIALDTK.G
225	232	2	951.52	5	1	30.1	20.1	95.00%	R.AEDVIHIR.E		R.AEDVIHIR.E
77	96	2	2025.08	2.4	1	40.5	16.3	95.00%	K.ASATNPLFPLAIALDTKGPE.I		K.ASATNPLFPLAIALDTKGPEIR.T
57	75	3	2254	4.4	1	44.4	24.3	95.00%	R.MNFSHGSYEYHQSVIDNAR.K		R.MNFSHGSYEYHQSVIDNAR.K
28	37	2	1088.6	5	0	46.3	18.4	95.00%	R.TSIICTIGPK.S	Carbamidomethyl (+57)	R.TSIICTIGPK.S
364	374	2	1226.59	3.2	0	47.3	21.8	95.00%	E.ASIPYGSLYQE.M		R.VAEASIPYGSLYQEMFGLVR.R

468	477	2	1186.55	5.3	0	54.8	21.9	95.00%	R.VAYGCQQAYK.M	Carbamidomethyl (+57)	R.VAYGCQQAYK.M
272	288	2	1770.96	2.9	1	71.4	16.6	95.00%	R.GDLGIEIPASQVFVAQK.M		R.GDLGIEIPASQVFVAQK.M
294	319	4	2965.41	3.9	1	47.2	22.5	95.00%	K.CNIAGKPVACATQMLESMTYNPR PTR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CNIAGKPVACATQMLESMTYNPR PTR.A
405	417	2	1287.72	5.7	0	62	16.5	95.00%	K.AIVVLSTSGNTAR.L		K.AIVVLSTSGNTAR.L
76	93	2	1870.06	4.2	1	70.7	11.1	95.00%	R.KASATNPLFPLAIALDTK.G		R.KASATNPLFPLAIALDTK.G
212	223	2	1368.69	4.2	0	39.8	20.4	95.00%	K.NGVDMIFASFIR.R		K.NGVDMIFASFIR.R
294	309	2	1761.83	2.8	0	75.3	22.8	95.00%	K.CNIAGKPVACATQMLE.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CNIAGKPVACATQMLESMTYNPR PTR.A
99	115	2	1689.79	3.2	0	69.5	23	95.00%	R.TGLTVGGTDYPISSGHE.M		R.TGLTVGGTDYPISSGHEMIFTTDD AYAEK.C
389	404	2	1503.78	2.7	1	64.5	20	95.00%	E.TTAVAAIGASIESDAK.A		R.RPLECATETTAVAAIGASIESDAK. A
47	56	3	1143.62	4.2	1	26	20.4	95.00%	K.LRDAGMNIVR.M		K.LRDAGMNIVR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
6	EF1A1_SCHPO	41.09%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
267	286	2	1988.07	2.8	0	31	16.7	95.00%	E.TGVIKPGMIVTFAPAGVTTE.V		R.VETGVIKPGMIVTFAPAGVTTEVK .S
136	146	2	1184.7	2.7	0	35.5	15.8	95.00%	E.HALLAYTLGVK.Q		R.EHALLAYTLGVK.Q
402	421	2	2268.08	4	1	67.5	22	95.00%	K.MVPSKPMCVEAFTDYAPLGR.F	Carbamidomethyl (+57)	K.MVPSKPMCVEAFTDYAPLGR.F
296	311	2	1601.81	2.4	0	73.2	20.5	95.00%	E.SLDAGLPGDNVGFNVK.N		K.SVEMHHESLDAGLPGDNVGFNV K.N
147	154	2	883.55	5.8	0	26.4	16.3	92.50%	K.QLIVAVNK.M		K.QLIVAVNK.M
254	264	2	1024.61	4.2	0	65.4	12.8	95.00%	K.IGGIGTVPVGR.V		K.IGGIGTVPVGR.V
6	20	2	1529.84	4.6	0	62.9	16.7	95.00%	K.GHINVVVIGHVDSGK.S		K.GHINVVVIGHVDSGK.S
185	214	3	3453.63	3.7	0	49.2	21.7	95.00%	K.TVPFVPVSGFQGDNMIEPTTNMP WYQGWQK.E		K.TVPFVPVSGFQGDNMIEPTTNMP WYQGWQK.E
85	100	2	1843.96	3.2	1	30.6	19.3	95.00%	K.YNVTVIDAPGHRDFIK.N		K.YNVTVIDAPGHRDFIK.N
225	245	3	2331.29	2.6	1	34.8	13.2	95.00%	K.TLLEAIDSIEPPARPTDKPLR.L		K.TLLEAIDSIEPPARPTDKPLR.L
265	286	2	2216.18	3.1	1	49.6	16.1	95.00%	R.VETGVIKPGMIVTFAPAGVTTE.V		R.VETGVIKPGMIVTFAPAGVTTEVK .S
155	164	2	1151.51	6.4	0	75.8	21.9	95.00%	K.MDTTGWSQAR.F		K.MDTTGWSQAR.F
85	96	2	1340.69	4.4	0	66.1	19.8	95.00%	K.YNVTVIDAPGHR.D		K.YNVTVIDAPGHR.D
246	253	2	974.55	4.1	0	32.1	18.8	95.00%	R.LPLQDVYK.I		R.LPLQDVYK.I
135	146	2	1313.74	3.9	1	45.8	17.4	95.00%	R.EHALLAYTLGVK.Q		R.EHALLAYTLGVK.Q
402	411	2	1176.54	3.1	0	28	21.7	94.60%	K.MVPSKPMCVE.A	Carbamidomethyl (+57)	K.MVPSKPMCVEAFTDYAPLGR.F
412	421	2	1109.55	3.4	0	43.6	21.3	95.00%	E.AFTDYAPLGR.F		K.MVPSKPMCVEAFTDYAPLGR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
7	ALF_SCHPO	67.60%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
207	234	3	2951.53	3.4	1	40.6	18.6	95.00%	R.ELSSVTPYFSIAAAFGNVHGVYK PGNVK.L		R.ELSSVTPYFSIAAAFGNVHGVYK PGNVK.L
253	275	2	2528.21	2	1	93.7	21.5	95.00%	K.TTNDKPVFFVFHGGSGSSVNEFR .T		K.TTNDKPVFFVFHGGSGSSVNEFR .T
94	112	2	2098.02	4.1	0	63.5	21.2	95.00%	R.SIAPFFGVPVVMHSDHCAK.K	Carbamidomethyl (+57)	R.SIAPFFGVPVVMHSDHCAK.K
2	19	2	1823.05	3.8	0	65.3	10.8	95.00%	M.GILDIVPTGVITGDNVLK.L		-.MGILDIVPTGVITGDNVLK.L
345	358	2	1597.83	4.2	1	60.4	19.5	95.00%	R.VLTALEDFYTVNTL.-		R.VLTALEDFYTVNTL.-
194	206	2	1696.81	2.4	1	51.8	22.3	95.00%	E.LYTQPEDIWDVYR.E		K.IWIEMEIGITGGEEDGVDNSHVSH TELYTQPEDIWDVYR.E
26	47	2	2198.13	3.4	1	51.9	18.6	95.00%	R.EHGFAIPAINVTSSSTAIAALE.A		R.EHGFAIPAINVTSSSTAIAALEAAR .E
285	300	2	1825.89	3.9	1	73.6	22	95.00%	K.VNIDTDTQFAYVEGVR.D		K.VNIDTDTQFAYVEGVR.D

306	318	2	1525.72	2.5	1	53.6	23.2	95.00%	K.YKDYLMTPVGNPE.G		K.YKDYLMTPVGNPEGADKPNK.K
113	123	2	1365.65	3.6	1	34.2	22.7	95.00%	K.KLLPWMDGMFE.A		K.KLLPWMDGMFEADEAYFK.I
253	273	2	2225.05	2.9	0	58.6	22.6	95.00%	K.TTNDKPVFFVFHGGSGSSVNE.F		K.TTNDKPVFFVFHGGSGSSVNEFR.T
114	123	2	1237.56	3.9	0	34	22.4	95.00%	K.LLPWMDGMFE.A		K.LLPWMDGMFEADEAYFK.I
235	248	2	1564.88	2.5	0	66.9	12.8	95.00%	K.LQPALLGQHQAYVK.E		K.LQPALLGQHQAYVK.E
54	71	2	1843.96	2.8	0	95.8	19.3	95.00%	R.SPIILQTSNGGAHFFAGK.E		R.SPIILQTSNGGAHFFAGK.E
94	113	5	2226.12	3.2	1	16.5	20	95.00%	R.SIAPFFGVPVVMHSDHCAKK.L	Carbamidomethyl (+57)	R.SIAPFFGVPVVMHSDHCAKK.L
131	149	3	2165.05	3.2	1	36.1	21.9	95.00%	K.IHGEPLFSSHMLDLSEEPK.K		K.IHGEPLFSSHMLDLSEEPK.K
80	93	2	1399.76	5.1	0	89.1	17.2	95.00%	K.ASIAGSIAAAHYIR.S		K.ASIAGSIAAAHYIR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
8	PDC2_SCHPO	41.75%	100%	24

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
379	393	2	1650.82	2.9	0	34.5	22.1	95.00%	R.QIQGLVDSNTTLYAE.T		R.QIQGLVDSNTTLYAETGDSWFNGLQMK.L
204	214	2	1130.62	4.6	1	53.5	18.8	95.00%	K.ATDIAAELISK.K		K.ATDIAAELISK.K
440	461	2	2409.21	3.3	1	90.9	18.9	95.00%	R.TIVMVGDGSFQLTGQEISQMIR.H		R.TIVMVGDGSFQLTGQEISQMIR.H
238	253	2	1690.85	4.5	1	52.2	21.1	95.00%	K.LAEALNCAAFIMPAAK.G	Deamidation (+1)/ Carbamidomethyl (+57)	K.LAEALNCAAFIMPAAK.G
228	237	2	949.49	5	1	30.2	21.6	95.00%	R.AAGAESAFVK.L		R.AAGAESAFVK.L
57	68	2	1341.62	3.6	1	36.9	22	95.00%	E.LNCAFAAEGYAR.S	Carbamidomethyl (+57)	R.LLDFLEYYPGLSEIGCCNELNCAFAAEGYAR.S
7	18	2	1326.66	2	0	44.7	20.9	95.00%	E.STMTVGTYLAQR.L		K.DAESTMTVGTYLAQR.L
304	328	2	2694.37	3	0	65.1	17.9	95.00%	R.AAPNPNILLNSDYTSVSIPGYVFSR.V		R.AAPNPNILLNSDYTSVSIPGYVFSR.V
147	159	2	1436.71	2.7	1	61.7	21.9	95.00%	R.AEDAPVMIDHAIR.Q		R.AEDAPVMIDHAIR.Q
480	489	3	1211.61	3.6	0	24.1	21.2	95.00%	E.IQIHDGPYNR.I		R.GYTIEIQIHDGPYNR.I
241	253	2	1376.7	4.1	0	60.3	20.9	95.00%	E.ALNCAAFIMPAAK.G	Carbamidomethyl (+57)	K.LAEALNCAAFIMPAAK.G
379	405	2	3015.43	1.6	1	70.1	22.1	95.00%	R.QIQGLVDSNTTLYAETGDSWFNGLQMK.L		R.QIQGLVDSNTTLYAETGDSWFNGLQMK.L
137	146	2	1101.64	5.4	1	51.2	16.4	95.00%	K.LTCAAVAIKR.A	Carbamidomethyl (+57)	K.LTCAAVAIKR.A
394	405	2	1398.63	3.6	0	46	22.8	95.00%	E.TGDSWFNGLQMK.L	Oxidation (+16)	R.QIQGLVDSNTTLYAETGDSWFNGLQMK.L
19	25	2	770.49	4.3	1	34.4	14.8	95.00%	R.LVEIGIK.N		R.LVEIGIK.N
462	474	3	1575.97	4.8	1	29.2	3.01	95.00%	R.HKLPVLIFLLNNR.G		R.HKLPVLIFLLNNR.G
149	159	2	1236.63	2.6	0	46.5	21.1	95.00%	E.DAPVMIDHAIR.Q		R.AEDAPVMIDHAIR.Q
26	37	2	1429.72	4.2	0	38.3	21.1	95.00%	K.NHFVVPGDYNLR.L		K.NHFVVPGDYNLR.L
464	474	2	1310.81	4.6	0	66.2	7.78	95.00%	K.LPVLIFLLNNR.G		K.LPVLIFLLNNR.G
136	145	2	1073.63	3.9	1	39.6	13	95.00%	K.KLTCAAVAIK.R	Carbamidomethyl (+57)	K.KLTCAAVAIK.R
4	18	2	1641.77	4.2	1	65.2	23.5	95.00%	K.DAESTMTVGTYLAQR.L		K.DAESTMTVGTYLAQR.L
172	194	3	2388.19	2.4	0	27	20.1	95.00%	E.IPTNMANQPCPVPGPISAVISPE.I	Carbamidomethyl (+57)	R.QAILQHKPVYIEIPTNMANQPCPVPGPISAVISPEISDK.E
539	549	2	1326.48	3.7	0	55.8	20.9	95.00%	E.CAIDTDDCTQE.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.EGPTLIECAIDTDDCTQELVDWGK.A
216	225	3	1064.66	3.8	1	29.3	11.8	95.00%	K.EKPILLAGPK.L		K.EKPILLAGPK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
9	ADH4_SCHPO	42.18%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
375	385	3	1245.76	3.9	0	37.6	6.02	95.00%	K.IRPHLVDLGVK.E		K.IRPHLVDLGVK.E
210	221	2	1351.65	4.3	0	53.4	22.8	95.00%	K.HTMPILSVNDPE.T		K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
76	87	2	1282.76	5.2	0	44.2	13.6	95.00%	K.NTLIVTDPGIIK.V		K.NTLIVTDPGIIK.V

245	261	2	1750.86	4.2	0	72.4	22	95.00%	E.AYVSTAANPITDACAVK.C	Carbamidomethyl (+57)	K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
366	374	2	1027.63	6.6	1	37.3	13	95.00%	R.ISQLVLEVK.I		R.ISQLVLEVK.I
149	159	2	1014.58	4.8	0	36.7	19.4	95.00%	K.GIALLATNGGK.I	Deamidation (+1)	K.GIALLATNGGK.I
169	188	2	1998.07	1.9	0	72.2	16.8	95.00%	K.SSKPQLPLIAINTTAGTASE.M		K.SSKPQLPLIAINTTAGTASEMTR.F
399	413	2	1624.69	6.5	0	46.4	23.3	95.00%	K.DACGATNPIQPTHDE.V	Carbamidomethyl (+57)	K.DACGATNPIQPTHDEVK.A
345	356	2	1359.62	2.6	1	56.5	22.9	95.00%	R.LGDIAFHLGCEE.H	Carbamidomethyl (+57)	R.LGDIAFHLGCEEHTAEAALDR.I
101	125	3	2678.34	2.6	0	43.6	20.3	95.00%	E.QSITVHLYDGVQPNPTVGNVNQGLE.I		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K
399	415	2	1851.85	4.5	1	49.6	23.2	95.00%	K.DACGATNPIQPTHDEVK.A	Carbamidomethyl (+57)	K.DACGATNPIQPTHDEVK.A
100	125	3	2807.38	3.2	1	28.6	20.9	95.00%	E.EQSITVHLYDGVQPNPTVGNVNQGLE.I		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K
169	191	2	2386.26	3.6	1	87.6	17.2	95.00%	K.SSKPQLPLIAINTTAGTASEMTR.F		K.SSKPQLPLIAINTTAGTASEMTR.F
130	148	2	1993.8	3.7	1	87.9	23.9	95.00%	K.ENCDSMVSIGGGSAHDCAK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.ENCDSMVSIGGGSAHDCAK.G
160	168	2	1008.48	5	1	40.9	22.5	95.00%	K.IADYEGVDK.S		K.IADYEGVDK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
10	THI3_SCHPO	48.55%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	127	2	1090.54	4.7	0	29.6	21.8	95.00%	K.IQLDDLCSK.F	Carbamidomethyl (+57)	K.IQLDDLCSK.F
74	95	2	2353.27	4.3	0	93.8	15.3	95.00%	R.GYPVTSFGSLLNEPFTGLITLK.G		R.GYPVTSFGSLLNEPFTGLITLK.G
128	139	2	1325.67	4.2	0	42.4	20.9	95.00%	K.FGLSPSDYTAIR.C		K.FGLSPSDYTAIR.C
37	56	2	1981.08	3.1	0	75.4	14.1	95.00%	E.VAILEPTNPSDVTALIGSGK.V		R.EGIEVAILEPTNPSDVTALIGSGK.V
6	27	2	2631.39	2.4	1	78.6	15.8	95.00%	K.ITFLTNWEATPYHLPIFLAQTR.G		K.ITFLTNWEATPYHLPIFLAQTR.G
63	71	2	954.54	4.5	0	51.1	14.8	95.00%	K.AMIHTLAAK.A		K.AMIHTLAAK.A
222	239	2	2030.06	3.2	1	79.8	19.1	95.00%	R.AIHSATLDMLKDPVQTYK.E		R.AIHSATLDMLKDPVQTYK.E
110	118	2	968.5	4.9	1	27.7	19.8	94.30%	R.IGYVGEFGK.I		R.IGYVGEFGK.I
14	27	2	1626.89	2.4	0	40.2	16.8	95.00%	E.ATPYHLPIFLAQTR.G		K.ITFLTNWEATPYHLPIFLAQTR.G
330	339	2	992.51	5.7	0	44.3	21.9	95.00%	K.GGVFSGNSLR.Y		K.GGVFSGNSLR.Y
189	211	3	2788.29	2.8	1	29.7	23.2	95.00%	R.LANLGCCCFCTILYIAHDEFIAK.H	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.LANLGCCCFCTILYIAHDEFIAK.H
260	273	2	1711.79	4.7	0	88.7	22.9	95.00%	R.CFAYFSHDISNVPR.D	Carbamidomethyl (+57)	R.CFAYFSHDISNVPR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
11	PMGY_SCHPO	52.61%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
176	185	2	1085.62	3.6	1	56.7	17.2	95.00%	E.GLTGDQIVKR.E		R.ALIMDLEGLTGDQIVKR.E
169	184	2	1714.92	4	1	69.3	17.2	95.00%	R.ALIMDLEGLTGDQIVK.R		R.ALIMDLEGLTGDQIVK.R
111	120	2	1271.65	5.7	1	79.8	21.1	95.00%	K.WGAEQVQIWR.R		K.WGAEQVQIWR.R
23	36	2	1589.81	3.1	1	55.6	20.2	95.00%	K.LNLFTGWKDPALSE.T		K.LNLFTGWKDPALSETGIK.E
95	108	2	1626.77	3.9	1	67.7	23.3	95.00%	R.YYGDLQGLNKDDAR.K		R.YYGDLQGLNKDDAR.K
186	199	2	1553.85	2.4	1	50.2	16.3	95.00%	R.ELATGVPIVYHLDK.D		R.ELATGVPIVYHLDK.D
2	14	2	1439.81	5.3	1	52	15.3	95.00%	M.TTEAAPNLLVLTR.H	Acetyl (+42)	-.MTTEAAPNLLVLTR.H
158	168	2	1149.67	4.5	0	26.5	13.2	92.80%	K.VLIAAHGNSLR.A		K.VLIAAHGNSLR.A
187	202	2	1724.95	2.1	1	35.8	17	95.00%	E.LATGVPIVYHLDKDGK.Y		R.ELATGVPIVYHLDKDGK.Y
95	104	2	1169.58	4.8	0	46.4	20.6	95.00%	R.YYGDLQGLNK.D		R.YYGDLQGLNK.D
1	14	2	1528.84	4.4	1	53	16.6	95.00%	-.MTTEAAPNLLVLTR.H		-.MTTEAAPNLLVLTR.H
53	66	2	1615.84	4.6	1	43.1	19.7	95.00%	R.GYKFDIAFTSALQR.A		R.GYKFDIAFTSALQR.A
5	14	2	1066.65	3.4	0	61.9	4.77	95.00%	E.AAPNLLVLTR.H		-.MTTEAAPNLLVLTR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
12	TPIS_SCHPO	54.22%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
223	239	2	1800.91	3	0	83.6	21	95.00%	K.FHDIDGFLVGGASLKPE.F		K.FHDIDGFLVGGASLKPEFHNIVNVHSL.-
160	174	2	1615.9	3.1	0	71.1	14.8	95.00%	K.IVIAYEPVWAIGTGK.T		K.IVIAYEPVWAIGTGK.T
58	70	2	1389.73	3.4	1	50	19.8	95.00%	K.DIGVGAQNVFDKK.N		K.DIGVGAQNVFDKK.N
78	98	2	2233.11	3.5	1	99	21.5	95.00%	E.NSAQSLIDAGITYTLTGHSER.R		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R
32	52	2	2422.27	3.5	1	66.1	17.3	95.00%	K.LNVGDVETVIFPQNMYLITTR.Q		K.LNVGDVETVIFPQNMYLITTR.Q
206	219	2	1453.66	3.6	1	63.9	23.2	95.00%	R.VIYGGSVNGGNCKE.F	Deamidation (+1)/ Carbamidomethyl (+57)	R.VIYGGSVNGGNCKEFLK.F
39	52	2	1695.91	2.9	0	51.5	17.8	95.00%	E.TVIFPQNMYLITTR.Q		K.LNVGDVETVIFPQNMYLITTR.Q
146	159	2	1613.86	4.5	1	61.4	19.4	95.00%	R.QLNAIADKVQNWSK.I		R.QLNAIADKVQNWSK.I
196	205	2	971.55	5.3	1	76.1	19.1	95.00%	K.LGASVAEGLR.V		K.LGASVAEGLR.V
223	249	3	2961.52	3.2	1	45.2	17.9	95.00%	K.FHDIDGFLVGGASLKPEFHNIVNVHSL.-		K.FHDIDGFLVGGASLKPEFHNIVNVHSL.-
206	218	2	1324.61	4.4	0	76.9	22.9	95.00%	R.VIYGGSVNGGNCK.E	Deamidation (+1)/ Carbamidomethyl (+57)	R.VIYGGSVNGGNCK.E
78	97	2	2077	3.3	0	101	22	95.00%	E.NSAQSLIDAGITYTLTGHSE.R		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
13	GLYD_SCHPO	47.54%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
146	159	2	1649.78	3.9	1	75	22.8	95.00%	K.ISAVSTYFESMPYR.V		K.ISAVSTYFESMPYR.V
124	145	3	2354.18	2.8	1	40.7	20	95.00%	R.LMGLDLPSGGHLSHGYQTDTKK.I		R.LMGLDLPSGGHLSHGYQTDTKK.I
233	243	2	1234.63	6.3	0	29	20.5	95.00%	E.YADVVTTTTHK.S		R.QIADSVNAYLVVDMAHISGLVSAGVIPSPFEYADVVTTTTHK.S
183	193	2	1209.62	4.5	0	57.8	20.3	95.00%	K.ILVAGTSAYCR.L	Carbamidomethyl (+57)	K.ILVAGTSAYCR.L
361	371	2	1254.76	4.6	1	48.8	9.54	95.00%	R.VLELINIVTNK.N		R.VLELINIVTNK.N
97	123	3	2996.43	3.4	0	55	21.4	95.00%	K.WGVNVQCLSGSPANMQVYQAIMPPHGR.L	Carbamidomethyl (+57)	K.WGVNVQCLSGSPANMQVYQAIMPPHGR.L
86	96	2	1129.62	5.1	0	54.8	20	95.00%	R.ALAAFNLDPAK.W		R.ALAAFNLDPAK.W
59	67	2	998.45	5.1	1	32.9	22	95.00%	K.YSEGYPGAR.Y		K.YSEGYPGAR.Y
277	302	3	2725.45	2.8	0	25.2	15.9	95.00%	K.INFSVFPGHQGGPHNHTITALAVALK.Q		K.INFSVFPGHQGGPHNHTITALAVALK.Q
413	422	2	1075.61	4.3	0	49.9	17.6	95.00%	R.ALTFAANLQK.E		R.ALTFAANLQK.E
46	58	2	1321.64	4.2	0	41.4	22.8	95.00%	R.AVMDALGSVMSNK.Y		R.AVMDALGSVMSNK.Y
160	182	3	2686.31	2.9	1	31.8	21.6	95.00%	R.VDPNTGLIDYDMLEHDAQLFRPK.I		R.VDPNTGLIDYDMLEHDAQLFRPK.I
145	154	2	1143.58	2.7	1	27.4	20.3	93.90%	K.KISAVSTYFE.S		K.KISAVSTYFESMPYR.V
334	349	2	1669.84	3.9	0	85	21.1	95.00%	K.LAADGTDSHMVLVDVK.S		K.LAADGTDSHMVLVDVK.S
457	467	2	1306.64	3.2	1	69.2	22.6	95.00%	E.WASSFPLADKW.-		K.EVAEWASSFPLADKW.-
406	412	2	878.45	4.3	0	35.8	21.5	95.00%	R.VVDYIDR.A		R.VVDYIDR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
14	THI2_SCHPO	27.13%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
175	187	2	1431.8	4.7	1	52.1	14.8	95.00%	K.LFNATAVEDLIVK.E		K.LFNATAVEDLIVK.E
2	15	2	1400.77	3.8	0	74.5	17.5	95.00%	M.APATAVVTPQTAFK.T		-.MAPATAVVTPQTAFK.T
244	263	3	2296.15	3.2	0	39.6	20.3	95.00%	R.LASAQLVSNLHDMRPLDMNR.A	Oxidation (+16)	R.LASAQLVSNLHDMRPLDMNR.A
39	55	2	1962.95	4.7	1	48.4	22.6	95.00%	K.AYPTYSLDESFSFAPIR.E		K.AYPTYSLDESFSFAPIR.E
1	15	2	1573.82	4.5	0	31.2	20	95.00%	-.MAPATAVVTPQTAFK.T	Acetyl (+42)	-.MAPATAVVTPQTAFK.T
295	308	2	1459.67	4	0	71.7	22.5	95.00%	R.MGPTFGGMMFSGIK.A		R.MGPTFGGMMFSGIK.A
243	263	4	2436.26	3.2	1	17.4	18.1	92.00%	K.RLASAQLVSNLHDMRPLDMNR.A		K.RLASAQLVSNLHDMRPLDMNR.A
131	139	2	1045.55	2.9	0	37	20.7	95.00%	R.KPADLFLNE.I		R.KPADLFLNEIGVPYEDEGDYVVVK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
15	SAHH_SCHPO	36.03%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
407	427	2	2266.18	3.4	0	77.1	18.3	95.00%	K.LTTLTSVQSDYLGIPVDGPYK.A		K.LTTLTSVQSDYLGIPVDGPYK.A
314	328	3	1665.93	5.5	1	30.5	14.8	95.00%	K.ANAKDVVNIKPQVDR.Y		K.ANAKDVVNIKPQVDR.Y
26	35	2	1114.58	2.7	1	38.1	19.8	95.00%	E.NEMPGLIAVR.E	Oxidation (+16)	K.ELEIAENEMPGLIAVR.E
8	18	2	1118.61	3.2	0	77.1	18.3	95.00%	K.VADISLAAFGR.K		K.VADISLAAFGR.K
216	227	2	1117.62	4.3	0	46.5	18.3	95.00%	K.VAVVAGFGDVGK.G		K.VAVVAGFGDVGK.G
269	280	2	1367.66	4	1	40.1	22.3	95.00%	K.EGQIFVTTTGCR.D	Carbamidomethyl (+57)	K.EGQIFVTTTGCR.D
119	143	3	2681.36	3.6	1	80.1	18.9	95.00%	K.SFPSGKPLNMILDDGGDLTALVHER.H		K.SFPSGKPLNMILDDGGDLTALVHER.H
176	187	2	1255.68	4.6	0	42.1	17.6	95.00%	K.VPAINVNDSVTK.S		K.VPAINVNDSVTK.S
336	344	2	1006.6	5	0	31.2	13	95.00%	R.HIILLADGR.L		R.HIILLADGR.L
174	187	3	1496.86	5	1	47.8	14.3	95.00%	K.LKVPAINVNDSVTK.S		K.LKVPAINVNDSVTK.S
318	328	2	1281.71	3.7	0	30.2	18	95.00%	K.DVVNIKPQVDR.Y		K.DVVNIKPQVDR.Y
318	330	2	1573.81	3	1	55.2	19.7	95.00%	K.DVVNIKPQVDRYE.L		K.DVVNIKPQVDRYELK.N
28	35	2	855.5	2.7	0	45.4	15.6	95.00%	E.MPGLIAVR.E		K.ELEIAENEMPGLIAVR.E
270	280	2	1238.61	4.1	0	45.8	21.9	95.00%	E.GQIFVTTTGCR.D	Carbamidomethyl (+57)	K.EGQIFVTTTGCR.D
245	259	2	1589.75	3.7	0	80.2	23.1	95.00%	E.VDPINALQAAMDGFE.V		R.VIVTEVDPINALQAAMDGFEVTTMEEAVK.E
158	167	2	1132.59	3.8	0	33.1	19.9	95.00%	E.TTTGVHNLYK.M		R.GISEETTTGVHNLYK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
16	METK_SCHPO	46.86%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
147	155	2	931.5	4.5	0	58	22	95.00%	K.LNAAMSVAR.R		K.LNAAMSVAR.R
20	40	3	2423.15	4	1	37.1	22.2	95.00%	K.ICDQISDAILDACLKDDPFSK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.ICDQISDAILDACLKDDPFSK.V
137	146	3	1117.73	2.5	0	31	3.01	95.00%	K.LPLTILLAHK.L		K.LPLTILLAHK.L
99	112	2	1612.79	3.3	1	48.1	22.1	95.00%	E.QQSPDIAQGLHYEK.A		K.TCNVLVAIEQQSPDIAQGLHYEK.A
2	10	2	1042.5	4.3	0	43.9	21.9	95.00%	M.AQTFLFTSE.S		-.MAQTFLFTSESVGEGHPDK.I
237	251	2	1429.74	3.6	0	73.6	19.7	95.00%	R.FVVGGPQGDAGLTGR.K		R.FVVGGPQGDAGLTGR.K
339	349	2	1256.73	4.3	0	36.5	15.2	95.00%	K.NFDLRPGVLVK.S		K.NFDLRPGVLVK.S
117	135	2	1970.86	2.7	1	82	23.5	95.00%	E.LGAGDQGIMFGYATDETPE.K		K.ALEELGAGDQGIMFGYATDETPEK.L
252	272	3	2077.05	3.9	1	61	20.4	95.00%	R.KIIVDTYGGWGAHGGGAFSGK.D		R.KIIVDTYGGWGAHGGGAFSGK.D
353	378	3	3055.48	3	1	68	20.7	95.00%	K.LQTPFYLSTASYGHFTDQSKPWEQPK.E		K.LQTPFYLSTASYGHFTDQSKPWEQPK.E
291	299	2	856.52	4.2	0	28.1	16.9	94.70%	K.SLVAAGLAR.R		K.SLVAAGLAR.R
213	226	2	1572.93	2.5	1	38.8	9.54	95.00%	K.IIKPTVPAHLLDEK.T		K.IIKPTVPAHLLDEK.T
253	272	2	1948.95	4	0	80.8	22.5	95.00%	K.IIVDTYGGWGAHGGGAFSGK.D		K.IIVDTYGGWGAHGGGAFSGK.D
136	146	3	1245.82	2.6	1	40.5	6.02	95.00%	E.KLPLTILLAHK.L		K.ALEELGAGDQGIMFGYATDETPEKLPLTILLAHK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
17	HSP72_SCHPO	29.37%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
327	340	2	1400.77	3.9	1	39.7	17.7	95.00%	K.ASVNEIVLVGGSTR.I		K.ASVNEIVLVGGSTR.I
4	25	3	2425.14	2.4	1	30.6	22.9	95.00%	K.SIGIDLGTTYSCVGHFSNNRVE.I	Carbamidomethyl (+57)	K.SIGIDLGTTYSCVGHFSNNRVEIIANDQGNR.T
538	548	2	1351.66	4.4	1	37.5	21.6	95.00%	K.NHLESYAYSLR.N		K.NHLESYAYSLR.N
137	153	2	1880.93	4	0	55	20.6	95.00%	K.VTDAVVTVPAYFNDSQR.Q		K.VTDAVVTVPAYFNDSQR.Q
76	86	2	1309.56	4.9	1	34.7	23.1	95.00%	K.FDDPEVQSDMK.H		K.FDDPEVQSDMK.H
170	185	2	1686.9	2.7	0	94.2	18.9	95.00%	R.IINEPTAAAIAYGLDR.S		R.IINEPTAAAIAYGLDR.S
578	589	2	1349.61	3.4	1	58.5	23.3	95.00%	E.WLDSNTTAAKDE.F		K.ETIEWLDSNTTAAKDEFEAK.Q
219	234	2	1647.72	4.3	1	72.5	23.9	95.00%	K.ATAGDTHLGGEDFDSR.L		K.ATAGDTHLGGEDFDSR.L

55	69	2	1698.82	4.2	0	74.8	22	95.00%	K.NQVAMNPHNTIFDAK.R			K.NQVAMNPHNTIFDAK.R
457	467	2	1182.65	4.4	1	28.3	16.8	94.90%	K.FELSGIPPAPR.G			K.FELSGIPPAPR.G
235	244	2	1273.69	4.3	1	25.1	19.4	90.40%	R.LVNHFIQEFK.R			R.LVNHFIQEFK.R
35	47	2	1486.7	4.2	1	60.5	22.9	95.00%	R.TTPSYVAFTDTER.L			R.TTPSYVAFTDTER.L
24	34	2	1227.63	5.8	1	33.2	20.7	95.00%	R.VEIIANDQGNR.T			R.VEIIANDQGNR.T
347	359	2	1539.75	4.6	1	52.1	22.7	95.00%	K.LVSDFFNGKEPCK.S	Carbamidomethyl (+57)		K.LVSDFFNGKEPCK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
18	A1EGU1_SCHPO	40.88%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
457	479	2	2580.33	3.2	0	77.6	18.8	95.00%	K.YVISQCNNALLYPALGVACVLSR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.YVISQCNNALLYPALGVACVLSR.C
258	292	4	3747.95	3.3	0	51.5	16.8	95.00%	R.ILDHYRPDIACFNDDIQGTGAVLAAIIGALHVTK.S	Carbamidomethyl (+57)	R.ILDHYRPDIACFNDDIQGTGAVLAAIIGALHVTK.S
44	57	2	1634.91	4.4	1	89.1	15.7	95.00%	R.LPPIVETLQQQVDR.C		R.LPPIVETLQQQVDR.C
535	547	2	1391.67	3.8	1	33.3	22.8	95.00%	E.GMSTVDLPKDDAK.L	Oxidation (+16)	K.QAVSEGMSTVDLPKDDAK.L
377	396	2	2009.14	2.3	0	38.5	10.4	95.00%	E.SAIALVKPTILLGCSGQPGK.F	Carbamidomethyl (+57)	K.EVPSGDINLESAIALVKPTILLGCSGQPGK.F
408	425	2	2093.11	3.5	1	62.5	17.4	95.00%	K.HVERPIIFPISNPTTLME.A		K.HVERPIIFPISNPTTLMEAKPDQIDK.W
501	517	2	1828.94	4.1	1	33.1	21	95.00%	R.SLFAADEALLPDLNNAR.E		R.SLFAADEALLPDLNNAR.E
123	137	2	1824.84	2.4	0	67.2	23	95.00%	E.GCYLDIDHNDLSYIK.Q	Carbamidomethyl (+57)	R.YPEGCYLDIDHNDLSYIK.Q
439	452	2	1418.83	2.4	0	44	10.8	95.00%	K.ALIATGSPLPPLNR.N		K.ALIATGSPLPPLNR.N
508	517	2	1095.61	3.2	0	30.6	17.1	95.00%	E.ALLPDLNNAR.E		R.SLFAADEALLPDLNNAR.E
490	500	2	1070.58	4.5	0	54.7	19	95.00%	K.AASDALATVPR.S		K.AASDALATVPR.S
15	23	2	955.55	4.9	0	32.8	17.4	95.00%	K.GVTLLNSPR.Y		K.GVTLLNSPR.Y
332	339	2	964.49	5	0	34.3	20	95.00%	R.GNLFMIDR.C		R.GNLFMIDR.C
456	479	3	2708.42	2.8	1	36.7	16.6	95.00%	K.KYVISQCNNALLYPALGVACVLSR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.KYVISQCNNALLYPALGVACVLSR.C
222	234	2	1526.73	2.5	1	68.3	23.2	95.00%	R.GEQYDSFLDNVIK.A		R.GEQYDSFLDNVIK.A
178	191	2	1553.75	3.5	0	59.3	22.2	95.00%	K.GHLMTLCAGLDPNR.F	Carbamidomethyl (+57)	K.GHLMTLCAGLDPNR.F
243	248	2	762.37	2.6	0	31.4	22.4	95.00%	E.AFIHFE.D		R.EVFPEAFIHFEDFGLANAK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
19	HSP90_SCHPO	27.27%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
516	525	2	1100.61	3	1	32.4	19.5	95.00%	K.LVNITKDGLE.L		K.LVNITKDGLELEETDEEK.A
48	60	2	1444.65	3	0	41.9	22.1	95.00%	R.YQSLSDPHALDAE.K		R.YQSLSDPHALDAEK.D
465	474	2	1170.6	4.5	1	29.7	20.8	95.00%	K.NIYFITGESK.Q		K.NIYFITGESK.Q
645	663	2	2011.99	3.1	0	76.3	21.4	95.00%	E.TALLSSGFTLDDPSAYAQR.I		K.DLATILYETALLSSGFTLDDPSAYAQR.I
567	587	2	2339.12	5.7	1	92.3	22.7	95.00%	K.IVGSPCLLTTGQYGWSANMER.I	Carbamidomethyl (+57)	K.IVGSPCLLTTGQYGWSANMER.I
440	458	2	2199.07	3.1	1	92.7	21.6	95.00%	R.YNSLNSPDDLISLEDYITK.M		R.YNSLNSPDDLISLEDYITK.M
596	606	2	1234.5	4.9	0	67.2	22.3	95.00%	R.DTSMSAYMSSR.K		R.DTSMSAYMSSR.K
88	99	2	1282.73	5.3	0	55.5	15.1	95.00%	K.NDLINNLGVIAK.S		K.NDLINNLGVIAK.S
34	45	2	1274.64	4	1	41.6	21.2	95.00%	R.ELISNASDALDK.I		R.ELISNASDALDK.I
362	375	2	1512.78	3.1	1	77.4	19.7	95.00%	K.GVVDSEDLPLNLSR.E		K.GVVDSEDLPLNLSR.E
80	99	2	2086.12	2.8	1	60.5	16.2	95.00%	R.DTGIGMTKNDLINNLGVIAK.S		R.DTGIGMTKNDLINNLGVIAK.S
198	212	2	1787.96	4.4	1	31.7	17.7	95.00%	K.HSEFISYPIQLVVTR.E		K.HSEFISYPIQLVVTR.E
440	453	2	1578.75	2.4	0	33.1	22.6	95.00%	R.YNSLNSPDDLISLE.D		R.YNSLNSPDDLISLEDYITK.M
422	436	2	1574.86	4	1	34.5	17.6	95.00%	K.LGIHEDAANRPALAK.L		K.LGIHEDAANRPALAK.L
290	302	2	1526.74	4	1	75.7	22.4	95.00%	K.SLTNDWEDHLAVK.H		K.SLTNDWEDHLAVK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
20	ILV5_SCHPO	28.71%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
145	159	2	1561.77	4	0	41	20.5	95.00%	K.GSIIMNLLSDAAQTE.T		K.GSIIMNLLSDAAQTETWPK.I
144	159	2	1705.86	3.3	1	44.9	20.3	95.00%	K.KGSIIMNLLSDAAQTE.T	Oxidation (+16)	K.KGSIIMNLLSDAAQTETWPK.I

84	104	2	2141.07	4.6	0	90.4	21.2	95.00%	K.NDTLAIIGYGSQGHGQGLNAR.D		K.NDTLAIIGYGSQGHGQGLNAR.D
330	337	2	914.47	6	0	41.2	19.8	95.00%	R.GAIDWTPR.F		R.GAIDWTPR.F
314	328	2	1725.76	3.8	0	69	24.5	95.00%	K.YGLDYMFAACSTTAR.R	Carbamidomethyl (+57)	K.YGLDYMFAACSTTAR.R
145	163	2	2074.05	4.2	1	75.2	20.1	95.00%	K.GSIIMNLLSDAAQTETWPK.I		K.GSIIMNLLSDAAQTETWPK.I
57	65	2	996.46	3.5	1	30.4	22.7	95.00%	R.VMDFAGTKE.N		R.VMDFAGTKENVWER.S
362	372	2	1312.61	4.6	1	61.6	22.7	95.00%	R.SLEYNSAPNYR.E		R.SLEYNSAPNYR.E
123	133	2	1198.6	4.3	1	28.6	20.9	95.00%	K.QAIEDGWVPGK.T		K.QAIEDGWVPGK.T
78	104	3	2906.47	2.4	1	96.6	19.4	95.00%	K.LVDYFKNDTLAIIGYGSQGHGQGLNAR.D		K.LVDYFKNDTLAIIGYGSQGHGQGLNAR.D
190	204	3	1639.97	3.2	1	31.2	9.03	95.00%	K.IHPPKDVDVILVAPK.G		K.IHPPKDVDVILVAPK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
21	6PGD_SCHPO	36.18%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
156	166	3	1228.76	4.8	0	32.1	6.99	95.00%	R.IKPIFQTLAAK.A		R.IKPIFQTLAAK.A
140	155	2	1669.81	3.2	0	31.9	22.5	95.00%	R.YGPSLMPGGNPAAWPR.I		R.YGPSLMPGGNPAAWPR.I
97	114	3	1943.94	3.4	1	32.4	22.3	95.00%	E.KGDIIVDGGNSHYPDTTR.R		K.AGKPVDYLIEGLAPLLEKGDIIVDGGNSHYPDTTR.R
467	492	3	2753.31	3.6	1	22.6	22.1	93.50%	K.SLPADKDIHINWTGHGGNISATTYDA.-		K.SLPADKDIHINWTGHGGNISATTYDA.-
98	115	3	1971.95	5.1	1	35.5	21.5	95.00%	K.GDIIVDGGNSHYPDTTRR.C		K.GDIIVDGGNSHYPDTTRR.C
320	333	2	1592.8	4.1	1	67.9	20.8	95.00%	K.QLIDDLEDALYASK.I		K.QLIDDLEDALYASK.I
437	449	2	1379.79	4.1	0	52	11.8	95.00%	R.SAVLPANLLQAQR.D		R.SAVLPANLLQAQR.D
410	436	3	2839.48	3.6	1	74.2	17.1	95.00%	R.RVVAQAAMLGIPVPATSTGLSFYDGYR.S		R.RVVAQAAMLGIPVPATSTGLSFYDGYR.S
98	114	2	1815.85	4.4	0	91.7	23.4	95.00%	K.GDIIVDGGNSHYPDTTR.R		K.GDIIVDGGNSHYPDTTR.R
450	458	2	1112.51	4.7	0	24.9	22.6	90.10%	R.DYFGAHTFR.V		R.DYFGAHTFR.V
29	37	2	1175.49	3.9	0	36.7	23.2	95.00%	K.GFTVCCYNR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GFTVCCYNR.T
5	28	2	2457.3	3	1	76	15.9	95.00%	K.EVADFGLIGLAVMGQNLILNGADK.G		K.EVADFGLIGLAVMGQNLILNGADK.G
80	89	2	1103.59	4.9	0	27.6	20.4	94.10%	K.AGKPVDYLIE.G		K.AGKPVDYLIEGLAPLLEK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
22	EF3_SCHPO	14.14%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	46	2	1245.63	3.4	1	39.5	21.4	95.00%	K.ALASFVNGPIEE.Q		K.ALASFVNGPIEEQDAPSQVFSAISK.Q
596	621	4	2935.49	3.5	1	34.9	19.3	95.00%	K.DVSSIIVSHDSGFLDHVVQAIIHYER.F		K.DVSSIIVSHDSGFLDHVVQAIIHYER.F
47	59	2	1376.7	2.6	0	79.4	21.2	95.00%	E.QDAPSQVFSAISK.Q		K.ALASFVNGPIEEQDAPSQVFSAISK.Q
281	294	2	1550.88	4.1	1	60.5	14.5	95.00%	K.LVEDPQVVAPFLPK.L		K.LVEDPQVVAPFLPK.L
78	95	2	1839.91	2.9	0	31.1	22	95.00%	E.AVANHGSVAADVEPYLVE.L		K.GLEAVANHGSVAADVEPYLVELLPAVIAK.V
757	765	2	1178.58	7.8	1	24.9	21.5	90.00%	K.TPSEYIQWR.F		K.TPSEYIQWR.F
479	493	2	1636.88	3.9	1	73.9	18	95.00%	R.AIVNGQVEGFPTHLR.T		R.AIVNGQVEGFPTHLR.T
133	147	2	1550.87	3.9	1	70.6	14.1	95.00%	K.AIVPSVLESIHTTGK.W		K.AIVPSVLESIHTTGK.W
541	554	2	1471.79	3.2	0	44.7	19	95.00%	E.LINMPIGSLSGGWK.M		K.ENSFTDELINMPIGSLSGGWK.M
202	213	2	1359.69	4.1	0	43.2	21	95.00%	K.VCTLIANADIDR.F	Carbamidomethyl (+57)	K.VCTLIANADIDR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
23	K6PF_SCHPO	20.49%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
364	380	3	1831.88	4.2	1	50.7	23.4	95.00%	R.ICEAVDSISSTAISHSR.A	Carbamidomethyl (+57)	R.ICEAVDSISSTAISHSR.A
613	628	3	1700.87	4.5	0	49.7	20.4	95.00%	R.GHTPLAIDNGFSGFLR.H		R.GHTPLAIDNGFSGFLR.H
419	431	2	1592.73	4.2	1	27.5	22.7	94.00%	K.WQDELCNSLSSVR.K	Carbamidomethyl (+57)	K.WQDELCNSLSSVR.K

283	308	2	2620.33	3.9	0	86.3	18.8	95.00%	K.NLISAGIDSIIVCGGDGSLTGADIFR.S	Carbamidomethyl (+57)	K.NLISAGIDSIIVCGGDGSLTGADIFR.S
586	603	3	1720.91	2.5	0	50.1	18.3	95.00%	R.VAIIHVGAPAGGMNSATR.A		R.VAIIHVGAPAGGMNSATR.A
798	806	2	934.49	4	1	31.5	20	95.00%	K.ATFALEAGR.N		K.ATFALEAGR.N
880	896	2	1696.88	4.3	0	74.6	19.5	95.00%	R.ANDLGNDPSSAVVIGIR.G		R.ANDLGNDPSSAVVIGIR.G
254	267	2	1400.75	3.4	1	49.7	19.4	95.00%	R.GWLAEGGTLIGTAR.C		R.GWLAEGGTLIGTAR.C
844	861	2	1860.9	4.7	0	42.3	22.3	95.00%	R.TAVPGHVQQGGNPTPMDR.A		R.TAVPGHVQQGGNPTPMDR.A
5	19	2	1635.76	3.2	0	50.9	23.5	95.00%	E.TVHGISCYSVVANTE.D	Carbamidomethyl (+57)	-.MSGETVHGISCYSVVANTEDTYNQTLDFYQK.L
927	938	2	1323.7	4.7	0	53.3	19	95.00%	R.DMHNLVNILAGK.T		R.DMHNLVNILAGK.T
197	214	2	1760.86	3.9	0	86.3	21.8	95.00%	K.IAVMTSGGDSPGMNAVVR.A		K.IAVMTSGGDSPGMNAVVR.A
367	380	2	1429.72	3.3	0	102	20.7	95.00%	E.AVDSISSTAISHSR.A		R.ICEAVDSISSTAISHSR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
24	HSP75_SCHPO	31.16%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	173	2	1168.66	5	0	34.3	15.6	95.00%	K.DAGAIAGLNVLR.I		K.DAGAIAGLNVLR.I
364	385	2	2201.14	3	1	96.5	18.6	95.00%	K.SINPDEAVAYGAAVQAAVLTNK.A		K.SINPDEAVAYGAAVQAAVLTNK.A
501	517	3	1779.92	5.5	1	60.6	19	95.00%	R.SAHIEITNSVGHLSSTK.I		R.SAHIEITNSVGHLSSTK.I
121	128	2	861.5	3.2	0	25.3	18.5	90.80%	E.ISAMVLTK.M		K.QFTAQEISAMVLTK.M
554	564	2	1265.6	3.5	0	31.7	22.5	95.00%	E.TTISEPNVMMK.L	Oxidation (+16)	K.SQLESYISNIETTISEPNVMMK.L
370	385	2	1545.86	2.7	0	56.1	17.5	95.00%	E.AVAYGAAVQAAVLTNK.A		K.SINPDEAVAYGAAVQAAVLTNK.A
253	260	2	929.45	5.3	0	25	20.3	90.30%	K.IDISDDPR.A		K.IDISDDPR.A
144	157	2	1552.8	4.6	0	33.7	20.1	95.00%	K.AVITVPAYFSDSQR.A		K.AVITVPAYFSDSQR.A
331	344	2	1437.76	3.8	0	34.4	18.7	95.00%	K.ADVHDIVLVGGSTR.I		K.ADVHDIVLVGGSTR.I
586	595	2	1146.56	3.6	1	61.2	22.2	95.00%	E.LEDTNTDALR.K		K.IEAQLAECMSQLELEDTNTDALR.K
115	128	2	1565.81	1.4	1	60	19.8	95.00%	K.QFTAQEISAMVLTK.M		K.QFTAQEISAMVLTK.M
506	517	2	1242.66	3.7	0	25	18.8	90.20%	E.ITNSVGHLSSTK.I		R.SAHIEITNSVGHLSSTK.I
174	190	2	1729.93	3.9	0	82.9	16.8	95.00%	R.IINEPTAAAIAYGLDAK.S		R.IINEPTAAAIAYGLDAK.S
221	241	2	2143.01	2.9	1	59.2	23.2	95.00%	E.VLATAGDTHLGGEDFDNALVE.H		K.IQGGVFEVLATAGDTHLGGEDFDNALVEHFIQEFK.R
410	419	2	1103.56	4.5	0	33.8	20.9	95.00%	E.GNVFGVVCPR.N	Carbamidomethyl (+57)	K.TQDLLLLDVVPLSLGVAMEGNVFGVVCPR.N
430	450	2	2374.16	5.6	1	61.9	21.3	95.00%	R.TFTTVADNQTTVTFPVYQGER.V		R.TFTTVADNQTTVTFPVYQGER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
25	EF2_SCHPO	20.78%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
272	283	2	1498.77	4.2	0	53.9	20.5	95.00%	R.AFNMFILDPIYR.I		R.AFNMFILDPIYR.I
466	479	2	1474.71	3.7	1	72.8	21.9	95.00%	K.SGTLTTSEVAHNMK.V		K.SGTLTTSEVAHNMK.V
565	578	2	1451.69	4.3	1	44.5	23.4	95.00%	R.ESVSEPSSMTALSK.S		R.ESVSEPSSMTALSK.S
623	631	2	1065.49	3	0	25.8	21.3	91.60%	E.FGWDVTDAR.K		R.IMADEFGWDVTDAR.K
632	651	3	2235.11	2.7	1	41.5	21.9	95.00%	R.KIWCFGPDTTGANVVVDQTK.A	Carbamidomethyl (+57)	R.KIWCFGPDTTGANVVVDQTK.A
633	651	2	2107.01	3.2	0	108	22.2	95.00%	K.IWCFGPDTTGANVVVDQTK.A	Carbamidomethyl (+57)	K.IWCFGPDTTGANVVVDQTK.A
284	292	2	1051.52	4.5	0	27.5	21.3	94.00%	R.IFDAVMNSR.K		R.IFDAVMNSR.K
244	253	2	1266.61	5.9	1	30	21.9	95.00%	R.LWGENYFNPK.T		R.LWGENYFNPK.T
151	162	3	1392.86	5.8	1	25.2	6.99	95.00%	R.IRPVVVVNKVDR.A		R.IRPVVVVNKVDR.A
544	555	2	1334.69	3.5	1	47.4	20.9	95.00%	K.DLQEDHAGIPLK.I		K.DLQEDHAGIPLK.I
371	384	2	1594.76	4.1	0	55	22.5	95.00%	R.NCDANAPLMIYVSK.M	Carbamidomethyl (+57)	R.NCDANAPLMIYVSK.M
327	346	2	2192.18	2.4	1	55.9	15.8	95.00%	K.FLPAADALMEMIVLHLPSPK.T		K.FLPAADALMEMIVLHLPSPK.T
442	465	2	2595.37	4.3	1	74.7	16	95.00%	R.IEPIEDCPAGNIIGLVGVDQFLVK.S	Carbamidomethyl (+57)	R.IEPIEDCPAGNIIGLVGVDQFLVK.S
337	346	2	1133.67	3.3	0	46	12.6	95.00%	E.MIVLHLPSPK.T		K.FLPAADALMEMIVLHLPSPK.T
618	631	2	1624.73	4.2	1	45	23.4	95.00%	R.IMADEFGWDVTDAR.K		R.IMADEFGWDVTDAR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
26	ACT_SCHPO	31.47%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
277	284	2	926.46	4	0	27.3	20.1	93.80%	E.ATYNSIMK.C		R.APEALFQPSALGLENAGIHEATYNSIMK.C
148	167	2	2073.03	3.1	0	65.7	21.2	95.00%	R.TTGIVLDSGDGVTHTVPIYE.G		R.TTGIVLDSGDGVTHTVPIYEGYALPHAIMR.L
85	95	3	1514.75	5.5	1	36	21	95.00%	K.IWHHTFYNELR.V		K.IWHHTFYNELR.V
292	312	2	2216.04	5	0	63.1	23.1	95.00%	K.DLYGNVVMSGGTTMYPGIADR.M		K.DLYGNVVMSGGTTMYPGIADR.M
227	238	2	1261.66	3.8	1	49.8	20.2	95.00%	E.LQTAAQSSSLEK.S		K.LCYVALDFEQELQTAAQSSSLEK.S
197	206	2	1131.53	5.1	1	41.4	22.8	95.00%	R.GYTFSTTAER.E		R.GYTFSTTAER.E
148	177	3	3182.62	3.4	1	67.2	18.3	95.00%	R.TTGIVLDSGDGVTHTVPIYEGYALPHAIMR.L		R.TTGIVLDSGDGVTHTVPIYEGYALPHAIMR.L
5	18	2	1448.7	1.9	0	73.1	22.6	95.00%	E.IAALVIDNGSGMCK.A	Deamidation (+1)/ Carbamidomethyl (+57)	-.MEEEIAALVIDNGSGMCK.A
73	84	2	1456.64	2.7	1	54	23.6	95.00%	E.HGIVNNWDDMEK.I		K.YPIEHGIVNNWDDMEK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
27	TSA1_SCHPO	44.79%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	147	2	1224.69	4.4	0	43.5	15.8	95.00%	R.QITINDLPVGR.S		R.QITINDLPVGR.S
90	107	2	1786.96	3	1	26.4	17.4	92.60%	K.EGGLGGINIPLLADPSHK.V		K.EGGLGGINIPLLADPSHK.V
125	132	2	901.53	4.7	0	35.7	18.9	95.00%	R.GLFLIDPK.G		R.GLFLIDPK.G
66	88	2	2576.29	0.89	1	97.3	19.9	95.00%	R.NAQVILTSTDSEYSHLAFINTPR.K		R.NAQVILTSTDSEYSHLAFINTPR.K
111	124	2	1523.77	4.1	1	79.7	21	95.00%	R.DYGVLIEDAGVAFR.G		R.DYGVLIEDAGVAFR.G
91	107	2	1657.92	2.6	0	37.2	16.3	95.00%	E.GGLGGINIPLLADPSHK.V		K.EGGLGGINIPLLADPSHK.V
78	88	2	1317.69	2.9	0	46.6	20.4	95.00%	E.YSHLAFINTPR.K		R.NAQVILTSTDSEYSHLAFINTPR.K
2	13	2	1341.74	4.1	0	36.9	17.6	95.00%	M.SLQIGKPAPDFK.G	Acetyl (+42)	-.MSLQIGKPAPDFK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
28	TKT_SCHPO	31.97%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
325	336	2	1449.68	6.5	1	28.4	22.7	95.00%	K.QSYPDLSNQLER.I	Deamidation (+1)	K.QSYPDLSNQLER.I
2	18	2	1869.94	3.1	0	81	21.3	95.00%	M.TSSSYTDIDTLAINTIR.T		-.MTSSSYTDIDTLAINTIR.T
238	252	2	1719.86	5	1	57.2	21.5	95.00%	R.EAMSCTDKPTLINLK.T	Carbamidomethyl (+57)	R.EAMSCTDKPTLINLK.T
395	407	2	1418.65	3.9	1	52.7	22.6	95.00%	R.WEGAADFQPPSSK.L		R.WEGAADFQPPSSK.L
653	663	3	1249.63	4.3	0	20.8	20.3	90.40%	K.FHFTTSGVAQR.A		K.FHFTTSGVAQR.A
261	275	2	1585.83	3.3	0	32.4	20.3	95.00%	E.LQGTHSVHGSPLKPE.D		K.TTIGYGSELQGTHSVHGSPLKPEDCVHVK.K
380	394	2	1499.8	3.8	0	44.4	17.9	95.00%	E.LVGGSADLTPSNLTR.W		K.LSEIVLDALCPVLPELVGGSADLTPSNLTR.W
510	531	2	2288.16	3.4	0	82.6	19.5	95.00%	E.TSAAYYSALTSDSTPSILALTR.Q		R.AMPNINCWRPADGNETSAAYYSALTSDSTPSILALTR.Q
182	193	2	1385.74	4.7	0	41.9	20.1	95.00%	K.LSNLIAVWDNNK.I		K.LSNLIAVWDNNK.I
118	137	2	1736.98	3.1	0	41.5	12	95.00%	E.TGAGPLGQGIASAVGLAIGK.A		K.TPGHPETHNPDLNIETGAGPLGQGIASAVGLAIGK.A
630	648	3	2046.93	3.6	1	34	23.7	95.00%	R.YVHEAFGMHTFGDSGPAPK.L		R.YVHEAFGMHTFGDSGPAPK.L
495	509	2	1743.75	2.6	0	47.3	23.5	95.00%	R.AMPNINCWRPADGNE.T	Carbamidomethyl (+57)	R.AMPNINCWRPADGNETSAAYYSALTSDSTPSILALTR.Q
495	531	3	4013.9	2.8	1	63.2	20.6	95.00%	R.AMPNINCWRPADGNETSAAYYSALTSDSTPSILALTR.Q	Carbamidomethyl (+57)	R.AMPNINCWRPADGNETSAAYYSALTSDSTPSILALTR.Q
291	303	2	1603.8	4	1	26.8	21.3	93.10%	K.TFQVPPEVYAYYK.E		K.TFQVPPEVYAYYK.E
30	49	3	1972.02	2.7	0	42.7	19.8	95.00%	K.SGHPGAPMGLAPAAHVLFSR.I		K.SGHPGAPMGLAPAAHVLFSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
29	HXK2_SCHPO	35.82%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
434	449	2	1529.79	4.8	0	96.2	20	95.00%	K.DGSGIGAALCALQAVK.E	Carbamidomethyl (+57)	K.DGSGIGAALCALQAVK.E
193	205	2	1357.76	2.9	0	85.5	16.9	95.00%	E.AVINDTVGTLVTR.A		R.IEAVINDTVGTLVTR.A
392	403	2	1203.6	2.8	1	35.6	21.8	95.00%	K.KSDVGVDGSLVE.H		K.KSDVGVDGSLVEHYPHFVDMLR.E
61	75	2	1595.8	3.5	0	61	21.3	95.00%	E.TGDFLALDFGGTNLR.V		K.NGEVLAMAPAFISTLPTGAETGDFLALDFGGTNLR.V
76	86	2	1287.67	3.9	0	30.3	20.6	95.00%	R.VCWIQLLGDGK.Y	Carbamidomethyl (+57)	R.VCWIQLLGDGK.Y
286	296	2	1240.63	5.9	1	25.6	20.1	91.30%	R.VGGMYLGELFR.R		R.VGGMYLGELFR.R
253	265	3	1536.68	3.5	0	32	23.6	95.00%	E.WGATDFSCLHSTR.Y	Carbamidomethyl (+57)	K.CTGDHMLINMEWGATDFSCLHSTR.Y
374	388	2	1564.83	4.1	0	56.1	19.1	95.00%	R.MSAVPIASLYLSTGR.A		R.MSAVPIASLYLSTGR.A
103	118	3	1858.88	2.9	1	35.7	23.2	95.00%	R.NESVKPIIDFMSDHVE.L		R.NESVKPIIDFMSDHVELFIK.E
44	60	2	1687.89	2.8	0	45.2	19.1	95.00%	E.VLAMAPAFISTLPTGAE.T		K.NGEVLAMAPAFISTLPTGAETGDFLALDFGGTNLR.V
404	413	3	1313.64	1.7	0	23.5	22.6	94.70%	E.HYPHFVDMLR.E		K.SDVGVDGSLVEHYPHFVDMLR.E
266	279	2	1598.77	2.6	0	50.7	22.7	95.00%	R.YDLLLDHDTPNAGR.Q		R.YDLLLDHDTPNAGR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
30	PUR9_SCHPO	24.27%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
138	153	2	1755.86	2.6	0	97.6	20.9	95.00%	R.VTILSDPADYATFTDK.F		R.VTILSDPADYATFTDK.F
551	565	2	1519.75	4.1	0	63.8	21.9	95.00%	K.YVAAPGGSVMDQAVR.D		K.YVAAPGGSVMDQAVR.D
526	543	2	2131.98	3.7	0	65.5	24.4	95.00%	K.DVVCASDAFFPFPDNIYR.L	Carbamidomethyl (+57)	K.DVVCASDAFFPFPDNIYR.L
223	244	2	2446.25	3.4	0	45.9	19	95.00%	K.VLCGSPGYINLMDALNSWPLVK.E	Carbamidomethyl (+57)	K.VLCGSPGYINLMDALNSWPLVK.E
354	362	2	1152.54	4.8	0	28.8	23.5	95.00%	K.YCVLQMDPK.Y	Carbamidomethyl (+57)	K.YCVLQMDPK.Y
201	215	2	1646.72	4.4	0	36.4	23.2	95.00%	R.YGANPHQSPAQAFME.Q		R.YGANPHQSPAQAFMEQGPLPFK.V
248	259	2	1216.65	4.7	1	30.2	19.1	95.00%	R.ENIGIPAAASFK.H		R.ENIGIPAAASFK.H
260	277	2	1745.93	1.6	1	43.5	17.6	95.00%	K.HVSPAGAAVGLPLSDVEK.K		K.HVSPAGAAVGLPLSDVEK.K
120	129	2	1055.64	2.9	0	65.9	15.3	95.00%	E.IDIGGVTLLR.A		R.ETIAKPNVTIPEAVEEIDIGGVTLLR.A
201	222	3	2414.16	4	1	23.8	21.7	95.00%	R.YGANPHQSPAQAFMEQGPLPFK.V		R.YGANPHQSPAQAFMEQGPLPFK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
31	IPYR_SCHPO	47.75%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
203	212	2	1145.48	2.9	1	32.2	22.8	95.00%	E.NSFAFSGECK.N	Carbamidomethyl (+57)	K.IPDGKPENSFAFSGECK.N
240	280	3	4115.08	2.7	1	89.4	17.6	95.00%	K.SDFSLVNVSVTGSVANDPSVSSTIPPAQELAPAPVDPSVHK.W		K.SDFSLVNVSVTGSVANDPSVSSTIPPAQELAPAPVDPSVHK.W
114	125	2	1304.56	3.5	1	33.5	23.8	95.00%	K.AKGDSDPLDVCE.I	Carbamidomethyl (+57)	K.AKGDSDPLDVCEIGEAR.G
186	192	2	922.44	6	1	35.4	21.7	95.00%	R.ATNEWFR.I		R.ATNEWFR.I
9	23	2	1710.89	3.8	1	56.7	19	95.00%	E.VGALNTLDYQVYVEK.N		R.EVGALNTLDYQVYVEK.N
157	169	2	1391.81	3	0	38.1	11.5	95.00%	K.VIVIDVNDPLAPK.L		K.VIVIDVNDPLAPK.L
24	42	2	2113.02	3.6	1	72.8	22.5	95.00%	K.NGTPISSWHDIPLYANAEK.T	Deamidation (+1)	K.NGTPISSWHDIPLYANAEK.T
43	53	2	1283.73	4	1	66.7	15.9	95.00%	K.TILNMVVEIPR.W		K.TILNMVVEIPR.W
193	202	2	1158.63	3.7	1	26.3	20	92.40%	R.IYKIPDGKPE.N		R.IYKIPDGKPENSFAFSGECK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
32	HSP60_SCHPO	24.74%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
112	128	2	1705.86	4.1	1	84.3	21.2	95.00%	K.TNEVAGDGTTTATVLTR.A		K.TNEVAGDGTTTATVLTR.A
115	128	2	1361.72	3.8	0	53.5	20.2	95.00%	E.VAGDGTTTATVLTR.A		K.TNEVAGDGTTTATVLTR.A
137	148	2	1316.6	4	0	27.4	23.3	93.90%	R.NVAAGCNPMDLR.R	Carbamidomethyl (+57)	R.NVAAGCNPMDLR.R

437	453	2	1588.85	4.6	1	29.9	18.9	95.00%	K.AAVSEGVLPGAGTSFVK.A		K.AAVSEGVLPGAGTSFVK.A
68	79	2	1313.7	4.3	0	39.3	19.4	95.00%	R.NVLIDQPFGSPK.I		R.NVLIDQPFGSPK.I
520	533	2	1570.87	4.4	1	87.2	15.3	95.00%	R.FVDLNEIGVLDPLK.V		R.FVDLNEIGVLDPLK.V
258	275	2	1937.07	4.4	1	74.7	14.9	95.00%	K.VSAVQDILPSLELAAQQR.R		K.VSAVQDILPSLELAAQQR.R
276	288	2	1424.76	2.7	1	45.2	19	95.00%	R.RPLVIIAEDVDGE.A		R.RPLVIIAEDVDGEALAACILNK.L
229	240	2	1401.72	4.3	0	35	20.5	95.00%	R.GYISPYFITDVK.S		R.GYISPYFITDVK.S
45	56	2	1215.69	4.9	0	52.6	16.8	95.00%	R.ASLLTGVDTLAR.A		R.ASLLTGVDTLAR.A
175	191	2	1712.82	0.57	0	41.8	23	95.00%	E.ISQVATISANGDTHIGE.L	Deamidation (+1)	R.DITTSEEISQVATISANGDTHIGELLAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
33	LYS9_SCHPO	34.22%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
177	183	2	740.49	4.7	0	33.1	9.03	95.00%	R.GVLLALR.N		R.GVLLALR.N
122	135	2	1509.82	2.4	0	40.2	16.9	95.00%	E.IGVDPGIDHLYAIK.T		K.AGSICMNEIGVDPGIDHLYAIK.T
38	49	2	1259.66	4.1	1	41.7	19.9	95.00%	K.AEAFINGIPNSK.A		K.AEAFINGIPNSK.A
149	170	2	2385.11	5.2	1	60.2	22.9	95.00%	K.SFLSYCGGLPAPEDSNNPLGYK.F	Carbamidomethyl (+57)	K.SFLSYCGGLPAPEDSNNPLGYK.F
2	22	3	2269.25	3.1	1	39	13	95.00%	M.PSILLLGSGFVAHPTLEYLSR.R		-.MPSILLLGSGFVAHPTLEYLSR.R
379	396	2	1989.93	4.3	0	76.6	23	95.00%	R.TCTLLDYGVPNGYTSMAK.L	Carbamidomethyl (+57)	R.TCTLLDYGVPNGYTSMAK.L
114	135	3	2372.16	2.8	1	47.3	21.4	95.00%	K.AGSICMNEIGVDPGIDHLYAIK.T	Carbamidomethyl (+57)	K.AGSICMNEIGVDPGIDHLYAIK.T
2	18	2	1749.97	2.7	0	44.8	15.7	95.00%	M.PSILLLGSGFVAHPTLE.Y		-.MPSILLLGSGFVAHPTLEYLSR.R
397	426	3	3075.62	3.2	0	47.3	14.3	95.00%	K.LVGVPCGVATQQILDGVINTPGVLAPNDMK.L	Carbamidomethyl (+57)	K.LVGVPCGVATQQILDGVINTPGVLAPNDMK.L
64	85	3	2488.28	3.3	1	39.1	17.6	95.00%	K.AVSEHDLTISLIPYTYHATVMK.A		K.AVSEHDLTISLIPYTYHATVMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
34	G6PI_SCHPO	23.64%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
208	216	2	992.59	2.7	0	42.3	11.8	95.00%	E.TTLFLIASK.T		K.CDPETTLFLIASK.T
217	228	2	1343.61	5.2	1	37.3	22.6	95.00%	K.TFTTAETCTNAK.S	Carbamidomethyl (+57)	K.TFTTAETCTNAK.S
372	382	2	1171.52	5.1	0	67.7	22.5	95.00%	R.SGDMVNYTTGK.I		R.SGDMVNYTTGK.I
464	477	2	1502.83	4	0	36.9	16.4	95.00%	K.TFVGNRPSNSIIAK.K		K.TFVGNRPSNSIIAK.K
534	547	2	1559.76	2.5	0	29.7	22.4	95.00%	E.NHDSSTNGLINLFK.N	Deamidation (+1)	K.GDVENHDSSTNGLINLFK.N
2	24	2	2548.27	3.8	1	60.7	19.4	95.00%	M.SFSLASTLPAWQAVQTHYESVGK.H	Acetyl (+42)	-.MSFSLASTLPAWQAVQTHYESVGK.H
118	128	2	1170.59	4.1	0	35.5	21.3	95.00%	K.VNGQDVMPGVR.K		K.VNGQDVMPGVR.K
204	216	2	1493.75	4.3	1	51.5	21.7	95.00%	K.CDPETTLFLIASK.T	Carbamidomethyl (+57)	K.CDPETTLFLIASK.T
429	445	2	1870.94	4.8	1	69.7	21.1	95.00%	R.MLFSNFAAQTEALMLGK.T		R.MLFSNFAAQTEALMLGK.T
353	367	2	1711.83	4.2	1	71.8	22.6	95.00%	R.FPAYLQQLSMESNGK.A		R.FPAYLQQLSMESNGK.A
2	20	2	2177.05	3	0	63.8	22.4	95.00%	M.SFSLASTLPAWQAVQTHYE.S	Acetyl (+42)	-.MSFSLASTLPAWQAVQTHYESVGK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
35	CYPH_SCHPO	44.44%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
90	123	3	3611.83	4	0	56	18.1	95.00%	K.HNKPGLLSMANAGPNTNGSQFFITTVVTPWLDGK.H		K.HNKPGLLSMANAGPNTNGSQFFITTVVTPWLDGK.H
2	17	2	1835.87	3.2	0	50.7	22	95.00%	M.SNCFFDVIANGQPLGR.I	Acetyl (+42)/ Carbamidomethyl (+57)	-.MSNCFFDVIANGQPLGR.I
22	29	2	931.51	4	0	29.7	20.8	95.00%	K.LFDDVVPK.T		K.LFDDVVPK.T
54	67	2	1607.82	3	0	74.1	20.1	95.00%	R.VIPQFMLQGGDFTR.G		R.VIPQFMLQGGDFTR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
36	GPD1_SCHPO	35.58%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
281	296	2	1692.8	2.7	0	52.8	22.8	95.00%	E.QSCGIADLVTSCLGGR.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.TMVEQSCGIADLVTSCLGGR.N
203	232	3	3092.63	2.8	1	70.4	16.2	95.00%	R.EQIAAVFDRPYFSVVSVDDVAGV ALGGALK.N		R.EQIAAVFDRPYFSVVSVDDVAGV ALGGALK.N
2	20	2	1989	3.8	0	99.4	21.1	95.00%	M.SGYGQQGVSAANIDSIRPK.K	Acetyl (+42)	-.MSGYGQQGVSAANIDSIRPK.K
87	104	2	2008.05	2	1	53.9	18.6	95.00%	K.YLPGIECPPNVIAVPDVR.E	Carbamidomethyl (+57)	K.YLPGIECPPNVIAVPDVR.E
277	296	2	2153	2.6	1	93.7	23.3	95.00%	R.TMVEQSCGIADLVTSCLGGR.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.TMVEQSCGIADLVTSCLGGR.N
188	202	2	1668.85	2	1	35.5	20.2	95.00%	E.TTIGFNPPNEVDIPR.E		R.EQFCETTIGFNPPNEVDIPR.E
125	144	2	2172.13	3.4	0	50.8	19.2	95.00%	R.VCDQMVGLIRPGAVGISCIK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VCDQMVGLIRPGAVGISCIK.G
317	331	2	1484.82	2.6	1	67.7	16.7	95.00%	K.ELLGGQLLQGAATSK.D		K.ELLGGQLLQGAATSK.D
318	331	2	1355.78	2.7	0	75.3	15.1	95.00%	E.LLGGQLLQGAATSK.D		K.ELLGGQLLQGAATSK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
37	SERA_SCHPO	25.54%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
275	284	2	1108.56	4.3	1	25.6	21.2	91.30%	K.EGSYLINASR.G		K.EGSYLINASR.G
338	351	2	1479.76	2.9	1	33.9	21.1	95.00%	K.NIILTPHIGGSTEE.A		K.NIILTPHIGGSTEEAQYNIGIEVSE ALTR.Y
410	421	2	1468.77	4	1	31.9	19.6	95.00%	R.QVNELFIDHNIK.S		R.QVNELFIDHNIK.S
248	260	2	1367.68	2.8	0	27.6	21.8	94.20%	R.ADFVSLHVPASPE.T		R.ADFVSLHVPASPETK.N
302	319	2	1729.86	2.3	0	51	21.4	95.00%	K.IAGAAIDVYPSEPAGNGK.D	Deamidation (+1)	K.IAGAAIDVYPSEPAGNGK.D
47	57	3	1247.68	3.8	1	25.6	17.9	95.00%	R.TLKPFASEDIK.I		R.TLKPFASEDIK.I
63	75	2	1430.7	3.1	1	64.8	21.2	95.00%	E.NVNQSALSNLKDE.G		K.ILLLENVNQSALSNLKDEGYQVEF LK.T
248	262	2	1596.82	4.1	1	50.8	20	95.00%	R.ADFVSLHVPASPETK.N		R.ADFVSLHVPASPETK.N
142	154	2	1394.7	4.8	0	57.8	20.3	95.00%	R.GIAVFNSPYANSR.S		R.GIAVFNSPYANSR.S
302	321	3	1972.98	1.9	1	39.1	21.5	95.00%	K.IAGAAIDVYPSEPAGNGKDK.F	Deamidation (+1)	K.IAGAAIDVYPSEPAGNGKDK.F
237	247	3	1291.73	4.7	1	20.7	16	90.20%	K.QLSSLPELLHR.A		K.QLSSLPELLHR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
38	PPA1_SCHPO	13.47%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
418	427	2	1194.64	3.5	0	51.1	18.4	95.00%	E.LYAYLNSPVR.V		R.HLVNEEVFPLSDCGFGPSNTSD GMCELYAYLNSPVR.V
40	59	3	2404.13	2.5	0	63.3	22.2	95.00%	R.SPYHKPYFYGPSIDFPTTCK.I	Carbamidomethyl (+57)	R.SPYHKPYFYGPSIDFPTTCK.I
260	270	2	1372.64	3.1	1	48.1	23.9	95.00%	E.IALQDYSEFCK.L	Carbamidomethyl (+57)	R.LNPYFSNYNLTNDDILNLYGICSY EIALQDYSEFCK.L
73	92	2	2047	4	0	113	22.1	95.00%	R.NPTGGNAAFDAVGIANFQQR.L		R.NPTGGNAAFDAVGIANFQQR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
39	THIL_SCHPO	25.06%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
291	301	2	1160.65	4.8	0	33.2	18	95.00%	R.FTTSPSLAIPK.A		R.FTTSPSLAIPK.A
321	331	2	1105.62	4.1	0	54.1	18.3	95.00%	E.AFSVVAVANTK.I		K.HAGIEASQVDYYEINEAFSVVAVA NTK.I
14	30	2	1654.81	3.1	0	81.5	21.8	95.00%	R.TPMGSFGGSFASLPATK.L		R.TPMGSFGGSFASLPATK.L
53	69	2	1772.9	3.2	0	64.8	20.1	95.00%	E.VFMGNVVSANLGQNPAR.Q		R.VNIKPSDVDEVFMGNVVSANLGQ NPAR.Q
339	359	3	2023.01	2.6	1	28.1	21.1	95.00%	E.RVNINGGGVAMGHPLGSSGSR.I	Deamidation (+1)	K.ILGLDPERVNINGGGVAMGHPLG SSGSR.I
43	52	2	1114.55	3.7	0	37.8	21.7	95.00%	R.VNIKPSDVDE.V		R.VNIKPSDVDEVFMGNVVSANLGQ NPAR.Q
43	69	3	2869.45	3.7	1	43	17.9	95.00%	R.VNIKPSDVDEVFMGNVVSANLGQ NPAR.Q		R.VNIKPSDVDEVFMGNVVSANLGQ NPAR.Q
360	371	2	1405.81	4.5	0	73.2	14.5	95.00%	R.IICTLAYILAQK.D	Carbamidomethyl (+57)	R.IICTLAYILAQK.D

340	359	3	1865.93	4.8	0	31	22	95.00%	R.VNINGGGVAMGHPLGSSGSR.I		R.VNINGGGVAMGHPLGSSGSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
40	FAS2_SCHPO	7.27%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1569	1579	2	1292.61	5	1	41.1	22.5	95.00%	R.NADNIDEYLAR.F		R.NADNIDEYLAR.F
488	502	3	1650.8	4.5	1	35.5	22.1	95.00%	K.NVNHPTAPSTTIDER.G		K.NVNHPTAPSTTIDER.G
31	44	2	1510.8	2.5	1	35.4	18.9	95.00%	E.TQDVILSPPVSAER.I		R.WIETQDVILSPPVSAER.I
1200	1215	2	1488.78	3.2	0	46	20.2	95.00%	E.LGNTVGSGIGGMSALR.G		K.YIHVSELGNTVGSGIGGMSALR.G
381	394	2	1509.83	2.8	0	56.5	16.9	95.00%	E.FYASGIAPIFSPLK.A		R.AQLDLWNEEHGEFYASGIAPIFSPLK.A
114	146	3	3020.56	3.1	1	35.9	17.8	95.00%	K.VETAAAAAPAATPAPAPAQTSAPAAALPDEPPK.A		K.VETAAAAAPAATPAPAPAQTSAPAAALPDEPPK.A
1300	1311	2	1181.56	4.5	0	45.3	22.4	95.00%	E.FANMGATSNAAK.E		R.ICISGGYDDFSEEGSYEFANMGATSNAAK.E
397	406	2	1310.58	5.6	0	36.9	23	95.00%	R.VYDSDWNWAR.Q		R.VYDSDWNWAR.Q
1393	1401	2	994.61	4.5	0	27.6	9.54	94.20%	K.TPLPIVDLK.F		K.TPLPIVDLK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
41	PDX1_SCHPO	22.97%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
71	83	2	1355.75	4.3	1	66.7	17.6	95.00%	K.EIQAAVSIPVMAK.V		K.EIQAAVSIPVMAK.V
38	49	2	1218.59	2.4	1	61.2	21.8	95.00%	E.AAGACAVMALER.V	Carbamidomethyl (+57)	R.IAEAAGACAVMALER.V
21	34	2	1457.74	4	1	89.6	20.6	95.00%	K.GGVIMDVVNAEQAR.I		K.GGVIMDVVNAEQAR.I
121	132	3	1383.7	4.4	1	31	21	95.00%	K.SKFTVPFVCGSR.N	Carbamidomethyl (+57)	K.SKFTVPFVCGSR.N
272	280	2	887.47	3.2	0	35	22.9	95.00%	E.NLGAAMVGR.S		K.ILAEVSENLGAAMVGR.S
13	20	2	830.47	4.2	0	38.8	20.1	95.00%	K.AGLAQMLK.G		K.AGLAQMLK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
42	C1TC_SCHPO	9.82%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
689	707	3	1923.15	3.9	0	37.5	6.99	95.00%	R.TSGLKPDAIVIVATVQALK.L		R.TSGLKPDAIVIVATVQALK.L
2	12	2	1184.68	4.9	1	55.8	15.9	95.00%	M.ALLLEGTSLAR.K	Acetyl (+42)	-.MALLLEGTSLAR.K
776	792	2	1697.77	3.6	0	38.7	23.5	95.00%	E.ALAAGATDAVDSNHWAE.G		R.EEALAAGATDAVDSNHWAEGGK.G
324	336	2	1299.71	5.1	1	59.2	18.9	95.00%	K.NIGDLASEIGIAK.S		K.NIGDLASEIGIAK.S
381	396	2	1629.9	3.4	0	106	16.1	95.00%	K.STLTAGLVQALSNLDK.L		K.STLTAGLVQALSNLDK.L
77	84	2	947.57	3.3	0	42.8	14.3	95.00%	E.YDLLLAIK.G		R.AANEAGISCEHVNFPEDITEYDLLLAIK.G
349	356	2	983.58	5.3	1	46.2	14.6	95.00%	K.VNLEILQR.L		K.VNLEILQR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
43	HSP7M_SCHPO	20.47%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
366	376	2	1188.6	3.6	1	38.2	21	95.00%	R.ALKDANLQTSE.I		R.ALKDANLQTSEINEVILVGGMTR.M
204	215	2	1124.67	4.6	0	48.3	12.8	95.00%	K.AAGAIAGLNVLR.V		K.AAGAIAGLNVLR.V
322	337	2	1645.86	3.4	0	41.2	19.7	95.00%	K.TDISLPFITADATGPK.H		K.TDISLPFITADATGPK.H
465	480	2	1637.79	2.7	1	39.2	22.3	95.00%	R.KSQVFSTAADGQTAVE.I		R.KSQVFSTAADGQTAVEIR.V
105	118	2	1578.81	4.5	1	81.4	20.7	95.00%	R.QAVINPENTFFATK.R		R.QAVINPENTFFATK.R
185	199	2	1679.83	4.3	0	62.1	21.8	95.00%	K.NAVVTVPAYFNDSQR.Q		K.NAVVTVPAYFNDSQR.Q
496	510	2	1538.89	4.2	0	77.2	14	95.00%	K.LIGNFQLTGIAPAPK.G		K.LIGNFQLTGIAPAPK.G
380	388	2	944.55	3.8	0	32.7	17.6	95.00%	E.VILVGGMTR.M		K.DANLQTSEINEVILVGGMTR.M
157	170	2	1496.8	5.1	0	59.3	19.2	95.00%	K.TYSPSQIGGFILSK.M		K.TYSPSQIGGFILSK.M
216	231	2	1630.86	3.8	0	78.5	19.3	95.00%	R.VVNEPTAAALAYGLDK.K		R.VVNEPTAAALAYGLDK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
44	GBLP_SCHPO	43.31%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
156	172	2	1893.9	4.3	0	71.3	22.2	95.00%	R.FSPNPDNLTFVSAGWDK.A		R.FSPNPDNLTFVSAGWDK.A
140	155	2	1851.83	4.1	0	53.9	23.1	95.00%	K.YTITDGGHSDWVSCVR.F	Carbamidomethyl (+57)	K.YTITDGGHSDWVSCVR.F
13	36	3	2480.24	2.9	1	45.8	20.5	95.00%	E.GHSGWVTSLSTAPENPDILLSGSR.D		R.ATLEGHSGWVTSLSTAPENPDILLSGSR.D
270	280	2	1161.68	3.2	1	36.3	14	95.00%	E.LTVDFVGVGKK.S		K.VDELTVDFVGVGKK.S
48	57	2	1135.53	4.7	0	43.2	22.3	95.00%	R.DDVNYGVAQR.R		R.DDVNYGVAQR.R
186	212	3	2736.26	2.5	0	50.4	23.4	95.00%	R.TSHYGHTGYVSAVTISPDGSLCASGGR.D	Carbamidomethyl (+57)	R.TSHYGHTGYVSAVTISPDGSLCASGGR.D
234	245	2	1314.71	3.1	0	32.5	18.9	95.00%	K.ANINALVFSPNR.Y		K.ANINALVFSPNR.Y
176	185	2	1264.65	5.4	1	30.1	21.5	95.00%	K.VWDLETFSLR.T		K.VWDLETFSLR.T
39	47	2	1112.68	5.9	0	27.8	12.6	94.30%	K.SIILWNLVR.D		K.SIILWNLVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
45	OAT_SCHPO	23.06%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
5	14	2	1147.56	3.7	0	25.3	21.8	90.80%	E.SLLHNTFSTE.Q		-.MSAESLLHNTFSTEQIEVLENEYAAHNYHPLPVCFSK.A
386	398	3	1374.81	3.3	0	27.4	11.8	95.00%	R.GVLAKPTHGNIIR.F		R.GVLAKPTHGNIIR.F
154	167	2	1493.69	4.9	0	59.2	23.2	95.00%	R.TMGIISMSTDPDAR.D		R.TMGIISMSTDPDAR.D
238	247	2	1127.56	2.7	0	34.4	20.2	95.00%	K.AHNVLFIADE.V		K.AHNVLFIADEVQTGVAR.T
141	153	2	1500.75	2.5	0	39	21	95.00%	E.AIILSCVDNFHGR.T	Carbamidomethyl (+57)	K.IPTDEAIILSCVDNFHGR.T
276	291	2	1561.85	3.1	0	55.6	17.1	95.00%	K.AISGGVYPVSAVLSSR.E		K.AISGGVYPVSAVLSSR.E
238	254	2	1838.97	4.4	1	78.8	18.6	95.00%	K.AHNVLFIADEVQTGVAR.T		K.AHNVLFIADEVQTGVAR.T
258	275	3	2051.1	4.3	1	30.2	15.9	95.00%	K.MLCIEHSNVKPDVVILGK.A	Carbamidomethyl (+57)	K.MLCIEHSNVKPDVVILGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
46	HXK1_SCHPO	16.12%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
231	246	2	1800.86	2.5	1	40.5	22.4	95.00%	E.IGVIFGTGCNACYIEK.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.LNAILSDTTGTLVASNYASPGTEIGVIFGTGCNACYIEK.F
283	291	2	1052.51	4.4	1	31.2	23.5	95.00%	R.TKYDVAIDE.E		R.TKYDVAIDEESPRPGLQTYEK.M
304	315	2	1380.7	5.1	0	25.3	21	90.80%	K.MIAGCYLGDILR.R	Carbamidomethyl (+57)	K.MIAGCYLGDILR.R
2	12	3	1409.65	4.4	0	25.1	22.2	95.00%	M.SLHDAYHWPSR.T	Acetyl (+42)	-.MSLHDAYHWPSR.T
406	426	3	2369.2	3.6	1	22.8	20.3	93.90%	R.KMNKPSMIVGTDGSVYNLYPR.F		R.KMNKPSMIVGTDGSVYNLYPR.F
352	360	2	1076.47	4	1	26.6	23.1	92.80%	E.VDPFENLDE.T		R.DPLAMDTSVLSAIEVDPFENLDETQTLFEETYGLK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
47	RL4A_SCHPO	32.23%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
122	140	2	1845.04	4.3	0	48.1	11.1	95.00%	R.YAISSAVAASGVPSLLLAR.G		R.YAISSAVAASGVPSLLLAR.G
147	163	2	1883.01	3.5	1	77	17.2	95.00%	E.IPEVPLVVDDAVQSFQK.T		R.IEEIPEVPLVVDDAVQSFQK.T
2	13	2	1304.71	4.5	0	25.5	17.9	91.20%	M.AAARPTVSIYSK.D	Acetyl (+42)	-.MAAARPTVSIYSK.D
235	248	3	1457.85	3	0	35.4	13	95.00%	R.LNLLQLAPGGHLGR.F		R.LNLLQLAPGGHLGR.F
282	291	2	1101.58	3.1	0	43.7	20.2	95.00%	E.NIISNADVTR.L		K.NYFLPENIISNADVTR.L
292	303	2	1357.75	4	1	43.8	18.1	95.00%	R.LINSDEIQSIVK.A		R.LINSDEIQSIVK.A
14	29	2	1695.88	4.2	1	38.3	19.4	95.00%	K.DGSVSSETIALPFVFK.A		K.DGSVSSETIALPFVFK.A
276	291	2	1864.94	4.5	1	39	21.7	95.00%	K.NYFLPENIISNADVTR.L		K.NYFLPENIISNADVTR.L
87	97	2	1197.51	4.4	0	32.6	22.8	95.00%	R.SGQAAFGNMCR.S	Carbamidomethyl (+57)	R.SGQAAFGNMCR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
48	ADH_SCHPO	36.00%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
25	35	2	1168.53	5.2	1	32.3	23	95.00%	E.EVPVAEPGQDE.V		K.FEEVPVAEPGQDEVLVNIK.Y
236	253	2	1681.87	1.6	0	68.5	18.9	95.00%	K.AATNGGAHGTLVLSTSPK.S	Deamidation (+1)	K.AATNGGAHGTLVLSTSPK.S

254	278	3	2513.21	3.1	1	41.5	21.5	95.00%	K.SYEQAAGFARPGSTMVTVSMPAGAK.L		K.SYEQAAGFARPGSTMVTVSMPAGAK.L
170	194	3	2506.29	2.9	1	37.4	17.2	95.00%	K.VGPGEWICIPGAGGGLGHLAVQYAK.A	Carbamidomethyl (+57)	K.VGPGEWICIPGAGGGLGHLAVQYAK.A
150	163	2	1581.75	4.4	0	41	22.7	95.00%	E.VAAPIMCAGITCYR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.AEETICPHIQLSGYTVDGTFQHYCIANATHATIIPESVPLEVAAPIMCAGITCYR.A
42	62	3	2378.15	2.1	0	31.5	22.1	95.00%	K.YTGVCHTDLHALQGDWPLPAK.M	Carbamidomethyl (+57)	K.YTGVCHTDLHALQGDWPLPAK.M
200	211	2	1231.6	1.6	1	31.2	22.3	95.00%	R.VVAIDTGDDKAE.L		R.VVAIDTGDDKAELVK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
49	CYSD_SCHPO	41.03%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
132	147	2	1732.75	1.5	0	34.8	24.1	95.00%	K.FVNGDDPNDLAAQIDE.N	Deamidation (+1)	K.FVNGDDPNDLAAQIDENTK.A
47	59	2	1541.79	2.4	0	34.4	19.4	95.00%	R.LFGLQEPGYIYSR.M		R.LFGLQEPGYIYSR.M
27	39	2	1486.79	4	0	44	18.3	95.00%	R.AVPIYATTSYVFR.D		R.AVPIYATTSYVFR.D
378	395	2	2014.03	2.6	1	31	19.9	95.00%	K.TLVIAPAYTTHLQLTDEE.Q		K.TLVIAPAYTTHLQLTDEEQISAGVTK.D
72	100	3	2787.49	3.3	1	49.9	14.9	95.00%	R.IAALEHGAAAIATSSGTSALFMALTTLAK.A		R.IAALEHGAAAIATSSGTSALFMALTTLAK.A
10	26	2	1780.88	3.8	0	81.2	21.8	95.00%	E.TLQLHAGQEPDAATSSR.A		-.MPVESEHFETLQLHAGQEPDAATSSR.A
156	169	2	1637.75	2.4	1	70.3	23.5	95.00%	E.SIGNPMYNVPDFER.I		K.AVYVESIGNPMYNVPDFER.I
366	377	2	1185.64	4.4	0	34.5	17.8	95.00%	K.LASQLANVGDAK.T		K.LASQLANVGDAK.T
170	210	4	4156.13	4.3	1	53.9	16.1	95.00%	R.IAEVAHAAGVPLMVDNTFGGGGYLVRPIDHGADIVTHSATK.W		R.IAEVAHAAGVPLMVDNTFGGGGYLVRPIDHGADIVTHSATK.W
132	150	2	2074.95	4.2	1	127	23.3	95.00%	K.FVNGDDPNDLAAQIDENTK.A		K.FVNGDDPNDLAAQIDENTK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
50	CARB_SCHPO	10.17%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
730	744	2	1630.79	2.5	1	53	21.8	95.00%	K.VLGTDPLMIDSAEDR.H		K.VLGTDPLMIDSAEDR.H
968	975	2	1019.52	4.9	0	24.9	20	90.10%	K.VPQFSWTR.L		K.VPQFSWTR.L
932	943	2	1304.72	5.6	0	35.2	17.9	95.00%	K.TLGVNFIDVATR.S		K.TLGVNFIDVATR.S
1016	1031	2	1630.91	2.3	0	65.7	15.8	95.00%	K.IPLPGQGILLGGDRPE.L		K.IPLPGQGILLGGDRPELAGIAADLSK.L
773	798	3	2736.49	2.9	0	51	14.1	95.00%	K.FANAVGYPVLVRPSYVLSGAAMSVIR.D		K.FANAVGYPVLVRPSYVLSGAAMSVIR.D
418	433	2	1784.89	3.2	0	42	20.9	95.00%	K.TTTANFEPSLDYVVTK.I		K.TTTANFEPSLDYVVTK.I
575	584	2	1057.58	4.7	1	32.1	19.7	95.00%	K.LVGASELDVR.A		K.LVGASELDVR.A
809	823	2	1533.82	3.7	0	37.1	18.7	95.00%	E.NASAVSPDHPVVITK.F		K.LENASAVSPDHPVVITK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
51	STI1_SCHPO	28.93%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
214	229	2	1577.73	4.7	0	54.1	23.5	95.00%	E.FAPSSSTPSADSAKPE.T		K.EEFAPSSSTPSADSAKPETTNPPPQPQPASEPMEEDK.T
543	560	2	1893.06	3.4	0	42.4	12.8	95.00%	E.VLGILQDPAMQAILGQAR.E		K.DPEVLGILQDPAMQAILGQAR.E
115	132	2	1692.83	2.8	0	75.2	22.8	95.00%	E.AAQTQAASGAGGFNPFAK.L		K.SVEAAQTQAASGAGGFNPFAK.L
146	164	2	1935.97	6.4	1	78.1	21.2	95.00%	K.LASNPETASLLADSAFMAK.L		K.LASNPETASLLADSAFMAK.L
76	90	3	1463.79	4.4	1	44.6	18.6	95.00%	R.KGAALHGLGDLDAAR.S		R.KGAALHGLGDLDAAR.S
112	132	2	2007.97	4.2	1	89.9	22.1	95.00%	K.SVEAAQTQAASGAGGFNPFAK.L		K.SVEAAQTQAASGAGGFNPFAK.L
168	183	2	1781.88	4.3	1	66.6	21.6	95.00%	K.IQQNPGSIMAELNDPR.M		K.IQQNPGSIMAELNDPR.M

96	111	3	1705.92	3	1	22.5	18.1	93.50%	E.GLKHDANNAQLLNGLK.S	Deamidation (+1)	R.SAYEEGLKHDANNAQLLNGLK.S
20	34	2	1711.85	3.9	1	70.3	21.7	95.00%	K.TAIDYFTQAIGLDER.N		K.TAIDYFTQAIGLDER.N
230	245	2	1751.78	5	1	42.7	24	95.00%	E.TTNPPPQPQASEPMEE.D		K.EEFAPSSSTPSADSAKPETTNPPPQPQASEPMEEDK.T
371	377	2	800.44	3.8	0	29.8	21.2	95.00%	R.TPDILSR.L		R.TPDILSR.L
311	322	2	1466.61	3.5	1	38.3	23.6	95.00%	E.ADQLDDCIKTCE.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.DITYLNNLAAAYFEADQLDDCIKTCEDAIEQGR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
52	EF1B_SCHPO	30.84%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
14	26	2	1580.81	2.8	1	34.3	20.4	95.00%	K.QLNDFLLDKSFIE.G		K.QLNDFLLDKSFIEGYEPSQADAVVFK.A
14	22	2	1104.59	4.8	0	36.2	19.8	95.00%	K.QLNDFLLDK.S		K.QLNDFLLDK.S
59	73	2	1561.84	4.2	0	60.9	18.5	95.00%	K.QIATYDLATLPGTAK.E		K.QIATYDLATLPGTAK.E
153	165	2	1432.74	3.9	0	44.3	20.2	95.00%	R.SIQMDGLVWGLSK.L		R.SIQMDGLVWGLSK.L
2	13	2	1209.59	3.7	0	57.4	22.5	95.00%	M.GFSDLTSDAGLK.Q		-.MGFSDLTSDAGLK.Q
23	39	2	1885.92	3.6	1	50.9	22.2	95.00%	K.SFIEGYEPSQADAVVFK.A		K.SFIEGYEPSQADAVVFK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
53	DHAS_SCHPO	32.21%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
19	28	2	1170.6	2.9	0	37.2	20.8	95.00%	R.FITLLSDHPEF.K		R.FITLLSDHPEFK.I
229	240	2	1375.66	3.5	0	63.9	22.4	95.00%	E.LTDNVVSAQCNR.V	Carbamidomethyl (+57)	K.ILGSVNSTISGYELTDNVVSAQCNR.V
112	132	3	2341.31	2.7	1	53.3	9.54	95.00%	R.REPTVPLVVPTVNTDHLDVIK.Y		R.REPTVPLVVPTVNTDHLDVIK.Y
31	39	2	856.52	4.9	0	28.2	16.9	94.80%	K.IAVLGASAR.S		K.IAVLGASAR.S
287	303	3	2003.98	4.2	0	33.9	22.1	95.00%	K.QAIYVFDDSTPDRPQPR.L		K.QAIYVFDDSTPDRPQPR.L
19	30	3	1445.76	4.9	1	23.3	20.3	94.40%	R.FITLLSDHPEFK.I		R.FITLLSDHPEFK.I
143	161	2	2003.03	3.7	0	89.2	20.5	95.00%	R.GCIITNSNCSTAAVVVPLK.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GCIITNSNCSTAAVVVPLK.A
267	278	2	1375.7	3.8	1	37.2	21.1	95.00%	R.EVLANYVSEPQK.L		R.EVLANYVSEPQK.L
6	18	2	1227.7	3.7	0	35.6	17.2	95.00%	K.VGILGATGTVGQR.F		K.VGILGATGTVGQR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
54	IF5A1_SCHPO	29.30%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
14	28	2	1608.78	2.9	0	40.8	22.3	95.00%	E.AGASLTFPMQCSALR.K	Carbamidomethyl (+57)	-.MAEEEHVDFEGGEAGASLTFPMQCSALR.K
11	28	2	1851.87	4.1	1	44.5	22.9	95.00%	E.GGEAGASLTFPMQCSALR.K	Carbamidomethyl (+57)	-.MAEEEHVDFEGGEAGASLTFPMQCSALR.K
73	87	2	1655.77	2.4	0	39.8	23	95.00%	E.DMSPSTHNMDVPVVK.R		K.YEDMSPSTHNMDVPVVK.R
14	29	3	1736.88	3.2	1	27.5	21.2	95.00%	E.AGASLTFPMQCSALRK.N	Carbamidomethyl (+57)	-.MAEEEHVDFEGGEAGASLTFPMQCSALRK.N
58	69	2	1352.76	4.3	0	43.7	15.3	95.00%	K.VHIVALDIFNGR.K		K.VHIVALDIFNGR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
55	UGPA1_SCHPO	21.94%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
494	506	2	1495.75	3.1	1	53.3	21.4	95.00%	E.NCVITGNLNILEH.-	Carbamidomethyl (+57)	R.IDIPNGSVLENCVITGNLNILEH.-
1	10	2	1166.63	4.6	0	24.9	18.5	90.00%	-.MDLAPRPLGR.Q	Acetyl (+42)	-.MDLAPRPLGR.Q
15	34	2	2047.96	2.6	0	127	23.2	95.00%	K.SQSAFAFDNTATSIAASTMK.N		K.SQSAFAFDNTATSIAASTMK.N
202	216	2	1577.8	4.4	0	26.8	21.6	93.10%	E.TLLPVPHTADSAIDE.W		K.ETLLPVPHTADSAIDEWYPPGHGDVFEALTNSGIIDTLIAQGK.E
185	194	2	1205.65	4.7	0	32.1	19.1	95.00%	K.IDILTFNQSR.Y		K.IDILTFNQSR.Y

228	243	2	1613.9	2.9	0	32.5	15.3	95.00%	E.ALTNSGIIDTLIAQGK.E		K.ETLLPVPHTADSAIDEWYPPGHG DVFEALTNSGIIDTLIAQGK.E
115	129	2	1460.72	4.2	0	48.3	21.8	95.00%	K.LNGGLGTTMGCVGPK.S	Carbamidomethyl (+57)	K.LNGGLGTTMGCVGPK.S
287	298	2	1278.63	4.4	0	55.1	21.4	95.00%	K.GGTLIDYDGNVR.L		K.GGTLIDYDGNVR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
56	RS18_SCHPO	29.61%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	78	2	1386.79	4	0	45.2	15.7	95.00%	R.IVTIIQNPSQFK.I		R.IVTIIQNPSQFK.I
2	14	2	1578.86	2.6	0	40.5	16	95.00%	M.SLVVPDNFQHILR.L	Acetyl (+42)	-.MSLVVPDNFQHILR.L
79	86	2	1031.56	6	0	52.6	18.7	95.00%	K.IPSWFLNR.Q		K.IPSWFLNR.Q
95	106	2	1334.69	4.9	0	24.9	20.3	90.00%	K.SFQLLANNVDSK.L		K.SFQLLANNVDSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
57	PUT2_SCHPO	21.72%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
406	422	2	1852.92	4.3	1	57.5	21.4	95.00%	K.ADDSEGFFVEPTVLLSK.N		K.ADDSEGFFVEPTVLLSK.N
362	384	3	2428.26	3.2	0	27	17.2	95.00%	K.VGAPLTDFANFVGPVIHQASFNK. L		K.VGAPLTDFANFVGPVIHQASFNK. L
254	274	3	2393.15	4.4	1	52.3	22	95.00%	K.VCFNHPEFAGLHFTGSTAVFR.S	Carbamidomethyl (+57)	K.VCFNHPEFAGLHFTGSTAVFR.S
275	288	2	1444.74	4.6	1	37.7	21	95.00%	R.SLWGTIGENVANGK.Y		R.SLWGTIGENVANGK.Y
495	509	2	1504.71	3.5	1	49.3	22	95.00%	K.CTGAVVGEQPFGGAR.A	Carbamidomethyl (+57)	K.CTGAVVGEQPFGGAR.A
531	548	2	2036.98	5	1	47.4	22	95.00%	R.SIKDTFAYADSVLYPSNF.-		R.SIKDTFAYADSVLYPSNF.-
484	494	2	1225.58	4.6	0	28	22.7	94.60%	R.NAAGNFYINDK.C		R.NAAGNFYINDK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
58	ACON_SCHPO	9.25%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
435	452	2	1870.93	6.6	0	37.9	21.3	95.00%	K.AGGIVLANACGPCIGQWK.R	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.AGGIVLANACGPCIGQWK.R
532	549	2	1853.89	4.6	0	68.9	22	95.00%	K.GYDPGSNTYVAPSSVNVK.D		K.GYDPGSNTYVAPSSVNVK.D
392	402	2	1203.6	5.2	0	35.2	21.6	95.00%	R.AASICQQAIDK.G	Carbamidomethyl (+57)	R.AASICQQAIDK.G
65	80	3	1895.95	4.5	1	26.2	21.6	95.00%	K.ILYGHLDDPVNQDIER.G		K.ILYGHLDDPVNQDIER.G
462	470	2	1052.53	5	0	36.5	21.1	95.00%	K.NSIVTSYNR.N		K.NSIVTSYNR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
59	MET3_SCHPO	16.33%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
427	440	2	1651.86	4	1	77.5	19.6	95.00%	R.LDAISVFYAQELQR.A		R.LDAISVFYAQELQR.A
42	58	2	1850.93	3.2	0	62.1	20.7	95.00%	E.LILNGGFSPLDGFMNQK.D	Deamidation (+1)	R.QFCDVELILNGGFSPLDGFMNQK .D
350	359	2	1102.6	3.9	1	29.9	19.2	95.00%	R.TLNISGTELR.R		R.TLNISGTELR.R
59	68	2	1233.64	5.6	1	40.5	20.6	95.00%	K.DYLNVVENLR.L		K.DYLNVVENLR.L
254	262	2	1012.62	5.1	0	33.5	12.6	95.00%	K.LSLLPLAMR.M		K.LSLLPLAMR.M
217	236	4	2231.2	3.6	0	31	13.4	95.00%	R.VLIHPVVGMTKPGDIDHFTR.V		R.VLIHPVVGMTKPGDIDHFTR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
60	YL8C_SCHPO	21.12%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
217	232	2	1745.96	4.4	1	53	15.1	95.00%	K.GTALQYITSNILPEVK.N		K.GTALQYITSNILPEVK.N
7	33	4	3045.57	3.9	1	29.7	16.9	95.00%	K.TNNLPTLDTLQMVISDVDGTLLDK HHR.F		K.TNNLPTLDTLQMVISDVDGTLLDK HHR.F
70	90	3	2326.19	3.3	0	38.3	19.8	95.00%	R.IPLDLDAFPAAHVNGCVLYNK.G	Carbamidomethyl (+57)	R.IPLDLDAFPAAHVNGCVLYNK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
61	FAS1_SCHPO	4.68%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

1870	1881	2	1266.57	5.2	0	37.8	23	95.00%	R.SDYGMVAANPSR.V		R.SDYGMVAANPSR.V
971	984	2	1619.76	2.6	1	47	22.9	95.00%	E.NFEDLNDPYPVAAR.F		K.TTLIENFEDLNDPYPVAAR.F
824	839	2	1635.84	2.6	1	26.1	19.6	92.10%	E.KTYDGPTGGIVTVLSE.L		K.GVDDSEWEKTYDGPTGGIVTVLSELGEPIHK.L
1778	1806	3	3141.54	1.9	1	40.3	20.5	95.00%	K.DSTSFSFTHPSGLLSATQFTQPALTLMEK.S		K.DSTSFSFTHPSGLLSATQFTQPALTLMEK.S
781	794	2	1545.81	3.9	0	42.1	20	95.00%	K.LPPMPFDGILFGSR.L		K.LPPMPFDGILFGSR.L
1041	1052	2	1199.62	3.4	1	58.5	19.2	95.00%	E.DLAAVVGEDVGR.V		K.DSLWQSEDLAAVVGEDVGR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
62	HSP7F_SCHPO	9.03%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
174	189	2	1665.85	4	0	78.4	20.6	95.00%	R.LMNDNAAAALTYGITK.T		R.LMNDNAAAALTYGITK.T
5	16	2	1249.64	6.5	0	29.4	20.5	95.00%	R.TNVVGIDFGNSK.T		R.TNVVGIDFGNSK.T
38	48	2	1194.59	3.8	1	34	22.2	95.00%	R.STPSLVSYGER.S		R.STPSLVSYGER.S
159	173	2	1534.89	4	1	42.9	10	95.00%	R.ALLEAANIAGLNPLR.L		R.ALLEAANIAGLNPLR.L
96	106	2	1134.6	4	1	31.7	21.5	95.00%	K.LTEVDGFVGAK.V		K.LTEVDGFVGAK.V
163	173	2	1108.64	2.8	0	26	14.9	91.90%	E.AANIAGLNPLR.L		R.ALLEAANIAGLNPLR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
63	HOSM_SCHPO	18.90%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	204	2	1315.66	4	0	40.8	22	95.00%	R.VGIADTVGCATPR.Q	Carbamidomethyl (+57)	R.VGIADTVGCATPR.Q
11	31	3	2302.11	0.95	0	47.3	21.6	95.00%	E.TIKPPMNGNPYGPNPSDFLSR.V	Deamidation (+1)	-.MSVSEANGTETIKPPMNGNPYGPNPSDFLSR.V
172	182	2	1264.7	4.6	0	43.4	17.3	95.00%	R.SDLVDLLSLYK.A		R.SDLVDLLSLYK.A
401	411	2	1290.55	4.4	1	41	23	95.00%	R.EYHADLSDADR.I		R.EYHADLSDADR.I
75	85	2	1173.6	4.3	1	33.3	21.3	95.00%	E.LTSPVASEQSR.Q		K.ALDNFGVDYIELTSPVASEQSR.Q
32	43	2	1391.75	4.9	1	68.1	19	95.00%	R.VNNFSIIESTLR.E		R.VNNFSIIESTLR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
64	YHY6_SCHPO	14.25%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
161	187	3	2608.39	2.9	0	29.8	15.6	95.00%	K.SVGVNPIIVDFSAPGSATAPSKPAAQK.K		K.SVGVNPIIVDFSAPGSATAPSKPAAQK.K
303	314	2	1339.7	2.9	0	48.3	20.3	95.00%	E.LDEPIAIRPTSE.T		R.AGTSELDEPIAIRPTSETVMYPYYAK.W
147	160	2	1522.84	2.6	0	33.7	14.3	95.00%	K.TVFVSPAAVQTYLK.S		K.TVFVSPAAVQTYLK.S
161	188	4	2736.49	3.7	1	29.1	14	95.00%	K.SVGVNPIIVDFSAPGSATAPSKPAAQKK.K		K.SVGVNPIIVDFSAPGSATAPSKPAAQKK.K
492	511	2	2075.19	2.9	0	50.2	7.78	95.00%	K.LPPAIALVQSVVVPCGITNK.T	Carbamidomethyl (+57)	K.LPPAIALVQSVVVPCGITNK.T
387	398	2	1343.81	4.3	0	30.5	9.03	95.00%	R.IYTDLLAVPVIK.G		R.IYTDLLAVPVIK.G
426	441	3	1703.81	4.5	0	20.8	22.5	90.30%	R.GIQGATSHCLGQNFSK.M	Carbamidomethyl (+57)	R.GIQGATSHCLGQNFSK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
65	ILV3_SCHPO	17.56%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
247	265	2	1882.89	3.5	1	50.3	22.9	95.00%	E.AMGMTLPGSSSYLAGSPEK.F		R.HACPGGGACGGMYTANTMASCAEAMGMTLPGSSSYLAGSPEK.F
372	384	2	1273.69	3	0	57.7	19.5	95.00%	E.GLIDGSNITVTGK.T		K.YLHAEGLIDGSNITVTGK.T
40	48	2	994.5	5.2	1	30.6	22.5	95.00%	K.YSETITGPK.S		K.YSETITGPK.S
141	159	2	2167.97	3	0	57.6	23.8	95.00%	E.TVMQGQWYDANVSIPGCDK.N	Carbamidomethyl (+57)	R.EIIADSIETVMQGQWYDANVSIPGCDK.N
526	542	2	1679.88	2.4	0	28	19.4	94.60%	E.AQVGGPIALVQDGDVIE.I		R.FSGGSHGFLIGHVDPEAQVGGPIALVQDGDVIEINAVK.N

185	212	3	3007.42	3.5	1	69.2	22.3	95.00%	R.AGHSPCQNNAPIDIVSAFQSYGEFITGK.I	Carbamidomethyl (+57)	R.AGHSPCQNNAPIDIVSAFQSYGEFITGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
66	ECM17_SCHPO	5.50%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
314	325	2	1337.8	4.6	0	39.3	10	95.00%	R.LTVLEPITSLPR.K		R.LTVLEPITSLPR.K
1449	1466	2	1680.8	2.9	1	32.1	22.7	95.00%	R.AGIITAVENGGANGAVHE.G	Deamidation (+1)/ Deamidation (+1)	R.AGIITAVENGGANGAVHEGVSPEAF.-
886	900	3	1738.91	3.3	1	31.2	18.7	95.00%	E.IDIDEPKPITNEDIK.Q		K.ALGLDNVEIDIDEPKPITNEDIK.Q
801	810	2	1058.57	5.4	1	27.5	20.2	94.00%	K.GADLNLSELK.Y		K.GADLNLSELK.Y
611	636	3	2801.42	3.9	1	43.3	19	95.00%	K.GPSVVLAYLPYHSADDDAITVLQETK.K		K.GPSVVLAYLPYHSADDDAITVLQETK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
67	NACA_SCHPO	38.73%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	75	2	1164.62	5.8	0	59.3	19.3	95.00%	K.SSNNAYIVLGK.V		K.SSNNAYIVLGK.V
52	64	2	1540.93	4.4	0	50.2	7.78	95.00%	K.NILLIINEPIVYK.S		K.NILLIINEPIVYK.S
14	26	2	1308.71	4.4	1	53	17.5	95.00%	E.LPAGSTTVVHAEK.A		K.ISELPAGSTTVVHAEK.A
141	150	2	1087.58	3.2	0	29.8	20	95.00%	E.LVMAQANVSR.A		K.DIELVMAQANVSR.A
132	140	2	946.46	2.2	1	26.2	22.6	92.30%	E.TGVDAKDIE.L		K.AVDETGVDAKDIELVMAQANVSR.A
76	86	2	1189.58	4.9	1	47.2	22.4	95.00%	K.VTVEDMAAQAR.A		K.VTVEDMAAQAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
68	RL8_SCHPO	25.48%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
211	225	2	1491.8	2.7	0	49.8	19	95.00%	E.LASIVSAVDANFSAK.Y		K.NELASIVSAVDANFSAK.Y
24	32	2	1084.62	4.7	0	29.3	18.1	95.00%	K.NPLFVSRPR.S		K.NPLFVSRPR.S
33	43	2	1188.62	4.1	0	26.8	20.2	93.10%	R.SFGIGQDIQPK.R		R.SFGIGQDIQPK.R
81	92	2	1364.74	3.7	1	46.2	20	95.00%	K.TLDKNTATQVFK.L		K.TLDKNTATQVFK.L
134	146	2	1425.8	4.3	1	45.6	14.9	95.00%	K.YGLNHVVALIEAK.K		K.YGLNHVVALIEAK.K
52	57	2	862.44	5.9	1	26.5	20.6	92.80%	K.WPEYIR.L		K.WPEYIR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
69	YF19_SCHPO	24.45%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
122	132	2	1208.53	4.1	0	34.4	22.5	95.00%	R.GDVQAAADCFR.Y	Carbamidomethyl (+57)	R.GDVQAAADCFR.Y
195	208	2	1516.82	4.7	1	34.9	18	95.00%	K.TAELTPLSALCLTK.F	Carbamidomethyl (+57)	K.TAELTPLSALCLTK.F
333	349	2	1794.85	3.3	1	65.9	23.1	95.00%	K.VGDPFAEDTFQGAQVSK.Q		K.VGDPFAEDTFQGAQVSK.Q
5	17	2	1406.78	4.6	1	33	15.7	95.00%	K.LVDHVEITVPTGK.T		K.LVDHVEITVPTGK.T
18	39	3	2450.25	2.3	0	25.5	19.2	95.00%	K.TYIQPVGLFINNQHVDSVHGGR.V		K.TYIQPVGLFINNQHVDSVHGGR.V
422	443	3	2229.12	4.1	0	21.2	20.4	91.10%	R.GNNSTYGLAAGVHTNNITNAIK.V		R.GNNSTYGLAAGVHTNNITNAIK.V
71	80	2	1161.56	3.7	0	28.3	22.2	94.90%	R.AAFQTDAPWR.K		R.AAFQTDAPWR.K
181	194	2	1439.82	3.6	0	42.9	14.8	95.00%	K.IAPAVACGNTIILK.T	Carbamidomethyl (+57)	K.IAPAVACGNTIILK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
70	EF1G_SCHPO	24.94%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
93	115	3	2635.36	2.2	1	28.8	16.5	95.00%	K.VLQYCSFTNSELPGAFRPIIAPR.V	Carbamidomethyl (+57)	K.VLQYCSFTNSELPGAFRPIIAPR.V
207	216	2	1182.71	4	0	27.1	14.1	93.60%	K.FIDQPLPIIK.A		K.FIDQPLPIIK.A
253	267	2	1583.71	2.7	1	54.4	23.2	95.00%	K.HPLASAPNGSFDIEE.Y	Deamidation (+1)	K.HPLASAPNGSFDIEEYK.R
355	375	3	2372.08	3.3	0	25.1	23.6	95.00%	K.GHDYVPAFDVAPDWGSYTFTK.L		K.GHDYVPAFDVAPDWGSYTFTK.L

389	400	2	1442.7	1.8	1	40.6	22.1	95.00%	E.DAWAWDKPIEGR.E		K.AFIEDAWAWDKPIEGR.E
198	216	3	2163.26	3	1	38	4.77	95.00%	K.LDAITEPLKFIDQPLPIIK.A		K.LDAITEPLKFIDQPLPIIK.A
116	127	2	1294.63	4.3	1	26.2	21.5	92.30%	R.VFGAPYDEQAAK.E		R.VFGAPYDEQAAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
71	IF4A_SCHPO	17.60%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
58	69	2	1173.61	5	0	69	21.1	95.00%	R.DVLAQAQSGTGK.T		R.DVLAQAQSGTGK.T
33	48	2	1854.94	3.8	1	30.4	21.1	95.00%	R.GIYAYGFERPSAIQQR.A		R.GIYAYGFERPSAIQQR.A
12	29	2	2157.95	2.7	1	77.3	24.2	95.00%	E.TNYDEVIDTFDDMNLKPE.L		-.MVDQLEDSVIETNYDEVIDTFDDMNLKPELLR.G
255	268	2	1608.83	2.2	0	54.2	19.8	95.00%	E.TVTVTQAVIFCNTR.R	Carbamidomethyl (+57)	K.LDTLCDLYETVTVTQAVIFCNTR.R
17	29	2	1535.72	3.2	0	53.5	22.7	95.00%	E.VIDTFDDMNLKPE.L		-.MVDQLEDSVIETNYDEVIDTFDDMNLKPELLR.G
384	392	2	1016.51	2.9	0	27	21.9	93.40%	E.MPMNIADLI.-		R.EIEQFYNTHIEEMPMNIADLI.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
72	GLNA_SCHPO	28.69%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
60	91	3	3497.64	3.1	0	54.8	22	95.00%	R.VWNFDGSSTGQAPGNNSDTLLKPVAMYNDPFR.R		R.VWNFDGSSTGQAPGNNSDTLLKPVAMYNDPFR.R
338	354	2	1830.98	3.4	0	62.8	17.2	95.00%	R.RPASSIDPYLVTGIITE.T		R.RPASSIDPYLVTGIITETMFEH.-
153	170	2	1809.83	4.4	0	40.7	23.2	95.00%	K.GGFPGPQGPFYCGVGTGR.V	Carbamidomethyl (+57)	K.GGFPGPQGPFYCGVGTGR.V
237	260	4	2635.31	3.2	0	28.9	20.3	95.00%	K.ISFHPKPILGDWNGAGCHTNVSTK.D	Carbamidomethyl (+57)	K.ISFHPKPILGDWNGAGCHTNVSTK.D
285	296	2	1386.66	2.2	0	34.8	22.1	95.00%	E.HIAVYGDDNDLR.L		K.EHIAVYGDDNDLR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
73	RS2_SCHPO	28.85%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
242	251	2	1210.6	4.7	1	50.8	22.2	95.00%	E.YADILMQTEK.K		K.AAFAAASLTYGILTPNLWAERPFGQTPIEEYADILMQTEK.K
64	74	2	1441.73	5.7	1	25.1	20.7	90.40%	K.EYQIVDYFLPR.L		K.EYQIVDYFLPR.L
55	64	2	1237.7	3	1	42.2	15.9	95.00%	E.IYLYSLPIKE.Y		K.SIEEIYLYSLPIKEYQIVDYFLPR.L
174	185	3	1138.69	4.8	1	25.2	10	95.00%	R.GAGLVAAPVTKR.F		R.GAGLVAAPVTKR.F
186	200	2	1799.86	4.8	1	102	22.5	95.00%	R.FLQLAGIEDCYTQSR.G	Carbamidomethyl (+57)	R.FLQLAGIEDCYTQSR.G
141	156	3	1696.87	4.8	0	37.6	20.5	95.00%	R.GYWGTALGDPHTVPVK.V		R.GYWGTALGDPHTVPVK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
74	TAL1_SCHPO	16.15%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
27	44	2	1917.03	3.2	0	67.5	17.3	95.00%	K.YKPQDATTNPSLILAASK.K		K.YKPQDATTNPSLILAASK.K
9	26	2	1795.89	4.5	1	86.8	21.4	95.00%	K.ATGTVVVSDTGDFESIAK.Y		K.ATGTVVVSDTGDFESIAK.Y
45	60	2	1721.91	3.6	0	82.8	18.1	95.00%	K.KPQYAALVDAAVDYAK.A		K.KPQYAALVDAAVDYAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
75	VIPI_SCHPO	33.07%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
69	94	2	2433.11	4.4	1	121	23.3	95.00%	K.IQITSEDGGAASTTDQGGAGGDQAAR.Q		K.IQITSEDGGAASTTDQGGAGGDQAAR.Q
55	68	2	1496.86	2.9	0	66.8	14.6	95.00%	K.TALLLQDALLGQNK.I		K.TALLLQDALLGQNK.I
101	110	2	1087.63	5.8	1	34.3	15.9	95.00%	R.SAIISELLSR.G		R.SAIISELLSR.G
122	134	2	1410.71	4.2	0	61.1	21.2	95.00%	K.SIQLDQSYGVSSK.F		K.SIQLDQSYGVSSK.F
111	121	2	1260.64	3.7	1	31.8	20.5	95.00%	R.GYHLSDVTLEK.S		R.GYHLSDVTLEK.S
137	147	2	1100.62	4.3	1	27.7	18.4	94.30%	K.GILESALSGVR.S		K.GILESALSGVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
76	LYS12_SCHPO	24.59%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
197	208	2	1324.65	5.3	0	41.8	22.1	95.00%	K.SNVMSVTDGLFR.E		K.SNVMSVTDGLFR.E
298	307	2	1044.58	4.6	0	32.2	19.6	95.00%	R.GIANPVATFR.S		R.GIANPVATFR.S
213	228	2	1744.8	2.6	0	34.4	24.1	95.00%	R.HAQSLDPSYASINVDE.Q		R.HAQSLDPSYASINVDEQIVDSMVYR.L
315	331	3	1851.85	2.3	0	25.1	23.2	95.00%	E.FMGHQDAAADIYTAVDK.V		R.SVALMLEFMGHQDAAADIYTAVDK.V
188	196	3	1047.69	4.7	0	25.1	3.01	95.00%	K.KPLVTIIHK.S		K.KPLVTIIHK.S
86	97	2	1231.7	4.7	0	25.9	15.2	91.90%	K.VAGYSSPIVALR.K		K.VAGYSSPIVALR.K
7	19	2	1264.78	2.8	0	28.4	8.45	94.90%	R.IVLGLIPADGIGK.E		R.IVLGLIPADGIGK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
77	THI4_SCHPO	19.88%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
310	338	3	3045.65	3.6	0	44.4	12.8	95.00%	K.TYIHAAQVNNDLARPVILDPVAVGATTAR.S		K.TYIHAAQVNNDLARPVILDPVAVGATTAR.S
373	385	2	1353.71	4.1	0	37.5	19.4	95.00%	R.GVDSISQHTLAAR.I		R.GVDSISQHTLAAR.I
121	140	2	2014.96	4.4	1	70	23	95.00%	K.AAADGADYVGIGSIYETNTK.D		K.AAADGADYVGIGSIYETNTK.D
249	265	3	1917.09	2.6	1	41.5	11.5	95.00%	K.LKDFTPLIHHLTNAVAK.N		K.LKDFTPLIHHLTNAVAK.N
237	248	2	1322.76	4.7	0	31.5	13	95.00%	K.DLLNQIPAALQK.L		K.DLLNQIPAALQK.L
31	42	2	1248.73	2.6	0	37.7	12.3	95.00%	E.GILGGVTLVQHR.E		R.QVEEGILGGVTLVQHR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
78	LEUC_SCHPO	13.72%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
633	649	2	2002.01	4.5	0	59.4	21.4	95.00%	R.VIIAPSFADIFFNNCFK.N	Carbamidomethyl (+57)	R.VIIAPSFADIFFNNCFK.N
603	619	3	1826.86	5.3	0	37.3	22.5	95.00%	R.HATVLVAHDNFGCGSSR.E	Carbamidomethyl (+57)	R.HATVLVAHDNFGCGSSR.E
62	77	3	1759.96	3.1	1	30.6	16.3	95.00%	E.LALATVDHNIPTDPRK.D		R.HPELALATVDHNIPTDPRK.D
477	493	2	1811.86	0.53	1	39.7	22.8	95.00%	R.EFFGDVSNGSPSIITNK.N	Deamidation (+1)	R.EFFGDVSNGSPSIITNK.N
650	667	2	2027	4	1	40.9	20.6	95.00%	K.NGMLPIPTPIEQVNDMMK.A		K.NGMLPIPTPIEQVNDMMK.A
545	563	2	1963.09	2.8	1	45.3	12.6	95.00%	E.GIAAPLPMANVDTDKIIPK.Q		K.FTVVEGIAAPLPMANVDTDKIIPK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
79	O59743_SCHPO	15.29%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
127	136	2	1252.56	3.6	0	33.8	23	95.00%	E.YYHLSAPDCK.S	Carbamidomethyl (+57)	K.LKPVPTSWEQALQDNKPEEYYHLSAPDCK.S
210	225	2	1690.88	3.5	0	52.7	20.2	95.00%	R.SIQDVPFTSATVDIAK.K		R.SIQDVPFTSATVDIAK.K
1	11	2	1319.72	3	1	34.6	19	95.00%	-.MDPYTVAIIKK.L	Acetyl (+42)	-.MDPYTVAIIKK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
80	VATA_SCHPO	14.38%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
150	165	2	1620.75	3.4	0	40.8	23.2	95.00%	R.IGDHVSGGDVFGSVFE.N		R.IGDHVSGGDVFGSVFENSLFNDHK.I
128	136	2	1002.51	5	1	25.2	21.1	90.70%	R.GINTESLNR.E		R.GINTESLNR.E
77	88	2	1228.64	2.8	0	42.5	20.2	95.00%	E.TSGLTVGDPVQR.T		K.CTIQVYEETSGLTVGDPVQR.T
373	389	2	1752.85	8	1	36.9	21.8	95.00%	R.LAEMPADSGYPAYLGAK.L		R.LAEMPADSGYPAYLGAK.L
317	331	2	1544.81	4.6	0	49.4	19.5	95.00%	R.TTLVANTSNMPVAAR.E		R.TTLVANTSNMPVAAR.E
221	240	3	2105.14	4.1	0	35.3	16.8	95.00%	R.AARPVADNLTANQPLLTGQR.V		R.AARPVADNLTANQPLLTGQR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
81	GCSP_SCHPO	12.19%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
953	965	2	1458.76	1.1	0	43.1	19.1	95.00%	K.DNNLLVNAPHPQK.D		K.DNNLLVNAPHPQK.D

657	684	3	2835.49	3.5	0	29.7	14.9	95.00%	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C	Carbamidomethyl (+57)	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C
114	126	2	1433.73	2.5	0	61.8	21.3	95.00%	E.FTTLANNVANQNK.L		K.NPPVNYSESEFTTLANNVANQNK.L
379	412	3	3679.8	2.3	1	51.4	19.4	95.00%	K.ATSNICTAQALLANMSAFYAIYHGPNGLQEIANR.I	Carbamidomethyl (+57)	K.ATSNICTAQALLANMSAFYAIYHGPNGLQEIANR.I
1000	1017	2	2072.93	3.3	1	36.4	23.4	95.00%	R.LDDAYGDKNLFCTCSPVV.-	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.LDDAYGDKNLFCTCSPVV.-
583	600	2	2083.04	3.9	0	43.2	20.3	95.00%	E.MMPITNPLFANIHPYVPE.E		K.LNAVTEMMPITNPLFANIHPYVPEEQAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
82	CDC48_SCHPO	11.41%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
221	230	2	1110.48	4.2	0	29.6	22.1	95.00%	E.VGYDDIGGCR.R	Carbamidomethyl (+57)	R.EDEESSLAEVGYDDIGGCR.R
550	563	2	1522.75	3.6	1	43.8	21.2	95.00%	K.AIANECSANFISVK.G	Carbamidomethyl (+57)	K.AIANECSANFISVK.G
588	604	2	1817.93	4.3	1	57.6	20.9	95.00%	R.AAAPCVVFLDELDSIAK.A	Carbamidomethyl (+57)	R.AAAPCVVFLDELDSIAK.A
116	129	2	1553.82	3.8	0	45.7	18.3	95.00%	R.LGDIVTINPCPDIK.Y	Carbamidomethyl (+57)	R.LGDIVTINPCPDIK.Y
359	379	3	2280.22	3.2	1	32.5	17.1	95.00%	R.SNVVVMAATNRPNSIDPALRR.F		R.SNVVVMAATNRPNSIDPALRR.F
316	332	2	1841.99	4.4	1	39.8	17.9	95.00%	K.NSPAIIFIDEIDSIAPK.R		K.NSPAIIFIDEIDSIAPK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
83	BCA1_SCHPO	12.37%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
315	331	2	1670.97	4.2	1	59.5	11.5	95.00%	R.LLEVFGAGTAALVSPVK.A		R.LLEVFGAGTAALVSPVK.A
37	49	3	1581.74	4.5	1	25.4	22.9	95.00%	K.FGENFTDHMLIMK.W		K.FGENFTDHMLIMK.W
318	331	2	1315.75	3	0	59.7	15.8	95.00%	E.VFGAGTAALVSPVK.A		R.LLEVFGAGTAALVSPVK.A
262	278	2	1795	2.5	1	50.2	14	95.00%	K.EIITAPLDGMILPGVTR.D		K.EIITAPLDGMILPGVTR.D
263	278	2	1665.95	2.8	0	62.8	12	95.00%	E.IITAPLDGMILPGVTR.D		K.EIITAPLDGMILPGVTR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
84	SPI1_SCHPO	23.15%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
203	216	2	1458.62	3	1	31	22.8	95.00%	E.AAAMPLPDEDDADL.-	Oxidation (+16)	K.LVGNPNLEFVASPALAPPEVQVDQQLLAQYQQEMNEAAAMPLPDEDDADL.-
110	122	2	1514.77	4.6	1	58.5	21	95.00%	R.VCENIPIVLCGNK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VCENIPIVLCGNK.V
152	165	3	1783.91	4.6	1	29.2	20.2	95.00%	K.SNYNFEKPFLWLAR.K		K.SNYNFEKPFLWLAR.K
166	174	2	982.55	3.8	1	31.6	16.7	95.00%	R.KLVGNPNLE.F		R.KLVGNPNLEFVASPALAPPEVQVDQQLLAQYQQEMNEAAAMPLPDEDDADL.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
85	RL1B_SCHPO	24.54%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
54	75	3	2486.26	2.6	0	38.3	19.8	95.00%	K.LPNVPRPNMAICILGDAHDLDR.A	Carbamidomethyl (+57)	K.LPNVPRPNMAICILGDAHDLDR.A
78	91	3	1486.72	4.2	1	36.5	22.9	95.00%	K.HGGVDAMSVDDLKK.L	Oxidation (+16)	K.HGGVDAMSVDDLKK.L
130	146	3	1787.89	3.6	1	25.5	21	95.00%	K.AGKFPSPVSHADDLYGK.I		K.AGKFPSPVSHADDLYGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
86	RS8A_SCHPO	35.50%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
60	74	2	1568.72	4.4	1	94.1	23.2	95.00%	R.LDSGNFSWGSEGVSK.K		R.LDSGNFSWGSEGVSK.K
165	178	2	1475.79	4.1	0	33.2	18.5	95.00%	R.LYAVVSSRPGQSGR.C		R.LYAVVSSRPGQSGR.C
152	164	2	1363.68	4.8	1	51.3	21.6	95.00%	K.VDSALETQFAAGR.L		K.VDSALETQFAAGR.L
78	92	2	1751.94	3.1	1	29	17.7	95.00%	R.IIQVAYHPSNNELVR.T		R.IIQVAYHPSNNELVR.T

111	124	3	1682.82	4.5	1	23.1	22	94.20%	R.VWYETHYGILMGSK.G		R.VWYETHYGILMGSK.G
78	89	2	1383.68	3.5	0	39	21.7	95.00%	R.IIQVAYHPSNNE.L		R.IIQVAYHPSNNELVR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
87	PUR8_SCHPO	10.17%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
226	242	2	1930.91	3.5	0	32.6	23.4	95.00%	K.LSGFDNVYPVTGQTYDR.K		K.LSGFDNVYPVTGQTYDR.K
437	449	2	1392.73	3.4	0	47.2	20.1	95.00%	E.LDSLLDASTFVGR.A		K.NTPYFAPIYDELDSLLDASTFVGR.A
243	261	3	2023.12	4.2	1	51.4	14.6	95.00%	R.KIDIDVLQPLASFGATAHK.I		R.KIDIDVLQPLASFGATAHK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
88	YDG7_SCHPO	11.53%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
7	23	3	1939.91	3.9	1	22.9	22.8	93.90%	K.YFENAQNVHFTLADGSK.I		K.YFENAQNVHFTLADGSK.I
53	65	2	1416.62	2.9	1	53.8	22.7	95.00%	R.HIDAAAIYGNEDE.V		R.HIDAAAIYGNEDEVGDGIK.E
293	299	2	771.46	3.5	0	26.3	19	92.40%	E.INSIGIR.A		K.EDMDEINSIGIR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
89	PURA_SCHPO	14.98%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
295	304	2	1080.57	4.3	0	28	19.1	94.60%	E.IGDHLQSVGR.E		R.VGAGPFPTEQLNEIGDHLQSVGR.E
206	224	3	2169.16	3.6	1	37.8	15.7	95.00%	R.LKPFVIDAVAFMYEALQSK.K		R.LKPFVIDAVAFMYEALQSK.K
268	276	2	899.55	4.9	0	44.5	17.2	95.00%	R.IANSIGVVK.A		R.IANSIGVVK.A
388	401	2	1610.74	2.8	0	29	23.1	95.00%	K.VPTTGITHWDQMPE.N		K.VPTTGITHWDQMPENAK.K
282	294	2	1357.66	2.8	1	28.4	22	94.90%	R.VGAGPFPTEQLNE.I		R.VGAGPFPTEQLNEIGDHLQSVGR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
90	THI22_SCHPO	8.53%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
134	151	2	1829.99	4.1	0	72.6	16.6	95.00%	K.LVVDPVMVATSGDSLVTK.D		K.LVVDPVMVATSGDSLVTK.D
9	18	2	1149.55	3.1	0	30.4	22.2	95.00%	E.SLSNQFDPSR.I		-.MPYNPLYESLSNQFDPSR.I
181	197	2	1890.88	4.9	1	111	22.6	95.00%	K.NQGLDISNINSVSDMER.C		K.NQGLDISNINSVSDMER.C
9	20	2	1391.67	3.6	1	36.3	22.7	95.00%	E.SLSNQFDPSRIE.T		-.MPYNPLYESLSNQFDPSRIETVLDPMGYTIK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
91	RS6B_SCHPO	19.67%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	115	2	1739.01	3.8	0	65.7	12.3	95.00%	R.GCIVGQDLAVLALAIVK.Q	Carbamidomethyl (+57)	R.GCIVGQDLAVLALAIVK.Q
116	131	2	1695.88	3.9	1	43.6	19.3	95.00%	K.QGEQDIPGLTDVTVPK.R		K.QGEQDIPGLTDVTVPK.R
59	72	3	1625.86	4.7	0	32.2	19.7	95.00%	K.QGFPMFQGVLLPHR.V		K.QGFPMFQGVLLPHR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
92	RL13_SCHPO	25.96%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
172	183	2	1398.66	5.4	1	54	22.9	95.00%	K.NFNAFSTLSNER.A		K.NFNAFSTLSNER.A
118	128	3	1326.79	4.7	0	51.2	12.3	95.00%	K.VYLAHLIVFPR.K		K.VYLAHLIVFPR.K
46	64	4	2080.27	3.1	1	20	0	95.00%	K.IAPRPVEAIRPAVKPPTIR.Y		K.IAPRPVEAIRPAVKPPTIR.Y
89	100	2	1263.7	3.9	0	28.9	18.6	95.00%	R.VASTIGIPVDHR.R		R.VASTIGIPVDHR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
93	RS14_SCHPO	35.25%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
76	84	2	950.59	3.1	0	33.9	6.99	95.00%	E.VGITALHIK.I		K.EVGITALHIK.I
117	129	2	1442.73	3.7	1	46.5	21.3	95.00%	R.IEDVTPIPTDSTR.R		R.IEDVTPIPTDSTR.R

57	72	2	1564.76	1.8	0	80.1	22.7	95.00%	E.SSPYAAMLAAQDAAAK.C		R.DESSPYAAMLAAQDAAAK.C
95	105	2	1037.57	5.3	0	47.1	18.2	95.00%	K.TPGPGAQAALR.A		K.TPGPGAQAALR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
94	AROG_SCHPO	19.09%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
199	226	3	2704.36	2.1	0	47.7	19.4	95.00%	K.NGTDGTVGVAIDAIGATAHPHTMLGVTK.Q	Deamidation (+1)	K.NGTDGTVGVAIDAIGATAHPHTMLGVTK.Q
350	363	2	1528.76	2.7	1	53.1	21.9	95.00%	E.QTAPMLDDLAEAVR.A		K.YGVSITDACVSWEQTAPMLDDLAEAVR.A
187	198	2	1235.7	3.5	0	49.3	16	95.00%	E.LASALSFPVGFK.N		R.ELASALSFPVGFK.N
118	133	2	1672.85	3.1	0	52.2	20.6	95.00%	K.GLVNDPNLDGSFAINK.G		K.GLVNDPNLDGSFAINK.G
186	198	2	1364.74	4.4	1	39.9	19.5	95.00%	R.ELASALSFPVGFK.N		R.ELASALSFPVGFK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
95	MMF1_SCHPO	35.80%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
59	75	2	1747.86	2.8	0	34.8	21.7	95.00%	K.ANGVIYCSGQIPVANGK.V	Carbamidomethyl (+57)/ Deamidation (+1)	K.ANGVIYCSGQIPVANGK.V
109	124	2	1781.87	4.4	0	46.5	22.1	95.00%	K.VNIFLADMDDFAAVNK.V		K.VNIFLADMDDFAAVNK.V
125	137	2	1483.81	3.9	1	42.4	16.6	95.00%	K.VYTEVLPDPKPAR.S		K.VYTEVLPDPKPAR.S
47	58	2	1247.66	5.3	0	27.4	19.2	93.90%	K.LSSAGPYNQAIK.A		K.LSSAGPYNQAIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
96	RS23_SCHPO	20.98%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
80	96	2	1946.93	3	1	39.2	22.1	95.00%	K.KVTAFVPHDGCLNFVDE.N	Carbamidomethyl (+57)	K.KVTAFVPHDGCLNFVDENDEVLLSGFGR.K
125	137	2	1326.74	4.4	1	55.5	17.4	95.00%	K.VAGVGLSALFHEK.K		K.VAGVGLSALFHEK.K
81	96	2	1818.83	3	0	37.2	23.7	95.00%	K.VTAFVPHDGCLNFVDE.N	Carbamidomethyl (+57)	K.VTAFVPHDGCLNFVDENDEVLLSGFGR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
97	SYKC_SCHPO	8.12%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
581	591	2	1169.63	4.1	1	60.1	18.8	95.00%	E.VQAAEPTVVKE.-		R.EVLLFPHMKPEVQAAEPTVVKE.-
15	28	2	1454.8	4	1	41.2	16.8	95.00%	K.ALVLDPVTGEQVSK.T		K.ALVLDPVTGEQVSK.T
154	176	4	2682.24	3.7	1	34.1	23.3	95.00%	K.LQVMCQAQDADTVDFAAQHEHLR.R	Carbamidomethyl (+57)	K.LQVMCQAQDADTVDFAAQHEHLR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
98	YA03_SCHPO	18.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
82	97	2	1778.89	2.6	1	48.9	21.3	95.00%	E.GGPDKVPVYISPFFQE.V		K.YLAEGGPDKVPVYISPFFQEVGHLPCDIGLELDK.L
181	194	2	1560.83	4.5	0	43.8	19.8	95.00%	K.AADIDFLPPQLSFK.N		K.AADIDFLPPQLSFK.N
98	108	2	1208.59	4.3	0	35.9	22.2	95.00%	E.VGHLPCDIGLE.L	Carbamidomethyl (+57)	K.VPVYISPFFQEVGHLPCDIGLELDK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
99	RAD24_SCHPO	9.63%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
109	120	2	1236.65	4.7	1	29.1	19.1	95.00%	K.HLIPNAASAESK.V		K.HLIPNAASAESK.V
95	108	2	1659.88	3.3	1	76	19	95.00%	E.LDTICQDILTVLEK.H	Carbamidomethyl (+57)	K.IEQELDTICQDILTVLEK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
100	RL15A_SCHPO	19.90%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

115	128	2	1699.83	4.1	0	73.6	21.7	95.00%	R.VLNSYWVNQDATYK.F		R.VLNSYWVNQDATYK.F
78	93	3	1761.94	4.8	0	23.7	19.4	95.00%	K.GQTYGKPVHQGVNHLK.Y		K.GQTYGKPVHQGVNHLK.Y
148	157	3	1218.69	4.4	0	24.4	16	95.00%	R.INWIVNPVHK.H		R.INWIVNPVHK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
101	LEU1_SCHPO	11.47%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
379	392	2	1593.77	3.5	0	28.7	21	95.00%	K.VPYLPLDPHDVNSE.Y		K.VPYLPLDPHDVNSEYAAIIR.V
464	479	2	1742.82	4.9	0	69.1	22.8	95.00%	R.FSVNDYTLSSNGPQSK.C		R.FSVNDYTLSSNGPQSK.C
341	362	3	2346.15	2.9	0	44.7	21.6	95.00%	R.HPYAGNLVFTAFSGSHQDAISK.G		R.HPYAGNLVFTAFSGSHQDAISK.G
137	151	3	1761.87	4	0	33.2	22.6	95.00%	K.NATVHLYNACSPLFR.E	Carbamidomethyl (+57)	K.NATVHLYNACSPLFR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
102	RL6_SCHPO	22.05%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	64	2	1497.84	5	0	33.1	16.2	95.00%	R.ASLAPGTVCILLAGR.F	Carbamidomethyl (+57)	R.ASLAPGTVCILLAGR.F
78	87	2	1091.59	3.1	0	30.9	20	95.00%	E.DTLVVTGPYK.V		R.VVVLSQLEDTLVVTGPYK.V
70	87	2	1959.1	3.1	1	33.6	14.3	95.00%	R.VVVLSQLEDTLVVTGPYK.V		R.VVVLSQLEDTLVVTGPYK.V
109	118	2	1031.56	5.5	1	31.2	19.9	95.00%	K.IDVSGVSVEK.F		K.IDVSGVSVEK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
103	ACL1_SCHPO	6.50%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
369	381	2	1420.73	4.5	1	44	20.7	95.00%	R.GSELTYNNVPISK.V		R.GSELTYNNVPISK.V
171	182	3	1338.74	4.8	0	23.6	16.8	94.80%	K.LYRPGSVAYVSK.S		K.LYRPGSVAYVSK.S
156	170	2	1506.72	3.3	0	45.7	23.3	95.00%	K.IGNTGGMMDNIVASK.L		K.IGNTGGMMDNIVASK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
104	GCST_SCHPO	16.54%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
34	51	2	1940.98	2.9	1	54.1	20	95.00%	K.EGATIVPFAGFSMPVQYK.G		K.EGATIVPFAGFSMPVQYK.G
165	180	2	1623.93	4	1	75.8	12.8	95.00%	R.ALIAIQGPETASVVQK.L		R.ALIAIQGPETASVVQK.L
330	344	2	1486.75	3.5	0	41.1	20.3	95.00%	E.VGQVTSGCPSPTLGK.N	Carbamidomethyl (+57)	R.HGSAVEVDGVEVGQVTSGCPSPTLGK.N
113	127	2	1603.8	3.8	1	53.2	21.3	95.00%	E.TGGIIDDTIISKQDE.N		K.ELKPFHSTLSAFTNETGGIIDDTIISKQDENTYYIVTNAACSEK.D
113	124	2	1231.67	1.5	0	37.3	19.2	95.00%	E.TGGIIDDTIISK.Q		K.ELKPFHSTLSAFTNETGGIIDDTIISK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
105	HMCS_SCHPO	14.77%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
264	277	2	1505.69	2.8	0	27.9	22.9	94.50%	R.LLYTDSAAEPSNPE.L		R.LLYTDSAAEPSNPELEGVR.E
155	183	3	2859.53	3.9	0	40.5	14.9	95.00%	K.GNARPTGGAGCVALLVGPNAPIVFEPGLR.G	Carbamidomethyl (+57)	K.GNARPTGGAGCVALLVGPNAPIVFEPGLR.G
382	392	3	1300.68	5.1	1	26	20	95.00%	K.KTNLVNDLDNR.H		K.KTNLVNDLDNR.H
217	228	2	1325.64	3.7	0	38.4	22.9	95.00%	K.ALDGAYANYNVR.D		K.ALDGAYANYNVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
106	TCTP_SCHPO	16.07%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
6	21	2	1737.84	4.2	1	86.5	23.1	95.00%	K.DVISGDELVSDAYDLK.E		K.DVISGDELVSDAYDLK.E
13	22	2	1151.58	3.5	1	27.4	22.1	94.00%	E.LVSDAYDLKE.V		K.DVISGDELVSDAYDLKEVDDIVYEADCQMVTVK.Q
64	73	2	1211.63	3	0	55.5	20.2	95.00%	E.TVNNLVYSFR.L		K.QGGDVDIGANPSAEDAEENAEEGTETVNNLVYSFR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
107	RL27A_SCHPO	29.41%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	48	3	1461.76	5.9	1	42.8	19.7	95.00%	K.SHPFGHAVVAGVER.Y		K.SHPFGHAVVAGVER.Y
23	34	2	1269.74	4.4	0	65.4	14.1	95.00%	K.VVILQAIDQGSK.S		K.VVILQAIDQGSK.S
94	107	2	1575.83	3.5	1	46.7	20.2	95.00%	K.GLITADTFKEPTQR.S		K.GLITADTFKEPTQR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
108	RL23_SCHPO	25.18%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
15	34	2	2090	3.5	0	78.6	22.5	95.00%	R.MTLGLPVQAIMNCADNSGAK.N	Carbamidomethyl (+57)	R.MTLGLPVQAIMNCADNSGAK.N
51	65	2	1531.78	3.4	0	55.2	20.6	95.00%	R.LPAASCGDMVLATVK.K	Carbamidomethyl (+57)	R.LPAASCGDMVLATVK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
109	TRP_SCHPO	14.49%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
382	393	2	1355.77	4.5	0	47.2	17	95.00%	K.INNCIGQILLAK.R	Carbamidomethyl (+57)	K.INNCIGQILLAK.R
400	419	3	1938.01	4.3	1	37.5	18.9	95.00%	R.IIAETGAGQHGVATAICAAK.F	Carbamidomethyl (+57)	R.IIAETGAGQHGVATAICAAK.F
275	302	3	2928.48	4.6	1	34.9	19.2	95.00%	K.QFQSGGSVATAPPAAVVEPINEMYLPQK.Y		K.QFQSGGSVATAPPAAVVEPINEMYLPQK.Y
445	461	2	1739.99	4	1	48.6	13.4	95.00%	R.LLGAEVVPVTSGTQTLR.D		R.LLGAEVVPVTSGTQTLR.D
91	114	2	2617.33	5.8	0	82.3	19.1	95.00%	R.DAGVTIPIILMGYYNPIFSYGDAK.T		R.DAGVTIPIILMGYYNPIFSYGDAK.T
450	461	2	1256.71	3.7	0	63.1	16.8	95.00%	E.VVPVTSGTQTLR.D		R.LLGAEVVPVTSGTQTLR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
110	SERC_SCHPO	10.28%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
376	385	2	1147.65	4.7	1	32.8	14.5	95.00%	R.LIDLLESFAK.A		R.LIDLLESFAK.A
216	228	2	1299.74	5	0	37	14.9	95.00%	K.NAGPAGITVVFVR.D		K.NAGPAGITVVFVR.D
189	199	2	1282.6	4.3	0	67	22.5	95.00%	R.VCDVSSNFISR.K	Carbamidomethyl (+57)	R.VCDVSSNFISR.K
324	329	2	766.38	5.3	0	26.2	20	92.30%	R.MNVTFR.I		R.MNVTFR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
111	RL10A_SCHPO	20.36%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	128	3	1265.71	4.6	0	30	16	95.00%	R.HAFGKPNGLVAR.V		R.HAFGKPNGLVAR.V
41	56	2	1798.86	2.8	1	44.4	22.2	95.00%	R.AGVDEFPLCIHLVSNE.Y	Carbamidomethyl (+57)	R.AGVDEFPLCIHLVSNEYEQITSEALEAAR.I
129	139	2	1228.7	4.7	0	40	16.9	95.00%	R.VNIGQILMSVR.T		R.VNIGQILMSVR.T
33	38	2	719.4	4.8	0	27.1	17.3	93.50%	R.IFDLGR.K		R.IFDLGR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
112	RS22_SCHPO	27.69%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
98	108	2	1171.7	4.9	0	29.1	13.2	95.00%	R.QVGVIVLTTSR.G		R.QVGVIVLTTSR.G
4	19	2	1814.9	4.5	1	77.6	21.1	95.00%	R.QSVLADCLNNIVNAER.R	Carbamidomethyl (+57)	R.QSVLADCLNNIVNAER.R
89	97	2	1111.62	5.6	0	31.9	15.9	95.00%	K.WVNQLLPSR.Q		K.WVNQLLPSR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
113	YI75_SCHPO	11.76%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
54	65	2	1279.67	5.1	1	47	20.3	95.00%	K.SFIGLDALTESK.G		K.SFIGLDALTESK.G
30	41	3	1413.76	4.8	1	20.9	17.9	90.50%	R.LRGPHCGTYLLK.V	Carbamidomethyl (+57)	R.LRGPHCGTYLLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
114	AATR1_SCHPO	15.19%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
305	317	2	1562.83	3.7	1	52.6	19.5	95.00%	R.VGWFTAQPLFIER.G		R.VGWFTAQPLFIER.G

424	438	2	1702.83	3.4	0	32.4	22.1	95.00%	E.GVNLACGNWFVVDPR.V	Carbamidomethyl (+57)	K.IHAEAVEEGVNLACGNWFVVDPR.V
275	288	2	1577.78	4.4	1	46.4	22	95.00%	K.ELIPSFLSMDVDGR.V		K.ELIPSFLSMDVDGR.V
38	54	2	1856.03	4.5	1	36.8	13.8	95.00%	K.IISLAGGLPNPEYFPIR.E		K.IISLAGGLPNPEYFPIR.E
7	19	3	1436.71	5.4	1	43.2	22.2	95.00%	K.DLSHHLSVESASR.K		K.DLSHHLSVESASR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
115	GLT1_SCHPO	1.94%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1897	1918	3	2189.08	3.9	1	55	21.2	95.00%	K.GKDVIVIGGGDTGNDCLGTSVR.H	Carbamidomethyl (+57)	K.GKDVIVIGGGDTGNDCLGTSVR.H
1758	1776	2	1792.99	3.1	0	90.7	15.8	95.00%	R.VAIIGSGPAGLAAADQLNR.A		R.VAIIGSGPAGLAAADQLNR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
116	PYC_SCHPO	7.59%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
829	838	2	1275.63	4.5	1	27.7	21.6	94.20%	K.QLEFDNNQLR.E		K.QLEFDNNQLR.E
525	546	3	2378.22	3	1	36.4	17.9	95.00%	E.IVMPVLLDSTGNQIDVSHPSEK.G		K.SEIVMPVLLDSTGNQIDVSHPSEK.G
1109	1129	3	2088.05	4.4	1	38.2	20.4	95.00%	R.ADPGNPGHVAAPMSGTIVEIR.V		R.ADPGNPGHVAAPMSGTIVEIR.V
917	929	2	1447.76	4.7	0	42.2	19.7	95.00%	K.VVGDLAQFMVQNK.L		K.VVGDLAQFMVQNK.L
302	315	2	1628.75	2	1	37.3	23.4	95.00%	K.YCNAGTAEFLLDQK.G	Carbamidomethyl (+57)	K.YCNAGTAEFLLDQK.G
839	848	2	1297.58	4.8	1	38.2	22.4	95.00%	R.EIDSYWAQMR.L		R.EIDSYWAQMR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
117	PMP20_SCHPO	26.92%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
30	55	2	2747.41	5.1	1	44.7	18.5	95.00%	K.FIIVGVPGAFTPPCSSQVPGYIANEK.Q	Carbamidomethyl (+57)	K.FIIVGVPGAFTPPCSSQVPGYIANEK.Q
141	156	2	1647.86	3	1	43.2	20.3	95.00%	E.VTDVDISSADKVLSSL.-		K.VFIENEVTDVDISSADKVLSSL.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
118	PYR1_SCHPO	1.74%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1135	1145	2	1229.6	4.3	0	46.2	22.2	95.00%	R.MLDDIGVDQPK.W		R.MLDDIGVDQPK.W
1758	1770	2	1371.7	4.4	0	56.2	21.2	95.00%	K.FVGNTAFTGFGVR.E		K.FVGNTAFTGFGVR.E
1804	1818	3	1724.81	5.5	1	27.4	22.6	95.00%	R.LHDQDDSGVQLEVDR.S		R.LHDQDDSGVQLEVDR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
119	YCO6_SCHPO	11.45%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
15	36	3	2140.01	3.2	0	36.7	22.5	95.00%	K.MSAAPTPHNTPSGTSAPNFGAK.A		K.MSAAPTPHNTPSGTSAPNFGAK.A
57	66	2	1068.58	2.8	0	40.9	16.5	95.00%	K.LGSLLHLTSE.G		K.LGSLLHLTSEGVSELPEAVQR.R
233	245	2	1434.65	4.4	0	35.8	22.7	95.00%	E.SGPSNVFLYDHAE.G		K.TYYYMEESGPSNVFLYDHAEGDK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
120	ASNS_SCHPO	3.23%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
516	523	2	1035.55	6.3	1	30	18.5	95.00%	K.LFDEIFPR.Q		K.LFDEIFPR.Q
399	408	2	1120.54	4.9	1	26.3	20.4	92.40%	K.STMAWGLEAR.V		K.STMAWGLEAR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
121	THRC_SCHPO	16.54%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

188	215	3	3177.45	3.2	0	25	22.4	95.00%	E.AQMTTVTDPNVHCITVNGVFDDCQDLVK.Q	Carbamidomethyl (+57)/ Deamidation (+1)/ Carbamidomethyl (+57)	R.VSPIQEAQMTTVTDPNVHCITVNGVFDDCQDLVK.Q
265	282	2	1945.01	4.9	0	46.3	19.8	95.00%	R.FIVPTGNFGDILAGYYAK.R		R.FIVPTGNFGDILAGYYAK.R
437	454	3	2061.03	4.7	1	31.2	20.3	95.00%	K.TKDQDITYICLSTAHPAK.F	Carbamidomethyl (+57)	K.TKDQDITYICLSTAHPAK.F
313	327	2	1443.73	4.4	0	39.8	21.5	95.00%	K.ADSTQVSPSGPISAK.E		K.ADSTQVSPSGPISAK.E
182	215	3	3829.81	3.8	1	34.2	21.6	95.00%	R.VSPIQEAQMTTVTDPNVHCITVNGVFDDCQDLVK.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VSPIQEAQMTTVTDPNVHCITVNGVFDDCQDLVK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
122	TRX1_SCHPO	27.18%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	79	2	1466.74	3	0	25.9	21.3	91.80%	E.AGVHAMPSFFLYK.N		K.VDVDQLSEIAAEAGVHAMPSFFLYK.N
40	54	2	1796.83	4.6	1	68.4	23.3	95.00%	K.FEQFSNTYSDATFIK.V		K.FEQFSNTYSDATFIK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
123	RS0B_SCHPO	32.75%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	88	4	2453.26	4	1	67.3	19.5	95.00%	R.VIATIENPADVCVISSRPYGHR.A	Carbamidomethyl (+57)	R.VIATIENPADVCVISSRPYGHR.A
4	31	4	2920.54	3.3	1	44.1	15.4	95.00%	E.SIARPSVLNATDDDIKNLLAADSHIGSK.N		-.MAESIARPSVLNATDDDIKNLLAADSHIGSK.N
139	169	3	3390.76	4.3	1	25.4	14.6	95.00%	K.EASFVNIPVIALCDTDSILNHVDVAIPINNK.G	Carbamidomethyl (+57)	K.EASFVNIPVIALCDTDSILNHVDVAIPINNK.G
231	243	2	1319.64	5.5	1	36.9	21.8	95.00%	E.AQLAAQTAAAEFE.V		K.AAAAAAAEEEAQLAAQTAAAEFEVTDSAAGTVDPTILDNATAGQVGQTTWEGDAEWNITGAAPSEWA.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
124	SYRC_SCHPO	6.80%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
163	180	2	1987.02	4.1	1	33.9	19.1	95.00%	R.STIIGSFLANLHESQGWK.V		R.STIIGSFLANLHESQGWK.V
480	489	2	1284.6	5.9	0	39.4	22.3	95.00%	R.INNYAFDWSR.M		R.INNYAFDWSR.M
11	24	2	1544.86	4.5	0	46.7	16.1	95.00%	K.SLSTLGLQDLPVFR.E		K.SLSTLGLQDLPVFR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
125	COFI_SCHPO	22.63%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
108	124	2	1827.87	3.4	1	38.2	22.6	95.00%	R.RAFTGIGTDIQATDFSE.V		R.RAFTGIGTDIQATDFSEVAYETVLEK.V
109	124	2	1671.77	2.5	0	66.2	23	95.00%	R.AFTGIGTDIQATDFSE.V		R.AFTGIGTDIQATDFSEVAYETVLEK.V
81	94	2	1584.9	4.1	0	54.1	15.7	95.00%	K.IIFISWSPDVAPIK.S		K.IIFISWSPDVAPIK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
126	RL12_SCHPO	36.97%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
68	83	2	1538.91	3.4	0	50.5	11.8	95.00%	R.QAAVSVVPSASALVIK.A		R.QAAVSVVPSASALVIK.A
95	108	2	1483.7	3.7	1	31.6	22.7	95.00%	K.DKNVAHSGNVSLDE.I		K.DKNVAHSGNVSLDEIIEVAR.T
97	108	2	1240.57	4.9	0	25.3	22.5	90.90%	K.NVAHSGNVSLDE.I		K.NVAHSGNVSLDEIIEVAR.T
17	31	2	1312.7	3.6	1	46	16.6	95.00%	R.AVGGEVAGGSTLAPK.I		R.AVGGEVAGGSTLAPK.I
131	146	2	1652.81	4	1	45.9	21	95.00%	K.EILGTAFSVGCTVDGK.N	Carbamidomethyl (+57)	K.EILGTAFSVGCTVDGK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
127	SODC_SCHPO	40.26%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

98	116	2	1984.04	4.4	0	72.6	18.1	95.00%	K.TTFSDSVISLFGANSIIGR.T		K.TTFSDSVISLFGANSIIGR.T
81	97	2	1765.87	4	1	72.3	21.9	95.00%	R.HVGDLGNLESDAQGNIK.T		R.HVGDLGNLESDAQGNIK.T
45	70	3	2825.25	4.3	1	41.5	23.6	95.00%	R.GFHIHQFGDNTNGCTSAGPHFNPEGK.T	Carbamidomethyl (+57)	R.GFHIHQFGDNTNGCTSAGPHFNPEGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
128	RL3A_SCHPO	16.75%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
214	222	2	1002.56	2.7	0	28.8	19.4	95.00%	E.MIDVIGVTR.G		K.STFEQNEMIDVIGVTR.G
11	19	2	982.54	4.3	0	27.2	18.1	93.70%	R.HGSLGFLPR.K		R.HGSLGFLPR.K
181	193	2	1315.67	3.2	1	50.5	21.4	95.00%	E.IQVNGGSVADKVE.W	Deamidation (+1)	K.AHLMEIQVNGGSVADKVEWAR.E
319	334	2	1715.87	2.3	1	34.3	21.1	95.00%	E.NDFVMLNGATPGPVKR.V	Deamidation (+1)	R.YGVVENDFVMLNGATPGPVKR.V
249	266	3	2035.03	4.4	0	29.3	21	95.00%	K.VACIGAWHPANVQWTVAR.A	Carbamidomethyl (+57)	K.VACIGAWHPANVQWTVAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
129	VATB_SCHPO	12.72%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
48	59	2	1295.72	2.9	0	39.2	16.3	95.00%	E.IVNLNLPDGSVR.S		R.RPQYNEIVNLNLPDGSVR.S
439	449	2	1284.62	4.2	1	36.9	21.6	95.00%	K.TFISQGAYENR.T		K.TFISQGAYENR.T
146	162	2	1774.94	5.8	0	71.2	19.1	95.00%	E.MIQTGISSIDGLNSIAR.G		R.IYPEEMIQTGISSIDGLNSIAR.G
108	125	2	1840.96	2.3	1	33.6	19.4	95.00%	R.VFNGSGLPIDKGPNLLAE.D	Deamidation (+1)	R.VFNGSGLPIDKGPNLLAEDYLDINGSPINPYAR.I
42	59	3	2083.09	4.5	1	23.6	18.3	94.90%	R.RPQYNEIVNLNLPDGSVR.S		R.RPQYNEIVNLNLPDGSVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
130	DHE4_SCHPO	13.75%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
417	439	2	2411.16	5.2	0	85.7	21.5	95.00%	K.YCDSGSNNIPSLVDGANIAGFLK.V	Carbamidomethyl (+57)	K.YCDSGSNNIPSLVDGANIAGFLK.V
356	367	2	1231.57	4.5	1	27.7	22.1	94.20%	R.ASGEGCWLAPGK.A	Carbamidomethyl (+57)	R.ASGEGCWLAPGK.A
93	101	2	1127.61	5.6	1	29.2	19.5	95.00%	K.FLGFEQIFK.N		K.FLGFEQIFK.N
399	416	2	1950.98	3.3	1	85	20.8	95.00%	K.LAGIMQNIFEQSTDVASK.Y		K.LAGIMQNIFEQSTDVASK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
131	ADK_SCHPO	15.29%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
253	267	2	1483.87	4.5	0	69.4	13.6	95.00%	R.VVVITQGADATIVAK.D		R.VVVITQGADATIVAK.D
126	138	2	1424.68	5.2	0	51	21.6	95.00%	R.SLCTNLGAANNYK.L	Carbamidomethyl (+57)	R.SLCTNLGAANNYK.L
41	64	3	2620.16	3.6	1	40.7	24	95.00%	E.SQMGIYKEPCVSYSAGGAAQNSCR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.SNDAVLASESQMGIYKEPCVSYSAGGAAQNSCR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
132	TBB_SCHPO	11.61%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
126	154	3	2876.43	3.5	0	64.1	20	95.00%	E.ACDALQGFQLTHSLGGGTGSGMGTLLLSK.I	Carbamidomethyl (+57)	R.EAEACDALQGFQLTHSLGGGTGSGMGTLLLSK.I
163	174	2	1249.62	3.9	0	41.3	20.6	95.00%	R.MMATFSVAPAPK.S		R.MMATFSVAPAPK.S
206	216	2	1163.66	5.1	0	35	15.8	95.00%	E.ALSSIFANTLK.I		K.SSDTVVEPYNATLSMHQLVENSDETFCIDNEALSSIFANTLK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
133	SYLC_SCHPO	3.78%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
382	398	2	1730.97	1.4	0	47.3	12.8	95.00%	K.GQDLIGALVNAPLSVHK.Q		K.GQDLIGALVNAPLSVHK.Q
226	241	2	1922.92	5.8	0	66.1	23.3	95.00%	R.SFITTDVNPYYDSFVR.W		R.SFITTDVNPYYDSFVR.W
779	787	2	927.55	4	0	33.4	16	95.00%	E.ALANSAILR.L		R.LALADAGDTVDDANFEEALANSAILR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
134	IMDH_SCHPO	12.21%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
303	313	2	1155.67	4.5	0	51.3	15.6	95.00%	K.IDVIAGNVVTR.E		K.IDVIAGNVVTR.E
214	234	3	2311.28	3.6	1	29.3	12	95.00%	K.LPVVDKDDNLVALLSLTDLMK.N		K.LPVVDKDDNLVALLSLTDLMK.N
419	433	2	1421.67	3.9	1	52.2	23.3	95.00%	R.GMGSIAAMEGTGVNK.N		R.GMGSIAAMEGTGVNK.N
342	358	2	1771.88	4.7	0	38.8	21.5	95.00%	E.VMACGRPQATAIAQVAE.F	Carbamidomethyl (+57)	R.VGMGSGSACITQEVMACGRPQATAIAQVAEFASQFGIGVIADGGIQNVGHMVK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
135	RL2_SCHPO	17.79%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
92	108	2	1725.87	4	1	46.3	21.6	95.00%	K.NAALTVGNVLPVGEMPE.G	Oxidation (+16)	K.NAALTVGNVLPVGEMPEGTIISNVEEK.A
128	144	2	1759.88	3	0	42.2	21.3	95.00%	R.SSGNYVIIVGHDVDTGK.T		R.SSGNYVIIVGHDVDTGK.T
163	173	2	940.55	4.3	0	54.6	11.8	95.00%	R.GVVGIVAGGGR.I		R.GVVGIVAGGGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
136	YDMC_SCHPO	3.71%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
82	91	2	1136.53	5	0	33.4	22.5	95.00%	R.NADNSVTNFR.D		R.NADNSVTNFR.D
485	495	2	1254.64	4	1	25.4	21.2	90.90%	K.VTKVEPEPIDE.E		K.VTKVEPEPIDEEEAFSDDEEEEPEEIK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
137	PMM_SCHPO	15.56%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
210	220	2	1282.6	2.9	0	37.3	22.5	95.00%	E.GFDTIHFFGDK.T		K.EGFDTIHFFGDK.T
45	58	2	1347.75	4.4	0	41.6	17.1	95.00%	K.VVAIGFVGGSDLSK.Q		K.VVAIGFVGGSDLSK.Q
236	250	2	1568.74	2.3	0	26.5	22.9	92.70%	R.TIGHSVTNPDDTIAE.L		R.TIGHSVTNPDDTIAELK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
138	PDI1_SCHPO	5.28%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	136	3	1350.87	5.1	1	30.4	0	95.00%	R.KQLLPTVKPISK.D		R.KQLLPTVKPISK.D
188	201	2	1436.77	4.3	0	45.1	17.4	95.00%	K.SLGSNFPGIVAFTK.D		K.SLGSNFPGIVAFTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
139	RS10B_SCHPO	23.13%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	44	3	1428.82	4.9	1	23.6	16	94.80%	K.HPEVGVPNLQVIK.A		K.HPEVGVPNLQVIK.A
10	24	2	1621.94	2.8	0	62.3	13.2	95.00%	K.AIHQALFQQGVLVAK.K		K.AIHQALFQQGVLVAK.K
26	31	2	732.38	5.5	0	30.1	20.4	95.00%	K.DFNLPK.H		K.DFNLPK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
140	RS4B_SCHPO	8.40%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
222	233	2	1232.68	5.6	1	42.4	17.6	95.00%	R.LSNVFVIGEAGK.S		R.LSNVFVIGEAGK.S
40	49	2	1258.72	4.7	1	26.1	16.8	92.20%	R.ECLPLIVFLR.N	Carbamidomethyl (+57)	R.ECLPLIVFLR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
141	RS17A_SCHPO	23.66%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	59	3	1133.6	4.6	0	24.5	19.6	95.00%	K.IAGYTTHLMK.R		K.IAGYTTHLMK.R
34	44	2	1156.68	4.8	1	51	15.2	95.00%	R.IVDEVAIIASK.R		R.IVDEVAIIASK.R
24	33	2	1234.67	4.6	1	36.3	17.9	95.00%	R.LTLDFQTNKR.I		R.LTLDFQTNKR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
142	RLA2_SCHPO	34.55%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
62	88	2	2220.11	4.1	1	89.7	20.7	95.00%	K.LATVPTGGAASAAPAAAAGGAAPAAEE.A		K.LATVPTGGAASAAPAAAAGGAAPAAEEAAK.E
25	35	2	1103.58	5.1	1	36.4	21.1	95.00%	E.SVLSTVGIEAE.S		K.DSPSASDIESVLSTVGIEAESER.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
143	Q76N21_SCHPO	35.37%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	140	3	2329.12	1.9	1	21.7	22.3	92.00%	K.GASDGGLFIPHSPNRFPGFDIE.T		K.YEGVTEPEGEFELTEAIEDGPRPFK.V
13	22	2	1195.61	4.9	0	30.3	22	95.00%	R.FVTCQIVSSR.V	Carbamidomethyl (+57)	K.SSPYFSRYQTKYRR.R
23	39	3	1864.91	3.1	1	21.6	22.2	91.90%	R.VNGDYVLAHAHSSELPR.Y	Deamidation (+1)	R.RREGKTDYYARKRLIAQAK.N
67	74	2	893.45	4.1	1	25	21.8	90.30%	K.VGLADKYE.G		R.FVTCQIVSSRVNGDYVLAHAHSSELPR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
144	ODPB_SCHPO	16.12%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
331	360	3	3021.51	4	1	35.4	18.5	95.00%	R.VSMADVPMPYSHPVEAASVPNADVVVAAAK.K		R.VSMADVPMPYSHPVEAASVPNADVVVAAAK.K
318	330	2	1496.68	3.3	1	47.1	22.7	95.00%	E.SDAFDYLDAPVER.V		R.IVTVDQAYSQHGIGSEIAAQIMESDAFDYLDAPVER.V
295	310	2	1702.82	2.8	0	41.5	22.3	95.00%	R.IVTVDQAYSQHGIGSE.I		R.IVTVDQAYSQHGIGSEIAAQIMESDAFDYLDAPVER.V
346	360	2	1381.76	3.3	0	30.5	16.2	95.00%	E.AASVPNADVVVAAAK.K		R.VSMADVPMPYSHPVEAASVPNADVVVAAAK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
145	SYTC_SCHPO	6.40%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
160	174	2	1703.8	4.7	1	71.1	23	95.00%	R.VITNDDYSSIESYAK.Q		R.VITNDDYSSIESYAK.Q
248	258	2	1187.55	4.2	0	47.1	22.3	95.00%	K.NSSSYFLGDAK.N		K.NSSSYFLGDAK.N
8	26	3	2136.14	4.2	1	27.4	16.1	95.00%	K.GVQASLDNLSLEIPFIQHR.L		K.GVQASLDNLSLEIPFIQHR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
146	CH10_SCHPO	28.85%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	84	2	1230.7	4	0	31.7	16.1	95.00%	R.VLLPAYGGSNIK.V		R.VLLPAYGGSNIK.V
62	72	2	1111.6	4.5	0	30.9	17.7	95.00%	K.LAQPSVAVGDR.V		K.LAQPSVAVGDR.V
98	104	2	798.52	3	1	36.8	11.1	95.00%	E.LLAIIKE.-		R.DHELLAIIKE.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
147	YHZ8_SCHPO	42.42%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
75	103	3	3217.69	3	0	57.2	16.4	95.00%	K.TSNPFLAFANYLTSTHAPLAEPLQLLNFK.V		K.TSNPFLAFANYLTSTHAPLAEPLQLLNFK.V
144	164	3	2285.2	2.8	0	38.6	18.5	95.00%	K.ADTSLIIHSLDDPSLYAVVTR.Y		K.ADTSLIIHSLDDPSLYAVVTR.Y
2	13	2	1361.7	3.8	0	57.2	20.6	95.00%	M.SFPASTHVYIAK.I	Acetyl (+42)	-.MSFPASTHVYIAK.I
177	198	3	2279.2	3.7	0	43.3	18.6	95.00%	E.ISGATSVSQQVIYSGVGFLNRP.-		K.SGIEPGPAEISGATSVSQQVIYSGVGFLNRP.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
148	NACB_SCHPO	17.22%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	72	2	876.45	3.6	0	26.8	20.4	93.20%	E.DGGVINFR.A		K.EDGGVINFR.A
73	90	3	1884.97	4	1	45.6	21.1	95.00%	R.APTVHSSLPNETTAIYGK.A		R.APTVHSSLPNETTAIYGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
149	SYDC_SCHPO	11.72%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
281	294	2	1356.6	4.8	1	27.5	22.6	94.00%	K.MSGASSEGGSNVFK.I		K.MSGASSEGGSNVFK.I
522	554	3	3334.69	3.2	1	85.5	18.1	95.00%	K.ALGVSPDVGLQQYIDAFAIGCPPHAGGGIGLER.V	Carbamidomethyl (+57)	K.ALGVSPDVGLQQYIDAFAIGCPPHAGGGIGLER.V
200	210	2	1229.65	4.9	1	29.1	19.6	95.00%	K.NLPFLVEDAGR.S		K.NLPFLVEDAGR.S
490	499	2	1300.55	3.9	0	26.9	22.9	93.30%	R.YSNSYDFFMK.G		R.YSNSYDFFMK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
150	RL14_SCHPO	11.94%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
103	110	2	993.46	6	0	29.1	22	95.00%	R.SQLNDFDR.F		R.SQLNDFDR.F
87	94	2	905.44	5.7	0	30.4	21.3	95.00%	K.WASSAWAK.K		K.WASSAWAK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
151	DAK1_SCHPO	10.00%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
45	66	3	2123.05	5.3	0	21	20.3	90.90%	K.NVSVISGGGAGHEPTHSSFVGK.G		K.NVSVISGGGAGHEPTHSSFVGK.G
503	526	3	2700.3	3.7	1	23.8	21.5	95.00%	K.YTPARPGDSTMCDALVPFVETFVK.T	Carbamidomethyl (+57)	K.YTPARPGDSTMCDALVPFVETFVK.T
388	399	2	1358.73	4.4	1	25.9	19.2	91.90%	R.QAIVNSMENLIK.A		R.QAIVNSMENLIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
152	SYIC_SCHPO	2.73%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
312	326	2	1426.69	3.9	0	40.6	22.3	95.00%	E.GSGTGIVHQAPAFGE.A		K.LYSADYVEEGSGTGIVHQAPAFGEADYDAAWAAGIIDADHQPPCPVDEQGLLTSEITDFAGQYVK.D
1050	1063	2	1559.87	3.9	0	68.2	14	95.00%	E.QDVQGATFLLSLLR.-		K.ETGADESNIIASEEQDVQGATFLLSLLR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
153	MPG1_SCHPO	14.33%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
270	287	2	1775.99	2.9	0	43.2	14.1	95.00%	K.IGPNVVIGPNVTIGDGVR.L		K.IGPNVVIGPNVTIGDGVR.L
144	154	2	1262.6	2.2	0	32	22	95.00%	K.YGVVVHYPNSE.S		K.YGVVVHYPNSESLIER.F
244	266	2	2263.29	2.8	0	71.4	9.54	95.00%	E.ILAPASSNIIGNVLIDPSATIGK.N		K.HKPEILAPASSNIIGNVLIDPSATIGK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
154	ACAC_SCHPO	2.28%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1972	1994	3	2667.36	3.2	1	27.8	18.3	95.00%	K.TAQAINDFNHGEQLPLFILANWR.G		K.TAQAINDFNHGEQLPLFILANWR.G
1856	1873	2	2026.93	3	1	31.8	23.4	95.00%	R.NNPVPISPSSDTWDRDVE.F		R.NNPVPISPSSDTWDRDVEFYPSQNGYDPR.W
197	207	2	1131.63	6.1	0	34.7	15.8	95.00%	K.ISSTIVAQSAR.V		K.ISSTIVAQSAR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
155	ACL2_SCHPO	13.01%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
193	209	2	1822.94	2.8	1	27.1	20.5	93.60%	R.ATIASTLLSDIPVEQHE.S		R.ATIASTLLSDIPVEQHESLVDFIIR.L
326	334	2	985.56	4.7	1	36	18.4	95.00%	K.LTILNAEGR.V		K.LTILNAEGR.V
382	389	2	947.52	4.5	0	26.9	20.6	93.30%	K.TVLDLMTR.G		K.TVLDLMTR.G

32	61	3	3211.76	3.3	1	47.1	13.8	95.00%	K.TVSATPAVQLAQIQFPLPTLVIPAESTTYR.E		K.TVSATPAVQLAQIQFPLPTLVIPAESTTYR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
156	RL7C_SCHPO	12.75%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
169	183	2	1497.85	4.8	1	75.4	16.2	95.00%	R.IALSDNAIIEAALGK.Y		R.IALSDNAIIEAALGK.Y
134	150	2	1963.05	2.3	0	83.2	16	95.00%	E.MLQVVEPYVTYGIPNLK.T		K.EMLQVVEPYVTYGIPNLK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
157	SPEE_SCHPO	8.39%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	12	2	1291.72	4.1	1	43.5	17.3	95.00%	M.SVQELSHPLIK.D	Acetyl (+42)	-.MSVQELSHPLIK.D
18	31	2	1631.79	4.6	1	31.2	22.1	95.00%	R.EINNMWPGQAMTLK.V		R.EINNMWPGQAMTLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
158	DYR_SCHPO	9.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
164	183	3	2062.15	3.7	0	25.4	12.3	95.00%	K.LTTPSLHIAGTSDTLVPLAR.S		K.LTTPSLHIAGTSDTLVPLAR.S
191	212	3	2537.31	3.6	1	37.3	18.9	95.00%	R.CENAHVLLHPGQHIVPQQAVYK.T	Carbamidomethyl (+57)	R.CENAHVLLHPGQHIVPQQAVYK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
159	APE1_SCHPO	6.69%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
850	867	2	1936.98	1.7	0	73.5	21.2	95.00%	R.ALQQSLDTISANSSFIDK.S		R.ALQQSLDTISANSSFIDK.S
253	269	2	1912.97	5	0	42.1	19.8	95.00%	K.TLDFFSGVFGEPYPLPK.C		K.TLDFFSGVFGEPYPLPK.C
137	149	2	1467.71	4.6	0	42.2	22.1	95.00%	K.YLATTQMEPTSAR.R		K.YLATTQMEPTSAR.R
487	497	2	1220.6	4.1	1	27.7	21.6	94.20%	R.FLSTGDVKPEE.D		R.FLSTGDVKPEEDTVIYWAPLK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
160	DLDH_SCHPO	8.81%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
113	128	2	1663.83	1.7	0	25	21.6	90.30%	R.GIDVSGVSVNLSQMMK.A		R.GIDVSGVSVNLSQMMK.A
155	168	2	1448.76	3.8	0	31.8	19.6	95.00%	K.GTGSFIDPQTLSVK.G		K.GTGSFIDPQTLSVK.G
248	262	2	1516.76	2.7	0	32.3	20.7	95.00%	E.FLPAVGGPMDADISK.A		R.LGAEVTVVEFLPAVGGPMDADISK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
161	RL31_SCHPO	21.24%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
91	105	2	1650.87	4.2	0	39.3	18.8	95.00%	K.ALYTYVQAVDVANPK.M		K.ALYTYVQAVDVANPK.M
7	15	2	986.56	5	0	39.5	18.5	95.00%	K.SAINQVVTR.D		K.SAINQVVTR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
162	KAD1_SCHPO	12.73%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	74	2	2135.02	3.9	1	83.2	21.2	95.00%	K.IMDQGGLVSDDIVTGMIKDE.I		K.IMDQGGLVSDDIVTGMIKDEILNNPECK.N
211	218	2	912.57	4	1	30.1	14.9	95.00%	E.QIVAILEK.A		K.WAAVDAAQKPEQVWEQIVAILEK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
163	RS13_SCHPO	23.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
44	55	2	1244.66	3.8	0	40.8	19.9	95.00%	K.GMSPSQIGVTLR.D		K.GMSPSQIGVTLR.D
28	39	2	1286.68	5	1	56.1	20	95.00%	K.ADADSVVEQILK.F		K.ADADSVVEQILK.F
10	20	2	1132.63	4.4	0	38.6	18.1	95.00%	K.GIASSALPYVR.S		K.GIASSALPYVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
164	RL30A_SCHPO	28.44%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
71	89	2	1997.95	6	0	62.5	22.3	95.00%	K.ANVHHYAGTNIDLGTACGK.L	Carbamidomethyl (+57)	K.ANVHHYAGTNIDLGTACGK.L
47	58	2	1335.77	2.6	0	25.2	13	90.70%	K.LILIAGNCPPLR.K	Carbamidomethyl (+57)	K.LILIAGNCPPLR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
165	RS3_SCHPO	13.65%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
154	175	3	2381.12	3.9	0	33.3	23	95.00%	K.FADGFMIHSGQPAVDFIDSATR.H		K.FADGFMIHSGQPAVDFIDSATR.H
97	108	2	1362.64	3.8	1	61	22.9	95.00%	R.GLCAVAQCESLR.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GLCAVAQCESLR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
166	PABP_SCHPO	4.75%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
258	266	2	1068.57	4.8	0	26.6	18.4	92.90%	K.ANFTNVYIK.N		K.ANFTNVYIK.N
447	456	2	1142.61	4.9	1	33.9	19.3	95.00%	R.SQLEAQIQAR.N		R.SQLEAQIQAR.N
99	110	2	1272.72	4.2	0	25.9	14.9	91.80%	E.LFNSIGPVASIR.V		K.AEEPEAAAEPSESTSTPTNASSV ATPSGTAPTSASLYVGELDPSVTEA MLFELFNSIGPVASIR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
167	PGM_SCHPO	4.33%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	49	2	1634.8	3.7	0	51.2	21.8	95.00%	E.NFVQATMDVVEPSAK.G		K.VTVFEQPNYVENFVQATMDVVE PSAK.G
350	358	2	1160.54	5.2	0	29	23	95.00%	K.FFCNLFDAK.R	Carbamidomethyl (+57)	K.FFCNLFDAK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
168	RL18A_SCHPO	12.30%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
81	93	2	1390.7	3.8	1	57.3	21.7	95.00%	K.TTVVVGTVTDDER.M		K.TTVVVGTVTDDER.M
56	65	3	1111.64	5.1	0	26.6	15.8	95.00%	K.TNRPPISISK.I		K.TNRPPISISK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
169	RL11_SCHPO	14.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
36	49	2	1531.83	4.2	1	63.5	17.2	95.00%	K.VLEQLSGQTPVFSK.A		K.VLEQLSGQTPVFSK.A
154	164	2	1349.67	4.1	1	39.8	21	95.00%	K.INAEDTINWFK.Q		K.INAEDTINWFK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
170	RS11_SCHPO	17.76%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	64	2	1161.6	4.7	0	33.4	20.9	95.00%	K.CPFVGQVSIR.G	Carbamidomethyl (+57)	K.CPFVGQVSIR.G
114	130	2	1870.97	4.9	1	41.5	19.8	95.00%	R.INEGDVVTVGQCRPLSK.T	Carbamidomethyl (+57)	R.INEGDVVTVGQCRPLSK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
171	YBS7_SCHPO	6.02%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
128	146	2	1760.86	5.1	0	31.6	21.8	95.00%	R.TSGSSTGLSNAPPSANVSK.A		R.TSGSSTGLSNAPPSANVSK.A
168	185	2	1942.99	3.8	0	36.8	19	95.00%	E.VCVPLNPDTGSVPLIHPE.Q	Carbamidomethyl (+57)	R.ATPEVCVPLNPDTGSVPLIHPEQ TDR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
172	SYG_SCHPO	6.90%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
216	232	3	1983.01	5	1	28	18.4	95.00%	K.GYLRPETAQGQFLNFSR.L		K.GYLRPETAQGQFLNFSR.L

492	506	2	1649.85	4.8	0	35.7	20.3	95.00%	R.TYTPNVIEPSFGLGR.I		R.TYTPNVIEPSFGLGR.I
526	538	2	1298.77	3.9	0	28.2	13.4	94.80%	R.GVLSFPASIAPIK.A		R.GVLSFPASIAPIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
173	IDHP_SCHPO	7.42%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
402	409	2	907.47	3.8	1	25.2	21.9	90.60%	E.FLDAVKSE.L		K.SPNGYVDTFEFLDAVKSELDSELVNIA.-
151	163	2	1272.66	3	1	35.7	21.2	95.00%	K.STDLVASGPGKLE.L		K.STDLVASGPGKLELSFTPK.G
392	407	2	1800.87	4.4	1	48.7	22.3	95.00%	K.SPNGYVDTFEFLDAVK.S		K.SPNGYVDTFEFLDAVK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
174	SYFA_SCHPO	4.61%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
128	138	2	1219.56	4.9	1	33.3	22.7	95.00%	K.NTDSITDETPK.V		K.NTDSITDETPK.V
280	291	2	1267.63	3.6	1	50.3	21.2	95.00%	K.VPASTDKLPDPE.Y		K.VPASTDKLPDPEYVAR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
175	FUMH_SCHPO	8.71%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
326	341	2	1622.87	2.2	0	39.6	16.7	95.00%	E.LILPANEPGSSIMPGK.V		R.CGLGELILPANEPGSSIMPGK.V
131	142	2	1157.67	3.6	1	43.3	16.5	95.00%	R.AIEILGGTLGSK.K		R.AIEILGGTLGSK.K
218	231	2	1574.78	2.6	1	35.6	21.1	95.00%	E.FSGYVTQVGYGIER.I		R.THMQDATPLSLGQEFSGYVTQVGYGIER.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
176	ASSY_SCHPO	6.34%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
320	332	2	1601.77	4.2	0	39.6	23	95.00%	K.ILYNGQFFSPCTR.M	Carbamidomethyl (+57)	K.ILYNGQFFSPCTR.M
193	205	2	1354.69	3.3	1	38.8	20.6	95.00%	E.AGILEDPSMTPPK.D		K.KPWSMDENIVHCSYEAGILEDPSMTPPK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
177	Q1L854_SCHPO	11.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
271	280	2	1070.53	3.8	0	25.8	19.9	91.70%	K.TQQAPPTLSE.T		K.TQQAPPTLSETDFPALA.-
143	160	2	1856.82	3.7	1	42.3	23.7	95.00%	R.GWGDLVNSAANPDVAENE.G		R.GWGDLVNSAANPDVAENEGNTPSGAQTPAAEEENVK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
178	RHP23_SCHPO	7.61%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
211	225	2	1515.76	3.9	0	38.8	21.5	95.00%	E.ALAPTSTGQPANLFE.Q		R.EESAAALAAQQQQSEALAPTSTGQPANLFEQAALSENENQEQPSNTVGDDPLGFLR.S
198	210	2	1301.63	3.9	0	52.9	21.7	95.00%	E.SAAALAAQQQQSE.A		R.EESAAALAAQQQQSEALAPTSTGQPANLFEQAALSENENQEQPSNTVGDDPLGFLR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
179	YET4_SCHPO	6.80%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
190	216	3	2686.32	5.5	1	58	21.4	95.00%	R.NDEQLGNSPASITSKPATTSAAQPSSK.V		R.NDEQLGNSPASITSKPATTSAAQPSSK.V
487	503	3	1712.87	4.4	0	27.8	21	95.00%	R.KPSSTGQEPTTPSTPAK.S		R.KPSSTGQEPTTPSTPAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
180	FIMB_SCHPO	4.89%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

508	524	2	1796.81	3.5	0	38.6	23.3	95.00%	K.TLSDSDMVAWANSMAAK.G		K.TLSDSDMVAWANSMAAK.G
158	170	2	1485.74	3.7	1	44.6	23	95.00%	K.LINDSVPDTIDER.V		K.LINDSVPDTIDER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
181	SCE3_SCHPO	15.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
46	66	2	2113.97	4.9	1	94.2	23.1	95.00%	R.ATPSSADAGYNAPSSTFESVR.S		R.ATPSSADAGYNAPSSTFESVR.S
272	289	3	1956.03	4.3	1	43	18.8	95.00%	K.RDPFGGAKPVDNTSVLQR.V		K.RDPFGGAKPVDNTSVLQR.V
250	271	3	2195.06	2.9	1	28.5	22.3	95.00%	R.SSSNVNTEATPSATTTTSSKPK.R		R.SSSNVNTEATPSATTTTSSKPK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
182	SLBR2_SCHPO	5.41%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
134	143	2	1115.56	4.3	1	27.1	21.4	93.60%	R.NIESSVQPSR.E		R.NIESSVQPSR.E
149	157	2	1075.63	4.5	0	33	16.5	95.00%	K.LLDQIYALK.H		K.LLDQIYALK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
183	YEI3_SCHPO	12.24%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
81	97	3	1834.04	4	1	21.8	10.4	92.20%	K.SRVPAFLTVFDIAGLTK.G		K.SRVPAFLTVFDIAGLTK.G
98	114	2	1641.86	2.2	0	35.5	19.2	95.00%	K.GASTGVGLGNAFLSHVR.A		K.GASTGVGLGNAFLSHVR.A
329	342	2	1482.75	2.8	1	41.2	21	95.00%	K.APQAAGVIHTDFEK.A		K.APQAAGVIHTDFEK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
184	KAPS_SCHPO	12.87%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
39	52	2	1664.86	3.8	1	65.6	20.6	95.00%	K.STIACALEQYLLQR.G	Carbamidomethyl (+57)	K.STIACALEQYLLQR.G
173	184	2	1327.67	3.8	1	29.6	20.9	95.00%	E.IVVSSHTQSIEE.C		K.EFTGISAPYEAPISPEIVVSSHTQSIEECVEK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
185	SYEC_SCHPO	6.15%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
190	206	2	1731.84	3.9	1	51.4	22.7	95.00%	K.SSGPNYEIGLPDAIDGK.V		K.SSGPNYEIGLPDAIDGK.V
295	309	2	1657.7	4.5	1	93.6	23.7	95.00%	K.SGQAYADDTDVETMR.H		K.SGQAYADDTDVETMR.H
66	77	2	1393.77	4.3	0	31.9	15.7	95.00%	K.LALQTFSQVYPK.L		K.LALQTFSQVYPK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
186	LYS4_SCHPO	4.30%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
149	159	2	1179.57	4.4	0	26	21.8	92.00%	K.GQGIDFYPAGR.G		K.GQGIDFYPAGR.G
470	489	2	1872.04	4.8	1	47.2	14.6	95.00%	R.EALAYLASPAVVAASAIAGK.I		R.EALAYLASPAVVAASAIAGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
187	CISY_SCHPO	7.82%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
91	101	2	1155.59	4.2	1	28.1	19.2	94.70%	E.GSVLDPNEGIR.F		R.SLIWEGSVLDPNEGIR.F
167	192	4	2838.39	2.4	1	38.1	20.5	95.00%	R.CPPTLHPMAQFSLAVTALEHDSAFAK.A	Carbamidomethyl (+57)	R.CPPTLHPMAQFSLAVTALEHDSAFAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
188	CARA_SCHPO	10.84%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
324	358	4	3743.79	2.8	1	17.6	21	92.60%	R.GHNIPALDIASGNCHITSQNHGYAVDASTLPAEWK.A	Carbamidomethyl (+57)	R.GHNIPALDIASGNCHITSQNHGYAVDASTLPAEWK.A
203	212	2	1101.62	2.8	0	53	17.6	95.00%	E.VNLVSQVSTR.E		K.ISIGEEYDANDDEAFINPEEVNLVSQVSTR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
189	ARO1_SCHPO	4.77%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
677	703	3	2950.41	2.7	1	45.4	21.4	95.00%	R.FACDVLRPMGCTVEQTATSTTVQGPPK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.FACDVLRPMGCTVEQTATSTTVQGPPK.G
162	172	2	1299.72	4.7	0	45.2	18.9	95.00%	K.NLVGAFWQPLR.V		K.NLVGAFWQPLR.V
1232	1247	2	1833.96	4.6	0	44.8	18.7	95.00%	R.ITNSMDIPLILFNMGR.F		R.ITNSMDIPLILFNMGR.F
640	660	2	2079.08	2.7	1	62.8	18.1	95.00%	E.IESDASSATYPLAIAAITGTK.C		K.YQNPPHYEIESDASSATYPLAIAAITGTK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
190	DED1_SCHPO	3.14%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
37	51	2	1398.63	3.2	0	39.7	23.1	95.00%	R.DKPSAGAAPAVGDDE.S		R.DKPSAGAAPAVGDDESVSSR.G
37	56	3	1914.9	5	1	49.2	23.3	95.00%	R.DKPSAGAAPAVGDDESVSSR.G		R.DKPSAGAAPAVGDDESVSSR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
191	YBB2_SCHPO	6.76%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
254	268	2	1518.81	3.9	0	38.1	18.2	95.00%	K.TAGSAVPANSLYLQK.A		K.TAGSAVPANSLYLQK.A
269	281	2	1442.67	3.7	0	41.2	22.9	95.00%	K.AYHDGTLPKPDTE.A		K.AYHDGTLPKPDTEAEIIQPVFIHPNAIVSK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
192	PNPP_SCHPO	13.42%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
196	213	2	1882.01	3.2	0	65.8	17.3	95.00%	K.FLPGSGAISYPLIFSTGR.Q		K.FLPGSGAISYPLIFSTGR.Q
145	166	3	2359.15	3.2	0	61.7	21.7	95.00%	K.IGPDPSVGAVLCGMDMHVTYLK.Y	Carbamidomethyl (+57)	K.IGPDPSVGAVLCGMDMHVTYLK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
193	PUR2_SCHPO	7.87%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
224	248	3	2494.13	2.5	1	37.1	22.9	95.00%	R.AFDGDKGPNTGGMGCYAPTPVASPK.L	Carbamidomethyl (+57)	R.AFDGDKGPNTGGMGCYAPTPVASPK.L
483	501	2	1913.96	3.4	0	24.9	21.3	90.00%	K.QAGWNDPLLVSATDGVGSK.L		K.QAGWNDPLLVSATDGVGSK.L
31	48	2	1678.78	1.8	1	54.6	23	95.00%	K.VYVAPGNGGTASNGAESK.M	Deamidation (+1)	K.VYVAPGNGGTASNGAESK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
194	SYSC_SCHPO	6.89%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
234	250	2	1864.89	2.8	1	68.1	22.2	95.00%	R.YLIATSEQPISAYHSGE.W		R.YLIATSEQPISAYHSGEWFEKPSEQLPLK.Y
358	371	2	1717.71	4.8	1	59.1	24.2	95.00%	K.ELVSCSNCTDYQSR.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.ELVSCSNCTDYQSR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
195	SODM_SCHPO	20.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	173	2	1303.7	4.2	0	48.8	19.3	95.00%	R.ITTTANQDTIVK.S		R.ITTTANQDTIVK.S
26	48	2	2502.32	2.9	1	32.8	15.8	95.00%	K.ATLPPLPYAYNALEPALSETIMK.L		K.ATLPPLPYAYNALEPALSETIMK.L
127	135	2	1108.52	5	1	34	22.6	95.00%	K.WGSLEDFQK.E		K.WGSLEDFQK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
196	ATPB_SCHPO	6.67%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	140	2	2064.13	2.7	0	58.4	14.8	95.00%	R.GTAVIDTGSPISIPVGPGTLGR.I		R.GTAVIDTGSPISIPVGPGTLGR.I
210	222	2	1501.86	4.8	1	34.9	14.3	95.00%	K.TVFIQELINNIAK.A		K.TVFIQELINNIAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
197	G3P2_SCHPO	34.03%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	79	2	1446.71	2.9	0	41.5	21.9	95.00%	K.LVIDGHSIDVHNE.R		K.LVIDGHSIDVHNER.D
249	259	3	1290.69	4.5	1	28.4	19.9	95.00%	K.LAKPTNYEDIK.A		K.LAKPTNYEDIK.A
235	248	2	1467.82	3.7	0	76.5	15.2	95.00%	R.VPTPDVSVVDLTVK.L		R.VPTPDVSVVDLTVK.L
173	186	2	1458.75	2.9	0	84.3	18.9	95.00%	E.GLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK.T
146	162	2	1818.91	4.5	0	75	21.7	95.00%	K.VISNASCTTNCLAPLAK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.VISNASCTTNCLAPLAK.V
324	335	2	1279.67	5	1	52.3	20.3	95.00%	R.VVDLVAYTASKD.-		R.VVDLVAYTASKD.-
163	172	2	1135.54	2.8	1	34.2	21.9	95.00%	K.VINDTFGIEE.G		K.VINDTFGIEEGLMTTVHATTATQK.T
172	186	2	1587.8	2.8	1	36.4	21.5	95.00%	E.EGLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK.T
6	13	2	819.43	6.2	0	38.4	19.6	95.00%	K.VGINGFGR.I	Deamidation (+1)	K.VGINGFGR.I
201	215	2	1343.71	4.7	0	69.9	19.5	95.00%	R.GASANIIPSSTGAAK.A		R.GASANIIPSSTGAAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
198	PPA2_SCHPO	5.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
138	143	2	719.4	4.8	0	27.1	17.3	93.50%	E.LFDLGR.Q		R.IELFDLGR.Q
152	167	2	1869.88	2.1	1	85.1	23.3	95.00%	E.LFDTDVYDINTAAQER.V		R.YYELFDTDVYDINTAAQER.V
136	143	2	961.53	5.4	1	31.9	19.8	95.00%	R.IELFDLGR.Q		R.IELFDLGR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
199	RLA5_SCHPO	20.18%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
38	48	2	1273.71	4	0	36.7	18	95.00%	E.VEPIWATIFAK.A		K.AGNVEVEPIWATIFAK.A
22	32	2	1217.73	2.7	1	26.1	12.8	92.10%	E.ITSDKLLSLTK.A		-.MSASELATSYAALILADEGIEITSDKLLSLTK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
200	DHOM_SCHPO	12.50%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	138	2	1568.79	4.5	0	56.7	21	95.00%	K.AFSASNDVYQNIIK.A		K.AFSASNDVYQNIIK.A
57	67	2	1391.68	4.7	1	33.1	21.7	95.00%	K.DYQPINLSEWK.N		K.DYQPINLSEWK.N
89	110	2	2284.21	4.5	1	95.1	18.1	95.00%	K.SPLPAILVDNTASEAIAQSYPK.F		K.SPLPAILVDNTASEAIAQSYPK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
201	RL28A_SCHPO	11.49%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
94	110	2	1787.95	3.9	1	37.3	18.9	95.00%	K.NTEVAPVINVLQSGYGK.V		K.NTEVAPVINVLQSGYGK.V
97	110	2	1443.81	3	0	72.5	14.8	95.00%	E.VAPVINVLQSGYGK.V		K.NTEVAPVINVLQSGYGK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
202	PRS6A_SCHPO	7.31%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
250	265	2	1657.89	4.1	0	53.8	18.1	95.00%	K.LAAPQLVQMFIGDGAK.L		K.LAAPQLVQMFIGDGAK.L
7	22	2	1661.72	7	0	42	24.1	95.00%	E.LDALDQSQQGGSSNNE.G		-.MSTLEELDALDQSQQGGSSNNEGLDGIEQEILAAGIDELNSR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
203	ACBP_SCHPO	34.48%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	13	2	1294.61	4.4	1	38.3	22.7	95.00%	M.SSTFEQAAADVK.E	Acetyl (+42)	-.MSSTFEQAAADVK.E
33	50	3	1912	4.1	1	25.6	18.5	95.00%	K.QATVGDNNTEKPGLLDLK.G		K.QATVGDNNTEKPGLLDLK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
204	Q9P7B4_SCHPO	13.13%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
234	256	3	2522.27	2.7	1	34.8	19.4	95.00%	R.ENVVIADTLVFPSHQGGANHVYR.K		R.ENVVIADTLVFPSHQGGANHVYR.K
163	173	2	1163.64	5.6	0	26.5	17.4	92.70%	K.SALAQFTSALR.K		K.SALAQFTSALR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
205	CYSK1_SCHPO	9.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
10	23	2	1341.78	3.9	0	59.1	14.9	95.00%	K.VPGIVSGFIGAIGR.T		K.VPGIVSGFIGAIGR.T
180	200	2	2019.93	5.1	0	71.4	24.1	95.00%	K.GTVDGFTCSTGTGGTFAGVTK.Y	Carbamidomethyl (+57)	K.GTVDGFTCSTGTGGTFAGVTK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
206	RLA0_SCHPO	15.06%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
133	144	2	1308.71	5.2	0	29.1	16.9	95.00%	K.TSFFQALGIPTK.I		K.TSFFQALGIPTK.I
98	132	3	3513.88	2.7	1	45.6	16.4	95.00%	R.ETIIANVIAAPARPNAIAPLDVFVPAGNTGMEPGK.T		R.ETIIANVIAAPARPNAIAPLDVFVPAGNTGMEPGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
207	CLH_SCHPO	1.32%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
64	76	3	1431.83	4.6	0	23.4	12	94.60%	R.RPISADSVILHPK.K		R.RPISADSVILHPK.K
212	220	2	955.58	2.1	0	28.5	13.4	95.00%	E.VQVLALASR.L		K.VSQPLESHASAFAVIQPEGVDHEVQVLALASR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
208	SUB2_SCHPO	7.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	76	2	1288.56	3.4	1	48.4	23.6	95.00%	R.AITDSGFEHPSE.V		R.AITDSGFEHPSEVQQVCIPQSILGTDVLCQAK.S
77	96	2	2256.17	2.9	0	79.6	18.1	95.00%	E.VQQVCIPQSILGTDVLCQAK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.AITDSGFEHPSEVQQVCIPQSILGTDVLCQAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
209	GUAA_SCHPO	10.76%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
232	254	3	2183.1	3.2	0	22.3	19.7	93.10%	K.MIGPSDHVIGAVSGGVDSTVASK.V		K.MIGPSDHVIGAVSGGVDSTVASK.V
170	203	4	3715.11	3.7	1	22.3	15.2	95.00%	K.NSPFAVIAHVTKPIIGLQFHPEVTHTPLGLQLIK.N		K.NSPFAVIAHVTKPIIGLQFHPEVTHTPLGLQLIK.N
231	254	4	2311.19	3.1	1	17.8	18.6	93.10%	R.KMIGPSDHVIGAVSGGVDSTVASK.V		R.KMIGPSDHVIGAVSGGVDSTVASK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
210	RL7B_SCHPO	14.00%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	21	2	2002.11	4.4	1	37	14.6	95.00%	M.VASSTVPSVASIFAPESLLK.K		-.MVASSTVPSVASIFAPESLLK.K
168	182	2	1523.86	4.4	1	56.2	14.5	95.00%	R.IPLSDNAIIEAALGK.Y		R.IPLSDNAIIEAALGK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
211	EIF3E_SCHPO	6.39%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
267	284	3	2029.08	4.4	0	22.1	17.6	92.80%	R.YLTVAVVTNQNNANQKPR.N		R.YLTVAVVTNQNNANQKPR.N		
418	431	2	1463.71	4.6	0	63.7	22	95.00%	E.STSTNVVADDLITE.A		R.NNPSVAAASNVAADQSTEDESIESTSTNVVADDLITEAETATEAEEPEPEVQFGFK.A		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
212	TBA1_SCHPO	8.13%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
291	304	2	1770.81	2.9	0	35.8	22.9	95.00%	E.ITNQCFEPYNQMVK.C	Carbamidomethyl (+57)	K.AFHESNSVQEITNQCFEPYNQMVK.C		
65	79	2	1758.92	3.8	0	35	18.9	95.00%	R.SIYVDLEPNVIDQVR.T		K.FVPRSIYVDLEPNVIDQVR.T		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
213	P5CR_SCHPO	13.83%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
116	129	2	1566.76	5	1	85.9	21.4	95.00%	K.TISSLQSMLDESTR.V		K.TISSLQSMLDESTR.V		
74	98	3	2668.4	2.5	1	41.7	17.4	95.00%	E.MAAISNVLLLSCKPQAAEDVLNSPK.M	Carbamidomethyl (+57)	K.ENAEMAAISNVLLLSCKPQAAEDVLNSPK.M		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
214	RS21_SCHPO	29.89%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
51	60	2	1113.59	4.5	0	33.8	19.7	95.00%	K.TTYAISGFVR.S		K.TTYAISGFVR.S		
72	87	2	1864.94	4.3	1	65.3	21.7	95.00%	R.LTTQDGLLEGVWSYQR.-		R.LTTQDGLLEGVWSYQR.-		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
215	RL24A_SCHPO	12.75%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
81	91	2	1097.65	4.7	0	29.4	14.3	95.00%	R.GIVGANLDVIK.E		R.GIVGANLDVIK.E		
36	43	2	978.52	4.9	1	29.5	21.1	95.00%	K.SESLFLQR.K		K.SESLFLQR.K		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
216	6PGL_SCHPO	8.95%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
46	55	2	1083.61	5.4	1	52.4	17.6	95.00%	K.VLAEGLAQQR.G		K.VLAEGLAQQR.G		
209	221	2	1488.81	4	1	42.1	16.7	95.00%	K.DILPIVIEDFTSK.L		K.DILPIVIEDFTSK.L		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
217	ARP3_SCHPO	8.20%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
178	198	2	2066.06	2.9	0	35.6	19.6	95.00%	R.SLTGTVVDSGDGVTHIIPVAE.G		R.SLTGTVVDSGDGVTHIIPVAEGYVIGSSIK.T		
310	323	2	1539.83	4.3	0	42.7	17.4	95.00%	E.LVDNVVQSSPIDVR.K		R.FLAPEIFFNPEIASSDFLTPLPELVDNVVQSSPIDVR.K		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
218	UBC4_SCHPO	25.85%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
102	128	3	3017.59	3.1	1	65.3	15.2	95.00%	K.VLLSICSLLTDPNPDDPLVPEIAHVYK.T	Carbamidomethyl (+57)	K.VLLSICSLLTDPNPDDPLVPEIAHVYK.T		
91	101	2	1244.65	4.6	0	28.4	20.3	95.00%	R.DQWSPALTISK.V		R.DQWSPALTISK.V		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
219	RS24A_SCHPO	20.15%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
21	32	3	1363.77	4	1	39.5	16.1	95.00%	R.KQMVVDILHPGK.A		R.KQMVVDILHPGK.A		
69	83	2	1672.81	4.3	1	28.6	22.9	95.00%	R.TTGFALIYDDVEAMK.K		R.TTGFALIYDDVEAMK.K		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
220	CAPZB_SCHPO	11.94%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
135	150	2	1722.76	4.9	0	29.6	23.6	95.00%	K.ASTSNSSGWDSIHVFE.C		K.ASTSNSSGWDSIHVFECLPTTETNVYDYR.L
245	260	2	1696.85	4.1	0	68.8	20.8	95.00%	R.SIQPVSDAQPNDSALR.S		R.SIQPVSDAQPNDSALR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
221	ARPC1_SCHPO	5.84%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	23	4	2564.32	3.3	1	37.1	17.8	95.00%	M.ATSQVLHILPKPSYEHAFNSQR.T	Acetyl (+42)	-.MATSQVLHILPKPSYEHAFNSQR.T
2	16	2	1723.92	3.4	0	48	18.6	95.00%	M.ATSQVLHILPKPSYE.H	Acetyl (+42)	-.MATSQVLHILPKPSYEHAFNSQR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
222	ARG56_SCHPO	6.33%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
487	524	4	4077.04	3.3	0	36.4	15.9	95.00%	K.FIQSDKPFADAIIQTQSTKPPTASSTTNNPSSSQINQK.R		K.FIQSDKPFADAIIQTQSTKPPTASSTTNNPSSSQINQK.R
861	878	2	1923.87	2.6	0	39.3	23.6	95.00%	K.GAATQALQNLNLSCGYDE.Y	Carbamidomethyl (+57)	K.GAATQALQNLNLSCGYDEYAGIHLD.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
223	YNY8_SCHPO	7.44%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
221	230	2	1165.62	2	0	28.6	19.8	95.00%	E.LYATFLDPAR.V		R.VSAVVNTADISENYTFDAPANELYATFLDPAR.V
2	16	2	1783.84	4.8	0	36.8	22.9	95.00%	M.SATSINPNNWHWTSK.D	Acetyl (+42)	-.MSATSINPNNWHWTSK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
224	ELF1_SCHPO	2.37%	99%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
776	784	2	1178.58	7.8	0	24.9	21.5	90.00%	K.TPSQYIQWR.Y	Deamidation (+1)	K.TPSQYIQWR.Y
156	171	2	1540.89	3.4	0	68.8	12.8	95.00%	K.VAALQLLGSLASSSPK.A		K.VAALQLLGSLASSSPK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
225	PPID_SCHPO	5.90%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
214	226	2	1432.74	4.4	0	72	20.3	95.00%	K.QFAQQNLDTAVAK.W		K.QFAQQNLDTAVAK.W
23	30	2	931.51	4.1	0	29.7	20.8	95.00%	E.LFDNVVPK.T	Deamidation (+1)	K.IQPTIYFELFDNVVPK.T

Supplementary Table S2: All "Scaffold" validated proteins and peptides identified from solprotSP (*S.pombe*) and from SCVMprot (*S.cerevisiae*) samples

***S.pombe* - Glu-C digest of large tryptic peptides (replicate C)**

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
1	G3P1_SCHPO	55.95%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
249	259	3	1290.69	4.5	1	28.4	19.9	95.00%	K.LAKPTNYEDIK.A		K.LAKPTNYEDIK.A
67	79	2	1407.7	2.6	0	86.4	22	95.00%	K.LVIDGNAIDVHNE.R		K.LVIDGNAIDVHNER.D
235	248	2	1467.82	3.7	0	76.5	15.2	95.00%	R.VPTPDVSVVDLTVK.L		R.VPTPDVSVVDLTVK.L
87	97	2	1226.55	2.8	0	34.8	23.1	95.00%	K.WSTSGADYVIE.S		K.WSTSGADYVIESTGVFTTQETAS AHLK.G
323	334	2	1304.75	5.7	1	40.6	12.8	95.00%	R.RVVDLVAYTAAK.D		R.RVVDLVAYTAAK.D
98	106	2	968.45	3.6	0	39.5	22.7	95.00%	E.STGVFTTQE.T		K.WSTSGADYVIESTGVFTTQETAS AHLK.G
173	186	2	1458.75	2.3	0	87.8	19	95.00%	E.GLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK. T
146	162	2	1818.91	4.5	0	75	21.7	95.00%	K.VISNASCTTNCLAPLAK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.VISNASCTTNCLAPLAK.V
324	334	2	1148.65	6.2	0	55.4	16.6	95.00%	R.VVDLVAYTAAK.D		R.VVDLVAYTAAK.D
49	61	2	1468.63	3.7	1	66.1	23.1	95.00%	K.YDSTHGRFDGSVE.I		K.YDSTHGRFDGSVEIK.D
27	41	2	1685.89	3.2	0	36.6	18.6	95.00%	K.TIQVVAINDPFIDLE.Y		K.TIQVVAINDPFIDLEYMAYMFK.Y
42	48	2	952.42	3.8	0	29	22.4	95.00%	E.YMAYMFK.Y		K.TIQVVAINDPFIDLEYMAYMFK.Y
324	336	2	1377.72	3.8	1	68.7	20	95.00%	R.VVDLVAYTAAKDN.-		R.VVDLVAYTAAKDN.-
172	186	2	1587.8	2.9	1	49.3	21.3	95.00%	E.EGLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK. T
98	113	2	1676.84	2.7	1	48	20.7	95.00%	E.STGVFTTQETASAHLK.G		K.WSTSGADYVIESTGVFTTQETAS AHLK.G
6	13	2	819.43	6.2	0	38.4	19.6	95.00%	K.VGINGFGR.I	Deamidation (+1)	K.VGINGFGR.I
201	215	2	1343.71	4.7	0	69.9	19.5	95.00%	R.GASANIIPSSTGAAK.A		R.GASANIIPSSTGAAK.A
119	137	2	2004.03	2.8	1	47.4	20.1	95.00%	R.VIISAPSKDAPMYVVGVNE.E	Oxidation (+16)	R.VIISAPSKDAPMYVVGVNEEK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
2	PGK_SCHPO	60.14%	100%	27

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
383	398	2	1528.71	3.1	1	38.5	23.3	95.00%	K.EDALSHVSTGGGASLE.L		K.EDALSHVSTGGGASLELLEGK.A
359	378	2	1917.95	4	1	118	21	95.00%	K.TCEAGNVVIVGGGDTATVAK.K	Carbamidomethyl (+57)	K.TCEAGNVVIVGGGDTATVAK.K
7	15	2	986.57	5.4	0	41.1	17.3	95.00%	K.LAITDVDLK.G		K.LAITDVDLK.G
302	316	2	1646.71	2.6	1	59	23.1	95.00%	E.EGIPDGWMGLDCGPK.S	Oxidation (+16)/ Carbamidomethyl (+57)	K.VGSATAEEGIPDGWMGLDCGPK. S
273	288	2	1805.93	4.9	1	56.9	20.3	95.00%	K.NNVEVFLPVDFVTADK.F		K.NNVEVFLPVDFVTADK.F
200	213	2	1423.83	2.3	0	37	11.8	95.00%	E.NPARPFLAILGGAK.V		K.ALENPARPFLAILGGAK.V
362	379	2	1655.93	2.5	1	41.8	16.4	95.00%	E.AGNVVIVGGGDTATVAKK.Y		K.TCEAGNVVIVGGGDTATVAKK.Y
384	398	2	1399.66	3.1	0	59.3	23.1	95.00%	E.DALSHVSTGGGASLE.L		K.EDALSHVSTGGGASLELLEGK.A
23	39	2	1914.96	3	1	41.9	21.4	95.00%	R.VDFNVPLDGDRITNNAR.I		R.VDFNVPLDGDRITNNAR.I
57	71	2	1591.87	2.9	0	46.2	17.5	95.00%	K.AVILMSHLGRPNGAR.V	Deamidation (+1)	K.AVILMSHLGRPNGAR.V
23	33	2	1245.61	6.8	0	62.1	21.6	95.00%	R.VDFNVPLDGDR.I		R.VDFNVPLDGDR.I
40	48	2	910.59	3.6	0	25.3	6.99	91.00%	R.IVGALPTIK.Y		R.IVGALPTIK.Y
330	347	2	2010.99	4.7	1	67	21.3	95.00%	K.TIVWNGPAGVFEFDNFAK.G		K.TIVWNGPAGVFEFDNFAK.G
303	316	2	1501.67	2	0	52.4	23	95.00%	E.GIPDGWMGLDCGPK.S	Carbamidomethyl (+57)	K.VGSATAEEGIPDGWMGLDCGPK. S
250	261	2	1237.59	4.5	1	61.5	22	95.00%	K.IGDSLFDEAGSK.N		K.IGDSLFDEAGSK.N
218	227	2	1183.69	5.5	0	39.2	16	95.00%	K.IQLIDNLLDK.V		K.IQLIDNLLDK.V

218	230	3	1552.9	4.8	1	31.7	11.8	95.00%	K.IQLIDNLLDKVNR.L		K.IQLIDNLLDKVNR.L
404	414	2	1040.63	5.6	0	39.4	16.1	95.00%	K.ALPGVVALSSK.-		K.ALPGVVALSSK.-
277	291	2	1739.92	3	1	45	18.8	95.00%	E.VFLPVDFVTADKFDK.D		K.NNVEVFLPVDFVTADKFDK.D
321	329	2	994.54	5.5	1	50.2	18.6	95.00%	K.FAEVITTSK.T		K.FAEVITTSK.T
75	86	3	1304.74	4.3	1	59.4	15.2	95.00%	K.YSLKPVAAELSK.L		K.YSLKPVAAELSK.L
197	213	2	1737	2.8	1	60.3	11.1	95.00%	K.ALENPARPFLAILGGAK.V		K.ALENPARPFLAILGGAK.V
151	169	2	2020.01	5.9	0	113	21	95.00%	K.SLTSLGDIFVNDAFGTAHR.A		K.SLTSLGDIFVNDAFGTAHR.A
362	378	2	1527.83	3.3	0	80.3	16.5	95.00%	E.AGNVVIVGGGDTATVAK.K		K.TCEAGNVVIVGGGDTATVAK.K
170	181	2	1267.64	4	0	58.7	21.1	95.00%	R.AHSSMVGVDLPR.V		R.AHSSMVGVDLPR.V
150	169	3	2148.1	3.4	1	64.2	19.6	95.00%	R.KSLTSLGDIFVNDAFGTAHR.A		R.KSLTSLGDIFVNDAFGTAHR.A
214	227	2	1596.91	2.2	1	62.5	13.8	95.00%	K.VADKIQLIDNLLDK.V		K.VADKIQLIDNLLDK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
3	ENO11_SCHPO	58.09%	100%	27

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
80	92	2	1388.65	3.7	1	47.5	23.3	95.00%	K.ANLDVTDQKAADE.F		K.ANLDVTDQKAADEFLLK.L
258	263	2	765.39	4.7	0	25.9	21.6	92.00%	K.YDLDIK.A		K.YDLDIK.A
212	230	2	1978.03	3.5	1	54.4	19.1	95.00%	E.GGIAPDLQTPQEALDLIVE.A		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
361	374	3	1608.73	4.7	1	47.1	23.9	95.00%	R.MSYEAGWGVMVSHR.S		R.MSYEAGWGVMVSHR.S
185	194	2	1204.59	5.4	1	34	22.3	95.00%	R.WGAETYHTLK.S		R.WGAETYHTLK.S
346	360	2	1585.85	6	1	90.8	17.3	95.00%	K.VNQIGSVTESLNAVR.M		K.VNQIGSVTESLNAVR.M
346	354	2	945.48	3.9	0	40.1	21	95.00%	K.VNQIGSVTE.S		K.VNQIGSVTESLNAVR.M
423	432	2	929.48	4.4	0	35.6	22.9	95.00%	E.GVYAGAHAGK.Y		R.IEEELGSEGVYAGAHAGK.Y
201	223	2	2261.02	3	1	89.1	23.4	95.00%	R.YGSSAGNVGDEGGIAPDLQTPQE.A		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
365	374	2	1098.54	3.1	0	66.4	21.2	95.00%	E.AGWGVMVSHR.S		R.MSYEAGWGVMVSHR.S
311	328	2	1963.98	4.2	1	93.2	21.3	95.00%	K.AETDFQIVGDDLTVTNVK.R		K.AETDFQIVGDDLTVTNVK.R
313	329	2	1920	3.2	1	78	19.2	95.00%	E.TDFQIVGDDLTVTNVKR.L		K.AETDFQIVGDDLTVTNVKR.L
289	310	3	2679.2	3	1	73.2	24	95.00%	K.YPIVSIEDPFDQDDWSAWTHMK.A		K.YPIVSIEDPFDQDDWSAWTHMK.A
65	79	2	1477.87	4	0	73.7	6.99	95.00%	K.AVGNVNNIIAPAVVK.A		K.AVGNVNNIIAPAVVK.A
313	328	2	1763.9	2.8	0	61	21.3	95.00%	E.TDFQIVGDDLTVTNVK.R		K.AETDFQIVGDDLTVTNVK.R
106	120	2	1560.82	4.2	0	61.3	19.9	95.00%	K.LGANAILGVSMAICR.A	Oxidation (+16)/ Carbamidomethyl (+57)	K.LGANAILGVSMAICR.A
378	396	2	1928.04	3.5	0	74.4	15.8	95.00%	E.TADTFISHLTVGIGAGQLK.S		R.SGETADTFISHLTVGIGAGQLK.S
169	184	2	1769.85	3	1	50.3	22.2	95.00%	E.FMILPTGAPSFSEAMR.W	Oxidation (+16)	K.GPYVLPVPSFNVLNGGSHAGGDLAFQEFMILPTGAPSFSEAMR.W
169	181	2	1395.68	5.9	0	44.5	22.5	95.00%	E.FMILPTGAPSFSE.A		K.GPYVLPVPSFNVLNGGSHAGGDLAFQEFMILPTGAPSFSEAMR.W
212	223	2	1224.6	3	0	49.7	21.8	95.00%	E.GGIAPDLQTPQE.A		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
273	287	2	1812.96	4.5	1	75.4	17.7	95.00%	K.LTYQQLTDLYVELSK.K		K.LTYQQLTDLYVELSK.K
243	257	2	1598.79	4.2	1	56.6	21.4	95.00%	K.IGLDVASSEFYVDGK.Y		K.IGLDVASSEFYVDGK.Y
338	345	2	901.51	4.7	0	31.4	19.4	95.00%	K.CANALLLK.V	Carbamidomethyl (+57)	K.CANALLLK.V
409	414	2	806.43	5.7	1	29.4	21.4	95.00%	K.YNELLR.I		K.YNELLR.I
375	396	2	2201.14	2.9	1	122	18.6	95.00%	R.SGETADTFISHLTVGIGAGQLK.S		R.SGETADTFISHLTVGIGAGQLK.S
89	96	2	905.49	4.7	1	57.4	20.4	95.00%	K.AADEFLLK.L		K.AADEFLLK.L
80	88	2	1002.5	4.3	0	41.9	20.3	95.00%	K.ANLDVTDQK.A		K.ANLDVTDQK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
4	METE_SCHPO	53.40%	100%	31

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
325	349	2	2643.33	5	1	39.9	19.7	95.00%	R.VQVASSSSILHIPHSLSGEDQINPE.I		R.VQVASSSSILHIPHSLSGEDQINPEIK.R

104	118	2	1384.69	3.8	1	65.1	21.6	95.00%	R.AATADKAAVDVPAGE.M		R.AATADKAAVDVPAGEMVK.W
577	595	2	2108.02	2.7	1	92.5	21.5	95.00%	R.DDVHDSVQAQQIALGLRDE.V		R.DDVHDSVQAQQIALGLRDEVLDLEK.A
638	667	3	3497.61	3.2	0	56.4	22.9	95.00%	R.LATAAVQDDTQIHSHFCYSDFNDIFDAIQR.L	Carbamidomethyl (+57)	R.LATAAVQDDTQIHSHFCYSDFNDIFDAIQR.L
561	571	2	1184.7	5.1	0	40.5	15.3	95.00%	K.GMLTAPITILR.W		K.GMLTAPITILR.W
434	449	2	1746.96	2.9	0	80.4	14.6	95.00%	K.LPLFPTTTIGSFPQTK.E		K.LPLFPTTTIGSFPQTK.E
486	498	2	1418.75	1.7	1	27.7	20	94.40%	E.VGLDVLVHGEPER.N		K.FQEEVGLDVLVHGEPER.N
4	11	2	845.48	4.8	0	33.3	20.1	95.00%	K.SAVLGFPR.I		K.SAVLGFPR.I
707	714	2	901.49	4.3	1	27.7	21.4	94.30%	R.VPPVSEFK.E		R.VPPVSEFK.E
684	690	2	813.51	5.6	0	34.2	17.2	95.00%	K.LLNVLSR.Y		K.LLNVLSR.Y
691	706	2	1818.88	3.8	0	84	22.1	95.00%	R.YTSCIGPGLFDIHSPR.V	Carbamidomethyl (+57)	R.YTSCIGPGLFDIHSPR.V
499	508	2	1257.55	4.4	1	53.6	23.2	95.00%	R.NDMVQYFGER.M		R.NDMVQYFGER.M
243	260	2	1982.08	3.5	0	54.1	14.5	95.00%	K.LILTTYFGSLQSNADVLK.G		K.LILTTYFGSLQSNADVLK.G
727	738	2	1466.7	3.1	0	48.9	23.3	95.00%	K.DHLWLNPDCGLK.T	Carbamidomethyl (+57)	K.DHLWLNPDCGLK.T
468	473	2	783.39	3.4	0	26.5	18.8	92.90%	E.YDAFIR.K		K.GLISQEEYDAFIR.K
428	449	3	2402.33	4.8	1	46	11.1	95.00%	K.QQASLKLPLFPTTTIGSFPQTK.E		K.QQASLKLPLFPTTTIGSFPQTK.E
261	273	2	1330.78	4	0	55.7	11.8	95.00%	K.GLPIAGVHVDVVR.A		K.GLPIAGVHVDVVR.A
468	474	2	911.49	3.1	1	25.9	18.1	91.90%	E.YDAFIRK.E		K.GLISQEEYDAFIRK.E
122	133	2	1609.74	3.8	0	28.1	23.8	94.80%	K.WFDSNYHFLRPE.V		K.WFDSNYHFLRPEVSEETDFK.L
281	299	2	1881.08	4.8	1	87.4	10	95.00%	R.ALAVLGENQIISVGVVSGR.N		R.ALAVLGENQIISVGVVSGR.N
723	738	3	1927.98	4	1	24.5	19	95.00%	K.HVPKDHLWLNPDCGLK.T	Carbamidomethyl (+57)	K.HVPKDHLWLNPDCGLK.T
288	299	2	1227.7	2.8	0	33.2	17.2	95.00%	E.NQIISVGVVSGR.N		R.ALAVLGENQIISVGVVSGR.N
361	369	2	1017.56	4.9	1	30.5	18.3	95.00%	K.CAELAILTK.A	Carbamidomethyl (+57)	K.CAELAILTK.A
547	560	2	1596.79	3.6	1	50.8	22	95.00%	K.ESQYAQSITSKPMK.G		K.ESQYAQSITSKPMK.G
606	615	2	1199.6	4.3	0	55.1	21.4	95.00%	K.VIQCDEPALR.E	Carbamidomethyl (+57)	K.VIQCDEPALR.E
668	679	2	1288.66	3.8	1	37	20.8	95.00%	R.LDADVVSIENSK.S		R.LDADVVSIENSK.S
527	546	3	2267.24	3.3	0	44.5	14.1	95.00%	R.CVRPPIIVGDVYRPAPMTVK.E	Carbamidomethyl (+57)	R.CVRPPIIVGDVYRPAPMTVK.E
631	637	2	877.45	5.9	0	49	21.3	95.00%	K.WAIDAFR.L		K.WAIDAFR.L
85	99	2	1616.79	4.1	0	63.5	22.1	95.00%	R.LSGLSSLDTYFAMGR.G		R.LSGLSSLDTYFAMGR.G
156	176	3	2256.33	3.9	1	51.3	6.99	95.00%	K.EAGIITRPVLVGPVTYLFIAK.A		K.EAGIITRPVLVGPVTYLFIAK.A
52	82	3	3521.71	3.5	0	48.3	19.9	95.00%	K.AQGVDIIPSNDFSLYDQIMDHSFSFNVIPPR.Y		K.AQGVDIIPSNDFSLYDQIMDHSFSFNVIPPR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
5	EF1A1_SCHPO	41.09%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
267	286	2	1988.07	2.5	0	33.9	16.8	95.00%	E.TGVIKPGMIVTFAPAGVTTE.V		R.VETGVIKPGMIVTFAPAGVTTEVK.S
136	146	2	1184.7	3	0	26.2	15.9	92.30%	E.HALLAYTLGVK.Q		R.EHALLAYTLGVK.Q
402	421	2	2268.08	4	1	67.5	22	95.00%	K.MVPSKPMCVEAFTDYAPLGR.F	Carbamidomethyl (+57)	K.MVPSKPMCVEAFTDYAPLGR.F
296	311	2	1601.81	2.8	0	67.1	20.6	95.00%	E.SLDAGLPGDNVGFNVK.N		K.SVEMHHESLDAGLPGDNVGFNVK.N
147	154	2	883.55	5.8	0	26.4	16.3	92.60%	K.QLIVAVNK.M		K.QLIVAVNK.M
254	264	2	1024.61	4.2	0	65.4	12.8	95.00%	K.IGGIGTVPVGR.V		K.IGGIGTVPVGR.V
6	20	2	1529.84	4.6	0	62.9	16.7	95.00%	K.GHINVVVIGHVDSGK.S		K.GHINVVVIGHVDSGK.S
185	214	3	3453.63	4.5	0	55	21.8	95.00%	K.TVPFVPVSGFQGDNMIEPTTNMPWYQGWQK.E		K.TVPFVPVSGFQGDNMIEPTTNMPWYQGWQK.E
85	100	2	1843.96	3.1	1	43.3	19.3	95.00%	K.YNVTVIDAPGHRDFIK.N		K.YNVTVIDAPGHRDFIK.N
265	286	2	2216.19	4	1	48.3	15.9	95.00%	R.VETGVIKPGMIVTFAPAGVTTE.V		R.VETGVIKPGMIVTFAPAGVTTEVK.S
229	253	3	2831.56	3.3	1	30.8	12.6	95.00%	E.AIDSIEPPARPTDKPLRLPLQDVYK.I		K.TLLEAIDSIEPPARPTDKPLRLPLQDVYK.I
225	245	3	2331.29	2.6	1	34.8	13.2	95.00%	K.TLLEAIDSIEPPARPTDKPLR.L		K.TLLEAIDSIEPPARPTDKPLR.L
155	164	2	1151.51	6.4	0	75.8	21.9	95.00%	K.MDTTGWSQAR.F		K.MDTTGWSQAR.F
85	96	2	1340.69	4.4	0	66.1	19.8	95.00%	K.YNVTVIDAPGHR.D		K.YNVTVIDAPGHR.D
246	253	2	974.55	4.1	0	32.1	18.8	95.00%	R.LPLQDVYK.I		R.LPLQDVYK.I

135	146	2	1313.74	3.9	1	45.8	17.4	95.00%	R.EHALLAYTLGVK.Q		R.EHALLAYTLGVK.Q
412	421	2	1109.55	2.9	0	31.7	21.1	95.00%	E.AFTDYAPLGR.F		K.MVPSKPMCVEAFTDYAPLGR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
6	KPYK_SCHPO	57.76%	100%	27

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
191	201	2	1186.61	4.4	1	25.5	20.9	91.30%	K.TDVDLPALSEK.D		K.TDVDLPALSEK.D
487	497	2	1053.66	5.9	0	39.5	10.4	95.00%	K.IIVLQGAVGGK.G		K.IIVLQGAVGGK.G
454	462	2	1129.58	2.7	1	42.5	19.7	95.00%	E.KEPLSDWQK.D		R.GVYPVIYEKEPLSDWQK.D
116	127	2	1403.63	2.7	1	52.2	23.3	95.00%	E.MIFTTDDAYAEK.C		R.TGLTVGGTDYPISSGHEMIFTTDDAYAEK.C
422	433	3	1430.81	4.2	0	47.6	13.4	95.00%	K.YRPSIPIVMVTR.C		K.YRPSIPIVMVTR.C
10	26	2	1880.98	3.7	1	90.9	18.7	95.00%	K.QWVAGLNSELDIPAVNR.R		K.QWVAGLNSELDIPAVNR.R
278	288	2	1186.68	3.4	0	68.1	16.9	95.00%	E.IPASQVFVAQK.M		R.GDLGIEIPASQVFVAQK.M
66	75	2	1201.59	4.1	0	42.1	21.6	95.00%	E.YHQSVIDNAR.K		R.MNFSHGSYEYHQSVIDNAR.K
128	138	2	1447.65	4.4	1	38.9	23.7	95.00%	K.CNDKVMYIDYK.N	Carbamidomethyl (+57)	K.CNDKVMYIDYK.N
345	357	2	1415.63	2.8	1	47.1	23.5	95.00%	K.GSYPVEAVTYMAE.T		K.GSYPVEAVTYMAETAR.V
248	271	2	2647.3	4.5	1	77.3	20.1	95.00%	K.IENQQGVNNFDSILDVTDGIMVAR.G		K.IENQQGVNNFDSILDVTDGIMVAR.G
77	93	2	1741.97	3.8	0	39.2	16.6	95.00%	K.ASATNPLFPLAIALDTK.G		K.ASATNPLFPLAIALDTK.G
225	232	2	951.52	5	1	30.1	20.1	95.00%	R.AEDVIHIR.E		R.AEDVIHIR.E
250	271	2	2405.18	4.4	0	94.5	21.1	95.00%	E.NQQGVNNFDSILDVTDGIMVAR.G		K.IENQQGVNNFDSILDVTDGIMVAR.G
77	96	2	2025.08	2.4	1	46	16.3	95.00%	K.ASATNPLFPLAIALDTKGPE.I		K.ASATNPLFPLAIALDTKGPEIR.T
57	75	3	2254	4.4	1	44.4	24.3	95.00%	R.MNFSHGSYEYHQSVIDNAR.K		R.MNFSHGSYEYHQSVIDNAR.K
28	37	2	1088.6	5	0	46.3	18.4	95.00%	R.TSIICTIGPK.S	Carbamidomethyl (+57)	R.TSIICTIGPK.S
364	374	2	1226.59	3	0	50.6	21.8	95.00%	E.ASIPYGSLYQE.M		R.VAEASIPYGSLYQEMFGLVR.R
468	477	2	1186.55	5.3	0	54.8	21.9	95.00%	R.VAYGCQQAYK.M	Carbamidomethyl (+57)	R.VAYGCQQAYK.M
272	288	2	1770.96	3.8	1	69.1	16.3	95.00%	R.GDLGIEIPASQVFVAQK.M		R.GDLGIEIPASQVFVAQK.M
294	319	4	2965.41	2.8	1	54	22.7	95.00%	K.CNIAGKPVACATQMLESMTYNPRPTR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CNIAGKPVACATQMLESMTYNPRPTR.A
405	417	2	1287.72	5.7	0	62	16.5	95.00%	K.AIVVLSTSGNTAR.L		K.AIVVLSTSGNTAR.L
76	93	2	1870.06	4.2	1	70.7	11.1	95.00%	R.KASATNPLFPLAIALDTK.G		R.KASATNPLFPLAIALDTK.G
212	223	2	1368.69	4.2	0	39.8	20.4	95.00%	K.NGVDMIFASFIR.R		K.NGVDMIFASFIR.R
294	309	2	1761.83	3.2	0	74.7	22.5	95.00%	K.CNIAGKPVACATQMLE.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CNIAGKPVACATQMLESMTYNPRPTR.A
99	115	2	1689.79	2.7	0	64.3	23	95.00%	R.TGLTVGGTDYPISSGHE.M		R.TGLTVGGTDYPISSGHEMIFTTDDAYAEK.C
47	56	3	1143.62	4.2	1	26	20.4	95.00%	K.LRDAGMNIVR.M		K.LRDAGMNIVR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
7	ALF_SCHPO	67.88%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
207	234	4	2951.53	3.2	1	31.9	18.8	95.00%	R.ELSSVTPYFSIAAAFGNVHGVYKPGNVK.L		R.ELSSVTPYFSIAAAFGNVHGVYKPGNVK.L
253	275	2	2528.21	2	1	93.7	21.5	95.00%	K.TTNDKPVFFVFHGGSGSSVNEFR.T		K.TTNDKPVFFVFHGGSGSSVNEFR.T
94	112	2	2098.02	3.1	0	68.9	21.5	95.00%	R.SIAPFFGVPVVMHSDHCAK.K	Carbamidomethyl (+57)	R.SIAPFFGVPVVMHSDHCAK.K
2	19	2	1823.05	3.8	0	65.3	10.8	95.00%	M.GILDIVPTGVITGDNVLK.L		-.MGILDIVPTGVITGDNVLK.L
345	358	2	1597.83	4.2	1	60.4	19.5	95.00%	R.VLTALEDFYTVNTL.-		R.VLTALEDFYTVNTL.-
194	206	2	1696.81	2.9	1	58	22.1	95.00%	E.LYTQPEDIWDVYR.E		K.IWIEMEIGITGGEEDGVDNSHVSHTELYTQPEDIWDVYR.E
26	47	2	2198.13	4.3	1	40.2	18.8	95.00%	R.EHGFAIPAINVTSSSTAIAALE.A		R.EHGFAIPAINVTSSSTAIAALEAAR.E
285	300	2	1825.89	3.9	1	73.6	22	95.00%	K.VNIDTDTQFAYVEGVR.D		K.VNIDTDTQFAYVEGVR.D
235	249	2	1693.92	4.5	1	32	16	95.00%	K.LQPALLGQHQAYVKE.Q		K.LQPALLGQHQAYVKEQLK.T
306	318	2	1525.72	2.2	1	51.9	23.3	95.00%	K.YKDYLMTPVGNPE.G		K.YKDYLMTPVGNPEGADKPNK.K

113	123	2	1365.65	3.1	1	31	22.7	95.00%	K.KLLPWMDGMFE.A		K.KLLPWMDGMFEADEAYFK.I
253	273	2	2225.05	2.9	0	67.9	22.6	95.00%	K.TTNDKPVFFVFHGGSGSSVNE.F		K.TTNDKPVFFVFHGGSGSSVNEFR.T
114	123	2	1237.56	3.3	0	24.9	22.4	90.20%	K.LLPWMDGMFE.A		K.LLPWMDGMFEADEAYFK.I
235	248	2	1564.88	2.9	0	71.3	12	95.00%	K.LQPALLGQHQAYVK.E		K.LQPALLGQHQAYVK.E
54	71	2	1844.94	-0.021	0	96.7	21.1	95.00%	R.SPIILQTSNGGAHFFAGK.E	Deamidation (+1)	R.SPIILQTSNGGAHFFAGK.E
94	113	5	2226.12	3.2	1	16.5	20	95.00%	R.SIAPFFGVPVVMHSDHCAKK.L	Carbamidomethyl (+57)	R.SIAPFFGVPVVMHSDHCAKK.L
131	149	3	2165.05	2.8	1	41.7	21.9	95.00%	K.IHGEPLFSSHMLDLSEEPK.K		K.IHGEPLFSSHMLDLSEEPK.K
80	93	2	1399.76	5.1	0	89.1	17.2	95.00%	K.ASIAGSIAAAHYIR.S		K.ASIAGSIAAAHYIR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
8	PDC2_SCHPO	40.07%	100%	23

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
379	393	2	1650.82	2.9	0	49.4	22.1	95.00%	R.QIQGLVDSNTTLYAE.T		R.QIQGLVDSNTTLYAETGDSWFNGLQMK.L
204	214	2	1130.62	4.6	1	53.5	18.8	95.00%	K.ATDIAAELISK.K		K.ATDIAAELISK.K
440	461	2	2409.21	3.3	1	90.9	18.9	95.00%	R.TIVMVGDGSFQLTGQEISQMIR.H		R.TIVMVGDGSFQLTGQEISQMIR.H
238	253	2	1690.85	4.5	1	52.2	21.1	95.00%	K.LAEALNCAAFIMPAAK.G	Deamidation (+1)/ Carbamidomethyl (+57)	K.LAEALNCAAFIMPAAK.G
228	237	2	949.49	5	1	30.2	21.6	95.00%	R.AAGAESAFVK.L		R.AAGAESAFVK.L
57	68	2	1341.62	2.5	1	33.5	22.2	95.00%	E.LNCAFAAEGYAR.S	Carbamidomethyl (+57)	R.LLDFLEYYPGLSEIGCCNELNCAFAAEGYAR.S
7	18	2	1342.66	3.6	0	41.7	22.3	95.00%	E.STMTVGTYLAQR.L	Oxidation (+16)	K.DAESTMTVGTYLAQR.L
304	328	2	2694.38	3.7	0	76.3	18.2	95.00%	R.AAPNPNILLNSDYTSVSIPGYVFSR.V		R.AAPNPNILLNSDYTSVSIPGYVFSR.V
147	159	2	1436.71	3	1	71.4	21.9	95.00%	R.AEDAPVMIDHAIR.Q		R.AEDAPVMIDHAIR.Q
241	253	2	1376.7	3.4	0	72.4	21.1	95.00%	E.ALNCAAFIMPAAK.G	Carbamidomethyl (+57)	K.LAEALNCAAFIMPAAK.G
379	405	2	3015.43	1.6	1	70.1	22.1	95.00%	R.QIQGLVDSNTTLYAETGDSWFNGLQMK.L		R.QIQGLVDSNTTLYAETGDSWFNGLQMK.L
137	146	2	1101.64	5.4	1	51.2	16.4	95.00%	K.LTCAAVAIKR.A	Carbamidomethyl (+57)	K.LTCAAVAIKR.A
394	405	2	1382.63	3	0	49.4	23	95.00%	E.TGDSWFNGLQMK.L		R.QIQGLVDSNTTLYAETGDSWFNGLQMK.L
19	25	2	770.49	4.3	1	34.4	14.8	95.00%	R.LVEIGIK.N		R.LVEIGIK.N
462	474	3	1575.97	4.8	1	29.2	3.01	95.00%	R.HKLPVLIFLLNNR.G		R.HKLPVLIFLLNNR.G
149	159	2	1252.63	2.8	0	34.9	21.9	95.00%	E.DAPVMIDHAIR.Q	Oxidation (+16)	R.AEDAPVMIDHAIR.Q
26	37	2	1429.72	4.2	0	38.3	21.1	95.00%	K.NHFVVPGDYNLR.L		K.NHFVVPGDYNLR.L
464	474	2	1310.81	4.6	0	66.2	7.78	95.00%	K.LPVLIFLLNNR.G		K.LPVLIFLLNNR.G
136	145	2	1073.63	3.9	1	39.6	13	95.00%	K.KLTCAAVAIK.R	Carbamidomethyl (+57)	K.KLTCAAVAIK.R
4	18	2	1641.77	4.2	1	65.2	23.5	95.00%	K.DAESTMTVGTYLAQR.L		K.DAESTMTVGTYLAQR.L
172	194	3	2404.19	5.5	0	22.7	20.9	93.40%	E.IPTNMANQPCPVPGPISAVISPE.I	Oxidation (+16)/ Carbamidomethyl (+57)	R.QAILQHKPVYIEIPTNMANQPCPVPGPISAVISPEISDK.E
539	549	2	1326.47	3.1	0	59.5	20.9	95.00%	E.CAIDTDDCTQE.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.EGPTLIECAIDTDDCTQELVDWGK.A
216	225	3	1064.66	3.8	1	29.3	11.8	95.00%	K.EKPILLAGPK.L		K.EKPILLAGPK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
9	ADH4_SCHPO	42.18%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
375	385	3	1245.76	3.9	0	37.6	6.02	95.00%	K.IRPHLVDLGVK.E		K.IRPHLVDLGVK.E
210	221	2	1351.65	4.3	0	50.7	22.8	95.00%	K.HTMPILSVNDPE.T		K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
76	87	2	1282.76	5.2	0	44.2	13.6	95.00%	K.NTLIVTDPGIIK.V		K.NTLIVTDPGIIK.V
245	261	2	1750.86	4.8	0	75.8	22	95.00%	E.AYVSTAANPITDACAVK.C	Carbamidomethyl (+57)	K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
366	374	2	1027.63	6.6	1	37.3	13	95.00%	R.ISQLVLEVK.I		R.ISQLVLEVK.I
149	159	2	1014.58	4.8	0	36.7	19.4	95.00%	K.GIALLATNGGK.I	Deamidation (+1)	K.GIALLATNGGK.I

169	188	2	1998.07	2.9	0	57.9	16.6	95.00%	K.SSKPQLPLIAINTTAGTASE.M			K.SSKPQLPLIAINTTAGTASEMTR.F
399	413	2	1624.68	3.3	0	40.3	23.4	95.00%	K.DACGATNPIQPTHDE.V	Carbamidomethyl (+57)		K.DACGATNPIQPTHDEVK.A
345	356	2	1359.62	3.2	1	45.5	23.3	95.00%	R.LGDIAFHLGCEE.H	Carbamidomethyl (+57)		R.LGDIAFHLGCEEHTAEAALDR.I
101	125	3	2678.34	2.4	0	35.9	20.3	95.00%	E.QSITVHLYDGVQPNPTVGNVNQGLE.I			K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K
399	415	2	1851.85	4.5	1	49.6	23.2	95.00%	K.DACGATNPIQPTHDEVK.A	Carbamidomethyl (+57)		K.DACGATNPIQPTHDEVK.A
100	125	3	2807.38	4.1	1	34.5	20.8	95.00%	E.EQSITVHLYDGVQPNPTVGNVNQGLE.I			K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K
169	191	2	2386.26	3.6	1	98.1	17.2	95.00%	K.SSKPQLPLIAINTTAGTASEMTR.F			K.SSKPQLPLIAINTTAGTASEMTR.F
130	148	2	1993.8	3.7	1	87.9	23.9	95.00%	K.ENCDSMVSIGGGSAHDCAK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)		K.ENCDSMVSIGGGSAHDCAK.G
160	168	2	1008.48	5	1	40.9	22.5	95.00%	K.IADYEGVDK.S			K.IADYEGVDK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
10	THI3_SCHPO	48.55%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	127	2	1090.54	4.7	0	29.6	21.8	95.00%	K.IQLDDLCSK.F	Carbamidomethyl (+57)	K.IQLDDLCSK.F
74	95	2	2353.27	3.5	0	91.4	15.3	95.00%	R.GYPVTSFGSLLNEPFTGLITLK.G		R.GYPVTSFGSLLNEPFTGLITLK.G
128	139	2	1325.67	4.2	0	42.4	20.9	95.00%	K.FGLSPSDYTAIR.C		K.FGLSPSDYTAIR.C
6	13	2	1022.51	3.6	0	32.2	21.5	95.00%	K.ITFLTNWE.A		K.ITFLTNWEATPYHLPIFLAQTR.G
37	56	2	1981.08	3.4	0	87.8	14.3	95.00%	E.VAILEPTNPSDVTALIGSGK.V		R.EGIEVAILEPTNPSDVTALIGSGK.V
6	27	2	2631.39	2.4	1	78.6	15.8	95.00%	K.ITFLTNWEATPYHLPIFLAQTR.G		K.ITFLTNWEATPYHLPIFLAQTR.G
63	71	2	954.54	4.5	0	51.1	14.8	95.00%	K.AMIHTLAAK.A		K.AMIHTLAAK.A
222	239	2	2030.06	3.2	1	79.8	19.1	95.00%	R.AIHSATLDMLKDPVQTYK.E		R.AIHSATLDMLKDPVQTYK.E
110	118	2	968.5	4.9	1	27.7	19.8	94.40%	R.IGYVGEFGK.I		R.IGYVGEFGK.I
14	27	3	1626.89	3.3	0	38.5	16.4	95.00%	E.ATPYHLPIFLAQTR.G		K.ITFLTNWEATPYHLPIFLAQTR.G
330	339	2	992.51	5.7	0	44.3	21.9	95.00%	K.GGVFSGNSLR.Y		K.GGVFSGNSLR.Y
189	211	3	2788.29	2.8	1	29.7	23.2	95.00%	R.LANLGCCCFCTILYIAHDEFIAK.H	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.LANLGCCCFCTILYIAHDEFIAK.H
260	273	2	1711.79	4.7	0	88.7	22.9	95.00%	R.CFAYFSHDISNVPR.D	Carbamidomethyl (+57)	R.CFAYFSHDISNVPR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
11	PMGY_SCHPO	57.35%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
176	185	2	1085.62	3.2	1	53.3	17.2	95.00%	E.GLTGDQIVKR.E		R.ALIMDLEGLTGDQIVKR.E
169	184	2	1714.92	4	1	69.3	17.2	95.00%	R.ALIMDLEGLTGDQIVK.R		R.ALIMDLEGLTGDQIVK.R
78	87	2	1098.6	3.1	1	27.1	18.4	93.60%	E.VGEPNLETIK.S		K.TCQIILEEVGEPNLETIK.S
111	120	2	1271.65	5.7	1	79.8	21.1	95.00%	K.WGAEQVQIWR.R		K.WGAEQVQIWR.R
23	36	2	1589.81	2.8	1	40.1	20.2	95.00%	K.LNLFTGWKDPALSE.T		K.LNLFTGWKDPALSETGIK.E
95	108	2	1626.77	3.9	1	67.7	23.3	95.00%	R.YYGDLQGLNKDDAR.K		R.YYGDLQGLNKDDAR.K
186	199	2	1553.85	2.9	1	49.8	16.1	95.00%	R.ELATGVPIVYHLDK.D		R.ELATGVPIVYHLDK.D
2	14	2	1439.81	5.3	1	52	15.3	95.00%	M.TTEAAPNLLVLTR.H	Acetyl (+42)	-.MTTEAAPNLLVLTR.H
158	168	2	1149.67	4.5	0	26.5	13.2	92.90%	K.VLIAAHGNSLR.A		K.VLIAAHGNSLR.A
95	104	2	1169.58	4.8	0	46.4	20.6	95.00%	R.YYGDLQGLNK.D		R.YYGDLQGLNK.D
187	202	2	1724.95	3	1	49.3	16.9	95.00%	E.LATGVPIVYHLDKDGK.Y		R.ELATGVPIVYHLDKDGK.Y
1	14	2	1528.84	4.4	1	53	16.6	95.00%	-.MTTEAAPNLLVLTR.H		-.MTTEAAPNLLVLTR.H
53	66	2	1615.84	4.6	1	43.1	19.7	95.00%	R.GYKFDIAFTSALQR.A		R.GYKFDIAFTSALQR.A
5	14	2	1066.65	3.1	0	56.6	6.02	95.00%	E.AAPNLLVLTR.H		-.MTTEAAPNLLVLTR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
12	THI2_SCHPO	32.93%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
175	187	2	1431.8	4.7	1	52.1	14.8	95.00%	K.LFNATAVEDLIVK.E		K.LFNATAVEDLIVK.E

2	15	2	1400.77	3.8	0	74.5	17.5	95.00%	M.APATAVVTPQTAFK.T		-.MAPATAVVTPQTAFK.T
286	294	2	1007.47	4.1	1	27.4	21.8	94.00%	E.LSEFDGANR.M		R.EVFPGMIVGGMELSEFDGANR.M
274	285	2	1264.59	3.5	1	31.4	22.6	95.00%	R.EVFPGMIVGGME.L		R.EVFPGMIVGGMELSEFDGANR.M
244	263	3	2296.15	3.2	0	39.6	20.3	95.00%	R.LASAQLVSNLHDMRPLDMNR.A	Oxidation (+16)	R.LASAQLVSNLHDMRPLDMNR.A
39	55	2	1962.95	4.7	1	48.4	22.6	95.00%	K.AYPTYSLDESFSFAPIR.E		K.AYPTYSLDESFSFAPIR.E
295	308	2	1459.67	4	0	71.7	22.5	95.00%	R.MGPTFGGMMFSGIK.A		R.MGPTFGGMMFSGIK.A
48	55	2	923.49	3	0	28.1	20.8	94.70%	E.SFSFAPIR.E		K.AYPTYSLDESFSFAPIR.E
131	139	2	1045.55	3.5	0	29	20.7	95.00%	R.KPADLFLNE.I		R.KPADLFLNEIGVPYEDEGDYVVV K.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
13	SAHH_SCHPO	36.03%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
407	427	2	2266.18	3.4	0	80.7	18.3	95.00%	K.LTTLTSVQSDYLGIPVDGPYK.A		K.LTTLTSVQSDYLGIPVDGPYK.A
314	328	3	1665.93	5.5	1	30.5	14.8	95.00%	K.ANAKDVVNIKPQVDR.Y		K.ANAKDVVNIKPQVDR.Y
26	35	2	1114.58	3.8	1	33.1	19.6	95.00%	E.NEMPGLIAVR.E	Oxidation (+16)	K.ELEIAENEMPGLIAVR.E
8	18	2	1118.61	3.2	0	77.1	18.3	95.00%	K.VADISLAAFGR.K		K.VADISLAAFGR.K
216	227	2	1117.62	4.3	0	46.5	18.3	95.00%	K.VAVVAGFGDVGK.G		K.VAVVAGFGDVGK.G
269	280	2	1367.66	4	1	40.1	22.3	95.00%	K.EGQIFVTTTGCR.D	Carbamidomethyl (+57)	K.EGQIFVTTTGCR.D
119	143	3	2681.36	3	1	73.1	19.4	95.00%	K.SFPSGKPLNMILDDGGDLTALVH ER.H		K.SFPSGKPLNMILDDGGDLTALVH ER.H
176	187	2	1255.68	4.6	0	42.1	17.6	95.00%	K.VPAINVNDSVTK.S		K.VPAINVNDSVTK.S
336	344	2	1006.6	5	0	31.2	13	95.00%	R.HIILLADGR.L		R.HIILLADGR.L
174	187	3	1496.86	5	1	47.8	14.3	95.00%	K.LKVPAINVNDSVTK.S		K.LKVPAINVNDSVTK.S
318	328	2	1281.71	3.7	0	30.2	18	95.00%	K.DVVNIKPQVDR.Y		K.DVVNIKPQVDR.Y
318	330	2	1573.82	3.2	1	38.4	19.7	95.00%	K.DVVNIKPQVDRYE.L		K.DVVNIKPQVDRYELK.N
28	35	2	871.5	2.9	0	30.8	19	95.00%	E.MPGLIAVR.E	Oxidation (+16)	K.ELEIAENEMPGLIAVR.E
270	280	2	1238.61	3.6	0	52.2	22	95.00%	E.GQIFVTTTGCR.D	Carbamidomethyl (+57)	K.EGQIFVTTTGCR.D
245	259	2	1589.75	3.3	0	76.3	23.2	95.00%	E.VDPINALQAAMDGFE.V		R.VIVTEVDPINALQAAMDGFEVTT MEEAVK.E
158	167	2	1132.59	3.6	0	38.2	19.9	95.00%	E.TTTGVHNLYK.M		R.GISEETTTGVHNLYK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
14	GLYD_SCHPO	47.54%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
146	159	2	1649.78	3.9	1	75	22.8	95.00%	K.ISAVSTYFESMPYR.V		K.ISAVSTYFESMPYR.V
233	243	2	1234.63	5.7	0	38.2	20.7	95.00%	E.YADVVTTTTHK.S		R.QIADSVNAYLVVDMAHISGLVSA GVIPSPFEYADVVTTTTHK.S
183	193	2	1209.62	4.5	0	57.8	20.3	95.00%	K.ILVAGTSAYCR.L	Carbamidomethyl (+57)	K.ILVAGTSAYCR.L
361	371	2	1254.76	4.6	1	48.8	9.54	95.00%	R.VLELINIVTNK.N		R.VLELINIVTNK.N
97	123	3	2996.43	3.4	0	55	21.4	95.00%	K.WGVNVQCLSGSPANMQVYQAIM PPHGR.L	Carbamidomethyl (+57)	K.WGVNVQCLSGSPANMQVYQAIM PPHGR.L
86	96	2	1129.62	5.1	0	54.8	20	95.00%	R.ALAAFNLDPAK.W		R.ALAAFNLDPAK.W
59	67	2	998.45	5.1	1	32.9	22	95.00%	K.YSEGYPGAR.Y		K.YSEGYPGAR.Y
277	302	3	2725.45	2.8	0	25.2	15.9	95.00%	K.INFSVFPGHQGGPHNHTITALAVA LK.Q		K.INFSVFPGHQGGPHNHTITALAVA LK.Q
413	422	2	1075.61	4.3	0	49.9	17.6	95.00%	R.ALTFAANLQK.E		R.ALTFAANLQK.E
124	144	2	2226.08	4.1	0	30.3	22	95.00%	R.LMGLDLPSGGHLSHGYQTDTK.K		R.LMGLDLPSGGHLSHGYQTDTK.K
46	58	2	1321.64	4.2	0	41.4	22.8	95.00%	R.AVMDALGSVMSNK.Y		R.AVMDALGSVMSNK.Y
160	182	3	2686.31	2.9	1	31.8	21.6	95.00%	R.VDPNTGLIDYDMLEHDAQLFRPK. I		R.VDPNTGLIDYDMLEHDAQLFRPK. I
145	154	2	1143.59	4.8	1	28.8	20.5	95.00%	K.KISAVSTYFE.S		K.KISAVSTYFESMPYR.V
334	349	2	1669.84	3.9	0	85	21.1	95.00%	K.LAADGTDSHMVLVDVK.S		K.LAADGTDSHMVLVDVK.S
457	467	2	1306.64	2.7	1	51.6	22.3	95.00%	E.WASSFPLADKW.-		K.EVAEWASSFPLADKW.-
406	412	2	878.45	4.3	0	35.8	21.5	95.00%	R.VVDYIDR.A		R.VVDYIDR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
15	TPIS_SCHPO	54.22%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
223	239	2	1800.91	3.1	0	62.8	20.9	95.00%	K.FHDIDGFLVGGASLKPE.F		K.FHDIDGFLVGGASLKPEFHNIVNVHSL.-
160	174	2	1615.9	2.9	0	70.1	14.5	95.00%	K.IVIAYEPVWAIGTGK.T		K.IVIAYEPVWAIGTGK.T
58	70	2	1389.73	3.4	1	50	19.8	95.00%	K.DIGVGAQNVFDKK.N		K.DIGVGAQNVFDKK.N
78	98	2	2233.11	3.5	1	94.9	21.5	95.00%	E.NSAQSLIDAGITYTLTGHSER.R		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R
32	52	2	2422.27	3.5	1	66.1	17.3	95.00%	K.LNVGDVETVIFPQNMYLITTR.Q		K.LNVGDVETVIFPQNMYLITTR.Q
206	219	2	1453.66	3.2	1	81.1	22.9	95.00%	R.VIYGGSVNGGNCKE.F	Deamidation (+1)/ Carbamidomethyl (+57)	R.VIYGGSVNGGNCKEFLK.F
39	52	2	1695.91	3.4	0	49.2	17.5	95.00%	E.TVIFPQNMYLITTR.Q		K.LNVGDVETVIFPQNMYLITTR.Q
146	159	2	1613.86	4.5	1	61.4	19.4	95.00%	R.QLNAIADKVQNWSK.I		R.QLNAIADKVQNWSK.I
196	205	2	971.55	5.3	1	76.1	19.1	95.00%	K.LGASVAEGLR.V		K.LGASVAEGLR.V
223	249	3	2961.52	3.2	1	45.2	17.9	95.00%	K.FHDIDGFLVGGASLKPEFHNIVNVHSL.-		K.FHDIDGFLVGGASLKPEFHNIVNVHSL.-
206	218	2	1324.61	4.4	0	76.9	22.9	95.00%	R.VIYGGSVNGGNCK.E	Deamidation (+1)/ Carbamidomethyl (+57)	R.VIYGGSVNGGNCK.E
78	97	2	2077	3.3	0	115	22	95.00%	E.NSAQSLIDAGITYTLTGHSE.R		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
16	METK_SCHPO	51.57%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
147	155	2	931.5	4.5	0	58	22	95.00%	K.LNAAMSVAR.R		K.LNAAMSVAR.R
20	40	3	2423.15	4	1	37.1	22.2	95.00%	K.ICDQISDAILDACLKDDPFSK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.ICDQISDAILDACLKDDPFSK.V
137	146	2	1117.73	3.3	0	34.2	3.01	95.00%	K.LPLTILLAHK.L		K.LPLTILLAHK.L
99	112	2	1612.79	3.3	1	49.5	22.1	95.00%	E.QQSPDIAQGLHYEK.A		K.TCNVLVAIEQQSPDIAQGLHYEK.A
2	10	2	1084.51	5.8	0	35.8	22.3	95.00%	M.AQTFLFTSE.S	Acetyl (+42)	-.MAQTFLFTSESVGEGHPDK.I
186	203	2	1926.97	1.9	1	55.4	21	95.00%	R.RVDTIVVSAQHADSISTE.D		R.RVDTIVVSAQHADSISTEDLR.S
237	251	2	1429.74	3.6	0	73.6	19.7	95.00%	R.FVVGGPQGDAGLTGR.K		R.FVVGGPQGDAGLTGR.K
339	349	2	1256.73	2.5	0	38.2	15.7	95.00%	K.NFDLRPGVLVK.S		K.NFDLRPGVLVK.S
117	135	2	1970.86	3	1	62	23.5	95.00%	E.LGAGDQGIMFGYATDETPE.K		K.ALEELGAGDQGIMFGYATDETPEK.L
252	272	3	2077.05	3.9	1	61	20.4	95.00%	R.KIIVDTYGGWGAHGGGAFSGK.D		R.KIIVDTYGGWGAHGGGAFSGK.D
353	378	3	3055.48	3	1	68	20.7	95.00%	K.LQTPFYLSTASYGHFTDQSKPWEQPK.E		K.LQTPFYLSTASYGHFTDQSKPWEQPK.E
237	252	2	1557.83	3.3	1	44	17.9	95.00%	R.FVVGGPQGDAGLTGRK.I		R.FVVGGPQGDAGLTGRK.I
291	299	2	856.52	4.2	0	28.1	16.9	94.80%	K.SLVAAGLAR.R		K.SLVAAGLAR.R
213	226	3	1572.93	4.6	1	37.1	6.99	95.00%	K.IIKPTVPAHLLDEK.T		K.IIKPTVPAHLLDEK.T
253	272	2	1948.95	4	0	80.8	22.5	95.00%	K.IIVDTYGGWGAHGGGAFSGK.D		K.IIVDTYGGWGAHGGGAFSGK.D
136	146	3	1245.82	2.6	1	50.1	6.02	95.00%	E.KLPLTILLAHK.L		K.ALEELGAGDQGIMFGYATDETPEKLPLTILLAHK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
17	HSP72_SCHPO	31.07%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
327	340	2	1400.77	3.9	1	39.7	17.7	95.00%	K.ASVNEIVLVGGSTR.I		K.ASVNEIVLVGGSTR.I
4	25	3	2425.14	3.6	1	38.6	22.7	95.00%	K.SIGIDLGTTYSCVGHFSNNRVE.I	Carbamidomethyl (+57)	K.SIGIDLGTTYSCVGHFSNNRVEIIANDQGNR.T
538	548	2	1351.66	4.4	1	37.5	21.6	95.00%	K.NHLESYAYSLR.N		K.NHLESYAYSLR.N
137	153	2	1880.93	4	0	55	20.6	95.00%	K.VTDAVVTVPAYFNDSQR.Q		K.VTDAVVTVPAYFNDSQR.Q
76	86	2	1309.56	4.9	1	34.7	23.1	95.00%	K.FDDPEVQSDMK.H		K.FDDPEVQSDMK.H
403	413	2	1086.62	4.3	0	27.6	17.4	94.20%	E.TAGGVMTPLIK.R		K.TQDLLLLDVAPLSMGIETAGGVMTPLIK.R

332	340	2	900.54	3.2	0	34.5	16.2	95.00%	E.IVLVGGSTR.I		K.ASVNEIVLVGGSTR.I
170	185	2	1686.9	4	0	94.1	18.7	95.00%	R.IINEPTAAAIAYGLDR.S		R.IINEPTAAAIAYGLDR.S
578	589	2	1349.61	3.1	1	58.2	23.3	95.00%	E.WLDSNTTAAKDE.F		K.ETIEWLDSNTTAAKDEFEAK.Q
219	234	2	1647.72	4.3	1	72.5	23.9	95.00%	K.ATAGDTHLGGEDFDSR.L		K.ATAGDTHLGGEDFDSR.L
55	69	2	1698.82	4.2	0	74.8	22	95.00%	K.NQVAMNPHNTIFDAK.R		K.NQVAMNPHNTIFDAK.R
457	467	2	1182.65	4.4	1	28.3	16.8	95.00%	K.FELSGIPPAPR.G		K.FELSGIPPAPR.G
235	244	2	1273.69	4.3	1	25.1	19.4	90.60%	R.LVNHFIQEFK.R		R.LVNHFIQEFK.R
35	47	2	1486.7	4.2	1	60.5	22.9	95.00%	R.TTPSYVAFTDTER.L		R.TTPSYVAFTDTER.L
24	34	2	1227.63	5.8	1	33.2	20.7	95.00%	R.VEIIANDQGNR.T		R.VEIIANDQGNR.T
347	359	2	1539.75	4.6	1	52.1	22.7	95.00%	K.LVSDFFNGKEPCK.S	Carbamidomethyl (+57)	K.LVSDFFNGKEPCK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
18	A1EGU1_SCHPO	43.19%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
457	479	2	2580.33	3.9	0	83.6	18.9	95.00%	K.YVISQCNNALLYPALGVACVLSR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.YVISQCNNALLYPALGVACVLSR.C
258	292	4	3747.95	3.3	0	51.5	16.8	95.00%	R.ILDHYRPDIACFNDDIQGTGAVALAAIIGALHVTK.S	Carbamidomethyl (+57)	R.ILDHYRPDIACFNDDIQGTGAVALAAIIGALHVTK.S
44	57	2	1634.91	4.4	1	89.1	15.7	95.00%	R.LPPIVETLQQQVDR.C		R.LPPIVETLQQQVDR.C
535	547	2	1375.67	3	1	44	22	95.00%	E.GMSTVDLPKDDAK.L		K.QAVSEGMSTVDLPKDDAK.L
377	396	3	2009.14	4.4	0	33.3	10.8	95.00%	E.SAIALVKPTILLGCSGQPGK.F	Carbamidomethyl (+57)	K.EVPSGDINLESAIALVKPTILLGCSGQPGK.F
408	425	2	2093.1	2.5	1	51.1	17.6	95.00%	K.HVERPIIFPISNPTTLME.A		K.HVERPIIFPISNPTTLMEAKPDQIDK.W
501	517	2	1828.94	4.1	1	33.1	21	95.00%	R.SLFAADEALLPDLNNAR.E		R.SLFAADEALLPDLNNAR.E
123	137	2	1824.84	2.3	0	68.8	23	95.00%	E.GCYLDIDHNDLSYIK.Q	Carbamidomethyl (+57)	R.YPEGCYLDIDHNDLSYIK.Q
439	452	2	1418.83	4.1	0	43.8	10.4	95.00%	K.ALIATGSPLPPLNR.N		K.ALIATGSPLPPLNR.N
490	500	2	1070.58	4.5	0	54.7	19	95.00%	K.AASDALATVPR.S		K.AASDALATVPR.S
15	23	2	955.55	4.9	0	32.8	17.4	95.00%	K.GVTLLNSPR.Y		K.GVTLLNSPR.Y
332	339	2	964.49	5	0	34.3	20	95.00%	R.GNLFMIDR.C		R.GNLFMIDR.C
456	479	3	2708.42	3.9	1	41.3	16.6	95.00%	K.KYVISQCNNALLYPALGVACVLSR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.KYVISQCNNALLYPALGVACVLSR.C
222	234	2	1526.73	2.5	1	68.3	23.2	95.00%	R.GEQYDSFLDNVIK.A		R.GEQYDSFLDNVIK.A
178	191	2	1553.75	3.5	0	59.3	22.2	95.00%	K.GHLMTLCAGLDPNR.F	Carbamidomethyl (+57)	K.GHLMTLCAGLDPNR.F
159	177	2	1752.02	2.8	0	46.1	10.4	95.00%	E.GILGIGDQGVGGVLISVAK.G		K.SDSVEYIIITDSEGILGIGDQGVGGVLISVAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
19	HSP90_SCHPO	27.27%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
516	525	2	1100.61	3.5	1	30.6	19.5	95.00%	K.LVNITKDGLE.L		K.LVNITKDGLELEETDEEK.A
48	60	2	1444.65	3.1	0	36.7	22.1	95.00%	R.YQSLSDPHALDAE.K		R.YQSLSDPHALDAEK.D
465	474	2	1170.6	4.5	1	29.7	20.8	95.00%	K.NIYFITGESK.Q		K.NIYFITGESK.Q
645	663	2	2011.99	3.1	0	76.6	21.4	95.00%	E.TALLSSGFTLDDPSAYAQR.I		K.DLATILYETALLSSGFTLDDPSAYAQR.I
567	587	2	2339.12	5.7	1	92.3	22.7	95.00%	K.IVGSPCLLTTGQYGWSANMER.I	Carbamidomethyl (+57)	K.IVGSPCLLTTGQYGWSANMER.I
201	212	2	1434.83	3.3	0	28.7	10.4	95.00%	E.FISYPIQLVVTR.E		K.HSEFISYPIQLVVTR.E
440	458	2	2199.07	3.1	1	92.7	21.6	95.00%	R.YNSLNSPDDLISLEDYITK.M		R.YNSLNSPDDLISLEDYITK.M
596	606	2	1234.5	4.9	0	67.2	22.3	95.00%	R.DTSMSAYMSSR.K		R.DTSMSAYMSSR.K
88	99	2	1282.73	5.3	0	55.5	15.1	95.00%	K.NDLINNLGVIAK.S		K.NDLINNLGVIAK.S
34	45	2	1274.64	4	1	41.6	21.2	95.00%	R.ELISNASDALDK.I		R.ELISNASDALDK.I
362	375	2	1512.78	3.1	1	77.4	19.7	95.00%	K.GVVDSEDLPLNLSR.E		K.GVVDSEDLPLNLSR.E
80	99	2	2086.12	2.8	1	41.3	16.2	95.00%	R.DTGIGMTKNDLINNLGVIAK.S		R.DTGIGMTKNDLINNLGVIAK.S
198	212	2	1787.96	4.4	1	31.7	17.7	95.00%	K.HSEFISYPIQLVVTR.E		K.HSEFISYPIQLVVTR.E
440	453	2	1578.74	1.3	0	29.6	22.7	95.00%	R.YNSLNSPDDLISLE.D		R.YNSLNSPDDLISLEDYITK.M
422	436	2	1574.86	4	1	34.5	17.6	95.00%	K.LGIHEDAANRPALAK.L		K.LGIHEDAANRPALAK.L
290	302	2	1526.74	4	1	75.7	22.4	95.00%	K.SLTNDWEDHLAVK.H		K.SLTNDWEDHLAVK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
20	6PGD_SCHPO	34.15%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
156	166	3	1228.76	4.8	0	32.1	6.99	95.00%	R.IKPIFQTLAAK.A		R.IKPIFQTLAAK.A
140	155	2	1669.81	4.7	0	28.8	22.6	95.00%	R.YGPSLMPGGNPAAWPR.I		R.YGPSLMPGGNPAAWPR.I
97	114	3	1943.94	2.6	1	43.8	22.3	95.00%	E.KGDIIVDGGNSHYPDTTR.R		K.AGKPVDYLIEGLAPLLEKGDIIVDGGNSHYPDTTR.R
467	492	3	2753.31	3.6	1	22.6	22.1	93.30%	K.SLPADKDIHINWTGHGGNISATTYDA.-		K.SLPADKDIHINWTGHGGNISATTYDA.-
98	115	3	1971.95	5.1	1	35.5	21.5	95.00%	K.GDIIVDGGNSHYPDTTRR.C		K.GDIIVDGGNSHYPDTTRR.C
320	333	2	1592.8	4.1	1	67.9	20.8	95.00%	K.QLIDDLEDALYASK.I		K.QLIDDLEDALYASK.I
437	449	2	1379.79	4.1	0	52	11.8	95.00%	R.SAVLPANLLQAQR.D		R.SAVLPANLLQAQR.D
410	436	3	2839.48	3.6	1	74.2	17.1	95.00%	R.RVVAQAAMLGIPVPATSTGLSFYDGYR.S		R.RVVAQAAMLGIPVPATSTGLSFYDGYR.S
98	114	2	1815.85	4.4	0	91.7	23.4	95.00%	K.GDIIVDGGNSHYPDTTR.R		K.GDIIVDGGNSHYPDTTR.R
450	458	2	1112.51	4.7	0	24.9	22.6	90.20%	R.DYFGAHTFR.V		R.DYFGAHTFR.V
29	37	2	1175.49	3.9	0	36.7	23.2	95.00%	K.GFTVCCYNR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GFTVCCYNR.T
5	28	2	2457.3	3	1	76	15.9	95.00%	K.EVADFGLIGLAVMGQNLILNGADK.G		K.EVADFGLIGLAVMGQNLILNGADK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
21	ILV5_SCHPO	33.91%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
144	159	2	1689.87	3.5	1	44.3	20.2	95.00%	K.KGSIIMNLLSDAAQTE.T		K.KGSIIMNLLSDAAQTETWPK.I
84	104	2	2141.07	4.6	0	90.4	21.2	95.00%	K.NDTLAIIGYGSQGHGQGLNAR.D		K.NDTLAIIGYGSQGHGQGLNAR.D
330	337	2	914.47	6	0	41.2	19.8	95.00%	R.GAIDWTPR.F		R.GAIDWTPR.F
314	328	2	1725.76	3.8	0	69	24.5	95.00%	K.YGLDYMFAACSTTAR.R	Carbamidomethyl (+57)	K.YGLDYMFAACSTTAR.R
145	163	2	2074.05	4.2	1	75.2	20.1	95.00%	K.GSIIMNLLSDAAQTETWPK.I		K.GSIIMNLLSDAAQTETWPK.I
57	65	2	996.46	3.7	1	25.1	22.7	90.50%	R.VMDFAGTKE.N		R.VMDFAGTKENVWER.S
362	372	2	1312.61	4.6	1	61.6	22.7	95.00%	R.SLEYNSAPNYR.E		R.SLEYNSAPNYR.E
123	133	2	1198.6	4.3	1	28.6	20.9	95.00%	K.QAIEDGWVPGK.T		K.QAIEDGWVPGK.T
303	313	2	1189.67	2.7	0	28.8	17.3	95.00%	E.ATQSLYPLIGK.Y		R.GHSPAEAFNETVEEATQSLYPLIGK.Y
78	104	3	2906.47	2.4	1	96.6	19.4	95.00%	K.LVDYFKNDTLAIIGYGSQGHGQGLNAR.D		K.LVDYFKNDTLAIIGYGSQGHGQGLNAR.D
349	358	2	1166.48	3	1	24.9	22.1	90.10%	E.LYDNVENGNE.A	Deamidation (+1)	K.VLNELYDNVENGNEAK.R
190	204	2	1639.97	3.6	1	26.8	9.54	93.20%	K.IHPPKDVDVILVAPK.G		K.IHPPKDVDVILVAPK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
22	K6PF_SCHPO	20.49%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
364	380	3	1831.88	4.2	1	50.7	23.4	95.00%	R.ICEAVDSISSTAISHSR.A	Carbamidomethyl (+57)	R.ICEAVDSISSTAISHSR.A
613	628	3	1700.87	4.5	0	49.7	20.4	95.00%	R.GHTPLAIDNGFSGFLR.H		R.GHTPLAIDNGFSGFLR.H
419	431	2	1592.73	4.2	1	27.5	22.7	94.10%	K.WQDELCNSLSSVR.K	Carbamidomethyl (+57)	K.WQDELCNSLSSVR.K
283	308	2	2620.33	3.9	0	86.3	18.8	95.00%	K.NLISAGIDSIIVCGGDGSLTGADIFR.S	Carbamidomethyl (+57)	K.NLISAGIDSIIVCGGDGSLTGADIFR.S
586	603	3	1720.91	2.7	0	60.8	18.3	95.00%	R.VAIIHVGAPAGGMNSATR.A		R.VAIIHVGAPAGGMNSATR.A
798	806	2	934.49	4	1	31.5	20	95.00%	K.ATFALEAGR.N		K.ATFALEAGR.N
880	896	2	1696.88	4.3	0	74.6	19.5	95.00%	R.ANDLGNDPSSAVVIGIR.G		R.ANDLGNDPSSAVVIGIR.G
254	267	2	1400.75	3.4	1	49.7	19.4	95.00%	R.GWLAEGGTLIGTAR.C		R.GWLAEGGTLIGTAR.C
844	861	2	1860.9	4.7	0	42.3	22.3	95.00%	R.TAVPGHVQQGGNPTPMDR.A		R.TAVPGHVQQGGNPTPMDR.A
5	19	2	1635.76	2.8	0	35.1	23.6	95.00%	E.TVHGISCYSVVANTE.D	Carbamidomethyl (+57)	-.MSGETVHGISCYSVVANTEDTYNQTLDFYQK.L
927	938	2	1323.7	4.7	0	53.3	19	95.00%	R.DMHNLVNILAGK.T		R.DMHNLVNILAGK.T
197	214	2	1760.86	3.3	0	86.3	21.8	95.00%	K.IAVMTSGGDSPGMNAVVR.A		K.IAVMTSGGDSPGMNAVVR.A
367	380	2	1429.72	4	0	61.4	20.8	95.00%	E.AVDSISSTAISHSR.A		R.ICEAVDSISSTAISHSR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
23	EF3_SCHPO	15.09%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	46	2	1245.63	4.1	1	38.5	21.4	95.00%	K.ALASFVNGPIEE.Q		K.ALASFVNGPIEEQDAPSQVFSAISK.Q
596	621	4	2935.49	3.5	1	34.9	19.3	95.00%	K.DVSSIIVSHDSGFLDHVVQAIIHYER.F		K.DVSSIIVSHDSGFLDHVVQAIIHYER.F
47	59	2	1376.7	3	0	81	21	95.00%	E.QDAPSQVFSAISK.Q		K.ALASFVNGPIEEQDAPSQVFSAISK.Q
281	294	2	1550.88	4.1	1	60.5	14.5	95.00%	K.LVEDPQVVAPFLPK.L		K.LVEDPQVVAPFLPK.L
78	95	2	1839.91	3.8	0	33	22	95.00%	E.AVANHGSVAADVEPYLVE.L		K.GLEAVANHGSVAADVEPYLVELLPAVIAK.V
757	765	2	1178.58	7.8	1	24.9	21.5	90.10%	K.TPSEYIQWR.F		K.TPSEYIQWR.F
479	493	2	1636.88	3.9	1	73.9	18	95.00%	R.AIVNGQVEGFPTHLR.T		R.AIVNGQVEGFPTHLR.T
20	29	2	1143.49	4.3	1	35.9	22.3	95.00%	K.HLTVCDAAEE.A	Carbamidomethyl (+57)	K.HLTVCDAAEEADAAK.A
133	147	2	1550.87	3.9	1	70.6	14.1	95.00%	K.AIVPSVLESIHTTGK.W		K.AIVPSVLESIHTTGK.W
541	554	2	1471.79	3	0	50.2	19	95.00%	E.LINMPIGSLSGGWK.M		K.ENSFTDELINMPIGSLSGGWK.M
202	213	2	1359.69	4.1	0	43.2	21	95.00%	K.VCTLIANADIDR.F	Carbamidomethyl (+57)	K.VCTLIANADIDR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
24	TSA1_SCHPO	44.79%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	147	2	1224.69	4.4	0	43.5	15.8	95.00%	R.QITINDLPVGR.S		R.QITINDLPVGR.S
90	107	2	1786.96	2.6	1	28.2	17.4	94.90%	K.EGGLGGINIPLLADPSHK.V		K.EGGLGGINIPLLADPSHK.V
125	132	2	901.53	4.7	0	35.7	18.9	95.00%	R.GLFLIDPK.G		R.GLFLIDPK.G
66	88	2	2576.29	0.89	1	97.3	19.9	95.00%	R.NAQVILTSTDSEYSHLAFINTPR.K		R.NAQVILTSTDSEYSHLAFINTPR.K
111	124	2	1523.77	4.1	1	79.7	21	95.00%	R.DYGVLIEDAGVAFR.G		R.DYGVLIEDAGVAFR.G
91	107	2	1657.92	2.7	0	55.9	16.3	95.00%	E.GGLGGINIPLLADPSHK.V		K.EGGLGGINIPLLADPSHK.V
78	88	2	1317.69	2.8	0	36.2	20.4	95.00%	E.YSHLAFINTPR.K		R.NAQVILTSTDSEYSHLAFINTPR.K
2	13	2	1341.74	4.1	0	36.9	17.6	95.00%	M.SLQIGKPAPDFK.G	Acetyl (+42)	-.MSLQIGKPAPDFK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
25	HSP75_SCHPO	32.79%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	173	2	1168.66	5	0	34.3	15.6	95.00%	K.DAGAIAGLNVLR.I		K.DAGAIAGLNVLR.I
501	517	3	1779.92	5.5	1	60.6	19	95.00%	R.SAHIEITNSVGHLSSTK.I		R.SAHIEITNSVGHLSSTK.I
370	385	2	1545.86	4.9	0	30.4	16.6	95.00%	E.AVAYGAAVQAAVLTNK.A		K.SINPDEAVAYGAAVQAAVLTNK.A
253	260	2	929.45	5.3	0	25	20.3	90.40%	K.IDISDDPR.A		K.IDISDDPR.A
144	157	2	1552.8	4.6	0	33.7	20.1	95.00%	K.AVITVPAYFSDSQR.A		K.AVITVPAYFSDSQR.A
331	344	2	1437.76	3.8	0	34.4	18.7	95.00%	K.ADVHDIVLVGGSTR.I		K.ADVHDIVLVGGSTR.I
586	595	2	1146.56	3.8	1	45.3	22.1	95.00%	E.LEDTNTDALR.K		K.IEAQLAECMSQLELEDTNTDALR.K
115	128	2	1565.81	1.4	1	60	19.8	95.00%	K.QFTAQEISAMVLTK.M		K.QFTAQEISAMVLTK.M
506	517	2	1242.66	4.3	0	48.5	18.6	95.00%	E.ITNSVGHLSSTK.I		R.SAHIEITNSVGHLSSTK.I
174	190	2	1729.93	3.1	0	88	17.1	95.00%	R.IINEPTAAAIAYGLDAK.S		R.IINEPTAAAIAYGLDAK.S
221	241	2	2143.02	3.8	1	45.4	23.2	95.00%	E.VLATAGDTHLGGEDFDNALVE.H		K.IQGGVFEVLATAGDTHLGGEDFDNALVEHFIQEFK.R
410	419	2	1103.56	3.4	0	30.3	20.9	95.00%	E.GNVFGVVCPR.N	Carbamidomethyl (+57)	K.TQDLLLLDVVPLSLGVAMEGNVFGVVCPR.N
286	301	2	1696.83	2.8	0	56.2	21.4	95.00%	E.VDSLSNGIDFSSSITR.A		R.ALSSVTQTTVEVDSLSNGIDFSSSITR.A
462	472	2	1255.68	3.2	0	32.3	19.1	95.00%	E.FQLTGIPPMPR.G		R.VNCAENEPLGEFQLTGIPPMPR.G

430	450	2	2374.16	5.6	1	61.9	21.3	95.00%	R.TFTTVADNQTTVTFPVYQGER.V		R.TFTTVADNQTTVTFPVYQGER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
26	EF2_SCHPO	20.78%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
272	283	2	1498.77	4.2	0	53.9	20.5	95.00%	R.AFNMFILDPIYR.I		R.AFNMFILDPIYR.I
466	479	2	1474.71	3.7	1	72.8	21.9	95.00%	K.SGTLTTSEVAHNMK.V		K.SGTLTTSEVAHNMK.V
565	578	2	1451.69	4.3	1	44.5	23.4	95.00%	R.ESVSEPSSMTALSK.S		R.ESVSEPSSMTALSK.S
623	631	2	1065.49	2.6	0	26.9	21.2	93.40%	E.FGWDVTDAR.K		R.IMADEFGWDVTDAR.K
632	651	3	2235.11	2.7	1	41.5	21.9	95.00%	R.KIWCFGPDTTGANVVVDQTK.A	Carbamidomethyl (+57)	R.KIWCFGPDTTGANVVVDQTK.A
633	651	2	2107.01	3.2	0	108	22.2	95.00%	K.IWCFGPDTTGANVVVDQTK.A	Carbamidomethyl (+57)	K.IWCFGPDTTGANVVVDQTK.A
284	292	2	1051.52	4.5	0	27.5	21.3	94.10%	R.IFDAVMNSR.K		R.IFDAVMNSR.K
244	253	2	1266.61	5.9	1	30	21.9	95.00%	R.LWGENYFNPK.T		R.LWGENYFNPK.T
151	162	3	1392.86	5.8	1	25.2	6.99	95.00%	R.IRPVVVVNKVDR.A		R.IRPVVVVNKVDR.A
544	555	2	1334.69	3.5	1	47.4	20.9	95.00%	K.DLQEDHAGIPLK.I		K.DLQEDHAGIPLK.I
371	384	2	1594.76	4.1	0	55	22.5	95.00%	R.NCDANAPLMIYVSK.M	Carbamidomethyl (+57)	R.NCDANAPLMIYVSK.M
327	346	2	2192.18	2.4	1	55.9	15.8	95.00%	K.FLPAADALMEMIVLHLPSPK.T		K.FLPAADALMEMIVLHLPSPK.T
442	465	2	2595.37	4.3	1	74.7	16	95.00%	R.IEPIEDCPAGNIIGLVGVDQFLVK.S	Carbamidomethyl (+57)	R.IEPIEDCPAGNIIGLVGVDQFLVK.S
337	346	2	1133.67	2.8	0	35.8	13.8	95.00%	E.MIVLHLPSPK.T		K.FLPAADALMEMIVLHLPSPK.T
618	631	2	1624.73	4.2	1	45	23.4	95.00%	R.IMADEFGWDVTDAR.K		R.IMADEFGWDVTDAR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
27	ACT_SCHPO	32.27%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
148	167	2	2073.03	3.1	0	60.1	21.2	95.00%	R.TTGIVLDSGDGVTHTVPIYE.G		R.TTGIVLDSGDGVTHTVPIYEGYALPHAIMR.L
260	270	2	1144.62	3.4	0	27.1	21.1	93.70%	E.ALFQPSALGLE.N		R.APEALFQPSALGLENAGIHEATYNSIMK.C
85	95	3	1514.75	5.5	1	36	21	95.00%	K.IWHHTFYNELR.V		K.IWHHTFYNELR.V
292	312	2	2216.04	5	0	63.1	23.1	95.00%	K.DLYGNVVMSGGTTMYPGIADR.M		K.DLYGNVVMSGGTTMYPGIADR.M
227	238	2	1261.66	3.6	1	63.8	20.2	95.00%	E.LQTAAQSSSLEK.S		K.LCYVALDFEQELQTAAQSSSLEK.S
197	206	2	1131.53	5.1	1	41.4	22.8	95.00%	R.GYTFSTTAER.E		R.GYTFSTTAER.E
148	177	3	3182.62	3.4	1	67.2	18.3	95.00%	R.TTGIVLDSGDGVTHTVPIYEGYALPHAIMR.L		R.TTGIVLDSGDGVTHTVPIYEGYALPHAIMR.L
5	18	2	1448.7	1.5	0	82.2	22.4	95.00%	E.IAALVIDNGSGMCK.A	Deamidation (+1)/ Carbamidomethyl (+57)	-.MEEEIAALVIDNGSGMCK.A
73	84	2	1456.64	2.3	1	44	23.6	95.00%	E.HGIVNNWDDMEK.I		K.YPIEHGIVNNWDDMEK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
28	TKT_SCHPO	31.97%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
325	336	2	1449.68	6.5	1	28.4	22.7	95.00%	K.QSYPDLSNQLER.I	Deamidation (+1)	K.QSYPDLSNQLER.I
2	18	2	1869.94	2.8	0	92.7	21.3	95.00%	M.TSSSYTDIDTLAINTIR.T		-.MTSSSYTDIDTLAINTIR.T
238	252	2	1719.86	5	1	57.2	21.5	95.00%	R.EAMSCTDKPTLINLK.T	Carbamidomethyl (+57)	R.EAMSCTDKPTLINLK.T
395	407	2	1418.65	3.9	1	52.7	22.6	95.00%	R.WEGAADFQPPSSK.L		R.WEGAADFQPPSSK.L
653	663	2	1249.63	3.9	0	24.8	20.3	90.00%	K.FHFTTSGVAQR.A		K.FHFTTSGVAQR.A
261	275	2	1585.83	3.8	0	27.7	20.4	94.30%	E.LQGTHSVHGSPLKPE.D		K.TTIGYGSELQGTHSVHGSPLKPEDCVHVK.K
380	394	2	1499.8	3	0	41.5	18	95.00%	E.LVGGSADLTPSNLTR.W		K.LSEIVLDALCPVLPELVGGSADLTPSNLTR.W
510	531	2	2288.16	3.4	0	112	19.5	95.00%	E.TSAAYYSALTSDSTPSILALTR.Q		R.AMPNINCWRPADGNETSAAYYSALTSDSTPSILALTR.Q
182	193	2	1385.74	4.7	0	41.9	20.1	95.00%	K.LSNLIAVWDNNK.I		K.LSNLIAVWDNNK.I
118	137	2	1736.98	1.5	0	43.4	12	95.00%	E.TGAGPLGQGIASAVGLAIGK.A		K.TPGHPETHNPDLNIETGAGPLGQGIASAVGLAIGK.A

630	648	3	2046.93	3.6	1	34	23.7	95.00%	R.YVHEAFGMHTFGDSGPAPK.L		R.YVHEAFGMHTFGDSGPAPK.L
495	509	2	1743.75	2.4	0	33	23.6	95.00%	R.AMPNINCWRPADGNE.T	Carbamidomethyl (+57)	R.AMPNINCWRPADGNETSAAYYSALTSDSTPSILALTR.Q
495	531	3	4013.9	2.8	1	63.2	20.6	95.00%	R.AMPNINCWRPADGNETSAAYYSALTSDSTPSILALTR.Q	Carbamidomethyl (+57)	R.AMPNINCWRPADGNETSAAYYSALTSDSTPSILALTR.Q
291	303	2	1603.8	4	1	26.8	21.3	93.20%	K.TFQVPPEVYAYYK.E		K.TFQVPPEVYAYYK.E
30	49	3	1972.02	3.4	0	54.7	19.8	95.00%	K.SGHPGAPMGLAPAAHVLFSR.I		K.SGHPGAPMGLAPAAHVLFSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
29	HSP60_SCHPO	23.71%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
112	128	2	1705.86	4.1	1	84.3	21.2	95.00%	K.TNEVAGDGTTTATVLTR.A		K.TNEVAGDGTTTATVLTR.A
115	128	2	1361.72	3.1	0	53.2	20.5	95.00%	E.VAGDGTTTATVLTR.A		K.TNEVAGDGTTTATVLTR.A
336	342	2	802.45	3.1	1	28.3	20.9	94.90%	E.IDVSIEK.A		R.NMLGDLAVLTDSAVFNDEIDVSIEK.A
137	148	2	1316.6	4	0	27.4	23.3	94.00%	R.NVAAGCNPMDLR.R	Carbamidomethyl (+57)	R.NVAAGCNPMDLR.R
437	453	2	1588.85	4.6	1	29.9	18.9	95.00%	K.AAVSEGVLPGAGTSFVK.A		K.AAVSEGVLPGAGTSFVK.A
68	79	2	1313.7	4.3	0	39.3	19.4	95.00%	R.NVLIDQPFGSPK.I		R.NVLIDQPFGSPK.I
520	533	2	1570.87	4.4	1	87.2	15.3	95.00%	R.FVDLNEIGVLDPLK.V		R.FVDLNEIGVLDPLK.V
258	275	2	1937.07	4.4	1	74.7	14.9	95.00%	K.VSAVQDILPSLELAAQQR.R		K.VSAVQDILPSLELAAQQR.R
229	240	2	1401.72	4.3	0	35	20.5	95.00%	R.GYISPYFITDVK.S		R.GYISPYFITDVK.S
45	56	2	1215.69	4.9	0	52.6	16.8	95.00%	R.ASLLTGVDTLAR.A		R.ASLLTGVDTLAR.A
175	191	2	1712.83	2.9	0	40.9	22.7	95.00%	E.ISQVATISANGDTHIGE.L	Deamidation (+1)	R.DITTSEEISQVATISANGDTHIGELLAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
30	HXK2_SCHPO	33.19%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
105	118	2	1615.8	2.6	0	39.8	21.8	95.00%	E.SVKPIIDFMSDHVE.L		R.NESVKPIIDFMSDHVELFIK.E
434	449	2	1529.79	4.8	0	96.2	20	95.00%	K.DGSGIGAALCALQAVK.E	Carbamidomethyl (+57)	K.DGSGIGAALCALQAVK.E
193	205	2	1357.76	2.5	0	67.1	16.9	95.00%	E.AVINDTVGTLVTR.A		R.IEAVINDTVGTLVTR.A
61	75	2	1595.8	2	0	64.7	21.6	95.00%	E.TGDFLALDFGGTNLR.V		K.NGEVLAMAPAFISTLPTGAETGDFLALDFGGTNLR.V
76	86	2	1287.67	3.9	0	30.3	20.6	95.00%	R.VCWIQLLGDGK.Y	Carbamidomethyl (+57)	R.VCWIQLLGDGK.Y
286	296	2	1240.63	5.9	1	25.6	20.1	91.40%	R.VGGMYLGELFR.R		R.VGGMYLGELFR.R
253	265	3	1536.68	2.4	0	31.9	23.2	95.00%	E.WGATDFSCLHSTR.Y	Carbamidomethyl (+57)	K.CTGDHMLINMEWGATDFSCLHSTR.Y
374	388	2	1564.83	4.1	0	56.1	19.1	95.00%	R.MSAVPIASLYLSTGR.A		R.MSAVPIASLYLSTGR.A
103	118	3	1858.88	3.3	1	33.3	23.1	95.00%	R.NESVKPIIDFMSDHVE.L		R.NESVKPIIDFMSDHVELFIK.E
44	60	2	1687.89	3.1	0	54.5	19	95.00%	E.VLAMAPAFISTLPTGAE.T		K.NGEVLAMAPAFISTLPTGAETGDFLALDFGGTNLR.V
404	413	3	1313.64	1.9	0	41.1	22.6	95.00%	E.HYPHFVDMLR.E		K.SDVGVDGSLVEHYPHFVDMLR.E
266	279	2	1598.77	3.1	0	53	22.6	95.00%	R.YDLLLDHDTPNAGR.Q		R.YDLLLDHDTPNAGR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
31	IPYR_SCHPO	47.75%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
203	212	2	1145.49	3.4	1	28.2	22.8	94.80%	E.NSFAFSGECK.N	Carbamidomethyl (+57)	K.IPDGKPENSFAFSGECK.N
240	280	3	4115.08	2.7	1	89.4	17.6	95.00%	K.SDFSLVNVSVTGSVANDPSVSSTIPPAQELAPAPVDPSVHK.W		K.SDFSLVNVSVTGSVANDPSVSSTIPPAQELAPAPVDPSVHK.W
114	125	2	1304.56	2.5	1	40.8	23.4	95.00%	K.AKGDSDPLDVCE.I	Carbamidomethyl (+57)	K.AKGDSDPLDVCEIGEAR.G
186	192	2	922.44	6	1	35.4	21.7	95.00%	R.ATNEWFR.I		R.ATNEWFR.I
9	23	2	1710.89	4.7	1	31.3	19	95.00%	E.VGALNTLDYQVYVEK.N		R.EVGALNTLDYQVYVEK.N
157	169	2	1391.81	4.1	0	37.4	11.8	95.00%	K.VIVIDVNDPLAPK.L		K.VIVIDVNDPLAPK.L
24	42	2	2113.02	2.7	1	73.6	22.6	95.00%	K.NGTPISSWHDIPLYANAEK.T	Deamidation (+1)	K.NGTPISSWHDIPLYANAEK.T
43	53	2	1283.73	4	1	66.7	15.9	95.00%	K.TILNMVVEIPR.W		K.TILNMVVEIPR.W
193	202	2	1158.63	3.2	1	25.1	20	90.50%	R.IYKIPDGKPE.N		R.IYKIPDGKPENSFAFSGECK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
32	PUR9_SCHPO	26.32%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
										Acetyl (+42)/ Carbamidomethyl (+57)/	

464	477	2	1502.83	4	0	36.9	16.4	95.00%	K.TFVGNRPSNSIIAK.K		K.TFVGNRPSNSIIAK.K
42	51	2	1189.57	2.2	1	28.3	22.8	95.00%	K.FSFTFNGLKE.E	Deamidation (+1)	K.FSFTFNGLKEEDGPILFDFSK.N
534	547	2	1559.76	2	0	32.8	22.5	95.00%	E.NHDSSTNGLINLFK.N	Deamidation (+1)	K.GDVENHDSSTNGLINLFK.N
2	24	2	2548.27	3.8	1	60.7	19.4	95.00%	M.SFSLASTLPAWQAVQTHYESVGK.H	Acetyl (+42)	-.MSFSLASTLPAWQAVQTHYESVGK.H
118	128	2	1170.59	4.1	0	35.5	21.3	95.00%	K.VNGQDVMPGVR.K		K.VNGQDVMPGVR.K
204	216	2	1493.75	4.3	1	51.5	21.7	95.00%	K.CDPETTLFLIASK.T	Carbamidomethyl (+57)	K.CDPETTLFLIASK.T
429	445	2	1870.94	4.8	1	69.7	21.1	95.00%	R.MLFSNFAAQTEALMLGK.T		R.MLFSNFAAQTEALMLGK.T
353	367	2	1711.83	4.2	1	71.8	22.6	95.00%	R.FPAYLQQLSMESNGK.A		R.FPAYLQQLSMESNGK.A
2	20	2	2177.05	3.9	0	52.6	22.4	95.00%	M.SFSLASTLPAWQAVQTHYE.S	Acetyl (+42)	-.MSFSLASTLPAWQAVQTHYESVGK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
36	SERA_SCHPO	23.18%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
275	284	2	1108.56	4.3	1	25.6	21.2	91.40%	K.EGSYLINASR.G		K.EGSYLINASR.G
338	351	2	1479.76	2.2	1	40	21.1	95.00%	K.NIILTPHIGGSTEE.A		K.NIILTPHIGGSTEEAQYNIGIEVSEALTR.Y
410	421	2	1468.77	4	1	31.9	19.6	95.00%	R.QVNELFIDHNIK.S		R.QVNELFIDHNIK.S
302	319	2	1728.88	4.5	0	48	20.8	95.00%	K.IAGAAIDVYPSEPAGNGK.D		K.IAGAAIDVYPSEPAGNGK.D
47	57	3	1247.68	3.8	1	25.6	17.9	95.00%	R.TLKPFASEDIK.I		R.TLKPFASEDIK.I
63	75	2	1430.7	2.7	1	60.7	21	95.00%	E.NVNQSALSNLKDE.G		K.ILLLENVNQSALSNLKDEGYQVEFLK.T
248	262	2	1596.82	4.1	1	50.8	20	95.00%	R.ADFVSLHVPASPETK.N		R.ADFVSLHVPASPETK.N
142	154	2	1394.7	4.8	0	57.8	20.3	95.00%	R.GIAVFNSPYANSR.S		R.GIAVFNSPYANSR.S
302	321	3	1972.98	2.5	1	34.2	21.5	95.00%	K.IAGAAIDVYPSEPAGNGKDK.F	Deamidation (+1)	K.IAGAAIDVYPSEPAGNGKDK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
37	GPD1_SCHPO	35.58%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
281	296	2	1692.8	3.3	0	57.4	22.7	95.00%	E.QSCGIADLVTSCLGGR.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.TMVEQSCGIADLVTSCLGGR.N
203	232	3	3092.63	2.8	1	70.4	16.2	95.00%	R.EQIAAVFDRPYFSVVSVDDVAGVALGGALK.N		R.EQIAAVFDRPYFSVVSVDDVAGVALGGALK.N
2	20	2	1989	3.8	0	99.4	21.1	95.00%	M.SGYGQQGVSAANIDSIRPK.K	Acetyl (+42)	-.MSGYGQQGVSAANIDSIRPK.K
87	104	2	2008.05	3	1	51.1	18.4	95.00%	K.YLPGIECPPNVIAVPDVR.E	Carbamidomethyl (+57)	K.YLPGIECPPNVIAVPDVR.E
277	296	2	2153	2.6	1	93.7	23.3	95.00%	R.TMVEQSCGIADLVTSCLGGR.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.TMVEQSCGIADLVTSCLGGR.N
188	202	2	1668.85	2.8	1	38.6	20.3	95.00%	E.TTIGFNPPNEVDIPR.E		R.EQFCETTIGFNPPNEVDIPR.E
125	144	2	2172.13	2.5	0	66	19.3	95.00%	R.VCDQMVGLIRPGAVGISCIK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VCDQMVGLIRPGAVGISCIK.G
317	331	2	1484.82	2.8	1	67	16.7	95.00%	K.ELLGGQLLQGAATSK.D		K.ELLGGQLLQGAATSK.D
318	331	2	1355.78	2.6	0	61.4	15.1	95.00%	E.LLGGQLLQGAATSK.D		K.ELLGGQLLQGAATSK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
38	LYS9_SCHPO	34.22%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
177	183	2	740.49	4.7	0	33.1	9.03	95.00%	R.GVLLALR.N		R.GVLLALR.N
122	135	2	1509.82	2.5	0	41.6	16.9	95.00%	E.IGVDPGIDHLYAIK.T		K.AGSICMNEIGVDPGIDHLYAIK.T
38	49	2	1259.66	4.1	1	41.7	19.9	95.00%	K.AEAFINGIPNSK.A		K.AEAFINGIPNSK.A
149	170	2	2385.11	5.2	1	60.2	22.9	95.00%	K.SFLSYCGGLPAPEDSNNPLGYK.F	Carbamidomethyl (+57)	K.SFLSYCGGLPAPEDSNNPLGYK.F
2	22	3	2269.25	3.1	1	39	13	95.00%	M.PSILLLGSGFVAHPTLEYLSR.R		-.MPSILLLGSGFVAHPTLEYLSR.R
379	396	2	1989.93	4.3	0	76.6	23	95.00%	R.TCTLLDYGVPNGYTSMAK.L	Carbamidomethyl (+57)	R.TCTLLDYGVPNGYTSMAK.L
114	135	3	2372.16	2.8	1	47.3	21.4	95.00%	K.AGSICMNEIGVDPGIDHLYAIK.T	Carbamidomethyl (+57)	K.AGSICMNEIGVDPGIDHLYAIK.T

2	18	2	1749.97	2.9	0	41.8	15.2	95.00%	M.PSILLLGSGFVAHPTLE.Y		-.MPSILLLGSGFVAHPTLEYLSR.R
397	426	3	3075.62	3.2	0	49	14.3	95.00%	K.LVGVPCGVATQQILDGVINTPGVLAPNDMK.L	Carbamidomethyl (+57)	K.LVGVPCGVATQQILDGVINTPGVLAPNDMK.L
64	85	3	2488.28	3.3	1	39.1	17.6	95.00%	K.AVSEHDLTISLIPYTYHATVMK.A		K.AVSEHDLTISLIPYTYHATVMK.A
68	85	3	2102.09	2.4	0	22.6	19.2	93.40%	E.HDLTISLIPYTYHATVMK.A		K.AVSEHDLTISLIPYTYHATVMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
39	PPA1_SCHPO	19.43%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
418	427	2	1194.64	4	0	44.5	18.5	95.00%	E.LYAYLNSPVR.V		R.HLVNEEVFPLSDCGFGPSNTSDGMCELYAYLNSPVR.V
40	59	3	2404.13	2.5	0	63.3	22.2	95.00%	R.SPYHKPYFYGPSIDFPTTCK.I	Carbamidomethyl (+57)	R.SPYHKPYFYGPSIDFPTTCK.I
260	270	2	1372.64	2.5	1	48.9	23.8	95.00%	E.IALQDYSEFCK.L	Carbamidomethyl (+57)	R.LNPYFSNYNLTNDDILNLYGICSYEIALQDYSEFCK.L
73	92	2	2047	4	0	100	22.1	95.00%	R.NPTGGNAAFDAVGIANFQQR.L		R.NPTGGNAAFDAVGIANFQQR.L
339	365	4	3018.43	3.4	1	22.7	21.9	95.00%	E.TALGFFTDNTPENPLPTSYQVHSHSMK.A		R.SVENNTQQVFFAFTHDANIIPVETALGFFTDNTPENPLPTSYQVHSHSMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
40	PDX1_SCHPO	22.97%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
71	83	2	1355.75	4.3	1	66.7	17.6	95.00%	K.EIQAAVSIPVMAK.V		K.EIQAAVSIPVMAK.V
38	49	2	1218.59	3	1	60.6	21.5	95.00%	E.AAGACAVMALER.V	Carbamidomethyl (+57)	R.IAEAAGACAVMALER.V
21	34	2	1457.74	4	1	89.6	20.6	95.00%	K.GGVIMDVVNAEQAR.I		K.GGVIMDVVNAEQAR.I
121	132	3	1383.7	4.4	1	31	21	95.00%	K.SKFTVPFVCGSR.N	Carbamidomethyl (+57)	K.SKFTVPFVCGSR.N
272	280	2	887.47	3.5	0	36.1	22.9	95.00%	E.NLGAAMVGR.S		K.ILAEVSENLGAAMVGR.S
13	20	2	830.47	4.2	0	38.8	20.1	95.00%	K.AGLAQMLK.G		K.AGLAQMLK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
41	HSP7M_SCHPO	20.47%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
366	376	2	1188.6	3.9	1	41.4	20.9	95.00%	R.ALKDANLQTSE.I		R.ALKDANLQTSEINEVILVGGMTR.M
204	215	2	1124.67	4.6	0	48.3	12.8	95.00%	K.AAGAIAGLNVLR.V		K.AAGAIAGLNVLR.V
322	337	2	1645.86	3.4	0	41.2	19.7	95.00%	K.TDISLPFITADATGPK.H		K.TDISLPFITADATGPK.H
465	480	2	1637.8	3.3	1	52.4	22.3	95.00%	R.KSQVFSTAADGQTAVE.I		R.KSQVFSTAADGQTAVEIR.V
105	118	2	1578.81	4.5	1	81.4	20.7	95.00%	R.QAVINPENTFFATK.R		R.QAVINPENTFFATK.R
185	199	2	1679.83	4.3	0	62.1	21.8	95.00%	K.NAVVTVPAYFNDSQR.Q		K.NAVVTVPAYFNDSQR.Q
496	510	2	1538.89	4.2	0	77.2	14	95.00%	K.LIGNFQLTGIAPAPK.G		K.LIGNFQLTGIAPAPK.G
380	388	2	944.55	3.4	0	24.8	17.6	90.00%	E.VILVGGMTR.M		K.DANLQTSEINEVILVGGMTR.M
157	170	2	1496.8	5.1	0	59.3	19.2	95.00%	K.TYSPSQIGGFILSK.M		K.TYSPSQIGGFILSK.M
216	231	2	1630.86	2.7	0	84.1	19.2	95.00%	R.VVNEPTAAALAYGLDK.K		R.VVNEPTAAALAYGLDK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
42	THIL_SCHPO	27.85%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
291	301	2	1160.65	4.8	0	33.2	18	95.00%	R.FTTSPSLAIPK.A		R.FTTSPSLAIPK.A
321	331	2	1105.62	3.2	0	39.6	17.9	95.00%	E.AFSVVAVANTK.I		K.HAGIEASQVDYYEINEAFSVVAVANTK.I
14	30	2	1654.81	3.5	0	82.9	21.8	95.00%	R.TPMGSFGGSFASLPATK.L		R.TPMGSFGGSFASLPATK.L
53	69	2	1772.91	5.5	0	58.9	19.5	95.00%	E.VFMGNVVSANLGQNPAR.Q		R.VNIKPSDVDEVFMGNVVSANLGQNPAR.Q
339	359	3	2023.01	2.9	1	25.4	21.2	95.00%	E.RVNINGGGVAMGHPLGSSGSR.I	Deamidation (+1)	K.ILGLDPERVNINGGGVAMGHPLGSSGSR.I

43	52	2	1114.55	3.3	0	25.4	21.1	91.10%	R.VNIKPSDVDE.V			R.VNIKPSDVDEVFMGNVVSANLGQNPAR.Q
43	69	3	2869.45	3.7	1	43	17.9	95.00%	R.VNIKPSDVDEVFMGNVVSANLGQNPAR.Q			R.VNIKPSDVDEVFMGNVVSANLGQNPAR.Q
119	129	2	1227.56	4.1	0	27.5	23	94.20%	E.SMSNAPYYAPK.N			K.ATILGAQTIMTGNAEIVVAGGTESMSNAPYYAPK.N
360	371	2	1405.81	4.5	0	73.2	14.5	95.00%	R.IICTLAYILAQK.D	Carbamidomethyl (+57)		R.IICTLAYILAQK.D
340	359	3	1865.93	4.8	0	31	22	95.00%	R.VNINGGGVAMGHPLGSSGSR.I			R.VNINGGGVAMGHPLGSSGSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
43	C1TC_SCHPO	12.27%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
689	707	3	1923.15	3.9	0	37.5	6.99	95.00%	R.TSGLKPDAIVIVATVQALK.L		R.TSGLKPDAIVIVATVQALK.L
2	12	2	1184.68	4.9	1	55.8	15.9	95.00%	M.ALLLEGTSLAR.K	Acetyl (+42)	-.MALLLEGTSLAR.K
749	760	2	1299.79	2.5	1	29.8	6.02	95.00%	R.KYGLPVVVAINK.F		R.KYGLPVVVAINK.F
776	792	2	1697.77	3.5	0	61.6	23.5	95.00%	E.ALAAGATDAVDSNHWAE.G		R.EEALAAGATDAVDSNHWAEGGK.G
324	336	2	1299.71	5.1	1	59.2	18.9	95.00%	K.NIGDLASEIGIAK.S		K.NIGDLASEIGIAK.S
381	396	2	1629.9	3.4	0	106	16.1	95.00%	K.STLTAGLVQALSNLDK.L		K.STLTAGLVQALSNLDK.L
77	84	2	947.57	3.5	0	34.9	14.3	95.00%	E.YDLLLAIK.G		R.AANEAGISCEHVNFPEDITEYDLLLAIK.G
817	827	2	1354.72	3.8	1	37	19.1	95.00%	R.LLYDVHEPIEK.K		R.LLYDVHEPIEK.K
349	356	2	983.58	5.3	1	46.2	14.6	95.00%	K.VNLEILQR.L		K.VNLEILQR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
44	ADH_SCHPO	38.29%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
257	278	3	2134.07	2.9	0	23.3	19.7	94.30%	E.QAAGFARPGSTMVTVSMPAGAK.L		K.SYEQAAGFARPGSTMVTVSMPAGAK.L
25	35	2	1168.53	5.4	1	25.2	23	90.70%	E.EVPVAEPGQDE.V		K.FEEVPVAEPGQDEVLVNIK.Y
236	253	2	1681.87	4.1	0	56	18.8	95.00%	K.AATNGGAHGTLVLSTSPK.S	Deamidation (+1)	K.AATNGGAHGTLVLSTSPK.S
254	278	3	2513.21	3.1	1	41.5	21.5	95.00%	K.SYEQAAGFARPGSTMVTVSMPAGAK.L		K.SYEQAAGFARPGSTMVTVSMPAGAK.L
170	194	3	2506.29	2.7	1	36.6	17.2	95.00%	K.VGPGEWICIPGAGGGLGHLAVQYAK.A	Carbamidomethyl (+57)	K.VGPGEWICIPGAGGGLGHLAVQYAK.A
150	163	2	1581.75	4.3	0	42.8	22.7	95.00%	E.VAAPIMCAGITCYR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.AEETICPHIQLSGYTVDGTFQHYCIANATHATIIPESVPLEVAAPIMCAGITCYR.A
42	62	3	2378.15	2.1	0	31.5	22.1	95.00%	K.YTGVCHTDLHALQGDWPLPAK.M	Carbamidomethyl (+57)	K.YTGVCHTDLHALQGDWPLPAK.M
200	211	2	1231.6	3.9	1	26.5	21.9	92.90%	R.VVAIDTGDDKAE.L		R.VVAIDTGDDKAELVK.S
63	70	2	852.42	3.4	0	28.2	21.8	94.90%	K.MPLIGGHE.G		K.MPLIGGHEGAGVVVK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
45	GBLP_SCHPO	38.22%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
156	172	2	1893.9	4.3	0	71.3	22.2	95.00%	R.FSPNPDNLTFVSAGWDK.A		R.FSPNPDNLTFVSAGWDK.A
13	36	3	2480.24	2.3	1	65.2	20.5	95.00%	E.GHSGWVTSLSTAPENPDILLSGSR.D		R.ATLEGHSGWVTSLSTAPENPDILLSGSR.D
270	280	2	1161.68	2.8	1	36.2	13.8	95.00%	E.LTVDFVGVGKK.S		K.VDELTVDFVGVGKK.S
48	57	2	1135.53	4.7	0	43.2	22.3	95.00%	R.DDVNYGVAQR.R		R.DDVNYGVAQR.R
186	212	3	2736.26	2.6	0	43.2	23.4	95.00%	R.TSHYGHTGYVSAVTISPDGSLCASGGR.D	Carbamidomethyl (+57)	R.TSHYGHTGYVSAVTISPDGSLCASGGR.D
234	245	2	1314.71	3.1	0	32.5	18.9	95.00%	K.ANINALVFSPNR.Y		K.ANINALVFSPNR.Y
176	185	2	1264.65	5.4	1	30.1	21.5	95.00%	K.VWDLETFSLR.T		K.VWDLETFSLR.T
39	47	2	1112.68	5.9	0	27.8	12.6	94.40%	K.SIILWNLVR.D		K.SIILWNLVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
46	PUT2_SCHPO	21.72%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
406	422	2	1852.92	4.3	1	57.5	21.4	95.00%	K.ADDSEGFFVEPTVLLSK.N		K.ADDSEGFFVEPTVLLSK.N
362	384	3	2428.26	2.6	0	29.8	17.2	95.00%	K.VGAPLTDFANFVGPVIHQASFNK.L		K.VGAPLTDFANFVGPVIHQASFNK.L
254	274	3	2393.15	4.4	1	52.3	22	95.00%	K.VCFNHPEFAGLHFTGSTAVFR.S	Carbamidomethyl (+57)	K.VCFNHPEFAGLHFTGSTAVFR.S
275	288	2	1444.74	4.6	1	37.7	21	95.00%	R.SLWGTIGENVANGK.Y		R.SLWGTIGENVANGK.Y
495	509	2	1504.71	3.5	1	49.3	22	95.00%	K.CTGAVVGEQPFGGAR.A	Carbamidomethyl (+57)	K.CTGAVVGEQPFGGAR.A
531	548	2	2036.98	5	1	47.4	22	95.00%	R.SIKDTFAYADSVLYPSNF.-		R.SIKDTFAYADSVLYPSNF.-
484	494	2	1225.58	4.6	0	28	22.7	94.70%	R.NAAGNFYINDK.C		R.NAAGNFYINDK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
47	CYSD_SCHPO	41.03%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
77	100	3	2290.21	3.4	0	23.4	16.6	94.40%	E.HGAAAIATSSGTSALFMALTTLAK.A		R.IAALEHGAAAIATSSGTSALFMALTTLAK.A
132	147	2	1731.76	1.9	0	26.1	24.6	92.30%	K.FVNGDDPNDLAAQIDE.N		K.FVNGDDPNDLAAQIDENTK.A
47	59	2	1541.79	3.4	0	41.8	19.3	95.00%	R.LFGLQEPGYIYSR.M		R.LFGLQEPGYIYSR.M
27	39	2	1486.79	3.4	0	44.8	18.1	95.00%	R.AVPIYATTSYVFR.D		R.AVPIYATTSYVFR.D
378	395	2	2014.03	2.6	1	27.1	19.9	93.70%	K.TLVIAPAYTTHLQLTDEE.Q		K.TLVIAPAYTTHLQLTDEEQISAGVTK.D
72	100	3	2787.49	3.3	1	49.9	14.9	95.00%	R.IAALEHGAAAIATSSGTSALFMALTTLAK.A		R.IAALEHGAAAIATSSGTSALFMALTTLAK.A
156	169	2	1637.76	2.5	1	65.7	23.4	95.00%	E.SIGNPMYNVPDFER.I		K.AVYVESIGNPMYNVPDFER.I
10	26	2	1780.88	3.9	0	38.9	21.8	95.00%	E.TLQLHAGQEPDAATSSR.A		-.MPVESEHFETLQLHAGQEPDAATSSR.A
366	377	2	1185.64	4.4	0	34.5	17.8	95.00%	K.LASQLANVGDAK.T		K.LASQLANVGDAK.T
170	210	4	4156.13	4.3	1	53.9	16.1	95.00%	R.IAEVAHAAGVPLMVDNTFGGGGYLVRPIDHGADIVTHSATK.W		R.IAEVAHAAGVPLMVDNTFGGGGYLVRPIDHGADIVTHSATK.W
132	150	2	2074.95	4.2	1	127	23.3	95.00%	K.FVNGDDPNDLAAQIDENTK.A		K.FVNGDDPNDLAAQIDENTK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
48	RL4A_SCHPO	32.23%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
122	140	2	1845.04	4.3	0	48.1	11.1	95.00%	R.YAISSAVAASGVPSLLLAR.G		R.YAISSAVAASGVPSLLLAR.G
147	163	2	1883.01	3.2	1	69	17.6	95.00%	E.IPEVPLVVDDAVQSFQK.T		R.IEEIPEVPLVVDDAVQSFQK.T
2	13	2	1304.71	4.5	0	25.5	17.9	91.30%	M.AAARPTVSIYSK.D	Acetyl (+42)	-.MAAARPTVSIYSK.D
235	248	3	1457.85	3	0	51.8	13	95.00%	R.LNLLQLAPGGHLGR.F		R.LNLLQLAPGGHLGR.F
282	291	2	1101.58	3.2	0	54.2	20.2	95.00%	E.NIISNADVTR.L		K.NYFLPENIISNADVTR.L
292	303	2	1357.75	4	1	43.8	18.1	95.00%	R.LINSDEIQSIVK.A		R.LINSDEIQSIVK.A
14	29	2	1695.88	4.2	1	38.3	19.4	95.00%	K.DGSVSSETIALPFVFK.A		K.DGSVSSETIALPFVFK.A
276	291	2	1864.94	4.5	1	39	21.7	95.00%	K.NYFLPENIISNADVTR.L		K.NYFLPENIISNADVTR.L
87	97	2	1197.51	4.4	0	32.6	22.8	95.00%	R.SGQAAFGNMCR.S	Carbamidomethyl (+57)	R.SGQAAFGNMCR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
49	EF1B_SCHPO	38.32%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
14	26	2	1580.81	3.4	1	32.2	20.2	95.00%	K.QLNDFLLDKSFIE.G		K.QLNDFLLDKSFIEGYEPSQADAVVFK.A
14	22	2	1104.59	4.8	0	36.2	19.8	95.00%	K.QLNDFLLDK.S		K.QLNDFLLDK.S
40	55	2	1586.81	3.9	1	29.7	21.1	95.00%	K.AVGVAPDTAKYPNGAR.W	Deamidation (+1)	K.AVGVAPDTAKYPNGAR.W
59	73	2	1561.84	4.2	0	60.9	18.5	95.00%	K.QIATYDLATLPGTAK.E		K.QIATYDLATLPGTAK.E
153	165	2	1432.74	3.9	0	44.3	20.2	95.00%	R.SIQMDGLVWGLSK.L		R.SIQMDGLVWGLSK.L
2	13	2	1209.59	3.7	0	57.4	22.5	95.00%	M.GFSDLTSDAGLK.Q		-.MGFSDLTSDAGLK.Q
23	39	2	1885.92	3.6	1	50.9	22.2	95.00%	K.SFIEGYEPSQADAVVFK.A		K.SFIEGYEPSQADAVVFK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
50	IF4A_SCHPO	17.60%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
58	69	2	1173.61	5	0	69	21.1	95.00%	R.DVLAQAQSGTGK.T		R.DVLAQAQSGTGK.T
33	48	2	1854.94	3.8	1	30.4	21.1	95.00%	R.GIYAYGFERPSAIQQR.A		R.GIYAYGFERPSAIQQR.A
12	29	2	2157.95	2.7	1	71.2	24.2	95.00%	E.TNYDEVIDTFDDMNLKPE.L		-.MVDQLEDSVIETNYDEVIDTFDDMNLKPELLR.G
255	268	2	1608.83	3.2	0	44.1	19.3	95.00%	E.TVTVTQAVIFCNTR.R	Carbamidomethyl (+57)	K.LDTLCDLYETVTVTQAVIFCNTR.R
17	29	2	1535.72	2.6	0	36.8	22.8	95.00%	E.VIDTFDDMNLKPE.L		-.MVDQLEDSVIETNYDEVIDTFDDMNLKPELLR.G
384	392	2	1016.51	3.1	0	28.8	21.9	95.00%	E.MPMNIADLI.-		R.EIEQFYNTHIEEMPMNIADLI.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
51	DHAS_SCHPO	32.21%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
19	28	2	1170.59	1.7	0	28	20.7	94.60%	R.FITLLSDHPE.F		R.FITLLSDHPEFK.I
229	240	2	1375.66	3.4	0	48.3	22.5	95.00%	E.LTDNVVSAQCNR.V	Carbamidomethyl (+57)	K.ILGSVNSTISGYELTDNVVSAQCNR.V
112	132	3	2341.31	2.7	1	53.3	9.54	95.00%	R.REPTVPLVVPTVNTDHLDVIK.Y		R.REPTVPLVVPTVNTDHLDVIK.Y
31	39	2	856.52	4.9	0	28.2	16.9	94.90%	K.IAVLGASAR.S		K.IAVLGASAR.S
287	303	3	2003.98	4.2	0	33.9	22.1	95.00%	K.QAIYVFDDSTPDRPQPR.L		K.QAIYVFDDSTPDRPQPR.L
19	30	3	1445.76	4.9	1	23.3	20.3	94.20%	R.FITLLSDHPEFK.I		R.FITLLSDHPEFK.I
143	161	2	2003.03	3.7	0	71.4	20.5	95.00%	R.GCIITNSNCSTAAVVVPLK.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GCIITNSNCSTAAVVVPLK.A
267	278	2	1375.7	3.8	1	37.2	21.1	95.00%	R.EVLANYVSEPQK.L		R.EVLANYVSEPQK.L
6	18	2	1227.7	3.7	0	35.6	17.2	95.00%	K.VGILGATGTVGQR.F		K.VGILGATGTVGQR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
52	CARB_SCHPO	10.17%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
730	744	2	1630.79	2.5	1	66.8	21.8	95.00%	K.VLGTDPLMIDSAEDR.H		K.VLGTDPLMIDSAEDR.H
968	975	2	1019.52	4.9	0	24.9	20	90.20%	K.VPQFSWTR.L		K.VPQFSWTR.L
932	943	2	1304.72	5.6	0	35.2	17.9	95.00%	K.TLGVNFIDVATR.S		K.TLGVNFIDVATR.S
1016	1031	2	1630.91	2.7	0	79	15.9	95.00%	K.IPLPGQGILLGGDRPE.L		K.IPLPGQGILLGGDRPELAGIAADLSK.L
773	798	3	2736.49	2.9	0	51	14.1	95.00%	K.FANAVGYPVLVRPSYVLSGAAMSVIR.D		K.FANAVGYPVLVRPSYVLSGAAMSVIR.D
418	433	2	1784.89	3.7	0	45.1	21.1	95.00%	K.TTTANFEPSLDYVVTK.I		K.TTTANFEPSLDYVVTK.I
575	584	2	1057.58	4.7	1	32.1	19.7	95.00%	K.LVGASELDVR.A		K.LVGASELDVR.A
809	823	2	1533.82	3.3	0	40	18.8	95.00%	E.NASAVSPDHPVVITK.F		K.LENASAVSPDHPVVITK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
53	OAT_SCHPO	20.78%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
386	398	3	1374.82	4.6	0	23.2	11.8	94.10%	R.GVLAKPTHGNIIR.F		R.GVLAKPTHGNIIR.F
154	167	2	1493.69	4.9	0	59.2	23.2	95.00%	R.TMGIISMSTDPDAR.D		R.TMGIISMSTDPDAR.D
141	153	2	1500.76	2.8	0	51.5	21	95.00%	E.AIILSCVDNFHGR.T	Carbamidomethyl (+57)	K.IPTDEAIILSCVDNFHGR.T
276	291	2	1561.85	4	0	53	16.7	95.00%	K.AISGGVYPVSAVLSSR.E		K.AISGGVYPVSAVLSSR.E
238	254	2	1838.97	4.4	1	78.8	18.6	95.00%	K.AHNVLFIADEVQTGVAR.T		K.AHNVLFIADEVQTGVAR.T
258	275	3	2051.1	4.3	1	30.2	15.9	95.00%	K.MLCIEHSNVKPDVVILGK.A	Carbamidomethyl (+57)	K.MLCIEHSNVKPDVVILGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
54	STI1_SCHPO	23.52%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
214	229	2	1577.73	5.9	0	42.9	23.1	95.00%	E.FAPSSSTPSADSAKPE.T		K.EEFAPSSSTPSADSAKPETTNPPPQPQASEPMEEDK.T
543	560	2	1893.06	2.9	0	54.7	13	95.00%	E.VLGILQDPAMQAILGQAR.E		K.DPEVLGILQDPAMQAILGQAR.E

115	132	2	1692.83	2.6	0	67.5	22.8	95.00%	E.AAQTQAASGAGGFNPFAK.L		K.SVEAAQTQAASGAGGFNPFAK.L
146	164	2	1935.97	6.4	1	78.1	21.2	95.00%	K.LASNPETASLLADSAFMAK.L		K.LASNPETASLLADSAFMAK.L
76	90	3	1463.79	4.4	1	44.6	18.6	95.00%	R.KGAALHGLGDLDAAR.S		R.KGAALHGLGDLDAAR.S
112	132	2	2007.97	4.2	1	89.9	22.1	95.00%	K.SVEAAQTQAASGAGGFNPFAK.L		K.SVEAAQTQAASGAGGFNPFAK.L
168	183	2	1781.88	4.3	1	66.6	21.6	95.00%	K.IQQNPGSIMAELNDPR.M		K.IQQNPGSIMAELNDPR.M
20	34	2	1711.85	3.9	1	70.3	21.7	95.00%	K.TAIDYFTQAIGLDER.N		K.TAIDYFTQAIGLDER.N
371	377	2	800.44	3.8	0	29.8	21.2	95.00%	R.TPDILSR.L		R.TPDILSR.L
311	322	2	1466.61	3	1	25.6	23.5	91.50%	E.ADQLDDCIKTCE.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.DITYLNNLAAAYFEADQLDDCIKTCEDAIEQGR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
55	UGPA1_SCHPO	22.13%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
494	506	2	1495.75	2.6	1	57.8	21.4	95.00%	E.NCVITGNLNILEH.-	Carbamidomethyl (+57)	R.IDIPNGSVLENCVITGNLNILEH.-
1	10	2	1166.63	4.6	0	24.9	18.5	90.10%	-.MDLAPRPLGR.Q	Acetyl (+42)	-.MDLAPRPLGR.Q
201	216	2	1706.84	2.4	1	25.4	22.3	91.20%	K.ETLLPVPHTADSAIDE.W		K.ETLLPVPHTADSAIDEWYPPGHGDVFEALTNSGIIDTLIAQGK.E
15	34	2	2047.96	2.6	0	135	23.2	95.00%	K.SQSAFAFDNTATSIAASTMK.N		K.SQSAFAFDNTATSIAASTMK.N
202	216	2	1577.8	4.5	0	33.1	21.6	95.00%	E.TLLPVPHTADSAIDE.W		K.ETLLPVPHTADSAIDEWYPPGHGDVFEALTNSGIIDTLIAQGK.E
185	194	2	1205.65	4.7	0	32.1	19.1	95.00%	K.IDILTFNQSR.Y		K.IDILTFNQSR.Y
228	243	2	1613.91	4.3	0	38	15.1	95.00%	E.ALTNSGIIDTLIAQGK.E		K.ETLLPVPHTADSAIDEWYPPGHGDVFEALTNSGIIDTLIAQGK.E
115	129	2	1460.72	4.2	0	48.3	21.8	95.00%	K.LNGGLGTTMGCVGPK.S	Carbamidomethyl (+57)	K.LNGGLGTTMGCVGPK.S
287	298	2	1278.63	4.4	0	55.1	21.4	95.00%	K.GGTLIDYDGNVR.L		K.GGTLIDYDGNVR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
56	RS18_SCHPO	29.61%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	78	2	1386.79	4	0	45.2	15.7	95.00%	R.IVTIIQNPSQFK.I		R.IVTIIQNPSQFK.I
2	14	2	1578.86	2.4	0	36.1	16	95.00%	M.SLVVPDNFQHILR.L	Acetyl (+42)	-.MSLVVPDNFQHILR.L
79	86	2	1031.56	6	0	52.6	18.7	95.00%	K.IPSWFLNR.Q		K.IPSWFLNR.Q
95	106	2	1334.69	4.9	0	24.9	20.3	90.20%	K.SFQLLANNVDSK.L		K.SFQLLANNVDSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
57	MET3_SCHPO	16.33%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
427	440	2	1651.86	4	1	77.5	19.6	95.00%	R.LDAISVFYAQELQR.A		R.LDAISVFYAQELQR.A
42	58	2	1850.93	2	0	72.1	20.8	95.00%	E.LILNGGFSPLDGFMNQK.D	Deamidation (+1)	R.QFCDVELILNGGFSPLDGFMNQK.D
350	359	2	1102.6	3.9	1	29.9	19.2	95.00%	R.TLNISGTELR.R		R.TLNISGTELR.R
59	68	2	1233.64	5.6	1	40.5	20.6	95.00%	K.DYLNVVENLR.L		K.DYLNVVENLR.L
254	262	2	1012.62	5.1	0	33.5	12.6	95.00%	K.LSLLPLAMR.M		K.LSLLPLAMR.M
217	236	4	2231.2	3.6	0	31	13.4	95.00%	R.VLIHPVVGMTKPGDIDHFTR.V		R.VLIHPVVGMTKPGDIDHFTR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
58	HOSM_SCHPO	20.10%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
242	257	2	1609.85	4.5	1	28.1	17.9	94.70%	E.AGATHIDTSILGIGER.N		R.GVVSCDIECHFHNDTGMAIANAYCALEAGATHIDTSILGIGER.N
192	204	2	1315.66	4	0	40.8	22	95.00%	R.VGIADTVGCATPR.Q	Carbamidomethyl (+57)	R.VGIADTVGCATPR.Q
11	31	3	2302.11	1.5	0	48.5	21.5	95.00%	E.TIKPPMNGNPYGPNPSDFLSR.V	Deamidation (+1)	-.MSVSEANGTETIKPPMNGNPYGPNPSDFLSR.V
172	182	2	1264.7	4.6	0	43.4	17.3	95.00%	R.SDLVDLLSLYK.A		R.SDLVDLLSLYK.A
401	411	2	1290.55	4.4	1	41	23	95.00%	R.EYHADLSDADR.I		R.EYHADLSDADR.I
32	43	2	1391.75	4.9	1	68.1	19	95.00%	R.VNNFSIIESTLR.E		R.VNNFSIIESTLR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
59	YHY6_SCHPO	12.29%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
161	187	3	2608.39	2.9	0	26.8	15.6	95.00%	K.SVGVNPIIVDFSAPGSATAPSKPAAQK.K		K.SVGVNPIIVDFSAPGSATAPSKPAAQK.K
303	314	2	1339.7	3	0	53.2	20.3	95.00%	E.LDEPIAIRPTSE.T		R.AGTSELDEPIAIRPTSETVMYPYYAK.W
161	188	4	2736.49	3.7	1	29.1	14	95.00%	K.SVGVNPIIVDFSAPGSATAPSKPAAQKK.K		K.SVGVNPIIVDFSAPGSATAPSKPAAQKK.K
492	511	2	2075.19	4.8	0	44	8.45	95.00%	K.LPPAIALVQSVVVPCGITNK.T	Carbamidomethyl (+57)	K.LPPAIALVQSVVVPCGITNK.T
387	398	2	1343.81	4.3	0	30.5	9.03	95.00%	R.IYTDLLAVPVIK.G		R.IYTDLLAVPVIK.G
426	441	3	1703.81	4.5	0	20.8	22.5	90.00%	R.GIQGATSHCLGQNFSK.M	Carbamidomethyl (+57)	R.GIQGATSHCLGQNFSK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
60	FAS1_SCHPO	4.73%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1870	1881	2	1266.57	5.2	0	37.8	23	95.00%	R.SDYGMVAANPSR.V		R.SDYGMVAANPSR.V
971	984	2	1619.76	2.7	1	48.2	22.9	95.00%	E.NFEDLNDPYPVAAR.F		K.TTLIENFEDLNDPYPVAAR.F
1676	1692	2	1824.86	3.9	1	52.4	23.4	95.00%	E.VEQPVSAYVFTGQGSQE.Q		K.VEVLNQETSEPVLVGTAEVEQPVSAYVFTGQGSQEQGMGMDLYASSPVAR.K
1778	1806	3	3141.54	1.9	1	40.3	20.5	95.00%	K.DSTSFSFTHPSGLLSATQFTQPALTLMEK.S		K.DSTSFSFTHPSGLLSATQFTQPALTLMEK.S
781	794	2	1545.81	3.9	0	42.1	20	95.00%	K.LPPMPFDGILFGSR.L		K.LPPMPFDGILFGSR.L
1041	1052	2	1199.62	3.4	1	42.6	19.2	95.00%	E.DLAAVVGEDVGR.V		K.DSLWQSEDLAAVVGEDVGR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
61	HXK1_SCHPO	12.40%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
231	246	2	1800.86	2.7	1	34.9	22.2	95.00%	E.IGVIFGTGCNACYIEK.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.LNAILSDTTGTLVASNYASPGTEIGVIFGTGCNACYIEK.F
304	315	2	1380.7	5.1	0	25.3	21	90.90%	K.MIAGCYLGDILR.R	Carbamidomethyl (+57)	K.MIAGCYLGDILR.R
2	12	3	1409.65	4.4	0	25.1	22.2	95.00%	M.SLHDAYHWPSR.T	Acetyl (+42)	-.MSLHDAYHWPSR.T
406	426	3	2369.2	3.6	1	22.8	20.3	93.60%	R.KMNKPSMIVGTDGSVYNLYPR.F		R.KMNKPSMIVGTDGSVYNLYPR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
62	ILV3_SCHPO	17.56%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
247	265	2	1882.89	3.2	1	53.8	23	95.00%	E.AMGMTLPGSSSYLAGSPEK.F		R.HACPGGGACGGMYTANTMASCAEAMGMTLPGSSSYLAGSPEK.F
372	384	2	1273.69	2.7	0	48.8	19.5	95.00%	E.GLIDGSNITVTGK.T		K.YLHAEGLIDGSNITVTGK.T
40	48	2	994.5	5.2	1	30.6	22.5	95.00%	K.YSETITGPK.S		K.YSETITGPK.S
141	159	2	2167.98	3.9	0	56.4	23.9	95.00%	E.TVMQGQWYDANVSIPGCDK.N	Carbamidomethyl (+57)	R.EIIADSIETVMQGQWYDANVSIPGCDK.N
526	542	2	1679.88	2.4	0	32.1	19.4	95.00%	E.AQVGGPIALVQDGDVIE.I		R.FSGGSHGFLIGHVDPEAQVGGPIALVQDGDVIEINAVK.N
185	212	3	3007.42	3.5	1	69.2	22.3	95.00%	R.AGHSPCQNNAPIDIVSAFQSYGEFITGK.I	Carbamidomethyl (+57)	R.AGHSPCQNNAPIDIVSAFQSYGEFITGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
63	GCSP_SCHPO	15.14%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
953	965	2	1458.76	1.1	0	43.1	19.1	95.00%	K.DNNLLVNAPHPQK.D		K.DNNLLVNAPHPQK.D
464	476	2	1412.68	3.3	1	39.2	22.2	95.00%	R.KVDDSHVGLSLDE.T		R.KVDDSHVGLSLDETVCDK.D
657	684	3	2835.49	3.7	0	27.8	14.9	95.00%	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C	Carbamidomethyl (+57)	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C

114	126	2	1433.73	3.1	0	62	21.4	95.00%	E.FTTLANNVANQNK.L			K.NPPVNYSESEFTTLANNVANQNK.L
790	806	3	1819.91	2	0	21.1	21.2	90.60%	K.HLADFLPSHPVVSCGGK.N	Carbamidomethyl (+57)		K.HLADFLPSHPVVSCGGK.N
379	412	3	3679.8	2.3	1	51.4	19.4	95.00%	K.ATSNICTAQALLANMSAFYAIYHGPNGLQEIANR.I	Carbamidomethyl (+57)		K.ATSNICTAQALLANMSAFYAIYHGPNGLQEIANR.I
1000	1017	2	2072.93	3.3	1	54	23.4	95.00%	R.LDDAYGDKNLFCTCSPVV.-	Carbamidomethyl (+57)/ Carbamidomethyl (+57)		R.LDDAYGDKNLFCTCSPVV.-
583	600	2	2083.03	2	0	30.8	20.5	95.00%	E.MMPITNPLFANIHPYVPE.E			K.LNAVTEMMPITNPLFANIHPYVPEEQAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
64	RS6B_SCHPO	19.67%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	115	2	1739.01	3.8	0	65.7	12.3	95.00%	R.GCIVGQDLAVLALAIVK.Q	Carbamidomethyl (+57)	R.GCIVGQDLAVLALAIVK.Q
116	131	2	1695.88	3.9	1	43.6	19.3	95.00%	K.QGEQDIPGLTDVTVPK.R		K.QGEQDIPGLTDVTVPK.R
59	72	3	1625.86	4.7	0	32.2	19.7	95.00%	K.QGFPMFQGVLLPHR.V		K.QGFPMFQGVLLPHR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
65	IF5A1_SCHPO	28.66%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
14	28	2	1608.78	2.6	0	41.7	22.2	95.00%	E.AGASLTFPMQCSALR.K	Carbamidomethyl (+57)	-.MAEEEHVDFEGGEAGASLTFPMQCSALR.K
11	28	2	1851.87	3.1	1	43.6	22.9	95.00%	E.GGEAGASLTFPMQCSALR.K	Carbamidomethyl (+57)	-.MAEEEHVDFEGGEAGASLTFPMQCSALR.K
73	87	2	1655.77	3.1	0	36.4	23.1	95.00%	E.DMSPSTHNMDVPVVK.R		K.YEDMSPSTHNMDVPVVK.R
58	69	2	1352.76	3.7	0	43.9	15.7	95.00%	K.VHIVALDIFNGR.K		K.VHIVALDIFNGR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
66	SPI1_SCHPO	23.15%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
203	216	2	1442.63	4.4	1	35.2	23.2	95.00%	E.AAAMPLPDEDDADL.-		K.LVGNPNLEFVASPALAPPEVQVDQQLLAQYQQEMNEAAAMPLPDEDDADL.-
110	122	2	1514.77	4.6	1	58.5	21	95.00%	R.VCENIPIVLCGNK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VCENIPIVLCGNK.V
152	165	3	1783.91	4.6	1	29.2	20.2	95.00%	K.SNYNFEKPFLWLAR.K		K.SNYNFEKPFLWLAR.K
166	174	2	982.55	4.9	1	27.3	16.7	93.90%	R.KLVGNPNLE.F		R.KLVGNPNLEFVASPALAPPEVQVDQQLLAQYQQEMNEAAAMPLPDEDDADL.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
67	ACON_SCHPO	10.93%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
435	452	2	1870.92	2.4	0	57.3	21.7	95.00%	K.AGGIVLANACGPCIGQWK.R	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.AGGIVLANACGPCIGQWK.R
532	549	2	1853.89	4.6	0	68.9	22	95.00%	K.GYDPGSNTYVAPSSVNVK.D		K.GYDPGSNTYVAPSSVNVK.D
392	402	2	1203.6	5.2	0	35.2	21.6	95.00%	R.AASICQQAIDK.G	Carbamidomethyl (+57)	R.AASICQQAIDK.G
65	80	3	1895.95	4.5	1	26.2	21.6	95.00%	K.ILYGHLDDPVNQDIER.G		K.ILYGHLDDPVNQDIER.G
462	470	2	1052.53	5	0	36.5	21.1	95.00%	K.NSIVTSYNR.N		K.NSIVTSYNR.N
286	298	2	1419.76	4.1	0	59.4	18.7	95.00%	E.IGATTSIFPFNPR.M		K.GGTGAIVEYFGPGVESLSCTGMGTICNMGAEIGATTSIFPFNPR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
68	YF19_SCHPO	22.07%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
122	132	2	1208.53	4.1	0	34.4	22.5	95.00%	R.GDVQAAADCFR.Y	Carbamidomethyl (+57)	R.GDVQAAADCFR.Y
195	208	2	1516.82	4.7	1	34.9	18	95.00%	K.TAELTPLSALCLTK.F	Carbamidomethyl (+57)	K.TAELTPLSALCLTK.F

333	349	2	1794.85	2.9	1	66	23.1	95.00%	K.VGDPFAEDTFQGAQVSK.Q		K.VGDPFAEDTFQGAQVSK.Q
5	17	2	1406.78	4.6	1	33	15.7	95.00%	K.LVDHVEITVPTGK.T		K.LVDHVEITVPTGK.T
402	411	2	1055.68	5.5	0	30.5	11.1	95.00%	E.IFGPVLAVIK.F		K.EEIFGPVLAVIK.F
422	443	3	2229.12	4.1	0	21.2	20.4	90.80%	R.GNNSTYGLAAGVHTNNITNAIK.V		R.GNNSTYGLAAGVHTNNITNAIK.V
71	80	2	1161.56	3.7	0	28.3	22.2	95.00%	R.AAFQTDAPWR.K		R.AAFQTDAPWR.K
181	194	2	1439.82	3.6	0	42.9	14.8	95.00%	K.IAPAVACGNTIILK.T	Carbamidomethyl (+57)	K.IAPAVACGNTIILK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
69	GLNA_SCHPO	28.69%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
60	91	3	3497.64	3.1	0	54.8	22	95.00%	R.VWNFDGSSTGQAPGNNSDTLLKPVAMYNDPFR.R		R.VWNFDGSSTGQAPGNNSDTLLKPVAMYNDPFR.R
338	354	2	1830.98	3.4	0	57.7	17.2	95.00%	R.RPASSIDPYLVTGIITE.T		R.RPASSIDPYLVTGIITETMFEH.-
153	170	2	1809.83	4.4	0	40.7	23.2	95.00%	K.GGFPGPQGPFYCGVGTGR.V	Carbamidomethyl (+57)	K.GGFPGPQGPFYCGVGTGR.V
237	260	4	2635.31	3.2	0	28.9	20.3	95.00%	K.ISFHPKPILGDWNGAGCHTNVSTK.D	Carbamidomethyl (+57)	K.ISFHPKPILGDWNGAGCHTNVSTK.D
285	296	2	1386.66	2.9	0	45.9	21.9	95.00%	E.HIAVYGDDNDLR.L		K.EHIAVYGDDNDLR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
70	RL8_SCHPO	25.48%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
211	225	2	1491.8	2.3	0	59.2	19.1	95.00%	E.LASIVSAVDANFSAK.Y		K.NELASIVSAVDANFSAK.Y
24	32	2	1084.62	4.7	0	29.3	18.1	95.00%	K.NPLFVSRPR.S		K.NPLFVSRPR.S
33	43	2	1188.62	4.1	0	26.8	20.2	93.20%	R.SFGIGQDIQPK.R		R.SFGIGQDIQPK.R
81	92	2	1364.74	3.7	1	46.2	20	95.00%	K.TLDKNTATQVFK.L		K.TLDKNTATQVFK.L
134	146	2	1425.8	4.3	1	45.6	14.9	95.00%	K.YGLNHVVALIEAK.K		K.YGLNHVVALIEAK.K
52	57	2	862.44	5.9	1	26.5	20.6	92.90%	K.WPEYIR.L		K.WPEYIR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
71	TAL1_SCHPO	16.15%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
27	44	2	1917.03	2.7	0	76.1	17.2	95.00%	K.YKPQDATTNPSLILAASK.K		K.YKPQDATTNPSLILAASK.K
9	26	2	1795.89	4.5	1	86.8	21.4	95.00%	K.ATGTVVVSDTGDFESIAK.Y		K.ATGTVVVSDTGDFESIAK.Y
45	60	2	1721.9	2.5	0	84.9	18.3	95.00%	K.KPQYAALVDAAVDYAK.A		K.KPQYAALVDAAVDYAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
72	AROG_SCHPO	24.73%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
199	226	3	2704.36	2.1	0	47.7	19.4	95.00%	K.NGTDGTVGVAIDAIGATAHPHTMLGVTK.Q	Deamidation (+1)	K.NGTDGTVGVAIDAIGATAHPHTMLGVTK.Q
350	363	2	1528.76	3.2	1	35.2	21.8	95.00%	E.QTAPMLDDLAEAVR.A		K.YGVSITDACVSWEQTAPMLDDLAEAVR.A
187	198	2	1235.7	3.2	0	37.1	16	95.00%	E.LASALSFPVGFK.N		R.ELASALSFPVGFK.N
118	133	2	1672.85	4.2	0	37.9	20.1	95.00%	K.GLVNDPNLDGSFAINK.G		K.GLVNDPNLDGSFAINK.G
22	42	2	2235.22	3.7	1	32.5	13.6	95.00%	R.VLGYNPLVPAALVQQEIPVSE.T		R.VLGYNPLVPAALVQQEIPVSETSR.K
186	198	2	1364.74	3.2	1	44	19.4	95.00%	R.ELASALSFPVGFK.N		R.ELASALSFPVGFK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
73	LYS12_SCHPO	23.20%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
197	208	2	1324.65	5.3	0	41.8	22.1	95.00%	K.SNVMSVTDGLFR.E		K.SNVMSVTDGLFR.E
298	307	2	1044.58	4.6	0	32.2	19.6	95.00%	R.GIANPVATFR.S		R.GIANPVATFR.S
315	331	3	1851.85	1.9	0	27	23.2	95.00%	E.FMGHQDAAADIYTAVDK.V		R.SVALMLEFMGHQDAAADIYTAVDK.V
188	196	3	1047.69	4.7	0	25.1	3.01	95.00%	K.KPLVTIIHK.S		K.KPLVTIIHK.S
86	97	2	1231.7	4.7	0	25.9	15.2	92.00%	K.VAGYSSPIVALR.K		K.VAGYSSPIVALR.K
352	362	2	1179.63	3.2	0	34.2	19.5	95.00%	E.ITDAVLANIHN.-		K.SGTNEITDAVLANIHN.-

7	19	2	1264.78	2.4	0	32.2	8.45	95.00%	R.IVLGLIPADGIGK.E		R.IVLGLIPADGIGK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
74	CDC48_SCHPO	13.01%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
221	230	2	1110.48	4.3	0	28.4	22.1	95.00%	E.VGYDDIGGCR.R	Carbamidomethyl (+57)	R.EDEESSLAEVGYDDIGGCR.R
550	563	2	1522.75	3.6	1	43.8	21.2	95.00%	K.AIANECSANFISVK.G	Carbamidomethyl (+57)	K.AIANECSANFISVK.G
588	604	2	1817.93	4.3	1	57.6	20.9	95.00%	R.AAAPCVVFLDELDSIAK.A	Carbamidomethyl (+57)	R.AAAPCVVFLDELDSIAK.A
116	129	2	1553.82	3.7	0	42.7	18.3	95.00%	R.LGDIVTINPCPDIK.Y	Carbamidomethyl (+57)	R.LGDIVTINPCPDIK.Y
359	379	3	2280.22	4.2	1	31.5	16.8	95.00%	R.SNVVVMAATNRPNSIDPALRR.F		R.SNVVVMAATNRPNSIDPALRR.F
316	332	2	1841.99	4.4	1	39.8	17.9	95.00%	K.NSPAIIFIDEIDSIAPK.R		K.NSPAIIFIDEIDSIAPK.R
461	473	2	1465.73	2.9	0	77.6	22.1	95.00%	E.VLDSLGVTMDNFR.F		K.MDMIDLDEDEIDAEVLDSLGVTMDNFR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
75	YL8C_SCHPO	24.42%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
217	232	2	1745.96	4.4	1	53	15.1	95.00%	K.GTALQYITSNILPEVK.N		K.GTALQYITSNILPEVK.N
7	33	4	3045.57	3.9	1	29.7	16.9	95.00%	K.TNNLPTLDTLQMVISDVDGTLLDKHHR.F		K.TNNLPTLDTLQMVISDVDGTLLDKHHR.F
70	90	3	2326.19	3.3	0	38.3	19.8	95.00%	R.IPLDLDAFPAAHVNGCVLYNK.G	Carbamidomethyl (+57)	R.IPLDLDAFPAAHVNGCVLYNK.G
93	102	2	1183.63	3	0	26.1	18.6	92.30%	K.IVYADHLKPE.V		K.IVYADHLKPEVVMEVVEATK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
76	VIPI_SCHPO	33.07%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
69	94	2	2433.11	4.4	1	121	23.3	95.00%	K.IQITSEDGGAASTTDQGGAGGDQAAR.Q		K.IQITSEDGGAASTTDQGGAGGDQAAR.Q
55	68	2	1496.86	2.7	0	61	14.6	95.00%	K.TALLLQDALLGQNK.I		K.TALLLQDALLGQNK.I
101	110	2	1087.63	5.8	1	34.3	15.9	95.00%	R.SAIISELLSR.G		R.SAIISELLSR.G
122	134	2	1410.71	4.2	0	61.1	21.2	95.00%	K.SIQLDQSYGVSSK.F		K.SIQLDQSYGVSSK.F
111	121	2	1260.64	3.7	1	31.8	20.5	95.00%	R.GYHLSDVTLEK.S		R.GYHLSDVTLEK.S
137	147	2	1100.62	4.3	1	27.7	18.4	94.40%	K.GILESALSGVR.S		K.GILESALSGVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
77	RL3A_SCHPO	16.75%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
214	222	2	1002.56	3.1	0	28.5	19.4	95.00%	E.MIDVIGVTR.G		K.STFEQNEMIDVIGVTR.G
11	19	2	982.54	4.3	0	27.2	18.1	93.70%	R.HGSLGFLPR.K		R.HGSLGFLPR.K
181	193	2	1315.67	3.2	1	41	21.4	95.00%	E.IQVNGGSVADKVE.W	Deamidation (+1)	K.AHLMEIQVNGGSVADKVEWAR.E
319	334	2	1715.87	2.9	1	30	21.1	95.00%	E.NDFVMLNGATPGPVKR.V	Deamidation (+1)	R.YGVVENDFVMLNGATPGPVKR.V
249	266	2	2035.03	4.1	0	30.3	20.9	95.00%	K.VACIGAWHPANVQWTVAR.A	Carbamidomethyl (+57)	K.VACIGAWHPANVQWTVAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
78	ECM17_SCHPO	3.26%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
314	325	2	1337.8	4.6	0	39.3	10	95.00%	R.LTVLEPITSLPR.K		R.LTVLEPITSLPR.K
801	810	2	1058.57	5.4	1	27.5	20.2	94.10%	K.GADLNLSELK.Y		K.GADLNLSELK.Y
611	636	3	2801.42	3.9	1	43.3	19	95.00%	K.GPSVVLAYLPYHSADDDAITVLQETK.K		K.GPSVVLAYLPYHSADDDAITVLQETK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
79	HSP7F_SCHPO	9.03%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
174	189	2	1665.85	4	0	78.4	20.6	95.00%	R.LMNDNAAAALTYGITK.T		R.LMNDNAAAALTYGITK.T

5	16	2	1249.64	6.5	0	29.4	20.5	95.00%	R.TNVVGIDFGNSK.T		R.TNVVGIDFGNSK.T
38	48	2	1194.59	3.8	1	34	22.2	95.00%	R.STPSLVSYGER.S		R.STPSLVSYGER.S
159	173	2	1534.89	4	1	42.9	10	95.00%	R.ALLEAANIAGLNPLR.L		R.ALLEAANIAGLNPLR.L
96	106	2	1134.6	4	1	31.7	21.5	95.00%	K.LTEVDGFVGAK.V		K.LTEVDGFVGAK.V
163	173	2	1108.64	2.4	0	42.8	14.1	95.00%	E.AANIAGLNPLR.L		R.ALLEAANIAGLNPLR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
80	THI4_SCHPO	19.88%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
310	338	3	3045.65	3.6	0	44.4	12.8	95.00%	K.TYIHAAQVNNDLARPVILDPVAVGATTAR.S		K.TYIHAAQVNNDLARPVILDPVAVGATTAR.S
373	385	2	1353.71	4.1	0	37.5	19.4	95.00%	R.GVDSISQHTLAAR.I		R.GVDSISQHTLAAR.I
121	140	2	2014.96	4.4	1	70	23	95.00%	K.AAADGADYVGIGSIYETNTK.D		K.AAADGADYVGIGSIYETNTK.D
249	265	4	1917.09	3.2	1	33.8	11.8	95.00%	K.LKDFTPLIHHLTNAVAK.N		K.LKDFTPLIHHLTNAVAK.N
237	248	2	1322.76	4.7	0	31.5	13	95.00%	K.DLLNQIPAALQK.L		K.DLLNQIPAALQK.L
31	42	2	1248.73	2.2	0	37.3	12.3	95.00%	E.GILGGVTLVQHR.E		R.QVEEGILGGVTLVQHR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
81	BCA1_SCHPO	12.37%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
315	331	2	1670.97	4.2	1	59.5	11.5	95.00%	R.LLEVFGAGTAALVSPVK.A		R.LLEVFGAGTAALVSPVK.A
37	49	3	1581.74	4.5	1	25.4	22.9	95.00%	K.FGENFTDHMLIMK.W		K.FGENFTDHMLIMK.W
318	331	2	1315.75	2.9	0	72.2	15.8	95.00%	E.VFGAGTAALVSPVK.A		R.LLEVFGAGTAALVSPVK.A
262	278	2	1795	4.2	1	43.3	14	95.00%	K.EIITAPLDGMILPGVTR.D		K.EIITAPLDGMILPGVTR.D
263	278	2	1665.95	2.9	0	77.6	12	95.00%	E.IITAPLDGMILPGVTR.D		K.EIITAPLDGMILPGVTR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
82	VATA_SCHPO	11.79%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
128	136	2	1002.51	5	1	25.2	21.1	90.80%	R.GINTESLNR.E		R.GINTESLNR.E
77	88	2	1228.64	2.5	0	36.4	20.2	95.00%	E.TSGLTVGDPVQR.T		K.CTIQVYEETSGLTVGDPVQR.T
373	389	2	1752.85	8	1	36.9	21.8	95.00%	R.LAEMPADSGYPAYLGAK.L		R.LAEMPADSGYPAYLGAK.L
317	331	2	1544.81	4.6	0	49.4	19.5	95.00%	R.TTLVANTSNMPVAAR.E		R.TTLVANTSNMPVAAR.E
221	240	3	2105.14	4.1	0	35.3	16.8	95.00%	R.AARPVADNLTANQPLLTGQR.V		R.AARPVADNLTANQPLLTGQR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
83	O59743_SCHPO	19.01%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
127	136	2	1252.56	3	0	38.4	22.9	95.00%	E.YYHLSAPDCK.S	Carbamidomethyl (+57)	K.LKPVPTSWEQALQDNKPEEYYHLSAPDCK.S
108	116	2	1055.57	2.4	0	31.2	19.2	95.00%	K.LKPVPTSWE.Q		K.LKPVPTSWEQALQDNKPEEYYHLSAPDCK.S
210	225	2	1690.88	3.5	0	52.7	20.2	95.00%	R.SIQDVPFTSATVDIAK.K		R.SIQDVPFTSATVDIAK.K
1	11	2	1319.72	4	1	28	19.1	94.70%	-.MDPYTVAIIKK.L	Acetyl (+42)	-.MDPYTVAIIKK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
84	EF1G_SCHPO	16.14%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
93	115	3	2635.37	2.6	1	32	16.4	95.00%	K.VLQYCSFTNSELPGAFRPIIAPR.V	Carbamidomethyl (+57)	K.VLQYCSFTNSELPGAFRPIIAPR.V
207	216	2	1182.71	4	0	27.1	14.1	93.70%	K.FIDQPLPIIK.A		K.FIDQPLPIIK.A
355	375	3	2372.08	3.3	0	25.1	23.6	95.00%	K.GHDYVPAFDVAPDWGSYTFTK.L		K.GHDYVPAFDVAPDWGSYTFTK.L
116	127	2	1294.63	4.3	1	26.2	21.5	92.40%	R.VFGAPYDEQAAK.E		R.VFGAPYDEQAAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
85	LEUC_SCHPO	9.10%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
633	649	2	2002.01	4.5	0	59.4	21.4	95.00%	R.VIIAPSFADIFFNNCFK.N	Carbamidomethyl (+57)	R.VIIAPSFADIFFNNCFK.N

603	619	3	1826.86	5.3	0	37.3	22.5	95.00%	R.HATVLVAHDNFGCGSSR.E	Carbamidomethyl (+57)	R.HATVLVAHDNFGCGSSR.E
477	493	2	1811.86	0.087	1	43.9	22.8	95.00%	R.EFFGDVSNGSPSIITNK.N	Deamidation (+1)	R.EFFGDVSNGSPSIITNK.N
650	667	2	2027	4	1	40.9	20.6	95.00%	K.NGMLPIPTPIEQVNDMMK.A		K.NGMLPIPTPIEQVNDMMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
86	NACA_SCHPO	38.73%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	75	2	1164.62	5.8	0	59.3	19.3	95.00%	K.SSNNAYIVLGK.V		K.SSNNAYIVLGK.V
52	64	2	1540.93	4.4	0	50.2	7.78	95.00%	K.NILLIINEPIVYK.S		K.NILLIINEPIVYK.S
14	26	2	1308.71	3	1	47.8	17.8	95.00%	E.LPAGSTTVVHAEK.A		K.ISELPAGSTTVVHAEK.A
141	150	2	1087.58	3.6	0	28.3	19.9	95.00%	E.LVMAQANVSR.A		K.DIELVMAQANVSR.A
132	140	2	946.46	3	1	27.2	22.2	93.80%	E.TGVDAKDIE.L		K.AVDETGVDAKDIELVMAQANVSR.A
76	86	2	1189.58	4.9	1	47.2	22.4	95.00%	K.VTVEDMAAQAR.A		K.VTVEDMAAQAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
87	SERC_SCHPO	12.85%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
175	184	2	1155.6	2.6	0	41	20.4	95.00%	E.FNEPPTNIPK.G		K.FTPDGETSLVYYCDNETVHGVEFNEPPTNIPK.G
376	385	2	1147.65	4.7	1	32.8	14.5	95.00%	R.LIDLLESFAK.A		R.LIDLLESFAK.A
216	228	2	1299.74	5	0	37	14.9	95.00%	K.NAGPAGITVVFVR.D		K.NAGPAGITVVFVR.D
189	199	2	1282.6	4.3	0	67	22.5	95.00%	R.VCDVSSNFISR.K	Carbamidomethyl (+57)	R.VCDVSSNFISR.K
324	329	2	766.38	5.3	0	26.2	20	92.40%	R.MNVTFR.I		R.MNVTFR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
88	RS0B_SCHPO	32.75%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	88	4	2453.26	4	1	67.3	19.5	95.00%	R.VIATIENPADVCVISSRPYGHR.A	Carbamidomethyl (+57)	R.VIATIENPADVCVISSRPYGHR.A
4	31	4	2920.53	2.9	1	66.1	15.4	95.00%	E.SIARPSVLNATDDDIKNLLAADSHIGSK.N		-.MAESIARPSVLNATDDDIKNLLAADSHIGSK.N
139	169	3	3390.76	4.3	1	25.4	14.6	95.00%	K.EASFVNIPVIALCDTDSILNHVDVAIPINNK.G	Carbamidomethyl (+57)	K.EASFVNIPVIALCDTDSILNHVDVAIPINNK.G
231	243	2	1319.64	5.1	1	28.6	21.8	95.00%	E.AQLAAQTAAAEFE.V		K.AAAAAAAEEEAQLAAQTAAAEFEVTDSAAGTVDPTILDNATAGQVGQTTWEGDAEWNITGAAPSEWA.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
89	MMF1_SCHPO	35.80%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
59	75	2	1747.86	2.8	0	34.8	21.7	95.00%	K.ANGVIYCSGQIPVANGK.V	Carbamidomethyl (+57)/ Deamidation (+1)	K.ANGVIYCSGQIPVANGK.V
109	124	2	1781.87	4.4	0	46.5	22.1	95.00%	K.VNIFLADMDDFAAVNK.V		K.VNIFLADMDDFAAVNK.V
125	137	2	1483.81	3.9	1	42.4	16.6	95.00%	K.VYTEVLPDPKPAR.S		K.VYTEVLPDPKPAR.S
47	58	2	1247.66	5.3	0	27.4	19.2	94.00%	K.LSSAGPYNQAIK.A		K.LSSAGPYNQAIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
90	RAD24_SCHPO	9.63%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
109	120	2	1236.65	4.7	1	29.1	19.1	95.00%	K.HLIPNAASAESK.V		K.HLIPNAASAESK.V
95	108	2	1659.88	3.7	1	64.3	19.1	95.00%	E.LDTICQDILTVLEK.H	Carbamidomethyl (+57)	K.IEQELDTICQDILTVLEK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
91	LEU1_SCHPO	11.47%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
379	392	2	1593.77	3.1	0	25.8	21.1	91.70%	K.VPYLPLDPHDVNSE.Y		K.VPYLPLDPHDVNSEYAAIIR.V

464	479	2	1742.82	4.9	0	69.1	22.8	95.00%	R.FSVNDYTLSSNGPQSK.C		R.FSVNDYTLSSNGPQSK.C
341	362	3	2346.15	2.9	0	44.7	21.6	95.00%	R.HPYAGNLVFTAFSGSHQDAISK.G		R.HPYAGNLVFTAFSGSHQDAISK.G
137	151	3	1761.87	4	0	33.2	22.6	95.00%	K.NATVHLYNACSPLFR.E	Carbamidomethyl (+57)	K.NATVHLYNACSPLFR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
92	RL1B_SCHPO	16.67%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
54	75	3	2486.26	2.6	0	38.3	19.8	95.00%	K.LPNVPRPNMAICILGDAHDLDR.A	Carbamidomethyl (+57)	K.LPNVPRPNMAICILGDAHDLDR.A
78	91	3	1486.72	4.2	1	36.5	22.9	95.00%	K.HGGVDAMSVDDLKK.L	Oxidation (+16)	K.HGGVDAMSVDDLKK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
93	PYC_SCHPO	8.19%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
829	838	2	1275.63	4.5	1	27.7	21.6	94.30%	K.QLEFDNNQLR.E		K.QLEFDNNQLR.E
525	546	3	2378.22	2.4	1	21.2	17.8	90.90%	E.IVMPVLLDSTGNQIDVSHPSEK.G		K.SEIVMPVLLDSTGNQIDVSHPSEK.G
1041	1047	2	894.46	3.4	0	39	21.4	95.00%	K.FFLSRPE.M		K.FFLSRPEMNEEMHVEIDQGK.T
1109	1129	3	2088.05	4.4	1	38.2	20.4	95.00%	R.ADPGNPGHVAAPMSGTIVEIR.V		R.ADPGNPGHVAAPMSGTIVEIR.V
917	929	2	1447.76	4.7	0	42.2	19.7	95.00%	K.VVGDLAQFMVQNK.L		K.VVGDLAQFMVQNK.L
302	315	2	1628.75	2	1	37.3	23.4	95.00%	K.YCNAGTAEFLLDQK.G	Carbamidomethyl (+57)	K.YCNAGTAEFLLDQK.G
839	848	2	1297.58	4.8	1	38.2	22.4	95.00%	R.EIDSYWAQMR.L		R.EIDSYWAQMR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
94	RL13_SCHPO	25.96%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
172	183	2	1398.66	5.4	1	54	22.9	95.00%	K.NFNAFSTLSNER.A		K.NFNAFSTLSNER.A
118	128	3	1326.79	4.7	0	51.2	12.3	95.00%	K.VYLAHLIVFPR.K		K.VYLAHLIVFPR.K
46	64	4	2080.27	3.1	1	20	0	95.00%	K.IAPRPVEAIRPAVKPPTIR.Y		K.IAPRPVEAIRPAVKPPTIR.Y
89	100	2	1263.7	3.9	0	28.9	18.6	95.00%	R.VASTIGIPVDHR.R		R.VASTIGIPVDHR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
95	THI22_SCHPO	10.53%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
134	151	2	1829.99	3.3	0	87.1	17.1	95.00%	K.LVVDPVMVATSGDSLVTK.D		K.LVVDPVMVATSGDSLVTK.D
9	18	2	1149.55	3.1	0	30.4	22.2	95.00%	E.SLSNQFDPSR.I		-.MPYNPLYESLSNQFDPSR.I
181	197	2	1890.88	4.9	1	111	22.6	95.00%	K.NQGLDISNINSVSDMER.C		K.NQGLDISNINSVSDMER.C
9	20	2	1391.67	3.2	1	25.1	22.5	90.50%	E.SLSNQFDPSRIE.T		-.MPYNPLYESLSNQFDPSRIETVLDPMGYTIK.R
21	31	2	1236.65	3.2	0	25.3	20.2	90.90%	E.TVLDPMGYTIK.R		R.IETVLDPMGYTIK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
96	PURA_SCHPO	9.68%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
206	224	3	2169.16	3.6	1	37.8	15.7	95.00%	R.LKPFVIDAVAFMYEALQSK.K		R.LKPFVIDAVAFMYEALQSK.K
268	276	2	899.55	4.9	0	44.5	17.2	95.00%	R.IANSIGVVK.A		R.IANSIGVVK.A
388	401	2	1610.74	2.7	0	33.1	22.9	95.00%	K.VPTTGITHWDQMPE.N		K.VPTTGITHWDQMPENAK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
97	RS2_SCHPO	28.85%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
242	251	2	1210.6	4.4	1	66.5	22	95.00%	E.YADILMQTEK.K		K.AAFAAASLTYGILTPNLWAERPFGQTPIEEYADILMQTEK.K
64	74	2	1441.73	5.7	1	25.1	20.7	90.50%	K.EYQIVDYFLPR.L		K.EYQIVDYFLPR.L
55	64	2	1237.7	3	1	49	15.9	95.00%	E.IYLYSLPIKE.Y		K.SIEEIYLYSLPIKEYQIVDYFLPR.L

174	185	3	1138.69	4.8	1	25.2	10	95.00%	R.GAGLVAAPVTKR.F		R.GAGLVAAPVTKR.F
186	200	2	1799.86	4.8	1	102	22.5	95.00%	R.FLQLAGIEDCYTQSR.G	Carbamidomethyl (+57)	R.FLQLAGIEDCYTQSR.G
141	156	3	1696.87	4.8	0	37.6	20.5	95.00%	R.GYWGTALGDPHTVPVK.V		R.GYWGTALGDPHTVPVK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
98	RS14_SCHPO	35.25%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
76	84	2	950.59	2.1	0	28.5	6.99	95.00%	E.VGITALHIK.I		K.EVGITALHIK.I
117	129	2	1442.73	3.7	1	46.5	21.3	95.00%	R.IEDVTPIPTDSTR.R		R.IEDVTPIPTDSTR.R
57	72	2	1564.76	2.1	0	75.1	22.8	95.00%	E.SSPYAAMLAAQDAAAK.C		R.DESSPYAAMLAAQDAAAK.C
95	105	2	1037.57	5.3	0	47.1	18.2	95.00%	K.TPGPGAQAALR.A		K.TPGPGAQAALR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
99	RL10A_SCHPO	20.36%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	128	3	1265.71	4.6	0	30	16	95.00%	R.HAFGKPNGLVAR.V		R.HAFGKPNGLVAR.V
41	56	2	1798.86	2.7	1	38.7	22.2	95.00%	R.AGVDEFPLCIHLVSNE.Y	Carbamidomethyl (+57)	R.AGVDEFPLCIHLVSNEYEQITSEALEAAR.I
129	139	2	1228.7	4.7	0	40	16.9	95.00%	R.VNIGQILMSVR.T		R.VNIGQILMSVR.T
33	38	2	719.4	4.8	0	27.1	17.3	93.60%	R.IFDLGR.K		R.IFDLGR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
100	SYTC_SCHPO	6.40%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
160	174	2	1703.8	4.7	1	71.1	23	95.00%	R.VITNDDYSSIESYAK.Q		R.VITNDDYSSIESYAK.Q
248	258	2	1187.55	4.2	0	47.1	22.3	95.00%	K.NSSSYFLGDAK.N		K.NSSSYFLGDAK.N
8	26	3	2136.14	4.2	1	27.4	16.1	95.00%	K.GVQASLDNLSLEIPFIQHR.L		K.GVQASLDNLSLEIPFIQHR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
101	PUR8_SCHPO	10.17%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
226	242	2	1930.91	3.5	0	32.6	23.4	95.00%	K.LSGFDNVYPVTGQTYDR.K		K.LSGFDNVYPVTGQTYDR.K
437	449	2	1392.73	2.9	0	25.2	19.8	90.70%	E.LDSLLDASTFVGR.A		K.NTPYFAPIYDELDSLLDASTFVGR.A
243	261	3	2023.12	2.7	1	59.1	14.5	95.00%	R.KIDIDVLQPLASFGATAHK.I		R.KIDIDVLQPLASFGATAHK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
102	RS4B_SCHPO	8.40%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
222	233	2	1232.68	5.6	1	42.4	17.6	95.00%	R.LSNVFVIGEAGK.S		R.LSNVFVIGEAGK.S
40	49	2	1258.72	4.7	1	26.1	16.8	92.30%	R.ECLPLIVFLR.N	Carbamidomethyl (+57)	R.ECLPLIVFLR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
103	PYR1_SCHPO	2.27%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1135	1145	2	1229.6	4.3	0	46.2	22.2	95.00%	R.MLDDIGVDQPK.W		R.MLDDIGVDQPK.W
1804	1815	2	1354.6	2.7	0	39.4	23.1	95.00%	R.LHDQDDSGVQLE.V		R.LHDQDDSGVQLEVDR.S
234	245	2	1342.75	2.4	1	27.7	17.8	94.30%	E.NLTSQVSIKEPK.L		K.NPNTENLTSQVSIKEPK.L
1758	1770	2	1371.7	4.4	0	56.2	21.2	95.00%	K.FVGNTAFTGFGVR.E		K.FVGNTAFTGFGVR.E
1804	1818	3	1724.81	5.5	1	27.4	22.6	95.00%	R.LHDQDDSGVQLEVDR.S		R.LHDQDDSGVQLEVDR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
104	GCST_SCHPO	16.54%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
34	51	2	1940.98	2.3	1	30	20.1	95.00%	K.EGATIVPFAGFSMPVQYK.G		K.EGATIVPFAGFSMPVQYK.G
165	180	2	1623.93	4	1	75.8	12.8	95.00%	R.ALIAIQGPETASVVQK.L		R.ALIAIQGPETASVVQK.L
330	344	2	1486.75	3.6	0	52.3	20.3	95.00%	E.VGQVTSGCPSPTLGK.N	Carbamidomethyl (+57)	R.HGSAVEVDGVEVGQVTSGCPSPTLGK.N

113	127	2	1603.8	3.8	1	47.7	21.3	95.00%	E.TGGIIDDTIISKQDE.N		K.ELKPFHSTLSAFTNETGGIIDDTIISKQDENTYYIVTNAACSEK.D
113	124	2	1231.67	1.2	0	36	19.2	95.00%	E.TGGIIDDTIISK.Q		K.ELKPFHSTLSAFTNETGGIIDDTIISK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
105	HMCS_SCHPO	11.63%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
155	183	3	2859.53	3.9	0	40.5	14.9	95.00%	K.GNARPTGGAGCVALLVGPNAPIVFEPGLR.G	Carbamidomethyl (+57)	K.GNARPTGGAGCVALLVGPNAPIVFEPGLR.G
382	392	3	1300.68	5.1	1	26	20	95.00%	K.KTNLVNDLDNR.H		K.KTNLVNDLDNR.H
217	228	2	1325.64	3.7	0	38.4	22.9	95.00%	K.ALDGAYANYNVR.D		K.ALDGAYANYNVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
106	YHEF_SCHPO	19.70%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
113	125	2	1421.69	3.1	0	28.8	21.9	95.00%	E.NAMIPFVNTVTSE.I		K.TCNPQSIENAMIPFVNTVTSEISFDAWAYTAQNSSR.I
54	65	2	1279.67	5.1	1	47	20.3	95.00%	K.SFIGLDALTESK.G		K.SFIGLDALTESKGEFFQR.M
30	41	3	1413.76	4.8	1	20.9	17.9	90.20%	R.LRGPHCGTYLLK.V	Carbamidomethyl (+57)	R.LRGPHCGTYLLKVVGTNATYVGEK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
107	TRP_SCHPO	14.49%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
382	393	2	1355.77	4.5	0	47.2	17	95.00%	K.INNCIGQILLAK.R	Carbamidomethyl (+57)	K.INNCIGQILLAK.R
400	419	3	1938.01	4.3	1	37.5	18.9	95.00%	R.IIAETGAGQHGVATAICAAK.F	Carbamidomethyl (+57)	R.IIAETGAGQHGVATAICAAK.F
275	302	3	2928.48	4.6	1	34.9	19.2	95.00%	K.QFQSGGSVATAPPAAVVEPINEMYLPQK.Y		K.QFQSGGSVATAPPAAVVEPINEMYLPQK.Y
445	461	2	1739.99	4	1	48.6	13.4	95.00%	R.LLGAEVVPVTSGTQTLR.D		R.LLGAEVVPVTSGTQTLR.D
91	114	2	2617.33	5.8	0	82.3	19.1	95.00%	R.DAGVTIPIILMGYYNPIFSYGDAK.T		R.DAGVTIPIILMGYYNPIFSYGDAK.T
450	461	2	1256.71	3.1	0	30.1	16.8	95.00%	E.VVPVTSGTQTLR.D		R.LLGAEVVPVTSGTQTLR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
108	RL15A_SCHPO	19.90%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
115	128	2	1699.83	4.1	0	73.6	21.7	95.00%	R.VLNSYWVNQDATYK.F		R.VLNSYWVNQDATYK.F
78	93	3	1761.94	4.8	0	23.7	19.4	94.70%	K.GQTYGKPVHQGVNHLK.Y		K.GQTYGKPVHQGVNHLK.Y
148	157	3	1218.69	4.4	0	24.4	16	95.00%	R.INWIVNPVHK.H		R.INWIVNPVHK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
109	ACL1_SCHPO	11.87%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
369	381	2	1420.73	4.5	1	44	20.7	95.00%	R.GSELTYNNVPISK.V		R.GSELTYNNVPISK.V
171	182	3	1338.74	4.8	0	23.6	16.8	94.60%	K.LYRPGSVAYVSK.S		K.LYRPGSVAYVSK.S
190	203	2	1574.76	3.9	0	27.3	22	93.90%	E.LNNIISHTTDGVYE.G		K.SGGMSNELNNIISHTTDGVYEGIAIGGDR.Y
156	170	2	1506.72	3.3	0	45.7	23.3	95.00%	K.IGNTGGMMDNIVASK.L		K.IGNTGGMMDNIVASK.L
137	155	2	1926.08	2.7	0	50.8	9.54	95.00%	K.NVVIIGPATVGGIKPGCFK.I	Carbamidomethyl (+57)	K.NVVIIGPATVGGIKPGCFK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
110	PMP20_SCHPO	26.92%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
30	55	2	2747.41	3.6	1	43.5	18.9	95.00%	K.FIIVGVPGAFTPPCSSQVPGYIANEK.Q	Carbamidomethyl (+57)	K.FIIVGVPGAFTPPCSSQVPGYIANEK.Q
141	156	2	1647.86	3	1	55.9	20.3	95.00%	E.VTDVDISSADKVLSSL.-		K.VFIENEVTDVDISSADKVLSSL.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
111	RS8A_SCHPO	35.50%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
60	74	2	1568.72	4.4	1	94.1	23.2	95.00%	R.LDSGNFSWGSEGVSK.K		R.LDSGNFSWGSEGVSK.K
165	178	2	1475.79	4.1	0	33.2	18.5	95.00%	R.LYAVVSSRPGQSGR.C		R.LYAVVSSRPGQSGR.C
152	164	2	1363.68	4.8	1	51.3	21.6	95.00%	K.VDSALETQFAAGR.L		K.VDSALETQFAAGR.L
78	92	2	1751.94	4.6	1	25.6	16.8	91.50%	R.IIQVAYHPSNNELVR.T		R.IIQVAYHPSNNELVR.T
111	124	3	1682.82	4.5	1	23.1	22	94.00%	R.VWYETHYGILMGSK.G		R.VWYETHYGILMGSK.G
78	89	2	1383.68	3.6	0	35.5	21.7	95.00%	R.IIQVAYHPSNNE.L		R.IIQVAYHPSNNELVR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
112	SYKC_SCHPO	8.12%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
581	591	2	1169.63	3.6	1	50.5	18.8	95.00%	E.VQAAEPTVVKE.-		R.EVLLFPHMKPEVQAAEPTVVKE.-
15	28	2	1454.8	4	1	41.2	16.8	95.00%	K.ALVLDPVTGEQVSK.T		K.ALVLDPVTGEQVSK.T
154	176	4	2682.24	3.7	1	34.1	23.3	95.00%	K.LQVMCQAQDADTVDFAAQHEHLR.R	Carbamidomethyl (+57)	K.LQVMCQAQDADTVDFAAQHEHLR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
113	MPG1_SCHPO	14.60%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
270	287	2	1775.99	2.5	0	42	14	95.00%	K.IGPNVVIGPNVTIGDGVR.L		K.IGPNVVIGPNVTIGDGVR.L
244	266	2	2263.29	3.7	0	64.2	9.54	95.00%	E.ILAPASSNIIGNVLIDPSATIGK.N		K.HKPEILAPASSNIIGNVLIDPSATIGK.N
338	349	2	1297.71	2.8	0	27.3	18.1	93.80%	E.IYVNGGSILPHK.S	Deamidation (+1)	R.LENVSVLGDDVVVNDEIYVNGGSILPHK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
114	RL27A_SCHPO	29.41%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	48	3	1461.76	5.9	1	42.8	19.7	95.00%	K.SHPFGHAVVAGVER.Y		K.SHPFGHAVVAGVER.Y
23	34	2	1269.74	4.4	0	65.4	14.1	95.00%	K.VVILQAIDQGSK.S		K.VVILQAIDQGSK.S
94	107	2	1575.83	3.5	1	46.7	20.2	95.00%	K.GLITADTFKEPTQR.S		K.GLITADTFKEPTQR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
115	TCTP_SCHPO	21.43%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
6	21	2	1737.84	4.2	1	86.5	23.1	95.00%	K.DVISGDELVSDAYDLK.E		K.DVISGDELVSDAYDLK.E
13	22	2	1151.57	3.2	1	27.5	22.1	94.10%	E.LVSDAYDLKE.V		K.DVISGDELVSDAYDLKEVDDIVYEADCQMVTVK.Q
30	38	2	1050.49	3.7	0	33.5	21.8	95.00%	E.ADCQMVTVK.Q	Carbamidomethyl (+57)	K.EVDDIVYEADCQMVTVK.Q
64	73	2	1211.63	3.2	0	38.7	20.2	95.00%	E.TVNNLVYSFR.L		K.QGGDVDIGANPSAEDAEENAEEGTETVNNLVYSFR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
116	DHE4_SCHPO	19.29%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
417	439	2	2411.16	5.2	0	85.7	21.5	95.00%	K.YCDSGSNNIPSLVDGANIAGFLK.V	Carbamidomethyl (+57)	K.YCDSGSNNIPSLVDGANIAGFLK.V
381	394	2	1620.7	2.2	0	39.5	23.3	95.00%	E.MAQNAQFSTWTHAE.V		K.AANAGGVAVSGLEMAQNAQFSTWTHAEVDAK.L
356	367	2	1231.57	4.5	1	27.7	22.1	94.30%	R.ASGEGCWLAPGK.A	Carbamidomethyl (+57)	R.ASGEGCWLAPGK.A
93	101	2	1127.61	5.6	1	29.2	19.5	95.00%	K.FLGFEQIFK.N		K.FLGFEQIFK.N
399	416	2	1950.98	4.6	1	78.4	20.5	95.00%	K.LAGIMQNIFEQSTDVASK.Y		K.LAGIMQNIFEQSTDVASK.Y
195	205	2	1218.63	2.6	0	29.6	20.3	95.00%	E.ATGYGVVYYVK.H		K.HMLTGGSNIRPEATGYGVVYYVK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
117	RS23_SCHPO	25.87%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
100	107	2	847.49	3	0	28.4	16.7	95.00%	E.VLLSGFGR.K		K.VTAFVPHDGCLNFVDENDEVLLSGFGR.K
125	137	2	1326.74	4.4	1	55.5	17.4	95.00%	K.VAGVGLSALFHEK.K		K.VAGVGLSALFHEK.K
81	96	2	1818.83	2.7	0	29.4	23.7	95.00%	K.VTAFVPHDGCLNFVDE.N	Carbamidomethyl (+57)	K.VTAFVPHDGCLNFVDENDEVLLSGFGR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
118	YA03_SCHPO	18.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
82	97	2	1778.89	2.6	1	45.2	21.3	95.00%	E.GGPDKVPVYISPFFQE.V		K.YLAEGGPDKVPVYISPFFQEVGHLPCDIGLELDK.L
181	194	2	1560.83	4.5	0	43.8	19.8	95.00%	K.AADIDFLPPQLSFK.N		K.AADIDFLPPQLSFK.N
98	108	2	1208.59	2.7	0	31.6	22.4	95.00%	E.VGHLPCDIGLE.L	Carbamidomethyl (+57)	K.VPVYISPFFQEVGHLPCDIGLELDK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
119	PABP_SCHPO	4.75%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
258	266	2	1068.57	4.8	0	26.6	18.4	93.00%	K.ANFTNVYIK.N		K.ANFTNVYIK.N
447	456	2	1142.61	4.9	1	33.9	19.3	95.00%	R.SQLEAQIQAR.N		R.SQLEAQIQAR.N
99	110	2	1272.73	5.5	0	37.9	14.9	95.00%	E.LFNSIGPVASIR.V		K.AEEPEAAAEPSESTSTPTNASSVATPSGTAPTSASLYVGELDPSVTEAMLFELFNSIGPVASIR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
120	YDG7_SCHPO	7.48%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
7	23	3	1939.91	3.9	1	22.9	22.8	93.70%	K.YFENAQNVHFTLADGSK.I		K.YFENAQNVHFTLADGSK.I
293	299	2	771.46	3	0	25.2	19	90.80%	E.INSIGIR.A		K.EDMDEINSIGIR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
121	RS22_SCHPO	27.69%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
98	108	2	1171.7	4.9	0	29.1	13.2	95.00%	R.QVGVIVLTTSR.G		R.QVGVIVLTTSR.G
4	19	2	1814.9	4.5	1	77.6	21.1	95.00%	R.QSVLADCLNNIVNAER.R	Carbamidomethyl (+57)	R.QSVLADCLNNIVNAER.R
89	97	2	1111.62	5.6	0	31.9	15.9	95.00%	K.WVNQLLPSR.Q		K.WVNQLLPSR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
122	RL6_SCHPO	22.05%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	64	2	1497.84	5	0	33.1	16.2	95.00%	R.ASLAPGTVCILLAGR.F	Carbamidomethyl (+57)	R.ASLAPGTVCILLAGR.F
78	87	2	1091.59	3.5	0	38.3	20.1	95.00%	E.DTLVVTGPYK.V		R.VVVLSQLEDTLVVTGPYK.V
70	87	2	1959.1	3.1	1	33.6	14.3	95.00%	R.VVVLSQLEDTLVVTGPYK.V		R.VVVLSQLEDTLVVTGPYK.V
109	118	2	1031.56	5.5	1	31.2	19.9	95.00%	K.IDVSGVSVEK.F		K.IDVSGVSVEK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
123	VATB_SCHPO	9.15%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
48	59	2	1295.72	2.8	0	26.4	16.3	92.70%	E.IVNLNLPDGSVR.S		R.RPQYNEIVNLNLPDGSVR.S
439	449	2	1284.62	4.2	1	36.9	21.6	95.00%	K.TFISQGAYENR.T		K.TFISQGAYENR.T
146	162	2	1774.93	3.2	0	81.9	19.8	95.00%	E.MIQTGISSIDGLNSIAR.G		R.IYPEEMIQTGISSIDGLNSIAR.G
42	59	3	2083.09	4.5	1	23.6	18.3	94.60%	R.RPQYNEIVNLNLPDGSVR.S		R.RPQYNEIVNLNLPDGSVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
124	TRX1_SCHPO	27.18%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	79	2	1466.74	2.3	0	30.5	21.3	95.00%	E.AGVHAMPSFFLYK.N		K.VDVDQLSEIAAEAGVHAMPSFFLYK.N

40	54	2	1796.83	4.6	1	68.4	23.3	95.00%	K.FEQFSNTYSDATFIK.V		K.FEQFSNTYSDATFIK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
125	DAK1_SCHPO	10.00%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
45	66	3	2123.05	5.3	0	21	20.3	90.60%	K.NVSVISGGGAGHEPTHSSFVGK.G		K.NVSVISGGGAGHEPTHSSFVGK.G
503	526	3	2700.3	3.7	1	23.8	21.5	94.80%	K.YTPARPGDSTMCDALVPFVETFVK.T	Carbamidomethyl (+57)	K.YTPARPGDSTMCDALVPFVETFVK.T
388	399	2	1358.73	4.4	1	25.9	19.2	92.00%	R.QAIVNSMENLIK.A		R.QAIVNSMENLIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
126	RL23_SCHPO	25.18%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
15	34	2	2090	3.5	0	108	22.5	95.00%	R.MTLGLPVQAIMNCADNSGAK.N	Carbamidomethyl (+57)	R.MTLGLPVQAIMNCADNSGAK.N
51	65	2	1531.78	3.4	0	55.2	20.6	95.00%	R.LPAASCGDMVLATVK.K	Carbamidomethyl (+57)	R.LPAASCGDMVLATVK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
127	TBB_SCHPO	11.38%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
126	154	3	2876.43	3.2	0	68.3	20.1	95.00%	E.ACDALQGFQLTHSLGGGTGSGMGTLLLSK.I	Carbamidomethyl (+57)	R.EAEACDALQGFQLTHSLGGGTGSGMGTLLLSK.I
163	174	2	1249.62	3.9	0	41.3	20.6	95.00%	R.MMATFSVAPAPK.S		R.MMATFSVAPAPK.S
112	121	2	1069.62	2.8	0	28.3	15.9	95.00%	E.LADAVLDVVR.R		K.GHYTEGAELADAVLDVVR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
128	YHZ8_SCHPO	42.42%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
75	103	3	3217.69	3	0	57.2	16.4	95.00%	K.TSNPFLAFANYLTSTHAPLAEPLQLLNFK.V		K.TSNPFLAFANYLTSTHAPLAEPLQLLNFK.V
144	164	3	2285.2	4.3	0	37.3	18.2	95.00%	K.ADTSLIIHSLDDPSLYAVVTR.Y		K.ADTSLIIHSLDDPSLYAVVTR.Y
2	13	2	1361.7	3.8	0	57.2	20.6	95.00%	M.SFPASTHVYIAK.I	Acetyl (+42)	-.MSFPASTHVYIAK.I
177	198	2	2279.2	1.9	0	93	18.6	95.00%	E.ISGATSVSQQVIYSGVGFLNRP.-		K.SGIEPGPAEISGATSVSQQVIYSGVGFLNRP.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
129	SODC_SCHPO	40.26%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
98	116	2	1984.04	4.4	0	72.6	18.1	95.00%	K.TTFSDSVISLFGANSIIGR.T		K.TTFSDSVISLFGANSIIGR.T
81	97	2	1765.87	4	1	72.3	21.9	95.00%	R.HVGDLGNLESDAQGNIK.T		R.HVGDLGNLESDAQGNIK.T
45	70	3	2825.25	4.3	1	41.5	23.6	95.00%	R.GFHIHQFGDNTNGCTSAGPHFNPEGK.T	Carbamidomethyl (+57)	R.GFHIHQFGDNTNGCTSAGPHFNPEGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
130	ODPB_SCHPO	16.12%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
331	360	3	3021.51	4	1	35.4	18.5	95.00%	R.VSMADVPMPYSHPVEAASVPNADVVVAAAK.K		R.VSMADVPMPYSHPVEAASVPNADVVVAAAK.K
318	330	2	1496.68	2.9	1	50.1	22.7	95.00%	E.SDAFDYLDAPVER.V		R.IVTVDQAYSQHGIGSEIAAQIMESDAFDYLDAPVER.V
295	310	2	1702.82	2.3	0	58.9	22.4	95.00%	R.IVTVDQAYSQHGIGSE.I		R.IVTVDQAYSQHGIGSEIAAQIMESDAFDYLDAPVER.V
346	360	2	1381.76	2.9	0	33	16.4	95.00%	E.AASVPNADVVVAAAK.K		R.VSMADVPMPYSHPVEAASVPNADVVVAAAK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
131	RS17A_SCHPO	23.66%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	59	3	1133.6	4.6	0	24.5	19.6	95.00%	K.IAGYTTHLMK.R		K.IAGYTTHLMK.R

34	44	2	1156.68	4.8	1	51	15.2	95.00%	R.IVDEVAIIASK.R		R.IVDEVAIIASK.R
24	33	2	1234.67	4.6	1	36.3	17.9	95.00%	R.LTLDFQTNKR.I		R.LTLDFQTNKR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
132	THRC_SCHPO	19.46%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
265	282	2	1945.01	4.9	0	46.3	19.8	95.00%	R.FIVPTGNFGDILAGYYAK.R		R.FIVPTGNFGDILAGYYAK.R
437	454	3	2061.03	4.7	1	31.2	20.3	95.00%	K.TKDQDITYICLSTAHPAK.F	Carbamidomethyl (+57)	K.TKDQDITYICLSTAHPAK.F
313	327	2	1443.73	4.4	0	39.8	21.5	95.00%	K.ADSTQVSPSGPISAK.E		K.ADSTQVSPSGPISAK.E
414	428	2	1651.79	3.7	0	36.7	22.8	95.00%	E.SDHYIIDPHTAVGVE.T		K.IYESDHYIIDPHTAVGVETGLR.C
182	215	3	3829.81	3.8	1	34.2	21.6	95.00%	R.VSPIQEAQMTTVTDPNVHCITVNGVFDDCQDLVK.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VSPIQEAQMTTVTDPNVHCITVNGVFDDCQDLVK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
133	YCO6_SCHPO	11.45%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
15	36	3	2140.01	3.2	0	36.1	22.5	95.00%	K.MSAAPTPHNTPSGTSAPNFGAK.A		K.MSAAPTPHNTPSGTSAPNFGAK.A
57	66	2	1068.59	4.1	0	38.4	16.1	95.00%	K.LGSLLHLTSE.G		K.LGSLLHLTSEGVSELPEAVQR.R
233	245	2	1434.65	4.2	0	47.9	22.7	95.00%	E.SGPSNVFLYDHAE.G		K.TYYYMEESGPSNVFLYDHAEGDK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
134	PMM_SCHPO	15.56%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
210	220	2	1282.6	3.6	0	34.2	22.5	95.00%	E.GFDTIHFFGDK.T		K.EGFDTIHFFGDK.T
45	58	2	1347.75	4.4	0	41.6	17.1	95.00%	K.VVAIGFVGGSDLSK.Q		K.VVAIGFVGGSDLSK.Q
236	250	2	1568.74	2.4	0	29.7	22.9	95.00%	R.TIGHSVTNPDDTIAE.L		R.TIGHSVTNPDDTIAELK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
135	ARGD_SCHPO	12.24%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
104	129	3	2885.5	2.4	1	31.8	17.5	95.00%	K.LVHSSNLFYNEPAIELSNVINNSLAK.N		K.LVHSSNLFYNEPAIELSNVINNSLAK.N
283	310	3	2746.56	2.7	0	43.2	8.45	95.00%	K.DVASPDIITVAKPLANGLPIGATIVSSK.I		K.DVASPDIITVAKPLANGLPIGATIVSSK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
136	RL12_SCHPO	36.97%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
68	83	2	1538.91	3.4	0	50.5	11.8	95.00%	R.QAAVSVVPSASALVIK.A		R.QAAVSVVPSASALVIK.A
95	108	2	1483.7	4	1	38.6	22.7	95.00%	K.DKNVAHSGNVSLDE.I		K.DKNVAHSGNVSLDEIIEVAR.T
97	108	2	1240.57	3.8	0	28.9	22.6	95.00%	K.NVAHSGNVSLDE.I		K.NVAHSGNVSLDEIIEVAR.T
17	31	2	1312.7	3.6	1	46	16.6	95.00%	R.AVGGEVAGGSTLAPK.I		R.AVGGEVAGGSTLAPK.I
131	146	2	1652.81	4	1	45.9	21	95.00%	K.EILGTAFSVGCTVDGK.N	Carbamidomethyl (+57)	K.EILGTAFSVGCTVDGK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
137	RLA2_SCHPO	34.55%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
62	88	2	2220.11	3.2	1	78.8	20.6	95.00%	K.LATVPTGGAASAAPAAAAGGAAPAAEE.A		K.LATVPTGGAASAAPAAAAGGAAPAAEEAAK.E
25	35	2	1103.58	4.7	1	37.7	20.9	95.00%	E.SVLSTVGIEAE.S		K.DSPSASDIESVLSTVGIEAESER.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
138	RS13_SCHPO	23.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
44	55	2	1244.66	3.8	0	40.8	19.9	95.00%	K.GMSPSQIGVTLR.D		K.GMSPSQIGVTLR.D

28	39	2	1286.68	5	1	56.1	20	95.00%	K.ADADSVVEQILK.F		K.ADADSVVEQILK.F
10	20	2	1132.63	4.4	0	38.6	18.1	95.00%	K.GIASSALPYVR.S		K.GIASSALPYVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
139	SYLC_SCHPO	4.68%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
843	852	2	1272.56	5	0	24.8	23.4	90.00%	K.SCFYDLQNAR.D	Carbamidomethyl (+57)	K.SCFYDLQNAR.D
382	398	2	1730.97	1.3	0	53.1	12.8	95.00%	K.GQDLIGALVNAPLSVHK.Q		K.GQDLIGALVNAPLSVHK.Q
226	241	2	1922.92	5.8	0	66.1	23.3	95.00%	R.SFITTDVNPYYDSFVR.W		R.SFITTDVNPYYDSFVR.W
779	787	2	927.55	3.3	0	40.5	16	95.00%	E.ALANSAILR.L		R.LALADAGDTVDDANFEEALANSAILR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
140	NACB_SCHPO	23.84%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
47	58	2	1357.71	2.4	1	36.7	19.4	95.00%	K.KLNMQNLAGIQE.V		K.KLNMQNLAGIQEVNMFK.E
59	64	2	766.37	3.2	1	31.3	20.1	95.00%	E.VNMFKE.D		K.LNMQNLAGIQEVNMFKEDGGVINFR.A
73	90	3	1884.97	4	1	45.6	21.1	95.00%	R.APTVHSSLPNETTAIYGK.A		R.APTVHSSLPNETTAIYGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
141	SYRC_SCHPO	6.80%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
163	180	2	1987.02	4.1	1	33.9	19.1	95.00%	R.STIIGSFLANLHESQGWK.V		R.STIIGSFLANLHESQGWK.V
480	489	2	1284.6	5.9	0	39.4	22.3	95.00%	R.INNYAFDWSR.M		R.INNYAFDWSR.M
11	24	2	1544.86	3.1	0	51.8	16.2	95.00%	K.SLSTLGLQDLPVFR.E		K.SLSTLGLQDLPVFR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
142	GLT1_SCHPO	1.94%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1897	1918	3	2189.08	3.9	1	55	21.2	95.00%	K.GKDVIVIGGGDTGNDCLGTSVR.H	Carbamidomethyl (+57)	K.GKDVIVIGGGDTGNDCLGTSVR.H
1758	1776	2	1792.98	2.6	0	91.3	15.8	95.00%	R.VAIIGSGPAGLAAADQLNR.A		R.VAIIGSGPAGLAAADQLNR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
143	SYDC_SCHPO	11.72%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
281	294	2	1356.6	4.8	1	27.5	22.6	94.10%	K.MSGASSEGGSNVFK.I		K.MSGASSEGGSNVFK.I
522	554	3	3334.69	3.2	1	85.5	18.1	95.00%	K.ALGVSPDVGLQQYIDAFAIGCPPHAGGGIGLER.V	Carbamidomethyl (+57)	K.ALGVSPDVGLQQYIDAFAIGCPPHAGGGIGLER.V
200	210	2	1229.65	4.9	1	29.1	19.6	95.00%	K.NLPFLVEDAGR.S		K.NLPFLVEDAGR.S
490	499	2	1300.55	3.9	0	26.9	22.9	93.40%	R.YSNSYDFFMK.G		R.YSNSYDFFMK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
144	AATR1_SCHPO	15.19%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
305	317	2	1562.83	3.7	1	52.6	19.5	95.00%	R.VGWFTAQPLFIER.G		R.VGWFTAQPLFIER.G
424	438	2	1702.83	3.1	0	48.9	22.1	95.00%	E.GVNLACGNWFVVDPR.V	Carbamidomethyl (+57)	K.IHAEAVEEGVNLACGNWFVVDPR.V
275	288	2	1577.78	4.4	1	46.4	22	95.00%	K.ELIPSFLSMDVDGR.V		K.ELIPSFLSMDVDGR.V
38	54	2	1856.03	4.5	1	36.8	13.8	95.00%	K.IISLAGGLPNPEYFPIR.E		K.IISLAGGLPNPEYFPIR.E
7	19	3	1436.71	5.4	1	43.2	22.2	95.00%	K.DLSHHLSVESASR.K		K.DLSHHLSVESASR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
145	DLDH_SCHPO	8.81%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
113	128	2	1663.83	1.7	0	25	21.6	90.40%	R.GIDVSGVSVNLSQMMK.A		R.GIDVSGVSVNLSQMMK.A
155	168	2	1448.76	3.8	0	31.8	19.6	95.00%	K.GTGSFIDPQTLSVK.G		K.GTGSFIDPQTLSVK.G

248	262	2	1516.76	2.4	0	31.4	20.8	95.00%	E.FLPAVGGPMDADISK.A		R.LGAEVTVVEFLPAVGGPMDADISK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
146	ADK_SCHPO	15.29%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
253	267	2	1483.87	4.5	0	69.4	13.6	95.00%	R.VVVITQGADATIVAK.D		R.VVVITQGADATIVAK.D
126	138	2	1424.68	5.2	0	51	21.6	95.00%	R.SLCTNLGAANNYK.L	Carbamidomethyl (+57)	R.SLCTNLGAANNYK.L
41	64	3	2620.15	2	1	48.7	23.9	95.00%	E.SQMGIYKEPCVSYSAGGAAQNSCR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.SNDAVLASESQMGIYKEPCVSYSAGGAAQNSCR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
147	RL36A_SCHPO	19.19%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	11	2	966.59	4.6	0	38.2	12.6	95.00%	M.APGLVVGLNK.G		-.MAPGLVVGLNK.G
88	96	2	989.55	3.7	0	44	17.2	95.00%	E.LTSVIQSSR.L		K.IEELTSVIQSSR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
148	KAD1_SCHPO	15.91%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	74	2	2135.02	2.9	1	87.4	21.5	95.00%	K.IMDQGGLVSDDIVTGMIKDE.I		K.IMDQGGLVSDDIVTGMIKDEILNNPECK.N
196	210	2	1726.84	3.2	1	48.2	22.7	95.00%	K.WAAVDAAQKPEQVWE.Q		K.WAAVDAAQKPEQVWEQIVAILEK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
149	SLBR2_SCHPO	12.25%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
134	143	2	1115.56	4.3	1	27.1	21.4	93.70%	R.NIESSVQPSR.E		R.NIESSVQPSR.E
222	245	3	2655.29	2.5	1	22.5	21	93.10%	R.HLLNLIDDTPVTPGEARPAYDGYE.T		R.HLLNLIDDTPVTPGEARPAYDGYETSR.Q
149	157	2	1075.63	4.5	0	33	16.5	95.00%	K.LLDQIYALK.H		K.LLDQIYALK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
150	DYR_SCHPO	9.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
164	183	3	2062.15	3.7	0	25.4	12.3	95.00%	K.LTTPSLHIAGTSDTLVPLAR.S		K.LTTPSLHIAGTSDTLVPLAR.S
191	212	3	2537.31	3.6	1	37.3	18.9	95.00%	R.CENAHVLLHPGQHIVPQQAVYK.T	Carbamidomethyl (+57)	R.CENAHVLLHPGQHIVPQQAVYK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
151	IMDH_SCHPO	8.97%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
303	313	2	1155.67	4.5	0	51.3	15.6	95.00%	K.IDVIAGNVVTR.E		K.IDVIAGNVVTR.E
214	234	3	2311.28	3.6	1	29.3	12	95.00%	K.LPVVDKDDNLVALLSLTDLMK.N		K.LPVVDKDDNLVALLSLTDLMK.N
419	433	2	1421.67	3.9	1	52.2	23.3	95.00%	R.GMGSIAAMEGTGVNK.N		R.GMGSIAAMEGTGVNK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
152	ACL2_SCHPO	13.01%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
193	209	2	1822.94	3.2	1	58	20.4	95.00%	R.ATIASTLLSDIPVEQHE.S		R.ATIASTLLSDIPVEQHESLVDFIIR.L
326	334	2	985.56	4.7	1	36	18.4	95.00%	K.LTILNAEGR.V		K.LTILNAEGR.V
382	389	2	947.52	4.5	0	26.9	20.6	93.40%	K.TVLDLMTR.G		K.TVLDLMTR.G
32	61	3	3211.76	3.3	1	47.1	13.8	95.00%	K.TVSATPAVQLAQIQFPLPTLVIPAESTTYR.E		K.TVSATPAVQLAQIQFPLPTLVIPAESTTYR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
153	RL14_SCHPO	11.94%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
103	110	2	993.46	6	0	29.1	22	95.00%	R.SQLNDFDR.F		R.SQLNDFDR.F
87	94	2	905.44	5.7	0	30.4	21.3	95.00%	K.WASSAWAK.K		K.WASSAWAK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
154	ASNS_SCHPO	3.23%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
516	523	2	1035.55	6.3	1	30	18.5	95.00%	K.LFDEIFPR.Q		K.LFDEIFPR.Q
399	408	2	1120.54	4.9	1	26.3	20.4	92.50%	K.STMAWGLEAR.V		K.STMAWGLEAR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
155	DHOM_SCHPO	12.50%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	138	2	1568.79	4.5	0	56.7	21	95.00%	K.AFSASNDVYQNIIK.A		K.AFSASNDVYQNIIK.A
57	67	2	1391.68	4.7	1	33.1	21.7	95.00%	K.DYQPINLSEWK.N		K.DYQPINLSEWK.N
89	110	2	2284.21	4.5	1	95.1	18.1	95.00%	K.SPLPAILVDNTASEAIAQSYPK.F		K.SPLPAILVDNTASEAIAQSYPK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
156	SCE3_SCHPO	15.72%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
46	66	2	2113.97	4.9	1	94.2	23.1	95.00%	R.ATPSSADAGYNAPSSTFESVR.S		R.ATPSSADAGYNAPSSTFESVR.S
46	63	2	1771.76	3.3	0	45.5	23.7	95.00%	R.ATPSSADAGYNAPSSTFE.S		R.ATPSSADAGYNAPSSTFESVR.S
272	289	3	1956.03	4.3	1	43	18.8	95.00%	K.RDPFGGAKPVDNTSVLQR.V		K.RDPFGGAKPVDNTSVLQR.V
250	271	3	2195.06	2.9	1	28.5	22.3	95.00%	R.SSSNVNTEATPSATTTTSSKPK.R		R.SSSNVNTEATPSATTTTSSKPK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
157	ASSY_SCHPO	6.34%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
320	332	2	1601.77	4.2	0	39.6	23	95.00%	K.ILYNGQFFSPCTR.M	Carbamidomethyl (+57)	K.ILYNGQFFSPCTR.M
193	205	2	1354.68	2.4	1	38.8	20.5	95.00%	E.AGILEDPSMTPPK.D		K.KPWSMDENIVHCSYEAGILEDPS MTPPK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
158	RL31_SCHPO	21.24%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
91	105	2	1650.87	3.4	0	46.6	18.9	95.00%	K.ALYTYVQAVDVANPK.M		K.ALYTYVQAVDVANPK.M
7	15	2	986.56	5	0	39.5	18.5	95.00%	K.SAINQVVTR.D		K.SAINQVVTR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
159	COFI_SCHPO	27.74%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
109	124	2	1671.77	2.1	0	59.6	23.1	95.00%	R.AFTGIGTDIQATDFSE.V		R.AFTGIGTDIQATDFSEVAYETVLE K.V
81	94	2	1584.9	4.1	0	54.1	15.7	95.00%	K.IIFISWSPDVAPIK.S		K.IIFISWSPDVAPIK.S
71	78	2	890.46	3.1	1	25.2	20.8	90.80%	E.FNLGEGVR.N		R.YAIYDFEFNLGEGVR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
160	PNPP_SCHPO	17.45%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
196	213	2	1882	2.9	0	59.1	17.2	95.00%	K.FLPGSGAISYPLIFSTGR.Q		K.FLPGSGAISYPLIFSTGR.Q
145	166	3	2359.15	3.2	0	61.7	21.7	95.00%	K.IGPDPSVGAVLCGMDMHVTYLK. Y	Carbamidomethyl (+57)	K.IGPDPSVGAVLCGMDMHVTYLK. Y
278	289	2	1393.68	4.6	1	25.3	22.5	90.90%	E.KDAPVVPDYYVE.S		K.EEEILEKDAPVVPDYYVESLAK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
161	RL21B_SCHPO	19.38%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
145	160	2	1782.88	2.4	0	44.9	21.5	95.00%	E.NNEPVTLHPVAYDTTI.-		R.QPAPPATAHFVSTENNEPVTLHPVAYDTTI.-
130	144	2	1607.81	2.6	1	28.9	20.5	95.00%	R.RQPAPPATAHFVSTE.N		R.RQPAPPATAHFVSTENNEPVTLHPVAYDTTI.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
162	SYEC_SCHPO	6.15%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
190	206	2	1731.84	3.9	1	51.4	22.7	95.00%	K.SSGPNYEIGLPDAIDGK.V		K.SSGPNYEIGLPDAIDGK.V
295	309	2	1657.7	4.5	1	93.6	23.7	95.00%	K.SGQAYADDTDVETMR.H		K.SGQAYADDTDVETMR.H
66	77	2	1393.77	4.3	0	31.9	15.7	95.00%	K.LALQTFSQVYPK.L		K.LALQTFSQVYPK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
163	YBS7_SCHPO	6.02%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
128	146	2	1760.86	5.1	0	31.6	21.8	95.00%	R.TSGSSTGLSNAPPSANVSK.A		R.TSGSSTGLSNAPPSANVSK.A
168	185	2	1942.99	2.8	0	36.3	19.3	95.00%	E.VCVPLNPDTGSVPLIHPE.Q	Carbamidomethyl (+57)	R.ATPEVCVPLNPDTGSVPLIHPEQTDR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
164	CISY_SCHPO	7.82%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
91	101	2	1155.59	3	1	29.2	19.9	95.00%	E.GSVLDPNEGIR.F		R.SLIWEGSVLDPNEGIR.F
167	192	4	2838.39	2.4	1	38.1	20.5	95.00%	R.CPPTLHPMAQFSLAVTALEHDSAFAK.A	Carbamidomethyl (+57)	R.CPPTLHPMAQFSLAVTALEHDSAFAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
165	RS10A_SCHPO	23.61%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	44	3	1428.82	4.9	1	23.6	16	94.60%	K.HPEVGVPNLQVIK.A		K.HPEVGVPNLQVIK.A
10	24	3	1580.91	4.1	0	31.3	11.5	95.00%	K.AIHQALFSQGVLVAK.K		K.AIHQALFSQGVLVAK.K
26	31	2	732.38	5.5	0	30.1	20.4	95.00%	K.DFNLPK.H		K.DFNLPK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
166	PDI1_SCHPO	5.28%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	136	3	1350.87	5.1	1	30.4	0	95.00%	R.KQLLPTVKPISK.D		R.KQLLPTVKPISK.D
188	201	2	1436.77	4.3	0	45.1	17.4	95.00%	K.SLGSNFPGIVAFTK.D		K.SLGSNFPGIVAFTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
167	Q1L854_SCHPO	11.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
271	280	2	1070.53	3.3	0	27.9	20.3	94.50%	K.TQQAPPTLSE.T		K.TQQAPPTLSETDFPALA.-
143	160	2	1856.82	2.7	1	46.7	23.7	95.00%	R.GWGDLVNSAANPDVAENE.G		R.GWGDLVNSAANPDVAENEGNTPSGAQTPAAEEENVK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
168	O13797_SCHPO	9.15%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
197	214	2	1831.84	5.2	0	74	23.7	95.00%	K.QLNQPSDSSATSGADQAR.T		K.QLNQPSDSSATSGADQAR.T
33	43	2	1265.61	3.3	0	35.3	22.2	95.00%	E.VAAQCIQDSFK.I	Carbamidomethyl (+57)	K.ESLEVAAQCIQDSFK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
169	RS3_SCHPO	20.08%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

154	175	3	2381.12	2.1	0	33.9	22.8	95.00%	K.FADGFMIHSGQPAVDFIDSATR.H		K.FADGFMIHSGQPAVDFIDSATR.H
97	108	2	1362.64	3.8	1	61	22.9	95.00%	R.GLCAVAQCESLR.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GLCAVAQCESLR.Y
215	230	2	1855.96	3.2	1	44.2	19.9	95.00%	E.EEPITKPYTVINQPVE.A		K.EEEPITKPYTVINQPVEAAAAAGQEVVAEQETAVAY.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
170	YET4_SCHPO	8.96%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
328	341	2	1393.69	4.6	1	28.2	22.5	94.90%	E.ESPIALGQGGVTHE.A		K.EINTTHDQAAATTTAAVASASTTATAESHAVADGIMNDNVLESIGENVQQETVFEDASDIPHADVIPHTTTVTVEEESPIALGQGGVTHEATTSAR.A
190	216	3	2686.32	5.5	1	58	21.4	95.00%	R.NDEQLGNSPASITSKPATTSAAQPSSK.V		R.NDEQLGNSPASITSKPATTSAAQPSSK.V
487	503	3	1712.87	4.4	0	27.8	21	95.00%	R.KPSSTGQEPTTPSTPAK.S		R.KPSSTGQEPTTPSTPAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
171	CH10_SCHPO	28.85%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	84	2	1230.7	4	0	31.7	16.1	95.00%	R.VLLPAYGGSNIK.V		R.VLLPAYGGSNIK.V
62	72	2	1111.6	4.5	0	30.9	17.7	95.00%	K.LAQPSVAVGDR.V		K.LAQPSVAVGDR.V
98	104	2	798.52	3	1	33.5	11.1	95.00%	E.LLAIIKE.-		R.DHELLAIIKE.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
172	RL28A_SCHPO	11.49%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
94	110	2	1787.95	3.9	1	37.3	18.9	95.00%	K.NTEVAPVINVLQSGYGK.V		K.NTEVAPVINVLQSGYGK.V
97	110	2	1443.81	3	0	47.9	14.8	95.00%	E.VAPVINVLQSGYGK.V		K.NTEVAPVINVLQSGYGK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
173	SODM_SCHPO	20.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	173	2	1303.7	4.2	0	48.8	19.3	95.00%	R.ITTTANQDTIVK.S		R.ITTTANQDTIVK.S
26	48	2	2502.32	2.9	1	32.8	15.8	95.00%	K.ATLPPLPYAYNALEPALSETIMK.L		K.ATLPPLPYAYNALEPALSETIMK.L
127	135	2	1108.52	5	1	34	22.6	95.00%	K.WGSLEDFQK.E		K.WGSLEDFQK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
174	PGM_SCHPO	4.33%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	49	2	1634.8	3.2	0	49.1	21.7	95.00%	E.NFVQATMDVVEPSAK.G		K.VTVFEQPNYVENFVQATMDVVEPSAK.G
350	358	2	1160.54	5.2	0	29	23	95.00%	K.FFCNLFDAK.R	Carbamidomethyl (+57)	K.FFCNLFDAK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
175	RL18A_SCHPO	12.30%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
81	93	2	1390.7	3.8	1	57.3	21.7	95.00%	K.TTVVVGTVTDDER.M		K.TTVVVGTVTDDER.M
56	65	3	1111.64	5.1	0	26.6	15.8	95.00%	K.TNRPPISISK.I		K.TNRPPISISK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
176	RS11_SCHPO	17.76%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	64	2	1161.6	4.7	0	33.4	20.9	95.00%	K.CPFVGQVSIR.G	Carbamidomethyl (+57)	K.CPFVGQVSIR.G
114	130	2	1870.97	4.9	1	41.5	19.8	95.00%	R.INEGDVVTVGQCRPLSK.T	Carbamidomethyl (+57)	R.INEGDVVTVGQCRPLSK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
177	RL2_SCHPO	17.79%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
92	108	2	1709.87	2.7	1	50.2	20.5	95.00%	K.NAALTVGNVLPVGEMPE.G		K.NAALTVGNVLPVGEMPEGTIISNVEEK.A
128	144	3	1759.88	4.2	0	23	21.4	93.90%	R.SSGNYVIIVGHDVDTGK.T		R.SSGNYVIIVGHDVDTGK.T
163	173	2	940.55	4.3	0	54.6	11.8	95.00%	R.GVVGIVAGGGR.I		R.GVVGIVAGGGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
178	RS12A_SCHPO	8.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	111	2	1486.76	2.4	1	27.9	19.4	94.50%	K.VLGEWAGLCVLDR.D	Carbamidomethyl (+57)	K.VLGEWAGLCVLDR.D
103	111	2	1088.55	2.9	0	29.4	20.9	95.00%	E.WAGLCVLDR.D	Carbamidomethyl (+57)	K.VLGEWAGLCVLDR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
179	SPEE_SCHPO	13.09%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
91	104	3	1338.8	2.7	1	28.2	10.8	95.00%	K.KVLVIGGGDGGVLR.E		K.KVLVIGGGDGGVLR.E
2	12	2	1291.72	4.1	1	43.5	17.3	95.00%	M.SVQELSHPLIK.D	Acetyl (+42)	-.MSVQELSHPLIK.D
18	31	2	1631.79	4.6	1	31.2	22.1	95.00%	R.EINNMWPGQAMTLK.V		R.EINNMWPGQAMTLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
180	SYG_SCHPO	6.90%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
216	232	3	1983.01	5	1	28	18.4	95.00%	K.GYLRPETAQGQFLNFSR.L		K.GYLRPETAQGQFLNFSR.L
492	506	2	1649.85	4.8	0	35.7	20.3	95.00%	R.TYTPNVIEPSFGLGR.I		R.TYTPNVIEPSFGLGR.I
526	538	2	1298.77	3.9	0	28.2	13.4	94.90%	R.GVLSFPASIAPIK.A		R.GVLSFPASIAPIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
181	SYFA_SCHPO	4.61%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
128	138	2	1219.56	4.9	1	33.3	22.7	95.00%	K.NTDSITDETPK.V		K.NTDSITDETPK.V
280	291	2	1267.63	2.8	1	49.3	21.7	95.00%	K.VPASTDKLPDPE.Y		K.VPASTDKLPDPEYVAR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
182	FUMH_SCHPO	8.71%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
326	341	2	1622.87	2.6	0	34.7	16.6	95.00%	E.LILPANEPGSSIMPGK.V		R.CGLGELILPANEPGSSIMPGK.V
131	142	2	1157.67	3.6	1	43.3	16.5	95.00%	R.AIEILGGTLGSK.K		R.AIEILGGTLGSK.K
218	231	2	1574.78	2.6	1	30.5	21.1	95.00%	E.FSGYVTQVGYGIER.I		R.THMQDATPLSLGQEFSGYVTQVGYGIER.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
183	Q76N21_SCHPO	21.77%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	140	3	2329.11	0.51	1	21.1	22.6	90.70%	K.GASDGGLFIPHSPNRFPGFDIE.T		K.YEGVTEPEGEFELTEAIEDGPRPFK.V
13	22	2	1195.61	4.9	0	30.3	22	95.00%	R.FVTCQIVSSR.V	Carbamidomethyl (+57)	K.SSPYFSRYQTKYRR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
184	RHP23_SCHPO	7.61%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
211	225	2	1515.76	4.5	0	40.8	21.2	95.00%	E.ALAPTSTGQPANLFE.Q		R.EESAAALAAQQQQSEALAPTSTGQPANLFEQAALSENENQEQPSNTVGDDPLGFLR.S
198	210	2	1301.63	4.7	0	45.1	21.7	95.00%	E.SAAALAAQQQQSE.A		R.EESAAALAAQQQQSEALAPTSTGQPANLFEQAALSENENQEQPSNTVGDDPLGFLR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
185	FIMB_SCHPO	4.89%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
508	524	2	1796.81	3.8	0	57	23.3	95.00%	K.TLSDSDMVAWANSMAAK.G		K.TLSDSDMVAWANSMAAK.G
158	170	2	1485.74	3.7	1	44.6	23	95.00%	K.LINDSVPDTIDER.V		K.LINDSVPDTIDER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
186	RL11_SCHPO	14.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
36	49	2	1531.83	4.2	1	63.5	17.2	95.00%	K.VLEQLSGQTPVFSK.A		K.VLEQLSGQTPVFSK.A
154	164	2	1349.67	4.1	1	39.8	21	95.00%	K.INAEDTINWFK.Q		K.INAEDTINWFK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
187	ACAC_SCHPO	2.11%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1972	1994	3	2667.36	3.2	1	27.8	18.3	95.00%	K.TAQAINDFNHGEQLPLFILANWR.G		K.TAQAINDFNHGEQLPLFILANWR.G
1792	1805	2	1391.82	2.5	0	32	10.8	95.00%	E.GQPIILTGAPALNK.V		R.AVQIEGQPIILTGAPALNK.V
197	207	2	1131.63	6.1	0	34.7	15.8	95.00%	K.ISSTIVAQSAR.V		K.ISSTIVAQSAR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
188	CYSK1_SCHPO	9.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
10	23	2	1341.78	3.9	0	59.1	14.9	95.00%	K.VPGIVSGFIGAIGR.T		K.VPGIVSGFIGAIGR.T
180	200	2	2019.93	3.1	0	77.1	24.3	95.00%	K.GTVDGFTCSTGTGGTFAGVTK.Y	Carbamidomethyl (+57)	K.GTVDGFTCSTGTGGTFAGVTK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
189	YEI3_SCHPO	7.91%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
81	97	3	1834.04	4	1	21.8	10.4	92.00%	K.SRVPAFLTVFDIAGLTK.G		K.SRVPAFLTVFDIAGLTK.G
329	342	2	1482.75	2.8	1	41.2	21	95.00%	K.APQAAGVIHTDFEK.A		K.APQAAGVIHTDFEK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
190	SYNC_SCHPO	5.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
48	57	2	1167.56	4	0	26.7	21.9	93.10%	E.TDANCTIFVK.K	Carbamidomethyl (+57)	K.TAIHALETDANCTIFVK.K
447	465	3	2338.25	2.9	1	23.4	16	94.30%	K.MTDQINRPIFLTYFPLEIK.S		K.MTDQINRPIFLTYFPLEIK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
191	SUB2_SCHPO	7.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	76	2	1288.56	3.1	1	44.2	23.6	95.00%	R.AITDSGFEHPSE.V		R.AITDSGFEHPSEVQQVCIPQSILGTDVLCQAK.S
77	96	2	2256.17	5.5	0	63.4	17.8	95.00%	E.VQQVCIPQSILGTDVLCQAK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.AITDSGFEHPSEVQQVCIPQSILGTDVLCQAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
192	LYS4_SCHPO	4.30%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
149	159	2	1179.57	4.4	0	26	21.8	92.10%	K.GQGIDFYPAGR.G		K.GQGIDFYPAGR.G
470	489	2	1872.04	4.8	1	47.2	14.6	95.00%	R.EALAYLASPAVVAASAIAGK.I		R.EALAYLASPAVVAASAIAGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
193	G3P2_SCHPO	31.34%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	79	2	1446.71	2.9	0	28.6	21.9	95.00%	K.LVIDGHSIDVHNE.R		K.LVIDGHSIDVHNER.D
249	259	3	1290.69	4.5	1	28.4	19.9	95.00%	K.LAKPTNYEDIK.A		K.LAKPTNYEDIK.A
235	248	2	1467.82	3.7	0	76.5	15.2	95.00%	R.VPTPDVSVVDLTVK.L		R.VPTPDVSVVDLTVK.L

173	186	2	1458.75	2.3	0	87.8	19	95.00%	E.GLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK.T
146	162	2	1818.91	4.5	0	75	21.7	95.00%	K.VISNASCTTNCLAPLAK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.VISNASCTTNCLAPLAK.V
324	335	2	1279.67	5	1	52.3	20.3	95.00%	R.VVDLVAYTASKD.-		R.VVDLVAYTASKD.-
172	186	2	1587.8	2.9	1	49.3	21.3	95.00%	E.EGLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK.T
6	13	2	819.43	6.2	0	38.4	19.6	95.00%	K.VGINGFGR.I	Deamidation (+1)	K.VGINGFGR.I
201	215	2	1343.71	4.7	0	69.9	19.5	95.00%	R.GASANIIPSSTGAAK.A		R.GASANIIPSSTGAAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
194	EIF3E_SCHPO	9.98%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
267	284	3	2029.08	4.4	0	22.1	17.6	92.50%	R.YLTVAVVTNQNNANQKPR.N		R.YLTVAVVTNQNNANQKPR.N
395	412	2	1744.79	4.6	0	68.1	24.1	95.00%	R.NNPSVAAASNVAADQSTE.D		R.NNPSVAAASNVAADQSTEDESIESTSTNVVADDLITEAETATEAEEPEPEVQFGFK.A
418	431	2	1463.71	4.2	0	43.8	22	95.00%	E.STSTNVVADDLITE.A		R.NNPSVAAASNVAADQSTEDESIESTSTNVVADDLITEAETATEAEEPEPEVQFGFK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
195	TBA1_SCHPO	8.13%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
291	304	2	1770.81	3.1	0	35.2	23	95.00%	E.ITNQCFEPYNQMVK.C	Carbamidomethyl (+57)	K.AFHESNSVQEITNQCFEPYNQMVK.C
65	79	2	1758.92	3.8	0	35	18.9	95.00%	R.SIYVDLEPNVIDQVR.T		K.FVPRSIYVDLEPNVIDQVR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
196	ARO1_SCHPO	4.77%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
677	703	3	2950.41	2.7	1	45.4	21.4	95.00%	R.FACDVLRPMGCTVEQTATSTTVQGPPK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.FACDVLRPMGCTVEQTATSTTVQGPPK.G
162	172	2	1299.72	4.7	0	45.2	18.9	95.00%	K.NLVGAFWQPLR.V		K.NLVGAFWQPLR.V
1232	1247	2	1833.96	4.6	0	44.8	18.7	95.00%	R.ITNSMDIPLILFNMGR.F		R.ITNSMDIPLILFNMGR.F
640	660	2	2079.08	3.7	1	45.5	17.6	95.00%	E.IESDASSATYPLAIAAITGTK.C		K.YQNPPHYEIESDASSATYPLAIAAITGTK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
197	DED1_SCHPO	3.14%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
37	51	2	1398.63	4	0	42.3	23	95.00%	R.DKPSAGAAPAVGDDE.S		R.DKPSAGAAPAVGDDESVSSR.G
37	56	3	1914.9	5	1	49.2	23.3	95.00%	R.DKPSAGAAPAVGDDESVSSR.G		R.DKPSAGAAPAVGDDESVSSR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
198	YBB2_SCHPO	6.76%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
254	268	2	1518.81	3.9	0	38.1	18.2	95.00%	K.TAGSAVPANSLYLQK.A		K.TAGSAVPANSLYLQK.A
269	281	2	1442.67	3.7	0	39.1	22.9	95.00%	K.AYHDGTLPKPDTE.A		K.AYHDGTLPKPDTEAEIIQPVFIHPNAIVSK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
199	KAPS_SCHPO	12.87%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
39	52	2	1664.86	3.8	1	65.6	20.6	95.00%	K.STIACALEQYLLQR.G	Carbamidomethyl (+57)	K.STIACALEQYLLQR.G
173	184	2	1327.67	3.1	1	42.1	21.4	95.00%	E.IVVSSHTQSIEE.C		K.EFTGISAPYEAPISPEIVVSSHTQSIEECVEK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
200	LYS1_SCHPO	8.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
274	304	3	3531.6	2.7	0	51.5	22.9	95.00%	R.VVCDVSCDTTNPNNPIPIYNVNTTFDHPTVE.V	Carbamidomethyl (+57)/Carbamidomethyl (+57)	R.VVCDVSCDTTNPNNPIPIYNVNTTFDHPTVEVK.G
274	306	3	3758.77	3.3	1	76.7	21.5	95.00%	R.VVCDVSCDTTNPNNPIPIYNVNTTFDHPTVEVK.G	Carbamidomethyl (+57)/Carbamidomethyl (+57)	R.VVCDVSCDTTNPNNPIPIYNVNTTFDHPTVEVK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
201	PPA2_SCHPO	5.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
138	143	2	719.4	4.8	0	27.1	17.3	93.60%	E.LFDLGR.Q		R.IELFDLGR.Q
152	167	2	1869.88	3.3	1	90.6	23.2	95.00%	E.LFDTDVYDINTAAQER.V		R.YYELFDTDVYDINTAAQER.V
136	143	2	961.53	5.4	1	31.9	19.8	95.00%	R.IELFDLGR.Q		R.IELFDLGR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
202	Q9P7B4_SCHPO	13.13%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
234	256	3	2522.27	2.7	1	34.8	19.4	95.00%	R.ENVVIADTLVFPSHQGGANHVYR.K		R.ENVVIADTLVFPSHQGGANHVYR.K
163	173	2	1163.64	5.6	0	26.5	17.4	92.80%	K.SALAQFTSALR.K		K.SALAQFTSALR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
203	RLA0_SCHPO	15.06%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
133	144	2	1308.71	5.2	0	29.1	16.9	95.00%	K.TSFFQALGIPTK.I		K.TSFFQALGIPTK.I
98	132	3	3513.88	2.7	1	45.6	16.4	95.00%	R.ETIIANVIAAPARPNAIAPLDVFVPAGNTGMEPGK.T		R.ETIIANVIAAPARPNAIAPLDVFVPAGNTGMEPGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
204	SYSC_SCHPO	6.89%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
234	250	2	1864.89	2.9	1	57.3	22.3	95.00%	R.YLIATSEQPISAYHSGE.W		R.YLIATSEQPISAYHSGEWFEKPSEQLPLK.Y
358	371	2	1717.71	4.8	1	59.1	24.2	95.00%	K.ELVSCSNCTDYQSR.N	Carbamidomethyl (+57)/Carbamidomethyl (+57)	K.ELVSCSNCTDYQSR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
205	ARP3_SCHPO	11.01%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
298	309	2	1288.66	3.7	0	42.2	21	95.00%	E.IASSDFLTPLPE.L		R.FLAPEIFFNPEIASSDFLTPLPELVDNVVQSSPIDVR.K
178	198	2	2066.06	2.9	0	28.7	19.6	95.00%	R.SLTGTVVDSGDGVTHIIPVAE.G		R.SLTGTVVDSGDGVTHIIPVAEGYVIGSSIK.T
310	323	2	1539.83	4.7	0	45	17.6	95.00%	E.LVDNVVQSSPIDVR.K		R.FLAPEIFFNPEIASSDFLTPLPELVDNVVQSSPIDVR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
206	IDHP_SCHPO	6.94%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
151	163	2	1272.66	3	1	45	21.2	95.00%	K.STDLVASGPGKLE.L		K.STDLVASGPGKLELSFTPK.G
392	407	2	1800.87	4.4	1	48.7	22.3	95.00%	K.SPNGYVDTFEFLDAVK.S		K.SPNGYVDTFEFLDAVK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
207	CARA_SCHPO	10.84%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
324	358	4	3743.79	2.8	1	17.6	21	91.30%	R.GHNIPALDIASGNCHITSQNHGYAVDASTLPAEWK.A	Carbamidomethyl (+57)	R.GHNIPALDIASGNCHITSQNHGYAVDASTLPAEWK.A

203	212	2	1101.62	3.5	0	42.5	16.6	95.00%	E.VNLVSQVSTR.E		K.ISIGEEYDANDDEAFINPEEVNLV SQVSTR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
208	PRS6A_SCHPO	7.31%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
250	265	2	1657.89	4.1	0	43	18.1	95.00%	K.LAAPQLVQMFIGDGAK.L		K.LAAPQLVQMFIGDGAK.L
7	22	2	1661.72	5.1	0	28	24.1	94.70%	E.LDALDQSQQGGSSNNE.G		- .MSTLEELDALDQSQQGGSSNNEG LDGIEQEILAAGIDELNSR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
209	APE1_SCHPO	3.40%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
253	269	2	1912.97	5	0	42.1	19.8	95.00%	K.TLDFFSGVFGEPYPLPK.C		K.TLDFFSGVFGEPYPLPK.C
137	149	2	1467.71	4.6	0	42.2	22.1	95.00%	K.YLATTQMEPTSAR.R		K.YLATTQMEPTSAR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
210	ACBP_SCHPO	34.48%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	13	2	1294.61	4.4	1	38.3	22.7	95.00%	M.SSTFEQAAADVK.E	Acetyl (+42)	-.MSSTFEQAAADVK.E
33	50	3	1912	4.1	1	25.6	18.5	95.00%	K.QATVGDNNTEKPGLLDLK.G		K.QATVGDNNTEKPGLLDLK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
211	RS0A_SCHPO	10.96%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
16	30	3	1666.89	3.3	1	21.3	16.4	91.10%	E.DIKQLLAANCHIGSK.N	Carbamidomethyl (+57)	- .MAQVGRPNILNATDEDIKQLLAAN CHIGSK.N
66	82	2	1842.96	3.2	1	38.3	20.1	95.00%	R.VIATIENPADVCVVSTR.T	Carbamidomethyl (+57)	R.VIATIENPADVCVVSTR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
212	CLH_SCHPO	1.56%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
64	76	3	1431.83	4.6	0	23.4	12	94.40%	R.RPISADSVILHPK.K		R.RPISADSVILHPK.K
232	244	3	1442.73	4.6	1	21.9	20.5	92.30%	E.VDRNPNNPAFATK.T		K.LSIVEVDRNPNNPAFATK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
213	RL24A_SCHPO	12.75%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
81	91	2	1097.65	4.7	0	29.4	14.3	95.00%	R.GIVGANLDVIK.E		R.GIVGANLDVIK.E
36	43	2	978.52	4.9	1	29.5	21.1	95.00%	K.SESLFLQR.K		K.SESLFLQR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
214	PUR2_SCHPO	5.46%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
224	248	3	2494.13	2.7	1	24.2	23	95.00%	R.AFDGDKGPNTGGMGCYAPTPVA SPK.L	Carbamidomethyl (+57)	R.AFDGDKGPNTGGMGCYAPTPVA SPK.L
31	48	2	1678.78	1.8	1	54.6	23	95.00%	K.VYVAPGNGGTASNGAESK.M	Deamidation (+1)	K.VYVAPGNGGTASNGAESK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
215	RS21_SCHPO	29.89%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
51	60	2	1113.59	4.5	0	33.8	19.7	95.00%	K.TTYAISGFVR.S		K.TTYAISGFVR.S
72	87	2	1864.94	4.3	1	65.3	21.7	95.00%	R.LTTQDGLLEGVWSYQR.-		R.LTTQDGLLEGVWSYQR.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
216	6PGL_SCHPO	8.95%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

46	55	2	1083.61	5.4	1	52.4	17.6	95.00%	K.VLAEGLAQQR.G		K.VLAEGLAQQR.G
209	221	2	1488.81	4	1	42.1	16.7	95.00%	K.DILPIVIEDFTSK.L		K.DILPIVIEDFTSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
217	UBC4_SCHPO	25.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
102	128	3	3017.59	3.1	1	65.3	15.2	95.00%	K.VLLSICSLLTDPNPDDPLVPEIAHVYK.T	Carbamidomethyl (+57)	K.VLLSICSLLTDPNPDDPLVPEIAHVYK.T
91	101	2	1244.65	4.6	0	28.4	20.3	95.00%	R.DQWSPALTISK.V		R.DQWSPALTISK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
218	RS24A_SCHPO	20.15%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
21	32	3	1363.77	4	1	39.5	16.1	95.00%	R.KQMVVDILHPGK.A		R.KQMVVDILHPGK.A
69	83	2	1672.81	4.3	1	28.6	22.9	95.00%	R.TTGFALIYDDVEAMK.K		R.TTGFALIYDDVEAMK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
219	SUI1_SCHPO	41.28%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	30	3	3239.53	4	0	72.2	21.3	95.00%	M.SAIQNFNTVDPFADTGDDDAQPLNNIHIR.I	Acetyl (+42)	-.MSAIQNFNTVDPFADTGDDDAQPLNNIHIR.I
62	77	2	1768.75	3.2	1	37.2	23.7	95.00%	K.DFACNGTIVKDDDLGE.V	Carbamidomethyl (+57)/ Deamidation (+1)	K.DFACNGTIVKDDDLGEVIQLQGDQR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
220	PPID_SCHPO	5.90%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
214	226	2	1432.74	4.4	0	72	20.3	95.00%	K.QFAQQNLDTAVAK.W		K.QFAQQNLDTAVAK.W
23	30	2	931.51	4.1	0	29.7	20.8	95.00%	E.LFDNVVPK.T	Deamidation (+1)	K.IQPTIYFELFDNVVPK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
221	RL7B_SCHPO	14.00%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	21	2	2002.11	4.4	1	37	14.6	95.00%	M.VASSTVPSVASIFAPESLLK.K		-.MVASSTVPSVASIFAPESLLK.K
168	182	2	1523.86	4.4	1	56.2	14.5	95.00%	R.IPLSDNAIIEAALGK.Y		R.IPLSDNAIIEAALGK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
222	ARPC1_SCHPO	5.84%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	23	4	2564.32	3.3	1	37.1	17.8	95.00%	M.ATSQVLHILPKPSYEHAFNSQR.T	Acetyl (+42)	-.MATSQVLHILPKPSYEHAFNSQR.T
2	16	2	1723.92	2.9	0	47.1	18.5	95.00%	M.ATSQVLHILPKPSYE.H	Acetyl (+42)	-.MATSQVLHILPKPSYEHAFNSQR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
223	RLA1_SCHPO	24.77%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
33	48	2	1743.93	4.8	0	29.5	19	95.00%	K.AANVDVEPIWATIFAK.A		K.AANVDVEPIWATIFAK.A
22	32	3	1217.73	2.6	1	27.8	12.8	95.00%	E.ITSDKLLSLTK.A		-.MSASELATSYSALILADEGIEITSDKLLSLTK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
224	YNY8_SCHPO	7.44%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

221	230	2	1165.62	3.1	0	27.2	20.3	93.80%	E.LYATFLDPAR.V		R.VSAVVNTADISENYTFDAPANELY ATFLDPAR.V
2	16	2	1783.84	4.8	0	36.8	22.9	95.00%	M.SATSINPNNWHWTSK.D	Acetyl (+42)	-.MSATSINPNNWHWTSK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
225	CATA_SCHPO	3.71%	99%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
431	439	2	1061.57	5.6	0	35.4	19.5	95.00%	R.AFWQNVLGK.K		R.AFWQNVLGK.K
331	340	2	1082.61	4	0	24.8	15.4	90.00%	E.VSADPVLQVR.T		R.FTLNQNPTNFFADIEQAGFSPSH MVPGIEVSADPVLQVR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
226	ELF1_SCHPO	2.37%	99%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
776	784	2	1178.58	7.8	0	24.9	21.5	90.10%	K.TPSQYIQWR.Y	Deamidation (+1)	K.TPSQYIQWR.Y
156	171	2	1540.89	3.7	0	42.9	12.3	95.00%	K.VAALQLLGSLASSSPK.A		K.VAALQLLGSLASSSPK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
227	GUAA_SCHPO	10.76%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
170	203	4	3715.11	3.7	1	22.3	15.2	95.00%	K.NSPFAVIAHVTKPIIGLQFHPEVTH TPLGLQLIK.N		K.NSPFAVIAHVTKPIIGLQFHPEVTH TPLGLQLIK.N
231	254	4	2311.19	3.1	1	17.8	18.6	91.90%	R.KMIGPSDHVIGAVSGGVDSTVAS K.V		R.KMIGPSDHVIGAVSGGVDSTVAS K.V

Supplementary Table S2: All "Scaffold" validated proteins and peptides identified from solprotSP (*S.pombe*) and from SCVMprot (*S.cerevisiae*) samples

S.pombe **- Chymotrypsin digest of large tryptic peptides (replicate A)**

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
1	PGK_SCHPO	74.40%	100%	35

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
359	379	2	2046.05	4.7	1	96.9	23.6	95.00%	K.TCEAGNVVIVGGGDTATVAKK.Y	Carbamidomethyl (+57)	K.TCEAGNVVIVGGGDTATVAKK.Y
359	378	2	1917.95	4	0	118	25	95.00%	K.TCEAGNVVIVGGGDTATVAK.K	Carbamidomethyl (+57)	K.TCEAGNVVIVGGGDTATVAK.K
138	149	3	1262.67	4.1	2	23.6	23.6	92.30%	K.VKADASAVEAFR.K		K.VKADASAVEAFR.K
138	148	2	1106.56	-1.7	2	41.5	24.1	95.00%	K.VKADASAVEAF.R		K.VKADASAVEAFR.K
279	289	2	1250.65	-0.026	2	33.1	24	95.00%	F.LPVDFVTADKF.D		K.NNVEVFLPVDFVTADKFDK.D
250	269	3	2127.99	3.6	1	36.8	27	95.00%	K.IGDSLFDEAGSKNVESMMAK.A		K.IGDSLFDEAGSKNVESMMAK.A
273	288	2	1805.93	4.9	1	56.9	24.3	95.00%	K.NNVEVFLPVDFVTADK.F		K.NNVEVFLPVDFVTADK.F
140	150	2	1163.6	4.3	1	57.5	24.3	95.00%	K.ADASAVEAFRK.S		K.ADASAVEAFRK.S
23	39	2	1914.95	-1.8	1	39.7	25.4	95.00%	R.VDFNVPLDGDRITNNAR.I		R.VDFNVPLDGDRITNNAR.I
57	71	2	1591.87	2.9	0	46.2	21.1	95.00%	K.AVILMSHLGRPNGAR.V	Deamidation (+1)	K.AVILMSHLGRPNGAR.V
23	33	2	1245.61	6.8	1	62.1	25.1	95.00%	R.VDFNVPLDGDR.I		R.VDFNVPLDGDR.I
112	122	2	1211.69	4.5	0	57.3	16.6	95.00%	K.GGEVILLENLR.F		K.GGEVILLENLR.F
40	48	2	910.59	3.6	0	25.3	9.54	90.40%	R.IVGALPTIK.Y		R.IVGALPTIK.Y
206	213	2	741.47	-1.6	0	36.2	18	95.00%	F.LAILGGAK.V		K.ALENPARPFLAILGGAK.V
250	261	2	1237.59	4.5	1	61.5	25.5	95.00%	K.IGDSLFDEAGSK.N		K.IGDSLFDEAGSK.N
218	227	2	1183.69	5.5	0	39.2	19.1	95.00%	K.IQLIDNLLDK.V		K.IQLIDNLLDK.V
218	230	3	1552.9	4.8	1	31.7	15.8	95.00%	K.IQLIDNLLDKVNR.L		K.IQLIDNLLDKVNR.L
76	86	3	1141.67	-0.53	0	30.7	17.8	95.00%	Y.SLKPVAAELSK.L		K.YSLKPVAAELSK.L
94	105	2	1406.64	3.6	1	56.7	26	95.00%	K.FLDDCVGPEVEK.A	Carbamidomethyl (+57)	K.FLDDCVGPEVEK.A
197	213	2	1736.99	-0.082	1	57.8	15.1	95.00%	K.ALENPARPFLAILGGAK.V		K.ALENPARPFLAILGGAK.V
170	181	2	1267.64	4	0	58.7	24.3	95.00%	R.AHSSMVGVDLPR.V		R.AHSSMVGVDLPR.V
123	136	3	1544.76	5.8	1	28.5	25.4	95.00%	R.FHIEEEGSAKVDGK.K		R.FHIEEEGSAKVDGK.K
214	230	3	1966.12	-1.8	1	76.2	16.7	95.00%	K.VADKIQLIDNLLDKVNR.L		K.VADKIQLIDNLLDKVNR.L
7	15	2	986.57	5.4	0	41.1	21.4	95.00%	K.LAITDVDLK.G		K.LAITDVDLK.G
123	132	3	1145.54	4.7	1	33.9	25.6	95.00%	R.FHIEEEGSAK.V		R.FHIEEEGSAK.V
197	205	2	1013.53	-1	1	35.9	21.8	95.00%	K.ALENPARPF.L		K.ALENPARPFLAILGGAK.V
341	347	2	869.39	-0.85	1	35.6	24.1	95.00%	F.EFDNFAK.G		K.TIVWNGPAGVFEFDNFAK.G
404	414	2	1040.63	5.6	0	39.4	17.4	95.00%	K.ALPGVVALSSK.-		K.ALPGVVALSSK.-
380	403	3	2417.21	2.5	1	72	24.1	95.00%	K.YGKEDALSHVSTGGGASLELLEGK.A		K.YGKEDALSHVSTGGGASLELLEGK.A
383	403	2	2069.04	3.6	0	81.1	24.4	95.00%	K.EDALSHVSTGGGASLELLEGK.A		K.EDALSHVSTGGGASLELLEGK.A
321	329	2	994.54	5.5	1	50.2	21.9	95.00%	K.FAEVITTSK.T		K.FAEVITTSK.T
75	86	3	1304.74	4.3	1	59.4	19.6	95.00%	K.YSLKPVAAELSK.L		K.YSLKPVAAELSK.L
151	169	2	2020.01	5.9	1	113	24.8	95.00%	K.SLTSLGDIFVNDAFGTAHR.A		K.SLTSLGDIFVNDAFGTAHR.A
295	316	2	2246.01	3.8	1	60.5	27.3	95.00%	K.VGSATAEEGIPDGWMGLDCGPK.S	Carbamidomethyl (+57)	K.VGSATAEEGIPDGWMGLDCGPK.S
214	227	2	1596.91	-1.6	1	61.3	18.1	95.00%	K.VADKIQLIDNLLDK.V		K.VADKIQLIDNLLDK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
2	ENO11_SCHPO	74.72%	100%	28

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
258	263	2	765.39	4.7	1	25.9	24.3	91.50%	K.YDLDIK.A		K.YDLDIK.A
415	425	2	1223.55	-1.6	1	50.7	25.3	95.00%	R.IEEELGSEGVY.A		R.IEEELGSEGVYAGAHAGK.Y
361	374	2	1608.72	-1.2	1	51	26.4	95.00%	R.MSYEAGWGVMVSHR.S		R.MSYEAGWGVMVSHR.S
94	103	2	1129.63	-1.3	1	28.6	21	94.90%	F.LLKLDGTENK.S		K.AADEFLLKLDGTENK.S
311	328	2	1963.98	4.2	1	93.2	25.2	95.00%	K.AETDFQIVGDDLTVTNVK.R		K.AETDFQIVGDDLTVTNVK.R
65	79	2	1477.87	4	0	73.7	15.3	95.00%	K.AVGNVNNIIAPAVVK.A		K.AVGNVNNIIAPAVVK.A
106	120	2	1560.82	4.2	0	61.3	23.8	95.00%	K.LGANAILGVSMAICR.A	Oxidation (+16)/ Carbamidomethyl (+57)	K.LGANAILGVSMAICR.A

170	184	2	1606.79	1.5	1	59.1	26.1	95.00%	F.MILPTGAPSFSEAMR.W		K.GPYVLPVPSFNVLNGGSHAGGDLAFQEFMILPTGAPSFSEAMR.W
170	179	2	1032.53	2.2	1	49.5	23.9	95.00%	F.MILPTGAPSF.S		K.GPYVLPVPSFNVLNGGSHAGGDLAFQEFMILPTGAPSFSEAMR.W
273	287	2	1812.96	4.5	1	75.4	22.6	95.00%	K.LTYQQLTDLYVELSK.K		K.LTYQQLTDLYVELSK.K
200	234	3	3596.81	3.8	2	68.4	21.1	95.00%	K.RYGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A		K.RYGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
243	257	2	1598.79	4.2	1	56.6	25	95.00%	K.IGLDVASSEFYVDGK.Y		K.IGLDVASSEFYVDGK.Y
409	414	2	806.43	5.7	1	29.4	25.1	95.00%	K.YNELLR.I		K.YNELLR.I
375	396	2	2201.14	2.9	1	122	22.5	95.00%	R.SGETADTFISHLTVGIGAGQLK.S		R.SGETADTFISHLTVGIGAGQLK.S
89	96	2	905.49	4.7	1	57.4	23.5	95.00%	K.AADEFLLK.L		K.AADEFLLK.L
80	88	2	1002.5	4.3	0	41.9	22.7	95.00%	K.ANLDVTDQK.A		K.ANLDVTDQK.A
185	194	2	1204.59	5.4	1	34	24.9	95.00%	R.WGAETYHTLK.S		R.WGAETYHTLK.S
346	360	2	1585.85	6	0	90.8	21.9	95.00%	K.VNQIGSVTESLNAVR.M		K.VNQIGSVTESLNAVR.M
288	303	2	1965.9	0.55	2	53.7	26.6	95.00%	K.KYPIVSIEDPFDQDDW.S		K.KYPIVSIEDPFDQDDWSAWTHMK.A
89	103	2	1662.85	3.3	1	74.4	24.4	95.00%	K.AADEFLLKLDGTENK.S		K.AADEFLLKLDGTENK.S
145	169	2	2572.27	3.7	1	56.5	24.4	95.00%	Y.VLPVPSFNVLNGGSHAGGDLAFQEF.M	Deamidation (+1)	K.GPYVLPVPSFNVLNGGSHAGGDLAFQEFMILPTGAPSFSEAMR.W
201	234	3	3440.71	3.8	1	65	22.1	95.00%	R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
311	329	2	2120.09	4.8	1	105	23.7	95.00%	K.AETDFQIVGDDLTVTNVKR.L		K.AETDFQIVGDDLTVTNVKR.L
16	32	2	1837.91	-1.8	0	95	25.4	95.00%	R.GNPTVEVDLTTETGIHR.A		R.GNPTVEVDLTTETGIHR.A
33	50	2	1886.97	4.8	1	105	24.3	95.00%	R.AIVPSGASTGIWEALEMR.D		R.AIVPSGASTGIWEALEMR.D
338	345	2	901.51	4.7	0	31.4	21.6	95.00%	K.CANALLLK.V	Carbamidomethyl (+57)	K.CANALLLK.V
415	432	2	1815.87	5.1	1	83.2	25.9	95.00%	R.IEEELGSEGVYAGAHAGK.Y		R.IEEELGSEGVYAGAHAGK.Y
383	396	2	1392.81	-0.94	0	64.3	16.4	95.00%	F.ISHLTVGIGAGQLK.S		R.SGETADTFISHLTVGIGAGQLK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
3	G3P1_SCHPO	60.71%	100%	20

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
169	186	2	1886.94	0.74	0	70.3	25.2	95.00%	F.GIEEGLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK.T
67	86	3	2203.13	3.8	1	43.2	23.2	95.00%	K.LVIDGNAIDVHNERDPADIK.W		K.LVIDGNAIDVHNERDPADIK.W
249	263	4	1673.93	-1.3	1	32.6	20.1	95.00%	K.LAKPTNYEDIKAAIK.A		K.LAKPTNYEDIKAAIK.A
132	145	2	1574.79	-1.7	2	42.5	24.9	95.00%	Y.VVGVNEEKFNPSEK.V		K.DAPMYVVGVNEEKFNPSEK.V
272	295	2	2589.13	0.12	1	55.4	27.3	95.00%	K.GVLGYTEDAVVSTDFCGDNHSSIF.D	Carbamidomethyl (+57)	K.GVLGYTEDAVVSTDFCGDNHSSIFDASAGIQLSPQFVK.L
119	139	2	2245.18	4	2	70	21.7	95.00%	R.VIISAPSKDAPMYVVGVNEEK.F		R.VIISAPSKDAPMYVVGVNEEK.F
127	139	2	1449.69	3.7	1	45.1	25.6	95.00%	K.DAPMYVVGVNEEK.F		K.DAPMYVVGVNEEK.F
146	162	2	1819.88	-1.9	0	82.7	26	95.00%	K.VISNASCTTNCLAPLAK.V	Carbamidomethyl (+57)/ Deamidation (+1)/ Carbamidomethyl (+57)	K.VISNASCTTNCLAPLAK.V
6	13	2	819.43	6.2	1	38.4	23.6	95.00%	K.VGINGFGR.I	Deamidation (+1)	K.VGINGFGR.I
234	248	2	1623.93	3.7	1	72.7	18.6	95.00%	F.RVPTPDVSVVDLTVK.L		K.LTGMAFRVPTPDVSVVDLTVK.L
249	259	3	1290.69	4.5	1	28.4	24	95.00%	K.LAKPTNYEDIK.A		K.LAKPTNYEDIK.A
56	66	2	1193.6	4.2	1	61.8	25.3	95.00%	R.FDGSVEIKDGK.L		R.FDGSVEIKDGK.L
235	248	2	1467.82	3.7	0	76.5	18.6	95.00%	R.VPTPDVSVVDLTVK.L		R.VPTPDVSVVDLTVK.L
64	86	3	2503.28	3.2	1	25.1	23.4	94.20%	K.DGKLVIDGNAIDVHNERDPADIK.W		K.DGKLVIDGNAIDVHNERDPADIK.W
296	309	2	1459.77	1.2	1	63.1	23.7	95.00%	F.DASAGIQLSPQFVK.L		K.GVLGYTEDAVVSTDFCGDNHSSIFDASAGIQLSPQFVK.L

323	334	2	1304.75	5.7	2	40.6	17.6	95.00%	R.RVVDLVAYTAAK.D	R.RVVDLVAYTAAK.D
324	334	2	1148.65	6.2	1	55.4	19.8	95.00%	R.VVDLVAYTAAK.D	R.VVDLVAYTAAK.D
163	186	2	2576.28	-0.043	1	100	24.2	95.00%	K.VINDTFGIEEGLMTTVHATTATQK.T	K.VINDTFGIEEGLMTTVHATTATQK.T
324	336	2	1377.72	3.8	1	68.7	24.4	95.00%	R.VVDLVAYTAAKDN.-	R.VVDLVAYTAAKDN.-
201	215	2	1343.71	4.7	0	69.9	22.9	95.00%	R.GASANIIPSSTGAAK.A	R.GASANIIPSSTGAAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
4	METE_SCHPO	59.42%	100%	44

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
638	653	2	1752.84	0.79	1	72.8	25.9	95.00%	R.LATAAVQDDTQIHSHF.C		R.LATAAVQDDTQIHSHFCYSDFNDIFDAIQR.L
434	449	2	1746.96	0.042	1	67.8	20.7	95.00%	K.LPLFPTTTIGSFPQTK.E		K.LPLFPTTTIGSFPQTK.E
128	141	2	1732.84	0.5	1	32.6	25.7	95.00%	Y.HFLRPEVSEETDFK.L		K.WFDSNYHFLRPEVSEETDFK.L
482	504	3	2702.27	0.079	2	26.7	26.5	94.30%	K.FQEEVGLDVLVHGEPERNDMVQY.F		K.FQEEVGLDVLVHGEPERNDMVQYFGER.M
156	171	2	1683.96	0.76	1	42.3	17.3	95.00%	K.EAGIITRPVLVGPVTY.L		K.EAGIITRPVLVGPVTYLFIAK.A
684	690	2	813.51	5.6	0	34.2	20.8	95.00%	K.LLNVLSR.Y		K.LLNVLSR.Y
393	404	2	1284.67	4.4	0	68.2	21.8	95.00%	R.AESPITNVEAVR.E		R.AESPITNVEAVR.E
707	716	3	1186.64	4.9	1	25.6	23	94.70%	R.VPPVSEFKER.I		R.VPPVSEFKER.I
391	404	2	1511.81	4	1	42.1	22.1	95.00%	K.ARAESPITNVEAVR.E		K.ARAESPITNVEAVR.E
67	76	2	1225.51	0.64	1	31.4	26	95.00%	Y.DQIMDHSFSF.N		K.AQGVDIIPSNDFSLYDQIMDHSFSFNVIPPR.Y
325	351	3	2884.5	3.5	0	47.3	20	95.00%	R.VQVASSSSILHIPHSLSGEDQINPEIK.R		R.VQVASSSSILHIPHSLSGEDQINPEIK.R
325	352	3	3040.6	0.27	1	79.7	18.3	95.00%	R.VQVASSSSILHIPHSLSGEDQINPEIKR.W		R.VQVASSSSILHIPHSLSGEDQINPEIKR.W
261	273	2	1330.77	-2.1	0	58.6	18.6	95.00%	K.GLPIAGVHVDVVR.A		K.GLPIAGVHVDVVR.A
104	121	2	1742.9	4.6	1	66.3	23.7	95.00%	R.AATADKAAVDVPAGEMVK.W		R.AATADKAAVDVPAGEMVK.W
128	140	2	1604.75	0.41	1	36.6	26.5	95.00%	Y.HFLRPEVSEETDF.K		K.WFDSNYHFLRPEVSEETDFK.L
281	299	2	1881.07	-1.5	0	98.4	17	95.00%	R.ALAVLGENQIISVGVVSGR.N		R.ALAVLGENQIISVGVVSGR.N
147	155	2	1034.53	5.7	1	36.8	24.9	95.00%	K.ALDEFLEAK.E		K.ALDEFLEAK.E
547	560	2	1596.79	3.6	1	50.8	25.3	95.00%	K.ESQYAQSITSKPMK.G		K.ESQYAQSITSKPMK.G
461	473	2	1539.76	4.1	1	67.2	24.8	95.00%	K.GLISQEEYDAFIR.K		K.GLISQEEYDAFIR.K
668	679	2	1288.66	3.8	0	37	24.7	95.00%	R.LDADVVSIENSK.S		R.LDADVVSIENSK.S
527	546	3	2267.24	3.3	1	44.5	19.1	95.00%	R.CVRPPIIVGDVYRPAPMTVK.E	Carbamidomethyl (+57)	R.CVRPPIIVGDVYRPAPMTVK.E
631	637	2	877.45	5.9	1	49	23.7	95.00%	K.WAIDAFR.L		K.WAIDAFR.L
577	601	3	2805.42	3	1	36.5	22.2	95.00%	R.DDVHDSVQAQQIALGLRDEVLDLEK.A		R.DDVHDSVQAQQIALGLRDEVLDLEK.A
156	176	3	2256.33	3.9	1	51.3	9.03	95.00%	K.EAGIITRPVLVGPVTYLFIAK.A		K.EAGIITRPVLVGPVTYLFIAK.A
656	667	2	1439.67	0.67	1	40.4	26.4	95.00%	Y.SDFNDIFDAIQR.L		R.LATAAVQDDTQIHSHFCYSDFNDIFDAIQR.L
561	571	2	1184.7	5.1	0	40.5	18.9	95.00%	K.GMLTAPITILR.W		K.GMLTAPITILR.W
4	11	2	845.48	4.8	1	33.3	22.7	95.00%	K.SAVLGFPR.I		K.SAVLGFPR.I
707	714	2	901.49	4.3	1	27.7	24.3	94.00%	R.VPPVSEFK.E		R.VPPVSEFK.E
691	706	2	1818.88	3.8	1	84	25.8	95.00%	R.YTSCIGPGLFDIHSPR.V	Carbamidomethyl (+57)	R.YTSCIGPGLFDIHSPR.V
499	508	2	1257.55	4.4	1	53.6	26	95.00%	R.NDMVQYFGER.M		R.NDMVQYFGER.M
243	260	2	1982.08	3.5	1	54.1	18.9	95.00%	K.LILTTYFGSLQSNADVLK.G		K.LILTTYFGSLQSNADVLK.G
85	95	2	1201.59	-1.1	1	28.7	25.4	94.70%	R.LSGLSSLDTYF.A		R.LSGLSSLDTYFAMGR.G
75	82	2	928.51	1.3	1	28.9	22.2	95.00%	F.SFNVIPPR.Y		K.AQGVDIIPSNDFSLYDQIMDHSFSFNVIPPR.Y
727	738	2	1466.7	4.2	1	48	26.1	95.00%	K.DHLWLNPDCGLK.T	Carbamidomethyl (+57)	K.DHLWLNPDCGLK.T
428	449	3	2402.33	4.8	2	46	15.8	95.00%	K.QQASLKLPLFPTTTIGSFPQTK.E		K.QQASLKLPLFPTTTIGSFPQTK.E
249	260	2	1277.66	-1.7	1	40	24.8	95.00%	Y.FGSLQSNADVLK.G		K.LILTTYFGSLQSNADVLK.G
527	538	2	1386.74	1.8	1	48.6	22.8	95.00%	R.CVRPPIIVGDVY.R	Carbamidomethyl (+57)	R.CVRPPIIVGDVYRPAPMTVK.E
64	74	2	1354.59	0.73	1	28.1	25.8	93.60%	F.SLYDQIMDHSF.S		K.AQGVDIIPSNDFSLYDQIMDHSFSFNVIPPR.Y
723	738	3	1927.98	4	2	24.5	23.9	93.50%	K.HVPKDHLWLNPDCGLK.T	Carbamidomethyl (+57)	K.HVPKDHLWLNPDCGLK.T

361	369	2	1017.56	4.9	0	30.5	22.3	95.00%	K.CAELAILTK.A	Carbamidomethyl (+57)	K.CAELAILTK.A
606	615	2	1199.6	4.3	0	55.1	23.2	95.00%	K.VIQCDEPALR.E	Carbamidomethyl (+57)	K.VIQCDEPALR.E
67	74	2	991.41	0.79	1	29.7	25.4	95.00%	Y.DQIMDHSF.S		K.AQGVDIIPSNDFSLYDQIMDHSFSFNVIPPR.Y
85	99	2	1616.79	4.1	1	63.5	25.7	95.00%	R.LSGLSSLDTYFAMGR.G		R.LSGLSSLDTYFAMGR.G
30	40	2	1132.6	4.2	0	58.1	23.1	95.00%	K.TSAEELLATAK.Q		K.TSAEELLATAK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
5	EF1A1_SCHPO	53.70%	100%	23

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
265	288	2	2443.34	0.61	1	51.8	17.4	95.00%	R.VETGVIKPGMIVTFAPAGVTTEVK.S		R.VETGVIKPGMIVTFAPAGVTTEVK.S
289	308	2	2109.94	0.32	1	46	27.3	95.00%	K.SVEMHHESLDAGLPGDNVGF.N		K.SVEMHHESLDAGLPGDNVGFNVK.N
195	208	2	1632.69	0.24	1	29.2	27.4	92.80%	F.QGDNMIEPTTNMPW.Y		K.TVPFVPVSGFQGDNMIEPTTNMPWYQGWQK.E
223	245	4	2516.4	3.1	1	25	14.9	95.00%	K.GKTLLEAIDSIEPPARPTDKPLR.L		K.GKTLLEAIDSIEPPARPTDKPLR.L
356	369	2	1607.76	0.9	0	30.9	26	95.00%	Y.SPVLDCHTAHIACK.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.NDPPMGCASFTAQVIILNHPGQISAGYSPVLDCHTAHIACK.F
279	288	2	971.53	-0.23	0	29.2	21.3	95.00%	F.APAGVTTEVK.S		R.VETGVIKPGMIVTFAPAGVTTEVK.S
320	338	3	2067.86	0.85	2	32.7	27.9	95.00%	R.RGNVCGDSKNDPPMGCASF.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.RGNVCGDSKNDPPMGCASFTAQVIILNHPGQISAGYSPVLDCHTAHIACK.F
135	146	2	1313.74	3.9	1	45.8	20.8	95.00%	R.EHALLAYTLGVK.Q		R.EHALLAYTLGVK.Q
370	376	2	848.47	4.7	1	25.9	22.7	91.40%	K.FAELIEK.I		K.FAELIEK.I
329	338	2	1094.42	2	1	34.3	23.7	95.00%	K.NDPPMGCASF.T	Carbamidomethyl (+57)	K.NDPPMGCASFTAQVIILNHPGQISAGYSPVLDCHTAHIACK.F
265	278	2	1489.82	0.12	1	49.4	21	95.00%	R.VETGVIKPGMIVTF.A		R.VETGVIKPGMIVTFAPAGVTTEVK.S
402	421	2	2268.08	4	1	67.5	26.2	95.00%	K.MVPSKPMCVEAFTDYAPLGR.F	Carbamidomethyl (+57)	K.MVPSKPMCVEAFTDYAPLGR.F
339	355	2	1780.95	1.5	1	55.8	21.8	95.00%	F.TAQVIILNHPGQISAGY.S		K.NDPPMGCASFTAQVIILNHPGQISAGYSPVLDCHTAHIACK.F
147	154	2	883.55	5.8	0	26.4	16.7	92.20%	K.QLIVAVNK.M		K.QLIVAVNK.M
254	264	2	1024.61	4.2	0	65.4	15.1	95.00%	K.IGGIGTVPVGR.V		K.IGGIGTVPVGR.V
6	20	2	1529.84	4.6	0	62.9	21.8	95.00%	K.GHINVVVIGHVDSGK.S		K.GHINVVVIGHVDSGK.S
289	311	3	2451.16	4	1	64.2	26.2	95.00%	K.SVEMHHESLDAGLPGDNVGFNVK.N		K.SVEMHHESLDAGLPGDNVGFNVK.N
321	338	2	1911.76	2.3	2	40	27.2	95.00%	R.GNVCGDSKNDPPMGCASF.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GNVCGDSKNDPPMGCASFTAQVIILNHPGQISAGYSPVLDCHTAHIACK.F
185	208	2	2663.24	1.2	1	51.8	26.4	95.00%	K.TVPFVPVSGFQGDNMIEPTTNMPW.Y		K.TVPFVPVSGFQGDNMIEPTTNMPWYQGWQK.E
225	245	3	2331.28	0.63	0	38.4	16.6	95.00%	K.TLLEAIDSIEPPARPTDKPLR.L		K.TLLEAIDSIEPPARPTDKPLR.L
155	164	2	1151.51	6.4	1	75.8	24.7	95.00%	K.MDTTGWSQAR.F		K.MDTTGWSQAR.F
85	96	2	1340.69	4.4	1	66.1	23.6	95.00%	K.YNVTVIDAPGHR.D		K.YNVTVIDAPGHR.D
246	253	2	974.55	4.1	1	32.1	22.3	95.00%	R.LPLQDVYK.I		R.LPLQDVYK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
6	KPYK_SCHPO	68.96%	100%	31

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
233	243	2	1214.66	3.9	1	28.5	22.1	94.90%	R.EVLGEEGKNIK.I		R.EVLGEEGKNIK.I
57	64	2	941.37	-0.65	1	41.1	23.1	95.00%	R.MNFSHGSY.E		R.MNFSHGSYEYHQSVIDNAR.K
422	433	3	1430.8	-1.9	1	46	19	95.00%	K.YRPSIPIVMVTR.C		K.YRPSIPIVMVTR.C
248	271	2	2647.29	0.75	1	80.8	24.7	95.00%	K.IENQQGVNNFDSILDVTDGIMVAR.G		K.IENQQGVNNFDSILDVTDGIMVAR.G
191	207	2	1884.98	-2.3	1	63.4	23.2	95.00%	K.TDVDLPALSEKDKADLR.F		K.TDVDLPALSEKDKADLR.F

77	98	3	2294.27	0.95	1	50.3	17.9	95.00%	K.ASATNPLFPLAIALDTKGPEIR.T		K.ASATNPLFPLAIALDTKGPEIR.T
65	75	2	1330.63	-0.99	1	45.2	26.1	95.00%	Y.EYHQSVIDNAR.K		R.MNFSHGSYEYHQSVIDNAR.K
468	477	2	1186.55	5.3	1	54.8	24.9	95.00%	R.VAYGCQQAYK.M	Carbamidomethyl (+57)	R.VAYGCQQAYK.M
294	319	4	2965.41	3.9	1	47.2	25.4	95.00%	K.CNIAGKPVACATQMLESMTYNPR PTR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CNIAGKPVACATQMLESMTYNPR PTR.A
405	417	2	1287.72	5.7	0	62	20.8	95.00%	K.AIVVLSTSGNTAR.L		K.AIVVLSTSGNTAR.L
212	223	2	1368.69	4.2	1	39.8	24.3	95.00%	K.NGVDMIFASFIR.R		K.NGVDMIFASFIR.R
381	404	2	2460.23	3.5	0	76.2	23.4	95.00%	R.RPLECATETTAVAAIGASIESDAK. A	Carbamidomethyl (+57)	R.RPLECATETTAVAAIGASIESDAK. A
191	201	2	1186.61	4.4	0	25.5	23.3	90.70%	K.TDVDLPALSEK.D		K.TDVDLPALSEK.D
487	497	2	1053.66	5.9	0	39.5	13	95.00%	K.IIVLQGAVGGK.G		K.IIVLQGAVGGK.G
446	460	2	1793.89	-0.062	2	35.4	25.6	95.00%	R.GVYPVIYEKEPLSDW.Q		R.GVYPVIYEKEPLSDWQK.D
294	313	2	2244.01	0.25	1	97.2	27.2	95.00%	K.CNIAGKPVACATQMLESMTY.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CNIAGKPVACATQMLESMTYNPR PTR.A
224	232	3	1107.62	3.9	1	57.7	19.8	95.00%	R.RAEDVIHIR.E		R.RAEDVIHIR.E
10	26	2	1880.98	3.7	1	90.9	22.6	95.00%	K.QWVAGLNSELDIPAVNR.R		K.QWVAGLNSELDIPAVNR.R
77	93	2	1741.96	-0.82	1	41.5	20.9	95.00%	K.ASATNPLFPLAIALDTK.G		K.ASATNPLFPLAIALDTK.G
225	232	2	951.52	5	0	30.1	22.5	95.00%	R.AEDVIHIR.E		R.AEDVIHIR.E
76	98	3	2422.36	0.36	2	80.9	15.1	95.00%	R.KASATNPLFPLAIALDTKGPEIR.T		R.KASATNPLFPLAIALDTKGPEIR.T
28	37	2	1088.6	5	0	46.3	21.8	95.00%	R.TSIICTIGPK.S	Carbamidomethyl (+57)	R.TSIICTIGPK.S
191	203	2	1429.74	3.8	1	45.1	24	95.00%	K.TDVDLPALSEKDK.A		K.TDVDLPALSEKDK.A
345	360	2	1743.82	5.3	1	80.9	27	95.00%	K.GSYPVEAVTYMAETAR.V		K.GSYPVEAVTYMAETAR.V
272	288	2	1770.96	3.8	1	69.1	20.9	95.00%	R.GDLGIEIPASQVFVAQK.M		R.GDLGIEIPASQVFVAQK.M
76	93	2	1870.06	4.2	2	70.7	17.4	95.00%	R.KASATNPLFPLAIALDTK.G		R.KASATNPLFPLAIALDTK.G
99	118	2	2080.98	-0.2	1	49.3	26.8	95.00%	R.TGLTVGGTDYPISSGHEMIF.T		R.TGLTVGGTDYPISSGHEMIFTTDD AYAEK.C
10	27	3	2037.08	4.1	1	30.7	21.6	95.00%	K.QWVAGLNSELDIPAVNRR.T		K.QWVAGLNSELDIPAVNRR.T
320	344	2	2490.22	0.48	0	105	25	95.00%	R.AEVSDVGNAVLDGADLVMLSGE TTK.G		R.AEVSDVGNAVLDGADLVMLSGE TTK.G
99	127	3	3075.41	2.5	1	69.9	25.7	95.00%	R.TGLTVGGTDYPISSGHEMIFTTDD AYAEK.C		R.TGLTVGGTDYPISSGHEMIFTTDD AYAEK.C
47	56	3	1143.62	4.2	1	26	23	95.00%	K.LRDAGMNIVR.M		K.LRDAGMNIVR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
7	ALF_SCHPO	58.94%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
26	50	2	2496.3	0.87	1	83.6	22	95.00%	R.EHGFAIPAINVTSSSTAIAALEAAR .E		R.EHGFAIPAINVTSSSTAIAALEAAR .E
253	261	2	1067.53	0.91	1	35.2	24.6	95.00%	K.TTNDKPVFF.V		K.TTNDKPVFFVFHGGSGSSVNEFR .T
262	275	2	1478.69	1	1	35.4	25.9	95.00%	F.VFHGGSGSSVNEFR.T		K.TTNDKPVFFVFHGGSGSSVNEFR .T
94	112	2	2098.02	4.1	1	63.5	26	95.00%	R.SIAPFFGVPVVMHSDHCAK.K	Carbamidomethyl (+57)	R.SIAPFFGVPVVMHSDHCAK.K
2	19	2	1823.05	3.8	0	65.3	16.3	95.00%	M.GILDIVPTGVITGDNVLK.L		-.MGILDIVPTGVITGDNVLK.L
99	112	2	1582.74	0.45	1	54	26.7	95.00%	F.FGVPVVMHSDHCAK.K	Carbamidomethyl (+57)	R.SIAPFFGVPVVMHSDHCAK.K
285	300	2	1825.89	3.9	1	73.6	25.6	95.00%	K.VNIDTDTQFAYVEGVR.D		K.VNIDTDTQFAYVEGVR.D
294	302	2	1070.5	1.3	2	30.8	23.9	95.00%	F.AYVEGVRDY.V		K.VNIDTDTQFAYVEGVRDYVLK.Y
235	248	2	1564.88	4	1	58.4	17.8	95.00%	K.LQPALLGQHQAYVK.E		K.LQPALLGQHQAYVK.E
54	71	2	1843.96	-1.7	1	94.9	23.4	95.00%	R.SPIILQTSNGGAHFFAGK.E		R.SPIILQTSNGGAHFFAGK.E
54	67	2	1441.72	-1.5	1	67.8	24.4	95.00%	R.SPIILQTSNGGAHF.F	Deamidation (+1)	R.SPIILQTSNGGAHFFAGK.E
131	149	3	2165.05	0.88	1	42.2	25.5	95.00%	K.IHGEPLFSSHMLDLSEEPK.K		K.IHGEPLFSSHMLDLSEEPK.K
80	93	2	1399.76	5.1	1	89.1	21.2	95.00%	K.ASIAGSIAAAHYIR.S		K.ASIAGSIAAAHYIR.S
310	326	2	1794.93	-0.85	1	41.3	23	95.00%	Y.LMTPVGNPEGADKPNKK.K		K.DYLMTPVGNPEGADKPNKK.K
30	50	2	2026.11	0.78	0	96.8	19	95.00%	F.AIPAINVTSSSTAIAALEAAR.E		R.EHGFAIPAINVTSSSTAIAALEAAR .E
345	358	2	1597.83	4.2	1	60.4	23.4	95.00%	R.VLTALEDFYTVNTL.-		R.VLTALEDFYTVNTL.-

196	206	2	1420.66	1.4	1	35.4	26	95.00%	Y.TQPEDIWDVYR.E		K.IWIEMEIGITGGEEDGVDNSHVSHTELYTQPEDIWDVYR.E
131	150	4	2293.15	3.4	1	21.8	24.1	95.00%	K.IHGEPLFSSHMLDLSEEPKK.E		K.IHGEPLFSSHMLDLSEEPKK.E
310	325	2	1666.83	-1	0	50	25.4	95.00%	Y.LMTPVGNPEGADKPNK.K		K.DYLMTPVGNPEGADKPNK.K
54	68	2	1587.8	-1.3	1	86.4	24.7	95.00%	R.SPIILQTSNGGAHFF.A		R.SPIILQTSNGGAHFFAGK.E
80	91	2	1130.57	-1.5	1	60.4	23.6	95.00%	K.ASIAGSIAAAHY.I		K.ASIAGSIAAAHYIR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
8	ADH4_SCHPO	51.66%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
76	87	2	1282.76	5.2	0	44.2	16	95.00%	K.NTLIVTDPGIIK.V		K.NTLIVTDPGIIK.V
366	374	2	1027.63	6.6	0	37.3	18.6	95.00%	R.ISQLVLEVK.I		R.ISQLVLEVK.I
386	398	2	1545.75	-2	2	63.9	26.1	95.00%	K.EKDFDVLVDHAMK.D		K.EKDFDVLVDHAMK.D
169	191	2	2386.26	3.6	0	87.6	21.4	95.00%	K.SSKPQLPLIAINTTAGTASEMTR.F		K.SSKPQLPLIAINTTAGTASEMTR.F
192	200	2	1078.57	4	1	35.5	23.3	95.00%	R.FAIITEETR.H		R.FAIITEETR.H
160	191	3	3376.73	2.5	1	83.5	19.6	95.00%	K.IADYEGVDKSSKPQLPLIAINTTAGTASEMTR.F		K.IADYEGVDKSSKPQLPLIAINTTAGTASEMTR.F
96	129	3	3701.97	2.4	1	70.9	16.3	95.00%	K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVKK.E		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVKK.E
129	148	3	2121.89	-0.81	1	66.3	27.6	95.00%	K.KENCDSMVSIGGGSAHDCAK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.KENCDSMVSIGGGSAHDCAK.G
351	365	2	1707.76	0.58	0	73.6	26.8	95.00%	F.HLGCEEHTAEAALDR.I	Carbamidomethyl (+57)	R.LGDIAFHLGCEEHTAEAALDR.I
345	365	3	2324.09	0.18	1	51.3	27.1	95.00%	R.LGDIAFHLGCEEHTAEAALDR.I	Carbamidomethyl (+57)	R.LGDIAFHLGCEEHTAEAALDR.I
375	385	3	1245.75	-1.6	0	42.6	13.6	95.00%	K.IRPHLVDLGVK.E		K.IRPHLVDLGVK.E
388	415	4	3122.45	0.6	1	19.7	24.9	94.10%	K.DFDVLVDHAMKDACGATNPIQPTHDEVK.A	Carbamidomethyl (+57)	K.DFDVLVDHAMKDACGATNPIQPTHDEVK.A
247	261	2	1516.76	1.9	0	55.8	24.8	95.00%	Y.VSTAANPITDACAVK.C	Carbamidomethyl (+57)	K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
149	159	2	1014.58	4.8	0	36.7	22.1	95.00%	K.GIALLATNGGK.I	Deamidation (+1)	K.GIALLATNGGK.I
210	224	2	1778.79	2.3	1	36.5	26.8	95.00%	K.HTMPILSVNDPETMY.G	Oxidation (+16)/ Oxidation (+16)	K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
109	128	2	2077.08	0.38	0	74.4	22.8	95.00%	Y.DGVQPNPTVGNVNQGLEIVK.K		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K
399	415	2	1851.85	4.5	0	49.6	26.8	95.00%	K.DACGATNPIQPTHDEVK.A	Carbamidomethyl (+57)	K.DACGATNPIQPTHDEVK.A
96	128	3	3573.88	3.6	1	56.5	17.6	95.00%	K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K
109	129	2	2205.18	1.7	1	56	20.5	95.00%	Y.DGVQPNPTVGNVNQGLEIVKK.E		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVKK.E
130	148	2	1993.8	3.7	0	87.9	27.1	95.00%	K.ENCDSMVSIGGGSAHDCAK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.ENCDSMVSIGGGSAHDCAK.G
160	168	2	1008.48	5	1	40.9	25.4	95.00%	K.IADYEGVDK.S		K.IADYEGVDK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
9	PDC2_SCHPO	47.98%	100%	28

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
204	214	2	1130.62	4.6	0	53.5	22.6	95.00%	K.ATDIAAELISK.K		K.ATDIAAELISK.K
516	525	2	1047.55	4.8	0	31.2	23.9	95.00%	K.TGEELTSAIK.V		K.TGEELTSAIK.V
228	237	2	949.49	5	1	30.2	24.5	95.00%	R.AAGAESAFVK.L		R.AAGAESAFVK.L
532	555	2	2764.23	2.9	1	69.2	27.2	95.00%	K.EGPTLIECAIDTDDCTQELVDWGK.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.EGPTLIECAIDTDDCTQELVDWGK.A
147	159	2	1436.71	3.9	0	60.9	25.7	95.00%	R.AEDAPVMIDHAIR.Q		R.AEDAPVMIDHAIR.Q
329	340	2	1425.76	4.3	1	95.2	22.6	95.00%	R.VYMAEFLELLAK.K		R.VYMAEFLELLAK.K
146	159	3	1592.81	-1.1	1	59	25	95.00%	K.RAEDAPVMIDHAIR.Q		K.RAEDAPVMIDHAIR.Q
369	378	2	1157.64	5	1	28	22.1	94.40%	K.AALNRVEVMR.Q		K.AALNRVEVMR.Q
137	146	2	1101.64	5.4	1	51.2	19.8	95.00%	K.LTCAAVAIKR.A	Carbamidomethyl (+57)	K.LTCAAVAIKR.A
26	37	2	1429.72	4.2	1	38.3	24.3	95.00%	K.NHFVVPGDYNLR.L		K.NHFVVPGDYNLR.L

2	14	2	1402.63	-1.6	2	67.7	27	95.00%	M.TKDAESTMTVGTY.L		-.MTKDAESTMTVGTYLAQR.L
464	474	2	1310.81	4.6	1	66.2	13.2	95.00%	K.LPVLIFLLNNR.G		K.LPVLIFLLNNR.G
450	461	2	1402.72	0.57	0	51.5	23.6	95.00%	F.QLTGQEISQMIR.H		R.TIVMVGDGSFQLTGQEISQMIR.H
216	225	3	1064.66	3.8	0	29.3	12	95.00%	K.EKPILLAGPK.L		K.EKPILLAGPK.L
136	146	3	1229.73	4.2	1	53.3	17.2	95.00%	K.KLTCAAVAIKR.A	Carbamidomethyl (+57)	K.KLTCAAVAIKR.A
160	203	4	4837.52	3.1	1	48.7	20.2	95.00%	R.QAILQHKPVYIEIPTNMANQPCPVPGPISAVISPEISDKESLEK.A	Carbamidomethyl (+57)	R.QAILQHKPVYIEIPTNMANQPCPVPGPISAVISPEISDKESLEK.A
440	461	2	2409.21	3.3	1	90.9	24	95.00%	R.TIVMVGDGSFQLTGQEISQMIR.H		R.TIVMVGDGSFQLTGQEISQMIR.H
238	253	2	1690.85	4.5	1	52.2	24.4	95.00%	K.LAEALNCAAFIMPAAK.G	Deamidation (+1)/ Carbamidomethyl (+57)	K.LAEALNCAAFIMPAAK.G
264	278	2	1599.74	-1.6	1	76.2	27	95.00%	Y.AGVYWGEVSSSETTK.A		K.NYAGVYWGEVSSSETTK.A
204	215	2	1258.72	4.6	1	64.8	20.6	95.00%	K.ATDIAAELISKK.E		K.ATDIAAELISKK.E
304	316	2	1400.69	0.13	1	26.4	25.1	92.20%	R.AAPNPNILLNSDY.T		R.AAPNPNILLNSDYTSVSIPGYVFSR.V
19	25	2	770.49	4.3	0	34.4	16	95.00%	R.LVEIGIK.N		R.LVEIGIK.N
462	474	3	1575.97	4.8	2	29.2	7.78	95.00%	R.HKLPVLIFLLNNR.G		R.HKLPVLIFLLNNR.G
2	18	2	1870.92	4.3	2	129	25.4	95.00%	M.TKDAESTMTVGTYLAQR.L		-.MTKDAESTMTVGTYLAQR.L
392	405	2	1583.69	-1.6	1	80.7	26.5	95.00%	Y.AETGDSWFNGLQMK.L	Deamidation (+1)	R.QIQGLVDSNTTLYAETGDSWFNGLQMK.L
136	145	2	1073.63	3.9	1	39.6	17.2	95.00%	K.KLTCAAVAIK.R	Carbamidomethyl (+57)	K.KLTCAAVAIK.R
4	18	2	1641.77	4.2	1	65.2	26.2	95.00%	K.DAESTMTVGTYLAQR.L		K.DAESTMTVGTYLAQR.L
268	278	2	1209.55	1.4	1	49.4	25.4	95.00%	Y.WGEVSSSETTK.A		K.NYAGVYWGEVSSSETTK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
10	GLYD_SCHPO	57.60%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
160	179	2	2321.05	-0.48	1	35.9	27.2	95.00%	R.VDPNTGLIDYDMLEHDAQLF.R	Oxidation (+16)	R.VDPNTGLIDYDMLEHDAQLFRPK.I
232	243	2	1363.66	0.87	1	30.4	25.3	95.00%	F.EYADVVTTTTHK.S		R.QIADSVNAYLVVDMAHISGLVSAGVIPSPFEYADVVTTTTHK.S
97	123	3	2996.43	3.4	1	55	25.2	95.00%	K.WGVNVQCLSGSPANMQVYQAIMPPHGR.L	Carbamidomethyl (+57)	K.WGVNVQCLSGSPANMQVYQAIMPPHGR.L
59	67	2	998.45	5.1	1	32.9	24.3	95.00%	K.YSEGYPGAR.Y		K.YSEGYPGAR.Y
277	302	3	2725.45	2.8	1	25.2	18.4	94.30%	K.INFSVFPGHQGGPHNHTITALAVALK.Q		K.INFSVFPGHQGGPHNHTITALAVALK.Q
124	139	2	1652.8	0.059	1	39.3	25.9	95.00%	R.LMGLDLPSGGHLSHGY.Q		R.LMGLDLPSGGHLSHGYQTDTK.K
334	349	2	1669.84	3.9	0	85	24.1	95.00%	K.LAADGTDSHMVLVDVK.S		K.LAADGTDSHMVLVDVK.S
303	312	2	1314.55	-0.51	2	36.4	25.9	95.00%	K.QCQEPAYKEY.Q	Carbamidomethyl (+57)	K.QCQEPAYKEYQAQVVK.N
2	24	2	2616.28	-0.15	1	57.4	24.7	95.00%	M.SSNDSIMLTPLKEQDPTVAEIMR.H	Acetyl (+42)	-.MSSNDSIMLTPLKEQDPTVAEIMR.H
183	193	2	1209.62	4.5	1	57.8	24.1	95.00%	K.ILVAGTSAYCR.L	Carbamidomethyl (+57)	K.ILVAGTSAYCR.L
453	467	2	1734.83	4.4	2	41.4	26	95.00%	K.EVAEWASSFPLADKW.-		K.EVAEWASSFPLADKW.-
361	371	2	1254.76	4.6	0	48.8	16.3	95.00%	R.VLELINIVTNK.N		R.VLELINIVTNK.N
458	467	2	1120.55	-1.2	2	61.9	24.1	95.00%	W.ASSFPLADKW.-		K.EVAEWASSFPLADKW.-
74	85	2	1550.75	4.7	1	96.3	26	95.00%	K.FIDQIETLCQER.A	Carbamidomethyl (+57)	K.FIDQIETLCQER.A
86	96	2	1129.62	5.1	1	54.8	23.3	95.00%	R.ALAAFNLDPAK.W		R.ALAAFNLDPAK.W
413	422	2	1075.61	4.3	1	49.9	21.1	95.00%	R.ALTFAANLQK.E		R.ALTFAANLQK.E
438	452	2	1729.9	3.9	1	75.9	22.5	95.00%	K.LGEGEQYPELVQLQK.E		K.LGEGEQYPELVQLQK.E
46	58	2	1321.64	4.2	0	41.4	25.9	95.00%	R.AVMDALGSVMSNK.Y		R.AVMDALGSVMSNK.Y
160	182	3	2686.31	2.9	1	31.8	24.1	95.00%	R.VDPNTGLIDYDMLEHDAQLFRPK.I		R.VDPNTGLIDYDMLEHDAQLFRPK.I
436	452	2	1929.02	-1.6	2	61	22.8	95.00%	K.AKLGEGEQYPELVQLQK.E		K.AKLGEGEQYPELVQLQK.E
406	412	2	878.45	4.3	1	35.8	24	95.00%	R.VVDYIDR.A		R.VVDYIDR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
11	PMGY_SCHPO	68.25%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
122	139	2	1962.92	-0.12	1	81.3	27	95.00%	R.SYDIAPPNGESLKDTAER.V	Deamidation (+1)	R.SYDIAPPNGESLKDTAER.V
111	120	2	1271.65	5.7	1	79.8	23.6	95.00%	K.WGAEQVQIWR.R		K.WGAEQVQIWR.R
30	40	2	1157.63	0.84	1	26.7	22.9	92.70%	W.KDPALSETGIK.E		K.LNLFTGWKDPALSETGIK.E
70	90	2	2429.25	3.7	1	89.6	23.2	95.00%	K.TCQIILEEVGEPNLETIKSEK.L	Carbamidomethyl (+57)	K.TCQIILEEVGEPNLETIKSEK.L
27	40	3	1501.78	1.3	1	45.3	23.6	95.00%	F.TGWKDPALSETGIK.E		K.LNLFTGWKDPALSETGIK.E
146	157	2	1320.78	4.4	1	36.9	14.3	95.00%	K.STIVPHILKGEK.V		K.STIVPHILKGEK.V
2	14	2	1439.81	5.3	0	52	18.1	95.00%	M.TTEAAPNLLVLTR.H	Acetyl (+42)	-.MTTEAAPNLLVLTR.H
70	87	2	2085.08	4.2	0	96.7	23.3	95.00%	K.TCQIILEEVGEPNLETIK.S	Carbamidomethyl (+57)	K.TCQIILEEVGEPNLETIK.S
169	184	2	1714.92	4	0	69.3	21.5	95.00%	R.ALIMDLEGLTGDQIVK.R		R.ALIMDLEGLTGDQIVK.R
169	185	2	1871.02	2.9	1	111	19.8	95.00%	R.ALIMDLEGLTGDQIVKR.E		R.ALIMDLEGLTGDQIVKR.E
158	168	2	1149.67	4.5	0	26.5	16.4	92.50%	K.VLIAAHGNSLR.A		K.VLIAAHGNSLR.A
95	104	2	1169.58	4.8	1	46.4	24.2	95.00%	R.YYGDLQGLNK.D		R.YYGDLQGLNK.D
186	202	2	1854	4.1	1	68.2	20.9	95.00%	R.ELATGVPIVYHLDKDGK.Y		R.ELATGVPIVYHLDKDGK.Y
1	14	2	1528.84	4.4	0	53	21.9	95.00%	-.MTTEAAPNLLVLTR.H		-.MTTEAAPNLLVLTR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
12	SAHH_SCHPO	49.19%	100%	20

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
20	35	2	1782.92	-1.1	0	79.9	23.9	95.00%	K.ELEIAENEMPGLIAVR.E		K.ELEIAENEMPGLIAVR.E
216	227	2	1117.62	4.3	1	46.5	22.5	95.00%	K.VAVVAGFGDVGK.G		K.VAVVAGFGDVGK.G
119	143	3	2681.36	2.8	1	63.5	22.9	95.00%	K.SFPSGKPLNMILDDGGDLTALVHER.H		K.SFPSGKPLNMILDDGGDLTALVHER.H
176	187	2	1255.68	4.6	0	42.1	21.2	95.00%	K.VPAINVNDSVTK.S		K.VPAINVNDSVTK.S
318	328	2	1281.71	3.7	0	30.2	20.1	95.00%	K.DVVNIKPQVDR.Y		K.DVVNIKPQVDR.Y
345	357	2	1371.66	2.2	1	29.5	24.8	95.00%	R.LVNLGCATGHPSF.V	Carbamidomethyl (+57)	R.LVNLGCATGHPSFVMSCSFTNQVLAQIALWTDNTSYPLGVHMLPK.K
407	427	2	2266.17	-0.085	1	81.4	22.6	95.00%	K.LTTLTSVQSDYLGIPVDGPYK.A		K.LTTLTSVQSDYLGIPVDGPYK.A
314	328	3	1665.93	5.5	1	30.5	18.1	95.00%	K.ANAKDVVNIKPQVDR.Y		K.ANAKDVVNIKPQVDR.Y
8	18	2	1118.61	3.2	1	77.1	22.5	95.00%	K.VADISLAAFGR.K		K.VADISLAAFGR.K
269	280	2	1367.66	4	1	40.1	26.3	95.00%	K.EGQIFVTTTGCR.D	Carbamidomethyl (+57)	K.EGQIFVTTTGCR.D
153	167	2	1647.82	4.5	1	70.1	25.3	95.00%	R.GISEETTTGVHNLYK.M		R.GISEETTTGVHNLYK.M
19	35	2	1911.02	4.5	1	76.1	20.7	95.00%	R.KELEIAENEMPGLIAVR.E		R.KELEIAENEMPGLIAVR.E
336	344	2	1006.6	5	0	31.2	14.6	95.00%	R.HIILLADGR.L		R.HIILLADGR.L
174	187	3	1496.86	5	1	47.8	17.9	95.00%	K.LKVPAINVNDSVTK.S		K.LKVPAINVNDSVTK.S
103	118	2	2053.94	4.3	1	72.2	26.8	95.00%	K.GETEEEYLWCIEQQLK.S	Carbamidomethyl (+57)	K.GETEEEYLWCIEQQLK.S
240	268	3	3119.56	4.6	1	62	22.3	95.00%	R.VIVTEVDPINALQAAMDGFEVTTMEEAVK.E		R.VIVTEVDPINALQAAMDGFEVTTMEEAVK.E
318	332	3	1815	4.1	2	25.1	20	94.20%	K.DVVNIKPQVDRYELK.N		K.DVVNIKPQVDRYELK.N
314	329	3	1828.98	1.4	2	32.3	21.3	95.00%	K.ANAKDVVNIKPQVDRY.E		K.ANAKDVVNIKPQVDRYELK.N
153	166	2	1519.71	-1.6	1	32.4	25.7	95.00%	R.GISEETTTGVHNLY.K		R.GISEETTTGVHNLYK.M
318	329	3	1444.77	-1.2	2	27	23.1	95.00%	K.DVVNIKPQVDRY.E		K.DVVNIKPQVDRYELK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
13	TPIS_SCHPO	64.66%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
160	174	2	1615.9	-1.2	1	67.6	19.3	95.00%	K.IVIAYEPVWAIGTGK.T		K.IVIAYEPVWAIGTGK.T
175	189	2	1678.84	4.6	0	84.5	25.2	95.00%	K.TATPEQAQEVHAEIR.K		K.TATPEQAQEVHAEIR.K
135	145	2	1242.66	4.7	0	39.7	22.2	95.00%	R.EANETINVVVR.Q		R.EANETINVVVR.Q
175	190	2	1806.92	-0.84	1	66.8	24.5	95.00%	K.TATPEQAQEVHAEIRK.W		K.TATPEQAQEVHAEIRK.W
71	90	2	2043.94	-0.59	1	69.5	27.2	95.00%	K.NGAYTGENSAQSLIDAGITY.T		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R
206	218	2	1324.61	4.4	1	76.9	26.4	95.00%	R.VIYGGSVNGGNCK.E	Deamidation (+1)/ Carbamidomethyl (+57)	R.VIYGGSVNGGNCK.E
71	98	3	2925.39	4	1	98.2	24.9	95.00%	K.NGAYTGENSAQSLIDAGITYTLTGHSER.R		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R
58	70	2	1389.73	3.4	1	50	23.5	95.00%	K.DIGVGAQNVFDKK.N		K.DIGVGAQNVFDKK.N

115	134	3	2176.12	2.2	1	34.6	23.6	95.00%	K.FALEQGLTVVACIGETLAER.E	Carbamidomethyl (+57)	K.FALEQGLTVVACIGETLAER.E
32	52	2	2422.27	3.5	1	66.1	21.6	95.00%	K.LNVGDVETVIFPQNMYLITTR.Q		K.LNVGDVETVIFPQNMYLITTR.Q
146	159	2	1613.86	4.5	2	61.4	22.6	95.00%	R.QLNAIADKVQNWSK.I		R.QLNAIADKVQNWSK.I
196	205	2	971.55	5.3	0	76.1	21.5	95.00%	K.LGASVAEGLR.V		K.LGASVAEGLR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
14	THI3_SCHPO	40.17%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	127	2	1090.54	4.7	0	29.6	24	95.00%	K.IQLDDLCSK.F	Carbamidomethyl (+57)	K.IQLDDLCSK.F
74	95	2	2353.27	3.5	1	91.4	20.1	95.00%	R.GYPVTSFGSLLNEPFTGLITLK.G		R.GYPVTSFGSLLNEPFTGLITLK.G
316	327	2	1385.71	3.6	0	53.6	23.8	95.00%	K.QEAIAEIQDEIK.Q		K.QEAIAEIQDEIK.Q
128	139	2	1325.67	4.2	1	42.4	24.2	95.00%	K.FGLSPSDYTAIR.C		K.FGLSPSDYTAIR.C
222	238	3	1901.96	0.17	2	23.1	25.2	91.20%	R.AIHSATLDMLKDPVQTY.K		R.AIHSATLDMLKDPVQTYK.E
316	329	2	1641.86	3.3	1	68.9	22.9	95.00%	K.QEAIAEIQDEIKQK.G		K.QEAIAEIQDEIKQK.G
63	71	2	954.54	4.5	0	51.1	16.2	95.00%	K.AMIHTLAAK.A		K.AMIHTLAAK.A
222	239	2	2030.06	3.2	2	79.8	21.9	95.00%	R.AIHSATLDMLKDPVQTYK.E		R.AIHSATLDMLKDPVQTYK.E
110	118	2	968.5	4.9	1	27.7	22.7	94.00%	R.IGYVGEFGK.I		R.IGYVGEFGK.I
330	339	2	992.51	5.7	1	44.3	24.5	95.00%	K.GGVFSGNSLR.Y		K.GGVFSGNSLR.Y
89	95	2	744.48	0.38	0	41.2	11.1	95.00%	F.TGLITLK.G		R.GYPVTSFGSLLNEPFTGLITLK.G
304	327	3	2756.31	1.7	1	46.1	25.4	95.00%	W.ELDPDEKDPMGKQEAIAEIQDEIK.Q	Oxidation (+16)	R.LGIIPQDFEPNCTNGYLTWELDPDEKDPMGKQEAIAEIQDEIK.Q
81	95	2	1601.9	0.67	1	77	18.5	95.00%	F.GSLLNEPFTGLITLK.G		R.GYPVTSFGSLLNEPFTGLITLK.G
33	56	2	2409.27	3	0	74.8	20.1	95.00%	R.EGIEVAILEPTNPSDVTALIGSGK.V		R.EGIEVAILEPTNPSDVTALIGSGK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
15	METK_SCHPO	63.35%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
252	258	2	850.48	-0.37	2	25.5	18.6	90.70%	R.KIIVDTY.G		R.KIIVDTYGGWGAHGGGAFSGK.D
186	206	3	2311.19	3.8	1	67.9	23.5	95.00%	R.RVDTIVVSAQHADSISTEDLR.S		R.RVDTIVVSAQHADSISTEDLR.S
339	349	2	1256.73	4.3	1	36.5	19.9	95.00%	K.NFDLRPGVLVK.S		K.NFDLRPGVLVK.S
127	146	3	2209.2	1.2	1	30.4	19.1	95.00%	F.GYATDETPEKLPLTILLAHK.L		K.ALEELGAGDQGIMFGYATDETPEKLPLTILLAHK.L
6	19	2	1501.7	-0.95	1	57.7	26.4	95.00%	F.LFTSESVGEGHPDK.I		-.MAQTFLFTSESVGEGHPDK.I
129	146	3	1989.12	2.1	1	25.1	16.3	94.30%	Y.ATDETPEKLPLTILLAHK.L		K.ALEELGAGDQGIMFGYATDETPEKLPLTILLAHK.L
169	185	2	1946.97	4.5	1	49.1	25.2	95.00%	K.TQVTIEYEEENGAVIPR.R		K.TQVTIEYEEENGAVIPR.R
147	155	2	931.5	4.5	0	58	23.1	95.00%	K.LNAAMSVAR.R		K.LNAAMSVAR.R
20	40	3	2423.15	4	2	37.1	26	95.00%	K.ICDQISDAILDACLKDDPFSK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.ICDQISDAILDACLKDDPFSK.V
113	126	2	1465.68	1.4	1	33.8	26	95.00%	K.ALEELGAGDQGIMF.G	Oxidation (+16)	K.ALEELGAGDQGIMFGYATDETPEK.L
237	251	2	1429.74	3.6	1	73.6	23.6	95.00%	R.FVVGGPQGDAGLTGR.K		R.FVVGGPQGDAGLTGR.K
90	112	3	2612.3	3.4	1	62.4	23.8	95.00%	K.TCNVLVAIEQQSPDIAQGLHYEK.A	Carbamidomethyl (+57)	K.TCNVLVAIEQQSPDIAQGLHYEK.A
328	338	2	1257.74	4.7	1	49.3	18.9	95.00%	K.TSAELVEIIRK.N		K.TSAELVEIIRK.N
365	374	2	1201.55	-1.4	1	35.3	25	95.00%	Y.GHFTDQSKPW.E		K.LQTPFYLSTASYGHFTDQSKPWEQPK.E
308	327	2	2053.08	5	1	69	22.2	95.00%	Y.AIGVAEPLSIFVNTYGTSSK.T		R.CLVQLSYAIGVAEPLSIFVNTYGTSSK.T
186	212	4	3010.56	2.5	1	34.2	20.5	95.00%	R.RVDTIVVSAQHADSISTEDLRSEILEK.I		R.RVDTIVVSAQHADSISTEDLRSEILEK.I
291	299	2	856.52	4.2	0	28.1	20.3	94.50%	K.SLVAAGLAR.R		K.SLVAAGLAR.R
213	226	2	1572.92	-2	0	43.5	15.7	95.00%	K.IIKPTVPAHLLDEK.T		K.IIKPTVPAHLLDEK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
16	EF3_SCHPO	36.39%	100%	28

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
333	350	2	1970	-1.1	0	93.9	23.9	95.00%	K.IPEVSTAANPEVCLETLK.A	Carbamidomethyl (+57)	K.IPEVSTAANPEVCLETLK.A
596	621	4	2935.49	3.5	1	34.9	21.6	95.00%	K.DVSSIIVSHDSGFLDHVVQAIIHYER.F		K.DVSSIIVSHDSGFLDHVVQAIIHYER.F
514	530	2	1948.1	2.5	1	29.8	14.1	95.00%	F.ILQDPAVPIKDRDEIVK.A		R.TVYVEHDIDESEADTPSVDFILQDPAVPIKDRDEIVK.A
920	933	2	1664.89	1.2	1	33.1	21.8	95.00%	W.LRPHVIVLDEPTNY.L		K.LVLAACTWLRPHVIVLDEPTNYLDR.D
995	1004	2	1194.54	-0.023	2	26.8	25.1	92.70%	R.IQEKEEGDTF.D		R.IQEKEEGDTFDAFGNK.I
75	92	2	1797.86	1	1	40.3	26.5	95.00%	K.GLEAVANHGSVAADVEPY.L		K.GLEAVANHGSVAADVEPYLVELLPAVIAK.V
75	103	3	2944.6	3.2	1	47.9	17.2	95.00%	K.GLEAVANHGSVAADVEPYLVELLPAVIAK.V		K.GLEAVANHGSVAADVEPYLVELLPAVIAK.V
972	994	3	2347.05	0.13	1	51.1	27.8	95.00%	W.AVNNGHMTPSGHNWVSGQGSGPR.I	Deamidation (+1)	R.EFTEGLTEEVWAVNNGHMTPSGHNWVSGQGSGPR.I
20	34	2	1599.73	5	0	78.4	27.1	95.00%	K.HLTVCDAAEEADAAK.A	Carbamidomethyl (+57)	K.HLTVCDAAEEADAAK.A
202	213	2	1359.69	4.1	0	43.2	24.4	95.00%	K.VCTLIANADIDR.F	Carbamidomethyl (+57)	K.VCTLIANADIDR.F
172	188	2	1929	4.2	1	43.7	23	95.00%	Y.SLPQIIPVVSESMWDTK.A		K.MNSLQLLDVLVEVAPSQLSYSLPQIIPVVSESMWDTK.A
859	870	2	1330.7	4.7	1	35.3	23.3	95.00%	K.MVAEVDRAEALK.S		K.MVAEVDRAEALK.S
35	59	2	2604.32	3.9	1	66.4	23	95.00%	K.ALASFVNGPIEEQDAPSQVFSAISK.Q		K.ALASFVNGPIEEQDAPSQVFSAISK.Q
351	367	2	1809.03	4.2	1	72.9	16.3	95.00%	K.AVLGEIKVPTNEEVIAK.Y		K.AVLGEIKVPTNEEVIAK.Y
281	294	2	1550.88	4.1	1	60.5	18.1	95.00%	K.LVEDPQVVAPFLPK.L		K.LVEDPQVVAPFLPK.L
40	54	2	1628.77	0.05	1	66.7	26.2	95.00%	F.VNGPIEEQDAPSQVF.S		K.ALASFVNGPIEEQDAPSQVFSAISK.Q
655	666	3	1346.72	0.73	2	24.4	22.9	93.40%	F.KFPEPGFLEGVK.T		K.SYYELGASEMEFKFPEPGFLEGVK.T
479	493	2	1636.88	3.9	1	73.9	22.1	95.00%	R.AIVNGQVEGFPTHLR.T		R.AIVNGQVEGFPTHLR.T
419	447	3	3168.34	2.9	1	77.1	26.5	95.00%	K.IPGGASHAEEEEEGEDLCNCEFSLAYGAK.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.IPGGASHAEEEEEGEDLCNCEFSLAYGAK.I
419	440	2	2477.96	0.17	1	58.6	26.6	95.00%	K.IPGGASHAEEEEEGEDLCNCEF.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.IPGGASHAEEEEEGEDLCNCEFSLAYGAK.I
133	147	2	1550.87	3.9	0	70.6	18.5	95.00%	K.AIVPSVLESIHTTGK.W		K.AIVPSVLESIHTTGK.W
766	777	2	1368.59	4	1	45.5	26.3	95.00%	R.FQSGEDLEAMDK.A		R.FQSGEDLEAMDK.A
881	900	3	2293.11	2.6	0	44.8	25.5	95.00%	K.EIEEHCSLLGLDAELVSHSR.I	Carbamidomethyl (+57)	K.EIEEHCSLLGLDAELVSHSR.I
494	513	2	2266.98	0.83	1	60.3	27.4	95.00%	R.TVYVEHDIDESEADTPSVDF.I		R.TVYVEHDIDESEADTPSVDFILQDPAVPIK.D
358	367	2	1098.6	4.8	0	47.3	20.5	95.00%	K.VPTNEEVIAK.Y		K.VPTNEEVIAK.Y
35	54	2	2118.03	0.18	1	61.1	26	95.00%	K.ALASFVNGPIEEQDAPSQVF.S		K.ALASFVNGPIEEQDAPSQVFSAISK.Q
880	900	3	2421.2	2	1	49.3	25.1	95.00%	R.KEIEEHCSLLGLDAELVSHSR.I	Carbamidomethyl (+57)	R.KEIEEHCSLLGLDAELVSHSR.I
325	350	3	2738.42	3.2	1	45.8	20.7	95.00%	R.VGNVVDGKIPEVSTAANPEVCLETLK.A	Carbamidomethyl (+57)	R.VGNVVDGKIPEVSTAANPEVCLETLK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
17	HSP90_SCHPO	34.38%	100%	20

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
522	533	2	1405.62	4.2	0	49.6	26.5	95.00%	K.DGLELEETDEEK.A		K.DGLELEETDEEK.A
275	287	2	1499.68	-1	2	55.1	27.2	95.00%	R.NPSEVTKEEYASF.Y		R.NPSEVTKEEYASFYK.S
465	474	2	1170.6	4.5	1	29.7	22.9	95.00%	K.NIYFITGESK.Q		K.NIYFITGESK.Q
567	587	2	2339.12	5.7	1	92.3	26.3	95.00%	K.IVGSPCLLTTGQYGWSANMER.I	Carbamidomethyl (+57)	K.IVGSPCLLTTGQYGWSANMER.I
440	458	2	2199.07	3.1	1	92.7	26.3	95.00%	R.YNSLNSPDDLISLEDYITK.M		R.YNSLNSPDDLISLEDYITK.M
596	606	2	1234.5	4.9	1	67.2	25.9	95.00%	R.DTSMSAYMSSR.K		R.DTSMSAYMSSR.K
362	375	2	1512.78	3.1	0	77.4	23.1	95.00%	K.GVVDSEDLPLNLSR.E		K.GVVDSEDLPLNLSR.E
516	536	3	2372.21	2.8	1	83.5	23.3	95.00%	K.LVNITKDGLELEETDEEKAAR.E		K.LVNITKDGLELEETDEEKAAR.E

198	212	2	1787.96	4.4	1	31.7	22.1	95.00%	K.HSEFISYPIQLVVTR.E	K.HSEFISYPIQLVVTR.E
522	536	2	1703.78	-1.1	1	77.2	27.3	95.00%	K.DGLELEETDEEKAAR.E	K.DGLELEETDEEKAAR.E
290	302	2	1526.74	4	1	75.7	26.1	95.00%	K.SLTNDWEDHLAVK.H	K.SLTNDWEDHLAVK.H
475	487	2	1548.8	4.5	1	76.3	24	95.00%	K.QAVENSPFLEIFR.A	K.QAVENSPFLEIFR.A
88	99	2	1282.73	5.3	0	55.5	17.7	95.00%	K.NDLINNLGVIAK.S	K.NDLINNLGVIAK.S
34	45	2	1274.64	4	0	41.6	24.4	95.00%	R.ELISNASDALDK.I	R.ELISNASDALDK.I
255	267	2	1520.76	4.6	1	46.2	25	95.00%	K.VKETTTETEELNK.T	K.VKETTTETEELNK.T
321	330	2	1176.6	4.2	2	27.8	24.2	94.10%	R.RAPMDLFEAK.R	R.RAPMDLFEAK.R
422	436	2	1574.85	-1.5	0	43.5	21	95.00%	K.LGIHEDAANRPALAK.L	K.LGIHEDAANRPALAK.L
48	64	2	1947.92	0.3	2	38.9	26.1	95.00%	R.YQSLSDPHALDAEKDLF.I	R.YQSLSDPHALDAEKDLFIR.I
34	47	2	1543.83	3.9	1	76.1	22.7	95.00%	R.ELISNASDALDKIR.Y	R.ELISNASDALDKIR.Y
504	514	2	1248.67	1.8	2	28.4	22	94.80%	Y.AVTQLKEFEGK.K	K.FDVLFMVDPIDEYAVTQLKEFEGK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
18	HSP72_SCHPO	48.07%	100%	25

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
327	340	2	1400.77	3.9	0	39.7	21.7	95.00%	K.ASVNEIVLVGGSTR.I		K.ASVNEIVLVGGSTR.I
55	66	2	1384.65	-0.66	1	29.8	26.3	94.80%	K.NQVAMNPHNTIF.D		K.NQVAMNPHNTIFDAK.R
170	181	2	1245.66	-1.7	1	39.3	22.9	95.00%	R.IINEPTAAAIAY.G		R.IINEPTAAAIAYGLDR.S
125	136	2	1324.65	4.5	2	66.6	25.3	95.00%	K.MRETAEAYLGGK.V		K.MRETAEAYLGGK.V
96	110	2	1689.9	5	1	31.8	22.8	95.00%	K.DGKPVLQVEYKGETK.T		K.DGKPVLQVEYKGETK.T
370	385	2	1516.77	0.91	0	85.7	24.3	95.00%	Y.GAAVQAAVLTGDTSEK.T		K.SINPDEAVAYGAAVQAAVLTGDTSEK.T
448	457	3	1194.61	0.53	2	35.9	24.3	95.00%	R.TKDCNLLGKF.E	Carbamidomethyl (+57)	R.TKDCNLLGKFELSGIPPAPR.G
219	234	2	1647.72	4.3	1	72.5	27.2	95.00%	K.ATAGDTHLGGEDFDSR.L		K.ATAGDTHLGGEDFDSR.L
20	34	2	1698.84	1.5	1	60.1	25	95.00%	F.SNNRVEIIANDQGNR.T		K.SIGIDLGTTYSCVGHFSNNRVEIIANDQGNR.T
324	340	2	1742.95	-1.9	1	83.5	21.1	95.00%	K.VDKASVNEIVLVGGSTR.I		K.VDKASVNEIVLVGGSTR.I
457	467	2	1182.65	4.4	1	28.3	19.8	94.70%	K.FELSGIPPAPR.G		K.FELSGIPPAPR.G
235	244	2	1273.69	4.3	1	25.1	22.4	90.00%	R.LVNHFIQEFK.R		R.LVNHFIQEFK.R
35	47	2	1486.7	4.2	1	60.5	26.3	95.00%	R.TTPSYVAFTDTER.L		R.TTPSYVAFTDTER.L
608	647	3	3499.6	0.71	1	45.4	25.5	95.00%	K.IYQAGGAPGGMPGAAPGAAPGAAPGAAPGAAPGGDNGPEVEEVD.-		K.IYQAGGAPGGMPGAAPGAAPGAAPGAAPGAAPGGDNGPEVEEVD.-
579	593	2	1638.77	-0.022	2	30.5	26	95.00%	W.LDSNTTAAKDEFEAK.Q		K.ETIEWLDSNTTAAKDEFEAK.Q
111	124	2	1611.8	4	1	69	25.2	95.00%	K.TFTPEEISSMVLMK.M		K.TFTPEEISSMVLMK.M
594	607	2	1556.83	4.2	1	73.7	22.8	95.00%	K.QKELESVANPIMAK.I		K.QKELESVANPIMAK.I
538	548	2	1351.66	4.4	1	37.5	25.4	95.00%	K.NHLESYAYSLR.N		K.NHLESYAYSLR.N
137	153	2	1880.93	4	1	55	25.1	95.00%	K.VTDAVVTVPAYFNDSQR.Q		K.VTDAVVTVPAYFNDSQR.Q
76	86	2	1309.56	4.9	1	34.7	25.9	95.00%	K.FDDPEVQSDMK.H		K.FDDPEVQSDMK.H
516	523	2	939.44	-0.77	2	29.5	25.6	95.00%	R.MVAEAEKY.K		R.MVAEAEKYK.A
170	185	2	1686.9	4	1	94.1	22.1	95.00%	R.IINEPTAAAIAYGLDR.S		R.IINEPTAAAIAYGLDR.S
55	69	2	1698.82	4.2	1	74.8	25.6	95.00%	K.NQVAMNPHNTIFDAK.R		K.NQVAMNPHNTIFDAK.R
430	445	2	1786.89	0.27	1	77	24.9	95.00%	Y.SDNQPGVLIQVFEGER.A		K.SEIFSTYSDNQPGVLIQVFEGER.A
24	34	2	1227.63	5.8	0	33.2	24.3	95.00%	R.VEIIANDQGNR.T		R.VEIIANDQGNR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
19	THI2_SCHPO	37.50%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
175	187	2	1431.8	-0.99	1	73.7	20.4	95.00%	K.LFNATAVEDLIVK.E		K.LFNATAVEDLIVK.E
309	320	2	1332.68	5.8	1	60	24.4	95.00%	K.AAQEALAIFDER.K		K.AAQEALAIFDER.K
137	154	2	2037	0.49	1	66.4	26	95.00%	F.LNEIGVPYEDEGDYVVVK.H		R.KPADLFLNEIGVPYEDEGDYVVVK.H
2	15	2	1400.77	3.8	1	74.5	21.2	95.00%	M.APATAVVTPQTAFK.T		-.MAPATAVVTPQTAFK.T
244	263	3	2296.15	3.2	0	39.6	24.6	95.00%	R.LASAQLVSNLHDMRPLDMNR.A	Oxidation (+16)	R.LASAQLVSNLHDMRPLDMNR.A
175	190	3	1745.96	4.6	1	37.2	20.4	95.00%	K.LFNATAVEDLIVKEGK.D		K.LFNATAVEDLIVKEGK.D
309	321	2	1460.76	-0.85	1	70.4	23.6	95.00%	K.AAQEALAIFDERK.A		K.AAQEALAIFDERK.A

244	270	3	3048.6	3.6	1	30.2	18.5	95.00%	R.LASAQLVSNLHDMRPLDMNRAEDLIVK.G		R.LASAQLVSNLHDMRPLDMNRAEDLIVK.G
295	308	2	1459.66	-1.5	1	75.4	26.4	95.00%	R.MGPTFGGMMFSGIK.A		R.MGPTFGGMMFSGIK.A
274	294	2	2254.05	3.3	1	79.8	26.7	95.00%	R.EVFPGMIVGGMELSEFDGANR.M		R.EVFPGMIVGGMELSEFDGANR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
20	A1EGU1_SCHPO	46.55%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
457	479	2	2580.33	2.4	1	74	22.4	95.00%	K.YVISQCNNALLYPALGVACVLSR.C	Carbamidomethyl (+57)/Carbamidomethyl (+57)	K.YVISQCNNALLYPALGVACVLSR.C
408	433	3	2988.58	2.9	1	71.1	18.6	95.00%	K.HVERPIIFPISNPTTLMEAKPDQIDK.W		K.HVERPIIFPISNPTTLMEAKPDQIDK.W
44	57	2	1634.91	4.4	0	89.1	19.9	95.00%	R.LPPIVETLQQQVDR.C		R.LPPIVETLQQQVDR.C
439	452	2	1418.82	-1.6	0	64.8	16.8	95.00%	K.ALIATGSPLPPLNR.N		K.ALIATGSPLPPLNR.N
408	438	5	3561.84	2.8	2	46.8	19.2	95.00%	K.HVERPIIFPISNPTTLMEAKPDQIDKWSDGK.A		K.HVERPIIFPISNPTTLMEAKPDQIDKWSDGK.A
490	500	2	1070.58	4.5	0	54.7	21.4	95.00%	K.AASDALATVPR.S		K.AASDALATVPR.S
15	23	2	955.55	4.9	0	32.8	17.6	95.00%	K.GVTLLNSPR.Y		K.GVTLLNSPR.Y
456	479	3	2708.42	2.3	2	27.2	20.9	95.00%	K.KYVISQCNNALLYPALGVACVLSR.C	Carbamidomethyl (+57)/Carbamidomethyl (+57)	K.KYVISQCNNALLYPALGVACVLSR.C
362	396	4	3654.89	2.7	1	43.8	18.7	95.00%	K.DSDFKEVPSGDINLESAIALVKPTILLGCSGQPGK.F	Carbamidomethyl (+57)	K.DSDFKEVPSGDINLESAIALVKPTILLGCSGQPGK.F
258	292	4	3747.95	3.3	1	51.5	18.5	95.00%	R.ILDHYRPDIACFNDDIQGTGAVALAAIIGALHVTK.S	Carbamidomethyl (+57)	R.ILDHYRPDIACFNDDIQGTGAVALAAIIGALHVTK.S
501	517	2	1828.93	-0.46	1	40.1	24.4	95.00%	R.SLFAADEALLPDLNNAR.E		R.SLFAADEALLPDLNNAR.E
367	396	3	3062.63	0.14	0	30.9	17.2	95.00%	K.EVPSGDINLESAIALVKPTILLGCSGQPGK.F	Carbamidomethyl (+57)	K.EVPSGDINLESAIALVKPTILLGCSGQPGK.F
530	547	2	1889.9	-1.2	1	64.1	26.1	95.00%	K.QAVSEGMSTVDLPKDDAK.L		K.QAVSEGMSTVDLPKDDAK.L
548	555	2	1085.63	3.7	2	31.8	20.6	95.00%	K.LKEWIIER.E		K.LKEWIIER.E
332	339	2	964.49	5	1	34.3	23.5	95.00%	R.GNLFMIDR.C		R.GNLFMIDR.C
245	256	2	1360.68	0.71	1	38.3	24.9	95.00%	F.IHFEDFGLANAK.R		R.EVFPEAFIHFEDFGLANAK.R
178	191	2	1553.75	3.5	0	59.3	26.2	95.00%	K.GHLMTLCAGLDPNR.F	Carbamidomethyl (+57)	K.GHLMTLCAGLDPNR.F
222	234	2	1526.73	2.5	1	68.3	26.6	95.00%	R.GEQYDSFLDNVIK.A		R.GEQYDSFLDNVIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
21	K6PF_SCHPO	33.44%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
159	183	3	2544.33	0.75	1	24.3	21.2	93.20%	K.KSEESGAASNLESGLATPVVETLKK.A		K.KSEESGAASNLESGLATPVVETLKK.A
364	380	3	1831.87	-0.9	0	58.9	26.4	95.00%	R.ICEAVDSISSTAISHSR.A	Carbamidomethyl (+57)	R.ICEAVDSISSTAISHSR.A
822	839	4	2058.08	3.2	1	52.7	21.6	95.00%	K.VYTTEVIGNIISEEAHKR.F		K.VYTTEVIGNIISEEAHKR.F
419	431	2	1592.73	4.2	1	27.5	26.3	91.90%	K.WQDELCNSLSSVR.K	Carbamidomethyl (+57)	K.WQDELCNSLSSVR.K
586	603	3	1736.9	-1	0	42.6	23.6	95.00%	R.VAIIHVGAPAGGMNSATR.A	Oxidation (+16)	R.VAIIHVGAPAGGMNSATR.A
534	545	2	1352.73	-0.83	1	43.5	21.2	95.00%	K.LTHEVADAIEKK.Q		K.LTHEVADAIEKK.Q
880	896	2	1696.87	-1.7	0	74.8	23.8	95.00%	R.ANDLGNDPSSAVVIGIR.G		R.ANDLGNDPSSAVVIGIR.G
903	918	2	1837.8	-0.95	0	97.3	27	95.00%	F.SSVADVENNETEIEMR.R	Oxidation (+16)	R.GTGVSFSSVADVENNETEIEMR.R
927	938	2	1323.7	4.7	0	53.3	22.2	95.00%	R.DMHNLVNILAGK.T		R.DMHNLVNILAGK.T
77	94	2	1954.97	4.6	1	62	24.9	95.00%	R.LVPGELSLSPAAEDSEWR.G		R.LVPGELSLSPAAEDSEWR.G
50	74	3	2845.31	0.82	2	35.4	26.3	95.00%	R.VCNESLREDWMHVAGNNSAESVTIK.F	Carbamidomethyl (+57)	R.VCNESLREDWMHVAGNNSAESVTIK.F
613	628	3	1700.87	4.5	1	49.7	23.9	95.00%	R.GHTPLAIDNGFSGFLR.H		R.GHTPLAIDNGFSGFLR.H
283	308	2	2620.33	3.9	1	86.3	23.1	95.00%	K.NLISAGIDSIIVCGGDGSLTGADIFR.S	Carbamidomethyl (+57)	K.NLISAGIDSIIVCGGDGSLTGADIFR.S
50	59	2	1306.56	0.92	2	34.2	26.2	95.00%	R.VCNESLREDW.M	Carbamidomethyl (+57)	R.VCNESLREDWMHVAGNNSAESVTIK.F
160	183	3	2416.24	3.9	1	44	22.9	95.00%	K.SEESGAASNLESGLATPVVETLKK.A		K.SEESGAASNLESGLATPVVETLKK.A

798	806	2	934.49	4	1	31.5	23.8	95.00%	K.ATFALEAGR.N		K.ATFALEAGR.N
438	460	2	2448.28	0.97	0	67.2	21.9	95.00%	K.SIVIVAEGAIDSELNHISPEDIK.N		K.SIVIVAEGAIDSELNHISPEDIK.N
254	267	2	1400.75	3.4	1	49.7	22.8	95.00%	R.GWLAEGGTLIGTAR.C		R.GWLAEGGTLIGTAR.C
844	861	2	1860.9	4.7	0	42.3	25.9	95.00%	R.TAVPGHVQQGGNPTPMDR.A		R.TAVPGHVQQGGNPTPMDR.A
197	214	2	1760.86	4.1	0	84.8	25	95.00%	K.IAVMTSGGDSPGMNAVVR.A		K.IAVMTSGGDSPGMNAVVR.A
822	838	2	1901.98	4.1	1	50.4	24.2	95.00%	K.VYTTEVIGNIISEEAHK.R		K.VYTTEVIGNIISEEAHK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
22	ILV5_SCHPO	34.90%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
84	104	2	2141.07	4.6	1	90.4	24.7	95.00%	K.NDTLAIIGYGSQGHGQGLNAR.D		K.NDTLAIIGYGSQGHGQGLNAR.D
330	337	2	914.47	6	1	41.2	21.8	95.00%	R.GAIDWTPR.F		R.GAIDWTPR.F
287	313	3	2972.46	2	2	25.8	23.9	94.90%	R.ERGHSPAEAFNETVEEATQSLYPLIGK.Y		R.ERGHSPAEAFNETVEEATQSLYPLIGK.Y
145	163	2	2074.05	4.2	1	75.2	24.7	95.00%	K.GSIIMNLLSDAAQTETWPK.I		K.GSIIMNLLSDAAQTETWPK.I
345	361	2	1975.97	4.3	1	90.3	25.7	95.00%	K.VLNELYDNVENGNEAKR.S		K.VLNELYDNVENGNEAKR.S
345	360	2	1819.85	-5	1	45.9	26.6	95.00%	K.VLNELYDNVENGNEAK.R		K.VLNELYDNVENGNEAK.R
373	383	2	1435.73	4.6	1	44.1	25	95.00%	R.ELYDKELEEIR.N		R.ELYDKELEEIR.N
123	133	2	1198.6	4.3	1	28.6	23.3	95.00%	K.QAIEDGWVPGK.T		K.QAIEDGWVPGK.T
144	163	2	2202.15	4.4	2	56.2	22.3	95.00%	K.KGSIIMNLLSDAAQTETWPK.I		K.KGSIIMNLLSDAAQTETWPK.I
362	372	2	1312.61	4.6	1	61.6	25.5	95.00%	R.SLEYNSAPNYR.E		R.SLEYNSAPNYR.E
289	313	2	2687.31	-0.23	1	88.9	24.5	95.00%	R.GHSPAEAFNETVEEATQSLYPLIGK.Y		R.GHSPAEAFNETVEEATQSLYPLIGK.Y
190	204	2	1639.97	3.6	1	26.8	14.8	92.80%	K.IHPPKDVDVILVAPK.G		K.IHPPKDVDVILVAPK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
23	6PGD_SCHPO	52.85%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
188	209	3	2659.19	3.5	1	32.6	26.8	95.00%	K.MVHNGIEYGDMQLICETYDIMK.R	Carbamidomethyl (+57)	K.MVHNGIEYGDMQLICETYDIMK.R
156	166	3	1228.76	4.8	1	32.1	12.3	95.00%	R.IKPIFQTLAAK.A		R.IKPIFQTLAAK.A
167	185	2	2119.81	-1.9	1	54.9	26.7	95.00%	K.AGNNEPCCDWVGEQGAGHY.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.AGNNEPCCDWVGEQGAGHYVK.M
98	115	3	1971.95	5.1	1	35.5	26.1	95.00%	K.GDIIVDGGNSHYPDTTRR.C		K.GDIIVDGGNSHYPDTTRR.C
54	67	2	1501.78	4.1	1	57.5	23.7	95.00%	K.SIVGAHSLEEFVSK.L		K.SIVGAHSLEEFVSK.L
188	205	2	2171.93	0.29	1	75.8	27.6	95.00%	K.MVHNGIEYGDMQLICETY.D	Carbamidomethyl (+57)	K.MVHNGIEYGDMQLICETYDIMK.R
98	114	2	1815.85	4.4	1	91.7	26.6	95.00%	K.GDIIVDGGNSHYPDTTR.R		K.GDIIVDGGNSHYPDTTR.R
29	37	2	1175.49	3.9	1	36.7	26.2	95.00%	K.GFTVCCYNR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GFTVCCYNR.T
122	139	3	1718.9	4.5	2	31	23.4	95.00%	K.KGILFVGSGVSGGEEGAR.Y		K.KGILFVGSGVSGGEEGAR.Y
38	51	2	1579.79	4.7	2	35.6	25.6	95.00%	R.TTSRVDEFLANEAK.G		R.TTSRVDEFLANEAK.G
42	51	2	1134.56	4.5	1	47.7	24.7	95.00%	R.VDEFLANEAK.G		R.VDEFLANEAK.G
123	139	2	1590.81	3.9	1	62.7	24.1	95.00%	K.GILFVGSGVSGGEEGAR.Y		K.GILFVGSGVSGGEEGAR.Y
80	114	4	3722.93	3.7	2	47.4	18.6	95.00%	K.AGKPVDYLIEGLAPLLEKGDIIVDGGNSHYPDTTR.R		K.AGKPVDYLIEGLAPLLEKGDIIVDGGNSHYPDTTR.R
211	225	2	1669.74	4.6	1	69.2	26.9	95.00%	R.GLGMSCDEIADVFEK.W	Carbamidomethyl (+57)	R.GLGMSCDEIADVFEK.W
140	155	2	1669.81	4.7	1	28.8	25.5	94.60%	R.YGPSLMPGGNPAAWPR.I		R.YGPSLMPGGNPAAWPR.I
269	291	2	2504.28	3.2	1	92.8	23.3	95.00%	K.WTAQNALEMGTPVSLITEAVFAR.C		K.WTAQNALEMGTPVSLITEAVFAR.C
320	333	2	1592.8	4.1	1	67.9	25	95.00%	K.QLIDDLEDALYASK.I		K.QLIDDLEDALYASK.I
437	449	2	1379.79	4.1	0	52	17.2	95.00%	R.SAVLPANLLQAQR.D		R.SAVLPANLLQAQR.D
80	97	2	1925.09	0.35	1	66.9	17.5	95.00%	K.AGKPVDYLIEGLAPLLEK.G		K.AGKPVDYLIEGLAPLLEK.G
467	478	2	1407.72	0.27	2	37.7	24.9	95.00%	K.SLPADKDIHINW.T		K.SLPADKDIHINWTGHGGNISATTYDA.-
5	28	2	2457.3	3	1	76	20.5	95.00%	K.EVADFGLIGLAVMGQNLILNGADK.G		K.EVADFGLIGLAVMGQNLILNGADK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
24	EF2_SCHPO	27.55%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
565	578	2	1451.69	4.3	0	44.5	26.5	95.00%	R.ESVSEPSSMTALSK.S		R.ESVSEPSSMTALSK.S
353	370	2	2024.89	3.6	1	81.7	27.6	95.00%	R.AETLYEGPMDDECAVGIR.N	Carbamidomethyl (+57)	R.AETLYEGPMDDECAVGIR.N
371	384	2	1594.76	4.1	1	55	26.1	95.00%	R.NCDANAPLMIYVSK.M	Carbamidomethyl (+57)	R.NCDANAPLMIYVSK.M
327	346	2	2192.18	2.4	1	55.9	20.7	95.00%	K.FLPAADALMEMIVLHLPSPK.T		K.FLPAADALMEMIVLHLPSPK.T
442	465	2	2595.37	4.3	1	74.7	18.9	95.00%	R.IEPIEDCPAGNIIGLVGVDQFLVK.S	Carbamidomethyl (+57)	R.IEPIEDCPAGNIIGLVGVDQFLVK.S
466	479	2	1474.71	3.7	0	72.8	25.6	95.00%	K.SGTLTTSEVAHNMK.V		K.SGTLTTSEVAHNMK.V
633	651	2	2107.01	3.2	1	108	25.8	95.00%	K.IWCFGPDTTGANVVVDQTK.A	Carbamidomethyl (+57)	K.IWCFGPDTTGANVVVDQTK.A
284	292	2	1051.52	4.5	1	27.5	24.3	93.80%	R.IFDAVMNSR.K		R.IFDAVMNSR.K
293	302	2	1178.66	4.6	2	62.3	20.3	95.00%	R.KDEVFTLLSK.L		R.KDEVFTLLSK.L
151	162	3	1392.85	-1.3	1	32.3	10.8	95.00%	R.IRPVVVVNKVDR.A		R.IRPVVVVNKVDR.A
544	555	2	1334.69	3.5	0	47.4	24.4	95.00%	K.DLQEDHAGIPLK.I		K.DLQEDHAGIPLK.I
827	838	2	1426.66	-2	2	28.4	26.6	92.80%	K.GLKENVPDYTEY.Y		K.GLKENVPDYTEYYDR.L
303	317	3	1726.94	3.8	1	43.5	20.8	95.00%	K.LEVTIKPDEKELEGK.A		K.LEVTIKPDEKELEGK.A
326	346	3	2320.28	3.2	2	27.9	17	95.00%	R.KFLPAADALMEMIVLHLPSPK.T		R.KFLPAADALMEMIVLHLPSPK.T
635	651	2	1807.84	-1	1	72.9	26.7	95.00%	W.CFGPDTTGANVVVDQTK.A	Carbamidomethyl (+57)	K.IWCFGPDTTGANVVVDQTK.A
586	609	3	2657.29	3.5	1	32.6	25.1	95.00%	R.IFMTAEPMSEELSVAIETGHVNPR.D		R.IFMTAEPMSEELSVAIETGHVNPR.D
618	631	2	1624.72	-1.2	1	57.3	26.9	95.00%	R.IMADEFGWDVTDAR.K		R.IMADEFGWDVTDAR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
25	TSA1_SCHPO	68.75%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	132	2	901.53	4.7	1	35.7	21.9	95.00%	R.GLFLIDPK.G		R.GLFLIDPK.G
155	173	2	2260.03	0.62	1	39.6	27.1	95.00%	R.LLDAFQFVEEHGEVCPANW.H	Carbamidomethyl (+57)	R.LLDAFQFVEEHGEVCPANWHK.G
89	107	2	1915.06	3.5	1	58	19.5	95.00%	R.KEGGLGGINIPLLADPSHK.V		R.KEGGLGGINIPLLADPSHK.V
66	88	2	2576.29	0.89	1	97.3	23.8	95.00%	R.NAQVILTSTDSEYSHLAFINTPR.K		R.NAQVILTSTDSEYSHLAFINTPR.K
111	124	2	1523.77	4.1	1	79.7	25.1	95.00%	R.DYGVLIEDAGVAFR.G		R.DYGVLIEDAGVAFR.G
66	83	2	1994.96	0.048	1	73.8	26	95.00%	R.NAQVILTSTDSEYSHLAF.I		R.NAQVILTSTDSEYSHLAFINTPR.K
2	13	2	1341.74	4.1	1	36.9	21.1	95.00%	M.SLQIGKPAPDFK.G	Acetyl (+42)	-.MSLQIGKPAPDFK.G
137	147	2	1224.69	4.4	0	43.5	18.2	95.00%	R.QITINDLPVGR.S		R.QITINDLPVGR.S
176	188	2	1466.69	-2.3	2	27	26.3	91.20%	K.GSDTIDTKNPEKY.F		K.GSDTIDTKNPEKYFSK.H
14	26	2	1333.69	3.6	1	40.1	24.2	95.00%	K.GTAVVNGAFEEIK.L		K.GTAVVNGAFEEIK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
26	HSP75_SCHPO	36.22%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	173	2	1168.66	5	0	34.3	19.3	95.00%	K.DAGAIAGLNVLR.I		K.DAGAIAGLNVLR.I
501	517	3	1779.91	-1.1	0	62.2	24.6	95.00%	R.SAHIEITNSVGHLSSTK.I		R.SAHIEITNSVGHLSSTK.I
174	185	2	1245.66	-1.7	1	39.3	22.9	95.00%	R.IINEPTAAAIAY.G		R.IINEPTAAAIAYGLDAK.S
451	462	2	1377.58	-2.3	1	37.8	26.7	95.00%	R.VNCAENEPLGEF.Q	Carbamidomethyl (+57)	R.VNCAENEPLGEFQLTGIPPMPR.G
331	344	2	1437.76	3.8	0	34.4	22.8	95.00%	K.ADVHDIVLVGGSTR.I		K.ADVHDIVLVGGSTR.I
115	128	2	1565.81	1.4	1	60	23.6	95.00%	K.QFTAQEISAMVLTK.M		K.QFTAQEISAMVLTK.M
39	51	2	1484.72	4.2	1	50.9	25.7	95.00%	R.TTPSFVAFTETER.L		R.TTPSFVAFTETER.L
430	450	2	2374.16	5.6	1	61.9	25.4	95.00%	R.TFTTVADNQTTVTFPVYQGER.V		R.TFTTVADNQTTVTFPVYQGER.V
96	113	2	1987.03	4.2	1	58.5	22.3	95.00%	K.VIDNNGIPTIEVNYLGEK.K		K.VIDNNGIPTIEVNYLGEK.K
451	472	2	2468.2	5.8	1	62.2	26.3	95.00%	R.VNCAENEPLGEFQLTGIPPMPR.G	Carbamidomethyl (+57)	R.VNCAENEPLGEFQLTGIPPMPR.G
571	596	3	2992.45	-0.52	1	56.8	24.8	95.00%	K.SKIEAQLAECMSQLELEDTNTDALRK.A	Carbamidomethyl (+57)	K.SKIEAQLAECMSQLELEDTNTDALRK.A
144	157	2	1552.8	4.6	1	33.7	24.1	95.00%	K.AVITVPAYFSDSQR.A		K.AVITVPAYFSDSQR.A

543	564	2	2513.21	3.3	1	64.4	25.7	95.00%	K.SQLESYISNIETTISEPNVMMK.L		K.SQLESYISNIETTISEPNVMMK.L
174	190	2	1729.93	3.9	1	82.9	21.3	95.00%	R.IINEPTAAAIAYGLDAK.S		R.IINEPTAAAIAYGLDAK.S
114	128	2	1693.91	3.7	2	42.8	20.6	95.00%	K.KQFTAQEISAMVLTK.M		K.KQFTAQEISAMVLTK.M
571	595	3	2864.36	3.4	1	74	25.7	95.00%	K.SKIEAQLAECMSQLELEDTNTDALR.K	Carbamidomethyl (+57)	K.SKIEAQLAECMSQLELEDTNTDALR.K
518	528	2	1336.63	-0.17	2	29.8	25.4	95.00%	K.IQEMIENADKF.K		K.IQEMIENADKFK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
27	ACT_SCHPO	51.47%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
292	312	2	2216.04	5	1	63.1	26.9	95.00%	K.DLYGNVVMSGGTTMYPGIADR.M		K.DLYGNVVMSGGTTMYPGIADR.M
257	279	2	2398.18	1.2	1	46.8	24.8	95.00%	R.APEALFQPSALGLENAGIHEATY.N		R.APEALFQPSALGLENAGIHEATYNSIMK.C
96	113	2	2014.03	3.9	0	59.4	23.7	95.00%	R.VAPEEHPCLLTEAPLNPK.S	Carbamidomethyl (+57)	R.VAPEEHPCLLTEAPLNPK.S
69	84	2	1958.89	3.6	1	64.1	27.3	95.00%	K.YPIEHGIVNNWDDMEK.I		K.YPIEHGIVNNWDDMEK.I
197	206	2	1131.53	5.1	1	41.4	25.6	95.00%	R.GYTFSTTAER.E		R.GYTFSTTAER.E
148	169	2	2293.11	-0.13	1	54.3	25.3	95.00%	R.TTGIVLDSGDGVTHTVPIYEGY.A		R.TTGIVLDSGDGVTHTVPIYEGYALPHAIMR.L
216	238	2	2629.27	3.5	1	106	25.4	95.00%	K.LCYVALDFEQELQTAAQSSSLEK.S	Carbamidomethyl (+57)	K.LCYVALDFEQELQTAAQSSSLEK.S
257	284	3	2971.48	3	1	43.9	22.9	95.00%	R.APEALFQPSALGLENAGIHEATYNSIMK.C		R.APEALFQPSALGLENAGIHEATYNSIMK.C
219	238	2	2193.08	0.54	1	93.1	25.1	95.00%	Y.VALDFEQELQTAAQSSSLEK.S		K.LCYVALDFEQELQTAAQSSSLEK.S
1	18	2	2007.9	4	0	79.9	27.5	95.00%	-.MEEEIAALVIDNGSGMCK.A	Acetyl (+42)/ Carbamidomethyl (+57)	-.MEEEIAALVIDNGSGMCK.A
239	254	2	1789.89	5.1	1	75.2	25.3	95.00%	K.SYELPDGQVITIGNER.F		K.SYELPDGQVITIGNER.F
148	177	3	3182.62	3.4	1	67.2	20.8	95.00%	R.TTGIVLDSGDGVTHTVPIYEGYALPHAIMR.L		R.TTGIVLDSGDGVTHTVPIYEGYALPHAIMR.L
360	372	2	1511.7	3.8	1	34.6	26.6	95.00%	K.QEYDESGPGIVYR.K		K.QEYDESGPGIVYR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
28	SERA_SCHPO	34.12%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
410	421	2	1468.77	4	1	31.9	22.6	95.00%	R.QVNELFIDHNIK.S		R.QVNELFIDHNIK.S
355	366	2	1300.7	1.1	0	45.8	22.7	95.00%	Y.NIGIEVSEALTR.Y		K.NIILTPHIGGSTEEAQYNIGIEVSEALTR.Y
302	319	2	1728.88	4.5	1	48	24.1	95.00%	K.IAGAAIDVYPSEPAGNGK.D		K.IAGAAIDVYPSEPAGNGK.D
248	262	2	1596.82	4.1	1	50.8	23.4	95.00%	R.ADFVSLHVPASPETK.N		R.ADFVSLHVPASPETK.N
142	154	2	1394.7	4.8	1	57.8	24.8	95.00%	R.GIAVFNSPYANSR.S		R.GIAVFNSPYANSR.S
434	452	2	2053.02	0.059	0	60.4	25.8	95.00%	Y.LVADISDCTPGSLEALHQK.L	Carbamidomethyl (+57)	R.GDIAYLVADISDCTPGSLEALHQK.L
275	284	2	1108.56	4.3	1	25.6	24.5	90.90%	K.EGSYLINASR.G		K.EGSYLINASR.G
367	385	2	2078.05	3.9	1	76.6	23.9	95.00%	R.YINEGNSIGAVNFPEVSLR.S		R.YINEGNSIGAVNFPEVSLR.S
338	354	2	1841.92	-0.17	1	49.9	25.4	95.00%	K.NIILTPHIGGSTEEAQY.N		K.NIILTPHIGGSTEEAQYNIGIEVSEALTR.Y
47	57	3	1247.68	3.8	1	25.6	22	94.80%	R.TLKPFASEDIK.I		R.TLKPFASEDIK.I
302	321	2	1972.97	-2.6	1	37.9	25.7	95.00%	K.IAGAAIDVYPSEPAGNGKDK.F	Deamidation (+1)	K.IAGAAIDVYPSEPAGNGKDK.F
237	247	3	1291.72	-1.3	0	26	20.2	95.00%	K.QLSSLPELLHR.A		K.QLSSLPELLHR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
29	HXK2_SCHPO	41.98%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
12	24	2	1581.76	-1.8	1	66.6	26.4	95.00%	K.LVNDFEYPTESLR.E		K.LVNDFEYPTESLR.E
11	24	2	1709.86	-1.7	2	55.3	24.4	95.00%	K.KLVNDFEYPTESLR.E		K.KLVNDFEYPTESLR.E
142	156	2	1705.78	-0.82	1	37.4	27	95.00%	F.TFSYPANQVSITESY.L		K.FGCPEEEYLPMGFTFSYPANQVSITESYLLR.W

392	413	3	2499.23	3.2	2	59.6	25	95.00%	K.KSDVGVDGSLVEHYPHFVDMLR.E		K.KSDVGVDGSLVEHYPHFVDMLR.E
76	87	2	1450.73	-0.88	2	39.3	25.1	95.00%	R.VCWIQLLGDGKY.E	Carbamidomethyl (+57)	R.VCWIQLLGDGKYEMK.H
103	122	3	2360.22	3.5	1	42.1	22.6	95.00%	R.NESVKPIIDFMSDHVELFIK.E		R.NESVKPIIDFMSDHVELFIK.E
360	369	2	1108.58	0.88	1	35.3	23.6	95.00%	Y.LWDAAHAIGR.R		R.SDEEALYLWDAAHAIGR.R
374	388	2	1564.83	4.1	1	56.1	22.5	95.00%	R.MSAVPIASLYLSTGR.A		R.MSAVPIASLYLSTGR.A
103	120	2	2119.03	1.7	1	45.5	25.7	95.00%	R.NESVKPIIDFMSDHVELF.I		R.NESVKPIIDFMSDHVELFIK.E
1	11	2	1334.67	4.1	1	29.9	25.4	95.00%	-.MEANFQQAVKK.L	Acetyl (+42)	-.MEANFQQAVKK.L
266	279	2	1598.78	3.9	1	49.6	25.7	95.00%	R.YDLLLDHDTPNAGR.Q		R.YDLLLDHDTPNAGR.Q
434	449	2	1529.79	4.8	0	96.2	24	95.00%	K.DGSGIGAALCALQAVK.E	Carbamidomethyl (+57)	K.DGSGIGAALCALQAVK.E
221	237	2	1806.86	0.11	1	36.1	26.2	95.00%	F.GTGTNGAYVEQMNQIPK.L		K.ESDTFMGIIFGTGTNGAYVEQMNQIPK.L
76	86	2	1287.67	3.9	1	30.3	24	95.00%	R.VCWIQLLGDGK.Y	Carbamidomethyl (+57)	R.VCWIQLLGDGK.Y
286	296	2	1240.63	5.9	1	25.6	23.1	90.90%	R.VGGMYLGELFR.R		R.VGGMYLGELFR.R
216	237	2	2369.14	-0.18	1	92.3	26	95.00%	F.MGIIFGTGTNGAYVEQMNQIPK.L	Deamidation (+1)	K.ESDTFMGIIFGTGTNGAYVEQMNQIPK.L
25	34	2	1234.62	4.3	2	29.8	24.8	95.00%	R.EAVKEFDELR.Q		R.EAVKEFDELR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
30	PUR9_SCHPO	41.54%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
76	91	2	1843.91	3.7	1	36	25.2	95.00%	R.DIPSDEKDLVEQSIEK.I		R.DIPSDEKDLVEQSIEK.I
328	347	2	2128.09	-1.3	1	46.9	24.1	95.00%	R.EVSDGVIAPGYEPEALELLK.K		R.EVSDGVIAPGYEPEALELLK.K
138	153	2	1755.86	4.1	1	89.5	25.2	95.00%	R.VTILSDPADYATFTDK.F		R.VTILSDPADYATFTDK.F
551	565	2	1519.75	4.1	1	63.8	25.7	95.00%	K.YVAAPGGSVMDQAVR.D		K.YVAAPGGSVMDQAVR.D
39	60	2	2231.08	4.2	0	97.7	25.9	95.00%	R.ESGMEVADVSSITNAPEILGGR.V		R.ESGMEVADVSSITNAPEILGGR.V
248	259	2	1216.65	4.7	1	30.2	23.6	95.00%	R.ENIGIPAAASFK.H		R.ENIGIPAAASFK.H
104	129	3	2776.53	2.1	0	22.6	15.8	90.50%	R.ETIAKPNVTIPEAVEEIDIGGVTLLR.A		R.ETIAKPNVTIPEAVEEIDIGGVTLLR.A
480	498	2	2018	3.8	1	84.7	25.3	95.00%	K.SNAIDLYVLDAVPAEGSER.E		K.SNAIDLYVLDAVPAEGSER.E
260	278	3	1874.03	3.8	1	46.3	18.9	95.00%	K.HVSPAGAAVGLPLSDVEKK.V		K.HVSPAGAAVGLPLSDVEKK.V
526	543	2	2131.98	3.7	1	65.5	27.4	95.00%	K.DVVCASDAFFPFPDNIYR.L	Carbamidomethyl (+57)	K.DVVCASDAFFPFPDNIYR.L
223	244	2	2446.24	1.8	1	57.4	23.8	95.00%	K.VLCGSPGYINLMDALNSWPLVK.E	Carbamidomethyl (+57)	K.VLCGSPGYINLMDALNSWPLVK.E
566	581	2	1881.9	4.3	1	55.8	26.3	95.00%	R.DTANEFNMVFSEIPLR.L		R.DTANEFNMVFSEIPLR.L
201	213	2	1386.63	-1	1	27	26.5	90.90%	R.YGANPHQSPAQAF.M		R.YGANPHQSPAQAFMEQGPLPFK.V
354	362	2	1152.54	4.8	1	28.8	25.5	94.70%	K.YCVLQMDPK.Y	Carbamidomethyl (+57)	K.YCVLQMDPK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
31	IPYR_SCHPO	58.48%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
240	280	3	4115.08	2.7	1	89.4	18.9	95.00%	K.SDFSLVNVSVTGSVANDPSVSSTIPPAQELAPAPVDPSVHK.W		K.SDFSLVNVSVTGSVANDPSVSSTIPPAQELAPAPVDPSVHK.W
32	42	2	1269.63	-0.8	1	44.2	24.5	95.00%	W.HDIPLYANAEK.T		K.NGTPISSWHDIPLYANAEK.T
186	192	2	922.44	6	1	35.4	24.5	95.00%	R.ATNEWFR.I		R.ATNEWFR.I
94	113	2	2305.07	0.95	1	33.5	26.3	95.00%	W.NYGAFPQTYEDPNVVHPETK.A		R.NCFPHHGYIWNYGAFPQTYEDPNVVHPETK.A
141	156	2	1774.89	4.3	1	77	25	95.00%	K.VLGVMALLDEGETDWK.V		K.VLGVMALLDEGETDWK.V
24	42	2	2112.04	4.6	1	50.5	25.5	95.00%	K.NGTPISSWHDIPLYANAEK.T		K.NGTPISSWHDIPLYANAEK.T
114	130	2	1830.85	4	1	98.5	26.8	95.00%	K.AKGDSDPLDVCEIGEAR.G	Carbamidomethyl (+57)	K.AKGDSDPLDVCEIGEAR.G
170	178	2	1101.53	3.9	0	49.3	23.4	95.00%	K.LNDIEDVER.H		K.LNDIEDVER.H
43	53	2	1283.73	4	0	66.7	19.5	95.00%	K.TILNMVVEIPR.W		K.TILNMVVEIPR.W
157	169	2	1391.81	4.1	0	37.4	15.2	95.00%	K.VIVIDVNDPLAPK.L		K.VIVIDVNDPLAPK.L
8	23	2	1839.93	4.1	1	74	24.1	95.00%	R.EVGALNTLDYQVYVEK.N		R.EVGALNTLDYQVYVEK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
32	TKT_SCHPO	27.88%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
364	394	3	3276.78	4.5	1	70.7	14.8	95.00%	R.KLSEIVLDALCPVLPELVGGSADLTPSNLTR.W	Carbamidomethyl (+57)	R.KLSEIVLDALCPVLPELVGGSADLTPSNLTR.W
325	336	2	1449.68	6.5	1	28.4	25.2	94.60%	K.QSYPDLSNQLER.I	Deamidation (+1)	K.QSYPDLSNQLER.I
2	18	2	1869.94	4.3	1	66.2	24.3	95.00%	M.TSSSYTDIDTLAINTIR.T		-.MTSSSYTDIDTLAINTIR.T
238	252	2	1719.86	5	0	57.2	25.3	95.00%	R.EAMSCTDKPTLINLK.T	Carbamidomethyl (+57)	R.EAMSCTDKPTLINLK.T
395	407	2	1418.65	3.9	1	52.7	26	95.00%	R.WEGAADFQPPSSK.L		R.WEGAADFQPPSSK.L
182	193	2	1385.74	4.7	1	41.9	22.7	95.00%	K.LSNLIAVWDNNK.I		K.LSNLIAVWDNNK.I
532	547	2	1810.95	4.2	0	72.5	22.4	95.00%	R.QNLPQLENSTIENALK.G		R.QNLPQLENSTIENALK.G
253	281	3	3132.54	2.9	1	59.8	23.1	95.00%	K.TTIGYGSELQGTHSVHGSPLKPEDCVHVK.K	Carbamidomethyl (+57)	K.TTIGYGSELQGTHSVHGSPLKPEDCVHVK.K
636	648	3	1300.59	-0.16	1	33.7	26	95.00%	F.GMHTFGDSGPAPK.L		R.YVHEAFGMHTFGDSGPAPK.L
306	318	2	1423.73	4.8	1	73.3	24.6	95.00%	R.VAIASSAEEEYKK.M		R.VAIASSAEEEYKK.M
30	49	3	1972.02	3.9	1	31.5	23.3	95.00%	K.SGHPGAPMGLAPAAHVLFSR.I		K.SGHPGAPMGLAPAAHVLFSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
33	G6PI_SCHPO	32.55%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
217	228	2	1343.61	5.2	1	37.3	26.3	95.00%	K.TFTTAETCTNAK.S	Carbamidomethyl (+57)	K.TFTTAETCTNAK.S
464	477	2	1502.83	4	1	36.9	20.6	95.00%	K.TFVGNRPSNSIIAK.K		K.TFVGNRPSNSIIAK.K
63	75	2	1499.85	3.9	0	37.5	19.3	95.00%	K.NLITEETVELLVK.L		K.NLITEETVELLVK.L
446	463	3	1916.98	-1.8	1	54.9	23.8	95.00%	K.TPAEVKAEGTPDEIVPHK.T		K.TPAEVKAEGTPDEIVPHK.T
118	128	2	1170.59	4.1	0	35.5	23.6	95.00%	K.VNGQDVMPGVR.K		K.VNGQDVMPGVR.K
429	445	2	1870.94	4.8	1	69.7	24.7	95.00%	R.MLFSNFAAQTEALMLGK.T		R.MLFSNFAAQTEALMLGK.T
110	128	3	2084.06	4.5	1	31.6	23.7	95.00%	R.NVSEKPMKVNGQDVMPGVR.K		R.NVSEKPMKVNGQDVMPGVR.K
530	547	3	1959.91	-5.3	1	25.9	27.2	92.40%	K.GDVENHDSSTNGLINLFK.N	Deamidation (+1)	K.GDVENHDSSTNGLINLFK.N
406	425	2	2259.19	-0.37	1	49.1	22.1	95.00%	K.LIPADFLIPIESHNPIDNNK.H		K.LIPADFLIPIESHNPIDNNK.H
372	382	2	1171.52	5.1	1	67.7	25.6	95.00%	R.SGDMVNYTTGK.I		R.SGDMVNYTTGK.I
435	445	2	1131.59	-1.2	0	53.6	22.9	95.00%	F.AAQTEALMLGK.T		R.MLFSNFAAQTEALMLGK.T
204	216	2	1493.75	4.3	1	51.5	25.6	95.00%	K.CDPETTLFLIASK.T	Carbamidomethyl (+57)	K.CDPETTLFLIASK.T
521	547	3	2955.5	3	2	45.6	21.4	95.00%	K.NVLAQLETKGDVENHDSSTNGLINLFK.N		K.NVLAQLETKGDVENHDSSTNGLINLFK.N
353	367	2	1711.83	4.2	1	71.8	25.8	95.00%	R.FPAYLQQLSMESNGK.A		R.FPAYLQQLSMESNGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
34	GPD1_SCHPO	38.44%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
87	104	2	2008.04	-0.99	1	59.7	22.7	95.00%	K.YLPGIECPPNVIAVPDVR.E	Carbamidomethyl (+57)	K.YLPGIECPPNVIAVPDVR.E
277	296	2	2153	2.6	0	93.7	26.8	95.00%	R.TMVEQSCGIADLVTSCLGGR.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.TMVEQSCGIADLVTSCLGGR.N
73	86	2	1656.85	-1.2	2	56.6	24.2	95.00%	R.KLTEVFNEAHENVK.Y		R.KLTEVFNEAHENVK.Y
74	86	2	1528.75	-1.1	1	69.9	25.1	95.00%	K.LTEVFNEAHENVK.Y		K.LTEVFNEAHENVK.Y
2	20	2	1989	3.8	1	99.4	24.5	95.00%	M.SGYGQQGVSAANIDSIRPK.K	Acetyl (+42)	-.MSGYGQQGVSAANIDSIRPK.K
310	331	3	2285.25	0.4	1	27.1	19.2	95.00%	K.SLETLEKELLGGQLLQGAATSK.D		K.SLETLEKELLGGQLLQGAATSK.D
183	202	2	2362.1	3.9	1	116	26.6	95.00%	R.EQFCETTIGFNPPNEVDIPR.E	Carbamidomethyl (+57)	R.EQFCETTIGFNPPNEVDIPR.E
168	182	2	1515.74	-2	0	74.9	25.6	95.00%	Y.CGVLSGANVANEVAR.E	Carbamidomethyl (+57)	K.LGIYCGVLSGANVANEVAR.E
125	144	3	2172.12	-1.5	0	35.1	22.6	95.00%	R.VCDQMVGLIRPGAVGISCIK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VCDQMVGLIRPGAVGISCIK.G
317	331	2	1484.82	-1.3	0	73.8	21.4	95.00%	K.ELLGGQLLQGAATSK.D		K.ELLGGQLLQGAATSK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
35	LYS9_SCHPO	42.22%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
177	183	2	740.49	4.7	0	33.1	11.8	95.00%	R.GVLLALR.N		R.GVLLALR.N
194	209	3	1820.92	0.77	2	45.1	24.7	95.00%	K.LVEIDGKDLMETAKPY.F		K.LVEIDGKDLMETAKPYFIYPGYAFVCYPNR.D
290	301	2	1276.66	4.3	1	31	23.5	95.00%	K.AESSSEADLIKK.I		K.AESSSEADLIKK.I

38	49	2	1259.66	4.1	1	41.7	23.9	95.00%	K.AEAFINGIPNSK.A		K.AEAFINGIPNSK.A
379	396	2	1990.9	-0.8	1	77.3	26.8	95.00%	R.TCTLLDYGVPNGYTSMAK.L	Carbamidomethyl (+57)/ Deamidation (+1)	R.TCTLLDYGVPNGYTSMAK.L
287	301	3	1616.9	-0.37	1	32.9	19.7	95.00%	R.VIKAESSSEADLIKK.I		R.VIKAESSSEADLIKK.I
397	426	3	3075.61	0.31	0	50	19	95.00%	K.LVGVPCGVATQQILDGVINTPGVLAPNDMK.L	Carbamidomethyl (+57)	K.LVGVPCGVATQQILDGVINTPGVLAPNDMK.L
64	85	3	2488.28	3.3	1	39.1	22.3	95.00%	K.AVSEHDLTISLIPYTYHATVMK.A		K.AVSEHDLTISLIPYTYHATVMK.A
2	22	3	2269.25	3.1	1	39	17.6	95.00%	M.PSILLLGSGFVAHPTLEYLSR.R		-.MPSILLLGSGFVAHPTLEYLSR.R
114	135	3	2372.16	2.8	1	47.3	25.4	95.00%	K.AGSICMNEIGVDPGIDHLYAIK.T	Carbamidomethyl (+57)	K.AGSICMNEIGVDPGIDHLYAIK.T
104	113	2	1103.56	4	0	29.1	23.7	95.00%	K.MAELEEAAIK.A		K.MAELEEAAIK.A
114	132	2	2059.94	0.4	1	52.7	27.2	95.00%	K.AGSICMNEIGVDPGIDHLY.A	Carbamidomethyl (+57)	K.AGSICMNEIGVDPGIDHLYAIK.T
154	170	2	1787.81	-1.7	1	51.6	26.8	95.00%	Y.CGGLPAPEDSNNPLGYK.F	Carbamidomethyl (+57)	K.SFLSYCGGLPAPEDSNNPLGYK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
36	PDX1_SCHPO	30.74%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	49	2	1547.75	3.7	0	51.8	25.4	95.00%	R.IAEAAGACAVMALER.V	Carbamidomethyl (+57)/ Oxidation (+16)	R.IAEAAGACAVMALER.V
265	280	2	1628.86	4	0	87.2	22.8	95.00%	K.ILAEVSENLGAAMVGR.S		K.ILAEVSENLGAAMVGR.S
71	83	2	1355.75	4.3	0	66.7	21.3	95.00%	K.EIQAAVSIPVMAK.V		K.EIQAAVSIPVMAK.V
150	164	2	1487.76	3.9	1	69.3	23.8	95.00%	R.TKGEAGTGDVVEAVR.H		R.TKGEAGTGDVVEAVR.H
21	34	2	1457.74	4	0	89.6	24.3	95.00%	K.GGVIMDVVNAEQAR.I		K.GGVIMDVVNAEQAR.I
140	149	2	1102.6	4.8	1	28.6	23	95.00%	R.RISEGAAMIR.T		R.RISEGAAMIR.T
13	20	2	830.47	4.2	0	38.8	21.5	95.00%	K.AGLAQMLK.G		K.AGLAQMLK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
37	HSP60_SCHPO	31.79%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	148	2	1316.6	4	0	27.4	26.5	91.30%	R.NVAAGCNPMDLR.R	Carbamidomethyl (+57)	R.NVAAGCNPMDLR.R
244	256	2	1529.84	4	1	44.5	21.4	95.00%	K.VEFENPLILLSEK.K		K.VEFENPLILLSEK.K
382	396	2	1722.82	4	1	31.1	26	95.00%	R.GVMADPNLTEYEKEK.L		R.GVMADPNLTEYEKEK.L
258	275	2	1937.07	4.4	0	74.7	18.9	95.00%	K.VSAVQDILPSLELAAQQR.R		K.VSAVQDILPSLELAAQQR.R
45	56	2	1215.69	4.9	0	52.6	21.2	95.00%	R.ASLLTGVDTLAR.A		R.ASLLTGVDTLAR.A
257	275	3	2065.15	-1.5	1	37.8	16.7	95.00%	K.KVSAVQDILPSLELAAQQR.R		K.KVSAVQDILPSLELAAQQR.R
112	128	2	1705.86	4.1	0	84.3	25.3	95.00%	K.TNEVAGDGTTTATVLTR.A		K.TNEVAGDGTTTATVLTR.A
437	453	2	1588.85	4.6	1	29.9	22.3	95.00%	K.AAVSEGVLPGAGTSFVK.A		K.AAVSEGVLPGAGTSFVK.A
478	500	3	2377.34	2.9	0	22.4	14.8	90.20%	K.AITRPAQTILENAGLEGNLIVGK.L		K.AITRPAQTILENAGLEGNLIVGK.L
241	256	2	1873.03	4.6	2	56.5	20	95.00%	K.SQKVEFENPLILLSEK.K		K.SQKVEFENPLILLSEK.K
168	195	3	2912.47	2.9	0	40.6	22.9	95.00%	R.DITTSEEISQVATISANGDTHIGELLAK.A		R.DITTSEEISQVATISANGDTHIGELLAK.A
68	79	2	1313.7	4.3	1	39.3	21.8	95.00%	R.NVLIDQPFGSPK.I		R.NVLIDQPFGSPK.I
520	533	2	1570.87	4.4	1	87.2	21.1	95.00%	R.FVDLNEIGVLDPLK.V		R.FVDLNEIGVLDPLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
38	YL8C_SCHPO	48.51%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
217	232	2	1745.96	4.4	1	53	20.4	95.00%	K.GTALQYITSNILPEVK.N		K.GTALQYITSNILPEVK.N
275	288	2	1456.71	-1.1	0	66.7	25.3	95.00%	R.VGNEEGAVGEVLER.I		R.VGNEEGAVGEVLER.I
7	33	4	3045.57	3.9	1	29.7	20.8	95.00%	K.TNNLPTLDTLQMVISDVDGTLLDKHHR.F		K.TNNLPTLDTLQMVISDVDGTLLDKHHR.F
96	112	3	1893.99	0.26	0	49.5	23	95.00%	Y.ADHLKPEVVMEVVEATK.G		K.IVYADHLKPEVVMEVVEATK.G
70	88	2	2085.02	-1.4	1	41	25.8	95.00%	R.IPLDLDAFPAAHVNGCVLY.N	Deamidation (+1)/ Carbamidomethyl (+57)	R.IPLDLDAFPAAHVNGCVLYNK.G
173	186	2	1645.79	3.6	1	65.2	26.3	95.00%	K.MAVCEDPDKLDVVR.D	Carbamidomethyl (+57)	K.MAVCEDPDKLDVVR.D
93	112	3	2269.21	1.5	1	46.5	20.6	95.00%	K.IVYADHLKPEVVMEVVEATK.G		K.IVYADHLKPEVVMEVVEATK.G

47	60	2	1575.87	4.2	2	37.4	19.7	95.00%	R.EKYPNFPIVLATGK.Q		R.EKYPNFPIVLATGK.Q
113	128	2	1865.86	0.59	1	40.2	26.7	95.00%	K.GNPNIANVVYDEHYVY.A		K.GNPNIANVVYDEHYVYALTPGR.E
70	90	3	2326.19	3.3	1	38.3	23.7	95.00%	R.IPLDLDAFPAAHVNGCVLYNK.G	Carbamidomethyl (+57)	R.IPLDLDAFPAAHVNGCVLYNK.G
2	33	4	3587.84	2.8	1	81.1	19.2	95.00%	M.SAVDKTNNLPTLDTLQMVISDVDGTLLDKHHR.F	Acetyl (+42)	-.MSAVDKTNNLPTLDTLQMVISDVDGTLLDKHHR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
39	CYPH_SCHPO	40.74%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	17	2	1835.86	-0.63	1	67.8	26.3	95.00%	M.SNCFFDVIANGQPLGR.I	Acetyl (+42)/ Carbamidomethyl (+57)	-.MSNCFFDVIANGQPLGR.I
112	123	2	1328.73	0.29	1	47.3	21.4	95.00%	F.ITTVVTPWLDGK.H		K.HNKPGLLSMANAGPNTNGSQFFITTVVTPWLDGK.H
59	67	2	1023.48	-1.3	1	26.7	25.3	92.10%	F.MLQGGDFTR.G		R.VIPQFMLQGGDFTR.G
124	139	3	1772.92	4.1	1	60.2	23.5	95.00%	K.HVVFGEVTEGMDVVKK.V		K.HVVFGEVTEGMDVVKK.V
54	67	2	1607.82	4.3	1	67.2	24.7	95.00%	R.VIPQFMLQGGDFTR.G		R.VIPQFMLQGGDFTR.G
124	138	2	1644.83	4.4	1	86.7	24.7	95.00%	K.HVVFGEVTEGMDVVK.K		K.HVVFGEVTEGMDVVK.K
22	29	2	931.51	4	1	29.7	23.4	95.00%	K.LFDDVVPK.T		K.LFDDVVPK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
40	CARB_SCHPO	13.62%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1016	1041	3	2570.45	0.58	0	45.5	12.6	95.00%	K.IPLPGQGILLGGDRPELAGIAADLSK.L		K.IPLPGQGILLGGDRPELAGIAADLSK.L
418	433	2	1784.89	3.2	1	42	24.9	95.00%	K.TTTANFEPSLDYVVTK.I		K.TTTANFEPSLDYVVTK.I
575	584	2	1057.58	4.7	0	32.1	22.6	95.00%	K.LVGASELDVR.A		K.LVGASELDVR.A
799	823	4	2678.39	3.7	1	43.2	21.4	95.00%	R.DESSLKDKLENASAVSPDHPVVITK.F		R.DESSLKDKLENASAVSPDHPVVITK.F
730	744	2	1630.78	-2.2	0	82.7	25.3	95.00%	K.VLGTDPLMIDSAEDR.H		K.VLGTDPLMIDSAEDR.H
932	943	2	1304.72	5.6	1	35.2	21.5	95.00%	K.TLGVNFIDVATR.S		K.TLGVNFIDVATR.S
1056	1070	2	1655.91	-1.6	1	47.5	20.6	95.00%	K.LLQPTSAEVVEFPVK.D		K.LLQPTSAEVVEFPVK.D
773	798	3	2736.49	2.9	1	51	17.3	95.00%	K.FANAVGYPVLVRPSYVLSGAAMSVIR.D		K.FANAVGYPVLVRPSYVLSGAAMSVIR.D
261	273	3	1432.7	2.1	1	31.6	25	95.00%	F.ANNKEELQSMAAK.S		R.SAYSLGGLGSGFANNKEELQSMAAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
41	PPA1_SCHPO	15.23%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	92	2	2047	4	1	99.4	25.8	95.00%	R.NPTGGNAAFDAVGIANFQQR.L		R.NPTGGNAAFDAVGIANFQQR.L
47	59	2	1531.7	0.46	1	62.7	26.4	95.00%	Y.FYGPSIDFPTTCK.I	Carbamidomethyl (+57)	R.SPYHKPYFYGPSIDFPTTCK.I
373	387	2	1723.81	-2.1	1	53.5	26.5	95.00%	F.AGNLITELFQCEDSK.Y	Carbamidomethyl (+57)	K.ASEFVPFAGNLITELFQCEDSK.Y
373	388	2	1886.87	0.86	2	63.7	27	95.00%	F.AGNLITELFQCEDSKY.Y	Carbamidomethyl (+57)	K.ASEFVPFAGNLITELFQCEDSKYYVR.H
205	224	2	2206.96	0.13	1	90.8	27.6	95.00%	Y.NACPASDADDFTTPALEAWR.N	Carbamidomethyl (+57)	R.VVDSALWYGYGMFGEDVHNFTNYILVSENATAGSNSLSSYNACPASDADDFTTPALEAWR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
42	PUT2_SCHPO	27.01%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
33	52	2	2197.23	0.22	1	54.3	16.9	95.00%	K.AYKELEAELPVTIPVIIDGK.E		K.AYKELEAELPVTIPVIIDGK.E
406	422	2	1852.92	4.3	1	57.5	25.6	95.00%	K.ADDSEGFFVEPTVLLSK.N		K.ADDSEGFFVEPTVLLSK.N
233	253	2	2068.09	4.4	1	68.9	22.3	95.00%	R.EAGLPAGALQFIPGDAVEVSK.V		R.EAGLPAGALQFIPGDAVEVSK.V

495	509	2	1504.71	3.5	1	49.3	26	95.00%	K.CTGAVVGEQPFGGAR.A	Carbamidomethyl (+57)	K.CTGAVVGEQPFGGAR.A
388	405	2	1773.9	-1.8	0	121	24.2	95.00%	K.VLESAASDSEIEVLAGGK.A		K.VLESAASDSEIEVLAGGK.A
82	92	2	1222.64	4.6	0	32.1	23.7	95.00%	K.HVEDAIEAALR.G		K.HVEDAIEAALR.G
275	288	2	1444.74	4.6	1	37.7	24.2	95.00%	R.SLWGTIGENVANGK.Y		R.SLWGTIGENVANGK.Y
373	382	2	1053.56	0.84	1	70.6	21.5	95.00%	F.VGPVIHQASF.N		K.VGAPLTDFANFVGPVIHQASFNK.L
36	63	3	3091.63	0.58	1	52.2	18.1	95.00%	K.ELEAELPVTIPVIIDGKEVETNTIGEQR.C		K.ELEAELPVTIPVIIDGKEVETNTIGEQR.C
484	494	2	1225.58	4.6	1	28	25.8	93.40%	R.NAAGNFYINDK.C		R.NAAGNFYINDK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
43	OAT_SCHPO	44.75%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
211	234	2	2621.26	-0.0035	1	49.3	25.2	95.00%	F.LVEPIQGEAGVMVPDDGYLEEAYK.L		K.VAAFLVEPIQGEAGVMVPDDGYLEEAYK.L
2	11	2	1159.55	2.2	1	34	25.6	95.00%	M.SAESLLHNTF.S	Acetyl (+42)	-.MSAESLLHNTFSTEQIEVLENEYAAHNYHPLPVCFSK.A
386	398	3	1374.82	4.6	0	23.2	15.4	91.60%	R.GVLAKPTHGNIIR.F		R.GVLAKPTHGNIIR.F
154	167	2	1493.69	4.9	0	59.2	26	95.00%	R.TMGIISMSTDPDAR.D		R.TMGIISMSTDPDAR.D
292	306	2	1694.76	1.3	1	33.4	26.1	95.00%	R.EIMLNFEPGTHGSTY.G		R.EIMLNFEPGTHGSTYGGNPLGAAVSIAALEVVK.E
135	153	3	2184.11	3	2	28.6	24.1	95.00%	K.KIPTDEAIILSCVDNFHGR.T	Carbamidomethyl (+57)	K.KIPTDEAIILSCVDNFHGR.T
276	291	2	1561.85	4	1	53	21.1	95.00%	K.AISGGVYPVSAVLSSR.E		K.AISGGVYPVSAVLSSR.E
238	254	2	1838.97	4.4	1	78.8	22	95.00%	K.AHNVLFIADEVQTGVAR.T		K.AHNVLFIADEVQTGVAR.T
258	275	3	2051.09	0.31	0	44.7	21.2	95.00%	K.MLCIEHSNVKPDVVILGK.A	Carbamidomethyl (+57)	K.MLCIEHSNVKPDVVILGK.A
307	327	3	2051.13	0.58	1	22.5	18.9	90.30%	Y.GGNPLGAAVSIAALEVVKEEK.L		R.EIMLNFEPGTHGSTYGGNPLGAAVSIAALEVVKEEK.L
70	80	2	1268.71	4.2	0	28.4	18.6	94.70%	K.IIEALVEQAQR.V		K.IIEALVEQAQR.V
107	124	2	1949.89	1	0	65.5	26.4	95.00%	Y.EMVIPMNTGAEAVETACK.L	Carbamidomethyl (+57)	K.YITEYFGYEMVIPMNTGAEAVETACK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
44	RAD24_SCHPO	50.74%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
228	267	3	4032.79	4.4	1	129	23.8	95.00%	R.DNLTLWTSDAEYSAAAAGGNTEGAQENAPSNAPEGEAEPK.A		R.DNLTLWTSDAEYSAAAAGGNTEGAQENAPSNAPEGEAEPK.A
15	30	3	1896.88	4.4	2	24.8	26.7	91.40%	K.LAEQAERYEGMVENMK.S		K.LAEQAERYEGMVENMK.S
156	172	2	1746.93	4.5	0	64.4	21.7	95.00%	K.AASEIATAELAPTHPIR.L		K.AASEIATAELAPTHPIR.L
240	270	3	2881.27	2.4	1	36.9	26.7	95.00%	Y.SAAAAGGNTEGAQENAPSNAPEGEAEPKADA.-		R.DNLTLWTSDAEYSAAAAGGNTEGAQENAPSNAPEGEAEPKADA.-
109	120	2	1236.65	4.7	0	29.1	22.7	95.00%	K.HLIPNAASAESK.V		K.HLIPNAASAESK.V
31	44	2	1562.75	4.1	0	82.9	26.1	95.00%	K.SVASTDQELTVEER.N		K.SVASTDQELTVEER.N
240	267	3	2624.16	0.37	0	51	27.2	95.00%	Y.SAAAAGGNTEGAQENAPSNAPEGEAEPK.A		R.DNLTLWTSDAEYSAAAAGGNTEGAQENAPSNAPEGEAEPK.A
2	14	2	1481.74	4.3	2	46.8	25.2	95.00%	M.STTSREDAVYLAK.L	Acetyl (+42)	-.MSTTSREDAVYLAK.L
64	85	3	2429.31	3.8	1	57.6	18.8	95.00%	R.IVSSIEQKEESKGNTAQVELIK.E		R.IVSSIEQKEESKGNTAQVELIK.E
234	267	3	3290.41	1.7	1	64.7	26.1	95.00%	W.TSDAEYSAAAAGGNTEGAQENAPSNAPEGEAEPK.A		R.DNLTLWTSDAEYSAAAAGGNTEGAQENAPSNAPEGEAEPK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
45	C1TC_SCHPO	14.62%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
689	707	3	1923.14	0.32	0	39.5	9.54	95.00%	R.TSGLKPDAIVIVATVQALK.L		R.TSGLKPDAIVIVATVQALK.L
204	219	2	1649.95	-0.62	1	31.1	14.9	95.00%	R.TADIVVAAIGIPHFVK.A		R.TADIVVAAIGIPHFVK.A
57	84	3	3131.52	3.1	1	32.8	23.6	95.00%	R.AANEAGISCEHVNFPEDITEYDLLLAIK.G	Carbamidomethyl (+57)	R.AANEAGISCEHVNFPEDITEYDLLLAIK.G

349	356	2	983.58	5.3	0	46.2	17.4	95.00%	K.VNLEILQR.L	K.VNLEILQR.L
835	849	2	1592.78	4.3	1	53.3	25.8	95.00%	K.EMYGADGIELSPLAK.E	K.EMYGADGIELSPLAK.E
2	12	2	1184.68	4.9	0	55.8	20.5	95.00%	M.ALLLEGTSLAR.K (Acetyl (+42))	-.MALLLEGTSLAR.K
536	546	2	1228.67	4.9	1	27.4	22	93.60%	R.KITIGENPTEK.G	R.KITIGENPTEK.G
324	336	2	1299.71	5.1	0	59.2	21.9	95.00%	K.NIGDLASEIGIAK.S	K.NIGDLASEIGIAK.S
381	396	2	1629.9	3.4	0	106	20.9	95.00%	K.STLTAGLVQALSNLDK.L	K.STLTAGLVQALSNLDK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
46	FAS2_SCHPO	8.09%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1569	1579	2	1292.61	5	1	41.1	25.6	95.00%	R.NADNIDEYLAR.F		R.NADNIDEYLAR.F
114	146	3	3020.56	3.1	0	35.9	21.2	95.00%	K.VETAAAAAPAATPAPAPAQTSAPAAALPDEPPK.A		K.VETAAAAAPAATPAPAPAQTSAPAAALPDEPPK.A
517	527	2	1319.7	5.4	2	32	23.6	95.00%	R.KLTHYVTEMAK.G		R.KLTHYVTEMAK.G
28	44	2	1939.01	4.4	1	67.5	22.9	95.00%	R.WIETQDVILSPPVSAER.I		R.WIETQDVILSPPVSAER.I
488	502	3	1650.8	4.5	0	35.5	26.1	95.00%	K.NVNHPTAPSTTIDER.G		K.NVNHPTAPSTTIDER.G
914	937	3	2504.19	3.1	1	37.5	26.2	95.00%	R.AVAAETAFDHSITNGPDSEAVFQK.T		R.AVAAETAFDHSITNGPDSEAVFQK.T
1393	1401	2	994.61	4.5	0	27.6	12	93.90%	K.TPLPIVDLK.F		K.TPLPIVDLK.F
1785	1813	3	2858.5	0.66	1	46.7	19.8	95.00%	K.GAAAPLKDIEIISSESGAPEVVLHGEAAK.A		K.GAAAPLKDIEIISSESGAPEVVLHGEAAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
47	HOSM_SCHPO	33.01%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	31	3	3218.5	4.8	1	47.5	25.2	95.00%	M.SVSEANGTETIKPPMNGNPYGPNPSDFLSR.V	Acetyl (+42)/ Deamidation (+1)	-.MSVSEANGTETIKPPMNGNPYGPNPSDFLSR.V
215	225	2	1321.55	2	1	33.5	25.7	95.00%	R.GVVSCDIECHF.H	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GVVSCDIECHFHNDTGMAIANAYCALEAGATHIDTSILGIGER.N
22	31	2	1088.53	1.3	1	50.8	23.8	95.00%	Y.GPNPSDFLSR.V		-.MSVSEANGTETIKPPMNGNPYGPNPSDFLSR.V
360	375	3	1793.94	-1.3	1	34.9	22.6	95.00%	K.SRAEQLNLHLTDAQAK.E		K.SRAEQLNLHLTDAQAK.E
192	204	2	1315.66	4	0	40.8	24.6	95.00%	R.VGIADTVGCATPR.Q	Carbamidomethyl (+57)	R.VGIADTVGCATPR.Q
64	85	2	2410.17	0.86	1	150	25.5	95.00%	K.ALDNFGVDYIELTSPVASEQSR.Q		K.ALDNFGVDYIELTSPVASEQSR.Q
172	182	2	1264.7	4.6	1	43.4	20.1	95.00%	R.SDLVDLLSLYK.A		R.SDLVDLLSLYK.A
401	411	2	1290.55	4.4	1	41	26.7	95.00%	R.EYHADLSDADR.I		R.EYHADLSDADR.I
32	43	2	1391.75	4.9	1	68.1	21.6	95.00%	R.VNNFSIIESTLR.E		R.VNNFSIIESTLR.E
333	344	3	1420.7	1	1	24.6	24.7	93.60%	Y.EILKPEDFGMSR.Y		K.AILANPSTYEILKPEDFGMSR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
48	HSP7F_SCHPO	23.75%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
174	189	2	1665.85	4	1	78.4	24.5	95.00%	R.LMNDNAAAALTYGITK.T		R.LMNDNAAAALTYGITK.T
539	558	3	2226.18	2.9	1	45	21.4	95.00%	K.VADLSVSVQEDRLPTEVLEK.Y		K.VADLSVSVQEDRLPTEVLEK.Y
561	580	4	2283.16	4.6	1	33.5	23.3	95.00%	R.EAEHQMIATDKLVAETVDRK.N		R.EAEHQMIATDKLVAETVDRK.N
581	591	2	1385.65	4	1	31.1	26.5	95.00%	K.NALEEYIYDTR.A		K.NALEEYIYDTR.A
694	720	3	3003.37	3.5	1	48	26.2	95.00%	R.APPPPPAEEVAPENEEVETMEIDEQKE.-		R.APPPPPAEEVAPENEEVETMEIDEQKE.-
38	48	2	1194.59	3.8	1	34	24.7	95.00%	R.STPSLVSYGER.S		R.STPSLVSYGER.S
96	106	2	1134.6	4	1	31.7	24.7	95.00%	K.LTEVDGFVGAK.V		K.LTEVDGFVGAK.V
305	318	3	1743.95	-0.81	2	24.7	21.3	93.70%	K.RSDFEELIKPLLER.L		K.RSDFEELIKPLLER.L
306	318	3	1587.85	-1.3	1	23.8	22.5	92.50%	R.SDFEELIKPLLER.L		R.SDFEELIKPLLER.L
5	16	2	1249.64	6.5	1	29.4	24.3	95.00%	R.TNVVGIDFGNSK.T		R.TNVVGIDFGNSK.T
159	173	2	1534.88	-1.5	0	47	14.8	95.00%	R.ALLEAANIAGLNPLR.L		R.ALLEAANIAGLNPLR.L
617	630	2	1684.72	4	1	75.9	26.8	95.00%	K.AEDWLYEEGEDTTK.A		K.AEDWLYEEGEDTTK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
49	HSP7M_SCHPO	24.33%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
637	647	2	1313.76	3.4	1	27.8	18.8	94.10%	K.KIDEIQQLSLK.V		K.KIDEIQQLSLK.V
366	388	3	2471.31	-0.16	1	28	20.6	95.00%	R.ALKDANLQTSEINEVILVGGMTR.M		R.ALKDANLQTSEINEVILVGGMTR.M
622	635	2	1464.65	3.4	0	88.6	26.6	95.00%	K.VNAGDEGITSEDMK.K		K.VNAGDEGITSEDMK.K
204	215	2	1124.67	4.6	0	48.3	15.1	95.00%	K.AAGAIAGLNVLR.V		K.AAGAIAGLNVLR.V
322	337	2	1645.86	3.4	1	41.2	22.9	95.00%	K.TDISLPFITADATGPK.H		K.TDISLPFITADATGPK.H
105	118	2	1578.81	4.5	1	81.4	24.5	95.00%	R.QAVINPENTFFATK.R		R.QAVINPENTFFATK.R
185	199	2	1679.83	4.3	1	62.1	25.8	95.00%	K.NAVVTVPAYFNDSQR.Q		K.NAVVTVPAYFNDSQR.Q
496	510	2	1538.89	4.2	1	77.2	15.4	95.00%	K.LIGNFQLTGIAPAPK.G		K.LIGNFQLTGIAPAPK.G
622	636	2	1592.74	5	1	80.4	25.9	95.00%	K.VNAGDEGITSEDMKK.K		K.VNAGDEGITSEDMKK.K
157	170	2	1496.8	5.1	1	59.3	21.7	95.00%	K.TYSPSQIGGFILSK.M		K.TYSPSQIGGFILSK.M
470	482	2	1317.65	-1	0	37	24.7	95.00%	F.STAADGQTAVEIR.V		K.SQVFSTAADGQTAVEIR.V
216	231	2	1630.86	3.8	1	78.5	22.3	95.00%	R.VVNEPTAAALAYGLDK.K		R.VVNEPTAAALAYGLDK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
50	VIPI_SCHPO	52.53%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
69	94	2	2433.11	4.4	0	121	26.9	95.00%	K.IQITSEDGGAASTTDQGGAGGDQAAR.Q		K.IQITSEDGGAASTTDQGGAGGDQAAR.Q
55	68	2	1496.85	-1.9	0	55.4	18.5	95.00%	K.TALLLQDALLGQNK.I		K.TALLLQDALLGQNK.I
199	218	3	2268.13	4	1	49.3	24.5	95.00%	K.VQNAYEDGKNQLLGIHNEAR.R		K.VQNAYEDGKNQLLGIHNEAR.R
101	110	2	1087.63	5.8	0	34.3	20.8	95.00%	R.SAIISELLSR.G		R.SAIISELLSR.G
225	254	3	2955.39	-0.58	1	59.5	25.4	95.00%	K.NQAEGTASPASSTPTAPAEKEPTAPTTESK.T		K.NQAEGTASPASSTPTAPAEKEPTAPTTESK.T
111	121	2	1260.64	3.7	1	31.8	24.1	95.00%	R.GYHLSDVTLEK.S		R.GYHLSDVTLEK.S
122	134	2	1410.71	4.2	1	61.1	24.7	95.00%	K.SIQLDQSYGVSSK.F		K.SIQLDQSYGVSSK.F
137	147	2	1100.62	4.3	0	27.7	22	94.00%	K.GILESALSGVR.S		K.GILESALSGVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
51	DHAS_SCHPO	40.34%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
112	132	3	2341.3	0.13	1	62	16.3	95.00%	R.REPTVPLVVPTVNTDHLDVIK.Y		R.REPTVPLVVPTVNTDHLDVIK.Y
19	30	3	1445.76	4.9	1	23.3	23.7	91.70%	R.FITLLSDHPEFK.I		R.FITLLSDHPEFK.I
143	161	2	2003.01	-2.3	0	80.2	24.1	95.00%	R.GCIITNSNCSTAAVVVPLK.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GCIITNSNCSTAAVVVPLK.A
304	318	3	1662.81	4.5	2	31.3	25.6	95.00%	R.LDRNNENGYAVSVGR.I		R.LDRNNENGYAVSVGR.I
215	227	2	1337.71	-9	2	30.8	23.4	95.00%	R.KILGSVNSTISGY.E		R.KILGSVNSTISGYELTDNVVSAQCNR.V
228	240	2	1504.7	1.2	0	65.8	26.9	95.00%	Y.ELTDNVVSAQCNR.V	Carbamidomethyl (+57)	K.ILGSVNSTISGYELTDNVVSAQCNR.V
31	39	2	856.52	4.9	0	28.2	20.3	94.60%	K.IAVLGASAR.S		K.IAVLGASAR.S
287	303	3	2003.98	4.2	1	33.9	25.8	95.00%	K.QAIYVFDDSTPDRPQPR.L		K.QAIYVFDDSTPDRPQPR.L
267	278	2	1375.7	3.8	1	37.2	23.7	95.00%	R.EVLANYVSEPQK.L		R.EVLANYVSEPQK.L
6	18	2	1227.7	3.7	0	35.6	20.5	95.00%	K.VGILGATGTVGQR.F		K.VGILGATGTVGQR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
52	HXK1_SCHPO	29.55%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	12	3	1409.65	4.4	1	25.1	25.7	93.40%	M.SLHDAYHWPSR.T	Acetyl (+42)	-.MSLHDAYHWPSR.T
447	469	2	2153.16	0.59	0	107	20.2	95.00%	K.VVTIPAEDGSGVGAALVSALEAK.G		K.VVTIPAEDGSGVGAALVSALEAK.G
26	47	3	2676.35	2.8	1	37.5	23.5	95.00%	K.TLQDHLDELEEQFTIPTELLHR.V		K.TLQDHLDELEEQFTIPTELLHR.V
304	315	2	1380.7	5.1	1	25.3	24.5	90.30%	K.MIAGCYLGDILR.R	Carbamidomethyl (+57)	K.MIAGCYLGDILR.R
87	97	2	1141.65	1.8	0	59.4	19.9	95.00%	Y.LALDLGGTNLR.V		K.GLTTNPGDVPMVPTWIIGTPDGNEHGSYLALDLGGTNLR.V

283	301	3	2181.06	1.1	2	34.3	25.7	95.00%	R.TKYDVAIDEESPRPGLQTY.E		R.TKYDVAIDEESPRPGLQTYEK.M
472	484	2	1423.77	-1.3	1	25.9	21.3	91.40%	K.ALTSDILAEHLKN.-		K.ALTSDILAEHLKN.-
406	426	3	2369.2	3.6	2	22.8	23.8	91.00%	R.KMNKPSMIVGTDGSVYNLYPR.F		R.KMNKPSMIVGTDGSVYNLYPR.F
236	246	2	1271.53	1.8	1	38.6	25.4	95.00%	F.GTGCNACYIEK.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.LNAILSDTTGTLVASNYASPGTEI GVIFGTGCNACYIEK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
53	THIL_SCHPO	35.95%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
196	210	2	1667.89	-2	1	41.8	22	95.00%	K.AFEQEIVPVEVPVGR.G		K.AFEQEIVPVEVPVGR.G
360	371	2	1405.81	4.5	1	73.2	17.9	95.00%	R.IICTLAYILAQK.D	Carbamidomethyl (+57)	R.IICTLAYILAQK.D
340	359	3	1865.93	4.8	0	31	25.8	95.00%	R.VNINGGGVAMGHPLGSSGSR.I		R.VNINGGGVAMGHPLGSSGSR.I
291	301	2	1160.65	4.8	1	33.2	21.1	95.00%	R.FTTSPSLAIPK.A		R.FTTSPSLAIPK.A
14	30	2	1654.8	-1.5	1	77.5	25.7	95.00%	R.TPMGSFGGSFASLPATK.L		R.TPMGSFGGSFASLPATK.L
43	69	3	2869.44	0.35	1	53.2	22.2	95.00%	R.VNIKPSDVDEVFMGNVVSANLGQ NPAR.Q		R.VNIKPSDVDEVFMGNVVSANLGQ NPAR.Q
278	290	2	1440.71	4.1	1	44.3	25.5	95.00%	K.IIGWGEAAQDPER.F		K.IIGWGEAAQDPER.F
55	69	2	1526.76	1.5	0	73.4	25.2	95.00%	F.MGNVVSANLGQNPAR.Q		R.VNIKPSDVDEVFMGNVVSANLGQ NPAR.Q
148	174	3	2905.25	0.63	1	52.7	26.8	95.00%	R.DGLSDAYDGLPMGNAAELCAEE HSIDR.A	Carbamidomethyl (+57)	R.DGLSDAYDGLPMGNAAELCAEE HSIDR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
54	EF1B_SCHPO	40.19%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
14	22	2	1104.59	4.8	1	36.2	23.2	95.00%	K.QLNDFLLDK.S		K.QLNDFLLDK.S
153	165	2	1432.74	3.9	1	44.3	24.2	95.00%	R.SIQMDGLVWGLSK.L		R.SIQMDGLVWGLSK.L
2	13	2	1209.59	3.7	1	57.4	25.4	95.00%	M.GFSDLTSDAGLK.Q		-.MGFSDLTSDAGLK.Q
40	55	2	1586.8	-0.47	2	49.3	24.9	95.00%	K.AVGVAPDTAKYPNGAR.W	Deamidation (+1)	K.AVGVAPDTAKYPNGAR.W
59	73	2	1561.84	4.2	1	60.9	22.2	95.00%	K.QIATYDLATLPGTAK.E		K.QIATYDLATLPGTAK.E
129	149	2	2459.18	0.48	1	72.3	26.2	95.00%	K.SLVTLDVKPWDDETPMDELEK.A		K.SLVTLDVKPWDDETPMDELEK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
55	GBLP_SCHPO	36.31%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
18	36	2	1956.02	0.86	0	45.6	22.9	95.00%	W.VTSLSTAPENPDILLSGSR.D		R.ATLEGHSGWVTSLSTAPENPDIL LSGSR.D
48	57	2	1135.53	4.7	1	43.2	24.9	95.00%	R.DDVNYGVAQR.R		R.DDVNYGVAQR.R
9	17	2	956.44	1.4	1	26.6	24.7	92.60%	R.ATLEGHSGW.V		R.ATLEGHSGWVTSLSTAPENPDIL LSGSR.D
186	212	3	2736.26	2.6	1	43.2	26.6	95.00%	R.TSHYGHTGYVSAVTISPDGSLCA SGGR.D	Carbamidomethyl (+57)	R.TSHYGHTGYVSAVTISPDGSLCA SGGR.D
9	36	3	2894.45	2.9	1	38.1	22.6	95.00%	R.ATLEGHSGWVTSLSTAPENPDIL LSGSR.D		R.ATLEGHSGWVTSLSTAPENPDIL LSGSR.D
300	308	2	1060.53	1.1	1	29.3	23.6	95.00%	F.SGWTDNLIR.V		K.SSEPECISLTWSPDGQTLFSGWT DNLIR.V
220	228	2	1090.49	1.2	1	33.4	24.5	95.00%	W.DLNESTHLY.S		R.DGTLMLWDLNESTHLYSLEAK.A
234	245	2	1314.71	3.1	1	32.5	22.6	95.00%	K.ANINALVFSPNR.Y		K.ANINALVFSPNR.Y
176	185	2	1264.65	5.4	1	30.1	24.6	95.00%	K.VWDLETFSLR.T		K.VWDLETFSLR.T
39	47	2	1112.68	5.9	1	27.8	17.4	94.10%	K.SIILWNLVR.D		K.SIILWNLVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
56	UGPA1_SCHPO	27.27%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
299	314	3	1876.02	4.4	1	30	20.3	95.00%	R.LLEIAQVPPQHVEEFK.S		R.LLEIAQVPPQHVEEFK.S

20	34	2	1527.72	-2	1	85.7	26.7	95.00%	F.AFDNTATSIAASTMK.N		K.SQSAFAFDNTATSIAASTMK.N
162	175	2	1539.72	0.57	1	36.7	26.2	95.00%	F.VLMNSFNTDEATAK.V		K.YNVNVPFVLMNSFNTDEATAK.V
74	104	3	3417.67	3.9	1	69	22.6	95.00%	R.GSEINWDLVESPKPEQVVEYDTITEAGGLSR.D		R.GSEINWDLVESPKPEQVVEYDTITEAGGLSR.D
185	194	2	1205.65	4.7	1	32.1	23.3	95.00%	K.IDILTFNQSR.Y		K.IDILTFNQSR.Y
408	419	2	1380.66	-0.3	0	40.5	26	95.00%	Y.SINHGQVEMNPR.R		K.SDLYSINHGQVEMNPR.R
437	449	3	1380.74	-1.2	1	27	22.1	95.00%	K.VADFSAHIPSIPK.I		K.VADFSAHIPSIPK.I
115	129	2	1460.72	4.2	0	48.3	25.1	95.00%	K.LNGGLGTTMGCVGPK.S	Carbamidomethyl (+57)	K.LNGGLGTTMGCVGPK.S
287	298	2	1278.63	4.4	1	55.1	24.9	95.00%	K.GGTLIDYDGNVR.L		K.GGTLIDYDGNVR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
57	ECM17_SCHPO	11.20%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
66	90	3	2646.29	0.37	1	34	24.7	95.00%	K.SHADPFAHIADAILAEEEVASTQPK.Q		K.SHADPFAHIADAILAEEEVASTQPK.Q
314	325	2	1337.8	4.6	0	39.3	13.4	95.00%	R.LTVLEPITSLPR.K		R.LTVLEPITSLPR.K
878	900	3	2550.31	0.19	0	32.4	22.9	95.00%	K.ALGLDNVEIDIDEPKPITNEDIK.Q		K.ALGLDNVEIDIDEPKPITNEDIK.Q
1053	1078	3	3057.48	0.0045	1	39.6	24.5	95.00%	K.QISNELLPTTSSYHEIWIEDPETVEK.R		K.QISNELLPTTSSYHEIWIEDPETVEK.R
611	636	3	2801.42	3.9	1	43.3	22.6	95.00%	K.GPSVVLAYLPYHSADDDAITVLQETK.K		K.GPSVVLAYLPYHSADDDAITVLQETK.K
1382	1390	2	945.5	-0.41	0	51.4	23.4	95.00%	W.VAEIACVGK.A	Carbamidomethyl (+57)	R.MTGCPNGCSRPWVAEIACVGK.A
1031	1048	2	2075.92	-2.2	1	46.5	27.3	95.00%	R.NVTCSSTPNNETIHDQLF.A	Carbamidomethyl (+57)	R.NVTCSSTPNNETIHDQLFAVSK.Q
801	810	2	1058.57	5.4	0	27.5	22.5	93.70%	K.GADLNLSELK.Y		K.GADLNLSELK.Y
759	774	2	1850.85	3.7	1	75.5	26.9	95.00%	K.IMAMDDFPIEELGNEK.N		K.IMAMDDFPIEELGNEK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
58	RS7_SCHPO	30.26%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	140	2	2393.32	-0.64	1	49.2	15.8	95.00%	R.TLTAVHNAILEDIVFPTEIIGK.R		R.TLTAVHNAILEDIVFPTEIIGK.R
59	70	2	1322.84	4	1	46.5	6.99	95.00%	K.AIVVFVPQPLLK.A		K.AIVVFVPQPLLK.A
119	141	3	2549.42	0.31	1	62.4	14.3	95.00%	R.TLTAVHNAILEDIVFPTEIIGKR.T		R.TLTAVHNAILEDIVFPTEIIGKR.T
11	34	2	2657.25	4.3	1	84.1	26.4	95.00%	R.SSSQPTETDLLVAQCLYDLESSSK.D	Carbamidomethyl (+57)	R.SSSQPTETDLLVAQCLYDLESSSK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
59	ADH_SCHPO	38.00%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
109	122	2	1616.75	1.6	1	31	26	95.00%	K.AEETICPHIQLSGY.T	Carbamidomethyl (+57)	K.AEETICPHIQLSGYTVDGTFQHYCIANATHATIIPESVPLEVAAPIMCAGITCYR.A
236	253	2	1681.87	4.1	0	56	23.2	95.00%	K.AATNGGAHGTLVLSTSPK.S	Deamidation (+1)	K.AATNGGAHGTLVLSTSPK.S
254	278	3	2513.21	3.1	1	41.5	25.7	95.00%	K.SYEQAAGFARPGSTMVTVSMPAGAK.L		K.SYEQAAGFARPGSTMVTVSMPAGAK.L
170	194	3	2506.29	3.6	1	33.6	22	95.00%	K.VGPGEWICIPGAGGGLGHLAVQYAK.A	Carbamidomethyl (+57)	K.VGPGEWICIPGAGGGLGHLAVQYAK.A
42	62	3	2378.15	2.1	1	31.5	25.6	95.00%	K.YTGVCHTDLHALQGDWPLPAK.M	Carbamidomethyl (+57)	K.YTGVCHTDLHALQGDWPLPAK.M
200	214	2	1571.84	-2.1	1	75.2	23.2	95.00%	R.VVAIDTGDDKAELVK.S		R.VVAIDTGDDKAELVK.S
63	77	3	1462.8	-1.1	0	27	21.8	95.00%	K.MPLIGGHEGAGVVVK.V		K.MPLIGGHEGAGVVVK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
60	MET3_SCHPO	25.10%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
427	440	2	1651.86	4	1	77.5	23.2	95.00%	R.LDAISVFYAQELQR.A		R.LDAISVFYAQELQR.A

350	359	2	1102.6	3.9	0	29.9	22.6	95.00%	R.TLNISGTELR.R		R.TLNISGTELR.R
69	92	2	2586.35	1.6	1	44	21.6	95.00%	R.LSTGEVFPIPITLDLNESQADSLK.A		R.LSTGEVFPIPITLDLNESQADSLK.A
59	68	2	1233.64	5.6	1	40.5	23.7	95.00%	K.DYLNVVENLR.L		K.DYLNVVENLR.L
254	262	2	1012.62	5.1	0	33.5	17.2	95.00%	K.LSLLPLAMR.M		K.LSLLPLAMR.M
217	234	3	1974.04	0.26	1	29.6	22.4	95.00%	R.VLIHPVVGMTKPGDIDHF.T		R.VLIHPVVGMTKPGDIDHFTR.V
364	382	2	2159.15	2.7	1	56.8	21.5	95.00%	R.VGANIPEWFSYPEVVAILR.Q		R.VGANIPEWFSYPEVVAILR.Q
13	29	2	1924	2.8	1	48.1	23.5	95.00%	R.DAPLREQLEQEATSLPK.I		R.DAPLREQLEQEATSLPK.I
217	236	4	2231.2	3.6	1	31	20.1	95.00%	R.VLIHPVVGMTKPGDIDHFTR.V		R.VLIHPVVGMTKPGDIDHFTR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
61	TRP_SCHPO	28.26%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
382	393	2	1355.77	4.5	0	47.2	19.5	95.00%	K.INNCIGQILLAK.R	Carbamidomethyl (+57)	K.INNCIGQILLAK.R
247	261	2	1623.75	3.4	1	47.6	26.5	95.00%	K.AEPGTAATVVEEYCK.Y	Carbamidomethyl (+57)	K.AEPGTAATVVEEYCK.Y
400	419	3	1938.01	4.3	0	37.5	22.6	95.00%	R.IIAETGAGQHGVATAICAAK.F	Carbamidomethyl (+57)	R.IIAETGAGQHGVATAICAAK.F
616	631	2	1825.87	3	1	57.5	26.5	95.00%	R.AEFIAVTDAQCLEGFR.A	Carbamidomethyl (+57)	R.AEFIAVTDAQCLEGFR.A
445	461	2	1739.99	4	0	48.6	17.7	95.00%	R.LLGAEVVPVTSGTQTLR.D		R.LLGAEVVPVTSGTQTLR.D
543	560	2	1822.79	-2.3	0	48.2	27.3	95.00%	K.SVMMLGCEAGGDGVDTPK.H	Carbamidomethyl (+57)	K.SVMMLGCEAGGDGVDTPK.H
673	690	3	1893.03	4.4	1	34.8	19.7	95.00%	R.GDKDVQSVAEQLPILGPK.I		R.GDKDVQSVAEQLPILGPK.I
275	302	3	2928.48	4.6	1	34.9	22.4	95.00%	K.QFQSGGSVATAPPAAVVEPINEMYLPQK.Y		K.QFQSGGSVATAPPAAVVEPINEMYLPQK.Y
24	36	2	1478.71	1.3	1	37.8	25.6	95.00%	F.VTCGFPNVDETIK.I	Carbamidomethyl (+57)	K.NVLVTFVTCGFPNVDETIK.I
56	67	2	1232.57	1.4	0	36.6	25.1	95.00%	F.SDAVADGPTICK.G	Carbamidomethyl (+57)	K.IMQGLQNGGAGIIELGIPFSDAVADGPTICK.G
584	611	3	2954.42	2.6	1	50.2	24.8	95.00%	R.EDGQIQDTHSISAGLDYPGVGPELSELK.Y		R.EDGQIQDTHSISAGLDYPGVGPELSELK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
62	CDC48_SCHPO	16.07%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
28	38	2	1146.59	0.93	0	47.3	24	95.00%	Y.SAEDTATAILR.K		K.DTYSAEDTATAILR.K
550	563	2	1522.75	3.6	1	43.8	25.1	95.00%	K.AIANECSANFISVK.G	Carbamidomethyl (+57)	K.AIANECSANFISVK.G
287	297	2	1247.66	0.22	1	44	23	95.00%	F.FLINGPEIMSK.M		R.AVANETGAFFFLINGPEIMSK.M
359	379	3	2280.22	4.2	1	31.5	20	95.00%	R.SNVVVMAATNRPNSIDPALRR.F		R.SNVVVMAATNRPNSIDPALRR.F
316	332	2	1841.99	4.4	1	39.8	20.9	95.00%	K.NSPAIIFIDEIDSIAPK.R		K.NSPAIIFIDEIDSIAPK.R
410	426	2	1858.86	0.91	1	56.4	27.7	95.00%	K.LADDVDLEQIAAETHGY.V		K.LADDVDLEQIAAETHGYVGSDLASLCSEAAMQQIR.E
588	604	2	1817.93	4.3	1	57.6	24.6	95.00%	R.AAAPCVVFLDELDSIAK.A	Carbamidomethyl (+57)	R.AAAPCVVFLDELDSIAK.A
116	129	2	1553.81	-2.2	0	40.9	23.2	95.00%	R.LGDIVTINPCPDIK.Y	Carbamidomethyl (+57)	R.LGDIVTINPCPDIK.Y
664	672	2	1024.52	1.3	0	27.4	23.8	93.60%	Y.VPLPDEEAR.F		R.LDQLIYVPLPDEEAR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
63	IF4A_SCHPO	27.04%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
156	165	2	1091.53	0.53	1	43	25	95.00%	R.ALPTDAVQMF.V		R.ALPTDAVQMFVLDEADEMLSR.G
58	69	2	1173.61	5	0	69	23.5	95.00%	R.DVLAQAQSGTGK.T		R.DVLAQAQSGTGK.T
49	69	3	2154.15	3.1	1	31.7	20.5	95.00%	R.AIMPILGERDVLAQAQSGTGK.T		R.AIMPILGERDVLAQAQSGTGK.T
378	392	2	1739.82	0.33	0	37	26.8	95.00%	Y.NTHIEEMPMNIADLI.-		R.EIEQFYNTHIEEMPMNIADLI.-
155	176	3	2506.23	3.9	2	41.3	24.8	95.00%	R.RALPTDAVQMFVLDEADEMLSR.G		R.RALPTDAVQMFVLDEADEMLSR.G
2	32	3	3667.76	4	1	58	22.9	95.00%	M.VDQLEDSVIETNYDEVIDTFDDMNLKPELLR.G		-.MVDQLEDSVIETNYDEVIDTFDDMNLKPELLR.G
372	392	2	2549.19	2.9	1	26.7	26.2	90.70%	R.EIEQFYNTHIEEMPMNIADLI.-		R.EIEQFYNTHIEEMPMNIADLI.-
38	48	2	1287.67	-0.95	1	28.7	23.7	95.00%	Y.GFERPSAIQQR.A		R.GIYAYGFERPSAIQQR.A

166	176	2	1276.6	0.92	0	61.5	24.7	95.00%	F.VLDEADEMLSR.G		R.ALPTDAVQMFVLDEADEMLSR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
64	RS18_SCHPO	28.95%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	66	2	1246.61	4	0	41.5	25.2	95.00%	R.AGELTTEELER.I		R.AGELTTEELER.I
67	78	2	1386.79	4	1	45.2	19.3	95.00%	R.IVTIIQNPSQFK.I		R.IVTIIQNPSQFK.I
2	14	2	1578.85	-2.1	1	32.2	21.6	95.00%	M.SLVVPDNFQHILR.L	Acetyl (+42)	-.MSLVVPDNFQHILR.L
79	86	2	1031.56	6	1	52.6	22.4	95.00%	K.IPSWFLNR.Q		K.IPSWFLNR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
65	RL8_SCHPO	28.19%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
24	32	2	1084.62	4.7	1	29.3	21.1	95.00%	K.NPLFVSRPR.S		K.NPLFVSRPR.S
109	120	2	1171.61	4.7	0	55.2	22.9	95.00%	R.LVAEAEAVANGK.S	Deamidation (+1)	R.LVAEAEAVANGK.S
134	146	2	1425.8	4.3	1	45.6	17.5	95.00%	K.YGLNHVVALIEAK.K		K.YGLNHVVALIEAK.K
69	78	2	1082.65	-0.67	2	26.4	17	92.20%	R.LKVPPAIAQF.Q		R.LKVPPAIAQFQK.T
33	43	2	1188.62	4.1	1	26.8	24.2	92.80%	R.SFGIGQDIQPK.R		R.SFGIGQDIQPK.R
81	92	2	1364.74	3.7	2	46.2	22.3	95.00%	K.TLDKNTATQVFK.L		K.TLDKNTATQVFK.L
52	57	2	862.44	5.9	1	26.5	23.4	92.40%	K.WPEYIR.L		K.WPEYIR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
66	LYS12_SCHPO	30.39%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
7	26	3	1987.19	3.6	1	23.5	9.03	92.00%	R.IVLGLIPADGIGKEVVPAAR.R		R.IVLGLIPADGIGKEVVPAAR.R
282	297	3	1637.79	1.2	0	45.8	26.2	95.00%	F.VMSEPVHGSAPDIAGR.G	Oxidation (+16)	R.EPECFDVVVAPNLYGDILSDGAASLIGSLGLVPSANVGDNFVMSEPVHGSAPDIAGR.G
86	97	2	1231.7	4.7	1	25.9	20.9	91.50%	K.VAGYSSPIVALR.K		K.VAGYSSPIVALR.K
197	208	2	1324.65	5.3	1	41.8	25.5	95.00%	K.SNVMSVTDGLFR.E		K.SNVMSVTDGLFR.E
298	307	2	1044.58	4.6	1	32.2	22.4	95.00%	R.GIANPVATFR.S		R.GIANPVATFR.S
188	196	3	1047.69	4.7	0	25.1	3.01	94.30%	K.KPLVTIIHK.S		K.KPLVTIIHK.S
127	138	2	1568.72	4	1	44	26	95.00%	R.ENTECLYVKEER.M	Carbamidomethyl (+57)	R.ENTECLYVKEER.M
67	85	3	2071.06	4.3	2	52.5	23.8	95.00%	R.LKTECNAALFGAVQSPTHK.V	Carbamidomethyl (+57)	R.LKTECNAALFGAVQSPTHK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
67	LEUC_SCHPO	17.94%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
59	77	4	2123.12	3.9	1	27	21.1	95.00%	R.HPELALATVDHNIPTDPRK.D		R.HPELALATVDHNIPTDPRK.D
540	563	3	2538.38	0.82	1	52.2	17	95.00%	K.FTVVEGIAAPLPMANVDTDKIIPK.Q		K.FTVVEGIAAPLPMANVDTDKIIPK.Q
417	436	3	2355.02	4.1	1	24.9	27.4	90.20%	R.EAGCSMCLGMNPDQLKPYER.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.EAGCSMCLGMNPDQLKPYER.C
303	323	3	2168.13	1.8	0	30.1	22.8	95.00%	W.GTSPQDVIPINGNIPDPAHVK.D		K.YDIEVEINAADVLPTVTWGTSPQDVIPINGNIPDPAHVK.D
603	619	3	1826.86	5.3	1	37.3	26.9	95.00%	R.HATVLVAHDNFGCGSSR.E	Carbamidomethyl (+57)	R.HATVLVAHDNFGCGSSR.E
477	493	2	1810.88	4.1	1	36.5	25.9	95.00%	R.EFFGDVSNGSPSIITNK.N		R.EFFGDVSNGSPSIITNK.N
650	667	2	2027	4	0	40.9	25.3	95.00%	K.NGMLPIPTPIEQVNDMMK.A		K.NGMLPIPTPIEQVNDMMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
68	CYSD_SCHPO	39.63%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
72	100	3	2787.49	3.3	1	49.9	18.1	95.00%	R.IAALEHGAAAIATSSGTSALFMALTTLAK.A		R.IAALEHGAAAIATSSGTSALFMALTTLAK.A
366	377	2	1185.64	4.4	0	34.5	21.8	95.00%	K.LASQLANVGDAK.T		K.LASQLANVGDAK.T
170	210	4	4156.13	4.3	1	53.9	19.3	95.00%	R.IAEVAHAAGVPLMVDNTFGGGGYLVRPIDHGADIVTHSATK.W		R.IAEVAHAAGVPLMVDNTFGGGGYLVRPIDHGADIVTHSATK.W
132	150	2	2074.95	4.2	1	127	26.7	95.00%	K.FVNGDDPNDLAAQIDENTK.A		K.FVNGDDPNDLAAQIDENTK.A

378	403	3	2798.48	2.5	1	42.6	20.2	95.00%	K.TLVIAPAYTTHLQLTDEEQISAGVTK.D		K.TLVIAPAYTTHLQLTDEEQISAGVTK.D
2	26	3	2735.28	-0.11	1	48.3	26.2	95.00%	M.PVESEHFETLQLHAGQEPDAATSSR.A		-.MPVESEHFETLQLHAGQEPDAATSSR.A
211	228	3	1752.91	-1	1	29	22.7	95.00%	K.WIGGHGTTIGGVIVDSGK.F		K.WIGGHGTTIGGVIVDSGK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
69	PYR1_SCHPO	5.79%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1135	1145	2	1229.6	4.3	0	46.2	25	95.00%	R.MLDDIGVDQPK.W		R.MLDDIGVDQPK.W
1771	1784	2	1494.85	4.1	0	35.2	17.2	95.00%	R.EAIPLLLTAVNEGR.L		R.EAIPLLLTAVNEGR.L
228	245	3	2026.07	0.4	1	50.3	21.6	95.00%	W.KNPNTENLTSQVSIKEPK.L		K.DWSTAFEDIPWKNPNTENLTSQVSIKEPK.L
457	466	2	1084.56	6.1	0	38.9	23	95.00%	K.LPGGTIEENR.S		K.LPGGTIEENR.S
1880	1906	3	2689.36	3.3	1	28.6	22.9	95.00%	K.VSALMSPGLPHAAPSLAEAFGQAPENK.A		K.VSALMSPGLPHAAPSLAEAFGQAPENK.A
1426	1442	2	1819.78	1.3	1	39	27.5	95.00%	F.ATAGTSDYFMESGVPCK.Y	Carbamidomethyl (+57)	K.LYENNYNIFATAGTSDYFMESGVPCK.Y
580	597	2	2032.07	0.085	2	57.1	22.1	95.00%	K.VLGTPIDTIITTEDRELF.A		K.VLGTPIDTIITTEDRELFAR.A
1804	1818	3	1724.81	5.5	0	27.4	26.4	95.00%	R.LHDQDDSGVQLEVDR.S		R.LHDQDDSGVQLEVDR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
70	RL4A_SCHPO	33.88%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
141	161	3	2348.2	1.4	2	51	22.7	95.00%	R.GHRIEEIPEVPLVVDDAVQSF.Q		R.GHRIEEIPEVPLVVDDAVQSFQK.T
122	140	2	1845.04	4.3	1	48.1	16.9	95.00%	R.YAISSAVAASGVPSLLLAR.G		R.YAISSAVAASGVPSLLLAR.G
2	13	2	1304.71	4.5	1	25.5	21.8	90.80%	M.AAARPTVSIYSK.D	Acetyl (+42)	-.MAAARPTVSIYSK.D
14	29	2	1695.88	4.2	1	38.3	23.2	95.00%	K.DGSVSSETIALPFVFK.A		K.DGSVSSETIALPFVFK.A
144	163	2	2254.18	3.5	1	34.1	21.6	95.00%	R.IEEIPEVPLVVDDAVQSFQK.T		R.IEEIPEVPLVVDDAVQSFQK.T
276	291	2	1864.93	-0.82	1	74.5	25.4	95.00%	K.NYFLPENIISNADVTR.L		K.NYFLPENIISNADVTR.L
235	248	3	1457.85	-0.96	0	34.9	17.6	95.00%	R.LNLLQLAPGGHLGR.F		R.LNLLQLAPGGHLGR.F
292	303	2	1357.75	4	0	43.8	21.6	95.00%	R.LINSDEIQSIVK.A		R.LINSDEIQSIVK.A
87	97	2	1197.51	4.4	1	32.6	26.1	95.00%	R.SGQAAFGNMCR.S	Carbamidomethyl (+57)	R.SGQAAFGNMCR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
71	RS3B_SCHPO	17.86%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
200	213	2	1513.87	4.8	1	38.9	18.5	95.00%	R.ATGSIFPLQNVLVR.K		R.ATGSIFPLQNVLVR.K
65	81	2	1955.98	-0.52	2	25.1	24.4	90.00%	R.ILEVSLADLQKDEEHAF.R		R.ILEVSLADLQKDEEHAFR.K
228	241	2	1524.79	4.4	0	71.2	23.4	95.00%	K.LLELHGESQDVGTK.V		K.LLELHGESQDVGTK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
72	FAS1_SCHPO	5.07%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1068	1087	3	2303.16	0.17	2	23.8	24.4	92.60%	K.VNEPAKELLDGINETHIQHF.I		K.VNEPAKELLDGINETHIQHFIK.K
1117	1130	2	1421.7	4.7	0	59.8	25.6	95.00%	K.SLESVSVTEEAGSK.V		K.SLESVSVTEEAGSK.V
2	12	2	1294.67	5.2	0	53.5	24.5	95.00%	M.VEAEQVHQSLR.S		-.MVEAEQVHQSLR.S
966	984	2	2177.07	4.2	1	92.2	25.1	95.00%	K.TTLIENFEDLNDPYPVAAR.F		K.TTLIENFEDLNDPYPVAAR.F
1870	1881	2	1266.57	5.2	1	37.8	25.8	95.00%	R.SDYGMVAANPSR.V		R.SDYGMVAANPSR.V
210	224	3	1723.91	5.4	1	36.5	22	95.00%	K.GLNVLDWLAGERPER.D		K.GLNVLDWLAGERPER.D
781	794	2	1545.81	3.9	1	42.1	23.7	95.00%	K.LPPMPFDGILFGSR.L		K.LPPMPFDGILFGSR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
73	YHY6_SCHPO	14.66%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
678	698	2	2257.13	4.5	0	51.2	24.5	95.00%	K.SLCIPLEQPSGEDAIIEGTTK.C	Carbamidomethyl (+57)	K.SLCIPLEQPSGEDAIIEGTTK.C

161	188	4	2736.49	3.7	1	29.1	17.2	95.00%	K.SVGVNPIIVDFSAPGSATAPSKPAAQKK.K		K.SVGVNPIIVDFSAPGSATAPSKPAAQKK.K
161	187	3	2608.39	2.9	1	26.8	19.5	95.00%	K.SVGVNPIIVDFSAPGSATAPSKPAAQK.K		K.SVGVNPIIVDFSAPGSATAPSKPAAQK.K
298	323	3	2901.42	3	1	27.8	24	95.00%	R.AGTSELDEPIAIRPTSETVMYPYYAK.W		R.AGTSELDEPIAIRPTSETVMYPYYAK.W
660	677	3	1900.86	4.5	1	43.4	27	95.00%	R.QVNGDEPEDEKAPSMGAK.S		R.QVNGDEPEDEKAPSMGAK.S
387	398	2	1343.81	4.3	1	30.5	13.8	95.00%	R.IYTDLLAVPVIK.G		R.IYTDLLAVPVIK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
74	NACA_SCHPO	54.91%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	75	2	1164.62	5.8	1	59.3	23.1	95.00%	K.SSNNAYIVLGK.V		K.SSNNAYIVLGK.V
100	118	2	1931.86	-1.4	0	38.5	27.7	95.00%	K.EEAAITEESGDAQPADTAK.I		K.EEAAITEESGDAQPADTAK.I
94	118	3	2590.19	-0.43	1	75.2	26.8	95.00%	K.QATETKEEAAITEESGDAQPADTAK.I		K.QATETKEEAAITEESGDAQPADTAK.I
119	137	3	2123	4.4	1	54.2	26.1	95.00%	K.IEESFEQEKAVDETGVDAK.D		K.IEESFEQEKAVDETGVDAK.D
11	26	2	1637.87	4.6	0	55.2	22.4	95.00%	K.ISELPAGSTTVVHAEK.A		K.ISELPAGSTTVVHAEK.A
52	64	2	1540.93	4.4	1	50.2	11.8	95.00%	K.NILLIINEPIVYK.S		K.NILLIINEPIVYK.S
76	86	2	1189.58	4.9	0	47.2	24.9	95.00%	K.VTVEDMAAQAR.A		K.VTVEDMAAQAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
75	ILV3_SCHPO	13.55%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
49	68	2	2142.97	5.2	1	90.3	27.1	95.00%	K.SQGASQAMLYATGLNEEDMK.K		K.SQGASQAMLYATGLNEEDMK.K
69	78	2	1144.57	0.71	1	26.8	23.1	92.90%	K.KPQVGIASCW.Y	Carbamidomethyl (+57)	K.KPQVGIASCWYEGNPCNMHLLDLGR.R
402	417	4	1843.09	3.6	1	32.1	12.6	95.00%	K.IIRPLSNPIKTEGHLR.V		K.IIRPLSNPIKTEGHLR.V
40	48	2	994.5	5.2	1	30.6	24.9	95.00%	K.YSETITGPK.S		K.YSETITGPK.S
266	278	3	1408.68	4.8	1	24.2	25.9	91.80%	K.FAECEAAGSAIKR.L	Carbamidomethyl (+57)	K.FAECEAAGSAIKR.L
224	236	2	1293.47	1.2	1	26.5	25.1	92.30%	R.HACPGGGACGGMY.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.HACPGGGACGGMYTANTMASCAEAMGMTLPGSSSYLAGSPEK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
76	RL13_SCHPO	43.75%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
172	183	2	1398.66	5.4	1	54	26.1	95.00%	K.NFNAFSTLSNER.A		K.NFNAFSTLSNER.A
46	64	4	2080.27	3.1	0	20	6.02	94.50%	K.IAPRPVEAIRPAVKPPTIR.Y		K.IAPRPVEAIRPAVKPPTIR.Y
118	128	3	1326.79	4.7	1	51.2	17.9	95.00%	K.VYLAHLIVFPR.K		K.VYLAHLIVFPR.K
135	171	3	3809.91	-0.053	1	64.2	20.2	95.00%	K.KGDATDVSGAEQTDVAAVLPITQEAVEEAKPITEEAK.N		K.KGDATDVSGAEQTDVAAVLPITQEAVEEAKPITEEAK.N
89	100	2	1263.7	3.9	0	28.9	20.6	95.00%	R.VASTIGIPVDHR.R		R.VASTIGIPVDHR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
77	SODC_SCHPO	57.14%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	144	4	2825.43	3.9	1	21.6	23	95.00%	R.TIVIHAGEDDLGKGTSEESLKTGNAGAR.N		R.TIVIHAGEDDLGKGTSEESLKTGNAGAR.N
81	97	2	1765.86	-0.97	0	77.3	26	95.00%	R.HVGDLGNLESDAQGNIK.T		R.HVGDLGNLESDAQGNIK.T
117	137	3	2198.12	3.9	1	49.5	24	95.00%	R.TIVIHAGEDDLGKGTSEESLK.T		R.TIVIHAGEDDLGKGTSEESLK.T
98	116	2	1984.04	4.4	1	72.6	22	95.00%	K.TTFSDSVISLFGANSIIGR.T		K.TTFSDSVISLFGANSIIGR.T
47	70	4	2621.15	2.2	1	39.6	26.9	95.00%	F.HIHQFGDNTNGCTSAGPHFNPEGK.T	Carbamidomethyl (+57)	R.GFHIHQFGDNTNGCTSAGPHFNPEGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
78	YF19_SCHPO	17.89%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

333	349	2	1794.84	-1.1	1	42	26.7	95.00%	K.VGDPFAEDTFQGAQVSK.Q		K.VGDPFAEDTFQGAQVSK.Q
181	194	2	1439.82	3.6	0	42.9	17.9	95.00%	K.IAPAVACGNTIILK.T	Carbamidomethyl (+57)	K.IAPAVACGNTIILK.T
122	132	2	1208.53	4.1	1	34.4	25.2	95.00%	R.GDVQAAADCFR.Y	Carbamidomethyl (+57)	R.GDVQAAADCFR.Y
195	208	2	1516.82	4.7	0	34.9	22.6	95.00%	K.TAELTPLSALCLTK.F	Carbamidomethyl (+57)	K.TAELTPLSALCLTK.F
5	17	2	1406.78	4.6	0	33	20	95.00%	K.LVDHVEITVPTGK.T		K.LVDHVEITVPTGK.T
71	80	2	1161.56	3.7	1	28.3	24.4	94.70%	R.AAFQTDAPWR.K		R.AAFQTDAPWR.K
105	115	2	1159.61	0.84	0	35.6	24.4	95.00%	Y.LASIETLDNGK.S		R.LADCIEQNLEYLASIETLDNGK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
79	ACON_SCHPO	11.95%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
532	549	2	1853.89	4.6	1	68.9	26.5	95.00%	K.GYDPGSNTYVAPSSVNVK.D		K.GYDPGSNTYVAPSSVNVK.D
613	626	2	1430.68	-1.8	0	51.7	26.2	95.00%	Y.MIGAINAENGEANK.L		R.GHLQNISNNYMIGAINAENGEANK.L
392	402	2	1203.6	5.2	0	35.2	24.5	95.00%	R.AASICQQAIDK.G	Carbamidomethyl (+57)	R.AASICQQAIDK.G
65	80	3	1895.95	4.5	1	26.2	25.3	95.00%	K.ILYGHLDDPVNQDIER.G		K.ILYGHLDDPVNQDIER.G
652	666	2	1665.78	3.4	1	67.3	26.5	95.00%	R.WVTLGEQNFGEGSSR.E		R.WVTLGEQNFGEGSSR.E
462	470	2	1052.53	5	1	36.5	24.7	95.00%	K.NSIVTSYNR.N		K.NSIVTSYNR.N
476	485	2	1056.46	0.54	1	48	24.9	95.00%	R.NDANPATHAF.V		R.NDANPATHAFVTSPDIVTAMVFSGDMNFNPLTDTLK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
80	THI4_SCHPO	23.94%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
356	372	2	1817.84	-2.3	0	71	26.8	95.00%	K.GNEGEIMNLAGEQGLMR.G		K.GNEGEIMNLAGEQGLMR.G
373	385	2	1353.71	4.1	0	37.5	23.1	95.00%	R.GVDSISQHTLAAR.I		R.GVDSISQHTLAAR.I
121	140	2	2014.95	-1.5	1	87.6	26.8	95.00%	K.AAADGADYVGIGSIYETNTK.D		K.AAADGADYVGIGSIYETNTK.D
249	265	4	1917.09	3.2	2	33.8	16	95.00%	K.LKDFTPLIHHLTNAVAK.N		K.LKDFTPLIHHLTNAVAK.N
27	42	3	1733.95	4.6	0	28	20	95.00%	R.QVEEGILGGVTLVQHR.E		R.QVEEGILGGVTLVQHR.E
310	338	3	3045.65	3.6	1	44.4	14.6	95.00%	K.TYIHAAQVNNDLARPVILDPVAVGATTAR.S		K.TYIHAAQVNNDLARPVILDPVAVGATTAR.S
237	248	2	1322.76	4.7	0	31.5	17.5	95.00%	K.DLLNQIPAALQK.L		K.DLLNQIPAALQK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
81	O59743_SCHPO	27.27%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
210	225	2	1690.88	3.5	1	52.7	24	95.00%	R.SIQDVPFTSATVDIAK.K		R.SIQDVPFTSATVDIAK.K
116	127	2	1462.66	1	1	27.8	26.6	91.90%	W.EQALQDNKPEEY.Y		K.LKPVPTSWEQALQDNKPEEYYHLSAPDCK.S
81	94	2	1543.81	1.1	1	25.6	23.9	90.90%	F.LGAYNVITPELAHF.E		K.EALDLFLGAYNVITPELAHFEAR.C
1	11	2	1319.72	4	1	28	22.8	94.40%	-.MDPYTVAIIKK.L	Acetyl (+42)	-.MDPYTVAIIKK.L
11	24	2	1515.81	-1.1	1	72.1	22.9	95.00%	K.KLGIEEQVETAATK.S		K.KLGIEEQVETAATK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
82	DHOM_SCHPO	23.40%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
42	56	2	1619.8	0.74	1	59.3	25.3	95.00%	F.NVVAISSMEGHYVSK.D		K.GFNENASTNGTTSFNVVAISSMEGHYVSK.D
57	67	2	1391.68	4.7	1	33.1	24.6	95.00%	K.DYQPINLSEWK.N		K.DYQPINLSEWK.N
238	252	2	1526.81	-2.2	1	47.2	23.1	95.00%	R.IAGVHVESASSFPVK.S		R.IAGVHVESASSFPVK.S
125	138	2	1568.79	4.5	1	56.7	23.9	95.00%	K.AFSASNDVYQNIIK.A		K.AFSASNDVYQNIIK.A
89	110	2	2284.21	4.5	1	95.1	21.9	95.00%	K.SPLPAILVDNTASEAIAQSYPK.F		K.SPLPAILVDNTASEAIAQSYPK.F
78	88	2	1190.66	1.2	1	43.1	21.5	95.00%	Y.SLDALVDFLAK.S		K.NLTSQNQGAYSLDALVDFLAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
83	YHZ8_SCHPO	50.51%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
168	189	2	2189.09	0.96	1	50.3	24.9	95.00%	K.SGIEPGPAEISGATSVSQQVIY.S		K.SGIEPGPAEISGATSVSQQVIYSGVGFLNRP.-
18	30	3	1414.8	-0.56	1	28.6	20.4	95.00%	K.KGEGDKILDLLSK.V		K.KGEGDKILDLLSK.V
144	164	3	2285.2	4.3	1	37.3	22.2	95.00%	K.ADTSLIIHSLDDPSLYAVVTR.Y		K.ADTSLIIHSLDDPSLYAVVTR.Y
104	121	3	1969.94	0.36	2	24.6	26.3	91.80%	K.VVDGHLDKDNLGPDAKDY.V		K.VVDGHLDKDNLGPDAKDYVLYTEYTGDSATLK.Q
122	135	2	1559.77	0.77	1	73.7	25.3	95.00%	Y.VLYTEYTGDSATLK.Q		K.DYVLYTEYTGDSATLK.Q
2	13	2	1361.7	3.8	1	57.2	24.5	95.00%	M.SFPASTHVYIAK.I	Acetyl (+42)	-.MSFPASTHVYIAK.I
144	159	2	1758.87	0.34	1	42.4	25	95.00%	K.ADTSLIIHSLDDPSLY.A		K.ADTSLIIHSLDDPSLYAVVTR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
84	RS22_SCHPO	38.46%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
44	57	3	1745.76	-1.3	1	48.4	27.5	95.00%	K.HGYIDEFTEIDDHR.S		K.HGYIDEFTEIDDHR.S
98	108	2	1171.7	4.9	0	29.1	18	95.00%	R.QVGVIVLTTSR.G		R.QVGVIVLTTSR.G
4	19	2	1814.89	-2.1	0	87.4	25.3	95.00%	R.QSVLADCLNNIVNAER.R	Carbamidomethyl (+57)	R.QSVLADCLNNIVNAER.R
89	97	2	1111.62	5.6	1	31.9	18.8	95.00%	K.WVNQLLPSR.Q		K.WVNQLLPSR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
85	RS6B_SCHPO	25.94%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	115	2	1739.01	3.8	0	65.7	16.6	95.00%	R.GCIVGQDLAVLALAIVK.Q	Carbamidomethyl (+57)	R.GCIVGQDLAVLALAIVK.Q
59	72	3	1625.86	4.7	1	32.2	22.4	95.00%	K.QGFPMFQGVLLPHR.V		K.QGFPMFQGVLLPHR.V
116	131	2	1695.88	3.9	0	43.6	23.4	95.00%	K.QGEQDIPGLTDVTVPK.R		K.QGEQDIPGLTDVTVPK.R
204	217	2	1606.78	4.3	2	54.8	26.1	95.00%	K.NREEAAEFAQLMAK.R		K.NREEAAEFAQLMAK.R
116	132	3	1851.97	-1.7	1	26.9	23.5	95.00%	K.QGEQDIPGLTDVTVPKR.L		K.QGEQDIPGLTDVTVPKR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
86	SERC_SCHPO	21.85%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
376	385	2	1147.65	-0.37	1	38.2	21.5	95.00%	R.LIDLLESFAK.A		R.LIDLLESFAK.A
164	184	3	2459.11	0.17	1	50.5	27.3	95.00%	Y.YCDNETVHGVEFNEPPTNIPK.G	Carbamidomethyl (+57)	K.FTPDGETSLVYYCDNETVHGVEFNEPPTNIPK.G
216	228	2	1299.74	5	1	37	19.3	95.00%	K.NAGPAGITVVFVR.D		K.NAGPAGITVVFVR.D
324	329	2	766.38	5.3	1	26.2	23.1	91.90%	R.MNVTFR.I		R.MNVTFR.I
330	352	5	2716.42	3.7	1	22	20.5	95.00%	R.IEPQELESEFLAEAEKHHLVQLK.G		R.IEPQELESEFLAEAEKHHLVQLK.G
375	385	2	1303.76	4	2	26.3	17.9	92.10%	R.RLIDLLESFAK.A		R.RLIDLLESFAK.A
189	199	2	1282.6	4.3	1	67	26.1	95.00%	R.VCDVSSNFISR.K	Carbamidomethyl (+57)	R.VCDVSSNFISR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
87	IF5A1_SCHPO	36.94%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	29	3	3107.41	2.7	1	84.1	26.2	95.00%	M.AEEEHVDFEGGEAGASLTFPMQCSALRK.N	Acetyl (+42)/ Carbamidomethyl (+57)	-.MAEEEHVDFEGGEAGASLTFPMQCSALRK.N
2	28	3	2979.31	4	1	77.3	26.7	95.00%	M.AEEEHVDFEGGEAGASLTFPMQCSALR.K	Acetyl (+42)/ Carbamidomethyl (+57)	-.MAEEEHVDFEGGEAGASLTFPMQCSALR.K
70	87	3	2075.97	4.1	2	55.3	26.8	95.00%	R.KYEDMSPSTHNMDVPVVK.R		R.KYEDMSPSTHNMDVPVVK.R
58	69	2	1352.76	4.3	1	43.7	18.5	95.00%	K.VHIVALDIFNGR.K		K.VHIVALDIFNGR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
88	HMCS_SCHPO	25.95%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
264	282	2	2060	-1.4	1	68.2	26	95.00%	R.LLYTDSAAEPSNPELEGVR.E		R.LLYTDSAAEPSNPELEGVR.E
393	407	3	1858.89	-1.8	1	41.2	26.5	95.00%	R.HCLTPTQYEEAIELR.H	Carbamidomethyl (+57)	R.HCLTPTQYEEAIELR.H

155	183	3	2859.53	3.9	1	40.5	18.8	95.00%	K.GNARPTGGAGCVALLVGPNAPIVFEPGLR.G	Carbamidomethyl (+57)	K.GNARPTGGAGCVALLVGPNAPIVFEPGLR.G
17	37	3	2214.06	0.46	1	71.6	26.1	95.00%	Y.TPNQYVEQAALEAHDGVSTGK.Y		K.GLVLYTPNQYVEQAALEAHDGVSTGK.Y
264	291	3	3030.55	2.7	1	23.5	21.3	92.00%	R.LLYTDSAAEPSNPELEGVRELLSTLDAK.K		R.LLYTDSAAEPSNPELEGVRELLSTLDAK.K
382	392	3	1300.68	5.1	1	26	23.3	95.00%	K.KTNLVNDLDNR.H		K.KTNLVNDLDNR.H
217	228	2	1325.64	3.7	1	38.4	25.8	95.00%	K.ALDGAYANYNVR.D		K.ALDGAYANYNVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
89	RS14_SCHPO	41.73%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	129	2	1442.73	3.7	0	46.5	24.9	95.00%	R.IEDVTPIPTDSTR.R		R.IEDVTPIPTDSTR.R
117	130	3	1598.84	5.4	1	24.2	22.5	93.10%	R.IEDVTPIPTDSTRR.K		R.IEDVTPIPTDSTRR.K
52	72	3	2181.01	3.8	2	31.5	27.2	95.00%	K.TDRDESSPYAAMLAAQDAAAK.C		K.TDRDESSPYAAMLAAQDAAAK.C
61	72	2	1130.57	-0.55	0	43.2	23.8	95.00%	Y.AAMLAAQDAAAK.C		R.DESSPYAAMLAAQDAAAK.C
95	105	2	1037.57	5.3	0	47.1	21.8	95.00%	K.TPGPGAQAALR.A		K.TPGPGAQAALR.A
73	84	3	1367.77	4	1	24.2	18.4	93.10%	K.CKEVGITALHIK.I	Carbamidomethyl (+57)	K.CKEVGITALHIK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
90	BCA1_SCHPO	22.63%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
315	331	2	1670.97	4.2	1	59.5	16.5	95.00%	R.LLEVFGAGTAALVSPVK.A		R.LLEVFGAGTAALVSPVK.A
37	49	3	1581.74	4.5	1	25.4	26.1	93.30%	K.FGENFTDHMLIMK.W		K.FGENFTDHMLIMK.W
262	278	2	1794.99	-0.63	0	56.8	20	95.00%	K.EIITAPLDGMILPGVTR.D		K.EIITAPLDGMILPGVTR.D
337	359	2	2462.16	4.4	1	42.7	26	95.00%	K.GTEYEIPMPEGQEAGPITSEISK.W		K.GTEYEIPMPEGQEAGPITSEISK.W
115	130	2	1769.96	3.9	1	43.7	20.6	95.00%	R.ISLPSFDPAELAEIIR.K		R.ISLPSFDPAELAEIIR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
91	ASNS_SCHPO	10.05%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
51	69	2	1853.97	-1.9	0	65.4	22.5	95.00%	R.LAIVGVESGAQPLVSDDGK.L		R.LAIVGVESGAQPLVSDDGK.L
456	463	2	1039.58	0.75	1	49.6	18.8	95.00%	Y.LPQDILWR.Q		K.AFDTTHDSSLQPYLPQDILWR.Q
516	523	2	1035.55	6.3	1	30	21.9	95.00%	K.LFDEIFPR.Q		K.LFDEIFPR.Q
399	408	2	1120.54	4.9	1	26.3	23.4	92.10%	K.STMAWGLEAR.V		K.STMAWGLEAR.V
464	474	2	1256.57	1.4	2	31.4	26.3	95.00%	R.QKEQFSDGVGY.S		R.QKEQFSDGVGYSWIDALK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
92	SYDC_SCHPO	13.10%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
281	294	2	1356.6	4.8	1	27.5	25.9	92.60%	K.MSGASSEGGSNVFK.I		K.MSGASSEGGSNVFK.I
522	554	3	3334.69	3.2	1	85.5	20.1	95.00%	K.ALGVSPDVGLQQYIDAFAIGCPPHAGGGIGLER.V	Carbamidomethyl (+57)	K.ALGVSPDVGLQQYIDAFAIGCPPHAGGGIGLER.V
200	210	2	1229.65	4.9	1	29.1	22.9	95.00%	K.NLPFLVEDAGR.S		K.NLPFLVEDAGR.S
211	228	2	2006.87	0.43	1	39.1	27.4	95.00%	R.SEEQIRESEENAAEGDSK.F		R.SEEQIRESEENAAEGDSK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
93	GLNA_SCHPO	20.61%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
33	42	3	1269.66	-1.3	1	23.7	22.8	92.50%	Y.IWIDGFNHLR.S		K.VMAEYIWIDGFNHLR.S
153	170	2	1809.83	4.4	1	40.7	26.4	95.00%	K.GGFPGPQGPFYCGVGTGR.V	Carbamidomethyl (+57)	K.GGFPGPQGPFYCGVGTGR.V
237	260	4	2635.31	3.2	1	28.9	24.7	95.00%	K.ISFHPKPILGDWNGAGCHTNVSTK.D	Carbamidomethyl (+57)	K.ISFHPKPILGDWNGAGCHTNVSTK.D
338	359	3	2476.24	4.1	1	26.8	23.6	95.00%	R.RPASSIDPYLVTGIITETMFEH.-		R.RPASSIDPYLVTGIITETMFEH.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
94	ACL2_SCHPO	16.26%	100%	6									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
163	176	2	1433.61	1.2	0	59.8	26.5	95.00%	F.CNEGGVDVGDVDAK.A	Carbamidomethyl (+57)	R.EGDWILFCNEGGVDVGDVDAK.A		
382	389	2	947.52	4.5	0	26.9	23.4	93.00%	K.TVLDLMTR.G		K.TVLDLMTR.G		
149	155	2	814.47	0.96	0	27.6	21.6	93.90%	Y.ININSVR.E		K.VQHAVGYLTTFLVEPFVPHPPNTEYYININSVR.E		
255	266	2	1367.61	3.7	1	48.5	26	95.00%	K.LDQTAEFECGAK.W	Carbamidomethyl (+57)	K.LDQTAEFECGAK.W		
326	334	2	985.56	4.7	0	36	21.4	95.00%	K.LTILNAEGR.V		K.LTILNAEGR.V		
32	61	3	3211.76	3.3	1	47.1	14.8	95.00%	K.TVSATPAVQLAQIQFPLPTLVIPAESTTYR.E		K.TVSATPAVQLAQIQFPLPTLVIPAESTTYR.E		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
95	MMF1_SCHPO	47.53%	100%	5									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
109	124	2	1781.86	-0.75	1	52	26.1	95.00%	K.VNIFLADMDDFAAVNK.V		K.VNIFLADMDDFAAVNK.V		
59	75	2	1747.86	2.8	1	34.8	25.3	95.00%	K.ANGVIYCSGQIPVANGK.V	Carbamidomethyl (+57)/ Deamidation (+1)	K.ANGVIYCSGQIPVANGK.V		
87	105	2	2116.09	4.6	0	131	22.9	95.00%	R.QCLLNLQEVLTEAGSSLNK.I	Carbamidomethyl (+57)	R.QCLLNLQEVLTEAGSSLNK.I		
125	137	2	1483.81	3.9	1	42.4	20.4	95.00%	K.VYTEVLPDPKPAR.S		K.VYTEVLPDPKPAR.S		
47	58	2	1247.66	5.3	1	27.4	23	93.60%	K.LSSAGPYNQAIK.A		K.LSSAGPYNQAIK.A		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
96	RL1B_SCHPO	17.59%	100%	3									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
54	75	3	2486.26	2.6	0	38.3	23.4	95.00%	K.LPNVPRPNMAICILGDAHDLDR.A	Carbamidomethyl (+57)	K.LPNVPRPNMAICILGDAHDLDR.A		
78	91	3	1470.71	-0.94	1	68.7	25.9	95.00%	K.HGGVDAMSVDDLKK.L		K.HGGVDAMSVDDLKK.L		
76	91	4	1669.85	4.6	1	27.7	23.8	95.00%	R.AKHGGVDAMSVDDLKK.L		R.AKHGGVDAMSVDDLKK.L		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
97	DYR_SCHPO	15.40%	100%	4									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
164	183	3	2062.15	3.7	0	25.4	16.2	94.60%	K.LTTPSLHIAGTSDTLVPLAR.S		K.LTTPSLHIAGTSDTLVPLAR.S		
191	212	3	2537.31	3.6	1	37.3	21.9	95.00%	R.CENAHVLLHPGQHIVPQQAVYK.T	Carbamidomethyl (+57)	R.CENAHVLLHPGQHIVPQQAVYK.T		
446	457	2	1300.66	1.1	1	45.3	23.8	95.00%	Y.GKNDDVNVALEK.L		K.EEVEIEFELYGKNDDVNVALEK.L		
265	281	2	1722.79	-0.24	0	66	27.1	95.00%	F.ANVTSSTESSGQLEEGK.S		K.QEMAYFANVTSSTESSGQLEEGK.S		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
98	GLT1_SCHPO	6.06%	100%	7									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
1442	1464	3	2335.04	4.9	1	32.4	27.3	95.00%	R.NSGAIAVVEGVGDHGCEYMTGGR.V	Carbamidomethyl (+57)	R.NSGAIAVVEGVGDHGCEYMTGGR.V		
1897	1918	3	2189.08	3.9	1	55	25.1	95.00%	K.GKDVIVIGGGDTGNDCLGTSVR.H	Carbamidomethyl (+57)	K.GKDVIVIGGGDTGNDCLGTSVR.H		
672	685	2	1555.69	5.3	1	68	26.5	95.00%	R.ICSEADTAVNEGYK.A	Carbamidomethyl (+57)	R.ICSEADTAVNEGYK.A		
624	638	2	1701.91	4.2	1	45.5	22.6	95.00%	R.MPTPILTVEEFNALK.N		R.MPTPILTVEEFNALK.N		
1690	1707	2	2063.08	4.1	1	61.9	22.4	95.00%	K.EALTQLLLTNNFPEFTGR.V		K.EALTQLLLTNNFPEFTGR.V		
1022	1038	3	1639.81	4.9	0	25.7	25.9	93.90%	K.MAQGAKPGEGGELPGNK.V		K.MAQGAKPGEGGELPGNK.V		
1758	1776	2	1792.98	-1.5	0	87.3	20.5	95.00%	R.VAIIGSGPAGLAAADQLNR.A		R.VAIIGSGPAGLAAADQLNR.A		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
99	YDG7_SCHPO	24.61%	100%	4									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
53	77	3	2611.26	3.8	1	72.1	24.9	95.00%	R.HIDAAAIYGNEDEVGDGIKESGVPR.K		R.HIDAAAIYGNEDEVGDGIKESGVPR.K		

308	321	2	1490.7	-2.6	1	36.4	26.1	95.00%	F.SNEPVFAGLEDGRT.-	R.FNQATFSNEPVFAGLEDGRT.-
282	299	3	2106.08	4.5	1	37.8	23.8	95.00%	K.YIPLTKEDMDEINSIGIR.A	K.YIPLTKEDMDEINSIGIR.A
183	204	3	2603.37	3.4	1	27.8	19.9	95.00%	K.VKPAVHQMELHPFLPQTEFVEK.H	K.VKPAVHQMELHPFLPQTEFVEK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
100	ASSY_SCHPO	15.61%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	205	2	1483.72	0.047	0	43.5	25.4	95.00%	Y.EAGILEDPSMTPPK.D		K.KPWSMDENIVHCSYEAGILEDPSMTPPK.D
181	191	2	1353.53	1.1	1	38.2	26	95.00%	W.SMDENIVHCSY.E	Carbamidomethyl (+57)	K.KPWSMDENIVHCSYEAGILEDPSMTPPK.D
103	122	3	2242.08	-1.9	1	34.6	25.9	95.00%	R.QIQIAEKENCIAVSHGCTGK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.QIQIAEKENCIAVSHGCTGK.G
333	350	2	1884.01	-1.7	0	80.4	21.3	95.00%	R.MLLAANNVSQEVVNGVVK.L		R.MLLAANNVSQEVVNGVVK.L
102	122	4	2398.2	5	1	39.2	24.1	95.00%	R.RQIQIAEKENCIAVSHGCTGK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.RQIQIAEKENCIAVSHGCTGK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
101	PABP_SCHPO	18.53%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
572	586	2	1603.82	-1.9	1	32	23.7	95.00%	R.FTAADLAAVPEESRK.Q		R.FTAADLAAVPEESRK.Q
258	266	2	1068.57	4.8	1	26.6	21	92.50%	K.ANFTNVYIK.N		K.ANFTNVYIK.N
101	110	2	1012.57	2.2	0	26.3	19.5	92.10%	F.NSIGPVASIR.V		K.AEEPEAAAEPSESTSTPTNASSVATPSGTAPTSASLYVGELDPSVTEAMLFELFNSIGPVASIR.V
9	46	4	4050.84	4.1	1	18.5	23.7	91.60%	K.QADAAVESDVNTNNEAVESSTKEESSNTPSTETQPEKK.A		K.QADAAVESDVNTNNEAVESSTKEESSNTPSTETQPEKK.A
447	456	2	1142.61	4.9	0	33.9	22.4	95.00%	R.SQLEAQIQAR.N		R.SQLEAQIQAR.N
9	45	3	3922.74	2	1	63.3	24.3	95.00%	K.QADAAVESDVNTNNEAVESSTKEESSNTPSTETQPEK.K		K.QADAAVESDVNTNNEAVESSTKEESSNTPSTETQPEK.K
536	571	3	3524.72	4.6	0	28.7	22.5	95.00%	R.GPVPAQGRPMMMPGSVPSAGPAEAEAVPAVPGMPER.F		R.GPVPAQGRPMMMPGSVPSAGPAEAEAVPAVPGMPER.F
98	110	2	1401.76	1.5	1	37.2	22.6	95.00%	F.ELFNSIGPVASIR.V		K.AEEPEAAAEPSESTSTPTNASSVATPSGTAPTSASLYVGELDPSVTEAMLFELFNSIGPVASIR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
102	TAL1_SCHPO	16.15%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
27	44	3	1917.03	4	1	42	22.1	95.00%	K.YKPQDATTNPSLILAASK.K		K.YKPQDATTNPSLILAASK.K
9	26	2	1795.89	4.5	1	86.8	25.2	95.00%	K.ATGTVVVSDTGDFESIAK.Y		K.ATGTVVVSDTGDFESIAK.Y
45	60	2	1721.9	-1.8	1	89.8	23.4	95.00%	K.KPQYAALVDAAVDYAK.A		K.KPQYAALVDAAVDYAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
103	VATA_SCHPO	16.80%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
89	114	4	2751.53	2.9	1	22.2	15.6	95.00%	R.TGKPLSVELGPGLAETIYDGIQRPLK.Q		R.TGKPLSVELGPGLAETIYDGIQRPLK.Q
373	389	2	1752.85	8	1	36.9	25.5	95.00%	R.LAEMPADSGYPAYLGAK.L		R.LAEMPADSGYPAYLGAK.L
317	331	2	1544.81	4.6	0	49.4	24.3	95.00%	R.TTLVANTSNMPVAAR.E		R.TTLVANTSNMPVAAR.E
182	198	2	1838.88	4.6	1	73	26.6	95.00%	R.GTVTYIAEAGSYHVDEK.L		R.GTVTYIAEAGSYHVDEK.L
221	240	3	2105.14	4.1	0	35.3	20.6	95.00%	R.AARPVADNLTANQPLLTGQR.V		R.AARPVADNLTANQPLLTGQR.V
128	136	2	1002.51	5	0	25.2	22.7	90.20%	R.GINTESLNR.E		R.GINTESLNR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
104	RL10A_SCHPO	26.24%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
129	139	2	1228.7	4.7	0	40	20.8	95.00%	R.VNIGQILMSVR.T		R.VNIGQILMSVR.T

58	69	2	1316.66	0.74	0	77.6	24.2	95.00%	Y.EQITSEALEAAR.I		R.AGVDEFPLCIHLVSNEYEQITSEALEAAR.I
41	69	3	3260.58	4	1	68.1	23.6	95.00%	R.AGVDEFPLCIHLVSNEYEQITSEALEAAR.I	Carbamidomethyl (+57)	R.AGVDEFPLCIHLVSNEYEQITSEALEAAR.I
117	128	3	1265.71	4.6	1	30	18.9	95.00%	R.HAFGKPNGLVAR.V		R.HAFGKPNGLVAR.V
33	38	2	719.4	4.8	1	27.1	21.4	93.20%	R.IFDLGR.K		R.IFDLGR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
105	AATR1_SCHPO	9.28%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
275	288	2	1577.78	4.4	1	46.4	25.6	95.00%	K.ELIPSFLSMDVDGR.V		K.ELIPSFLSMDVDGR.V
38	54	2	1856.03	4.5	1	36.8	19	95.00%	K.IISLAGGLPNPEYFPIR.E		K.IISLAGGLPNPEYFPIR.E
7	19	3	1436.71	5.4	0	43.2	25.8	95.00%	K.DLSHHLSVESASR.K		K.DLSHHLSVESASR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
106	PYC_SCHPO	5.74%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1109	1129	3	2088.05	4.4	0	38.2	24.2	95.00%	R.ADPGNPGHVAAPMSGTIVEIR.V		R.ADPGNPGHVAAPMSGTIVEIR.V
839	848	2	1297.58	4.8	1	38.2	25.9	95.00%	R.EIDSYWAQMR.L		R.EIDSYWAQMR.L
829	838	2	1275.63	4.5	1	27.7	24.9	94.00%	K.QLEFDNNQLR.E		K.QLEFDNNQLR.E
917	929	2	1447.76	4.7	1	42.2	24.4	95.00%	K.VVGDLAQFMVQNK.L		K.VVGDLAQFMVQNK.L
302	315	2	1628.75	2	1	37.3	27	95.00%	K.YCNAGTAEFLLDQK.G	Carbamidomethyl (+57)	K.YCNAGTAEFLLDQK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
107	AROG_SCHPO	18.82%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
199	226	3	2704.36	2.1	0	47.7	23.5	95.00%	K.NGTDGTVGVAIDAIGATAHPHTMLGVTK.Q	Deamidation (+1)	K.NGTDGTVGVAIDAIGATAHPHTMLGVTK.Q
186	198	2	1364.74	4.4	1	39.9	22	95.00%	R.ELASALSFPVGFK.N		R.ELASALSFPVGFK.N
349	363	2	1657.8	-1	0	48.1	25.9	95.00%	W.EQTAPMLDDLAEAVR.A		K.YGVSITDACVSWEQTAPMLDDLAEAVR.A
250	263	3	1525.76	-0.59	2	31.5	25.1	95.00%	K.KGPNYDAEHVAAVR.K		K.KGPNYDAEHVAAVR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
108	VATB_SCHPO	14.12%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
415	427	2	1417.68	4.9	0	78	25.7	95.00%	K.SVVGEEALSQEDR.L		K.SVVGEEALSQEDR.L
439	449	2	1284.62	4.2	1	36.9	25.3	95.00%	K.TFISQGAYENR.T		K.TFISQGAYENR.T
485	503	2	2015.89	5.3	1	57.2	27.3	95.00%	R.SSAYTESSKDVIDNTPESS.-		R.SSAYTESSKDVIDNTPESS.-
350	359	2	1176.62	2	1	44.2	23.8	95.00%	Y.ITEGQIFVDR.Q		R.NGSITQIPILTMPNDDITHPIPDLTGYITEGQIFVDR.Q
42	59	3	2083.09	4.5	1	23.6	22.1	92.30%	R.RPQYNEIVNLNLPDGSVR.S		R.RPQYNEIVNLNLPDGSVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
109	SYKC_SCHPO	12.86%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
15	28	2	1454.8	-1.7	0	50.7	21.8	95.00%	K.ALVLDPVTGEQVSK.T		K.ALVLDPVTGEQVSK.T
570	591	3	2490.32	-0.44	1	36.5	21	95.00%	R.EVLLFPHMKPEVQAAEPTVVKE.-		R.EVLLFPHMKPEVQAAEPTVVKE.-
498	513	2	1999.9	4.4	1	72.7	27.2	95.00%	K.EICNAYTELNDIFDQR.A	Carbamidomethyl (+57)	K.EICNAYTELNDIFDQR.A
153	176	4	2810.33	3.8	2	33.2	25.1	95.00%	K.KLQVMCQAQDADTVDFAAQHEHLR.R	Carbamidomethyl (+57)	K.KLQVMCQAQDADTVDFAAQHEHLR.R
154	176	4	2682.24	3.7	1	34.1	26.4	95.00%	K.LQVMCQAQDADTVDFAAQHEHLR.R	Carbamidomethyl (+57)	K.LQVMCQAQDADTVDFAAQHEHLR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
110	PMP20_SCHPO	44.23%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

40	55	2	1746.83	1.6	1	49.9	26.1	95.00%	F.TPPCSSQVPGYIANEK.Q	Carbamidomethyl (+57)	K.FIIVGVPGAFTPPCSSQVPGYIANEK.Q
82	93	2	1265.53	-1.5	1	49.4	25.9	95.00%	K.SFDGGEQSGVHF.V		K.SFDGGEQSGVHFVADWNGEFTK.A
11	29	3	2215.13	4.2	1	34.9	23.8	95.00%	K.VTLWENKPEEVVEFPSQGK.F		K.VTLWENKPEEVVEFPSQGK.F
135	156	2	2379.21	3.2	1	61.1	23.8	95.00%	K.VFIENEVTDVDISSADKVLSSL.-		K.VFIENEVTDVDISSADKVLSSL.-
135	151	2	1879.91	3.7	1	64.2	26	95.00%	K.VFIENEVTDVDISSADK.V		K.VFIENEVTDVDISSADK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
111	SYTC_SCHPO	8.25%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
248	258	2	1187.55	4.2	1	47.1	26	95.00%	K.NSSSYFLGDAK.N		K.NSSSYFLGDAK.N
94	106	2	1502.78	0.07	0	37.2	23.7	95.00%	W.DLTRPLEASCTLK.L	Carbamidomethyl (+57)	R.VTVAIVNGEPWDLTRPLEASCTLK.L
8	26	3	2136.14	4.2	1	27.4	21.3	95.00%	K.GVQASLDNLSLEIPFIQHR.L		K.GVQASLDNLSLEIPFIQHR.L
160	174	2	1703.8	4.7	1	71.1	26.8	95.00%	R.VITNDDYSSIESYAK.Q		R.VITNDDYSSIESYAK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
112	EF1G_SCHPO	10.51%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
207	216	2	1182.71	4	1	27.1	15.7	93.30%	K.FIDQPLPIIK.A		K.FIDQPLPIIK.A
128	139	2	1303.72	4.6	1	40.7	21.9	95.00%	K.EAETAIALIFAR.F		K.EAETAIALIFAR.F
198	216	3	2163.26	1.1	2	36.3	12.3	95.00%	K.LDAITEPLKFIDQPLPIIK.A		K.LDAITEPLKFIDQPLPIIK.A
116	127	2	1294.63	4.3	1	26.2	25.4	91.40%	R.VFGAPYDEQAAK.E		R.VFGAPYDEQAAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
113	THRC_SCHPO	20.23%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
437	454	3	2061.03	4.7	2	31.2	24.5	95.00%	K.TKDQDITYICLSTAHPAK.F	Carbamidomethyl (+57)	K.TKDQDITYICLSTAHPAK.F
313	327	2	1443.73	4.4	0	39.8	24.6	95.00%	K.ADSTQVSPSGPISAK.E		K.ADSTQVSPSGPISAK.E
418	432	2	1576.86	-0.077	0	58.2	22	95.00%	Y.IIDPHTAVGVETGLR.C		K.IYESDHYIIDPHTAVGVETGLR.C
182	215	3	3829.81	3.8	1	34.2	23.2	95.00%	R.VSPIQEAQMTTVTDPNVHCITVNGVFDDCQDLVK.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VSPIQEAQMTTVTDPNVHCITVNGVFDDCQDLVK.Q
399	410	2	1331.7	3.6	1	37.5	23.8	95.00%	R.VSNDETIDAIKK.I		R.VSNDETIDAIKK.I
493	502	3	1083.63	-1.6	0	34.6	18.5	95.00%	F.SGKPNIDILK.Q		R.TCIFSGKPNIDILK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
114	RS0B_SCHPO	28.92%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	31	3	3162.63	3.2	1	83.6	21.1	95.00%	M.AESIARPSVLNATDDDIKNLLAADSHIGSK.N	Acetyl (+42)	-.MAESIARPSVLNATDDDIKNLLAADSHIGSK.N
67	88	4	2453.26	4	1	67.3	22.5	95.00%	R.VIATIENPADVCVISSRPYGHR.A	Carbamidomethyl (+57)	R.VIATIENPADVCVISSRPYGHR.A
139	169	3	3390.76	4.3	1	25.4	18.4	94.50%	K.EASFVNIPVIALCDTDSILNHVDVAIPINNK.G	Carbamidomethyl (+57)	K.EASFVNIPVIALCDTDSILNHVDVAIPINNK.G
67	85	2	2103.07	0.15	1	93.3	24.7	95.00%	R.VIATIENPADVCVISSRPY.G	Carbamidomethyl (+57)	R.VIATIENPADVCVISSRPYGHR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
115	DHE4_SCHPO	21.29%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
279	291	3	1405.74	5	1	27.9	22.8	95.00%	K.RASIADSASLCKK.H	Carbamidomethyl (+57)	K.RASIADSASLCKK.H
417	439	2	2411.16	5.2	1	85.7	25.8	95.00%	K.YCDSGSNNIPSLVDGANIAGFLK.V	Carbamidomethyl (+57)	K.YCDSGSNNIPSLVDGANIAGFLK.V
356	367	2	1231.57	4.5	1	27.7	25	94.00%	R.ASGEGCWLAPGK.A	Carbamidomethyl (+57)	R.ASGEGCWLAPGK.A
399	416	2	1950.97	-1.2	1	95.2	25.5	95.00%	K.LAGIMQNIFEQSTDVASK.Y		K.LAGIMQNIFEQSTDVASK.Y
334	353	2	2102.96	4.2	1	111	27.3	95.00%	R.YVAEGSNMGSSAEAVEVFEK.S		R.YVAEGSNMGSSAEAVEVFEK.S

25	34	3	1266.71	4.3	1	33.7	18.5	95.00%	K.LFEVHPELKR.V		K.LFEVHPELKR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
116	YA03_SCHPO	35.16%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
181	194	2	1560.82	-1	1	50.7	23.8	95.00%	K.AADIDFLPPQLSFK.N		K.AADIDFLPPQLSFK.N
14	47	4	3763.78	4.5	1	35.9	22.9	95.00%	R.HGQAQHNVGPDEDHNIRDPVLTSEGIEQCEALAK.E	Carbamidomethyl (+57)	R.HGQAQHNVGPDEDHNIRDPVLTSEGIEQCEALAK.E
154	170	2	1807	-0.17	1	29.1	18.5	95.00%	Y.LAALPQQQIAVITHSAF.I		K.EALEYLAALPQQQIAVITHSAFIR.F
66	77	3	1430.83	3.8	1	35.5	16.4	95.00%	R.RTLQTMEIALKK.Y		R.RTLQTMEIALKK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
117	RL12_SCHPO	40.00%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
138	165	3	3106.45	-0.21	1	26.3	25.4	95.00%	F.SVGCTVDGKNPHDVQKEIDNGEIEIPQE.-	Carbamidomethyl (+57)	K.EILGTAFSVGCTVDGKNPHDVQKEIDNGEIEIPQE.-
68	83	2	1538.91	3.4	0	50.5	14.5	95.00%	R.QAAVSVVPSASALVIK.A		R.QAAVSVVPSASALVIK.A
138	153	3	1739.83	0.54	1	41.8	26.9	95.00%	F.SVGCTVDGKNPHDVQK.E	Carbamidomethyl (+57)	K.EILGTAFSVGCTVDGKNPHDVQK.E
17	31	2	1312.7	3.6	0	46	21.3	95.00%	R.AVGGEVAGGSTLAPK.I		R.AVGGEVAGGSTLAPK.I
131	146	2	1652.81	4	1	45.9	25.2	95.00%	K.EILGTAFSVGCTVDGK.N	Carbamidomethyl (+57)	K.EILGTAFSVGCTVDGK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
118	SLBR2_SCHPO	24.79%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
134	143	2	1115.56	4.3	0	27.1	23.9	93.30%	R.NIESSVQPSR.E		R.NIESSVQPSR.E
166	192	3	3060.53	3.6	1	43.6	22.3	95.00%	R.LVTMEQELVREEAACLVAEAQLSNTTR.E	Carbamidomethyl (+57)	R.LVTMEQELVREEAACLVAEAQLSNTTR.E
222	248	3	2999.47	2.8	1	39.6	24	95.00%	R.HLLNLIDDTPVTPGEARPAYDGYETSR.Q		R.HLLNLIDDTPVTPGEARPAYDGYETSR.Q
271	284	2	1570.76	0.69	0	42.2	25.9	95.00%	F.VKPQIEDDAQSDAR.S		R.QIVMDAEHALSSWVPSQPAVNFVKPQIEDDAQSDAR.S
149	157	2	1075.63	4.5	1	33	19.2	95.00%	K.LLDQIYALK.H		K.LLDQIYALK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
119	COFI_SCHPO	29.20%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	44	3	1533.82	5.2	1	36.4	23	95.00%	K.MNDTKTEIVVEKK.S		K.MNDTKTEIVVEKK.S
81	94	2	1584.9	4.1	1	54.1	19.2	95.00%	K.IIFISWSPDVAPIK.S		K.IIFISWSPDVAPIK.S
32	43	2	1405.72	4.4	1	32.5	24.4	95.00%	K.MNDTKTEIVVEK.K		K.MNDTKTEIVVEK.K
8	20	2	1548.76	4.6	1	71.2	25.7	95.00%	K.VSPECLEAFQELK.L	Carbamidomethyl (+57)	K.VSPECLEAFQELK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
120	GCST_SCHPO	23.51%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
132	148	4	1889.95	0.98	1	20.2	24.6	94.90%	Y.IVTNAACSEKDEANLKK.H	Carbamidomethyl (+57)	K.QDENTYYIVTNAACSEKDEANLKK.H
165	180	2	1623.93	4	0	75.8	18.3	95.00%	R.ALIAIQGPETASVVQK.L		R.ALIAIQGPETASVVQK.L
81	97	2	1779.9	3.9	1	64.1	25.2	95.00%	R.GENATAYLESITPSSLK.E		R.GENATAYLESITPSSLK.E
319	344	3	2566.25	4.5	0	41.9	25.4	95.00%	R.HGSAVEVDGVEVGQVTSGCPSPTLGK.N	Carbamidomethyl (+57)	R.HGSAVEVDGVEVGQVTSGCPSPTLGK.N
110	124	2	1575.8	0.053	0	74.1	24.9	95.00%	F.TNETGGIIDDTIISK.Q		K.ELKPFHSTLSAFTNETGGIIDDTIISK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
121	GCSP_SCHPO	6.78%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
953	965	2	1458.76	1.1	0	43.1	23.9	95.00%	K.DNNLLVNAPHPQK.D		K.DNNLLVNAPHPQK.D

657	684	3	2835.49	3.7	1	27.8	19.3	95.00%	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C	Carbamidomethyl (+57)	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C
577	597	2	2385.19	-0.34	1	38.6	24.5	95.00%	K.LNAVTEMMPITNPLFANIHPY.V		K.LNAVTEMMPITNPLFANIHPYVPEEQAK.G
577	604	3	3166.6	3.7	1	40.5	22.4	95.00%	K.LNAVTEMMPITNPLFANIHPYVPEEQAK.G		K.LNAVTEMMPITNPLFANIHPYVPEEQAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
122	PURA_SCHPO	13.13%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
421	434	3	1498.78	0.47	1	30.9	22.7	95.00%	F.IGVGPGRDEMLVKE.-		K.FVGVPITFIGVGPGRDEMLVKE.-R.IANSIGVVK.A
268	276	2	899.55	4.9	0	44.5	21.5	95.00%	R.IANSIGVVK.A		
282	304	3	2420.22	4.2	1	27.4	23.9	95.00%	R.VGAGPFPTEQLNEIGDHLQSVGR.E		R.VGAGPFPTEQLNEIGDHLQSVGR.E
126	136	2	1129.57	4.6	0	38.6	22.9	95.00%	R.ADALNEAELGK.Q		R.ADALNEAELGK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
123	RAD25_SCHPO	22.59%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
63	74	2	1417.75	4.9	1	43.2	23.2	95.00%	R.IISSIEQKEESR.G		R.IISSIEQKEESR.G
244	261	3	1846.84	4.4	0	24	26.7	90.00%	K.EEAPAAAAASENEHPEPK.E		K.EEAPAAAAASENEHPEPK.E
88	107	3	2369.22	3.8	1	24.6	23.4	93.60%	R.KKIEDELSDICHDVLSVLEK.H	Carbamidomethyl (+57)	R.KKIEDELSDICHDVLSVLEK.H
233	261	3	3041.36	2.8	1	53.5	27.1	95.00%	W.TSDAEYNQSAKEEAPAAAAASENEHPEPK.E		R.DNLTLWTSDAEYNQSAKEEAPAAAAASENEHPEPK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
124	ADK_SCHPO	26.47%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
126	138	2	1424.68	5.2	1	51	26.2	95.00%	R.SLCTNLGAANNYK.L	Carbamidomethyl (+57)	R.SLCTNLGAANNYK.L
253	267	2	1483.87	4.5	0	69.4	17.2	95.00%	R.VVVITQGADATIVAK.D		R.VVVITQGADATIVAK.D
86	96	2	1295.61	3.7	1	43.7	26.2	95.00%	K.FADMLLESNEK.A		K.FADMLLESNEK.A
230	245	2	1688.89	3.8	0	56.9	23.5	95.00%	K.STDVQEIALALSSVEK.V		K.STDVQEIALALSSVEK.V
32	46	2	1583.72	0.95	1	52.7	26.4	95.00%	K.SNDAVLASESQMGIY.K		K.SNDAVLASESQMGIYK.E
8	27	2	2181.09	1.4	1	71.6	25.3	95.00%	F.GLENPLLDYYVGGETATLEK.Y		-.MSSYILFGLENPLLDYYVGGETATLEK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
125	RS17A_SCHPO	24.43%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	59	3	1133.6	4.6	1	24.5	23.1	93.50%	K.IAGYTTHLMK.R		K.IAGYTTHLMK.R
34	45	3	1312.77	-0.91	1	22.4	19	90.10%	R.IVDEVAIIASKR.L		R.IVDEVAIIASKR.L
24	33	2	1234.67	4.6	1	36.3	22.3	95.00%	R.LTLDFQTNKR.I		R.LTLDFQTNKR.I
34	44	2	1156.68	4.8	0	51	20	95.00%	R.IVDEVAIIASK.R		R.IVDEVAIIASK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
126	THI22_SCHPO	8.71%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
423	435	2	1516.6	5.3	1	56.7	25.8	95.00%	K.SCEESPACTAYSR.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.SCEESPACTAYSR.Y
181	197	2	1890.88	4.9	0	111	26.6	95.00%	K.NQGLDISNINSVSDMER.C		K.NQGLDISNINSVSDMER.C
134	151	2	1829.98	-2	0	82.6	22	95.00%	K.LVVDPVMVATSGDSLVTK.D		K.LVVDPVMVATSGDSLVTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
127	STI1_SCHPO	15.74%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
146	164	2	1935.97	6.4	1	78.1	25.2	95.00%	K.LASNPETASLLADSAFMAK.L		K.LASNPETASLLADSAFMAK.L
168	183	2	1781.88	4.3	0	66.6	25.8	95.00%	K.IQQNPGSIMAELNDPR.M		K.IQQNPGSIMAELNDPR.M
20	34	2	1711.85	3.9	1	70.3	24.9	95.00%	K.TAIDYFTQAIGLDER.N		K.TAIDYFTQAIGLDER.N

371	377	2	800.44	3.8	0	29.8	23.1	95.00%	R.TPDILSR.L		R.TPDILSR.L
76	90	3	1463.79	4.4	1	44.6	21.9	95.00%	R.KGAALHGLGDLDAAR.S		R.KGAALHGLGDLDAAR.S
112	132	2	2007.97	4.2	1	89.9	26.5	95.00%	K.SVEAAQTQAASGAGGFNPFAK.L		K.SVEAAQTQAASGAGGFNPFAK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
128	DAK1_SCHPO	8.28%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
388	399	2	1358.73	4.4	0	25.9	23.3	91.50%	R.QAIVNSMENLIK.A		R.QAIVNSMENLIK.A
557	580	3	2355.27	-0.17	2	25.2	19.3	94.30%	Y.VGDDVKVPDAGALGVVAIVEGFTK.-		R.AVYVGDDVKVPDAGALGVVAIVEGFTK.-
527	538	2	1301.63	4.7	0	60.8	25.2	95.00%	K.TNDLNAAVEEAR.K		K.TNDLNAAVEEAR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
129	RL31_SCHPO	21.24%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
91	105	2	1650.87	4.2	1	39.3	22.9	95.00%	K.ALYTYVQAVDVANPK.M		K.ALYTYVQAVDVANPK.M
7	15	2	986.56	5	0	39.5	22.3	95.00%	K.SAINQVVTR.D		K.SAINQVVTR.D
94	105	2	1303.68	-0.93	1	63	24.1	95.00%	Y.TYVQAVDVANPK.M		K.ALYTYVQAVDVANPK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
130	SYLC_SCHPO	2.61%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
382	398	3	1730.98	4.6	0	32.6	17.9	95.00%	K.GQDLIGALVNAPLSVHK.Q		K.GQDLIGALVNAPLSVHK.Q
530	541	2	1389.69	-0.58	1	44.4	24	95.00%	F.VYNEPEGQVISR.S		K.ELIDQGLAFVYNEPEGQVISR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
131	PMM_SCHPO	22.57%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
29	43	2	1728.92	4.2	0	56.6	22	95.00%	R.LSVSPEMLETLQNLR.K		R.LSVSPEMLETLQNLR.K
236	253	4	1938.02	4.7	1	21.7	22.3	95.00%	R.TIGHSVTNPDDTIAELKK.I		R.TIGHSVTNPDDTIAELKK.I
77	87	2	1211.59	0.63	1	27.9	25.2	94.00%	Y.AFAENGLTAYR.Y		K.QQEQLSVNGENVIDSFDYAFAENGLTAYR.Y
45	58	2	1347.75	4.4	1	41.6	21.3	95.00%	K.VVAIGFVGGSDLSK.Q		K.VVAIGFVGGSDLSK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
132	RS2_SCHPO	22.13%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
186	200	2	1799.86	4.8	1	102	26.4	95.00%	R.FLQLAGIEDCYTQSR.G	Carbamidomethyl (+57)	R.FLQLAGIEDCYTQSR.G
51	63	2	1566.86	4.2	1	34.6	19.5	95.00%	K.SIEEIYLYSLPIK.E		K.SIEEIYLYSLPIK.E
174	185	3	1138.69	4.8	1	25.2	13	94.30%	R.GAGLVAAPVTKR.F		R.GAGLVAAPVTKR.F
141	156	3	1696.87	4.8	1	37.6	24.2	95.00%	R.GYWGTALGDPHTVPVK.V		R.GYWGTALGDPHTVPVK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
133	ACL1_SCHPO	11.87%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
369	381	2	1420.73	4.5	1	44	24.3	95.00%	R.GSELTYNNVPISK.V		R.GSELTYNNVPISK.V
171	182	3	1338.74	4.8	1	23.6	20	92.30%	K.LYRPGSVAYVSK.S		K.LYRPGSVAYVSK.S
313	326	2	1570.9	3.9	1	58.3	18.2	95.00%	K.LPALLQEVYEGLVK.K		K.LPALLQEVYEGLVK.K
137	154	2	1797.98	-1.2	1	33	21.5	95.00%	K.NVVIIGPATVGGIKPGCF.K	Carbamidomethyl (+57)	K.NVVIIGPATVGGIKPGCFK.I
156	170	2	1506.72	3.3	0	45.7	26.1	95.00%	K.IGNTGGMMDNIVASK.L		K.IGNTGGMMDNIVASK.L
313	327	3	1699	4	1	30.3	13.8	95.00%	K.LPALLQEVYEGLVKK.G		K.LPALLQEVYEGLVKK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
134	RL15A_SCHPO	12.94%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
78	93	3	1761.94	4.8	1	23.7	22.7	92.40%	K.GQTYGKPVHQGVNHLK.Y		K.GQTYGKPVHQGVNHLK.Y
148	157	3	1218.69	4.4	1	24.4	19.5	93.40%	R.INWIVNPVHK.H		R.INWIVNPVHK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
135	PUR8_SCHPO	16.18%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
410	423	3	1571.79	4.9	1	22.5	24.5	90.40%	R.VVKEEGGDNDLIER.I		R.VVKEEGGDNDLIER.I
226	242	2	1930.91	3.5	1	32.6	26.9	95.00%	K.LSGFDNVYPVTGQTYDR.K		K.LSGFDNVYPVTGQTYDR.K
243	261	3	2023.12	4.2	2	51.4	18.6	95.00%	R.KIDIDVLQPLASFGATAHK.I		R.KIDIDVLQPLASFGATAHK.I
450	460	2	1248.61	5.4	1	26.4	24.4	92.30%	R.APEQTESFVNK.D		R.APEQTESFVNK.D
372	388	2	1909.94	4.9	1	55.7	25.3	95.00%	R.AELPFMATENIIMAMTK.H		R.AELPFMATENIIMAMTK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
136	ARO1_SCHPO	6.10%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
677	703	3	2950.41	2.7	1	45.4	24.6	95.00%	R.FACDVLRPMGCTVEQTATSTTVQGPPK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.FACDVLRPMGCTVEQTATSTTVQGPPK.G
1232	1247	2	1833.96	4.6	1	44.8	23.3	95.00%	R.ITNSMDIPLILFNMGR.F		R.ITNSMDIPLILFNMGR.F
1326	1338	2	1509.69	1.3	1	54.4	26.3	95.00%	Y.EAFETDTVDEVQK.V		R.SPILHSTAYELLGLPHTYEAFETDTVDEVQK.V
632	660	3	3107.51	1.4	1	44.5	23.6	95.00%	K.YQNPPHYEIESDASSATYPLAIAAITGTK.C		K.YQNPPHYEIESDASSATYPLAIAAITGTK.C
162	172	2	1299.72	4.7	1	45.2	22.1	95.00%	K.NLVGAFWQPLR.V		K.NLVGAFWQPLR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
137	SYG_SCHPO	6.13%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
187	198	2	1297.63	5.4	0	37	25.7	95.00%	R.NPATNGELETPR.Q		R.NPATNGELETPR.Q
492	506	2	1649.85	4.8	1	35.7	24.3	95.00%	R.TYTPNVIEPSFGLGR.I		R.TYTPNVIEPSFGLGR.I
526	538	2	1298.76	-1.6	1	29.7	17.9	95.00%	R.GVLSFPASIAPIK.A		R.GVLSFPASIAPIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
138	Q1L854_SCHPO	21.25%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
143	178	3	3637.66	4	1	78.1	25.6	95.00%	R.GWGDLVNSAANPDVAENEGNTPSGAQTPAAEEENVK.T		R.GWGDLVNSAANPDVAENEGNTPSGAQTPAAEEENVK.T
10	28	2	2077.07	4.4	1	50.2	23.6	95.00%	K.NLFDLLGEETPAATTTEKK.T		K.NLFDLLGEETPAATTTEKK.T
10	27	2	1948.96	-1.8	1	75.9	25.6	95.00%	K.NLFDLLGEETPAATTTEK.K		K.NLFDLLGEETPAATTTEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
139	KAD1_SCHPO	23.64%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
196	218	3	2621.39	2.8	1	47.7	19.3	95.00%	K.WAAVDAAQKPEQVWEQIVAILEK.A		K.WAAVDAAQKPEQVWEQIVAILEK.A
54	82	3	3231.58	-0.63	1	66.9	22.8	95.00%	K.KIMDQGGLVSDDIVTGMIKDEILNNPECK.N	Carbamidomethyl (+57)	K.KIMDQGGLVSDDIVTGMIKDEILNNPECK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
140	ARGD_SCHPO	14.97%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
311	332	3	2276.09	4.8	1	39.5	26	95.00%	K.IAAEIHPGEHGSTFGGNPVACR.V	Carbamidomethyl (+57)	K.IAAEIHPGEHGSTFGGNPVACR.V
283	310	3	2746.56	2.7	0	43.2	12.8	95.00%	K.DVASPDIITVAKPLANGLPIGATIVSSK.I		K.DVASPDIITVAKPLANGLPIGATIVSSK.I
139	154	2	1784.85	4.1	1	92.8	26.6	95.00%	K.IFFANCGTEANETALK.F	Carbamidomethyl (+57)	K.IFFANCGTEANETALK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
141	RL2_SCHPO	21.74%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
92	118	3	2780.44	3.2	0	52	21.5	95.00%	K.NAALTVGNVLPVGEMPEGTIISNVEEK.A		K.NAALTVGNVLPVGEMPEGTIISNVEEK.A
133	144	2	1251.68	-1.2	0	42.3	21	95.00%	Y.VIIVGHDVDTGK.T		R.SSGNYVIIVGHDVDTGK.T

128	144	3	1759.88	4.2	1	23	24.5	91.30%	R.SSGNYVIIVGHDVDTGK.T		R.SSGNYVIIVGHDVDTGK.T
163	173	2	940.55	4.3	0	54.6	14.8	95.00%	R.GVVGIVAGGGR.I		R.GVVGIVAGGGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
142	RANG_SCHPO	32.56%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
88	98	2	1353.6	4	1	43.5	26.3	95.00%	K.TNEEEETVEFK.M		K.TNEEEETVEFK.M
188	198	2	1253.61	5.8	1	35.7	25.3	95.00%	R.FANSENANLFK.E		R.FANSENANLFK.E
49	80	3	3379.58	3.1	2	28.6	24.6	95.00%	K.SGASTNDEKKPAEGDEDAEPASPEVHFEPIVK.L		K.SGASTNDEKKPAEGDEDAEPASPEVHFEPIVK.L
169	184	2	1622.73	1.2	1	41.3	26.6	95.00%	W.TVAADVSEGEPTAETF.A		R.SWVWTVAADVSEGEPTAETFAIR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
143	NACB_SCHPO	47.68%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	88	2	1699.84	-1.5	1	34.9	25.3	95.00%	R.APTVHSSLPNETTAIY.G		R.APTVHSSLPNETTAIYGK.A
73	90	3	1884.97	4	1	45.6	23.7	95.00%	R.APTVHSSLPNETTAIYGK.A		R.APTVHSSLPNETTAIYGK.A
130	151	2	2376.03	2.8	2	68.7	27.6	95.00%	K.GADAQADDGEIPDLVEKFDEQD.-		K.GADAQADDGEIPDLVEKFDEQD.-
63	72	2	1133.59	1.7	2	28.5	23.7	94.80%	F.KEDGGVINFR.A		K.LNMQNLAGIQEVNMFKEDGGVINFR.A
95	116	2	2320.31	3	0	52.8	14.1	95.00%	K.TLSEILPGILNNLGPESLTALR.Q		K.TLSEILPGILNNLGPESLTALR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
144	SYRC_SCHPO	10.03%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
163	180	2	1987.02	4.1	1	33.9	22.7	95.00%	R.STIIGSFLANLHESQGWK.V		R.STIIGSFLANLHESQGWK.V
225	238	2	1588.76	3.6	1	45.2	25.9	95.00%	K.VNADATEEDEKIQK.D		K.VNADATEEDEKIQK.D
11	24	2	1544.86	4.5	1	46.7	20.3	95.00%	K.SLSTLGLQDLPVFR.E		K.SLSTLGLQDLPVFR.E
452	467	2	1759.87	3.7	1	55	24.8	95.00%	K.YAQVENPEEVADIVGK.T		K.YAQVENPEEVADIVGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
145	RS12A_SCHPO	46.90%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	111	2	1486.76	2.4	1	27.9	23.6	94.20%	K.VLGEWAGLCVLDR.D	Carbamidomethyl (+57)	K.VLGEWAGLCVLDR.D
79	93	2	1671.88	4.1	0	73.8	22.7	95.00%	K.LVEALCAESETPLIK.V	Carbamidomethyl (+57)	K.LVEALCAESETPLIK.V
61	78	3	2208.97	4.2	1	36.3	27.3	95.00%	R.QAHLCVLCESCDQEAYVK.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.QAHLCVLCESCDQEAYVK.L
117	138	3	2356.1	-1.5	2	60.7	27	95.00%	R.KVVGCSCVAVTDYGEDSAALQK.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.KVVGCSCVAVTDYGEDSAALQK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
146	RS4B_SCHPO	11.07%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
222	233	2	1232.68	5.6	1	42.4	22.1	95.00%	R.LSNVFVIGEAGK.S		R.LSNVFVIGEAGK.S
246	252	2	846.45	4.8	0	45.4	23.7	95.00%	K.LSITEER.D		K.LSITEER.D
40	49	2	1258.72	4.7	1	26.1	20.6	91.80%	R.ECLPLIVFLR.N	Carbamidomethyl (+57)	R.ECLPLIVFLR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
147	SCE3_SCHPO	21.65%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
250	271	3	2195.06	2.9	0	28.5	26.2	95.00%	R.SSSNVNTEATPSATTTTSSKPK.R		R.SSSNVNTEATPSATTTTSSKPK.R
46	66	2	2113.97	4.9	1	94.2	27.3	95.00%	R.ATPSSADAGYNAPSSTFESVR.S		R.ATPSSADAGYNAPSSTFESVR.S
272	289	3	1956.03	4.3	2	43	22.6	95.00%	K.RDPFGGAKPVDNTSVLQR.V		K.RDPFGGAKPVDNTSVLQR.V

359	381	2	2403.05	5.1	1	111	27.7	95.00%	K.TPATEDAPATNAGEAEEEEGWTK.I		K.TPATEDAPATNAGEAEEEEGWTK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
148	SYEC_SCHPO	10.89%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
278	288	2	1354.61	1.9	1	34.9	26.5	95.00%	Y.TSDYLDTIHQY.C		K.ENSEFQDAILEDVALLGIKPDVVTYTSDYLDTIHQYCVDMIK.S
66	77	2	1393.77	4.3	1	31.9	20.3	95.00%	K.LALQTFSQVYPK.L		K.LALQTFSQVYPK.L
190	206	2	1731.84	3.9	1	51.4	25.5	95.00%	K.SSGPNYEIGLPDAIDGK.V		K.SSGPNYEIGLPDAIDGK.V
322	344	3	2559.28	1.2	1	45.9	23.9	95.00%	R.DRPIEESLEILSEMDKGSDVGLK.N		R.DRPIEESLEILSEMDKGSDVGLK.N
295	309	2	1657.7	4.5	1	93.6	26.8	95.00%	K.SGQAYADDTDVETMR.H		K.SGQAYADDTDVETMR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
149	IMDH_SCHPO	17.75%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
169	187	3	2214.08	4.5	1	37	26	95.00%	R.DVQFHKDTNTPVTEVMTPR.E		R.DVQFHKDTNTPVTEVMTPR.E
2	15	2	1636.88	4	1	27	21.7	93.10%	M.SAFKPYTEALEVLK.K	Acetyl (+42)	-.MSAFKPYTEALEVLK.K
303	313	2	1155.67	4.5	0	51.3	19.6	95.00%	K.IDVIAGNVVTR.E		K.IDVIAGNVVTR.E
214	234	3	2311.28	3.6	1	29.3	16.8	95.00%	K.LPVVDKDDNLVALLSLTDLMK.N		K.LPVVDKDDNLVALLSLTDLMK.N
129	139	3	1179.63	1.3	0	29.1	23	95.00%	F.SPQHTVGDVLK.I		K.YENGFILDPVVFSPQHTVGDVLK.I
212	234	4	2496.4	3.3	1	24	15.4	95.00%	K.GKLPVVDKDDNLVALLSLTDLMK.N		K.GKLPVVDKDDNLVALLSLTDLMK.N
419	433	2	1421.67	3.9	0	52.2	26.3	95.00%	R.GMGSIAAMEGTGVNK.N		R.GMGSIAAMEGTGVNK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
150	KAPS_SCHPO	22.77%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
166	188	3	2567.24	-0.26	0	41	25.6	95.00%	Y.EAPISPEIVVSSHTQSIEECVEK.I	Carbamidomethyl (+57)	K.EFTGISAPYEAPISPEIVVSSHTQSIEECVEK.I
157	188	3	3532.7	3.1	1	32.4	22.1	95.00%	K.EFTGISAPYEAPISPEIVVSSHTQSIEECVEK.I	Carbamidomethyl (+57)	K.EFTGISAPYEAPISPEIVVSSHTQSIEECVEK.I
39	52	2	1664.86	3.8	1	65.6	24	95.00%	K.STIACALEQYLLQR.G	Carbamidomethyl (+57)	K.STIACALEQYLLQR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
151	TRXB_SCHPO	18.63%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
78	89	2	1323.7	5	1	25.2	22.3	90.20%	R.FGTEIITETVSK.L		R.FGTEIITETVSK.L
154	175	3	2201.13	-1.1	1	36.6	23.1	95.00%	R.NKPLAVVGGGDSAAEEAQFLTK.Y		R.NKPLAVVGGGDSAAEEAQFLTK.Y
99	124	3	2801.32	3.2	1	61.8	25.7	95.00%	K.YWLEGAEEEEPHTADSVILATGASAR.R		K.YWLEGAEEEEPHTADSVILATGASAR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
152	RL36A_SCHPO	24.24%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
83	96	2	1545.84	4.6	1	75.1	21.3	95.00%	K.GKIEELTSVIQSSR.L		K.GKIEELTSVIQSSR.L
85	96	2	1360.73	3.8	0	56.4	23.5	95.00%	K.IEELTSVIQSSR.L		K.IEELTSVIQSSR.L
2	11	2	966.59	4.6	0	38.2	15.1	95.00%	M.APGLVVGLNK.G		-.MAPGLVVGLNK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
153	LEU1_SCHPO	13.18%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
82	99	2	1998.98	4.3	1	62	25.3	95.00%	K.EIEVGFPSASQTDFAFVR.H		K.EIEVGFPSASQTDFAFVR.H
464	479	2	1742.82	4.9	1	69.1	26.4	95.00%	R.FSVNDYTLSSNGPQSK.C		R.FSVNDYTLSSNGPQSK.C
137	151	3	1761.87	4	1	33.2	25.6	95.00%	K.NATVHLYNACSPLFR.E	Carbamidomethyl (+57)	K.NATVHLYNACSPLFR.E

268	295	3	2788.37	3.6	2	73.8	24.5	95.00%	R.GTAVAAAELGQLAGGDRIEGCLFGNGER.T	Carbamidomethyl (+57)	R.GTAVAAAELGQLAGGDRIEGCLFGNGER.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
154	LYS4_SCHPO	7.91%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
405	418	2	1316.66	-0.7	0	56.5	24.4	95.00%	Y.VGAASSEVEAAAQK.N		K.VADGVEFYVGAASSEVEAAAQK.N
149	159	2	1179.57	4.4	1	26	25.1	91.50%	K.GQGIDFYPAGR.G		K.GQGIDFYPAGR.G
189	200	2	1184.64	1.7	0	34.5	21.6	95.00%	Y.GGVGCLGTPIVR.T	Carbamidomethyl (+57)	R.GIGHQIMVEQGYAMPGSMAVASDSHSNTYGGVGCLGTPIVR.T
470	489	2	1872.04	4.8	1	47.2	18.7	95.00%	R.EALAYLASPAVVAASAIAGK.I		R.EALAYLASPAVVAASAIAGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
155	P25_SCHPO	17.82%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
36	52	2	1976.06	4.7	1	48.2	21.4	95.00%	K.AVIYQFPETLSPEILEK.M		K.AVIYQFPETLSPEILEK.M
2	20	2	2064.09	-0.8	1	82.6	22	95.00%	M.STANTVAIVIYSTYGHVVK.L	Acetyl (+42)	-.MSTANTVAIVIYSTYGHVVK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
156	SYNC_SCHPO	6.16%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
223	235	2	1382.68	0.92	1	41.1	25.3	95.00%	Y.QILHAAPTGEEAF.T		K.SAPGNHELVVDYYQILHAAPTGEEAFTNR.L
447	465	3	2338.25	2.9	1	23.4	20.2	91.90%	K.MTDQINRPIFLTYFPLEIK.S		K.MTDQINRPIFLTYFPLEIK.S
223	238	3	1753.88	0.62	1	41.8	25	95.00%	Y.QILHAAPTGEEAFTNR.L		K.SAPGNHELVVDYYQILHAAPTGEEAFTNR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
157	TBB_SCHPO	16.52%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
104	121	3	1913.96	4.4	1	33.4	25.1	95.00%	K.GHYTEGAELADAVLDVVR.R		K.GHYTEGAELADAVLDVVR.R
123	154	3	3205.55	2.6	1	82.9	24.4	95.00%	R.EAEACDALQGFQLTHSLGGGTGSGMGTLLLSK.I	Carbamidomethyl (+57)	R.EAEACDALQGFQLTHSLGGGTGSGMGTLLLSK.I
163	174	2	1249.62	3.9	1	41.3	24.6	95.00%	R.MMATFSVAPAPK.S		R.MMATFSVAPAPK.S
295	306	2	1319.56	1.2	0	26.8	26.2	90.80%	F.DANNMMVAADPR.H	Oxidation (+16)	R.LHFFMVGFAPLAAIGSSSFQAVSVPELTQQMFDANNMMVAADPR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
158	RL30A_SCHPO	17.43%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
77	89	2	1276.61	-1.2	0	58.2	24.9	95.00%	Y.AGTNIDLGTACGK.L	Carbamidomethyl (+57)	K.ANVHHYAGTNIDLGTACGK.L
71	89	2	1997.95	6	1	62.5	26.5	95.00%	K.ANVHHYAGTNIDLGTACGK.L	Carbamidomethyl (+57)	K.ANVHHYAGTNIDLGTACGK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
159	RL27A_SCHPO	32.35%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
23	34	2	1269.74	4.4	0	65.4	18	95.00%	K.VVILQAIDQGSK.S		K.VVILQAIDQGSK.S
35	48	3	1461.76	5.9	1	42.8	23.5	95.00%	K.SHPFGHAVVAGVER.Y		K.SHPFGHAVVAGVER.Y
35	52	4	1963.05	4.3	2	23.2	21.1	95.00%	K.SHPFGHAVVAGVERYPLK.V		K.SHPFGHAVVAGVERYPLK.V
94	107	2	1575.83	3.5	1	46.7	23.7	95.00%	K.GLITADTFKEPTQR.S		K.GLITADTFKEPTQR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
160	SPEE_SCHPO	18.79%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
185	193	2	1061.59	1.5	1	26.7	22	92.70%	Y.FQLLSDALR.G		K.FLQDYQNTFDVIITDSSDPDGPAEALFQKPYFQLLSDALR.G

105	126	3	2641.27	3.1	1	46.8	25.6	95.00%	R.EVVKHECVEEAILCDIDEDVIK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.EVVKHECVEEAILCDIDEDVIK.V
2	12	2	1291.72	4.1	0	43.5	20	95.00%	M.SVQELSHPLIK.D	Acetyl (+42)	-.MSVQELSHPLIK.D
18	31	2	1631.79	4.6	1	31.2	25.2	95.00%	R.EINNMWPGQAMTLK.V		R.EINNMWPGQAMTLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
161	SYYC_SCHPO	10.22%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
368	395	3	2695.3	1.2	2	53.7	24.9	95.00%	K.KAGTTNASIAAESGAAPATESQTAESFK.K		K.KAGTTNASIAAESGAAPATESQTAESFK.K
2	14	2	1605.82	-2.4	2	49.4	24.1	95.00%	M.SLTPDEKYELITR.N	Acetyl (+42)	-.MSLTPDEKYELITR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
162	UBA1_SCHPO	4.45%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
82	92	2	1260.64	0.77	1	26.1	24	91.80%	Y.FLTEDDIGVPR.A		R.IEDLSSQYFLTEDDIGVPR.A
566	588	3	2468.18	-1.4	1	39	26.4	95.00%	K.GNTQVVVPHLTESYGSSQDPPEK.S		K.GNTQVVVPHLTESYGSSQDPPEK.S
361	371	2	1083.63	0.63	0	32.3	20	95.00%	F.LGGAVAQEVLK.A		R.GDLVAMSAFLGGAVAQEVLK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
163	RL19A_SCHPO	21.24%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
118	128	3	1386.74	5	1	32.3	22.9	95.00%	K.HLYHTLYLEAK.G		K.HLYHTLYLEAK.G
182	193	2	1422.69	3.6	1	31.8	25.9	95.00%	R.EQLYTAAEKIEE.-		R.EQLYTAAEKIEE.-
21	38	3	2088.99	-1.2	2	29.6	26.6	95.00%	R.KVWMDPNEISEISNANSR.Q		R.KVWMDPNEISEISNANSR.Q
22	38	2	1960.89	-1.2	1	79.5	26.9	95.00%	K.VWMDPNEISEISNANSR.Q		K.VWMDPNEISEISNANSR.Q
182	193	2	1422.69	3.6	1	31.8	25.9	95.00%	R.EQIYTAAEKIEE.-		R.EQLYTAAEKIEE.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
164	PDI1_SCHPO	8.33%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
398	412	2	1637.79	4.8	1	66.2	26.4	95.00%	K.LAEEYSDDSNVVVAK.I		K.LAEEYSDDSNVVVAK.I
125	136	3	1350.87	5.1	1	30.4	6.99	95.00%	R.KQLLPTVKPISK.D		R.KQLLPTVKPISK.D
188	201	2	1436.77	4.3	1	45.1	21.9	95.00%	K.SLGSNFPGIVAFTK.D		K.SLGSNFPGIVAFTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
165	RS8A_SCHPO	28.50%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
60	74	2	1568.72	4.4	1	94.1	26	95.00%	R.LDSGNFSWGSEGVSK.K		R.LDSGNFSWGSEGVSK.K
165	178	2	1475.79	4.1	1	33.2	22.9	95.00%	R.LYAVVSSRPGQSGR.C		R.LYAVVSSRPGQSGR.C
152	164	2	1363.68	4.8	1	51.3	24.8	95.00%	K.VDSALETQFAAGR.L		K.VDSALETQFAAGR.L
78	92	2	1751.94	4.6	1	25.6	21.1	90.90%	R.IIQVAYHPSNNELVR.T		R.IIQVAYHPSNNELVR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
166	RL7C_SCHPO	8.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
169	183	2	1497.85	4.8	0	75.4	18.6	95.00%	R.IALSDNAIIEAALGK.Y		R.IALSDNAIIEAALGK.Y
110	115	2	772.46	1	0	29.6	18.4	95.00%	K.IMQLLR.L		K.IMQLLR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
167	RL18B_SCHPO	18.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	65	3	1111.64	5.1	0	26.6	16.7	95.00%	K.TNRPPISISK.I		K.TNRPPISISK.I
132	142	2	1127.63	4.1	0	42.3	21	95.00%	R.APTGSNTVLLR.G		R.APTGSNTVLLR.G
118	131	2	1454.81	-1.2	0	54.4	20.6	95.00%	K.AGGEVLTLDQLALR.A		K.AGGEVLTLDQLALR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
168	RS11_SCHPO	17.76%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	64	2	1161.6	4.7	1	33.4	23.9	95.00%	K.CPFVGQVSIR.G	Carbamidomethyl (+57)	K.CPFVGQVSIR.G
114	130	2	1870.97	4.9	0	41.5	23.5	95.00%	R.INEGDVVTVGQCRPLSK.T	Carbamidomethyl (+57)	R.INEGDVVTVGQCRPLSK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
169	FUMH_SCHPO	11.83%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
131	142	2	1157.67	3.6	0	43.3	20.5	95.00%	R.AIEILGGTLGSK.K		R.AIEILGGTLGSK.K
392	417	3	2921.34	2.7	1	27.9	26.5	95.00%	R.LLGDACESFTDHCVVGIEPNYEGIAR.H	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.LLGDACESFTDHCVVGIEPNYEGIAR.H
112	130	2	2006.91	0.95	0	52.6	27.3	95.00%	F.QTGSGTQSNMNSNEVIANR.A		R.LDDNFPLVVFQTGSGTQSNMNSNEVIANR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
170	YCO6_SCHPO	10.69%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
37	56	2	2127	-0.81	0	112	27	95.00%	K.APQVNTIDEGDENLEAIDGK.L		K.APQVNTIDEGDENLEAIDGK.L
15	36	3	2140	-1.5	1	31.1	27	95.00%	K.MSAAPTPHNTPSGTSAPNFGAK.A		K.MSAAPTPHNTPSGTSAPNFGAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
171	CAP_SCHPO	4.54%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
499	509	2	1122.58	5.1	0	31.4	24	95.00%	K.SSLSSEVVTSK.S		K.SSLSSEVVTSK.S
339	352	2	1443.77	1.4	1	39.8	23.6	95.00%	F.AEINKGEGITSGLR.K		K.GDMGAVFAEINKGEGITSGLR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
172	RL3A_SCHPO	11.08%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
249	262	2	1607.76	-2.4	1	28.5	25.7	94.10%	K.VACIGAWHPANVQW.T	Carbamidomethyl (+57)	K.VACIGAWHPANVQWTVAR.A
207	222	2	1837.9	4.3	1	73.9	26	95.00%	K.STFEQNEMIDVIGVTR.G		K.STFEQNEMIDVIGVTR.G
11	19	2	982.54	4.3	1	27.2	19	93.40%	R.HGSLGFLPR.K		R.HGSLGFLPR.K
249	266	3	2035.03	4.4	1	29.3	24.6	95.00%	K.VACIGAWHPANVQWTVAR.A	Carbamidomethyl (+57)	K.VACIGAWHPANVQWTVAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
173	YFHH_SCHPO	5.21%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
504	529	4	3037.42	4.5	1	22.9	25.6	95.00%	K.EEERPLPSEPSQNQPAEYRDTPDTPR.N		K.EEERPLPSEPSQNQPAEYRDTPDTPR.N
307	340	4	3584.77	4.2	2	20.1	21.8	94.80%	R.VAKDDDPFVVSNTANSDEPASSSKPAKPLTDLNR.A		R.VAKDDDPFVVSNTANSDEPASSSKPAKPLTDLNR.A
711	734	3	2663.2	-1.3	1	40.2	27	95.00%	R.ISEVTEDSIDEDKQNEVDPSTSAR.A		R.ISEVTEDSIDEDKQNEVDPSTSAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
174	TCTP_SCHPO	18.45%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
6	21	2	1737.84	4.2	1	86.5	26.3	95.00%	K.DVISGDELVSDAYDLK.E		K.DVISGDELVSDAYDLK.E
5	18	2	1509.72	0.39	2	42.9	26.6	95.00%	Y.KDVISGDELVSDAY.D		-.MLLYKDVISGDELVSDAYDLK.E
99	112	2	1670.86	-0.5	2	38.7	23.4	95.00%	R.LQESNPERVPVFEK.N		R.LQESNPERVPVFEK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
175	FKBP_SCHPO	13.39%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
44	58	2	1602.86	4.3	1	59	22.9	95.00%	R.GSPFVCTIGVGQLIR.G	Carbamidomethyl (+57)	R.GSPFVCTIGVGQLIR.G
48	58	2	1214.68	-1.7	0	59.5	21.2	95.00%	F.VCTIGVGQLIR.G	Carbamidomethyl (+57)	R.GSPFVCTIGVGQLIR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
176	YDMC_SCHPO	11.66%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
370	385	2	1877	4	1	39.4	21.8	95.00%	K.LTSLMESIFPEQTIIR.S		K.LTSLMESIFPEQTIIR.S
109	122	2	1458.75	1	1	73.3	24.3	95.00%	Y.SANPVNVEGQIGFK.I		K.SHDELTLHHCHYSANPVNVEGQIGFK.I
488	513	3	3117.34	3.1	1	64.3	27	95.00%	K.VEPEPIDEEEAFSDDEEEEPEEIKER.I		K.VEPEPIDEEEAFSDDEEEEPEEIKER.I
82	91	2	1136.53	5	1	33.4	25.4	95.00%	R.NADNSVTNFR.D		R.NADNSVTNFR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
177	ACBP_SCHPO	34.48%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
33	50	3	1912	4.1	0	25.6	22.8	94.70%	K.QATVGDNNTEKPGLLDLK.G		K.QATVGDNNTEKPGLLDLK.G
2	13	2	1294.61	4.4	1	38.3	25.5	95.00%	M.SSTFEQAAADVK.E	Acetyl (+42)	-.MSSTFEQAAADVK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
178	RS13_SCHPO	23.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
10	20	2	1132.63	4.4	1	38.6	21.9	95.00%	K.GIASSALPYVR.S		K.GIASSALPYVR.S
44	55	2	1244.66	3.8	0	40.8	23	95.00%	K.GMSPSQIGVTLR.D		K.GMSPSQIGVTLR.D
28	39	2	1286.68	5	0	56.1	23	95.00%	K.ADADSVVEQILK.F		K.ADADSVVEQILK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
179	RL6_SCHPO	22.05%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
70	87	2	1959.1	3.1	1	33.6	16.6	95.00%	R.VVVLSQLEDTLVVTGPYK.V		R.VVVLSQLEDTLVVTGPYK.V
50	64	2	1497.84	5	0	33.1	19.4	95.00%	R.ASLAPGTVCILLAGR.F	Carbamidomethyl (+57)	R.ASLAPGTVCILLAGR.F
109	118	2	1031.56	5.5	0	31.2	23.6	95.00%	K.IDVSGVSVEK.F		K.IDVSGVSVEK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
180	PUR7_SCHPO	13.71%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
159	174	3	1746.79	5.6	0	25.2	26.9	91.80%	K.AAEGHDENIHPDEVSK.I		K.AAEGHDENIHPDEVSK.I
258	282	3	2764.43	3.8	1	38.4	21	95.00%	R.NWLTANNLANKPNVSLPEDVVEATR.R		R.NWLTANNLANKPNVSLPEDVVEATR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
181	RL23_SCHPO	28.06%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
15	34	2	2090	3.5	0	65.5	25.9	95.00%	R.MTLGLPVQAIMNCADNSGAK.N	Carbamidomethyl (+57)	R.MTLGLPVQAIMNCADNSGAK.N
48	66	3	2043.11	4.2	1	47.8	20.5	95.00%	R.LNRLPAASCGDMVLATVKK.G	Carbamidomethyl (+57)	R.LNRLPAASCGDMVLATVKK.G
51	65	2	1531.78	3.4	0	55.2	24.6	95.00%	R.LPAASCGDMVLATVK.K	Carbamidomethyl (+57)	R.LPAASCGDMVLATVK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
182	MPG1_SCHPO	11.02%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
270	287	2	1776	4.2	0	35.2	18.4	95.00%	K.IGPNVVIGPNVTIGDGVR.L		K.IGPNVVIGPNVTIGDGVR.L
138	159	4	2530.28	3.4	2	22.1	23.2	95.00%	K.VEEPSKYGVVVHYPNSESLIER.F		K.VEEPSKYGVVVHYPNSESLIER.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
183	RL14_SCHPO	11.94%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
103	110	2	993.46	6	1	29.1	24.7	95.00%	R.SQLNDFDR.F		R.SQLNDFDR.F
87	94	2	905.44	5.7	1	30.4	23.9	95.00%	K.WASSAWAK.K		K.WASSAWAK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
184	RS15A_SCHPO	20.92%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
90	108	2	2033.08	3.1	1	80.9	21.7	95.00%	R.NMIILPEMVGSVVGIYNGK.L		R.NMIILPEMVGSVVGIYNGK.L
73	85	2	1396.76	4.6	0	40.4	20.4	95.00%	K.TEAPLNEKPATVK.T		K.TEAPLNEKPATVK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
185	SYH_SCHPO	7.25%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
24	38	3	1603.81	4.1	1	23.8	24.1	92.60%	K.SQGASKEDIDKEVAK.L		K.SQGASKEDIDKEVAK.L
364	387	3	2316.06	2.7	1	56.7	26.7	95.00%	K.SADPEADRSNDDSIGVGSIAAGGR.Y		K.SADPEADRSNDDSIGVGSIAAGGR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
186	SODM_SCHPO	20.18%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
34	48	2	1649.83	0.048	1	30.2	24.6	95.00%	Y.AYNALEPALSETIMK.L		K.ATLPPLPYAYNALEPALSETIMK.L
162	173	2	1303.7	4.2	0	48.8	23.1	95.00%	R.ITTTANQDTIVK.S		R.ITTTANQDTIVK.S
26	48	2	2502.32	2.9	1	32.8	21.7	95.00%	K.ATLPPLPYAYNALEPALSETIMK.L		K.ATLPPLPYAYNALEPALSETIMK.L
127	135	2	1108.52	5	1	34	24.8	95.00%	K.WGSLEDFQK.E		K.WGSLEDFQK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
187	RL33B_SCHPO	24.07%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
33	45	2	1574.65	-1.6	2	27.8	26.3	92.30%	K.IEGCDSKEEAQFY.L	Carbamidomethyl (+57)	K.IEGCDSKEEAQFYLGK.R
20	32	4	1401.82	4.5	1	28.1	16.4	95.00%	R.SKHVIHPGTSIVK.I		R.SKHVIHPGTSIVK.I
33	44	2	1411.59	-0.92	2	33.8	26.2	95.00%	K.IEGCDSKEEAQF.Y	Carbamidomethyl (+57)	K.IEGCDSKEEAQFYLGK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
188	RL11_SCHPO	14.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
154	164	2	1349.67	4.1	1	39.8	24.3	95.00%	K.INAEDTINWFK.Q		K.INAEDTINWFK.Q
36	49	2	1531.83	4.2	1	63.5	21.9	95.00%	K.VLEQLSGQTPVFSK.A		K.VLEQLSGQTPVFSK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
189	PNPP_SCHPO	18.12%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
145	166	3	2359.15	3.2	1	61.7	25.7	95.00%	K.IGPDPSVGAVLCGMDMHVTYLK.Y	Carbamidomethyl (+57)	K.IGPDPSVGAVLCGMDMHVTYLK.Y
196	213	2	1882	-0.65	1	57.4	21.7	95.00%	K.FLPGSGAISYPLIFSTGR.Q		K.FLPGSGAISYPLIFSTGR.Q
182	195	2	1535.75	-1.3	1	52.8	25.5	95.00%	F.LLTNQDSTFPTNGK.F	Deamidation (+1)	K.YCMAFQYLQDPNCAFLLTNQDSTFPTNGK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
190	RS28_SCHPO	36.76%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
47	62	3	1838.98	4.7	1	27.2	21.1	95.00%	K.GPVREDDILVLLESER.E		K.GPVREDDILVLLESER.E
1	9	2	1031.54	3.7	1	25.7	23.6	91.10%	-.MDSSKVPVK.L	Acetyl (+42)	-.MDSSKVPVK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
191	PUR4_SCHPO	3.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
298	334	4	3616.77	4.4	1	38.1	21.7	95.00%	K.VETHNHPTAVSPFPGAATGSGGEIRDEGAVGQGSLSK.A		K.VETHNHPTAVSPFPGAATGSGGEIRDEGAVGQGSLSK.A
412	425	3	1426.76	5.3	1	35.9	22.9	95.00%	R.GYHKPIMAAGGIGR.I		R.GYHKPIMAAGGIGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
192	PPID_SCHPO	13.48%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

64	72	2	1023.48	-1.3	1	26.7	25.3	92.10%	F.MLQGGDFTR.G			K.NFMLQGGDFTR.G
214	226	2	1432.74	4.4	1	72	24.1	95.00%	K.QFAQQNLDTAVAK.W			K.QFAQQNLDTAVAK.W
144	169	3	2959.42	-0.045	1	35.9	25.6	95.00%	R.TIENLETKNDDPVVPVVIEECGTCTK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)		R.TIENLETKNDDPVVPVVIEECGTCTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
193	YLF4_SCHPO	9.56%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
115	133	2	2193.13	3	1	72.8	23.3	95.00%	K.AFSPIETQSIVEQLDEFLK.S		K.AFSPIETQSIVEQLDEFLK.S
292	315	4	2593.24	3.1	2	34.2	25.8	95.00%	K.AVKHPNADSLYVSTIHCGDAEGPR.T	Carbamidomethyl (+57)	K.AVKHPNADSLYVSTIHCGDAEGPR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
194	Q9P7B4_SCHPO	20.08%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
234	256	3	2522.27	2.7	1	34.8	23.7	95.00%	R.ENVVIADTLVFPSHQGGANHVYR.K		R.ENVVIADTLVFPSHQGGANHVYR.K
233	256	4	2678.38	4.3	2	40.7	21.6	95.00%	R.RENVVIADTLVFPSHQGGANHVYR.K		R.RENVVIADTLVFPSHQGGANHVYR.K
183	199	2	1918.98	6.8	1	60.8	23.8	95.00%	R.IMEVDPGLVETEFSVVR.F		R.IMEVDPGLVETEFSVVR.F
163	173	2	1163.64	5.6	1	26.5	21.7	92.40%	K.SALAQFTSALR.K		K.SALAQFTSALR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
195	YBS7_SCHPO	17.72%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
442	471	4	3134.5	-0.033	1	26.4	24.5	95.00%	K.EQPPNKAEPAVPTEASSTKPSEAAEESTPR.F		K.EQPPNKAEPAVPTEASSTKPSEAAEESTPR.F
353	386	4	3399.65	2.3	1	59.5	23.6	95.00%	K.HTGPSLSSASQPSAASSSSSSEPSNLDKINDVKK.N		K.HTGPSLSSASQPSAASSSSSSEPSNLDKINDVKK.N
128	146	2	1760.86	5.1	0	31.6	25	95.00%	R.TSGSSTGLSNAPPSANVSK.A		R.TSGSSTGLSNAPPSANVSK.A
164	189	3	2841.41	3.2	0	29.4	23.9	95.00%	R.ATPEVCVPLNPDTGSVPLIHPEQTDR.G	Carbamidomethyl (+57)	R.ATPEVCVPLNPDTGSVPLIHPEQTDR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
196	PGM_SCHPO	9.03%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	21	3	2330.21	3.2	1	23.9	22.6	92.70%	-.MIETIPTKPYEGQRPGTSGLR.K		-.MIETIPTKPYEGQRPGTSGLR.K
423	435	2	1529.66	4.3	1	62.5	26.5	95.00%	R.YDYEELENEAAGK.V		R.YDYEELENEAAGK.V
127	142	2	1631.79	4.4	1	81.8	25.2	95.00%	K.YNLGNGGPAPESVTEK.I		K.YNLGNGGPAPESVTEK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
197	RS10B_SCHPO	34.01%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
10	24	3	1621.94	4.8	1	31.6	16.6	95.00%	K.AIHQALFQQGVLVAK.K		K.AIHQALFQQGVLVAK.K
26	31	2	732.38	5.5	1	30.1	22.6	95.00%	K.DFNLPK.H		K.DFNLPK.H
32	44	3	1428.82	4.9	0	23.6	19.8	92.30%	K.HPEVGVPNLQVIK.A		K.HPEVGVPNLQVIK.A
78	93	4	1859.01	4	1	23	19.4	95.00%	R.EYLHLPAEVVPATHKR.Q		R.EYLHLPAEVVPATHKR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
198	ATPB_SCHPO	7.43%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
160	185	3	2859.38	0.39	1	40.6	25.3	95.00%	K.YSPIHADAPSFEEQSTTPEILETGIK.V		K.YSPIHADAPSFEEQSTTPEILETGIK.V
210	222	2	1501.85	-0.74	1	46.5	18.7	95.00%	K.TVFIQELINNIAK.A		K.TVFIQELINNIAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
199	DPNP_SCHPO	16.43%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

224	243	3	2206.97	4.4	1	57.3	27.7	95.00%	K.FCEGVEAGHSMQGTQEEIAK.Y	Carbamidomethyl (+57)	K.FCEGVEAGHSMQGTQEEIAK.Y
334	350	3	1840.98	4.8	2	23.8	21.8	92.60%	K.VIEATAAVTSKDPHFQK.V		K.VIEATAAVTSKDPHFQK.V
200	220	4	2473.24	1.3	1	17.9	24.4	90.10%	Y.SLHNEKLEPVQVHMQDVQNTK.D		R.NHGCFQYSLHNEKLEPVQVHMQDVQNTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
200	RPE_SCHPO	17.54%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
6	20	2	1557.84	-0.66	1	46.3	22.7	95.00%	K.IAPSLLAGDFANLEK.E		K.IAPSLLAGDFANLEK.E
202	214	2	1421.73	1.3	0	25.9	25.2	91.10%	F.HAQSPEEVISGLR.N		K.TVDAAADAGANVIVAGTAVFHAQSPEEVISGLR.N
123	134	2	1369.79	-0.6	1	31.4	19.5	95.00%	K.TPVEVILPFVEK.L		K.TPVEVILPFVEK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
201	RL21A_SCHPO	14.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
138	160	3	2554.23	-0.27	1	37.1	25.1	95.00%	K.AHFVSTENNEPVTLHPVAYDTTI.-		K.AHFVSTENNEPVTLHPVAYDTTI.-
141	156	2	1768.87	1.1	1	26.5	26	90.70%	F.VSTENNEPVTLHPVAY.D		K.AHFVSTENNEPVTLHPVAYDTTI.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
202	FIMB_SCHPO	4.89%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
508	524	2	1796.81	3.5	1	38.6	27.1	95.00%	K.TLSDSDMVAWANSMAAK.G		K.TLSDSDMVAWANSMAAK.G
158	170	2	1485.74	3.7	0	44.6	25.3	95.00%	K.LINDSVPDTIDER.V		K.LINDSVPDTIDER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
203	SEC31_SCHPO	2.70%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
985	1000	2	1627.82	1.3	1	68.1	24.6	95.00%	Y.TPIAVASSTVNPAHTY.K		R.ISSSPNMPPSNPYTPIAVASSTVNPAHTYKPHGGSQIVPPPK.Q
404	420	2	1859.86	-1.3	0	59.5	27.3	95.00%	K.EVTITSAPDEVEQDEAK.S		K.EVTITSAPDEVEQDEAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
204	YEI3_SCHPO	8.67%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
329	342	2	1482.75	2.8	1	41.2	24.8	95.00%	K.APQAAGVIHTDFEK.A		K.APQAAGVIHTDFEK.A
43	62	2	2148.03	-2	1	63.5	25.8	95.00%	K.SVLGNPANYPYATIDPEEAK.V		K.SVLGNPANYPYATIDPEEAK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
205	CARA_SCHPO	6.99%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
347	358	2	1286.65	1.5	1	39.8	24.1	95.00%	Y.AVDASTLPAEWK.A		R.GHNIPALDIASGNCHITSQNHGYAVDASTLPAEWK.A
74	90	2	1842.89	0.32	1	73.5	26.7	95.00%	F.TTSPVGYVESLTDPSYK.Q		R.NVSGEAVFTTSPVGYVESLTDPSYK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
206	CH10_SCHPO	22.12%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	84	2	1230.7	4	1	31.7	20.5	95.00%	R.VLLPAYGGSNIK.V		R.VLLPAYGGSNIK.V
62	72	2	1111.6	4.5	0	30.9	19.8	95.00%	K.LAQPSVAVGDR.V		K.LAQPSVAVGDR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
207	DLDH_SCHPO	6.07%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
203	219	3	1743.02	4.9	1	25.6	13.4	94.70%	K.KIVSSTGALSLSEVPKK.M		K.KIVSSTGALSLSEVPKK.M

155	168	2	1448.76	3.8	1	31.8	23.7	95.00%	K.GTGSFIDPQTLSVK.G		K.GTGSFIDPQTLSVK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
208	CAN_SCHPO	18.44%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
84	101	3	2033.14	2.7	1	42.8	18.1	95.00%	R.VPETTILNLLPGEVFVHR.N		R.VPETTILNLLPGEVFVHR.N
9	34	4	2766.34	3.9	1	21.8	25.1	95.00%	R.IEEIDHQDEIIDREASTASPVSGAGK.I		R.IEEIDHQDEIIDREASTASPVSGAGK.I
8	34	4	2922.44	2.7	1	21.1	23.5	95.00%	R.RIEEIDHQDEIIDREASTASPVSGAGK.I		R.RIEEIDHQDEIIDREASTASPVSGAGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
209	O13797_SCHPO	23.66%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
16	43	3	3097.48	-0.4	2	39.9	25.1	95.00%	K.QAITTGSISEEEKESLEVAAQCIQDSFK.I	Carbamidomethyl (+57)	K.QAITTGSISEEEKESLEVAAQCIQDSFK.I
197	214	2	1831.84	5.2	0	74	26.7	95.00%	K.QLNQPSDSSATSGADQAR.T		K.QLNQPSDSSATSGADQAR.T
124	152	4	3210.53	3.2	1	60.9	24.3	95.00%	R.AAAYNQLGQFENAVEDALTCLSLDPHHAR.A	Carbamidomethyl (+57)	R.AAAYNQLGQFENAVEDALTCLSLDPHHAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
210	LYS1_SCHPO	13.86%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
274	306	3	3758.77	3.3	1	76.7	23.8	95.00%	R.VVCDVSCDTTNPNNPIPIYNVNTTFDHPTVEVK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VVCDVSCDTTNPNNPIPIYNVNTTFDHPTVEVK.G
329	346	2	1904.02	3.7	1	28.9	21.2	95.00%	R.ESSEAFSEALIPSLLALK.D		R.ESSEAFSEALIPSLLALK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
211	GPD2_SCHPO	15.01%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
170	186	2	1731.85	1.4	0	60.7	25.3	95.00%	Y.CGVLSGANIASEVAQEK.F	Carbamidomethyl (+57)	R.LFSDIIEENTGMYCGVLSGANIASEVAQEK.F
67	88	4	2626.25	3.3	2	19.3	25.5	92.40%	K.IQHEGKECNLTEVFNTTHENVK.Y	Carbamidomethyl (+57)	K.IQHEGKECNLTEVFNTTHENVK.Y
311	327	3	1907.98	3	0	33.8	23.9	95.00%	K.TGKPMHVVEQELLDGQK.L		K.TGKPMHVVEQELLDGQK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
212	TPM_SCHPO	21.74%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
69	86	3	2087.06	4.7	1	48.9	24	95.00%	R.LKADNEDIQKTEAEQLSR.K		R.LKADNEDIQKTEAEQLSR.K
49	65	3	1948.91	-1.3	1	42.3	26.4	95.00%	R.KSEAAESQLEELEEETK.Q		R.KSEAAESQLEELEEETK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
213	PUR2_SCHPO	4.44%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
31	48	2	1678.78	1.8	1	54.6	26.3	95.00%	K.VYVAPGNGGTASNGAESK.M	Deamidation (+1)	K.VYVAPGNGGTASNGAESK.M
581	597	3	1742.76	0.056	1	55.9	27	95.00%	Y.HDGHYDANGTSVGAVSR.D	Deamidation (+1)	K.QAGCALVGGETSEMPGLYHDGHYDANGTSVGAVSR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
214	SUB2_SCHPO	10.14%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	96	3	3526.72	3.8	1	60.2	22.5	95.00%	R.AITDSGFEHPSEVQQVCIPQSILGTDVLCQAK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.AITDSGFEHPSEVQQVCIPQSILGTDVLCQAK.S
399	410	2	1336.6	-0.83	0	50	26	95.00%	F.SSSEEDSQILDK.I		K.GLAITFSSSEEDSQILDK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
215	RL25A_SCHPO	19.86%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

125	137	2	1329.66	4	0	94.2	25.3	95.00%	K.LSADADALDVANR.I		K.LSADADALDVANR.I
74	88	4	1806.97	3	2	20.6	22	95.00%	K.KIEDDNTLVFHVHLK.A		K.KIEDDNTLVFHVHLK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
216	RLA0_SCHPO	15.06%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
133	144	2	1308.71	5.2	1	29.1	21.1	95.00%	K.TSFFQALGIPTK.I		K.TSFFQALGIPTK.I
98	132	3	3513.88	2.7	1	45.6	16.2	95.00%	R.ETIIANVIAAPARPNAIAPLDVFVP AGNTGMEPGK.T		R.ETIIANVIAAPARPNAIAPLDVFVP AGNTGMEPGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
217	RS3_SCHPO	10.04%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
30	42	2	1513.64	4.2	1	70.9	26.5	95.00%	R.ELSEEGYSGCEVR.V	Carbamidomethyl (+57)	R.ELSEEGYSGCEVR.V
97	108	2	1362.64	3.8	0	61	25.1	95.00%	R.GLCAVAQCESLR.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GLCAVAQCESLR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
218	YB64_SCHPO	6.51%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
231	241	2	1124.54	2.2	1	27.8	25.4	93.70%	Y.FGGDVDTSTVK.V		K.SGGPVVEQATHFCDLSIYFGGDV DTSTVK.V
49	62	2	1567.85	-2.7	0	28.9	20.8	95.00%	R.VTALINPLINESER.V		R.VTALINPLINESER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
219	Q9URK9_SCHPO	23.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	66	3	1455.8	4.9	1	38.8	21.2	95.00%	R.ELLTLDEKDPKR.L		R.ELLTLDEKDPKRLFEGNAIIR.R
152	168	3	1785.9	4.3	1	38.7	24.4	95.00%	K.HIDFALSSPYGGGRPGR.C		K.HIDFALSSPYGGGRPGRCKRK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
220	6PGL_SCHPO	8.95%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
46	55	2	1083.61	5.4	0	52.4	19.8	95.00%	K.VLAEGLAQQR.G		K.VLAEGLAQQR.G
209	221	2	1488.81	4	1	42.1	21.6	95.00%	K.DILPIVIEDFTSK.L		K.DILPIVIEDFTSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
221	YET4_SCHPO	13.60%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
190	216	3	2686.32	5.5	0	58	23.9	95.00%	R.NDEQLGNSPASITSKPATTSAAQ PSSK.V		R.NDEQLGNSPASITSKPATTSAAQ PSSK.V
419	462	4	4557.19	2.7	1	18.1	20	90.70%	K.NEVNVPSTIPTESENPVAVGGTT AEHPVQEAVTAPTETAHDFSK.E		K.NEVNVPSTIPTESENPVAVGGTT AEHPVQEAVTAPTETAHDFSK.E
487	503	3	1712.87	4.4	0	27.8	24.6	95.00%	R.KPSSTGQEPTTPSTPAK.S		R.KPSSTGQEPTTPSTPAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
222	RL24A_SCHPO	20.81%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	12	2	1357.64	4.1	2	34.6	26	95.00%	-.MKVEVCSFSGSK.V	Carbamidomethyl (+57)	-.MKVEVCSFSGSK.V
81	91	2	1097.65	4.7	0	29.4	18.3	95.00%	R.GIVGANLDVIK.E		R.GIVGANLDVIK.E
36	43	2	978.52	4.9	1	29.5	24.4	95.00%	K.SESLFLQR.K		K.SESLFLQR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
223	RL7B_SCHPO	16.40%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	21	2	2002.11	4.4	1	37	18.8	95.00%	M.VASSTVPSVASIFAPESLLK.K		-.MVASSTVPSVASIFAPESLLK.K
109	114	2	772.46	1	0	29.6	18.4	95.00%	K.IMQLLR.L		K.IMQLLR.L
168	182	2	1523.86	4.4	0	56.2	16.5	95.00%	R.IPLSDNAIIEAALGK.Y		R.IPLSDNAIIEAALGK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
224	MUG64_SCHPO	11.19%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
224	238	3	1767.86	4.9	0	44.3	26.4	95.00%	K.LDVESAKPENLEHCK.S	Carbamidomethyl (+57)	K.LDVESAKPENLEHCK.S
108	125	2	1851.02	3.8	0	41.3	19.5	95.00%	R.NLGNLTPLEQTPLASVGK.N		R.NLGNLTPLEQTPLASVGK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
225	RS24A_SCHPO	20.15%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
21	32	3	1363.77	4	1	39.5	19.4	95.00%	R.KQMVVDILHPGK.A		R.KQMVVDILHPGK.A
69	83	2	1672.81	4.3	1	28.6	26.2	93.60%	R.TTGFALIYDDVEAMK.K		R.TTGFALIYDDVEAMK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
226	GUAA_SCHPO	8.91%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	130	2	1549.73	-1.6	1	43.7	26.3	95.00%	R.EYGPATVSMEPEIK.T		R.EYGPATVSMEPEIK.T
170	203	4	3715.11	3.7	1	22.3	19.8	95.00%	K.NSPFAVIAHVTKPIIGLQFHPEVTHTPLGLQLIK.N		K.NSPFAVIAHVTKPIIGLQFHPEVTHTPLGLQLIK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
227	ACAC_SCHPO	1.05%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
197	207	2	1131.63	6.1	0	34.7	20.8	95.00%	K.ISSTIVAQSAR.V		K.ISSTIVAQSAR.V
899	911	2	1475.7	-0.72	0	48.4	25.5	95.00%	Y.CDGQNLATTQQLK.V	Carbamidomethyl (+57)	K.QLEVAIQTYCDGQNLATTQQLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
228	TBA1_SCHPO	9.23%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	79	2	1758.92	3.8	1	35	23.6	95.00%	R.SIYVDLEPNVIDQVR.T		K.FVPRSIYVDLEPNVIDQVR.T
281	299	2	2298.99	1	1	32.4	27.6	95.00%	K.AFHESNSVQEITNQCFEPY.N	Carbamidomethyl (+57)	R.IHFPLVTYSPIVSAAKAFHESNSVQEITNQCFEPYNQMVK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
229	AROF_SCHPO	10.05%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
252	265	2	1338.61	4.9	1	41	26	95.00%	K.SGTNFDADSVAGAK.A		K.SGTNFDADSVAGAK.A
266	288	4	2617.24	3.5	1	24.8	25.9	95.00%	K.AKLEECNKLPSIMIDCSHGNSSK.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.AKLEECNKLPSIMIDCSHGNSSK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
230	AROC_SCHPO	11.14%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
328	340	2	1331.68	5.2	0	55.6	24.3	95.00%	K.SPATIGVEQSTSR.Y		K.SPATIGVEQSTSR.Y
161	191	3	3385.69	2.7	1	61.9	21.1	95.00%	K.IAIPLHETASSAILDPEDDTFESPITAEYLK.F		K.IAIPLHETASSAILDPEDDTFESPITAEYLK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
231	HIS1_SCHPO	9.03%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	10	2	1282.6	4.8	0	34.4	26.1	95.00%	-.MDLVNHLEDR.L	Acetyl (+42)	-.MDLVNHLEDR.L
211	228	2	2047.02	-2.1	0	48.4	25.1	95.00%	R.SSNCSSELEPLLQTIITR.I	Carbamidomethyl (+57)	R.SSNCSSELEPLLQTIITR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
232	WOS2_SCHPO	23.66%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

155	186	3	3261.4	0.94	1	79.2	26.3	95.00%	F.GNLGGAGAGEDASDSEPELEEEEEVGSNEKKE.-		R.WVDEDEQEAQPEVSPFGAGGMPDLSALGGMGGMDFSQFGNLGGAGAGEDASDSEPELEEEEEVGSNEKKE.-
28	39	2	1279.74	0.14	0	33.9	16.1	95.00%	Y.LTVLIPDAVDPK.I		K.NVIYLTVLIPDAVDPK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
233	ERF3_SCHPO	2.72%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
534	551	3	1939.96	5.4	2	34.4	25.4	95.00%	R.VRGDDSDVQTGYVLTSTK.N		R.VRGDDSDVQTGYVLTSTK.N
534	545	2	1310.57	-0.61	2	26.5	26	90.90%	R.VRGDDSDVQTGY.V		R.VRGDDSDVQTGYVLTSTK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
234	RL35_SCHPO	19.67%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
11	24	2	1684.85	4.2	0	72	24.4	95.00%	K.QSQENLAEQLQELR.Q		K.QSQENLAEQLQELR.Q
56	65	2	1157.65	4.3	0	33.6	22	95.00%	R.ILTVINESNR.L		R.ILTVINESNR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
235	RS21_SCHPO	48.28%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
51	60	2	1113.59	4.5	1	33.8	21.7	95.00%	K.TTYAISGFVR.S		K.TTYAISGFVR.S
1	16	2	1902.96	5.9	1	43.5	24.6	95.00%	-.MENEAGQLVDLYVPRK.C	Acetyl (+42)	-.MENEAGQLVDLYVPRK.C
72	87	2	1864.94	4.3	1	65.3	25.3	95.00%	R.LTTQDGLLEGVWSYQR.-		R.LTTQDGLLEGVWSYQR.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
236	RS3A_SCHPO	11.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
228	241	2	1510.76	-1	0	47.3	24.5	95.00%	K.LLELHGESQDVGSK.V		K.LLELHGESQDVGSK.V
200	213	2	1647.88	5.1	1	47.9	22.3	95.00%	K.ATNNIYPLQNVFVR.K		K.ATNNIYPLQNVFVR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
237	PPA2_SCHPO	5.18%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
136	143	2	961.53	5.4	1	31.9	23.3	95.00%	R.IELFDLGR.Q		R.IELFDLGR.Q
73	88	2	1640.68	-1.3	1	53.2	26.7	95.00%	R.NPTGDDTATDVSSAQY.I		R.NPTGDDTATDVSSAQYIDIFQNK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
238	KGUA_SCHPO	12.38%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
134	147	2	1596.89	0.36	1	29.2	18.9	95.00%	Y.VFLAPPSIEQLEVR.L		K.ASPIDAQYVFLAPPSIEQLEVR.L
2	12	2	1103.59	4.9	0	34.4	22.8	95.00%	M.TPQLSSSVASK.L		-.MTPQLSSSVASK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
239	EIF3G_SCHPO	12.77%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
104	120	3	1804.87	0.88	1	28	25.8	95.00%	W.TTTKEEEQDEAALAAAK.V		R.LQLGWTTTKEEEQDEAALAAAK.V
147	165	2	1934.99	-2.3	0	57.8	24.4	95.00%	K.SIIGPVDEPPLDASPVSSR.A		K.SIIGPVDEPPLDASPVSSR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
240	SYFA_SCHPO	4.81%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	14	2	1558.9	4.5	2	64.1	15.4	95.00%	M.SKLEALQVFLLEK.L	Acetyl (+42)	-.MSKLEALQVFLLEK.L
128	138	2	1219.56	4.9	0	33.3	25.8	95.00%	K.NTDSITDETPK.V		K.NTDSITDETPK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
241	UBC4_SCHPO	25.85%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
91	101	2	1244.65	4.6	1	28.4	23.7	94.80%	R.DQWSPALTISK.V		R.DQWSPALTISK.V	
102	128	3	3017.59	3.1	1	65.3	19.2	95.00%	K.VLLSICSLLTDPNPDDPLVPEIAHVYK.T	Carbamidomethyl (+57)	K.VLLSICSLLTDPNPDDPLVPEIAHVYK.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
242	SYQ_SCHPO	3.95%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
757	773	3	1760.83	5.2	1	28.1	26.6	95.00%	K.TDSSAGVDKAENPESVR.F		K.TDSSAGVDKAENPESVR.F	
52	66	2	1574.91	4.6	1	39.6	15.1	95.00%	R.TIGNLLFTLANASLK.Q		R.TIGNLLFTLANASLK.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
243	RPN11_SCHPO	10.71%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
73	92	2	2046.01	0.044	1	51.4	25.1	95.00%	F.AMPQSGTGVSVEAVDPVFQK.N		R.VVDVFAMPQSGTGVSVEAVDPVFQK.N	
258	270	2	1511.8	3.2	0	34.5	22.4	95.00%	R.VQNEVTLSPEQLR.I		R.VQNEVTLSPEQLR.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
244	SEC13_SCHPO	11.11%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
154	172	2	1721.9	1.2	0	72.1	23.4	95.00%	W.SPPSLSGSVVGQSPAAGPK.K		R.IFTAHEPGCNAVCWSPPSLSGSVVGQSPAAGPK.K	
140	172	3	3364.61	3	1	43.1	23.6	95.00%	R.IFTAHEPGCNAVCWSPPSLSGSVVGQSPAAGPK.K	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.IFTAHEPGCNAVCWSPPSLSGSVVGQSPAAGPK.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
245	RLA1_SCHPO	29.36%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
11	26	2	1673.87	0.11	0	90.5	23.4	95.00%	Y.SALILADEGIEITSDK.L		-.MSASELATSYSALILADEGIEITSDK.L	
33	48	2	1743.93	4.8	1	29.5	22.4	95.00%	K.AANVDVEPIWATIFAK.A		K.AANVDVEPIWATIFAK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
246	P5CR_SCHPO	15.25%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
70	98	3	3111.57	2.6	0	41.3	21.7	95.00%	K.ENAEMAAISNVLLLSCKPQAAEDVLNSPK.M	Carbamidomethyl (+57)	K.ENAEMAAISNVLLLSCKPQAAEDVLNSPK.M	
116	129	2	1566.76	5	0	85.9	25.9	95.00%	K.TISSLQSMLDESTR.V		K.TISSLQSMLDESTR.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
247	CYSK1_SCHPO	9.97%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
10	23	2	1341.78	3.9	1	59.1	18.5	95.00%	K.VPGIVSGFIGAIGR.T		K.VPGIVSGFIGAIGR.T	
180	200	2	2019.93	5.1	1	71.4	26.9	95.00%	K.GTVDGFTCSTGTGGTFAGVTK.Y	Carbamidomethyl (+57)	K.GTVDGFTCSTGTGGTFAGVTK.Y	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
248	YBN4_SCHPO	12.62%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
182	203	4	2693.39	2.2	1	23.4	21.8	95.00%	K.VKPTIHQMELHPYLPQTEYLEK.H		K.VKPTIHQMELHPYLPQTEYLEK.H	
52	70	4	2151.08	3	1	29.4	25.2	95.00%	R.HIDTAHIYGNEKEIGEGIR.E		R.HIDTAHIYGNEKEIGEGIR.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
249	ODP2_SCHPO	10.56%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	

215	238	4	2577.46	3.9	2	20.4	13.4	95.00%	R.IIKVDIENFKPVVAPKPSNEAAAK.A		R.IIKVDIENFKPVVAPKPSNEAAAK.A
49	75	3	2873.43	2.8	1	41.8	23.9	95.00%	K.NYPAHTVINMPALSPTMTTGNIGAFQK.K		K.NYPAHTVINMPALSPTMTTGNIGAFQK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
250	ODPB_SCHPO	12.30%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
220	234	2	1634.86	4.6	1	26.5	22.7	92.50%	K.EALSEDFVLPFGLAK.V		K.EALSEDFVLPFGLAK.V
331	360	3	3021.51	4	1	35.4	23.2	95.00%	R.VSMADVPMPYSHPVEAASVPNADVVVAAAK.K		R.VSMADVPMPYSHPVEAASVPNADVVVAAAK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
251	EIF3E_SCHPO	2.99%	99%	1

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
477	491	2	1679.84	3.6	1	46.3	25.6	95.00%	K.SLSFESQNLEQSLAK.S		K.SLSFESQNLEQSLAK.S

Supplementary Table S2: All "Scaffold" validated proteins and peptides identified from solprotSP (*S.pombe*) and from SCVMprot (*S.cerevisiae*) samples

S.pombe **- Chymotrypsin digest of large tryptic peptides (replicate B)**

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
1	PGK_SCHPO	72.95%	100%	35

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
359	379	2	2046.05	4.7	1	96.9	23.6	95.00%	K.TCEAGNVVIVGGGDTATVAKK.Y	Carbamidomethyl (+57)	K.TCEAGNVVIVGGGDTATVAKK.Y
359	378	2	1917.95	4	0	118	25	95.00%	K.TCEAGNVVIVGGGDTATVAK.K	Carbamidomethyl (+57)	K.TCEAGNVVIVGGGDTATVAK.K
138	149	3	1262.67	4.1	2	23.6	23.6	92.00%	K.VKADASAVEAFR.K		K.VKADASAVEAFR.K
138	148	2	1106.56	-1.6	2	39	24.1	95.00%	K.VKADASAVEAF.R		K.VKADASAVEAFR.K
279	289	2	1250.66	0.61	2	26.5	23.7	92.10%	F.LPVDFVTADKF.D		K.NNVEVFLPVDFVTADKFDK.D
250	269	3	2127.99	3.6	1	36.8	27	95.00%	K.IGDSLFDEAGSKNVESMMAK.A		K.IGDSLFDEAGSKNVESMMAK.A
273	288	2	1805.93	4.9	1	56.9	24.3	95.00%	K.NNVEVFLPVDFVTADK.F		K.NNVEVFLPVDFVTADK.F
140	150	2	1163.6	4.3	1	57.5	24.3	95.00%	K.ADASAVEAFRK.S		K.ADASAVEAFRK.S
23	39	2	1914.95	-1.2	1	42.5	25.3	95.00%	R.VDFNVPLDGDRITNNAR.I		R.VDFNVPLDGDRITNNAR.I
57	71	2	1591.87	2.9	0	46.2	21.1	95.00%	K.AVILMSHLGRPNGAR.V	Deamidation (+1)	K.AVILMSHLGRPNGAR.V
23	33	2	1245.61	6.8	1	62.1	25.1	95.00%	R.VDFNVPLDGDR.I		R.VDFNVPLDGDR.I
112	122	2	1211.69	4.5	0	57.3	16.6	95.00%	K.GGEVILLENLR.F		K.GGEVILLENLR.F
206	213	2	741.47	-0.57	0	31.7	18	95.00%	F.LAILGGAK.V		K.ALENPARPFLAILGGAK.V
40	48	2	910.59	3.6	0	25.3	9.54	90.10%	R.IVGALPTIK.Y		R.IVGALPTIK.Y
250	261	2	1237.59	4.5	1	61.5	25.5	95.00%	K.IGDSLFDEAGSK.N		K.IGDSLFDEAGSK.N
218	227	2	1183.69	5.5	0	39.2	19.1	95.00%	K.IQLIDNLLDK.V		K.IQLIDNLLDK.V
218	230	3	1552.9	4.8	1	31.7	15.8	95.00%	K.IQLIDNLLDKVNR.L		K.IQLIDNLLDKVNR.L
76	86	3	1141.67	-1.3	0	32.4	17.8	95.00%	Y.SLKPVAAELSK.L		K.YSLKPVAAELSK.L
94	105	2	1406.64	3.6	1	56.7	26	95.00%	K.FLDDCVGPEVEK.A	Carbamidomethyl (+57)	K.FLDDCVGPEVEK.A
272	283	2	1419.74	0.54	2	26.3	23.9	91.80%	K.KNNVEVFLPVDF.V		K.KNNVEVFLPVDFVTADK.F
197	213	2	1736.99	-0.89	1	55.5	15.3	95.00%	K.ALENPARPFLAILGGAK.V		K.ALENPARPFLAILGGAK.V
170	181	2	1267.64	4	0	58.7	24.3	95.00%	R.AHSSMVGVDLPR.V		R.AHSSMVGVDLPR.V
123	136	3	1544.76	5.8	1	28.5	25.4	95.00%	R.FHIEEEGSAKVDGK.K		R.FHIEEEGSAKVDGK.K
214	230	3	1966.12	-2	1	69	16.7	95.00%	K.VADKIQLIDNLLDKVNR.L		K.VADKIQLIDNLLDKVNR.L
7	15	2	986.57	5.4	0	41.1	21.4	95.00%	K.LAITDVDLK.G		K.LAITDVDLK.G
123	132	3	1145.54	4.7	1	33.9	25.6	95.00%	R.FHIEEEGSAK.V		R.FHIEEEGSAK.V
197	205	2	1013.53	-0.44	1	29.4	21.8	95.00%	K.ALENPARPF.L		K.ALENPARPFLAILGGAK.V
404	414	2	1040.63	5.6	0	39.4	17.4	95.00%	K.ALPGVVALSSK.-		K.ALPGVVALSSK.-
380	403	3	2417.21	2.5	1	72	24.1	95.00%	K.YGKEDALSHVSTGGGASLELLEGK.A		K.YGKEDALSHVSTGGGASLELLEGK.A
383	403	2	2069.04	3.6	0	81.1	24.4	95.00%	K.EDALSHVSTGGGASLELLEGK.A		K.EDALSHVSTGGGASLELLEGK.A
321	329	2	994.54	5.5	1	50.2	21.9	95.00%	K.FAEVITTSK.T		K.FAEVITTSK.T
75	86	3	1304.74	4.3	1	59.4	19.6	95.00%	K.YSLKPVAAELSK.L		K.YSLKPVAAELSK.L
151	169	2	2020	-1.1	1	120	25.3	95.00%	K.SLTSLGDIFVNDAFGTAHR.A		K.SLTSLGDIFVNDAFGTAHR.A
295	316	2	2245.99	-2.4	1	70.9	27.3	95.00%	K.VGSATAEEGIPDGWMGLDCGPK.S	Carbamidomethyl (+57)	K.VGSATAEEGIPDGWMGLDCGPK.S
214	227	2	1596.91	-1.6	1	59.1	18.1	95.00%	K.VADKIQLIDNLLDK.V		K.VADKIQLIDNLLDK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
2	ENO11_SCHPO	74.72%	100%	28

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
258	263	2	765.39	4.7	1	25.9	24.3	91.20%	K.YDLDIK.A		K.YDLDIK.A
415	425	2	1223.55	-1.2	1	56.6	25.2	95.00%	R.IEEELGSEGVY.A		R.IEEELGSEGVYAGAHAGK.Y
361	374	3	1608.73	4.7	1	47.1	26.2	95.00%	R.MSYEAGWGVMVSHR.S		R.MSYEAGWGVMVSHR.S
94	103	2	1129.63	-1.2	1	27.8	21	93.90%	F.LLKLDGTENK.S		K.AADEFLLKLDGTENK.S
311	328	2	1963.97	-1.7	1	93.4	25.6	95.00%	K.AETDFQIVGDDLTVTNVK.R		K.AETDFQIVGDDLTVTNVK.R
65	79	2	1477.87	4	0	73.7	15.3	95.00%	K.AVGNVNNIIAPAVVK.A		K.AVGNVNNIIAPAVVK.A
106	120	2	1560.82	4.2	0	61.3	23.8	95.00%	K.LGANAILGVSMAICR.A	Oxidation (+16)/ Carbamidomethyl (+57)	K.LGANAILGVSMAICR.A

170	184	2	1606.79	1.1	1	63.6	26.1	95.00%	F.MILPTGAPSFSEAMR.W		K.GPYVLPVPSFNVLNGGSHAGGDLAFQEFMILPTGAPSFSEAMR.W
170	179	2	1032.53	2	1	47.6	23.9	95.00%	F.MILPTGAPSF.S		K.GPYVLPVPSFNVLNGGSHAGGDLAFQEFMILPTGAPSFSEAMR.W
273	287	2	1812.96	4.5	1	75.4	22.6	95.00%	K.LTYQQLTDLYVELSK.K		K.LTYQQLTDLYVELSK.K
200	234	3	3596.81	3.8	2	68.4	21.1	95.00%	K.RYGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A		K.RYGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
243	257	2	1598.78	-2.2	1	56.8	25.5	95.00%	K.IGLDVASSEFYVDGK.Y		K.IGLDVASSEFYVDGK.Y
409	414	2	806.43	5.7	1	29.4	25.1	95.00%	K.YNELLR.I		K.YNELLR.I
375	396	2	2201.14	2.9	1	122	22.5	95.00%	R.SGETADTFISHLTVGIGAGQLK.S		R.SGETADTFISHLTVGIGAGQLK.S
89	96	2	905.49	4.7	1	57.4	23.5	95.00%	K.AADEFLLK.L		K.AADEFLLK.L
80	88	2	1002.5	4.3	0	41.9	22.7	95.00%	K.ANLDVTDQK.A		K.ANLDVTDQK.A
185	194	2	1204.59	5.4	1	34	24.9	95.00%	R.WGAETYHTLK.S		R.WGAETYHTLK.S
346	360	2	1585.85	6	0	90.8	21.9	95.00%	K.VNQIGSVTESLNAVR.M		K.VNQIGSVTESLNAVR.M
288	303	2	1965.9	-0.06	2	59	26.7	95.00%	K.KYPIVSIEDPFDQDDW.S		K.KYPIVSIEDPFDQDDWSAWTHMK.A
89	103	2	1662.85	3.3	1	74.4	24.4	95.00%	K.AADEFLLKLDGTENK.S		K.AADEFLLKLDGTENK.S
145	169	2	2572.26	-0.21	1	29.2	24.7	95.00%	Y.VLPVPSFNVLNGGSHAGGDLAFQEF.M	Deamidation (+1)	K.GPYVLPVPSFNVLNGGSHAGGDLAFQEFMILPTGAPSFSEAMR.W
201	234	3	3440.71	3.8	1	65	22.1	95.00%	R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
311	329	2	2120.09	4.8	1	105	23.7	95.00%	K.AETDFQIVGDDLTVTNVKR.L		K.AETDFQIVGDDLTVTNVKR.L
16	32	2	1837.92	4	0	84.2	25	95.00%	R.GNPTVEVDLTTETGIHR.A		R.GNPTVEVDLTTETGIHR.A
33	50	2	1886.95	-1.9	1	113	24.8	95.00%	R.AIVPSGASTGIWEALEMR.D		R.AIVPSGASTGIWEALEMR.D
338	345	2	901.51	4.7	0	31.4	21.6	95.00%	K.CANALLLK.V	Carbamidomethyl (+57)	K.CANALLLK.V
415	432	2	1815.87	5.1	1	83.2	25.9	95.00%	R.IEEELGSEGVYAGAHAGK.Y		R.IEEELGSEGVYAGAHAGK.Y
383	396	2	1392.81	-1.4	0	72.2	16.4	95.00%	F.ISHLTVGIGAGQLK.S		R.SGETADTFISHLTVGIGAGQLK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
3	G3P1_SCHPO	60.71%	100%	20							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	86	2	2203.12	-1	1	43.5	23.5	95.00%	K.LVIDGNAIDVHNERDPADIK.W		K.LVIDGNAIDVHNERDPADIK.W
169	186	2	1886.94	-0.43	0	78	25.2	95.00%	F.GIEEGLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK.T
249	263	4	1673.93	-1.3	1	31	20.1	95.00%	K.LAKPTNYEDIKAAIK.A		K.LAKPTNYEDIKAAIK.A
132	145	2	1574.79	-1.5	2	59.4	24.9	95.00%	Y.VVGVNEEKFNPSEK.V		K.DAPMYVVGVNEEKFNPSEK.V
272	295	2	2589.14	0.9	1	78.8	27.4	95.00%	K.GVLGYTEDAVVSTDFCGDNHSSIF.D	Carbamidomethyl (+57)	K.GVLGYTEDAVVSTDFCGDNHSSIFDASAGIQLSPQFVK.L
119	139	2	2245.18	4	2	70	21.7	95.00%	R.VIISAPSKDAPMYVVGVNEEK.F		R.VIISAPSKDAPMYVVGVNEEK.F
127	139	2	1449.69	3.7	1	45.1	25.6	95.00%	K.DAPMYVVGVNEEK.F		K.DAPMYVVGVNEEK.F
146	162	2	1818.91	4.5	0	75	25.3	95.00%	K.VISNASCTTNCLAPLAK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.VISNASCTTNCLAPLAK.V
6	13	2	819.43	6.2	1	38.4	23.6	95.00%	K.VGINGFGR.I	Deamidation (+1)	K.VGINGFGR.I
234	248	2	1623.93	3.7	1	72.7	18.6	95.00%	F.RVPTPDVSVVDLTVK.L		K.LTGMAFRVPTPDVSVVDLTVK.L
249	259	3	1290.69	4.5	1	28.4	24	95.00%	K.LAKPTNYEDIK.A		K.LAKPTNYEDIK.A
56	66	2	1193.6	4.2	1	61.8	25.3	95.00%	R.FDGSVEIKDGK.L		R.FDGSVEIKDGK.L
235	248	2	1467.82	3.7	0	76.5	18.6	95.00%	R.VPTPDVSVVDLTVK.L		R.VPTPDVSVVDLTVK.L
296	309	2	1459.77	1.4	1	62.3	23.7	95.00%	F.DASAGIQLSPQFVK.L		K.GVLGYTEDAVVSTDFCGDNHSSIFDASAGIQLSPQFVK.L
323	334	2	1304.75	5.7	2	40.6	17.6	95.00%	R.RVVDLVAYTAAK.D		R.RVVDLVAYTAAK.D
64	86	3	2503.28	3.2	1	25.1	23.4	94.00%	K.DGKLVIDGNAIDVHNERDPADIK.W		K.DGKLVIDGNAIDVHNERDPADIK.W

324	334	2	1148.65	6.2	1	55.4	19.8	95.00%	R.VVDLVAYTAAK.D		R.VVDLVAYTAAK.D
163	186	2	2576.28	0.73	1	102	24	95.00%	K.VINDTFGIEEGLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK.T
324	336	2	1377.72	3.8	1	68.7	24.4	95.00%	R.VVDLVAYTAAKDN.-		R.VVDLVAYTAAKDN.-
201	215	2	1343.71	4.7	0	69.9	22.9	95.00%	R.GASANIIPSSTGAAK.A		R.GASANIIPSSTGAAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
4	METE_SCHPO	59.42%	100%	42

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
638	653	2	1752.84	0.45	1	64.1	25.9	95.00%	R.LATAAVQDDTQIHSHF.C		R.LATAAVQDDTQIHSHFCYSDFNDIFDAIQR.L
434	449	2	1746.96	-0.072	1	73	20.7	95.00%	K.LPLFPTTTIGSFPQTK.E		K.LPLFPTTTIGSFPQTK.E
128	141	2	1732.84	0.61	1	48.3	25.7	95.00%	Y.HFLRPEVSEETDFK.L		K.WFDSNYHFLRPEVSEETDFK.L
482	504	3	2702.27	0.41	2	29.9	26.4	95.00%	K.FQEEVGLDVLVHGEPERNDMVQY.F		K.FQEEVGLDVLVHGEPERNDMVQYFGER.M
156	171	2	1683.96	0.049	1	39	17.3	95.00%	K.EAGIITRPVLVGPVTY.L		K.EAGIITRPVLVGPVTYLFIAK.A
684	690	2	813.51	5.6	0	34.2	20.8	95.00%	K.LLNVLSR.Y		K.LLNVLSR.Y
393	404	2	1284.67	4.4	0	68.2	21.8	95.00%	R.AESPITNVEAVR.E		R.AESPITNVEAVR.E
707	716	3	1186.64	4.9	1	25.6	23	94.50%	R.VPPVSEFKER.I		R.VPPVSEFKER.I
391	404	2	1511.81	4	1	42.1	22.1	95.00%	K.ARAESPITNVEAVR.E		K.ARAESPITNVEAVR.E
67	76	2	1225.51	0.48	1	38.7	26	95.00%	Y.DQIMDHSFSF.N		K.AQGVDIIPSNDFSLYDQIMDHSFSFNVIPPR.Y
325	351	3	2884.5	3.5	0	47.3	20	95.00%	R.VQVASSSSILHIPHSLSGEDQINPEIK.R		R.VQVASSSSILHIPHSLSGEDQINPEIK.R
325	352	3	3040.6	0.27	1	78.3	18.3	95.00%	R.VQVASSSSILHIPHSLSGEDQINPEIKR.W		R.VQVASSSSILHIPHSLSGEDQINPEIKR.W
261	273	2	1330.77	-1.4	0	67.2	18.3	95.00%	K.GLPIAGVHVDVVR.A		K.GLPIAGVHVDVVR.A
104	121	2	1742.9	4.6	1	66.3	23.7	95.00%	R.AATADKAAVDVPAGEMVK.W		R.AATADKAAVDVPAGEMVK.W
128	140	2	1604.75	0.16	1	35.2	26.5	95.00%	Y.HFLRPEVSEETDF.K		K.WFDSNYHFLRPEVSEETDFK.L
281	299	2	1881.07	-1.4	0	91.8	17	95.00%	R.ALAVLGENQIISVGVVSGR.N		R.ALAVLGENQIISVGVVSGR.N
147	155	2	1034.53	5.7	1	36.8	24.9	95.00%	K.ALDEFLEAK.E		K.ALDEFLEAK.E
547	560	2	1596.79	3.6	1	50.8	25.3	95.00%	K.ESQYAQSITSKPMK.G		K.ESQYAQSITSKPMK.G
461	473	2	1539.76	4.1	1	67.2	24.8	95.00%	K.GLISQEEYDAFIR.K		K.GLISQEEYDAFIR.K
668	679	2	1288.66	3.8	0	37	24.7	95.00%	R.LDADVVSIENSK.S		R.LDADVVSIENSK.S
527	546	3	2267.24	3.3	1	44.5	19.1	95.00%	R.CVRPPIIVGDVYRPAPMTVK.E	Carbamidomethyl (+57)	R.CVRPPIIVGDVYRPAPMTVK.E
631	637	2	877.45	5.9	1	49	23.7	95.00%	K.WAIDAFR.L		K.WAIDAFR.L
577	601	3	2805.42	3	1	36.5	22.2	95.00%	R.DDVHDSVQAQQIALGLRDEVLDLEK.A		R.DDVHDSVQAQQIALGLRDEVLDLEK.A
156	176	3	2256.33	3.9	1	51.3	9.03	95.00%	K.EAGIITRPVLVGPVTYLFIAK.A		K.EAGIITRPVLVGPVTYLFIAK.A
656	667	2	1439.67	0.26	1	38	26.5	95.00%	Y.SDFNDIFDAIQR.L		R.LATAAVQDDTQIHSHFCYSDFNDIFDAIQR.L
561	571	2	1184.7	5.1	0	40.5	18.9	95.00%	K.GMLTAPITILR.W		K.GMLTAPITILR.W
4	11	2	845.48	4.8	1	33.3	22.7	95.00%	K.SAVLGFPR.I		K.SAVLGFPR.I
707	714	2	901.49	4.3	1	27.7	24.3	93.80%	R.VPPVSEFK.E		R.VPPVSEFK.E
691	706	2	1818.88	3.8	1	84	25.8	95.00%	R.YTSCIGPGLFDIHSPR.V	Carbamidomethyl (+57)	R.YTSCIGPGLFDIHSPR.V
499	508	2	1257.55	4.4	1	53.6	26	95.00%	R.NDMVQYFGER.M		R.NDMVQYFGER.M
243	260	2	1982.07	0.4	1	73.8	18.5	95.00%	K.LILTTYFGSLQSNADVLK.G		K.LILTTYFGSLQSNADVLK.G
75	82	2	928.51	0.61	1	26	22.2	91.40%	F.SFNVIPPR.Y		K.AQGVDIIPSNDFSLYDQIMDHSFSFNVIPPR.Y
727	738	2	1466.7	4.2	1	48	26.1	95.00%	K.DHLWLNPDCGLK.T	Carbamidomethyl (+57)	K.DHLWLNPDCGLK.T
428	449	3	2402.33	4.8	2	46	15.8	95.00%	K.QQASLKLPLFPTTTIGSFPQTK.E		K.QQASLKLPLFPTTTIGSFPQTK.E
527	538	2	1386.73	1.2	1	41.3	23.2	95.00%	R.CVRPPIIVGDVY.R	Carbamidomethyl (+57)	R.CVRPPIIVGDVYRPAPMTVK.E
64	74	2	1354.59	0.29	1	43.3	25.7	95.00%	F.SLYDQIMDHSF.S		K.AQGVDIIPSNDFSLYDQIMDHSFSFNVIPPR.Y
723	738	3	1927.98	4	2	24.5	23.9	93.20%	K.HVPKDHLWLNPDCGLK.T	Carbamidomethyl (+57)	K.HVPKDHLWLNPDCGLK.T
361	369	2	1017.56	4.9	0	30.5	22.3	95.00%	K.CAELAILTK.A	Carbamidomethyl (+57)	K.CAELAILTK.A
606	615	2	1199.6	4.3	0	55.1	23.2	95.00%	K.VIQCDEPALR.E	Carbamidomethyl (+57)	K.VIQCDEPALR.E

67	74	2	991.41	0.59	1	29.6	25.4	95.00%	Y.DQIMDHSF.S		K.AQGVDIIPSNDFSLYDQIMDHSFSFNVIPPR.Y
85	99	2	1616.79	4.1	1	63.5	25.7	95.00%	R.LSGLSSLDTYFAMGR.G		R.LSGLSSLDTYFAMGR.G
30	40	2	1132.6	4.2	0	58.1	23.1	95.00%	K.TSAEELLATAK.Q		K.TSAEELLATAK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
5	EF1A1_SCHPO	53.70%	100%	22

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
265	288	2	2443.34	-0.21	1	51.7	17.5	95.00%	R.VETGVIKPGMIVTFAPAGVTTEVK.S		R.VETGVIKPGMIVTFAPAGVTTEVK.S
289	308	2	2109.94	-0.63	1	49.2	27.3	95.00%	K.SVEMHHESLDAGLPGDNVGF.N		K.SVEMHHESLDAGLPGDNVGFNVK.N
223	245	4	2516.4	3.1	1	25	14.9	95.00%	K.GKTLLEAIDSIEPPARPTDKPLR.L		K.GKTLLEAIDSIEPPARPTDKPLR.L
356	369	2	1607.76	0.65	0	30.1	26.1	95.00%	Y.SPVLDCHTAHIACK.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.NDPPMGCASFTAQVIILNHPGQISAGYSPVLDCHTAHIACK.F
279	288	2	971.53	0.39	0	42.5	21.3	95.00%	F.APAGVTTEVK.S		R.VETGVIKPGMIVTFAPAGVTTEVK.S
320	338	3	2067.86	1.1	2	25.5	27.9	90.30%	R.RGNVCGDSKNDPPMGCASF.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.RGNVCGDSKNDPPMGCASFTAQVIILNHPGQISAGYSPVLDCHTAHIACK.F
135	146	2	1313.74	3.9	1	45.8	20.8	95.00%	R.EHALLAYTLGVK.Q		R.EHALLAYTLGVK.Q
370	376	2	848.47	4.7	1	25.9	22.7	91.20%	K.FAELIEK.I		K.FAELIEK.I
329	338	2	1094.42	1.3	1	47.5	23.9	95.00%	K.NDPPMGCASF.T	Carbamidomethyl (+57)	K.NDPPMGCASFTAQVIILNHPGQISAGYSPVLDCHTAHIACK.F
265	278	2	1489.82	0.93	1	58.8	20.9	95.00%	R.VETGVIKPGMIVTF.A		R.VETGVIKPGMIVTFAPAGVTTEVK.S
402	421	2	2268.08	4	1	67.5	26.2	95.00%	K.MVPSKPMCVEAFTDYAPLGR.F	Carbamidomethyl (+57)	K.MVPSKPMCVEAFTDYAPLGR.F
339	355	2	1780.95	1.3	1	48.3	22.1	95.00%	F.TAQVIILNHPGQISAGY.S		K.NDPPMGCASFTAQVIILNHPGQISAGYSPVLDCHTAHIACK.F
147	154	2	883.55	5.8	0	26.4	16.7	91.90%	K.QLIVAVNK.M		K.QLIVAVNK.M
254	264	2	1024.61	4.2	0	65.4	15.1	95.00%	K.IGGIGTVPVGR.V		K.IGGIGTVPVGR.V
6	20	2	1529.84	4.6	0	62.9	21.8	95.00%	K.GHINVVVIGHVDSGK.S		K.GHINVVVIGHVDSGK.S
289	311	3	2451.16	4	1	64.2	26.2	95.00%	K.SVEMHHESLDAGLPGDNVGFNVK.N		K.SVEMHHESLDAGLPGDNVGFNVK.N
321	338	2	1911.75	-0.29	2	43.7	27	95.00%	R.GNVCGDSKNDPPMGCASF.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GNVCGDSKNDPPMGCASFTAQVIILNHPGQISAGYSPVLDCHTAHIACK.F
185	208	2	2663.24	0.44	1	56	26.5	95.00%	K.TVPFVPVSGFQGDNMIEPTTNMPW.Y		K.TVPFVPVSGFQGDNMIEPTTNMPWYQGWQK.E
225	245	3	2331.29	2.6	0	34.8	16.7	95.00%	K.TLLEAIDSIEPPARPTDKPLR.L		K.TLLEAIDSIEPPARPTDKPLR.L
155	164	2	1151.51	6.4	1	75.8	24.7	95.00%	K.MDTTGWSQAR.F		K.MDTTGWSQAR.F
85	96	2	1340.69	4.4	1	66.1	23.6	95.00%	K.YNVTVIDAPGHR.D		K.YNVTVIDAPGHR.D
246	253	2	974.55	4.1	1	32.1	22.3	95.00%	R.LPLQDVYK.I		R.LPLQDVYK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
6	KPYK_SCHPO	68.37%	100%	33

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
233	243	2	1214.66	3.9	1	28.5	22.1	94.70%	R.EVLGEEGKNIK.I		R.EVLGEEGKNIK.I
57	64	2	941.37	-1.3	1	37.2	23.1	95.00%	R.MNFSHGSY.E		R.MNFSHGSYEYHQSVIDNAR.K
422	433	3	1430.81	4.6	1	41.1	18	95.00%	K.YRPSIPIVMVTR.C		K.YRPSIPIVMVTR.C
12	26	2	1566.83	-1.5	0	40	21.3	95.00%	W.VAGLNSELDIPAVNR.R		K.QWVAGLNSELDIPAVNR.R
248	271	2	2647.29	-0.0022	1	82.3	24.8	95.00%	K.IENQQGVNNFDSILDVTDGIMVAR.G		K.IENQQGVNNFDSILDVTDGIMVAR.G
191	207	2	1884.99	4	1	51.4	22.8	95.00%	K.TDVDLPALSEKDKADLR.F		K.TDVDLPALSEKDKADLR.F
77	98	3	2294.27	3.2	1	35.9	17.7	95.00%	K.ASATNPLFPLAIALDTKGPEIR.T		K.ASATNPLFPLAIALDTKGPEIR.T
345	354	2	1084.51	-0.93	1	40.2	24.5	95.00%	K.GSYPVEAVTY.M		K.GSYPVEAVTYMAETAR.V
468	477	2	1186.55	5.3	1	54.8	24.9	95.00%	R.VAYGCQQAYK.M	Carbamidomethyl (+57)	R.VAYGCQQAYK.M

65	75	2	1330.63	-0.68	1	49.1	26.1	95.00%	Y.EYHQSVIDNAR.K		R.MNFSHGSYEYHQSVIDNAR.K
294	319	4	2965.4	-0.14	1	53.9	25.7	95.00%	K.CNIAGKPVACATQMLESMTYNPR PTR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CNIAGKPVACATQMLESMTYNPR PTR.A
405	417	2	1287.72	5.7	0	62	20.8	95.00%	K.AIVVLSTSGNTAR.L		K.AIVVLSTSGNTAR.L
212	223	2	1368.69	4.2	1	39.8	24.3	95.00%	K.NGVDMIFASFIR.R		K.NGVDMIFASFIR.R
381	404	2	2460.23	3.5	0	76.2	23.4	95.00%	R.RPLECATETTAVAAIGASIESDAK. A	Carbamidomethyl (+57)	R.RPLECATETTAVAAIGASIESDAK. A
191	201	2	1186.61	4.4	0	25.5	23.3	90.40%	K.TDVDLPALSEK.D		K.TDVDLPALSEK.D
487	497	2	1053.66	5.9	0	39.5	13	95.00%	K.IIVLQGAVGGK.G		K.IIVLQGAVGGK.G
294	313	2	2244.01	0.25	1	84.6	27.2	95.00%	K.CNIAGKPVACATQMLESMTY.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CNIAGKPVACATQMLESMTYNPR PTR.A
224	232	3	1107.62	3.9	1	57.7	19.8	95.00%	R.RAEDVIHIR.E		R.RAEDVIHIR.E
10	26	2	1880.98	3.7	1	90.9	22.6	95.00%	K.QWVAGLNSELDIPAVNR.R		K.QWVAGLNSELDIPAVNR.R
77	93	2	1741.96	-1.5	1	51.2	20.7	95.00%	K.ASATNPLFPLAIALDTK.G		K.ASATNPLFPLAIALDTK.G
225	232	2	951.52	5	0	30.1	22.5	95.00%	R.AEDVIHIR.E		R.AEDVIHIR.E
76	98	3	2422.36	-0.13	2	81.2	15.3	95.00%	R.KASATNPLFPLAIALDTKGPEIR.T		R.KASATNPLFPLAIALDTKGPEIR.T
28	37	2	1088.6	5	0	46.3	21.8	95.00%	R.TSIICTIGPK.S	Carbamidomethyl (+57)	R.TSIICTIGPK.S
191	203	2	1429.74	3.8	1	45.1	24	95.00%	K.TDVDLPALSEKDK.A		K.TDVDLPALSEKDK.A
345	360	2	1743.82	5.3	1	80.9	27	95.00%	K.GSYPVEAVTYMAETAR.V		K.GSYPVEAVTYMAETAR.V
272	288	2	1770.96	3.8	1	69.1	20.9	95.00%	R.GDLGIEIPASQVFVAQK.M		R.GDLGIEIPASQVFVAQK.M
76	93	2	1870.06	0.3	2	86.6	18.2	95.00%	R.KASATNPLFPLAIALDTK.G		R.KASATNPLFPLAIALDTK.G
99	118	2	2080.98	-1.2	1	50.5	26.9	95.00%	R.TGLTVGGTDYPISSGHEMIF.T		R.TGLTVGGTDYPISSGHEMIFTTDD AYAEK.C
10	27	3	2037.08	4.1	1	30.7	21.6	95.00%	K.QWVAGLNSELDIPAVNRR.T		K.QWVAGLNSELDIPAVNRR.T
320	344	2	2490.22	0.48	0	105	25	95.00%	R.AEVSDVGNAVLDGADLVMLSGE TTK.G		R.AEVSDVGNAVLDGADLVMLSGE TTK.G
99	127	3	3075.41	2.5	1	69.9	25.7	95.00%	R.TGLTVGGTDYPISSGHEMIFTTDD AYAEK.C		R.TGLTVGGTDYPISSGHEMIFTTDD AYAEK.C
369	380	2	1398.7	-1.2	1	42.4	24.5	95.00%	Y.GSLYQEMFGLVR.R		R.VAEASIPYGSLYQEMFGLVR.R
47	56	3	1143.62	4.2	1	26	23	94.90%	K.LRDAGMNIVR.M		K.LRDAGMNIVR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
7	ALF_SCHPO	58.94%	100%	22

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
26	50	2	2496.3	0.87	1	73.3	22	95.00%	R.EHGFAIPAINVTSSSTAIAALEAAR .E		R.EHGFAIPAINVTSSSTAIAALEAAR .E
253	261	2	1067.53	0.91	1	34.3	24.6	95.00%	K.TTNDKPVFF.V		K.TTNDKPVFFVFHGGSGSSVNEFR .T
262	275	2	1478.69	1.9	1	32.5	26.1	95.00%	F.VFHGGSGSSVNEFR.T		K.TTNDKPVFFVFHGGSGSSVNEFR .T
94	112	2	2098.02	4.1	1	63.5	26	95.00%	R.SIAPFFGVPVVMHSDHCAK.K	Carbamidomethyl (+57)	R.SIAPFFGVPVVMHSDHCAK.K
2	19	2	1823.05	3.8	0	65.3	16.3	95.00%	M.GILDIVPTGVITGDNVLK.L		-.MGILDIVPTGVITGDNVLK.L
99	112	2	1582.74	-0.053	1	53.7	26.5	95.00%	F.FGVPVVMHSDHCAK.K	Carbamidomethyl (+57)	R.SIAPFFGVPVVMHSDHCAK.K
285	300	2	1825.89	3.9	1	73.6	25.6	95.00%	K.VNIDTDTQFAYVEGVR.D		K.VNIDTDTQFAYVEGVR.D
285	293	2	1051.48	0.08	1	28.8	24.7	95.00%	K.VNIDTDTQF.A		K.VNIDTDTQFAYVEGVR.D
294	302	2	1070.5	0.55	2	36.2	23.9	95.00%	F.AYVEGVRDY.V		K.VNIDTDTQFAYVEGVRDYVLK.Y
235	248	2	1564.88	4	1	58.4	17.8	95.00%	K.LQPALLGQHQAYVK.E		K.LQPALLGQHQAYVK.E
54	71	2	1843.95	-1.9	1	86.6	23.4	95.00%	R.SPIILQTSNGGAHFFAGK.E		R.SPIILQTSNGGAHFFAGK.E
54	67	2	1441.72	-2.4	1	73.8	24.3	95.00%	R.SPIILQTSNGGAHF.F	Deamidation (+1)	R.SPIILQTSNGGAHFFAGK.E
131	149	3	2165.05	0.18	1	48.5	25.4	95.00%	K.IHGEPLFSSHMLDLSEEPK.K		K.IHGEPLFSSHMLDLSEEPK.K
80	93	2	1399.76	5.1	1	89.1	21.2	95.00%	K.ASIAGSIAAAHYIR.S		K.ASIAGSIAAAHYIR.S
310	326	2	1794.93	0.93	1	27	22.8	93.00%	Y.LMTPVGNPEGADKPNKK.K		K.DYLMTPVGNPEGADKPNKK.K
30	50	2	2026.11	-0.21	0	105	19.2	95.00%	F.AIPAINVTSSSTAIAALEAAR.E		R.EHGFAIPAINVTSSSTAIAALEAAR .E
345	358	2	1597.82	-1.5	1	71	23.9	95.00%	R.VLTALEDFYTVNTL.-		R.VLTALEDFYTVNTL.-
196	206	2	1420.66	1.4	1	28.2	26	93.30%	Y.TQPEDIWDVYR.E		K.IWIEMEIGITGGEEDGVDNSHVSH TELYTQPEDIWDVYR.E

131	150	4	2293.14	0.23	1	24.1	24.2	95.00%	K.IHGEPLFSSHMLDLSEEPKK.E		K.IHGEPLFSSHMLDLSEEPKK.E
310	325	2	1682.83	-0.98	0	57.8	25.9	95.00%	Y.LMTPVGNPEGADKPNK.K	Oxidation (+16)	K.DYLMTPVGNPEGADKPNK.K
54	68	2	1587.8	-1.8	1	80.4	24.6	95.00%	R.SPIILQTSNGGAHFF.A		R.SPIILQTSNGGAHFFAGK.E
80	91	2	1130.57	-0.81	1	68.7	24.1	95.00%	K.ASIAGSIAAAHY.I		K.ASIAGSIAAAHYIR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
8	ADH4_SCHPO	58.29%	100%	22

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
76	87	2	1282.76	5.2	0	44.2	16	95.00%	K.NTLIVTDPGIIK.V		K.NTLIVTDPGIIK.V
366	374	2	1027.63	6.6	0	37.3	18.6	95.00%	R.ISQLVLEVK.I		R.ISQLVLEVK.I
204	224	3	2450.16	0.73	2	25.1	26.3	92.30%	K.MAIIDKHTMPILSVNDPETMY.G	Oxidation (+16)/ Oxidation (+16)	K.MAIIDKHTMPILSVNDPETMYGLP PSLTAATGMDALTHAVEAYVSTAA NPITDACAVK.C
386	398	2	1545.76	3.9	2	63.6	25.9	95.00%	K.EKDFDVLVDHAMK.D		K.EKDFDVLVDHAMK.D
169	191	2	2386.26	3.6	0	87.6	21.4	95.00%	K.SSKPQLPLIAINTTAGTASEMTR.F		K.SSKPQLPLIAINTTAGTASEMTR.F
192	200	2	1078.57	4	1	35.5	23.3	95.00%	R.FAIITEETR.H		R.FAIITEETR.H
160	191	3	3376.73	2.5	1	83.5	19.6	95.00%	K.IADYEGVDKSSKPQLPLIAINTTAG TASEMTR.F		K.IADYEGVDKSSKPQLPLIAINTTAG TASEMTR.F
96	129	3	3701.97	2.4	1	70.9	16.3	95.00%	K.ALLEEQSITVHLYDGVQPNPTVG NVNQGLEIVKK.E		K.ALLEEQSITVHLYDGVQPNPTVG NVNQGLEIVKK.E
129	148	3	2121.89	-0.81	1	65.8	27.6	95.00%	K.KENCDSMVSIGGGSAHDCAK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.KENCDSMVSIGGGSAHDCAK.G
351	365	2	1707.77	1.1	0	75.9	26.8	95.00%	F.HLGCEEHTAEAALDR.I	Carbamidomethyl (+57)	R.LGDIAFHLGCEEHTAEAALDR.I
345	365	3	2324.09	3.1	1	49.5	26.7	95.00%	R.LGDIAFHLGCEEHTAEAALDR.I	Carbamidomethyl (+57)	R.LGDIAFHLGCEEHTAEAALDR.I
375	385	3	1245.75	-1.4	0	42.3	13.6	95.00%	K.IRPHLVDLGVK.E		K.IRPHLVDLGVK.E
247	261	2	1516.76	1.2	0	62	24.6	95.00%	Y.VSTAANPITDACAVK.C	Carbamidomethyl (+57)	K.HTMPILSVNDPETMYGLPPSLTA ATGMDALTHAVEAYVSTAANPITDA CAVK.C
149	159	2	1014.58	4.8	0	36.7	22.1	95.00%	K.GIALLATNGGK.I	Deamidation (+1)	K.GIALLATNGGK.I
210	224	2	1778.79	1.4	1	36.8	26.8	95.00%	K.HTMPILSVNDPETMY.G	Oxidation (+16)/ Oxidation (+16)	K.HTMPILSVNDPETMYGLPPSLTA ATGMDALTHAVEAYVSTAANPITDA CAVK.C
109	128	2	2077.08	0.38	0	67.9	22.8	95.00%	Y.DGVQPNPTVGNVNQGLEIVK.K		K.ALLEEQSITVHLYDGVQPNPTVG NVNQGLEIVK.K
399	415	2	1851.85	4.5	0	49.6	26.8	95.00%	K.DACGATNPIQPTHDEVK.A	Carbamidomethyl (+57)	K.DACGATNPIQPTHDEVK.A
96	128	3	3573.88	3.6	1	56.5	17.6	95.00%	K.ALLEEQSITVHLYDGVQPNPTVG NVNQGLEIVK.K		K.ALLEEQSITVHLYDGVQPNPTVG NVNQGLEIVK.K
109	129	2	2205.18	2.6	1	32.8	20.4	95.00%	Y.DGVQPNPTVGNVNQGLEIVKK.E		K.ALLEEQSITVHLYDGVQPNPTVG NVNQGLEIVKK.E
130	148	2	1993.8	3.7	0	87.9	27.1	95.00%	K.ENCDSMVSIGGGSAHDCAK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.ENCDSMVSIGGGSAHDCAK.G
225	246	2	2185.07	0.31	1	42.7	25.9	95.00%	Y.GLPPSLTAATGMDALTHAVEAY.V		K.HTMPILSVNDPETMYGLPPSLTA ATGMDALTHAVEAYVSTAANPITDA CAVK.C
160	168	2	1008.48	5	1	40.9	25.4	95.00%	K.IADYEGVDK.S		K.IADYEGVDK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
9	PDC2_SCHPO	53.03%	100%	31

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
204	214	2	1130.62	4.6	0	53.5	22.6	95.00%	K.ATDIAAELISK.K		K.ATDIAAELISK.K
516	525	2	1047.55	4.8	0	31.2	23.9	95.00%	K.TGEELTSAIK.V		K.TGEELTSAIK.V
228	237	2	949.49	5	1	30.2	24.5	95.00%	R.AAGAESAFVK.L		R.AAGAESAFVK.L
532	555	2	2764.23	2.9	1	69.2	27.2	95.00%	K.EGPTLIECAIDTDDCTQELVDWG K.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.EGPTLIECAIDTDDCTQELVDWG K.A
147	159	2	1436.71	-2.2	0	63.4	26.1	95.00%	R.AEDAPVMIDHAIR.Q		R.AEDAPVMIDHAIR.Q
329	340	2	1425.76	4.3	1	95.2	22.6	95.00%	R.VYMAEFLELLAK.K		R.VYMAEFLELLAK.K
146	159	3	1592.82	5.1	1	58.6	24.9	95.00%	K.RAEDAPVMIDHAIR.Q		K.RAEDAPVMIDHAIR.Q
369	378	2	1157.64	5	1	28	22.1	94.20%	K.AALNRVEVMR.Q		K.AALNRVEVMR.Q

137	146	2	1101.64	5.4	1	51.2	19.8	95.00%	K.LTCAAVAIKR.A	Carbamidomethyl (+57)	K.LTCAAVAIKR.A
26	37	2	1429.72	4.2	1	38.3	24.3	95.00%	K.NHFVVPGDYNLR.L		K.NHFVVPGDYNLR.L
2	14	2	1402.63	-1.6	2	68.8	27	95.00%	M.TKDAESTMTVGTY.L		-.MTKDAESTMTVGTYLAQR.L
464	474	2	1310.81	4.6	1	66.2	13.2	95.00%	K.LPVLIFLLNNR.G		K.LPVLIFLLNNR.G
238	247	2	1078.51	-0.65	1	36.4	24.8	95.00%	K.LAEALNCAAF.I	Carbamidomethyl (+57)	K.LAEALNCAAFIMPAAK.G
450	461	2	1402.73	0.71	0	58.4	23.6	95.00%	F.QLTGQEISQMIR.H		R.TIVMVGDGSFQLTGQEISQMIR.H
216	225	3	1064.66	3.8	0	29.3	12	95.00%	K.EKPILLAGPK.L		K.EKPILLAGPK.L
80	94	2	1397.68	0.99	1	45.2	25.8	95.00%	Y.SVGALTAFDGIGGAY.A		R.SNGIACAVVTYSVGALTAFDGIGGAYAENLPVILVSGSPNTNDLSSGHLLHHTLGTHDFEYQMEIAK.K
136	146	3	1229.73	4.2	1	53.3	17.2	95.00%	K.KLTCAAVAIKR.A	Carbamidomethyl (+57)	K.KLTCAAVAIKR.A
160	203	4	4837.52	3.1	1	48.7	20.2	95.00%	R.QAILQHKPVYIEIPTNMANQPCPVPGPISAVISPEISDKESLEK.A	Carbamidomethyl (+57)	R.QAILQHKPVYIEIPTNMANQPCPVPGPISAVISPEISDKESLEK.A
440	461	2	2409.21	3.3	1	90.9	24	95.00%	R.TIVMVGDGSFQLTGQEISQMIR.H		R.TIVMVGDGSFQLTGQEISQMIR.H
238	253	2	1690.85	4.5	1	52.2	24.4	95.00%	K.LAEALNCAAFIMPAAK.G	Deamidation (+1)/ Carbamidomethyl (+57)	K.LAEALNCAAFIMPAAK.G
264	278	2	1599.74	-0.0054	1	73.2	27	95.00%	Y.AGVYWGEVSSSETTK.A		K.NYAGVYWGEVSSSETTK.A
204	215	2	1258.72	4.6	1	64.8	20.6	95.00%	K.ATDIAAELISKK.E		K.ATDIAAELISKK.E
304	316	2	1400.69	0.41	1	47	25.1	95.00%	R.AAPNPNILLNSDY.T		R.AAPNPNILLNSDYTSVSIPGYVFSR.V
19	25	2	770.49	4.3	0	34.4	16	95.00%	R.LVEIGIK.N		R.LVEIGIK.N
462	474	3	1575.97	4.8	2	29.2	7.78	95.00%	R.HKLPVLIFLLNNR.G		R.HKLPVLIFLLNNR.G
494	508	2	1645.69	-1.7	1	84.9	26.8	95.00%	W.DFAAFCESLNGETGK.A	Carbamidomethyl (+57)/ Deamidation (+1)	R.IQNWDFAAFCESLNGETGK.A
2	18	2	1870.92	4.3	2	129	25.4	95.00%	M.TKDAESTMTVGTYLAQR.L		-.MTKDAESTMTVGTYLAQR.L
392	405	2	1583.69	-0.21	1	70.2	26.5	95.00%	Y.AETGDSWFNGLQMK.L	Deamidation (+1)	R.QIQGLVDSNTTLYAETGDSWFNGLQMK.L
136	145	2	1073.63	3.9	1	39.6	17.2	95.00%	K.KLTCAAVAIK.R	Carbamidomethyl (+57)	K.KLTCAAVAIK.R
4	18	2	1641.77	4.2	1	65.2	26.2	95.00%	K.DAESTMTVGTYLAQR.L		K.DAESTMTVGTYLAQR.L
268	278	2	1209.55	1.2	1	56.3	25.4	95.00%	Y.WGEVSSSETTK.A		K.NYAGVYWGEVSSSETTK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
10	PMGY_SCHPO	68.25%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
122	139	2	1962.92	-0.12	1	81.3	27	95.00%	R.SYDIAPPNGESLKDTAER.V	Deamidation (+1)	R.SYDIAPPNGESLKDTAER.V
111	120	2	1271.65	5.7	1	79.8	23.6	95.00%	K.WGAEQVQIWR.R		K.WGAEQVQIWR.R
30	40	3	1157.63	0.6	1	33.4	22.9	95.00%	W.KDPALSETGIK.E		K.LNLFTGWKDPALSETGIK.E
70	90	2	2429.25	3.7	1	89.6	23.2	95.00%	K.TCQIILEEVGEPNLETIKSEK.L	Carbamidomethyl (+57)	K.TCQIILEEVGEPNLETIKSEK.L
27	40	3	1501.78	0.73	1	51.2	23.6	95.00%	F.TGWKDPALSETGIK.E		K.LNLFTGWKDPALSETGIK.E
146	157	2	1320.78	4.4	1	36.9	14.3	95.00%	K.STIVPHILKGEK.V		K.STIVPHILKGEK.V
2	14	2	1439.81	5.3	0	52	18.1	95.00%	M.TTEAAPNLLVLTR.H	Acetyl (+42)	-.MTTEAAPNLLVLTR.H
70	87	2	2085.08	4.2	0	96.7	23.3	95.00%	K.TCQIILEEVGEPNLETIK.S	Carbamidomethyl (+57)	K.TCQIILEEVGEPNLETIK.S
169	184	2	1730.91	-1.1	0	85.6	22.7	95.00%	R.ALIMDLEGLTGDQIVK.R	Oxidation (+16)	R.ALIMDLEGLTGDQIVK.R
169	185	2	1871.02	2.9	1	111	19.8	95.00%	R.ALIMDLEGLTGDQIVKR.E		R.ALIMDLEGLTGDQIVKR.E
158	168	2	1149.67	4.5	0	26.5	16.4	92.20%	K.VLIAAHGNSLR.A		K.VLIAAHGNSLR.A
95	104	2	1169.58	4.8	1	46.4	24.2	95.00%	R.YYGDLQGLNK.D		R.YYGDLQGLNK.D
186	202	2	1854	4.1	1	68.2	20.9	95.00%	R.ELATGVPIVYHLDKDGK.Y		R.ELATGVPIVYHLDKDGK.Y
1	14	2	1528.84	4.4	0	53	21.9	95.00%	-.MTTEAAPNLLVLTR.H		-.MTTEAAPNLLVLTR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
11	GLYD_SCHPO	55.03%	100%	20

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
160	179	2	2321.05	-0.48	1	35.6	27.2	95.00%	R.VDPNTGLIDYDMLEHDAQLF.R	Oxidation (+16)	R.VDPNTGLIDYDMLEHDAQLFRPK.I
97	123	3	2996.43	3.4	1	55	25.2	95.00%	K.WGVNVQCLSGSPANMQVYQAIMPPHGR.L	Carbamidomethyl (+57)	K.WGVNVQCLSGSPANMQVYQAIMPPHGR.L
59	67	2	998.45	5.1	1	32.9	24.3	95.00%	K.YSEGYPGAR.Y		K.YSEGYPGAR.Y

277	302	3	2725.45	2.8	1	25.2	18.4	94.10%	K.INFSVFPGHQGGPHNHTITALAVALK.Q		K.INFSVFPGHQGGPHNHTITALAVALK.Q
124	139	2	1652.8	-0.062	1	49.2	25.9	95.00%	R.LMGLDLPSGGHLSHGY.Q		R.LMGLDLPSGGHLSHGYQTDTK.K
334	349	2	1669.84	3.9	0	85	24.1	95.00%	K.LAADGTDSHMVLVDVK.S		K.LAADGTDSHMVLVDVK.S
303	312	2	1314.55	-0.66	2	31.3	25.9	95.00%	K.QCQEPAYKEY.Q	Carbamidomethyl (+57)	K.QCQEPAYKEYQAQVVK.N
2	24	2	2616.28	0.62	1	54	24.6	95.00%	M.SSNDSIMLTPLKEQDPTVAEIMR.H	Acetyl (+42)	-.MSSNDSIMLTPLKEQDPTVAEIMR.H
183	193	2	1209.62	4.5	1	57.8	24.1	95.00%	K.ILVAGTSAYCR.L	Carbamidomethyl (+57)	K.ILVAGTSAYCR.L
453	467	2	1734.83	4.4	2	41.4	26	95.00%	K.EVAEWASSFPLADKW.-		K.EVAEWASSFPLADKW.-
361	371	2	1254.76	4.6	0	48.8	16.3	95.00%	R.VLELINIVTNK.N		R.VLELINIVTNK.N
458	467	2	1120.55	-1.5	2	37	23.8	95.00%	W.ASSFPLADKW.-		K.EVAEWASSFPLADKW.-
74	85	2	1550.75	4.7	1	96.3	26	95.00%	K.FIDQIETLCQER.A	Carbamidomethyl (+57)	K.FIDQIETLCQER.A
86	96	2	1129.62	5.1	1	54.8	23.3	95.00%	R.ALAAFNLDPAK.W		R.ALAAFNLDPAK.W
413	422	2	1075.61	4.3	1	49.9	21.1	95.00%	R.ALTFAANLQK.E		R.ALTFAANLQK.E
438	452	2	1729.9	3.9	1	75.9	22.5	95.00%	K.LGEGEQYPELVQLQK.E		K.LGEGEQYPELVQLQK.E
46	58	2	1321.64	4.2	0	41.4	25.9	95.00%	R.AVMDALGSVMSNK.Y		R.AVMDALGSVMSNK.Y
160	182	3	2686.31	2.9	1	31.8	24.1	95.00%	R.VDPNTGLIDYDMLEHDAQLFRPK.I		R.VDPNTGLIDYDMLEHDAQLFRPK.I
436	452	2	1929.02	-2.6	2	56.2	22.8	95.00%	K.AKLGEGEQYPELVQLQK.E		K.AKLGEGEQYPELVQLQK.E
406	412	2	878.45	4.3	1	35.8	24	95.00%	R.VVDYIDR.A		R.VVDYIDR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
12	SAHH_SCHPO	49.19%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
20	35	2	1782.92	-1.5	0	79	23.9	95.00%	K.ELEIAENEMPGLIAVR.E		K.ELEIAENEMPGLIAVR.E
216	227	2	1117.62	4.3	1	46.5	22.5	95.00%	K.VAVVAGFGDVGK.G		K.VAVVAGFGDVGK.G
119	143	3	2681.36	2.8	1	63.5	22.9	95.00%	K.SFPSGKPLNMILDDGGDLTALVHER.H		K.SFPSGKPLNMILDDGGDLTALVHER.H
176	187	2	1255.68	4.6	0	42.1	21.2	95.00%	K.VPAINVNDSVTK.S		K.VPAINVNDSVTK.S
318	328	2	1281.71	3.7	0	30.2	20.1	95.00%	K.DVVNIKPQVDR.Y		K.DVVNIKPQVDR.Y
345	357	2	1371.66	2.5	1	32.2	24.8	95.00%	R.LVNLGCATGHPSF.V	Carbamidomethyl (+57)	R.LVNLGCATGHPSFVMSCSFTNQVLAQIALWTDNTSYPLGVHMLPK.K
407	427	2	2266.17	-0.97	1	80.6	22.7	95.00%	K.LTTLTSVQSDYLGIPVDGPYK.A		K.LTTLTSVQSDYLGIPVDGPYK.A
314	328	3	1665.93	5.5	1	30.5	18.1	95.00%	K.ANAKDVVNIKPQVDR.Y		K.ANAKDVVNIKPQVDR.Y
8	18	2	1118.61	3.2	1	77.1	22.5	95.00%	K.VADISLAAFGR.K		K.VADISLAAFGR.K
269	280	2	1367.66	4	1	40.1	26.3	95.00%	K.EGQIFVTTTGCR.D	Carbamidomethyl (+57)	K.EGQIFVTTTGCR.D
153	167	2	1647.81	-2.2	1	74.6	25.8	95.00%	R.GISEETTTGVHNLYK.M		R.GISEETTTGVHNLYK.M
19	35	2	1911.01	-0.28	1	83.7	21.4	95.00%	R.KELEIAENEMPGLIAVR.E		R.KELEIAENEMPGLIAVR.E
336	344	2	1006.6	5	0	31.2	14.6	95.00%	R.HIILLADGR.L		R.HIILLADGR.L
174	187	3	1496.86	5	1	47.8	17.9	95.00%	K.LKVPAINVNDSVTK.S		K.LKVPAINVNDSVTK.S
103	118	2	2053.94	4.3	1	72.2	26.8	95.00%	K.GETEEEYLWCIEQQLK.S	Carbamidomethyl (+57)	K.GETEEEYLWCIEQQLK.S
240	268	3	3119.56	4.6	1	62	22.3	95.00%	R.VIVTEVDPINALQAAMDGFEVTTMEEAVK.E		R.VIVTEVDPINALQAAMDGFEVTTMEEAVK.E
318	332	3	1815	4.1	2	25.1	20	93.90%	K.DVVNIKPQVDRYELK.N		K.DVVNIKPQVDRYELK.N
314	329	2	1828.98	0.54	2	44.6	21.3	95.00%	K.ANAKDVVNIKPQVDRY.E		K.ANAKDVVNIKPQVDRYELK.N
153	166	2	1519.71	-1.4	1	34.8	25.8	95.00%	R.GISEETTTGVHNLY.K		R.GISEETTTGVHNLYK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
13	TPIS_SCHPO	65.46%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
160	174	2	1615.9	-0.32	1	77	19.6	95.00%	K.IVIAYEPVWAIGTGK.T		K.IVIAYEPVWAIGTGK.T
175	189	2	1678.83	-1.4	0	90	25.6	95.00%	K.TATPEQAQEVHAEIR.K		K.TATPEQAQEVHAEIR.K
135	145	2	1242.66	4.7	0	39.7	22.2	95.00%	R.EANETINVVVR.Q		R.EANETINVVVR.Q
175	190	2	1806.92	-1.5	1	69	24.6	95.00%	K.TATPEQAQEVHAEIRK.W		K.TATPEQAQEVHAEIRK.W
71	90	2	2043.94	-0.59	1	56	27.2	95.00%	K.NGAYTGENSAQSLIDAGITY.T		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R

206	218	2	1324.61	4.4	1	76.9	26.4	95.00%	R.VIYGGSVNGGNCK.E	Deamidation (+1)/ Carbamidomethyl (+57)	R.VIYGGSVNGGNCK.E
71	98	3	2925.39	4	1	98.2	24.9	95.00%	K.NGAYTGENSAQSLIDAGITYTLTGHSER.R		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R
58	70	2	1389.73	3.4	1	50	23.5	95.00%	K.DIGVGAQNVFDKK.N		K.DIGVGAQNVFDKK.N
115	134	3	2176.12	2.2	1	34.6	23.6	95.00%	K.FALEQGLTVVACIGETLAER.E	Carbamidomethyl (+57)	K.FALEQGLTVVACIGETLAER.E
32	52	2	2422.27	3.5	1	66.1	21.6	95.00%	K.LNVGDVETVIFPQNMYLITTR.Q		K.LNVGDVETVIFPQNMYLITTR.Q
146	159	2	1613.86	4.5	2	61.4	22.6	95.00%	R.QLNAIADKVQNWSK.I		R.QLNAIADKVQNWSK.I
196	205	2	971.55	5.3	0	76.1	21.5	95.00%	K.LGASVAEGLR.V		K.LGASVAEGLR.V
206	220	2	1599.74	0.012	2	32.8	26.8	95.00%	R.VIYGGSVNGGNCKEF.L	Carbamidomethyl (+57)	R.VIYGGSVNGGNCKEFLK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
14	THI3_SCHPO	40.17%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	127	2	1090.54	4.7	0	29.6	24	95.00%	K.IQLDDLCSK.F	Carbamidomethyl (+57)	K.IQLDDLCSK.F
74	95	2	2353.26	0.93	1	95.1	20.4	95.00%	R.GYPVTSFGSLLNEPFTGLITLK.G		R.GYPVTSFGSLLNEPFTGLITLK.G
316	327	2	1385.71	3.6	0	53.6	23.8	95.00%	K.QEAIAEIQDEIK.Q		K.QEAIAEIQDEIK.Q
222	238	2	1901.96	-0.26	2	38	25.3	95.00%	R.AIHSATLDMLKDPVQTY.K		R.AIHSATLDMLKDPVQTYK.E
128	139	2	1325.67	4.2	1	42.4	24.2	95.00%	K.FGLSPSDYTAIR.C		K.FGLSPSDYTAIR.C
316	329	2	1641.86	3.3	1	68.9	22.9	95.00%	K.QEAIAEIQDEIKQK.G		K.QEAIAEIQDEIKQK.G
63	71	2	954.54	4.5	0	51.1	16.2	95.00%	K.AMIHTLAAK.A		K.AMIHTLAAK.A
222	239	2	2030.06	3.2	2	79.8	21.9	95.00%	R.AIHSATLDMLKDPVQTYK.E		R.AIHSATLDMLKDPVQTYK.E
110	118	2	968.5	4.9	1	27.7	22.7	93.80%	R.IGYVGEFGK.I		R.IGYVGEFGK.I
330	339	2	992.51	5.7	1	44.3	24.5	95.00%	K.GGVFSGNSLR.Y		K.GGVFSGNSLR.Y
89	95	2	744.47	-0.43	0	43.8	11.1	95.00%	F.TGLITLK.G		R.GYPVTSFGSLLNEPFTGLITLK.G
304	327	3	2740.31	0.65	1	49.1	25.4	95.00%	W.ELDPDEKDPMGKQEAIAEIQDEIK.Q		R.LGIIPQDFEPNCTNGYLTWELDPDEKDPMGKQEAIAEIQDEIK.Q
304	315	3	1372.62	0.94	1	40.5	27	95.00%	W.ELDPDEKDPMGK.Q		R.LGIIPQDFEPNCTNGYLTWELDPDEKDPMGK.Q
81	95	2	1601.9	-0.33	1	71.4	18.8	95.00%	F.GSLLNEPFTGLITLK.G		R.GYPVTSFGSLLNEPFTGLITLK.G
33	56	2	2409.27	1.3	0	76.4	20.6	95.00%	R.EGIEVAILEPTNPSDVTALIGSGK.V		R.EGIEVAILEPTNPSDVTALIGSGK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
15	METK_SCHPO	60.99%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
186	206	3	2311.19	3.8	1	67.9	23.5	95.00%	R.RVDTIVVSAQHADSISTEDLR.S		R.RVDTIVVSAQHADSISTEDLR.S
339	349	2	1256.73	4.3	1	36.5	19.9	95.00%	K.NFDLRPGVLVK.S		K.NFDLRPGVLVK.S
6	19	2	1501.7	-2	1	68.7	26.1	95.00%	F.LFTSESVGEGHPDK.I		-.MAQTFLFTSESVGEGHPDK.I
129	146	3	1989.12	1.3	1	27.4	16.3	95.00%	Y.ATDETPEKLPLTILLAHK.L		K.ALEELGAGDQGIMFGYATDETPEKLPLTILLAHK.L
169	185	2	1946.97	4.5	1	49.1	25.2	95.00%	K.TQVTIEYEEENGAVIPR.R		K.TQVTIEYEEENGAVIPR.R
147	155	2	931.5	4.5	0	58	23.1	95.00%	K.LNAAMSVAR.R		K.LNAAMSVAR.R
20	40	3	2423.15	4	2	37.1	26	95.00%	K.ICDQISDAILDACLKDDPFSK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.ICDQISDAILDACLKDDPFSK.V
113	126	2	1465.68	1.3	1	39.9	25.8	95.00%	K.ALEELGAGDQGIMF.G	Oxidation (+16)	K.ALEELGAGDQGIMFGYATDETPEK.L
237	251	2	1429.74	3.6	1	73.6	23.6	95.00%	R.FVVGGPQGDAGLTGR.K		R.FVVGGPQGDAGLTGR.K
90	112	3	2612.3	3.4	1	62.4	23.8	95.00%	K.TCNVLVAIEQQSPDIAQGLHYEK.A	Carbamidomethyl (+57)	K.TCNVLVAIEQQSPDIAQGLHYEK.A
328	338	2	1257.74	4.7	1	49.3	18.9	95.00%	K.TSAELVEIIRK.N		K.TSAELVEIIRK.N
365	374	2	1201.55	0.4	1	33.4	25.6	95.00%	Y.GHFTDQSKPW.E		K.LQTPFYLSTASYGHFTDQSKPWEQPK.E
308	327	2	2053.08	5	1	69	22.2	95.00%	Y.AIGVAEPLSIFVNTYGTSSK.T		R.CLVQLSYAIGVAEPLSIFVNTYGTSSK.T

186	212	4	3010.56	2.5	1	34.2	20.5	95.00%	R.RVDTIVVSAQHADSISTEDLRSEILEK.I		R.RVDTIVVSAQHADSISTEDLRSEILEK.I
291	299	2	856.52	4.2	0	28.1	20.3	94.30%	K.SLVAAGLAR.R		K.SLVAAGLAR.R
213	226	3	1572.93	4.6	0	37.1	14.1	95.00%	K.IIKPTVPAHLLDEK.T		K.IIKPTVPAHLLDEK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
16	THI2_SCHPO	40.85%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
175	187	2	1431.8	-1.3	1	71.2	20.3	95.00%	K.LFNATAVEDLIVK.E		K.LFNATAVEDLIVK.E
309	320	2	1332.68	5.8	1	60	24.4	95.00%	K.AAQEALAIFDER.K		K.AAQEALAIFDER.K
137	154	2	2036.99	-0.49	1	60.2	26	95.00%	F.LNEIGVPYEDEGDYVVVK.H		R.KPADLFLNEIGVPYEDEGDYVVVK.H
39	49	2	1291.56	-1.1	1	45.2	26.2	95.00%	K.AYPTYSLDESF.S		K.AYPTYSLDESFSFAPIR.E
2	15	2	1400.77	3.8	1	74.5	21.2	95.00%	M.APATAVVTPQTAFK.T		-.MAPATAVVTPQTAFK.T
244	263	3	2296.15	3.2	0	39.6	24.6	95.00%	R.LASAQLVSNLHDMRPLDMNR.A	Oxidation (+16)	R.LASAQLVSNLHDMRPLDMNR.A
175	190	3	1745.96	4.6	1	37.2	20.4	95.00%	K.LFNATAVEDLIVKEGK.D		K.LFNATAVEDLIVKEGK.D
309	321	2	1460.77	4.2	1	58.6	22.9	95.00%	K.AAQEALAIFDERK.A		K.AAQEALAIFDERK.A
244	270	3	3048.6	3.6	1	30.2	18.5	95.00%	R.LASAQLVSNLHDMRPLDMNRAEDLIVK.G		R.LASAQLVSNLHDMRPLDMNRAEDLIVK.G
295	308	2	1459.67	4	1	71.7	26.5	95.00%	R.MGPTFGGMMFSGIK.A		R.MGPTFGGMMFSGIK.A
177	187	2	1171.64	-1.5	0	26.9	20.9	92.70%	F.NATAVEDLIVK.E		K.LFNATAVEDLIVK.E
274	294	2	2254.05	3.3	1	79.8	26.7	95.00%	R.EVFPGMIVGGMELSEFDGANR.M		R.EVFPGMIVGGMELSEFDGANR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
17	HSP90_SCHPO	34.38%	100%	20

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
522	533	2	1405.62	4.2	0	49.6	26.5	95.00%	K.DGLELEETDEEK.A		K.DGLELEETDEEK.A
275	287	2	1499.68	-1.4	2	50.6	26.9	95.00%	R.NPSEVTKEEYASF.Y		R.NPSEVTKEEYASFYK.S
465	474	2	1170.6	4.5	1	29.7	22.9	95.00%	K.NIYFITGESK.Q		K.NIYFITGESK.Q
567	587	2	2339.12	5.7	1	92.3	26.3	95.00%	K.IVGSPCLLTTGQYGWSANMER.I	Carbamidomethyl (+57)	K.IVGSPCLLTTGQYGWSANMER.I
440	458	2	2199.07	3.1	1	92.7	26.3	95.00%	R.YNSLNSPDDLISLEDYITK.M		R.YNSLNSPDDLISLEDYITK.M
596	606	2	1234.5	4.9	1	67.2	25.9	95.00%	R.DTSMSAYMSSR.K		R.DTSMSAYMSSR.K
362	375	2	1512.78	3.1	0	77.4	23.1	95.00%	K.GVVDSEDLPLNLSR.E		K.GVVDSEDLPLNLSR.E
516	536	3	2372.21	2.8	1	83.5	23.3	95.00%	K.LVNITKDGLELEETDEEKAAR.E		K.LVNITKDGLELEETDEEKAAR.E
198	212	2	1787.96	4.4	1	31.7	22.1	95.00%	K.HSEFISYPIQLVVTR.E		K.HSEFISYPIQLVVTR.E
522	536	2	1703.78	-1.8	1	80.6	27.4	95.00%	K.DGLELEETDEEKAAR.E		K.DGLELEETDEEKAAR.E
290	302	2	1526.74	4	1	75.7	26.1	95.00%	K.SLTNDWEDHLAVK.H		K.SLTNDWEDHLAVK.H
475	487	2	1548.8	4.5	1	76.3	24	95.00%	K.QAVENSPFLEIFR.A		K.QAVENSPFLEIFR.A
88	99	2	1282.73	5.3	0	55.5	17.7	95.00%	K.NDLINNLGVIAK.S		K.NDLINNLGVIAK.S
34	45	2	1274.64	4	0	41.6	24.4	95.00%	R.ELISNASDALDK.I		R.ELISNASDALDK.I
255	267	2	1520.76	4.6	1	46.2	25	95.00%	K.VKETTTETEELNK.T		K.VKETTTETEELNK.T
321	330	2	1176.6	4.2	2	27.8	24.2	93.90%	R.RAPMDLFEAK.R		R.RAPMDLFEAK.R
422	436	2	1574.85	-0.91	0	44	21.9	95.00%	K.LGIHEDAANRPALAK.L		K.LGIHEDAANRPALAK.L
48	64	2	1947.92	-0.11	2	26.8	26.1	90.80%	R.YQSLSDPHALDAEKDLF.I		R.YQSLSDPHALDAEKDLFIR.I
34	47	2	1543.83	3.9	1	76.1	22.7	95.00%	R.ELISNASDALDKIR.Y		R.ELISNASDALDKIR.Y
504	514	2	1248.67	1.3	2	29.2	22	95.00%	Y.AVTQLKEFEGK.K		K.FDVLFMVDPIDEYAVTQLKEFEGK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
18	HSP72_SCHPO	42.97%	100%	22

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
327	340	2	1400.77	3.9	0	39.7	21.7	95.00%	K.ASVNEIVLVGGSTR.I		K.ASVNEIVLVGGSTR.I
55	66	2	1384.65	-0.66	1	40.5	26.3	95.00%	K.NQVAMNPHNTIF.D		K.NQVAMNPHNTIFDAK.R
170	181	2	1245.66	-1.1	1	38.1	22.9	95.00%	R.IINEPTAAAIAY.G		R.IINEPTAAAIAYGLDR.S
125	136	2	1324.65	4.5	2	66.6	25.3	95.00%	K.MRETAEAYLGGK.V		K.MRETAEAYLGGK.V
96	110	2	1689.9	5	1	31.8	22.8	95.00%	K.DGKPVLQVEYKGETK.T		K.DGKPVLQVEYKGETK.T

370	385	2	1516.77	0.38	0	77	24.5	95.00%	Y.GAAVQAAVLTGDTSEK.T		K.SINPDEAVAYGAAVQAAVLTGDTSEK.T
448	457	2	1194.61	0.26	2	39.7	24.7	95.00%	R.TKDCNLLGKF.E	Carbamidomethyl (+57)	R.TKDCNLLGKFELSGIPPAPR.G
219	234	2	1647.72	4.3	1	72.5	27.2	95.00%	K.ATAGDTHLGGEDFDSR.L		K.ATAGDTHLGGEDFDSR.L
20	34	3	1699.82	-1.1	1	46.4	26	95.00%	F.SNNRVEIIANDQGNR.T	Deamidation (+1)	K.SIGIDLGTTYSCVGHFSNNRVEIIANDQGNR.T
324	340	2	1742.96	4.2	1	81.9	20.6	95.00%	K.VDKASVNEIVLVGGSTR.I		K.VDKASVNEIVLVGGSTR.I
457	467	2	1182.65	4.4	1	28.3	19.8	94.50%	K.FELSGIPPAPR.G		K.FELSGIPPAPR.G
35	47	2	1486.7	4.2	1	60.5	26.3	95.00%	R.TTPSYVAFTDTER.L		R.TTPSYVAFTDTER.L
608	647	3	3499.6	0.71	1	41.9	25.5	95.00%	K.IYQAGGAPGGMPGAAPGAAPGAAPGAAPGGDNGPEVEEVD.-		K.IYQAGGAPGGMPGAAPGAAPGAAPGAAPGGDNGPEVEEVD.-
111	124	2	1611.8	4	1	69	25.2	95.00%	K.TFTPEEISSMVLMK.M		K.TFTPEEISSMVLMK.M
538	548	2	1351.66	4.4	1	37.5	25.4	95.00%	K.NHLESYAYSLR.N		K.NHLESYAYSLR.N
594	607	2	1556.83	4.2	1	73.7	22.8	95.00%	K.QKELESVANPIMAK.I		K.QKELESVANPIMAK.I
137	153	2	1880.93	4	1	55	25.1	95.00%	K.VTDAVVTVPAYFNDSQR.Q		K.VTDAVVTVPAYFNDSQR.Q
76	86	2	1309.56	4.9	1	34.7	25.9	95.00%	K.FDDPEVQSDMK.H		K.FDDPEVQSDMK.H
170	185	2	1686.9	4	1	94.1	22.1	95.00%	R.IINEPTAAAIAYGLDR.S		R.IINEPTAAAIAYGLDR.S
55	69	2	1698.82	4.2	1	74.8	25.6	95.00%	K.NQVAMNPHNTIFDAK.R		K.NQVAMNPHNTIFDAK.R
430	445	2	1786.89	0.61	1	64.8	25	95.00%	Y.SDNQPGVLIQVFEGER.A		K.SEIFSTYSDNQPGVLIQVFEGER.A
24	34	2	1227.63	5.8	0	33.2	24.3	95.00%	R.VEIIANDQGNR.T		R.VEIIANDQGNR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
19	EF3_SCHPO	35.63%	100%	27

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
333	350	2	1970	-0.81	0	88.4	23.7	95.00%	K.IPEVSTAANPEVCLETLK.A	Carbamidomethyl (+57)	K.IPEVSTAANPEVCLETLK.A
596	621	4	2935.49	3.5	1	34.9	21.6	95.00%	K.DVSSIIVSHDSGFLDHVVQAIIHYER.F		K.DVSSIIVSHDSGFLDHVVQAIIHYER.F
920	933	2	1664.89	1.4	1	27.4	21.7	93.40%	W.LRPHVIVLDEPTNY.L		K.LVLAACTWLRPHVIVLDEPTNYLDR.D
514	530	3	1948.1	0.67	1	27.1	14.1	95.00%	F.ILQDPAVPIKDRDEIVK.A		R.TVYVEHDIDESEADTPSVDFILQDPAVPIKDRDEIVK.A
75	92	2	1797.85	0.16	1	43.5	26.6	95.00%	K.GLEAVANHGSVAADVEPY.L		K.GLEAVANHGSVAADVEPYLVELLPAVIAK.V
75	103	3	2944.6	3.2	1	47.9	17.2	95.00%	K.GLEAVANHGSVAADVEPYLVELLPAVIAK.V		K.GLEAVANHGSVAADVEPYLVELLPAVIAK.V
972	994	3	2346.07	0.65	1	44.6	27.2	95.00%	W.AVNNGHMTPSGHNWVSGQGSGPR.I		R.EFTEGLTEEVWAVNNGHMTPSGHNWVSGQGSGPR.I
20	34	2	1599.73	5	0	78.4	27.1	95.00%	K.HLTVCDAAEEADAAK.A	Carbamidomethyl (+57)	K.HLTVCDAAEEADAAK.A
202	213	2	1359.69	4.1	0	43.2	24.4	95.00%	K.VCTLIANADIDR.F	Carbamidomethyl (+57)	K.VCTLIANADIDR.F
172	188	2	1928.99	-1.4	1	43.8	23.8	95.00%	Y.SLPQIIPVVSESMWDTK.A		K.MNSLQLLDVLVEVAPSQLSYSLPQIIPVVSESMWDTK.A
859	870	2	1330.7	4.7	1	35.3	23.3	95.00%	K.MVAEVDRAEALK.S		K.MVAEVDRAEALK.S
35	59	2	2604.32	3.9	1	66.4	23	95.00%	K.ALASFVNGPIEEQDAPSQVFSAISK.Q		K.ALASFVNGPIEEQDAPSQVFSAISK.Q
351	367	2	1809.03	4.2	1	72.9	16.3	95.00%	K.AVLGEIKVPTNEEVIAK.Y		K.AVLGEIKVPTNEEVIAK.Y
281	294	2	1550.87	-1.7	1	64.8	19.1	95.00%	K.LVEDPQVVAPFLPK.L		K.LVEDPQVVAPFLPK.L
40	54	2	1628.77	0.29	1	48.7	26.3	95.00%	F.VNGPIEEQDAPSQVF.S		K.ALASFVNGPIEEQDAPSQVFSAISK.Q
479	493	2	1636.88	3.9	1	73.9	22.1	95.00%	R.AIVNGQVEGFPTHLR.T		R.AIVNGQVEGFPTHLR.T
419	440	2	2477.96	-0.64	1	69	26.5	95.00%	K.IPGGASHAEEEEEGEDLCNCEF.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.IPGGASHAEEEEEGEDLCNCEFSLAYGAK.I
419	447	3	3168.34	2.9	1	77.1	26.5	95.00%	K.IPGGASHAEEEEEGEDLCNCEFSLAYGAK.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.IPGGASHAEEEEEGEDLCNCEFSLAYGAK.I
836	849	2	1688.78	-1.7	1	38.1	27.2	95.00%	R.WVPMMSSDNAWLPR.G		R.WVPMMSSDNAWLPR.G
133	147	2	1550.87	3.9	0	70.6	18.5	95.00%	K.AIVPSVLESIHTTGK.W		K.AIVPSVLESIHTTGK.W
766	777	2	1368.59	4	1	45.5	26.3	95.00%	R.FQSGEDLEAMDK.A		R.FQSGEDLEAMDK.A
881	900	3	2293.11	2.6	0	44.8	25.5	95.00%	K.EIEEHCSLLGLDAELVSHSR.I	Carbamidomethyl (+57)	K.EIEEHCSLLGLDAELVSHSR.I

494	513	2	2266.98	-0.052	1	43.2	27.3	95.00%	R.TVYVEHDIDESEADTPSVDF.I		R.TVYVEHDIDESEADTPSVDFILQDPAVPIK.D
358	367	2	1098.6	4.8	0	47.3	20.5	95.00%	K.VPTNEEVIAK.Y		K.VPTNEEVIAK.Y
35	54	2	2118.03	0.18	1	63.2	26	95.00%	K.ALASFVNGPIEEQDAPSQVF.S		K.ALASFVNGPIEEQDAPSQVFSAISK.Q
880	900	3	2421.2	2	1	49.3	25.1	95.00%	R.KEIEEHCSLLGLDAELVSHSR.I	Carbamidomethyl (+57)	R.KEIEEHCSLLGLDAELVSHSR.I
325	350	3	2738.42	3.2	1	45.8	20.7	95.00%	R.VGNVVDGKIPEVSTAANPEVCLETLK.A	Carbamidomethyl (+57)	R.VGNVVDGKIPEVSTAANPEVCLETLK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
20	A1EGU1_SCHPO	46.55%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
457	479	2	2580.33	2.4	1	74	22.4	95.00%	K.YVISQCNNALLYPALGVACVLSR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.YVISQCNNALLYPALGVACVLSR.C
408	433	3	2988.58	2.9	1	71.1	18.6	95.00%	K.HVERPIIFPISNPTTLMEAKPDQIDK.W		K.HVERPIIFPISNPTTLMEAKPDQIDK.W
44	57	2	1634.91	4.4	0	89.1	19.9	95.00%	R.LPPIVETLQQQVDR.C		R.LPPIVETLQQQVDR.C
439	452	2	1418.82	-2.1	0	62.7	16.8	95.00%	K.ALIATGSPLPPLNR.N		K.ALIATGSPLPPLNR.N
408	438	5	3561.84	2.8	2	46.8	19.2	95.00%	K.HVERPIIFPISNPTTLMEAKPDQIDKWSDGK.A		K.HVERPIIFPISNPTTLMEAKPDQIDKWSDGK.A
490	500	2	1070.58	4.5	0	54.7	21.4	95.00%	K.AASDALATVPR.S		K.AASDALATVPR.S
15	23	2	955.55	4.9	0	32.8	17.6	95.00%	K.GVTLLNSPR.Y		K.GVTLLNSPR.Y
456	479	3	2708.42	2.3	2	27.2	20.9	95.00%	K.KYVISQCNNALLYPALGVACVLSR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.KYVISQCNNALLYPALGVACVLSR.C
362	396	4	3654.89	2.7	1	43.8	18.7	95.00%	K.DSDFKEVPSGDINLESAIALVKPTILLGCSGQPGK.F	Carbamidomethyl (+57)	K.DSDFKEVPSGDINLESAIALVKPTILLGCSGQPGK.F
258	292	4	3747.95	3.3	1	51.5	18.5	95.00%	R.ILDHYRPDIACFNDDIQGTGAVALAAIIGALHVTK.S	Carbamidomethyl (+57)	R.ILDHYRPDIACFNDDIQGTGAVALAAIIGALHVTK.S
501	517	2	1828.93	-1.4	1	46.8	24.4	95.00%	R.SLFAADEALLPDLNNAR.E		R.SLFAADEALLPDLNNAR.E
367	396	3	3062.64	3.1	0	30.5	16.6	95.00%	K.EVPSGDINLESAIALVKPTILLGCSGQPGK.F	Carbamidomethyl (+57)	K.EVPSGDINLESAIALVKPTILLGCSGQPGK.F
530	547	2	1889.9	-1.4	1	77	26.3	95.00%	K.QAVSEGMSTVDLPKDDAK.L		K.QAVSEGMSTVDLPKDDAK.L
548	555	2	1085.63	3.7	2	31.8	20.6	95.00%	K.LKEWIIER.E		K.LKEWIIER.E
332	339	2	964.49	5	1	34.3	23.5	95.00%	R.GNLFMIDR.C		R.GNLFMIDR.C
245	256	2	1360.68	0.27	1	25.6	24.7	90.60%	F.IHFEDFGLANAK.R		R.EVFPEAFIHFEDFGLANAK.R
178	191	2	1553.75	3.5	0	59.3	26.2	95.00%	K.GHLMTLCAGLDPNR.F	Carbamidomethyl (+57)	K.GHLMTLCAGLDPNR.F
222	234	2	1526.73	2.5	1	68.3	26.6	95.00%	R.GEQYDSFLDNVIK.A		R.GEQYDSFLDNVIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
21	6PGD_SCHPO	56.30%	100%	23

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
188	209	3	2659.19	3.5	1	32.6	26.8	95.00%	K.MVHNGIEYGDMQLICETYDIMK.R	Carbamidomethyl (+57)	K.MVHNGIEYGDMQLICETYDIMK.R
156	166	3	1228.76	4.8	1	32.1	12.3	95.00%	R.IKPIFQTLAAK.A		R.IKPIFQTLAAK.A
167	185	2	2119.81	-1.9	1	66	26.7	95.00%	K.AGNNEPCCDWVGEQGAGHY.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.AGNNEPCCDWVGEQGAGHYVK.M
98	115	3	1971.95	5.1	1	35.5	26.1	95.00%	K.GDIIVDGGNSHYPDTTRR.C		K.GDIIVDGGNSHYPDTTRR.C
10	28	2	1896.05	0.21	0	51.8	18.3	95.00%	F.GLIGLAVMGQNLILNGADK.G		K.EVADFGLIGLAVMGQNLILNGADK.G
54	67	2	1501.78	4.1	1	57.5	23.7	95.00%	K.SIVGAHSLEEFVSK.L		K.SIVGAHSLEEFVSK.L
188	205	2	2172.91	-1.6	1	64.1	27.5	95.00%	K.MVHNGIEYGDMQLICETY.D	Deamidation (+1)/ Carbamidomethyl (+57)	K.MVHNGIEYGDMQLICETYDIMK.R
98	114	2	1815.85	4.4	1	91.7	26.6	95.00%	K.GDIIVDGGNSHYPDTTR.R		K.GDIIVDGGNSHYPDTTR.R
29	37	2	1175.49	3.9	1	36.7	26.2	95.00%	K.GFTVCCYNR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GFTVCCYNR.T
122	139	3	1718.9	4.5	2	31	23.4	95.00%	K.KGILFVGSGVSGGEEGAR.Y		K.KGILFVGSGVSGGEEGAR.Y
38	51	2	1579.79	4.7	2	35.6	25.6	95.00%	R.TTSRVDEFLANEAK.G		R.TTSRVDEFLANEAK.G
42	51	2	1134.56	4.5	1	47.7	24.7	95.00%	R.VDEFLANEAK.G		R.VDEFLANEAK.G

377	393	2	2007.98	0.13	2	41.3	26.4	95.00%	K.DITEAFREDPNLESILF.H		K.DITEAFREDPNLESILFHPFFTNGVEK.A
123	139	2	1590.81	3.9	1	62.7	24.1	95.00%	K.GILFVGSGVSGGEEGAR.Y		K.GILFVGSGVSGGEEGAR.Y
80	114	4	3722.93	3.7	2	47.4	18.6	95.00%	K.AGKPVDYLIEGLAPLLEKGDIIVDGGNSHYPDTTR.R		K.AGKPVDYLIEGLAPLLEKGDIIVDGGNSHYPDTTR.R
211	225	2	1669.74	4.6	1	69.2	26.9	95.00%	R.GLGMSCDEIADVFEK.W	Carbamidomethyl (+57)	R.GLGMSCDEIADVFEK.W
140	155	2	1669.81	4.7	1	28.8	25.5	94.50%	R.YGPSLMPGGNPAAWPR.I		R.YGPSLMPGGNPAAWPR.I
269	291	2	2504.28	3.2	1	92.8	23.3	95.00%	K.WTAQNALEMGTPVSLITEAVFAR.C		K.WTAQNALEMGTPVSLITEAVFAR.C
320	333	2	1592.8	4.1	1	67.9	25	95.00%	K.QLIDDLEDALYASK.I		K.QLIDDLEDALYASK.I
437	449	2	1379.79	4.1	0	52	17.2	95.00%	R.SAVLPANLLQAQR.D		R.SAVLPANLLQAQR.D
80	97	2	1925.09	-0.48	1	65.5	17.8	95.00%	K.AGKPVDYLIEGLAPLLEK.G		K.AGKPVDYLIEGLAPLLEK.G
467	478	2	1407.72	0.84	2	25.7	24.9	90.90%	K.SLPADKDIHINW.T		K.SLPADKDIHINWTGHGGNISATTYDA.-
5	28	2	2457.3	3	1	76	20.5	95.00%	K.EVADFGLIGLAVMGQNLILNGADK.G		K.EVADFGLIGLAVMGQNLILNGADK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
22	K6PF_SCHPO	35.14%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
364	380	3	1831.87	-1.2	0	65.1	26.4	95.00%	R.ICEAVDSISSTAISHSR.A	Carbamidomethyl (+57)	R.ICEAVDSISSTAISHSR.A
822	839	4	2058.08	3.2	1	52.7	21.6	95.00%	K.VYTTEVIGNIISEEAHKR.F		K.VYTTEVIGNIISEEAHKR.F
419	431	2	1592.73	4.2	1	27.5	26.3	91.70%	K.WQDELCNSLSSVR.K	Carbamidomethyl (+57)	K.WQDELCNSLSSVR.K
129	145	2	1903.96	0.2	1	30	24.6	95.00%	K.KPDEVYVEDPLGNLIGF.S		K.KPDEVYVEDPLGNLIGFSDR.Y
586	603	3	1736.9	-1	0	54.2	23.6	95.00%	R.VAIIHVGAPAGGMNSATR.A	Oxidation (+16)	R.VAIIHVGAPAGGMNSATR.A
534	545	2	1352.73	-0.68	1	39.3	21.2	95.00%	K.LTHEVADAIEKK.Q		K.LTHEVADAIEKK.Q
880	896	2	1696.88	4.3	0	74.6	23.1	95.00%	R.ANDLGNDPSSAVVIGIR.G		R.ANDLGNDPSSAVVIGIR.G
903	918	2	1837.8	-0.95	0	100	27	95.00%	F.SSVADVENNETEIEMR.R	Oxidation (+16)	R.GTGVSFSSVADVENNETEIEMR.R
927	938	2	1323.7	4.7	0	53.3	22.2	95.00%	R.DMHNLVNILAGK.T		R.DMHNLVNILAGK.T
77	94	2	1954.96	-1.2	1	64.2	25.6	95.00%	R.LVPGELSLSPAAEDSEWR.G		R.LVPGELSLSPAAEDSEWR.G
50	74	3	2845.31	0.51	2	40.3	26.2	95.00%	R.VCNESLREDWMHVAGNNSAESVTIK.F	Carbamidomethyl (+57)	R.VCNESLREDWMHVAGNNSAESVTIK.F
613	628	3	1700.87	4.5	1	49.7	23.9	95.00%	R.GHTPLAIDNGFSGFLR.H		R.GHTPLAIDNGFSGFLR.H
283	308	2	2620.33	3.9	1	86.3	23.1	95.00%	K.NLISAGIDSIIVCGGDGSLTGADIFR.S	Carbamidomethyl (+57)	K.NLISAGIDSIIVCGGDGSLTGADIFR.S
160	183	3	2416.24	3.9	1	44	22.9	95.00%	K.SEESGAASNLESGLATPVVETLKK.A		K.SEESGAASNLESGLATPVVETLKK.A
798	806	2	934.49	4	1	31.5	23.8	95.00%	K.ATFALEAGR.N		K.ATFALEAGR.N
438	460	2	2448.28	0.16	0	67.9	21.9	95.00%	K.SIVIVAEGAIDSELNHISPEDIK.N		K.SIVIVAEGAIDSELNHISPEDIK.N
160	182	2	2288.13	-2.2	0	74.8	25.2	95.00%	K.SEESGAASNLESGLATPVVETLK.K		K.SEESGAASNLESGLATPVVETLK.K
254	267	2	1400.75	3.4	1	49.7	22.8	95.00%	R.GWLAEGGTLIGTAR.C		R.GWLAEGGTLIGTAR.C
844	861	2	1860.9	4.7	0	42.3	25.9	95.00%	R.TAVPGHVQQGGNPTPMDR.A		R.TAVPGHVQQGGNPTPMDR.A
197	214	2	1760.86	4.1	0	84.8	25	95.00%	K.IAVMTSGGDSPGMNAVVR.A		K.IAVMTSGGDSPGMNAVVR.A
822	838	2	1901.97	-1.3	1	52.7	24.4	95.00%	K.VYTTEVIGNIISEEAHK.R		K.VYTTEVIGNIISEEAHK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
23	ILV5_SCHPO	34.90%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
84	104	2	2141.07	4.6	1	90.4	24.7	95.00%	K.NDTLAIIGYGSQGHGQGLNAR.D		K.NDTLAIIGYGSQGHGQGLNAR.D
330	337	2	914.47	6	1	41.2	21.8	95.00%	R.GAIDWTPR.F		R.GAIDWTPR.F
287	313	3	2972.45	-0.74	2	60.9	24.1	95.00%	R.ERGHSPAEAFNETVEEATQSLYPLIGK.Y		R.ERGHSPAEAFNETVEEATQSLYPLIGK.Y
145	163	2	2074.05	4.2	1	75.2	24.7	95.00%	K.GSIIMNLLSDAAQTETWPK.I		K.GSIIMNLLSDAAQTETWPK.I
345	361	2	1975.97	4.3	1	90.3	25.7	95.00%	K.VLNELYDNVENGNEAKR.S		K.VLNELYDNVENGNEAKR.S
345	360	2	1819.85	-4.8	1	42.9	26.7	95.00%	K.VLNELYDNVENGNEAK.R		K.VLNELYDNVENGNEAK.R
373	383	2	1435.72	-1.8	1	46.7	25.3	95.00%	R.ELYDKELEEIR.N		R.ELYDKELEEIR.N

123	133	2	1198.6	4.3	1	28.6	23.3	94.90%	K.QAIEDGWVPGK.T		K.QAIEDGWVPGK.T
144	163	2	2202.15	4.4	2	56.2	22.3	95.00%	K.KGSIIMNLLSDAAQTETWPK.I		K.KGSIIMNLLSDAAQTETWPK.I
362	372	2	1312.61	4.6	1	61.6	25.5	95.00%	R.SLEYNSAPNYR.E		R.SLEYNSAPNYR.E
289	313	2	2687.32	3.5	1	76.3	24.3	95.00%	R.GHSPAEAFNETVEEATQSLYPLIGK.Y		R.GHSPAEAFNETVEEATQSLYPLIGK.Y
190	204	2	1639.97	3.6	1	26.8	14.8	92.60%	K.IHPPKDVDVILVAPK.G		K.IHPPKDVDVILVAPK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
24	EF2_SCHPO	27.55%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
565	578	2	1451.69	4.3	0	44.5	26.5	95.00%	R.ESVSEPSSMTALSK.S		R.ESVSEPSSMTALSK.S
353	370	2	2024.89	3.6	1	81.7	27.6	95.00%	R.AETLYEGPMDDECAVGIR.N	Carbamidomethyl (+57)	R.AETLYEGPMDDECAVGIR.N
371	384	2	1594.76	4.1	1	55	26.1	95.00%	R.NCDANAPLMIYVSK.M	Carbamidomethyl (+57)	R.NCDANAPLMIYVSK.M
327	346	2	2192.18	0.63	1	93	20.9	95.00%	K.FLPAADALMEMIVLHLPSPK.T		K.FLPAADALMEMIVLHLPSPK.T
442	465	2	2595.37	4.3	1	74.7	18.9	95.00%	R.IEPIEDCPAGNIIGLVGVDQFLVK.S	Carbamidomethyl (+57)	R.IEPIEDCPAGNIIGLVGVDQFLVK.S
466	479	2	1474.71	3.7	0	72.8	25.6	95.00%	K.SGTLTTSEVAHNMK.V		K.SGTLTTSEVAHNMK.V
633	651	2	2107.01	3.2	1	108	25.8	95.00%	K.IWCFGPDTTGANVVVDQTK.A	Carbamidomethyl (+57)	K.IWCFGPDTTGANVVVDQTK.A
284	292	2	1051.52	4.5	1	27.5	24.3	93.60%	R.IFDAVMNSR.K		R.IFDAVMNSR.K
293	302	2	1178.66	4.6	2	62.3	20.3	95.00%	R.KDEVFTLLSK.L		R.KDEVFTLLSK.L
151	162	3	1392.85	-1.3	1	27.9	10.8	95.00%	R.IRPVVVVNKVDR.A		R.IRPVVVVNKVDR.A
544	555	2	1334.69	3.5	0	47.4	24.4	95.00%	K.DLQEDHAGIPLK.I		K.DLQEDHAGIPLK.I
827	838	2	1426.66	-1.6	2	34.7	26.6	95.00%	K.GLKENVPDYTEY.Y		K.GLKENVPDYTEYYDR.L
303	317	3	1726.94	3.8	1	43.5	20.8	95.00%	K.LEVTIKPDEKELEGK.A		K.LEVTIKPDEKELEGK.A
326	346	3	2320.27	0.64	2	56.6	17.9	95.00%	R.KFLPAADALMEMIVLHLPSPK.T		R.KFLPAADALMEMIVLHLPSPK.T
635	651	2	1807.84	-2.3	1	90.7	26.7	95.00%	W.CFGPDTTGANVVVDQTK.A	Carbamidomethyl (+57)	K.IWCFGPDTTGANVVVDQTK.A
586	609	3	2657.29	3.5	1	32.6	25.1	95.00%	R.IFMTAEPMSEELSVAIETGHVNPR.D		R.IFMTAEPMSEELSVAIETGHVNPR.D
618	631	2	1624.72	-1.8	1	61.8	26.9	95.00%	R.IMADEFGWDVTDAR.K		R.IMADEFGWDVTDAR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
25	PUR9_SCHPO	43.93%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
76	91	2	1843.9	-2	1	51.3	25.5	95.00%	R.DIPSDEKDLVEQSIEK.I		R.DIPSDEKDLVEQSIEK.I
328	347	2	2128.1	0.55	1	39.5	24.2	95.00%	R.EVSDGVIAPGYEPEALELLK.K		R.EVSDGVIAPGYEPEALELLK.K
405	418	2	1427.86	-0.78	0	46.5	13.6	95.00%	K.SALIDLVIATTALK.Y		K.SALIDLVIATTALK.Y
138	153	2	1755.86	4.1	1	89.5	25.2	95.00%	R.VTILSDPADYATFTDK.F		R.VTILSDPADYATFTDK.F
551	565	2	1519.75	4.1	1	63.8	25.7	95.00%	K.YVAAPGGSVMDQAVR.D		K.YVAAPGGSVMDQAVR.D
39	60	2	2231.08	4.2	0	97.7	25.9	95.00%	R.ESGMEVADVSSITNAPEILGGR.V		R.ESGMEVADVSSITNAPEILGGR.V
248	259	2	1216.65	4.7	1	30.2	23.6	95.00%	R.ENIGIPAAASFK.H		R.ENIGIPAAASFK.H
104	129	3	2776.52	0.29	0	23.3	16	91.50%	R.ETIAKPNVTIPEAVEEIDIGGVTLLR.A		R.ETIAKPNVTIPEAVEEIDIGGVTLLR.A
480	498	2	2018	3.8	1	84.7	25.3	95.00%	K.SNAIDLYVLDAVPAEGSER.E		K.SNAIDLYVLDAVPAEGSER.E
260	278	3	1874.03	3.8	1	46.3	18.9	95.00%	K.HVSPAGAAVGLPLSDVEKK.V		K.HVSPAGAAVGLPLSDVEKK.V
526	543	2	2131.98	3.7	1	65.5	27.4	95.00%	K.DVVCASDAFFPFPDNIYR.L	Carbamidomethyl (+57)	K.DVVCASDAFFPFPDNIYR.L
223	244	2	2446.24	0.95	1	79.8	23.8	95.00%	K.VLCGSPGYINLMDALNSWPLVK.E	Carbamidomethyl (+57)	K.VLCGSPGYINLMDALNSWPLVK.E
566	581	2	1881.9	4.3	1	55.8	26.3	95.00%	R.DTANEFNMVFSEIPLR.L		R.DTANEFNMVFSEIPLR.L
201	213	2	1386.63	-0.59	1	40	26.5	95.00%	R.YGANPHQSPAQAF.M		R.YGANPHQSPAQAFMEQGPLPFK.V
354	362	2	1152.54	4.8	1	28.8	25.5	94.50%	K.YCVLQMDPK.Y	Carbamidomethyl (+57)	K.YCVLQMDPK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
26	TSA1_SCHPO	68.75%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	132	2	901.53	4.7	1	35.7	21.9	95.00%	R.GLFLIDPK.G		R.GLFLIDPK.G
155	173	2	2260.03	0.62	1	35.6	27.1	95.00%	R.LLDAFQFVEEHGEVCPANW.H	Carbamidomethyl (+57)	R.LLDAFQFVEEHGEVCPANWHK.G

89	107	2	1915.06	3.5	1	58	19.5	95.00%	R.KEGGLGGINIPLLADPSHK.V		R.KEGGLGGINIPLLADPSHK.V
66	88	2	2576.29	0.89	1	97.3	23.8	95.00%	R.NAQVILTSTDSEYSHLAFINTPR.K		R.NAQVILTSTDSEYSHLAFINTPR.K
111	124	2	1523.77	4.1	1	79.7	25.1	95.00%	R.DYGVLIEDAGVAFR.G		R.DYGVLIEDAGVAFR.G
66	83	2	1994.96	0.35	1	72.8	26	95.00%	R.NAQVILTSTDSEYSHLAF.I		R.NAQVILTSTDSEYSHLAFINTPR.K
2	13	2	1341.74	4.1	1	36.9	21.1	95.00%	M.SLQIGKPAPDFK.G	Acetyl (+42)	-.MSLQIGKPAPDFK.G
137	147	2	1224.69	4.4	0	43.5	18.2	95.00%	R.QITINDLPVGR.S		R.QITINDLPVGR.S
176	188	2	1466.69	-1	2	27.1	26.5	90.60%	K.GSDTIDTKNPEKY.F		K.GSDTIDTKNPEKYFSK.H
14	26	2	1333.69	3.6	1	40.1	24.2	95.00%	K.GTAVVNGAFEEIK.L		K.GTAVVNGAFEEIK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
27	ACT_SCHPO	51.47%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
292	312	2	2216.04	5	1	63.1	26.9	95.00%	K.DLYGNVVMSGGTTMYPGIADR.M		K.DLYGNVVMSGGTTMYPGIADR.M
257	279	2	2398.18	-0.51	1	60.3	24.8	95.00%	R.APEALFQPSALGLENAGIHEATY.N		R.APEALFQPSALGLENAGIHEATYNSIMK.C
96	113	2	2014.03	3.9	0	59.4	23.7	95.00%	R.VAPEEHPCLLTEAPLNPK.S	Carbamidomethyl (+57)	R.VAPEEHPCLLTEAPLNPK.S
69	84	2	1958.89	3.6	1	64.1	27.3	95.00%	K.YPIEHGIVNNWDDMEK.I		K.YPIEHGIVNNWDDMEK.I
197	206	2	1131.53	5.1	1	41.4	25.6	95.00%	R.GYTFSTTAER.E		R.GYTFSTTAER.E
148	169	2	2293.11	0.74	1	61.9	25.2	95.00%	R.TTGIVLDSGDGVTHTVPIYEGY.A		R.TTGIVLDSGDGVTHTVPIYEGYALPHAIMR.L
216	238	2	2629.27	3.5	1	106	25.4	95.00%	K.LCYVALDFEQELQTAAQSSSLEK.S	Carbamidomethyl (+57)	K.LCYVALDFEQELQTAAQSSSLEK.S
257	284	3	2971.48	3	1	43.9	22.9	95.00%	R.APEALFQPSALGLENAGIHEATYNSIMK.C		R.APEALFQPSALGLENAGIHEATYNSIMK.C
219	238	2	2193.08	-0.37	1	93.1	25.2	95.00%	Y.VALDFEQELQTAAQSSSLEK.S		K.LCYVALDFEQELQTAAQSSSLEK.S
1	18	2	2007.9	4	0	79.9	27.5	95.00%	-.MEEEIAALVIDNGSGMCK.A	Acetyl (+42)/ Carbamidomethyl (+57)	-.MEEEIAALVIDNGSGMCK.A
239	254	2	1789.89	5.1	1	75.2	25.3	95.00%	K.SYELPDGQVITIGNER.F		K.SYELPDGQVITIGNER.F
148	177	3	3182.62	3.4	1	67.2	20.8	95.00%	R.TTGIVLDSGDGVTHTVPIYEGYALPHAIMR.L		R.TTGIVLDSGDGVTHTVPIYEGYALPHAIMR.L
360	372	2	1511.7	3.8	1	34.6	26.6	95.00%	K.QEYDESGPGIVYR.K		K.QEYDESGPGIVYR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
28	HSP75_SCHPO	36.05%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	173	2	1168.66	5	0	34.3	19.3	95.00%	K.DAGAIAGLNVLR.I		K.DAGAIAGLNVLR.I
501	517	3	1779.92	5.5	0	60.6	23.6	95.00%	R.SAHIEITNSVGHLSSTK.I		R.SAHIEITNSVGHLSSTK.I
174	185	2	1245.66	-1.1	1	38.1	22.9	95.00%	R.IINEPTAAAIAY.G		R.IINEPTAAAIAYGLDAK.S
331	344	2	1437.76	-1.9	0	37.7	23.1	95.00%	K.ADVHDIVLVGGSTR.I		K.ADVHDIVLVGGSTR.I
115	128	2	1565.81	1.4	1	60	23.6	95.00%	K.QFTAQEISAMVLTK.M		K.QFTAQEISAMVLTK.M
39	51	2	1484.72	4.2	1	50.9	25.7	95.00%	R.TTPSFVAFTETER.L		R.TTPSFVAFTETER.L
96	113	2	1987.02	-1.8	1	74.8	22.9	95.00%	K.VIDNNGIPTIEVNYLGEK.K		K.VIDNNGIPTIEVNYLGEK.K
430	450	2	2374.14	-0.34	1	69.9	25.9	95.00%	R.TFTTVADNQTTVTFPVYQGER.V		R.TFTTVADNQTTVTFPVYQGER.V
451	472	2	2468.2	5.8	1	62.2	26.3	95.00%	R.VNCAENEPLGEFQLTGIPPMPR.G	Carbamidomethyl (+57)	R.VNCAENEPLGEFQLTGIPPMPR.G
144	157	2	1552.8	4.6	1	33.7	24.1	95.00%	K.AVITVPAYFSDSQR.A		K.AVITVPAYFSDSQR.A
543	564	2	2513.2	0.16	1	64.9	26	95.00%	K.SQLESYISNIETTISEPNVMMK.L		K.SQLESYISNIETTISEPNVMMK.L
174	190	2	1729.93	3.9	1	82.9	21.3	95.00%	R.IINEPTAAAIAYGLDAK.S		R.IINEPTAAAIAYGLDAK.S
114	128	2	1693.91	3.7	2	42.8	20.6	95.00%	K.KQFTAQEISAMVLTK.M		K.KQFTAQEISAMVLTK.M
571	595	3	2864.36	3.4	1	74	25.7	95.00%	K.SKIEAQLAECMSQLELEDTNTDALR.K	Carbamidomethyl (+57)	K.SKIEAQLAECMSQLELEDTNTDALR.K
518	528	2	1336.63	0.58	2	38.3	25.5	95.00%	K.IQEMIENADKF.K		K.IQEMIENADKFK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

29	SERA_SCHPO	36.70%	100%	13									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
410	421	2	1468.77	4	1	31.9	22.6	95.00%	R.QVNELFIDHNIK.S		R.QVNELFIDHNIK.S		
355	366	2	1300.7	0.98	0	63.9	22.7	95.00%	Y.NIGIEVSEALTR.Y		K.NIILTPHIGGSTEEAQYNIGIEVSEALTR.Y		
302	319	2	1729.84	-4.9	1	52.3	25.3	95.00%	K.IAGAAIDVYPSEPAGNGK.D	Deamidation (+1)	K.IAGAAIDVYPSEPAGNGK.D		
248	262	2	1596.82	4.1	1	50.8	23.4	95.00%	R.ADFVSLHVPASPETK.N		R.ADFVSLHVPASPETK.N		
142	154	2	1394.7	4.8	1	57.8	24.8	95.00%	R.GIAVFNSPYANSR.S		R.GIAVFNSPYANSR.S		
434	452	2	2053.01	-0.91	0	52.4	25.8	95.00%	Y.LVADISDCTPGSLEALHQK.L	Carbamidomethyl (+57)	R.GDIAYLVADISDCTPGSLEALHQK.L		
275	284	2	1108.56	4.3	1	25.6	24.5	90.60%	K.EGSYLINASR.G		K.EGSYLINASR.G		
367	385	2	2078.05	3.9	1	76.6	23.9	95.00%	R.YINEGNSIGAVNFPEVSLR.S		R.YINEGNSIGAVNFPEVSLR.S		
338	354	2	1841.92	-0.059	1	56.2	25.4	95.00%	K.NIILTPHIGGSTEEAQY.N		K.NIILTPHIGGSTEEAQYNIGIEVSEALTR.Y		
422	433	2	1344.6	0.44	2	28.5	27.2	91.90%	K.SQFSDSRGDIAY.L		K.SQFSDSRGDIAYLVADISDCTPGSLEALHQK.L		
47	57	3	1247.68	3.8	1	25.6	22	94.60%	R.TLKPFASEDIK.I		R.TLKPFASEDIK.I		
302	321	3	1972.97	-2.8	1	43.3	25.6	95.00%	K.IAGAAIDVYPSEPAGNGKDK.F	Deamidation (+1)	K.IAGAAIDVYPSEPAGNGKDK.F		
237	247	3	1291.72	-1.3	0	25.4	20.2	94.20%	K.QLSSLPELLHR.A		K.QLSSLPELLHR.A		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
30	GPD1_SCHPO	46.75%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
87	104	2	2008.06	5	1	48.8	21.6	95.00%	K.YLPGIECPPNVIAVPDVR.E	Carbamidomethyl (+57)	K.YLPGIECPPNVIAVPDVR.E
341	353	2	1544.76	0.63	2	33.5	25.6	95.00%	K.DMVKDFPLFTAVY.N		K.DMVKDFPLFTAVYNISYEDMDPK.D
214	232	3	1802.98	1.8	1	33.3	20.9	95.00%	Y.FSVVSVDDVAGVALGGALK.N		R.EQIAAVFDRPYFSVVSVDDVAGVALGGALK.N
277	296	2	2153	2.6	0	93.7	26.8	95.00%	R.TMVEQSCGIADLVTSCLGGR.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.TMVEQSCGIADLVTSCLGGR.N
73	86	3	1656.85	-0.85	2	40.6	24.2	95.00%	R.KLTEVFNEAHENVK.Y		R.KLTEVFNEAHENVK.Y
74	86	2	1528.76	4.4	1	69.8	24.4	95.00%	K.LTEVFNEAHENVK.Y		K.LTEVFNEAHENVK.Y
2	20	2	1989	3.8	1	99.4	24.5	95.00%	M.SGYGQQGVSAANIDSIRPK.K	Acetyl (+42)	-.MSGYGQQGVSAANIDSIRPK.K
310	331	3	2285.25	0.0069	1	35.9	19.4	95.00%	K.SLETLEKELLGGQLLQGAATSK.D		K.SLETLEKELLGGQLLQGAATSK.D
183	202	2	2362.1	3.9	1	116	26.6	95.00%	R.EQFCETTIGFNPPNEVDIPR.E	Carbamidomethyl (+57)	R.EQFCETTIGFNPPNEVDIPR.E
168	182	2	1515.74	-2.3	0	75.1	25.8	95.00%	Y.CGVLSGANVANEVAR.E	Carbamidomethyl (+57)	K.LGIYCGVLSGANVANEVAR.E
125	144	3	2172.12	-1.8	0	28.9	22.7	95.00%	R.VCDQMVGLIRPGAVGISCIK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VCDQMVGLIRPGAVGISCIK.G
317	331	2	1484.82	-2	0	58.2	21.4	95.00%	K.ELLGGQLLQGAATSK.D		K.ELLGGQLLQGAATSK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
31	IPYR_SCHPO	58.48%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
240	280	3	4115.08	2.7	1	89.4	18.9	95.00%	K.SDFSLVNVSVTGSVANDPSVSSTIPPAQELAPAPVDPSVHK.W		K.SDFSLVNVSVTGSVANDPSVSSTIPPAQELAPAPVDPSVHK.W
32	42	2	1269.63	-0.8	1	39.6	24.5	95.00%	W.HDIPLYANAEK.T		K.NGTPISSWHDIPLYANAEK.T
186	192	2	922.44	6	1	35.4	24.5	95.00%	R.ATNEWFR.I		R.ATNEWFR.I
94	113	2	2305.06	-0.79	1	41.9	26.5	95.00%	W.NYGAFPQTYEDPNVVHPETK.A		R.NCFPHHGYIWNYGAFPQTYEDPNVVHPETK.A
141	156	2	1774.88	-1.8	1	81.3	25.3	95.00%	K.VLGVMALLDEGETDWK.V		K.VLGVMALLDEGETDWK.V
24	42	2	2112.04	4.6	1	50.5	25.5	95.00%	K.NGTPISSWHDIPLYANAEK.T		K.NGTPISSWHDIPLYANAEK.T
114	130	2	1830.85	4	1	98.5	26.8	95.00%	K.AKGDSDPLDVCEIGEAR.G	Carbamidomethyl (+57)	K.AKGDSDPLDVCEIGEAR.G
170	178	2	1101.53	3.9	0	49.3	23.4	95.00%	K.LNDIEDVER.H		K.LNDIEDVER.H
43	53	2	1283.73	4	0	66.7	19.5	95.00%	K.TILNMVVEIPR.W		K.TILNMVVEIPR.W
157	169	2	1391.8	-1.3	0	45.1	15.7	95.00%	K.VIVIDVNDPLAPK.L		K.VIVIDVNDPLAPK.L
8	23	2	1839.93	4.1	1	74	24.1	95.00%	R.EVGALNTLDYQVYVEK.N		R.EVGALNTLDYQVYVEK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
32	HXK2_SCHPO	40.88%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
12	24	2	1581.77	4.1	1	62.3	25.8	95.00%	K.LVNDFEYPTESLR.E		K.LVNDFEYPTESLR.E
11	24	2	1709.86	-1.6	2	72.1	24.4	95.00%	K.KLVNDFEYPTESLR.E		K.KLVNDFEYPTESLR.E
142	156	2	1705.78	-0.12	1	34.6	27	95.00%	F.TFSYPANQVSITESY.L		K.FGCPEEEYLPMGFTFSYPANQVSITESYLLR.W
392	413	3	2499.22	-0.035	2	65.5	25.2	95.00%	K.KSDVGVDGSLVEHYPHFVDMLR.E		K.KSDVGVDGSLVEHYPHFVDMLR.E
76	87	2	1450.73	-2	2	43.9	25.2	95.00%	R.VCWIQLLGDGKY.E	Carbamidomethyl (+57)	R.VCWIQLLGDGKYEMK.H
103	122	3	2360.22	3.5	1	42.1	22.6	95.00%	R.NESVKPIIDFMSDHVELFIK.E		R.NESVKPIIDFMSDHVELFIK.E
360	369	2	1108.58	1.2	1	46.8	23.6	95.00%	Y.LWDAAHAIGR.R		R.SDEEALYLWDAAHAIGR.R
374	388	2	1564.83	4.1	1	56.1	22.5	95.00%	R.MSAVPIASLYLSTGR.A		R.MSAVPIASLYLSTGR.A
103	120	2	2119.03	0.79	1	36.4	25.8	95.00%	R.NESVKPIIDFMSDHVELF.I		R.NESVKPIIDFMSDHVELFIK.E
1	11	2	1334.67	4.1	1	29.9	25.4	95.00%	-.MEANFQQAVKK.L	Acetyl (+42)	-.MEANFQQAVKK.L
266	279	2	1598.78	3.9	1	49.6	25.7	95.00%	R.YDLLLDHDTPNAGR.Q		R.YDLLLDHDTPNAGR.Q
434	449	2	1529.79	4.8	0	96.2	24	95.00%	K.DGSGIGAALCALQAVK.E	Carbamidomethyl (+57)	K.DGSGIGAALCALQAVK.E
221	237	2	1806.86	0.44	1	54.6	26.2	95.00%	F.GTGTNGAYVEQMNQIPK.L		K.ESDTFMGIIFGTGTNGAYVEQMNQIPK.L
76	86	2	1287.67	3.9	1	30.3	24	95.00%	R.VCWIQLLGDGK.Y	Carbamidomethyl (+57)	R.VCWIQLLGDGK.Y
286	296	2	1240.63	5.9	1	25.6	23.1	90.60%	R.VGGMYLGELFR.R		R.VGGMYLGELFR.R
25	34	2	1234.62	4.3	2	29.8	24.8	95.00%	R.EAVKEFDELR.Q		R.EAVKEFDELR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
33	HSP60_SCHPO	27.84%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	148	2	1316.6	4	0	27.4	26.5	91.10%	R.NVAAGCNPMDLR.R	Carbamidomethyl (+57)	R.NVAAGCNPMDLR.R
244	256	2	1529.84	4	1	44.5	21.4	95.00%	K.VEFENPLILLSEK.K		K.VEFENPLILLSEK.K
382	396	2	1722.82	4	1	31.1	26	95.00%	R.GVMADPNLTEYEKEK.L		R.GVMADPNLTEYEKEK.L
258	275	2	1937.07	4.4	0	74.7	18.9	95.00%	K.VSAVQDILPSLELAAQQR.R		K.VSAVQDILPSLELAAQQR.R
45	56	2	1215.69	4.9	0	52.6	21.2	95.00%	R.ASLLTGVDTLAR.A		R.ASLLTGVDTLAR.A
257	275	3	2065.16	4	1	35.3	16.2	95.00%	K.KVSAVQDILPSLELAAQQR.R		K.KVSAVQDILPSLELAAQQR.R
112	128	2	1705.86	4.1	0	84.3	25.3	95.00%	K.TNEVAGDGTTTATVLTR.A		K.TNEVAGDGTTTATVLTR.A
437	453	2	1588.85	4.6	1	29.9	22.3	95.00%	K.AAVSEGVLPGAGTSFVK.A		K.AAVSEGVLPGAGTSFVK.A
241	256	2	1873.03	4.6	2	56.5	20	95.00%	K.SQKVEFENPLILLSEK.K		K.SQKVEFENPLILLSEK.K
168	195	3	2912.46	-1.3	0	45.7	23.7	95.00%	R.DITTSEEISQVATISANGDTHIGELLAK.A		R.DITTSEEISQVATISANGDTHIGELLAK.A
68	79	2	1313.7	4.3	1	39.3	21.8	95.00%	R.NVLIDQPFGSPK.I		R.NVLIDQPFGSPK.I
520	533	2	1570.87	4.4	1	87.2	21.1	95.00%	R.FVDLNEIGVLDPLK.V		R.FVDLNEIGVLDPLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
34	G6PI_SCHPO	35.82%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
217	228	2	1343.61	5.2	1	37.3	26.3	95.00%	K.TFTTAETCTNAK.S	Carbamidomethyl (+57)	K.TFTTAETCTNAK.S
464	477	2	1502.83	4	1	36.9	20.6	95.00%	K.TFVGNRPSNSIIAK.K		K.TFVGNRPSNSIIAK.K
383	397	2	1718.81	1.4	1	30	26.5	94.80%	K.ILWGEPGTNSQHSFF.Q		K.ILWGEPGTNSQHSFFQLIHQGTK.L
63	75	2	1499.85	3.9	0	37.5	19.3	95.00%	K.NLITEETVELLVK.L		K.NLITEETVELLVK.L
446	463	3	1916.98	-1.7	1	51.4	23.8	95.00%	K.TPAEVKAEGTPDEIVPHK.T		K.TPAEVKAEGTPDEIVPHK.T
79	90	2	1332.67	0.27	2	35.7	24.5	95.00%	K.EANVEGLRDALF.A		K.EANVEGLRDALFAGEHINFTEDR.A
118	128	2	1170.59	4.1	0	35.5	23.6	95.00%	K.VNGQDVMPGVR.K		K.VNGQDVMPGVR.K
429	445	2	1870.94	4.8	1	69.7	24.7	95.00%	R.MLFSNFAAQTEALMLGK.T		R.MLFSNFAAQTEALMLGK.T
110	128	3	2084.06	4.5	1	31.6	23.7	95.00%	R.NVSEKPMKVNGQDVMPGVR.K		R.NVSEKPMKVNGQDVMPGVR.K
91	101	3	1287.59	0.92	1	31.1	26.4	95.00%	F.AGEHINFTEDR.A		R.DALFAGEHINFTEDR.A
372	382	2	1171.52	5.1	1	67.7	25.6	95.00%	R.SGDMVNYTTGK.I		R.SGDMVNYTTGK.I
435	445	2	1131.59	-1.2	0	37.5	22.9	95.00%	F.AAQTEALMLGK.T		R.MLFSNFAAQTEALMLGK.T
204	216	2	1493.75	4.3	1	51.5	25.6	95.00%	K.CDPETTLFLIASK.T	Carbamidomethyl (+57)	K.CDPETTLFLIASK.T

521	547	3	2955.5	3	2	45.6	21.4	95.00%	K.NVLAQLETKGDVENHDSSTNGLINLFK.N			K.NVLAQLETKGDVENHDSSTNGLINLFK.N
353	367	2	1711.83	4.2	1	71.8	25.8	95.00%	R.FPAYLQQLSMESNGK.A			R.FPAYLQQLSMESNGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
35	LYS9_SCHPO	42.22%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
177	183	2	740.49	4.7	0	33.1	11.8	95.00%	R.GVLLALR.N		R.GVLLALR.N
194	209	3	1820.92	0.61	2	31.4	24.7	95.00%	K.LVEIDGKDLMETAKPY.F		K.LVEIDGKDLMETAKPYFIYPGYAFVCYPNR.D
290	301	2	1276.66	4.3	1	31	23.5	95.00%	K.AESSSEADLIKK.I		K.AESSSEADLIKK.I
38	49	2	1259.66	4.1	1	41.7	23.9	95.00%	K.AEAFINGIPNSK.A		K.AEAFINGIPNSK.A
379	396	2	1989.93	4.3	1	76.6	26.5	95.00%	R.TCTLLDYGVPNGYTSMAK.L	Carbamidomethyl (+57)	R.TCTLLDYGVPNGYTSMAK.L
287	301	3	1616.91	5.4	1	31	19	95.00%	R.VIKAESSSEADLIKK.I		R.VIKAESSSEADLIKK.I
397	426	3	3075.61	0.31	0	42.1	19	95.00%	K.LVGVPCGVATQQILDGVINTPGVLAPNDMK.L	Carbamidomethyl (+57)	K.LVGVPCGVATQQILDGVINTPGVLAPNDMK.L
64	85	3	2488.28	3.3	1	39.1	22.3	95.00%	K.AVSEHDLTISLIPYTYHATVMK.A		K.AVSEHDLTISLIPYTYHATVMK.A
2	22	3	2269.25	3.1	1	39	17.6	95.00%	M.PSILLLGSGFVAHPTLEYLSR.R		-.MPSILLLGSGFVAHPTLEYLSR.R
114	135	3	2372.16	2.8	1	47.3	25.4	95.00%	K.AGSICMNEIGVDPGIDHLYAIK.T	Carbamidomethyl (+57)	K.AGSICMNEIGVDPGIDHLYAIK.T
104	113	2	1103.56	4	0	29.1	23.7	95.00%	K.MAELEEAAIK.A		K.MAELEEAAIK.A
114	132	2	2059.94	0.4	1	63.1	27.2	95.00%	K.AGSICMNEIGVDPGIDHLY.A	Carbamidomethyl (+57)	K.AGSICMNEIGVDPGIDHLYAIK.T
154	170	2	1787.81	-1.7	1	56.6	26.8	95.00%	Y.CGGLPAPEDSNNPLGYK.F	Carbamidomethyl (+57)	K.SFLSYCGGLPAPEDSNNPLGYK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
36	TKT_SCHPO	29.05%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
364	394	3	3276.78	4.5	1	70.7	14.8	95.00%	R.KLSEIVLDALCPVLPELVGGSADLTPSNLTR.W	Carbamidomethyl (+57)	R.KLSEIVLDALCPVLPELVGGSADLTPSNLTR.W
325	336	2	1449.68	6.5	1	28.4	25.2	94.50%	K.QSYPDLSNQLER.I	Deamidation (+1)	K.QSYPDLSNQLER.I
2	18	2	1869.93	-1.4	1	70	24.8	95.00%	M.TSSSYTDIDTLAINTIR.T		-.MTSSSYTDIDTLAINTIR.T
238	252	2	1719.86	5	0	57.2	25.3	95.00%	R.EAMSCTDKPTLINLK.T	Carbamidomethyl (+57)	R.EAMSCTDKPTLINLK.T
395	407	2	1418.65	3.9	1	52.7	26	95.00%	R.WEGAADFQPPSSK.L		R.WEGAADFQPPSSK.L
495	515	2	2400.03	1.3	1	40.9	27.5	95.00%	R.AMPNINCWRPADGNETSAAYY.S	Carbamidomethyl (+57)	R.AMPNINCWRPADGNETSAAYYSALTSDSTPSILALTR.Q
182	193	2	1385.74	4.7	1	41.9	22.7	95.00%	K.LSNLIAVWDNNK.I		K.LSNLIAVWDNNK.I
532	547	2	1810.95	4.2	0	72.5	22.4	95.00%	R.QNLPQLENSTIENALK.G		R.QNLPQLENSTIENALK.G
253	281	3	3132.54	2.9	1	59.8	23.1	95.00%	K.TTIGYGSELQGTHSVHGSPLKPEDCVHVK.K	Carbamidomethyl (+57)	K.TTIGYGSELQGTHSVHGSPLKPEDCVHVK.K
306	318	2	1423.73	4.8	1	73.3	24.6	95.00%	R.VAIASSAEEEYKK.M		R.VAIASSAEEEYKK.M
30	49	3	1972.02	3.9	1	31.5	23.3	95.00%	K.SGHPGAPMGLAPAAHVLFSR.I		K.SGHPGAPMGLAPAAHVLFSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
37	PDX1_SCHPO	30.74%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	49	2	1547.75	3.7	0	51.8	25.4	95.00%	R.IAEAAGACAVMALER.V	Carbamidomethyl (+57)/ Oxidation (+16)	R.IAEAAGACAVMALER.V
265	280	2	1628.86	4	0	87.2	22.8	95.00%	K.ILAEVSENLGAAMVGR.S		K.ILAEVSENLGAAMVGR.S
71	83	2	1355.75	4.3	0	66.7	21.3	95.00%	K.EIQAAVSIPVMAK.V		K.EIQAAVSIPVMAK.V
150	164	2	1487.76	3.9	1	69.3	23.8	95.00%	R.TKGEAGTGDVVEAVR.H		R.TKGEAGTGDVVEAVR.H
21	34	2	1457.74	4	0	89.6	24.3	95.00%	K.GGVIMDVVNAEQAR.I		K.GGVIMDVVNAEQAR.I
140	149	2	1102.6	4.8	1	28.6	23	94.80%	R.RISEGAAMIR.T		R.RISEGAAMIR.T
13	20	2	830.47	4.2	0	38.8	21.5	95.00%	K.AGLAQMLK.G		K.AGLAQMLK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
38	PPA1_SCHPO	18.32%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

73	92	2	2047	4	1	99.4	25.8	95.00%	R.NPTGGNAAFDAVGIANFQQR.L		R.NPTGGNAAFDAVGIANFQQR.L
47	59	2	1531.7	-1.6	1	57.5	26.3	95.00%	Y.FYGPSIDFPTTCK.I	Carbamidomethyl (+57)	R.SPYHKPYFYGPSIDFPTTCK.I
373	387	2	1723.81	-1.1	1	62.1	26.5	95.00%	F.AGNLITELFQCEDSK.Y	Carbamidomethyl (+57)	K.ASEFVPFAGNLITELFQCEDSK.Y
373	388	2	1886.87	-0.096	2	58.4	27.1	95.00%	F.AGNLITELFQCEDSKY.Y	Carbamidomethyl (+57)	K.ASEFVPFAGNLITELFQCEDSKYYVR.H
344	357	2	1594.72	0.11	1	34.2	26.6	95.00%	F.FTDNTPENPLPTSY.Q		R.SVENNTQQVFFAFTHDANIIPVETALGFFTDNTPENPLPTSYQVHSHSMK.A
205	224	2	2206.96	1.9	1	82.9	27.7	95.00%	Y.NACPASDADDFTTPALEAWR.N	Carbamidomethyl (+57)	R.VVDSALWYGYGMFGEDVHNFTNYILVSENATAGSNSLSSYNACPASDADDFTTPALEAWR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
39	YL8C_SCHPO	48.51%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
217	232	2	1745.96	4.4	1	53	20.4	95.00%	K.GTALQYITSNILPEVK.N		K.GTALQYITSNILPEVK.N
275	288	2	1456.71	-1.4	0	68.9	25.3	95.00%	R.VGNEEGAVGEVLER.I		R.VGNEEGAVGEVLER.I
7	33	4	3045.57	3.9	1	29.7	20.8	95.00%	K.TNNLPTLDTLQMVISDVDGTLLDKHHR.F		K.TNNLPTLDTLQMVISDVDGTLLDKHHR.F
96	112	3	1893.99	0.9	0	50.3	22.8	95.00%	Y.ADHLKPEVVMEVVEATK.G		K.IVYADHLKPEVVMEVVEATK.G
70	88	2	2085.02	-1.4	1	56.6	25.8	95.00%	R.IPLDLDAFPAAHVNGCVLY.N	Deamidation (+1)/ Carbamidomethyl (+57)	R.IPLDLDAFPAAHVNGCVLYNK.G
173	186	2	1645.79	3.6	1	65.2	26.3	95.00%	K.MAVCEDPDKLDVVR.D	Carbamidomethyl (+57)	K.MAVCEDPDKLDVVR.D
93	112	3	2269.21	3.4	1	35.2	20.1	95.00%	K.IVYADHLKPEVVMEVVEATK.G		K.IVYADHLKPEVVMEVVEATK.G
47	60	2	1575.87	4.2	2	37.4	19.7	95.00%	R.EKYPNFPIVLATGK.Q		R.EKYPNFPIVLATGK.Q
113	128	2	1865.86	-0.054	1	59.8	26.7	95.00%	K.GNPNIANVVYDEHYVY.A		K.GNPNIANVVYDEHYVYALTPGR.E
70	90	3	2326.19	3.3	1	38.3	23.7	95.00%	R.IPLDLDAFPAAHVNGCVLYNK.G	Carbamidomethyl (+57)	R.IPLDLDAFPAAHVNGCVLYNK.G
2	33	4	3587.84	2.8	1	81.1	19.2	95.00%	M.SAVDKTNNLPTLDTLQMVISDVDGTLLDKHHR.F	Acetyl (+42)	-.MSAVDKTNNLPTLDTLQMVISDVDGTLLDKHHR.F
223	232	2	1112.64	-1.1	0	25.5	17.2	90.40%	Y.ITSNILPEVK.N		K.GTALQYITSNILPEVK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
40	CYPH_SCHPO	40.74%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	17	2	1835.87	3.9	1	50	26.1	95.00%	M.SNCFFDVIANGQPLGR.I	Acetyl (+42)/ Carbamidomethyl (+57)	-.MSNCFFDVIANGQPLGR.I
112	123	2	1328.74	0.59	1	43.2	21.4	95.00%	F.ITTVVTPWLDGK.H		K.HNKPGLLSMANAGPNTNGSQFFITTVVTPWLDGK.H
124	139	3	1772.92	4.1	1	60.2	23.5	95.00%	K.HVVFGEVTEGMDVVKK.V		K.HVVFGEVTEGMDVVKK.V
54	67	2	1607.82	4.3	1	67.2	24.7	95.00%	R.VIPQFMLQGGDFTR.G		R.VIPQFMLQGGDFTR.G
124	138	2	1644.83	4.4	1	86.7	24.7	95.00%	K.HVVFGEVTEGMDVVK.K		K.HVVFGEVTEGMDVVK.K
22	29	2	931.51	4	1	29.7	23.4	95.00%	K.LFDDVVPK.T		K.LFDDVVPK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
41	FAS2_SCHPO	10.42%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1569	1579	2	1292.61	5	1	41.1	25.6	95.00%	R.NADNIDEYLAR.F		R.NADNIDEYLAR.F
114	146	3	3020.56	3.1	0	35.9	21.2	95.00%	K.VETAAAAAPAATPAPAPAQTSAPAAALPDEPPK.A		K.VETAAAAAPAATPAPAPAQTSAPAAALPDEPPK.A
421	431	3	1279.72	-0.62	1	24.3	19.2	93.00%	R.LKHVDTEIVAR.C		R.LKHVDTEIVAR.C
517	527	2	1319.7	5.4	2	32	23.6	95.00%	R.KLTHYVTEMAK.G		R.KLTHYVTEMAK.G
967	986	2	2145.09	1.7	2	54.5	24.2	95.00%	R.GMVDLEKVPVVTGFSEVGPW.G		R.GMVDLEKVPVVTGFSEVGPWGNSR.T
28	44	2	1939.01	4.4	1	67.5	22.9	95.00%	R.WIETQDVILSPPVSAER.I		R.WIETQDVILSPPVSAER.I
488	502	3	1650.8	4.5	0	35.5	26.1	95.00%	K.NVNHPTAPSTTIDER.G		K.NVNHPTAPSTTIDER.G

914	937	3	2504.19	3.1	1	37.5	26.2	95.00%	R.AVAAETAFDHSITNGPDSEAVFQK.T		R.AVAAETAFDHSITNGPDSEAVFQK.T
1393	1401	2	994.61	4.5	0	27.6	12	93.70%	K.TPLPIVDLK.F		K.TPLPIVDLK.F
383	394	2	1199.69	0.23	1	26.2	20.7	91.60%	Y.ASGIAPIFSPLK.A		R.AQLDLWNEEHGEFYASGIAPIFSPLK.A
1785	1813	3	2858.5	0.14	1	62.6	19.8	95.00%	K.GAAAPLKDIEIISSESGAPEVVLHGEAAK.A		K.GAAAPLKDIEIISSESGAPEVVLHGEAAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
42	CARB_SCHPO	12.50%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1016	1041	3	2570.44	0.12	0	38.4	12.6	95.00%	K.IPLPGQGILLGGDRPELAGIAADLSK.L		K.IPLPGQGILLGGDRPELAGIAADLSK.L
418	433	2	1784.89	3.2	1	42	24.9	95.00%	K.TTTANFEPSLDYVVTK.I		K.TTTANFEPSLDYVVTK.I
575	584	2	1057.58	4.7	0	32.1	22.6	95.00%	K.LVGASELDVR.A		K.LVGASELDVR.A
799	823	4	2678.38	-0.47	1	49.6	22	95.00%	R.DESSLKDKLENASAVSPDHPVVITK.F		R.DESSLKDKLENASAVSPDHPVVITK.F
730	744	2	1630.79	-1.2	0	88.3	25.4	95.00%	K.VLGTDPLMIDSAEDR.H		K.VLGTDPLMIDSAEDR.H
932	943	2	1304.72	5.6	1	35.2	21.5	95.00%	K.TLGVNFIDVATR.S		K.TLGVNFIDVATR.S
1056	1070	2	1655.91	-0.56	1	42.6	20.4	95.00%	K.LLQPTSAEVVEFPVK.D		K.LLQPTSAEVVEFPVK.D
773	798	3	2736.49	2.9	1	51	17.3	95.00%	K.FANAVGYPVLVRPSYVLSGAAMSVIR.D		K.FANAVGYPVLVRPSYVLSGAAMSVIR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
43	PUT2_SCHPO	28.47%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
406	422	2	1852.92	4.3	1	57.5	25.6	95.00%	K.ADDSEGFFVEPTVLLSK.N		K.ADDSEGFFVEPTVLLSK.N
233	253	2	2068.09	4.4	1	68.9	22.3	95.00%	R.EAGLPAGALQFIPGDAVEVSK.V		R.EAGLPAGALQFIPGDAVEVSK.V
495	509	2	1504.71	3.5	1	49.3	26	95.00%	K.CTGAVVGEQPFGGAR.A	Carbamidomethyl (+57)	K.CTGAVVGEQPFGGAR.A
362	372	2	1150.57	0.75	1	37.5	24.4	95.00%	K.VGAPLTDFANF.V		K.VGAPLTDFANFVGPVIHQASFNK.L
388	405	2	1773.91	3.9	0	102	24	95.00%	K.VLESAASDSEIEVLAGGK.A		K.VLESAASDSEIEVLAGGK.A
82	92	2	1222.64	4.6	0	32.1	23.7	95.00%	K.HVEDAIEAALR.G		K.HVEDAIEAALR.G
275	288	2	1444.74	4.6	1	37.7	24.2	95.00%	R.SLWGTIGENVANGK.Y		R.SLWGTIGENVANGK.Y
373	382	2	1053.56	0.84	1	55.7	21.5	95.00%	F.VGPVIHQASF.N		K.VGAPLTDFANFVGPVIHQASFNK.L
36	63	3	3091.64	3.5	1	24.8	17.6	93.60%	K.ELEAELPVTIPVIIDGKEVETNTIGEQR.C		K.ELEAELPVTIPVIIDGKEVETNTIGEQR.C
484	494	2	1225.58	4.6	1	28	25.8	93.20%	R.NAAGNFYINDK.C		R.NAAGNFYINDK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
44	RAD24_SCHPO	50.74%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
228	267	3	4032.79	4.4	1	129	23.8	95.00%	R.DNLTLWTSDAEYSAAAAGGNTEGAQENAPSNAPEGEAEPK.A		R.DNLTLWTSDAEYSAAAAGGNTEGAQENAPSNAPEGEAEPK.A
15	30	3	1896.88	4.4	2	24.8	26.7	91.10%	K.LAEQAERYEGMVENMK.S		K.LAEQAERYEGMVENMK.S
156	172	2	1746.92	-2.1	0	68.5	21.9	95.00%	K.AASEIATAELAPTHPIR.L		K.AASEIATAELAPTHPIR.L
240	270	3	2881.26	0.96	1	33.5	26.7	95.00%	Y.SAAAAGGNTEGAQENAPSNAPEGEAEPKADA.-		R.DNLTLWTSDAEYSAAAAGGNTEGAQENAPSNAPEGEAEPKADA.-
109	120	2	1236.65	4.7	0	29.1	22.7	95.00%	K.HLIPNAASAESK.V		K.HLIPNAASAESK.V
31	44	2	1562.75	4.1	0	82.9	26.1	95.00%	K.SVASTDQELTVEER.N		K.SVASTDQELTVEER.N
240	267	3	2624.16	0.94	0	53.7	27.2	95.00%	Y.SAAAAGGNTEGAQENAPSNAPEGEAEPK.A		R.DNLTLWTSDAEYSAAAAGGNTEGAQENAPSNAPEGEAEPK.A
2	14	2	1481.74	4.3	2	46.8	25.2	95.00%	M.STTSREDAVYLAK.L	Acetyl (+42)	-.MSTTSREDAVYLAK.L
64	85	3	2429.31	3.8	1	57.6	18.8	95.00%	R.IVSSIEQKEESKGNTAQVELIK.E		R.IVSSIEQKEESKGNTAQVELIK.E

234	267	3	3290.41	1.7	1	71.3	26.1	95.00%	W.TSDAEYSAAAAGGNTEGAQENAPSNAPEGEAEPK.A		R.DNLTLWTSDAEYSAAAAGGNTEGAQENAPSNAPEGEAEPK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
45	HSP7M_SCHPO	31.31%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
637	647	2	1313.76	3.4	1	27.8	18.8	93.90%	K.KIDEIQQLSLK.V		K.KIDEIQQLSLK.V
366	388	3	2471.31	0.21	1	33.1	20.8	95.00%	R.ALKDANLQTSEINEVILVGGMTR.M		R.ALKDANLQTSEINEVILVGGMTR.M
582	609	3	3240.56	-0.048	1	41.1	23.7	95.00%	R.AESVCTDIESNLDIHKDKLDQQAVEDLR.S	Carbamidomethyl (+57)	R.AESVCTDIESNLDIHKDKLDQQAVEDLR.S
622	635	2	1464.65	3.4	0	88.6	26.6	95.00%	K.VNAGDEGITSEDMK.K		K.VNAGDEGITSEDMK.K
204	215	2	1124.67	4.6	0	48.3	15.1	95.00%	K.AAGAIAGLNVLR.V		K.AAGAIAGLNVLR.V
322	337	2	1645.86	3.4	1	41.2	22.9	95.00%	K.TDISLPFITADATGPK.H		K.TDISLPFITADATGPK.H
105	118	2	1578.81	4.5	1	81.4	24.5	95.00%	R.QAVINPENTFFATK.R		R.QAVINPENTFFATK.R
263	281	3	2002.92	-3.4	1	36.4	26.9	95.00%	R.STNGDTHLGGEDFDVALVR.H	Deamidation (+1)	R.STNGDTHLGGEDFDVALVR.H
185	199	2	1679.83	4.3	1	62.1	25.8	95.00%	K.NAVVTVPAYFNDSQR.Q		K.NAVVTVPAYFNDSQR.Q
496	510	2	1538.88	-2.2	1	82.3	16.6	95.00%	K.LIGNFQLTGIAPAPK.G		K.LIGNFQLTGIAPAPK.G
622	636	2	1592.74	5	1	80.4	25.9	95.00%	K.VNAGDEGITSEDMKK.K		K.VNAGDEGITSEDMKK.K
157	170	2	1496.8	5.1	1	59.3	21.7	95.00%	K.TYSPSQIGGFILSK.M		K.TYSPSQIGGFILSK.M
470	482	2	1317.65	-0.55	0	58.9	24.7	95.00%	F.STAADGQTAVEIR.V		K.SQVFSTAADGQTAVEIR.V
216	231	2	1630.86	3.8	1	78.5	22.3	95.00%	R.VVNEPTAAALAYGLDK.K		R.VVNEPTAAALAYGLDK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
46	HXK1_SCHPO	20.66%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	12	3	1409.65	4.4	1	25.1	25.7	93.20%	M.SLHDAYHWPSR.T	Acetyl (+42)	-.MSLHDAYHWPSR.T
447	469	2	2153.17	3.4	0	105	19.9	95.00%	K.VVTIPAEDGSGVGAALVSALEAK.G		K.VVTIPAEDGSGVGAALVSALEAK.G
26	47	3	2676.35	2.8	1	37.5	23.5	95.00%	K.TLQDHLDELEEQFTIPTELLHR.V		K.TLQDHLDELEEQFTIPTELLHR.V
304	315	2	1380.7	5.1	1	25.3	24.5	90.00%	K.MIAGCYLGDILR.R	Carbamidomethyl (+57)	K.MIAGCYLGDILR.R
87	97	2	1141.65	2.2	0	59.8	20.1	95.00%	Y.LALDLGGTNLR.V		K.GLTTNPGDVPMVPTWIIGTPDGNEHGSYLALDLGGTNLR.V
406	426	3	2369.2	3.6	2	22.8	23.8	90.70%	R.KMNKPSMIVGTDGSVYNLYPR.F		R.KMNKPSMIVGTDGSVYNLYPR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
47	VIPI_SCHPO	58.75%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
69	94	2	2433.11	4.4	0	121	26.9	95.00%	K.IQITSEDGGAASTTDQGGAGGDQAAR.Q		K.IQITSEDGGAASTTDQGGAGGDQAAR.Q
55	68	2	1496.85	-1.5	0	50.1	18.5	95.00%	K.TALLLQDALLGQNK.I		K.TALLLQDALLGQNK.I
199	218	3	2268.13	4	1	49.3	24.5	95.00%	K.VQNAYEDGKNQLLGIHNEAR.R		K.VQNAYEDGKNQLLGIHNEAR.R
101	110	2	1087.63	5.8	0	34.3	20.8	95.00%	R.SAIISELLSR.G		R.SAIISELLSR.G
225	254	3	2955.41	4.7	1	54.3	25.2	95.00%	K.NQAEGTASPASSTPTAPAEKEPTAPTTESK.T		K.NQAEGTASPASSTPTAPAEKEPTAPTTESK.T
111	121	2	1260.64	3.7	1	31.8	24.1	95.00%	R.GYHLSDVTLEK.S		R.GYHLSDVTLEK.S
2	17	2	1798.93	-1.9	0	33.5	24	95.00%	M.SNQVIVTNISPEVTEK.Q	Acetyl (+42)	-.MSNQVIVTNISPEVTEK.Q
122	134	2	1410.71	4.2	1	61.1	24.7	95.00%	K.SIQLDQSYGVSSK.F		K.SIQLDQSYGVSSK.F
137	147	2	1100.62	4.3	0	27.7	22	93.90%	K.GILESALSGVR.S		K.GILESALSGVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
48	C1TC_SCHPO	12.91%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
689	707	3	1923.15	3.9	0	37.5	9.03	95.00%	R.TSGLKPDAIVIVATVQALK.L		R.TSGLKPDAIVIVATVQALK.L
57	84	3	3131.52	3.1	1	32.8	23.6	95.00%	R.AANEAGISCEHVNFPEDITEYDLLLAIK.G	Carbamidomethyl (+57)	R.AANEAGISCEHVNFPEDITEYDLLLAIK.G
349	356	2	983.58	5.3	0	46.2	17.4	95.00%	K.VNLEILQR.L		K.VNLEILQR.L
835	849	2	1592.77	-1.3	1	65.3	25.6	95.00%	K.EMYGADGIELSPLAK.E		K.EMYGADGIELSPLAK.E

2	12	2	1184.68	4.9	0	55.8	20.5	95.00%	M.ALLLEGTSLAR.K	Acetyl (+42)	-.MALLLEGTSLAR.K
536	546	2	1228.67	4.9	1	27.4	22	93.40%	R.KITIGENPTEK.G		R.KITIGENPTEK.G
324	336	2	1299.71	5.1	0	59.2	21.9	95.00%	K.NIGDLASEIGIAK.S		K.NIGDLASEIGIAK.S
381	396	2	1629.9	3.4	0	106	20.9	95.00%	K.STLTAGLVQALSNLDK.L		K.STLTAGLVQALSNLDK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
49	OAT_SCHPO	39.95%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
211	234	2	2621.26	-0.0035	1	62.5	25.2	95.00%	F.LVEPIQGEAGVMVPDDGYLEEAYK.L		K.VAAFLVEPIQGEAGVMVPDDGYLEEAYK.L
2	11	2	1159.55	3.4	1	35.4	25.6	95.00%	M.SAESLLHNTF.S	Acetyl (+42)	-.MSAESLLHNTFSTEQIEVLENEYAAHNYHPLPVCFSK.A
386	398	3	1374.82	4.6	0	23.2	15.4	91.30%	R.GVLAKPTHGNIIR.F		R.GVLAKPTHGNIIR.F
154	167	2	1493.69	4.9	0	59.2	26	95.00%	R.TMGIISMSTDPDAR.D		R.TMGIISMSTDPDAR.D
292	306	2	1694.76	2.2	1	49.4	26.1	95.00%	R.EIMLNFEPGTHGSTY.G		R.EIMLNFEPGTHGSTYGGNPLGAAVSIAALEVVK.E
135	153	3	2184.11	3	2	28.6	24.1	95.00%	K.KIPTDEAIILSCVDNFHGR.T	Carbamidomethyl (+57)	K.KIPTDEAIILSCVDNFHGR.T
276	291	2	1561.85	4	1	53	21.1	95.00%	K.AISGGVYPVSAVLSSR.E		K.AISGGVYPVSAVLSSR.E
238	254	2	1838.97	4.4	1	78.8	22	95.00%	K.AHNVLFIADEVQTGVAR.T		K.AHNVLFIADEVQTGVAR.T
258	275	3	2051.1	4.3	0	30.2	21	95.00%	K.MLCIEHSNVKPDVVILGK.A	Carbamidomethyl (+57)	K.MLCIEHSNVKPDVVILGK.A
70	80	2	1268.71	4.2	0	28.4	18.6	94.60%	K.IIEALVEQAQR.V		K.IIEALVEQAQR.V
107	124	2	1949.89	0.11	0	67.4	26.5	95.00%	Y.EMVIPMNTGAEAVETACK.L	Carbamidomethyl (+57)	K.YITEYFGYEMVIPMNTGAEAVETACK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
50	THIL_SCHPO	38.99%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
196	210	2	1667.89	-1.2	1	44.4	21.9	95.00%	K.AFEQEIVPVEVPVGR.G		K.AFEQEIVPVEVPVGR.G
360	371	2	1405.81	4.5	1	73.2	17.9	95.00%	R.IICTLAYILAQK.D	Carbamidomethyl (+57)	R.IICTLAYILAQK.D
340	359	3	1865.93	4.8	0	31	25.8	95.00%	R.VNINGGGVAMGHPLGSSGSR.I		R.VNINGGGVAMGHPLGSSGSR.I
291	301	2	1160.65	4.8	1	33.2	21.1	95.00%	R.FTTSPSLAIPK.A		R.FTTSPSLAIPK.A
14	30	2	1654.81	3.8	1	74.4	25.7	95.00%	R.TPMGSFGGSFASLPATK.L		R.TPMGSFGGSFASLPATK.L
43	69	3	2869.45	3.7	1	43	21.6	95.00%	R.VNIKPSDVDEVFMGNVVSANLGQNPAR.Q		R.VNIKPSDVDEVFMGNVVSANLGQNPAR.Q
136	147	2	1346.72	-1.4	1	39.8	23.4	95.00%	K.YGNVELVDGLLR.D		K.YGNVELVDGLLR.D
278	290	2	1440.71	4.1	1	44.3	25.5	95.00%	K.IIGWGEAAQDPER.F		K.IIGWGEAAQDPER.F
55	69	2	1526.76	0.58	0	83.3	25.2	95.00%	F.MGNVVSANLGQNPAR.Q		R.VNIKPSDVDEVFMGNVVSANLGQNPAR.Q
148	174	3	2905.26	3	1	42.8	26.8	95.00%	R.DGLSDAYDGLPMGNAAELCAEEHSIDR.A	Carbamidomethyl (+57)	R.DGLSDAYDGLPMGNAAELCAEEHSIDR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
51	ADH_SCHPO	36.29%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
109	122	2	1616.75	1.6	1	35.5	26	95.00%	K.AEETICPHIQLSGY.T	Carbamidomethyl (+57)	K.AEETICPHIQLSGYTVDGTFQHYCIANATHATIIPESVPLEVAAPIMCAGITCYR.A
236	253	2	1681.87	4.1	0	56	23.2	95.00%	K.AATNGGAHGTLVLSTSPK.S	Deamidation (+1)	K.AATNGGAHGTLVLSTSPK.S
254	278	3	2513.21	3.1	1	41.5	25.7	95.00%	K.SYEQAAGFARPGSTMVTVSMPAGAK.L		K.SYEQAAGFARPGSTMVTVSMPAGAK.L
170	194	3	2506.29	3.6	1	33.6	22	95.00%	K.VGPGEWICIPGAGGGLGHLAVQYAK.A	Carbamidomethyl (+57)	K.VGPGEWICIPGAGGGLGHLAVQYAK.A
123	131	2	1066.47	1.3	1	30.4	24.3	95.00%	Y.TVDGTFQHY.C		K.AEETICPHIQLSGYTVDGTFQHYCIANATHATIIPESVPLEVAAPIMCAGITCYR.A
42	62	3	2378.15	2.1	1	31.5	25.6	95.00%	K.YTGVCHTDLHALQGDWPLPAK.M	Carbamidomethyl (+57)	K.YTGVCHTDLHALQGDWPLPAK.M
200	214	2	1571.84	-1.5	1	61	22.9	95.00%	R.VVAIDTGDDKAELVK.S		R.VVAIDTGDDKAELVK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
52	HOSM_SCHPO	33.49%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
144	156	2	1447.79	-1.6	1	43.1	21.5	95.00%	Y.IIDSATEVINFVK.S		K.DMTYIIDSATEVINFVK.S
2	31	3	3218.5	4.8	1	47.5	25.2	95.00%	M.SVSEANGTETIKPPMNGNPYGPNPSDFLSR.V	Acetyl (+42)/ Deamidation (+1)	-.MSVSEANGTETIKPPMNGNPYGPNPSDFLSR.V
22	31	2	1088.53	0.8	1	57.8	24.7	95.00%	Y.GPNPSDFLSR.V		-.MSVSEANGTETIKPPMNGNPYGPNPSDFLSR.V
360	375	3	1793.94	-1.5	1	34.8	22.6	95.00%	K.SRAEQLNLHLTDAQAK.E		K.SRAEQLNLHLTDAQAK.E
192	204	2	1315.66	4	0	40.8	24.6	95.00%	R.VGIADTVGCATPR.Q	Carbamidomethyl (+57)	R.VGIADTVGCATPR.Q
64	85	2	2410.16	-0.79	1	150	25.7	95.00%	K.ALDNFGVDYIELTSPVASEQSR.Q		K.ALDNFGVDYIELTSPVASEQSR.Q
172	182	2	1264.7	4.6	1	43.4	20.1	95.00%	R.SDLVDLLSLYK.A		R.SDLVDLLSLYK.A
401	411	2	1290.55	4.4	1	41	26.7	95.00%	R.EYHADLSDADR.I		R.EYHADLSDADR.I
32	43	2	1391.75	4.9	1	68.1	21.6	95.00%	R.VNNFSIIESTLR.E		R.VNNFSIIESTLR.E
333	344	3	1420.7	0.2	1	28.1	24.7	95.00%	Y.EILKPEDFGMSR.Y		K.AILANPSTYEILKPEDFGMSR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
53	CDC48_SCHPO	14.97%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
28	38	2	1146.59	0.59	0	40.8	24	95.00%	Y.SAEDTATAILR.K		K.DTYSAEDTATAILR.K
550	563	2	1522.75	3.6	1	43.8	25.1	95.00%	K.AIANECSANFISVK.G	Carbamidomethyl (+57)	K.AIANECSANFISVK.G
287	297	2	1247.66	-0.26	1	36.6	23	95.00%	F.FLINGPEIMSK.M		R.AVANETGAFFFLINGPEIMSK.M
359	379	3	2280.22	4.2	1	31.5	20	95.00%	R.SNVVVMAATNRPNSIDPALRR.F		R.SNVVVMAATNRPNSIDPALRR.F
316	332	2	1841.98	-1.5	1	44.7	21.7	95.00%	K.NSPAIIFIDEIDSIAPK.R		K.NSPAIIFIDEIDSIAPK.R
410	426	2	1858.86	0.69	1	65.7	27.7	95.00%	K.LADDVDLEQIAAETHGY.V		K.LADDVDLEQIAAETHGYVGSDLASLCSEAAMQQIR.E
588	604	2	1817.92	-1.2	1	61.3	24.7	95.00%	R.AAAPCVVFLDELDSIAK.A	Carbamidomethyl (+57)	R.AAAPCVVFLDELDSIAK.A
116	129	2	1553.81	-1.9	0	42.1	23.3	95.00%	R.LGDIVTINPCPDIK.Y	Carbamidomethyl (+57)	R.LGDIVTINPCPDIK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
54	HSP7F_SCHPO	23.61%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
174	189	2	1665.85	4	1	78.4	24.5	95.00%	R.LMNDNAAAALTYGITK.T		R.LMNDNAAAALTYGITK.T
539	558	3	2226.18	2.9	1	45	21.4	95.00%	K.VADLSVSVQEDRLPTEVLEK.Y		K.VADLSVSVQEDRLPTEVLEK.Y
561	580	4	2283.16	4.6	1	33.5	23.3	95.00%	R.EAEHQMIATDKLVAETVDRK.N		R.EAEHQMIATDKLVAETVDRK.N
581	591	2	1385.65	4	1	31.1	26.5	95.00%	K.NALEEYIYDTR.A		K.NALEEYIYDTR.A
694	720	3	3003.35	-0.51	1	48.9	26.3	95.00%	R.APPPPPAEEVAPENEEVETMEIDEQKE.-		R.APPPPPAEEVAPENEEVETMEIDEQKE.-
38	48	2	1194.59	3.8	1	34	24.7	95.00%	R.STPSLVSYGER.S		R.STPSLVSYGER.S
96	106	2	1134.6	4	1	31.7	24.7	95.00%	K.LTEVDGFVGAK.V		K.LTEVDGFVGAK.V
306	318	3	1587.85	-0.89	1	29.8	22.8	95.00%	R.SDFEELIKPLLER.L		R.SDFEELIKPLLER.L
5	16	2	1249.64	6.5	1	29.4	24.3	95.00%	R.TNVVGIDFGNSK.T		R.TNVVGIDFGNSK.T
159	173	2	1534.89	4	0	42.9	14.3	95.00%	R.ALLEAANIAGLNPLR.L		R.ALLEAANIAGLNPLR.L
617	630	2	1684.72	4	1	75.9	26.8	95.00%	K.AEDWLYEEGEDTTK.A		K.AEDWLYEEGEDTTK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
55	UGPA1_SCHPO	24.70%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
299	314	3	1876.02	4.4	1	30	20.3	95.00%	R.LLEIAQVPPQHVEEFK.S		R.LLEIAQVPPQHVEEFK.S
20	34	2	1527.72	-2.3	1	87.4	26.7	95.00%	F.AFDNTATSIAASTMK.N		K.SQSAFAFDNTATSIAASTMK.N
162	175	2	1539.72	-1.2	1	54.7	26.5	95.00%	F.VLMNSFNTDEATAK.V		K.YNVNVPFVLMNSFNTDEATAK.V
74	104	3	3417.67	3.9	1	69	22.6	95.00%	R.GSEINWDLVESPKPEQVVEYDTITEAGGLSR.D		R.GSEINWDLVESPKPEQVVEYDTITEAGGLSR.D

185	194	2	1205.65	4.7	1	32.1	23.3	95.00%	K.IDILTFNQSR.Y		K.IDILTFNQSR.Y
408	419	2	1380.66	-0.011	0	32.7	26	95.00%	Y.SINHGQVEMNPR.R		K.SDLYSINHGQVEMNPR.R
115	129	2	1460.72	4.2	0	48.3	25.1	95.00%	K.LNGGLGTTMGCVGPK.S	Carbamidomethyl (+57)	K.LNGGLGTTMGCVGPK.S
287	298	2	1278.63	4.4	1	55.1	24.9	95.00%	K.GGTLIDYDGNVR.L		K.GGTLIDYDGNVR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
56	DHAS_SCHPO	36.69%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
112	132	3	2341.31	2.7	1	53.3	16.3	95.00%	R.REPTVPLVVPTVNTDHLDVIK.Y		R.REPTVPLVVPTVNTDHLDVIK.Y
19	30	3	1445.76	4.9	1	23.3	23.7	91.40%	R.FITLLSDHPEFK.I		R.FITLLSDHPEFK.I
143	161	2	2003.01	-2.3	0	76.7	24.1	95.00%	R.GCIITNSNCSTAAVVVPLK.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GCIITNSNCSTAAVVVPLK.A
304	318	3	1662.81	4.5	2	31.3	25.6	95.00%	R.LDRNNENGYAVSVGR.I		R.LDRNNENGYAVSVGR.I
228	240	2	1504.7	1.2	0	47.5	26.9	95.00%	Y.ELTDNVVSAQCNR.V	Carbamidomethyl (+57)	K.ILGSVNSTISGYELTDNVVSAQCNR.V
31	39	2	856.52	4.9	0	28.2	20.3	94.40%	K.IAVLGASAR.S		K.IAVLGASAR.S
287	303	3	2003.98	4.2	1	33.9	25.8	95.00%	K.QAIYVFDDSTPDRPQPR.L		K.QAIYVFDDSTPDRPQPR.L
291	303	3	1528.73	-0.27	1	26.6	26.1	94.40%	Y.VFDDSTPDRPQPR.L		K.QAIYVFDDSTPDRPQPR.L
267	278	2	1375.7	3.8	1	37.2	23.7	95.00%	R.EVLANYVSEPQK.L		R.EVLANYVSEPQK.L
6	18	2	1227.7	3.7	0	35.6	20.5	95.00%	K.VGILGATGTVGQR.F		K.VGILGATGTVGQR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
57	RS7_SCHPO	30.26%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	140	2	2393.32	1	1	58.4	15.1	95.00%	R.TLTAVHNAILEDIVFPTEIIGK.R		R.TLTAVHNAILEDIVFPTEIIGK.R
59	70	2	1322.84	4	1	46.5	6.99	95.00%	K.AIVVFVPQPLLK.A		K.AIVVFVPQPLLK.A
119	141	3	2549.42	0.31	1	60.9	14.3	95.00%	R.TLTAVHNAILEDIVFPTEIIGKR.T		R.TLTAVHNAILEDIVFPTEIIGKR.T
11	34	2	2657.25	4.3	1	84.1	26.4	95.00%	R.SSSQPTETDLLVAQCLYDLESSSK.D	Carbamidomethyl (+57)	R.SSSQPTETDLLVAQCLYDLESSSK.D
11	27	2	1910.89	-0.56	1	48.5	26.8	95.00%	R.SSSQPTETDLLVAQCLY.D	Carbamidomethyl (+57)	R.SSSQPTETDLLVAQCLYDLESSSK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
58	PYR1_SCHPO	7.66%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1135	1145	2	1229.6	4.3	0	46.2	25	95.00%	R.MLDDIGVDQPK.W		R.MLDDIGVDQPK.W
1771	1784	2	1494.85	4.1	0	35.2	17.2	95.00%	R.EAIPLLLTAVNEGR.L		R.EAIPLLLTAVNEGR.L
228	245	3	2026.07	0.4	1	42.6	21.6	95.00%	W.KNPNTENLTSQVSIKEPK.L		K.DWSTAFEDIPWKNPNTENLTSQVSIKEPK.L
457	466	2	1084.56	6.1	0	38.9	23	95.00%	K.LPGGTIEENR.S		K.LPGGTIEENR.S
1880	1906	3	2689.36	3.3	1	28.6	22.9	95.00%	K.VSALMSPGLPHAAPSLAEAFGQAPENK.A		K.VSALMSPGLPHAAPSLAEAFGQAPENK.A
511	525	2	1625.94	0.36	0	33.7	17	95.00%	Y.TILINPNIATIQTSK.G		R.EEGIYTILINPNIATIQTSK.G
1192	1208	3	1859.07	1.2	1	23.1	14.8	91.20%	Y.LQQAVAINKDHPVVISK.Y		K.FCDTVGYPVLVRPSYVLSGAAMNTVYSQSDLHSYLQQAVAINKDHPVVISK.Y
1426	1442	2	1819.78	0.12	1	35	27.5	95.00%	F.ATAGTSDYFMESGVPCK.Y	Carbamidomethyl (+57)	K.LYENNYNIFATAGTSDYFMESGVPCK.Y
662	671	2	1112.62	1.6	0	31.9	19.6	95.00%	F.ATSPQVLIER.S		R.AAYALGGLGSGFADNEAELIDLCTLAFATSPQVLIER.S
580	597	2	2032.07	0.085	2	44.3	22.1	95.00%	K.VLGTPIDTIITTEDRELF.A		K.VLGTPIDTIITTEDRELFAR.A
1804	1818	3	1724.81	5.5	0	27.4	26.4	94.90%	R.LHDQDDSGVQLEVDR.S		R.LHDQDDSGVQLEVDR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
59	LEUC_SCHPO	17.55%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
57	77	5	2378.29	3.8	1	17.4	18.5	90.00%	K.VRHPELALATVDHNIPTDPRK.D		K.VRHPELALATVDHNIPTDPRK.D
59	77	4	2123.12	3.9	1	27	21.1	95.00%	R.HPELALATVDHNIPTDPRK.D		R.HPELALATVDHNIPTDPRK.D

540	563	3	2538.39	3.4	1	28.2	16.8	95.00%	K.FTVVEGIAAPLPMANVDTDKIIPK.Q		K.FTVVEGIAAPLPMANVDTDKIIPK.Q
675	689	2	1698.84	-1.8	1	52.2	25.2	95.00%	K.FSVDLVNQTITYGDK.Q		K.FSVDLVNQTITYGDK.Q
303	323	3	2168.13	2	0	56.5	22.8	95.00%	W.GTSPQDVIPINGNIPDPAHVK.D		K.YDIEVEINAADVLPTVTWGTSPQDVIPINGNIPDPAHVK.D
603	619	3	1826.86	5.3	1	37.3	26.9	95.00%	R.HATVLVAHDNFGCGSSR.E	Carbamidomethyl (+57)	R.HATVLVAHDNFGCGSSR.E
477	493	2	1810.88	4.1	1	36.5	25.9	95.00%	R.EFFGDVSNGSPSIITNK.N		R.EFFGDVSNGSPSIITNK.N
650	667	2	2027	4	0	40.9	25.3	95.00%	K.NGMLPIPTPIEQVNDMMK.A		K.NGMLPIPTPIEQVNDMMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
60	EF1B_SCHPO	47.66%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
14	22	2	1104.59	4.8	1	36.2	23.2	95.00%	K.QLNDFLLDK.S		K.QLNDFLLDK.S
153	165	2	1432.74	3.9	1	44.3	24.2	95.00%	R.SIQMDGLVWGLSK.L		R.SIQMDGLVWGLSK.L
64	73	2	985.54	-1	0	27.3	21	93.40%	Y.DLATLPGTAK.E		K.QIATYDLATLPGTAK.E
2	13	2	1209.59	3.7	1	57.4	25.4	95.00%	M.GFSDLTSDAGLK.Q		-.MGFSDLTSDAGLK.Q
59	73	2	1561.84	4.2	1	60.9	22.2	95.00%	K.QIATYDLATLPGTAK.E		K.QIATYDLATLPGTAK.E
40	55	2	1586.8	-1.4	2	38.5	24.7	95.00%	K.AVGVAPDTAKYPNGAR.W	Deamidation (+1)	K.AVGVAPDTAKYPNGAR.W
129	149	2	2459.19	2.9	1	66.3	26.2	95.00%	K.SLVTLDVKPWDDETPMDELEK.A		K.SLVTLDVKPWDDETPMDELEK.A
23	38	2	1757.81	-1	1	28	26.6	92.00%	K.SFIEGYEPSQADAVVF.K		K.SFIEGYEPSQADAVVFK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
61	GBLP_SCHPO	33.44%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
18	36	2	1956.02	0.55	0	56.9	23	95.00%	W.VTSLSTAPENPDILLSGSR.D		R.ATLEGHSGWVTSLSTAPENPDILLSGSR.D
48	57	2	1135.53	4.7	1	43.2	24.9	95.00%	R.DDVNYGVAQR.R		R.DDVNYGVAQR.R
9	17	2	956.44	1.2	1	33.4	24.7	95.00%	R.ATLEGHSGW.V		R.ATLEGHSGWVTSLSTAPENPDILLSGSR.D
186	212	3	2736.26	2.6	1	43.2	26.6	95.00%	R.TSHYGHTGYVSAVTISPDGSLCASGGR.D	Carbamidomethyl (+57)	R.TSHYGHTGYVSAVTISPDGSLCASGGR.D
9	36	3	2894.45	2.9	1	38.1	22.6	95.00%	R.ATLEGHSGWVTSLSTAPENPDILLSGSR.D		R.ATLEGHSGWVTSLSTAPENPDILLSGSR.D
300	308	2	1060.53	0.36	1	36.1	23.7	95.00%	F.SGWTDNLIR.V		K.SSEPECISLTWSPDGQTLFSGWTDNLIR.V
234	245	2	1314.71	3.1	1	32.5	22.6	95.00%	K.ANINALVFSPNR.Y		K.ANINALVFSPNR.Y
176	185	2	1264.65	5.4	1	30.1	24.6	95.00%	K.VWDLETFSLR.T		K.VWDLETFSLR.T
39	47	2	1112.68	5.9	1	27.8	17.4	93.90%	K.SIILWNLVR.D		K.SIILWNLVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
62	RS18_SCHPO	28.95%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	66	2	1246.61	4	0	41.5	25.2	95.00%	R.AGELTTEELER.I		R.AGELTTEELER.I
67	78	2	1386.79	4	1	45.2	19.3	95.00%	R.IVTIIQNPSQFK.I		R.IVTIIQNPSQFK.I
2	14	2	1578.85	-1.8	1	29.2	21.6	95.00%	M.SLVVPDNFQHILR.L	Acetyl (+42)	-.MSLVVPDNFQHILR.L
79	86	2	1031.56	6	1	52.6	22.4	95.00%	K.IPSWFLNR.Q		K.IPSWFLNR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
63	TRP_SCHPO	29.70%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
382	393	2	1355.77	4.5	0	47.2	19.5	95.00%	K.INNCIGQILLAK.R	Carbamidomethyl (+57)	K.INNCIGQILLAK.R
247	261	2	1623.75	3.4	1	47.6	26.5	95.00%	K.AEPGTAATVVEEYCK.Y	Carbamidomethyl (+57)	K.AEPGTAATVVEEYCK.Y
217	239	3	2325.14	1.1	1	43.4	24.9	95.00%	F.GVNTSEHFHQVGSVSDGVVVGSK.I		K.FAGDTPLAVGFGVNTSEHFHQVGSVSDGVVVGSK.I
400	419	3	1938.01	4.3	0	37.5	22.6	95.00%	R.IIAETGAGQHGVATAICAAK.F	Carbamidomethyl (+57)	R.IIAETGAGQHGVATAICAAK.F
616	631	2	1825.87	3	1	57.5	26.5	95.00%	R.AEFIAVTDAQCLEGFR.A	Carbamidomethyl (+57)	R.AEFIAVTDAQCLEGFR.A
445	461	2	1739.99	4	0	48.6	17.7	95.00%	R.LLGAEVVPVTSGTQTLR.D		R.LLGAEVVPVTSGTQTLR.D
543	560	2	1822.79	-2.2	0	39	27.2	95.00%	K.SVMMLGCEAGGDGVDTPK.H	Carbamidomethyl (+57)	K.SVMMLGCEAGGDGVDTPK.H

673	690	3	1893.03	4.4	1	34.8	19.7	95.00%	R.GDKDVQSVAEQLPILGPK.I		R.GDKDVQSVAEQLPILGPK.I
275	302	3	2928.48	4.6	1	34.9	22.4	95.00%	K.QFQSGGSVATAPPAAVVEPINEMYLPQK.Y		K.QFQSGGSVATAPPAAVVEPINEMYLPQK.Y
56	67	2	1232.57	0.74	0	32.7	24.7	95.00%	F.SDAVADGPTICK.G	Carbamidomethyl (+57)	K.IMQGLQNGGAGIIELGIPFSDAVADGPTICK.G
584	611	3	2954.42	2.6	1	50.2	24.8	95.00%	R.EDGQIQDTHSISAGLDYPGVGPELSELK.Y		R.EDGQIQDTHSISAGLDYPGVGPELSELK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
64	ECM17_SCHPO	11.20%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
66	90	4	2646.3	0.95	1	22.7	24.8	95.00%	K.SHADPFAHIADAILAEEEVASTQPK.Q		K.SHADPFAHIADAILAEEEVASTQPK.Q
314	325	2	1337.8	4.6	0	39.3	13.4	95.00%	R.LTVLEPITSLPR.K		R.LTVLEPITSLPR.K
878	900	3	2550.31	-0.28	0	30.1	22.8	95.00%	K.ALGLDNVEIDIDEPKPITNEDIK.Q		K.ALGLDNVEIDIDEPKPITNEDIK.Q
1053	1078	3	3057.49	0.99	1	43.1	24.4	95.00%	K.QISNELLPTTSSYHEIWIEDPETVEK.R		K.QISNELLPTTSSYHEIWIEDPETVEK.R
611	636	3	2801.42	3.9	1	43.3	22.6	95.00%	K.GPSVVLAYLPYHSADDDAITVLQETK.K		K.GPSVVLAYLPYHSADDDAITVLQETK.K
1382	1390	2	945.5	-0.41	0	56.1	23.4	95.00%	W.VAEIACVGK.A	Carbamidomethyl (+57)	R.MTGCPNGCSRPWVAEIACVGK.A
1031	1048	2	2075.92	-1.2	1	49.3	27.3	95.00%	R.NVTCSSTPNNETIHDQLF.A	Carbamidomethyl (+57)	R.NVTCSSTPNNETIHDQLFAVSK.Q
801	810	2	1058.57	5.4	0	27.5	22.5	93.50%	K.GADLNLSELK.Y		K.GADLNLSELK.Y
759	774	2	1850.85	3.7	1	75.5	26.9	95.00%	K.IMAMDDFPIEELGNEK.N		K.IMAMDDFPIEELGNEK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
65	MET3_SCHPO	27.55%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
427	440	2	1651.86	4	1	77.5	23.2	95.00%	R.LDAISVFYAQELQR.A		R.LDAISVFYAQELQR.A
350	359	2	1102.6	3.9	0	29.9	22.6	95.00%	R.TLNISGTELR.R		R.TLNISGTELR.R
69	92	2	2586.35	1.6	1	44	21.6	95.00%	R.LSTGEVFPIPITLDLNESQADSLK.A		R.LSTGEVFPIPITLDLNESQADSLK.A
59	68	2	1233.64	5.6	1	40.5	23.7	95.00%	K.DYLNVVENLR.L		K.DYLNVVENLR.L
254	262	2	1012.62	5.1	0	33.5	17.2	95.00%	K.LSLLPLAMR.M		K.LSLLPLAMR.M
479	490	2	1293.64	-1.5	1	26	24.8	91.30%	F.AVLSQLSDEGYL.-		K.DSVSEVTFAVLSQLSDEGYL.-
217	234	3	1974.04	0.26	1	33.6	22.4	95.00%	R.VLIHPVVGMTKPGDIDHF.T		R.VLIHPVVGMTKPGDIDHFTR.V
364	382	2	2159.15	2.7	1	56.8	21.5	95.00%	R.VGANIPEWFSYPEVVAILR.Q		R.VGANIPEWFSYPEVVAILR.Q
13	29	2	1924	2.8	1	48.1	23.5	95.00%	R.DAPLREQLEQEATSLPK.I		R.DAPLREQLEQEATSLPK.I
217	236	4	2231.2	3.6	1	31	20.1	95.00%	R.VLIHPVVGMTKPGDIDHFTR.V		R.VLIHPVVGMTKPGDIDHFTR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
66	FAS1_SCHPO	5.79%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1068	1087	3	2303.16	0.3	2	23.4	24.4	91.70%	K.VNEPAKELLDGINETHIQHF.I		K.VNEPAKELLDGINETHIQHFIK.K
1117	1130	2	1421.7	4.7	0	59.8	25.6	95.00%	K.SLESVSVTEEAGSK.V		K.SLESVSVTEEAGSK.V
2	12	2	1294.67	5.2	0	53.5	24.5	95.00%	M.VEAEQVHQSLR.S		-.MVEAEQVHQSLR.S
966	984	2	2177.07	4.2	1	92.2	25.1	95.00%	K.TTLIENFEDLNDPYPVAAR.F		K.TTLIENFEDLNDPYPVAAR.F
520	534	2	1580.77	-1.5	1	75.9	26.4	95.00%	R.VIVADSFESLDMGAK.F		R.VIVADSFESLDMGAK.F
1870	1881	2	1266.57	5.2	1	37.8	25.8	95.00%	R.SDYGMVAANPSR.V		R.SDYGMVAANPSR.V
210	224	3	1723.91	5.4	1	36.5	22	95.00%	K.GLNVLDWLAGERPER.D		K.GLNVLDWLAGERPER.D
781	794	2	1545.81	3.9	1	42.1	23.7	95.00%	K.LPPMPFDGILFGSR.L		K.LPPMPFDGILFGSR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
67	RL8_SCHPO	28.19%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
24	32	2	1084.62	4.7	1	29.3	21.1	95.00%	K.NPLFVSRPR.S		K.NPLFVSRPR.S
109	120	2	1171.61	4.7	0	55.2	22.9	95.00%	R.LVAEAEAVANGK.S	Deamidation (+1)	R.LVAEAEAVANGK.S

134	146	2	1425.8	4.3	1	45.6	17.5	95.00%	K.YGLNHVVALIEAK.K		K.YGLNHVVALIEAK.K
69	78	2	1082.65	-1.2	2	35.5	17	95.00%	R.LKVPPAIAQF.Q		R.LKVPPAIAQFQK.T
33	43	2	1188.62	4.1	1	26.8	24.2	92.60%	R.SFGIGQDIQPK.R		R.SFGIGQDIQPK.R
81	92	2	1364.74	3.7	2	46.2	22.3	95.00%	K.TLDKNTATQVFK.L		K.TLDKNTATQVFK.L
52	57	2	862.44	5.9	1	26.5	23.4	92.20%	K.WPEYIR.L		K.WPEYIR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
68	YHY6_SCHPO	17.46%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
678	698	2	2257.13	4.5	0	51.2	24.5	95.00%	K.SLCIPLEQPSGEDAIIEGTTK.C	Carbamidomethyl (+57)	K.SLCIPLEQPSGEDAIIEGTTK.C
161	188	4	2736.49	3.7	1	29.1	17.2	95.00%	K.SVGVNPIIVDFSAPGSATAPSKPAAQKK.K		K.SVGVNPIIVDFSAPGSATAPSKPAAQKK.K
298	320	2	2539.22	-0.0067	1	25.9	24.9	91.10%	R.AGTSELDEPIAIRPTSETVMYPYY.YAK.W		R.AGTSELDEPIAIRPTSETVMYPYYAK.W
161	187	3	2608.39	2.9	1	26.8	19.5	95.00%	K.SVGVNPIIVDFSAPGSATAPSKPAAQK.K		K.SVGVNPIIVDFSAPGSATAPSKPAAQK.K
298	323	3	2901.42	3	1	27.8	24	95.00%	R.AGTSELDEPIAIRPTSETVMYPYYAK.W		R.AGTSELDEPIAIRPTSETVMYPYYAK.W
492	511	2	2075.18	-2.9	0	37.1	14.9	95.00%	K.LPPAIALVQSVVVPCGITNK.T	Carbamidomethyl (+57)	K.LPPAIALVQSVVVPCGITNK.T
660	677	3	1900.86	4.5	1	43.4	27	95.00%	R.QVNGDEPEDEKAPSMGAK.S		R.QVNGDEPEDEKAPSMGAK.S
387	398	2	1343.81	4.3	1	30.5	13.8	95.00%	R.IYTDLLAVPVIK.G		R.IYTDLLAVPVIK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
69	RL4A_SCHPO	33.88%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
141	161	3	2348.2	0.89	2	49.5	22.7	95.00%	R.GHRIEEIPEVPLVVDDAVQSF.Q		R.GHRIEEIPEVPLVVDDAVQSFQK.T
122	140	2	1845.03	-1.5	1	55.8	17.7	95.00%	R.YAISSAVAASGVPSLLLAR.G		R.YAISSAVAASGVPSLLLAR.G
2	13	2	1304.71	4.5	1	25.5	21.8	90.50%	M.AAARPTVSIYSK.D	Acetyl (+42)	-.MAAARPTVSIYSK.D
14	29	2	1695.88	4.2	1	38.3	23.2	95.00%	K.DGSVSSETIALPFVFK.A		K.DGSVSSETIALPFVFK.A
144	163	2	2254.18	3.5	1	34.1	21.6	95.00%	R.IEEIPEVPLVVDDAVQSFQK.T		R.IEEIPEVPLVVDDAVQSFQK.T
276	291	2	1864.93	-1.1	1	69.3	25.4	95.00%	K.NYFLPENIISNADVTR.L		K.NYFLPENIISNADVTR.L
235	248	3	1457.85	4.2	0	28.5	17.5	95.00%	R.LNLLQLAPGGHLGR.F		R.LNLLQLAPGGHLGR.F
292	303	2	1357.75	4	0	43.8	21.6	95.00%	R.LINSDEIQSIVK.A		R.LINSDEIQSIVK.A
87	97	2	1197.51	4.4	1	32.6	26.1	95.00%	R.SGQAAFGNMCR.S	Carbamidomethyl (+57)	R.SGQAAFGNMCR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
70	CYSD_SCHPO	39.63%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
72	100	3	2787.49	1.5	1	58.7	18	95.00%	R.IAALEHGAAAIATSSGTSALFMALTTLAK.A		R.IAALEHGAAAIATSSGTSALFMALTTLAK.A
366	377	2	1185.64	4.4	0	34.5	21.8	95.00%	K.LASQLANVGDAK.T		K.LASQLANVGDAK.T
170	210	4	4156.13	4.3	1	53.9	19.3	95.00%	R.IAEVAHAAGVPLMVDNTFGGGGYLVRPIDHGADIVTHSATK.W		R.IAEVAHAAGVPLMVDNTFGGGGYLVRPIDHGADIVTHSATK.W
132	150	2	2074.95	4.2	1	127	26.7	95.00%	K.FVNGDDPNDLAAQIDENTK.A		K.FVNGDDPNDLAAQIDENTK.A
378	403	3	2798.48	2.5	1	42.6	20.2	95.00%	K.TLVIAPAYTTHLQLTDEEQISAGVTK.D		K.TLVIAPAYTTHLQLTDEEQISAGVTK.D
193	210	3	1929.05	1.1	0	30	20.8	95.00%	Y.LVRPIDHGADIVTHSATK.W		R.IAEVAHAAGVPLMVDNTFGGGGYLVRPIDHGADIVTHSATK.W
2	26	3	2735.28	-0.11	1	59.1	26.2	95.00%	M.PVESEHFETLQLHAGQEPDAATSSR.A		-.MPVESEHFETLQLHAGQEPDAATSSR.A
211	228	3	1752.92	0.18	1	23.5	22.7	91.90%	K.WIGGHGTTIGGVIVDSGK.F		K.WIGGHGTTIGGVIVDSGK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
71	LYS12_SCHPO	30.39%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
7	26	3	1987.19	3.6	1	23.5	9.03	91.70%	R.IVLGLIPADGIGKEVVPAAR.R		R.IVLGLIPADGIGKEVVPAAR.R

282	297	2	1621.79	0.29	0	40.6	25.6	95.00%	F.VMSEPVHGSAPDIAGR.G		R.EPECFDVVVAPNLYGDILSDGAASLIGSLGLVPSANVGDNFVMSEPVHGSAPDIAGR.G
86	97	2	1231.7	4.7	1	25.9	20.9	91.20%	K.VAGYSSPIVALR.K		K.VAGYSSPIVALR.K
197	208	2	1324.65	5.3	1	41.8	25.5	95.00%	K.SNVMSVTDGLFR.E		K.SNVMSVTDGLFR.E
298	307	2	1044.58	4.6	1	32.2	22.4	95.00%	R.GIANPVATFR.S		R.GIANPVATFR.S
188	196	3	1047.69	4.7	0	25.1	3.01	94.00%	K.KPLVTIIHK.S		K.KPLVTIIHK.S
127	138	2	1568.72	4	1	44	26	95.00%	R.ENTECLYVKEER.M	Carbamidomethyl (+57)	R.ENTECLYVKEER.M
67	85	3	2071.06	4.3	2	52.5	23.8	95.00%	R.LKTECNAALFGAVQSPTHK.V	Carbamidomethyl (+57)	R.LKTECNAALFGAVQSPTHK.V
7	19	2	1264.77	-1.4	0	35.3	13.6	95.00%	R.IVLGLIPADGIGK.E		R.IVLGLIPADGIGK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
72	IF4A_SCHPO	24.23%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
156	165	2	1091.53	0.9	1	45.5	25	95.00%	R.ALPTDAVQMF.V		R.ALPTDAVQMFVLDEADEMLSR.G
58	69	2	1173.61	5	0	69	23.5	95.00%	R.DVLAQAQSGTGK.T		R.DVLAQAQSGTGK.T
49	69	3	2154.15	3.1	1	31.7	20.5	95.00%	R.AIMPILGERDVLAQAQSGTGK.T		R.AIMPILGERDVLAQAQSGTGK.T
378	392	2	1739.82	-0.011	0	35.8	26.7	95.00%	Y.NTHIEEMPMNIADLI.-		R.EIEQFYNTHIEEMPMNIADLI.-
155	176	3	2506.23	3.9	2	41.3	24.8	95.00%	R.RALPTDAVQMFVLDEADEMLSR.G		R.RALPTDAVQMFVLDEADEMLSR.G
2	32	3	3667.76	4	1	58	22.9	95.00%	M.VDQLEDSVIETNYDEVIDTFDDMNLKPELLR.G		-.MVDQLEDSVIETNYDEVIDTFDDMNLKPELLR.G
372	392	2	2549.19	2.9	1	26.7	26.2	90.40%	R.EIEQFYNTHIEEMPMNIADLI.-		R.EIEQFYNTHIEEMPMNIADLI.-
166	176	2	1276.6	0.14	0	52.7	24.9	95.00%	F.VLDEADEMLSR.G		R.ALPTDAVQMFVLDEADEMLSR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
73	ACON_SCHPO	13.62%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
532	549	2	1853.89	4.6	1	68.9	26.5	95.00%	K.GYDPGSNTYVAPSSVNVK.D		K.GYDPGSNTYVAPSSVNVK.D
613	626	2	1430.68	-1	0	45.1	26.4	95.00%	Y.MIGAINAENGEANK.L		R.GHLQNISNNYMIGAINAENGEANK.L
392	402	2	1203.6	5.2	0	35.2	24.5	95.00%	R.AASICQQAIDK.G	Carbamidomethyl (+57)	R.AASICQQAIDK.G
65	80	3	1895.94	-1.3	1	27.1	25.4	95.00%	K.ILYGHLDDPVNQDIER.G		K.ILYGHLDDPVNQDIER.G
652	666	2	1665.78	3.4	1	67.3	26.5	95.00%	R.WVTLGEQNFGEGSSR.E		R.WVTLGEQNFGEGSSR.E
462	470	2	1052.53	5	1	36.5	24.7	95.00%	K.NSIVTSYNR.N		K.NSIVTSYNR.N
476	485	2	1056.46	2	1	30.3	24.5	95.00%	R.NDANPATHAF.V		R.NDANPATHAFVTSPDIVTAMVFSGDMNFNPLTDTLK.D
519	531	2	1327.72	1.5	2	27.5	22	93.60%	F.KFEPPTGAGLPSK.G		K.DGNDFKFEPPTGAGLPSK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
74	GLT1_SCHPO	7.15%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1442	1464	3	2335.04	4.9	1	32.4	27.3	95.00%	R.NSGAIAVVEGVGDHGCEYMTGGR.V	Carbamidomethyl (+57)	R.NSGAIAVVEGVGDHGCEYMTGGR.V
1897	1918	3	2189.08	3.9	1	55	25.1	95.00%	K.GKDVIVIGGGDTGNDCLGTSVR.H	Carbamidomethyl (+57)	K.GKDVIVIGGGDTGNDCLGTSVR.H
672	685	2	1555.69	5.3	1	68	26.5	95.00%	R.ICSEADTAVNEGYK.A	Carbamidomethyl (+57)	R.ICSEADTAVNEGYK.A
624	638	2	1701.91	4.2	1	45.5	22.6	95.00%	R.MPTPILTVEEFNALK.N		R.MPTPILTVEEFNALK.N
1664	1675	2	1427.58	-0.73	1	38.1	26	95.00%	F.CQSDYGCPISNK.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.CMDCGTPFCQSDYGCPISNK.I
1690	1707	2	2063.08	4.1	1	61.9	22.4	95.00%	K.EALTQLLLTNNFPEFTGR.V		K.EALTQLLLTNNFPEFTGR.V
1022	1038	3	1639.81	4.9	0	25.7	25.9	93.60%	K.MAQGAKPGEGGELPGNK.V		K.MAQGAKPGEGGELPGNK.V
1011	1021	2	1293.64	-1.2	1	33.8	25.4	95.00%	W.YLSDADELQIK.M		R.FGVTSWYLSDADELQIK.M
1442	1459	2	1832.8	-1.7	1	72.4	27.1	95.00%	R.NSGAIAVVEGVGDHGCEY.M	Carbamidomethyl (+57)	R.NSGAIAVVEGVGDHGCEYMTGGR.V
1758	1776	2	1792.98	-1.9	0	90.9	20.6	95.00%	R.VAIIGSGPAGLAAADQLNR.A		R.VAIIGSGPAGLAAADQLNR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
75	NACA_SCHPO	54.91%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	75	2	1164.62	5.8	1	59.3	23.1	95.00%	K.SSNNAYIVLGK.V		K.SSNNAYIVLGK.V
100	118	2	1931.86	-0.22	0	30.2	27.6	93.70%	K.EEAAITEESGDAQPADTAK.I		K.EEAAITEESGDAQPADTAK.I
94	118	3	2590.19	-1.1	1	59.9	26.8	95.00%	K.QATETKEEAAITEESGDAQPADTAK.I		K.QATETKEEAAITEESGDAQPADTAK.I
119	137	3	2123	4.4	1	54.2	26.1	95.00%	K.IEESFEQEKAVDETGVDAK.D		K.IEESFEQEKAVDETGVDAK.D
11	26	2	1637.87	4.6	0	55.2	22.4	95.00%	K.ISELPAGSTTVVHAEK.A		K.ISELPAGSTTVVHAEK.A
52	64	2	1540.93	4.4	1	50.2	11.8	95.00%	K.NILLIINEPIVYK.S		K.NILLIINEPIVYK.S
76	86	2	1189.58	4.9	0	47.2	24.9	95.00%	K.VTVEDMAAQAR.A		K.VTVEDMAAQAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
76	SODC_SCHPO	41.56%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	144	4	2825.43	3.9	1	21.6	23	95.00%	R.TIVIHAGEDDLGKGTSEESLKTGNAGAR.N		R.TIVIHAGEDDLGKGTSEESLKTGNAGAR.N
81	97	2	1765.87	4	0	72.3	25.7	95.00%	R.HVGDLGNLESDAQGNIK.T		R.HVGDLGNLESDAQGNIK.T
117	137	3	2198.12	3.9	1	49.5	24	95.00%	R.TIVIHAGEDDLGKGTSEESLK.T		R.TIVIHAGEDDLGKGTSEESLK.T
98	116	2	1984.04	4.4	1	72.6	22	95.00%	K.TTFSDSVISLFGANSIIGR.T		K.TTFSDSVISLFGANSIIGR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
77	DHOM_SCHPO	26.60%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
42	56	2	1619.8	0.12	1	52.1	25.4	95.00%	F.NVVAISSMEGHYVSK.D		K.GFNENASTNGTTSFNVVAISSMEGHYVSK.D
57	67	2	1391.68	4.7	1	33.1	24.6	95.00%	K.DYQPINLSEWK.N		K.DYQPINLSEWK.N
238	252	2	1526.81	-1.8	1	35.8	23.1	95.00%	R.IAGVHVESASSFPVK.S		R.IAGVHVESASSFPVK.S
125	138	2	1568.79	4.5	1	56.7	23.9	95.00%	K.AFSASNDVYQNIIK.A		K.AFSASNDVYQNIIK.A
89	110	2	2284.19	-1.7	1	98.4	22.5	95.00%	K.SPLPAILVDNTASEAIAQSYPK.F		K.SPLPAILVDNTASEAIAQSYPK.F
320	331	2	1307.64	0.22	1	27.4	25.8	92.30%	F.ANLQSSDNIISF.T		K.YDASHPFANLQSSDNIISFTTK.R
78	88	2	1190.66	0.15	1	42.8	21.8	95.00%	Y.SLDALVDFLAK.S		K.NLTSQNQGAYSLDALVDFLAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
78	ILV3_SCHPO	16.89%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
446	459	2	1608.78	-1.3	1	70.8	26.2	95.00%	R.VFDAENDFIAALER.G		R.VFDAENDFIAALER.G
49	68	2	2142.97	5.2	1	90.3	27.1	95.00%	K.SQGASQAMLYATGLNEEDMK.K		K.SQGASQAMLYATGLNEEDMK.K
69	78	2	1144.57	0.37	1	42	23.1	95.00%	K.KPQVGIASCW.Y	Carbamidomethyl (+57)	K.KPQVGIASCWYEGNPCNMHLLDLGR.R
402	417	4	1843.09	3.6	1	32.1	12.6	95.00%	K.IIRPLSNPIKTEGHLR.V		K.IIRPLSNPIKTEGHLR.V
40	48	2	994.5	5.2	1	30.6	24.9	95.00%	K.YSETITGPK.S		K.YSETITGPK.S
266	278	3	1408.68	4.8	1	24.2	25.9	91.50%	K.FAECEAAGSAIKR.L	Carbamidomethyl (+57)	K.FAECEAAGSAIKR.L
108	126	2	1970.92	-0.1	1	54.9	27.2	95.00%	F.QFNTIGVSDGISMGTTGMR.Y		K.AGLTGFQFNTIGVSDGISMGTTGMR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
79	BCA1_SCHPO	22.63%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
315	331	2	1670.97	4.2	1	59.5	16.5	95.00%	R.LLEVFGAGTAALVSPVK.A		R.LLEVFGAGTAALVSPVK.A
37	49	3	1581.74	4.5	1	25.4	26.1	93.00%	K.FGENFTDHMLIMK.W		K.FGENFTDHMLIMK.W
262	278	2	1794.99	-1.9	0	48.3	20	95.00%	K.EIITAPLDGMILPGVTR.D		K.EIITAPLDGMILPGVTR.D
337	359	2	2462.15	-1.3	1	48.2	26.5	95.00%	K.GTEYEIPMPEGQEAGPITSEISK.W		K.GTEYEIPMPEGQEAGPITSEISK.W

115	130	2	1769.95	-2	1	46.8	21.7	95.00%	R.ISLPSFDPAELAEIIR.K		R.ISLPSFDPAELAEIIR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
80	RL13_SCHPO	43.75%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
172	183	2	1398.66	5.4	1	54	26.1	95.00%	K.NFNAFSTLSNER.A		K.NFNAFSTLSNER.A
46	64	4	2080.27	3.1	0	20	6.02	94.60%	K.IAPRPVEAIRPAVKPPTIR.Y		K.IAPRPVEAIRPAVKPPTIR.Y
118	128	3	1326.79	4.7	1	51.2	17.9	95.00%	K.VYLAHLIVFPR.K		K.VYLAHLIVFPR.K
135	171	3	3809.91	-0.053	1	86.8	20.2	95.00%	K.KGDATDVSGAEQTDVAAVLPITQEAVEEAKPITEEAK.N		K.KGDATDVSGAEQTDVAAVLPITQEAVEEAKPITEEAK.N
89	100	2	1263.7	3.9	0	28.9	20.6	95.00%	R.VASTIGIPVDHR.R		R.VASTIGIPVDHR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
81	RS22_SCHPO	38.46%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
44	57	3	1745.76	-0.63	1	29.2	27.5	95.00%	K.HGYIDEFTEIDDHR.S		K.HGYIDEFTEIDDHR.S
98	108	2	1171.7	4.9	0	29.1	18	95.00%	R.QVGVIVLTTSR.G		R.QVGVIVLTTSR.G
4	19	2	1814.89	-1.5	0	81.5	25.2	95.00%	R.QSVLADCLNNIVNAER.R	Carbamidomethyl (+57)	R.QSVLADCLNNIVNAER.R
89	97	2	1111.62	5.6	1	31.9	18.8	95.00%	K.WVNQLLPSR.Q		K.WVNQLLPSR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
82	PMP20_SCHPO	44.23%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
40	55	2	1746.83	0.35	1	59.5	26.1	95.00%	F.TPPCSSQVPGYIANEK.Q	Carbamidomethyl (+57)	K.FIIVGVPGAFTPPCSSQVPGYIANEK.Q
82	93	2	1265.53	-1.5	1	37.6	25.9	95.00%	K.SFDGGEQSGVHF.V		K.SFDGGEQSGVHFVADWNGEFTK.A
11	29	3	2215.13	4.2	1	34.9	23.8	95.00%	K.VTLWENKPEEVVEFPSQGK.F		K.VTLWENKPEEVVEFPSQGK.F
135	156	2	2379.21	3.2	1	61.1	23.8	95.00%	K.VFIENEVTDVDISSADKVLSSL.-		K.VFIENEVTDVDISSADKVLSSL.-
135	151	2	1879.9	-1.6	1	68.2	26.5	95.00%	K.VFIENEVTDVDISSADK.V		K.VFIENEVTDVDISSADK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
83	THI4_SCHPO	23.94%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
356	372	2	1817.84	-1.8	0	71.4	26.8	95.00%	K.GNEGEIMNLAGEQGLMR.G		K.GNEGEIMNLAGEQGLMR.G
373	385	2	1353.71	4.1	0	37.5	23.1	95.00%	R.GVDSISQHTLAAR.I		R.GVDSISQHTLAAR.I
121	140	2	2014.95	-0.55	1	79.8	26.7	95.00%	K.AAADGADYVGIGSIYETNTK.D		K.AAADGADYVGIGSIYETNTK.D
249	265	4	1917.09	3.2	2	33.8	16	95.00%	K.LKDFTPLIHHLTNAVAK.N		K.LKDFTPLIHHLTNAVAK.N
27	42	3	1733.95	4.6	0	28	20	95.00%	R.QVEEGILGGVTLVQHR.E		R.QVEEGILGGVTLVQHR.E
310	338	3	3045.64	0.66	1	51.5	15.3	95.00%	K.TYIHAAQVNNDLARPVILDPVAVGATTAR.S		K.TYIHAAQVNNDLARPVILDPVAVGATTAR.S
237	248	2	1322.76	4.7	0	31.5	17.5	95.00%	K.DLLNQIPAALQK.L		K.DLLNQIPAALQK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
84	SERC_SCHPO	21.85%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
376	385	2	1147.65	4.7	1	32.8	20.8	95.00%	R.LIDLLESFAK.A		R.LIDLLESFAK.A
164	184	3	2459.11	0.3	1	42.8	27.3	95.00%	Y.YCDNETVHGVEFNEPPTNIPK.G	Carbamidomethyl (+57)	K.FTPDGETSLVYYCDNETVHGVEFNEPPTNIPK.G
216	228	2	1299.74	5	1	37	19.3	95.00%	K.NAGPAGITVVFVR.D		K.NAGPAGITVVFVR.D
324	329	2	766.38	5.3	1	26.2	23.1	91.60%	R.MNVTFR.I		R.MNVTFR.I
330	352	5	2716.42	3.7	1	22	20.5	95.00%	R.IEPQELESEFLAEAEKHHLVQLK.G		R.IEPQELESEFLAEAEKHHLVQLK.G
375	385	2	1303.75	-1.3	2	48.9	19.2	95.00%	R.RLIDLLESFAK.A		R.RLIDLLESFAK.A
189	199	2	1282.6	4.3	1	67	26.1	95.00%	R.VCDVSSNFISR.K	Carbamidomethyl (+57)	R.VCDVSSNFISR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
85	ASNS_SCHPO	10.05%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

51	69	2	1853.97	-0.6	0	70.4	22	95.00%	R.LAIVGVESGAQPLVSDDGK.L		R.LAIVGVESGAQPLVSDDGK.L
456	463	2	1039.58	0.56	1	31.7	18.8	95.00%	Y.LPQDILWR.Q		K.AFDTTHDSSLQPYLPQDILWR.Q
516	523	2	1035.55	6.3	1	30	21.9	95.00%	K.LFDEIFPR.Q		K.LFDEIFPR.Q
399	408	2	1120.54	4.9	1	26.3	23.4	91.80%	K.STMAWGLEAR.V		K.STMAWGLEAR.V
464	474	2	1256.57	1.3	2	40.6	26.3	95.00%	R.QKEQFSDGVGY.S		R.QKEQFSDGVGYSWIDALK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
86	RS6B_SCHPO	25.52%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	115	2	1739.01	3.8	0	65.7	16.6	95.00%	R.GCIVGQDLAVLALAIVK.Q	Carbamidomethyl (+57)	R.GCIVGQDLAVLALAIVK.Q
59	72	3	1625.86	4.7	1	32.2	22.4	95.00%	K.QGFPMFQGVLLPHR.V		K.QGFPMFQGVLLPHR.V
116	131	2	1695.87	-1.5	0	47.2	23.6	95.00%	K.QGEQDIPGLTDVTVPK.R		K.QGEQDIPGLTDVTVPK.R
204	217	2	1606.78	4.3	2	54.8	26.1	95.00%	K.NREEAAEFAQLMAK.R		K.NREEAAEFAQLMAK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
87	YHZ8_SCHPO	39.39%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
18	30	3	1414.8	-1.6	1	24	20.5	92.50%	K.KGEGDKILDLLSK.V		K.KGEGDKILDLLSK.V
144	164	3	2285.2	4.3	1	37.3	22.2	95.00%	K.ADTSLIIHSLDDPSLYAVVTR.Y		K.ADTSLIIHSLDDPSLYAVVTR.Y
104	121	3	1969.94	0.21	2	33.1	26.3	95.00%	K.VVDGHLDKDNLGPDAKDY.V		K.VVDGHLDKDNLGPDAKDYVLYTEYTGDSATLK.Q
122	135	2	1559.77	0.13	1	73.8	25.4	95.00%	Y.VLYTEYTGDSATLK.Q		K.DYVLYTEYTGDSATLK.Q
2	13	2	1361.7	3.8	1	57.2	24.5	95.00%	M.SFPASTHVYIAK.I	Acetyl (+42)	-.MSFPASTHVYIAK.I
144	159	2	1758.87	0.11	1	37.8	25	95.00%	K.ADTSLIIHSLDDPSLY.A		K.ADTSLIIHSLDDPSLYAVVTR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
88	RS3B_SCHPO	11.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
200	213	2	1513.87	4.8	1	38.9	18.5	95.00%	R.ATGSIFPLQNVLVR.K		R.ATGSIFPLQNVLVR.K
228	241	2	1524.79	4.4	0	71.2	23.4	95.00%	K.LLELHGESQDVGTK.V		K.LLELHGESQDVGTK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
89	HMCS_SCHPO	25.95%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
264	282	2	2060	-1.4	1	68.3	26	95.00%	R.LLYTDSAAEPSNPELEGVR.E		R.LLYTDSAAEPSNPELEGVR.E
393	407	3	1858.89	-0.14	1	45.4	26.5	95.00%	R.HCLTPTQYEEAIELR.H	Carbamidomethyl (+57)	R.HCLTPTQYEEAIELR.H
155	183	3	2859.53	3.9	1	40.5	18.8	95.00%	K.GNARPTGGAGCVALLVGPNAPIVFEPGLR.G	Carbamidomethyl (+57)	K.GNARPTGGAGCVALLVGPNAPIVFEPGLR.G
17	37	2	2214.05	-0.91	1	98	26.3	95.00%	Y.TPNQYVEQAALEAHDGVSTGK.Y		K.GLVLYTPNQYVEQAALEAHDGVSTGK.Y
264	291	3	3030.55	2.7	1	23.5	21.3	91.70%	R.LLYTDSAAEPSNPELEGVRELLSTLDAK.K		R.LLYTDSAAEPSNPELEGVRELLSTLDAK.K
382	392	3	1300.68	5.1	1	26	23.3	94.90%	K.KTNLVNDLDNR.H		K.KTNLVNDLDNR.H
217	228	2	1325.64	3.7	1	38.4	25.8	95.00%	K.ALDGAYANYNVR.D		K.ALDGAYANYNVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
90	RAD25_SCHPO	22.59%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
63	74	2	1417.75	4.9	1	43.2	23.2	95.00%	R.IISSIEQKEESR.G		R.IISSIEQKEESR.G
239	261	3	2375.1	0.71	1	32.3	27	95.00%	Y.NQSAKEEAPAAAAASENEHPEPK.E		R.DNLTLWTSDAEYNQSAKEEAPAAAAASENEHPEPK.E
88	107	3	2369.22	3.8	1	24.6	23.4	93.40%	R.KKIEDELSDICHDVLSVLEK.H	Carbamidomethyl (+57)	R.KKIEDELSDICHDVLSVLEK.H
233	261	3	3041.35	0.82	1	48.2	27	95.00%	W.TSDAEYNQSAKEEAPAAAAASENEHPEPK.E		R.DNLTLWTSDAEYNQSAKEEAPAAAAASENEHPEPK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
91	GLNA_SCHPO	20.61%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

153	170	2	1809.83	4.4	1	40.7	26.4	95.00%	K.GGFPGPQGPFYCGVGTGR.V	Carbamidomethyl (+57)	K.GGFPGPQGPFYCGVGTGR.V
237	260	4	2635.31	3.2	1	28.9	24.7	95.00%	K.ISFHPKPILGDWNGAGCHTNVSTK.D	Carbamidomethyl (+57)	K.ISFHPKPILGDWNGAGCHTNVSTK.D
139	148	2	1319.59	0.37	1	40.5	26.2	95.00%	Y.TMLDYYDRPF.G		K.ETWFGIEQEYTMLDYYDRPFGWPK.G
338	359	3	2476.24	4.1	1	26.8	23.6	95.00%	R.RPASSIDPYLVTGIITETMFEH.-		R.RPASSIDPYLVTGIITETMFEH.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
92	SYKC_SCHPO	12.86%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
15	28	2	1454.8	-0.69	0	48.9	21.7	95.00%	K.ALVLDPVTGEQVSK.T		K.ALVLDPVTGEQVSK.T
570	591	3	2490.33	2.8	1	30.8	20.8	95.00%	R.EVLLFPHMKPEVQAAEPTVVKE.-		R.EVLLFPHMKPEVQAAEPTVVKE.-
498	513	2	1999.9	4.4	1	72.7	27.2	95.00%	K.EICNAYTELNDIFDQR.A	Carbamidomethyl (+57)	K.EICNAYTELNDIFDQR.A
153	176	4	2810.33	3.8	2	33.2	25.1	95.00%	K.KLQVMCQAQDADTVDFAAQHEHLR.R	Carbamidomethyl (+57)	K.KLQVMCQAQDADTVDFAAQHEHLR.R
154	176	4	2682.24	3.7	1	34.1	26.4	95.00%	K.LQVMCQAQDADTVDFAAQHEHLR.R	Carbamidomethyl (+57)	K.LQVMCQAQDADTVDFAAQHEHLR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
93	MMF1_SCHPO	47.53%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
109	124	2	1781.86	-1.8	1	58.9	26.1	95.00%	K.VNIFLADMDDFAAVNK.V		K.VNIFLADMDDFAAVNK.V
59	75	2	1747.86	2.8	1	34.8	25.3	95.00%	K.ANGVIYCSGQIPVANGK.V	Carbamidomethyl (+57)/ Deamidation (+1)	K.ANGVIYCSGQIPVANGK.V
87	105	2	2116.09	4.6	0	131	22.9	95.00%	R.QCLLNLQEVLTEAGSSLNK.I	Carbamidomethyl (+57)	R.QCLLNLQEVLTEAGSSLNK.I
125	137	2	1483.81	3.9	1	42.4	20.4	95.00%	K.VYTEVLPDPKPAR.S		K.VYTEVLPDPKPAR.S
47	58	2	1247.66	5.3	1	27.4	23	93.40%	K.LSSAGPYNQAIK.A		K.LSSAGPYNQAIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
94	GCST_SCHPO	23.00%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
165	180	2	1623.93	4	0	75.8	18.3	95.00%	R.ALIAIQGPETASVVQK.L		R.ALIAIQGPETASVVQK.L
351	365	2	1557.86	0.96	0	26.9	20.9	92.80%	Y.ISTGLHQVGTPAHIK.V		K.NIAMGYISTGLHQVGTPAHIK.V
81	97	2	1779.9	3.9	1	64.1	25.2	95.00%	R.GENATAYLESITPSSLK.E		R.GENATAYLESITPSSLK.E
319	344	3	2566.25	4.5	0	41.9	25.4	95.00%	R.HGSAVEVDGVEVGQVTSGCPSPTLGK.N	Carbamidomethyl (+57)	R.HGSAVEVDGVEVGQVTSGCPSPTLGK.N
110	124	2	1575.8	-0.45	0	74.3	24.9	95.00%	F.TNETGGIIDDTIISK.Q		K.ELKPFHSTLSAFTNETGGIIDDTIISK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
95	YA03_SCHPO	35.16%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
181	194	2	1560.82	-2.1	1	45.7	23.9	95.00%	K.AADIDFLPPQLSFK.N		K.AADIDFLPPQLSFK.N
14	47	4	3763.76	-0.97	1	51.8	23.7	95.00%	R.HGQAQHNVGPDEDHNIRDPVLTSEGIEQCEALAK.E	Carbamidomethyl (+57)	R.HGQAQHNVGPDEDHNIRDPVLTSEGIEQCEALAK.E
154	170	2	1807	-0.83	1	25.3	18.8	90.00%	Y.LAALPQQQIAVITHSAF.I		K.EALEYLAALPQQQIAVITHSAFIR.F
66	77	3	1430.83	3.8	1	35.5	16.4	95.00%	R.RTLQTMEIALKK.Y		R.RTLQTMEIALKK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
96	RL1B_SCHPO	17.59%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
54	75	3	2486.26	2.6	0	38.3	23.4	95.00%	K.LPNVPRPNMAICILGDAHDLDR.A	Carbamidomethyl (+57)	K.LPNVPRPNMAICILGDAHDLDR.A
78	91	3	1470.71	-0.33	1	60.5	25.8	95.00%	K.HGGVDAMSVDDLKK.L		K.HGGVDAMSVDDLKK.L
76	91	4	1669.85	4.6	1	27.7	23.8	95.00%	R.AKHGGVDAMSVDDLKK.L		R.AKHGGVDAMSVDDLKK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

97	PYC_SCHPO	6.84%	100%	6									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
1109	1129	3	2088.05	4.4	0	38.2	24.2	95.00%	R.ADPGNPGHVAAPMSGTIVEIR.V		R.ADPGNPGHVAAPMSGTIVEIR.V		
839	848	2	1297.58	4.8	1	38.2	25.9	95.00%	R.EIDSYWAQMR.L		R.EIDSYWAQMR.L		
829	838	2	1275.63	4.5	1	27.7	24.9	93.80%	K.QLEFDNNQLR.E		K.QLEFDNNQLR.E		
917	929	2	1447.76	4.7	1	42.2	24.4	95.00%	K.VVGDLAQFMVQNK.L		K.VVGDLAQFMVQNK.L		
302	315	2	1628.75	2	1	37.3	27	95.00%	K.YCNAGTAEFLLDQK.G	Carbamidomethyl (+57)	K.YCNAGTAEFLLDQK.G		
867	879	3	1419.75	0.92	0	30.2	24	95.00%	Y.NHEIPGGQLTNLK.F		K.GTDSDVYNHEIPGGQLTNLK.F		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
98	YF19_SCHPO	14.51%	100%	6									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
181	194	2	1439.82	3.6	0	42.9	17.9	95.00%	K.IAPAVACGNTIILK.T	Carbamidomethyl (+57)	K.IAPAVACGNTIILK.T		
122	132	2	1208.53	4.1	1	34.4	25.2	95.00%	R.GDVQAAADCFR.Y	Carbamidomethyl (+57)	R.GDVQAAADCFR.Y		
195	208	2	1516.82	4.7	0	34.9	22.6	95.00%	K.TAELTPLSALCLTK.F	Carbamidomethyl (+57)	K.TAELTPLSALCLTK.F		
5	17	2	1406.78	4.6	0	33	20	95.00%	K.LVDHVEITVPTGK.T		K.LVDHVEITVPTGK.T		
71	80	2	1161.56	3.7	1	28.3	24.4	94.50%	R.AAFQTDAPWR.K		R.AAFQTDAPWR.K		
105	115	2	1159.61	0.33	0	31	24.4	95.00%	Y.LASIETLDNGK.S		R.LADCIEQNLEYLASIETLDNGK.S		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
99	O59743_SCHPO	20.66%	100%	4									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
210	225	2	1690.88	3.5	1	52.7	24	95.00%	R.SIQDVPFTSATVDIAK.K		R.SIQDVPFTSATVDIAK.K		
85	94	2	1139.6	0.76	1	29.2	22.6	95.00%	Y.NVITPELAHF.E		K.EALDLFLGAYNVITPELAHFEAR.C		
1	11	2	1319.72	4	1	28	22.8	94.20%	-.MDPYTVAIIKK.L	Acetyl (+42)	-.MDPYTVAIIKK.L		
11	24	2	1515.81	-2	1	68.9	23.2	95.00%	K.KLGIEEQVETAATK.S		K.KLGIEEQVETAATK.S		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
100	DYR_SCHPO	15.40%	100%	4									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
164	183	3	2062.15	3.7	0	25.4	16.2	94.30%	K.LTTPSLHIAGTSDTLVPLAR.S		K.LTTPSLHIAGTSDTLVPLAR.S		
191	212	3	2537.31	3.6	1	37.3	21.9	95.00%	R.CENAHVLLHPGQHIVPQQAVYK.T	Carbamidomethyl (+57)	R.CENAHVLLHPGQHIVPQQAVYK.T		
446	457	2	1300.66	1.1	1	51.9	23.8	95.00%	Y.GKNDDVNVALEK.L		K.EEVEIEFELYGKNDDVNVALEK.L		
265	281	2	1722.79	-0.24	0	80.7	27.1	95.00%	F.ANVTSSTESSGQLEEGK.S		K.QEMAYFANVTSSTESSGQLEEGK.S		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
101	IF5A1_SCHPO	36.94%	100%	4									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
2	29	3	3107.41	2.7	1	84.1	26.2	95.00%	M.AEEEHVDFEGGEAGASLTFPMQCSALRK.N	Acetyl (+42)/ Carbamidomethyl (+57)	-.MAEEEHVDFEGGEAGASLTFPMQCSALRK.N		
2	28	3	2979.31	4	1	77.3	26.7	95.00%	M.AEEEHVDFEGGEAGASLTFPMQCSALR.K	Acetyl (+42)/ Carbamidomethyl (+57)	-.MAEEEHVDFEGGEAGASLTFPMQCSALR.K		
70	87	3	2075.97	4.1	2	55.3	26.8	95.00%	R.KYEDMSPSTHNMDVPVVK.R		R.KYEDMSPSTHNMDVPVVK.R		
58	69	2	1352.76	4.3	1	43.7	18.5	95.00%	K.VHIVALDIFNGR.K		K.VHIVALDIFNGR.K		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
102	COFI_SCHPO	29.20%	100%	4									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
32	44	3	1533.82	5.2	1	36.4	23	95.00%	K.MNDTKTEIVVEKK.S		K.MNDTKTEIVVEKK.S		
81	94	2	1584.89	-0.96	1	54.5	19.1	95.00%	K.IIFISWSPDVAPIK.S		K.IIFISWSPDVAPIK.S		
32	43	2	1405.72	4.4	1	32.5	24.4	95.00%	K.MNDTKTEIVVEK.K		K.MNDTKTEIVVEK.K		

8	20	2	1548.76	4.6	1	71.2	25.7	95.00%	K.VSPECLEAFQELK.L	Carbamidomethyl (+57)	K.VSPECLEAFQELK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
103	NACB_SCHPO	47.68%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	88	2	1699.84	-1.5	1	37.7	25.3	95.00%	R.APTVHSSLPNETTAIY.G		R.APTVHSSLPNETTAIYGK.A
73	90	3	1884.97	4	1	45.6	23.7	95.00%	R.APTVHSSLPNETTAIYGK.A		R.APTVHSSLPNETTAIYGK.A
130	151	2	2376.02	-0.52	2	73.8	27.7	95.00%	K.GADAQADDGEIPDLVEKFDEQD.-		K.GADAQADDGEIPDLVEKFDEQD.-
63	72	2	1133.58	0.85	2	33.1	23.6	95.00%	F.KEDGGVINFR.A		K.LNMQNLAGIQEVNMFKEDGGVINFR.A
95	116	2	2320.3	0.38	0	67.4	14.6	95.00%	K.TLSEILPGILNNLGPESLTALR.Q		K.TLSEILPGILNNLGPESLTALR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
104	TAL1_SCHPO	16.15%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
27	44	3	1917.03	4	1	42	22.1	95.00%	K.YKPQDATTNPSLILAASK.K		K.YKPQDATTNPSLILAASK.K
9	26	2	1795.89	4.5	1	86.8	25.2	95.00%	K.ATGTVVVSDTGDFESIAK.Y		K.ATGTVVVSDTGDFESIAK.Y
45	60	2	1721.91	3.6	1	82.8	22.9	95.00%	K.KPQYAALVDAAVDYAK.A		K.KPQYAALVDAAVDYAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
105	RS14_SCHPO	41.73%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	129	2	1442.73	3.7	0	46.5	24.9	95.00%	R.IEDVTPIPTDSTR.R		R.IEDVTPIPTDSTR.R
117	130	3	1598.84	5.4	1	24.2	22.5	92.80%	R.IEDVTPIPTDSTRR.K		R.IEDVTPIPTDSTRR.K
52	72	3	2181.01	3.8	2	31.5	27.2	95.00%	K.TDRDESSPYAAMLAAQDAAAK.C		K.TDRDESSPYAAMLAAQDAAAK.C
61	72	2	1130.57	-0.73	0	60.6	23.8	95.00%	Y.AAMLAAQDAAAK.C		R.DESSPYAAMLAAQDAAAK.C
95	105	2	1037.57	5.3	0	47.1	21.8	95.00%	K.TPGPGAQAALR.A		K.TPGPGAQAALR.A
73	84	3	1367.77	4	1	24.2	18.4	92.90%	K.CKEVGITALHIK.I	Carbamidomethyl (+57)	K.CKEVGITALHIK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
106	AROG_SCHPO	22.31%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
92	104	2	1518.72	-1.4	0	51.1	25.9	95.00%	K.ADELQDALCVVMR.C	Carbamidomethyl (+57)	K.ADELQDALCVVMR.C
199	226	3	2704.36	2.1	0	47.7	23.5	95.00%	K.NGTDGTVGVAIDAIGATAHPHTMLGVTK.Q	Deamidation (+1)	K.NGTDGTVGVAIDAIGATAHPHTMLGVTK.Q
186	198	2	1364.74	4.4	1	39.9	22	95.00%	R.ELASALSFPVGFK.N		R.ELASALSFPVGFK.N
349	363	2	1657.8	0.17	0	32.8	26.3	95.00%	W.EQTAPMLDDLAEAVR.A		K.YGVSITDACVSWEQTAPMLDDLAEAVR.A
250	263	3	1525.76	-0.59	2	40.5	25.1	95.00%	K.KGPNYDAEHVAAVR.K		K.KGPNYDAEHVAAVR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
107	SLBR2_SCHPO	29.91%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
334	351	2	1799.89	-1.9	0	39.8	25.4	95.00%	R.IASESSDAVPQQTAVQVA.-		R.IASESSDAVPQQTAVQVA.-
134	143	2	1115.56	4.3	0	27.1	23.9	93.10%	R.NIESSVQPSR.E		R.NIESSVQPSR.E
166	192	3	3060.53	3.6	1	43.6	22.3	95.00%	R.LVTMEQELVREEAACLVAEAQLSNTTR.E	Carbamidomethyl (+57)	R.LVTMEQELVREEAACLVAEAQLSNTTR.E
222	248	3	2999.47	0.77	1	50	24.1	95.00%	R.HLLNLIDDTPVTPGEARPAYDGYETSR.Q		R.HLLNLIDDTPVTPGEARPAYDGYETSR.Q
271	284	2	1570.76	0.69	0	36.4	25.9	95.00%	F.VKPQIEDDAQSDAR.S		R.QIVMDAEHALSSWVPSQPAVNFVKPQIEDDAQSDAR.S
149	157	2	1075.63	4.5	1	33	19.2	95.00%	K.LLDQIYALK.H		K.LLDQIYALK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
108	ASSY_SCHPO	18.78%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

192	205	2	1483.72	0.18	0	51.7	25.4	95.00%	Y.EAGILEDPSMTPPK.D		K.KPWSMDENIVHCSYEAGILEDPSMTPPK.D
181	191	2	1353.53	1.1	1	39.3	26	95.00%	W.SMDENIVHCSY.E	Carbamidomethyl (+57)	K.KPWSMDENIVHCSYEAGILEDPSMTPPK.D
135	147	3	1491.86	0.33	1	23	17	91.00%	Y.ALKPDVQVIAPWR.L		R.FELAYYALKPDVQVIAPWR.L
333	350	2	1884.01	-1.1	0	96.8	21.1	95.00%	R.MLLAANNVSQEVVNGVVK.L		R.MLLAANNVSQEVVNGVVK.L
102	122	4	2398.2	5	1	39.2	24.1	95.00%	R.RQIQIAEKENCIAVSHGCTGK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.RQIQIAEKENCIAVSHGCTGK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
109	ACL1_SCHPO	11.87%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
369	381	2	1420.73	4.5	1	44	24.3	95.00%	R.GSELTYNNVPISK.V		R.GSELTYNNVPISK.V
171	182	3	1338.74	4.8	1	23.6	20	92.00%	K.LYRPGSVAYVSK.S		K.LYRPGSVAYVSK.S
313	326	2	1570.9	3.9	1	58.3	18.2	95.00%	K.LPALLQEVYEGLVK.K		K.LPALLQEVYEGLVK.K
137	154	2	1797.98	-1.1	1	35.1	21.4	95.00%	K.NVVIIGPATVGGIKPGCF.K	Carbamidomethyl (+57)	K.NVVIIGPATVGGIKPGCFK.I
156	170	2	1506.72	3.3	0	45.7	26.1	95.00%	K.IGNTGGMMDNIVASK.L		K.IGNTGGMMDNIVASK.L
313	327	3	1699	4	1	30.3	13.8	95.00%	K.LPALLQEVYEGLVKK.G		K.LPALLQEVYEGLVKK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
110	DAK1_SCHPO	11.38%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	18	3	2124.09	-0.36	2	35.6	22.8	95.00%	-.MDKHFINDPEVLVLDGLK.S	Acetyl (+42)	-.MDKHFINDPEVLVLDGLK.S
388	399	2	1358.73	4.4	0	25.9	23.3	91.20%	R.QAIVNSMENLIK.A		R.QAIVNSMENLIK.A
557	580	3	2355.27	0.21	2	32.1	19.4	95.00%	Y.VGDDVKVPDAGALGVVAIVEGFTK.-		R.AVYVGDDVKVPDAGALGVVAIVEGFTK.-
527	538	2	1301.63	4.7	0	60.8	25.2	95.00%	K.TNDLNAAVEEAR.K		K.TNDLNAAVEEAR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
111	SYLC_SCHPO	3.69%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
382	398	3	1730.98	4.6	0	32.6	17.9	95.00%	K.GQDLIGALVNAPLSVHK.Q		K.GQDLIGALVNAPLSVHK.Q
530	541	2	1389.69	-0.87	1	47.2	23.9	95.00%	F.VYNEPEGQVISR.S		K.ELIDQGLAFVYNEPEGQVISR.S
341	352	2	1380.66	1.4	1	36.2	26.1	95.00%	Y.GIYESNVPNELF.I		K.VCMIAATLRPETMYGQTNCYVGPNITYGIYESNVPNELFICTR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
112	YDG7_SCHPO	24.61%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
53	77	3	2611.25	-0.61	1	74.6	25.4	95.00%	R.HIDAAAIYGNEDEVGDGIKESGVPR.K		R.HIDAAAIYGNEDEVGDGIKESGVPR.K
308	321	2	1490.7	-2	1	34	26	95.00%	F.SNEPVFAGLEDGRT.-		R.FNQATFSNEPVFAGLEDGRT.-
282	299	3	2106.08	4.5	1	37.8	23.8	95.00%	K.YIPLTKEDMDEINSIGIR.A		K.YIPLTKEDMDEINSIGIR.A
183	204	3	2603.37	3.4	1	27.8	19.9	95.00%	K.VKPAVHQMELHPFLPQTEFVEK.H		K.VKPAVHQMELHPFLPQTEFVEK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
113	STI1_SCHPO	15.74%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
146	164	2	1935.97	6.4	1	78.1	25.2	95.00%	K.LASNPETASLLADSAFMAK.L		K.LASNPETASLLADSAFMAK.L
168	183	2	1781.88	4.3	0	66.6	25.8	95.00%	K.IQQNPGSIMAELNDPR.M		K.IQQNPGSIMAELNDPR.M
20	34	2	1711.84	-1.5	1	81.3	25.6	95.00%	K.TAIDYFTQAIGLDER.N		K.TAIDYFTQAIGLDER.N
371	377	2	800.44	3.8	0	29.8	23.1	95.00%	R.TPDILSR.L		R.TPDILSR.L
76	90	3	1463.79	4.4	1	44.6	21.9	95.00%	R.KGAALHGLGDLDAAR.S		R.KGAALHGLGDLDAAR.S
112	132	2	2007.97	4.2	1	89.9	26.5	95.00%	K.SVEAAQTQAASGAGGFNPFAK.L		K.SVEAAQTQAASGAGGFNPFAK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
114	SCE3_SCHPO	21.65%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
250	271	3	2195.05	-0.95	0	30.4	26.1	95.00%	R.SSSNVNTEATPSATTTTSSKPK.R		R.SSSNVNTEATPSATTTTSSKPK.R
46	66	2	2113.97	4.9	1	94.2	27.3	95.00%	R.ATPSSADAGYNAPSSTFESVR.S		R.ATPSSADAGYNAPSSTFESVR.S
272	289	3	1956.03	4.3	2	43	22.6	95.00%	K.RDPFGGAKPVDNTSVLQR.V		K.RDPFGGAKPVDNTSVLQR.V
359	381	2	2403.05	5.1	1	111	27.7	95.00%	K.TPATEDAPATNAGEAEEEEGWTK.I		K.TPATEDAPATNAGEAEEEEGWTK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
115	TBB_SCHPO	19.87%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
63	77	2	1556.81	-2.3	0	35	24.1	95.00%	R.AVLVDLEPGTMDAVK.S		R.AVLVDLEPGTMDAVK.S
104	121	3	1913.96	4.4	1	33.4	25.1	95.00%	K.GHYTEGAELADAVLDVVR.R		K.GHYTEGAELADAVLDVVR.R
123	154	3	3205.55	2.6	1	82.9	24.4	95.00%	R.EAEACDALQGFQLTHSLGGGTGSGMGTLLLSK.I	Carbamidomethyl (+57)	R.EAEACDALQGFQLTHSLGGGTGSGMGTLLLSK.I
163	174	2	1249.62	3.9	1	41.3	24.6	95.00%	R.MMATFSVAPAPK.S		R.MMATFSVAPAPK.S
295	306	2	1319.56	0.12	0	33.6	26.2	95.00%	F.DANNMMVAADPR.H	Oxidation (+16)	R.LHFFMVGFAPLAAIGSSSFQAVSVPELTQQMFDANNMMVAADPR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
116	ACL2_SCHPO	16.67%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
61	70	2	1190.63	1.7	2	25.9	23.1	91.20%	Y.REVVEDVFAK.V		K.TVSATPAVQLAQIQFPLPTLVIPAESTTYREVVEDVFAK.V
163	176	2	1433.61	-0.9	0	66.1	26.5	95.00%	F.CNEGGVDVGDVDAK.A	Carbamidomethyl (+57)	R.EGDWILFCNEGGVDVGDVDAK.A
382	389	2	947.52	4.5	0	26.9	23.4	92.80%	K.TVLDLMTR.G		K.TVLDLMTR.G
255	266	2	1367.61	3.7	1	48.5	26	95.00%	K.LDQTAEFECGAK.W	Carbamidomethyl (+57)	K.LDQTAEFECGAK.W
326	334	2	985.56	4.7	0	36	21.4	95.00%	K.LTILNAEGR.V		K.LTILNAEGR.V
32	61	3	3211.76	3.3	1	47.1	14.8	95.00%	K.TVSATPAVQLAQIQFPLPTLVIPAESTTYR.E		K.TVSATPAVQLAQIQFPLPTLVIPAESTTYR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
117	PABP_SCHPO	16.23%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
258	266	2	1068.57	4.8	1	26.6	21	92.30%	K.ANFTNVYIK.N		K.ANFTNVYIK.N
9	46	4	4050.84	4.1	1	18.5	23.7	91.70%	K.QADAAVESDVNTNNEAVESSTKEESSNTPSTETQPEKK.A		K.QADAAVESDVNTNNEAVESSTKEESSNTPSTETQPEKK.A
447	456	2	1142.61	4.9	0	33.9	22.4	95.00%	R.SQLEAQIQAR.N		R.SQLEAQIQAR.N
536	571	3	3524.72	4.6	0	28.7	22.5	95.00%	R.GPVPAQGRPMMMPGSVPSAGPAEAEAVPAVPGMPER.F		R.GPVPAQGRPMMMPGSVPSAGPAEAEAVPAVPGMPER.F
98	110	2	1401.76	1.7	1	28	22.6	94.20%	F.ELFNSIGPVASIR.V		K.AEEPEAAAEPSESTSTPTNASSVATPSGTAPTSASLYVGELDPSVTEAMLFELFNSIGPVASIR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
118	RL12_SCHPO	40.00%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
138	165	3	3106.45	-0.21	1	31.5	25.4	95.00%	F.SVGCTVDGKNPHDVQKEIDNGEIEIPQE.-	Carbamidomethyl (+57)	K.EILGTAFSVGCTVDGKNPHDVQKEIDNGEIEIPQE.-
68	83	2	1538.91	3.4	0	50.5	14.5	95.00%	R.QAAVSVVPSASALVIK.A		R.QAAVSVVPSASALVIK.A
138	153	3	1739.83	0.72	1	30.4	26.9	95.00%	F.SVGCTVDGKNPHDVQK.E	Carbamidomethyl (+57)	K.EILGTAFSVGCTVDGKNPHDVQK.E
17	31	2	1312.7	3.6	0	46	21.3	95.00%	R.AVGGEVAGGSTLAPK.I		R.AVGGEVAGGSTLAPK.I
131	146	2	1652.81	4	1	45.9	25.2	95.00%	K.EILGTAFSVGCTVDGK.N	Carbamidomethyl (+57)	K.EILGTAFSVGCTVDGK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

119	IMDH_SCHPO	18.32%	100%	7									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
169	187	3	2214.08	4.5	1	37	26	95.00%	R.DVQFHKDTNTPVTEVMTPR.E		R.DVQFHKDTNTPVTEVMTPR.E		
2	15	2	1636.88	4	1	27	21.7	92.80%	M.SAFKPYTEALEVLK.K	Acetyl (+42)	-.MSAFKPYTEALEVLK.K		
303	313	2	1155.67	4.5	0	51.3	19.6	95.00%	K.IDVIAGNVVTR.E		K.IDVIAGNVVTR.E		
214	234	3	2311.28	3.6	1	29.3	16.8	95.00%	K.LPVVDKDDNLVALLSLTDLMK.N		K.LPVVDKDDNLVALLSLTDLMK.N		
188	201	2	1559.8	-4.6	0	63.5	24.5	95.00%	R.EELITTAEGISLER.A		R.EELITTAEGISLER.A		
212	234	4	2496.4	3.3	1	24	15.4	95.00%	K.GKLPVVDKDDNLVALLSLTDLMK.N		K.GKLPVVDKDDNLVALLSLTDLMK.N		
419	433	2	1421.67	3.9	0	52.2	26.3	95.00%	R.GMGSIAAMEGTGVNK.N		R.GMGSIAAMEGTGVNK.N		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
120	RL10A_SCHPO	26.24%	100%	5									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
129	139	2	1228.7	4.7	0	40	20.8	95.00%	R.VNIGQILMSVR.T		R.VNIGQILMSVR.T		
58	69	2	1316.66	0.43	0	78	24.2	95.00%	Y.EQITSEALEAAR.I		R.AGVDEFPLCIHLVSNEYEQITSEALEAAR.I		
41	69	3	3260.58	4	1	68.1	23.6	95.00%	R.AGVDEFPLCIHLVSNEYEQITSEALEAAR.I	Carbamidomethyl (+57)	R.AGVDEFPLCIHLVSNEYEQITSEALEAAR.I		
117	128	3	1265.71	4.6	1	30	18.9	95.00%	R.HAFGKPNGLVAR.V		R.HAFGKPNGLVAR.V		
33	38	2	719.4	4.8	1	27.1	21.4	93.00%	R.IFDLGR.K		R.IFDLGR.K		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
121	PUR8_SCHPO	16.18%	100%	5									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
410	423	3	1571.79	4.9	1	22.5	24.5	90.10%	R.VVKEEGGDNDLIER.I		R.VVKEEGGDNDLIER.I		
226	242	2	1930.91	3.5	1	32.6	26.9	95.00%	K.LSGFDNVYPVTGQTYDR.K		K.LSGFDNVYPVTGQTYDR.K		
243	261	3	2023.12	4.2	2	51.4	18.6	95.00%	R.KIDIDVLQPLASFGATAHK.I		R.KIDIDVLQPLASFGATAHK.I		
450	460	2	1248.61	5.4	1	26.4	24.4	92.10%	R.APEQTESFVNK.D		R.APEQTESFVNK.D		
372	388	2	1909.94	4.9	1	55.7	25.3	95.00%	R.AELPFMATENIIMAMTK.H		R.AELPFMATENIIMAMTK.H		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
122	SYDC_SCHPO	13.10%	100%	4									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
281	294	2	1356.6	4.8	1	27.5	25.9	92.40%	K.MSGASSEGGSNVFK.I		K.MSGASSEGGSNVFK.I		
522	554	3	3334.69	3.2	1	85.5	20.1	95.00%	K.ALGVSPDVGLQQYIDAFAIGCPPHAGGGIGLER.V	Carbamidomethyl (+57)	K.ALGVSPDVGLQQYIDAFAIGCPPHAGGGIGLER.V		
200	210	2	1229.65	4.9	1	29.1	22.9	95.00%	K.NLPFLVEDAGR.S		K.NLPFLVEDAGR.S		
211	228	3	2006.87	-0.6	1	48.5	27.2	95.00%	R.SEEQIRESEENAAEGDSK.F		R.SEEQIRESEENAAEGDSK.F		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
123	AATR1_SCHPO	9.28%	100%	3									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
275	288	2	1577.78	4.4	1	46.4	25.6	95.00%	K.ELIPSFLSMDVDGR.V		K.ELIPSFLSMDVDGR.V		
38	54	2	1856.02	-1.6	1	50	20.6	95.00%	K.IISLAGGLPNPEYFPIR.E		K.IISLAGGLPNPEYFPIR.E		
7	19	3	1436.71	5.4	0	43.2	25.8	95.00%	K.DLSHHLSVESASR.K		K.DLSHHLSVESASR.K		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
124	EF1G_SCHPO	8.31%	100%	3									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
207	216	2	1182.71	4	1	27.1	15.7	93.10%	K.FIDQPLPIIK.A		K.FIDQPLPIIK.A		
128	139	2	1303.72	4.6	1	40.7	21.9	95.00%	K.EAETAIALIFAR.F		K.EAETAIALIFAR.F		
116	127	2	1294.63	4.3	1	26.2	25.4	91.10%	R.VFGAPYDEQAAK.E		R.VFGAPYDEQAAK.E		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
125	PURA_SCHPO	13.13%	100%	4									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
421	434	3	1498.78	0.27	1	26	22.7	94.90%	F.IGVGPGRDEMLVKE.-		K.FVGVPITFIGVGPGRDEMLVKE.-		
268	276	2	899.55	4.9	0	44.5	21.5	95.00%	R.IANSIGVVK.A		R.IANSIGVVK.A		

282	304	3	2420.22	4.2	1	27.4	23.9	95.00%	R.VGAGPFPTEQLNEIGDHLQSVGR.E		R.VGAGPFPTEQLNEIGDHLQSVGR.E
126	136	2	1129.57	4.6	0	38.6	22.9	95.00%	R.ADALNEAELGK.Q		R.ADALNEAELGK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
126	SYTC_SCHPO	8.25%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
248	258	2	1187.55	4.2	1	47.1	26	95.00%	K.NSSSYFLGDAK.N		K.NSSSYFLGDAK.N
94	106	2	1502.78	0.34	0	33.9	23.3	95.00%	W.DLTRPLEASCTLK.L	Carbamidomethyl (+57)	R.VTVAIVNGEPWDLTRPLEASCTLK.L
8	26	3	2136.14	4.2	1	27.4	21.3	95.00%	K.GVQASLDNLSLEIPFIQHR.L		K.GVQASLDNLSLEIPFIQHR.L
160	174	2	1703.8	4.7	1	71.1	26.8	95.00%	R.VITNDDYSSIESYAK.Q		R.VITNDDYSSIESYAK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
127	RS0B_SCHPO	28.92%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	31	3	3162.63	3.2	1	83.6	21.1	95.00%	M.AESIARPSVLNATDDDIKNLLAADSHIGSK.N	Acetyl (+42)	-.MAESIARPSVLNATDDDIKNLLAADSHIGSK.N
67	88	4	2453.26	4	1	67.3	22.5	95.00%	R.VIATIENPADVCVISSRPYGHR.A	Carbamidomethyl (+57)	R.VIATIENPADVCVISSRPYGHR.A
139	169	3	3390.76	4.3	1	25.4	18.4	94.30%	K.EASFVNIPVIALCDTDSILNHVDVAIPINNK.G	Carbamidomethyl (+57)	K.EASFVNIPVIALCDTDSILNHVDVAIPINNK.G
67	85	2	2103.07	0.15	1	97.6	24.7	95.00%	R.VIATIENPADVCVISSRPY.G	Carbamidomethyl (+57)	R.VIATIENPADVCVISSRPYGHR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
128	DHE4_SCHPO	21.29%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
279	291	3	1405.74	5	1	27.9	22.8	95.00%	K.RASIADSASLCKK.H	Carbamidomethyl (+57)	K.RASIADSASLCKK.H
417	439	2	2411.16	5.2	1	85.7	25.8	95.00%	K.YCDSGSNNIPSLVDGANIAGFLK.V	Carbamidomethyl (+57)	K.YCDSGSNNIPSLVDGANIAGFLK.V
356	367	2	1231.57	4.5	1	27.7	25	93.80%	R.ASGEGCWLAPGK.A	Carbamidomethyl (+57)	R.ASGEGCWLAPGK.A
399	416	2	1950.97	-1.8	1	103	25.5	95.00%	K.LAGIMQNIFEQSTDVASK.Y		K.LAGIMQNIFEQSTDVASK.Y
334	353	2	2102.94	-2.4	1	122	27.4	95.00%	R.YVAEGSNMGSSAEAVEVFEK.S		R.YVAEGSNMGSSAEAVEVFEK.S
25	34	3	1266.71	4.3	1	33.7	18.5	95.00%	K.LFEVHPELKR.V		K.LFEVHPELKR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
129	THRC_SCHPO	18.29%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
437	454	3	2061.03	4.7	2	31.2	24.5	95.00%	K.TKDQDITYICLSTAHPAK.F	Carbamidomethyl (+57)	K.TKDQDITYICLSTAHPAK.F
313	327	2	1443.73	4.4	0	39.8	24.6	95.00%	K.ADSTQVSPSGPISAK.E		K.ADSTQVSPSGPISAK.E
418	432	2	1576.86	0.049	0	40.8	22	95.00%	Y.IIDPHTAVGVETGLR.C		K.IYESDHYIIDPHTAVGVETGLR.C
182	215	3	3829.81	3.8	1	34.2	23.2	95.00%	R.VSPIQEAQMTTVTDPNVHCITVNGVFDDCQDLVK.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VSPIQEAQMTTVTDPNVHCITVNGVFDDCQDLVK.Q
399	410	2	1331.7	3.6	1	37.5	23.8	95.00%	R.VSNDETIDAIKK.I		R.VSNDETIDAIKK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
130	SYNC_SCHPO	6.16%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
223	235	2	1382.68	0.34	1	29.4	25.1	95.00%	Y.QILHAAPTGEEAF.T		K.SAPGNHELVVDYYQILHAAPTGEEAFTNR.L
447	465	3	2338.25	2.9	1	23.4	20.2	91.60%	K.MTDQINRPIFLTYFPLEIK.S		K.MTDQINRPIFLTYFPLEIK.S
223	238	3	1753.88	0.62	1	30.2	25	95.00%	Y.QILHAAPTGEEAFTNR.L		K.SAPGNHELVVDYYQILHAAPTGEEAFTNR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
131	ATPB_SCHPO	17.90%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
160	185	3	2859.38	0.39	1	46.5	25.3	95.00%	K.YSPIHADAPSFEEQSTTPEILETGIK.V		K.YSPIHADAPSFEEQSTTPEILETGIK.V
210	222	2	1501.85	-0.48	1	51.4	18.7	95.00%	K.TVFIQELINNIAK.A		K.TVFIQELINNIAK.A
141	156	3	1765.94	-1.2	1	29.2	22.2	95.00%	R.IMNVIGEPVDERGPIK.A		R.IMNVIGEPVDERGPIK.A
384	400	2	1802.93	-1.2	1	32.4	23.8	95.00%	R.SISELGIYPAVDPLDSK.S		R.SISELGIYPAVDPLDSK.S
119	140	2	2064.12	-1.2	0	66.3	18.3	95.00%	R.GTAVIDTGSPISIPVGPGTLGR.I		R.GTAVIDTGSPISIPVGPGTLGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
132	RS12A_SCHPO	46.90%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	111	2	1486.76	2.4	1	27.9	23.6	94.00%	K.VLGEWAGLCVLDR.D	Carbamidomethyl (+57)	K.VLGEWAGLCVLDR.D
79	93	2	1671.88	4.1	0	73.8	22.7	95.00%	K.LVEALCAESETPLIK.V	Carbamidomethyl (+57)	K.LVEALCAESETPLIK.V
61	76	2	1981.79	-1.3	1	36.3	27.1	95.00%	R.QAHLCVLCESCDQEAY.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.QAHLCVLCESCDQEAYVK.L
61	78	3	2208.97	4.2	1	36.3	27.3	95.00%	R.QAHLCVLCESCDQEAYVK.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.QAHLCVLCESCDQEAYVK.L
117	138	3	2356.1	-2.4	2	47.3	26.9	95.00%	R.KVVGCSCVAVTDYGEDSAALQK.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.KVVGCSCVAVTDYGEDSAALQK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
133	LYS4_SCHPO	11.93%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
405	418	2	1316.66	-0.092	0	36.2	24.2	95.00%	Y.VGAASSEVEAAAQK.N		K.VADGVEFYVGAASSEVEAAAQK.N
149	159	2	1179.57	4.4	1	26	25.1	91.30%	K.GQGIDFYPAGR.G		K.GQGIDFYPAGR.G
189	200	2	1184.64	1.4	0	35	21.6	95.00%	Y.GGVGCLGTPIVR.T	Carbamidomethyl (+57)	R.GIGHQIMVEQGYAMPGSMAVASDSHSNTYGGVGCLGTPIVR.T
281	292	2	1233.62	-0.75	1	31.2	24.1	95.00%	W.GALSGLFPTDEK.L		R.LTIANMTTEWGALSGLFPTDEK.L
172	188	2	1724.72	2.1	1	30.1	26.9	94.40%	Y.AMPGSMAVASDSHSNTY.G		R.GIGHQIMVEQGYAMPGSMAVASDSHSNTYGGVGCLGTPIVR.T
470	489	2	1872.04	4.8	1	47.2	18.7	95.00%	R.EALAYLASPAVVAASAIAGK.I		R.EALAYLASPAVVAASAIAGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
134	RL6_SCHPO	22.05%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
70	87	2	1959.1	3.1	1	33.6	16.6	95.00%	R.VVVLSQLEDTLVVTGPYK.V		R.VVVLSQLEDTLVVTGPYK.V
50	64	2	1497.83	-1.3	0	48.6	19.8	95.00%	R.ASLAPGTVCILLAGR.F	Carbamidomethyl (+57)	R.ASLAPGTVCILLAGR.F
109	118	2	1031.56	5.5	0	31.2	23.6	95.00%	K.IDVSGVSVEK.F		K.IDVSGVSVEK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
135	RS17A_SCHPO	23.66%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	59	3	1133.6	4.6	1	24.5	23.1	93.20%	K.IAGYTTHLMK.R		K.IAGYTTHLMK.R
24	33	2	1234.67	4.6	1	36.3	22.3	95.00%	R.LTLDFQTNKR.I		R.LTLDFQTNKR.I
34	44	2	1156.68	4.8	0	51	20	95.00%	R.IVDEVAIIASK.R		R.IVDEVAIIASK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
136	LEU1_SCHPO	13.18%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
82	99	2	1998.98	4.3	1	62	25.3	95.00%	K.EIEVGFPSASQTDFAFVR.H		K.EIEVGFPSASQTDFAFVR.H
464	479	2	1742.82	4.9	1	69.1	26.4	95.00%	R.FSVNDYTLSSNGPQSK.C		R.FSVNDYTLSSNGPQSK.C
137	151	3	1761.87	4	1	33.2	25.6	95.00%	K.NATVHLYNACSPLFR.E	Carbamidomethyl (+57)	K.NATVHLYNACSPLFR.E
268	295	3	2788.37	3.6	2	73.8	24.5	95.00%	R.GTAVAAAELGQLAGGDRIEGCLFGNGER.T	Carbamidomethyl (+57)	R.GTAVAAAELGQLAGGDRIEGCLFGNGER.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
137	VATA_SCHPO	15.35%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
89	114	4	2751.53	2.9	1	22.2	15.6	95.00%	R.TGKPLSVELGPGLAETIYDGIQRPLK.Q		R.TGKPLSVELGPGLAETIYDGIQRPLK.Q
373	389	2	1752.85	8	1	36.9	25.5	95.00%	R.LAEMPADSGYPAYLGAK.L		R.LAEMPADSGYPAYLGAK.L
317	331	2	1544.81	4.6	0	49.4	24.3	95.00%	R.TTLVANTSNMPVAAR.E		R.TTLVANTSNMPVAAR.E
182	198	2	1838.88	4.6	1	73	26.6	95.00%	R.GTVTYIAEAGSYHVDEK.L		R.GTVTYIAEAGSYHVDEK.L
221	240	3	2105.14	4.1	0	35.3	20.6	95.00%	R.AARPVADNLTANQPLLTGQR.V		R.AARPVADNLTANQPLLTGQR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
138	SYG_SCHPO	7.98%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
93	104	3	1423.66	0.44	2	27.6	26.1	95.00%	W.MCKDPATGEIFR.A	Carbamidomethyl (+57)	K.FADWMCKDPATGEIFR.A
187	198	2	1297.63	5.4	0	37	25.7	95.00%	R.NPATNGELETPR.Q		R.NPATNGELETPR.Q
492	506	2	1649.84	-0.98	1	46.3	24.7	95.00%	R.TYTPNVIEPSFGLGR.I		R.TYTPNVIEPSFGLGR.I
526	538	2	1298.76	-0.87	1	31.6	18.3	95.00%	R.GVLSFPASIAPIK.A		R.GVLSFPASIAPIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
139	KAPS_SCHPO	25.25%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
166	188	3	2567.24	-0.26	0	36.1	25.6	95.00%	Y.EAPISPEIVVSSHTQSIEECVEK.I	Carbamidomethyl (+57)	K.EFTGISAPYEAPISPEIVVSSHTQSIEECVEK.I
152	158	2	792.4	-0.55	2	28.1	22.9	94.30%	R.AGEIKEF.T		R.AGEIKEFTGISAPYEAPISPEIVVSSHTQSIEECVEK.I
157	188	3	3532.7	3.1	1	32.4	22.1	95.00%	K.EFTGISAPYEAPISPEIVVSSHTQSIEECVEK.I	Carbamidomethyl (+57)	K.EFTGISAPYEAPISPEIVVSSHTQSIEECVEK.I
39	52	2	1664.86	3.8	1	65.6	24	95.00%	K.STIACALEQYLLQR.G	Carbamidomethyl (+57)	K.STIACALEQYLLQR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
140	PMM_SCHPO	22.57%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
29	43	2	1728.91	-1.7	0	64.2	22.9	95.00%	R.LSVSPEMLETLQNLR.K		R.LSVSPEMLETLQNLR.K
236	253	4	1938.02	4.7	1	21.7	22.3	95.00%	R.TIGHSVTNPDDTIAELKK.I		R.TIGHSVTNPDDTIAELKK.I
77	87	2	1211.59	0.63	1	35.3	25.2	95.00%	Y.AFAENGLTAYR.Y		K.QQEQLSVNGENVIDSFDYAFAENGLTAYR.Y
45	58	2	1347.75	4.4	1	41.6	21.3	95.00%	K.VVAIGFVGGSDLSK.Q		K.VVAIGFVGGSDLSK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
141	RANG_SCHPO	32.56%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
88	98	2	1353.6	4	1	43.5	26.3	95.00%	K.TNEEEETVEFK.M		K.TNEEEETVEFK.M
188	198	2	1253.61	5.8	1	35.7	25.3	95.00%	R.FANSENANLFK.E		R.FANSENANLFK.E
49	80	3	3379.58	3.1	2	28.6	24.6	95.00%	K.SGASTNDEKKPAEGDEDAEPASPEVHFEPIVK.L		K.SGASTNDEKKPAEGDEDAEPASPEVHFEPIVK.L
169	184	2	1622.73	-0.39	1	35	26.6	95.00%	W.TVAADVSEGEPTAETF.A		R.SWVWTVAADVSEGEPTAETFAIR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
142	GCSP_SCHPO	6.78%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
953	965	2	1458.76	1.1	0	43.1	23.9	95.00%	K.DNNLLVNAPHPQK.D		K.DNNLLVNAPHPQK.D
657	684	3	2835.49	3.7	1	27.8	19.3	95.00%	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C	Carbamidomethyl (+57)	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C
577	597	2	2385.18	-1.2	1	42.8	24.4	95.00%	K.LNAVTEMMPITNPLFANIHPY.V		K.LNAVTEMMPITNPLFANIHPYVPEEQAK.G
577	604	3	3166.6	3.7	1	40.5	22.4	95.00%	K.LNAVTEMMPITNPLFANIHPYVPEEQAK.G		K.LNAVTEMMPITNPLFANIHPYVPEEQAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
143	RL15A_SCHPO	12.94%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
78	93	3	1761.94	4.8	1	23.7	22.7	92.20%	K.GQTYGKPVHQGVNHLK.Y		K.GQTYGKPVHQGVNHLK.Y
148	157	3	1218.69	4.4	1	24.4	19.5	93.10%	R.INWIVNPVHK.H		R.INWIVNPVHK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
144	RL31_SCHPO	21.24%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
91	105	2	1650.87	4.2	1	39.3	22.9	95.00%	K.ALYTYVQAVDVANPK.M		K.ALYTYVQAVDVANPK.M
7	15	2	986.56	5	0	39.5	22.3	95.00%	K.SAINQVVTR.D		K.SAINQVVTR.D
94	105	2	1303.68	-0.93	1	64.4	24.1	95.00%	Y.TYVQAVDVANPK.M		K.ALYTYVQAVDVANPK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
145	VATB_SCHPO	14.12%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
415	427	2	1417.68	4.9	0	78	25.7	95.00%	K.SVVGEEALSQEDR.L		K.SVVGEEALSQEDR.L
439	449	2	1284.62	4.2	1	36.9	25.3	95.00%	K.TFISQGAYENR.T		K.TFISQGAYENR.T
485	503	2	2015.89	5.3	1	57.2	27.3	95.00%	R.SSAYTESSKDVIDNTPESS.-		R.SSAYTESSKDVIDNTPESS.-
350	359	2	1176.61	0.32	1	38.9	23.8	95.00%	Y.ITEGQIFVDR.Q		R.NGSITQIPILTMPNDDITHPIPDLTGYITEGQIFVDR.Q
42	59	3	2083.09	4.5	1	23.6	22.1	92.00%	R.RPQYNEIVNLNLPDGSVR.S		R.RPQYNEIVNLNLPDGSVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
146	RS2_SCHPO	22.13%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
186	200	2	1799.86	4.8	1	102	26.4	95.00%	R.FLQLAGIEDCYTQSR.G	Carbamidomethyl (+57)	R.FLQLAGIEDCYTQSR.G
51	63	2	1566.86	4.2	1	34.6	19.5	95.00%	K.SIEEIYLYSLPIK.E		K.SIEEIYLYSLPIK.E
174	185	3	1138.69	4.8	1	25.2	13	94.00%	R.GAGLVAAPVTKR.F		R.GAGLVAAPVTKR.F
141	156	3	1696.86	-1	1	39.5	24.6	95.00%	R.GYWGTALGDPHTVPVK.V		R.GYWGTALGDPHTVPVK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
147	SYRC_SCHPO	10.03%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
163	180	2	1987.02	4.1	1	33.9	22.7	95.00%	R.STIIGSFLANLHESQGWK.V		R.STIIGSFLANLHESQGWK.V
225	238	2	1588.76	3.6	1	45.2	25.9	95.00%	K.VNADATEEDEKIQK.D		K.VNADATEEDEKIQK.D
11	24	2	1544.86	4.5	1	46.7	20.3	95.00%	K.SLSTLGLQDLPVFR.E		K.SLSTLGLQDLPVFR.E
452	467	2	1759.87	3.7	1	55	24.8	95.00%	K.YAQVENPEEVADIVGK.T		K.YAQVENPEEVADIVGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
148	TRXB_SCHPO	22.67%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
256	270	2	1689.88	-2.4	1	59.7	23.7	95.00%	K.LVAEQIELDEAGYIK.T		K.LVAEQIELDEAGYIK.T
154	175	3	2202.13	7.2	1	22.8	22.8	90.60%	R.NKPLAVVGGGDSAAEEAQFLTK.Y	Deamidation (+1)	R.NKPLAVVGGGDSAAEEAQFLTK.Y
246	255	3	1069.59	0.85	1	27.5	19.7	95.00%	F.YAIGHIPATK.L		K.NTNTNEVSDLQVNGLFYAIGHIPATK.L
99	124	3	2801.32	3.2	1	61.8	25.7	95.00%	K.YWLEGAEEEEPHTADSVILATGASAR.R		K.YWLEGAEEEEPHTADSVILATGASAR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
149	PDI1_SCHPO	8.33%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
398	412	2	1637.79	4.8	1	66.2	26.4	95.00%	K.LAEEYSDDSNVVVAK.I		K.LAEEYSDDSNVVVAK.I
125	136	3	1350.87	5.1	1	30.4	6.99	95.00%	R.KQLLPTVKPISK.D		R.KQLLPTVKPISK.D
188	201	2	1436.77	4.3	1	45.1	21.9	95.00%	K.SLGSNFPGIVAFTK.D		K.SLGSNFPGIVAFTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
150	TCTP_SCHPO	28.57%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
6	21	2	1737.84	4.2	1	86.5	26.3	95.00%	K.DVISGDELVSDAYDLK.E		K.DVISGDELVSDAYDLK.E
5	18	2	1509.72	-0.14	2	37.1	26.5	95.00%	Y.KDVISGDELVSDAY.D		-.MLLYKDVISGDELVSDAYDLK.E
99	112	2	1670.86	-1.6	2	45.2	23.5	95.00%	R.LQESNPERVPVFEK.N		R.LQESNPERVPVFEK.N
22	38	2	2012.91	-0.93	1	61.6	27	95.00%	K.EVDDIVYEADCQMVTVK.Q	Carbamidomethyl (+57)	K.EVDDIVYEADCQMVTVK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
151	P25_SCHPO	17.82%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
36	52	2	1976.06	4.7	1	48.2	21.4	95.00%	K.AVIYQFPETLSPEILEK.M		K.AVIYQFPETLSPEILEK.M
40	52	2	1529.8	-1.9	1	40.7	24	95.00%	Y.QFPETLSPEILEK.M		K.AVIYQFPETLSPEILEK.M
2	20	2	2064.09	-0.8	1	83.2	22	95.00%	M.STANTVAIVIYSTYGHVVK.L	Acetyl (+42)	-.MSTANTVAIVIYSTYGHVVK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
152	ADK_SCHPO	16.18%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
126	138	2	1424.68	5.2	1	51	26.2	95.00%	R.SLCTNLGAANNYK.L	Carbamidomethyl (+57)	R.SLCTNLGAANNYK.L
253	267	2	1483.87	4.5	0	69.4	17.2	95.00%	R.VVVITQGADATIVAK.D		R.VVVITQGADATIVAK.D
86	96	2	1295.61	3.7	1	43.7	26.2	95.00%	K.FADMLLESNEK.A		K.FADMLLESNEK.A
230	245	2	1688.89	3.8	0	56.9	23.5	95.00%	K.STDVQEIALALSSVEK.V		K.STDVQEIALALSSVEK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
153	YBS7_SCHPO	20.98%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
442	471	4	3134.5	-0.033	1	26.4	24.5	95.00%	K.EQPPNKAEPAVPTEASSTKPSEAAEESTPR.F		K.EQPPNKAEPAVPTEASSTKPSEAAEESTPR.F
353	386	4	3399.65	2.3	1	59.5	23.6	95.00%	K.HTGPSLSSASQPSAASSSSSSEPSNLDKINDVKK.N		K.HTGPSLSSASQPSAASSSSSSEPSNLDKINDVKK.N
128	146	2	1760.86	5.1	0	31.6	25	95.00%	R.TSGSSTGLSNAPPSANVSK.A		R.TSGSSTGLSNAPPSANVSK.A
387	406	3	2245.17	-0.98	1	26.5	22	95.00%	K.NIEVSANEPQPRPVKEDVPK.S		K.NIEVSANEPQPRPVKEDVPK.S
164	189	3	2841.41	3.2	0	29.4	23.9	95.00%	R.ATPEVCVPLNPDTGSVPLIHPEQTDR.G	Carbamidomethyl (+57)	R.ATPEVCVPLNPDTGSVPLIHPEQTDR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
154	THI22_SCHPO	8.71%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
423	435	2	1516.6	5.3	1	56.7	25.8	95.00%	K.SCEESPACTAYSR.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.SCEESPACTAYSR.Y
181	197	2	1890.88	4.9	0	111	26.6	95.00%	K.NQGLDISNINSVSDMER.C		K.NQGLDISNINSVSDMER.C
134	151	2	1829.98	-1.3	0	78.1	21.8	95.00%	K.LVVDPVMVATSGDSLVTK.D		K.LVVDPVMVATSGDSLVTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
155	YDMC_SCHPO	11.66%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
370	385	2	1876.99	-1.9	1	48.5	22.6	95.00%	K.LTSLMESIFPEQTIIR.S		K.LTSLMESIFPEQTIIR.S
109	122	2	1458.75	0.055	1	47.1	24.2	95.00%	Y.SANPVNVEGQIGFK.I		K.SHDELTLHHCHYSANPVNVEGQIGFK.I
488	513	3	3117.34	3.1	1	64.3	27	95.00%	K.VEPEPIDEEEAFSDDEEEEPEEIKER.I		K.VEPEPIDEEEAFSDDEEEEPEEIKER.I
82	91	2	1136.53	5	1	33.4	25.4	95.00%	R.NADNSVTNFR.D		R.NADNSVTNFR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
156	YCO6_SCHPO	10.69%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
37	56	2	2127	-0.81	0	112	27	95.00%	K.APQVNTIDEGDENLEAIDGK.L		K.APQVNTIDEGDENLEAIDGK.L
15	36	3	2140	-1.3	1	28.4	26.9	95.00%	K.MSAAPTPHNTPSGTSAPNFGAK.A		K.MSAAPTPHNTPSGTSAPNFGAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
157	ARGD_SCHPO	14.97%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
311	332	3	2276.09	4.8	1	39.5	26	95.00%	K.IAAEIHPGEHGSTFGGNPVACR.V	Carbamidomethyl (+57)	K.IAAEIHPGEHGSTFGGNPVACR.V
283	310	3	2746.56	2.7	0	43.2	12.8	95.00%	K.DVASPDIITVAKPLANGLPIGATIVSSK.I		K.DVASPDIITVAKPLANGLPIGATIVSSK.I
139	154	2	1784.85	4.1	1	92.8	26.6	95.00%	K.IFFANCGTEANETALK.F	Carbamidomethyl (+57)	K.IFFANCGTEANETALK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
158	RL36A_SCHPO	24.24%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
83	96	2	1545.84	4.6	1	75.1	21.3	95.00%	K.GKIEELTSVIQSSR.L		K.GKIEELTSVIQSSR.L
85	96	2	1360.73	3.8	0	56.4	23.5	95.00%	K.IEELTSVIQSSR.L		K.IEELTSVIQSSR.L
2	11	2	966.59	4.6	0	38.2	15.1	95.00%	M.APGLVVGLNK.G		-.MAPGLVVGLNK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
159	YLF4_SCHPO	13.56%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
115	133	2	2193.13	2.1	1	76.8	23.4	95.00%	K.AFSPIETQSIVEQLDEFLK.S		K.AFSPIETQSIVEQLDEFLK.S
292	315	4	2593.24	3.1	2	34.2	25.8	95.00%	K.AVKHPNADSLYVSTIHCGDAEGPR.T	Carbamidomethyl (+57)	K.AVKHPNADSLYVSTIHCGDAEGPR.T
381	398	2	2063.97	-0.79	1	65.8	26.5	95.00%	R.LTFEGFDTEEPEAQLNPK.R		R.LTFEGFDTEEPEAQLNPK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
160	RL18B_SCHPO	18.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	65	3	1111.64	5.1	0	26.6	16.7	95.00%	K.TNRPPISISK.I		K.TNRPPISISK.I
132	142	2	1127.63	4.1	0	42.3	21	95.00%	R.APTGSNTVLLR.G		R.APTGSNTVLLR.G
118	131	2	1454.81	-1.2	0	54.2	20.6	95.00%	K.AGGEVLTLDQLALR.A		K.AGGEVLTLDQLALR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
161	RL23_SCHPO	28.06%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
15	34	2	2090	3.5	0	65.5	25.9	95.00%	R.MTLGLPVQAIMNCADNSGAK.N	Carbamidomethyl (+57)	R.MTLGLPVQAIMNCADNSGAK.N
48	66	3	2043.11	4.2	1	47.8	20.5	95.00%	R.LNRLPAASCGDMVLATVKK.G	Carbamidomethyl (+57)	R.LNRLPAASCGDMVLATVKK.G
51	65	2	1531.77	-2.2	0	57.1	25	95.00%	R.LPAASCGDMVLATVK.K	Carbamidomethyl (+57)	R.LPAASCGDMVLATVK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
162	RL30A_SCHPO	17.43%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
77	89	2	1276.61	-0.77	0	62.7	25	95.00%	Y.AGTNIDLGTACGK.L	Carbamidomethyl (+57)	K.ANVHHYAGTNIDLGTACGK.L
71	89	2	1997.95	6	1	62.5	26.5	95.00%	K.ANVHHYAGTNIDLGTACGK.L	Carbamidomethyl (+57)	K.ANVHHYAGTNIDLGTACGK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
163	RS11_SCHPO	17.76%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	64	2	1161.6	4.7	1	33.4	23.9	95.00%	K.CPFVGQVSIR.G	Carbamidomethyl (+57)	K.CPFVGQVSIR.G
114	130	2	1870.97	4.9	0	41.5	23.5	95.00%	R.INEGDVVTVGQCRPLSK.T	Carbamidomethyl (+57)	R.INEGDVVTVGQCRPLSK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
164	RL27A_SCHPO	32.35%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
23	34	2	1269.74	4.4	0	65.4	18	95.00%	K.VVILQAIDQGSK.S		K.VVILQAIDQGSK.S
35	48	3	1461.76	5.9	1	42.8	23.5	95.00%	K.SHPFGHAVVAGVER.Y		K.SHPFGHAVVAGVER.Y
35	52	4	1963.05	4.3	2	23.2	21.1	95.00%	K.SHPFGHAVVAGVERYPLK.V		K.SHPFGHAVVAGVERYPLK.V
94	107	2	1575.83	3.5	1	46.7	23.7	95.00%	K.GLITADTFKEPTQR.S		K.GLITADTFKEPTQR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
165	FUMH_SCHPO	15.15%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
131	142	2	1157.67	3.6	0	43.3	20.5	95.00%	R.AIEILGGTLGSK.K		R.AIEILGGTLGSK.K
86	101	2	1697.86	-1.7	0	73.1	24.5	95.00%	K.LADAIEQAAQEVIDGR.L		K.LADAIEQAAQEVIDGR.L
392	417	3	2921.34	2.7	1	27.9	26.5	95.00%	R.LLGDACESFTDHCVVGIEPNYEGIAR.H	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.LLGDACESFTDHCVVGIEPNYEGIAR.H
112	130	2	2006.91	0.95	0	53.6	27.3	95.00%	F.QTGSGTQSNMNSNEVIANR.A		R.LDDNFPLVVFQTGSGTQSNMNSNEVIANR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
166	SPEE_SCHPO	15.77%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
105	126	3	2641.27	3.1	1	46.8	25.6	95.00%	R.EVVKHECVEEAILCDIDEDVIK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.EVVKHECVEEAILCDIDEDVIK.V
2	12	2	1291.72	4.1	0	43.5	20	95.00%	M.SVQELSHPLIK.D	Acetyl (+42)	-.MSVQELSHPLIK.D
18	31	2	1631.79	4.6	1	31.2	25.2	95.00%	R.EINNMWPGQAMTLK.V		R.EINNMWPGQAMTLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
167	ARO1_SCHPO	4.26%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
677	703	3	2950.4	0.26	1	53.7	24.9	95.00%	R.FACDVLRPMGCTVEQTATSTTVQGPPK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.FACDVLRPMGCTVEQTATSTTVQGPPK.G
1232	1247	2	1833.96	4.6	1	44.8	23.3	95.00%	R.ITNSMDIPLILFNMGR.F		R.ITNSMDIPLILFNMGR.F
1326	1338	2	1509.68	0.38	1	66.2	26.4	95.00%	Y.EAFETDTVDEVQK.V		R.SPILHSTAYELLGLPHTYEAFETDTVDEVQK.V
162	172	2	1299.72	4.7	1	45.2	22.1	95.00%	K.NLVGAFWQPLR.V		K.NLVGAFWQPLR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
168	Q1L854_SCHPO	21.25%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
143	178	3	3637.66	4	1	78.1	25.6	95.00%	R.GWGDLVNSAANPDVAENEGNTPSGAQTPAAEEENVK.T		R.GWGDLVNSAANPDVAENEGNTPSGAQTPAAEEENVK.T
10	28	2	2077.07	4.4	1	50.2	23.6	95.00%	K.NLFDLLGEETPAATTTEKK.T		K.NLFDLLGEETPAATTTEKK.T
10	27	2	1948.97	3.6	1	75.2	25.5	95.00%	K.NLFDLLGEETPAATTTEK.K		K.NLFDLLGEETPAATTTEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
169	SYEC_SCHPO	7.68%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
278	288	2	1354.61	1.9	1	33.6	26.5	95.00%	Y.TSDYLDTIHQY.C		K.ENSEFQDAILEDVALLGIKPDVVTYTSDYLDTIHQYCVDMIK.S
66	77	2	1393.77	4.3	1	31.9	20.3	95.00%	K.LALQTFSQVYPK.L		K.LALQTFSQVYPK.L
190	206	2	1731.84	3.9	1	51.4	25.5	95.00%	K.SSGPNYEIGLPDAIDGK.V		K.SSGPNYEIGLPDAIDGK.V
295	309	2	1657.7	4.5	1	93.6	26.8	95.00%	K.SGQAYADDTDVETMR.H		K.SGQAYADDTDVETMR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
170	RS10B_SCHPO	34.01%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
10	24	3	1621.94	4.8	1	31.6	16.6	95.00%	K.AIHQALFQQGVLVAK.K		K.AIHQALFQQGVLVAK.K
26	31	2	732.38	5.5	1	30.1	22.6	95.00%	K.DFNLPK.H		K.DFNLPK.H
32	44	2	1428.81	-0.85	0	30.4	21.3	95.00%	K.HPEVGVPNLQVIK.A		K.HPEVGVPNLQVIK.A
78	93	4	1859.01	4	1	23	19.4	95.00%	R.EYLHLPAEVVPATHKR.Q		R.EYLHLPAEVVPATHKR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
171	TPM_SCHPO	41.61%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
69	86	3	2087.06	4.7	1	48.9	24	95.00%	R.LKADNEDIQKTEAEQLSR.K		R.LKADNEDIQKTEAEQLSR.K
49	65	3	1948.91	-0.82	1	32.5	26.3	95.00%	R.KSEAAESQLEELEEETK.Q		R.KSEAAESQLEELEEETK.Q
87	103	3	2070.12	0.91	1	34.2	20.2	95.00%	R.KVELLEEELETNDKLLR.E		R.KVELLEEELETNDKLLR.E
147	161	2	1707.87	-1.1	1	42.6	24.4	95.00%	K.VKAELDEVHQALEDL.-		K.VKAELDEVHQALEDL.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
172	RS8A_SCHPO	28.50%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
60	74	2	1568.72	4.4	1	94.1	26	95.00%	R.LDSGNFSWGSEGVSK.K		R.LDSGNFSWGSEGVSK.K
165	178	2	1475.79	4.1	1	33.2	22.9	95.00%	R.LYAVVSSRPGQSGR.C		R.LYAVVSSRPGQSGR.C
152	164	2	1363.68	4.8	1	51.3	24.8	95.00%	K.VDSALETQFAAGR.L		K.VDSALETQFAAGR.L
78	92	2	1751.94	4.6	1	25.6	21.1	90.70%	R.IIQVAYHPSNNELVR.T		R.IIQVAYHPSNNELVR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
173	RL2_SCHPO	21.74%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
92	118	3	2780.43	-0.25	0	53.8	22.2	95.00%	K.NAALTVGNVLPVGEMPEGTIISNVEEK.A		K.NAALTVGNVLPVGEMPEGTIISNVEEK.A
133	144	2	1251.68	-1.7	0	44.2	21.1	95.00%	Y.VIIVGHDVDTGK.T		R.SSGNYVIIVGHDVDTGK.T
128	144	3	1759.88	4.2	1	23	24.5	91.00%	R.SSGNYVIIVGHDVDTGK.T		R.SSGNYVIIVGHDVDTGK.T
163	173	2	940.55	4.3	0	54.6	14.8	95.00%	R.GVVGIVAGGGR.I		R.GVVGIVAGGGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
174	RL7C_SCHPO	8.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
169	183	2	1497.85	4.8	0	75.4	18.6	95.00%	R.IALSDNAIIEAALGK.Y		R.IALSDNAIIEAALGK.Y
110	115	2	772.46	-0.28	0	29.3	22.3	95.00%	K.IMQLLR.L		K.IMQLLR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
175	KAD1_SCHPO	23.64%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
196	218	3	2621.39	2.8	1	47.7	19.3	95.00%	K.WAAVDAAQKPEQVWEQIVAILEK.A		K.WAAVDAAQKPEQVWEQIVAILEK.A
54	82	3	3231.58	0.29	1	73.8	22.6	95.00%	K.KIMDQGGLVSDDIVTGMIKDEILNNPECK.N	Carbamidomethyl (+57)	K.KIMDQGGLVSDDIVTGMIKDEILNNPECK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
176	RS4B_SCHPO	11.07%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
222	233	2	1232.68	5.6	1	42.4	22.1	95.00%	R.LSNVFVIGEAGK.S		R.LSNVFVIGEAGK.S
246	252	2	846.45	4.8	0	45.4	23.7	95.00%	K.LSITEER.D		K.LSITEER.D
40	49	2	1258.72	4.7	1	26.1	20.6	91.60%	R.ECLPLIVFLR.N	Carbamidomethyl (+57)	R.ECLPLIVFLR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
177	RS28_SCHPO	41.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
47	65	3	2195.16	0.45	1	25	21.5	93.90%	K.GPVREDDILVLLESEREAR.R		K.GPVREDDILVLLESEREAR.R
47	62	3	1838.98	4.7	1	27.2	21.1	95.00%	K.GPVREDDILVLLESER.E		K.GPVREDDILVLLESER.E
1	9	2	1031.54	3.7	1	25.7	23.6	90.80%	-.MDSSKVPVK.L	Acetyl (+42)	-.MDSSKVPVK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
178	CAP_SCHPO	4.54%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
499	509	2	1122.58	5.1	0	31.4	24	95.00%	K.SSLSSEVVTSK.S		K.SSLSSEVVTSK.S
339	352	2	1443.77	0.74	1	26.5	23.6	92.10%	F.AEINKGEGITSGLR.K		K.GDMGAVFAEINKGEGITSGLR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
179	YFHH_SCHPO	5.21%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
504	529	4	3037.42	4.5	1	22.9	25.6	95.00%	K.EEERPLPSEPSQNQPAEYRDTPDTPR.N		K.EEERPLPSEPSQNQPAEYRDTPDTPR.N
307	340	4	3584.77	4.2	2	20.1	21.8	94.90%	R.VAKDDDPFVVSNTANSDEPASSSKPAKPLTDLNR.A		R.VAKDDDPFVVSNTANSDEPASSSKPAKPLTDLNR.A

711	734	3	2663.2	-1.4	1	42.2	26.9	95.00%	R.ISEVTEDSIDEDKQNEVDPSTSAR.A		R.ISEVTEDSIDEDKQNEVDPSTSAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
180	RL21A_SCHPO	14.37%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
138	160	3	2554.24	2	1	27.5	25	95.00%	K.AHFVSTENNEPVTLHPVAYDTTI.-		K.AHFVSTENNEPVTLHPVAYDTTI.-
138	156	3	2124.03	-0.092	1	27	26.2	94.80%	K.AHFVSTENNEPVTLHPVAY.D		K.AHFVSTENNEPVTLHPVAYDTTI.-
141	160	2	2199.07	0.81	1	46	26	95.00%	F.VSTENNEPVTLHPVAYDTTI.-		K.AHFVSTENNEPVTLHPVAYDTTI.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
181	ACBP_SCHPO	43.68%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
33	50	3	1911.99	-1.5	0	26.4	23.3	95.00%	K.QATVGDNNTEKPGLLDLK.G		K.QATVGDNNTEKPGLLDLK.G
74	81	2	949.51	-1.2	1	33	21.8	95.00%	Y.ISFVDELK.T		K.EDAASEYISFVDELK.T
2	13	2	1294.61	4.4	1	38.3	25.5	95.00%	M.SSTFEQAAADVK.E	Acetyl (+42)	-.MSSTFEQAAADVK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
182	RS15A_SCHPO	20.92%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
90	108	2	2033.08	3.1	1	80.9	21.7	95.00%	R.NMIILPEMVGSVVGIYNGK.L		R.NMIILPEMVGSVVGIYNGK.L
73	85	2	1396.76	4.6	0	40.4	20.4	95.00%	K.TEAPLNEKPATVK.T		K.TEAPLNEKPATVK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
183	RS13_SCHPO	23.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
10	20	2	1132.63	4.4	1	38.6	21.9	95.00%	K.GIASSALPYVR.S		K.GIASSALPYVR.S
44	55	2	1244.66	3.8	0	40.8	23	95.00%	K.GMSPSQIGVTLR.D		K.GMSPSQIGVTLR.D
28	39	2	1286.68	5	0	56.1	23	95.00%	K.ADADSVVEQILK.F		K.ADADSVVEQILK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
184	SODM_SCHPO	20.18%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
34	48	2	1649.84	0.9	1	36.4	24.8	95.00%	Y.AYNALEPALSETIMK.L		K.ATLPPLPYAYNALEPALSETIMK.L
162	173	2	1303.7	4.2	0	48.8	23.1	95.00%	R.ITTTANQDTIVK.S		R.ITTTANQDTIVK.S
26	48	2	2502.32	2.9	1	32.8	21.7	95.00%	K.ATLPPLPYAYNALEPALSETIMK.L		K.ATLPPLPYAYNALEPALSETIMK.L
127	135	2	1108.52	5	1	34	24.8	95.00%	K.WGSLEDFQK.E		K.WGSLEDFQK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
185	RL3A_SCHPO	11.08%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
207	222	2	1837.89	-1.6	1	85.4	26.3	95.00%	K.STFEQNEMIDVIGVTR.G		K.STFEQNEMIDVIGVTR.G
11	19	2	982.54	4.3	1	27.2	19	93.20%	R.HGSLGFLPR.K		R.HGSLGFLPR.K
249	266	3	2035.03	4.4	1	29.3	24.6	95.00%	K.VACIGAWHPANVQWTVAR.A	Carbamidomethyl (+57)	K.VACIGAWHPANVQWTVAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
186	APE1_SCHPO	3.51%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
850	867	2	1936.97	-1.1	1	72.5	25.1	95.00%	R.ALQQSLDTISANSSFIDK.S		R.ALQQSLDTISANSSFIDK.S
137	149	2	1467.71	4.6	1	42.2	25.7	95.00%	K.YLATTQMEPTSAR.R		K.YLATTQMEPTSAR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
187	SYYC_SCHPO	10.22%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

368	395	3	2695.3	3.6	2	45.5	24.9	95.00%	K.KAGTTNASIAAESGAAPATESQTAESFK.K		K.KAGTTNASIAAESGAAPATESQTAESFK.K
2	14	2	1605.83	4.1	2	47.4	23.6	95.00%	M.SLTPDEKYELITR.N	Acetyl (+42)	-.MSLTPDEKYELITR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
188	RL19A_SCHPO	20.73%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
118	128	3	1386.74	5	1	32.3	22.9	95.00%	K.HLYHTLYLEAK.G		K.HLYHTLYLEAK.G
182	193	2	1422.69	3.6	1	31.8	25.9	95.00%	R.EQLYTAAEKIEE.-		R.EQLYTAAEKIEE.-
22	38	2	1960.89	-0.42	1	79.3	26.9	95.00%	K.VWMDPNEISEISNANSR.Q		K.VWMDPNEISEISNANSR.Q
182	193	2	1422.69	3.6	1	31.8	25.9	95.00%	R.EQIYTAAEKIEE.-		R.EQLYTAAEKIEE.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
189	RS21_SCHPO	48.28%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
51	60	2	1113.59	4.5	1	33.8	21.7	95.00%	K.TTYAISGFVR.S		K.TTYAISGFVR.S
1	16	2	1902.96	5.9	1	43.5	24.6	95.00%	-.MENEAGQLVDLYVPRK.C	Acetyl (+42)	-.MENEAGQLVDLYVPRK.C
72	87	2	1864.94	4.3	1	65.3	25.3	95.00%	R.LTTQDGLLEGVWSYQR.-		R.LTTQDGLLEGVWSYQR.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
190	RL14_SCHPO	11.94%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
103	110	2	993.46	6	1	29.1	24.7	95.00%	R.SQLNDFDR.F		R.SQLNDFDR.F
87	94	2	905.44	5.7	1	30.4	23.9	95.00%	K.WASSAWAK.K		K.WASSAWAK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
191	UBA1_SCHPO	5.83%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
566	588	3	2468.19	4.9	1	37.5	26.5	95.00%	K.GNTQVVVPHLTESYGSSQDPPEK.S		K.GNTQVVVPHLTESYGSSQDPPEK.S
767	788	4	2497.23	-0.71	1	28.7	25	95.00%	K.IQVNENEEAPETAANKDKQELK.S		K.IQVNENEEAPETAANKDKQELK.S
529	542	2	1513.81	-1.2	0	62.8	22	95.00%	K.LSLVTNALDNVEAR.M		K.LSLVTNALDNVEAR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
192	RL33B_SCHPO	24.07%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
33	45	2	1574.65	-2	2	29.7	26	94.90%	K.IEGCDSKEEAQFY.L	Carbamidomethyl (+57)	K.IEGCDSKEEAQFYLGK.R
20	32	4	1401.82	4.5	1	28.1	16.4	95.00%	R.SKHVIHPGTSIVK.I		R.SKHVIHPGTSIVK.I
33	44	2	1411.59	-1.1	2	38.1	26.2	95.00%	K.IEGCDSKEEAQF.Y	Carbamidomethyl (+57)	K.IEGCDSKEEAQFYLGK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
193	RL11_SCHPO	14.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
154	164	2	1349.67	4.1	1	39.8	24.3	95.00%	K.INAEDTINWFK.Q		K.INAEDTINWFK.Q
36	49	2	1531.83	4.2	1	63.5	21.9	95.00%	K.VLEQLSGQTPVFSK.A		K.VLEQLSGQTPVFSK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
194	PNPP_SCHPO	12.08%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
145	166	3	2359.15	3.2	1	61.7	25.7	95.00%	K.IGPDPSVGAVLCGMDMHVTYLK.Y	Carbamidomethyl (+57)	K.IGPDPSVGAVLCGMDMHVTYLK.Y
182	195	2	1535.74	-2.3	1	48.4	25.5	95.00%	F.LLTNQDSTFPTNGK.F	Deamidation (+1)	K.YCMAFQYLQDPNCAFLLTNQDSTFPTNGK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
195	CH10_SCHPO	22.12%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	84	2	1230.7	4	1	31.7	20.5	95.00%	R.VLLPAYGGSNIK.V		R.VLLPAYGGSNIK.V

62	72	2	1111.6	4.5	0	30.9	19.8	95.00%	K.LAQPSVAVGDR.V		K.LAQPSVAVGDR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
196	CLH_SCHPO	1.50%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
64	76	3	1431.83	4.6	0	23.4	16.7	91.60%	R.RPISADSVILHPK.K		R.RPISADSVILHPK.K
1517	1528	2	1531.71	9.6	2	28.7	26.6	93.10%	W.TQSIELSKQDRF.Y	Phospho (+80)/ Deamidation (+1)	R.WTQSIELSKQDRFYK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
197	PPA2_SCHPO	5.18%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
136	143	2	961.53	5.4	1	31.9	23.3	95.00%	R.IELFDLGR.Q		R.IELFDLGR.Q
73	88	2	1640.68	-1	1	45.2	26.7	95.00%	R.NPTGDDTATDVSSAQY.I		R.NPTGDDTATDVSSAQYIDIFQNK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
198	SPI1_SCHPO	15.28%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
110	122	2	1514.77	4.6	0	58.5	24.5	95.00%	R.VCENIPIVLCGNK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VCENIPIVLCGNK.V
197	216	2	2217.91	2.2	0	29.3	27.7	92.40%	Y.QQEMNEAAAMPLPDEDDADL.-	Oxidation (+16)	K.LVGNPNLEFVASPALAPPEVQVDQQLLAQYQQEMNEAAAMPLPEDDADL.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
199	PGM_SCHPO	9.03%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	21	3	2330.21	3.2	1	23.9	22.6	92.40%	-.MIETIPTKPYEGQRPGTSGLR.K		-.MIETIPTKPYEGQRPGTSGLR.K
423	435	2	1529.66	4.3	1	62.5	26.5	95.00%	R.YDYEELENEAAGK.V		R.YDYEELENEAAGK.V
127	142	2	1631.79	4.4	1	81.8	25.2	95.00%	K.YNLGNGGPAPESVTEK.I		K.YNLGNGGPAPESVTEK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
200	PUR4_SCHPO	3.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
298	334	4	3616.77	4.4	1	38.1	21.7	95.00%	K.VETHNHPTAVSPFPGAATGSGGEIRDEGAVGQGSLSK.A		K.VETHNHPTAVSPFPGAATGSGGEIRDEGAVGQGSLSK.A
412	425	3	1426.76	5.3	1	35.9	22.9	95.00%	R.GYHKPIMAAGGIGR.I		R.GYHKPIMAAGGIGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
201	TBA1_SCHPO	7.47%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
69	83	2	1758.91	-0.86	1	76.8	23.8	95.00%	R.SIYVDLEPNVIDQVR.T		R.SIYVDLEPNVIDQVR.T
285	303	2	2298.99	1	1	53.9	27.6	95.00%	K.AFHESNSVQEITNQCFEPY.N	Carbamidomethyl (+57)	K.AFHESNSVQEITNQCFEPYNQMVK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
202	RL28A_SCHPO	20.27%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
94	110	2	1787.95	3.9	1	37.3	22.7	95.00%	K.NTEVAPVINVLQSGYGK.V		K.NTEVAPVINVLQSGYGK.V
115	127	3	1464.84	-0.14	1	24.8	17.3	93.60%	K.GRLPETPVIVQTR.Y		K.GRLPETPVIVQTR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
203	DPNP_SCHPO	10.48%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
224	243	3	2206.97	4.4	1	57.3	27.7	95.00%	K.FCEGVEAGHSMQGTQEEIAK.Y	Carbamidomethyl (+57)	K.FCEGVEAGHSMQGTQEEIAK.Y
334	350	3	1840.98	4.8	2	23.8	21.8	92.30%	K.VIEATAAVTSKDPHFQK.V		K.VIEATAAVTSKDPHFQK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
204	6PGL_SCHPO	8.95%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
46	55	2	1083.61	5.4	0	52.4	19.8	95.00%	K.VLAEGLAQQR.G		K.VLAEGLAQQR.G
209	221	2	1488.81	-1.8	1	51	22.9	95.00%	K.DILPIVIEDFTSK.L		K.DILPIVIEDFTSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
205	FKBP_SCHPO	13.39%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
44	58	2	1602.86	4.3	1	59	22.9	95.00%	R.GSPFVCTIGVGQLIR.G	Carbamidomethyl (+57)	R.GSPFVCTIGVGQLIR.G
48	58	2	1214.68	-0.72	0	56.5	21.6	95.00%	F.VCTIGVGQLIR.G	Carbamidomethyl (+57)	R.GSPFVCTIGVGQLIR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
206	YET4_SCHPO	13.60%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
190	216	3	2686.32	5.5	0	58	23.9	95.00%	R.NDEQLGNSPASITSKPATTSAAQPSSK.V		R.NDEQLGNSPASITSKPATTSAAQPSSK.V
419	462	4	4557.19	2.7	1	18.1	20	90.80%	K.NEVNVPSTIPTESENPVAVGGTTAEHPVQEAVTAPTETAHDFSK.E		K.NEVNVPSTIPTESENPVAVGGTTAEHPVQEAVTAPTETAHDFSK.E
487	503	3	1712.87	4.4	0	27.8	24.6	95.00%	R.KPSSTGQEPTTPSTPAK.S		R.KPSSTGQEPTTPSTPAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
207	SUB2_SCHPO	10.14%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	96	3	3526.72	3.8	1	60.2	22.5	95.00%	R.AITDSGFEHPSEVQQVCIPQSILGTDVLCQAK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.AITDSGFEHPSEVQQVCIPQSILGTDVLCQAK.S
399	410	2	1336.6	-0.98	0	66.6	26	95.00%	F.SSSEEDSQILDK.I		K.GLAITFSSSEEDSQILDK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
208	RPE_SCHPO	17.54%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
6	20	2	1557.84	-1.3	1	48.4	22.6	95.00%	K.IAPSLLAGDFANLEK.E		K.IAPSLLAGDFANLEK.E
202	214	2	1421.73	1	0	33.8	25.2	95.00%	F.HAQSPEEVISGLR.N		K.TVDAAADAGANVIVAGTAVFHAQSPEEVISGLR.N
123	134	2	1369.78	-1.5	1	51.7	19.4	95.00%	K.TPVEVILPFVEK.L		K.TPVEVILPFVEK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
209	SEC31_SCHPO	2.70%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
985	1000	2	1627.82	2.1	1	54.5	24.6	95.00%	Y.TPIAVASSTVNPAHTY.K		R.ISSSPNMPPSNPYTPIAVASSTVNPAHTYKPHGGSQIVPPPK.Q
404	420	2	1859.86	-1.1	0	65.5	27.2	95.00%	K.EVTITSAPDEVEQDEAK.S		K.EVTITSAPDEVEQDEAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
210	YEI3_SCHPO	8.67%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
329	342	2	1482.75	2.8	1	41.2	24.8	95.00%	K.APQAAGVIHTDFEK.A		K.APQAAGVIHTDFEK.A
43	62	2	2148.03	-2	1	66.2	25.8	95.00%	K.SVLGNPANYPYATIDPEEAK.V		K.SVLGNPANYPYATIDPEEAK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
211	GUAA_SCHPO	13.17%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	130	2	1549.73	-1.6	1	62.2	26.3	95.00%	R.EYGPATVSMEPEIK.T		R.EYGPATVSMEPEIK.T
232	254	3	2183.09	-1.7	0	26.1	25.2	94.80%	K.MIGPSDHVIGAVSGGVDSTVASK.V		K.MIGPSDHVIGAVSGGVDSTVASK.V
170	203	4	3715.11	3.7	1	22.3	19.8	95.00%	K.NSPFAVIAHVTKPIIGLQFHPEVTHTPLGLQLIK.N		K.NSPFAVIAHVTKPIIGLQFHPEVTHTPLGLQLIK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
212	CARA_SCHPO	6.99%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
347	358	2	1286.65	0.68	1	27.4	24.2	93.40%	Y.AVDASTLPAEWK.A		R.GHNIPALDIASGNCHITSQNHGYAVDASTLPAEWK.A
74	90	2	1842.89	0.97	1	70.6	26.6	95.00%	F.TTSPVGYVESLTDPSYK.Q		R.NVSGEAVFTTSPVGYVESLTDPSYK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
213	SRP2_SCHPO	11.78%	99%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
100	119	3	2388.2	0.3	1	22.5	24.3	90.10%	R.LIVENLSEDVSWQDLKDVMR.K		R.LIVENLSEDVSWQDLKDVMR.K
161	183	3	2460.23	4.1	1	47.5	23.3	95.00%	K.GQAVTLREDPDAANEPLPEVPSR.F		K.GQAVTLREDPDAANEPLPEVPSR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
214	CAN_SCHPO	18.44%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
84	101	3	2033.14	2.7	1	42.8	18.1	95.00%	R.VPETTILNLLPGEVFVHR.N		R.VPETTILNLLPGEVFVHR.N
9	34	4	2766.34	3.9	1	21.8	25.1	95.00%	R.IEEIDHQDEIIDREASTASPVSGAGK.I		R.IEEIDHQDEIIDREASTASPVSGAGK.I
8	34	4	2922.43	-0.34	1	23.1	23.9	95.00%	R.RIEEIDHQDEIIDREASTASPVSGAGK.I		R.RIEEIDHQDEIIDREASTASPVSGAGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
215	RL25A_SCHPO	19.86%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	137	2	1329.66	4	0	94.2	25.3	95.00%	K.LSADADALDVANR.I		K.LSADADALDVANR.I
74	88	4	1806.97	3	2	20.6	22	95.00%	K.KIEDDNTLVFHVHLK.A		K.KIEDDNTLVFHVHLK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
216	Q9P7B4_SCHPO	20.08%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
234	256	3	2522.27	2.7	1	34.8	23.7	95.00%	R.ENVVIADTLVFPSHQGGANHVYR.K		R.ENVVIADTLVFPSHQGGANHVYR.K
233	256	4	2678.38	4.3	2	40.7	21.6	95.00%	R.RENVVIADTLVFPSHQGGANHVYR.K		R.RENVVIADTLVFPSHQGGANHVYR.K
183	199	2	1918.98	6.8	1	60.8	23.8	95.00%	R.IMEVDPGLVETEFSVVR.F		R.IMEVDPGLVETEFSVVR.F
163	173	2	1163.64	5.6	1	26.5	21.7	92.20%	K.SALAQFTSALR.K		K.SALAQFTSALR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
217	MPG1_SCHPO	11.02%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
270	287	2	1776	4.2	0	35.2	18.4	95.00%	K.IGPNVVIGPNVTIGDGVR.L		K.IGPNVVIGPNVTIGDGVR.L
138	159	4	2530.28	3.4	2	22.1	23.2	95.00%	K.VEEPSKYGVVVHYPNSESLIER.F		K.VEEPSKYGVVVHYPNSESLIER.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
218	LYS1_SCHPO	13.86%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
274	306	3	3758.76	0.87	1	83.8	23.9	95.00%	R.VVCDVSCDTTNPNNPIPIYNVNTTFDHPTVEVK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VVCDVSCDTTNPNNPIPIYNVNTTFDHPTVEVK.G
329	346	2	1904.02	3.7	1	28.9	21.2	95.00%	R.ESSEAFSEALIPSLLALK.D		R.ESSEAFSEALIPSLLALK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
219	GPD2_SCHPO	15.01%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
170	186	2	1731.85	0.13	0	61.6	25.2	95.00%	Y.CGVLSGANIASEVAQEK.F	Carbamidomethyl (+57)	R.LFSDIIEENTGMYCGVLSGANIASEVAQEK.F
67	88	4	2626.25	3.3	2	19.3	25.5	92.50%	K.IQHEGKECNLTEVFNTTHENVK.Y	Carbamidomethyl (+57)	K.IQHEGKECNLTEVFNTTHENVK.Y

311	327	3	1907.98	3	0	33.8	23.9	95.00%	K.TGKPMHVVEQELLDGQK.L		K.TGKPMHVVEQELLDGQK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
220	FIMB_SCHPO	4.89%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
508	524	2	1796.81	3.5	1	38.6	27.1	95.00%	K.TLSDSDMVAWANSMAAK.G		K.TLSDSDMVAWANSMAAK.G
158	170	2	1485.74	3.7	0	44.6	25.3	95.00%	K.LINDSVPDTIDER.V		K.LINDSVPDTIDER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
221	DLDH_SCHPO	6.07%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
203	219	3	1743.02	4.9	1	25.6	13.4	94.50%	K.KIVSSTGALSLSEVPKK.M		K.KIVSSTGALSLSEVPKK.M
155	168	2	1448.76	3.8	1	31.8	23.7	95.00%	K.GTGSFIDPQTLSVK.G		K.GTGSFIDPQTLSVK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
222	PPID_SCHPO	10.96%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
214	226	2	1432.74	4.4	1	72	24.1	95.00%	K.QFAQQNLDTAVAK.W		K.QFAQQNLDTAVAK.W
144	169	3	2959.43	3.1	1	32.1	25.2	95.00%	R.TIENLETKNDDPVVPVVIEECGTCTK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.TIENLETKNDDPVVPVVIEECGTCTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
223	CATA_SCHPO	5.47%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
431	439	2	1061.57	5.6	1	35.4	23.1	95.00%	R.AFWQNVLGK.K		R.AFWQNVLGK.K
230	248	3	1936.88	-2.2	0	31.1	27.2	95.00%	K.GLTNEEAAALDGSNPDHAR.Q		K.GLTNEEAAALDGSNPDHAR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
224	RS3_SCHPO	10.04%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
30	42	2	1513.64	4.2	1	70.9	26.5	95.00%	R.ELSEEGYSGCEVR.V	Carbamidomethyl (+57)	R.ELSEEGYSGCEVR.V
97	108	2	1362.64	3.8	0	61	25.1	95.00%	R.GLCAVAQCESLR.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GLCAVAQCESLR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
225	RS24A_SCHPO	20.15%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
21	32	3	1363.76	-1.9	1	46.3	20	95.00%	R.KQMVVDILHPGK.A		R.KQMVVDILHPGK.A
69	83	2	1672.81	4.3	1	28.6	26.2	93.40%	R.TTGFALIYDDVEAMK.K		R.TTGFALIYDDVEAMK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
226	PUR7_SCHPO	18.39%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
159	174	3	1746.79	5.6	0	25.2	26.9	91.50%	K.AAEGHDENIHPDEVSK.I		K.AAEGHDENIHPDEVSK.I
222	235	2	1541.83	-1.8	0	26.6	22.2	92.40%	K.IVLVDEVLTPDSSR.F		K.IVLVDEVLTPDSSR.F
258	282	3	2764.43	3.8	1	38.4	21	95.00%	R.NWLTANNLANKPNVSLPEDVVEATR.R		R.NWLTANNLANKPNVSLPEDVVEATR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
227	ACON2_SCHPO	3.09%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
528	541	2	1500.77	1.3	1	26.4	23.7	92.00%	K.FRPPQGVELPSAGF.I		K.FRPPQGVELPSAGFIAGDSSYIPEPNPQPVPETEVTIDPK.S
313	326	2	1476.63	-1.4	1	49	26.7	95.00%	R.AEVADAASEVHSEY.N		R.AEVADAASEVHSEYNYLAADTGAK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
228	Q9URK9_SCHPO	23.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

55	66	3	1455.8	4.9	1	38.8	21.2	95.00%	R.ELLTLDEKDPKR.L		R.ELLTLDEKDPKRLFEGNAIIR.R
152	168	3	1785.9	4.3	1	38.7	24.4	95.00%	K.HIDFALSSPYGGGRPGR.C		K.HIDFALSSPYGGGRPGRCKRK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
229	RLA1_SCHPO	29.36%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
11	26	2	1673.87	0.11	0	91.5	23.4	95.00%	Y.SALILADEGIEITSDK.L		-.MSASELATSYSALILADEGIEITSDK.L
33	48	2	1743.93	4.8	1	29.5	22.4	95.00%	K.AANVDVEPIWATIFAK.A		K.AANVDVEPIWATIFAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
230	SYFA_SCHPO	4.81%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	14	2	1558.9	4.5	2	64.1	15.4	95.00%	M.SKLEALQVFLLEK.L	Acetyl (+42)	-.MSKLEALQVFLLEK.L
128	138	2	1219.56	4.9	0	33.3	25.8	95.00%	K.NTDSITDETPK.V		K.NTDSITDETPK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
231	RL24A_SCHPO	20.81%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	12	2	1357.64	4.1	2	34.6	26	95.00%	-.MKVEVCSFSGSK.V	Carbamidomethyl (+57)	-.MKVEVCSFSGSK.V
81	91	2	1097.65	4.7	0	29.4	18.3	95.00%	R.GIVGANLDVIK.E		R.GIVGANLDVIK.E
36	43	2	978.52	4.9	1	29.5	24.4	95.00%	K.SESLFLQR.K		K.SESLFLQR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
232	RL7B_SCHPO	16.40%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	21	2	2002.11	4.4	1	37	18.8	95.00%	M.VASSTVPSVASIFAPESLLK.K		-.MVASSTVPSVASIFAPESLLK.K
109	114	2	772.46	-0.28	0	29.3	22.3	95.00%	K.IMQLLR.L		K.IMQLLR.L
168	182	2	1523.86	4.4	0	56.2	16.5	95.00%	R.IPLSDNAIIEAALGK.Y		R.IPLSDNAIIEAALGK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
233	MUG64_SCHPO	11.19%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
224	238	3	1767.86	4.9	0	44.3	26.4	95.00%	K.LDVESAKPENLEHCK.S	Carbamidomethyl (+57)	K.LDVESAKPENLEHCK.S
108	125	2	1851.02	3.8	0	41.3	19.5	95.00%	R.NLGNLTPLEQTPLASVGK.N		R.NLGNLTPLEQTPLASVGK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
234	SYQ_SCHPO	3.95%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
757	773	3	1760.83	5.2	1	28.1	26.6	95.00%	K.TDSSAGVDKAENPESVR.F		K.TDSSAGVDKAENPESVR.F
52	66	2	1574.91	4.6	1	39.6	15.1	95.00%	R.TIGNLLFTLANASLK.Q		R.TIGNLLFTLANASLK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
235	CYSK1_SCHPO	16.24%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
249	270	3	2473.25	1.5	1	26.2	24.2	95.00%	R.ITGNVQPVYDLIDDAMKIPDEK.S		R.ITGNVQPVYDLIDDAMKIPDEK.S
10	23	2	1341.78	3.9	1	59.1	18.5	95.00%	K.VPGIVSGFIGAIGR.T		K.VPGIVSGFIGAIGR.T
180	200	2	2019.93	5.1	1	71.4	26.9	95.00%	K.GTVDGFTCSTGTGGTFAGVTK.Y	Carbamidomethyl (+57)	K.GTVDGFTCSTGTGGTFAGVTK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
236	ODPB_SCHPO	12.30%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
220	234	2	1634.86	4.6	1	26.5	22.7	92.20%	K.EALSEDFVLPFGLAK.V		K.EALSEDFVLPFGLAK.V
331	360	3	3021.51	4	1	35.4	23.2	95.00%	R.VSMADVPMPYSHPVEAASVPNADVVVAAAK.K		R.VSMADVPMPYSHPVEAASVPNADVVVAAAK.K

341	360	2	1931.01	1.7	0	57.8	22.8	95.00%	Y.SHPVEAASVPNADVVVAAAK.K		R.VSMADVPMPYSHPVEAASVPNADVVVAAAK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
237	PUR2_SCHPO	4.44%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
31	48	2	1678.78	1.8	1	54.6	26.3	95.00%	K.VYVAPGNGGTASNGAESK.M	Deamidation (+1)	K.VYVAPGNGGTASNGAESK.M
581	597	3	1741.78	1.1	1	36.5	27.2	95.00%	Y.HDGHYDANGTSVGAVSR.D		K.QAGCALVGGETSEMPGLYHDGHYDANGTSVGAVSR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
238	KGUA_SCHPO	12.38%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
134	147	2	1596.89	0.11	1	27.4	19.3	93.50%	Y.VFLAPPSIEQLEVR.L		K.ASPIDAQYVFLAPPSIEQLEVR.L
2	12	2	1103.59	4.9	0	34.4	22.8	95.00%	M.TPQLSSSVASK.L		-.MTPQLSSSVASK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
239	SYH_SCHPO	7.25%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
24	38	3	1603.81	4.1	1	23.8	24.1	92.30%	K.SQGASKEDIDKEVAK.L		K.SQGASKEDIDKEVAK.L
364	387	3	2316.06	2.7	1	56.7	26.7	95.00%	K.SADPEADRSNDDSIGVGSIAAGGR.Y		K.SADPEADRSNDDSIGVGSIAAGGR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
240	ACAC_SCHPO	1.05%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
197	207	2	1131.63	6.1	0	34.7	20.8	95.00%	K.ISSTIVAQSAR.V		K.ISSTIVAQSAR.V
899	911	2	1475.7	-0.18	0	53.1	25.6	95.00%	Y.CDGQNLATTQQLK.V	Carbamidomethyl (+57)	K.QLEVAIQTYCDGQNLATTQQLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
241	AROC_SCHPO	11.14%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
328	340	2	1331.68	5.2	0	55.6	24.3	95.00%	K.SPATIGVEQSTSR.Y		K.SPATIGVEQSTSR.Y
161	191	3	3385.69	2.7	1	61.9	21.1	95.00%	K.IAIPLHETASSAILDPEDDTFESPITAEYLK.F		K.IAIPLHETASSAILDPEDDTFESPITAEYLK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
242	O13797_SCHPO	14.83%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
197	214	2	1831.84	5.2	0	74	26.7	95.00%	K.QLNQPSDSSATSGADQAR.T		K.QLNQPSDSSATSGADQAR.T
124	152	4	3210.53	3.2	1	60.9	24.3	95.00%	R.AAAYNQLGQFENAVEDALTCLSLDPHHAR.A	Carbamidomethyl (+57)	R.AAAYNQLGQFENAVEDALTCLSLDPHHAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
243	RL35_SCHPO	19.67%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
11	24	2	1684.85	4.2	0	72	24.4	95.00%	K.QSQENLAEQLQELR.Q		K.QSQENLAEQLQELR.Q
56	65	2	1157.65	4.3	0	33.6	22	95.00%	R.ILTVINESNR.L		R.ILTVINESNR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
244	WOS2_SCHPO	12.90%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
28	39	2	1279.74	-0.017	0	46.3	16.1	95.00%	Y.LTVLIPDAVDPK.I		K.NVIYLTVLIPDAVDPK.I
16	27	2	1394.67	0.56	2	40.7	26.2	95.00%	R.SNKDDAEKNVIY.L		R.SNKDDAEKNVIYLTVLIPDAVDPK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
245	TCPQ_SCHPO	4.03%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
64	73	2	1086.61	1.8	0	57.1	21.8	95.00%	F.LTNDAATIIR.E		K.IVVNHLQQTFLTNDAATIIR.E
243	254	2	1377.64	-1.4	0	38.8	25.6	95.00%	F.SCPLDISQTETK.G	Carbamidomethyl (+57)	K.VAVFSCPLDISQTETK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
246	RLA0_SCHPO	15.06%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
133	144	2	1308.71	5.2	1	29.1	21.1	95.00%	K.TSFFQALGIPTK.I		K.TSFFQALGIPTK.I
98	132	3	3513.88	2.7	1	45.6	16.2	95.00%	R.ETIIANVIAAPARPNAIAPLDVFVPAGNTGMEPGK.T		R.ETIIANVIAAPARPNAIAPLDVFVPAGNTGMEPGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
247	UBC4_SCHPO	25.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
91	101	2	1244.65	4.6	1	28.4	23.7	94.70%	R.DQWSPALTISK.V		R.DQWSPALTISK.V
102	128	3	3017.59	3.1	1	65.3	19.2	95.00%	K.VLLSICSLLTDPNPDDPLVPEIAHVYK.T	Carbamidomethyl (+57)	K.VLLSICSLLTDPNPDDPLVPEIAHVYK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
248	AROF_SCHPO	10.05%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
252	265	2	1338.61	4.9	1	41	26	95.00%	K.SGTNFDADSVAGAK.A		K.SGTNFDADSVAGAK.A
266	288	4	2617.24	3.5	1	24.8	25.9	95.00%	K.AKLEECNKLPSIMIDCSHGNSSK.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.AKLEECNKLPSIMIDCSHGNSSK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
249	IDH2_SCHPO	7.94%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
314	330	2	1757.99	4.4	0	54.2	18.6	95.00%	K.GLANPTALLLSSVMMLK.H		K.GLANPTALLLSSVMMLK.H
301	313	2	1264.64	-0.1	0	35.5	25.6	95.00%	F.EAVHGTAPDIAGK.G		K.IVTDPVPYNNTVMVMPNLYGDIVSDMCAGLIGGLGLTPSGNIGNQASIFEAVHGTAPDIAGK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
250	SEC13_SCHPO	11.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
154	172	2	1721.9	0.28	0	75.7	23.5	95.00%	W.SPPSLSGSVVGQSPAAGPK.K		R.IFTAHEPGCNAVCWSPPSLSGSVVGQSPAAGPK.K
140	172	3	3364.61	3	1	43.1	23.6	95.00%	R.IFTAHEPGCNAVCWSPPSLSGSVVGQSPAAGPK.K	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.IFTAHEPGCNAVCWSPPSLSGSVVGQSPAAGPK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
251	P5CR_SCHPO	15.25%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
70	98	3	3111.57	2.6	0	41.3	21.7	95.00%	K.ENAEMAAISNVLLLSCKPQAAEDVLNSPK.M	Carbamidomethyl (+57)	K.ENAEMAAISNVLLLSCKPQAAEDVLNSPK.M
116	129	2	1566.76	5	0	85.9	25.9	95.00%	K.TISSLQSMLDESTR.V		K.TISSLQSMLDESTR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
252	YBN4_SCHPO	12.62%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
182	203	4	2693.39	2.2	1	23.4	21.8	95.00%	K.VKPTIHQMELHPYLPQTEYLEK.H		K.VKPTIHQMELHPYLPQTEYLEK.H
52	70	4	2151.08	3	1	29.4	25.2	95.00%	R.HIDTAHIYGNEKEIGEGIR.E		R.HIDTAHIYGNEKEIGEGIR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
253	ODP2_SCHPO	10.56%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

215	238	4	2577.46	3.9	2	20.4	13.4	95.00%	R.IIKVDIENFKPVVAPKPSNEAAAK.A	R.IIKVDIENFKPVVAPKPSNEAAAK.A
49	75	3	2873.43	2.8	1	41.8	23.9	95.00%	K.NYPAHTVINMPALSPTMTTGNIGAFQK.K	K.NYPAHTVINMPALSPTMTTGNIGAFQK.K

Supplementary Table S2: All "Scaffold" validated proteins and peptides identified from solprotSP (*S.pombe*) and from SCVMprot (*S.cerevisiae*) samples

***S.pombe* - Chymotrypsin digest of large tryptic peptides (replicate C)**

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
1	PGK_SCHPO	74.64%	100%	34

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
359	379	2	2046.05	4.7	1	96.9	23.6	95.00%	K.TCEAGNVVIVGGGDTATVAKK.Y	Carbamidomethyl (+57)	K.TCEAGNVVIVGGGDTATVAKK.Y
359	378	2	1917.95	4	0	118	25	95.00%	K.TCEAGNVVIVGGGDTATVAK.K	Carbamidomethyl (+57)	K.TCEAGNVVIVGGGDTATVAK.K
138	149	3	1262.67	4.1	2	23.6	23.6	92.20%	K.VKADASAVEAFR.K		K.VKADASAVEAFR.K
138	148	2	1106.56	-1.7	2	34.3	24.1	95.00%	K.VKADASAVEAF.R		K.VKADASAVEAFR.K
250	269	3	2127.98	0.19	1	38.2	27.2	95.00%	K.IGDSLFDEAGSKNVESMMAK.A		K.IGDSLFDEAGSKNVESMMAK.A
273	288	2	1805.93	4.9	1	56.9	24.3	95.00%	K.NNVEVFLPVDFVTADK.F		K.NNVEVFLPVDFVTADK.F
140	150	2	1163.6	4.3	1	57.5	24.3	95.00%	K.ADASAVEAFRK.S		K.ADASAVEAFRK.S
23	39	2	1914.95	-2.1	1	44	25.4	95.00%	R.VDFNVPLDGDRITNNAR.I		R.VDFNVPLDGDRITNNAR.I
57	71	2	1591.87	2.9	0	46.2	21.1	95.00%	K.AVILMSHLGRPNGAR.V	Deamidation (+1)	K.AVILMSHLGRPNGAR.V
23	33	2	1245.61	6.8	1	62.1	25.1	95.00%	R.VDFNVPLDGDR.I		R.VDFNVPLDGDR.I
112	122	2	1211.69	4.5	0	57.3	16.6	95.00%	K.GGEVILLENLR.F		K.GGEVILLENLR.F
206	213	2	741.47	-1.4	0	28.6	18	94.70%	F.LAILGGAK.V		K.ALENPARPFLAILGGAK.V
250	261	2	1237.59	4.5	1	61.5	25.5	95.00%	K.IGDSLFDEAGSK.N		K.IGDSLFDEAGSK.N
218	227	2	1183.69	5.5	0	39.2	19.1	95.00%	K.IQLIDNLLDK.V		K.IQLIDNLLDK.V
218	230	3	1552.9	4.8	1	31.7	15.8	95.00%	K.IQLIDNLLDKVNR.L		K.IQLIDNLLDKVNR.L
76	86	3	1141.67	-0.79	0	37.9	17.8	95.00%	Y.SLKPVAAELSK.L		K.YSLKPVAAELSK.L
94	105	2	1406.64	3.6	1	56.7	26	95.00%	K.FLDDCVGPEVEK.A	Carbamidomethyl (+57)	K.FLDDCVGPEVEK.A
197	213	2	1737	3.5	1	54.1	14.5	95.00%	K.ALENPARPFLAILGGAK.V		K.ALENPARPFLAILGGAK.V
170	181	2	1267.64	4	0	58.7	24.3	95.00%	R.AHSSMVGVDLPR.V		R.AHSSMVGVDLPR.V
123	136	3	1544.76	5.8	1	28.5	25.4	95.00%	R.FHIEEEGSAKVDGK.K		R.FHIEEEGSAKVDGK.K
214	230	2	1966.13	4.4	1	68.4	15.2	95.00%	K.VADKIQLIDNLLDKVNR.L		K.VADKIQLIDNLLDKVNR.L
7	15	2	986.57	5.4	0	41.1	21.4	95.00%	K.LAITDVDLK.G		K.LAITDVDLK.G
123	132	3	1145.54	4.7	1	33.9	25.6	95.00%	R.FHIEEEGSAK.V		R.FHIEEEGSAK.V
197	205	2	1013.53	-0.63	1	33.6	21.8	95.00%	K.ALENPARPF.L		K.ALENPARPFLAILGGAK.V
341	347	2	869.39	-0.85	1	27.2	24.1	93.10%	F.EFDNFAK.G		K.TIVWNGPAGVFEFDNFAK.G
404	414	2	1040.63	5.6	0	39.4	17.4	95.00%	K.ALPGVVALSSK.-		K.ALPGVVALSSK.-
380	403	3	2417.21	2.5	1	72	24.1	95.00%	K.YGKEDALSHVSTGGGASLELLEGK.A		K.YGKEDALSHVSTGGGASLELLEGK.A
321	329	2	994.54	5.5	1	50.2	21.9	95.00%	K.FAEVITTSK.T		K.FAEVITTSK.T
75	86	3	1304.74	4.3	1	59.4	19.6	95.00%	K.YSLKPVAAELSK.L		K.YSLKPVAAELSK.L
383	403	2	2069.04	3.6	0	81.1	24.4	95.00%	K.EDALSHVSTGGGASLELLEGK.A		K.EDALSHVSTGGGASLELLEGK.A
151	169	2	2020.01	5.9	1	113	24.8	95.00%	K.SLTSLGDIFVNDAFGTAHR.A		K.SLTSLGDIFVNDAFGTAHR.A
295	316	2	2246	-1.5	1	63.8	27.3	95.00%	K.VGSATAEEGIPDGWMGLDCGPK.S	Carbamidomethyl (+57)	K.VGSATAEEGIPDGWMGLDCGPK.S
214	227	2	1596.91	-1.9	1	58.8	18.1	95.00%	K.VADKIQLIDNLLDK.V		K.VADKIQLIDNLLDK.V
330	340	2	1159.6	-1.1	1	33.2	24.1	95.00%	K.TIVWNGPAGVF.E		K.TIVWNGPAGVFEFDNFAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
2	ENO11_SCHPO	74.72%	100%	27

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
258	263	2	765.39	4.7	1	25.9	24.3	91.10%	K.YDLDIK.A		K.YDLDIK.A
415	425	2	1223.55	-1.3	1	41.7	25.2	95.00%	R.IEEELGSEGVY.A		R.IEEELGSEGVYAGAHAGK.Y
361	374	2	1608.72	-1.6	1	61.8	26.4	95.00%	R.MSYEAGWGVMVSHR.S		R.MSYEAGWGVMVSHR.S
311	328	2	1963.98	4.2	1	93.2	25.2	95.00%	K.AETDFQIVGDDLTVTNVK.R		K.AETDFQIVGDDLTVTNVK.R
65	79	2	1477.87	4	0	73.7	15.3	95.00%	K.AVGNVNNIIAPAVVK.A		K.AVGNVNNIIAPAVVK.A
106	120	2	1560.82	4.2	0	61.3	23.8	95.00%	K.LGANAILGVSMAICR.A	Oxidation (+16)/ Carbamidomethyl (+57)	K.LGANAILGVSMAICR.A
170	184	2	1606.79	2.1	1	73.4	25.8	95.00%	F.MILPTGAPSFSEAMR.W		K.GPYVLPVPSFNVLNGGSHAGGDLAFQEFMILPTGAPSFSEAMR.W

170	179	2	1032.53	2.6	1	46.5	23.9	95.00%	F.MILPTGAPSF.S		K.GPYVLPVPSFNVLNGGSHAGGDLAFQEFMILPTGAPSFSEAMR.W
273	287	2	1812.95	-1.4	1	79.2	22.9	95.00%	K.LTYQQLTDLYVELSK.K		K.LTYQQLTDLYVELSK.K
200	234	3	3596.81	3.8	2	68.4	21.1	95.00%	K.RYGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A		K.RYGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
243	257	2	1598.78	-1.8	1	80.5	25.8	95.00%	K.IGLDVASSEFYVDGK.Y		K.IGLDVASSEFYVDGK.Y
409	414	2	806.43	5.7	1	29.4	25.1	95.00%	K.YNELLR.I		K.YNELLR.I
375	396	2	2201.14	2.9	1	122	22.5	95.00%	R.SGETADTFISHLTVGIGAGQLK.S		R.SGETADTFISHLTVGIGAGQLK.S
89	96	2	905.49	4.7	1	57.4	23.5	95.00%	K.AADEFLLK.L		K.AADEFLLK.L
80	88	2	1002.5	4.3	0	41.9	22.7	95.00%	K.ANLDVTDQK.A		K.ANLDVTDQK.A
185	194	2	1204.59	5.4	1	34	24.9	95.00%	R.WGAETYHTLK.S		R.WGAETYHTLK.S
346	360	2	1585.85	6	0	90.8	21.9	95.00%	K.VNQIGSVTESLNAVR.M		K.VNQIGSVTESLNAVR.M
288	303	2	1965.9	0.041	2	55	26.7	95.00%	K.KYPIVSIEDPFDQDDW.S		K.KYPIVSIEDPFDQDDWSAWTHMK.A
89	103	2	1662.85	3.3	1	74.4	24.4	95.00%	K.AADEFLLKLDGTENK.S		K.AADEFLLKLDGTENK.S
145	169	2	2572.26	0.57	1	50.1	24.8	95.00%	Y.VLPVPSFNVLNGGSHAGGDLAFQEF.M	Deamidation (+1)	K.GPYVLPVPSFNVLNGGSHAGGDLAFQEFMILPTGAPSFSEAMR.W
201	234	3	3440.71	3.8	1	65	22.1	95.00%	R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
311	329	2	2120.09	4.8	1	105	23.7	95.00%	K.AETDFQIVGDDLTVTNVKR.L		K.AETDFQIVGDDLTVTNVKR.L
16	32	2	1837.91	-1.6	0	89.9	25.4	95.00%	R.GNPTVEVDLTTETGIHR.A		R.GNPTVEVDLTTETGIHR.A
33	50	2	1886.97	4.8	1	105	24.3	95.00%	R.AIVPSGASTGIWEALEMR.D		R.AIVPSGASTGIWEALEMR.D
338	345	2	901.51	4.7	0	31.4	21.6	95.00%	K.CANALLLK.V	Carbamidomethyl (+57)	K.CANALLLK.V
415	432	2	1815.86	-0.67	1	89	26.1	95.00%	R.IEEELGSEGVYAGAHAGK.Y		R.IEEELGSEGVYAGAHAGK.Y
383	396	2	1392.81	0.5	0	77.7	16.3	95.00%	F.ISHLTVGIGAGQLK.S		R.SGETADTFISHLTVGIGAGQLK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
3	G3P1_SCHPO	68.45%	100%	22

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	86	3	2203.13	3.8	1	43.2	23.2	95.00%	K.LVIDGNAIDVHNERDPADIK.W		K.LVIDGNAIDVHNERDPADIK.W
169	186	2	1886.94	-0.0056	0	76.3	25.2	95.00%	F.GIEEGLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK.T
249	263	4	1673.93	-1.8	1	23.7	19.9	95.00%	K.LAKPTNYEDIKAAIK.A		K.LAKPTNYEDIKAAIK.A
132	145	2	1574.8	0.87	2	40.6	24.7	95.00%	Y.VVGVNEEKFNPSEK.V		K.DAPMYVVGVNEEKFNPSEK.V
272	295	2	2589.14	0.9	1	58.3	27.4	95.00%	K.GVLGYTEDAVVSTDFCGDNHSSIF.D	Carbamidomethyl (+57)	K.GVLGYTEDAVVSTDFCGDNHSSIFDASAGIQLSPQFVK.L
119	139	2	2245.17	-0.5	2	78.4	22.1	95.00%	R.VIISAPSKDAPMYVVGVNEEK.F		R.VIISAPSKDAPMYVVGVNEEK.F
127	139	2	1449.69	3.7	1	45.1	25.6	95.00%	K.DAPMYVVGVNEEK.F		K.DAPMYVVGVNEEK.F
103	113	3	1185.6	0.34	0	26.3	23.9	95.00%	F.TTQETASAHLK.G		K.WSTSGADYVIESTGVFTTQETASAHLK.G
146	162	2	1819.88	-1.6	0	85.1	26	95.00%	K.VISNASCTTNCLAPLAK.V	Carbamidomethyl (+57)/ Deamidation (+1)/ Carbamidomethyl (+57)	K.VISNASCTTNCLAPLAK.V
88	102	2	1531.71	1.7	1	29.8	26.6	94.30%	W.STSGADYVIESTGVF.T		K.WSTSGADYVIESTGVFTTQETASAHLK.G
6	13	2	819.43	6.2	1	38.4	23.6	95.00%	K.VGINGFGR.I	Deamidation (+1)	K.VGINGFGR.I
234	248	2	1623.93	3.7	1	72.7	18.6	95.00%	F.RVPTPDVSVVDLTVK.L		K.LTGMAFRVPTPDVSVVDLTVK.L
249	259	3	1290.69	4.5	1	28.4	24	95.00%	K.LAKPTNYEDIK.A		K.LAKPTNYEDIK.A
56	66	2	1193.6	4.2	1	61.8	25.3	95.00%	R.FDGSVEIKDGK.L		R.FDGSVEIKDGK.L
235	248	2	1467.82	3.7	0	76.5	18.6	95.00%	R.VPTPDVSVVDLTVK.L		R.VPTPDVSVVDLTVK.L
64	86	3	2503.28	3.2	1	25.1	23.4	94.10%	K.DGKLVIDGNAIDVHNERDPADIK.W		K.DGKLVIDGNAIDVHNERDPADIK.W

296	309	2	1459.77	0.26	1	67.2	23.7	95.00%	F.DASAGIQLSPQFVK.L		K.GVLGYTEDAVVSTDFCGDNHSSIFDASAGIQLSPQFVK.L
323	334	2	1304.75	5.7	2	40.6	17.6	95.00%	R.RVVDLVAYTAAK.D		R.RVVDLVAYTAAK.D
324	334	2	1148.65	6.2	1	55.4	19.8	95.00%	R.VVDLVAYTAAK.D		R.VVDLVAYTAAK.D
163	186	2	2576.28	1.5	1	96.3	24	95.00%	K.VINDTFGIEEGLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK.T
324	336	2	1377.72	3.8	1	68.7	24.4	95.00%	R.VVDLVAYTAAKDN.-		R.VVDLVAYTAAKDN.-
201	215	2	1343.71	4.7	0	69.9	22.9	95.00%	R.GASANIIPSSTGAAK.A		R.GASANIIPSSTGAAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
4	METE_SCHPO	59.42%	100%	43

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
638	653	2	1752.84	0.91	1	74.5	25.9	95.00%	R.LATAAVQDDTQIHSHF.C		R.LATAAVQDDTQIHSHFCYSDFNDIFDAIQR.L
434	449	2	1746.95	-2.1	1	73	20.9	95.00%	K.LPLFPTTTIGSFPQTK.E		K.LPLFPTTTIGSFPQTK.E
128	141	2	1732.84	0.5	1	45.4	25.7	95.00%	Y.HFLRPEVSEETDFK.L		K.WFDSNYHFLRPEVSEETDFK.L
482	504	3	2702.26	-0.14	2	27	26.5	94.60%	K.FQEEVGLDVLVHGEPERNDMVQY.F		K.FQEEVGLDVLVHGEPERNDMVQYFGER.M
156	171	2	1683.96	0.52	1	43.5	17.3	95.00%	K.EAGIITRPVLVGPVTY.L		K.EAGIITRPVLVGPVTYLFIAK.A
684	690	2	813.51	5.6	0	34.2	20.8	95.00%	K.LLNVLSR.Y		K.LLNVLSR.Y
393	404	2	1284.67	4.4	0	68.2	21.8	95.00%	R.AESPITNVEAVR.E		R.AESPITNVEAVR.E
707	716	3	1186.64	4.9	1	25.6	23	94.60%	R.VPPVSEFKER.I		R.VPPVSEFKER.I
391	404	2	1511.81	4	1	42.1	22.1	95.00%	K.ARAESPITNVEAVR.E		K.ARAESPITNVEAVR.E
67	76	2	1225.51	0.8	1	44.4	26	95.00%	Y.DQIMDHSFSF.N		K.AQGVDIIPSNDFSLYDQIMDHSFSFNVIPPR.Y
325	351	3	2884.5	3.5	0	47.3	20	95.00%	R.VQVASSSSILHIPHSLSGEDQINPEIK.R		R.VQVASSSSILHIPHSLSGEDQINPEIK.R
325	352	3	3040.6	2.2	1	77.8	18.1	95.00%	R.VQVASSSSILHIPHSLSGEDQINPEIKR.W		R.VQVASSSSILHIPHSLSGEDQINPEIKR.W
261	273	2	1330.77	-1.7	0	75.1	18.6	95.00%	K.GLPIAGVHVDVVR.A		K.GLPIAGVHVDVVR.A
104	121	2	1742.9	4.6	1	66.3	23.7	95.00%	R.AATADKAAVDVPAGEMVK.W		R.AATADKAAVDVPAGEMVK.W
128	140	2	1604.75	0.54	1	62.5	26.5	95.00%	Y.HFLRPEVSEETDF.K		K.WFDSNYHFLRPEVSEETDFK.L
281	299	2	1881.07	-1.4	0	88.4	17	95.00%	R.ALAVLGENQIISVGVVSGR.N		R.ALAVLGENQIISVGVVSGR.N
147	155	2	1034.53	5.7	1	36.8	24.9	95.00%	K.ALDEFLEAK.E		K.ALDEFLEAK.E
547	560	2	1596.79	3.6	1	50.8	25.3	95.00%	K.ESQYAQSITSKPMK.G		K.ESQYAQSITSKPMK.G
461	473	2	1539.75	-1.6	1	71.3	25.5	95.00%	K.GLISQEEYDAFIR.K		K.GLISQEEYDAFIR.K
668	679	2	1288.66	3.8	0	37	24.7	95.00%	R.LDADVVSIENSK.S		R.LDADVVSIENSK.S
527	546	3	2267.24	3.3	1	44.5	19.1	95.00%	R.CVRPPIIVGDVYRPAPMTVK.E	Carbamidomethyl (+57)	R.CVRPPIIVGDVYRPAPMTVK.E
631	637	2	877.45	5.9	1	49	23.7	95.00%	K.WAIDAFR.L		K.WAIDAFR.L
577	601	3	2805.42	3	1	36.5	22.2	95.00%	R.DDVHDSVQAQQIALGLRDEVLDLEK.A		R.DDVHDSVQAQQIALGLRDEVLDLEK.A
156	176	3	2256.33	3.9	1	51.3	9.03	95.00%	K.EAGIITRPVLVGPVTYLFIAK.A		K.EAGIITRPVLVGPVTYLFIAK.A
656	667	2	1439.67	0.67	1	47.4	26.4	95.00%	Y.SDFNDIFDAIQR.L		R.LATAAVQDDTQIHSHFCYSDFNDIFDAIQR.L
561	571	2	1184.69	-1.3	0	46	20	95.00%	K.GMLTAPITILR.W		K.GMLTAPITILR.W
4	11	2	845.48	4.8	1	33.3	22.7	95.00%	K.SAVLGFPR.I		K.SAVLGFPR.I
707	714	2	901.49	4.3	1	27.7	24.3	93.70%	R.VPPVSEFK.E		R.VPPVSEFK.E
691	706	2	1818.88	3.8	1	84	25.8	95.00%	R.YTSCIGPGLFDIHSPR.V	Carbamidomethyl (+57)	R.YTSCIGPGLFDIHSPR.V
499	508	2	1257.55	4.4	1	53.6	26	95.00%	R.NDMVQYFGER.M		R.NDMVQYFGER.M
243	260	2	1982.07	0.4	1	66.5	18.5	95.00%	K.LILTTYFGSLQSNADVLK.G		K.LILTTYFGSLQSNADVLK.G
75	82	2	928.51	0.61	1	28.7	22.2	94.80%	F.SFNVIPPR.Y		K.AQGVDIIPSNDFSLYDQIMDHSFSFNVIPPR.Y
727	738	2	1466.7	4.2	1	48	26.1	95.00%	K.DHLWLNPDCGLK.T	Carbamidomethyl (+57)	K.DHLWLNPDCGLK.T
428	449	3	2402.32	0.17	2	47	17.1	95.00%	K.QQASLKLPLFPTTTIGSFPQTK.E		K.QQASLKLPLFPTTTIGSFPQTK.E
527	538	2	1386.74	1.7	1	41.4	22.9	95.00%	R.CVRPPIIVGDVY.R	Carbamidomethyl (+57)	R.CVRPPIIVGDVYRPAPMTVK.E
64	74	2	1354.59	0.73	1	41.7	25.8	95.00%	F.SLYDQIMDHSF.S		K.AQGVDIIPSNDFSLYDQIMDHSFSFNVIPPR.Y
723	738	3	1927.98	4	2	24.5	23.9	93.40%	K.HVPKDHLWLNPDCGLK.T	Carbamidomethyl (+57)	K.HVPKDHLWLNPDCGLK.T

361	369	2	1017.56	4.9	0	30.5	22.3	95.00%	K.CAELAILTK.A	Carbamidomethyl (+57)	K.CAELAILTK.A
461	471	2	1270.57	-0.96	1	27	26	91.30%	K.GLISQEEYDAF.I		K.GLISQEEYDAFIR.K
606	615	2	1199.6	4.3	0	55.1	23.2	95.00%	K.VIQCDEPALR.E	Carbamidomethyl (+57)	K.VIQCDEPALR.E
67	74	2	991.41	0.99	1	27.3	25.4	92.60%	Y.DQIMDHSF.S		K.AQGVDIIPSNDFSLYDQIMDHSFS FNVIPPR.Y
85	99	2	1616.79	4.1	1	63.5	25.7	95.00%	R.LSGLSSLDTYFAMGR.G		R.LSGLSSLDTYFAMGR.G
30	40	2	1132.6	4.2	0	58.1	23.1	95.00%	K.TSAEELLATAK.Q		K.TSAEELLATAK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
5	EF1A1_SCHPO	54.78%	100%	22

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
265	288	2	2443.34	0.61	1	50.4	17.4	95.00%	R.VETGVIKPGMIVTFAPAGVTTEVK .S		R.VETGVIKPGMIVTFAPAGVTTEVK .S
289	308	2	2109.94	0.32	1	44.4	27.3	95.00%	K.SVEMHHESLDAGLPGDNVGF.N		K.SVEMHHESLDAGLPGDNVGFNV K.N
57	62	2	730.4	-1.9	1	25.8	24.2	90.80%	Y.AWVLDK.L		K.YAWVLDK.L
223	245	4	2516.4	3.1	1	25	14.9	95.00%	K.GKTLLEAIDSIEPPARPTDKPLR.L		K.GKTLLEAIDSIEPPARPTDKPLR.L
356	369	2	1607.76	0.53	0	53.5	26.1	95.00%	Y.SPVLDCHTAHIACK.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.NDPPMGCASFTAQVIILNHPGQIS AGYSPVLDCHTAHIACK.F
279	288	2	971.53	0.39	0	43	21.3	95.00%	F.APAGVTTEVK.S		R.VETGVIKPGMIVTFAPAGVTTEVK .S
135	146	2	1313.74	3.9	1	45.8	20.8	95.00%	R.EHALLAYTLGVK.Q		R.EHALLAYTLGVK.Q
370	376	2	848.47	4.7	1	25.9	22.7	91.00%	K.FAELIEK.I		K.FAELIEK.I
329	338	2	1094.42	1.5	1	44.3	23.9	95.00%	K.NDPPMGCASF.T	Carbamidomethyl (+57)	K.NDPPMGCASFTAQVIILNHPGQIS AGYSPVLDCHTAHIACK.F
265	278	2	1489.82	0.39	1	56	21	95.00%	R.VETGVIKPGMIVTF.A		R.VETGVIKPGMIVTFAPAGVTTEVK .S
402	421	2	2268.08	4	1	67.5	26.2	95.00%	K.MVPSKPMCVEAFTDYAPLGR.F	Carbamidomethyl (+57)	K.MVPSKPMCVEAFTDYAPLGR.F
339	355	2	1780.95	1.7	1	54	21.8	95.00%	F.TAQVIILNHPGQISAGY.S		K.NDPPMGCASFTAQVIILNHPGQIS AGYSPVLDCHTAHIACK.F
147	154	2	883.55	5.8	0	26.4	16.7	91.80%	K.QLIVAVNK.M		K.QLIVAVNK.M
254	264	2	1024.61	4.2	0	65.4	15.1	95.00%	K.IGGIGTVPVGR.V		K.IGGIGTVPVGR.V
6	20	2	1529.84	4.6	0	62.9	21.8	95.00%	K.GHINVVVIGHVDSGK.S		K.GHINVVVIGHVDSGK.S
289	311	3	2451.16	4	1	64.2	26.2	95.00%	K.SVEMHHESLDAGLPGDNVGFNV K.N		K.SVEMHHESLDAGLPGDNVGFNV K.N
321	338	2	1911.76	0.34	2	34.6	27	95.00%	R.GNVCGDSKNDPPMGCASF.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GNVCGDSKNDPPMGCASFTAQV IILNHPGQISAGYSPVLDCHTAHIAC K.F
185	208	2	2663.24	-0.31	1	50	26.6	95.00%	K.TVPFVPVSGFQGDNMIEPTTNMP W.Y		K.TVPFVPVSGFQGDNMIEPTTNMP WYQGWQK.E
225	245	3	2331.29	2.6	0	34.8	16.7	95.00%	K.TLLEAIDSIEPPARPTDKPLR.L		K.TLLEAIDSIEPPARPTDKPLR.L
155	164	2	1151.51	6.4	1	75.8	24.7	95.00%	K.MDTTGWSQAR.F		K.MDTTGWSQAR.F
85	96	2	1340.69	4.4	1	66.1	23.6	95.00%	K.YNVTVIDAPGHR.D		K.YNVTVIDAPGHR.D
246	253	2	974.55	4.1	1	32.1	22.3	95.00%	R.LPLQDVYK.I		R.LPLQDVYK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
6	KPYK_SCHPO	71.32%	100%	34

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
233	243	2	1214.66	3.9	1	28.5	22.1	94.60%	R.EVLGEEGKNIK.I		R.EVLGEEGKNIK.I
57	64	2	941.37	-0.22	1	44.7	22.9	95.00%	R.MNFSHGSY.E		R.MNFSHGSYEYHQSVIDNAR.K
422	433	3	1430.81	-0.83	1	41.6	19	95.00%	K.YRPSIPIVMVTR.C		K.YRPSIPIVMVTR.C
248	271	2	2647.29	0.75	1	83.9	24.7	95.00%	K.IENQQGVNNFDSILDVTDGIMVAR .G		K.IENQQGVNNFDSILDVTDGIMVAR .G
191	207	2	1884.98	-2.1	1	57.5	23.3	95.00%	K.TDVDLPALSEKDKADLR.F		K.TDVDLPALSEKDKADLR.F
77	98	3	2294.27	3.2	1	35.9	17.7	95.00%	K.ASATNPLFPLAIALDTKGPEIR.T		K.ASATNPLFPLAIALDTKGPEIR.T
272	284	2	1344.69	-2.5	1	32.1	23.2	95.00%	R.GDLGIEIPASQVF.V		R.GDLGIEIPASQVFVAQK.M
345	354	2	1084.51	-0.93	1	25.5	24.5	90.30%	K.GSYPVEAVTY.M		K.GSYPVEAVTYMAETAR.V

65	75	2	1330.63	-0.99	1	43.5	26.1	95.00%	Y.EYHQSVIDNAR.K		R.MNFSHGSYEYHQSVIDNAR.K
468	477	2	1186.55	5.3	1	54.8	24.9	95.00%	R.VAYGCQQAYK.M	Carbamidomethyl (+57)	R.VAYGCQQAYK.M
294	319	4	2965.41	0.81	1	59.4	25.7	95.00%	K.CNIAGKPVACATQMLESMTYNPR PTR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CNIAGKPVACATQMLESMTYNPR PTR.A
405	417	2	1287.72	5.7	0	62	20.8	95.00%	K.AIVVLSTSGNTAR.L		K.AIVVLSTSGNTAR.L
212	223	2	1368.69	4.2	1	39.8	24.3	95.00%	K.NGVDMIFASFIR.R		K.NGVDMIFASFIR.R
381	404	2	2460.23	3.5	0	76.2	23.4	95.00%	R.RPLECATETTAVAAIGASIESDAK. A	Carbamidomethyl (+57)	R.RPLECATETTAVAAIGASIESDAK. A
191	201	2	1186.61	4.4	0	25.5	23.3	90.30%	K.TDVDLPALSEK.D		K.TDVDLPALSEK.D
487	497	2	1053.66	5.9	0	39.5	13	95.00%	K.IIVLQGAVGGK.G		K.IIVLQGAVGGK.G
446	460	2	1793.89	0.94	2	29.3	25.4	95.00%	R.GVYPVIYEKEPLSDW.Q		R.GVYPVIYEKEPLSDWQK.D
294	313	2	2244.01	0.25	1	80.6	27.2	95.00%	K.CNIAGKPVACATQMLESMTY.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CNIAGKPVACATQMLESMTYNPR PTR.A
224	232	3	1107.62	3.9	1	57.7	19.8	95.00%	R.RAEDVIHIR.E		R.RAEDVIHIR.E
10	26	2	1880.98	3.7	1	90.9	22.6	95.00%	K.QWVAGLNSELDIPAVNR.R		K.QWVAGLNSELDIPAVNR.R
77	93	2	1741.96	-1.7	1	52.4	20.8	95.00%	K.ASATNPLFPLAIALDTK.G		K.ASATNPLFPLAIALDTK.G
225	232	2	951.52	5	0	30.1	22.5	95.00%	R.AEDVIHIR.E		R.AEDVIHIR.E
76	98	3	2422.36	-0.38	2	80.7	15.1	95.00%	R.KASATNPLFPLAIALDTKGPEIR.T		R.KASATNPLFPLAIALDTKGPEIR.T
28	37	2	1088.6	5	0	46.3	21.8	95.00%	R.TSIICTIGPK.S	Carbamidomethyl (+57)	R.TSIICTIGPK.S
191	203	2	1429.74	3.8	1	45.1	24	95.00%	K.TDVDLPALSEKDK.A		K.TDVDLPALSEKDK.A
345	360	2	1743.82	5.3	1	80.9	27	95.00%	K.GSYPVEAVTYMAETAR.V		K.GSYPVEAVTYMAETAR.V
272	288	2	1770.96	3.8	1	69.1	20.9	95.00%	R.GDLGIEIPASQVFVAQK.M		R.GDLGIEIPASQVFVAQK.M
76	93	2	1870.06	0.089	2	79.6	18.3	95.00%	R.KASATNPLFPLAIALDTK.G		R.KASATNPLFPLAIALDTK.G
99	118	2	2080.98	-0.2	1	48.5	26.8	95.00%	R.TGLTVGGTDYPISSGHEMIF.T		R.TGLTVGGTDYPISSGHEMIFTTDD AYAEK.C
10	27	3	2037.08	4.1	1	30.7	21.6	95.00%	K.QWVAGLNSELDIPAVNRR.T		K.QWVAGLNSELDIPAVNRR.T
320	344	2	2506.22	3.3	0	104	24.8	95.00%	R.AEVSDVGNAVLDGADLVMLSGE TTK.G	Oxidation (+16)	R.AEVSDVGNAVLDGADLVMLSGE TTK.G
99	127	3	3075.41	2.5	1	69.9	25.7	95.00%	R.TGLTVGGTDYPISSGHEMIFTTDD AYAEK.C		R.TGLTVGGTDYPISSGHEMIFTTDD AYAEK.C
369	380	2	1398.69	-1.9	1	67.2	24.6	95.00%	Y.GSLYQEMFGLVR.R		R.VAEASIPYGSLYQEMFGLVR.R
47	56	3	1143.62	4.2	1	26	23	95.00%	K.LRDAGMNIVR.M		K.LRDAGMNIVR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
7	ALF_SCHPO	58.66%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
26	50	2	2496.3	0.066	1	79.2	22.1	95.00%	R.EHGFAIPAINVTSSSTAIAALEAAR .E		R.EHGFAIPAINVTSSSTAIAALEAAR .E
253	261	2	1067.53	1.1	1	33.9	24.6	95.00%	K.TTNDKPVFF.V		K.TTNDKPVFFVFHGGSGSSVNEFR .T
262	275	2	1478.69	2.3	1	54.1	26.1	95.00%	F.VFHGGSGSSVNEFR.T		K.TTNDKPVFFVFHGGSGSSVNEFR .T
94	112	2	2098.02	4.1	1	63.5	26	95.00%	R.SIAPFFGVPVVMHSDHCAK.K	Carbamidomethyl (+57)	R.SIAPFFGVPVVMHSDHCAK.K
2	19	2	1823.05	3.8	0	65.3	16.3	95.00%	M.GILDIVPTGVITGDNVLK.L		-.MGILDIVPTGVITGDNVLK.L
99	112	2	1582.74	0.45	1	56.6	26.7	95.00%	F.FGVPVVMHSDHCAK.K	Carbamidomethyl (+57)	R.SIAPFFGVPVVMHSDHCAK.K
285	300	2	1825.89	3.9	1	73.6	25.6	95.00%	K.VNIDTDTQFAYVEGVR.D		K.VNIDTDTQFAYVEGVR.D
285	293	2	1051.48	0.65	1	30.3	25	95.00%	K.VNIDTDTQF.A		K.VNIDTDTQFAYVEGVR.D
294	302	2	1070.5	0.92	2	31.5	23.9	95.00%	F.AYVEGVRDY.V		K.VNIDTDTQFAYVEGVRDYVLK.Y
235	248	2	1564.88	4	1	58.4	17.8	95.00%	K.LQPALLGQHQAYVK.E		K.LQPALLGQHQAYVK.E
54	71	2	1844.94	0.85	1	86	24.4	95.00%	R.SPIILQTSNGGAHFFAGK.E	Deamidation (+1)	R.SPIILQTSNGGAHFFAGK.E
54	67	2	1441.72	-2.4	1	65.2	24.3	95.00%	R.SPIILQTSNGGAHF.F	Deamidation (+1)	R.SPIILQTSNGGAHFFAGK.E
131	149	3	2165.05	-0.23	1	41.3	25.6	95.00%	K.IHGEPLFSSHMLDLSEEPK.K		K.IHGEPLFSSHMLDLSEEPK.K
80	93	2	1399.76	5.1	1	89.1	21.2	95.00%	K.ASIAGSIAAAHYIR.S		K.ASIAGSIAAAHYIR.S
30	50	2	2026.11	0.78	0	91.9	19	95.00%	F.AIPAINVTSSSTAIAALEAAR.E		R.EHGFAIPAINVTSSSTAIAALEAAR .E
345	358	2	1597.83	4.2	1	60.4	23.4	95.00%	R.VLTALEDFYTVNTL.-		R.VLTALEDFYTVNTL.-

196	206	2	1420.66	1.5	1	35.7	25.9	95.00%	Y.TQPEDIWDVYR.E		K.IWIEMEIGITGGEEDGVDNSHVSHTELYTQPEDIWDVYR.E
131	150	4	2293.15	3.4	1	21.8	24.1	95.00%	K.IHGEPLFSSHMLDLSEEPKK.E		K.IHGEPLFSSHMLDLSEEPKK.E
310	325	2	1666.84	0.64	0	49.2	25.1	95.00%	Y.LMTPVGNPEGADKPNK.K		K.DYLMTPVGNPEGADKPNK.K
54	68	2	1588.78	-4.4	1	92.7	25.3	95.00%	R.SPIILQTSNGGAHFF.A	Deamidation (+1)	R.SPIILQTSNGGAHFFAGK.E
80	91	2	1130.57	-1.3	1	69.7	23.5	95.00%	K.ASIAGSIAAAHY.I		K.ASIAGSIAAAHYIR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
8	ADH4_SCHPO	59.72%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
76	87	2	1282.76	5.2	0	44.2	16	95.00%	K.NTLIVTDPGIIK.V		K.NTLIVTDPGIIK.V
366	374	2	1027.63	6.6	0	37.3	18.6	95.00%	R.ISQLVLEVK.I		R.ISQLVLEVK.I
305	316	2	1329.63	1.6	1	27.1	26.1	91.30%	Y.VHAMAHQLGGFY.G		R.DNMAYAEFLGGMAFNNASLGYVHAMAHQLGGFYGIPHGVCNAVLLAHVQK.F
386	398	2	1545.76	3.9	2	63.6	25.9	95.00%	K.EKDFDVLVDHAMK.D		K.EKDFDVLVDHAMK.D
169	191	2	2386.26	3.6	0	87.6	21.4	95.00%	K.SSKPQLPLIAINTTAGTASEMTR.F		K.SSKPQLPLIAINTTAGTASEMTR.F
192	200	2	1078.57	4	1	35.5	23.3	95.00%	R.FAIITEETR.H		R.FAIITEETR.H
160	191	3	3376.73	2.5	1	83.5	19.6	95.00%	K.IADYEGVDKSSKPQLPLIAINTTAGTASEMTR.F		K.IADYEGVDKSSKPQLPLIAINTTAGTASEMTR.F
96	129	3	3701.97	2.4	1	70.9	16.3	95.00%	K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVKK.E		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVKK.E
129	148	3	2121.88	-1.7	1	67.6	27.6	95.00%	K.KENCDSMVSIGGGSAHDCAK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.KENCDSMVSIGGGSAHDCAK.G
351	365	2	1707.77	1.1	0	77.3	26.8	95.00%	F.HLGCEEHTAEAALDR.I	Carbamidomethyl (+57)	R.LGDIAFHLGCEEHTAEAALDR.I
345	365	3	2324.09	3.1	1	49.5	26.7	95.00%	R.LGDIAFHLGCEEHTAEAALDR.I	Carbamidomethyl (+57)	R.LGDIAFHLGCEEHTAEAALDR.I
375	385	3	1245.76	3.9	0	37.6	10	95.00%	K.IRPHLVDLGVK.E		K.IRPHLVDLGVK.E
247	261	2	1516.76	1.3	0	69.8	24.6	95.00%	Y.VSTAANPITDACAVK.C	Carbamidomethyl (+57)	K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
149	159	2	1014.58	4.8	0	36.7	22.1	95.00%	K.GIALLATNGGK.I	Deamidation (+1)	K.GIALLATNGGK.I
210	224	2	1762.79	0.84	1	30.9	27.3	94.60%	K.HTMPILSVNDPETMY.G	Oxidation (+16)	K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
109	128	2	2077.08	1.3	0	67.6	22.5	95.00%	Y.DGVQPNPTVGNVNQGLEIVK.K		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K
399	415	2	1851.85	4.5	0	49.6	26.8	95.00%	K.DACGATNPIQPTHDEVK.A	Carbamidomethyl (+57)	K.DACGATNPIQPTHDEVK.A
96	128	3	3573.88	3.6	1	56.5	17.6	95.00%	K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K
130	148	2	1993.8	3.7	0	87.9	27.1	95.00%	K.ENCDSMVSIGGGSAHDCAK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.ENCDSMVSIGGGSAHDCAK.G
225	246	2	2185.07	0.31	1	54.4	25.9	95.00%	Y.GLPPSLTAATGMDALTHAVEAY.V		K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
160	168	2	1008.48	5	1	40.9	25.4	95.00%	K.IADYEGVDK.S		K.IADYEGVDK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
9	PDC2_SCHPO	48.32%	100%	29

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
204	214	2	1130.62	4.6	0	53.5	22.6	95.00%	K.ATDIAAELISK.K		K.ATDIAAELISK.K
516	525	2	1047.55	4.8	0	31.2	23.9	95.00%	K.TGEELTSAIK.V		K.TGEELTSAIK.V
228	237	2	949.49	5	1	30.2	24.5	95.00%	R.AAGAESAFVK.L		R.AAGAESAFVK.L
532	555	2	2764.22	0.74	1	74.3	27.2	95.00%	K.EGPTLIECAIDTDDCTQELVDWGK.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.EGPTLIECAIDTDDCTQELVDWGK.A
147	159	2	1436.71	3.9	0	60.9	25.7	95.00%	R.AEDAPVMIDHAIR.Q		R.AEDAPVMIDHAIR.Q
329	340	2	1425.76	4.3	1	95.2	22.6	95.00%	R.VYMAEFLELLAK.K		R.VYMAEFLELLAK.K
146	159	3	1592.82	5.1	1	58.6	24.9	95.00%	K.RAEDAPVMIDHAIR.Q		K.RAEDAPVMIDHAIR.Q
369	378	2	1157.64	5	1	28	22.1	94.10%	K.AALNRVEVMR.Q		K.AALNRVEVMR.Q

137	146	2	1101.64	5.4	1	51.2	19.8	95.00%	K.LTCAAVAIKR.A	Carbamidomethyl (+57)	K.LTCAAVAIKR.A
26	37	2	1429.72	4.2	1	38.3	24.3	95.00%	K.NHFVVPGDYNLR.L		K.NHFVVPGDYNLR.L
2	14	2	1402.63	-2.1	2	66.6	27	95.00%	M.TKDAESTMTVGTY.L		-.MTKDAESTMTVGTYLAQR.L
464	474	2	1310.81	4.6	1	66.2	13.2	95.00%	K.LPVLIFLLNNR.G		K.LPVLIFLLNNR.G
238	247	2	1078.51	-0.65	1	48.7	24.8	95.00%	K.LAEALNCAAF.I	Carbamidomethyl (+57)	K.LAEALNCAAFIMPAAK.G
450	461	2	1402.72	0.57	0	53	23.6	95.00%	F.QLTGQEISQMIR.H		R.TIVMVGDGSFQLTGQEISQMIR.H
216	225	3	1064.66	3.8	0	29.3	12	95.00%	K.EKPILLAGPK.L		K.EKPILLAGPK.L
80	94	2	1397.68	1.1	1	50.8	25.3	95.00%	Y.SVGALTAFDGIGGAY.A		R.SNGIACAVVTYSVGALTAFDGIGGAYAENLPVILVSGSPNTNDLSSGHLLHHTLGTHDFEYQMEIAK.K
136	146	3	1229.73	4.2	1	53.3	17.2	95.00%	K.KLTCAAVAIKR.A	Carbamidomethyl (+57)	K.KLTCAAVAIKR.A
160	203	4	4837.52	3.1	1	48.7	20.2	95.00%	R.QAILQHKPVYIEIPTNMANQPCPVPGPISAVISPEISDKESLEK.A	Carbamidomethyl (+57)	R.QAILQHKPVYIEIPTNMANQPCPVPGPISAVISPEISDKESLEK.A
440	461	2	2409.21	3.3	1	90.9	24	95.00%	R.TIVMVGDGSFQLTGQEISQMIR.H		R.TIVMVGDGSFQLTGQEISQMIR.H
238	253	2	1690.85	4.5	1	52.2	24.4	95.00%	K.LAEALNCAAFIMPAAK.G	Deamidation (+1)/ Carbamidomethyl (+57)	K.LAEALNCAAFIMPAAK.G
264	278	2	1599.74	0.49	1	82.7	27	95.00%	Y.AGVYWGEVSSSETTK.A		K.NYAGVYWGEVSSSETTK.A
204	215	2	1258.72	4.6	1	64.8	20.6	95.00%	K.ATDIAAELISKK.E		K.ATDIAAELISKK.E
19	25	2	770.49	4.3	0	34.4	16	95.00%	R.LVEIGIK.N		R.LVEIGIK.N
462	474	3	1575.97	4.8	2	29.2	7.78	95.00%	R.HKLPVLIFLLNNR.G		R.HKLPVLIFLLNNR.G
2	18	2	1870.92	4.3	2	129	25.4	95.00%	M.TKDAESTMTVGTYLAQR.L		-.MTKDAESTMTVGTYLAQR.L
392	405	2	1583.69	-3.4	1	68.9	26.3	95.00%	Y.AETGDSWFNGLQMK.L	Deamidation (+1)	R.QIQGLVDSNTTLYAETGDSWFNGLQMK.L
136	145	2	1073.63	3.9	1	39.6	17.2	95.00%	K.KLTCAAVAIK.R	Carbamidomethyl (+57)	K.KLTCAAVAIK.R
4	18	2	1641.77	4.2	1	65.2	26.2	95.00%	K.DAESTMTVGTYLAQR.L		K.DAESTMTVGTYLAQR.L
268	278	2	1209.55	0.9	1	56.5	25.4	95.00%	Y.WGEVSSSETTK.A		K.NYAGVYWGEVSSSETTK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
10	PMGY_SCHPO	68.25%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
122	139	2	1962.92	-0.12	1	81.3	27	95.00%	R.SYDIAPPNGESLKDTAER.V	Deamidation (+1)	R.SYDIAPPNGESLKDTAER.V
111	120	2	1271.65	5.7	1	79.8	23.6	95.00%	K.WGAEQVQIWR.R		K.WGAEQVQIWR.R
30	40	3	1157.63	0.86	1	24.5	22.9	93.30%	W.KDPALSETGIK.E		K.LNLFTGWKDPALSETGIK.E
70	90	2	2429.25	3.7	1	89.6	23.2	95.00%	K.TCQIILEEVGEPNLETIKSEK.L	Carbamidomethyl (+57)	K.TCQIILEEVGEPNLETIKSEK.L
27	40	2	1501.78	0.58	1	37	23.7	95.00%	F.TGWKDPALSETGIK.E		K.LNLFTGWKDPALSETGIK.E
146	157	2	1320.78	4.4	1	36.9	14.3	95.00%	K.STIVPHILKGEK.V		K.STIVPHILKGEK.V
2	14	2	1439.81	5.3	0	52	18.1	95.00%	M.TTEAAPNLLVLTR.H	Acetyl (+42)	-.MTTEAAPNLLVLTR.H
70	87	2	2085.08	4.2	0	96.7	23.3	95.00%	K.TCQIILEEVGEPNLETIK.S	Carbamidomethyl (+57)	K.TCQIILEEVGEPNLETIK.S
169	184	2	1714.91	-1.8	0	80.3	21.9	95.00%	R.ALIMDLEGLTGDQIVK.R		R.ALIMDLEGLTGDQIVK.R
169	185	2	1871.02	-0.11	1	120	20.3	95.00%	R.ALIMDLEGLTGDQIVKR.E		R.ALIMDLEGLTGDQIVKR.E
158	168	2	1149.67	4.5	0	26.5	16.4	92.10%	K.VLIAAHGNSLR.A		K.VLIAAHGNSLR.A
95	104	2	1169.58	4.8	1	46.4	24.2	95.00%	R.YYGDLQGLNK.D		R.YYGDLQGLNK.D
186	202	2	1854	4.1	1	68.2	20.9	95.00%	R.ELATGVPIVYHLDKDGK.Y		R.ELATGVPIVYHLDKDGK.Y
1	14	2	1528.84	4.4	0	53	21.9	95.00%	-.MTTEAAPNLLVLTR.H		-.MTTEAAPNLLVLTR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
11	GLYD_SCHPO	55.03%	100%	20

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
160	179	2	2305.06	-0.96	1	34.8	26.8	95.00%	R.VDPNTGLIDYDMLEHDAQLF.R		R.VDPNTGLIDYDMLEHDAQLFRPK.I
97	123	3	2996.43	3.4	1	55	25.2	95.00%	K.WGVNVQCLSGSPANMQVYQAIMPPHGR.L	Carbamidomethyl (+57)	K.WGVNVQCLSGSPANMQVYQAIMPPHGR.L
59	67	2	998.45	5.1	1	32.9	24.3	95.00%	K.YSEGYPGAR.Y		K.YSEGYPGAR.Y
277	302	3	2725.45	2.8	1	25.2	18.4	94.20%	K.INFSVFPGHQGGPHNHTITALAVALK.Q		K.INFSVFPGHQGGPHNHTITALAVALK.Q
124	139	2	1652.8	-0.062	1	37.9	25.9	95.00%	R.LMGLDLPSGGHLSHGY.Q		R.LMGLDLPSGGHLSHGYQTDTK.K

334	349	2	1669.84	3.9	0	85	24.1	95.00%	K.LAADGTDSHMVLVDVK.S		K.LAADGTDSHMVLVDVK.S
303	312	2	1314.55	-1.3	2	32.8	26.1	95.00%	K.QCQEPAYKEY.Q	Carbamidomethyl (+57)	K.QCQEPAYKEYQAQVVK.N
2	24	2	2616.28	-0.15	1	53.3	24.7	95.00%	M.SSNDSIMLTPLKEQDPTVAEIMR.H	Acetyl (+42)	-.MSSNDSIMLTPLKEQDPTVAEIMR.H
183	193	2	1209.62	4.5	1	57.8	24.1	95.00%	K.ILVAGTSAYCR.L	Carbamidomethyl (+57)	K.ILVAGTSAYCR.L
453	467	2	1734.83	4.4	2	41.4	26	95.00%	K.EVAEWASSFPLADKW.-		K.EVAEWASSFPLADKW.-
361	371	2	1254.76	4.6	0	48.8	16.3	95.00%	R.VLELINIVTNK.N		R.VLELINIVTNK.N
458	467	2	1120.55	-1.4	2	58.5	23.8	95.00%	W.ASSFPLADKW.-		K.EVAEWASSFPLADKW.-
74	85	2	1550.75	4.7	1	96.3	26	95.00%	K.FIDQIETLCQER.A	Carbamidomethyl (+57)	K.FIDQIETLCQER.A
86	96	2	1129.62	5.1	1	54.8	23.3	95.00%	R.ALAAFNLDPAK.W		R.ALAAFNLDPAK.W
413	422	2	1075.61	4.3	1	49.9	21.1	95.00%	R.ALTFAANLQK.E		R.ALTFAANLQK.E
438	452	2	1729.9	3.9	1	75.9	22.5	95.00%	K.LGEGEQYPELVQLQK.E		K.LGEGEQYPELVQLQK.E
46	58	2	1321.64	4.2	0	41.4	25.9	95.00%	R.AVMDALGSVMSNK.Y		R.AVMDALGSVMSNK.Y
160	182	3	2686.31	2.9	1	31.8	24.1	95.00%	R.VDPNTGLIDYDMLEHDAQLFRPK.I		R.VDPNTGLIDYDMLEHDAQLFRPK.I
436	452	2	1929.02	-1.7	2	64.2	22.8	95.00%	K.AKLGEGEQYPELVQLQK.E		K.AKLGEGEQYPELVQLQK.E
406	412	2	878.45	4.3	1	35.8	24	95.00%	R.VVDYIDR.A		R.VVDYIDR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
12	SAHH_SCHPO	49.19%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
20	35	2	1782.92	-1.8	0	73.9	23.8	95.00%	K.ELEIAENEMPGLIAVR.E		K.ELEIAENEMPGLIAVR.E
216	227	2	1117.62	4.3	1	46.5	22.5	95.00%	K.VAVVAGFGDVGK.G		K.VAVVAGFGDVGK.G
119	143	3	2681.36	2.8	1	63.5	22.9	95.00%	K.SFPSGKPLNMILDDGGDLTALVHER.H		K.SFPSGKPLNMILDDGGDLTALVHER.H
176	187	2	1255.68	4.6	0	42.1	21.2	95.00%	K.VPAINVNDSVTK.S		K.VPAINVNDSVTK.S
318	328	2	1281.71	3.7	0	30.2	20.1	95.00%	K.DVVNIKPQVDR.Y		K.DVVNIKPQVDR.Y
345	357	2	1371.66	2.3	1	40.2	24.8	95.00%	R.LVNLGCATGHPSF.V	Carbamidomethyl (+57)	R.LVNLGCATGHPSFVMSCSFTNQVLAQIALWTDNTSYPLGVHMLPK.K
407	427	2	2266.18	0.8	1	80.8	22.3	95.00%	K.LTTLTSVQSDYLGIPVDGPYK.A		K.LTTLTSVQSDYLGIPVDGPYK.A
314	328	3	1665.93	5.5	1	30.5	18.1	95.00%	K.ANAKDVVNIKPQVDR.Y		K.ANAKDVVNIKPQVDR.Y
8	18	2	1118.61	3.2	1	77.1	22.5	95.00%	K.VADISLAAFGR.K		K.VADISLAAFGR.K
269	280	2	1367.66	4	1	40.1	26.3	95.00%	K.EGQIFVTTTGCR.D	Carbamidomethyl (+57)	K.EGQIFVTTTGCR.D
153	167	2	1647.82	4.5	1	70.1	25.3	95.00%	R.GISEETTTGVHNLYK.M		R.GISEETTTGVHNLYK.M
19	35	2	1911.02	4.5	1	76.1	20.7	95.00%	R.KELEIAENEMPGLIAVR.E		R.KELEIAENEMPGLIAVR.E
336	344	2	1006.6	5	0	31.2	14.6	95.00%	R.HIILLADGR.L		R.HIILLADGR.L
174	187	3	1496.86	5	1	47.8	17.9	95.00%	K.LKVPAINVNDSVTK.S		K.LKVPAINVNDSVTK.S
103	118	2	2053.94	4.3	1	72.2	26.8	95.00%	K.GETEEEYLWCIEQQLK.S	Carbamidomethyl (+57)	K.GETEEEYLWCIEQQLK.S
240	268	3	3119.56	4.6	1	62	22.3	95.00%	R.VIVTEVDPINALQAAMDGFEVTTMEEAVK.E		R.VIVTEVDPINALQAAMDGFEVTTMEEAVK.E
314	329	3	1828.98	1.2	2	25.6	21.3	94.60%	K.ANAKDVVNIKPQVDRY.E		K.ANAKDVVNIKPQVDRYELK.N
318	332	3	1815	4.1	2	25.1	20	94.10%	K.DVVNIKPQVDRYELK.N		K.DVVNIKPQVDRYELK.N
318	329	3	1444.77	-1.4	2	25.1	23.1	94.10%	K.DVVNIKPQVDRY.E		K.DVVNIKPQVDRYELK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
13	TPIS_SCHPO	64.66%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
160	174	2	1615.9	-1.4	1	71.9	19.5	95.00%	K.IVIAYEPVWAIGTGK.T		K.IVIAYEPVWAIGTGK.T
175	189	2	1678.84	4.6	0	84.5	25.2	95.00%	K.TATPEQAQEVHAEIR.K		K.TATPEQAQEVHAEIR.K
135	145	2	1242.66	4.7	0	39.7	22.2	95.00%	R.EANETINVVVR.Q		R.EANETINVVVR.Q
175	190	2	1806.93	4.5	1	52	24	95.00%	K.TATPEQAQEVHAEIRK.W		K.TATPEQAQEVHAEIRK.W
75	98	3	2520.21	1.7	1	28.6	25.5	95.00%	Y.TGENSAQSLIDAGITYTLTGHSER.R		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R
71	90	2	2043.94	0.39	1	69	27.3	95.00%	K.NGAYTGENSAQSLIDAGITY.T		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R
206	218	2	1324.61	4.4	1	76.9	26.4	95.00%	R.VIYGGSVNGGNCK.E	Deamidation (+1)/ Carbamidomethyl (+57)	R.VIYGGSVNGGNCK.E

71	98	3	2925.39	4	1	98.2	24.9	95.00%	K.NGAYTGENSAQSLIDAGITYTLTGHSER.R		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R
58	70	2	1389.73	3.4	1	50	23.5	95.00%	K.DIGVGAQNVFDKK.N		K.DIGVGAQNVFDKK.N
115	134	3	2176.12	2.2	1	34.6	23.6	95.00%	K.FALEQGLTVVACIGETLAER.E	Carbamidomethyl (+57)	K.FALEQGLTVVACIGETLAER.E
32	52	2	2422.27	3.5	1	66.1	21.6	95.00%	K.LNVGDVETVIFPQNMYLITTR.Q		K.LNVGDVETVIFPQNMYLITTR.Q
146	159	2	1613.86	4.5	2	61.4	22.6	95.00%	R.QLNAIADKVQNWSK.I		R.QLNAIADKVQNWSK.I
196	205	2	971.55	5.3	0	76.1	21.5	95.00%	K.LGASVAEGLR.V		K.LGASVAEGLR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
14	THI3_SCHPO	45.09%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	127	2	1090.54	4.7	0	29.6	24	95.00%	K.IQLDDLCSK.F	Carbamidomethyl (+57)	K.IQLDDLCSK.F
74	95	2	2353.27	3.5	1	91.4	20.1	95.00%	R.GYPVTSFGSLLNEPFTGLITLK.G		R.GYPVTSFGSLLNEPFTGLITLK.G
316	327	2	1385.71	3.6	0	53.6	23.8	95.00%	K.QEAIAEIQDEIK.Q		K.QEAIAEIQDEIK.Q
222	238	2	1901.96	-0.26	2	29.1	25.3	95.00%	R.AIHSATLDMLKDPVQTY.K		R.AIHSATLDMLKDPVQTYK.E
128	139	2	1325.67	4.2	1	42.4	24.2	95.00%	K.FGLSPSDYTAIR.C		K.FGLSPSDYTAIR.C
316	329	2	1641.86	3.3	1	68.9	22.9	95.00%	K.QEAIAEIQDEIKQK.G		K.QEAIAEIQDEIKQK.G
63	71	2	954.54	4.5	0	51.1	16.2	95.00%	K.AMIHTLAAK.A		K.AMIHTLAAK.A
284	300	2	1992.94	1.9	2	33	26.5	95.00%	K.RLGIIPQDFEPNCTNGY.L	Carbamidomethyl (+57)	K.RLGIIPQDFEPNCTNGYLTWELDPDEK.D
222	239	2	2030.06	3.2	2	79.8	21.9	95.00%	R.AIHSATLDMLKDPVQTYK.E		R.AIHSATLDMLKDPVQTYK.E
110	118	2	968.5	4.9	1	27.7	22.7	93.70%	R.IGYVGEFGK.I		R.IGYVGEFGK.I
330	339	2	992.51	5.7	1	44.3	24.5	95.00%	K.GGVFSGNSLR.Y		K.GGVFSGNSLR.Y
89	95	2	744.47	0.11	0	41.8	11.1	95.00%	F.TGLITLK.G		R.GYPVTSFGSLLNEPFTGLITLK.G
304	327	3	2740.31	-0.33	1	44.1	25.5	95.00%	W.ELDPDEKDPMGKQEAIAEIQDEIK.Q		R.LGIIPQDFEPNCTNGYLTWELDPDEKDPMGKQEAIAEIQDEIK.Q
304	315	3	1372.62	0.94	1	26.5	27	93.40%	W.ELDPDEKDPMGK.Q		R.LGIIPQDFEPNCTNGYLTWELDPDEKDPMGK.Q
81	95	2	1601.9	0.42	1	85.5	18.5	95.00%	F.GSLLNEPFTGLITLK.G		R.GYPVTSFGSLLNEPFTGLITLK.G
33	56	2	2409.27	3	0	74.8	20.1	95.00%	R.EGIEVAILEPTNPSDVTALIGSGK.V		R.EGIEVAILEPTNPSDVTALIGSGK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
15	METK_SCHPO	63.35%	100%	20

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
308	318	2	1115.62	1.7	1	35.7	22	95.00%	Y.AIGVAEPLSIF.V		R.CLVQLSYAIGVAEPLSIFVNTYGTSSK.T
252	258	2	850.48	-0.6	2	34.3	18.6	95.00%	R.KIIVDTY.G		R.KIIVDTYGGWGAHGGGAFSGK.D
186	206	3	2311.19	3.8	1	67.9	23.5	95.00%	R.RVDTIVVSAQHADSISTEDLR.S		R.RVDTIVVSAQHADSISTEDLR.S
339	349	2	1256.73	4.3	1	36.5	19.9	95.00%	K.NFDLRPGVLVK.S		K.NFDLRPGVLVK.S
237	252	3	1557.82	-1.6	1	22.6	22.9	90.50%	R.FVVGGPQGDAGLTGRK.I		R.FVVGGPQGDAGLTGRK.I
127	146	3	2209.2	0.91	1	22.4	19.1	90.00%	F.GYATDETPEKLPLTILLAHK.L		K.ALEELGAGDQGIMFGYATDETPEKLPLTILLAHK.L
6	19	2	1501.7	-2.1	1	53.8	26.1	95.00%	F.LFTSESVGEGHPDK.I		-.MAQTFLFTSESVGEGHPDK.I
129	146	3	1989.12	2.1	1	32.2	16.3	95.00%	Y.ATDETPEKLPLTILLAHK.L		K.ALEELGAGDQGIMFGYATDETPEKLPLTILLAHK.L
169	185	2	1946.97	4.5	1	49.1	25.2	95.00%	K.TQVTIEYEEENGAVIPR.R		K.TQVTIEYEEENGAVIPR.R
147	155	2	931.5	4.5	0	58	23.1	95.00%	K.LNAAMSVAR.R		K.LNAAMSVAR.R
20	40	3	2423.15	4	2	37.1	26	95.00%	K.ICDQISDAILDACLKDDPFSK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.ICDQISDAILDACLKDDPFSK.V
113	126	2	1449.68	1.9	1	42.6	25.2	95.00%	K.ALEELGAGDQGIMF.G		K.ALEELGAGDQGIMFGYATDETPEK.L
237	251	2	1429.74	3.6	1	73.6	23.6	95.00%	R.FVVGGPQGDAGLTGR.K		R.FVVGGPQGDAGLTGR.K
90	112	3	2612.29	0.41	1	66.1	24.1	95.00%	K.TCNVLVAIEQQSPDIAQGLHYEK.A	Carbamidomethyl (+57)	K.TCNVLVAIEQQSPDIAQGLHYEK.A

328	338	2	1257.74	4.7	1	49.3	18.9	95.00%	K.TSAELVEIIRK.N		K.TSAELVEIIRK.N
365	374	2	1201.55	-1.6	1	28.4	26.2	93.10%	Y.GHFTDQSKPW.E		K.LQTPFYLSTASYGHFTDQSKPWEQPK.E
308	327	2	2053.08	5	1	69	22.2	95.00%	Y.AIGVAEPLSIFVNTYGTSSK.T		R.CLVQLSYAIGVAEPLSIFVNTYGTSSK.T
186	212	4	3010.56	2.5	1	34.2	20.5	95.00%	R.RVDTIVVSAQHADSISTEDLRSEILEK.I		R.RVDTIVVSAQHADSISTEDLRSEILEK.I
291	299	2	856.52	4.2	0	28.1	20.3	94.20%	K.SLVAAGLAR.R		K.SLVAAGLAR.R
213	226	3	1572.93	4.6	0	37.1	14.1	95.00%	K.IIKPTVPAHLLDEK.T		K.IIKPTVPAHLLDEK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
16	HSP72_SCHPO	44.20%	100%	24

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
327	340	2	1400.77	3.9	0	39.7	21.7	95.00%	K.ASVNEIVLVGGSTR.I		K.ASVNEIVLVGGSTR.I
96	105	2	1146.59	-1.9	1	30	23.5	95.00%	K.DGKPVLQVEY.K		K.DGKPVLQVEYK.G
170	181	2	1245.66	-1.1	1	38.4	22.9	95.00%	R.IINEPTAAAIAY.G		R.IINEPTAAAIAYGLDR.S
125	136	2	1324.65	4.5	2	66.6	25.3	95.00%	K.MRETAEAYLGGK.V		K.MRETAEAYLGGK.V
96	110	2	1689.9	5	1	31.8	22.8	95.00%	K.DGKPVLQVEYKGETK.T		K.DGKPVLQVEYKGETK.T
370	385	2	1516.77	-1.9	0	62.3	24.4	95.00%	Y.GAAVQAAVLTGDTSEK.T		K.SINPDEAVAYGAAVQAAVLTGDTSEK.T
448	457	3	1194.61	0.28	2	33.4	24.7	95.00%	R.TKDCNLLGKF.E	Carbamidomethyl (+57)	R.TKDCNLLGKFELSGIPPAPR.G
219	234	2	1647.72	4.3	1	72.5	27.2	95.00%	K.ATAGDTHLGGEDFDSR.L		K.ATAGDTHLGGEDFDSR.L
20	34	3	1699.82	-0.54	1	39.3	26	95.00%	F.SNNRVEIIANDQGNR.T	Deamidation (+1)	K.SIGIDLGTTYSCVGHFSNNRVEIIANDQGNR.T
324	340	2	1742.96	4.2	1	81.9	20.6	95.00%	K.VDKASVNEIVLVGGSTR.I		K.VDKASVNEIVLVGGSTR.I
457	467	2	1182.65	4.4	1	28.3	19.8	94.40%	K.FELSGIPPAPR.G		K.FELSGIPPAPR.G
35	47	2	1486.7	4.2	1	60.5	26.3	95.00%	R.TTPSYVAFTDTER.L		R.TTPSYVAFTDTER.L
608	647	3	3515.61	5.3	1	39.6	25.5	95.00%	K.IYQAGGAPGGMPGAAPGAAPGAAPGAAPGAAPGGDNGPEVEEVD.-	Oxidation (+16)	K.IYQAGGAPGGMPGAAPGAAPGAAPGAAPGAAPGGDNGPEVEEVD.-
610	647	3	3223.45	-0.039	0	29.8	26.1	95.00%	Y.QAGGAPGGMPGAAPGAAPGAAPGAAPGGDNGPEVEEVD.-		K.IYQAGGAPGGMPGAAPGAAPGAAPGAAPGAAPGGDNGPEVEEVD.-
111	124	2	1611.8	4	1	69	25.2	95.00%	K.TFTPEEISSMVLMK.M		K.TFTPEEISSMVLMK.M
594	607	2	1556.83	4.2	1	73.7	22.8	95.00%	K.QKELESVANPIMAK.I		K.QKELESVANPIMAK.I
538	548	2	1351.66	4.4	1	37.5	25.4	95.00%	K.NHLESYAYSLR.N		K.NHLESYAYSLR.N
137	153	2	1880.93	4	1	55	25.1	95.00%	K.VTDAVVTVPAYFNDSQR.Q		K.VTDAVVTVPAYFNDSQR.Q
76	86	2	1309.56	4.9	1	34.7	25.9	95.00%	K.FDDPEVQSDMK.H		K.FDDPEVQSDMK.H
516	523	2	939.44	-1.4	2	30.7	25.7	95.00%	R.MVAEAEKY.K		R.MVAEAEKYK.A
170	185	2	1686.9	4	1	94.1	22.1	95.00%	R.IINEPTAAAIAYGLDR.S		R.IINEPTAAAIAYGLDR.S
55	69	2	1698.82	4.2	1	74.8	25.6	95.00%	K.NQVAMNPHNTIFDAK.R		K.NQVAMNPHNTIFDAK.R
430	445	2	1786.88	-0.18	1	75.8	25.1	95.00%	Y.SDNQPGVLIQVFEGER.A		K.SEIFSTYSDNQPGVLIQVFEGER.A
24	34	2	1227.63	5.8	0	33.2	24.3	95.00%	R.VEIIANDQGNR.T		R.VEIIANDQGNR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
17	EF3_SCHPO	36.20%	100%	27

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
333	350	2	1970.01	4.8	0	86.5	23.5	95.00%	K.IPEVSTAANPEVCLETLK.A	Carbamidomethyl (+57)	K.IPEVSTAANPEVCLETLK.A
596	621	4	2935.49	3.5	1	34.9	21.6	95.00%	K.DVSSIIVSHDSGFLDHVVQAIIHYER.F		K.DVSSIIVSHDSGFLDHVVQAIIHYER.F
514	530	2	1948.1	1.6	1	26.2	14.1	91.50%	F.ILQDPAVPIKDRDEIVK.A		R.TVYVEHDIDESEADTPSVDFILQDPAVPIKDRDEIVK.A
920	933	2	1664.89	1.4	1	39.1	21.7	95.00%	W.LRPHVIVLDEPTNY.L		K.LVLAACTWLRPHVIVLDEPTNYLDR.D
75	92	2	1797.85	0.71	1	30.5	26.7	95.00%	K.GLEAVANHGSVAADVEPY.L		K.GLEAVANHGSVAADVEPYLVELLPAVIAK.V
719	738	3	2327.15	-2.2	1	22.8	25	90.80%	K.VLTGELLPTVGEIYQHENCR.I	Carbamidomethyl (+57)	K.VLTGELLPTVGEIYQHENCR.I
75	103	3	2944.6	3.2	1	47.9	17.2	95.00%	K.GLEAVANHGSVAADVEPYLVELLPAVIAK.V		K.GLEAVANHGSVAADVEPYLVELLPAVIAK.V

972	994	3	2346.07	0.65	1	55.6	27.2	95.00%	W.AVNNGHMTPSGHNWVSGQGSGPR.I		R.EFTEGLTEEVWAVNNGHMTPSGHNWVSGQGSGPR.I
20	34	2	1599.72	-1.6	0	80.8	27.4	95.00%	K.HLTVCDAAEEADAAK.A	Carbamidomethyl (+57)	K.HLTVCDAAEEADAAK.A
202	213	2	1359.69	4.1	0	43.2	24.4	95.00%	K.VCTLIANADIDR.F	Carbamidomethyl (+57)	K.VCTLIANADIDR.F
172	188	2	1928.99	-1.7	1	47	23.7	95.00%	Y.SLPQIIPVVSESMWDTK.A		K.MNSLQLLDVLVEVAPSQLSYSLPQIIPVVSESMWDTK.A
859	870	2	1330.7	4.7	1	35.3	23.3	95.00%	K.MVAEVDRAEALK.S		K.MVAEVDRAEALK.S
35	59	2	2604.32	3.9	1	66.4	23	95.00%	K.ALASFVNGPIEEQDAPSQVFSAISK.Q		K.ALASFVNGPIEEQDAPSQVFSAISK.Q
351	367	2	1809.03	4.2	1	72.9	16.3	95.00%	K.AVLGEIKVPTNEEVIAK.Y		K.AVLGEIKVPTNEEVIAK.Y
281	294	2	1550.88	4.1	1	60.5	18.1	95.00%	K.LVEDPQVVAPFLPK.L		K.LVEDPQVVAPFLPK.L
40	54	2	1628.77	-0.073	1	54.4	26.4	95.00%	F.VNGPIEEQDAPSQVF.S		K.ALASFVNGPIEEQDAPSQVFSAISK.Q
479	493	2	1636.88	3.9	1	73.9	22.1	95.00%	R.AIVNGQVEGFPTHLR.T		R.AIVNGQVEGFPTHLR.T
419	447	3	3168.34	2.9	1	77.1	26.5	95.00%	K.IPGGASHAEEEEEGEDLCNCEFSLAYGAK.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.IPGGASHAEEEEEGEDLCNCEFSLAYGAK.I
419	440	2	2477.96	0.98	1	65.1	26.6	95.00%	K.IPGGASHAEEEEEGEDLCNCEF.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.IPGGASHAEEEEEGEDLCNCEFSLAYGAK.I
133	147	2	1550.87	3.9	0	70.6	18.5	95.00%	K.AIVPSVLESIHTTGK.W		K.AIVPSVLESIHTTGK.W
766	777	2	1368.59	4	1	45.5	26.3	95.00%	R.FQSGEDLEAMDK.A		R.FQSGEDLEAMDK.A
881	900	3	2293.11	2.6	0	44.8	25.5	95.00%	K.EIEEHCSLLGLDAELVSHSR.I	Carbamidomethyl (+57)	K.EIEEHCSLLGLDAELVSHSR.I
494	513	2	2266.98	0.83	1	33	27.4	95.00%	R.TVYVEHDIDESEADTPSVDF.I		R.TVYVEHDIDESEADTPSVDFILQDPAVPIK.D
358	367	2	1098.6	4.8	0	47.3	20.5	95.00%	K.VPTNEEVIAK.Y		K.VPTNEEVIAK.Y
35	54	2	2118.03	0.18	1	56.3	26	95.00%	K.ALASFVNGPIEEQDAPSQVF.S		K.ALASFVNGPIEEQDAPSQVFSAISK.Q
880	900	3	2421.2	2	1	49.3	25.1	95.00%	R.KEIEEHCSLLGLDAELVSHSR.I	Carbamidomethyl (+57)	R.KEIEEHCSLLGLDAELVSHSR.I
325	350	3	2738.42	-0.023	1	56.6	21.5	95.00%	R.VGNVVDGKIPEVSTAANPEVCLETLK.A	Carbamidomethyl (+57)	R.VGNVVDGKIPEVSTAANPEVCLETLK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
18	A1EGU1_SCHPO	49.73%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
457	479	2	2580.33	2.4	1	74	22.4	95.00%	K.YVISQCNNALLYPALGVACVLSR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.YVISQCNNALLYPALGVACVLSR.C
408	433	3	2988.58	2.9	1	71.1	18.6	95.00%	K.HVERPIIFPISNPTTLMEAKPDQIDK.W		K.HVERPIIFPISNPTTLMEAKPDQIDK.W
44	57	2	1634.91	4.4	0	89.1	19.9	95.00%	R.LPPIVETLQQQVDR.C		R.LPPIVETLQQQVDR.C
120	137	3	2213.99	-2.5	1	29.6	27.3	95.00%	R.YPEGCYLDIDHNDLSYIK.Q	Carbamidomethyl (+57)	R.YPEGCYLDIDHNDLSYIK.Q
439	452	2	1418.83	4.1	0	43.8	15.2	95.00%	K.ALIATGSPLPPLNR.N		K.ALIATGSPLPPLNR.N
408	438	5	3561.84	2.8	2	46.8	19.2	95.00%	K.HVERPIIFPISNPTTLMEAKPDQIDKWSDGK.A		K.HVERPIIFPISNPTTLMEAKPDQIDKWSDGK.A
490	500	2	1070.58	4.5	0	54.7	21.4	95.00%	K.AASDALATVPR.S		K.AASDALATVPR.S
15	23	2	955.55	4.9	0	32.8	17.6	95.00%	K.GVTLLNSPR.Y		K.GVTLLNSPR.Y
456	479	3	2708.42	2.3	2	27.2	20.9	95.00%	K.KYVISQCNNALLYPALGVACVLSR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.KYVISQCNNALLYPALGVACVLSR.C
362	396	4	3654.89	2.7	1	43.8	18.7	95.00%	K.DSDFKEVPSGDINLESAIALVKPTILLGCSGQPGK.F	Carbamidomethyl (+57)	K.DSDFKEVPSGDINLESAIALVKPTILLGCSGQPGK.F
258	292	4	3747.95	3.3	1	51.5	18.5	95.00%	R.ILDHYRPDIACFNDDIQGTGAVALAAIIGALHVTK.S	Carbamidomethyl (+57)	R.ILDHYRPDIACFNDDIQGTGAVALAAIIGALHVTK.S
501	517	2	1828.93	-2.2	1	44.7	24.3	95.00%	R.SLFAADEALLPDLNNAR.E		R.SLFAADEALLPDLNNAR.E
367	396	3	3062.64	3.1	0	30.5	16.6	95.00%	K.EVPSGDINLESAIALVKPTILLGCSGQPGK.F	Carbamidomethyl (+57)	K.EVPSGDINLESAIALVKPTILLGCSGQPGK.F
530	547	2	1889.9	-1.9	1	76.9	26.2	95.00%	K.QAVSEGMSTVDLPKDDAK.L		K.QAVSEGMSTVDLPKDDAK.L
548	555	2	1085.63	3.7	2	31.8	20.6	95.00%	K.LKEWIIER.E		K.LKEWIIER.E
332	339	2	964.49	5	1	34.3	23.5	95.00%	R.GNLFMIDR.C		R.GNLFMIDR.C
245	256	2	1360.68	-0.027	1	30.6	24.7	95.00%	F.IHFEDFGLANAK.R		R.EVFPEAFIHFEDFGLANAK.R
178	191	2	1553.75	3.5	0	59.3	26.2	95.00%	K.GHLMTLCAGLDPNR.F	Carbamidomethyl (+57)	K.GHLMTLCAGLDPNR.F
222	234	2	1526.73	2.5	1	68.3	26.6	95.00%	R.GEQYDSFLDNVIK.A		R.GEQYDSFLDNVIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
19	HSP90_SCHPO	34.38%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
522	533	2	1405.62	4.2	0	49.6	26.5	95.00%	K.DGLELEETDEEK.A		K.DGLELEETDEEK.A
275	287	2	1499.68	-1.8	2	52	26.9	95.00%	R.NPSEVTKEEYASF.Y		R.NPSEVTKEEYASFYK.S
465	474	2	1170.6	4.5	1	29.7	22.9	95.00%	K.NIYFITGESK.Q		K.NIYFITGESK.Q
567	587	2	2339.12	5.7	1	92.3	26.3	95.00%	K.IVGSPCLLTTGQYGWSANMER.I	Carbamidomethyl (+57)	K.IVGSPCLLTTGQYGWSANMER.I
440	458	2	2199.07	3.1	1	92.7	26.3	95.00%	R.YNSLNSPDDLISLEDYITK.M		R.YNSLNSPDDLISLEDYITK.M
596	606	2	1234.5	4.9	1	67.2	25.9	95.00%	R.DTSMSAYMSSR.K		R.DTSMSAYMSSR.K
362	375	2	1512.78	3.1	0	77.4	23.1	95.00%	K.GVVDSEDLPLNLSR.E		K.GVVDSEDLPLNLSR.E
516	536	3	2372.21	2.8	1	83.5	23.3	95.00%	K.LVNITKDGLELEETDEEKAAR.E		K.LVNITKDGLELEETDEEKAAR.E
198	212	2	1787.96	4.4	1	31.7	22.1	95.00%	K.HSEFISYPIQLVVTR.E		K.HSEFISYPIQLVVTR.E
522	536	2	1703.78	-1.5	1	76.8	27.3	95.00%	K.DGLELEETDEEKAAR.E		K.DGLELEETDEEKAAR.E
290	302	2	1526.74	4	1	75.7	26.1	95.00%	K.SLTNDWEDHLAVK.H		K.SLTNDWEDHLAVK.H
580	587	2	949.41	-0.76	1	29.5	23.5	95.00%	Y.GWSANMER.I		K.IVGSPCLLTTGQYGWSANMER.I
475	487	2	1548.8	4.5	1	76.3	24	95.00%	K.QAVENSPFLEIFR.A		K.QAVENSPFLEIFR.A
88	99	2	1282.73	5.3	0	55.5	17.7	95.00%	K.NDLINNLGVIAK.S		K.NDLINNLGVIAK.S
34	45	2	1274.64	4	0	41.6	24.4	95.00%	R.ELISNASDALDK.I		R.ELISNASDALDK.I
255	267	2	1520.76	4.6	1	46.2	25	95.00%	K.VKETTTETEELNK.T		K.VKETTTETEELNK.T
321	330	2	1176.6	4.2	2	27.8	24.2	93.80%	R.RAPMDLFEAK.R		R.RAPMDLFEAK.R
422	436	2	1574.85	-1.2	0	38.9	21.9	95.00%	K.LGIHEDAANRPALAK.L		K.LGIHEDAANRPALAK.L
48	64	2	1947.92	-0.32	2	28.4	26.1	93.20%	R.YQSLSDPHALDAEKDLF.I		R.YQSLSDPHALDAEKDLFIR.I
34	47	2	1543.83	3.9	1	76.1	22.7	95.00%	R.ELISNASDALDKIR.Y		R.ELISNASDALDKIR.Y
504	514	2	1248.67	0.54	2	26.5	22.6	92.00%	Y.AVTQLKEFEGK.K		K.FDVLFMVDPIDEYAVTQLKEFEGK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
20	THI2_SCHPO	40.85%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
175	187	2	1431.79	-2.3	1	77.2	20.4	95.00%	K.LFNATAVEDLIVK.E		K.LFNATAVEDLIVK.E
309	320	2	1332.68	5.8	1	60	24.4	95.00%	K.AAQEALAIFDER.K		K.AAQEALAIFDER.K
137	154	2	2037	0.49	1	64.8	26	95.00%	F.LNEIGVPYEDEGDYVVVK.H		R.KPADLFLNEIGVPYEDEGDYVVVK.H
39	49	2	1291.56	-1.1	1	60.2	26.2	95.00%	K.AYPTYSLDESF.S		K.AYPTYSLDESFSFAPIR.E
2	15	2	1400.77	3.8	1	74.5	21.2	95.00%	M.APATAVVTPQTAFK.T		-.MAPATAVVTPQTAFK.T
244	263	3	2296.15	3.2	0	39.6	24.6	95.00%	R.LASAQLVSNLHDMRPLDMNR.A	Oxidation (+16)	R.LASAQLVSNLHDMRPLDMNR.A
175	190	3	1745.96	4.6	1	37.2	20.4	95.00%	K.LFNATAVEDLIVKEGK.D		K.LFNATAVEDLIVKEGK.D
309	321	2	1460.77	4.2	1	58.6	22.9	95.00%	K.AAQEALAIFDERK.A		K.AAQEALAIFDERK.A
244	270	3	3048.6	3.6	1	30.2	18.5	95.00%	R.LASAQLVSNLHDMRPLDMNRAEDLIVK.G		R.LASAQLVSNLHDMRPLDMNRAEDLIVK.G
295	308	2	1459.67	4	1	71.7	26.5	95.00%	R.MGPTFGGMMFSGIK.A		R.MGPTFGGMMFSGIK.A
177	187	2	1171.64	-1.6	0	27.7	20.9	93.70%	F.NATAVEDLIVK.E		K.LFNATAVEDLIVK.E
274	294	2	2254.05	3.3	1	79.8	26.7	95.00%	R.EVFPGMIVGGMELSEFDGANR.M		R.EVFPGMIVGGMELSEFDGANR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
21	6PGD_SCHPO	59.15%	100%	23

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
188	209	3	2659.19	3.5	1	32.6	26.8	95.00%	K.MVHNGIEYGDMQLICETYDIMK.R	Carbamidomethyl (+57)	K.MVHNGIEYGDMQLICETYDIMK.R
156	166	3	1228.76	4.8	1	32.1	12.3	95.00%	R.IKPIFQTLAAK.A		R.IKPIFQTLAAK.A
167	185	2	2119.81	-1.9	1	68.3	26.7	95.00%	K.AGNNEPCCDWVGEQGAGHY.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.AGNNEPCCDWVGEQGAGHYVK.M
98	115	3	1971.95	5.1	1	35.5	26.1	95.00%	K.GDIIVDGGNSHYPDTTRR.C		K.GDIIVDGGNSHYPDTTRR.C
54	67	2	1501.78	4.1	1	57.5	23.7	95.00%	K.SIVGAHSLEEFVSK.L		K.SIVGAHSLEEFVSK.L

188	205	2	2171.93	0.29	1	76	27.6	95.00%	K.MVHNGIEYGDMQLICETY.D	Carbamidomethyl (+57)	K.MVHNGIEYGDMQLICETYDIMK.R
98	114	2	1815.85	4.4	1	91.7	26.6	95.00%	K.GDIIVDGGNSHYPDTTR.R		K.GDIIVDGGNSHYPDTTR.R
29	37	2	1175.49	3.9	1	36.7	26.2	95.00%	K.GFTVCCYNR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GFTVCCYNR.T
122	139	3	1718.9	4.5	2	31	23.4	95.00%	K.KGILFVGSGVSGGEEGAR.Y		K.KGILFVGSGVSGGEEGAR.Y
38	51	2	1579.79	4.7	2	35.6	25.6	95.00%	R.TTSRVDEFLANEAK.G		R.TTSRVDEFLANEAK.G
479	492	2	1363.6	-1.7	1	28.5	26.2	93.10%	W.TGHGGNISATTYDA.-		K.DIHINWTGHGGNISATTYDA.-
42	51	2	1134.56	4.5	1	47.7	24.7	95.00%	R.VDEFLANEAK.G		R.VDEFLANEAK.G
377	393	2	2007.98	0.13	2	33.5	26.4	95.00%	K.DITEAFREDPNLESILF.H		K.DITEAFREDPNLESILFHPFFTNGVEK.A
123	139	2	1590.81	3.9	1	62.7	24.1	95.00%	K.GILFVGSGVSGGEEGAR.Y		K.GILFVGSGVSGGEEGAR.Y
80	114	4	3722.92	-0.045	2	48.8	18.8	95.00%	K.AGKPVDYLIEGLAPLLEKGDIIVDGGNSHYPDTTR.R		K.AGKPVDYLIEGLAPLLEKGDIIVDGGNSHYPDTTR.R
211	225	2	1669.74	4.6	1	69.2	26.9	95.00%	R.GLGMSCDEIADVFEK.W	Carbamidomethyl (+57)	R.GLGMSCDEIADVFEK.W
140	155	2	1669.81	4.7	1	28.8	25.5	94.30%	R.YGPSLMPGGNPAAWPR.I		R.YGPSLMPGGNPAAWPR.I
269	291	2	2504.28	3.2	1	92.8	23.3	95.00%	K.WTAQNALEMGTPVSLITEAVFAR.C		K.WTAQNALEMGTPVSLITEAVFAR.C
320	333	2	1592.8	4.1	1	67.9	25	95.00%	K.QLIDDLEDALYASK.I		K.QLIDDLEDALYASK.I
437	449	2	1379.79	4.1	0	52	17.2	95.00%	R.SAVLPANLLQAQR.D		R.SAVLPANLLQAQR.D
80	97	2	1925.09	0.14	1	64.7	17.5	95.00%	K.AGKPVDYLIEGLAPLLEK.G		K.AGKPVDYLIEGLAPLLEK.G
467	478	2	1407.72	0.84	2	25.9	24.9	90.90%	K.SLPADKDIHINW.T		K.SLPADKDIHINWTGHGGNISATTYDA.-
5	28	2	2457.3	3	1	76	20.5	95.00%	K.EVADFGLIGLAVMGQNLILNGADK.G		K.EVADFGLIGLAVMGQNLILNGADK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
22	ILV5_SCHPO	34.90%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
84	104	2	2141.07	4.6	1	90.4	24.7	95.00%	K.NDTLAIIGYGSQGHGQGLNAR.D		K.NDTLAIIGYGSQGHGQGLNAR.D
330	337	2	914.47	6	1	41.2	21.8	95.00%	R.GAIDWTPR.F		R.GAIDWTPR.F
287	313	3	2972.45	-0.34	2	40.3	24.2	95.00%	R.ERGHSPAEAFNETVEEATQSLYPLIGK.Y		R.ERGHSPAEAFNETVEEATQSLYPLIGK.Y
145	163	2	2074.05	4.2	1	75.2	24.7	95.00%	K.GSIIMNLLSDAAQTETWPK.I		K.GSIIMNLLSDAAQTETWPK.I
345	361	2	1975.97	4.3	1	90.3	25.7	95.00%	K.VLNELYDNVENGNEAKR.S		K.VLNELYDNVENGNEAKR.S
373	383	2	1435.72	-2	1	46.8	25.3	95.00%	R.ELYDKELEEIR.N		R.ELYDKELEEIR.N
123	133	2	1198.6	4.3	1	28.6	23.3	94.80%	K.QAIEDGWVPGK.T		K.QAIEDGWVPGK.T
144	163	2	2202.15	4.4	2	56.2	22.3	95.00%	K.KGSIIMNLLSDAAQTETWPK.I		K.KGSIIMNLLSDAAQTETWPK.I
362	372	2	1312.61	4.6	1	61.6	25.5	95.00%	R.SLEYNSAPNYR.E		R.SLEYNSAPNYR.E
289	313	2	2687.32	3.5	1	76.3	24.3	95.00%	R.GHSPAEAFNETVEEATQSLYPLIGK.Y		R.GHSPAEAFNETVEEATQSLYPLIGK.Y
190	204	2	1639.97	3.6	1	26.8	14.8	92.40%	K.IHPPKDVDVILVAPK.G		K.IHPPKDVDVILVAPK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
23	K6PF_SCHPO	33.33%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
364	380	3	1831.87	-1.7	0	52.5	26.5	95.00%	R.ICEAVDSISSTAISHSR.A	Carbamidomethyl (+57)	R.ICEAVDSISSTAISHSR.A
822	839	4	2058.08	3.2	1	52.7	21.6	95.00%	K.VYTTEVIGNIISEEAHKR.F		K.VYTTEVIGNIISEEAHKR.F
419	431	2	1592.73	4.2	1	27.5	26.3	91.50%	K.WQDELCNSLSSVR.K	Carbamidomethyl (+57)	K.WQDELCNSLSSVR.K
586	603	3	1720.91	4.2	0	35.8	22.6	95.00%	R.VAIIHVGAPAGGMNSATR.A		R.VAIIHVGAPAGGMNSATR.A
534	545	2	1352.73	-1.6	1	42.1	21.2	95.00%	K.LTHEVADAIEKK.Q		K.LTHEVADAIEKK.Q
880	896	2	1696.87	-0.9	0	78	23.5	95.00%	R.ANDLGNDPSSAVVIGIR.G		R.ANDLGNDPSSAVVIGIR.G
903	918	2	1837.8	-1.3	0	97.7	26.9	95.00%	F.SSVADVENNETEIEMR.R	Oxidation (+16)	R.GTGVSFSSVADVENNETEIEMR.R
927	938	2	1323.7	4.7	0	53.3	22.2	95.00%	R.DMHNLVNILAGK.T		R.DMHNLVNILAGK.T
77	94	2	1954.97	4.6	1	62	24.9	95.00%	R.LVPGELSLSPAAEDSEWR.G		R.LVPGELSLSPAAEDSEWR.G
50	74	3	2845.31	0.19	2	38.3	26.2	95.00%	R.VCNESLREDWMHVAGNNSAESVTIK.F	Carbamidomethyl (+57)	R.VCNESLREDWMHVAGNNSAESVTIK.F

613	628	3	1700.87	4.5	1	49.7	23.9	95.00%	R.GHTPLAIDNGFSGFLR.H		R.GHTPLAIDNGFSGFLR.H
283	308	2	2620.33	3.9	1	86.3	23.1	95.00%	K.NLISAGIDSIIVCGGDGSLTGADIFR.S	Carbamidomethyl (+57)	K.NLISAGIDSIIVCGGDGSLTGADIFR.S
160	183	3	2416.24	3.9	1	44	22.9	95.00%	K.SEESGAASNLESGLATPVVETLKK.A		K.SEESGAASNLESGLATPVVETLKK.A
798	806	2	934.49	4	1	31.5	23.8	95.00%	K.ATFALEAGR.N		K.ATFALEAGR.N
438	460	2	2448.28	3.4	0	60.2	21.5	95.00%	K.SIVIVAEGAIDSELNHISPEDIK.N		K.SIVIVAEGAIDSELNHISPEDIK.N
254	267	2	1400.75	3.4	1	49.7	22.8	95.00%	R.GWLAEGGTLIGTAR.C		R.GWLAEGGTLIGTAR.C
844	861	2	1860.9	4.7	0	42.3	25.9	95.00%	R.TAVPGHVQQGGNPTPMDR.A		R.TAVPGHVQQGGNPTPMDR.A
197	214	2	1760.86	4.1	0	84.8	25	95.00%	K.IAVMTSGGDSPGMNAVVR.A		K.IAVMTSGGDSPGMNAVVR.A
822	838	2	1901.97	-1.5	1	68.7	24.5	95.00%	K.VYTTEVIGNIISEEAHK.R		K.VYTTEVIGNIISEEAHK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
24	EF2_SCHPO	27.55%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
565	578	2	1451.69	4.3	0	44.5	26.5	95.00%	R.ESVSEPSSMTALSK.S		R.ESVSEPSSMTALSK.S
353	370	2	2024.89	3.6	1	81.7	27.6	95.00%	R.AETLYEGPMDDECAVGIR.N	Carbamidomethyl (+57)	R.AETLYEGPMDDECAVGIR.N
371	384	2	1594.76	4.1	1	55	26.1	95.00%	R.NCDANAPLMIYVSK.M	Carbamidomethyl (+57)	R.NCDANAPLMIYVSK.M
327	346	2	2192.18	2.4	1	55.9	20.7	95.00%	K.FLPAADALMEMIVLHLPSPK.T		K.FLPAADALMEMIVLHLPSPK.T
442	465	2	2595.37	4.3	1	74.7	18.9	95.00%	R.IEPIEDCPAGNIIGLVGVDQFLVK.S	Carbamidomethyl (+57)	R.IEPIEDCPAGNIIGLVGVDQFLVK.S
466	479	2	1474.71	3.7	0	72.8	25.6	95.00%	K.SGTLTTSEVAHNMK.V		K.SGTLTTSEVAHNMK.V
633	651	2	2107.01	3.2	1	108	25.8	95.00%	K.IWCFGPDTTGANVVVDQTK.A	Carbamidomethyl (+57)	K.IWCFGPDTTGANVVVDQTK.A
284	292	2	1051.52	4.5	1	27.5	24.3	93.50%	R.IFDAVMNSR.K		R.IFDAVMNSR.K
293	302	2	1178.66	4.6	2	62.3	20.3	95.00%	R.KDEVFTLLSK.L		R.KDEVFTLLSK.L
151	162	3	1392.86	-0.64	1	46.9	10	95.00%	R.IRPVVVVNKVDR.A		R.IRPVVVVNKVDR.A
544	555	2	1334.69	3.5	0	47.4	24.4	95.00%	K.DLQEDHAGIPLK.I		K.DLQEDHAGIPLK.I
827	838	2	1426.66	-2	2	27	26.6	90.00%	K.GLKENVPDYTEY.Y		K.GLKENVPDYTEYYDR.L
303	317	3	1726.94	3.8	1	43.5	20.8	95.00%	K.LEVTIKPDEKELEGK.A		K.LEVTIKPDEKELEGK.A
326	346	3	2320.27	0.51	2	29.8	17.9	95.00%	R.KFLPAADALMEMIVLHLPSPK.T		R.KFLPAADALMEMIVLHLPSPK.T
635	651	2	1807.84	-1.3	1	72.7	26.7	95.00%	W.CFGPDTTGANVVVDQTK.A	Carbamidomethyl (+57)	K.IWCFGPDTTGANVVVDQTK.A
586	609	3	2657.29	0.79	1	41.9	25.2	95.00%	R.IFMTAEPMSEELSVAIETGHVNPR.D		R.IFMTAEPMSEELSVAIETGHVNPR.D
618	631	2	1624.72	-1.3	1	46.8	26.9	95.00%	R.IMADEFGWDVTDAR.K		R.IMADEFGWDVTDAR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
25	TSA1_SCHPO	61.98%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	132	2	901.53	4.7	1	35.7	21.9	95.00%	R.GLFLIDPK.G		R.GLFLIDPK.G
155	173	2	2260.03	0.62	1	44.7	27.1	95.00%	R.LLDAFQFVEEHGEVCPANW.H	Carbamidomethyl (+57)	R.LLDAFQFVEEHGEVCPANWHK.G
89	107	2	1915.06	3.5	1	58	19.5	95.00%	R.KEGGLGGINIPLLADPSHK.V		R.KEGGLGGINIPLLADPSHK.V
66	88	2	2576.29	0.89	1	97.3	23.8	95.00%	R.NAQVILTSTDSEYSHLAFINTPR.K		R.NAQVILTSTDSEYSHLAFINTPR.K
111	124	2	1523.77	4.1	1	79.7	25.1	95.00%	R.DYGVLIEDAGVAFR.G		R.DYGVLIEDAGVAFR.G
66	83	2	1994.96	-0.052	1	63.9	25.9	95.00%	R.NAQVILTSTDSEYSHLAF.I		R.NAQVILTSTDSEYSHLAFINTPR.K
2	13	2	1341.74	4.1	1	36.9	21.1	95.00%	M.SLQIGKPAPDFK.G	Acetyl (+42)	-.MSLQIGKPAPDFK.G
137	147	2	1224.69	4.4	0	43.5	18.2	95.00%	R.QITINDLPVGR.S		R.QITINDLPVGR.S
14	26	2	1333.69	3.6	1	40.1	24.2	95.00%	K.GTAVVNGAFEEIK.L		K.GTAVVNGAFEEIK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
26	HSP75_SCHPO	36.05%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	173	2	1168.66	5	0	34.3	19.3	95.00%	K.DAGAIAGLNVLR.I		K.DAGAIAGLNVLR.I
501	517	3	1779.92	5.5	0	60.6	23.6	95.00%	R.SAHIEITNSVGHLSSTK.I		R.SAHIEITNSVGHLSSTK.I
174	185	2	1245.66	-1.1	1	38.4	22.9	95.00%	R.IINEPTAAAIAY.G		R.IINEPTAAAIAYGLDAK.S
331	344	2	1437.76	3.8	0	34.4	22.8	95.00%	K.ADVHDIVLVGGSTR.I		K.ADVHDIVLVGGSTR.I
115	128	2	1565.81	1.4	1	60	23.6	95.00%	K.QFTAQEISAMVLTK.M		K.QFTAQEISAMVLTK.M

39	51	2	1484.72	4.2	1	50.9	25.7	95.00%	R.TTPSFVAFTETER.L		R.TTPSFVAFTETER.L
96	113	2	1987.03	4.2	1	58.5	22.3	95.00%	K.VIDNNGIPTIEVNYLGEK.K		K.VIDNNGIPTIEVNYLGEK.K
430	450	2	2374.16	5.6	1	61.9	25.4	95.00%	R.TFTTVADNQTTVTFPVYQGER.V		R.TFTTVADNQTTVTFPVYQGER.V
451	472	2	2468.2	5.8	1	62.2	26.3	95.00%	R.VNCAENEPLGEFQLTGIPPMPR.G	Carbamidomethyl (+57)	R.VNCAENEPLGEFQLTGIPPMPR.G
144	157	2	1552.8	4.6	1	33.7	24.1	95.00%	K.AVITVPAYFSDSQR.A		K.AVITVPAYFSDSQR.A
543	564	2	2513.21	3.3	1	64.4	25.7	95.00%	K.SQLESYISNIETTISEPNVMMK.L		K.SQLESYISNIETTISEPNVMMK.L
174	190	2	1729.93	3.9	1	82.9	21.3	95.00%	R.IINEPTAAAIAYGLDAK.S		R.IINEPTAAAIAYGLDAK.S
114	128	2	1693.91	3.7	2	42.8	20.6	95.00%	K.KQFTAQEISAMVLTK.M		K.KQFTAQEISAMVLTK.M
571	595	3	2864.36	3.4	1	74	25.7	95.00%	K.SKIEAQLAECMSQLELEDTNTDALR.K	Carbamidomethyl (+57)	K.SKIEAQLAECMSQLELEDTNTDALR.K
518	528	2	1336.63	0.28	2	30.4	25.5	95.00%	K.IQEMIENADKF.K		K.IQEMIENADKFK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
27	ACT_SCHPO	51.47%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
292	312	2	2216.04	5	1	63.1	26.9	95.00%	K.DLYGNVVMSGGTTMYPGIADR.M		K.DLYGNVVMSGGTTMYPGIADR.M
257	279	2	2398.18	-0.51	1	64.6	24.8	95.00%	R.APEALFQPSALGLENAGIHEATY.N		R.APEALFQPSALGLENAGIHEATYNSIMK.C
96	113	2	2014.03	3.9	0	59.4	23.7	95.00%	R.VAPEEHPCLLTEAPLNPK.S	Carbamidomethyl (+57)	R.VAPEEHPCLLTEAPLNPK.S
69	84	2	1958.88	-2	1	66.1	27.3	95.00%	K.YPIEHGIVNNWDDMEK.I		K.YPIEHGIVNNWDDMEK.I
197	206	2	1131.53	5.1	1	41.4	25.6	95.00%	R.GYTFSTTAER.E		R.GYTFSTTAER.E
148	169	2	2293.11	0.74	1	55.6	25.2	95.00%	R.TTGIVLDSGDGVTHTVPIYEGY.A		R.TTGIVLDSGDGVTHTVPIYEGYALPHAIMR.L
216	238	2	2629.26	0.43	1	107	25.8	95.00%	K.LCYVALDFEQELQTAAQSSSLEK.S	Carbamidomethyl (+57)	K.LCYVALDFEQELQTAAQSSSLEK.S
257	284	3	2971.48	3	1	43.9	22.9	95.00%	R.APEALFQPSALGLENAGIHEATYNSIMK.C		R.APEALFQPSALGLENAGIHEATYNSIMK.C
219	238	2	2193.08	0.54	1	99.4	25.1	95.00%	Y.VALDFEQELQTAAQSSSLEK.S		K.LCYVALDFEQELQTAAQSSSLEK.S
1	18	2	2007.9	4	0	79.9	27.5	95.00%	-.MEEEIAALVIDNGSGMCK.A	Acetyl (+42)/ Carbamidomethyl (+57)	-.MEEEIAALVIDNGSGMCK.A
239	254	2	1789.89	5.1	1	75.2	25.3	95.00%	K.SYELPDGQVITIGNER.F		K.SYELPDGQVITIGNER.F
148	177	3	3182.62	3.4	1	67.2	20.8	95.00%	R.TTGIVLDSGDGVTHTVPIYEGYALPHAIMR.L		R.TTGIVLDSGDGVTHTVPIYEGYALPHAIMR.L
360	372	2	1511.7	3.8	1	34.6	26.6	95.00%	K.QEYDESGPGIVYR.K		K.QEYDESGPGIVYR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
28	SERA_SCHPO	34.12%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
410	421	2	1468.77	4	1	31.9	22.6	95.00%	R.QVNELFIDHNIK.S		R.QVNELFIDHNIK.S
355	366	2	1300.7	1.6	0	48.6	22.1	95.00%	Y.NIGIEVSEALTR.Y		K.NIILTPHIGGSTEEAQYNIGIEVSEALTR.Y
302	319	2	1729.85	-3.3	1	59.1	24.9	95.00%	K.IAGAAIDVYPSEPAGNGK.D	Deamidation (+1)	K.IAGAAIDVYPSEPAGNGK.D
248	262	2	1596.82	4.1	1	50.8	23.4	95.00%	R.ADFVSLHVPASPETK.N		R.ADFVSLHVPASPETK.N
142	154	2	1394.7	4.8	1	57.8	24.8	95.00%	R.GIAVFNSPYANSR.S		R.GIAVFNSPYANSR.S
434	452	2	2053.02	0.059	0	63.7	25.8	95.00%	Y.LVADISDCTPGSLEALHQK.L	Carbamidomethyl (+57)	R.GDIAYLVADISDCTPGSLEALHQK.L
275	284	2	1108.56	4.3	1	25.6	24.5	90.40%	K.EGSYLINASR.G		K.EGSYLINASR.G
367	385	2	2078.05	3.9	1	76.6	23.9	95.00%	R.YINEGNSIGAVNFPEVSLR.S		R.YINEGNSIGAVNFPEVSLR.S
338	354	2	1841.92	0.05	1	49	25.5	95.00%	K.NIILTPHIGGSTEEAQY.N		K.NIILTPHIGGSTEEAQYNIGIEVSEALTR.Y
47	57	3	1247.68	3.8	1	25.6	22	94.70%	R.TLKPFASEDIK.I		R.TLKPFASEDIK.I
302	321	3	1972.97	-2.3	1	49.3	25.8	95.00%	K.IAGAAIDVYPSEPAGNGKDK.F	Deamidation (+1)	K.IAGAAIDVYPSEPAGNGKDK.F
237	247	3	1291.72	-2.2	0	35.1	20	95.00%	K.QLSSLPELLHR.A		K.QLSSLPELLHR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
29	PUR9_SCHPO	43.08%	100%	15									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
76	91	2	1843.9	-1.7	1	42.6	25.6	95.00%	R.DIPSDEKDLVEQSIEK.I		R.DIPSDEKDLVEQSIEK.I		
328	347	2	2128.09	-0.39	1	34.2	24	95.00%	R.EVSDGVIAPGYEPEALELLK.K		R.EVSDGVIAPGYEPEALELLK.K		
138	153	2	1755.86	4.1	1	89.5	25.2	95.00%	R.VTILSDPADYATFTDK.F		R.VTILSDPADYATFTDK.F		
551	565	2	1519.75	4.1	1	63.8	25.7	95.00%	K.YVAAPGGSVMDQAVR.D		K.YVAAPGGSVMDQAVR.D		
39	60	2	2231.08	4.2	0	97.7	25.9	95.00%	R.ESGMEVADVSSITNAPEILGGR.V		R.ESGMEVADVSSITNAPEILGGR.V		
248	259	2	1216.65	4.7	1	30.2	23.6	95.00%	R.ENIGIPAAASFK.H		R.ENIGIPAAASFK.H		
104	129	3	2776.52	-0.038	0	24.4	16	93.20%	R.ETIAKPNVTIPEAVEEIDIGGVTLLR.A		R.ETIAKPNVTIPEAVEEIDIGGVTLLR.A		
480	498	2	2018	3.8	1	84.7	25.3	95.00%	K.SNAIDLYVLDAVPAEGSER.E		K.SNAIDLYVLDAVPAEGSER.E		
260	278	3	1874.03	3.8	1	46.3	18.9	95.00%	K.HVSPAGAAVGLPLSDVEKK.V		K.HVSPAGAAVGLPLSDVEKK.V		
526	543	2	2131.98	3.7	1	65.5	27.4	95.00%	K.DVVCASDAFFPFPDNIYR.L	Carbamidomethyl (+57)	K.DVVCASDAFFPFPDNIYR.L		
223	244	2	2446.24	0.95	1	74.8	23.8	95.00%	K.VLCGSPGYINLMDALNSWPLVK.E	Carbamidomethyl (+57)	K.VLCGSPGYINLMDALNSWPLVK.E		
214	222	2	1045.53	0.93	1	28.6	23.5	94.70%	F.MEQGPLPFK.V		R.YGANPHQSPAQAFMEQGPLPFK.V		
566	581	2	1881.9	4.3	1	55.8	26.3	95.00%	R.DTANEFNMVFSEIPLR.L		R.DTANEFNMVFSEIPLR.L		
201	213	2	1386.63	-1.2	1	28.6	26.5	92.90%	R.YGANPHQSPAQAF.M		R.YGANPHQSPAQAFMEQGPLPFK.V		
354	362	2	1152.54	4.8	1	28.8	25.5	94.40%	K.YCVLQMDPK.Y	Carbamidomethyl (+57)	K.YCVLQMDPK.Y		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
30	GPD1_SCHPO	42.86%	100%	11									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
87	104	2	2008.04	-2	1	54.4	22.9	95.00%	K.YLPGIECPPNVIAVPDVR.E	Carbamidomethyl (+57)	K.YLPGIECPPNVIAVPDVR.E		
277	296	2	2153	2.6	0	93.7	26.8	95.00%	R.TMVEQSCGIADLVTSCLGGR.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.TMVEQSCGIADLVTSCLGGR.N		
73	86	3	1656.86	5.1	2	38.6	23.6	95.00%	R.KLTEVFNEAHENVK.Y		R.KLTEVFNEAHENVK.Y		
74	86	2	1528.75	-1.8	1	77.2	25	95.00%	K.LTEVFNEAHENVK.Y		K.LTEVFNEAHENVK.Y		
2	20	2	1989	3.8	1	99.4	24.5	95.00%	M.SGYGQQGVSAANIDSIRPK.K	Acetyl (+42)	-.MSGYGQQGVSAANIDSIRPK.K		
310	331	3	2285.26	3	1	24.3	18.5	93.10%	K.SLETLEKELLGGQLLQGAATSK.D		K.SLETLEKELLGGQLLQGAATSK.D		
183	202	2	2362.1	3.9	1	116	26.6	95.00%	R.EQFCETTIGFNPPNEVDIPR.E	Carbamidomethyl (+57)	R.EQFCETTIGFNPPNEVDIPR.E		
23	39	2	1628.89	-1.9	1	27.7	22	93.70%	R.LSIGVVGSGNWGTAIAK.I		R.LSIGVVGSGNWGTAIAK.I		
168	182	2	1515.74	-2.3	0	75.4	25.8	95.00%	Y.CGVLSGANVANEVAR.E	Carbamidomethyl (+57)	K.LGIYCGVLSGANVANEVAR.E		
125	144	3	2172.13	4	0	27	22.4	95.00%	R.VCDQMVGLIRPGAVGISCIK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VCDQMVGLIRPGAVGISCIK.G		
317	331	2	1484.82	-2.6	0	87.3	21.7	95.00%	K.ELLGGQLLQGAATSK.D		K.ELLGGQLLQGAATSK.D		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
31	G6PI_SCHPO	34.36%	100%	15									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
217	228	2	1343.61	5.2	1	37.3	26.3	95.00%	K.TFTTAETCTNAK.S	Carbamidomethyl (+57)	K.TFTTAETCTNAK.S		
464	477	2	1502.83	4	1	36.9	20.6	95.00%	K.TFVGNRPSNSIIAK.K		K.TFVGNRPSNSIIAK.K		
63	75	2	1499.85	3.9	0	37.5	19.3	95.00%	K.NLITEETVELLVK.L		K.NLITEETVELLVK.L		
446	463	3	1916.98	-1.7	1	41.1	23.8	95.00%	K.TPAEVKAEGTPDEIVPHK.T		K.TPAEVKAEGTPDEIVPHK.T		
79	90	2	1332.67	0.72	2	28.3	24.6	94.40%	K.EANVEGLRDALF.A		K.EANVEGLRDALFAGEHINFTEDR.A		
2	19	2	2048	0.55	1	42.4	25.7	95.00%	M.SFSLASTLPAWQAVQTHY.E	Acetyl (+42)	-.MSFSLASTLPAWQAVQTHYESVGK.H		
118	128	2	1170.59	4.1	0	35.5	23.6	95.00%	K.VNGQDVMPGVR.K		K.VNGQDVMPGVR.K		
429	445	2	1870.94	4.8	1	69.7	24.7	95.00%	R.MLFSNFAAQTEALMLGK.T		R.MLFSNFAAQTEALMLGK.T		
110	128	3	2084.06	4.5	1	31.6	23.7	95.00%	R.NVSEKPMKVNGQDVMPGVR.K		R.NVSEKPMKVNGQDVMPGVR.K		
530	547	3	1959.91	-5.9	1	30.8	27.3	95.00%	K.GDVENHDSSTNGLINLFK.N	Deamidation (+1)	K.GDVENHDSSTNGLINLFK.N		
372	382	2	1171.52	5.1	1	67.7	25.6	95.00%	R.SGDMVNYTTGK.I		R.SGDMVNYTTGK.I		

435	445	2	1131.59	-1.5	0	41.7	22.9	95.00%	F.AAQTEALMLGK.T		R.MLFSNFAAQTEALMLGK.T
204	216	2	1493.75	4.3	1	51.5	25.6	95.00%	K.CDPETTLFLIASK.T	Carbamidomethyl (+57)	K.CDPETTLFLIASK.T
521	547	3	2955.5	3	2	45.6	21.4	95.00%	K.NVLAQLETKGDVENHDSSTNGLINLFK.N		K.NVLAQLETKGDVENHDSSTNGLINLFK.N
353	367	2	1712.8	-4.1	1	72.3	26.6	95.00%	R.FPAYLQQLSMESNGK.A	Deamidation (+1)	R.FPAYLQQLSMESNGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
32	HXK2_SCHPO	38.68%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
12	24	2	1581.77	4.1	1	62.3	25.8	95.00%	K.LVNDFEYPTESLR.E		K.LVNDFEYPTESLR.E
11	24	2	1709.86	-1.4	2	76.8	24.5	95.00%	K.KLVNDFEYPTESLR.E		K.KLVNDFEYPTESLR.E
392	413	3	2499.23	3.2	2	59.6	25	95.00%	K.KSDVGVDGSLVEHYPHFVDMLR.E		K.KSDVGVDGSLVEHYPHFVDMLR.E
76	87	2	1450.73	-1.3	2	56.6	25.1	95.00%	R.VCWIQLLGDGKY.E	Carbamidomethyl (+57)	R.VCWIQLLGDGKYEMK.H
103	122	3	2360.22	3.5	1	42.1	22.6	95.00%	R.NESVKPIIDFMSDHVELFIK.E		R.NESVKPIIDFMSDHVELFIK.E
360	369	2	1108.58	1.6	1	30.8	23.5	95.00%	Y.LWDAAHAIGR.R		R.SDEEALYLWDAAHAIGR.R
374	388	2	1564.83	4.1	1	56.1	22.5	95.00%	R.MSAVPIASLYLSTGR.A		R.MSAVPIASLYLSTGR.A
103	120	2	2119.03	0.79	1	38	25.8	95.00%	R.NESVKPIIDFMSDHVELF.I		R.NESVKPIIDFMSDHVELFIK.E
1	11	2	1334.67	4.1	1	29.9	25.4	95.00%	-.MEANFQQAVKK.L	Acetyl (+42)	-.MEANFQQAVKK.L
266	279	2	1598.78	3.9	1	49.6	25.7	95.00%	R.YDLLLDHDTPNAGR.Q		R.YDLLLDHDTPNAGR.Q
434	449	2	1529.79	4.8	0	96.2	24	95.00%	K.DGSGIGAALCALQAVK.E	Carbamidomethyl (+57)	K.DGSGIGAALCALQAVK.E
221	237	2	1806.86	0.99	1	35.9	26.2	95.00%	F.GTGTNGAYVEQMNQIPK.L		K.ESDTFMGIIFGTGTNGAYVEQMNQIPK.L
76	86	2	1287.67	3.9	1	30.3	24	95.00%	R.VCWIQLLGDGK.Y	Carbamidomethyl (+57)	R.VCWIQLLGDGK.Y
286	296	2	1240.63	5.9	1	25.6	23.1	90.40%	R.VGGMYLGELFR.R		R.VGGMYLGELFR.R
216	237	2	2369.14	-0.18	1	67.8	26	95.00%	F.MGIIFGTGTNGAYVEQMNQIPK.L	Deamidation (+1)	K.ESDTFMGIIFGTGTNGAYVEQMNQIPK.L
25	34	2	1234.62	4.3	2	29.8	24.8	95.00%	R.EAVKEFDELR.Q		R.EAVKEFDELR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
33	IPYR_SCHPO	58.48%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
240	280	3	4115.08	2.7	1	89.4	18.9	95.00%	K.SDFSLVNVSVTGSVANDPSVSSTIPPAQELAPAPVDPSVHK.W		K.SDFSLVNVSVTGSVANDPSVSSTIPPAQELAPAPVDPSVHK.W
32	42	2	1269.63	-1.6	1	30.7	24.6	95.00%	W.HDIPLYANAEK.T		K.NGTPISSWHDIPLYANAEK.T
186	192	2	922.44	6	1	35.4	24.5	95.00%	R.ATNEWFR.I		R.ATNEWFR.I
94	113	2	2305.07	0.079	1	39.3	26.5	95.00%	W.NYGAFPQTYEDPNVVHPETK.A		R.NCFPHHGYIWNYGAFPQTYEDPNVVHPETK.A
141	156	2	1774.88	-1.7	1	93.9	25.2	95.00%	K.VLGVMALLDEGETDWK.V		K.VLGVMALLDEGETDWK.V
24	42	2	2112.04	4.6	1	50.5	25.5	95.00%	K.NGTPISSWHDIPLYANAEK.T		K.NGTPISSWHDIPLYANAEK.T
114	130	2	1830.85	4	1	98.5	26.8	95.00%	K.AKGDSDPLDVCEIGEAR.G	Carbamidomethyl (+57)	K.AKGDSDPLDVCEIGEAR.G
170	178	2	1101.53	3.9	0	49.3	23.4	95.00%	K.LNDIEDVER.H		K.LNDIEDVER.H
43	53	2	1283.73	4	0	66.7	19.5	95.00%	K.TILNMVVEIPR.W		K.TILNMVVEIPR.W
157	169	2	1391.81	4.1	0	37.4	15.2	95.00%	K.VIVIDVNDPLAPK.L		K.VIVIDVNDPLAPK.L
8	23	2	1839.93	4.1	1	74	24.1	95.00%	R.EVGALNTLDYQVYVEK.N		R.EVGALNTLDYQVYVEK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
34	TKT_SCHPO	30.95%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
364	394	3	3276.78	4.5	1	70.7	14.8	95.00%	R.KLSEIVLDALCPVLPELVGGSADLTPSNLTR.W	Carbamidomethyl (+57)	R.KLSEIVLDALCPVLPELVGGSADLTPSNLTR.W
325	336	2	1449.68	6.5	1	28.4	25.2	94.40%	K.QSYPDLSNQLER.I	Deamidation (+1)	K.QSYPDLSNQLER.I
2	18	2	1869.93	-1.7	1	87.6	24.7	95.00%	M.TSSSYTDIDTLAINTIR.T		-.MTSSSYTDIDTLAINTIR.T
238	252	2	1719.86	5	0	57.2	25.3	95.00%	R.EAMSCTDKPTLINLK.T	Carbamidomethyl (+57)	R.EAMSCTDKPTLINLK.T
395	407	2	1418.65	3.9	1	52.7	26	95.00%	R.WEGAADFQPPSSK.L		R.WEGAADFQPPSSK.L
495	515	2	2400.03	0.46	1	33	27.4	95.00%	R.AMPNINCWRPADGNETSAAYY.S	Carbamidomethyl (+57)	R.AMPNINCWRPADGNETSAAYYSALTSDSTPSILALTR.Q
182	193	2	1385.74	4.7	1	41.9	22.7	95.00%	K.LSNLIAVWDNNK.I		K.LSNLIAVWDNNK.I
532	547	2	1810.95	4.2	0	72.5	22.4	95.00%	R.QNLPQLENSTIENALK.G		R.QNLPQLENSTIENALK.G

253	281	3	3132.54	2.9	1	59.8	23.1	95.00%	K.TTIGYGSELQGTHSVHGSPLKPEDCVHVK.K	Carbamidomethyl (+57)	K.TTIGYGSELQGTHSVHGSPLKPEDCVHVK.K
636	648	3	1300.59	-1.1	1	32.2	26.5	95.00%	F.GMHTFGDSGPAPK.L		R.YVHEAFGMHTFGDSGPAPK.L
306	318	2	1423.73	4.8	1	73.3	24.6	95.00%	R.VAIASSAEEEYKK.M		R.VAIASSAEEEYKK.M
30	49	3	1972.02	3.9	1	31.5	23.3	95.00%	K.SGHPGAPMGLAPAAHVLFSR.I		K.SGHPGAPMGLAPAAHVLFSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
35	LYS9_SCHPO	42.22%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
177	183	2	740.49	4.7	0	33.1	11.8	95.00%	R.GVLLALR.N		R.GVLLALR.N
194	209	3	1820.92	0.28	2	44	24.7	95.00%	K.LVEIDGKDLMETAKPY.F		K.LVEIDGKDLMETAKPYFIYPGYAFVCYPNR.D
290	301	2	1276.66	4.3	1	31	23.5	95.00%	K.AESSSEADLIKK.I		K.AESSSEADLIKK.I
38	49	2	1259.66	4.1	1	41.7	23.9	95.00%	K.AEAFINGIPNSK.A		K.AEAFINGIPNSK.A
379	396	2	1989.93	4.3	1	76.6	26.5	95.00%	R.TCTLLDYGVPNGYTSMAK.L	Carbamidomethyl (+57)	R.TCTLLDYGVPNGYTSMAK.L
287	301	3	1616.91	5.4	1	31	19	95.00%	R.VIKAESSSEADLIKK.I		R.VIKAESSSEADLIKK.I
397	426	3	3075.61	1.3	0	40.9	19	95.00%	K.LVGVPCGVATQQILDGVINTPGVLAPNDMK.L	Carbamidomethyl (+57)	K.LVGVPCGVATQQILDGVINTPGVLAPNDMK.L
64	85	3	2488.28	3.3	1	39.1	22.3	95.00%	K.AVSEHDLTISLIPYTYHATVMK.A		K.AVSEHDLTISLIPYTYHATVMK.A
2	22	3	2269.25	3.1	1	39	17.6	95.00%	M.PSILLLGSGFVAHPTLEYLSR.R		-.MPSILLLGSGFVAHPTLEYLSR.R
114	135	3	2372.16	2.8	1	47.3	25.4	95.00%	K.AGSICMNEIGVDPGIDHLYAIK.T	Carbamidomethyl (+57)	K.AGSICMNEIGVDPGIDHLYAIK.T
104	113	2	1103.56	4	0	29.1	23.7	95.00%	K.MAELEEAAIK.A		K.MAELEEAAIK.A
114	132	2	2059.94	0.4	1	55.7	27.2	95.00%	K.AGSICMNEIGVDPGIDHLY.A	Carbamidomethyl (+57)	K.AGSICMNEIGVDPGIDHLYAIK.T
154	170	2	1787.81	-1.8	1	57.9	26.8	95.00%	Y.CGGLPAPEDSNNPLGYK.F	Carbamidomethyl (+57)	K.SFLSYCGGLPAPEDSNNPLGYK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
36	CYPH_SCHPO	40.74%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	17	2	1835.86	-1.6	1	64.5	26.4	95.00%	M.SNCFFDVIANGQPLGR.I	Acetyl (+42)/ Carbamidomethyl (+57)	-.MSNCFFDVIANGQPLGR.I
112	123	2	1328.73	0.14	1	63.8	21.4	95.00%	F.ITTVVTPWLDGK.H		K.HNKPGLLSMANAGPNTNGSQFFITTVVTPWLDGK.H
124	139	3	1772.92	4.1	1	60.2	23.5	95.00%	K.HVVFGEVTEGMDVVKK.V		K.HVVFGEVTEGMDVVKK.V
54	67	2	1607.82	4.3	1	67.2	24.7	95.00%	R.VIPQFMLQGGDFTR.G		R.VIPQFMLQGGDFTR.G
124	138	2	1644.83	4.4	1	86.7	24.7	95.00%	K.HVVFGEVTEGMDVVK.K		K.HVVFGEVTEGMDVVK.K
22	29	2	931.51	4	1	29.7	23.4	95.00%	K.LFDDVVPK.T		K.LFDDVVPK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
37	HSP60_SCHPO	31.79%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	148	2	1316.6	4	0	27.4	26.5	90.90%	R.NVAAGCNPMDLR.R	Carbamidomethyl (+57)	R.NVAAGCNPMDLR.R
244	256	2	1529.83	-1.1	1	50.8	21.9	95.00%	K.VEFENPLILLSEK.K		K.VEFENPLILLSEK.K
382	396	2	1722.82	4	1	31.1	26	95.00%	R.GVMADPNLTEYEKEK.L		R.GVMADPNLTEYEKEK.L
258	275	2	1937.07	4.4	0	74.7	18.9	95.00%	K.VSAVQDILPSLELAAQQR.R		K.VSAVQDILPSLELAAQQR.R
45	56	2	1215.69	4.9	0	52.6	21.2	95.00%	R.ASLLTGVDTLAR.A		R.ASLLTGVDTLAR.A
257	275	3	2065.16	4	1	35.3	16.2	95.00%	K.KVSAVQDILPSLELAAQQR.R		K.KVSAVQDILPSLELAAQQR.R
112	128	2	1705.86	4.1	0	84.3	25.3	95.00%	K.TNEVAGDGTTTATVLTR.A		K.TNEVAGDGTTTATVLTR.A
437	453	2	1588.85	4.6	1	29.9	22.3	95.00%	K.AAVSEGVLPGAGTSFVK.A		K.AAVSEGVLPGAGTSFVK.A
478	500	3	2377.34	2.9	0	22.4	14.8	90.10%	K.AITRPAQTILENAGLEGNLIVGK.L		K.AITRPAQTILENAGLEGNLIVGK.L
241	256	2	1873.03	4.6	2	56.5	20	95.00%	K.SQKVEFENPLILLSEK.K		K.SQKVEFENPLILLSEK.K
168	195	3	2912.46	-0.2	0	44.6	23.4	95.00%	R.DITTSEEISQVATISANGDTHIGELLAK.A		R.DITTSEEISQVATISANGDTHIGELLAK.A
68	79	2	1313.7	4.3	1	39.3	21.8	95.00%	R.NVLIDQPFGSPK.I		R.NVLIDQPFGSPK.I
520	533	2	1570.87	4.4	1	87.2	21.1	95.00%	R.FVDLNEIGVLDPLK.V		R.FVDLNEIGVLDPLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
38	PDX1_SCHPO	30.74%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	49	2	1547.75	3.7	0	51.8	25.4	95.00%	R.IAEAAGACAVMALER.V	Carbamidomethyl (+57)/ Oxidation (+16)	R.IAEAAGACAVMALER.V
265	280	2	1628.86	4	0	87.2	22.8	95.00%	K.ILAEVSENLGAAMVGR.S		K.ILAEVSENLGAAMVGR.S
71	83	2	1355.75	4.3	0	66.7	21.3	95.00%	K.EIQAAVSIPVMAK.V		K.EIQAAVSIPVMAK.V
150	164	2	1487.76	-1.7	1	74.1	24.3	95.00%	R.TKGEAGTGDVVEAVR.H		R.TKGEAGTGDVVEAVR.H
21	34	2	1457.74	4	0	89.6	24.3	95.00%	K.GGVIMDVVNAEQAR.I		K.GGVIMDVVNAEQAR.I
140	149	2	1102.6	4.8	1	28.6	23	94.70%	R.RISEGAAMIR.T		R.RISEGAAMIR.T
13	20	2	830.47	4.2	0	38.8	21.5	95.00%	K.AGLAQMLK.G		K.AGLAQMLK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
39	PUT2_SCHPO	26.46%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
406	422	2	1852.91	-2.2	1	64.8	26.4	95.00%	K.ADDSEGFFVEPTVLLSK.N		K.ADDSEGFFVEPTVLLSK.N
233	253	2	2068.09	4.4	1	68.9	22.3	95.00%	R.EAGLPAGALQFIPGDAVEVSK.V		R.EAGLPAGALQFIPGDAVEVSK.V
495	509	2	1504.71	3.5	1	49.3	26	95.00%	K.CTGAVVGEQPFGGAR.A	Carbamidomethyl (+57)	K.CTGAVVGEQPFGGAR.A
388	405	2	1773.91	3.9	0	102	24	95.00%	K.VLESAASDSEIEVLAGGK.A		K.VLESAASDSEIEVLAGGK.A
82	92	2	1222.64	4.6	0	32.1	23.7	95.00%	K.HVEDAIEAALR.G		K.HVEDAIEAALR.G
275	288	2	1444.74	4.6	1	37.7	24.2	95.00%	R.SLWGTIGENVANGK.Y		R.SLWGTIGENVANGK.Y
373	382	2	1053.56	0.84	1	68.6	21.5	95.00%	F.VGPVIHQASF.N		K.VGAPLTDFANFVGPVIHQASFNK.L
36	63	3	3091.63	0.58	1	39.6	18.1	95.00%	K.ELEAELPVTIPVIIDGKEVETNTIGEQR.C		K.ELEAELPVTIPVIIDGKEVETNTIGEQR.C
484	494	2	1225.58	4.6	1	28	25.8	93.00%	R.NAAGNFYINDK.C		R.NAAGNFYINDK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
40	YL8C_SCHPO	48.51%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
217	232	2	1745.96	4.4	1	53	20.4	95.00%	K.GTALQYITSNILPEVK.N		K.GTALQYITSNILPEVK.N
275	288	2	1456.71	-1.5	0	71.2	25.3	95.00%	R.VGNEEGAVGEVLER.I		R.VGNEEGAVGEVLER.I
7	33	4	3045.57	3.9	1	29.7	20.8	95.00%	K.TNNLPTLDTLQMVISDVDGTLLDKHHR.F		K.TNNLPTLDTLQMVISDVDGTLLDKHHR.F
96	112	3	1893.99	0.11	0	63.5	23	95.00%	Y.ADHLKPEVVMEVVEATK.G		K.IVYADHLKPEVVMEVVEATK.G
70	88	2	2085.02	-1.4	1	48.4	25.8	95.00%	R.IPLDLDAFPAAHVNGCVLY.N	Deamidation (+1)/ Carbamidomethyl (+57)	R.IPLDLDAFPAAHVNGCVLYNK.G
173	186	2	1645.79	3.6	1	65.2	26.3	95.00%	K.MAVCEDPDKLDVVR.D	Carbamidomethyl (+57)	K.MAVCEDPDKLDVVR.D
93	112	3	2269.21	3.4	1	35.2	20.1	95.00%	K.IVYADHLKPEVVMEVVEATK.G		K.IVYADHLKPEVVMEVVEATK.G
47	60	2	1575.87	4.2	2	37.4	19.7	95.00%	R.EKYPNFPIVLATGK.Q		R.EKYPNFPIVLATGK.Q
113	128	2	1865.86	0.053	1	54.7	26.8	95.00%	K.GNPNIANVVYDEHYVY.A		K.GNPNIANVVYDEHYVYALTPGR.E
70	90	3	2326.19	3.3	1	38.3	23.7	95.00%	R.IPLDLDAFPAAHVNGCVLYNK.G	Carbamidomethyl (+57)	R.IPLDLDAFPAAHVNGCVLYNK.G
2	33	4	3587.84	2.8	1	81.1	19.2	95.00%	M.SAVDKTNNLPTLDTLQMVISDVDGTLLDKHHR.F	Acetyl (+42)	-.MSAVDKTNNLPTLDTLQMVISDVDGTLLDKHHR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
41	OAT_SCHPO	37.67%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
211	234	2	2621.26	-0.77	1	55	25.3	95.00%	F.LVEPIQGEAGVMVPDDGYLEEAYK.L		K.VAAFLVEPIQGEAGVMVPDDGYLEEAYK.L
386	398	3	1374.82	4.6	0	23.2	15.4	91.50%	R.GVLAKPTHGNIIR.F		R.GVLAKPTHGNIIR.F
154	167	2	1493.69	4.9	0	59.2	26	95.00%	R.TMGIISMSTDPDAR.D		R.TMGIISMSTDPDAR.D
292	306	2	1694.77	2.4	1	56.8	26.3	95.00%	R.EIMLNFEPGTHGSTY.G		R.EIMLNFEPGTHGSTYGGNPLGAAVSIAALEVVK.E
135	153	3	2184.11	3	2	28.6	24.1	95.00%	K.KIPTDEAIILSCVDNFHGR.T	Carbamidomethyl (+57)	K.KIPTDEAIILSCVDNFHGR.T

276	291	2	1561.85	4	1	53	21.1	95.00%	K.AISGGVYPVSAVLSSR.E		K.AISGGVYPVSAVLSSR.E
238	254	2	1838.97	4.4	1	78.8	22	95.00%	K.AHNVLFIADEVQTGVAR.T		K.AHNVLFIADEVQTGVAR.T
258	275	3	2051.09	0.023	0	51.5	21.2	95.00%	K.MLCIEHSNVKPDVVILGK.A	Carbamidomethyl (+57)	K.MLCIEHSNVKPDVVILGK.A
70	80	2	1268.71	4.2	0	28.4	18.6	94.50%	K.IIEALVEQAQR.V		K.IIEALVEQAQR.V
107	124	2	1949.89	0.31	0	70.9	26.5	95.00%	Y.EMVIPMNTGAEAVETACK.L	Carbamidomethyl (+57)	K.YITEYFGYEMVIPMNTGAEAVETACK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
42	GBLP_SCHPO	37.26%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
18	36	2	1956.02	0.042	0	59	23	95.00%	W.VTSLSTAPENPDILLSGSR.D		R.ATLEGHSGWVTSLSTAPENPDILLSGSR.D
48	57	2	1135.53	4.7	1	43.2	24.9	95.00%	R.DDVNYGVAQR.R		R.DDVNYGVAQR.R
9	17	2	956.44	1.2	1	35.7	24.7	95.00%	R.ATLEGHSGW.V		R.ATLEGHSGWVTSLSTAPENPDILLSGSR.D
186	212	3	2736.26	2.6	1	43.2	26.6	95.00%	R.TSHYGHTGYVSAVTISPDGSLCASGGR.D	Carbamidomethyl (+57)	R.TSHYGHTGYVSAVTISPDGSLCASGGR.D
9	36	3	2894.45	2.9	1	38.1	22.6	95.00%	R.ATLEGHSGWVTSLSTAPENPDILLSGSR.D		R.ATLEGHSGWVTSLSTAPENPDILLSGSR.D
66	77	2	1399.57	1.2	1	33.7	25.4	95.00%	F.VSDCALSFDSHY.A	Carbamidomethyl (+57)	R.LTGHSHFVSDCALSFDSHYALSASWDK.T
300	308	2	1060.53	0.92	1	40.9	23.6	95.00%	F.SGWTDNLIR.V		K.SSEPECISLTWSPDGQTLFSGWTDNLIR.V
234	245	2	1314.71	3.1	1	32.5	22.6	95.00%	K.ANINALVFSPNR.Y		K.ANINALVFSPNR.Y
176	185	2	1264.65	5.4	1	30.1	24.6	95.00%	K.VWDLETFSLR.T		K.VWDLETFSLR.T
39	47	2	1112.68	5.9	1	27.8	17.4	93.80%	K.SIILWNLVR.D		K.SIILWNLVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
43	HOSM_SCHPO	35.17%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	31	3	3218.5	4.8	1	47.5	25.2	95.00%	M.SVSEANGTETIKPPMNGNPYGPNPSDFLSR.V	Acetyl (+42)/ Deamidation (+1)	-.MSVSEANGTETIKPPMNGNPYGPNPSDFLSR.V
238	257	3	2083.04	1.6	0	40.6	24.7	95.00%	Y.CALEAGATHIDTSILGIGER.N	Carbamidomethyl (+57)	R.GVVSCDIECHFHNDTGMAIANAYCALEAGATHIDTSILGIGER.N
22	31	2	1088.53	0.8	1	51.9	24.7	95.00%	Y.GPNPSDFLSR.V		-.MSVSEANGTETIKPPMNGNPYGPNPSDFLSR.V
360	375	3	1793.94	-1.3	1	51.6	22.6	95.00%	K.SRAEQLNLHLTDAQAK.E		K.SRAEQLNLHLTDAQAK.E
192	204	2	1315.66	4	0	40.8	24.6	95.00%	R.VGIADTVGCATPR.Q	Carbamidomethyl (+57)	R.VGIADTVGCATPR.Q
64	85	2	2410.17	0.035	1	123	25.6	95.00%	K.ALDNFGVDYIELTSPVASEQSR.Q		K.ALDNFGVDYIELTSPVASEQSR.Q
172	182	2	1264.7	4.6	1	43.4	20.1	95.00%	R.SDLVDLLSLYK.A		R.SDLVDLLSLYK.A
401	411	2	1290.55	4.4	1	41	26.7	95.00%	R.EYHADLSDADR.I		R.EYHADLSDADR.I
32	43	2	1391.75	4.9	1	68.1	21.6	95.00%	R.VNNFSIIESTLR.E		R.VNNFSIIESTLR.E
333	344	3	1420.7	0.63	1	39.4	24.9	95.00%	Y.EILKPEDFGMSR.Y		K.AILANPSTYEILKPEDFGMSR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
44	RAD24_SCHPO	50.74%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
228	267	3	4032.79	4.4	1	129	23.8	95.00%	R.DNLTLWTSDAEYSAAAAGGNTEGAQENAPSNAPEGEAEPK.A		R.DNLTLWTSDAEYSAAAAGGNTEGAQENAPSNAPEGEAEPK.A
15	30	3	1896.87	-2.1	2	30.6	26.9	95.00%	K.LAEQAERYEGMVENMK.S		K.LAEQAERYEGMVENMK.S
156	172	2	1746.93	4.5	0	64.4	21.7	95.00%	K.AASEIATAELAPTHPIR.L		K.AASEIATAELAPTHPIR.L
240	270	3	2881.26	0.96	1	33.1	26.7	95.00%	Y.SAAAAGGNTEGAQENAPSNAPEGEAEPKADA.-		R.DNLTLWTSDAEYSAAAAGGNTEGAQENAPSNAPEGEAEPKADA.-
109	120	2	1236.65	4.7	0	29.1	22.7	95.00%	K.HLIPNAASAESK.V		K.HLIPNAASAESK.V
31	44	2	1562.75	4.1	0	82.9	26.1	95.00%	K.SVASTDQELTVEER.N		K.SVASTDQELTVEER.N

240	267	3	2624.16	0.37	0	57.2	27.2	95.00%	Y.SAAAAGGNTEGAQENAPSNAPEGEAEPK.A		R.DNLTLWTSDAEYSAAAAGGNTEGAQENAPSNAPEGEAEPK.A
2	14	2	1481.74	4.3	2	46.8	25.2	95.00%	M.STTSREDAVYLAK.L	Acetyl (+42)	-.MSTTSREDAVYLAK.L
64	85	3	2429.31	3.8	1	57.6	18.8	95.00%	R.IVSSIEQKEESKGNTAQVELIK.E		R.IVSSIEQKEESKGNTAQVELIK.E
234	267	3	3290.41	1.7	1	64.5	26.1	95.00%	W.TSDAEYSAAAAGGNTEGAQENAPSNAPEGEAEPK.A		R.DNLTLWTSDAEYSAAAAGGNTEGAQENAPSNAPEGEAEPK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
45	HSP7M_SCHPO	31.31%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
637	647	2	1313.76	3.4	1	27.8	18.8	93.80%	K.KIDEIQQLSLK.V		K.KIDEIQQLSLK.V
366	388	3	2471.31	0.57	1	38.9	20.9	95.00%	R.ALKDANLQTSEINEVILVGGMTR.M		R.ALKDANLQTSEINEVILVGGMTR.M
582	609	3	3240.55	-0.97	1	32.3	24	95.00%	R.AESVCTDIESNLDIHKDKLDQQAVEDLR.S	Carbamidomethyl (+57)	R.AESVCTDIESNLDIHKDKLDQQAVEDLR.S
622	635	2	1464.65	3.4	0	88.6	26.6	95.00%	K.VNAGDEGITSEDMK.K		K.VNAGDEGITSEDMK.K
204	215	2	1124.67	4.6	0	48.3	15.1	95.00%	K.AAGAIAGLNVLR.V		K.AAGAIAGLNVLR.V
322	337	2	1645.86	3.4	1	41.2	22.9	95.00%	K.TDISLPFITADATGPK.H		K.TDISLPFITADATGPK.H
105	118	2	1578.81	4.5	1	81.4	24.5	95.00%	R.QAVINPENTFFATK.R		R.QAVINPENTFFATK.R
263	281	3	2002.92	-3.2	1	28.6	26.9	95.00%	R.STNGDTHLGGEDFDVALVR.H	Deamidation (+1)	R.STNGDTHLGGEDFDVALVR.H
185	199	2	1679.83	4.3	1	62.1	25.8	95.00%	K.NAVVTVPAYFNDSQR.Q		K.NAVVTVPAYFNDSQR.Q
496	510	2	1538.89	4.2	1	77.2	15.4	95.00%	K.LIGNFQLTGIAPAPK.G		K.LIGNFQLTGIAPAPK.G
622	636	2	1592.74	5	1	80.4	25.9	95.00%	K.VNAGDEGITSEDMKK.K		K.VNAGDEGITSEDMKK.K
157	170	2	1496.8	5.1	1	59.3	21.7	95.00%	K.TYSPSQIGGFILSK.M		K.TYSPSQIGGFILSK.M
470	482	2	1317.65	-1.6	0	48	24.5	95.00%	F.STAADGQTAVEIR.V		K.SQVFSTAADGQTAVEIR.V
216	231	2	1630.86	3.8	1	78.5	22.3	95.00%	R.VVNEPTAAALAYGLDK.K		R.VVNEPTAAALAYGLDK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
46	CARB_SCHPO	11.38%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
418	433	2	1784.89	3.2	1	42	24.9	95.00%	K.TTTANFEPSLDYVVTK.I		K.TTTANFEPSLDYVVTK.I
575	584	2	1057.58	4.7	0	32.1	22.6	95.00%	K.LVGASELDVR.A		K.LVGASELDVR.A
799	823	3	2678.38	-0.41	1	51.7	22	95.00%	R.DESSLKDKLENASAVSPDHPVVITK.F		R.DESSLKDKLENASAVSPDHPVVITK.F
730	744	2	1630.78	-2.2	0	88.3	25.3	95.00%	K.VLGTDPLMIDSAEDR.H		K.VLGTDPLMIDSAEDR.H
932	943	2	1304.72	5.6	1	35.2	21.5	95.00%	K.TLGVNFIDVATR.S		K.TLGVNFIDVATR.S
1056	1070	2	1655.91	-1.6	1	42.7	20.6	95.00%	K.LLQPTSAEVVEFPVK.D		K.LLQPTSAEVVEFPVK.D
773	798	3	2736.49	2.9	1	51	17.3	95.00%	K.FANAVGYPVLVRPSYVLSGAAMSVIR.D		K.FANAVGYPVLVRPSYVLSGAAMSVIR.D
261	273	3	1432.7	3.3	1	25.5	25	94.50%	F.ANNKEELQSMAAK.S		R.SAYSLGGLGSGFANNKEELQSMAAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
47	C1TC_SCHPO	16.01%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
689	707	3	1923.15	3.9	0	37.5	9.03	95.00%	R.TSGLKPDAIVIVATVQALK.L		R.TSGLKPDAIVIVATVQALK.L
204	219	3	1649.95	-1.5	1	48.7	14.8	95.00%	R.TADIVVAAIGIPHFVK.A		R.TADIVVAAIGIPHFVK.A
57	84	3	3131.52	3.1	1	32.8	23.6	95.00%	R.AANEAGISCEHVNFPEDITEYDLLLAIK.G	Carbamidomethyl (+57)	R.AANEAGISCEHVNFPEDITEYDLLLAIK.G
349	356	2	983.58	5.3	0	46.2	17.4	95.00%	K.VNLEILQR.L		K.VNLEILQR.L
835	849	2	1592.77	-1.9	1	65.7	25.8	95.00%	K.EMYGADGIELSPLAK.E		K.EMYGADGIELSPLAK.E
2	12	2	1184.68	4.9	0	55.8	20.5	95.00%	M.ALLLEGTSLAR.K	Acetyl (+42)	-.MALLLEGTSLAR.K
536	546	2	1228.67	4.9	1	27.4	22	93.30%	R.KITIGENPTEK.G		R.KITIGENPTEK.G
457	469	2	1525.65	-1.9	1	38.5	26.5	95.00%	R.MFHENTQSDAALY.K		R.MFHENTQSDAALYK.R
324	336	2	1299.71	5.1	0	59.2	21.9	95.00%	K.NIGDLASEIGIAK.S		K.NIGDLASEIGIAK.S
381	396	2	1629.9	3.4	0	106	20.9	95.00%	K.STLTAGLVQALSNLDK.L		K.STLTAGLVQALSNLDK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
48	PPA1_SCHPO	16.78%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	92	2	2047	4	1	99.4	25.8	95.00%	R.NPTGGNAAFDAVGIANFQQR.L		R.NPTGGNAAFDAVGIANFQQR.L
47	59	2	1531.7	-1.4	1	62.8	26.3	95.00%	Y.FYGPSIDFPTTCK.I	Carbamidomethyl (+57)	R.SPYHKPYFYGPSIDFPTTCK.I
420	427	2	918.49	1.5	1	25.8	22.4	90.80%	Y.AYLNSPVR.V		R.HLVNEEVFPLSDCGFGPSNTSDGMCELYAYLNSPVR.V
373	387	2	1723.81	-2	1	64.7	26.5	95.00%	F.AGNLITELFQCEDSK.Y	Carbamidomethyl (+57)	K.ASEFVPFAGNLITELFQCEDSK.Y
205	224	2	2206.96	0.13	1	96.6	27.6	95.00%	Y.NACPASDADDFTTPALEAWR.N	Carbamidomethyl (+57)	R.VVDSALWYGYGMFGEDVHNFTNYILVSENATAGSNSLSSYNACPASDADDFTTPALEAWR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
49	FAS2_SCHPO	8.09%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1569	1579	2	1292.61	5	1	41.1	25.6	95.00%	R.NADNIDEYLAR.F		R.NADNIDEYLAR.F
114	146	3	3020.56	3.1	0	35.9	21.2	95.00%	K.VETAAAAAPAATPAPAPAQTSAPAAALPDEPPK.A		K.VETAAAAAPAATPAPAPAQTSAPAAALPDEPPK.A
517	527	2	1319.7	5.4	2	32	23.6	95.00%	R.KLTHYVTEMAK.G		R.KLTHYVTEMAK.G
28	44	2	1939.01	4.4	1	67.5	22.9	95.00%	R.WIETQDVILSPPVSAER.I		R.WIETQDVILSPPVSAER.I
488	502	3	1650.8	4.5	0	35.5	26.1	95.00%	K.NVNHPTAPSTTIDER.G		K.NVNHPTAPSTTIDER.G
914	937	3	2504.19	3.1	1	37.5	26.2	95.00%	R.AVAAETAFDHSITNGPDSEAVFQK.T		R.AVAAETAFDHSITNGPDSEAVFQK.T
1393	1401	2	994.61	4.5	0	27.6	12	93.60%	K.TPLPIVDLK.F		K.TPLPIVDLK.F
1785	1813	3	2858.5	0.14	1	54.3	19.8	95.00%	K.GAAAPLKDIEIISSESGAPEVVLHGEAAK.A		K.GAAAPLKDIEIISSESGAPEVVLHGEAAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
50	THIL_SCHPO	35.95%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
196	210	2	1667.89	-1.8	1	55.6	22	95.00%	K.AFEQEIVPVEVPVGR.G		K.AFEQEIVPVEVPVGR.G
360	371	2	1405.81	4.5	1	73.2	17.9	95.00%	R.IICTLAYILAQK.D	Carbamidomethyl (+57)	R.IICTLAYILAQK.D
340	359	3	1865.93	4.8	0	31	25.8	95.00%	R.VNINGGGVAMGHPLGSSGSR.I		R.VNINGGGVAMGHPLGSSGSR.I
291	301	2	1160.65	4.8	1	33.2	21.1	95.00%	R.FTTSPSLAIPK.A		R.FTTSPSLAIPK.A
14	30	2	1654.8	-2.6	1	79.2	25.5	95.00%	R.TPMGSFGGSFASLPATK.L		R.TPMGSFGGSFASLPATK.L
43	69	3	2869.44	-0.17	1	51.4	22.2	95.00%	R.VNIKPSDVDEVFMGNVVSANLGQNPAR.Q		R.VNIKPSDVDEVFMGNVVSANLGQNPAR.Q
278	290	2	1440.71	4.1	1	44.3	25.5	95.00%	K.IIGWGEAAQDPER.F		K.IIGWGEAAQDPER.F
55	69	2	1526.76	1.1	0	82.6	25.3	95.00%	F.MGNVVSANLGQNPAR.Q		R.VNIKPSDVDEVFMGNVVSANLGQNPAR.Q
148	174	3	2905.26	3	1	42.8	26.8	95.00%	R.DGLSDAYDGLPMGNAAELCAEEHSIDR.A	Carbamidomethyl (+57)	R.DGLSDAYDGLPMGNAAELCAEEHSIDR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
51	RS7_SCHPO	30.26%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	140	2	2393.32	1	1	47.3	15.1	95.00%	R.TLTAVHNAILEDIVFPTEIIGK.R		R.TLTAVHNAILEDIVFPTEIIGK.R
59	70	2	1322.84	4	1	46.5	6.99	95.00%	K.AIVVFVPQPLLK.A		K.AIVVFVPQPLLK.A
119	141	3	2549.42	0.19	1	49.2	14.3	95.00%	R.TLTAVHNAILEDIVFPTEIIGKR.T		R.TLTAVHNAILEDIVFPTEIIGKR.T
11	34	2	2657.25	4.3	1	84.1	26.4	95.00%	R.SSSQPTETDLLVAQCLYDLESSSK.D	Carbamidomethyl (+57)	R.SSSQPTETDLLVAQCLYDLESSSK.D
11	27	2	1910.89	-0.76	1	37.4	26.8	95.00%	R.SSSQPTETDLLVAQCLY.D	Carbamidomethyl (+57)	R.SSSQPTETDLLVAQCLYDLESSSK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
52	HSP7F_SCHPO	23.75%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
174	189	2	1665.85	4	1	78.4	24.5	95.00%	R.LMNDNAAAALTYGITK.T		R.LMNDNAAAALTYGITK.T
539	558	3	2226.18	2.9	1	45	21.4	95.00%	K.VADLSVSVQEDRLPTEVLEK.Y		K.VADLSVSVQEDRLPTEVLEK.Y

561	580	4	2283.16	4.6	1	33.5	23.3	95.00%	R.EAEHQMIATDKLVAETVDRK.N	R.EAEHQMIATDKLVAETVDRK.N
581	591	2	1385.65	4	1	31.1	26.5	95.00%	K.NALEEYIYDTR.A	K.NALEEYIYDTR.A
694	720	3	3003.37	3.5	1	48	26.2	95.00%	R.APPPPPAEEVAPENEEVETMEIDEQKE.-	R.APPPPPAEEVAPENEEVETMEIDEQKE.-
38	48	2	1194.59	3.8	1	34	24.7	95.00%	R.STPSLVSYGER.S	R.STPSLVSYGER.S
96	106	2	1134.6	4	1	31.7	24.7	95.00%	K.LTEVDGFVGAK.V	K.LTEVDGFVGAK.V
305	318	3	1743.95	-2	2	25.1	21.3	94.20%	K.RSDFEELIKPLLER.L	K.RSDFEELIKPLLER.L
306	318	3	1587.85	-1.6	1	24.4	22.9	93.20%	R.SDFEELIKPLLER.L	R.SDFEELIKPLLER.L
5	16	2	1249.64	6.5	1	29.4	24.3	95.00%	R.TNVVGIDFGNSK.T	R.TNVVGIDFGNSK.T
159	173	2	1534.88	-1.7	0	63.4	15.3	95.00%	R.ALLEAANIAGLNPLR.L	R.ALLEAANIAGLNPLR.L
617	630	2	1684.72	4	1	75.9	26.8	95.00%	K.AEDWLYEEGEDTTK.A	K.AEDWLYEEGEDTTK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
53	TRP_SCHPO	28.26%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
382	393	2	1355.77	4.5	0	47.2	19.5	95.00%	K.INNCIGQILLAK.R	Carbamidomethyl (+57)	K.INNCIGQILLAK.R
247	261	2	1623.75	3.4	1	47.6	26.5	95.00%	K.AEPGTAATVVEEYCK.Y	Carbamidomethyl (+57)	K.AEPGTAATVVEEYCK.Y
400	419	3	1938.01	4.3	0	37.5	22.6	95.00%	R.IIAETGAGQHGVATAICAAK.F	Carbamidomethyl (+57)	R.IIAETGAGQHGVATAICAAK.F
616	631	2	1825.87	3	1	57.5	26.5	95.00%	R.AEFIAVTDAQCLEGFR.A	Carbamidomethyl (+57)	R.AEFIAVTDAQCLEGFR.A
445	461	2	1739.99	4	0	48.6	17.7	95.00%	R.LLGAEVVPVTSGTQTLR.D		R.LLGAEVVPVTSGTQTLR.D
543	560	2	1822.79	-2.6	0	42.7	27.2	95.00%	K.SVMMLGCEAGGDGVDTPK.H	Carbamidomethyl (+57)	K.SVMMLGCEAGGDGVDTPK.H
673	690	3	1893.03	4.4	1	34.8	19.7	95.00%	R.GDKDVQSVAEQLPILGPK.I		R.GDKDVQSVAEQLPILGPK.I
275	302	3	2928.48	4.6	1	34.9	22.4	95.00%	K.QFQSGGSVATAPPAAVVEPINEMYLPQK.Y		K.QFQSGGSVATAPPAAVVEPINEMYLPQK.Y
24	36	2	1478.71	0.34	1	27.7	25.8	92.60%	F.VTCGFPNVDETIK.I	Carbamidomethyl (+57)	K.NVLVTFVTCGFPNVDETIK.I
56	67	2	1232.57	0.9	0	47.1	25.1	95.00%	F.SDAVADGPTICK.G	Carbamidomethyl (+57)	K.IMQGLQNGGAGIIELGIPFSDAVADGPTICK.G
584	611	3	2954.42	2.6	1	50.2	24.8	95.00%	R.EDGQIQDTHSISAGLDYPGVGPELSELK.Y		R.EDGQIQDTHSISAGLDYPGVGPELSELK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
54	VIPI_SCHPO	52.53%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
69	94	2	2433.1	-2.2	0	125	27.2	95.00%	K.IQITSEDGGAASTTDQGGAGGDQAAR.Q		K.IQITSEDGGAASTTDQGGAGGDQAAR.Q
55	68	2	1496.85	-1.8	0	63.6	18.5	95.00%	K.TALLLQDALLGQNK.I		K.TALLLQDALLGQNK.I
199	218	3	2268.13	4	1	49.3	24.5	95.00%	K.VQNAYEDGKNQLLGIHNEAR.R		K.VQNAYEDGKNQLLGIHNEAR.R
101	110	2	1087.63	5.8	0	34.3	20.8	95.00%	R.SAIISELLSR.G		R.SAIISELLSR.G
225	254	3	2955.41	4.7	1	54.3	25.2	95.00%	K.NQAEGTASPASSTPTAPAEKEPTAPTTESK.T		K.NQAEGTASPASSTPTAPAEKEPTAPTTESK.T
111	121	2	1260.64	3.7	1	31.8	24.1	95.00%	R.GYHLSDVTLEK.S		R.GYHLSDVTLEK.S
122	134	2	1410.71	4.2	1	61.1	24.7	95.00%	K.SIQLDQSYGVSSK.F		K.SIQLDQSYGVSSK.F
137	147	2	1100.62	4.3	0	27.7	22	93.70%	K.GILESALSGVR.S		K.GILESALSGVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
55	ECM17_SCHPO	12.76%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
66	90	4	2646.3	1.1	1	40.4	24.7	95.00%	K.SHADPFAHIADAILAEEEVASTQPK.Q		K.SHADPFAHIADAILAEEEVASTQPK.Q
314	325	2	1337.8	4.6	0	39.3	13.4	95.00%	R.LTVLEPITSLPR.K		R.LTVLEPITSLPR.K
878	900	3	2550.31	-0.042	0	26.1	22.8	95.00%	K.ALGLDNVEIDIDEPKPITNEDIK.Q		K.ALGLDNVEIDIDEPKPITNEDIK.Q
1053	1078	3	3057.48	0.0045	1	32.9	24.5	95.00%	K.QISNELLPTTSSYHEIWIEDPETVEK.R		K.QISNELLPTTSSYHEIWIEDPETVEK.R
908	931	2	2512.17	2	1	38.4	26.3	95.00%	R.GTIFEGLADESTGALAESDCQLTK.F	Carbamidomethyl (+57)	R.GTIFEGLADESTGALAESDCQLTK.F
611	636	3	2801.42	3.9	1	43.3	22.6	95.00%	K.GPSVVLAYLPYHSADDDAITVLQETK.K		K.GPSVVLAYLPYHSADDDAITVLQETK.K

1031	1048	2	2075.92	-1.2	1	50.2	27.3	95.00%	R.NVTCSSTPNNETIHDQLF.A	Carbamidomethyl (+57)	R.NVTCSSTPNNETIHDQLFAVSK.Q
173	180	2	899.49	2.3	1	25.9	19.8	91.10%	K.LNTGVLHF.Y		K.LNTGVLHFYSPVYDTTAALENIETLPSK.E
801	810	2	1058.57	5.4	0	27.5	22.5	93.40%	K.GADLNLSELK.Y		K.GADLNLSELK.Y
759	774	2	1850.84	-2	1	75.6	27.2	95.00%	K.IMAMDDFPIEELGNEK.N		K.IMAMDDFPIEELGNEK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
56	EF1B_SCHPO	32.71%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
14	22	2	1104.59	4.8	1	36.2	23.2	95.00%	K.QLNDFLLDK.S		K.QLNDFLLDK.S
153	165	2	1432.74	3.9	1	44.3	24.2	95.00%	R.SIQMDGLVWGLSK.L		R.SIQMDGLVWGLSK.L
64	73	2	985.54	-1.9	0	27.9	20.9	93.90%	Y.DLATLPGTAK.E		K.QIATYDLATLPGTAK.E
2	13	2	1209.59	3.7	1	57.4	25.4	95.00%	M.GFSDLTSDAGLK.Q		-.MGFSDLTSDAGLK.Q
59	73	2	1561.84	4.2	1	60.9	22.2	95.00%	K.QIATYDLATLPGTAK.E		K.QIATYDLATLPGTAK.E
129	149	2	2459.18	0.48	1	84.9	26.2	95.00%	K.SLVTLDVKPWDDETPMDELEK.A		K.SLVTLDVKPWDDETPMDELEK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
57	ADH_SCHPO	36.29%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
109	122	2	1616.75	1.9	1	43.8	26	95.00%	K.AEETICPHIQLSGY.T	Carbamidomethyl (+57)	K.AEETICPHIQLSGYTVDGTFQHYCIANATHATIIPESVPLEVAAPIMCAGITCYR.A
262	278	3	1659.85	0.85	0	24.2	24.9	93.10%	F.ARPGSTMVTVSMPAGAK.L		K.SYEQAAGFARPGSTMVTVSMPAGAK.L
236	253	2	1681.87	4.1	0	56	23.2	95.00%	K.AATNGGAHGTLVLSTSPK.S	Deamidation (+1)	K.AATNGGAHGTLVLSTSPK.S
254	278	3	2513.21	3.1	1	41.5	25.7	95.00%	K.SYEQAAGFARPGSTMVTVSMPAGAK.L		K.SYEQAAGFARPGSTMVTVSMPAGAK.L
170	194	3	2506.29	3.6	1	33.6	22	95.00%	K.VGPGEWICIPGAGGGLGHLAVQYAK.A	Carbamidomethyl (+57)	K.VGPGEWICIPGAGGGLGHLAVQYAK.A
123	131	2	1066.47	1.7	1	32.6	24.2	95.00%	Y.TVDGTFQHY.C		K.AEETICPHIQLSGYTVDGTFQHYCIANATHATIIPESVPLEVAAPIMCAGITCYR.A
42	62	3	2378.15	2.1	1	31.5	25.6	95.00%	K.YTGVCHTDLHALQGDWPLPAK.M	Carbamidomethyl (+57)	K.YTGVCHTDLHALQGDWPLPAK.M
200	214	2	1571.84	-2.1	1	90.8	23.2	95.00%	R.VVAIDTGDDKAELVK.S		R.VVAIDTGDDKAELVK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
58	DHAS_SCHPO	40.34%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
112	132	3	2341.31	2.7	1	53.3	16.3	95.00%	R.REPTVPLVVPTVNTDHLDVIK.Y		R.REPTVPLVVPTVNTDHLDVIK.Y
19	30	3	1445.76	4.9	1	23.3	23.7	91.60%	R.FITLLSDHPEFK.I		R.FITLLSDHPEFK.I
143	161	2	2003.03	3.7	0	71.4	23.7	95.00%	R.GCIITNSNCSTAAVVVPLK.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GCIITNSNCSTAAVVVPLK.A
304	318	3	1662.81	4.5	2	31.3	25.6	95.00%	R.LDRNNENGYAVSVGR.I		R.LDRNNENGYAVSVGR.I
215	227	2	1337.72	2.6	2	33.7	21.1	95.00%	R.KILGSVNSTISGY.E		R.KILGSVNSTISGYELTDNVVSAQCNR.V
228	240	2	1504.7	1.6	0	58.5	26.8	95.00%	Y.ELTDNVVSAQCNR.V	Carbamidomethyl (+57)	K.ILGSVNSTISGYELTDNVVSAQCNR.V
31	39	2	856.52	4.9	0	28.2	20.3	94.30%	K.IAVLGASAR.S		K.IAVLGASAR.S
287	303	3	2003.98	4.2	1	33.9	25.8	95.00%	K.QAIYVFDDSTPDRPQPR.L		K.QAIYVFDDSTPDRPQPR.L
267	278	2	1375.7	3.8	1	37.2	23.7	95.00%	R.EVLANYVSEPQK.L		R.EVLANYVSEPQK.L
6	18	2	1227.7	3.7	0	35.6	20.5	95.00%	K.VGILGATGTVGQR.F		K.VGILGATGTVGQR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
59	HXK1_SCHPO	27.07%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	12	3	1409.65	4.4	1	25.1	25.7	93.30%	M.SLHDAYHWPSR.T	Acetyl (+42)	-.MSLHDAYHWPSR.T

447	469	2	2153.17	3.4	0	105	19.9	95.00%	K.VVTIPAEDGSGVGAALVSALEAK.G			K.VVTIPAEDGSGVGAALVSALEAK.G
26	47	3	2676.35	2.8	1	37.5	23.5	95.00%	K.TLQDHLDELEEQFTIPTELLHR.V			K.TLQDHLDELEEQFTIPTELLHR.V
87	97	2	1141.65	1.8	0	56.2	19.9	95.00%	Y.LALDLGGTNLR.V			K.GLTTNPGDVPMVPTWIIGTPDGNEHGSYLALDLGGTNLR.V
283	301	3	2181.06	1.3	2	34.8	25.7	95.00%	R.TKYDVAIDEESPRPGLQTY.E			R.TKYDVAIDEESPRPGLQTYEK.M
472	484	2	1423.76	-2.1	1	34.3	21.3	95.00%	K.ALTSDILAEHLKN.-			K.ALTSDILAEHLKN.-
406	426	3	2369.2	3.6	2	22.8	23.8	90.90%	R.KMNKPSMIVGTDGSVYNLYPR.F			R.KMNKPSMIVGTDGSVYNLYPR.F
236	246	2	1271.53	0.67	1	29.7	25.5	95.00%	F.GTGCNACYIEK.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)		R.LNAILSDTTGTLVASNYASPGTEIGVIFGTGCNACYIEK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
60	UGPA1_SCHPO	24.70%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
299	314	3	1876.02	4.4	1	30	20.3	95.00%	R.LLEIAQVPPQHVEEFK.S		R.LLEIAQVPPQHVEEFK.S
20	34	2	1527.72	-2.4	1	92	26.8	95.00%	F.AFDNTATSIAASTMK.N		K.SQSAFAFDNTATSIAASTMK.N
162	175	2	1539.72	-1.8	1	41.1	26.4	95.00%	F.VLMNSFNTDEATAK.V		K.YNVNVPFVLMNSFNTDEATAK.V
74	104	3	3417.67	3.9	1	69	22.6	95.00%	R.GSEINWDLVESPKPEQVVEYDTITEAGGLSR.D		R.GSEINWDLVESPKPEQVVEYDTITEAGGLSR.D
185	194	2	1205.65	4.7	1	32.1	23.3	95.00%	K.IDILTFNQSR.Y		K.IDILTFNQSR.Y
408	419	2	1380.66	-0.88	0	33.5	26.1	95.00%	Y.SINHGQVEMNPR.R		K.SDLYSINHGQVEMNPR.R
115	129	2	1460.72	4.2	0	48.3	25.1	95.00%	K.LNGGLGTTMGCVGPK.S	Carbamidomethyl (+57)	K.LNGGLGTTMGCVGPK.S
287	298	2	1278.63	4.4	1	55.1	24.9	95.00%	K.GGTLIDYDGNVR.L		K.GGTLIDYDGNVR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
61	RL4A_SCHPO	33.88%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
141	161	3	2348.2	1.3	2	39.2	22.7	95.00%	R.GHRIEEIPEVPLVVDDAVQSF.Q		R.GHRIEEIPEVPLVVDDAVQSFQK.T
122	140	2	1845.04	4.3	1	48.1	16.9	95.00%	R.YAISSAVAASGVPSLLLAR.G		R.YAISSAVAASGVPSLLLAR.G
2	13	2	1304.71	4.5	1	25.5	21.8	90.30%	M.AAARPTVSIYSK.D	Acetyl (+42)	-.MAAARPTVSIYSK.D
14	29	2	1695.88	4.2	1	38.3	23.2	95.00%	K.DGSVSSETIALPFVFK.A		K.DGSVSSETIALPFVFK.A
144	163	2	2254.18	3.5	1	34.1	21.6	95.00%	R.IEEIPEVPLVVDDAVQSFQK.T		R.IEEIPEVPLVVDDAVQSFQK.T
276	291	2	1864.93	-0.92	1	81.3	25.4	95.00%	K.NYFLPENIISNADVTR.L		K.NYFLPENIISNADVTR.L
235	248	3	1457.84	-1.6	0	31.5	17.6	95.00%	R.LNLLQLAPGGHLGR.F		R.LNLLQLAPGGHLGR.F
292	303	2	1357.75	4	0	43.8	21.6	95.00%	R.LINSDEIQSIVK.A		R.LINSDEIQSIVK.A
87	97	2	1197.51	4.4	1	32.6	26.1	95.00%	R.SGQAAFGNMCR.S	Carbamidomethyl (+57)	R.SGQAAFGNMCR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
62	RS18_SCHPO	28.95%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	66	2	1246.61	4	0	41.5	25.2	95.00%	R.AGELTTEELER.I		R.AGELTTEELER.I
67	78	2	1386.79	4	1	45.2	19.3	95.00%	R.IVTIIQNPSQFK.I		R.IVTIIQNPSQFK.I
2	14	2	1578.85	-1.8	1	31.6	21.6	95.00%	M.SLVVPDNFQHILR.L	Acetyl (+42)	-.MSLVVPDNFQHILR.L
79	86	2	1031.56	6	1	52.6	22.4	95.00%	K.IPSWFLNR.Q		K.IPSWFLNR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
63	CDC48_SCHPO	15.09%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
28	38	2	1146.59	1.1	0	47.7	24	95.00%	Y.SAEDTATAILR.K		K.DTYSAEDTATAILR.K
550	563	2	1522.75	3.6	1	43.8	25.1	95.00%	K.AIANECSANFISVK.G	Carbamidomethyl (+57)	K.AIANECSANFISVK.G
287	297	2	1247.66	-0.1	1	43.9	23	95.00%	F.FLINGPEIMSK.M		R.AVANETGAFFFLINGPEIMSK.M
359	379	3	2280.22	4.2	1	31.5	20	95.00%	R.SNVVVMAATNRPNSIDPALRR.F		R.SNVVVMAATNRPNSIDPALRR.F
658	672	2	1769.92	-1.8	1	40.7	23.1	95.00%	R.LDQLIYVPLPDEEAR.F		R.LDQLIYVPLPDEEAR.F
316	332	2	1841.97	-2.9	1	50	21.6	95.00%	K.NSPAIIFIDEIDSIAPK.R		K.NSPAIIFIDEIDSIAPK.R

410	426	2	1858.86	0.69	1	68.7	27.7	95.00%	K.LADDVDLEQIAAETHGY.V		K.LADDVDLEQIAAETHGYVGSDLASLCSEAAMQQIR.E
588	604	2	1817.92	-1.2	1	76.6	24.7	95.00%	R.AAAPCVVFLDELDSIAK.A	Carbamidomethyl (+57)	R.AAAPCVVFLDELDSIAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
64	IF4A_SCHPO	24.23%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
156	165	2	1091.53	1.8	1	44	25	95.00%	R.ALPTDAVQMF.V		R.ALPTDAVQMFVLDEADEMLSR.G
58	69	2	1173.61	5	0	69	23.5	95.00%	R.DVLAQAQSGTGK.T		R.DVLAQAQSGTGK.T
49	69	3	2154.15	3.1	1	31.7	20.5	95.00%	R.AIMPILGERDVLAQAQSGTGK.T		R.AIMPILGERDVLAQAQSGTGK.T
378	392	2	1739.82	0.33	0	36.5	26.8	95.00%	Y.NTHIEEMPMNIADLI.-		R.EIEQFYNTHIEEMPMNIADLI.-
155	176	3	2506.23	3.9	2	41.3	24.8	95.00%	R.RALPTDAVQMFVLDEADEMLSR.G		R.RALPTDAVQMFVLDEADEMLSR.G
2	32	3	3667.76	4	1	58	22.9	95.00%	M.VDQLEDSVIETNYDEVIDTFDDMNLKPELLR.G		-.MVDQLEDSVIETNYDEVIDTFDDMNLKPELLR.G
372	392	2	2549.19	2.9	1	26.7	26.2	90.20%	R.EIEQFYNTHIEEMPMNIADLI.-		R.EIEQFYNTHIEEMPMNIADLI.-
166	176	2	1276.6	0.29	0	62.2	24.9	95.00%	F.VLDEADEMLSR.G		R.ALPTDAVQMFVLDEADEMLSR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
65	FAS1_SCHPO	5.79%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1068	1087	4	2303.16	0.7	2	20.8	24.6	95.00%	K.VNEPAKELLDGINETHIQHF.I		K.VNEPAKELLDGINETHIQHFIK.K
1117	1130	2	1421.7	4.7	0	59.8	25.6	95.00%	K.SLESVSVTEEAGSK.V		K.SLESVSVTEEAGSK.V
712	726	2	1655.88	-1.5	1	32.2	22.7	95.00%	K.ANPTFPIVLQWTGGR.A		K.ANPTFPIVLQWTGGR.A
2	12	2	1294.67	5.2	0	53.5	24.5	95.00%	M.VEAEQVHQSLR.S		-.MVEAEQVHQSLR.S
966	984	2	2177.07	4.2	1	92.2	25.1	95.00%	K.TTLIENFEDLNDPYPVAAR.F		K.TTLIENFEDLNDPYPVAAR.F
1870	1881	2	1266.57	5.2	1	37.8	25.8	95.00%	R.SDYGMVAANPSR.V		R.SDYGMVAANPSR.V
210	224	3	1723.91	5.4	1	36.5	22	95.00%	K.GLNVLDWLAGERPER.D		K.GLNVLDWLAGERPER.D
781	794	2	1545.81	3.9	1	42.1	23.7	95.00%	K.LPPMPFDGILFGSR.L		K.LPPMPFDGILFGSR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
66	RL8_SCHPO	28.19%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
24	32	2	1084.62	4.7	1	29.3	21.1	95.00%	K.NPLFVSRPR.S		K.NPLFVSRPR.S
109	120	2	1171.61	4.7	0	55.2	22.9	95.00%	R.LVAEAEAVANGK.S	Deamidation (+1)	R.LVAEAEAVANGK.S
134	146	2	1425.8	-1.1	1	55.2	18.9	95.00%	K.YGLNHVVALIEAK.K		K.YGLNHVVALIEAK.K
69	78	2	1082.65	-1.6	2	38.3	17	95.00%	R.LKVPPAIAQF.Q		R.LKVPPAIAQFQK.T
33	43	2	1188.62	4.1	1	26.8	24.2	92.40%	R.SFGIGQDIQPK.R		R.SFGIGQDIQPK.R
81	92	2	1364.74	3.7	2	46.2	22.3	95.00%	K.TLDKNTATQVFK.L		K.TLDKNTATQVFK.L
52	57	2	862.44	5.9	1	26.5	23.4	92.00%	K.WPEYIR.L		K.WPEYIR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
67	MET3_SCHPO	25.10%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
427	440	2	1651.86	4	1	77.5	23.2	95.00%	R.LDAISVFYAQELQR.A		R.LDAISVFYAQELQR.A
350	359	2	1102.6	3.9	0	29.9	22.6	95.00%	R.TLNISGTELR.R		R.TLNISGTELR.R
69	92	2	2586.35	1.6	1	44	21.6	95.00%	R.LSTGEVFPIPITLDLNESQADSLK.A		R.LSTGEVFPIPITLDLNESQADSLK.A
59	68	2	1233.64	5.6	1	40.5	23.7	95.00%	K.DYLNVVENLR.L		K.DYLNVVENLR.L
254	262	2	1012.62	5.1	0	33.5	17.2	95.00%	K.LSLLPLAMR.M		K.LSLLPLAMR.M
217	234	3	1974.04	0.41	1	38	22.1	95.00%	R.VLIHPVVGMTKPGDIDHF.T		R.VLIHPVVGMTKPGDIDHFTR.V
364	382	2	2159.15	2.7	1	56.8	21.5	95.00%	R.VGANIPEWFSYPEVVAILR.Q		R.VGANIPEWFSYPEVVAILR.Q
13	29	2	1924	2.8	1	48.1	23.5	95.00%	R.DAPLREQLEQEATSLPK.I		R.DAPLREQLEQEATSLPK.I
217	236	4	2231.2	3.6	1	31	20.1	95.00%	R.VLIHPVVGMTKPGDIDHFTR.V		R.VLIHPVVGMTKPGDIDHFTR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
68	YHY6_SCHPO	20.81%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
678	698	2	2257.13	4.5	0	51.2	24.5	95.00%	K.SLCIPLEQPSGEDAIIEGTTK.C	Carbamidomethyl (+57)	K.SLCIPLEQPSGEDAIIEGTTK.C
161	188	4	2736.49	3.7	1	29.1	17.2	95.00%	K.SVGVNPIIVDFSAPGSATAPSKPAAQKK.K		K.SVGVNPIIVDFSAPGSATAPSKPAAQKK.K
298	320	2	2539.22	1.6	1	29.3	24.8	95.00%	R.AGTSELDEPIAIRPTSETVMYPY.Y		R.AGTSELDEPIAIRPTSETVMYPYYAK.W
60	83	2	2367.33	-0.38	0	62.8	14.9	95.00%	K.SQTVVPIILAALETTSTPSGIAAK.A		K.SQTVVPIILAALETTSTPSGIAAK.A
161	187	3	2608.39	2.9	1	26.8	19.5	95.00%	K.SVGVNPIIVDFSAPGSATAPSKPAAQK.K		K.SVGVNPIIVDFSAPGSATAPSKPAAQK.K
298	323	3	2901.42	3	1	27.8	24	95.00%	R.AGTSELDEPIAIRPTSETVMYPYYAK.W		R.AGTSELDEPIAIRPTSETVMYPYYAK.W
492	511	2	2075.18	-2	0	29.3	15.1	95.00%	K.LPPAIALVQSVVVPCGITNK.T	Carbamidomethyl (+57)	K.LPPAIALVQSVVVPCGITNK.T
660	677	3	1900.86	4.5	1	43.4	27	95.00%	R.QVNGDEPEDEKAPSMGAK.S		R.QVNGDEPEDEKAPSMGAK.S
387	398	2	1343.81	4.3	1	30.5	13.8	95.00%	R.IYTDLLAVPVIK.G		R.IYTDLLAVPVIK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
69	PYR1_SCHPO	6.24%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1135	1145	2	1229.6	4.3	0	46.2	25	95.00%	R.MLDDIGVDQPK.W		R.MLDDIGVDQPK.W
1771	1784	2	1494.85	4.1	0	35.2	17.2	95.00%	R.EAIPLLLTAVNEGR.L		R.EAIPLLLTAVNEGR.L
228	245	3	2026.07	0.69	1	34.6	21.6	95.00%	W.KNPNTENLTSQVSIKEPK.L		K.DWSTAFEDIPWKNPNTENLTSQVSIKEPK.L
457	466	2	1084.56	6.1	0	38.9	23	95.00%	K.LPGGTIEENR.S		K.LPGGTIEENR.S
1880	1906	3	2689.36	3.3	1	28.6	22.9	95.00%	K.VSALMSPGLPHAAPSLAEAFGQAPENK.A		K.VSALMSPGLPHAAPSLAEAFGQAPENK.A
1426	1442	2	1819.78	-0.21	1	49.7	27.5	95.00%	F.ATAGTSDYFMESGVPCK.Y	Carbamidomethyl (+57)	K.LYENNYNIFATAGTSDYFMESGVPCK.Y
662	671	2	1112.62	1.4	0	27	19.6	92.80%	F.ATSPQVLIER.S		R.AAYALGGLGSGFADNEAELIDLCTLAFATSPQVLIER.S
580	597	2	2032.07	0.085	2	39.1	22.1	95.00%	K.VLGTPIDTIITTEDRELF.A		K.VLGTPIDTIITTEDRELFAR.A
1804	1818	3	1724.81	5.5	0	27.4	26.4	95.00%	R.LHDQDDSGVQLEVDR.S		R.LHDQDDSGVQLEVDR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
70	ILV3_SCHPO	17.22%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
446	459	2	1608.78	-1.6	1	59.8	26.2	95.00%	R.VFDAENDFIAALER.G		R.VFDAENDFIAALER.G
49	68	2	2142.97	5.2	1	90.3	27.1	95.00%	K.SQGASQAMLYATGLNEEDMK.K		K.SQGASQAMLYATGLNEEDMK.K
185	202	2	1896.88	0.059	1	41	26.6	95.00%	R.AGHSPCQNNAPIDIVSAF.Q	Carbamidomethyl (+57)	R.AGHSPCQNNAPIDIVSAFQSYGEFITGK.I
402	417	4	1843.09	3.6	1	32.1	12.6	95.00%	K.IIRPLSNPIKTEGHLR.V		K.IIRPLSNPIKTEGHLR.V
40	48	2	994.5	5.2	1	30.6	24.9	95.00%	K.YSETITGPK.S		K.YSETITGPK.S
266	278	3	1408.68	4.8	1	24.2	25.9	91.70%	K.FAECEAAGSAIKR.L	Carbamidomethyl (+57)	K.FAECEAAGSAIKR.L
224	236	2	1293.47	1.7	1	31	25.1	95.00%	R.HACPGGGACGGMY.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.HACPGGGACGGMYTANTMASCAEAMGMTLPGSSSYLAGSPEK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
71	LEUC_SCHPO	17.94%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
59	77	4	2123.12	3.9	1	27	21.1	95.00%	R.HPELALATVDHNIPTDPRK.D		R.HPELALATVDHNIPTDPRK.D
540	563	3	2538.39	3.4	1	28.2	16.8	95.00%	K.FTVVEGIAAPLPMANVDTDKIIPK.Q		K.FTVVEGIAAPLPMANVDTDKIIPK.Q
417	436	3	2355.02	4.1	1	24.9	27.4	90.10%	R.EAGCSMCLGMNPDQLKPYER.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.EAGCSMCLGMNPDQLKPYER.C
303	323	3	2168.13	1.5	0	27.4	22.9	95.00%	W.GTSPQDVIPINGNIPDPAHVK.D		K.YDIEVEINAADVLPTVTWGTSPQDVIPINGNIPDPAHVK.D

603	619	3	1826.86	5.3	1	37.3	26.9	95.00%	R.HATVLVAHDNFGCGSSR.E	Carbamidomethyl (+57)	R.HATVLVAHDNFGCGSSR.E
477	493	2	1810.88	4.1	1	36.5	25.9	95.00%	R.EFFGDVSNGSPSIITNK.N		R.EFFGDVSNGSPSIITNK.N
650	667	2	2027	4	0	40.9	25.3	95.00%	K.NGMLPIPTPIEQVNDMMK.A		K.NGMLPIPTPIEQVNDMMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
72	LYS12_SCHPO	30.39%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
7	26	3	1987.19	3.6	1	23.5	9.03	91.90%	R.IVLGLIPADGIGKEVVPAAR.R		R.IVLGLIPADGIGKEVVPAAR.R
282	297	3	1621.79	1.5	0	37.7	25.6	95.00%	F.VMSEPVHGSAPDIAGR.G		R.EPECFDVVVAPNLYGDILSDGAASLIGSLGLVPSANVGDNFVMSEPVHGSAPDIAGR.G
86	97	2	1231.7	4.7	1	25.9	20.9	91.00%	K.VAGYSSPIVALR.K		K.VAGYSSPIVALR.K
197	208	2	1324.65	5.3	1	41.8	25.5	95.00%	K.SNVMSVTDGLFR.E		K.SNVMSVTDGLFR.E
298	307	2	1044.58	4.6	1	32.2	22.4	95.00%	R.GIANPVATFR.S		R.GIANPVATFR.S
188	196	3	1047.69	4.7	0	25.1	3.01	94.20%	K.KPLVTIIHK.S		K.KPLVTIIHK.S
127	138	2	1568.72	4	1	44	26	95.00%	R.ENTECLYVKEER.M	Carbamidomethyl (+57)	R.ENTECLYVKEER.M
67	85	3	2071.06	4.3	2	52.5	23.8	95.00%	R.LKTECNAALFGAVQSPTHK.V	Carbamidomethyl (+57)	R.LKTECNAALFGAVQSPTHK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
73	CYSD_SCHPO	39.63%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
72	100	3	2787.49	3.3	1	49.9	18.1	95.00%	R.IAALEHGAAAIATSSGTSALFMALTTLAK.A		R.IAALEHGAAAIATSSGTSALFMALTTLAK.A
366	377	2	1185.64	4.4	0	34.5	21.8	95.00%	K.LASQLANVGDAK.T		K.LASQLANVGDAK.T
170	210	4	4156.13	4.3	1	53.9	19.3	95.00%	R.IAEVAHAAGVPLMVDNTFGGGGYLVRPIDHGADIVTHSATK.W		R.IAEVAHAAGVPLMVDNTFGGGGYLVRPIDHGADIVTHSATK.W
132	150	2	2074.95	4.2	1	127	26.7	95.00%	K.FVNGDDPNDLAAQIDENTK.A		K.FVNGDDPNDLAAQIDENTK.A
378	403	3	2798.48	2.5	1	42.6	20.2	95.00%	K.TLVIAPAYTTHLQLTDEEQISAGVTK.D		K.TLVIAPAYTTHLQLTDEEQISAGVTK.D
193	210	3	1929.04	0.52	0	23.4	20.8	91.80%	Y.LVRPIDHGADIVTHSATK.W		R.IAEVAHAAGVPLMVDNTFGGGGYLVRPIDHGADIVTHSATK.W
2	26	3	2735.28	1.1	1	59.6	26.1	95.00%	M.PVESEHFETLQLHAGQEPDAATSSR.A		-.MPVESEHFETLQLHAGQEPDAATSSR.A
211	228	3	1752.91	-1.7	1	26.2	22.8	95.00%	K.WIGGHGTTIGGVIVDSGK.F		K.WIGGHGTTIGGVIVDSGK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
74	RS3B_SCHPO	11.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
200	213	2	1513.86	-1.9	1	47	19.3	95.00%	R.ATGSIFPLQNVLVR.K		R.ATGSIFPLQNVLVR.K
228	241	2	1524.79	4.4	0	71.2	23.4	95.00%	K.LLELHGESQDVGTK.V		K.LLELHGESQDVGTK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
75	ACON_SCHPO	11.95%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
532	549	2	1853.89	4.6	1	68.9	26.5	95.00%	K.GYDPGSNTYVAPSSVNVK.D		K.GYDPGSNTYVAPSSVNVK.D
613	626	2	1430.68	-1.6	0	42.5	26.4	95.00%	Y.MIGAINAENGEANK.L		R.GHLQNISNNYMIGAINAENGEANK.L
392	402	2	1203.6	5.2	0	35.2	24.5	95.00%	R.AASICQQAIDK.G	Carbamidomethyl (+57)	R.AASICQQAIDK.G
65	80	3	1895.95	4.5	1	26.2	25.3	95.00%	K.ILYGHLDDPVNQDIER.G		K.ILYGHLDDPVNQDIER.G
652	666	2	1665.78	3.4	1	67.3	26.5	95.00%	R.WVTLGEQNFGEGSSR.E		R.WVTLGEQNFGEGSSR.E
462	470	2	1052.53	5	1	36.5	24.7	95.00%	K.NSIVTSYNR.N		K.NSIVTSYNR.N
476	485	2	1056.46	1.7	1	39	24.5	95.00%	R.NDANPATHAF.V		R.NDANPATHAFVTSPDIVTAMVFSGDMNFNPLTDTLK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
76	NACA_SCHPO	54.91%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	75	2	1164.62	5.8	1	59.3	23.1	95.00%	K.SSNNAYIVLGK.V		K.SSNNAYIVLGK.V

94	118	3	2590.19	-0.77	1	57.5	26.8	95.00%	K.QATETKEEAAITEESGDAQPADTAK.I		K.QATETKEEAAITEESGDAQPADTAK.I
119	137	3	2123	4.4	1	54.2	26.1	95.00%	K.IEESFEQEKAVDETGVDAK.D		K.IEESFEQEKAVDETGVDAK.D
11	26	2	1637.87	4.6	0	55.2	22.4	95.00%	K.ISELPAGSTTVVHAEK.A		K.ISELPAGSTTVVHAEK.A
52	64	2	1540.93	4.4	1	50.2	11.8	95.00%	K.NILLIINEPIVYK.S		K.NILLIINEPIVYK.S
76	86	2	1189.58	4.9	0	47.2	24.9	95.00%	K.VTVEDMAAQAR.A		K.VTVEDMAAQAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
77	GLT1_SCHPO	6.63%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1442	1464	3	2335.04	4.9	1	32.4	27.3	95.00%	R.NSGAIAVVEGVGDHGCEYMTGGR.V	Carbamidomethyl (+57)	R.NSGAIAVVEGVGDHGCEYMTGGR.V
1897	1918	3	2189.08	3.9	1	55	25.1	95.00%	K.GKDVIVIGGGDTGNDCLGTSVR.H	Carbamidomethyl (+57)	K.GKDVIVIGGGDTGNDCLGTSVR.H
672	685	2	1555.69	5.3	1	68	26.5	95.00%	R.ICSEADTAVNEGYK.A	Carbamidomethyl (+57)	R.ICSEADTAVNEGYK.A
624	638	2	1701.91	4.2	1	45.5	22.6	95.00%	R.MPTPILTVEEFNALK.N		R.MPTPILTVEEFNALK.N
1664	1675	2	1427.58	-0.87	1	37.1	26	95.00%	F.CQSDYGCPISNK.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.CMDCGTPFCQSDYGCPISNK.I
1690	1707	2	2063.08	4.1	1	61.9	22.4	95.00%	K.EALTQLLLTNNFPEFTGR.V		K.EALTQLLLTNNFPEFTGR.V
1022	1038	3	1639.81	4.9	0	25.7	25.9	93.80%	K.MAQGAKPGEGGELPGNK.V		K.MAQGAKPGEGGELPGNK.V
1442	1459	2	1832.8	-2	1	58.1	27.1	95.00%	R.NSGAIAVVEGVGDHGCEY.M	Carbamidomethyl (+57)	R.NSGAIAVVEGVGDHGCEYMTGGR.V
1758	1776	2	1792.97	-2.9	0	96.3	20.8	95.00%	R.VAIIGSGPAGLAAADQLNR.A		R.VAIIGSGPAGLAAADQLNR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
78	RAD25_SCHPO	34.07%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
63	74	2	1417.75	4.9	1	43.2	23.2	95.00%	R.IISSIEQKEESR.G		R.IISSIEQKEESR.G
155	171	2	1752.87	-2.2	0	31.5	25.5	95.00%	K.AASDIAVAELPPTDPMR.L		K.AASDIAVAELPPTDPMR.L
88	107	3	2369.22	3.8	1	24.6	23.4	93.50%	R.KKIEDELSDICHDVLSVLEK.H	Carbamidomethyl (+57)	R.KKIEDELSDICHDVLSVLEK.H
30	43	3	1633.81	-0.96	1	26.9	25.3	95.00%	K.KVACSNDKLSVEER.N	Carbamidomethyl (+57)	K.KVACSNDKLSVEER.N
233	261	3	3041.35	0.82	1	43.7	27	95.00%	W.TSDAEYNQSAKEEAPAAAAASENEHPEPK.E		R.DNLTLWTSDAEYNQSAKEEAPAAAAASENEHPEPK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
79	YF19_SCHPO	14.51%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
181	194	2	1439.82	3.6	0	42.9	17.9	95.00%	K.IAPAVACGNTIILK.T	Carbamidomethyl (+57)	K.IAPAVACGNTIILK.T
122	132	2	1208.53	4.1	1	34.4	25.2	95.00%	R.GDVQAAADCFR.Y	Carbamidomethyl (+57)	R.GDVQAAADCFR.Y
195	208	2	1516.82	4.7	0	34.9	22.6	95.00%	K.TAELTPLSALCLTK.F	Carbamidomethyl (+57)	K.TAELTPLSALCLTK.F
5	17	2	1406.78	4.6	0	33	20	95.00%	K.LVDHVEITVPTGK.T		K.LVDHVEITVPTGK.T
71	80	2	1161.56	3.7	1	28.3	24.4	94.40%	R.AAFQTDAPWR.K		R.AAFQTDAPWR.K
105	115	2	1159.61	0.67	0	42.2	24.4	95.00%	Y.LASIETLDNGK.S		R.LADCIEQNLEYLASIETLDNGK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
80	RL13_SCHPO	43.75%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
172	183	2	1398.66	5.4	1	54	26.1	95.00%	K.NFNAFSTLSNER.A		K.NFNAFSTLSNER.A
46	64	4	2080.27	3.1	0	20	6.02	94.80%	K.IAPRPVEAIRPAVKPPTIR.Y		K.IAPRPVEAIRPAVKPPTIR.Y
118	128	3	1326.79	4.7	1	51.2	17.9	95.00%	K.VYLAHLIVFPR.K		K.VYLAHLIVFPR.K
135	171	3	3809.91	1.5	1	74.6	20	95.00%	K.KGDATDVSGAEQTDVAAVLPITQEAVEEAKPITEEAK.N		K.KGDATDVSGAEQTDVAAVLPITQEAVEEAKPITEEAK.N
89	100	2	1263.7	3.9	0	28.9	20.6	95.00%	R.VASTIGIPVDHR.R		R.VASTIGIPVDHR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
81	O59743_SCHPO	21.49%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
210	225	2	1690.88	3.5	1	52.7	24	95.00%	R.SIQDVPFTSATVDIAK.K		R.SIQDVPFTSATVDIAK.K

116	127	2	1462.66	0.74	1	28.5	26.6	92.60%	W.EQALQDNKPEEY.Y		K.LKPVPTSWEQALQDNKPEEYYHLSAPDCK.S
1	11	2	1319.72	4	1	28	22.8	94.10%	-.MDPYTVAIIKK.L	Acetyl (+42)	-.MDPYTVAIIKK.L
11	24	2	1515.81	-2.1	1	77.1	23.2	95.00%	K.KLGIEEQVETAATK.S		K.KLGIEEQVETAATK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
82	THI4_SCHPO	23.94%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
356	372	2	1817.84	-1.9	0	74.9	26.9	95.00%	K.GNEGEIMNLAGEQGLMR.G		K.GNEGEIMNLAGEQGLMR.G
373	385	2	1353.71	4.1	0	37.5	23.1	95.00%	R.GVDSISQHTLAAR.I		R.GVDSISQHTLAAR.I
121	140	2	2014.95	-0.55	1	72.2	26.7	95.00%	K.AAADGADYVGIGSIYETNTK.D		K.AAADGADYVGIGSIYETNTK.D
249	265	4	1917.09	3.2	2	33.8	16	95.00%	K.LKDFTPLIHHLTNAVAK.N		K.LKDFTPLIHHLTNAVAK.N
27	42	3	1733.95	4.6	0	28	20	95.00%	R.QVEEGILGGVTLVQHR.E		R.QVEEGILGGVTLVQHR.E
310	338	3	3045.65	3.6	1	44.4	14.6	95.00%	K.TYIHAAQVNNDLARPVILDPVAVGATTAR.S		K.TYIHAAQVNNDLARPVILDPVAVGATTAR.S
237	248	2	1322.76	4.7	0	31.5	17.5	95.00%	K.DLLNQIPAALQK.L		K.DLLNQIPAALQK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
83	RS22_SCHPO	27.69%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
98	108	2	1171.7	4.9	0	29.1	18	95.00%	R.QVGVIVLTTSR.G		R.QVGVIVLTTSR.G
4	19	2	1814.89	-1.8	0	88.9	25.2	95.00%	R.QSVLADCLNNIVNAER.R	Carbamidomethyl (+57)	R.QSVLADCLNNIVNAER.R
89	97	2	1111.62	5.6	1	31.9	18.8	95.00%	K.WVNQLLPSR.Q		K.WVNQLLPSR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
84	MMF1_SCHPO	47.53%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
109	124	2	1781.86	-2	1	63.1	26.2	95.00%	K.VNIFLADMDDFAAVNK.V		K.VNIFLADMDDFAAVNK.V
59	75	2	1747.86	2.8	1	34.8	25.3	95.00%	K.ANGVIYCSGQIPVANGK.V	Carbamidomethyl (+57)/ Deamidation (+1)	K.ANGVIYCSGQIPVANGK.V
87	105	2	2116.09	4.6	0	131	22.9	95.00%	R.QCLLNLQEVLTEAGSSLNK.I	Carbamidomethyl (+57)	R.QCLLNLQEVLTEAGSSLNK.I
125	137	2	1483.81	3.9	1	42.4	20.4	95.00%	K.VYTEVLPDPKPAR.S		K.VYTEVLPDPKPAR.S
47	58	2	1247.66	5.3	1	27.4	23	93.30%	K.LSSAGPYNQAIK.A		K.LSSAGPYNQAIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
85	SODC_SCHPO	41.56%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	144	4	2825.43	3.9	1	21.6	23	95.00%	R.TIVIHAGEDDLGKGTSEESLKTGNAGAR.N		R.TIVIHAGEDDLGKGTSEESLKTGNAGAR.N
81	97	2	1765.87	4	0	72.3	25.7	95.00%	R.HVGDLGNLESDAQGNIK.T		R.HVGDLGNLESDAQGNIK.T
117	137	3	2198.12	3.9	1	49.5	24	95.00%	R.TIVIHAGEDDLGKGTSEESLK.T		R.TIVIHAGEDDLGKGTSEESLK.T
98	116	2	1984.04	4.4	1	72.6	22	95.00%	K.TTFSDSVISLFGANSIIGR.T		K.TTFSDSVISLFGANSIIGR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
86	SERC_SCHPO	21.85%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
376	385	2	1147.65	4.7	1	32.8	20.8	95.00%	R.LIDLLESFAK.A		R.LIDLLESFAK.A
164	184	3	2459.11	0.78	1	44.6	27.2	95.00%	Y.YCDNETVHGVEFNEPPTNIPK.G	Carbamidomethyl (+57)	K.FTPDGETSLVYYCDNETVHGVEFNEPPTNIPK.G
216	228	2	1299.74	5	1	37	19.3	95.00%	K.NAGPAGITVVFVR.D		K.NAGPAGITVVFVR.D
324	329	2	766.38	5.3	1	26.2	23.1	91.50%	R.MNVTFR.I		R.MNVTFR.I
330	352	5	2716.42	3.7	1	22	20.5	95.00%	R.IEPQELESEFLAEAEKHHLVQLK.G		R.IEPQELESEFLAEAEKHHLVQLK.G
375	385	2	1303.75	-0.87	2	37.6	19.2	95.00%	R.RLIDLLESFAK.A		R.RLIDLLESFAK.A
189	199	2	1282.6	4.3	1	67	26.1	95.00%	R.VCDVSSNFISR.K	Carbamidomethyl (+57)	R.VCDVSSNFISR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
87	PMP20_SCHPO	44.23%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

40	55	2	1746.83	0.58	1	49.3	26.2	95.00%	F.TPPCSSQVPGYIANEK.Q	Carbamidomethyl (+57)	K.FIIVGVPGAFTPPCSSQVPGYIANEK.Q
82	93	2	1265.53	-1.7	1	49.9	25.9	95.00%	K.SFDGGEQSGVHF.V		K.SFDGGEQSGVHFVADWNGEFTK.A
11	29	3	2215.13	4.2	1	34.9	23.8	95.00%	K.VTLWENKPEEVVEFPSQGK.F		K.VTLWENKPEEVVEFPSQGK.F
135	156	2	2379.21	3.2	1	61.1	23.8	95.00%	K.VFIENEVTDVDISSADKVLSSL.-		K.VFIENEVTDVDISSADKVLSSL.-
135	151	2	1879.9	-2.4	1	65.3	26.6	95.00%	K.VFIENEVTDVDISSADK.V		K.VFIENEVTDVDISSADK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
88	DHOM_SCHPO	22.61%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
42	56	2	1619.8	0.74	1	51.5	25.3	95.00%	F.NVVAISSMEGHYVSK.D		K.GFNENASTNGTTSFNVVAISSMEGHYVSK.D
57	67	2	1391.68	4.7	1	33.1	24.6	95.00%	K.DYQPINLSEWK.N		K.DYQPINLSEWK.N
125	138	2	1568.79	4.5	1	56.7	23.9	95.00%	K.AFSASNDVYQNIIK.A		K.AFSASNDVYQNIIK.A
89	110	2	2284.19	-1.7	1	95.3	22.5	95.00%	K.SPLPAILVDNTASEAIAQSYPK.F		K.SPLPAILVDNTASEAIAQSYPK.F
320	331	2	1307.64	0.83	1	31.5	25.5	95.00%	F.ANLQSSDNIISF.T		K.YDASHPFANLQSSDNIISFTTK.R
78	88	2	1190.66	0.99	1	43.8	21.5	95.00%	Y.SLDALVDFLAK.S		K.NLTSQNQGAYSLDALVDFLAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
89	YHZ8_SCHPO	39.39%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
18	30	3	1414.8	-1.4	1	33.5	20.5	95.00%	K.KGEGDKILDLLSK.V		K.KGEGDKILDLLSK.V
144	164	3	2285.2	4.3	1	37.3	22.2	95.00%	K.ADTSLIIHSLDDPSLYAVVTR.Y		K.ADTSLIIHSLDDPSLYAVVTR.Y
104	121	3	1969.94	1.6	2	27.5	26.2	95.00%	K.VVDGHLDKDNLGPDAKDY.V		K.VVDGHLDKDNLGPDAKDYVLYTEYTGDSATLK.Q
122	135	2	1559.77	0.51	1	64.2	25.3	95.00%	Y.VLYTEYTGDSATLK.Q		K.DYVLYTEYTGDSATLK.Q
2	13	2	1361.7	3.8	1	57.2	24.5	95.00%	M.SFPASTHVYIAK.I	Acetyl (+42)	-.MSFPASTHVYIAK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
90	EF1G_SCHPO	12.71%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
207	216	2	1182.71	4	1	27.1	15.7	92.90%	K.FIDQPLPIIK.A		K.FIDQPLPIIK.A
128	139	2	1303.72	4.6	1	40.7	21.9	95.00%	K.EAETAIALIFAR.F		K.EAETAIALIFAR.F
198	216	3	2163.26	0.64	2	34.5	12.3	95.00%	K.LDAITEPLKFIDQPLPIIK.A		K.LDAITEPLKFIDQPLPIIK.A
392	400	3	1070.55	-1.5	1	26.9	23.6	95.00%	W.AWDKPIEGR.E		K.AFIEDAWAWDKPIEGR.E
116	127	2	1294.63	4.3	1	26.2	25.4	90.90%	R.VFGAPYDEQAAK.E		R.VFGAPYDEQAAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
91	RS14_SCHPO	41.73%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	129	2	1442.73	3.7	0	46.5	24.9	95.00%	R.IEDVTPIPTDSTR.R		R.IEDVTPIPTDSTR.R
117	130	3	1598.84	5.4	1	24.2	22.5	93.00%	R.IEDVTPIPTDSTRR.K		R.IEDVTPIPTDSTRR.K
52	72	3	2181.01	3.8	2	31.5	27.2	95.00%	K.TDRDESSPYAAMLAAQDAAAK.C		K.TDRDESSPYAAMLAAQDAAAK.C
61	72	2	1130.58	1.7	0	50.2	23.7	95.00%	Y.AAMLAAQDAAAK.C		R.DESSPYAAMLAAQDAAAK.C
95	105	2	1037.57	5.3	0	47.1	21.8	95.00%	K.TPGPGAQAALR.A		K.TPGPGAQAALR.A
73	84	3	1367.77	4	1	24.2	18.4	93.00%	K.CKEVGITALHIK.I	Carbamidomethyl (+57)	K.CKEVGITALHIK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
92	DYR_SCHPO	15.40%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
164	183	3	2062.15	3.7	0	25.4	16.2	94.50%	K.LTTPSLHIAGTSDTLVPLAR.S		K.LTTPSLHIAGTSDTLVPLAR.S
191	212	3	2537.31	3.6	1	37.3	21.9	95.00%	R.CENAHVLLHPGQHIVPQQAVYK.T	Carbamidomethyl (+57)	R.CENAHVLLHPGQHIVPQQAVYK.T

446	457	2	1300.66	0.29	1	39	23.8	95.00%	Y.GKNDDVNVALEK.L		K.EEVEIEFELYGKNDDVNVALEK.L
265	281	2	1722.79	-1.5	0	74.1	27.1	95.00%	F.ANVTSSTESSGQLEEGK.S		K.QEMAYFANVTSSTESSGQLEEGK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
93	RS6B_SCHPO	25.52%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	115	2	1739.01	3.8	0	65.7	16.6	95.00%	R.GCIVGQDLAVLALAIVK.Q	Carbamidomethyl (+57)	R.GCIVGQDLAVLALAIVK.Q
59	72	3	1625.86	4.7	1	32.2	22.4	95.00%	K.QGFPMFQGVLLPHR.V		K.QGFPMFQGVLLPHR.V
116	131	2	1695.88	3.9	0	43.6	23.4	95.00%	K.QGEQDIPGLTDVTVPK.R		K.QGEQDIPGLTDVTVPK.R
204	217	2	1606.78	4.3	2	54.8	26.1	95.00%	K.NREEAAEFAQLMAK.R		K.NREEAAEFAQLMAK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
94	BCA1_SCHPO	22.63%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
315	331	2	1670.97	4.2	1	59.5	16.5	95.00%	R.LLEVFGAGTAALVSPVK.A		R.LLEVFGAGTAALVSPVK.A
37	49	3	1581.74	4.5	1	25.4	26.1	93.20%	K.FGENFTDHMLIMK.W		K.FGENFTDHMLIMK.W
262	278	2	1794.99	-1.3	0	55.7	20.1	95.00%	K.EIITAPLDGMILPGVTR.D		K.EIITAPLDGMILPGVTR.D
337	359	2	2462.15	-1.3	1	50.2	26.5	95.00%	K.GTEYEIPMPEGQEAGPITSEISK.W		K.GTEYEIPMPEGQEAGPITSEISK.W
115	130	2	1769.96	3.9	1	43.7	20.6	95.00%	R.ISLPSFDPAELAEIIR.K		R.ISLPSFDPAELAEIIR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
95	PYC_SCHPO	6.84%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1109	1129	3	2088.05	4.4	0	38.2	24.2	95.00%	R.ADPGNPGHVAAPMSGTIVEIR.V		R.ADPGNPGHVAAPMSGTIVEIR.V
839	848	2	1297.58	4.8	1	38.2	25.9	95.00%	R.EIDSYWAQMR.L		R.EIDSYWAQMR.L
829	838	2	1275.63	4.5	1	27.7	24.9	93.70%	K.QLEFDNNQLR.E		K.QLEFDNNQLR.E
917	929	2	1447.76	4.7	1	42.2	24.4	95.00%	K.VVGDLAQFMVQNK.L		K.VVGDLAQFMVQNK.L
302	315	2	1628.75	2	1	37.3	27	95.00%	K.YCNAGTAEFLLDQK.G	Carbamidomethyl (+57)	K.YCNAGTAEFLLDQK.G
867	879	2	1419.75	-0.011	0	28.1	24	94.10%	Y.NHEIPGGQLTNLK.F		K.GTDSDVYNHEIPGGQLTNLK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
96	ASNS_SCHPO	12.57%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
279	292	2	1349.76	-2	0	26.5	19	92.00%	F.AIGLPGSPDLLAAR.K		K.LHSFAIGLPGSPDLLAAR.K
51	69	2	1853.97	-0.28	0	83.9	22	95.00%	R.LAIVGVESGAQPLVSDDGK.L		R.LAIVGVESGAQPLVSDDGK.L
456	463	2	1039.58	0.75	1	57	18.8	95.00%	Y.LPQDILWR.Q		K.AFDTTHDSSLQPYLPQDILWR.Q
516	523	2	1035.55	6.3	1	30	21.9	95.00%	K.LFDEIFPR.Q		K.LFDEIFPR.Q
399	408	2	1120.54	4.9	1	26.3	23.4	91.70%	K.STMAWGLEAR.V		K.STMAWGLEAR.V
464	474	2	1256.57	0.95	2	28	26.5	92.10%	R.QKEQFSDGVGY.S		R.QKEQFSDGVGYSWIDALK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
97	HMCS_SCHPO	25.95%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
264	282	2	2060.02	4.4	1	63.4	25.8	95.00%	R.LLYTDSAAEPSNPELEGVR.E		R.LLYTDSAAEPSNPELEGVR.E
393	407	3	1858.89	-1.4	1	27.1	26.4	94.70%	R.HCLTPTQYEEAIELR.H	Carbamidomethyl (+57)	R.HCLTPTQYEEAIELR.H
155	183	3	2859.53	3.9	1	40.5	18.8	95.00%	K.GNARPTGGAGCVALLVGPNAPIVFEPGLR.G	Carbamidomethyl (+57)	K.GNARPTGGAGCVALLVGPNAPIVFEPGLR.G
17	37	3	2214.06	0.46	1	46.3	26.1	95.00%	Y.TPNQYVEQAALEAHDGVSTGK.Y		K.GLVLYTPNQYVEQAALEAHDGVSTGK.Y
264	291	3	3030.55	2.7	1	23.5	21.3	91.90%	R.LLYTDSAAEPSNPELEGVRELLSTLDAK.K		R.LLYTDSAAEPSNPELEGVRELLSTLDAK.K
382	392	3	1300.68	5.1	1	26	23.3	95.00%	K.KTNLVNDLDNR.H		K.KTNLVNDLDNR.H
217	228	2	1325.64	3.7	1	38.4	25.8	95.00%	K.ALDGAYANYNVR.D		K.ALDGAYANYNVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
98	IF5A1_SCHPO	36.94%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	29	3	3107.41	2.7	1	84.1	26.2	95.00%	M.AEEEHVDFEGGEAGASLTFPMQCSALRK.N	Acetyl (+42)/ Carbamidomethyl (+57)	-.MAEEEHVDFEGGEAGASLTFPMQCSALRK.N
2	28	3	2979.31	4	1	77.3	26.7	95.00%	M.AEEEHVDFEGGEAGASLTFPMQCSALR.K	Acetyl (+42)/ Carbamidomethyl (+57)	-.MAEEEHVDFEGGEAGASLTFPMQCSALR.K
70	87	3	2075.96	-1.8	2	58.3	27.2	95.00%	R.KYEDMSPSTHNMDVPVVK.R		R.KYEDMSPSTHNMDVPVVK.R
58	69	2	1352.76	4.3	1	43.7	18.5	95.00%	K.VHIVALDIFNGR.K		K.VHIVALDIFNGR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
99	TAL1_SCHPO	16.15%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
27	44	3	1917.03	4	1	42	22.1	95.00%	K.YKPQDATTNPSLILAASK.K		K.YKPQDATTNPSLILAASK.K
9	26	2	1795.89	4.5	1	86.8	25.2	95.00%	K.ATGTVVVSDTGDFESIAK.Y		K.ATGTVVVSDTGDFESIAK.Y
45	60	2	1721.9	-1.6	1	87.5	23.5	95.00%	K.KPQYAALVDAAVDYAK.A		K.KPQYAALVDAAVDYAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
100	GLNA_SCHPO	17.83%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
153	170	2	1809.83	4.4	1	40.7	26.4	95.00%	K.GGFPGPQPGPFYCGVGTGR.V	Carbamidomethyl (+57)	K.GGFPGPQGPFYCGVGTGR.V
237	260	4	2635.31	3.2	1	28.9	24.7	95.00%	K.ISFHPKPILGDWNGAGCHTNVSTK.D	Carbamidomethyl (+57)	K.ISFHPKPILGDWNGAGCHTNVSTK.D
338	359	3	2476.24	4.1	1	26.8	23.6	95.00%	R.RPASSIDPYLVTGIITETMFEH.-		R.RPASSIDPYLVTGIITETMFEH.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
101	SYDC_SCHPO	13.10%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
281	294	2	1356.6	4.8	1	27.5	25.9	92.20%	K.MSGASSEGGSNVFK.I		K.MSGASSEGGSNVFK.I
522	554	3	3334.69	3.2	1	85.5	20.1	95.00%	K.ALGVSPDVGLQQYIDAFAIGCPPHAGGGIGLER.V	Carbamidomethyl (+57)	K.ALGVSPDVGLQQYIDAFAIGCPPHAGGGIGLER.V
200	210	2	1229.65	4.9	1	29.1	22.9	95.00%	K.NLPFLVEDAGR.S		K.NLPFLVEDAGR.S
211	228	3	2006.87	-0.75	1	38.4	27.2	95.00%	R.SEEQIRESEENAAEGDSK.F		R.SEEQIRESEENAAEGDSK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
102	COFI_SCHPO	36.50%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	44	3	1533.82	5.2	1	36.4	23	95.00%	K.MNDTKTEIVVEKK.S		K.MNDTKTEIVVEKK.S
81	94	2	1584.89	-1.7	1	70.8	19.5	95.00%	K.IIFISWSPDVAPIK.S		K.IIFISWSPDVAPIK.S
32	43	2	1405.72	4.4	1	32.5	24.4	95.00%	K.MNDTKTEIVVEK.K		K.MNDTKTEIVVEK.K
8	20	2	1548.75	-1.1	1	78.7	25.9	95.00%	K.VSPECLEAFQELK.L	Carbamidomethyl (+57)	K.VSPECLEAFQELK.L
54	63	3	1201.58	0.35	1	37.9	25.5	95.00%	F.LGDLPEKDCR.Y	Carbamidomethyl (+57)	K.DFDTFLGDLPEKDCR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
103	NACB_SCHPO	47.68%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	88	2	1699.84	-2.4	1	43.2	25.5	95.00%	R.APTVHSSLPNETTAIY.G		R.APTVHSSLPNETTAIYGK.A
73	90	3	1884.97	4	1	45.6	23.7	95.00%	R.APTVHSSLPNETTAIYGK.A		R.APTVHSSLPNETTAIYGK.A
130	151	2	2376.03	2.8	2	68.7	27.6	95.00%	K.GADAQADDGEIPDLVEKFDEQD.-		K.GADAQADDGEIPDLVEKFDEQD.-
63	72	2	1133.58	0.5	2	35.1	23.7	95.00%	F.KEDGGVINFR.A		K.LNMQNLAGIQEVNMFKEDGGVINFR.A
95	116	2	2320.3	1.2	0	64.9	14.6	95.00%	K.TLSEILPGILNNLGPESLTALR.Q		K.TLSEILPGILNNLGPESLTALR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
104	RL10A_SCHPO	26.24%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

129	139	2	1228.7	4.7	0	40	20.8	95.00%	R.VNIGQILMSVR.T		R.VNIGQILMSVR.T
58	69	2	1316.66	0.74	0	77.5	24.2	95.00%	Y.EQITSEALEAAR.I		R.AGVDEFPLCIHLVSNEYEQITSEALEAAR.I
41	69	3	3260.58	4	1	68.1	23.6	95.00%	R.AGVDEFPLCIHLVSNEYEQITSEALEAAR.I	Carbamidomethyl (+57)	R.AGVDEFPLCIHLVSNEYEQITSEALEAAR.I
117	128	3	1265.71	4.6	1	30	18.9	95.00%	R.HAFGKPNGLVAR.V		R.HAFGKPNGLVAR.V
33	38	2	719.4	4.8	1	27.1	21.4	92.90%	R.IFDLGR.K		R.IFDLGR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
105	RS0B_SCHPO	28.92%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	31	3	3162.63	3.2	1	83.6	21.1	95.00%	M.AESIARPSVLNATDDDIKNLLAADSHIGSK.N	Acetyl (+42)	-.MAESIARPSVLNATDDDIKNLLAADSHIGSK.N
67	88	4	2453.26	4	1	67.3	22.5	95.00%	R.VIATIENPADVCVISSRPYGHR.A	Carbamidomethyl (+57)	R.VIATIENPADVCVISSRPYGHR.A
139	169	3	3390.76	4.3	1	25.4	18.4	94.40%	K.EASFVNIPVIALCDTDSILNHVDVAIPINNK.G	Carbamidomethyl (+57)	K.EASFVNIPVIALCDTDSILNHVDVAIPINNK.G
67	85	2	2103.07	0.15	1	76	24.7	95.00%	R.VIATIENPADVCVISSRPY.G	Carbamidomethyl (+57)	R.VIATIENPADVCVISSRPYGHR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
106	VATA_SCHPO	15.35%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
89	114	4	2751.53	2.9	1	22.2	15.6	95.00%	R.TGKPLSVELGPGLAETIYDGIQRPLK.Q		R.TGKPLSVELGPGLAETIYDGIQRPLK.Q
187	198	2	1317.62	-1.2	1	27.5	25.6	92.60%	Y.IAEAGSYHVDEK.L		R.GTVTYIAEAGSYHVDEK.L
373	389	2	1752.85	8.8	1	38.8	25.7	95.00%	R.LAEMPADSGYPAYLGAK.L		R.LAEMPADSGYPAYLGAK.L
317	331	2	1544.81	4.6	0	49.4	24.3	95.00%	R.TTLVANTSNMPVAAR.E		R.TTLVANTSNMPVAAR.E
182	198	2	1838.88	4.6	1	73	26.6	95.00%	R.GTVTYIAEAGSYHVDEK.L		R.GTVTYIAEAGSYHVDEK.L
221	240	3	2105.14	4.1	0	35.3	20.6	95.00%	R.AARPVADNLTANQPLLTGQR.V		R.AARPVADNLTANQPLLTGQR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
107	ACL2_SCHPO	14.84%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
163	176	2	1433.61	0.64	0	79.6	26.8	95.00%	F.CNEGGVDVGDVDAK.A	Carbamidomethyl (+57)	R.EGDWILFCNEGGVDVGDVDAK.A
382	389	2	947.52	4.5	0	26.9	23.4	92.60%	K.TVLDLMTR.G		K.TVLDLMTR.G
255	266	2	1367.61	3.7	1	48.5	26	95.00%	K.LDQTAEFECGAK.W	Carbamidomethyl (+57)	K.LDQTAEFECGAK.W
326	334	2	985.56	4.7	0	36	21.4	95.00%	K.LTILNAEGR.V		K.LTILNAEGR.V
32	61	3	3211.76	3.3	1	47.1	14.8	95.00%	K.TVSATPAVQLAQIQFPLPTLVIPAESTTYR.E		K.TVSATPAVQLAQIQFPLPTLVIPAESTTYR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
108	RL1B_SCHPO	17.59%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
54	75	3	2486.26	2.6	0	38.3	23.4	95.00%	K.LPNVPRPNMAICILGDAHDLDR.A	Carbamidomethyl (+57)	K.LPNVPRPNMAICILGDAHDLDR.A
78	91	3	1470.71	-0.94	1	69.2	25.9	95.00%	K.HGGVDAMSVDDLKK.L		K.HGGVDAMSVDDLKK.L
76	91	4	1669.85	4.6	1	27.7	23.8	95.00%	R.AKHGGVDAMSVDDLKK.L		R.AKHGGVDAMSVDDLKK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
109	SYTC_SCHPO	8.25%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
248	258	2	1187.55	4.2	1	47.1	26	95.00%	K.NSSSYFLGDAK.N		K.NSSSYFLGDAK.N
94	106	2	1502.78	0.74	0	36	23.2	95.00%	W.DLTRPLEASCTLK.L	Carbamidomethyl (+57)	R.VTVAIVNGEPWDLTRPLEASCTLK.L
8	26	3	2136.14	4.2	1	27.4	21.3	95.00%	K.GVQASLDNLSLEIPFIQHR.L		K.GVQASLDNLSLEIPFIQHR.L
160	174	2	1703.8	4.7	1	71.1	26.8	95.00%	R.VITNDDYSSIESYAK.Q		R.VITNDDYSSIESYAK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
110	DHE4_SCHPO	21.29%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
279	291	3	1405.74	5	1	27.9	22.8	95.00%	K.RASIADSASLCKK.H	Carbamidomethyl (+57)	K.RASIADSASLCKK.H
417	439	2	2411.16	5.2	1	85.7	25.8	95.00%	K.YCDSGSNNIPSLVDGANIAGFLK.V	Carbamidomethyl (+57)	K.YCDSGSNNIPSLVDGANIAGFLK.V
356	367	2	1231.57	4.5	1	27.7	25	93.70%	R.ASGEGCWLAPGK.A	Carbamidomethyl (+57)	R.ASGEGCWLAPGK.A
399	416	2	1950.97	-1.2	1	98.2	25.5	95.00%	K.LAGIMQNIFEQSTDVASK.Y		K.LAGIMQNIFEQSTDVASK.Y
334	353	2	2102.94	-1.5	1	126	27.5	95.00%	R.YVAEGSNMGSSAEAVEVFEK.S		R.YVAEGSNMGSSAEAVEVFEK.S
25	34	3	1266.71	4.3	1	33.7	18.5	95.00%	K.LFEVHPELKR.V		K.LFEVHPELKR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
111	PURA_SCHPO	14.06%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
46	63	2	1832.81	-0.76	1	36	27	95.00%	R.CQGGNNAGHTIVANGVTY.D	Carbamidomethyl (+57)/ Deamidation (+1)	R.CQGGNNAGHTIVANGVTYDFHILPSGLVNPK.C
268	276	2	899.55	4.9	0	44.5	21.5	95.00%	R.IANSIGVVK.A		R.IANSIGVVK.A
282	304	3	2420.21	-0.91	1	39.9	24.4	95.00%	R.VGAGPFPTEQLNEIGDHLQSVGR.E		R.VGAGPFPTEQLNEIGDHLQSVGR.E
126	136	2	1129.57	4.6	0	38.6	22.9	95.00%	R.ADALNEAELGK.Q		R.ADALNEAELGK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
112	SYKC_SCHPO	12.86%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
15	28	2	1454.8	-1.8	0	50.5	21.8	95.00%	K.ALVLDPVTGEQVSK.T		K.ALVLDPVTGEQVSK.T
570	591	3	2490.32	-0.56	1	33.2	20.9	95.00%	R.EVLLFPHMKPEVQAAEPTVVKE.-		R.EVLLFPHMKPEVQAAEPTVVKE.-
498	513	2	1999.9	4.4	1	72.7	27.2	95.00%	K.EICNAYTELNDIFDQR.A	Carbamidomethyl (+57)	K.EICNAYTELNDIFDQR.A
153	176	4	2810.33	3.8	2	33.2	25.1	95.00%	K.KLQVMCQAQDADTVDFAAQHEHLR.R	Carbamidomethyl (+57)	K.KLQVMCQAQDADTVDFAAQHEHLR.R
154	176	4	2682.24	3.7	1	34.1	26.4	95.00%	K.LQVMCQAQDADTVDFAAQHEHLR.R	Carbamidomethyl (+57)	K.LQVMCQAQDADTVDFAAQHEHLR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
113	ASSY_SCHPO	15.61%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	205	2	1483.72	0.72	0	32.2	25.3	95.00%	Y.EAGILEDPSMTPPK.D		K.KPWSMDENIVHCSYEAGILEDPSMTPPK.D
181	191	2	1353.53	0.24	1	41.4	26.2	95.00%	W.SMDENIVHCSY.E	Carbamidomethyl (+57)	K.KPWSMDENIVHCSYEAGILEDPSMTPPK.D
333	350	2	1884.01	-1.7	0	83.3	21.3	95.00%	R.MLLAANNVSQEVVNGVVK.L		R.MLLAANNVSQEVVNGVVK.L
102	122	4	2398.2	5	1	39.2	24.1	95.00%	R.RQIQIAEKENCIAVSHGCTGK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.RQIQIAEKENCIAVSHGCTGK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
114	DAK1_SCHPO	11.38%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	18	3	2124.09	-0.36	2	53.2	22.8	95.00%	-.MDKHFINDPEVLVLDGLK.S	Acetyl (+42)	-.MDKHFINDPEVLVLDGLK.S
388	399	2	1358.73	4.4	0	25.9	23.3	91.00%	R.QAIVNSMENLIK.A		R.QAIVNSMENLIK.A
557	580	3	2355.27	0.086	2	37.9	19.4	95.00%	Y.VGDDVKVPDAGALGVVAIVEGFTK.-		R.AVYVGDDVKVPDAGALGVVAIVEGFTK.-
527	538	2	1301.63	4.7	0	60.8	25.2	95.00%	K.TNDLNAAVEEAR.K		K.TNDLNAAVEEAR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
115	YDG7_SCHPO	24.61%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

53	77	3	2611.25	-0.27	1	75	25.4	95.00%	R.HIDAAAIYGNEDEVGDGIKESGVPR.K		R.HIDAAAIYGNEDEVGDGIKESGVPR.K
308	321	2	1490.7	-2.2	1	29.4	26	94.40%	F.SNEPVFAGLEDGRT.-		R.FNQATFSNEPVFAGLEDGRT.-
282	299	3	2106.08	4.5	1	37.8	23.8	95.00%	K.YIPLTKEDMDEINSIGIR.A		K.YIPLTKEDMDEINSIGIR.A
183	204	3	2603.37	3.4	1	27.8	19.9	95.00%	K.VKPAVHQMELHPFLPQTEFVEK.H		K.VKPAVHQMELHPFLPQTEFVEK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
116	GCST_SCHPO	19.12%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
165	180	2	1623.93	4	0	75.8	18.3	95.00%	R.ALIAIQGPETASVVQK.L		R.ALIAIQGPETASVVQK.L
81	97	2	1779.88	-2.5	1	66.9	25.8	95.00%	R.GENATAYLESITPSSLK.E		R.GENATAYLESITPSSLK.E
319	344	3	2566.23	-0.21	0	43.5	25.6	95.00%	R.HGSAVEVDGVEVGQVTSGCPSPTLGK.N	Carbamidomethyl (+57)	R.HGSAVEVDGVEVGQVTSGCPSPTLGK.N
110	124	2	1575.8	-0.073	0	62.3	24.9	95.00%	F.TNETGGIIDDTIISK.Q		K.ELKPFHSTLSAFTNETGGIIDDTIISK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
117	AROG_SCHPO	22.31%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
92	104	2	1518.71	-1.6	0	40	25.9	95.00%	K.ADELQDALCVVMR.C	Carbamidomethyl (+57)	K.ADELQDALCVVMR.C
199	226	3	2704.36	2.1	0	47.7	23.5	95.00%	K.NGTDGTVGVAIDAIGATAHPHTMLGVTK.Q	Deamidation (+1)	K.NGTDGTVGVAIDAIGATAHPHTMLGVTK.Q
186	198	2	1364.74	4.4	1	39.9	22	95.00%	R.ELASALSFPVGFK.N		R.ELASALSFPVGFK.N
349	363	2	1657.8	0.65	0	27.5	26.3	91.60%	W.EQTAPMLDDLAEAVR.A		K.YGVSITDACVSWEQTAPMLDDLAEAVR.A
250	263	3	1525.76	-0.79	2	29.3	25.1	95.00%	K.KGPNYDAEHVAAVR.K		K.KGPNYDAEHVAAVR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
118	YA03_SCHPO	34.70%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
79	94	2	1687.89	1.9	2	34.7	23.3	95.00%	Y.LAEGGPDKVPVYISPF.F		K.YLAEGGPDKVPVYISPFFQEVGHLPCDIGLELDK.L
181	194	2	1560.82	-1	1	54.6	23.8	95.00%	K.AADIDFLPPQLSFK.N		K.AADIDFLPPQLSFK.N
14	47	4	3763.78	4.5	1	35.9	22.9	95.00%	R.HGQAQHNVGPDEDHNIRDPVLTSEGIEQCEALAK.E	Carbamidomethyl (+57)	R.HGQAQHNVGPDEDHNIRDPVLTSEGIEQCEALAK.E
66	77	3	1430.83	3.8	1	35.5	16.4	95.00%	R.RTLQTMEIALKK.Y		R.RTLQTMEIALKK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
119	AATR1_SCHPO	9.28%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
275	288	2	1577.78	4.4	1	46.4	25.6	95.00%	K.ELIPSFLSMDVDGR.V		K.ELIPSFLSMDVDGR.V
38	54	2	1856.02	-1.5	1	47	20.6	95.00%	K.IISLAGGLPNPEYFPIR.E		K.IISLAGGLPNPEYFPIR.E
7	19	3	1436.71	5.4	0	43.2	25.8	95.00%	K.DLSHHLSVESASR.K		K.DLSHHLSVESASR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
120	PABP_SCHPO	21.90%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
46	83	3	3693.71	2.3	2	35	24.3	95.00%	K.KAEEPEAAAEPSESTSTPTNASSVATPSGTAPTSASLY.V		K.KAEEPEAAAEPSESTSTPTNASSVATPSGTAPTSASLYVGELDPSVTEAMLFELFNSIGPVASIR.V
258	266	2	1068.57	4.8	1	26.6	21	92.20%	K.ANFTNVYIK.N		K.ANFTNVYIK.N
9	46	4	4050.83	1.1	1	28.4	24.1	95.00%	K.QADAAVESDVNTNNEAVESSTKEESSNTPSTETQPEKK.A		K.QADAAVESDVNTNNEAVESSTKEESSNTPSTETQPEKK.A
447	456	2	1142.61	4.9	0	33.9	22.4	95.00%	R.SQLEAQIQAR.N		R.SQLEAQIQAR.N
536	571	3	3524.72	4.6	0	28.7	22.5	95.00%	R.GPVPAQGRPMMMPGSVPSAGPAEAEAVPAVPGMPER.F		R.GPVPAQGRPMMMPGSVPSAGPAEAEAVPAVPGMPER.F

98	110	2	1401.76	2.1	1	50.9	22.1	95.00%	F.ELFNSIGPVASIR.V		K.AEEPEAAAEPSESTSTPTNASSV ATPSGTAPTSASLYVGELDPSVTEA MLFELFNSIGPVASIR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
121	LEU1_SCHPO	15.75%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
82	99	2	1998.98	4.3	1	62	25.3	95.00%	K.EIEVGFPSASQTDFAFVR.H		K.EIEVGFPSASQTDFAFVR.H
464	479	2	1742.82	4.9	1	69.1	26.4	95.00%	R.FSVNDYTLSSNGPQSK.C		R.FSVNDYTLSSNGPQSK.C
379	393	2	1756.83	0.16	1	32.1	26.5	95.00%	K.VPYLPLDPHDVNSEY.A		K.VPYLPLDPHDVNSEYAAIIR.V
137	151	3	1761.87	4	1	33.2	25.6	95.00%	K.NATVHLYNACSPLFR.E	Carbamidomethyl (+57)	K.NATVHLYNACSPLFR.E
268	295	3	2788.37	3.6	2	73.8	24.5	95.00%	R.GTAVAAAELGQLAGGDRIEGCLF GNGER.T	Carbamidomethyl (+57)	R.GTAVAAAELGQLAGGDRIEGCLF GNGER.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
122	TBB_SCHPO	22.77%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
63	77	2	1556.81	-0.14	0	36	23.5	95.00%	R.AVLVDLEPGTMDAVK.S		R.AVLVDLEPGTMDAVK.S
104	121	3	1913.96	4.4	1	33.4	25.1	95.00%	K.GHYTEGAELADAVLDVVR.R		K.GHYTEGAELADAVLDVVR.R
123	154	3	3205.55	2.6	1	82.9	24.4	95.00%	R.EAEACDALQGFQLTHSLGGGTG SGMGTLLLSK.I	Carbamidomethyl (+57)	R.EAEACDALQGFQLTHSLGGGTG SGMGTLLLSK.I
163	174	2	1249.62	3.9	1	41.3	24.6	95.00%	R.MMATFSVAPAPK.S		R.MMATFSVAPAPK.S
295	306	2	1303.57	1.4	0	41.5	26	95.00%	F.DANNMMVAADPR.H		R.LHFFMVGFAPLAAIGSSSFQAVS VPELTQQMFDANNMMVAADPR.H
282	294	2	1476.73	-0.48	1	27.2	25.2	92.80%	F.QAVSVPELTQQMF.D		R.LHFFMVGFAPLAAIGSSSFQAVS VPELTQQMFDANNMMVAADPR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
123	ACL1_SCHPO	11.87%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
369	381	2	1420.73	4.5	1	44	24.3	95.00%	R.GSELTYNNVPISK.V		R.GSELTYNNVPISK.V
171	182	3	1338.74	4.8	1	23.6	20	92.20%	K.LYRPGSVAYVSK.S		K.LYRPGSVAYVSK.S
313	326	2	1570.9	3.9	1	58.3	18.2	95.00%	K.LPALLQEVYEGLVK.K		K.LPALLQEVYEGLVK.K
137	154	2	1797.98	-1.9	1	32.8	21.5	95.00%	K.NVVIIGPATVGGIKPGCF.K	Carbamidomethyl (+57)	K.NVVIIGPATVGGIKPGCFK.I
156	170	2	1506.72	3.3	0	45.7	26.1	95.00%	K.IGNTGGMMDNIVASK.L		K.IGNTGGMMDNIVASK.L
313	327	3	1699	4	1	30.3	13.8	95.00%	K.LPALLQEVYEGLVKK.G		K.LPALLQEVYEGLVKK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
124	SLBR2_SCHPO	24.79%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
134	143	2	1115.56	4.3	0	27.1	23.9	92.90%	R.NIESSVQPSR.E		R.NIESSVQPSR.E
166	192	3	3060.53	3.6	1	43.6	22.3	95.00%	R.LVTMEQELVREEAACLVAEAQLS NTTR.E	Carbamidomethyl (+57)	R.LVTMEQELVREEAACLVAEAQLS NTTR.E
222	248	3	2999.46	-0.23	1	47.6	24.3	95.00%	R.HLLNLIDDTPVTPGEARPAYDGY ETSR.Q		R.HLLNLIDDTPVTPGEARPAYDGY ETSR.Q
271	284	2	1570.76	0.051	0	30.6	25.6	95.00%	F.VKPQIEDDAQSDAR.S		R.QIVMDAEHALSSWVPSQPAVNF VKPQIEDDAQSDAR.S
149	157	2	1075.63	4.5	1	33	19.2	95.00%	K.LLDQIYALK.H		K.LLDQIYALK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
125	SYNC_SCHPO	9.68%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
223	235	2	1382.69	1.4	1	33.2	25.2	95.00%	Y.QILHAAPTGEEAF.T		K.SAPGNHELVVDYYQILHAAPTGE EAFTNR.L
447	465	3	2338.25	2.9	1	23.4	20.2	91.80%	K.MTDQINRPIFLTYFPLEIK.S		K.MTDQINRPIFLTYFPLEIK.S
223	238	3	1753.88	0.62	1	42.9	25	95.00%	Y.QILHAAPTGEEAFTNR.L		K.SAPGNHELVVDYYQILHAAPTGE EAFTNR.L

21	40	2	2052.89	-0.011	1	44.3	27.8	95.00%	Y.IDEASGNDETGNGSQTSPFK.T		K.SDVVFYIDEASGNDETGNGSQTSPFK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
126	PUR8_SCHPO	16.18%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
410	423	3	1571.79	4.9	1	22.5	24.5	90.30%	R.VVKEEGGDNDLIER.I		R.VVKEEGGDNDLIER.I
226	242	2	1930.91	3.5	1	32.6	26.9	95.00%	K.LSGFDNVYPVTGQTYDR.K		K.LSGFDNVYPVTGQTYDR.K
243	261	3	2023.12	4.2	2	51.4	18.6	95.00%	R.KIDIDVLQPLASFGATAHK.I		R.KIDIDVLQPLASFGATAHK.I
450	460	2	1248.61	5.4	1	26.4	24.4	91.90%	R.APEQTESFVNK.D		R.APEQTESFVNK.D
372	388	2	1909.94	4.9	1	55.7	25.3	95.00%	R.AELPFMATENIIMAMTK.H		R.AELPFMATENIIMAMTK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
127	SYLC_SCHPO	2.61%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
382	398	3	1730.98	4.6	0	32.6	17.9	95.00%	K.GQDLIGALVNAPLSVHK.Q		K.GQDLIGALVNAPLSVHK.Q
530	541	2	1389.69	-1.3	1	45	24.1	95.00%	F.VYNEPEGQVISR.S		K.ELIDQGLAFVYNEPEGQVISR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
128	Q1L854_SCHPO	21.25%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
143	178	3	3637.66	4	1	78.1	25.6	95.00%	R.GWGDLVNSAANPDVAENEGNTPSGAQTPAAEEENVK.T		R.GWGDLVNSAANPDVAENEGNTPSGAQTPAAEEENVK.T
10	28	2	2077.07	4.4	1	50.2	23.6	95.00%	K.NLFDLLGEETPAATTTEKK.T		K.NLFDLLGEETPAATTTEKK.T
10	27	2	1948.96	-1.8	1	83.4	25.6	95.00%	K.NLFDLLGEETPAATTTEK.K		K.NLFDLLGEETPAATTTEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
129	THRC_SCHPO	18.29%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
437	454	3	2061.03	4.7	2	31.2	24.5	95.00%	K.TKDQDITYICLSTAHPAK.F	Carbamidomethyl (+57)	K.TKDQDITYICLSTAHPAK.F
313	327	2	1443.73	4.4	0	39.8	24.6	95.00%	K.ADSTQVSPSGPISAK.E		K.ADSTQVSPSGPISAK.E
418	432	2	1576.86	-0.2	0	43	22	95.00%	Y.IIDPHTAVGVETGLR.C		K.IYESDHYIIDPHTAVGVETGLR.C
182	215	3	3829.81	3.8	1	34.2	23.2	95.00%	R.VSPIQEAQMTTVTDPNVHCITVNGVFDDCQDLVK.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VSPIQEAQMTTVTDPNVHCITVNGVFDDCQDLVK.Q
399	410	2	1331.7	3.6	1	37.5	23.8	95.00%	R.VSNDETIDAIKK.I		R.VSNDETIDAIKK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
130	VATB_SCHPO	12.13%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
415	427	2	1417.68	4.9	0	78	25.7	95.00%	K.SVVGEEALSQEDR.L		K.SVVGEEALSQEDR.L
439	449	2	1284.62	4.2	1	36.9	25.3	95.00%	K.TFISQGAYENR.T		K.TFISQGAYENR.T
485	503	2	2015.89	5.3	1	57.2	27.3	95.00%	R.SSAYTESSKDVIDNTPESS.-		R.SSAYTESSKDVIDNTPESS.-
42	59	3	2083.09	4.5	1	23.6	22.1	92.20%	R.RPQYNEIVNLNLPDGSVR.S		R.RPQYNEIVNLNLPDGSVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
131	SCE3_SCHPO	21.65%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
250	271	3	2195.05	-1.1	0	32.1	26.1	95.00%	R.SSSNVNTEATPSATTTTSSKPK.R		R.SSSNVNTEATPSATTTTSSKPK.R
46	66	2	2113.97	4.9	1	94.2	27.3	95.00%	R.ATPSSADAGYNAPSSTFESVR.S		R.ATPSSADAGYNAPSSTFESVR.S
272	289	3	1956.03	4.3	2	43	22.6	95.00%	K.RDPFGGAKPVDNTSVLQR.V		K.RDPFGGAKPVDNTSVLQR.V
359	381	2	2403.05	5.1	1	111	27.7	95.00%	K.TPATEDAPATNAGEAEEEEGWTK.I		K.TPATEDAPATNAGEAEEEEGWTK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
132	TRXB_SCHPO	20.19%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
205	221	2	1843.89	-2.6	1	44.2	25.6	95.00%	K.VEVLWNTVAEEAQGDGK.L		K.VEVLWNTVAEEAQGDGK.L

154	175	3	2202.13	6.5	1	23	23.2	91.20%	R.NKPLAVVGGGDSAAEEAQFLTK.Y	Deamidation (+1)	R.NKPLAVVGGGDSAAEEAQFLTK.Y	
99	124	3	2801.32	3.2	1	61.8	25.7	95.00%	K.YWLEGAEEEEPHTADSVILATGASAR.R		K.YWLEGAEEEEPHTADSVILATGASAR.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
133	P25_SCHPO	17.82%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
36	52	2	1976.06	4.7	1	48.2	21.4	95.00%	K.AVIYQFPETLSPEILEK.M		K.AVIYQFPETLSPEILEK.M
40	52	2	1529.8	-1.7	1	38.4	23.9	95.00%	Y.QFPETLSPEILEK.M		K.AVIYQFPETLSPEILEK.M
2	20	2	2064.09	2.1	1	77.6	21.8	95.00%	M.STANTVAIVIYSTYGHVVK.L	Acetyl (+42)	-.MSTANTVAIVIYSTYGHVVK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
134	PMM_SCHPO	18.29%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
29	43	2	1728.91	-1.5	0	60.3	22.9	95.00%	R.LSVSPEMLETLQNLR.K		R.LSVSPEMLETLQNLR.K
236	253	4	1938.02	4.7	1	21.7	22.3	95.00%	R.TIGHSVTNPDDTIAELKK.I		R.TIGHSVTNPDDTIAELKK.I
45	58	2	1347.75	4.4	1	41.6	21.3	95.00%	K.VVAIGFVGGSDLSK.Q		K.VVAIGFVGGSDLSK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
135	ATPB_SCHPO	10.67%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
160	185	3	2859.38	0.91	1	50	25.2	95.00%	K.YSPIHADAPSFEEQSTTPEILETGIK.V		K.YSPIHADAPSFEEQSTTPEILETGIK.V
210	222	2	1501.85	-1.5	1	41.1	18.6	95.00%	K.TVFIQELINNIAK.A		K.TVFIQELINNIAK.A
384	400	2	1802.93	-0.78	1	26.2	23.8	91.50%	R.SISELGIYPAVDPLDSK.S		R.SISELGIYPAVDPLDSK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
136	LYS4_SCHPO	10.26%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
405	418	2	1316.66	-0.85	0	45.2	24.3	95.00%	Y.VGAASSEVEAAAQK.N		K.VADGVEFYVGAASSEVEAAAQK.N
149	159	2	1179.57	4.4	1	26	25.1	91.10%	K.GQGIDFYPAGR.G		K.GQGIDFYPAGR.G
189	200	2	1184.64	1.4	0	40	21.6	95.00%	Y.GGVGCLGTPIVR.T	Carbamidomethyl (+57)	R.GIGHQIMVEQGYAMPGSMAVASDSHSNTYGGVGCLGTPIVR.T
172	188	2	1724.72	1.6	1	40.1	27	95.00%	Y.AMPGSMAVASDSHSNTY.G		R.GIGHQIMVEQGYAMPGSMAVASDSHSNTYGGVGCLGTPIVR.T
470	489	2	1872.04	4.8	1	47.2	18.7	95.00%	R.EALAYLASPAVVAASAIAGK.I		R.EALAYLASPAVVAASAIAGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
137	RL15A_SCHPO	12.94%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
78	93	3	1761.94	4.8	1	23.7	22.7	92.30%	K.GQTYGKPVHQGVNHLK.Y		K.GQTYGKPVHQGVNHLK.Y
148	157	3	1218.69	4.4	1	24.4	19.5	93.30%	R.INWIVNPVHK.H		R.INWIVNPVHK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
138	SYG_SCHPO	7.98%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
93	104	3	1423.66	0.86	2	27.4	25.9	95.00%	W.MCKDPATGEIFR.A	Carbamidomethyl (+57)	K.FADWMCKDPATGEIFR.A
187	198	2	1297.63	5.4	0	37	25.7	95.00%	R.NPATNGELETPR.Q		R.NPATNGELETPR.Q
492	506	2	1649.85	4.8	1	35.7	24.3	95.00%	R.TYTPNVIEPSFGLGR.I		R.TYTPNVIEPSFGLGR.I
526	538	2	1298.76	-2.3	1	40.9	18.3	95.00%	R.GVLSFPASIAPIK.A		R.GVLSFPASIAPIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
139	GCSP_SCHPO	6.78%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
953	965	2	1458.76	1.1	0	43.1	23.9	95.00%	K.DNNLLVNAPHPQK.D		K.DNNLLVNAPHPQK.D
657	684	3	2835.49	3.7	1	27.8	19.3	95.00%	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C	Carbamidomethyl (+57)	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C

577	604	3	3166.6	3.7	1	40.5	22.4	95.00%	K.LNAVTEMMPITNPLFANIHPYVPEEQAK.G		K.LNAVTEMMPITNPLFANIHPYVPEEQAK.G
657	678	2	2198.06	0.049	1	34.4	26.3	95.00%	R.NICLIPVSAHGTNPASAAMAGF.T	Carbamidomethyl (+57)	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
140	ARO1_SCHPO	6.10%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
677	703	3	2950.4	0.26	1	52.8	24.9	95.00%	R.FACDVLRPMGCTVEQTATSTTVQGPPK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.FACDVLRPMGCTVEQTATSTTVQGPPK.G
1232	1247	2	1833.96	4.6	1	44.8	23.3	95.00%	R.ITNSMDIPLILFNMGR.F		R.ITNSMDIPLILFNMGR.F
1326	1338	2	1509.69	1.6	1	55.9	26.4	95.00%	Y.EAFETDTVDEVQK.V		R.SPILHSTAYELLGLPHTYEAFETDTVDEVQK.V
632	660	3	3107.51	0.39	1	46.8	23.6	95.00%	K.YQNPPHYEIESDASSATYPLAIAAITGTK.C		K.YQNPPHYEIESDASSATYPLAIAAITGTK.C
162	172	2	1299.72	4.7	1	45.2	22.1	95.00%	K.NLVGAFWQPLR.V		K.NLVGAFWQPLR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
141	ARGD_SCHPO	19.05%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
112	129	2	1988.02	-0.11	1	75.8	23.3	95.00%	F.YNEPAIELSNVINNSLAK.N		K.LVHSSNLFYNEPAIELSNVINNSLAK.N
311	332	3	2276.09	4.8	1	39.5	26	95.00%	K.IAAEIHPGEHGSTFGGNPVACR.V	Carbamidomethyl (+57)	K.IAAEIHPGEHGSTFGGNPVACR.V
283	310	3	2746.56	2.7	0	43.2	12.8	95.00%	K.DVASPDIITVAKPLANGLPIGATIVSSK.I		K.DVASPDIITVAKPLANGLPIGATIVSSK.I
139	154	2	1784.85	4.1	1	92.8	26.6	95.00%	K.IFFANCGTEANETALK.F	Carbamidomethyl (+57)	K.IFFANCGTEANETALK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
142	RS17B_SCHPO	23.48%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	59	3	1133.6	4.6	1	24.5	23.1	93.40%	K.IAGYTTHLMK.R		K.IAGYTTHLMK.R
24	33	2	1234.67	4.6	1	36.3	22.3	95.00%	R.LTLDFQTNKR.I		R.LTLDFQTNKR.I
34	44	2	1156.68	4.8	0	51	20	95.00%	R.IVDEVAIIASK.R		R.IVDEVAIIASK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
143	IMDH_SCHPO	18.32%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
169	187	3	2214.08	4.5	1	37	26	95.00%	R.DVQFHKDTNTPVTEVMTPR.E		R.DVQFHKDTNTPVTEVMTPR.E
2	15	2	1636.88	4	1	27	21.7	92.70%	M.SAFKPYTEALEVLK.K	Acetyl (+42)	-.MSAFKPYTEALEVLK.K
303	313	2	1155.67	4.5	0	51.3	19.6	95.00%	K.IDVIAGNVVTR.E		K.IDVIAGNVVTR.E
214	234	3	2311.28	3.6	1	29.3	16.8	95.00%	K.LPVVDKDDNLVALLSLTDLMK.N		K.LPVVDKDDNLVALLSLTDLMK.N
188	201	2	1559.8	-1.6	0	60.1	23.9	95.00%	R.EELITTAEGISLER.A		R.EELITTAEGISLER.A
212	234	4	2496.4	3.3	1	24	15.4	95.00%	K.GKLPVVDKDDNLVALLSLTDLMK.N		K.GKLPVVDKDDNLVALLSLTDLMK.N
419	433	2	1421.67	3.9	0	52.2	26.3	95.00%	R.GMGSIAAMEGTGVNK.N		R.GMGSIAAMEGTGVNK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
144	STI1_SCHPO	15.74%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
146	164	2	1935.97	6.4	1	78.1	25.2	95.00%	K.LASNPETASLLADSAFMAK.L		K.LASNPETASLLADSAFMAK.L
168	183	2	1781.88	4.3	0	66.6	25.8	95.00%	K.IQQNPGSIMAELNDPR.M		K.IQQNPGSIMAELNDPR.M
20	34	2	1711.85	3.9	1	70.3	24.9	95.00%	K.TAIDYFTQAIGLDER.N		K.TAIDYFTQAIGLDER.N
371	377	2	800.44	3.8	0	29.8	23.1	95.00%	R.TPDILSR.L		R.TPDILSR.L
76	90	3	1463.79	4.4	1	44.6	21.9	95.00%	R.KGAALHGLGDLDAAR.S		R.KGAALHGLGDLDAAR.S
112	132	2	2007.97	4.2	1	89.9	26.5	95.00%	K.SVEAAQTQAASGAGGFNPFAK.L		K.SVEAAQTQAASGAGGFNPFAK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

145	SYRC_SCHPO	10.03%		100%		4							
Start	End	charge	Mr(expt)		ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
163	180	2	1987.02		4.1	1	33.9	22.7	95.00%	R.STIIGSFLANLHESQGWK.V		R.STIIGSFLANLHESQGWK.V	
225	238	2	1588.76		3.6	1	45.2	25.9	95.00%	K.VNADATEEDEKIQK.D		K.VNADATEEDEKIQK.D	
11	24	2	1544.86		4.5	1	46.7	20.3	95.00%	K.SLSTLGLQDLPVFR.E		K.SLSTLGLQDLPVFR.E	
452	467	2	1759.87		3.7	1	55	24.8	95.00%	K.YAQVENPEEVADIVGK.T		K.YAQVENPEEVADIVGK.T	
Index	AC	Coverage	Scaffold probability		Nb distinct peptides								
146	RANG_SCHPO	32.56%		100%		4							
Start	End	charge	Mr(expt)		ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
88	98	2	1353.6		4	1	43.5	26.3	95.00%	K.TNEEEETVEFK.M		K.TNEEEETVEFK.M	
188	198	2	1253.61		5.8	1	35.7	25.3	95.00%	R.FANSENANLFK.E		R.FANSENANLFK.E	
49	80	3	3379.58		3.1	2	28.6	24.6	95.00%	K.SGASTNDEKKPAEGDEDAEPASPEVHFEPIVK.L		K.SGASTNDEKKPAEGDEDAEPASPEVHFEPIVK.L	
169	184	2	1622.73		0.72	1	41	26.7	95.00%	W.TVAADVSEGEPTAETF.A		R.SWVWTVAADVSEGEPTAETFAIR.F	
Index	AC	Coverage	Scaffold probability		Nb distinct peptides								
147	RS2_SCHPO	22.13%		100%		4							
Start	End	charge	Mr(expt)		ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
186	200	2	1799.86		4.8	1	102	26.4	95.00%	R.FLQLAGIEDCYTQSR.G	Carbamidomethyl (+57)	R.FLQLAGIEDCYTQSR.G	
51	63	2	1566.86		4.2	1	34.6	19.5	95.00%	K.SIEEIYLYSLPIK.E		K.SIEEIYLYSLPIK.E	
174	185	3	1138.69		4.8	1	25.2	13	94.20%	R.GAGLVAAPVTKR.F		R.GAGLVAAPVTKR.F	
141	156	3	1696.87		4.8	1	37.6	24.2	95.00%	R.GYWGTALGDPHTVPVK.V		R.GYWGTALGDPHTVPVK.V	
Index	AC	Coverage	Scaffold probability		Nb distinct peptides								
148	RL36A_SCHPO	24.24%		100%		3							
Start	End	charge	Mr(expt)		ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
83	96	2	1545.83		-1.4	1	78.1	22.1	95.00%	K.GKIEELTSVIQSSR.L		K.GKIEELTSVIQSSR.L	
85	96	2	1360.73		3.8	0	56.4	23.5	95.00%	K.IEELTSVIQSSR.L		K.IEELTSVIQSSR.L	
2	11	2	966.59		4.6	0	38.2	15.1	95.00%	M.APGLVVGLNK.G		-.MAPGLVVGLNK.G	
Index	AC	Coverage	Scaffold probability		Nb distinct peptides								
149	RS12A_SCHPO	46.90%		100%		4							
Start	End	charge	Mr(expt)		ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
99	111	2	1486.76		2.4	1	27.9	23.6	93.90%	K.VLGEWAGLCVLDR.D	Carbamidomethyl (+57)	K.VLGEWAGLCVLDR.D	
79	93	2	1671.87		-1.8	0	75.5	23	95.00%	K.LVEALCAESETPLIK.V	Carbamidomethyl (+57)	K.LVEALCAESETPLIK.V	
61	78	3	2208.97		4.2	1	36.3	27.3	95.00%	R.QAHLCVLCESCDQEAYVK.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.QAHLCVLCESCDQEAYVK.L	
117	138	3	2356.1		-1.5	2	47	27	95.00%	R.KVVGCSCVAVTDYGEDSAALQK.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.KVVGCSCVAVTDYGEDSAALQK.L	
Index	AC	Coverage	Scaffold probability		Nb distinct peptides								
150	SYEC_SCHPO	10.89%		100%		5							
Start	End	charge	Mr(expt)		ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
278	288	2	1354.61		2.1	1	35.9	26.4	95.00%	Y.TSDYLDTIHQY.C		K.ENSEFQDAILEDVALLGIKPDVVTYTSDYLDTIHQYCVDMIK.S	
66	77	2	1393.77		4.3	1	31.9	20.3	95.00%	K.LALQTFSQVYPK.L		K.LALQTFSQVYPK.L	
190	206	2	1731.84		3.9	1	51.4	25.5	95.00%	K.SSGPNYEIGLPDAIDGK.V		K.SSGPNYEIGLPDAIDGK.V	
322	344	3	2559.28		2.3	1	48.8	23.9	95.00%	R.DRPIEESLEILSEMDKGSDVGLK.N		R.DRPIEESLEILSEMDKGSDVGLK.N	
295	309	2	1657.7		4.5	1	93.6	26.8	95.00%	K.SGQAYADDTDVETMR.H		K.SGQAYADDTDVETMR.H	
Index	AC	Coverage	Scaffold probability		Nb distinct peptides								
151	CAP_SCHPO	4.54%		100%		2							
Start	End	charge	Mr(expt)		ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
499	509	2	1122.58		5.1	0	31.4	24	95.00%	K.SSLSSEVVTSK.S		K.SSLSSEVVTSK.S	

339	352	2	1443.77	0.47	1	28	23.6	94.00%	F.AEINKGEGITSGLR.K		K.GDMGAVFAEINKGEGITSGLR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
152	ADK_SCHPO	16.18%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
126	138	2	1424.68	5.2	1	51	26.2	95.00%	R.SLCTNLGAANNYK.L	Carbamidomethyl (+57)	R.SLCTNLGAANNYK.L
253	267	2	1483.87	4.5	0	69.4	17.2	95.00%	R.VVVITQGADATIVAK.D		R.VVVITQGADATIVAK.D
86	96	2	1295.61	3.7	1	43.7	26.2	95.00%	K.FADMLLESNEK.A		K.FADMLLESNEK.A
230	245	2	1688.89	3.8	0	56.9	23.5	95.00%	K.STDVQEIALALSSVEK.V		K.STDVQEIALALSSVEK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
153	THI22_SCHPO	8.71%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
423	435	2	1516.6	5.3	1	56.7	25.8	95.00%	K.SCEESPACTAYSR.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.SCEESPACTAYSR.Y
181	197	2	1890.87	-1.3	0	123	27	95.00%	K.NQGLDISNINSVSDMER.C		K.NQGLDISNINSVSDMER.C
134	151	2	1829.98	-1.6	0	76.8	21.8	95.00%	K.LVVDPVMVATSGDSLVTK.D		K.LVVDPVMVATSGDSLVTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
154	YFHH_SCHPO	5.21%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
504	529	4	3037.42	4.5	1	22.9	25.6	95.00%	K.EEERPLPSEPSQNQPAEYRDTP DTPR.N		K.EEERPLPSEPSQNQPAEYRDTP DTPR.N
307	340	4	3584.77	4.2	2	20.1	21.8	95.00%	R.VAKDDDPFVVSNTANSDEPASSS KPAKPLTDLNR.A		R.VAKDDDPFVVSNTANSDEPASSS KPAKPLTDLNR.A
711	734	3	2663.22	4.7	1	32.8	26.9	95.00%	R.ISEVTEDSIDEDKQNEVDPSTSAR .A		R.ISEVTEDSIDEDKQNEVDPSTSAR .A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
155	RS11_SCHPO	17.76%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	64	2	1161.6	4.7	1	33.4	23.9	95.00%	K.CPFVGQVSIR.G	Carbamidomethyl (+57)	K.CPFVGQVSIR.G
114	130	2	1870.97	4.9	0	41.5	23.5	95.00%	R.INEGDVVTVGQCRPLSK.T	Carbamidomethyl (+57)	R.INEGDVVTVGQCRPLSK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
156	YDMC_SCHPO	11.66%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
370	385	2	1876.99	-1.7	1	42.9	22.5	95.00%	K.LTSLMESIFPEQTIIR.S		K.LTSLMESIFPEQTIIR.S
109	122	2	1458.75	0.47	1	60.9	24.3	95.00%	Y.SANPVNVEGQIGFK.I		K.SHDELTLHHCHYSANPVNVEGQI GFK.I
488	513	3	3117.34	3.1	1	64.3	27	95.00%	K.VEPEPIDEEEAFSDDEEEEPEEIK ER.I		K.VEPEPIDEEEAFSDDEEEEPEEIK ER.I
82	91	2	1136.53	5	1	33.4	25.4	95.00%	R.NADNSVTNFR.D		R.NADNSVTNFR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
157	RS28_SCHPO	41.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
47	65	3	2195.15	-0.23	1	34.8	21.7	95.00%	K.GPVREDDILVLLESEREAR.R		K.GPVREDDILVLLESEREAR.R
47	62	3	1838.98	4.7	1	27.2	21.1	95.00%	K.GPVREDDILVLLESER.E		K.GPVREDDILVLLESER.E
1	9	2	1031.54	3.7	1	25.7	23.6	90.70%	-.MDSSKVPVK.L	Acetyl (+42)	-.MDSSKVPVK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
158	KAD1_SCHPO	29.55%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
196	218	3	2621.39	2.8	1	47.7	19.3	95.00%	K.WAAVDAAQKPEQVWEQIVAILEK .A		K.WAAVDAAQKPEQVWEQIVAILEK .A
27	39	3	1416.72	-1.5	1	34.1	24.9	95.00%	K.YGIAHLATGDMLR.S		K.YGIAHLATGDMLR.S

54	82	4	3231.58	0.27	1	34.3	22.6	95.00%	K.KIMDQGGLVSDDIVTGMIKDEILNNPECK.N	Carbamidomethyl (+57)	K.KIMDQGGLVSDDIVTGMIKDEILNNPECK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
159	RL18B_SCHPO	18.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	65	3	1111.64	5.1	0	26.6	16.7	95.00%	K.TNRPPISISK.I		K.TNRPPISISK.I
132	142	2	1127.63	4.1	0	42.3	21	95.00%	R.APTGSNTVLLR.G		R.APTGSNTVLLR.G
118	131	2	1454.81	-2.7	0	46.3	20.5	95.00%	K.AGGEVLTLDQLALR.A		K.AGGEVLTLDQLALR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
160	RL27A_SCHPO	32.35%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
23	34	2	1269.74	4.4	0	65.4	18	95.00%	K.VVILQAIDQGSK.S		K.VVILQAIDQGSK.S
35	48	3	1461.76	5.9	1	42.8	23.5	95.00%	K.SHPFGHAVVAGVER.Y		K.SHPFGHAVVAGVER.Y
35	52	4	1963.05	4.3	2	23.2	21.1	95.00%	K.SHPFGHAVVAGVERYPLK.V		K.SHPFGHAVVAGVERYPLK.V
94	107	2	1575.83	3.5	1	46.7	23.7	95.00%	K.GLITADTFKEPTQR.S		K.GLITADTFKEPTQR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
161	TCTP_SCHPO	17.86%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
6	21	2	1737.84	4.2	1	86.5	26.3	95.00%	K.DVISGDELVSDAYDLK.E		K.DVISGDELVSDAYDLK.E
99	112	2	1670.86	-1.6	2	35	23.5	95.00%	R.LQESNPERVPVFEK.N		R.LQESNPERVPVFEK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
162	SPEE_SCHPO	15.77%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
105	126	3	2641.27	3.1	1	46.8	25.6	95.00%	R.EVVKHECVEEAILCDIDEDVIK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.EVVKHECVEEAILCDIDEDVIK.V
2	12	2	1291.72	4.1	0	43.5	20	95.00%	M.SVQELSHPLIK.D	Acetyl (+42)	-.MSVQELSHPLIK.D
18	31	2	1631.79	4.6	1	31.2	25.2	95.00%	R.EINNMWPGQAMTLK.V		R.EINNMWPGQAMTLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
163	ACBP_SCHPO	34.48%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
33	50	3	1911.99	-2.1	0	28	23.3	95.00%	K.QATVGDNNTEKPGLLDLK.G		K.QATVGDNNTEKPGLLDLK.G
2	13	2	1294.61	4.4	1	38.3	25.5	95.00%	M.SSTFEQAAADVK.E	Acetyl (+42)	-.MSSTFEQAAADVK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
164	SYYC_SCHPO	10.22%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
368	395	3	2695.3	0.63	2	53.5	24.9	95.00%	K.KAGTTNASIAAESGAAPATESQTAESFK.K		K.KAGTTNASIAAESGAAPATESQTAESFK.K
2	14	2	1605.83	4.1	2	47.4	23.6	95.00%	M.SLTPDEKYELITR.N	Acetyl (+42)	-.MSLTPDEKYELITR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
165	RL3A_SCHPO	11.08%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
249	262	2	1607.76	-1.7	1	37.9	26	95.00%	K.VACIGAWHPANVQW.T	Carbamidomethyl (+57)	K.VACIGAWHPANVQWTVAR.A
207	222	2	1837.88	-2.7	1	85.4	26.2	95.00%	K.STFEQNEMIDVIGVTR.G		K.STFEQNEMIDVIGVTR.G
11	19	2	982.54	4.3	1	27.2	19	93.00%	R.HGSLGFLPR.K		R.HGSLGFLPR.K
249	266	3	2035.03	4.4	1	29.3	24.6	95.00%	K.VACIGAWHPANVQWTVAR.A	Carbamidomethyl (+57)	K.VACIGAWHPANVQWTVAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
166	RS27_SCHPO	20.48%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	18	3	1937	-1.1	1	22.5	23.1	90.30%	M.VLAVDLLNPSHESEMRK.H		-.MVLAVDLLNPSHESEMRK.H
2	17	2	1808.91	-2.1	0	58.8	24.6	95.00%	M.VLAVDLLNPSHESEMR.K		-.MVLAVDLLNPSHESEMR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
167	PDI1_SCHPO	8.33%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
398	412	2	1637.79	4.8	1	66.2	26.4	95.00%	K.LAEEYSDDSNVVVAK.I		K.LAEEYSDDSNVVVAK.I
125	136	3	1350.87	5.1	1	30.4	6.99	95.00%	R.KQLLPTVKPISK.D		R.KQLLPTVKPISK.D
188	201	2	1436.77	4.3	1	45.1	21.9	95.00%	K.SLGSNFPGIVAFTK.D		K.SLGSNFPGIVAFTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
168	TPM_SCHPO	31.06%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
69	86	3	2087.06	4.7	1	48.9	24	95.00%	R.LKADNEDIQKTEAEQLSR.K		R.LKADNEDIQKTEAEQLSR.K
87	103	3	2070.12	0.91	1	46	20.2	95.00%	R.KVELLEEELETNDKLLR.E		R.KVELLEEELETNDKLLR.E
147	161	2	1707.87	-1.5	1	29.2	24.3	95.00%	K.VKAELDEVHQALEDL.-		K.VKAELDEVHQALEDL.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
169	RS8A_SCHPO	28.50%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
60	74	2	1568.72	4.4	1	94.1	26	95.00%	R.LDSGNFSWGSEGVSK.K		R.LDSGNFSWGSEGVSK.K
165	178	2	1475.79	4.1	1	33.2	22.9	95.00%	R.LYAVVSSRPGQSGR.C		R.LYAVVSSRPGQSGR.C
152	164	2	1363.68	4.8	1	51.3	24.8	95.00%	K.VDSALETQFAAGR.L		K.VDSALETQFAAGR.L
78	92	2	1751.94	4.6	1	25.6	21.1	90.50%	R.IIQVAYHPSNNELVR.T		R.IIQVAYHPSNNELVR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
170	RL19A_SCHPO	20.73%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
118	128	3	1386.74	5	1	32.3	22.9	95.00%	K.HLYHTLYLEAK.G		K.HLYHTLYLEAK.G
182	193	2	1422.69	3.6	1	31.8	25.9	95.00%	R.EQLYTAAEKIEE.-		R.EQLYTAAEKIEE.-
22	38	2	1960.89	-1.5	1	73.5	26.9	95.00%	K.VWMDPNEISEISNANSR.Q		K.VWMDPNEISEISNANSR.Q
182	193	2	1422.69	3.6	1	31.8	25.9	95.00%	R.EQIYTAAEKIEE.-		R.EQLYTAAEKIEE.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
171	RL30A_SCHPO	17.43%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
77	89	2	1276.61	-1.6	0	56.6	24.8	95.00%	Y.AGTNIDLGTACGK.L	Carbamidomethyl (+57)	K.ANVHHYAGTNIDLGTACGK.L
71	89	2	1997.95	6	1	62.5	26.5	95.00%	K.ANVHHYAGTNIDLGTACGK.L	Carbamidomethyl (+57)	K.ANVHHYAGTNIDLGTACGK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
172	RS4B_SCHPO	11.07%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
222	233	2	1232.68	5.6	1	42.4	22.1	95.00%	R.LSNVFVIGEAGK.S		R.LSNVFVIGEAGK.S
246	252	2	846.45	4.8	0	45.4	23.7	95.00%	K.LSITEER.D		K.LSITEER.D
40	49	2	1258.72	4.7	1	26.1	20.6	91.40%	R.ECLPLIVFLR.N	Carbamidomethyl (+57)	R.ECLPLIVFLR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
173	RL31_SCHPO	21.24%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
91	105	2	1650.87	4.2	1	39.3	22.9	95.00%	K.ALYTYVQAVDVANPK.M		K.ALYTYVQAVDVANPK.M
7	15	2	986.56	5	0	39.5	22.3	95.00%	K.SAINQVVTR.D		K.SAINQVVTR.D
94	105	2	1303.67	-1.8	1	58.8	23.9	95.00%	Y.TYVQAVDVANPK.M		K.ALYTYVQAVDVANPK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
174	RL12_SCHPO	28.48%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
68	83	2	1538.91	3.4	0	50.5	14.5	95.00%	R.QAAVSVVPSASALVIK.A		R.QAAVSVVPSASALVIK.A
17	31	2	1312.7	3.6	0	46	21.3	95.00%	R.AVGGEVAGGSTLAPK.I		R.AVGGEVAGGSTLAPK.I
131	146	2	1652.81	4	1	45.9	25.2	95.00%	K.EILGTAFSVGCTVDGK.N	Carbamidomethyl (+57)	K.EILGTAFSVGCTVDGK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
175	YBS7_SCHPO	22.44%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
442	471	4	3134.5	-0.033	1	26.4	24.5	95.00%	K.EQPPNKAEPAVPTEASSTKPSEAAEESTPR.F		K.EQPPNKAEPAVPTEASSTKPSEAAEESTPR.F
353	386	4	3399.65	2.3	1	59.5	23.6	95.00%	K.HTGPSLSSASQPSAASSSSSSEPSNLDKINDVKK.N		K.HTGPSLSSASQPSAASSSSSSEPSNLDKINDVKK.N
128	146	2	1760.86	5.1	0	31.6	25	95.00%	R.TSGSSTGLSNAPPSANVSK.A		R.TSGSSTGLSNAPPSANVSK.A
516	544	3	2894.33	1.5	1	30.7	26.3	95.00%	K.SPASGETSEAGVKETETTTSSESALPDAR.K		K.SPASGETSEAGVKETETTTSSESALPDAR.K
164	189	3	2841.41	3.2	0	29.4	23.9	95.00%	R.ATPEVCVPLNPDTGSVPLIHPEQTDR.G	Carbamidomethyl (+57)	R.ATPEVCVPLNPDTGSVPLIHPEQTDR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
176	RS10B_SCHPO	34.01%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
10	24	3	1621.94	4.8	1	31.6	16.6	95.00%	K.AIHQALFQQGVLVAK.K		K.AIHQALFQQGVLVAK.K
26	31	2	732.38	5.5	1	30.1	22.6	95.00%	K.DFNLPK.H		K.DFNLPK.H
32	44	2	1428.81	-1.7	0	27.7	21.3	93.70%	K.HPEVGVPNLQVIK.A		K.HPEVGVPNLQVIK.A
78	93	4	1859.01	4	1	23	19.4	95.00%	R.EYLHLPAEVVPATHKR.Q		R.EYLHLPAEVVPATHKR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
177	RL7C_SCHPO	8.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
169	183	2	1497.85	4.8	0	75.4	18.6	95.00%	R.IALSDNAIIEAALGK.Y		R.IALSDNAIIEAALGK.Y
110	115	2	772.46	-0.018	0	31.7	22.3	95.00%	K.IMQLLR.L		K.IMQLLR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
178	RL2_SCHPO	21.74%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
92	118	3	2780.44	3.2	0	52	21.5	95.00%	K.NAALTVGNVLPVGEMPEGTIISNVEEK.A		K.NAALTVGNVLPVGEMPEGTIISNVEEK.A
133	144	2	1251.68	-1.8	0	46.7	21.1	95.00%	Y.VIIVGHDVDTGK.T		R.SSGNYVIIVGHDVDTGK.T
128	144	3	1759.88	4.2	1	23	24.5	91.20%	R.SSGNYVIIVGHDVDTGK.T		R.SSGNYVIIVGHDVDTGK.T
163	173	2	940.55	4.3	0	54.6	14.8	95.00%	R.GVVGIVAGGGR.I		R.GVVGIVAGGGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
179	YCO6_SCHPO	10.69%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
37	56	2	2126.99	-1.8	0	106	26.9	95.00%	K.APQVNTIDEGDENLEAIDGK.L		K.APQVNTIDEGDENLEAIDGK.L
15	36	3	2140	-1.5	1	30.1	27	95.00%	K.MSAAPTPHNTPSGTSAPNFGAK.A		K.MSAAPTPHNTPSGTSAPNFGAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
180	MPG1_SCHPO	11.02%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
270	287	2	1776	4.2	0	35.2	18.4	95.00%	K.IGPNVVIGPNVTIGDGVR.L		K.IGPNVVIGPNVTIGDGVR.L
138	159	4	2530.28	3.4	2	22.1	23.2	95.00%	K.VEEPSKYGVVVHYPNSESLIER.F		K.VEEPSKYGVVVHYPNSESLIER.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
181	SUB2_SCHPO	10.14%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	96	3	3526.72	3.8	1	60.2	22.5	95.00%	R.AITDSGFEHPSEVQQVCIPQSILGTDVLCQAK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.AITDSGFEHPSEVQQVCIPQSILGTDVLCQAK.S
399	410	2	1336.6	-1.1	0	39.6	25.9	95.00%	F.SSSEEDSQILDK.I		K.GLAITFSSSEEDSQILDK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
182	RPE_SCHPO	17.54%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
6	20	2	1557.84	-1.8	1	49	22.7	95.00%	K.IAPSLLAGDFANLEK.E		K.IAPSLLAGDFANLEK.E

202	214	2	1421.73	0.48	0	45.2	25.1	95.00%	F.HAQSPEEVISGLR.N		K.TVDAAADAGANVIVAGTAVFHAQ SPEEVISGLR.N
123	134	2	1369.78	-1.8	1	38.9	19.4	95.00%	K.TPVEVILPFVEK.L		K.TPVEVILPFVEK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
183	RL21A_SCHPO	14.37%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
138	160	3	2554.23	0.32	1	32.7	25	95.00%	K.AHFVSTENNEPVTLHPVAYDTTI.-		K.AHFVSTENNEPVTLHPVAYDTTI.-
138	156	3	2124.03	0.47	1	30.3	26.2	95.00%	K.AHFVSTENNEPVTLHPVAY.D		K.AHFVSTENNEPVTLHPVAYDTTI.-
141	160	2	2199.07	0.81	1	40.6	26	95.00%	F.VSTENNEPVTLHPVAYDTTI.-		K.AHFVSTENNEPVTLHPVAYDTTI.-
141	156	2	1768.86	0.73	1	30.9	26.1	95.00%	F.VSTENNEPVTLHPVAY.D		K.AHFVSTENNEPVTLHPVAYDTTI.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
184	RL6_SCHPO	22.05%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
70	87	2	1959.1	3.1	1	33.6	16.6	95.00%	R.VVVLSQLEDTLVVTGPYK.V		R.VVVLSQLEDTLVVTGPYK.V
50	64	2	1497.84	5	0	33.1	19.4	95.00%	R.ASLAPGTVCILLAGR.F	Carbamidomethyl (+57)	R.ASLAPGTVCILLAGR.F
109	118	2	1031.56	5.5	0	31.2	23.6	95.00%	K.IDVSGVSVEK.F		K.IDVSGVSVEK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
185	RS13_SCHPO	23.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
10	20	2	1132.63	4.4	1	38.6	21.9	95.00%	K.GIASSALPYVR.S		K.GIASSALPYVR.S
44	55	2	1244.66	3.8	0	40.8	23	95.00%	K.GMSPSQIGVTLR.D		K.GMSPSQIGVTLR.D
28	39	2	1286.68	5	0	56.1	23	95.00%	K.ADADSVVEQILK.F		K.ADADSVVEQILK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
186	SODM_SCHPO	20.18%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
34	48	2	1649.84	1.4	1	34.3	24.7	95.00%	Y.AYNALEPALSETIMK.L		K.ATLPPLPYAYNALEPALSETIMK.L
162	173	2	1303.7	4.2	0	48.8	23.1	95.00%	R.ITTTANQDTIVK.S		R.ITTTANQDTIVK.S
26	48	2	2502.32	2.9	1	32.8	21.7	95.00%	K.ATLPPLPYAYNALEPALSETIMK.L		K.ATLPPLPYAYNALEPALSETIMK.L
127	135	2	1108.52	5	1	34	24.8	95.00%	K.WGSLEDFQK.E		K.WGSLEDFQK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
187	RL33A_SCHPO	24.07%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
33	45	2	1574.65	-1.9	2	29.9	26.3	94.60%	K.IEGCDSKEEAQFY.L	Carbamidomethyl (+57)	K.IEGCDSKEEAQFYLGK.R
20	32	4	1401.82	4.5	1	28.1	16.4	95.00%	R.SKHVIHPGTSIVK.I		R.SKHVIHPGTSLVK.I
33	44	2	1411.59	-0.92	2	39.9	26.2	95.00%	K.IEGCDSKEEAQF.Y	Carbamidomethyl (+57)	K.IEGCDSKEEAQFYLGK.R
20	32	4	1401.82	4.5	1	28.1	16.4	95.00%	R.SKHVIHPGTSLVK.I		R.SKHVIHPGTSLVK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
188	RL23_SCHPO	28.06%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
15	34	2	2090	3.5	0	65.5	25.9	95.00%	R.MTLGLPVQAIMNCADNSGAK.N	Carbamidomethyl (+57)	R.MTLGLPVQAIMNCADNSGAK.N
48	66	3	2043.11	4.2	1	47.8	20.5	95.00%	R.LNRLPAASCGDMVLATVKK.G	Carbamidomethyl (+57)	R.LNRLPAASCGDMVLATVKK.G
51	65	2	1531.78	3.4	0	55.2	24.6	95.00%	R.LPAASCGDMVLATVK.K	Carbamidomethyl (+57)	R.LPAASCGDMVLATVK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
189	KAPS_SCHPO	30.69%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

152	158	2	792.4	0.97	2	25.8	22.9	90.80%	R.AGEIKEF.T		R.AGEIKEFTGISAPYEAPISPEIVVSSHTQSIEECVEK.I
157	188	3	3532.7	3.1	1	32.4	22.1	95.00%	K.EFTGISAPYEAPISPEIVVSSHTQSIEECVEK.I	Carbamidomethyl (+57)	K.EFTGISAPYEAPISPEIVVSSHTQSIEECVEK.I
39	52	2	1664.86	3.8	1	65.6	24	95.00%	K.STIACALEQYLLQR.G	Carbamidomethyl (+57)	K.STIACALEQYLLQR.G
131	141	2	1314.62	0.61	0	42.3	26	95.00%	Y.VECPVEVAEQR.D	Carbamidomethyl (+57)	K.DGLPFIEVYVECPVEVAEQR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
190	GPD2_SCHPO	19.57%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
170	186	2	1731.85	0.7	0	62.5	25.3	95.00%	Y.CGVLSGANIASEVAQEK.F	Carbamidomethyl (+57)	R.LFSDIIEENTGMYCGVLSGANIASEVAQEK.F
67	88	4	2626.25	3.3	2	19.3	25.5	92.70%	K.IQHEGKECNLTEVFNTTHENVK.Y	Carbamidomethyl (+57)	K.IQHEGKECNLTEVFNTTHENVK.Y
220	236	2	1649.93	-2.7	0	27.8	15.7	93.80%	R.VNIVEDVPGVALGGALK.N		R.VNIVEDVPGVALGGALK.N
311	327	3	1907.98	3	0	33.8	23.9	95.00%	K.TGKPMHVVEQELLDGQK.L		K.TGKPMHVVEQELLDGQK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
191	RL14_SCHPO	11.94%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
103	110	2	993.46	6	1	29.1	24.7	95.00%	R.SQLNDFDR.F		R.SQLNDFDR.F
87	94	2	905.44	5.7	1	30.4	23.9	95.00%	K.WASSAWAK.K		K.WASSAWAK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
192	RS15A_SCHPO	20.92%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
90	108	2	2033.08	3.1	1	80.9	21.7	95.00%	R.NMIILPEMVGSVVGIYNGK.L		R.NMIILPEMVGSVVGIYNGK.L
73	85	2	1396.76	4.6	0	40.4	20.4	95.00%	K.TEAPLNEKPATVK.T		K.TEAPLNEKPATVK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
193	PGM_SCHPO	9.03%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	21	3	2330.21	3.2	1	23.9	22.6	92.60%	-.MIETIPTKPYEGQRPGTSGLR.K		-.MIETIPTKPYEGQRPGTSGLR.K
423	435	2	1529.66	4.3	1	62.5	26.5	95.00%	R.YDYEELENEAAGK.V		R.YDYEELENEAAGK.V
127	142	2	1631.79	4.4	1	81.8	25.2	95.00%	K.YNLGNGGPAPESVTEK.I		K.YNLGNGGPAPESVTEK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
194	SYH_SCHPO	7.25%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
24	38	3	1603.81	4.1	1	23.8	24.1	92.50%	K.SQGASKEDIDKEVAK.L		K.SQGASKEDIDKEVAK.L
364	387	3	2316.06	2.7	1	56.7	26.7	95.00%	K.SADPEADRSNDDSIGVGSIAAGGR.Y		K.SADPEADRSNDDSIGVGSIAAGGR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
195	6PGL_SCHPO	8.95%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
46	55	2	1083.61	5.4	0	52.4	19.8	95.00%	K.VLAEGLAQQR.G		K.VLAEGLAQQR.G
209	221	2	1488.81	-1.9	1	50.7	22.9	95.00%	K.DILPIVIEDFTSK.L		K.DILPIVIEDFTSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
196	RL11_SCHPO	14.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
154	164	2	1349.67	4.1	1	39.8	24.3	95.00%	K.INAEDTINWFK.Q		K.INAEDTINWFK.Q
36	49	2	1531.83	4.2	1	63.5	21.9	95.00%	K.VLEQLSGQTPVFSK.A		K.VLEQLSGQTPVFSK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
197	PNPP_SCHPO	12.08%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

145	166	3	2359.15	3.2	1	61.7	25.7	95.00%	K.IGPDPSVGAVLCGMDMHVTYLK.Y	Carbamidomethyl (+57)	K.IGPDPSVGAVLCGMDMHVTYLK.Y
182	195	2	1535.74	-2	1	41.8	25.6	95.00%	F.LLTNQDSTFPTNGK.F	Deamidation (+1)	K.YCMAFQYLQDPNCAFLLTNQDSTFPTNGK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
198	WOS2_SCHPO	32.26%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
155	186	3	3261.4	1.9	1	79.4	26.3	95.00%	F.GNLGGAGAGEDASDSEPELEEEEEVGSNEKKE.-		R.WVDEDEQEAQPEVSPFGAGGMPDLSALGGMGGMDFSQFGNLGGAGAGEDASDSEPELEEEEEVGSNEKKE.-
28	39	2	1279.74	0.45	0	49.8	15.9	95.00%	Y.LTVLIPDAVDPK.I		K.NVIYLTVLIPDAVDPK.I
117	132	2	1903.82	2	1	32.8	28	95.00%	R.WVDEDEQEAQPEVSPF.G		R.WVDEDEQEAQPEVSPFGAGGMPDLSALGGMGGMDFSQFGNLGGAGAGEDASDSEPELEEEEEVGSNEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
199	FUMH_SCHPO	11.83%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
131	142	2	1157.67	3.6	0	43.3	20.5	95.00%	R.AIEILGGTLGSK.K		R.AIEILGGTLGSK.K
392	417	3	2921.34	2.7	1	27.9	26.5	95.00%	R.LLGDACESFTDHCVVGIEPNYEGIAR.H	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.LLGDACESFTDHCVVGIEPNYEGIAR.H
112	130	2	2006.91	0.95	0	51	27.3	95.00%	F.QTGSGTQSNMNSNEVIANR.A		R.LDDNFPLVVFQTGSGTQSNMNSNEVIANR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
200	RL28A_SCHPO	20.27%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
94	110	2	1787.95	3.9	1	37.3	22.7	95.00%	K.NTEVAPVINVLQSGYGK.V		K.NTEVAPVINVLQSGYGK.V
115	127	3	1464.84	-1.2	1	24.4	17.2	93.20%	K.GRLPETPVIVQTR.Y		K.GRLPETPVIVQTR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
201	RS24B_SCHPO	26.12%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	83	2	1256.59	-2	1	29.5	26.1	94.50%	F.ALIYDSTESMK.K		R.STGFALIYDSTESMK.K
50	61	2	1381.64	4.3	1	28	26.4	92.30%	K.TDSECVQAFGLR.T	Carbamidomethyl (+57)	K.TDSECVQAFGLR.T
21	32	3	1363.77	4	1	39.5	19.4	95.00%	R.KQMVVDILHPGK.A		R.KQMVVDILHPGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
202	UBA1_SCHPO	3.36%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
566	588	3	2468.19	4.9	1	37.5	26.5	95.00%	K.GNTQVVVPHLTESYGSSQDPPEK.S		K.GNTQVVVPHLTESYGSSQDPPEK.S
361	371	2	1083.63	0.078	0	36.9	17.8	95.00%	F.LGGAVAQEVLK.A		R.GDLVAMSAFLGGAVAQEVLK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
203	DLDH_SCHPO	6.07%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
203	219	3	1743.02	4.9	1	25.6	13.4	94.60%	K.KIVSSTGALSLSEVPKK.M		K.KIVSSTGALSLSEVPKK.M
155	168	2	1448.76	3.8	1	31.8	23.7	95.00%	K.GTGSFIDPQTLSVK.G		K.GTGSFIDPQTLSVK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
204	Q9P7B4_SCHPO	20.08%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
234	256	3	2522.27	2.7	1	34.8	23.7	95.00%	R.ENVVIADTLVFPSHQGGANHVYR.K		R.ENVVIADTLVFPSHQGGANHVYR.K

233	256	4	2678.38	4.3	2	40.7	21.6	95.00%	R.RENVVIADTLVFPSHQGGANHVYR.K			R.RENVVIADTLVFPSHQGGANHVYR.K
183	199	2	1918.98	6.8	1	60.8	23.8	95.00%	R.IMEVDPGLVETEFSVVR.F			R.IMEVDPGLVETEFSVVR.F
163	173	2	1163.64	5.6	1	26.5	21.7	92.00%	K.SALAQFTSALR.K			K.SALAQFTSALR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
205	FKBP_SCHPO	13.39%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
44	58	2	1602.86	4.3	1	59	22.9	95.00%	R.GSPFVCTIGVGQLIR.G	Carbamidomethyl (+57)	R.GSPFVCTIGVGQLIR.G
48	58	2	1214.68	-1.4	0	58	21.5	95.00%	F.VCTIGVGQLIR.G	Carbamidomethyl (+57)	R.GSPFVCTIGVGQLIR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
206	YEI3_SCHPO	8.67%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
329	342	2	1482.75	2.8	1	41.2	24.8	95.00%	K.APQAAGVIHTDFEK.A		K.APQAAGVIHTDFEK.A
43	62	2	2148.04	-1	1	63.8	25.8	95.00%	K.SVLGNPANYPYATIDPEEAK.V		K.SVLGNPANYPYATIDPEEAK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
207	GUAA_SCHPO	13.36%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	130	2	1549.73	-1.9	1	46.3	26.4	95.00%	R.EYGPATVSMEPEIK.T		R.EYGPATVSMEPEIK.T
231	254	4	2311.19	3.1	1	17.8	22.9	90.20%	R.KMIGPSDHVIGAVSGGVDSTVASK.V		R.KMIGPSDHVIGAVSGGVDSTVASK.V
170	203	4	3715.11	3.7	1	22.3	19.8	95.00%	K.NSPFAVIAHVTKPIIGLQFHPEVTHTPLGLQLIK.N		K.NSPFAVIAHVTKPIIGLQFHPEVTHTPLGLQLIK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
208	CH10_SCHPO	22.12%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	84	2	1230.7	4	1	31.7	20.5	95.00%	R.VLLPAYGGSNIK.V		R.VLLPAYGGSNIK.V
62	72	2	1111.6	4.5	0	30.9	19.8	95.00%	K.LAQPSVAVGDR.V		K.LAQPSVAVGDR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
209	RL25A_SCHPO	19.86%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	137	2	1329.66	4	0	94.2	25.3	95.00%	K.LSADADALDVANR.I		K.LSADADALDVANR.I
74	88	4	1806.97	3	2	20.6	22	95.00%	K.KIEDDNTLVFHVHLK.A		K.KIEDDNTLVFHVHLK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
210	CAN_SCHPO	18.44%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
84	101	3	2033.14	2.7	1	42.8	18.1	95.00%	R.VPETTILNLLPGEVFVHR.N		R.VPETTILNLLPGEVFVHR.N
9	34	4	2766.34	3.9	1	21.8	25.1	95.00%	R.IEEIDHQDEIIDREASTASPVSGAGK.I		R.IEEIDHQDEIIDREASTASPVSGAGK.I
8	34	4	2922.44	2.7	1	21.1	23.5	95.00%	R.RIEEIDHQDEIIDREASTASPVSGAGK.I		R.RIEEIDHQDEIIDREASTASPVSGAGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
211	AROF_SCHPO	10.05%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
252	265	2	1338.61	4.9	1	41	26	95.00%	K.SGTNFDADSVAGAK.A		K.SGTNFDADSVAGAK.A
266	288	4	2617.24	3.5	1	24.8	25.9	95.00%	K.AKLEECNKLPSIMIDCSHGNSSK.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.AKLEECNKLPSIMIDCSHGNSSK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
212	LYS1_SCHPO	13.86%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
274	306	3	3758.77	3.3	1	76.7	23.8	95.00%	R.VVCDVSCDTTNPNNPIPIYNVNTTFDHPTVEVK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VVCDVSCDTTNPNNPIPIYNVNTTFDHPTVEVK.G

329	346	2	1904.02	3.7	1	28.9	21.2	95.00%	R.ESSEAFSEALIPSLLALK.D		R.ESSEAFSEALIPSLLALK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
213	FIMB_SCHPO	4.89%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
508	524	2	1796.81	3.5	1	38.6	27.1	95.00%	K.TLSDSDMVAWANSMAAK.G		K.TLSDSDMVAWANSMAAK.G
158	170	2	1485.74	3.7	0	44.6	25.3	95.00%	K.LINDSVPDTIDER.V		K.LINDSVPDTIDER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
214	Q9URK9_SCHPO	23.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	66	3	1455.79	-0.9	1	45.9	21.8	95.00%	R.ELLTLDEKDPKR.L		R.ELLTLDEKDPKRLFEGNAIIR.R
152	168	3	1785.9	4.3	1	38.7	24.4	95.00%	K.HIDFALSSPYGGGRPGR.C		K.HIDFALSSPYGGGRPGRCKRK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
215	PPA2_SCHPO	8.42%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
47	61	2	1654.77	2.3	1	41.9	26.6	95.00%	Y.FNGPTTSFPESCAIK.Q	Carbamidomethyl (+57)	K.DHLGTISVYHEPYFNGPTTSFPESCAIK.Q
136	143	2	961.53	5.4	1	31.9	23.3	95.00%	R.IELFDLGR.Q		R.IELFDLGR.Q
73	88	2	1640.68	-1	1	52.4	26.7	95.00%	R.NPTGDDTATDVSSAQY.I		R.NPTGDDTATDVSSAQYIDIFQNK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
216	PUR4_SCHPO	3.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
298	334	4	3616.77	4.4	1	38.1	21.7	95.00%	K.VETHNHPTAVSPFPGAATGSGGEIRDEGAVGQGSLSK.A		K.VETHNHPTAVSPFPGAATGSGGEIRDEGAVGQGSLSK.A
412	425	3	1426.76	5.3	1	35.9	22.9	95.00%	R.GYHKPIMAAGGIGR.I		R.GYHKPIMAAGGIGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
217	PUR7_SCHPO	18.39%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
159	174	3	1746.79	5.6	0	25.2	26.9	91.70%	K.AAEGHDENIHPDEVSK.I		K.AAEGHDENIHPDEVSK.I
222	235	2	1541.83	-2.3	0	29.7	22.2	95.00%	K.IVLVDEVLTPDSSR.F		K.IVLVDEVLTPDSSR.F
258	282	3	2764.43	3.8	1	38.4	21	95.00%	R.NWLTANNLANKPNVSLPEDVVEATR.R		R.NWLTANNLANKPNVSLPEDVVEATR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
218	AROC_SCHPO	11.14%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
328	340	2	1331.68	5.2	0	55.6	24.3	95.00%	K.SPATIGVEQSTSR.Y		K.SPATIGVEQSTSR.Y
161	191	3	3385.69	2.7	1	61.9	21.1	95.00%	K.IAIPLHETASSAILDPEDDTFESPITAEYLK.F		K.IAIPLHETASSAILDPEDDTFESPITAEYLK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
219	RS3_SCHPO	10.04%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
30	42	2	1513.64	4.2	1	70.9	26.5	95.00%	R.ELSEEGYSGCEVR.V	Carbamidomethyl (+57)	R.ELSEEGYSGCEVR.V
97	108	2	1362.64	3.8	0	61	25.1	95.00%	R.GLCAVAQCESLR.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GLCAVAQCESLR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
220	RLA1_SCHPO	29.36%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
11	26	2	1673.87	0.23	0	87.2	23.4	95.00%	Y.SALILADEGIEITSDK.L		-.MSASELATSYSALILADEGIEITSDK.L

33	48	2	1743.93	4.8	1	29.5	22.4	95.00%	K.AANVDVEPIWATIFAK.A		K.AANVDVEPIWATIFAK.A
33	46	2	1544.79	-1.2	1	27.8	24.8	93.80%	K.AANVDVEPIWATIF.A		K.AANVDVEPIWATIFAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
221	DPNP_SCHPO	10.48%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
224	243	3	2206.97	4.4	1	57.3	27.7	95.00%	K.FCEGVEAGHSMQGTQEEIAK.Y	Carbamidomethyl (+57)	K.FCEGVEAGHSMQGTQEEIAK.Y
334	350	3	1840.98	4.8	2	23.8	21.8	92.50%	K.VIEATAAVTSKDPHFQK.V		K.VIEATAAVTSKDPHFQK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
222	PP2C3_SCHPO	10.63%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
305	326	3	2364.03	-1.6	1	32.3	27.6	95.00%	R.VAANDGPCAPPEYAENHGPGWR.S	Carbamidomethyl (+57)	R.VAANDGPCAPPEYAENHGPGWR.S
106	127	3	2430.16	3.2	1	44.7	26.4	95.00%	K.AILDDDQFHTDPSGCTATVVLR.V	Carbamidomethyl (+57)	K.AILDDDQFHTDPSGCTATVVLR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
223	RL35_SCHPO	19.67%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
11	24	2	1684.85	4.2	0	72	24.4	95.00%	K.QSQENLAEQLQELR.Q		K.QSQENLAEQLQELR.Q
56	65	2	1157.65	4.3	0	33.6	22	95.00%	R.ILTVINESNR.L		R.ILTVINESNR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
224	HIS5_SCHPO	5.91%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
296	310	2	1715.8	-2.1	0	34.5	26.3	95.00%	R.NCPMADAPMLQVLEK.A	Carbamidomethyl (+57)	R.NCPMADAPMLQVLEK.A
203	219	2	1810.87	-1.1	1	59.4	26	95.00%	K.AFLTGNYEQPISGEASK.L		K.AFLTGNYEQPISGEASK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
225	YET4_SCHPO	13.60%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
190	216	3	2686.32	5.5	0	58	23.9	95.00%	R.NDEQLGNSPASITSKPATTSAAQPSSK.V		R.NDEQLGNSPASITSKPATTSAAQPSSK.V
419	462	4	4557.19	2.7	1	18.1	20	91.10%	K.NEVNVPSTIPTESENPVAVGGTTAEHPVQEAVTAPTETAHDFSK.E		K.NEVNVPSTIPTESENPVAVGGTTAEHPVQEAVTAPTETAHDFSK.E
487	503	3	1712.87	4.4	0	27.8	24.6	95.00%	R.KPSSTGQEPTTPSTPAK.S		R.KPSSTGQEPTTPSTPAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
226	ODP2_SCHPO	12.84%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
215	238	4	2577.46	3.9	2	20.4	13.4	95.00%	R.IIKVDIENFKPVVAPKPSNEAAAK.A		R.IIKVDIENFKPVVAPKPSNEAAAK.A
49	75	3	2873.43	2.8	1	41.8	23.9	95.00%	K.NYPAHTVINMPALSPTMTTGNIGAFQK.K		K.NYPAHTVINMPALSPTMTTGNIGAFQK.K
388	398	2	1267.61	2.3	1	32	25.9	95.00%	K.LKPEEYQGGTF.T		K.LKPEEYQGGTFTISNLGMFPVDQFTAIINPPQACILAVGTTVDTVVPDSTSEK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
227	SEC31_SCHPO	2.70%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
985	1000	2	1627.82	1.2	1	49.1	24.6	95.00%	Y.TPIAVASSTVNPAHTY.K		R.ISSSPNMPPSNPYTPIAVASSTVNPAHTYKPHGGSQIVPPPK.Q
404	420	2	1859.87	5.1	0	57.5	26.8	95.00%	K.EVTITSAPDEVEQDEAK.S		K.EVTITSAPDEVEQDEAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
228	PUR2_SCHPO	4.44%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
31	48	2	1678.78	1.8	1	54.6	26.3	95.00%	K.VYVAPGNGGTASNGAESK.M	Deamidation (+1)	K.VYVAPGNGGTASNGAESK.M
581	597	3	1741.78	0.58	1	44.2	27.1	95.00%	Y.HDGHYDANGTSVGAVSR.D		K.QAGCALVGGETSEMPGLYHDGH YDANGTSVGAVSR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
229	P5CR_SCHPO	22.70%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
70	98	3	3111.57	2.6	0	41.3	21.7	95.00%	K.ENAEMAAISNVLLLSCKPQAAED VLNSPK.M	Carbamidomethyl (+57)	K.ENAEMAAISNVLLLSCKPQAAED VLNSPK.M
241	261	2	2117.03	-1.9	0	67.9	25.9	95.00%	R.NDVSTPAGCTISGLLALEDGK.I	Carbamidomethyl (+57)	R.NDVSTPAGCTISGLLALEDGK.I
116	129	2	1566.76	5	0	85.9	25.9	95.00%	K.TISSLQSMLDESTR.V		K.TISSLQSMLDESTR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
230	RL7B_SCHPO	16.40%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	21	2	2002.11	4.4	1	37	18.8	95.00%	M.VASSTVPSVASIFAPESLLK.K		-.MVASSTVPSVASIFAPESLLK.K
109	114	2	772.46	-0.018	0	31.7	22.3	95.00%	K.IMQLLR.L		K.IMQLLR.L
168	182	2	1523.86	4.4	0	56.2	16.5	95.00%	R.IPLSDNAIIEAALGK.Y		R.IPLSDNAIIEAALGK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
231	MUG64_SCHPO	11.19%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
224	238	3	1767.86	4.9	0	44.3	26.4	95.00%	K.LDVESAKPENLEHCK.S	Carbamidomethyl (+57)	K.LDVESAKPENLEHCK.S
108	125	2	1851.02	3.8	0	41.3	19.5	95.00%	R.NLGNLTPLEQTPLASVGK.N		R.NLGNLTPLEQTPLASVGK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
232	ODPB_SCHPO	12.30%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
220	234	2	1634.86	4.6	1	26.5	22.7	92.10%	K.EALSEDFVLPFGLAK.V		K.EALSEDFVLPFGLAK.V
331	360	3	3021.51	4	1	35.4	23.2	95.00%	R.VSMADVPMPYSHPVEAASVPNA DVVVAAAK.K		R.VSMADVPMPYSHPVEAASVPNA DVVVAAAK.K
341	360	2	1931.01	-0.065	0	55.5	22.9	95.00%	Y.SHPVEAASVPNADVVVAAAK.K		R.VSMADVPMPYSHPVEAASVPNA DVVVAAAK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
233	CARA_SCHPO	4.10%	100%	1

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
74	90	2	1842.89	0.65	1	74.8	26.7	95.00%	F.TTSPVGYVESLTDPSYK.Q		R.NVSGEAVFTTSPVGYVESLTDPS YK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
234	ACAC_SCHPO	1.05%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
197	207	2	1131.63	6.1	0	34.7	20.8	95.00%	K.ISSTIVAQSAR.V		K.ISSTIVAQSAR.V
899	911	2	1475.7	-2.2	0	35.1	25.4	95.00%	Y.CDGQNLATTQQLK.V	Carbamidomethyl (+57)	K.QLEVAIQTYCDGQNLATTQQLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
235	HIS1_SCHPO	9.03%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	10	2	1282.6	4.8	0	34.4	26.1	95.00%	-.MDLVNHLEDR.L	Acetyl (+42)	-.MDLVNHLEDR.L
211	228	2	2047.02	-2.1	0	66.7	25.1	95.00%	R.SSNCSSELEPLLQTIITR.I	Carbamidomethyl (+57)	R.SSNCSSELEPLLQTIITR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
236	PPID_SCHPO	10.96%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
214	226	2	1432.74	4.4	1	72	24.1	95.00%	K.QFAQQNLDTAVAK.W		K.QFAQQNLDTAVAK.W

144	169	3	2959.43	3.1	1	32.1	25.2	95.00%	R.TIENLETKNDDPVVPVVIEECGTCTK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.TIENLETKNDDPVVPVVIEECGTCTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
237	O13797_SCHPO	14.83%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
197	214	2	1831.84	5.2	0	74	26.7	95.00%	K.QLNQPSDSSATSGADQAR.T		K.QLNQPSDSSATSGADQAR.T
124	152	4	3210.53	3.2	1	60.9	24.3	95.00%	R.AAAYNQLGQFENAVEDALTCLSLDPHHAR.A	Carbamidomethyl (+57)	R.AAAYNQLGQFENAVEDALTCLSLDPHHAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
238	RS21_SCHPO	48.28%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
51	60	2	1113.59	4.5	1	33.8	21.7	95.00%	K.TTYAISGFVR.S		K.TTYAISGFVR.S
1	16	2	1902.96	5.9	1	43.5	24.6	95.00%	-.MENEAGQLVDLYVPRK.C	Acetyl (+42)	-.MENEAGQLVDLYVPRK.C
72	87	2	1864.94	4.3	1	65.3	25.3	95.00%	R.LTTQDGLLEGVWSYQR.-		R.LTTQDGLLEGVWSYQR.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
239	RL24A_SCHPO	20.81%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	12	2	1357.64	4.1	2	34.6	26	95.00%	-.MKVEVCSFSGSK.V	Carbamidomethyl (+57)	-.MKVEVCSFSGSK.V
81	91	2	1097.65	4.7	0	29.4	18.3	95.00%	R.GIVGANLDVIK.E		R.GIVGANLDVIK.E
36	43	2	978.52	4.9	1	29.5	24.4	95.00%	K.SESLFLQR.K		K.SESLFLQR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
240	HIS7_SCHPO	14.81%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
199	213	2	1434.73	4.7	0	45	24.5	95.00%	R.AATSLTGSSEVPSTK.G		R.AATSLTGSSEVPSTK.G
24	40	2	1901.96	-1.4	1	39	24.9	95.00%	K.APLPEESNFIDELITSK.H		K.APLPEESNFIDELITSK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
241	RPN11_SCHPO	10.71%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	92	2	2046.01	1	1	59.3	25.1	95.00%	F.AMPQSGTGVSVEAVDPVFQK.N		R.VVDVFAMPQSGTGVSVEAVDPVFQK.N
258	270	2	1511.8	3.2	0	34.5	22.4	95.00%	R.VQNEVTLSPEQLR.I		R.VQNEVTLSPEQLR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
242	Q9USR1_SCHPO	11.72%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
181	198	3	1821	-0.99	1	24.7	19.8	93.70%	K.VHSIAITPVKGETSSAPK.T		K.VHSIAITPVKGETSSAPK.T
109	124	2	1403.73	4.8	0	51.6	24	95.00%	K.ATGTGALASSSSAPVK.G		K.ATGTGALASSSSAPVK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
243	KGUA_SCHPO	12.38%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
134	147	2	1596.89	0.61	1	29.1	19	95.00%	Y.VFLAPPSIEQLEVR.L		K.ASPIDAQYVFLAPPSIEQLEVR.L
2	12	2	1103.59	4.9	0	34.4	22.8	95.00%	M.TPQLSSSVASK.L		-.MTPQLSSSVASK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
244	SDS23_SCHPO	9.80%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	16	2	1491.72	4.8	0	80.7	25.2	95.00%	M.PLSTQSSDSLSSAGR.Q		-.MPLSTQSSDSLSSAGR.Q
50	74	3	2810.36	-1.2	0	22.5	24.5	90.20%	F.LHDNEIALIDPETSMEEASSILIDR.D		K.WQDIPVTFLHDNEIALIDPETSMEEASSILIDR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
245	YNY8_SCHPO	8.33%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
237	249	2	1394.73	0.41	1	25.6	22.9	90.50%	R.APPQLDVRPQGAF.S		R.APPQLDVRPQGAFSLFHGNVVG K.F
2	16	2	1783.84	4.8	1	36.8	26.3	95.00%	M.SATSINPNNWHWTSK.D	Acetyl (+42)	-.MSATSINPNNWHWTSK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
246	SYFA_SCHPO	4.81%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	14	2	1558.9	4.5	2	64.1	15.4	95.00%	M.SKLEALQVFLLEK.L	Acetyl (+42)	-.MSKLEALQVFLLEK.L
128	138	2	1219.56	4.9	0	33.3	25.8	95.00%	K.NTDSITDETPK.V		K.NTDSITDETPK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
247	ERF3_SCHPO	2.72%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
534	551	3	1939.96	5.4	2	34.4	25.4	95.00%	R.VRGDDSDVQTGYVLTSTK.N		R.VRGDDSDVQTGYVLTSTK.N
534	545	2	1310.57	-0.77	2	32.4	26	95.00%	R.VRGDDSDVQTGY.V		R.VRGDDSDVQTGYVLTSTK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
248	ERG19_SCHPO	8.14%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
5	20	2	1760.95	-1.6	1	28.5	21.9	94.60%	K.VYQCTVSAPVNIAVIK.Y	Carbamidomethyl (+57)	K.VYQCTVSAPVNIAVIK.Y
373	388	2	1670.87	-2	0	70.1	23.4	95.00%	R.VLTIDESLIDASGNPK.F		R.VLTIDESLIDASGNPK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
249	SEC13_SCHPO	11.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
154	172	2	1721.9	0.4	0	71.6	23.4	95.00%	W.SPPSLSGSVVGQSPAAGPK.K		R.IFTAHEPGCNAVCWSPPSLSGSV VGQSPAAGPK.K
140	172	3	3364.61	3	1	43.1	23.6	95.00%	R.IFTAHEPGCNAVCWSPPSLSGSV VGQSPAAGPK.K	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.IFTAHEPGCNAVCWSPPSLSGSV VGQSPAAGPK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
250	CYSK1_SCHPO	9.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
10	23	2	1341.78	3.9	1	59.1	18.5	95.00%	K.VPGIVSGFIGAIGR.T		K.VPGIVSGFIGAIGR.T
180	200	2	2019.93	5.1	1	71.4	26.9	95.00%	K.GTVDGFTCSTGTGGTFAGVTK.Y	Carbamidomethyl (+57)	K.GTVDGFTCSTGTGGTFAGVTK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
251	YBN4_SCHPO	12.62%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
182	203	4	2693.39	2.2	1	23.4	21.8	95.00%	K.VKPTIHQMELHPYLPQTEYLEK.H		K.VKPTIHQMELHPYLPQTEYLEK.H
52	70	4	2151.08	3	1	29.4	25.2	95.00%	R.HIDTAHIYGNEKEIGEGIR.E		R.HIDTAHIYGNEKEIGEGIR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
252	RLA0_SCHPO	15.06%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
133	144	2	1308.71	5.2	1	29.1	21.1	95.00%	K.TSFFQALGIPTK.I		K.TSFFQALGIPTK.I
98	132	3	3513.88	2.7	1	45.6	16.2	95.00%	R.ETIIANVIAAPARPNAIAPLDVFVP AGNTGMEPGK.T		R.ETIIANVIAAPARPNAIAPLDVFVP AGNTGMEPGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
253	SYQ_SCHPO	3.95%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
757	773	3	1760.83	5.2	1	28.1	26.6	95.00%	K.TDSSAGVDKAENPESVR.F		K.TDSSAGVDKAENPESVR.F
52	66	2	1574.91	4.6	1	39.6	15.1	95.00%	R.TIGNLLFTLANASLK.Q		R.TIGNLLFTLANASLK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
254	UBC4_SCHPO	25.85%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
91	101	2	1244.65	4.6	1	28.4	23.7	94.50%	R.DQWSPALTISK.V		R.DQWSPALTISK.V	
102	128	3	3017.59	3.1	1	65.3	19.2	95.00%	K.VLLSICSLLTDPNPDDPLVPEIAHVYK.T	Carbamidomethyl (+57)	K.VLLSICSLLTDPNPDDPLVPEIAHVYK.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
255	YB35_SCHPO	3.13%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
693	705	2	1475.72	4.7	0	26.1	25.2	91.00%	R.QESLPSQQTTETK.H		R.QESLPSQQTTETK.H	
339	366	5	3084.43	8.2	2	21.1	25.6	95.00%	K.KWIAAISSAIENDEEANKPNVTADNASF.G	Phospho (+80)	K.KWIAAISSAIENDEEANKPNVTADNASFGTHDLAPAAHK.F	

Supplementary Table S2: All "Scaffold" validated proteins and peptides identified from solprotSP (*S.pombe*) and from SCVMprot (*S.cerevisiae*) samples

***S.pombe* - Asp-N digest of large tryptic peptides (replicate A)**

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
1	ENO11_SCHPO	45.56%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
361	374	3	1608.73	4.7	1	47.1	24	95.00%	R.MSYEAGWGVMVSHR.S		R.MSYEAGWGVMVSHR.S
185	194	2	1204.59	5.4	1	34	22.9	95.00%	R.WGAETYHTLK.S		R.WGAETYHTLK.S
346	360	2	1585.85	6	1	90.8	18.6	95.00%	K.VNQIGSVTESLNAVR.M		K.VNQIGSVTESLNAVR.M
302	310	2	1160.51	2.5	0	27.7	24.3	95.00%	D.DWSAWTHMK.A		K.YPIVSIEDPFDQDDWSAWTHMK.A
364	374	2	1227.59	2.8	0	32.7	23.7	95.00%	Y.EAGWGVMVSHR.S		R.MSYEAGWGVMVSHR.S
65	79	2	1477.87	4	0	73.7	9.03	95.00%	K.AVGNVNNIIAPAVVK.A		K.AVGNVNNIIAPAVVK.A
106	120	2	1560.82	4.2	0	61.3	19.3	95.00%	K.LGANAILGVSMAICR.A	Oxidation (+16)/ Carbamidomethyl (+57)	K.LGANAILGVSMAICR.A
33	47	2	1470.78	3.2	1	47.8	19.1	95.00%	R.AIVPSGASTGIWEAL.E		R.AIVPSGASTGIWEALEMR.D
23	32	2	1141.58	3.2	1	42.4	21.6	95.00%	V.DLTTETGIHR.A		R.GNPTVEVDLTTETGIHR.A
380	396	2	1755.95	1.5	0	72.3	16	95.00%	A.DTFISHLTVGIGAGQLK.S		R.SGETADTFISHLTVGIGAGQLK.S
301	310	2	1275.54	2.6	1	48.7	24.5	95.00%	Q.DDWSAWTHMK.A		K.YPIVSIEDPFDQDDWSAWTHMK.A
338	345	2	901.51	4.7	0	31.4	20.4	95.00%	K.CANALLLK.V	Carbamidomethyl (+57)	K.CANALLLK.V
409	414	2	806.43	5.7	1	29.4	22.3	95.00%	K.YNELLR.I		K.YNELLR.I
142	162	2	2039.02	2	0	62.3	21	95.00%	K.GPYVLPVPSFNVLNGGSHAGG.D	Deamidation (+1)	K.GPYVLPVPSFNVLNGGSHAGGDLAFQEFMILPTGAPSFSEAMR.W
217	225	2	1013.51	2.1	1	29.2	21.5	95.00%	P.DLQTPQEAL.D		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
168	184	2	1898.89	2.1	1	58.9	22.9	95.00%	Q.EFMILPTGAPSFSEAMR.W	Oxidation (+16)	K.GPYVLPVPSFNVLNGGSHAGGDLAFQEFMILPTGAPSFSEAMR.W
226	234	2	1013.58	2.1	1	37.8	19	95.00%	L.DLIVEAINK.A		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
320	328	2	1003.52	3.1	1	49.4	22.6	95.00%	G.DDLTVTNVK.R		K.AETDFQIVGDDLTVTNVK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
2	G3P1_SCHPO	33.93%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	126	2	813.5	2.2	0	29.9	16.7	95.00%	R.VIISAPSK.D		R.VIISAPSK.D
39	48	2	1309.58	2.7	1	50.3	23.7	95.00%	I.DLEYMAYMFK.Y		K.TIQVVAINDPFIDLEYMAYMFK.Y
228	234	2	794.41	4.9	0	23.6	20.8	90.10%	K.LTGMAFR.V		K.LTGMAFR.V
118	126	2	969.6	2.8	1	33.5	12.6	95.00%	K.RVIISAPSK.D		K.RVIISAPSK.D
296	309	2	1459.77	2	0	65.9	20	95.00%	F.DASAGIQLSPQFVK.L		K.GVLGYTEDAVVSTDFCGDNHSSIFDASAGIQLSPQFVK.L
249	256	2	934.48	3.2	1	26.4	22.7	94.60%	K.LAKPTNYE.D		K.LAKPTNYEDIK.A
146	162	2	1818.91	4.5	0	75	21.9	95.00%	K.VISNASCTTNCLAPLAK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.VISNASCTTNCLAPLAK.V
324	334	2	1148.65	6.2	1	55.4	16.7	95.00%	R.VVDLVAYTAAK.D		R.VVDLVAYTAAK.D
172	186	2	1587.8	1.4	0	89.7	21.3	95.00%	E.EGLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK.T
6	13	2	819.43	6.2	0	38.4	21.6	95.00%	K.VGINGFGR.I	Deamidation (+1)	K.VGINGFGR.I
201	215	2	1343.71	4.7	0	69.9	20	95.00%	R.GASANIIPSSTGAAK.A		R.GASANIIPSSTGAAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
3	PGK_SCHPO	35.75%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	169	2	873.41	4.2	0	27.3	22.5	95.00%	N.DAFGTAHR.A		K.SLTSLGDIFVNDAFGTAHR.A

57	71	2	1591.87	2.9	0	46.2	17.9	95.00%	K.AVILMSHLGRPNGAR.V	Deamidation (+1)	K.AVILMSHLGRPNGAR.V
40	48	2	910.59	3.6	0	25.3	6.02	93.20%	R.IVGALPTIK.Y		R.IVGALPTIK.Y
384	400	2	1625.83	2.1	1	49.9	20.6	95.00%	E.DALSHVSTGGGASLELL.E		K.EDALSHVSTGGGASLELLEGK.A
276	286	2	1235.65	2.4	1	32.8	21.2	95.00%	V.EVFLPVDFVTA.D		K.NNVEVFLPVDFVTADK.F
49	56	2	975.51	4.7	1	23.5	21.6	90.00%	K.YALEQQPK.A		K.YALEQQPK.A
383	397	2	1399.66	2.7	1	65.8	24	95.00%	K.EDALSHVSTGGGASL.E		K.EDALSHVSTGGGASLELLEGK.A
384	397	2	1270.62	2.4	0	63.7	22.7	95.00%	E.DALSHVSTGGGASL.E		K.EDALSHVSTGGGASLELLEGK.A
359	371	2	1231.59	2.4	1	25.3	22.5	93.20%	K.TCEAGNVVIVGGG.D	Carbamidomethyl (+57)	K.TCEAGNVVIVGGGDTATVAK.K
404	414	2	1040.63	5.6	0	39.4	15.9	95.00%	K.ALPGVVALSSK.-		K.ALPGVVALSSK.-
321	329	2	994.54	5.5	1	50.2	20.3	95.00%	K.FAEVITTSK.T		K.FAEVITTSK.T
75	86	3	1304.74	4.3	1	59.4	14.8	95.00%	K.YSLKPVAAELSK.L		K.YSLKPVAAELSK.L
197	213	2	1737	3.5	1	54.1	10.8	95.00%	K.ALENPARPFLAILGGAK.V		K.ALENPARPFLAILGGAK.V
170	181	2	1267.64	4	1	58.7	22.2	95.00%	R.AHSSMVGVDLPR.V		R.AHSSMVGVDLPR.V
157	169	2	1461.7	2.4	1	48.2	23.4	95.00%	G.DIFVNDAFGTAHR.A		K.SLTSLGDIFVNDAFGTAHR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
4	METE_SCHPO	38.22%	100%	26

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
561	571	2	1184.7	5.1	0	40.5	15.3	95.00%	K.GMLTAPITILR.W		K.GMLTAPITILR.W
434	449	2	1746.96	2.8	0	60.3	14.3	95.00%	K.LPLFPTTTIGSFPQTK.E		K.LPLFPTTTIGSFPQTK.E
4	11	2	845.48	4.8	0	33.3	20.6	95.00%	K.SAVLGFPR.I		K.SAVLGFPR.I
325	343	2	1947.01	1.8	1	71.2	19.6	95.00%	R.VQVASSSSILHIPHSLSGE.D		R.VQVASSSSILHIPHSLSGEDQINPEIK.R
71	82	2	1414.7	1.9	0	44	22.1	95.00%	M.DHSFSFNVIPPR.Y		K.AQGVDIIPSNDFSLYDQIMDHSFSFNVIPPR.Y
707	714	2	901.49	4.3	1	27.7	23.1	95.00%	R.VPPVSEFK.E		R.VPPVSEFK.E
684	690	2	813.51	5.6	0	34.2	16.9	95.00%	K.LLNVLSR.Y		K.LLNVLSR.Y
691	706	2	1818.88	3.8	1	84	21.9	95.00%	R.YTSCIGPGLFDIHSPR.V	Carbamidomethyl (+57)	R.YTSCIGPGLFDIHSPR.V
344	351	2	955.5	1.9	1	29.6	20.5	95.00%	E.DQINPEIK.R		R.VQVASSSSILHIPHSLSGEDQINPEIK.R
243	260	2	1982.08	3.5	1	54.1	14.3	95.00%	K.LILTTYFGSLQSNADVLK.G		K.LILTTYFGSLQSNADVLK.G
261	269	2	861.51	2.9	0	32.5	16	95.00%	K.GLPIAGVHV.D		K.GLPIAGVHVDVVR.A
727	738	2	1466.7	4.2	1	48	23	95.00%	K.DHLWLNPDCGLK.T	Carbamidomethyl (+57)	K.DHLWLNPDCGLK.T
428	449	3	2402.33	2.8	1	51.8	12	95.00%	K.QQASLKLPLFPTTTIGSFPQTK.E		K.QQASLKLPLFPTTTIGSFPQTK.E
261	273	2	1330.78	4	1	55.7	11.5	95.00%	K.GLPIAGVHVDVVR.A		K.GLPIAGVHVDVVR.A
500	508	2	1143.51	2.7	1	43	23.7	95.00%	N.DMVQYFGER.M		R.NDMVQYFGER.M
281	299	2	1881.08	4.8	1	87.4	8.45	95.00%	R.ALAVLGENQIISVGVVSGR.N		R.ALAVLGENQIISVGVVSGR.N
92	99	2	959.42	3.4	0	33	23.2	95.00%	L.DTYFAMGR.G		R.LSGLSSLDTYFAMGR.G
361	369	2	1017.56	4.9	1	30.5	20.9	95.00%	K.CAELAILTK.A	Carbamidomethyl (+57)	K.CAELAILTK.A
547	560	2	1596.79	3.6	0	50.8	22.2	95.00%	K.ESQYAQSITSKPMK.G		K.ESQYAQSITSKPMK.G
536	546	2	1275.67	1.6	0	44.4	20.7	95.00%	G.DVYRPAPMTVK.E		R.CVRPPIIVGDVYRPAPMTVK.E
527	546	3	2267.24	3.3	1	44.5	14.3	95.00%	R.CVRPPIIVGDVYRPAPMTVK.E	Carbamidomethyl (+57)	R.CVRPPIIVGDVYRPAPMTVK.E
631	637	2	877.45	5.9	1	49	22.6	95.00%	K.WAIDAFR.L		K.WAIDAFR.L
85	99	2	1616.79	4.1	1	63.5	22.5	95.00%	R.LSGLSSLDTYFAMGR.G		R.LSGLSSLDTYFAMGR.G
221	231	2	1275.67	1.6	1	24.9	21.2	92.60%	L.DLPQEILASYK.E		K.LTEAGAEYIQIDEPILTLDLPQEILASYK.E
581	593	2	1397.77	2	0	78.8	17.5	95.00%	H.DSVQAQQIALGLR.D		R.DDVHDSVQAQQIALGLR.D
156	176	3	2256.33	3.9	0	51.3	6.02	95.00%	K.EAGIITRPVLVGPVTYLFIAK.A		K.EAGIITRPVLVGPVTYLFIAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
5	EF1A1_SCHPO	40.43%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
402	414	2	1495.69	1.9	1	23.5	23.1	90.00%	K.MVPSKPMCVEAFT.D	Carbamidomethyl (+57)	K.MVPSKPMCVEAFTDYAPLGR.F

197	214	2	2238	3.5	1	79.5	22.9	95.00%	G.DNMIEPTTNMPWYQGWQK.E		K.TVPFVPVSGFQGDNMIEPTTNMPWYQGWQK.E
415	421	2	790.4	2.2	0	23.8	21.6	90.60%	T.DYAPLGR.F		K.MVPSKPMCVEAFTDYAPLGR.F
147	154	2	883.55	5.8	0	26.4	15.7	94.50%	K.QLIVAVNK.M		K.QLIVAVNK.M
254	264	2	1024.61	4.2	0	65.4	14	95.00%	K.IGGIGTVPVGR.V		K.IGGIGTVPVGR.V
101	109	2	921.42	1.9	0	27.6	22.9	95.00%	K.NMITGTSQA.D		K.NMITGTSQADCAVLIIGGGTGEFEAGISK.D
304	311	2	891.45	2.7	0	35.4	22.5	95.00%	G.DNVGFNVK.N		K.SVEMHHESLDAGLPGDNVGFNVK.N
6	20	2	1529.84	4.6	1	62.9	17.6	95.00%	K.GHINVVVIGHVDSGK.S		K.GHINVVVIGHVDSGK.S
155	164	2	1151.51	6.4	1	75.8	23.4	95.00%	K.MDTTGWSQAR.F		K.MDTTGWSQAR.F
241	249	2	1078.65	1	1	31.6	11.5	95.00%	T.DKPLRLPLQ.D		K.TLLEAIDSIEPPARPTDKPLRLPLQDVYK.I
85	96	2	1340.69	4.4	1	66.1	20.6	95.00%	K.YNVTVIDAPGHR.D		K.YNVTVIDAPGHR.D
246	253	2	974.55	4.1	1	32.1	20.3	95.00%	R.LPLQDVYK.I		R.LPLQDVYK.I
265	285	2	2087.14	2.6	1	47.2	14.6	95.00%	R.VETGVIKPGMIVTFAPAGVTT.E		R.VETGVIKPGMIVTFAPAGVTTEVK.S
135	146	2	1313.74	2.6	0	52.8	17.8	95.00%	R.EHALLAYTLGVK.Q		R.EHALLAYTLGVK.Q
185	196	2	1233.64	1.9	0	23.6	21.9	90.20%	K.TVPFVPVSGFQG.D		K.TVPFVPVSGFQGDNMIEPTTNMPWYQGWQK.E
56	62	2	893.47	4.6	1	24.5	22.3	92.00%	K.YAWVLDK.L		K.YAWVLDK.L
231	240	2	1081.54	2.3	1	42.9	22.9	95.00%	I.DSIEPPARPT.D		K.TLLEAIDSIEPPARPTDKPLR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
6	KPYK_SCHPO	36.74%	100%	20

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
487	497	2	1053.66	5.9	0	39.5	11.1	95.00%	K.IIVLQGAVGGK.G		K.IIVLQGAVGGK.G
215	223	2	1114.55	2.9	0	43.6	23.3	95.00%	V.DMIFASFIR.R	Oxidation (+16)	K.NGVDMIFASFIR.R
77	90	2	1397.8	3.3	0	36.4	14.8	95.00%	K.ASATNPLFPLAIAL.D		K.ASATNPLFPLAIALDTK.G
422	433	3	1430.81	3.6	0	48.6	15.2	95.00%	K.YRPSIPIVMVTR.C		K.YRPSIPIVMVTR.C
334	344	2	1192.6	1.9	1	55.2	22.5	95.00%	A.DLVMLSGETTK.G		R.AEVSDVGNAVLDGADLVMLSGETTK.G
107	120	2	1596.72	2.2	1	29.2	23.8	95.00%	T.DYPISSGHEMIFTT.D		R.TGLTVGGTDYPISSGHEMIFTTDDAYAEK.C
265	271	2	760.39	2.1	0	34	24.8	95.00%	T.DGIMVAR.G		K.IENQQGVNNFDSILDVTDGIMVAR.G
77	93	2	1741.97	3.8	1	39.2	15.4	95.00%	K.ASATNPLFPLAIALDTK.G		K.ASATNPLFPLAIALDTK.G
309	319	2	1350.64	3.1	0	34.9	23	95.00%	L.ESMTYNPRPTR.A		K.CNIAGKPVACATQMLESMTYNPRPTR.A
57	71	2	1797.78	2.5	1	49.7	24.1	95.00%	R.MNFSHGSYEYHQSVI.D		R.MNFSHGSYEYHQSVIDNAR.K
28	37	2	1088.6	5	0	46.3	19.4	95.00%	R.TSIICTIGPK.S	Carbamidomethyl (+57)	R.TSIICTIGPK.S
468	477	2	1186.55	5.3	0	54.8	23	95.00%	R.VAYGCQQAYK.M	Carbamidomethyl (+57)	R.VAYGCQQAYK.M
294	319	4	2965.41	3.9	1	47.2	20.3	95.00%	K.CNIAGKPVACATQMLESMTYNPRPTR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CNIAGKPVACATQMLESMTYNPRPTR.A
294	308	2	1632.78	2.5	0	46.6	22.4	95.00%	K.CNIAGKPVACATQML.E	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CNIAGKPVACATQMLESMTYNPRPTR.A
405	417	2	1287.72	5.7	0	62	17.6	95.00%	K.AIVVLSTSGNTAR.L		K.AIVVLSTSGNTAR.L
248	257	2	1161.54	2.6	1	27.6	23.6	95.00%	K.IENQQGVNNF.D		K.IENQQGVNNFDSILDVTDGIMVAR.G
212	223	2	1368.69	4.2	1	39.8	21.8	95.00%	K.NGVDMIFASFIR.R		K.NGVDMIFASFIR.R
76	90	2	1525.89	2	1	50.5	14.1	95.00%	R.KASATNPLFPLAIAL.D		R.KASATNPLFPLAIALDTK.G
194	201	2	871.47	2.7	1	27.7	23.1	95.00%	V.DLPALSEK.D		K.TDVDLPALSEK.D
47	56	3	1143.62	4.2	1	26	21.5	95.00%	K.LRDAGMNIVR.M		K.LRDAGMNIVR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
7	ALF_SCHPO	56.70%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
351	358	2	971.46	3.7	0	26.4	22.7	94.70%	E.DFYTVNTL.-		R.VLTALEDFYTVNTL.-

256	272	2	1779.86	2.7	0	76.9	22	95.00%	N.DKPVFFVFHGGSGSSVN.E		K.TTNDKPVFFVFHGGSGSSVNEFR.T
26	50	2	2496.31	3.3	1	74.3	15.9	95.00%	R.EHGFAIPAINVTSSSTAIAALEAAR.E		R.EHGFAIPAINVTSSSTAIAALEAAR.E
207	234	4	2951.53	3.2	0	31.9	16.8	95.00%	R.ELSSVTPYFSIAAAFGNVHGVYKPGNVK.L		R.ELSSVTPYFSIAAAFGNVHGVYKPGNVK.L
290	300	2	1283.62	2.6	1	73.9	22.3	95.00%	T.DTQFAYVEGVR.D		K.VNIDTDTQFAYVEGVR.D
131	142	2	1366.67	2.9	1	34.3	23	95.00%	K.IHGEPLFSSHML.D		K.IHGEPLFSSHMLDLSEEPK.K
113	118	2	786.45	1.9	1	27.3	21.7	95.00%	K.KLLPWM.D		K.KLLPWMDGMFEADEAYFK.I
94	112	2	2098.02	4.1	1	63.5	21.8	95.00%	R.SIAPFFGVPVVMHSDHCAK.K	Carbamidomethyl (+57)	R.SIAPFFGVPVVMHSDHCAK.K
26	46	2	2069.08	1	0	30.1	18.8	95.00%	R.EHGFAIPAINVTSSSTAIAAL.E		R.EHGFAIPAINVTSSSTAIAALEAAR.E
5	19	2	1539.86	2.8	1	51.3	16.3	95.00%	L.DIVPTGVITGDNVLK.L		-.MGILDIVPTGVITGDNVLK.L
94	107	2	1486.77	2.7	0	59.4	20	95.00%	R.SIAPFFGVPVVMHS.D		R.SIAPFFGVPVVMHSDHCAK.K
308	320	2	1378.61	3.2	1	38.2	24.4	95.00%	K.DYLMTPVGNPEGA.D	Oxidation (+16)	K.DYLMTPVGNPEGADKPNK.K
256	275	3	2212.07	1.2	1	30.3	21.5	95.00%	N.DKPVFFVFHGGSGSSVNEFR.T		K.TTNDKPVFFVFHGGSGSSVNEFR.T
235	248	2	1564.88	3.1	0	70	14	95.00%	K.LQPALLGQHQAYVK.E		K.LQPALLGQHQAYVK.E
54	71	2	1844.94	-2.2	0	107	20.4	95.00%	R.SPIILQTSNGGAHFFAGK.E	Deamidation (+1)	R.SPIILQTSNGGAHFFAGK.E
80	93	2	1399.76	5.1	0	89.1	17.4	95.00%	K.ASIAGSIAAAHYIR.S		K.ASIAGSIAAAHYIR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
8	PDC2_SCHPO	28.96%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
238	253	2	1690.85	2.6	1	77	21.6	95.00%	K.LAEALNCAAFIMPAAK.G	Deamidation (+1)/ Carbamidomethyl (+57)	K.LAEALNCAAFIMPAAK.G
228	237	2	949.49	5	1	30.2	22.7	95.00%	R.AAGAESAFVK.L		R.AAGAESAFVK.L
304	328	2	2694.37	3	1	65.1	18.3	95.00%	R.AAPNPNILLNSDYTSVSIPGYVFSR.V		R.AAPNPNILLNSDYTSVSIPGYVFSR.V
215	225	3	1192.76	4.9	1	19	7.78	92.60%	K.KEKPILLAGPK.L		K.KEKPILLAGPK.L
446	461	2	1808.88	3	1	92.1	22.3	95.00%	G.DGSFQLTGQEISQMIR.H		R.TIVMVGDGSFQLTGQEISQMIR.H
315	328	2	1589.78	1.9	0	56	22.4	95.00%	S.DYTSVSIPGYVFSR.V		R.AAPNPNILLNSDYTSVSIPGYVFSR.V
137	146	2	1101.64	5.4	1	51.2	17.3	95.00%	K.LTCAAVAIKR.A	Carbamidomethyl (+57)	K.LTCAAVAIKR.A
19	25	2	770.49	4.3	1	34.4	15.4	95.00%	R.LVEIGIK.N		R.LVEIGIK.N
462	474	3	1575.97	4.8	1	29.2	3.01	95.00%	R.HKLPVLIFLLNNR.G		R.HKLPVLIFLLNNR.G
43	55	2	1560.62	1.2	1	34	23.5	95.00%	L.EYYPGLSEIGCCN.E	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.LLDFLEYYPGLSEIGCCNELNCAFAAEGYAR.S
26	37	2	1429.72	4.2	1	38.3	21.6	95.00%	K.NHFVVPGDYNLR.L		K.NHFVVPGDYNLR.L
304	314	2	1122.61	2	0	33.4	19	95.00%	R.AAPNPNILLNS.D		R.AAPNPNILLNSDYTSVSIPGYVFSR.V
464	474	2	1310.81	4.6	0	66.2	6.02	95.00%	K.LPVLIFLLNNR.G		K.LPVLIFLLNNR.G
136	145	2	1073.63	3.9	1	39.6	14	95.00%	K.KLTCAAVAIK.R	Carbamidomethyl (+57)	K.KLTCAAVAIK.R
56	68	2	1470.66	1.7	1	51.7	23.2	95.00%	N.ELNCAFAAEGYAR.S	Carbamidomethyl (+57)	R.LLDFLEYYPGLSEIGCCNELNCAFAAEGYAR.S
4	18	2	1641.77	4.2	1	65.2	23.8	95.00%	K.DAESTMTVGTYLAQR.L		K.DAESTMTVGTYLAQR.L
396	405	2	1224.56	2.3	0	34.8	24	95.00%	G.DSWFNGLQMK.L		R.QIQGLVDSNTTLYAETGDSWFNGLQMK.L
216	225	3	1064.66	3.8	0	29.3	12	95.00%	K.EKPILLAGPK.L		K.EKPILLAGPK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
9	ADH4_SCHPO	30.81%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
237	255	2	1942.97	2.6	1	25.3	20.8	93.20%	M.DALTHAVEAYVSTAANPIT.D		K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
375	385	3	1245.76	3.9	1	37.6	3.01	95.00%	K.IRPHLVDLGVK.E		K.IRPHLVDLGVK.E
399	411	2	1380.61	2.2	0	58.1	23.7	95.00%	K.DACGATNPIQPTH.D	Carbamidomethyl (+57)	K.DACGATNPIQPTHDEVK.A

76	87	2	1282.76	5.2	1	44.2	12.8	95.00%	K.NTLIVTDPGIIK.V		K.NTLIVTDPGIIK.V
366	374	2	1027.63	6.6	1	37.3	15.2	95.00%	R.ISQLVLEVK.I		R.ISQLVLEVK.I
149	159	2	1014.58	4.8	0	36.7	19.8	95.00%	K.GIALLATNGGK.I	Deamidation (+1)	K.GIALLATNGGK.I
109	128	2	2077.09	2.3	1	67.5	17.6	95.00%	Y.DGVQPNPTVGNVNQGLEIVK.K		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K
169	191	2	2386.26	3.6	1	87.6	17.2	95.00%	K.SSKPQLPLIAINTTAGTASEMTR.F		K.SSKPQLPLIAINTTAGTASEMTR.F
133	144	2	1116.49	3	0	64.2	24.3	95.00%	C.DSMVSIGGGSAH.D		K.ENCDSMVSIGGGSAHDCAK.G
169	187	2	1869.03	2.4	0	53.3	15.3	95.00%	K.SSKPQLPLIAINTTAGTAS.E		K.SSKPQLPLIAINTTAGTASEMTR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
10	PMGY_SCHPO	40.28%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
23	30	2	977.54	1.7	0	27.6	21.1	95.00%	K.LNLFTGWK.D		K.LNLFTGWK.D
111	120	2	1271.65	5.7	1	79.8	21.7	95.00%	K.WGAEQVQIWR.R		K.WGAEQVQIWR.R
2	14	2	1439.81	5.3	1	52	15.8	95.00%	M.TTEAAPNLLVLTR.H	Acetyl (+42)	-.MTTEAAPNLLVLTR.H
158	168	2	1149.67	4.5	0	26.5	13.8	94.80%	K.VLIAAHGNSLR.A		K.VLIAAHGNSLR.A
95	104	2	1169.58	4.8	1	46.4	21.9	95.00%	R.YYGDLQGLNK.D		R.YYGDLQGLNK.D
31	40	2	1029.54	2.3	1	33.2	22	95.00%	K.DPALSETGIK.E		K.DPALSETGIK.E
57	66	2	1120.59	3.5	0	57.8	20.1	95.00%	F.DIAFTSALQR.A		K.FDIAFTSALQR.A
1	14	2	1528.83	2.6	1	53.6	17.2	95.00%	-.MTTEAAPNLLVLTR.H		-.MTTEAAPNLLVLTR.H
186	197	2	1310.73	3	0	40.2	17.8	95.00%	R.ELATGVPIVYHL.D		R.ELATGVPIVYHLDK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
11	THI2_SCHPO	15.24%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	15	2	1400.77	3.8	0	74.5	18.3	95.00%	M.APATAVVTPQTAFK.T		-.MAPATAVVTPQTAFK.T
46	55	2	1167.56	3.2	1	63.3	23.1	95.00%	L.DESFSFAPIR.E		K.AYPTYSLDESFSFAPIR.E
295	308	2	1459.67	4	0	71.7	23.6	95.00%	R.MGPTFGGMMFSGIK.A		R.MGPTFGGMMFSGIK.A
243	254	2	1307.73	2.4	1	41.7	14.6	95.00%	K.RLASAQLVSNLH.D		K.RLASAQLVSNLHDMRPLDMNR.A
244	254	2	1151.63	1.9	0	68.5	17.3	95.00%	R.LASAQLVSNLH.D		R.LASAQLVSNLHDMRPLDMNR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
12	TPIS_SCHPO	48.59%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
206	222	2	1841.9	2.2	1	42.9	22	95.00%	R.VIYGGSVNGGNCKEFLK.F	Deamidation (+1)/ Carbamidomethyl (+57)	R.VIYGGSVNGGNCKEFLK.F
160	174	2	1615.9	2.3	1	70	15.3	95.00%	K.IVIAYEPVWAIGTGK.T		K.IVIAYEPVWAIGTGK.T
227	249	3	2449.28	1.9	1	19.5	17.2	93.50%	I.DGFLVGGASLKPEFHNIVNVHSL.-		K.FHDIDGFLVGGASLKPEFHNIVNVHSL.-
71	84	2	1424.64	1.7	1	55.3	23.7	95.00%	K.NGAYTGENSAQSLI.D	Deamidation (+1)	K.NGAYTGENSAQSLIDAGITYTLTGHSER.R
135	145	2	1242.66	4.7	1	39.7	19.3	95.00%	R.EANETINVVVR.Q		R.EANETINVVVR.Q
85	98	2	1519.73	2	1	55	22.1	95.00%	I.DAGITYTLTGHSER.R		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R
36	52	2	2055.04	2.2	1	65.8	19.2	95.00%	G.DVETVIFPQNMYLITTR.Q	Oxidation (+16)	K.LNVGDVETVIFPQNMYLITTR.Q
196	205	2	971.55	5.3	1	76.1	20.9	95.00%	K.LGASVAEGLR.V		K.LGASVAEGLR.V
206	218	2	1324.61	4.4	0	76.9	23.5	95.00%	R.VIYGGSVNGGNCK.E	Deamidation (+1)/ Carbamidomethyl (+57)	R.VIYGGSVNGGNCK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
13	GLYD_SCHPO	39.61%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
146	159	2	1649.78	3.9	1	75	23.1	95.00%	K.ISAVSTYFESMPYR.V		K.ISAVSTYFESMPYR.V
183	193	2	1209.62	4.5	0	57.8	21.2	95.00%	K.ILVAGTSAYCR.L	Carbamidomethyl (+57)	K.ILVAGTSAYCR.L
306	318	2	1551.8	2.6	1	23.9	20.9	90.70%	Q.EPAYKEYQAQVVK.N		K.QCQEPAYKEYQAQVVK.N
361	371	2	1254.76	3.3	1	84.2	9.03	95.00%	R.VLELINIVTNK.N		R.VLELINIVTNK.N

175	182	2	973.54	3	0	28.7	20	95.00%	H.DAQLFRPK.I		R.VDPNTGLIDYDMLEHDAQLFRPK.I
97	123	3	2996.43	3.4	0	55	19.8	95.00%	K.WGVNVQCLSGSPANMQVYQAIMPPHGR.L	Carbamidomethyl (+57)	K.WGVNVQCLSGSPANMQVYQAIMPPHGR.L
5	15	2	1273.66	1.9	1	34.3	22.1	95.00%	N.DSIMLTPLKEQ.D		-.MSSNDSIMLTPLKEQDPTVAEIMR.H
86	96	2	1129.62	5.1	1	54.8	20.3	95.00%	R.ALAAFNLDPAK.W		R.ALAAFNLDPAK.W
59	67	2	998.45	5.1	1	32.9	23.5	95.00%	K.YSEGYPGAR.Y		K.YSEGYPGAR.Y
277	302	3	2725.45	2.8	0	25.2	14.6	95.00%	K.INFSVFPGHQGGPHNHTITALAVALK.Q		K.INFSVFPGHQGGPHNHTITALAVALK.Q
413	422	2	1075.61	4.3	0	49.9	17.5	95.00%	R.ALTFAANLQK.E		R.ALTFAANLQK.E
250	256	2	840.44	5.4	0	24.1	19.8	91.20%	R.GAMIFFR.R		R.GAMIFFR.R
46	58	2	1321.64	4.2	1	41.4	23.4	95.00%	R.AVMDALGSVMSNK.Y		R.AVMDALGSVMSNK.Y
128	141	2	1467.68	1.1	0	47.5	23.5	95.00%	L.DLPSGGHLSHGYQT.D		R.LMGLDLPSGGHLSHGYQTDTK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
14	SAHH_SCHPO	25.17%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
246	255	2	1058.51	1.9	0	27.8	23.9	95.00%	V.DPINALQAAM.D	Oxidation (+16)	R.VIVTEVDPINALQAAMDGFEVTTMEEAVK.E
25	35	2	1227.63	2.9	1	33.9	20.9	95.00%	A.ENEMPGLIAVR.E		K.ELEIAENEMPGLIAVR.E
8	18	2	1118.61	3.2	1	77.1	19.2	95.00%	K.VADISLAAFGR.K		K.VADISLAAFGR.K
216	227	2	1117.62	4.3	1	46.5	19.6	95.00%	K.VAVVAGFGDVGK.G		K.VAVVAGFGDVGK.G
269	280	2	1367.65	1.8	0	48.4	22.9	95.00%	K.EGQIFVTTTGCR.D	Carbamidomethyl (+57)	K.EGQIFVTTTGCR.D
119	130	2	1302.7	2.2	0	46.3	19.3	95.00%	K.SFPSGKPLNMIL.D		K.SFPSGKPLNMILDDGGDLTALVHER.H
176	187	2	1255.68	4.6	1	42.1	18.7	95.00%	K.VPAINVNDSVTK.S		K.VPAINVNDSVTK.S
336	344	2	1006.6	5	1	31.2	12.6	95.00%	R.HIILLADGR.L		R.HIILLADGR.L
318	328	2	1281.71	3.7	1	30.2	18.2	95.00%	K.DVVNIKPQVDR.Y		K.DVVNIKPQVDR.Y
318	326	2	1010.58	3.4	0	35.5	16.1	95.00%	K.DVVNIKPQV.D		K.DVVNIKPQVDR.Y
135	143	2	1052.56	1.6	1	50.8	19.4	95.00%	G.DLTALVHER.H		K.SFPSGKPLNMILDDGGDLTALVHER.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
15	THI3_SCHPO	31.21%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
47	56	2	959.53	2.4	0	55.1	20.9	95.00%	S.DVTALIGSGK.V		R.EGIEVAILEPTNPSDVTALIGSGK.V
74	95	2	2353.26	1.8	1	91.8	15.6	95.00%	R.GYPVTSFGSLLNEPFTGLITLK.G		R.GYPVTSFGSLLNEPFTGLITLK.G
128	139	2	1325.67	4.2	1	42.4	21.6	95.00%	K.FGLSPSDYTAIR.C		K.FGLSPSDYTAIR.C
74	85	2	1253.63	1.1	0	65.8	22.1	95.00%	R.GYPVTSFGSLLN.E		R.GYPVTSFGSLLNEPFTGLITLK.G
6	27	2	2631.39	2.4	1	78.6	14.8	95.00%	K.ITFLTNWEATPYHLPIFLAQTR.G		K.ITFLTNWEATPYHLPIFLAQTR.G
63	71	2	954.54	4.5	0	51.1	15.9	95.00%	K.AMIHTLAAK.A		K.AMIHTLAAK.A
110	118	2	968.5	4.9	1	27.7	21.8	95.00%	R.IGYVGEFGK.I		R.IGYVGEFGK.I
330	339	2	992.51	5.7	0	44.3	22.7	95.00%	K.GGVFSGNSLR.Y		K.GGVFSGNSLR.Y
260	273	2	1711.79	4.7	1	88.7	23.2	95.00%	R.CFAYFSHDISNVPR.D	Carbamidomethyl (+57)	R.CFAYFSHDISNVPR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
16	METK_SCHPO	37.43%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
147	155	2	931.5	4.5	0	58	23.4	95.00%	K.LNAAMSVAR.R		K.LNAAMSVAR.R
137	146	3	1117.73	3.6	0	25.4	3.01	95.00%	K.LPLTILLAHK.L		K.LPLTILLAHK.L
256	272	2	1623.71	3.1	0	71.2	24.2	95.00%	V.DTYGGWGAHGGGAFSGK.D		K.IIVDTYGGWGAHGGGAFSGK.D
237	251	2	1429.74	3.6	1	73.6	20.9	95.00%	R.FVVGGPQGDAGLTGR.K		R.FVVGGPQGDAGLTGR.K
339	349	2	1256.73	4.3	1	36.5	14.8	95.00%	K.NFDLRPGVLVK.S		K.NFDLRPGVLVK.S

227	236	3	1156.6	4.8	0	18.7	20.6	91.90%	K.TVYHIQPSGR.F		K.TVYHIQPSGR.F
291	299	2	856.52	4.2	0	28.1	17.2	95.00%	K.SLVAAGLAR.R		K.SLVAAGLAR.R
253	272	2	1948.95	4	1	80.8	22.4	95.00%	K.IIVDTYGGWGAHGGGAFSGK.D		K.IIVDTYGGWGAHGGGAFSGK.D
369	378	2	1241.61	4	1	33.4	22.3	95.00%	T.DQSKPWEQPK.E		K.LQTPFYLSTASYGHFTDQSKPWEQPK.E
90	102	2	1457.72	2.1	1	37	22.1	95.00%	K.TCNVLVAIEQQSP.D	Carbamidomethyl (+57)	K.TCNVLVAIEQQSPDIAQGLHYEK.A
353	368	2	1831.88	1.5	0	84	22.9	95.00%	K.LQTPFYLSTASYGHFT.D		K.LQTPFYLSTASYGHFTDQSKPWEQPK.E
188	197	2	1039.53	3.3	0	33.7	20.5	95.00%	V.DTIVVSAQHA.D		R.VDTIVVSAQHADSISTEDLR.S
103	112	2	1172.59	2.8	1	40.5	21.9	95.00%	P.DIAQGLHYEK.A		K.TCNVLVAIEQQSPDIAQGLHYEK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
17	HSP90_SCHPO	13.78%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
368	375	2	926.52	3.4	0	36.6	18.1	95.00%	E.DLPLNLSR.E		K.GVVDSEDLPLNLSR.E
465	474	2	1170.6	4.5	1	29.7	21.9	95.00%	K.NIYFITGESK.Q		K.NIYFITGESK.Q
567	587	2	2339.12	5.7	1	92.3	21.4	95.00%	K.IVGSPCLLTTGQYGWSANMER.I	Carbamidomethyl (+57)	K.IVGSPCLLTTGQYGWSANMER.I
351	361	2	1343.75	2	1	34.8	16.6	95.00%	E.ELIPEWLGFIK.G		R.VFITDDCEELIPEWLGFIK.G
596	606	2	1234.5	4.9	0	67.2	23.7	95.00%	R.DTSMSAYMSSR.K		R.DTSMSAYMSSR.K
88	99	2	1282.73	5.3	1	55.5	15.2	95.00%	K.NDLINNLGVIAK.S		K.NDLINNLGVIAK.S
198	212	2	1787.96	4	1	56.2	18.2	95.00%	K.HSEFISYPIQLVVTR.E		K.HSEFISYPIQLVVTR.E
655	663	2	1021.45	3	1	50.1	23.1	95.00%	L.DDPSAYAQR.I		K.DLATILYETALLSSGFTLDDPSAYAQR.I
89	99	2	1168.69	3	0	31.8	14.5	95.00%	N.DLINNLGVIAK.S		K.NDLINNLGVIAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
18	A1EGU1_SCHPO	25.13%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
457	479	2	2580.33	3.2	0	74.9	18.2	95.00%	K.YVISQCNNALLYPALGVACVLSR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.YVISQCNNALLYPALGVACVLSR.C
372	396	3	2593.42	1.9	1	44.2	10.8	95.00%	G.DINLESAIALVKPTILLGCSGQPGK.F	Carbamidomethyl (+57)	K.EVPSGDINLESAIALVKPTILLGCSGQPGK.F
439	452	2	1418.83	2.4	0	46.2	9.54	95.00%	K.ALIATGSPLPPLNR.N		K.ALIATGSPLPPLNR.N
249	256	2	834.43	2.1	0	29.6	22.7	95.00%	E.DFGLANAK.R		R.EVFPEAFIHFEDFGLANAK.R
490	500	2	1070.58	4.5	1	54.7	19.7	95.00%	K.AASDALATVPR.S		K.AASDALATVPR.S
15	23	2	955.55	4.9	0	32.8	16.9	95.00%	K.GVTLLNSPR.Y		K.GVTLLNSPR.Y
332	339	2	964.49	5	1	34.3	21.6	95.00%	R.GNLFMIDR.C		R.GNLFMIDR.C
456	479	3	2708.42	2.5	1	50.2	14.9	95.00%	K.KYVISQCNNALLYPALGVACVLSR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.KYVISQCNNALLYPALGVACVLSR.C
44	55	2	1363.78	2.7	1	50.7	15.6	95.00%	R.LPPIVETLQQQV.D		R.LPPIVETLQQQVDR.C
178	191	2	1553.75	3.5	1	59.3	23	95.00%	K.GHLMTLCAGLDPNR.F	Carbamidomethyl (+57)	K.GHLMTLCAGLDPNR.F
408	424	2	1964.06	1.2	1	42.4	16.1	95.00%	K.HVERPIIFPISNPTTLM.E		K.HVERPIIFPISNPTTLMEAKPDQIDK.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
19	HSP72_SCHPO	15.92%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
327	340	2	1400.77	3.9	1	39.7	18.9	95.00%	K.ASVNEIVLVGGSTR.I		K.ASVNEIVLVGGSTR.I
55	66	2	1384.66	3.4	0	40.3	23.2	95.00%	K.NQVAMNPHNTIF.D		K.NQVAMNPHNTIFDAK.R
538	548	2	1351.66	4.4	1	37.5	22.2	95.00%	K.NHLESYAYSLR.N		K.NHLESYAYSLR.N
350	359	2	1241.54	3.2	1	26.6	23.7	94.90%	S.DFFNGKEPCK.S	Deamidation (+1)/ Carbamidomethyl (+57)	K.LVSDFFNGKEPCK.S
450	457	2	965.47	1.7	1	30.8	23.2	95.00%	K.DCNLLGKF.E	Carbamidomethyl (+57)	K.DCNLLGKFELSGIPPAPR.G
170	183	2	1415.77	3.3	1	27.1	18.3	95.00%	R.IINEPTAAAIAYGL.D		R.IINEPTAAAIAYGLDR.S
55	69	2	1698.82	4.2	1	74.8	21.8	95.00%	K.NQVAMNPHNTIFDAK.R		K.NQVAMNPHNTIFDAK.R
457	467	2	1182.65	4.4	1	28.3	17.7	95.00%	K.FELSGIPPAPR.G		K.FELSGIPPAPR.G

235	244	2	1273.69	4.3	1	25.1	19.5	92.90%	R.LVNHFIQEFK.R		R.LVNHFIQEFK.R
96	106	2	1274.69	4.5	1	24.7	19.8	92.20%	K.DGKPVLQVEYK.G		K.DGKPVLQVEYK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
20	ILV5_SCHPO	21.04%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
317	328	2	1392.58	2	0	58.5	24.6	95.00%	L.DYMFAACSTTAR.R	Carbamidomethyl (+57)	K.YGLDYMFAACSTTAR.R
84	104	2	2141.07	4.6	1	90.4	20.5	95.00%	K.NDTLAIIGYGSQGHGQGLNAR.D		K.NDTLAIIGYGSQGHGQGLNAR.D
330	337	2	914.47	6	1	41.2	21.2	95.00%	R.GAIDWTPR.F		R.GAIDWTPR.F
314	328	2	1725.76	3.8	1	69	24.2	95.00%	K.YGLDYMFAACSTTAR.R	Carbamidomethyl (+57)	K.YGLDYMFAACSTTAR.R
173	189	3	2017.04	2.6	1	19	19.9	92.50%	K.TLYFSHGFSVIFKDQTK.I		K.TLYFSHGFSVIFKDQTK.I
301	313	2	1447.76	1.2	1	25	20.5	92.80%	V.EEATQSLYPLIGK.Y		R.GHSPAEAFNETVEEATQSLYPLIGK.Y
362	372	2	1312.61	4.6	1	61.6	23.6	95.00%	R.SLEYNSAPNYR.E		R.SLEYNSAPNYR.E
302	313	2	1318.72	2.3	0	34.4	18.8	95.00%	E.EATQSLYPLIGK.Y		R.GHSPAEAFNETVEEATQSLYPLIGK.Y
85	104	3	2027.02	2.1	0	65.5	19.1	95.00%	N.DTLAIIGYGSQGHGQGLNAR.D		K.NDTLAIIGYGSQGHGQGLNAR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
21	K6PF_SCHPO	15.39%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
613	628	3	1700.87	4.5	1	49.7	19.8	95.00%	R.GHTPLAIDNGFSGFLR.H		R.GHTPLAIDNGFSGFLR.H
510	522	2	1357.66	2.4	0	64.7	22.8	95.00%	P.DTPSPMIAINGNK.I	Deamidation (+1)	R.MLATLQGVDAVDAVLASTPDTPSPMIAINGNK.I
586	603	3	1720.91	2.7	0	69.8	19.1	95.00%	R.VAIIHVGAPAGGMNSATR.A		R.VAIIHVGAPAGGMNSATR.A
369	380	2	1259.61	3.2	0	63.4	23.3	95.00%	V.DSISSTAISHSR.A		R.ICEAVDSISSTAISHSR.A
882	896	2	1511.8	2.6	1	47.4	19	95.00%	N.DLGNDPSSAVVIGIR.G		R.ANDLGNDPSSAVVIGIR.G
844	859	2	1589.77	1.9	0	35.7	22.6	95.00%	R.TAVPGHVQQGGNPTPM.D		R.TAVPGHVQQGGNPTPMDR.A
620	628	2	1012.46	2.3	0	31.4	23.1	95.00%	I.DNGFSGFLR.H	Deamidation (+1)	R.GHTPLAIDNGFSGFLR.H
798	806	2	934.49	4	1	31.5	20.6	95.00%	K.ATFALEAGR.N		K.ATFALEAGR.N
254	267	2	1400.75	3.4	1	49.7	19.2	95.00%	R.GWLAEGGTLIGTAR.C		R.GWLAEGGTLIGTAR.C
844	861	2	1860.9	4.7	1	42.3	22.5	95.00%	R.TAVPGHVQQGGNPTPMDR.A		R.TAVPGHVQQGGNPTPMDR.A
927	938	2	1323.7	4.7	0	53.3	19.7	95.00%	R.DMHNLVNILAGK.T		R.DMHNLVNILAGK.T
197	214	2	1760.86	4.1	1	84.8	21.3	95.00%	K.IAVMTSGGDSPGMNAVVR.A		K.IAVMTSGGDSPGMNAVVR.A
205	214	2	1044.51	2.7	0	27	23.1	95.00%	G.DSPGMNAVVR.A		K.IAVMTSGGDSPGMNAVVR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
22	6PGD_SCHPO	21.34%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
156	166	3	1228.76	4.8	0	32.1	7.78	95.00%	R.IKPIFQTLAAK.A		R.IKPIFQTLAAK.A
140	155	2	1669.81	3	0	38.4	22.3	95.00%	R.YGPSLMPGGNPAAWPR.I		R.YGPSLMPGGNPAAWPR.I
85	95	2	1215.68	2.7	1	24.2	18.1	91.40%	V.DYLIEGLAPLL.E		K.AGKPVDYLIEGLAPLLEK.G
73	79	2	843.53	4.4	0	24.3	11.1	91.60%	R.VCILLVK.A	Carbamidomethyl (+57)	R.VCILLVK.A
437	449	2	1379.79	4.1	0	52	13.8	95.00%	R.SAVLPANLLQAQR.D		R.SAVLPANLLQAQR.D
276	291	2	1719.89	2.3	1	63.5	20	95.00%	L.EMGTPVSLITEAVFAR.C		K.WTAQNALEMGTPVSLITEAVFAR.C
450	458	2	1112.51	4.7	0	24.9	23.9	92.60%	R.DYFGAHTFR.V		R.DYFGAHTFR.V
175	187	2	1444.68	2.3	1	48.4	23.6	95.00%	C.DWVGEQGAGHYVK.M		K.AGNNEPCCDWVGEQGAGHYVK.M
29	37	2	1175.49	3.9	0	36.7	24.4	95.00%	K.GFTVCCYNR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GFTVCCYNR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
23	EF2_SCHPO	11.64%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
272	283	2	1498.77	4.2	1	53.9	20.9	95.00%	R.AFNMFILDPIYR.I		R.AFNMFILDPIYR.I
466	479	2	1474.71	3.7	1	72.8	22.2	95.00%	K.SGTLTTSEVAHNMK.V		K.SGTLTTSEVAHNMK.V

565	578	2	1451.69	4.3	1	44.5	23.1	95.00%	R.ESVSEPSSMTALSK.S		R.ESVSEPSSMTALSK.S
284	292	2	1051.52	4.5	1	27.5	22.9	95.00%	R.IFDAVMNSR.K		R.IFDAVMNSR.K
336	346	2	1262.71	2.7	0	36	17.5	95.00%	M.EMIVLHLPSPK.T		K.FLPAADALMEMIVLHLPSPK.T
810	820	2	1200.58	1.6	0	37.4	22.8	95.00%	L.DPTSKPGQIVC.E	Carbamidomethyl (+57)	R.QATAGQAFPQLVFDHWSPMSG DPLDPTSKPGQIVCEAR.K
244	253	2	1266.61	5.9	1	30	23.2	95.00%	R.LWGENYFNPK.T		R.LWGENYFNPK.T
371	384	2	1594.76	4.1	1	55	22.8	95.00%	R.NCDANAPLMIYVSK.M	Carbamidomethyl (+57)	R.NCDANAPLMIYVSK.M
810	823	2	1556.76	1.7	1	38.8	22.1	95.00%	L.DPTSKPGQIVCEAR.K	Carbamidomethyl (+57)	R.QATAGQAFPQLVFDHWSPMSG DPLDPTSKPGQIVCEAR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
24	EF3_SCHPO	7.45%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
757	765	2	1178.58	7.8	1	24.9	22.3	92.50%	K.TPSEYIQWR.F		K.TPSEYIQWR.F
434	447	2	1646.71	2.1	1	58.7	23.4	95.00%	E.DLCNCEFSLAYGAK.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.IPGGASHAEEEEEGEDLCNCEFS LAYGAK.I
479	493	2	1636.88	3.9	1	73.9	18.3	95.00%	R.AIVNGQVEGFPTHLR.T		R.AIVNGQVEGFPTHLR.T
133	147	2	1550.87	3.9	1	70.6	14.1	95.00%	K.AIVPSVLESIHTTGK.W		K.AIVPSVLESIHTTGK.W
75	87	2	1194.6	2.3	1	24	22.6	91.10%	K.GLEAVANHGSVAA.D		K.GLEAVANHGSVAADVEPYLVELL PAVIAK.V
48	59	2	1248.64	2.4	0	68.6	21.9	95.00%	Q.DAPSQVFSAISK.Q		K.ALASFVNGPIEEQDAPSQVFSAIS K.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
25	TSA1_SCHPO	30.73%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	147	2	1224.69	4.4	1	43.5	16.5	95.00%	R.QITINDLPVGR.S		R.QITINDLPVGR.S
89	102	2	1350.79	2.9	1	25.1	11.1	92.90%	R.KEGGLGGINIPLLA.D		R.KEGGLGGINIPLLADPSHK.V
75	88	2	1648.79	1.5	1	53.6	22.9	95.00%	T.DSEYSHLAFINTPR.K		R.NAQVILTSTDSEYSHLAFINTPR.K
125	132	2	901.53	4.7	1	35.7	19.4	95.00%	R.GLFLIDPK.G		R.GLFLIDPK.G
2	13	2	1341.74	4.1	1	36.9	18	95.00%	M.SLQIGKPAPDFK.G	Acetyl (+42)	-.MSLQIGKPAPDFK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
26	TKT_SCHPO	15.77%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
238	252	2	1719.86	5	1	57.2	21.1	95.00%	R.EAMSCTDKPTLINLK.T	Carbamidomethyl (+57)	R.EAMSCTDKPTLINLK.T
8	18	2	1243.68	3.2	1	25	18.5	92.80%	T.DIDTLAINTIR.T		-.MTSSSYTDIDTLAINTIR.T
653	663	2	1249.63	3.9	0	24.8	22	92.40%	K.FHFTTSGVAQR.A		K.FHFTTSGVAQR.A
480	494	3	1751.84	1.3	1	25.4	22	95.00%	E.DGPTHQPIETFAHFR.A		R.VIYVATHDSIGLGEDGPTHQPIET FAHFR.A
182	193	2	1385.74	4.7	1	41.9	19.8	95.00%	K.LSNLIAVWDNNK.I		K.LSNLIAVWDNNK.I
521	531	2	1172.64	2	0	41	19.5	95.00%	S.DSTPSILALTR.Q		R.AMPNINCWRPADGNETSAAYYS ALTSDSTPSILALTR.Q
291	303	2	1603.8	4	1	26.8	22.2	95.00%	K.TFQVPPEVYAYYK.E		K.TFQVPPEVYAYYK.E
30	49	3	1972.02	3	0	44.1	18.4	95.00%	K.SGHPGAPMGLAPAAHVLFSR.I		K.SGHPGAPMGLAPAAHVLFSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
27	HSP75_SCHPO	18.27%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	173	2	1168.66	5	0	34.3	16.6	95.00%	K.DAGAIAGLNVLR.I		K.DAGAIAGLNVLR.I
335	344	2	1015.57	3.8	0	39.4	19.7	95.00%	H.DIVLVGGSTR.I		K.ADVHDIVLVGGSTR.I
501	517	2	1779.92	2.3	1	74.7	19	95.00%	R.SAHIEITNSVGHLSSTK.I		R.SAHIEITNSVGHLSSTK.I
144	157	2	1552.8	4.6	1	33.7	20.7	95.00%	K.AVITVPAYFSDSQR.A		K.AVITVPAYFSDSQR.A
457	472	2	1780.92	2.6	1	49.7	19.1	95.00%	N.EPLGEFQLTGIPPMPR.G		R.VNCAENEPLGEFQLTGIPPMPR. G
174	187	2	1415.77	3.3	1	27.1	18.3	95.00%	R.IINEPTAAAIAYGL.D		R.IINEPTAAAIAYGLDAK.S
115	128	2	1565.82	1.9	1	72.4	19.1	95.00%	K.QFTAQEISAMVLTK.M		K.QFTAQEISAMVLTK.M

436	450	2	1753.83	3.2	1	59.1	22.5	95.00%	A.DNQTTVTFPVYQGER.V		R.TFTTVADNQTTVTFPVYQGER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
28	ACT_SCHPO	22.67%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
244	254	2	1200.61	2.3	1	54.1	21	95.00%	P.DGQVITIGNER.F		K.SYELPDGQVITIGNER.F
85	95	3	1514.75	5.5	1	36	22.5	95.00%	K.IWHHTFYNELR.V		K.IWHHTFYNELR.V
69	79	2	1340.66	2.7	1	32.1	22.5	95.00%	K.YPIEHGIVNNW.D		K.YPIEHGIVNNWDDMEK.I
292	312	2	2216.04	5	1	63.1	21.7	95.00%	K.DLYGNVVMSGGTTMYPGIADR.M		K.DLYGNVVMSGGTTMYPGIADR.M
197	206	2	1131.53	5.1	1	41.4	23.9	95.00%	R.GYTFSTTAER.E		R.GYTFSTTAER.E
157	177	3	2339.18	1.6	1	63.2	18.4	95.00%	G.DGVTHTVPIYEGYALPHAIMR.L		R.TTGIVLDSGDGVTHTVPIYEGYALPHAIMR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
29	PUR9_SCHPO	22.05%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
121	129	2	942.55	2.1	0	30	18.9	95.00%	I.DIGGVTLLR.A		R.ETIAKPNVTIPEAVEEIDIGGVTLLR.A
284	297	2	1626.78	2.3	1	56.6	23	95.00%	S.DITEFTPLACAYAR.A	Carbamidomethyl (+57)	K.VYFVSDITEFTPLACAYAR.A
46	60	2	1527.79	2.9	1	72	20.8	95.00%	A.DVSSITNAPEILGGR.V		R.ESGMEVADVSSITNAPEILGGR.V
551	565	2	1519.75	4.1	1	63.8	21.9	95.00%	K.YVAAPGGSVMDQAVR.D		K.YVAAPGGSVMDQAVR.D
223	244	2	2446.25	3.4	1	45.9	18.8	95.00%	K.VLCGSPGYINLMDALNSWPLVK.E	Carbamidomethyl (+57)	K.VLCGSPGYINLMDALNSWPLVK.E
93	103	2	1394.7	2.1	0	30.8	21.7	95.00%	I.DIVVCNLYPFR.E	Carbamidomethyl (+57)	K.IDIVVCNLYPFR.E
354	362	2	1152.54	4.8	1	28.8	23.9	95.00%	K.YCVLQMDPK.Y	Carbamidomethyl (+57)	K.YCVLQMDPK.Y
248	259	2	1216.65	4.7	0	30.2	20.5	95.00%	R.ENIGIPAAASFK.H		R.ENIGIPAAASFK.H
201	222	3	2414.16	4	1	23.8	20	95.00%	R.YGANPHQSPAQAFMEQGPLPFK.V		R.YGANPHQSPAQAFMEQGPLPFK.V
201	214	2	1517.68	3	0	30.8	24.2	95.00%	R.YGANPHQSPAQAFM.E		R.YGANPHQSPAQAFMEQGPLPFK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
30	GPD1_SCHPO	28.57%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
220	232	2	1184.64	2.1	1	49.9	18.9	95.00%	V.DDVAGVALGGALK.N		R.EQIAAVFDRPYFSVVSVDDVAGVALGGALK.N
2	20	2	1989	3.8	1	99.4	20.8	95.00%	M.SGYGQQGVSAANIDSIRPK.K	Acetyl (+42)	-.MSGYGQQGVSAANIDSIRPK.K
287	296	2	1076.53	2.6	0	47.6	22.4	95.00%	A.DLVTSCLGGR.N	Carbamidomethyl (+57)	R.TMVEQSCGIADLVTSCLGGR.N
127	144	2	1913.03	2.2	0	59.4	15.4	95.00%	C.DQMVGLIRPGAVGISCIK.G	Carbamidomethyl (+57)	R.VCDQMVGLIRPGAVGISCIK.G
23	39	2	1628.89	2.5	0	23.8	17.6	90.60%	R.LSIGVVGSGNWGTAIAK.I		R.LSIGVVGSGNWGTAIAK.I
125	144	3	2172.13	2.1	1	29.7	18.9	95.00%	R.VCDQMVGLIRPGAVGISCIK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VCDQMVGLIRPGAVGISCIK.G
317	331	2	1484.82	2.8	0	75.6	17.5	95.00%	K.ELLGGQLLQGAATSK.D		K.ELLGGQLLQGAATSK.D
111	124	3	1710.95	2.5	1	18.4	14.5	91.10%	A.DILVFVVPHQFIER.V		R.ADILVFVVPHQFIER.V
315	331	2	1741.96	1.8	1	68.5	16.2	95.00%	L.EKELLGGQLLQGAATSK.D		K.SLETLEKELLGGQLLQGAATSK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
31	SERA_SCHPO	21.89%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
58	73	2	1768.01	1.3	1	103	11.5	95.00%	K.ILLLENVNQSALSNLK.D		K.ILLLENVNQSALSNLK.D
275	284	2	1108.56	4.3	0	25.6	22.9	93.60%	K.EGSYLINASR.G		K.EGSYLINASR.G
440	452	2	1454.69	1.8	1	48.8	23.6	95.00%	S.DCTPGSLEALHQK.L	Carbamidomethyl (+57)	R.GDIAYLVADISDCTPGSLEALHQK.L
324	337	2	1676.75	4	1	28.8	24	95.00%	V.DSLNSWTSELTHCK.N	Carbamidomethyl (+57)	K.FVDSLNSWTSELTHCK.N
308	319	2	1233.56	3.5	1	37.2	23	95.00%	I.DVYPSEPAGNGK.D	Deamidation (+1)	K.IAGAAIDVYPSEPAGNGK.D

338	350	2	1350.72	1.8	1	31.8	20.1	95.00%	K.NIILTPHIGGSTE.E		K.NIILTPHIGGSTEEAQYNIGIEVSEALTR.Y
142	154	2	1394.7	4.8	0	57.8	21.7	95.00%	R.GIAVFNSPYANSR.S		R.GIAVFNSPYANSR.S
237	247	3	1291.73	4.7	1	20.7	16	95.00%	K.QLSSLPELLHR.A		K.QLSSLPELLHR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
32	HXK2_SCHPO	18.02%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
434	449	2	1529.79	4.8	0	96.2	20.7	95.00%	K.DGSGIGAALCALQAVK.E	Carbamidomethyl (+57)	K.DGSGIGAALCALQAVK.E
197	205	2	960.53	2.2	0	28.9	20.6	95.00%	N.DTVGTLVTR.A		R.IEAVINDTVGTLVTR.A
76	86	2	1287.67	3.9	1	30.3	21.5	95.00%	R.VCWIQLLGDGK.Y	Carbamidomethyl (+57)	R.VCWIQLLGDGK.Y
286	296	2	1240.63	5.9	1	25.6	20.9	93.60%	R.VGGMYLGELFR.R		R.VGGMYLGELFR.R
257	265	2	1121.5	2.3	0	35.7	22.8	95.00%	T.DFSCLHSTR.Y	Carbamidomethyl (+57)	K.CTGDHMLINMEWGATDFSCLHSTR.Y
374	388	2	1564.83	4.1	0	56.1	18.1	95.00%	R.MSAVPIASLYLSTGR.A		R.MSAVPIASLYLSTGR.A
1	11	2	1334.67	4.1	1	29.9	22.5	95.00%	-.MEANFQQAVKK.L	Acetyl (+42)	-.MEANFQQAVKK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
33	LYS9_SCHPO	30.44%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
204	223	3	2455.17	1.8	0	33.3	21.6	95.00%	M.ETAKPYFIYPGYAFVCYPNR.D	Carbamidomethyl (+57)	K.DLMETAKPYFIYPGYAFVCYPNR.D
69	85	2	1965.03	2.3	0	24.8	18.2	92.40%	H.DLTISLIPYTYHATVMK.A		K.AVSEHDLTISLIPYTYHATVMK.A
177	183	2	740.49	4.7	0	33.1	10.4	95.00%	R.GVLLALR.N		R.GVLLALR.N
171	176	2	768.36	6.1	0	24.6	23.1	92.00%	K.FSWSSR.G		K.FSWSSR.G
397	410	2	1453.8	1.6	0	26.6	15.6	94.80%	K.LVGVPCGVATQQIL.D	Carbamidomethyl (+57)	K.LVGVPCGVATQQILDGVINTPGVLAPNDMK.L
38	49	2	1259.66	4.1	1	41.7	20	95.00%	K.AEAFINGIPNSK.A		K.AEAFINGIPNSK.A
2	22	3	2269.25	3.1	1	39	13.2	95.00%	M.PSILLLGSGFVAHPTLEYLSR.R		-.MPSILLLGSGFVAHPTLEYLSR.R
411	423	2	1265.66	2	0	30.9	20.6	95.00%	L.DGVINTPGVLAPN.D		K.LVGVPCGVATQQILDGVINTPGVLAPNDMK.L
379	396	2	1989.93	4.3	1	76.6	22.3	95.00%	R.TCTLLDYGVPNGYTSMAK.L	Carbamidomethyl (+57)	R.TCTLLDYGVPNGYTSMAK.L
162	170	2	1006.48	3	0	35	22.9	95.00%	E.DSNNPLGYK.F		K.SFLSYCGGLPAPEDSNNPLGYK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
34	G6PI_SCHPO	28.73%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
217	228	2	1343.61	5.2	1	37.3	24.3	95.00%	K.TFTTAETCTNAK.S	Carbamidomethyl (+57)	K.TFTTAETCTNAK.S
372	382	2	1171.52	5.1	1	67.7	24.3	95.00%	R.SGDMVNYTTGK.I		R.SGDMVNYTTGK.I
464	477	2	1502.83	4	0	36.9	16.5	95.00%	K.TFVGNRPSNSIIAK.K		K.TFVGNRPSNSIIAK.K
383	405	3	2624.32	2	1	23.6	18.3	95.00%	K.ILWGEPGTNSQHSFFQLIHQGTK.L		K.ILWGEPGTNSQHSFFQLIHQGTK.L
79	86	2	886.45	2.7	1	42	21.4	95.00%	K.EANVEGLR.D		K.EANVEGLR.D
2	24	2	2548.27	3.8	1	60.7	19.4	95.00%	M.SFSLASTLPAWQAVQTHYESVGK.H	Acetyl (+42)	-.MSFSLASTLPAWQAVQTHYESVGK.H
410	421	2	1393.73	2.2	1	25.3	20.4	93.20%	A.DFLIPIESHNPI.D		K.LIPADFLIPIESHNPIDNNK.H
118	128	2	1170.59	4.1	1	35.5	21.4	95.00%	K.VNGQDVMPGVR.K		K.VNGQDVMPGVR.K
429	445	2	1870.94	4.8	1	69.7	21.6	95.00%	R.MLFSNFAAQTEALMLGK.T		R.MLFSNFAAQTEALMLGK.T
536	547	2	1308.66	2.4	0	42.5	22.4	95.00%	H.DSSTNGLINLFK.N	Deamidation (+1)	K.GDVENHDSSTNGLINLFK.N
353	367	2	1711.83	4.2	1	71.8	22.7	95.00%	R.FPAYLQQLSMESNGK.A		R.FPAYLQQLSMESNGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
35	IPYR_SCHPO	13.15%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

104	113	3	1134.57	2.4	1	18.5	22	91.50%	E.DPNVVHPETK.A		R.NCFPHHGYIWNYGAFPQTYEDPNVVHPETK.A
186	192	2	922.44	6	1	35.4	23.7	95.00%	R.ATNEWFR.I		R.ATNEWFR.I
33	42	2	1132.58	2.9	1	26.5	21.7	94.70%	H.DIPLYANAEK.T		K.NGTPISSWHDIPLYANAEK.T
43	53	2	1283.73	4	1	66.7	15.1	95.00%	K.TILNMVVEIPR.W		K.TILNMVVEIPR.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
36	HSP60_SCHPO	12.89%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	148	2	1316.6	4	1	27.4	24.3	95.00%	R.NVAAGCNPMDLR.R	Carbamidomethyl (+57)	R.NVAAGCNPMDLR.R
437	453	2	1588.85	4.6	1	29.9	18.9	95.00%	K.AAVSEGVLPGAGTSFVK.A		K.AAVSEGVLPGAGTSFVK.A
68	79	2	1313.7	4.3	1	39.3	18.6	95.00%	R.NVLIDQPFGSPK.I		R.NVLIDQPFGSPK.I
229	240	2	1401.72	4.3	1	35	20.5	95.00%	R.GYISPYFITDVK.S		R.GYISPYFITDVK.S
186	195	3	1095.59	2.1	1	32.5	19	95.00%	G.DTHIGELLAK.A		R.DITTSEEISQVATISANGDTHIGELLAK.A
45	56	2	1215.69	4.9	1	52.6	16.7	95.00%	R.ASLLTGVDTLAR.A		R.ASLLTGVDTLAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
37	MET3_SCHPO	13.06%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
217	229	3	1346.78	2.1	0	30	14.1	95.00%	R.VLIHPVVGMTKPG.D		R.VLIHPVVGMTKPGDIDHFTR.V
350	359	2	1102.6	3.9	1	29.9	20.4	95.00%	R.TLNISGTELR.R		R.TLNISGTELR.R
59	68	2	1233.64	5.6	1	40.5	21.9	95.00%	K.DYLNVVENLR.L		K.DYLNVVENLR.L
254	262	2	1012.62	5.1	0	33.5	13	95.00%	K.LSLLPLAMR.M		K.LSLLPLAMR.M
73	81	2	1027.6	3	0	25.4	17.9	93.30%	G.EVFPIPITL.D		R.LSTGEVFPIPITLDLNESQADSLK.A
458	470	3	1481.83	3.4	1	29.3	15.4	95.00%	K.VPAEWTTVNIKPK.D		K.VPAEWTTVNIKPK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
38	THIL_SCHPO	26.08%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
291	301	2	1160.65	4.8	0	33.2	17.2	95.00%	R.FTTSPSLAIPK.A		R.FTTSPSLAIPK.A
51	69	2	2016.97	2.3	1	88.1	20.9	95.00%	V.DEVFMGNVVSANLGQNPAR.Q		R.VNIKPSDVDEVFMGNVVSANLGQNPAR.Q
14	30	2	1654.81	2.6	0	78	21.9	95.00%	R.TPMGSFGGSFASLPATK.L		R.TPMGSFGGSFASLPATK.L
267	277	2	1194.77	2.8	1	25.9	6.99	94.00%	K.VKELGLKPLAK.I		K.VKELGLKPLAK.I
360	371	2	1405.81	4.5	0	73.2	14.9	95.00%	R.IICTLAYILAQK.D	Carbamidomethyl (+57)	R.IICTLAYILAQK.D
254	266	2	1232.65	2.3	0	56.1	20.8	95.00%	N.DGASALVLMSAAK.V		K.SNGTVTAANASTLNDGASALVLMSAAK.V
340	359	3	1865.93	4.8	0	31	21.8	95.00%	R.VNINGGGVAMGHPLGSSGSR.I		R.VNINGGGVAMGHPLGSSGSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
39	RL4A_SCHPO	23.42%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
122	140	2	1845.04	4.3	0	48.1	10	95.00%	R.YAISSAVAASGVPSLLLAR.G		R.YAISSAVAASGVPSLLLAR.G
2	13	2	1304.71	4.5	0	25.5	18.4	93.50%	M.AAARPTVSIYSK.D	Acetyl (+42)	-.MAAARPTVSIYSK.D
276	287	2	1393.69	2.9	1	27.8	22.7	95.00%	K.NYFLPENIISNA.D		K.NYFLPENIISNADVTR.L
235	248	3	1457.85	2.7	0	52.9	13.4	95.00%	R.LNLLQLAPGGHLGR.F		R.LNLLQLAPGGHLGR.F
234	248	3	1613.95	3	1	24.8	6.02	95.00%	R.RLNLLQLAPGGHLGR.F		R.RLNLLQLAPGGHLGR.F
14	29	2	1695.88	3.2	1	47.7	19.6	95.00%	K.DGSVSSETIALPFVFK.A		K.DGSVSSETIALPFVFK.A
87	97	2	1197.51	4.4	0	32.6	24.2	95.00%	R.SGQAAFGNMCR.S	Carbamidomethyl (+57)	R.SGQAAFGNMCR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
40	PDX1_SCHPO	14.53%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
71	83	2	1355.75	4.3	0	66.7	18.3	95.00%	K.EIQAAVSIPVMAK.V		K.EIQAAVSIPVMAK.V
121	132	3	1383.7	4.4	1	31	21.8	95.00%	K.SKFTVPFVCGSR.N	Carbamidomethyl (+57)	K.SKFTVPFVCGSR.N
271	280	2	1016.51	3.4	0	44.4	23.2	95.00%	S.ENLGAAMVGR.S		K.ILAEVSENLGAAMVGR.S
13	20	2	830.47	4.2	0	38.8	20.6	95.00%	K.AGLAQMLK.G		K.AGLAQMLK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
41	C1TC_SCHPO	11.63%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
689	707	3	1923.15	3.9	1	37.5	6.02	95.00%	R.TSGLKPDAIVIVATVQALK.L		R.TSGLKPDAIVIVATVQALK.L
2	12	2	1184.68	4.9	1	55.8	16.5	95.00%	M.ALLLEGTSLAR.K	Acetyl (+42)	-.MALLLEGTSLAR.K
170	183	2	1555.88	2.9	1	29.9	13.2	95.00%	R.SNIVGRPMSILLEK.A		R.SNIVGRPMSILLEK.A
764	773	2	1100.55	2.2	1	38.8	21.8	95.00%	S.DSPNEISAIR.E		K.FSSDSPNEISAIR.E
381	396	2	1629.9	3.4	1	106	16.4	95.00%	K.STLTAGLVQALSNLDK.L		K.STLTAGLVQALSNLDK.L
349	356	2	983.58	5.3	1	46.2	15.8	95.00%	K.VNLEILQR.L		K.VNLEILQR.L
259	289	3	3121.66	4	1	20.6	12.6	95.00%	K.EVASAITPVPGSVGPMTVAMLLQNVVESAVR.F		K.EVASAITPVPGSVGPMTVAMLLQNVVESAVR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
42	HSP7M_SCHPO	13.20%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
204	215	2	1124.67	4.6	0	48.3	13.8	95.00%	K.AAGAIAGLNVLR.V		K.AAGAIAGLNVLR.V
379	388	2	1073.59	2	0	25.2	19.5	93.10%	N.EVILVGGMTR.M		K.DANLQTSEINEVILVGGMTR.M
474	482	2	987.5	3.6	1	24.5	20.7	91.90%	A.DGQTAVEIR.V		K.SQVFSTAADGQTAVEIR.V
105	118	2	1578.81	4.5	1	81.4	20.5	95.00%	R.QAVINPENTFFATK.R		R.QAVINPENTFFATK.R
185	199	2	1679.83	4.3	1	62.1	22	95.00%	K.NAVVTVPAYFNDSQR.Q		K.NAVVTVPAYFNDSQR.Q
496	510	2	1538.89	4.2	0	77.2	13	95.00%	K.LIGNFQLTGIAPAPK.G		K.LIGNFQLTGIAPAPK.G
157	170	2	1496.8	5.1	0	59.3	18.7	95.00%	K.TYSPSQIGGFILSK.M		K.TYSPSQIGGFILSK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
43	PUT2_SCHPO	15.33%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
368	384	2	1889.95	3.1	0	57.8	21	95.00%	T.DFANFVGPVIHQASFNK.L		K.VGAPLTDFANFVGPVIHQASFNK.L
362	384	3	2428.26	1.9	1	37	17.1	95.00%	K.VGAPLTDFANFVGPVIHQASFNK.L		K.VGAPLTDFANFVGPVIHQASFNK.L
254	274	3	2393.15	4.4	1	52.3	20.9	95.00%	K.VCFNHPEFAGLHFTGSTAVFR.S	Carbamidomethyl (+57)	K.VCFNHPEFAGLHFTGSTAVFR.S
275	288	2	1444.74	4.6	1	37.7	21.6	95.00%	R.SLWGTIGENVANGK.Y		R.SLWGTIGENVANGK.Y
495	509	2	1504.71	3.5	1	49.3	22.5	95.00%	K.CTGAVVGEQPFGGAR.A	Carbamidomethyl (+57)	K.CTGAVVGEQPFGGAR.A
484	494	2	1225.58	4.6	1	28	23.5	95.00%	R.NAAGNFYINDK.C		R.NAAGNFYINDK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
44	PPA1_SCHPO	19.87%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
413	427	2	1802.8	3	1	63.2	23.9	95.00%	S.DGMCELYAYLNSPVR.V	Oxidation (+16)/ Carbamidomethyl (+57)	R.HLVNEEVFPLSDCGFGPSNTSDGMCELYAYLNSPVR.V
40	59	3	2404.13	2.5	1	63.3	22.4	95.00%	R.SPYHKPYFYGPSIDFPTTCK.I	Carbamidomethyl (+57)	R.SPYHKPYFYGPSIDFPTTCK.I
417	427	2	1323.68	2	0	51.2	21.1	95.00%	C.ELYAYLNSPVR.V		R.HLVNEEVFPLSDCGFGPSNTSDGMCELYAYLNSPVR.V
73	92	2	2047	4	1	99.4	21.6	95.00%	R.NPTGGNAAFDAVGIANFQQR.L		R.NPTGGNAAFDAVGIANFQQR.L
331	345	2	1606.83	3.6	1	32.3	20	95.00%	H.DANIIPVETALGFFT.D		R.SVENNTQQVFFAFTHDANIIPVETALGFFTDNTPENPLPTSYQVHSHSMK.A
346	365	4	2281.05	2	1	19.9	22.2	95.00%	T.DNTPENPLPTSYQVHSHSMK.A		R.SVENNTQQVFFAFTHDANIIPVETALGFFTDNTPENPLPTSYQVHSHSMK.A
40	52	2	1554.75	1.6	0	38.6	22.9	95.00%	R.SPYHKPYFYGPSI.D		R.SPYHKPYFYGPSIDFPTTCK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
45	FAS2_SCHPO	1.25%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
689	702	2	1504.78	3.7	0	23.5	20.2	90.10%	R.GSCLIVVPFNQGSK.T	Carbamidomethyl (+57)	R.GSCLIVVPFNQGSK.T
1393	1401	2	994.61	4.5	1	27.6	10.4	95.00%	K.TPLPIVDLK.F		K.TPLPIVDLK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
46	YL8C_SCHPO	15.18%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
47	60	2	1575.87	2.6	1	42.8	16	95.00%	R.EKYPNFPIVLATGK.Q		R.EKYPNFPIVLATGK.Q
217	232	2	1745.96	4.4	1	53	15.1	95.00%	K.GTALQYITSNILPEVK.N		K.GTALQYITSNILPEVK.N
49	60	2	1318.74	5.4	0	24.4	17.3	91.70%	K.YPNFPIVLATGK.Q		K.YPNFPIVLATGK.Q
75	90	2	1775.83	0.95	0	56.9	23.2	95.00%	L.DAFPAAHVNGCVLYNK.G	Deamidation (+1)/ Carbamidomethyl (+57)	R.IPLDLDAFPAAHVNGCVLYNK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
47	HSP7F_SCHPO	9.44%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
174	189	2	1665.85	4	1	78.4	20.7	95.00%	R.LMNDNAAAALTYGITK.T		R.LMNDNAAAALTYGITK.T
5	16	2	1249.64	6.5	1	29.4	21.8	95.00%	R.TNVVGIDFGNSK.T		R.TNVVGIDFGNSK.T
38	48	2	1194.59	3.8	1	34	23	95.00%	R.STPSLVSYGER.S		R.STPSLVSYGER.S
377	390	2	1549.78	3.1	0	56.8	21.1	95.00%	R.GCALSCAILSPVFR.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GCALSCAILSPVFR.V
177	189	2	1307.68	3.7	0	33.3	21.1	95.00%	N.DNAAAALTYGITK.T		R.LMNDNAAAALTYGITK.T
159	173	2	1534.89	4	1	42.9	9.54	95.00%	R.ALLEAANIAGLNPLR.L		R.ALLEAANIAGLNPLR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
48	CYPH_SCHPO	43.83%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
83	89	2	835.41	2.6	1	26.6	22.3	94.80%	P.DENFALK.H		K.FPDENFALK.H
90	123	3	3611.83	4	1	56	16.4	95.00%	K.HNKPGLLSMANAGPNTNGSQFFITTVVTPWLDGK.H		K.HNKPGLLSMANAGPNTNGSQFFITTVVTPWLDGK.H
2	17	2	1835.87	3.9	1	50	22.6	95.00%	M.SNCFFDVIANGQPLGR.I	Acetyl (+42)/ Carbamidomethyl (+57)	-.MSNCFFDVIANGQPLGR.I
54	67	2	1607.82	4.3	1	67.2	20.8	95.00%	R.VIPQFMLQGGDFTR.G		R.VIPQFMLQGGDFTR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
49	ILV3_SCHPO	7.53%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
40	48	2	994.5	5.2	1	30.6	23.7	95.00%	K.YSETITGPK.S		K.YSETITGPK.S
246	265	2	2011.93	2.1	1	74.8	23.2	95.00%	A.EAMGMTLPGSSSYLAGSPEK.F		R.HACPGGGACGGMYTANTMASCAEAMGMTLPGSSSYLAGSPEK.F
197	212	2	1760.87	2.4	1	62.5	21.1	95.00%	I.DIVSAFQSYGEFITGK.I		R.AGHSPCQNNAPIDIVSAFQSYGEFITGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
50	RS18_SCHPO	29.61%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	78	2	1386.79	4	0	45.2	15.2	95.00%	R.IVTIIQNPSQFK.I		R.IVTIIQNPSQFK.I
2	14	2	1578.86	3.1	1	36	16.7	95.00%	M.SLVVPDNFQHILR.L	Acetyl (+42)	-.MSLVVPDNFQHILR.L
79	86	2	1031.56	6	0	52.6	20.6	95.00%	K.IPSWFLNR.Q		K.IPSWFLNR.Q
95	106	2	1334.69	4.9	1	24.9	20.8	92.60%	K.SFQLLANNVDSK.L		K.SFQLLANNVDSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
51	ADH_SCHPO	27.14%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
236	253	2	1681.87	4.1	0	56	18.3	95.00%	K.AATNGGAHGTLVLSTSPK.S	Deamidation (+1)	K.AATNGGAHGTLVLSTSPK.S
322	333	2	1420.74	4.6	1	23.7	19.8	90.30%	K.VQPFSTLPDVYR.L		K.VQPFSTLPDVYR.L
254	278	3	2513.21	3.1	1	41.5	20.2	95.00%	K.SYEQAAGFARPGSTMVTVSMPAGAK.L		K.SYEQAAGFARPGSTMVTVSMPAGAK.L
170	194	3	2506.29	3.6	1	33.6	16.1	95.00%	K.VGPGEWICIPGAGGGLGHLAVQYAK.A	Carbamidomethyl (+57)	K.VGPGEWICIPGAGGGLGHLAVQYAK.A
63	77	2	1462.8	2.7	1	48.2	17.1	95.00%	K.MPLIGGHEGAGVVVK.V		K.MPLIGGHEGAGVVVK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
52	CYSD_SCHPO	20.98%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
408	415	2	836.48	1.9	1	29.7	15.8	95.00%	R.VAVGIEHI.D		R.VAVGIEHIDDIIADFAQALEVA.-
47	59	2	1541.79	2.7	1	44.4	20.6	95.00%	R.LFGLQEPGYIYSR.M		R.LFGLQEPGYIYSR.M
27	39	2	1486.79	3.4	0	61.1	19	95.00%	R.AVPIYATTSYVFR.D		R.AVPIYATTSYVFR.D
72	100	3	2787.49	3.3	1	49.9	14.5	95.00%	R.IAALEHGAAAIATSSGTSALFMALTTLAK.A		R.IAALEHGAAAIATSSGTSALFMALTTLAK.A
151	165	2	1651.8	3.1	1	25.9	22.9	93.90%	K.AVYVESIGNPMYNVP.D		K.AVYVESIGNPMYNVPDFER.I
366	377	2	1185.64	4.4	1	34.5	19.6	95.00%	K.LASQLANVGDAK.T		K.LASQLANVGDAK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
53	YHY6_SCHPO	18.72%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
214	225	2	1537.76	2.5	0	47.6	21.5	95.00%	A.DFPNWYQQVLTK.S		K.DADFPNWYQQVLTK.S
161	187	3	2608.39	2.9	1	26.8	14.5	95.00%	K.SVGVNPIIVDFSAPGSATAPSKPAAQK.K		K.SVGVNPIIVDFSAPGSATAPSKPAAQK.K
147	160	2	1522.84	2.7	0	37.7	15.2	95.00%	K.TVFVSPAAVQTYLK.S		K.TVFVSPAAVQTYLK.S
335	343	2	1114.59	4.7	0	24.2	20.9	91.30%	K.LNQWNSVVR.W		K.LNQWNSVVR.W
492	511	3	2075.19	3	0	19.6	8.45	93.80%	K.LPPAIALVQSVVVPCGITNK.T	Carbamidomethyl (+57)	K.LPPAIALVQSVVVPCGITNK.T
387	398	2	1343.81	4.3	1	30.5	9.03	95.00%	R.IYTDLLAVPVIK.G		R.IYTDLLAVPVIK.G
426	441	3	1703.81	4.5	0	20.8	22.7	95.00%	R.GIQGATSHCLGQNFSK.M	Carbamidomethyl (+57)	R.GIQGATSHCLGQNFSK.M
60	83	3	2367.33	2.1	1	19.9	9.54	94.30%	K.SQTVVPIILAALETTSTPSGIAAK.A		K.SQTVVPIILAALETTSTPSGIAAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
54	UGPA1_SCHPO	16.60%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
22	34	2	1309.62	2.6	0	65.1	23.1	95.00%	F.DNTATSIAASTMK.N		K.SQSAFAFDNTATSIAASTMK.N
439	449	3	1210.64	3.2	0	18.4	20.4	91.20%	A.DFSAHIPSIPK.I		K.VADFSAHIPSIPK.I
493	506	2	1624.79	1.5	1	55.9	23	95.00%	L.ENCVITGNLNILEH.-	Carbamidomethyl (+57)	R.IDIPNGSVLENCVITGNLNILEH.-
1	10	2	1166.63	4.6	1	24.9	19.3	92.50%	-.MDLAPRPLGR.Q	Acetyl (+42)	-.MDLAPRPLGR.Q
185	194	2	1205.65	4.7	1	32.1	19.4	95.00%	K.IDILTFNQSR.Y		K.IDILTFNQSR.Y
94	104	2	1118.56	2	1	50.9	21.9	95.00%	Y.DTITEAGGLSR.D		R.GSEINWDLVESPKPEQVVEYDTITEAGGLSR.D
115	129	2	1460.72	4.2	0	48.3	22.8	95.00%	K.LNGGLGTTMGCVGPK.S	Carbamidomethyl (+57)	K.LNGGLGTTMGCVGPK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
55	GLNA_SCHPO	11.70%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
247	260	2	1546.65	-0.71	0	54.1	23.9	95.00%	G.DWNGAGCHTNVSTK.D	Deamidation (+1)/ Carbamidomethyl (+57)	K.ISFHPKPILGDWNGAGCHTNVSTK.D
153	170	2	1809.83	2.4	0	45.5	23.3	95.00%	K.GGFPGPQGPFYCGVGTGR.V	Carbamidomethyl (+57)	K.GGFPGPQGPFYCGVGTGR.V
237	260	4	2635.31	3.2	1	28.9	19.4	95.00%	K.ISFHPKPILGDWNGAGCHTNVSTK.D	Carbamidomethyl (+57)	K.ISFHPKPILGDWNGAGCHTNVSTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
56	OAT_SCHPO	6.62%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
386	398	3	1374.82	4.6	0	23.2	12.3	95.00%	R.GVLAKPTHGNIIR.F		R.GVLAKPTHGNIIR.F
276	291	2	1561.85	4	0	53	16.6	95.00%	K.AISGGVYPVSAVLSSR.E		K.AISGGVYPVSAVLSSR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
57	IF4A_SCHPO	9.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
58	69	2	1173.61	5	0	69	21.8	95.00%	R.DVLAQAQSGTGK.T		R.DVLAQAQSGTGK.T
33	48	2	1854.94	2.1	1	40.7	20.3	95.00%	R.GIYAYGFERPSAIQQR.A		R.GIYAYGFERPSAIQQR.A
298	305	2	1047.49	4.2	1	24.7	22.7	92.30%	R.DTLMHEFR.T		R.DTLMHEFR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
58	DHAS_SCHPO	18.21%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
307	318	2	1278.6	4.8	1	24.6	23.5	92.10%	R.NNENGYAVSVGR.I		R.NNENGYAVSVGR.I
31	39	2	856.52	4.9	0	28.2	17.2	95.00%	K.IAVLGASAR.S		K.IAVLGASAR.S
143	161	2	2003.03	3.7	0	71.4	19.5	95.00%	R.GCIITNSNCSTAAVVVPLK.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GCIITNSNCSTAAVVVPLK.A
267	278	2	1375.7	3.8	1	37.2	21.5	95.00%	R.EVLANYVSEPQK.L		R.EVLANYVSEPQK.L
6	18	2	1227.7	3.7	0	35.6	17.3	95.00%	K.VGILGATGTVGQR.F		K.VGILGATGTVGQR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
59	LEUC_SCHPO	9.37%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
633	649	2	2002.01	4.5	1	59.4	21.1	95.00%	R.VIIAPSFADIFFNNCFK.N	Carbamidomethyl (+57)	R.VIIAPSFADIFFNNCFK.N
603	619	3	1826.86	5.3	1	37.3	22.8	95.00%	R.HATVLVAHDNFGCGSSR.E	Carbamidomethyl (+57)	R.HATVLVAHDNFGCGSSR.E
477	493	2	1810.88	4.1	1	36.5	21.8	95.00%	R.EFFGDVSNGSPSIITNK.N		R.EFFGDVSNGSPSIITNK.N
520	539	2	1786.91	1.7	0	89.1	21	95.00%	A.DGIATNVAGSVSSGSAGIPK.F		K.NYDPSHDVEGDIGLSVDDATDAV TDADGIATNVAGSVSSGSAGIPK.F
481	493	2	1331.66	2.3	0	52.9	22.2	95.00%	G.DVSNGSPSIITNK.N	Deamidation (+1)	R.EFFGDVSNGSPSIITNK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
60	HOSM_SCHPO	11.48%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	204	2	1315.66	4	1	40.8	22.3	95.00%	R.VGIADTVGCATPR.Q	Carbamidomethyl (+57)	R.VGIADTVGCATPR.Q
258	269	2	1195.7	2.6	0	28	13.4	95.00%	R.NGITPLGALLAR.M	Deamidation (+1)	R.NGITPLGALLAR.M
146	156	2	1221.63	2.7	1	48	22.4	95.00%	I.DSATEVINFVK.S		K.DMTYIIDSATEVINFVK.S
32	43	2	1391.75	4.9	1	68.1	19.7	95.00%	R.VNNFSIIESTLR.E		R.VNNFSIIESTLR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
61	ECM17_SCHPO	2.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1031	1044	2	1572.69	3.1	1	77.8	23.6	95.00%	R.NVTCSSTPNNETIH.D	Carbamidomethyl (+57)	R.NVTCSSTPNNETIHDQLFAVSK.Q
314	325	2	1337.8	4.6	1	39.3	10.8	95.00%	R.LTVLEPITSLPR.K		R.LTVLEPITSLPR.K
1053	1066	2	1588.78	1.4	1	44.3	22.5	95.00%	K.QISNELLPTTSSYH.E		K.QISNELLPTTSSYHEIWIEDPETVE K.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
62	HXK1_SCHPO	9.09%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
36	47	2	1482.79	2.1	1	30.5	19	95.00%	E.EQFTIPTELLHR.V		K.TLQDHLDELEEQFTIPTELLHR.V
304	315	2	1380.7	5.1	1	25.3	22.1	93.10%	K.MIAGCYLGDILR.R	Carbamidomethyl (+57)	K.MIAGCYLGDILR.R
274	282	2	1076.58	2.5	0	43	20	95.00%	F.DNQHVVLPR.T		K.YDFPEDMNMIINCEWCDFDNQH VVLPR.T
2	12	3	1409.65	4.4	1	25.1	23.1	95.00%	M.SLHDAYHWPSR.T	Acetyl (+42)	-.MSLHDAYHWPSR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
63	EF1B_SCHPO	13.08%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
59	73	2	1561.84	4.2	1	60.9	18.5	95.00%	K.QIATYDLATLPGTAK.E		K.QIATYDLATLPGTAK.E
153	165	2	1432.74	3.9	1	44.3	21.2	95.00%	R.SIQMDGLVWGLSK.L		R.SIQMDGLVWGLSK.L
157	165	2	973.53	3.1	0	31.6	22.2	95.00%	M.DGLVWGLSK.L		R.SIQMDGLVWGLSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
64	VIPI_SCHPO	18.68%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	68	2	1496.86	4.3	1	41.7	13.6	95.00%	K.TALLLQDALLGQNK.I		K.TALLLQDALLGQNK.I

101	110	2	1087.63	5.8	1	34.3	16.6	95.00%	R.SAIISELLSR.G		R.SAIISELLSR.G
122	134	2	1410.71	4.2	1	61.1	21.6	95.00%	K.SIQLDQSYGVSSK.F		K.SIQLDQSYGVSSK.F
137	147	2	1100.62	4.3	1	27.7	18.8	95.00%	K.GILESALSGVR.S		K.GILESALSGVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
65	RS7_SCHPO	11.28%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
59	70	2	1322.84	4	0	46.5	4.77	95.00%	K.AIVVFVPQPLLK.A		K.AIVVFVPQPLLK.A
168	177	3	1123.57	4.2	0	19.7	22.8	94.00%	K.LGSFSSVYHK.L		K.LGSFSSVYHK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
66	GBLP_SCHPO	18.47%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
48	57	2	1135.53	4.7	1	43.2	22.9	95.00%	R.DDVNYGVAQR.R		R.DDVNYGVAQR.R
186	212	3	2736.26	2.6	1	43.2	22.2	95.00%	R.TSHYGHTGYVSAVTISPDGSLCASGGR.D	Carbamidomethyl (+57)	R.TSHYGHTGYVSAVTISPDGSLCASGGR.D
234	245	2	1314.71	3.1	0	32.5	19.4	95.00%	K.ANINALVFSPNR.Y		K.ANINALVFSPNR.Y
39	47	2	1112.68	5.9	0	27.8	13	95.00%	K.SIILWNLVR.D		K.SIILWNLVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
67	MMF1_SCHPO	30.25%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
94	105	2	1246.64	2.8	1	44.8	22	95.00%	Q.EVLTEAGSSLNK.I		R.QCLLNLQEVLTEAGSSLNK.I
59	75	2	1747.86	2.8	0	34.8	21.7	95.00%	K.ANGVIYCSGQIPVANGK.V	Carbamidomethyl (+57)/ Deamidation (+1)	K.ANGVIYCSGQIPVANGK.V
117	124	2	878.42	2.9	1	31	22.8	95.00%	M.DDFAAVNK.V		K.VNIFLADMDDFAAVNK.V
47	58	2	1247.66	5.3	0	27.4	19.6	95.00%	K.LSSAGPYNQAIK.A		K.LSSAGPYNQAIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
68	RS6B_SCHPO	18.41%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
39	51	2	1414.68	2.7	1	54	23.1	95.00%	G.DSVGPEFAGYVFK.I		R.MGQEVPGDSVGPEFAGYVFK.I
99	115	2	1739.01	3.8	1	65.7	11.1	95.00%	R.GCIVGQDLAVLALAIVK.Q	Carbamidomethyl (+57)	R.GCIVGQDLAVLALAIVK.Q
59	72	3	1625.86	3.4	0	35.4	19.5	95.00%	K.QGFPMFQGVLLPHR.V		K.QGFPMFQGVLLPHR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
69	RAD24_SCHPO	15.19%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
109	120	2	1236.65	4.7	1	29.1	20.3	95.00%	K.HLIPNAASAESK.V		K.HLIPNAASAESK.V
164	172	2	1032.57	3	0	29	16.2	95.00%	A.ELAPTHPIR.L		K.AASEIATAELAPTHPIR.L
76	85	2	1071.6	3.6	1	23.8	19.7	90.70%	K.GNTAQVELIK.E		K.GNTAQVELIK.E
218	227	2	1188.66	2.2	0	58.2	17.9	95.00%	K.DSTLIMQLLR.D		K.DSTLIMQLLR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
70	RL15A_SCHPO	19.90%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
115	128	2	1699.83	4.1	1	73.6	22.2	95.00%	R.VLNSYWVNQDATYK.F		R.VLNSYWVNQDATYK.F
78	93	3	1761.94	4.3	0	26	18.5	95.00%	K.GQTYGKPVHQGVNHLK.Y		K.GQTYGKPVHQGVNHLK.Y
148	157	3	1218.69	4.4	0	24.4	16.8	95.00%	R.INWIVNPVHK.H		R.INWIVNPVHK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
71	YF19_SCHPO	13.92%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
195	208	2	1516.82	2.8	1	70.9	17.8	95.00%	K.TAELTPLSALCLTK.F	Carbamidomethyl (+57)	K.TAELTPLSALCLTK.F
422	443	3	2229.12	4.1	0	21.2	19.3	95.00%	R.GNNSTYGLAAGVHTNNITNAIK.V		R.GNNSTYGLAAGVHTNNITNAIK.V
71	80	2	1161.56	3.7	1	28.3	23.5	95.00%	R.AAFQTDAPWR.K		R.AAFQTDAPWR.K
340	349	2	1079.53	2.6	0	31	23.3	95.00%	E.DTFQGAQVSK.Q		K.VGDPFAEDTFQGAQVSK.Q

181	194	2	1439.82	2.8	0	60.3	15.3	95.00%	K.IAPAVACGNTIILK.T	Carbamidomethyl (+57)	K.IAPAVACGNTIILK.T		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
72	DHOM_SCHPO	22.61%	100%	6									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
125	138	2	1568.79	4.5	1	56.7	21.1	95.00%	K.AFSASNDVYQNIIK.A		K.AFSASNDVYQNIIK.A		
57	67	2	1391.68	4.7	1	33.1	22.6	95.00%	K.DYQPINLSEWK.N		K.DYQPINLSEWK.N		
313	325	2	1435.64	2.7	1	43.2	24.2	95.00%	K.YDASHPFANLQSS.D		K.YDASHPFANLQSSDNIISFTTK.R		
238	252	2	1526.81	2.9	1	35	19.4	95.00%	R.IAGVHVESASSFPVK.S		R.IAGVHVESASSFPVK.S		
142	164	3	2293.24	2.2	1	29.9	14	95.00%	K.ESGALLMHEASVGAGLPIISTLK.E		K.ESGALLMHEASVGAGLPIISTLK.E		
102	110	2	1005.52	2.5	0	28	22	95.00%	S.EAIAQSYPK.F		K.SPLPAILVDNTASEAIAQSYPK.F		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
73	CARB_SCHPO	5.34%	100%	4									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
968	975	2	1019.52	4.9	0	24.9	23	92.60%	K.VPQFSWTR.L		K.VPQFSWTR.L		
932	943	2	1304.72	5.6	1	35.2	18.1	95.00%	K.TLGVNFIDVATR.S		K.TLGVNFIDVATR.S		
402	417	3	1672.96	2.4	1	32.7	12	95.00%	K.IALGHTLPELPNAVTK.T		K.IALGHTLPELPNAVTK.T		
773	798	3	2736.49	2.9	0	51	13.2	95.00%	K.FANAVGYPVLVRPSYVLSGAAMSVIR.D		K.FANAVGYPVLVRPSYVLSGAAMSVIR.D		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
74	RL8_SCHPO	15.06%	100%	4									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
24	32	2	1084.62	4.7	0	29.3	18.8	95.00%	K.NPLFVSRPR.S		K.NPLFVSRPR.S		
33	43	2	1188.62	4.1	1	26.8	21.3	95.00%	R.SFGIGQDIQPK.R		R.SFGIGQDIQPK.R		
134	146	2	1425.8	2.2	1	54.1	14.5	95.00%	K.YGLNHVVALIEAK.K		K.YGLNHVVALIEAK.K		
52	57	2	862.44	5.9	1	26.5	22.3	94.70%	K.WPEYIR.L		K.WPEYIR.L		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
75	TRP_SCHPO	10.47%	100%	4									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
382	393	2	1355.77	4.5	0	47.2	17.2	95.00%	K.INNCIGQILLAK.R	Carbamidomethyl (+57)	K.INNCIGQILLAK.R		
400	419	3	1938.01	4.3	1	37.5	19.2	95.00%	R.IIAETGAGQHGVATAICAAK.F	Carbamidomethyl (+57)	R.IIAETGAGQHGVATAICAAK.F		
445	461	2	1739.98	2.8	1	63.8	14	95.00%	R.LLGAEVVPVTSGTQTLR.D		R.LLGAEVVPVTSGTQTLR.D		
91	114	2	2617.33	5.8	1	82.3	18.2	95.00%	R.DAGVTIPIILMGYYNPIFSYGDAK.T		R.DAGVTIPIILMGYYNPIFSYGDAK.T		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
76	EF1G_SCHPO	13.20%	100%	4									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
290	298	2	1136.52	1.9	1	25.9	23	94.00%	F.DPENYSVWK.V		R.SGALPWFFEHFDPENYSVWK.V		
93	115	3	2635.36	2.4	1	47.1	15.7	95.00%	K.VLQYCSFTNSELPGAFRPIIAPR.V	Carbamidomethyl (+57)	K.VLQYCSFTNSELPGAFRPIIAPR.V		
207	216	2	1182.71	4	1	27.1	14.6	95.00%	K.FIDQPLPIIK.A		K.FIDQPLPIIK.A		
128	139	2	1303.72	4.6	1	40.7	18.6	95.00%	K.EAETAIALIFAR.F		K.EAETAIALIFAR.F		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
77	RS3B_SCHPO	5.56%	100%	1									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
200	213	2	1513.87	4.8	0	38.9	13.6	95.00%	R.ATGSIFPLQNVLVR.K		R.ATGSIFPLQNVLVR.K		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
78	RS23_SCHPO	21.68%	100%	3									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		

98	107	2	1091.56	2.2	1	47.6	22.2	95.00%	N.DEVLLSGFGR.K		K.VTAFVPHDGCLNFVDENDEVLLSGFGR.K
80	87	2	897.51	1.8	1	25.2	17.4	93.00%	K.KVTAFVPH.D		K.KVTAFVPHDGCLNFVDENDEVLLSGFGR.K
125	137	2	1326.74	4.4	1	55.5	17.2	95.00%	K.VAGVGLSALFHEK.K		K.VAGVGLSALFHEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
79	RS8A_SCHPO	21.50%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
165	178	2	1475.79	4.1	0	33.2	18.9	95.00%	R.LYAVVSSRPGQSGR.C		R.LYAVVSSRPGQSGR.C
78	92	2	1751.94	3.2	1	39.9	18.1	95.00%	R.IIQVAYHPSNNELVR.T		R.IIQVAYHPSNNELVR.T
111	124	3	1682.82	4.5	1	23.1	22.3	95.00%	R.VWYETHYGILMGSK.G		R.VWYETHYGILMGSK.G
78	88	2	1254.64	3.2	0	24.9	21.8	92.60%	R.IIQVAYHPSNN.E		R.IIQVAYHPSNNELVR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
80	PMP20_SCHPO	23.08%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
110	119	2	997.56	3	0	49.4	16.4	95.00%	F.DASGLLGPLR.S		K.AFDAGFDASGLLGPLR.S
30	55	2	2747.41	2.2	1	57.7	17.2	95.00%	K.FIIVGVPGAFTPPCSSQVPGYIANEK.Q	Carbamidomethyl (+57)	K.FIIVGVPGAFTPPCSSQVPGYIANEK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
81	PYR1_SCHPO	1.65%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1771	1784	2	1494.85	4.1	1	35.2	12.3	95.00%	R.EAIPLLLTAVNEGR.L		R.EAIPLLLTAVNEGR.L
1897	1906	2	1089.51	2.4	1	34.8	22.9	95.00%	A.EAFGQAPENK.A		K.VSALMSPGLPHAAPSLAEAFGQAPENK.A
1758	1770	2	1371.7	4.4	0	56.2	21.7	95.00%	K.FVGNTAFTGFGVR.E		K.FVGNTAFTGFGVR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
82	THI4_SCHPO	8.11%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
373	385	2	1353.71	4.1	1	37.5	19.8	95.00%	R.GVDSISQHTLAAR.I		R.GVDSISQHTLAAR.I
249	265	4	1917.09	3.2	1	33.8	10.4	95.00%	K.LKDFTPLIHHLTNAVAK.N		K.LKDFTPLIHHLTNAVAK.N
237	248	2	1322.76	4.7	0	31.5	13.2	95.00%	K.DLLNQIPAALQK.L		K.DLLNQIPAALQK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
83	FAS1_SCHPO	3.47%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
415	431	3	1929.06	4.4	0	19.3	14.8	93.20%	R.FLSISVPFHSPYLAPVR.S		R.FLSISVPFHSPYLAPVR.S
1870	1881	2	1266.57	5.2	1	37.8	24.2	95.00%	R.SDYGMVAANPSR.V		R.SDYGMVAANPSR.V
1778	1806	3	3141.54	1.9	1	40.3	18.6	95.00%	K.DSTSFSFTHPSGLLSATQFTQPALTLMEK.S		K.DSTSFSFTHPSGLLSATQFTQPALTLMEK.S
781	794	2	1545.81	3.9	1	42.1	20.3	95.00%	K.LPPMPFDGILFGSR.L		K.LPPMPFDGILFGSR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
84	VATA_SCHPO	9.37%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
227	240	2	1539.8	2.4	0	65.8	19.9	95.00%	A.DNLTANQPLLTGQR.V		R.AARPVADNLTANQPLLTGQR.V
128	136	2	1002.51	5	1	25.2	22.2	93.10%	R.GINTESLNR.E		R.GINTESLNR.E
317	331	2	1544.81	4.6	0	49.4	20.9	95.00%	R.TTLVANTSNMPVAAR.E		R.TTLVANTSNMPVAAR.E
221	240	3	2105.14	4.1	1	35.3	16	95.00%	R.AARPVADNLTANQPLLTGQR.V		R.AARPVADNLTANQPLLTGQR.V
182	195	2	1466.71	2.1	1	25.3	23.1	93.20%	R.GTVTYIAEAGSYHV.D		R.GTVTYIAEAGSYHVDEK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
85	RS22_SCHPO	23.85%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
9	19	2	1316.62	1.8	1	40.3	23.5	95.00%	A.DCLNNIVNAER.R	Carbamidomethyl (+57)	R.QSVLADCLNNIVNAER.R
98	108	2	1171.7	4.9	0	29.1	13.4	95.00%	R.QVGVIVLTTSR.G		R.QVGVIVLTTSR.G

89	97	2	1111.62	5.6	0	31.9	16.8	95.00%	K.WVNQLLPSR.Q		K.WVNQLLPSR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
86	CDC48_SCHPO	3.19%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
550	563	2	1522.75	3.6	1	43.8	21.7	95.00%	K.AIANECSANFISVK.G	Carbamidomethyl (+57)	K.AIANECSANFISVK.G
511	522	2	1424.67	4.6	1	24.4	23	91.70%	R.ETVQMPVMYAEK.F		R.ETVQMPVMYAEK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
87	ACON_SCHPO	4.88%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
532	549	2	1853.89	4.6	1	68.9	22	95.00%	K.GYDPGSNTYVAPSSVNVK.D		K.GYDPGSNTYVAPSSVNVK.D
392	402	2	1203.6	5.2	1	35.2	22.5	95.00%	R.AASICQQAIDK.G	Carbamidomethyl (+57)	R.AASICQQAIDK.G
462	470	2	1052.53	5	0	36.5	22.4	95.00%	K.NSIVTSYNR.N		K.NSIVTSYNR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
88	ASNS_SCHPO	3.59%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
156	165	2	1143.55	2.8	1	27.9	22.9	95.00%	P.DTAYFASELK.A		R.DPIGITTLYQGFSSDSPDTAYFASELK.A
399	408	2	1120.54	4.9	1	26.3	21.9	94.50%	K.STMAWGLEAR.V		K.STMAWGLEAR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
89	AROG_SCHPO	11.02%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
66	76	2	1192.67	2.6	0	33.6	17.8	95.00%	R.IIVVVGPCSIH.D	Carbamidomethyl (+57)	R.IIVVVGPCSIHDPK.L
210	226	3	1718.88	1.7	0	18.3	20.4	90.90%	I.DAIGATAHPHTMLGVTK.Q		K.NGTDGTVGVAIDAIGATAHPHTMLGVTK.Q
186	198	2	1364.74	3.3	0	69	18.8	95.00%	R.ELASALSFPVGFK.N		R.ELASALSFPVGFK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
90	RS10B_SCHPO	23.13%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	44	3	1428.81	3.4	1	30.9	16.5	95.00%	K.HPEVGVPNLQVIK.A		K.HPEVGVPNLQVIK.A
10	24	3	1621.94	3	0	33.8	14.1	95.00%	K.AIHQALFQQGVLVAK.K		K.AIHQALFQQGVLVAK.K
26	31	2	732.38	5.5	0	30.1	22.2	95.00%	K.DFNLPK.H		K.DFNLPK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
91	RL10A_SCHPO	13.12%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	128	3	1265.71	4.6	0	30	15.9	95.00%	R.HAFGKPNGLVAR.V		R.HAFGKPNGLVAR.V
129	139	2	1228.7	4.7	0	40	16.1	95.00%	R.VNIGQILMSVR.T		R.VNIGQILMSVR.T
33	38	2	719.4	4.8	1	27.1	17.8	95.00%	R.IFDLGR.K		R.IFDLGR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
92	RL13_SCHPO	25.96%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
172	183	2	1398.66	5.4	1	54	23.8	95.00%	K.NFNAFSTLSNER.A		K.NFNAFSTLSNER.A
118	128	3	1326.79	4.7	0	51.2	13.8	95.00%	K.VYLAHLIVFPR.K		K.VYLAHLIVFPR.K
46	64	4	2080.27	3.1	1	20	0	95.00%	K.IAPRPVEAIRPAVKPPTIR.Y		K.IAPRPVEAIRPAVKPPTIR.Y
89	100	2	1263.7	3.9	1	28.9	18.6	95.00%	R.VASTIGIPVDHR.R		R.VASTIGIPVDHR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
93	GCST_SCHPO	17.83%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
266	281	2	1688.87	2.1	1	47.2	20.5	95.00%	D.DTTSPVEGSLSWIIGK.R		R.LEAGMCLYGSDIDDTTSPVEGSLSWIIGK.R
34	51	2	1940.98	2.9	0	39	19.7	95.00%	K.EGATIVPFAGFSMPVQYK.G		K.EGATIVPFAGFSMPVQYK.G
165	180	2	1623.93	4	1	75.8	11.5	95.00%	R.ALIAIQGPETASVVQK.L		R.ALIAIQGPETASVVQK.L

326	344	2	1886.91	1.9	1	88.7	22.1	95.00%	V.DGVEVGQVTSGCPSPTLGK.N	Carbamidomethyl (+57)	R.HGSAVEVDGVEVGQVTSGCPSPTLGK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
94	LYS12_SCHPO	11.88%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
197	208	2	1324.65	5.3	1	41.8	23	95.00%	K.SNVMSVTDGLFR.E		K.SNVMSVTDGLFR.E
298	307	2	1044.58	4.6	0	32.2	20.9	95.00%	R.GIANPVATFR.S		R.GIANPVATFR.S
188	196	3	1047.69	4.7	0	25.1	3.01	95.00%	K.KPLVTIIHK.S		K.KPLVTIIHK.S
86	97	2	1231.7	4.7	0	25.9	16.7	94.00%	K.VAGYSSPIVALR.K		K.VAGYSSPIVALR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
95	RL3A_SCHPO	13.66%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
11	19	2	982.54	4.3	0	27.2	19	95.00%	R.HGSLGFLPR.K		R.HGSLGFLPR.K
320	334	3	1601.83	1.8	1	21.7	20.4	95.00%	N.DFVMLNGATPGPVKR.V	Deamidation (+1)	R.YGVVENDFVMLNGATPGPVKR.V
101	111	2	1242.63	2.2	1	33.1	22.2	95.00%	R.SLTTVWAEHLS.E		R.SLTTVWAEHLSEEVK.R
249	266	3	2035.03	4.4	0	29.3	20.6	95.00%	K.VACIGAWHPANVQWTVAR.A	Carbamidomethyl (+57)	K.VACIGAWHPANVQWTVAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
96	GCSP_SCHPO	9.05%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
953	965	2	1458.76	1.1	0	43.1	20.8	95.00%	K.DNNLLVNAPHPQK.D		K.DNNLLVNAPHPQK.D
657	684	3	2835.48	2	0	30.6	15.8	95.00%	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C	Carbamidomethyl (+57)	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C
379	412	3	3679.8	2.3	1	51.4	16.5	95.00%	K.ATSNICTAQALLANMSAFYAIYHGPNGLQEIANR.I	Carbamidomethyl (+57)	K.ATSNICTAQALLANMSAFYAIYHGPNGLQEIANR.I
560	576	2	1831.87	4.3	0	45.3	23.2	95.00%	K.DLSLAHAMTPLGSCTMK.L	Carbamidomethyl (+57)	K.DLSLAHAMTPLGSCTMK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
97	SODC_SCHPO	24.03%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
98	116	2	1984.04	4.4	1	72.6	17.4	95.00%	K.TTFSDSVISLFGANSIIGR.T		K.TTFSDSVISLFGANSIIGR.T
53	70	2	1902.78	0.62	1	68.5	23.8	95.00%	G.DNTNGCTSAGPHFNPEGK.T	Deamidation (+1)/ Carbamidomethyl (+57)	R.GFHIHQFGDNTNGCTSAGPHFNPEGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
98	RL27A_SCHPO	25.74%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	48	3	1461.76	5.9	1	42.8	20.6	95.00%	K.SHPFGHAVVAGVER.Y		K.SHPFGHAVVAGVER.Y
23	34	2	1269.74	4.4	1	65.4	15.8	95.00%	K.VVILQAIDQGSK.S		K.VVILQAIDQGSK.S
99	107	2	1120.56	3.4	1	24.3	22	91.50%	A.DTFKEPTQR.S		K.GLITADTFKEPTQR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
99	SPI1_SCHPO	12.50%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
110	122	2	1514.77	4.6	1	58.5	21.8	95.00%	R.VCENIPIVLCGNK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VCENIPIVLCGNK.V
152	165	2	1783.91	3.3	1	34.2	20.2	95.00%	K.SNYNFEKPFLWLAR.K		K.SNYNFEKPFLWLAR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
100	PYC_SCHPO	3.29%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
405	420	2	1618.76	1.1	1	47.3	23.5	95.00%	R.LDGANGFAGSVITPHY.D	Deamidation (+1)	R.LDGANGFAGSVITPHYDSMLVK.C
917	929	2	1447.76	4.7	1	42.2	20.4	95.00%	K.VVGDLAQFMVQNK.L		K.VVGDLAQFMVQNK.L
839	848	2	1297.58	4.8	1	38.2	24	95.00%	R.EIDSYWAQMR.L		R.EIDSYWAQMR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
101	PURA_SCHPO	8.53%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
268	276	2	899.55	4.9	0	44.5	18.9	95.00%	R.IANSIGVVK.A		R.IANSIGVVK.A
413	427	2	1514.86	2.2	0	30.3	14.1	95.00%	K.FVGVPITFIGVGPGR.D		K.FVGVPITFIGVGPGR.D
64	76	2	1435.79	2	0	31.6	17.3	95.00%	Y.DFHILPSGLVNPK.C		R.CQGGNNAGHTIVANGVTYDFHILPSGLVNPK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
102	STI1_SCHPO	4.74%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
112	132	2	2007.97	4.2	1	89.9	21.8	95.00%	K.SVEAAQTQAASGAGGFNPFAK.L		K.SVEAAQTQAASGAGGFNPFAK.L
371	377	2	800.44	3.8	1	29.8	23	95.00%	R.TPDILSR.L		R.TPDILSR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
103	BCA1_SCHPO	8.95%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
315	331	2	1670.97	4.2	1	59.5	12.3	95.00%	R.LLEVFGAGTAALVSPVK.A		R.LLEVFGAGTAALVSPVK.A
262	278	2	1795	4.2	1	43.3	12.3	95.00%	K.EIITAPLDGMILPGVTR.D		K.EIITAPLDGMILPGVTR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
104	SYEC_SCHPO	5.31%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
394	404	2	1196.62	1.7	1	36.3	21.5	95.00%	V.DSLEGVTHALR.T		R.AYPTYDFACPIVDSLEGVTHALR.T
652	666	2	1734.83	1.8	1	27.1	23.1	95.00%	K.DFLTPQTEFHSPVFA.D		K.DFLTPQTEFHSPVFADVGIK.N
66	77	2	1393.77	4.3	0	31.9	16.8	95.00%	K.LALQTFSQVYPK.L		K.LALQTFSQVYPK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
105	DHE4_SCHPO	6.87%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
430	439	2	1004.53	3.7	0	37	21.3	95.00%	V.DGANIAGFLK.V		K.YCDSGSNNIPSLVDGANIAGFLK.V
356	367	2	1231.57	4.5	1	27.7	23.5	95.00%	R.ASGEGCWLAPGK.A	Carbamidomethyl (+57)	R.ASGEGCWLAPGK.A
93	101	2	1127.61	5.6	1	29.2	20.5	95.00%	K.FLGFEQIFK.N		K.FLGFEQIFK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
106	RS4A_SCHPO	8.02%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
12	22	3	1285.7	4.9	1	18.7	18.9	91.90%	R.VAAPHHWLLDK.L		R.VAAPHHWLLDK.L
40	49	2	1258.72	4.7	0	26.1	17.2	94.30%	R.ECLPLIVFLR.N	Carbamidomethyl (+57)	R.ECLPLIVFLR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
107	ASSY_SCHPO	10.73%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
110	122	2	1431.63	3.7	0	47.3	23.4	95.00%	K.ENCIAVSHGCTGK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.ENCIAVSHGCTGK.G
333	350	2	1885	3.3	1	76	17.1	95.00%	R.MLLAANNVSQEVVNGVVK.L	Deamidation (+1)	R.MLLAANNVSQEVVNGVVK.L
320	332	2	1601.77	4.2	0	39.6	23.3	95.00%	K.ILYNGQFFSPCTR.M	Carbamidomethyl (+57)	K.ILYNGQFFSPCTR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
108	RL12_SCHPO	34.55%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
68	83	2	1538.91	3.4	0	50.5	11.8	95.00%	R.QAAVSVVPSASALVIK.A		R.QAAVSVVPSASALVIK.A
97	106	2	996.5	3.5	0	28.5	21.3	95.00%	K.NVAHSGNVSL.D		K.NVAHSGNVSLDEIIEVAR.T
17	31	2	1312.7	3.6	1	46	18.2	95.00%	R.AVGGEVAGGSTLAPK.I		R.AVGGEVAGGSTLAPK.I
131	146	2	1652.81	4	1	45.9	21.7	95.00%	K.EILGTAFSVGCTVDGK.N	Carbamidomethyl (+57)	K.EILGTAFSVGCTVDGK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
109	IMDH_SCHPO	7.25%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
303	313	2	1155.67	4.5	1	51.3	17.4	95.00%	K.IDVIAGNVVTR.E		K.IDVIAGNVVTR.E
124	135	2	1281.64	2.2	0	35	22.5	95.00%	L.DPVVFSPQHTVG.D		K.YENGFILDPVVFSPQHTVGDVLK.I
419	433	2	1421.67	3.9	1	52.2	23.9	95.00%	R.GMGSIAAMEGTGVNK.N		R.GMGSIAAMEGTGVNK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
110	RS14_SCHPO	16.55%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
95	105	2	1037.57	5.3	0	47.1	19.2	95.00%	K.TPGPGAQAALR.A		K.TPGPGAQAALR.A
73	84	3	1367.77	4	1	24.2	16.5	95.00%	K.CKEVGITALHIK.I	Carbamidomethyl (+57)	K.CKEVGITALHIK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
111	NACA_SCHPO	13.87%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	75	2	1164.62	5.8	0	59.3	21.2	95.00%	K.SSNNAYIVLGK.V		K.SSNNAYIVLGK.V
52	64	2	1540.93	4.4	1	50.2	4.77	95.00%	K.NILLIINEPIVYK.S		K.NILLIINEPIVYK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
112	SERC_SCHPO	11.31%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
216	228	2	1299.74	5	0	37	14.8	95.00%	K.NAGPAGITVVFVR.D		K.NAGPAGITVVFVR.D
229	242	3	1532.84	5.6	1	18.3	16.5	90.90%	R.DSVLARPTPAELHK.L		R.DSVLARPTPAELHK.L
189	199	2	1282.6	4.3	1	67	23.4	95.00%	R.VCDVSSNFISR.K	Carbamidomethyl (+57)	R.VCDVSSNFISR.K
324	329	2	766.38	5.3	0	26.2	21.3	94.30%	R.MNVTFR.I		R.MNVTFR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
113	RS11_SCHPO	15.13%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	64	2	1161.6	4.7	0	33.4	21.5	95.00%	K.CPFVGQVSIR.G	Carbamidomethyl (+57)	K.CPFVGQVSIR.G
118	130	2	1457.77	2.9	0	56.6	19.7	95.00%	G.DVVTVGQCRPLSK.T	Carbamidomethyl (+57)	R.INEGDVVTVGQCRPLSK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
114	PMM_SCHPO	9.34%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
19	28	2	1043.53	3.3	1	37	21.2	95.00%	F.DVDGTLTPAR.L		K.TLVLFDVDGTLTPAR.L
45	58	2	1347.75	4.4	1	41.6	18.1	95.00%	K.VVAIGFVGGSDLSK.Q		K.VVAIGFVGGSDLSK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
115	THRC_SCHPO	8.56%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
265	282	2	1945.01	4.9	1	46.3	19.4	95.00%	R.FIVPTGNFGDILAGYYAK.R		R.FIVPTGNFGDILAGYYAK.R
313	327	2	1443.73	4.4	1	39.8	22.1	95.00%	K.ADSTQVSPSGPISAK.E		K.ADSTQVSPSGPISAK.E
377	387	2	1184.64	2.5	1	27.9	18.9	95.00%	R.DGTVTVRPEVL.E		R.DGTVTVRPEVLEAAR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
116	LEU1_SCHPO	10.96%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
464	479	2	1742.82	4.9	1	69.1	23.3	95.00%	R.FSVNDYTLSSNGPQSK.C		R.FSVNDYTLSSNGPQSK.C
388	398	2	1249.63	1.6	1	53.9	21.7	95.00%	H.DVNSEYAAIIR.V		K.VPYLPLDPHDVNSEYAAIIR.V
341	362	3	2346.15	2.9	1	44.7	21.3	95.00%	R.HPYAGNLVFTAFSGSHQDAISK.G		R.HPYAGNLVFTAFSGSHQDAISK.G
137	151	3	1761.87	4	0	33.2	22.3	95.00%	K.NATVHLYNACSPLFR.E	Carbamidomethyl (+57)	K.NATVHLYNACSPLFR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
117	ACL1_SCHPO	8.46%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

369	381	2	1420.73	4.5	1	44	21.2	95.00%	R.GSELTYNNVPISK.V			R.GSELTYNNVPISK.V
171	182	3	1338.74	4.8	0	23.6	16.2	95.00%	K.LYRPGSVAYVSK.S			K.LYRPGSVAYVSK.S
586	597	3	1316.73	4.9	1	18	18.3	90.10%	R.SIGLIGHHLDQK.R			R.SIGLIGHHLDQK.R
156	170	2	1506.72	3.3	1	45.7	23.6	95.00%	K.IGNTGGMMDNIVASK.L			K.IGNTGGMMDNIVASK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
118	GLT1_SCHPO	1.75%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1690	1707	2	2063.08	4.1	1	61.9	18.1	95.00%	K.EALTQLLLTNNFPEFTGR.V		K.EALTQLLLTNNFPEFTGR.V
1758	1776	2	1792.99	3.3	1	78.8	15.4	95.00%	R.VAIIGSGPAGLAAADQLNR.A		R.VAIIGSGPAGLAAADQLNR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
119	YHZ8_SCHPO	31.31%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
154	164	2	1234.62	1.9	1	36.2	21.9	95.00%	L.DDPSLYAVVTR.Y		K.ADTSLIIHSLDDPSLYAVVTR.Y
75	103	3	3217.69	3	1	57.2	13.8	95.00%	K.TSNPFLAFANYLTSTHAPLAEPLQLLNFK.V		K.TSNPFLAFANYLTSTHAPLAEPLQLLNFK.V
2	13	2	1361.7	3.8	0	57.2	21.5	95.00%	M.SFPASTHVYIAK.I	Acetyl (+42)	-.MSFPASTHVYIAK.I
144	153	2	1068.58	2.4	1	40.3	17.4	95.00%	K.ADTSLIIHSL.D		K.ADTSLIIHSLDDPSLYAVVTR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
120	TAL1_SCHPO	5.59%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
27	44	3	1917.03	4	1	42	18.3	95.00%	K.YKPQDATTNPSLILAASK.K		K.YKPQDATTNPSLILAASK.K
31	44	2	1400.76	3	0	60	18.6	95.00%	Q.DATTNPSLILAASK.K		K.YKPQDATTNPSLILAASK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
121	AATR1_SCHPO	9.07%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
305	317	2	1562.83	3.7	1	52.6	18.7	95.00%	R.VGWFTAQPLFIER.G		R.VGWFTAQPLFIER.G
38	54	2	1856.03	4.5	1	36.8	14.3	95.00%	K.IISLAGGLPNPEYFPIR.E		K.IISLAGGLPNPEYFPIR.E
7	19	3	1436.71	5.4	1	43.2	22.8	95.00%	K.DLSHHLSVESASR.K		K.DLSHHLSVESASR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
122	RL23_SCHPO	25.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
15	34	2	2090	3.5	1	65.5	21.8	95.00%	R.MTLGLPVQAIMNCADNSGAK.N	Carbamidomethyl (+57)	R.MTLGLPVQAIMNCADNSGAK.N
15	28	2	1533.74	2.9	0	53	22.6	95.00%	R.MTLGLPVQAIMNCA.D	Oxidation (+16)/ Carbamidomethyl (+57)	R.MTLGLPVQAIMNCADNSGAK.N
51	65	2	1531.78	3.4	1	55.2	21.1	95.00%	R.LPAASCGDMVLATVK.K	Carbamidomethyl (+57)	R.LPAASCGDMVLATVK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
123	HMCS_SCHPO	9.17%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
155	183	3	2859.53	3.9	1	40.5	14.5	95.00%	K.GNARPTGGAGCVALLVGPNAPIVFEPGLR.G	Carbamidomethyl (+57)	K.GNARPTGGAGCVALLVGPNAPIVFEPGLR.G
217	228	2	1325.64	3.7	1	38.4	23.7	95.00%	K.ALDGAYANYNVR.D		K.ALDGAYANYNVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
124	RS13_SCHPO	15.23%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
44	55	2	1244.66	3.8	0	40.8	20.8	95.00%	K.GMSPSQIGVTLR.D		K.GMSPSQIGVTLR.D
10	20	2	1132.63	4.4	0	38.6	18.7	95.00%	K.GIASSALPYVR.S		K.GIASSALPYVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
125	DAK1_SCHPO	5.86%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
45	66	3	2123.05	5.3	1	21	20.2	95.00%	K.NVSVISGGGAGHEPTHSSFVGK.G		K.NVSVISGGGAGHEPTHSSFVGK.G

388	399	2	1358.73	4.4	1	25.9	20.7	94.00%	R.QAIVNSMENLIK.A		R.QAIVNSMENLIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
126	SYDC_SCHPO	4.14%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
281	294	2	1356.6	4.8	1	27.5	24	95.00%	K.MSGASSEGGSNVFK.I		K.MSGASSEGGSNVFK.I
490	499	2	1300.55	3.9	1	26.9	24.1	95.00%	R.YSNSYDFFMK.G		R.YSNSYDFFMK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
127	RS2_SCHPO	19.37%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
64	74	2	1441.73	5.7	1	25.1	21.5	92.90%	K.EYQIVDYFLPR.L		K.EYQIVDYFLPR.L
174	185	3	1138.69	4.8	1	25.2	11.8	95.00%	R.GAGLVAAPVTKR.F		R.GAGLVAAPVTKR.F
54	63	2	1237.7	2.8	0	34.5	14.6	95.00%	E.EIYLYSLPIK.E		K.SIEEIYLYSLPIK.E
141	156	3	1696.87	4.8	1	37.6	20.8	95.00%	R.GYWGTALGDPHTVPVK.V		R.GYWGTALGDPHTVPVK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
128	SYG_SCHPO	6.90%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
216	232	3	1983	3.5	1	46.6	19.8	95.00%	K.GYLRPETAQGQFLNFSR.L		K.GYLRPETAQGQFLNFSR.L
492	506	2	1649.85	2.7	1	54.5	20.9	95.00%	R.TYTPNVIEPSFGLGR.I		R.TYTPNVIEPSFGLGR.I
526	538	2	1298.77	3.9	0	28.2	14.3	95.00%	R.GVLSFPASIAPIK.A		R.GVLSFPASIAPIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
129	SYLC_SCHPO	2.43%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
843	852	2	1272.56	5	1	24.8	23.7	92.50%	K.SCFYDLQNAR.D	Carbamidomethyl (+57)	K.SCFYDLQNAR.D
382	398	3	1730.98	4.6	1	32.6	13.8	95.00%	K.GQDLIGALVNAPLSVHK.Q		K.GQDLIGALVNAPLSVHK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
130	DYR_SCHPO	11.93%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
164	183	3	2062.15	3.7	1	25.4	10.4	95.00%	K.LTTPSLHIAGTSDTLVPLAR.S		K.LTTPSLHIAGTSDTLVPLAR.S
191	212	3	2537.31	3.6	1	37.3	18.1	95.00%	R.CENAHVLLHPGQHIVPQQAVYK.T	Carbamidomethyl (+57)	R.CENAHVLLHPGQHIVPQQAVYK.T
34	46	2	1399.72	2.3	1	24.2	21.3	91.30%	K.YAELHFPTGPVVA.D		K.YAELHFPTGPVVADEEADPNDEEEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
131	YHEF_SCHPO	14.29%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
90	104	2	1731.88	2.6	0	49.8	20.6	95.00%	N.DTANFTPLTFTTYLK.T		R.LFTIAENDTANFTPLTFTTYLKTCNPQSIENAMIPFVNTVTSEISFDAWAYTAQNSSR.I
30	41	3	1413.76	4.8	1	20.9	18.8	95.00%	R.LRGPHCGTYLLK.V	Carbamidomethyl (+57)	R.LRGPHCGTYLLKVVGTNATYVGEK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
132	Q76N21_SCHPO	13.61%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
13	22	2	1195.61	4.9	0	30.3	22.2	95.00%	R.FVTCQIVSSR.V	Carbamidomethyl (+57)	K.SSPYFSRYQTKYRR.R
26	35	2	1098.51	3.9	0	29.6	23.5	95.00%	G.DYVLAHAHSS.E		R.EGKTDYYARKR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
133	TBB_SCHPO	8.71%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
128	154	3	2645.35	1.9	0	47.2	17.7	95.00%	C.DALQGFQLTHSLGGGTGSGMGTLLLSK.I		R.EAEACDALQGFQLTHSLGGGTGSGMGTLLLSK.I
163	174	2	1249.62	3.9	0	41.3	22	95.00%	R.MMATFSVAPAPK.S		R.MMATFSVAPAPK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
134	SPEE_SCHPO	8.39%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	12	2	1291.72	4.1	1	43.5	17.5	95.00%	M.SVQELSHPLIK.D	Acetyl (+42)	-.MSVQELSHPLIK.D
18	31	2	1631.79	4.6	0	31.2	22.5	95.00%	R.EINNMWPGQAMTLK.V		R.EINNMWPGQAMTLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
135	RL30A_SCHPO	28.44%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
71	89	2	1997.95	6	1	62.5	22	95.00%	K.ANVHHYAGTNIDLGTACGK.L	Carbamidomethyl (+57)	K.ANVHHYAGTNIDLGTACGK.L
47	58	2	1335.77	2.3	0	26.2	13.2	94.40%	K.LILIAGNCPPLR.K	Carbamidomethyl (+57)	K.LILIAGNCPPLR.K
71	81	2	1195.58	3.1	0	31	23.7	95.00%	K.ANVHHYAGTNI.D		K.ANVHHYAGTNIDLGTACGK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
136	SLBR2_SCHPO	5.41%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
134	143	2	1115.56	4.3	1	27.1	22.4	95.00%	R.NIESSVQPSR.E		R.NIESSVQPSR.E
149	157	2	1075.63	4.5	1	33	16.1	95.00%	K.LLDQIYALK.H		K.LLDQIYALK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
137	PDI1_SCHPO	5.28%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	136	3	1350.87	5.1	1	30.4	0	95.00%	R.KQLLPTVKPISK.D		R.KQLLPTVKPISK.D
188	201	2	1436.77	4.3	0	45.1	18.3	95.00%	K.SLGSNFPGIVAFTK.D		K.SLGSNFPGIVAFTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
138	EIF3B_SCHPO	2.62%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
478	487	2	1116.58	4.2	0	31.6	21.6	95.00%	N.DQVLNSTNVK.T		R.FAIISANDQVLNSTNVK.T
29	37	2	989.56	2.2	0	33.7	18.2	95.00%	K.LNVTKPVGY.D		K.LNVTKPVGYDTVVVIEGAPVVEEAK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
139	DLDH_SCHPO	9.20%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
113	128	2	1663.83	1.7	1	25	21.8	92.80%	R.GIDVSGVSVNLSQMMK.A		R.GIDVSGVSVNLSQMMK.A
155	168	2	1448.76	3.8	1	31.8	20.2	95.00%	K.GTGSFIDPQTLSVK.G		K.GTGSFIDPQTLSVK.G
47	63	2	1673.86	2.6	0	43	19.6	95.00%	Y.DLCVIGGGPGGYVAAIR.G	Carbamidomethyl (+57)	K.ASGNGEYDLCVIGGGPGGYVAAIR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
140	ARO1_SCHPO	4.39%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
643	660	2	1749.92	1.8	0	79.2	18.3	95.00%	S.DASSATYPLAIAAITGTK.C		K.YQNPPHYEIESDASSATYPLAIAAITGTK.C
162	172	2	1299.72	4.7	0	45.2	19.1	95.00%	K.NLVGAFWQPLR.V		K.NLVGAFWQPLR.V
680	703	3	2572.27	1.7	1	23.5	20.1	95.00%	C.DVLRPMGCTVEQTATSTTVQGPPK.G	Carbamidomethyl (+57)	R.FACDVLRPMGCTVEQTATSTTVQGPPK.G
1232	1247	2	1833.96	4.6	1	44.8	18.5	95.00%	R.ITNSMDIPLILFNMGR.F		R.ITNSMDIPLILFNMGR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
141	SYRC_SCHPO	6.80%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
163	180	2	1987.02	4.1	1	33.9	18.6	95.00%	R.STIIGSFLANLHESQGWK.V		R.STIIGSFLANLHESQGWK.V
480	489	2	1284.6	5.9	1	39.4	23	95.00%	R.INNYAFDWSR.M		R.INNYAFDWSR.M
11	24	2	1544.86	4.5	1	46.7	15.6	95.00%	K.SLSTLGLQDLPVFR.E		K.SLSTLGLQDLPVFR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
142	RL7C_SCHPO	11.55%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
173	183	2	1113.61	2.9	1	70	19.2	95.00%	S.DNAIIEAALGK.Y		R.IALSDNAIIEAALGK.Y
133	150	2	2092.1	1.8	1	51	17.1	95.00%	K.EMLQVVEPYVTYGIPNLK.T		K.EMLQVVEPYVTYGIPNLK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
143	YCO6_SCHPO	7.89%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
15	36	3	2140.01	5.3	0	26.3	21.7	95.00%	K.MSAAPTPHNTPSGTSAPNFGAK.A		K.MSAAPTPHNTPSGTSAPNFGAK.A
186	194	2	939.47	2.3	1	27.9	21.7	95.00%	E.DEGALSHLV.D		K.NVLSLSEMITPEDEGALSHLVDIR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
144	PUR4_SCHPO	1.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
323	334	2	1146.56	3.5	1	28.9	22.9	95.00%	R.DEGAVGQGSLSK.A		R.DEGAVGQGSLSK.A
412	425	3	1426.76	5.3	0	35.9	20.9	95.00%	R.GYHKPIMAAGGIGR.I		R.GYHKPIMAAGGIGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
145	PABP_SCHPO	5.05%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
258	266	2	1068.57	4.8	0	26.6	19.8	94.80%	K.ANFTNVYIK.N		K.ANFTNVYIK.N
447	456	2	1142.61	4.9	1	33.9	20.4	95.00%	R.SQLEAQIQAR.N		R.SQLEAQIQAR.N
428	441	3	1529.88	2.3	0	46.6	13.2	95.00%	R.MLAGKPLYVALAQR.K		R.MLAGKPLYVALAQR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
146	Q9P7B4_SCHPO	13.13%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
234	256	3	2522.27	2.7	1	34.8	18.7	95.00%	R.ENVVIADTLVFPSHQGGANHVYR.K		R.ENVVIADTLVFPSHQGGANHVYR.K
163	173	2	1163.64	5.6	0	26.5	18.9	94.70%	K.SALAQFTSALR.K		K.SALAQFTSALR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
147	ACL2_SCHPO	9.55%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
326	334	2	985.56	4.7	1	36	19.5	95.00%	K.LTILNAEGR.V		K.LTILNAEGR.V
382	389	2	947.52	4.5	1	26.9	20.9	95.00%	K.TVLDLMTR.G		K.TVLDLMTR.G
32	61	3	3211.76	3.3	1	47.1	14.5	95.00%	K.TVSATPAVQLAQIQFPLPTLVIPAESTTYR.E		K.TVSATPAVQLAQIQFPLPTLVIPAESTTYR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
148	RL2_SCHPO	8.70%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
128	138	2	1144.59	3.7	0	34.5	22.4	95.00%	R.SSGNYVIIVGH.D		R.SSGNYVIIVGHDVDTGK.T
163	173	2	940.55	4.3	0	54.6	13.2	95.00%	R.GVVGIVAGGGR.I		R.GVVGIVAGGGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
149	RS21_SCHPO	25.29%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
76	87	2	1421.7	3.1	1	52.6	23.2	95.00%	Q.DGLLEGVWSYQR.-		R.LTTQDGLLEGVWSYQR.-
51	60	2	1113.59	4.5	0	33.8	20.8	95.00%	K.TTYAISGFVR.S		K.TTYAISGFVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
150	ACAC_SCHPO	1.80%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
443	453	2	1404.64	2.8	1	32.7	23.3	95.00%	I.DFFFQNPESFK.V		R.DGDSEIDFFFQNPESFK.V
1787	1805	2	1932.11	1.7	1	65.2	9.54	95.00%	R.AVQIEGQPIILTGAPALNK.V		R.AVQIEGQPIILTGAPALNK.V
197	207	2	1131.63	6.1	0	34.7	17.5	95.00%	K.ISSTIVAQSAR.V		K.ISSTIVAQSAR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
151	ADK_SCHPO	8.24%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
253	267	2	1483.87	4.5	1	69.4	13.8	95.00%	R.VVVITQGADATIVAK.D		R.VVVITQGADATIVAK.D
126	138	2	1424.68	5.2	0	51	22.3	95.00%	R.SLCTNLGAANNYK.L	Carbamidomethyl (+57)	R.SLCTNLGAANNYK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
152	APE1_SCHPO	2.61%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	149	2	1467.71	4.6	1	42.2	22.8	95.00%	K.YLATTQMEPTSAR.R		K.YLATTQMEPTSAR.R
498	507	2	1204.65	2.9	0	25.3	19.6	93.20%	E.DTVIYWAPLK.L		R.FLSTGDVKPEEDTVIYWAPLK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
153	MPG1_SCHPO	8.82%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
336	349	3	1541.78	2.8	1	18.3	21.6	90.90%	N.DEIYVNGGSILPHK.S	Deamidation (+1)	R.LENVSVLGDDVVVNDEIYVNGGSILPHK.S
270	287	2	1776	4.2	1	35.2	14.1	95.00%	K.IGPNVVIGPNVTIGDGVR.L		K.IGPNVVIGPNVTIGDGVR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
154	RL31_SCHPO	21.24%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
91	105	2	1650.87	4.2	1	39.3	18.9	95.00%	K.ALYTYVQAVDVANPK.M		K.ALYTYVQAVDVANPK.M
7	15	2	986.56	5	0	39.5	20.5	95.00%	K.SAINQVVTR.D		K.SAINQVVTR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
155	RLA0_SCHPO	10.26%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
133	144	2	1308.71	5.2	0	29.1	16.9	95.00%	K.TSFFQALGIPTK.I		K.TSFFQALGIPTK.I
98	117	2	2014.16	2.9	0	31.3	9.54	95.00%	R.ETIIANVIAAPARPNAIAPL.D		R.ETIIANVIAAPARPNAIAPLDVFVPAGNTGMEPGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
156	ATPB_SCHPO	5.71%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
124	140	2	1622.87	3	0	25.9	17.2	94.00%	I.DTGSPISIPVGPGTLGR.I		R.GTAVIDTGSPISIPVGPGTLGR.I
210	222	2	1501.86	4.8	1	34.9	14.9	95.00%	K.TVFIQELINNIAK.A		K.TVFIQELINNIAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
157	LYS4_SCHPO	4.30%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
149	159	2	1179.57	4.4	1	26	23.1	94.10%	K.GQGIDFYPAGR.G		K.GQGIDFYPAGR.G
470	489	2	1872.04	4.8	0	47.2	14.6	95.00%	R.EALAYLASPAVVAASAIAGK.I		R.EALAYLASPAVVAASAIAGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
158	KAPS_SCHPO	13.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	14	2	1413.73	4.2	0	23.6	20.3	90.20%	M.ATNITFHPGSVTK.E	Acetyl (+42)	-.MATNITFHPGSVTK.E
39	52	2	1664.86	3.8	1	65.6	20.5	95.00%	K.STIACALEQYLLQR.G	Carbamidomethyl (+57)	K.STIACALEQYLLQR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
159	RL24A_SCHPO	12.75%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
81	91	2	1097.65	4.7	1	29.4	15.7	95.00%	R.GIVGANLDVIK.E		R.GIVGANLDVIK.E
36	43	2	978.52	4.9	1	29.5	21.8	95.00%	K.SESLFLQR.K		K.SESLFLQR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
160	CH10_SCHPO	22.12%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	84	2	1230.7	4	0	31.7	17.3	95.00%	R.VLLPAYGGSNIK.V		R.VLLPAYGGSNIK.V
62	72	2	1111.6	4.5	1	30.9	17.7	95.00%	K.LAQPSVAVGDR.V		K.LAQPSVAVGDR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
161	ACON2_SCHPO	3.98%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
485	503	2	1961	4.1	0	59.6	20.3	95.00%	N.DGNPSTMNFLTSPVIVAAK.I		R.NDGNPSTMNFLTSPVIVAAK.I
528	544	2	1741.92	2.9	1	26.3	18.9	94.40%	K.FRPPQGVELPSAGFIAG.D		K.FRPPQGVELPSAGFIAGDSSYIPE PNPQPVPETEVTIDPK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
162	BUT2_SCHPO	6.92%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
338	349	2	1493.65	4.2	1	37.5	23.5	95.00%	R.GCEYTQNIPCPR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GCEYTQNIPCPR.A
200	214	2	1679.86	3.1	1	78.4	20.6	95.00%	R.YYGNTEALSSLPLPR.N		R.YYGNTEALSSLPLPR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
163	CYSK1_SCHPO	9.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
10	23	2	1341.78	3.9	0	59.1	14.1	95.00%	K.VPGIVSGFIGAIGR.T		K.VPGIVSGFIGAIGR.T
180	200	2	2019.93	5.1	1	71.4	23.7	95.00%	K.GTVDGFTCSTGTGGTFAGVTK.Y	Carbamidomethyl (+57)	K.GTVDGFTCSTGTGGTFAGVTK.Y

Supplementary Table S2: All "Scaffold" validated proteins and peptides identified from solprotSP (*S.pombe*) and from SCVMprot (*S.cerevisiae*) samples

S.pombe **- Asp-N digest of large tryptic peptides (replicate B)**

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
1	ENO11_SCHPO	45.56%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
361	374	3	1608.73	4.7	1	47.1	24	95.00%	R.MSYEAGWGVMVSHR.S		R.MSYEAGWGVMVSHR.S
185	194	2	1204.59	5.4	1	34	22.9	95.00%	R.WGAETYHTLK.S		R.WGAETYHTLK.S
346	360	2	1586.83	4	1	90.8	20.1	95.00%	K.VNQIGSVTESLNAVR.M	Deamidation (+1)	K.VNQIGSVTESLNAVR.M
302	310	2	1160.51	3	0	27.2	24.2	95.00%	D.DWSAWTHMK.A		K.YPIVSIEDPFDQDDWSAWTHMK.A
364	374	2	1227.58	1.9	0	37	23.7	95.00%	Y.EAGWGVMVSHR.S		R.MSYEAGWGVMVSHR.S
65	79	2	1477.87	4	0	73.7	9.03	95.00%	K.AVGNVNNIIAPAVVK.A		K.AVGNVNNIIAPAVVK.A
106	120	2	1560.82	4.2	0	61.3	19.3	95.00%	K.LGANAILGVSMAICR.A	Oxidation (+16)/ Carbamidomethyl (+57)	K.LGANAILGVSMAICR.A
33	47	2	1470.78	3.7	1	45.9	19	95.00%	R.AIVPSGASTGIWEAL.E		R.AIVPSGASTGIWEALEMR.D
23	32	2	1141.58	2.9	1	44.8	21.2	95.00%	V.DLTTETGIHR.A		R.GNPTVEVDLTTETGIHR.A
380	396	2	1755.96	2.4	0	57.7	15.9	95.00%	A.DTFISHLTVGIGAGQLK.S		R.SGETADTFISHLTVGIGAGQLK.S
168	180	2	1395.68	2.6	0	36.4	23.4	95.00%	Q.EFMILPTGAPSFS.E		K.GPYVLPVPSFNVLNGGSHAGGDLAFQEFMILPTGAPSFSEAMR.W
301	310	3	1275.54	3.3	1	38.7	24.8	95.00%	Q.DDWSAWTHMK.A		K.YPIVSIEDPFDQDDWSAWTHMK.A
142	162	2	2039.02	2	0	64	21	95.00%	K.GPYVLPVPSFNVLNGGSHAGG.D	Deamidation (+1)	K.GPYVLPVPSFNVLNGGSHAGGDLAFQEFMILPTGAPSFSEAMR.W
338	345	2	901.51	4.7	0	31.4	20.4	95.00%	K.CANALLLK.V	Carbamidomethyl (+57)	K.CANALLLK.V
409	414	2	806.43	5.7	1	29.4	22.3	95.00%	K.YNELLR.I		K.YNELLR.I
217	225	2	1013.51	2.5	1	32.8	21.5	95.00%	P.DLQTPQEAL.D		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
168	184	2	1898.89	1.9	1	51.1	22.9	95.00%	Q.EFMILPTGAPSFSEAMR.W	Oxidation (+16)	K.GPYVLPVPSFNVLNGGSHAGGDLAFQEFMILPTGAPSFSEAMR.W
226	234	2	1013.58	2.3	1	40.8	19	95.00%	L.DLIVEAINK.A		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
320	328	2	1003.52	3.1	1	48.6	22.6	95.00%	G.DDLTVTNVK.R		K.AETDFQIVGDDLTVTNVK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
2	G3P1_SCHPO	36.61%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	126	2	813.5	1.9	0	26.6	16.7	94.80%	R.VIISAPSK.D		R.VIISAPSK.D
39	48	2	1309.58	2.5	1	38.5	23.7	95.00%	I.DLEYMAYMFK.Y		K.TIQVVAINDPFIDLEYMAYMFK.Y
228	234	2	794.41	4.9	0	23.6	20.8	90.00%	K.LTGMAFR.V		K.LTGMAFR.V
118	126	2	969.6	2.8	1	30.7	12.6	95.00%	K.RVIISAPSK.D		K.RVIISAPSK.D
296	309	2	1459.77	1.6	0	67.9	20	95.00%	F.DASAGIQLSPQFVK.L		K.GVLGYTEDAVVSTDFCGDNHSSIFDASAGIQLSPQFVK.L
249	256	2	934.48	3.2	1	26.8	22.7	95.00%	K.LAKPTNYE.D		K.LAKPTNYEDIK.A
146	162	2	1818.91	4.5	0	75	21.9	95.00%	K.VISNASCTTNCLAPLAK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.VISNASCTTNCLAPLAK.V
324	334	2	1148.65	6.2	1	55.4	16.7	95.00%	R.VVDLVAYTAAK.D		R.VVDLVAYTAAK.D
84	92	2	963.47	1.8	1	52.8	22.9	95.00%	A.DIKWSTSGA.D		R.DPADIKWSTSGADYVIESTGVFTTQETASAHLK.G
172	186	2	1587.8	2.6	0	79.6	21.3	95.00%	E.EGLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK.T
6	13	2	819.43	6.2	0	38.4	21.6	95.00%	K.VGINGFGR.I	Deamidation (+1)	K.VGINGFGR.I
201	215	2	1343.71	4.7	0	69.9	20	95.00%	R.GASANIIPSSTGAAK.A		R.GASANIIPSSTGAAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
3	PGK_SCHPO	33.82%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	169	2	873.41	4	0	24.2	22.5	91.20%	N.DAFGTAHR.A		K.SLTSLGDIFVNDAFGTAHR.A
57	71	2	1591.87	2.9	0	46.2	17.9	95.00%	K.AVILMSHLGRPNGAR.V	Deamidation (+1)	K.AVILMSHLGRPNGAR.V
40	48	2	910.59	3.6	0	25.3	6.02	93.10%	R.IVGALPTIK.Y		R.IVGALPTIK.Y
384	400	2	1625.83	2.3	1	51.5	20.7	95.00%	E.DALSHVSTGGGASLELL.E		K.EDALSHVSTGGGASLELLEGK.A
276	286	2	1235.65	3.5	1	27.7	21.1	95.00%	V.EVFLPVDFVTA.D		K.NNVEVFLPVDFVTADK.F
383	397	2	1399.66	2.8	1	67.1	24	95.00%	K.EDALSHVSTGGGASL.E		K.EDALSHVSTGGGASLELLEGK.A
384	397	2	1270.62	2.5	0	70	22.7	95.00%	E.DALSHVSTGGGASL.E		K.EDALSHVSTGGGASLELLEGK.A
359	371	2	1231.59	3.3	1	27.4	22.5	95.00%	K.TCEAGNVVIVGGG.D	Carbamidomethyl (+57)	K.TCEAGNVVIVGGGDTATVAK.K
404	414	2	1040.63	5.6	0	39.4	15.9	95.00%	K.ALPGVVALSSK.-		K.ALPGVVALSSK.-
321	329	2	994.54	5.5	1	50.2	20.3	95.00%	K.FAEVITTSK.T		K.FAEVITTSK.T
75	86	3	1304.74	4.3	1	59.4	14.8	95.00%	K.YSLKPVAAELSK.L		K.YSLKPVAAELSK.L
197	213	2	1737	3	1	56.5	11.8	95.00%	K.ALENPARPFLAILGGAK.V		K.ALENPARPFLAILGGAK.V
170	181	2	1267.64	4	1	58.7	22.2	95.00%	R.AHSSMVGVDLPR.V		R.AHSSMVGVDLPR.V
157	169	2	1461.7	2	1	44.4	23.5	95.00%	G.DIFVNDAFGTAHR.A		K.SLTSLGDIFVNDAFGTAHR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
4	METE_SCHPO	40.97%	100%	28

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
561	571	2	1184.7	5.1	0	40.5	15.3	95.00%	K.GMLTAPITILR.W		K.GMLTAPITILR.W
434	449	2	1746.96	2.6	0	68.8	14	95.00%	K.LPLFPTTTIGSFPQTK.E		K.LPLFPTTTIGSFPQTK.E
671	679	2	989.51	2.1	1	31.7	23	95.00%	A.DVVSIENSK.S		R.LDADVVSIENSK.S
4	11	2	845.48	4.8	0	33.3	20.6	95.00%	K.SAVLGFPR.I		K.SAVLGFPR.I
325	343	2	1947.01	2	1	60	19.5	95.00%	R.VQVASSSSILHIPHSLSGE.D		R.VQVASSSSILHIPHSLSGEDQINPEIK.R
71	82	2	1414.7	1.9	0	42.7	22.1	95.00%	M.DHSFSFNVIPPR.Y		K.AQGVDIIPSNDFSLYDQIMDHSFSFNVIPPR.Y
707	714	2	901.49	4.3	1	27.7	23.1	95.00%	R.VPPVSEFK.E		R.VPPVSEFK.E
684	690	2	813.51	5.6	0	34.2	16.9	95.00%	K.LLNVLSR.Y		K.LLNVLSR.Y
691	706	2	1818.88	3.8	1	84	21.9	95.00%	R.YTSCIGPGLFDIHSPR.V	Carbamidomethyl (+57)	R.YTSCIGPGLFDIHSPR.V
344	351	2	955.5	2.9	1	24.1	20.5	91.20%	E.DQINPEIK.R		R.VQVASSSSILHIPHSLSGEDQINPEIK.R
243	260	2	1982.08	3.5	1	54.1	14.3	95.00%	K.LILTTYFGSLQSNADVLK.G		K.LILTTYFGSLQSNADVLK.G
261	269	2	861.51	2.2	0	36.1	14.6	95.00%	K.GLPIAGVHV.D		K.GLPIAGVHVDVVR.A
727	738	2	1466.7	4.2	1	48	23	95.00%	K.DHLWLNPDCGLK.T	Carbamidomethyl (+57)	K.DHLWLNPDCGLK.T
428	449	3	2402.33	2.3	1	54.3	12.6	95.00%	K.QQASLKLPLFPTTTIGSFPQTK.E		K.QQASLKLPLFPTTTIGSFPQTK.E
261	273	2	1330.78	2.5	1	57.8	12.6	95.00%	K.GLPIAGVHVDVVR.A		K.GLPIAGVHVDVVR.A
500	508	2	1159.5	2.9	1	41.5	24	95.00%	N.DMVQYFGER.M	Oxidation (+16)	R.NDMVQYFGER.M
645	656	2	1508.6	2.6	1	27.2	22.9	95.00%	Q.DDTQIHSHFCYS.D	Carbamidomethyl (+57)	R.LATAAVQDDTQIHSHFCYSDFNDIFDAIQR.L
281	299	2	1881.08	4.8	1	87.4	8.45	95.00%	R.ALAVLGENQIISVGVVSGR.N		R.ALAVLGENQIISVGVVSGR.N
92	99	2	959.42	3.4	0	32.8	23.2	95.00%	L.DTYFAMGR.G		R.LSGLSSLDTYFAMGR.G
361	369	2	1017.56	4.9	1	30.5	20.9	95.00%	K.CAELAILTK.A	Carbamidomethyl (+57)	K.CAELAILTK.A
547	560	2	1596.79	3.6	0	50.8	22.2	95.00%	K.ESQYAQSITSKPMK.G		K.ESQYAQSITSKPMK.G
536	546	2	1275.67	1.6	0	33.8	20.7	95.00%	G.DVYRPAPMTVK.E		R.CVRPPIIVGDVYRPAPMTVK.E
527	546	3	2267.24	3.3	1	44.5	14.3	95.00%	R.CVRPPIIVGDVYRPAPMTVK.E	Carbamidomethyl (+57)	R.CVRPPIIVGDVYRPAPMTVK.E
631	637	2	877.45	5.9	1	49	22.6	95.00%	K.WAIDAFR.L		K.WAIDAFR.L
85	99	2	1616.79	4.1	1	63.5	22.5	95.00%	R.LSGLSSLDTYFAMGR.G		R.LSGLSSLDTYFAMGR.G
221	231	2	1275.68	3	1	34.3	20.8	95.00%	L.DLPQEILASYK.E		K.LTEAGAEYIQIDEPILTLDLPQEILASYK.E
581	593	2	1397.77	2	0	67.6	17.5	95.00%	H.DSVQAQQIALGLR.D		R.DDVHDSVQAQQIALGLR.D
156	176	3	2256.33	3.9	0	51.3	6.02	95.00%	K.EAGIITRPVLVGPVTYLFIAK.A		K.EAGIITRPVLVGPVTYLFIAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
5	EF1A1_SCHPO	40.43%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
402	414	2	1495.69	2.7	1	24.1	23.2	91.10%	K.MVPSKPMCVEAFT.D	Carbamidomethyl (+57)	K.MVPSKPMCVEAFTDYAPLGR.F
197	214	2	2253.99	2.2	1	74.9	23.4	95.00%	G.DNMIEPTTNMPWYQGWQK.E	Oxidation (+16)	K.TVPFVPVSGFQGDNMIEPTTNMPWYQGWQK.E
360	369	2	1211.52	3.3	0	28.9	24.5	95.00%	L.DCHTAHIACK.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.NDPPMGCASFTAQVIILNHPGQISAGYSPVLDCHTAHIACK.F
147	154	2	883.55	5.8	0	26.4	15.7	94.50%	K.QLIVAVNK.M		K.QLIVAVNK.M
254	264	2	1024.61	4.2	0	65.4	14	95.00%	K.IGGIGTVPVGR.V		K.IGGIGTVPVGR.V
6	20	2	1529.84	4.6	1	62.9	17.6	95.00%	K.GHINVVVIGHVDSGK.S		K.GHINVVVIGHVDSGK.S
304	311	2	891.45	2.7	0	33.6	22.5	95.00%	G.DNVGFNVK.N		K.SVEMHHESLDAGLPGDNVGFNVK.N
155	164	2	1151.51	6.4	1	75.8	23.4	95.00%	K.MDTTGWSQAR.F		K.MDTTGWSQAR.F
241	249	2	1078.65	2.7	1	32.8	11.5	95.00%	T.DKPLRLPLQ.D		K.TLLEAIDSIEPPARPTDKPLRLPLQDVYK.I
298	311	2	1401.69	1.5	1	31.8	22.5	95.00%	L.DAGLPGDNVGFNVK.N		K.SVEMHHESLDAGLPGDNVGFNVK.N
85	96	2	1340.69	4.4	1	66.1	20.6	95.00%	K.YNVTVIDAPGHR.D		K.YNVTVIDAPGHR.D
246	253	2	974.55	4.1	1	32.1	20.3	95.00%	R.LPLQDVYK.I		R.LPLQDVYK.I
265	285	2	2087.14	2.6	1	49.3	14.6	95.00%	R.VETGVIKPGMIVTFAPAGVTT.E		R.VETGVIKPGMIVTFAPAGVTTEVK.S
135	146	2	1313.74	3	0	53.9	17.8	95.00%	R.EHALLAYTLGVK.Q		R.EHALLAYTLGVK.Q
185	196	2	1233.64	2.4	0	27.8	22	95.00%	K.TVPFVPVSGFQG.D		K.TVPFVPVSGFQGDNMIEPTTNMPWYQGWQK.E
56	62	2	893.47	4.6	1	24.5	22.3	91.90%	K.YAWVLDK.L		K.YAWVLDK.L
231	240	2	1081.54	2.8	1	39	22.8	95.00%	I.DSIEPPARPT.D		K.TLLEAIDSIEPPARPTDKPLR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
6	ALF_SCHPO	56.70%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
351	358	2	971.46	3.1	0	26.5	21.5	94.70%	E.DFYTVNTL.-		R.VLTALEDFYTVNTL.-
256	272	2	1779.86	1.9	0	61.9	22	95.00%	N.DKPVFFVFHGGSGSSVN.E		K.TTNDKPVFFVFHGGSGSSVNEFR.T
26	50	2	2496.31	4.1	1	69.4	15.4	95.00%	R.EHGFAIPAINVTSSSTAIAALEAAR.E		R.EHGFAIPAINVTSSSTAIAALEAAR.E
207	234	4	2951.53	3.2	0	31.9	16.8	95.00%	R.ELSSVTPYFSIAAAFGNVHGVYKPGNVK.L		R.ELSSVTPYFSIAAAFGNVHGVYKPGNVK.L
290	300	2	1283.62	2.8	1	68.6	22.3	95.00%	T.DTQFAYVEGVR.D		K.VNIDTDTQFAYVEGVR.D
131	142	2	1366.67	2.8	1	38.2	22.8	95.00%	K.IHGEPLFSSHML.D		K.IHGEPLFSSHMLDLSEEPK.K
113	118	2	786.45	2.4	1	27.2	21.7	95.00%	K.KLLPWM.D		K.KLLPWMDGMFEADEAYFK.I
94	112	2	2098.02	4.1	1	63.5	21.8	95.00%	R.SIAPFFGVPVVMHSDHCAK.K	Carbamidomethyl (+57)	R.SIAPFFGVPVVMHSDHCAK.K
26	46	2	2069.09	2.9	0	48.1	18.3	95.00%	R.EHGFAIPAINVTSSSTAIAAL.E		R.EHGFAIPAINVTSSSTAIAALEAAR.E
5	19	2	1539.86	2.9	1	50.8	16.3	95.00%	L.DIVPTGVITGDNVLK.L		-.MGILDIVPTGVITGDNVLK.L
94	107	2	1486.77	2.8	0	53.2	20	95.00%	R.SIAPFFGVPVVMHS.D		R.SIAPFFGVPVVMHSDHCAK.K
308	320	2	1378.61	2.6	1	47.8	24.2	95.00%	K.DYLMTPVGNPEGA.D	Oxidation (+16)	K.DYLMTPVGNPEGADKPNK.K
256	275	3	2212.07	1.5	1	32.8	21.5	95.00%	N.DKPVFFVFHGGSGSSVNEFR.T		K.TTNDKPVFFVFHGGSGSSVNEFR.T
235	248	2	1564.88	2.6	0	63.9	15.1	95.00%	K.LQPALLGQHQAYVK.E		K.LQPALLGQHQAYVK.E
54	71	2	1843.96	2.8	0	95.4	18.7	95.00%	R.SPIILQTSNGGAHFFAGK.E		R.SPIILQTSNGGAHFFAGK.E
80	93	2	1399.76	5.1	0	89.1	17.4	95.00%	K.ASIAGSIAAAHYIR.S		K.ASIAGSIAAAHYIR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
7	KPYK_SCHPO	32.42%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
487	497	2	1053.66	5.9	0	39.5	11.1	95.00%	K.IIVLQGAVGGK.G		K.IIVLQGAVGGK.G

215	223	2	1098.56	4.9	0	36.7	20.8	95.00%	V.DMIFASFIR.R		K.NGVDMIFASFIR.R
77	90	2	1397.8	2.5	0	29.6	14.9	95.00%	K.ASATNPLFPLAIAL.D		K.ASATNPLFPLAIALDTK.G
422	433	3	1430.81	4.6	0	41.1	14.9	95.00%	K.YRPSIPIVMVTR.C		K.YRPSIPIVMVTR.C
334	344	2	1192.6	2.9	1	57.4	22.9	95.00%	A.DLVMLSGETTK.G		R.AEVSDVGNAVLDGADLVMLSGETTK.G
265	271	2	760.39	2.1	0	26.4	24.8	94.50%	T.DGIMVAR.G		K.IENQQGVNNFDSILDVTDGIMVAR.G
77	93	2	1741.97	3.8	1	39.2	15.4	95.00%	K.ASATNPLFPLAIALDTK.G		K.ASATNPLFPLAIALDTK.G
57	71	2	1797.78	2.7	1	37.7	24.1	95.00%	R.MNFSHGSYEYHQSVI.D		R.MNFSHGSYEYHQSVIDNAR.K
28	37	2	1088.6	5	0	46.3	19.4	95.00%	R.TSIICTIGPK.S	Carbamidomethyl (+57)	R.TSIICTIGPK.S
468	477	2	1186.55	5.3	0	54.8	23	95.00%	R.VAYGCQQAYK.M	Carbamidomethyl (+57)	R.VAYGCQQAYK.M
294	319	4	2965.41	2.6	1	60.2	20.5	95.00%	K.CNIAGKPVACATQMLESMTYNPRPTR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CNIAGKPVACATQMLESMTYNPRPTR.A
294	308	2	1632.78	2.7	0	68.9	22.6	95.00%	K.CNIAGKPVACATQML.E	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CNIAGKPVACATQMLESMTYNPRPTR.A
405	417	2	1287.72	5.7	0	62	17.6	95.00%	K.AIVVLSTSGNTAR.L		K.AIVVLSTSGNTAR.L
248	257	2	1161.54	2.7	1	28.9	23.6	95.00%	K.IENQQGVNNF.D		K.IENQQGVNNFDSILDVTDGIMVAR.G
212	223	2	1368.69	4.2	1	39.8	21.8	95.00%	K.NGVDMIFASFIR.R		K.NGVDMIFASFIR.R
76	90	2	1525.89	2	1	50.2	14.1	95.00%	R.KASATNPLFPLAIAL.D		R.KASATNPLFPLAIALDTK.G
47	56	3	1143.62	4.2	1	26	21.5	95.00%	K.LRDAGMNIVR.M		K.LRDAGMNIVR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
8	PDC2_SCHPO	29.29%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
238	253	2	1689.86	2.3	1	71.9	20.2	95.00%	K.LAEALNCAAFIMPAAK.G	Carbamidomethyl (+57)	K.LAEALNCAAFIMPAAK.G
228	237	2	949.49	5	1	30.2	22.7	95.00%	R.AAGAESAFVK.L		R.AAGAESAFVK.L
304	328	2	2694.37	2.3	1	69.6	18.3	95.00%	R.AAPNPNILLNSDYTSVSIPGYVFSR.V		R.AAPNPNILLNSDYTSVSIPGYVFSR.V
215	225	3	1192.76	4.9	1	19	7.78	92.00%	K.KEKPILLAGPK.L		K.KEKPILLAGPK.L
446	461	2	1808.88	2.3	1	79.6	22.2	95.00%	G.DGSFQLTGQEISQMIR.H		R.TIVMVGDGSFQLTGQEISQMIR.H
96	110	2	1552.81	2.6	0	58.2	19.7	95.00%	A.ENLPVILVSGSPNTN.D		R.SNGIACAVVTYSVGALTAFDGIGGAYAENLPVILVSGSPNTNDLSSGHLLHHTLGTHDFEYQMEIAK.K
315	328	2	1589.78	2.2	0	55.5	22.4	95.00%	S.DYTSVSIPGYVFSR.V		R.AAPNPNILLNSDYTSVSIPGYVFSR.V
137	146	2	1101.64	5.4	1	51.2	17.3	95.00%	K.LTCAAVAIKR.A	Carbamidomethyl (+57)	K.LTCAAVAIKR.A
19	25	2	770.49	4.3	1	34.4	15.4	95.00%	R.LVEIGIK.N		R.LVEIGIK.N
462	474	3	1575.97	4.8	1	29.2	3.01	95.00%	R.HKLPVLIFLLNNR.G		R.HKLPVLIFLLNNR.G
26	37	2	1429.72	4.2	1	38.3	21.6	95.00%	K.NHFVVPGDYNLR.L		K.NHFVVPGDYNLR.L
304	314	2	1122.61	2.7	0	30.5	18.9	95.00%	R.AAPNPNILLNS.D		R.AAPNPNILLNSDYTSVSIPGYVFSR.V
464	474	2	1310.81	4.6	0	66.2	6.02	95.00%	K.LPVLIFLLNNR.G		K.LPVLIFLLNNR.G
136	145	2	1073.63	3.9	1	39.6	14	95.00%	K.KLTCAAVAIK.R	Carbamidomethyl (+57)	K.KLTCAAVAIK.R
56	68	2	1470.66	2.1	1	76.3	23.3	95.00%	N.ELNCAFAAEGYAR.S	Carbamidomethyl (+57)	R.LLDFLEYYPGLSEIGCCNELNCAFAAEGYAR.S
4	18	2	1657.77	2.6	1	70.4	23.8	95.00%	K.DAESTMTVGTYLAQR.L	Oxidation (+16)	K.DAESTMTVGTYLAQR.L
396	405	2	1225.55	4.2	0	44.1	24.5	95.00%	G.DSWFNGLQMK.L	Deamidation (+1)	R.QIQGLVDSNTTLYAETGDSWFNGLQMK.L
216	225	3	1064.66	3.8	0	29.3	12	95.00%	K.EKPILLAGPK.L		K.EKPILLAGPK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
9	ADH4_SCHPO	39.81%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
237	255	2	1942.97	2.2	1	54	20.8	95.00%	M.DALTHAVEAYVSTAANPIT.D		K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
375	385	3	1245.76	3.9	1	37.6	3.01	95.00%	K.IRPHLVDLGVK.E		K.IRPHLVDLGVK.E

219	236	2	1882.84	2.4	1	65.2	23.2	95.00%	N.DPETMYGLPPSLTAATGM.D	Oxidation (+16)/ Oxidation (+16)	K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
208	218	2	1269.64	2	1	40	21.4	95.00%	I.DKHTMPILSVN.D	Oxidation (+16)	K.MAIIDKHTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
399	411	2	1380.61	2.5	0	54.2	23.7	95.00%	K.DACGATNPIQPTH.D	Carbamidomethyl (+57)	K.DACGATNPIQPTHDEVK.A
76	87	2	1282.76	5.2	1	44.2	12.8	95.00%	K.NTLIVTDPGIIK.V		K.NTLIVTDPGIIK.V
366	374	2	1027.63	6.6	1	37.3	15.2	95.00%	R.ISQLVLEVK.I		R.ISQLVLEVK.I
149	159	2	1014.58	4.8	0	36.7	19.8	95.00%	K.GIALLATNGGK.I	Deamidation (+1)	K.GIALLATNGGK.I
109	128	2	2077.09	2.3	1	61.8	17.6	95.00%	Y.DGVQPNPTVGNVNQGLEIVK.K		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K
100	108	2	1088.55	2.6	0	24	22.6	90.90%	E.EQSITVHLY.D		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K
109	124	2	1607.79	2.2	0	61.6	22.1	95.00%	Y.DGVQPNPTVGNVNQGL.E		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K
169	191	2	2386.26	3.6	1	87.6	17.2	95.00%	K.SSKPQLPLIAINTTAGTASEMTR.F		K.SSKPQLPLIAINTTAGTASEMTR.F
133	144	2	1116.49	3.4	0	59.9	24.3	95.00%	C.DSMVSIGGGSAH.D		K.ENCDSMVSIGGGSAHDCAK.G
244	255	2	1235.6	1	0	45.4	22.3	95.00%	V.EAYVSTAANPIT.D		K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
169	187	2	1869.03	3	0	46.4	14.8	95.00%	K.SSKPQLPLIAINTTAGTAS.E		K.SSKPQLPLIAINTTAGTASEMTR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
10	PMGY_SCHPO	40.28%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
23	30	2	977.54	2.3	0	32.5	20.8	95.00%	K.LNLFTGWK.D		K.LNLFTGWK.D
111	120	2	1271.65	5.7	1	79.8	21.7	95.00%	K.WGAEQVQIWR.R		K.WGAEQVQIWR.R
2	14	2	1439.81	5.3	1	52	15.8	95.00%	M.TTEAAPNLLVLTR.H	Acetyl (+42)	-.MTTEAAPNLLVLTR.H
158	168	2	1149.67	4.5	0	26.5	13.8	94.70%	K.VLIAAHGNSLR.A		K.VLIAAHGNSLR.A
95	104	2	1169.58	4.8	1	46.4	21.9	95.00%	R.YYGDLQGLNK.D		R.YYGDLQGLNK.D
31	40	2	1029.54	2.3	1	39.7	22	95.00%	K.DPALSETGIK.E		K.DPALSETGIK.E
57	66	2	1120.59	3.1	0	59.2	20.1	95.00%	F.DIAFTSALQR.A		K.FDIAFTSALQR.A
1	14	2	1528.83	2.9	1	57.2	17.2	95.00%	-.MTTEAAPNLLVLTR.H		-.MTTEAAPNLLVLTR.H
186	197	2	1310.73	3.4	0	37.9	17.8	95.00%	R.ELATGVPIVYHL.D		R.ELATGVPIVYHLDK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
11	THI2_SCHPO	21.95%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	15	2	1400.77	3.8	0	74.5	18.3	95.00%	M.APATAVVTPQTAFK.T		-.MAPATAVVTPQTAFK.T
233	242	2	1096.5	2.5	0	39.5	23.6	95.00%	H.DGPFGAFCVK.R	Carbamidomethyl (+57)	R.IAGVVTNWTLVSLNHGLQSCMDPNTINAHLVVSATGHDGPFGAFCVK.R
46	55	2	1167.56	2.9	1	56.5	23.4	95.00%	L.DESFSFAPIR.E		K.AYPTYSLDESFSFAPIR.E
155	166	3	1303.67	3.3	0	22.7	20.9	95.00%	K.HAALFTSTVMAR.T		K.HAALFTSTVMAR.T
295	308	2	1459.67	3.1	0	90.2	23.5	95.00%	R.MGPTFGGMMFSGIK.A		R.MGPTFGGMMFSGIK.A
243	254	2	1307.73	2.7	1	32.9	14.6	95.00%	K.RLASAQLVSNLH.D		K.RLASAQLVSNLHDMRPLDMNR.A
244	254	2	1151.63	2.4	0	75.9	17.5	95.00%	R.LASAQLVSNLH.D		R.LASAQLVSNLHDMRPLDMNR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
12	GLYD_SCHPO	39.61%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
146	159	2	1649.78	3.9	1	75	23.1	95.00%	K.ISAVSTYFESMPYR.V		K.ISAVSTYFESMPYR.V
183	193	2	1209.62	4.5	0	57.8	21.2	95.00%	K.ILVAGTSAYCR.L	Carbamidomethyl (+57)	K.ILVAGTSAYCR.L
306	318	2	1551.8	2	1	28.2	21.1	95.00%	Q.EPAYKEYQAQVVK.N		K.QCQEPAYKEYQAQVVK.N
361	371	2	1254.76	2.4	1	49.8	9.03	95.00%	R.VLELINIVTNK.N		R.VLELINIVTNK.N

175	182	2	973.54	2.2	0	27.2	20.1	95.00%	H.DAQLFRPK.I		R.VDPNTGLIDYDMLEHDAQLFRPK.I
97	123	3	2996.43	3.4	0	55	19.8	95.00%	K.WGVNVQCLSGSPANMQVYQAIMPPHGR.L	Carbamidomethyl (+57)	K.WGVNVQCLSGSPANMQVYQAIMPPHGR.L
5	15	2	1289.66	1.8	1	47.2	22	95.00%	N.DSIMLTPLKEQ.D	Oxidation (+16)	-.MSSNDSIMLTPLKEQDPTVAEIMR.H
86	96	2	1129.62	5.1	1	54.8	20.3	95.00%	R.ALAAFNLDPAK.W		R.ALAAFNLDPAK.W
59	67	2	998.45	5.1	1	32.9	23.5	95.00%	K.YSEGYPGAR.Y		K.YSEGYPGAR.Y
277	302	3	2725.45	2.8	0	25.2	14.6	95.00%	K.INFSVFPGHQGGPHNHTITALAVALK.Q		K.INFSVFPGHQGGPHNHTITALAVALK.Q
413	422	2	1075.61	4.3	0	49.9	17.5	95.00%	R.ALTFAANLQK.E		R.ALTFAANLQK.E
250	256	2	840.44	5.4	0	24.1	19.8	91.10%	R.GAMIFFR.R		R.GAMIFFR.R
46	58	2	1321.64	4.2	1	41.4	23.4	95.00%	R.AVMDALGSVMSNK.Y		R.AVMDALGSVMSNK.Y
128	141	2	1467.68	1.6	0	41.9	23.7	95.00%	L.DLPSGGHLSHGYQT.D		R.LMGLDLPSGGHLSHGYQTDTK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
13	TPIS_SCHPO	43.78%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
206	222	2	1841.9	2.2	1	42.9	22	95.00%	R.VIYGGSVNGGNCKEFLK.F	Deamidation (+1)/ Carbamidomethyl (+57)	R.VIYGGSVNGGNCKEFLK.F
160	174	2	1615.9	2.9	1	74.5	14.6	95.00%	K.IVIAYEPVWAIGTGK.T		K.IVIAYEPVWAIGTGK.T
71	84	2	1424.64	1.2	1	45	24	95.00%	K.NGAYTGENSAQSLI.D	Deamidation (+1)	K.NGAYTGENSAQSLIDAGITYTLTGHSER.R
135	145	2	1242.66	4.7	1	39.7	19.3	95.00%	R.EANETINVVVR.Q		R.EANETINVVVR.Q
57	67	2	1146.61	2.9	1	33.5	20.9	95.00%	K.KDIGVGAQNVF.D		K.KDIGVGAQNVFDK.K
85	98	2	1519.73	2.1	1	60.9	22.2	95.00%	I.DAGITYTLTGHSER.R		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R
36	52	2	2039.05	3.7	1	52.5	19.4	95.00%	G.DVETVIFPQNMYLITTR.Q		K.LNVGDVETVIFPQNMYLITTR.Q
196	205	2	971.55	5.3	1	76.1	20.9	95.00%	K.LGASVAEGLR.V		K.LGASVAEGLR.V
206	218	2	1324.61	4.4	0	76.9	23.5	95.00%	R.VIYGGSVNGGNCK.E	Deamidation (+1)/ Carbamidomethyl (+57)	R.VIYGGSVNGGNCK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
14	THI3_SCHPO	37.57%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
47	56	2	959.53	2.2	0	70	20.9	95.00%	S.DVTALIGSGK.V		R.EGIEVAILEPTNPSDVTALIGSGK.V
74	95	2	2353.27	3.5	1	91.4	15.3	95.00%	R.GYPVTSFGSLLNEPFTGLITLK.G		R.GYPVTSFGSLLNEPFTGLITLK.G
291	303	2	1616.65	2.8	1	36.1	23.6	95.00%	Q.DFEPNCTNGYLTW.E	Carbamidomethyl (+57)/ Deamidation (+1)	R.LGIIPQDFEPNCTNGYLTWELDPDEK.D
128	139	2	1325.67	4.2	1	42.4	21.6	95.00%	K.FGLSPSDYTAIR.C		K.FGLSPSDYTAIR.C
74	85	2	1253.63	2.5	0	59.5	22	95.00%	R.GYPVTSFGSLLN.E		R.GYPVTSFGSLLNEPFTGLITLK.G
6	27	2	2631.39	2.4	1	78.6	14.8	95.00%	K.ITFLTNWEATPYHLPIFLAQTR.G		K.ITFLTNWEATPYHLPIFLAQTR.G
63	71	2	954.54	4.5	0	51.1	15.9	95.00%	K.AMIHTLAAK.A		K.AMIHTLAAK.A
260	266	2	930.37	2.7	0	23.9	23.8	90.70%	R.CFAYFSH.D	Carbamidomethyl (+57)	R.CFAYFSHDISNVPR.D
293	305	2	1596.68	1.8	1	28.5	23.6	95.00%	F.EPNCTNGYLTWEL.D	Carbamidomethyl (+57)/ Deamidation (+1)	R.LGIIPQDFEPNCTNGYLTWELDPDEK.D
110	118	2	968.5	4.9	1	27.7	21.8	95.00%	R.IGYVGEFGK.I		R.IGYVGEFGK.I
330	339	2	992.51	5.7	0	44.3	22.7	95.00%	K.GGVFSGNSLR.Y		K.GGVFSGNSLR.Y
284	290	2	795.5	2.2	1	27.5	10	95.00%	K.RLGIIPQ.D		K.RLGIIPQDFEPNCTNGYLTWELDPDEK.D
86	95	2	1117.64	1.3	0	30	16.6	95.00%	N.EPFTGLITLK.G		R.GYPVTSFGSLLNEPFTGLITLK.G
260	273	2	1711.79	4.7	1	88.7	23.2	95.00%	R.CFAYFSHDISNVPR.D	Carbamidomethyl (+57)	R.CFAYFSHDISNVPR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
15	SAHH_SCHPO	25.64%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
246	255	2	1042.51	2.7	0	28.2	22.7	95.00%	V.DPINALQAAM.D		R.VIVTEVDPINALQAAMDGFEVTTMEEAVK.E
25	35	2	1227.63	2.9	1	39.1	20.9	95.00%	A.ENEMPGLIAVR.E		K.ELEIAENEMPGLIAVR.E
8	18	2	1118.61	3.2	1	77.1	19.2	95.00%	K.VADISLAAFGR.K		K.VADISLAAFGR.K
216	227	2	1117.62	4.3	1	46.5	19.6	95.00%	K.VAVVAGFGDVGK.G		K.VAVVAGFGDVGK.G
269	280	2	1367.65	2.1	0	59.7	22.9	95.00%	K.EGQIFVTTTGCR.D	Carbamidomethyl (+57)	K.EGQIFVTTTGCR.D
119	130	2	1302.7	2.2	0	31.9	19.3	95.00%	K.SFPSGKPLNMIL.D		K.SFPSGKPLNMILDDGGDLTALVHER.H
176	187	2	1255.68	4.6	1	42.1	18.7	95.00%	K.VPAINVNDSVTK.S		K.VPAINVNDSVTK.S
336	344	2	1006.6	5	1	31.2	12.6	95.00%	R.HIILLADGR.L		R.HIILLADGR.L
318	328	2	1281.71	3.7	1	30.2	18.2	95.00%	K.DVVNIKPQVDR.Y		K.DVVNIKPQVDR.Y
318	326	2	1010.58	3.3	0	31.5	16.2	95.00%	K.DVVNIKPQV.D		K.DVVNIKPQVDR.Y
135	143	2	1052.56	2.2	1	51.5	19.4	95.00%	G.DLTALVHER.H		K.SFPSGKPLNMILDDGGDLTALVHER.H
174	182	2	966.59	3.1	1	27.1	13.4	95.00%	K.LKVPAINVN.D		K.LKVPAINVNDSVTK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
16	METK_SCHPO	43.19%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
147	155	2	931.5	4.5	0	58	23.4	95.00%	K.LNAAMSVAR.R		K.LNAAMSVAR.R
121	130	2	1101.48	2.7	0	46.1	24.3	95.00%	G.DQGIMFGYAT.D		K.ALEELGAGDQGIMFGYATDETPEK.L
137	146	3	1117.73	2.8	0	44.7	3.01	95.00%	K.LPLTILLAHK.L		K.LPLTILLAHK.L
256	272	2	1623.71	2.1	0	75.3	24.3	95.00%	V.DTYGGWGAHGGGAFSGK.D		K.IIVDTYGGWGAHGGGAFSGK.D
237	251	2	1429.74	3.6	1	73.6	20.9	95.00%	R.FVVGGPQGDAGLTGR.K		R.FVVGGPQGDAGLTGR.K
2	13	2	1327.63	3	1	38.8	23	95.00%	M.AQTFLFTSESVG.E	Acetyl (+42)	-.MAQTFLFTSESVGEGHPDK.I
339	349	2	1256.73	4.3	1	36.5	14.8	95.00%	K.NFDLRPGVLVK.S		K.NFDLRPGVLVK.S
227	236	3	1156.6	4.8	0	18.7	20.6	91.30%	K.TVYHIQPSGR.F		K.TVYHIQPSGR.F
291	299	2	856.52	4.2	0	28.1	17.2	95.00%	K.SLVAAGLAR.R		K.SLVAAGLAR.R
253	272	2	1948.95	4	1	80.8	22.4	95.00%	K.IIVDTYGGWGAHGGGAFSGK.D		K.IIVDTYGGWGAHGGGAFSGK.D
369	378	2	1241.61	1.6	1	25	22.9	92.70%	T.DQSKPWEQPK.E		K.LQTPFYLSTASYGHFTDQSKPWEQPK.E
90	102	2	1457.72	2.3	1	44.1	22	95.00%	K.TCNVLVAIEQQSP.D	Carbamidomethyl (+57)	K.TCNVLVAIEQQSPDIAQGLHYEK.A
353	368	2	1831.88	2.5	0	75.3	22.8	95.00%	K.LQTPFYLSTASYGHFT.D		K.LQTPFYLSTASYGHFTDQSKPWEQPK.E
188	197	2	1039.53	3.3	0	39.5	20.5	95.00%	V.DTIVVSAQHA.D		R.VDTIVVSAQHADSISTEDLR.S
103	112	2	1172.59	3	1	39.8	21.8	95.00%	P.DIAQGLHYEK.A		K.TCNVLVAIEQQSPDIAQGLHYEK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
17	A1EGU1_SCHPO	26.55%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
457	479	2	2580.33	3.2	0	74.6	18.2	95.00%	K.YVISQCNNALLYPALGVACVLSR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.YVISQCNNALLYPALGVACVLSR.C
372	396	3	2593.42	2.1	1	40.3	10.8	95.00%	G.DINLESAIALVKPTILLGCSGQPGK.F	Carbamidomethyl (+57)	K.EVPSGDINLESAIALVKPTILLGCSGQPGK.F
439	452	2	1418.83	2.3	0	48.6	9.54	95.00%	K.ALIATGSPLPPLNR.N		K.ALIATGSPLPPLNR.N
249	256	2	834.43	2.8	0	39	22.7	95.00%	E.DFGLANAK.R		R.EVFPEAFIHFEDFGLANAK.R
490	500	2	1070.58	4.5	1	54.7	19.7	95.00%	K.AASDALATVPR.S		K.AASDALATVPR.S
15	23	2	955.55	4.9	0	32.8	16.9	95.00%	K.GVTLLNSPR.Y		K.GVTLLNSPR.Y
332	339	2	964.49	5	1	34.3	21.6	95.00%	R.GNLFMIDR.C		R.GNLFMIDR.C
456	479	3	2708.42	2.6	1	45.3	14.9	95.00%	K.KYVISQCNNALLYPALGVACVLSR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.KYVISQCNNALLYPALGVACVLSR.C
364	371	2	877.42	2	1	32.2	22.7	95.00%	S.DFKEVPSG.D		K.DSDFKEVPSGDINLESAIALVKPTILLGCSGQPGK.F

44	55	2	1363.77	2.3	1	45.2	16.1	95.00%	R.LPPIVETLQQQV.D		R.LPPIVETLQQQVDR.C
178	191	2	1553.75	3.5	1	59.3	23	95.00%	K.GHLMTLCAGLDPNR.F	Carbamidomethyl (+57)	K.GHLMTLCAGLDPNR.F
408	424	2	1964.06	3.1	1	37.8	14.9	95.00%	K.HVERPIIFPISNPTTLM.E		K.HVERPIIFPISNPTTLMEAKPDQID K.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
18	HSP90_SCHPO	13.78%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
368	375	2	926.52	2.8	0	32.6	18.2	95.00%	E.DLPLNLSR.E		K.GVVDSEDLPLNLSR.E
465	474	2	1170.6	4.5	1	29.7	21.9	95.00%	K.NIYFITGESK.Q		K.NIYFITGESK.Q
567	587	2	2339.12	5.7	1	92.3	21.4	95.00%	K.IVGSPCLLTTGQYGWSANMER.I	Carbamidomethyl (+57)	K.IVGSPCLLTTGQYGWSANMER.I
351	361	2	1343.75	2.3	1	31.1	16.6	95.00%	E.ELIPEWLGFIK.G		R.VFITDDCEELIPEWLGFIK.G
596	606	2	1234.5	4.9	0	67.2	23.7	95.00%	R.DTSMSAYMSSR.K		R.DTSMSAYMSSR.K
88	99	2	1282.73	5.3	1	55.5	15.2	95.00%	K.NDLINNLGVIAK.S		K.NDLINNLGVIAK.S
198	212	2	1787.96	3.3	1	45.4	18.1	95.00%	K.HSEFISYPIQLVVTR.E		K.HSEFISYPIQLVVTR.E
655	663	2	1021.45	3.6	1	49.9	23.3	95.00%	L.DDPSAYAQR.I		K.DLATILYETALLSSGFTLDDPSAY AQR.I
89	99	2	1168.69	3.1	0	26.3	14.5	94.40%	N.DLINNLGVIAK.S		K.NDLINNLGVIAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
19	HSP72_SCHPO	19.32%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
327	340	2	1400.77	3.9	1	39.7	18.9	95.00%	K.ASVNEIVLVGGSTR.I		K.ASVNEIVLVGGSTR.I
55	66	2	1384.66	2.9	0	41.8	23.4	95.00%	K.NQVAMNPHNTIF.D		K.NQVAMNPHNTIFDAK.R
84	91	3	1087.53	2.1	1	23.4	22.4	95.00%	S.DMKHWPFK.V		K.FDDPEVQSDMKHWPFK.V
538	548	2	1351.66	4.4	1	37.5	22.2	95.00%	K.NHLESYAYSLR.N		K.NHLESYAYSLR.N
350	359	2	1241.54	2.7	1	24.2	23.7	91.30%	S.DFFNGKEPCK.S	Deamidation (+1)/ Carbamidomethyl (+57)	K.LVSDFFNGKEPCK.S
170	183	2	1415.77	3.7	1	38	18.3	95.00%	R.IINEPTAAAIAYGL.D		R.IINEPTAAAIAYGLDR.S
55	69	2	1698.82	4.2	1	74.8	21.8	95.00%	K.NQVAMNPHNTIFDAK.R		K.NQVAMNPHNTIFDAK.R
457	467	2	1182.65	4.4	1	28.3	17.7	95.00%	K.FELSGIPPAPR.G		K.FELSGIPPAPR.G
235	244	2	1273.69	4.3	1	25.1	19.5	92.80%	R.LVNHFIQEFK.R		R.LVNHFIQEFK.R
96	106	2	1274.69	4.5	1	24.7	19.8	92.10%	K.DGKPVLQVEYK.G		K.DGKPVLQVEYK.G
331	340	2	1029.59	3.8	0	31.3	18	95.00%	N.EIVLVGGSTR.I		K.ASVNEIVLVGGSTR.I
393	413	2	2099.11	2.1	1	74.1	17	95.00%	L.DVAPLSMGIETAGGVMTPLIK.R		K.TQDLLLLDVAPLSMGIETAGGVM TPLIK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
20	ILV5_SCHPO	20.79%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
317	328	2	1392.58	2.3	0	72.3	24.6	95.00%	L.DYMFAACSTTAR.R	Carbamidomethyl (+57)	K.YGLDYMFAACSTTAR.R
84	104	2	2141.07	4.6	1	90.4	20.5	95.00%	K.NDTLAIIGYGSQGHGQGLNAR.D		K.NDTLAIIGYGSQGHGQGLNAR.D
330	337	2	914.47	6	1	41.2	21.2	95.00%	R.GAIDWTPR.F		R.GAIDWTPR.F
314	328	2	1725.76	3.8	1	69	24.2	95.00%	K.YGLDYMFAACSTTAR.R	Carbamidomethyl (+57)	K.YGLDYMFAACSTTAR.R
173	189	3	2017.04	2.6	1	19	19.9	92.00%	K.TLYFSHGFSVIFKDQTK.I		K.TLYFSHGFSVIFKDQTK.I
362	372	2	1312.61	4.6	1	61.6	23.6	95.00%	R.SLEYNSAPNYR.E		R.SLEYNSAPNYR.E
302	313	2	1318.72	3.8	0	27	18.6	95.00%	E.EATQSLYPLIGK.Y		R.GHSPAEAFNETVEEATQSLYPLI GK.Y
85	104	3	2027.02	2.7	0	55.7	19.1	95.00%	N.DTLAIIGYGSQGHGQGLNAR.D		K.NDTLAIIGYGSQGHGQGLNAR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
21	K6PF_SCHPO	15.71%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	146	2	1031.53	3.6	0	26.7	21.8	94.90%	E.DPLGNLIGFS.D		K.KPDEVYVEDPLGNLIGFSDR.Y
613	628	3	1700.87	4.5	1	49.7	19.8	95.00%	R.GHTPLAIDNGFSGFLR.H		R.GHTPLAIDNGFSGFLR.H

510	522	2	1357.66	2.1	0	54	22.6	95.00%	P.DTPSPMIAINGNK.I	Deamidation (+1)	R.MLATLQGVDAVDAVLASTPDTPSPMIAINGNK.I
586	603	3	1720.91	2.8	0	62.8	19.1	95.00%	R.VAIIHVGAPAGGMNSATR.A		R.VAIIHVGAPAGGMNSATR.A
369	380	2	1259.61	3.1	0	56.6	23.3	95.00%	V.DSISSTAISHSR.A		R.ICEAVDSISSTAISHSR.A
844	859	2	1589.77	3.1	0	26.6	22.6	94.70%	R.TAVPGHVQQGGNPTPM.D		R.TAVPGHVQQGGNPTPMDR.A
620	628	2	1012.46	2.5	0	39.7	23.1	95.00%	I.DNGFSGFLR.H	Deamidation (+1)	R.GHTPLAIDNGFSGFLR.H
573	580	2	957.46	1.8	1	36.7	22.4	95.00%	E.DESHFVPK.D		R.DPEFADYLHTWEGTTFIEDESHFVPK.D
798	806	2	934.49	4	1	31.5	20.6	95.00%	K.ATFALEAGR.N		K.ATFALEAGR.N
254	267	2	1400.75	3.4	1	49.7	19.2	95.00%	R.GWLAEGGTLIGTAR.C		R.GWLAEGGTLIGTAR.C
844	861	2	1860.9	4.7	1	42.3	22.5	95.00%	R.TAVPGHVQQGGNPTPMDR.A		R.TAVPGHVQQGGNPTPMDR.A
927	938	2	1323.7	4.7	0	53.3	19.7	95.00%	R.DMHNLVNILAGK.T		R.DMHNLVNILAGK.T
197	214	2	1760.86	4.1	1	84.8	21.3	95.00%	K.IAVMTSGGDSPGMNAVVR.A		K.IAVMTSGGDSPGMNAVVR.A
205	214	2	1044.51	3	0	25.3	22.9	93.10%	G.DSPGMNAVVR.A		K.IAVMTSGGDSPGMNAVVR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
22	EF2_SCHPO	12.59%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
272	283	2	1498.77	4.2	1	53.9	20.9	95.00%	R.AFNMFILDPIYR.I		R.AFNMFILDPIYR.I
466	479	2	1474.71	3.7	1	72.8	22.2	95.00%	K.SGTLTTSEVAHNMK.V		K.SGTLTTSEVAHNMK.V
565	578	2	1451.69	4.3	1	44.5	23.1	95.00%	R.ESVSEPSSMTALSK.S		R.ESVSEPSSMTALSK.S
284	292	2	1051.52	4.5	1	27.5	22.9	95.00%	R.IFDAVMNSR.K		R.IFDAVMNSR.K
810	820	2	1200.58	1.1	0	55	22.9	95.00%	L.DPTSKPGQIVC.E	Carbamidomethyl (+57)	R.QATAGQAFPQLVFDHWSPMSGDPLDPTSKPGQIVCEAR.K
244	253	2	1266.61	5.9	1	30	23.2	95.00%	R.LWGENYFNPK.T		R.LWGENYFNPK.T
110	120	2	1194.59	2.3	1	68.1	22.7	95.00%	V.DFSSEVTAALR.V		K.EPADGTDFLVNLIDSPGHVDFSSEVTAALR.V
371	384	2	1594.76	4.1	1	55	22.8	95.00%	R.NCDANAPLMIYVSK.M	Carbamidomethyl (+57)	R.NCDANAPLMIYVSK.M
810	823	2	1556.77	2.1	1	44.5	22.2	95.00%	L.DPTSKPGQIVCEAR.K	Carbamidomethyl (+57)	R.QATAGQAFPQLVFDHWSPMSGDPLDPTSKPGQIVCEAR.K
363	370	2	918.43	3.5	1	24.1	22.8	91.00%	D.DECAVGIR.N	Carbamidomethyl (+57)	R.AETLYEGPMDDECAVGIR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
23	6PGD_SCHPO	23.78%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
156	166	3	1228.76	2.4	0	38.8	7.78	95.00%	R.IKPIFQTLAAK.A		R.IKPIFQTLAAK.A
140	155	2	1685.8	3	0	49	22.4	95.00%	R.YGPSLMPGGNPAAWPR.I	Oxidation (+16)	R.YGPSLMPGGNPAAWPR.I
85	95	2	1215.68	2.4	1	30.6	18.1	95.00%	V.DYLIEGLAPLL.E		K.AGKPVDYLIEGLAPLLEK.G
99	110	2	1285.6	2.6	1	41.9	23.8	95.00%	G.DIIVDGGNSHYP.D		K.GDIIVDGGNSHYPDTTR.R
73	79	2	843.53	4.4	0	24.3	11.1	91.50%	R.VCILLVK.A	Carbamidomethyl (+57)	R.VCILLVK.A
437	449	2	1379.79	4.1	0	52	13.8	95.00%	R.SAVLPANLLQAQR.D		R.SAVLPANLLQAQR.D
276	291	2	1719.89	2.2	1	63.6	20.3	95.00%	L.EMGTPVSLITEAVFAR.C		K.WTAQNALEMGTPVSLITEAVFAR.C
450	458	2	1112.51	4.7	0	24.9	23.9	92.50%	R.DYFGAHTFR.V		R.DYFGAHTFR.V
175	187	2	1444.68	2.3	1	57.8	23.6	95.00%	C.DWVGEQGAGHYVK.M		K.AGNNEPCCDWVGEQGAGHYVK.M
29	37	2	1175.49	3.9	0	36.7	24.4	95.00%	K.GFTVCCYNR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GFTVCCYNR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
24	EF3_SCHPO	8.60%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
757	765	2	1178.58	7.8	1	24.9	22.3	92.40%	K.TPSEYIQWR.F		K.TPSEYIQWR.F
675	691	3	1960.95	2.2	0	22.6	22	95.00%	K.VQHMSFQYPGTSKPQLN.D		K.VQHMSFQYPGTSKPQLNDISFQVSLSSR.I
434	447	2	1646.71	2.3	1	53.7	23.5	95.00%	E.DLCNCEFSLAYGAK.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.IPGGASHAEEEEEGEDLCNCEFSLAYGAK.I
479	493	2	1636.88	3.9	1	73.9	18.3	95.00%	R.AIVNGQVEGFPTHLR.T		R.AIVNGQVEGFPTHLR.T
133	147	2	1550.87	3.9	1	70.6	14.1	95.00%	K.AIVPSVLESIHTTGK.W		K.AIVPSVLESIHTTGK.W

937	944	2	789.42	1.9	0	27.8	21.8	95.00%	R.DSLGALSK.G		R.DSLGALSK.G
48	59	2	1248.64	2.1	0	51	21.7	95.00%	Q.DAPSQVFSAISK.Q		K.ALASFVNGPIEEQDAPSQVFSAISK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
25	TSA1_SCHPO	30.73%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	147	2	1224.69	4.4	1	43.5	16.5	95.00%	R.QITINDLPVGR.S		R.QITINDLPVGR.S
89	102	2	1350.79	3.1	1	24.3	11.1	91.40%	R.KEGGLGGINIPLLA.D		R.KEGGLGGINIPLLADPSHK.V
75	88	2	1648.79	2	1	74.6	22.9	95.00%	T.DSEYSHLAFINTPR.K		R.NAQVILTSTDSEYSHLAFINTPR.K
125	132	2	901.53	4.7	1	35.7	19.4	95.00%	R.GLFLIDPK.G		R.GLFLIDPK.G
2	13	2	1341.74	4.1	1	36.9	18	95.00%	M.SLQIGKPAPDFK.G	Acetyl (+42)	-.MSLQIGKPAPDFK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
26	TKT_SCHPO	17.37%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
238	252	2	1719.86	5	1	57.2	21.1	95.00%	R.EAMSCTDKPTLINLK.T	Carbamidomethyl (+57)	R.EAMSCTDKPTLINLK.T
8	18	2	1243.68	3.4	1	31.7	18.5	95.00%	T.DIDTLAINTIR.T		-.MTSSSYTDIDTLAINTIR.T
653	663	2	1249.63	3.9	0	24.8	22	92.30%	K.FHFTTSGVAQR.A		K.FHFTTSGVAQR.A
480	494	3	1751.84	2.3	1	31.2	21.7	95.00%	E.DGPTHQPIETFAHFR.A		R.VIYVATHDSIGLGEDGPTHQPIETFAHFR.A
182	193	2	1385.74	4.7	1	41.9	19.8	95.00%	K.LSNLIAVWDNNK.I		K.LSNLIAVWDNNK.I
10	18	2	1015.57	3	0	25.7	19.8	93.60%	I.DTLAINTIR.T		-.MTSSSYTDIDTLAINTIR.T
521	531	2	1172.64	2.5	0	47.4	19.5	95.00%	S.DSTPSILALTR.Q		R.AMPNINCWRPADGNETSAAYYSALTSDSTPSILALTR.Q
291	303	2	1603.8	4	1	26.8	22.2	94.90%	K.TFQVPPEVYAYYK.E		K.TFQVPPEVYAYYK.E
495	505	2	1328.62	2.6	0	28	23.9	95.00%	R.AMPNINCWRPA.D	Carbamidomethyl (+57)	R.AMPNINCWRPADGNETSAAYYSALTSDSTPSILALTR.Q
30	49	3	1972.02	2.7	0	59.7	18.4	95.00%	K.SGHPGAPMGLAPAAHVLFSR.I		K.SGHPGAPMGLAPAAHVLFSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
27	ACT_SCHPO	22.67%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
244	254	2	1200.61	2.6	1	46.6	21.5	95.00%	P.DGQVITIGNER.F		K.SYELPDGQVITIGNER.F
85	95	3	1514.75	5.5	1	36	22.5	95.00%	K.IWHHTFYNELR.V		K.IWHHTFYNELR.V
69	79	2	1340.66	3	1	33.3	22.5	95.00%	K.YPIEHGIVNNW.D		K.YPIEHGIVNNWDDMEK.I
292	312	2	2216.04	5	1	63.1	21.7	95.00%	K.DLYGNVVMSGGTTMYPGIADR.M		K.DLYGNVVMSGGTTMYPGIADR.M
197	206	2	1131.53	5.1	1	41.4	23.9	95.00%	R.GYTFSTTAER.E		R.GYTFSTTAER.E
157	177	3	2339.18	2.2	1	62.2	18.3	95.00%	G.DGVTHTVPIYEGYALPHAIMR.L		R.TTGIVLDSGDGVTHTVPIYEGYALPHAIMR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
28	HSP75_SCHPO	18.27%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	173	2	1168.66	5	0	34.3	16.6	95.00%	K.DAGAIAGLNVLR.I		K.DAGAIAGLNVLR.I
335	344	2	1015.57	3	0	48.2	19.8	95.00%	H.DIVLVGGSTR.I		K.ADVHDIVLVGGSTR.I
501	517	2	1779.91	1.5	1	72.1	19.1	95.00%	R.SAHIEITNSVGHLSSTK.I		R.SAHIEITNSVGHLSSTK.I
144	157	2	1552.8	4.6	1	33.7	20.7	95.00%	K.AVITVPAYFSDSQR.A		K.AVITVPAYFSDSQR.A
457	472	2	1780.92	1.7	1	65.8	19.1	95.00%	N.EPLGEFQLTGIPPMPR.G		R.VNCAENEPLGEFQLTGIPPMPR.G
174	187	2	1415.77	3.7	1	38	18.3	95.00%	R.IINEPTAAAIAYGL.D		R.IINEPTAAAIAYGLDAK.S
115	128	2	1565.81	1.5	1	68.3	19.1	95.00%	K.QFTAQEISAMVLTK.M		K.QFTAQEISAMVLTK.M
436	450	2	1753.83	2.3	1	81.5	22.5	95.00%	A.DNQTTVTFPVYQGER.V		R.TFTTVADNQTTVTFPVYQGER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
29	SERA_SCHPO	19.10%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
58	73	2	1768.01	2.4	1	85.4	11.5	95.00%	K.ILLLENVNQSALSNLK.D		K.ILLLENVNQSALSNLK.D
275	284	2	1108.56	4.3	0	25.6	22.9	93.50%	K.EGSYLINASR.G		K.EGSYLINASR.G
440	452	2	1454.69	1.7	1	44.2	23.6	95.00%	S.DCTPGSLEALHQK.L	Carbamidomethyl (+57)	R.GDIAYLVADISDCTPGSLEALHQK.L
324	337	2	1676.75	2.9	1	35.6	24.1	95.00%	V.DSLNSWTSELTHCK.N	Carbamidomethyl (+57)	K.FVDSLNSWTSELTHCK.N
308	319	2	1233.56	3.2	1	37.7	23.1	95.00%	I.DVYPSEPAGNGK.D	Deamidation (+1)	K.IAGAAIDVYPSEPAGNGK.D
142	154	2	1394.7	4.8	0	57.8	21.7	95.00%	R.GIAVFNSPYANSR.S		R.GIAVFNSPYANSR.S
237	247	3	1291.73	3.1	1	34.4	16.5	95.00%	K.QLSSLPELLHR.A		K.QLSSLPELLHR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
30	GPD1_SCHPO	34.03%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
220	232	2	1184.64	2.8	1	56	19.5	95.00%	V.DDVAGVALGGALK.N		R.EQIAAVFDRPYFSVVSVDDVAGVALGGALK.N
2	20	2	1989	3.8	1	99.4	20.8	95.00%	M.SGYGQQGVSAANIDSIRPK.K	Acetyl (+42)	-.MSGYGQQGVSAANIDSIRPK.K
199	209	2	1257.67	2	1	46.1	20	95.00%	V.DIPREQIAAVF.D		R.EQFCETTIGFNPPNEVDIPREQIAAVFDRPYFSVVSVDDVAGVALGGALK.N
287	296	2	1076.53	2.2	0	49.8	22.4	95.00%	A.DLVTSCLGGR.N	Carbamidomethyl (+57)	R.TMVEQSCGIADLVTSCLGGR.N
127	144	2	1913.03	2.7	0	61.7	15.4	95.00%	C.DQMVGLIRPGAVGISCIK.G	Carbamidomethyl (+57)	R.VCDQMVGLIRPGAVGISCIK.G
23	39	2	1628.89	2.5	0	23.8	17.6	90.50%	R.LSIGVVGSGNWGTAIAK.I		R.LSIGVVGSGNWGTAIAK.I
125	144	3	2172.13	2.4	1	37	19	95.00%	R.VCDQMVGLIRPGAVGISCIK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VCDQMVGLIRPGAVGISCIK.G
111	124	2	1710.95	3.3	1	33.2	14.8	95.00%	A.DILVFVVPHQFIER.V		R.ADILVFVVPHQFIER.V
317	331	2	1484.83	3.6	0	57.3	17	95.00%	K.ELLGGQLLQGAATSK.D		K.ELLGGQLLQGAATSK.D
210	219	2	1167.59	2.1	0	29.4	21.7	95.00%	F.DRPYFSVVSV.D		R.EQIAAVFDRPYFSVVSVDDVAGVALGGALK.N
315	331	2	1741.96	3.1	1	60.2	16	95.00%	L.EKELLGGQLLQGAATSK.D		K.SLETLEKELLGGQLLQGAATSK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
31	HXK2_SCHPO	18.02%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
434	449	2	1529.79	4.8	0	96.2	20.7	95.00%	K.DGSGIGAALCALQAVK.E	Carbamidomethyl (+57)	K.DGSGIGAALCALQAVK.E
197	205	2	960.53	1.7	0	31.6	20.6	95.00%	N.DTVGTLVTR.A		R.IEAVINDTVGTLVTR.A
76	86	2	1287.67	3.9	1	30.3	21.5	95.00%	R.VCWIQLLGDGK.Y	Carbamidomethyl (+57)	R.VCWIQLLGDGK.Y
286	296	2	1240.63	5.9	1	25.6	20.9	93.50%	R.VGGMYLGELFR.R		R.VGGMYLGELFR.R
257	265	2	1121.5	2.5	0	30.2	22.9	95.00%	T.DFSCLHSTR.Y	Carbamidomethyl (+57)	K.CTGDHMLINMEWGATDFSCLHSTR.Y
374	388	2	1564.83	4.1	0	56.1	18.1	95.00%	R.MSAVPIASLYLSTGR.A		R.MSAVPIASLYLSTGR.A
1	11	2	1334.67	4.1	1	29.9	22.5	95.00%	-.MEANFQQAVKK.L	Acetyl (+42)	-.MEANFQQAVKK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
32	PUR9_SCHPO	24.44%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
235	244	2	1141.62	2.4	0	29.4	18.5	95.00%	M.DALNSWPLVK.E		K.VLCGSPGYINLMDALNSWPLVK.E
121	129	2	942.55	2.5	0	38	18.9	95.00%	I.DIGGVTLLR.A		R.ETIAKPNVTIPEAVEEIDIGGVTLLR.A
284	297	2	1626.77	2	1	41.2	23	95.00%	S.DITEFTPLACAYAR.A	Carbamidomethyl (+57)	K.VYFVSDITEFTPLACAYAR.A
46	60	2	1527.79	2.5	1	64.1	20.9	95.00%	A.DVSSITNAPEILGGR.V		R.ESGMEVADVSSITNAPEILGGR.V
551	565	2	1519.75	4.1	1	63.8	21.9	95.00%	K.YVAAPGGSVMDQAVR.D		K.YVAAPGGSVMDQAVR.D
260	273	2	1274.7	2.4	0	25.7	19.2	93.60%	K.HVSPAGAAVGLPLS.D		K.HVSPAGAAVGLPLSDVEK.K
223	244	2	2446.25	3.4	1	45.9	18.8	95.00%	K.VLCGSPGYINLMDALNSWPLVK.E	Carbamidomethyl (+57)	K.VLCGSPGYINLMDALNSWPLVK.E
93	103	2	1394.71	2.7	0	33.8	22	95.00%	I.DIVVCNLYPFR.E	Carbamidomethyl (+57)	K.IDIVVCNLYPFR.E
354	362	2	1152.54	4.8	1	28.8	23.9	95.00%	K.YCVLQMDPK.Y	Carbamidomethyl (+57)	K.YCVLQMDPK.Y

248	259	2	1216.65	4.7	0	30.2	20.5	95.00%	R.ENIGIPAAASFK.H		R.ENIGIPAAASFK.H
201	222	3	2414.16	4	1	23.8	20	95.00%	R.YGANPHQSPAQAFMEQGPLPFK.V		R.YGANPHQSPAQAFMEQGPLPFK.V
201	214	2	1517.68	2.6	0	33.5	24	95.00%	R.YGANPHQSPAQAFM.E		R.YGANPHQSPAQAFMEQGPLPFK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
33	HSP60_SCHPO	15.81%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	148	2	1316.6	4	1	27.4	24.3	95.00%	R.NVAAGCNPMDLR.R	Carbamidomethyl (+57)	R.NVAAGCNPMDLR.R
437	453	2	1588.85	4.6	1	29.9	18.9	95.00%	K.AAVSEGVLPGAGTSFVK.A		K.AAVSEGVLPGAGTSFVK.A
68	79	2	1313.7	4.3	1	39.3	18.6	95.00%	R.NVLIDQPFGSPK.I		R.NVLIDQPFGSPK.I
541	557	2	1680.77	2.3	1	54.5	22.9	95.00%	V.DASGVASLMGTTECAIV.D	Carbamidomethyl (+57)	R.TGLVDASGVASLMGTTECAIVDAPEESK.A
229	240	2	1401.72	4.3	1	35	20.5	95.00%	R.GYISPYFITDVK.S		R.GYISPYFITDVK.S
186	195	3	1095.6	2.9	1	40.1	18.9	95.00%	G.DTHIGELLAK.A		R.DITTSEEISQVATISANGDTHIGELLAK.A
45	56	2	1215.69	4.9	1	52.6	16.7	95.00%	R.ASLLTGVDTLAR.A		R.ASLLTGVDTLAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
34	IPYR_SCHPO	12.80%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
186	192	2	922.44	6	1	35.4	23.7	95.00%	R.ATNEWFR.I		R.ATNEWFR.I
256	274	2	1874.97	1.5	1	33.6	19.1	95.00%	N.DPSVSSTIPPAQELAPAPV.D		K.SDFSLVNVSVTGSVANDPSVSSTIPPAQELAPAPVDPSVHK.W
43	53	2	1283.73	4	1	66.7	15.1	95.00%	K.TILNMVVEIPR.W		K.TILNMVVEIPR.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
35	G6PI_SCHPO	24.55%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
217	228	2	1343.61	5.2	1	37.3	24.3	95.00%	K.TFTTAETCTNAK.S	Carbamidomethyl (+57)	K.TFTTAETCTNAK.S
372	382	2	1171.52	5.1	1	67.7	24.3	95.00%	R.SGDMVNYTTGK.I		R.SGDMVNYTTGK.I
464	477	2	1502.83	4	0	36.9	16.5	95.00%	K.TFVGNRPSNSIIAK.K		K.TFVGNRPSNSIIAK.K
79	86	2	886.45	1.3	1	33.4	21.5	95.00%	K.EANVEGLR.D		K.EANVEGLR.D
2	24	2	2548.27	3.8	1	60.7	19.4	95.00%	M.SFSLASTLPAWQAVQTHYESVGK.H	Acetyl (+42)	-.MSFSLASTLPAWQAVQTHYESVGK.H
410	421	2	1393.73	2.6	1	24.3	20.3	91.40%	A.DFLIPIESHNPI.D		K.LIPADFLIPIESHNPIDNNK.H
118	128	2	1170.59	4.1	1	35.5	21.4	95.00%	K.VNGQDVMPGVR.K		K.VNGQDVMPGVR.K
429	445	2	1870.94	4.8	1	69.7	21.6	95.00%	R.MLFSNFAAQTEALMLGK.T		R.MLFSNFAAQTEALMLGK.T
536	547	2	1308.66	2.1	0	36.5	22.6	95.00%	H.DSSTNGLINLFK.N	Deamidation (+1)	K.GDVENHDSSTNGLINLFK.N
353	367	2	1712.81	0.45	1	72.1	23.4	95.00%	R.FPAYLQQLSMESNGK.A	Deamidation (+1)	R.FPAYLQQLSMESNGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
36	THIL_SCHPO	26.08%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
291	301	2	1160.65	4.8	0	33.2	17.2	95.00%	R.FTTSPSLAIPK.A		R.FTTSPSLAIPK.A
51	69	2	2016.97	2.3	1	104	20.9	95.00%	V.DEVFMGNVVSANLGQNPAR.Q		R.VNIKPSDVDEVFMGNVVSANLGQNPAR.Q
14	30	2	1654.81	1.9	0	91	22.1	95.00%	R.TPMGSFGGSFASLPATK.L		R.TPMGSFGGSFASLPATK.L
267	277	3	1194.77	1.9	1	29.4	6.02	95.00%	K.VKELGLKPLAK.I		K.VKELGLKPLAK.I
360	371	2	1405.8	2.6	0	76.2	14.8	95.00%	R.IICTLAYILAQK.D	Carbamidomethyl (+57)	R.IICTLAYILAQK.D
254	266	2	1232.65	3.3	0	61.8	20.7	95.00%	N.DGASALVLMSAAK.V		K.SNGTVTAANASTLNDGASALVLMSAAK.V
340	359	2	1866.9	2	0	77.8	22.3	95.00%	R.VNINGGGVAMGHPLGSSGSR.I	Deamidation (+1)	R.VNINGGGVAMGHPLGSSGSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
37	HSP7M_SCHPO	12.02%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

204	215	2	1124.67	4.6	0	48.3	13.8	95.00%	K.AAGAIAGLNVLR.V		K.AAGAIAGLNVLR.V
474	482	2	987.5	4	1	28.2	21.6	95.00%	A.DGQTAVEIR.V		K.SQVFSTAADGQTAVEIR.V
105	118	2	1578.81	4.5	1	81.4	20.5	95.00%	R.QAVINPENTFFATK.R		R.QAVINPENTFFATK.R
185	199	2	1679.83	4.3	1	62.1	22	95.00%	K.NAVVTVPAYFNDSQR.Q		K.NAVVTVPAYFNDSQR.Q
496	510	2	1538.89	4.2	0	77.2	13	95.00%	K.LIGNFQLTGIAPAPK.G		K.LIGNFQLTGIAPAPK.G
157	170	2	1496.8	5.1	0	59.3	18.7	95.00%	K.TYSPSQIGGFILSK.M		K.TYSPSQIGGFILSK.M
155	170	2	1681.91	3.4	1	37.3	17.7	95.00%	R.GKTYSPSQIGGFILSK.M		R.GKTYSPSQIGGFILSK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
38	LYS9_SCHPO	19.11%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
177	183	2	740.49	4.7	0	33.1	10.4	95.00%	R.GVLLALR.N		R.GVLLALR.N
171	176	2	768.36	6.1	0	24.6	23.1	91.90%	K.FSWSSR.G		K.FSWSSR.G
38	49	2	1259.66	4.1	1	41.7	20	95.00%	K.AEAFINGIPNSK.A		K.AEAFINGIPNSK.A
2	22	3	2269.25	3.1	1	39	13.2	95.00%	M.PSILLLGSGFVAHPTLEYLSR.R		-.MPSILLLGSGFVAHPTLEYLSR.R
411	423	2	1265.66	0.38	0	36.7	21	95.00%	L.DGVINTPGVLAPN.D		K.LVGVPCGVATQQILDGVINTPGVLAPNDMK.L
379	396	2	1989.93	4.3	1	76.6	22.3	95.00%	R.TCTLLDYGVPNGYTSMAK.L	Carbamidomethyl (+57)	R.TCTLLDYGVPNGYTSMAK.L
162	170	2	1006.48	3.4	0	26.7	22.9	94.90%	E.DSNNPLGYK.F		K.SFLSYCGGLPAPEDSNNPLGYK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
39	MET3_SCHPO	13.67%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
217	229	2	1346.78	1.8	0	30.6	14.1	95.00%	R.VLIHPVVGMTKPG.D		R.VLIHPVVGMTKPGDIDHFTR.V
350	359	2	1102.6	3.9	1	29.9	20.4	95.00%	R.TLNISGTELR.R		R.TLNISGTELR.R
404	415	2	1225.7	3.2	1	24.9	16.1	92.40%	K.LLPSALVSALNE.D		K.LLPSALVSALNEDGR.R
59	68	2	1233.64	5.6	1	40.5	21.9	95.00%	K.DYLNVVENLR.L		K.DYLNVVENLR.L
254	262	2	1012.62	5.1	0	33.5	13	95.00%	K.LSLLPLAMR.M		K.LSLLPLAMR.M
217	231	3	1574.89	2.7	1	30.3	14.6	95.00%	R.VLIHPVVGMTKPGDI.D		R.VLIHPVVGMTKPGDIDHFTR.V
307	317	2	1326.61	1.5	1	65.4	24.3	95.00%	Y.DAQYLVEQYAQ.E		K.NSQGEDFYGPYDAQYLVEQYAQEIGITIVPFQMMTYLPDEDIYKPVDK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
40	YL8C_SCHPO	15.18%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
47	60	2	1575.87	2.9	1	43.6	15.9	95.00%	R.EKYPNFPIVLATGK.Q		R.EKYPNFPIVLATGK.Q
217	232	2	1745.96	4.4	1	53	15.1	95.00%	K.GTALQYITSNILPEVK.N		K.GTALQYITSNILPEVK.N
49	60	2	1318.74	5.4	0	24.4	17.3	91.60%	K.YPNFPIVLATGK.Q		K.YPNFPIVLATGK.Q
75	90	2	1775.83	0.62	0	72.7	23.1	95.00%	L.DAFPAAHVNGCVLYNK.G	Deamidation (+1)/ Carbamidomethyl (+57)	R.IPLDLDAFPAAHVNGCVLYNK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
41	RL4A_SCHPO	23.42%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
122	140	2	1845.04	4.3	0	48.1	10	95.00%	R.YAISSAVAASGVPSLLLAR.G		R.YAISSAVAASGVPSLLLAR.G
2	13	2	1304.71	4.5	0	25.5	18.4	93.40%	M.AAARPTVSIYSK.D	Acetyl (+42)	-.MAAARPTVSIYSK.D
276	287	2	1393.69	2.8	1	27.4	22.7	95.00%	K.NYFLPENIISNA.D		K.NYFLPENIISNADVTR.L
235	248	3	1457.85	3.4	0	54.2	13.4	95.00%	R.LNLLQLAPGGHLGR.F		R.LNLLQLAPGGHLGR.F
234	248	3	1613.95	3.4	1	26.9	6.02	95.00%	R.RLNLLQLAPGGHLGR.F		R.RLNLLQLAPGGHLGR.F
14	29	2	1695.88	4.2	1	38.3	19.3	95.00%	K.DGSVSSETIALPFVFK.A		K.DGSVSSETIALPFVFK.A
87	97	2	1197.51	4.4	0	32.6	24.2	95.00%	R.SGQAAFGNMCR.S	Carbamidomethyl (+57)	R.SGQAAFGNMCR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
42	PDX1_SCHPO	14.53%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
71	83	2	1355.75	4.3	0	66.7	18.3	95.00%	K.EIQAAVSIPVMAK.V		K.EIQAAVSIPVMAK.V

121	132	3	1383.7	4.4	1	31	21.8	95.00%	K.SKFTVPFVCGSR.N	Carbamidomethyl (+57)	K.SKFTVPFVCGSR.N
271	280	2	1016.51	2.6	0	29.1	23.4	95.00%	S.ENLGAAMVGR.S		K.ILAEVSENLGAAMVGR.S
13	20	2	830.47	4.2	0	38.8	20.6	95.00%	K.AGLAQMLK.G		K.AGLAQMLK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
43	C1TC_SCHPO	12.49%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
689	707	3	1923.15	3.9	1	37.5	6.02	95.00%	R.TSGLKPDAIVIVATVQALK.L		R.TSGLKPDAIVIVATVQALK.L
2	12	2	1184.68	4.9	1	55.8	16.5	95.00%	M.ALLLEGTSLAR.K	Acetyl (+42)	-.MALLLEGTSLAR.K
749	760	3	1299.8	2.7	1	22.8	7.78	95.00%	R.KYGLPVVVAINK.F		R.KYGLPVVVAINK.F
121	130	2	1139.49	2.2	1	32.9	23.4	95.00%	V.DGFCETNLGK.L	Carbamidomethyl (+57)	K.DVDGFCETNLGK.L
764	773	2	1100.55	2.3	1	32.1	21.8	95.00%	S.DSPNEISAIR.E		K.FSSDSPNEISAIR.E
381	396	2	1629.9	3.4	1	106	16.4	95.00%	K.STLTAGLVQALSNLDK.L		K.STLTAGLVQALSNLDK.L
349	356	2	983.58	5.3	1	46.2	15.8	95.00%	K.VNLEILQR.L		K.VNLEILQR.L
259	289	3	3121.66	4	1	20.6	12.6	95.00%	K.EVASAITPVPGSVGPMTVAMLLQNVVESAVR.F		K.EVASAITPVPGSVGPMTVAMLLQNVVESAVR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
44	CYPH_SCHPO	39.51%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
90	123	3	3611.83	4	1	56	16.4	95.00%	K.HNKPGLLSMANAGPNTNGSQFFITTVVTPWLDGK.H		K.HNKPGLLSMANAGPNTNGSQFFITTVVTPWLDGK.H
2	17	2	1835.87	3.9	1	50	22.6	95.00%	M.SNCFFDVIANGQPLGR.I	Acetyl (+42)/ Carbamidomethyl (+57)	-.MSNCFFDVIANGQPLGR.I
54	67	2	1607.82	4.3	1	67.2	20.8	95.00%	R.VIPQFMLQGGDFTR.G		R.VIPQFMLQGGDFTR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
45	ECM17_SCHPO	5.50%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
385	399	2	1570.79	2.5	1	31.6	21.1	95.00%	T.DGVSQVFVPTPPSIE.E		R.DNLSGALKPSLVCDFTDGVSQVFVPTPPSIEEAYHK.L
1031	1044	2	1572.69	2.8	1	55.2	23.6	95.00%	R.NVTCSSTPNNETIH.D	Carbamidomethyl (+57)	R.NVTCSSTPNNETIHDQLFAVSK.Q
1088	1100	2	1518.78	2.5	1	38.4	21.1	95.00%	Q.DVEPLYGPTYLPR.K		K.VAGEAVQDVEPLYGPTYLPR.K
314	325	2	1337.8	4.6	1	39.3	10.8	95.00%	R.LTVLEPITSLPR.K		R.LTVLEPITSLPR.K
1053	1066	2	1588.77	0.94	1	41.3	22.6	95.00%	K.QISNELLPTTSSYH.E		K.QISNELLPTTSSYHEIWIEDPETVEK.R
369	381	2	1372.71	2.9	0	41.6	21.1	95.00%	R.DNLSGALKPSLVC.D	Carbamidomethyl (+57)	R.DNLSGALKPSLVCDFTDGVSQVFVPTPPSIEEAYHK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
46	PUT2_SCHPO	15.33%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
368	384	2	1889.95	1.9	0	48.5	20.8	95.00%	T.DFANFVGPVIHQASFNK.L		K.VGAPLTDFANFVGPVIHQASFNK.L
362	384	3	2428.26	2.5	1	45.1	17.1	95.00%	K.VGAPLTDFANFVGPVIHQASFNK.L		K.VGAPLTDFANFVGPVIHQASFNK.L
254	274	3	2393.15	4.4	1	52.3	20.9	95.00%	K.VCFNHPEFAGLHFTGSTAVFR.S	Carbamidomethyl (+57)	K.VCFNHPEFAGLHFTGSTAVFR.S
275	288	2	1444.74	4.6	1	37.7	21.6	95.00%	R.SLWGTIGENVANGK.Y		R.SLWGTIGENVANGK.Y
495	509	2	1504.71	3.5	1	49.3	22.5	95.00%	K.CTGAVVGEQPFGGAR.A	Carbamidomethyl (+57)	K.CTGAVVGEQPFGGAR.A
484	494	2	1225.58	4.6	1	28	23.5	95.00%	R.NAAGNFYINDK.C		R.NAAGNFYINDK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
47	PPA1_SCHPO	15.45%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
413	427	2	1802.8	2.3	1	60.3	23.8	95.00%	S.DGMCELYAYLNSPVR.V	Oxidation (+16)/ Carbamidomethyl (+57)	R.HLVNEEVFPLSDCGFGPSNTSDGMCELYAYLNSPVR.V
40	59	3	2404.13	2.5	1	63.3	22.4	95.00%	R.SPYHKPYFYGPSIDFPTTCK.I	Carbamidomethyl (+57)	R.SPYHKPYFYGPSIDFPTTCK.I

417	427	2	1323.69	2.7	0	49.5	21	95.00%	C.ELYAYLNSPVR.V			R.HLVNEEVFPLSDCGFGPSNTSDGMCELYAYLNSPVR.V
73	92	2	2047	4	1	99.4	21.6	95.00%	R.NPTGGNAAFDAVGIANFQQR.L			R.NPTGGNAAFDAVGIANFQQR.L
331	345	2	1606.83	2.8	1	51.7	20	95.00%	H.DANIIPVETALGFFT.D			R.SVENNTQQVFFAFTHDANIIPVETALGFFTDNTPENPLPTSYQVHSHSMK.A
40	52	2	1554.75	2.4	0	32.2	23.1	95.00%	R.SPYHKPYFYGPSI.D			R.SPYHKPYFYGPSIDFPTTCK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
48	ADH_SCHPO	27.14%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
236	253	2	1681.87	4.1	0	56	18.3	95.00%	K.AATNGGAHGTLVLSTSPK.S	Deamidation (+1)	K.AATNGGAHGTLVLSTSPK.S
322	333	2	1420.74	4.6	1	23.7	19.8	90.20%	K.VQPFSTLPDVYR.L		K.VQPFSTLPDVYR.L
254	278	3	2513.21	2.1	1	48.3	20.3	95.00%	K.SYEQAAGFARPGSTMVTVSMPAGAK.L		K.SYEQAAGFARPGSTMVTVSMPAGAK.L
170	194	3	2506.29	3.6	1	33.6	16.1	95.00%	K.VGPGEWICIPGAGGGLGHLAVQYAK.A	Carbamidomethyl (+57)	K.VGPGEWICIPGAGGGLGHLAVQYAK.A
63	77	3	1462.8	2.8	1	20.8	17.1	95.00%	K.MPLIGGHEGAGVVVK.V		K.MPLIGGHEGAGVVVK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
49	HSP7F_SCHPO	11.25%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
174	189	2	1665.85	4	1	78.4	20.7	95.00%	R.LMNDNAAAALTYGITK.T		R.LMNDNAAAALTYGITK.T
422	434	2	1403.7	2.8	1	66	22.4	95.00%	L.EVFSEGNPIPSTK.I		R.EFHVHDVTTYPITFSWEPIPENPEEDSSLEVFSEGNPIPSTK.I
5	16	2	1249.64	6.5	1	29.4	21.8	95.00%	R.TNVVGIDFGNSK.T		R.TNVVGIDFGNSK.T
38	48	2	1194.59	3.8	1	34	23	95.00%	R.STPSLVSYGER.S		R.STPSLVSYGER.S
377	390	2	1549.78	3.8	0	45.7	21.1	95.00%	R.GCALSCAILSPVFR.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GCALSCAILSPVFR.V
177	189	2	1307.68	2.7	0	54	21.3	95.00%	N.DNAAAALTYGITK.T		R.LMNDNAAAALTYGITK.T
159	173	2	1534.89	2.6	1	54.1	10	95.00%	R.ALLEAANIAGLNPLR.L		R.ALLEAANIAGLNPLR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
50	FAS2_SCHPO	3.26%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
689	702	2	1504.78	3.7	0	23.5	20.2	90.00%	R.GSCLIVVPFNQGSK.T	Carbamidomethyl (+57)	R.GSCLIVVPFNQGSK.T
207	223	2	1753.83	3.6	1	64.9	22.6	95.00%	L.DELGAIMQSSFNGSLGK.Q	Deamidation (+1)	K.EFGATPEKPEEVPLDELGAIMQSSFNGSLGK.Q
774	793	3	2133.1	2.1	0	37.5	18.1	95.00%	M.DTRPAQVILPLSPNHGTFGN.D		R.GMDTRPAQVILPLSPNHGTFGNDGLYSESK.L
1393	1401	2	994.61	4.5	1	27.6	10.4	95.00%	K.TPLPIVDLK.F		K.TPLPIVDLK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
51	CYSD_SCHPO	24.94%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
47	59	2	1541.79	2.3	1	44	20.9	95.00%	R.LFGLQEPGYIYSR.M		R.LFGLQEPGYIYSR.M
27	39	2	1486.79	4.5	0	66.1	19.5	95.00%	R.AVPIYATTSYVFR.D		R.AVPIYATTSYVFR.D
184	197	2	1464.74	2.6	0	29	21.7	95.00%	V.DNTFGGGGYLVRPI.D		R.IAEVAHAAGVPLMVDNTFGGGGYLVRPIDHGADIVTHSATK.W
9	19	2	1221.6	2.5	1	28.7	22.8	95.00%	F.ETLQLHAGQEP.D		-.MPVESEHFETLQLHAGQEPDAATSSR.A
72	100	3	2787.49	3.3	1	49.9	14.5	95.00%	R.IAALEHGAAAIATSSGTSALFMALTTLAK.A		R.IAALEHGAAAIATSSGTSALFMALTTLAK.A
151	165	2	1651.8	2.8	1	40	22.9	95.00%	K.AVYVESIGNPMYNVP.D		K.AVYVESIGNPMYNVPDFER.I
366	377	2	1185.64	4.4	1	34.5	19.6	95.00%	K.LASQLANVGDAK.T		K.LASQLANVGDAK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
52	HOSM_SCHPO	12.92%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	204	2	1315.66	4	1	40.8	22.3	95.00%	R.VGIADTVGCATPR.Q	Carbamidomethyl (+57)	R.VGIADTVGCATPR.Q
248	257	2	1059.56	3	1	46.4	21.1	95.00%	I.DTSILGIGER.N		R.GVVSCDIECHFHNDTGMAIANAY CALEAGATHIDTSILGIGER.N
146	156	2	1221.63	2.7	1	49.3	22.4	95.00%	I.DSATEVINFVK.S		K.DMTYIIDSATEVINFVK.S
220	227	2	1070.43	2.8	1	25.8	22.6	93.70%	C.DIECHFHN.D	Carbamidomethyl (+57)	R.GVVSCDIECHFHNDTGMAIANAY CALEAGATHIDTSILGIGER.N
32	43	2	1391.75	4.9	1	68.1	19.7	95.00%	R.VNNFSIIESTLR.E		R.VNNFSIIESTLR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
53	LEUC_SCHPO	11.35%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
633	649	2	2002.01	4.5	1	59.4	21.1	95.00%	R.VIIAPSFADIFFNNCFK.N	Carbamidomethyl (+57)	R.VIIAPSFADIFFNNCFK.N
603	619	3	1826.86	5.3	1	37.3	22.8	95.00%	R.HATVLVAHDNFGCGSSR.E	Carbamidomethyl (+57)	R.HATVLVAHDNFGCGSSR.E
477	493	2	1810.88	4.1	1	36.5	21.8	95.00%	R.EFFGDVSNGSPSIITNK.N		R.EFFGDVSNGSPSIITNK.N
520	539	2	1786.91	2.5	0	71.4	20.6	95.00%	A.DGIATNVAGSVSSGSAGIPK.F		K.NYDPSHDVEGDIGLSVDDATDAV TDADGIATNVAGSVSSGSAGIPK.F
455	469	2	1450.8	1.8	0	26.7	17.2	94.90%	R.THLVSPAMAAAAAAIK.G		R.THLVSPAMAAAAAAIK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
54	DHAS_SCHPO	22.13%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
231	244	2	1569.8	2.2	1	38.8	20.9	95.00%	T.DNVVSAQCNRVPVI.D	Carbamidomethyl (+57)	K.ILGSVNSTISGYELTDNVVSAQCN RVPVIDGHLMCISVK.F
307	318	2	1278.6	4.8	1	24.6	23.5	92.00%	R.NNENGYAVSVGR.I		R.NNENGYAVSVGR.I
31	39	2	856.52	4.9	0	28.2	17.2	95.00%	K.IAVLGASAR.S		K.IAVLGASAR.S
143	161	2	2003.02	2.7	0	76.5	19.4	95.00%	R.GCIITNSNCSTAAVVVPLK.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GCIITNSNCSTAAVVVPLK.A
267	278	2	1375.7	3.8	1	37.2	21.5	95.00%	R.EVLANYVSEPQK.L		R.EVLANYVSEPQK.L
6	18	2	1227.7	3.7	0	35.6	17.3	95.00%	K.VGILGATGTVGQR.F		K.VGILGATGTVGQR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
55	GLNA_SCHPO	11.70%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
247	260	2	1546.65	1.5	0	48.4	24.3	95.00%	G.DWNGAGCHTNVSTK.D	Deamidation (+1)/ Carbamidomethyl (+57)	K.ISFHPKPILGDWNGAGCHTNVST K.D
153	170	2	1809.83	2.5	0	46.1	23.2	95.00%	K.GGFPGPQGPFYCGVGTGR.V	Carbamidomethyl (+57)	K.GGFPGPQGPFYCGVGTGR.V
237	246	2	1107.65	1.8	0	25.7	14.1	93.60%	K.ISFHPKPILG.D		K.ISFHPKPILGDWNGAGCHTNVST K.D
237	260	4	2635.31	3.2	1	28.9	19.4	95.00%	K.ISFHPKPILGDWNGAGCHTNVST K.D	Carbamidomethyl (+57)	K.ISFHPKPILGDWNGAGCHTNVST K.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
56	OAT_SCHPO	6.62%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
386	398	3	1374.81	2.2	0	28.4	13	95.00%	R.GVLAKPTHGNIIR.F		R.GVLAKPTHGNIIR.F
276	291	2	1561.85	4	0	53	16.6	95.00%	K.AISGGVYPVSAVLSSR.E		K.AISGGVYPVSAVLSSR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
57	RS18_SCHPO	29.61%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	78	2	1386.79	4	0	45.2	15.2	95.00%	R.IVTIIQNPSQFK.I		R.IVTIIQNPSQFK.I
2	14	2	1578.86	3.1	1	29.9	16.7	95.00%	M.SLVVPDNFQHILR.L	Acetyl (+42)	-.MSLVVPDNFQHILR.L
79	86	2	1031.56	6	0	52.6	20.6	95.00%	K.IPSWFLNR.Q		K.IPSWFLNR.Q
95	106	2	1334.69	4.9	1	24.9	20.8	92.50%	K.SFQLLANNVDSK.L		K.SFQLLANNVDSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
58	UGPA1_SCHPO	16.80%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
22	34	2	1309.62	2	0	66.1	23.2	95.00%	F.DNTATSIAASTMK.N		K.SQSAFAFDNTATSIAASTMK.N
493	506	2	1624.79	2.8	1	72.2	22.8	95.00%	L.ENCVITGNLNILEH.-	Carbamidomethyl (+57)	R.IDIPNGSVLENCVITGNLNILEH.-
1	10	2	1166.63	4.6	1	24.9	19.3	92.40%	-.MDLAPRPLGR.Q	Acetyl (+42)	-.MDLAPRPLGR.Q
185	194	2	1205.65	4.7	1	32.1	19.4	95.00%	K.IDILTFNQSR.Y		K.IDILTFNQSR.Y
94	104	2	1118.56	2.4	1	48.2	21.9	95.00%	Y.DTITEAGGLSR.D		R.GSEINWDLVESPKPEQVVEYDTITEAGGLSR.D
224	235	2	1277.65	3.4	1	23.6	21.7	90.10%	G.DVFEALTNSGII.D		K.ETLLPVPHTADSAIDEWYPPGHGDVFEALTNSGIIDTLIAQGK.E
115	129	2	1460.72	4.2	0	48.3	22.8	95.00%	K.LNGGLGTTMGCVGPK.S	Carbamidomethyl (+57)	K.LNGGLGTTMGCVGPK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
59	ILV3_SCHPO	10.87%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
116	126	2	1124.5	3	0	25.1	24	92.70%	S.DGISMGTTGMR.Y		K.AGLTGFQFNTIGVSDGISMGTTGMR.Y
539	547	2	999.56	2.1	1	28.7	20.6	95.00%	G.DVIEINAVK.N		R.FSGGSHGFLIGHVDPEAQVGGPIALVQDGDVIEINAVK.N
40	48	2	994.5	5.2	1	30.6	23.7	95.00%	K.YSETITGPK.S		K.YSETITGPK.S
246	265	2	2011.93	2.1	1	69.9	23.2	95.00%	A.EAMGMTLPGSSSYLAGSPEK.F		R.HACPGGGACGGMYTANTMASCAEAMGMTLPGSSSYLAGSPEK.F
197	212	2	1760.87	3.4	1	64.4	21.2	95.00%	I.DIVSAFQSYGEFITGK.I		R.AGHSPCQNNAPIDIVSAFQSYGEFITGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
60	HXK1_SCHPO	9.09%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
36	47	2	1482.79	2.5	1	25.4	18.7	93.30%	E.EQFTIPTELLHR.V		K.TLQDHLDELEEQFTIPTELLHR.V
304	315	2	1380.7	5.1	1	25.3	22.1	93.10%	K.MIAGCYLGDILR.R	Carbamidomethyl (+57)	K.MIAGCYLGDILR.R
274	282	2	1076.58	2.3	0	53.9	20	95.00%	F.DNQHVVLPR.T		K.YDFPEDMNMIINCEWCDFDNQHVVLPR.T
2	12	3	1409.65	4.4	1	25.1	23.1	95.00%	M.SLHDAYHWPSR.T	Acetyl (+42)	-.MSLHDAYHWPSR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
61	YF19_SCHPO	16.90%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
195	208	2	1516.82	1.5	1	41.6	18.1	95.00%	K.TAELTPLSALCLTK.F	Carbamidomethyl (+57)	K.TAELTPLSALCLTK.F
18	32	2	1741.92	2.3	0	35.6	18.9	95.00%	K.TYIQPVGLFINNQHV.D		K.TYIQPVGLFINNQHVDSVHGGR.V
422	443	3	2229.12	4.1	0	21.2	19.3	95.00%	R.GNNSTYGLAAGVHTNNITNAIK.V		R.GNNSTYGLAAGVHTNNITNAIK.V
71	80	2	1161.56	3.7	1	28.3	23.5	95.00%	R.AAFQTDAPWR.K		R.AAFQTDAPWR.K
340	349	2	1079.53	3.7	0	31.9	23.1	95.00%	E.DTFQGAQVSK.Q		K.VGDPFAEDTFQGAQVSK.Q
181	194	2	1439.82	2.4	0	54.2	15.3	95.00%	K.IAPAVACGNTIILK.T	Carbamidomethyl (+57)	K.IAPAVACGNTIILK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
62	RL8_SCHPO	15.06%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
24	32	2	1084.62	4.7	0	29.3	18.8	95.00%	K.NPLFVSRPR.S		K.NPLFVSRPR.S
33	43	2	1188.62	4.1	1	26.8	21.3	94.90%	R.SFGIGQDIQPK.R		R.SFGIGQDIQPK.R
134	146	2	1425.8	2	1	51.5	15.1	95.00%	K.YGLNHVVALIEAK.K		K.YGLNHVVALIEAK.K
52	57	2	862.44	5.9	1	26.5	22.3	94.70%	K.WPEYIR.L		K.WPEYIR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
63	PYR1_SCHPO	3.07%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
709	720	2	1229.65	1.9	0	34.6	19.5	95.00%	G.DSIVVAPSQTLT.D		R.DAFDNCITVCNMENFDPLGIHTGDSIVVAPSQTLTDEDYNMLR.T

1771	1784	2	1494.85	4.1	1	35.2	12.3	95.00%	R.EAIPLLLTAVNEGR.L		R.EAIPLLLTAVNEGR.L
689	700	2	1515.58	2.5	1	35.8	23.3	95.00%	F.DNCITVCNMENF.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.DAFDNCITVCNMENFDPLGIHTG DSIVVAPSQTLTDEDYNMLR.T
701	708	2	808.41	1.8	0	28.8	20.6	95.00%	F.DPLGIHTG.D		R.DAFDNCITVCNMENFDPLGIHTG DSIVVAPSQTLTDEDYNMLR.T
1771	1781	2	1152.68	2.8	0	26.5	14	94.60%	R.EAIPLLLTAVN.E		R.EAIPLLLTAVNEGR.L
1897	1906	2	1089.51	4.1	1	23.8	22.9	90.40%	A.EAFGQAPENK.A		K.VSALMSPGLPHAAPSLAEAFGQA PENK.A
1758	1770	2	1371.7	4.4	0	56.2	21.7	95.00%	K.FVGNTAFTGFGVR.E		K.FVGNTAFTGFGVR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
64	VIPI_SCHPO	18.68%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	68	2	1496.86	4.3	1	41.7	13.6	95.00%	K.TALLLQDALLGQNK.I		K.TALLLQDALLGQNK.I
101	110	2	1087.63	5.8	1	34.3	16.6	95.00%	R.SAIISELLSR.G		R.SAIISELLSR.G
122	134	2	1410.71	4.2	1	61.1	21.6	95.00%	K.SIQLDQSYGVSSK.F		K.SIQLDQSYGVSSK.F
137	147	2	1100.62	4.3	1	27.7	18.8	95.00%	K.GILESALSGVR.S		K.GILESALSGVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
65	IF4A_SCHPO	9.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
58	69	2	1173.61	5	0	69	21.8	95.00%	R.DVLAQAQSGTGK.T		R.DVLAQAQSGTGK.T
33	48	2	1854.94	2	1	30.9	20.3	95.00%	R.GIYAYGFERPSAIQQR.A		R.GIYAYGFERPSAIQQR.A
298	305	2	1047.49	4.2	1	24.7	22.7	92.20%	R.DTLMHEFR.T		R.DTLMHEFR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
66	RL15A_SCHPO	19.90%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
115	128	2	1699.83	4.1	1	73.6	22.2	95.00%	R.VLNSYWVNQDATYK.F		R.VLNSYWVNQDATYK.F
78	93	3	1761.94	5.1	0	24	18.2	95.00%	K.GQTYGKPVHQGVNHLK.Y		K.GQTYGKPVHQGVNHLK.Y
148	157	3	1218.69	4.4	0	24.4	16.8	95.00%	R.INWIVNPVHK.H		R.INWIVNPVHK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
67	GBLP_SCHPO	18.47%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
48	57	2	1135.53	4.7	1	43.2	22.9	95.00%	R.DDVNYGVAQR.R		R.DDVNYGVAQR.R
186	212	3	2736.26	2.6	1	43.2	22.2	95.00%	R.TSHYGHTGYVSAVTISPDGSLCA SGGR.D	Carbamidomethyl (+57)	R.TSHYGHTGYVSAVTISPDGSLCA SGGR.D
234	245	2	1314.71	3.1	0	32.5	19.4	95.00%	K.ANINALVFSPNR.Y		K.ANINALVFSPNR.Y
39	47	2	1112.68	5.9	0	27.8	13	95.00%	K.SIILWNLVR.D		K.SIILWNLVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
68	EF1B_SCHPO	13.08%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
59	73	2	1561.84	4.2	1	60.9	18.5	95.00%	K.QIATYDLATLPGTAK.E		K.QIATYDLATLPGTAK.E
153	165	2	1432.74	3.9	1	44.3	21.2	95.00%	R.SIQMDGLVWGLSK.L		R.SIQMDGLVWGLSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
69	RS7_SCHPO	15.90%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
59	70	2	1322.84	4	0	46.5	4.77	95.00%	K.AIVVFVPQPLLK.A		K.AIVVFVPQPLLK.A
168	177	3	1123.57	4.2	0	19.7	22.8	93.50%	K.LGSFSSVYHK.L		K.LGSFSSVYHK.L
19	27	2	1093.55	3.6	0	24.9	21.4	92.50%	T.DLLVAQCLY.D	Carbamidomethyl (+57)	R.SSSQPTETDLLVAQCLYDLESSS K.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
70	TRP_SCHPO	11.76%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
382	393	2	1355.77	4.5	0	47.2	17.2	95.00%	K.INNCIGQILLAK.R	Carbamidomethyl (+57)	K.INNCIGQILLAK.R

400	419	2	1938	1.9	1	69.3	19.5	95.00%	R.IIAETGAGQHGVATAICAAK.F	Carbamidomethyl (+57)	R.IIAETGAGQHGVATAICAAK.F
445	461	2	1739.98	1.9	1	49.2	14.5	95.00%	R.LLGAEVVPVTSGTQTLR.D		R.LLGAEVVPVTSGTQTLR.D
590	598	2	899.44	2.3	0	26.8	21.4	95.00%	Q.DTHSISAGL.D		R.EDGQIQDTHSISAGLDYPGVGPELSELK.Y
91	114	2	2617.33	5.8	1	82.3	18.2	95.00%	R.DAGVTIPIILMGYYNPIFSYGDAK.T		R.DAGVTIPIILMGYYNPIFSYGDAK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
71	RAD24_SCHPO	15.19%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
109	120	2	1236.65	4.7	1	29.1	20.3	95.00%	K.HLIPNAASAESK.V		K.HLIPNAASAESK.V
164	172	2	1032.58	3.4	0	30.7	17.8	95.00%	A.ELAPTHPIR.L		K.AASEIATAELAPTHPIR.L
76	85	2	1071.6	3.6	1	23.8	19.7	90.60%	K.GNTAQVELIK.E		K.GNTAQVELIK.E
218	227	2	1204.65	2.1	0	54	19.6	95.00%	K.DSTLIMQLLR.D	Oxidation (+16)	K.DSTLIMQLLR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
72	RS23_SCHPO	21.68%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
98	107	2	1091.56	2.4	1	53.5	22.2	95.00%	N.DEVLLSGFGR.K		K.VTAFVPHDGCLNFVDENDEVLLSGFGR.K
80	87	2	897.51	1.1	1	30.4	17.5	95.00%	K.KVTAFVPH.D		K.KVTAFVPHDGCLNFVDENDEVLLSGFGR.K
125	137	2	1326.74	4.4	1	55.5	17.2	95.00%	K.VAGVGLSALFHEK.K		K.VAGVGLSALFHEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
73	CDC48_SCHPO	5.03%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
550	563	2	1522.75	3.6	1	43.8	21.7	95.00%	K.AIANECSANFISVK.G	Carbamidomethyl (+57)	K.AIANECSANFISVK.G
511	522	2	1424.67	4.6	1	24.4	23	91.60%	R.ETVQMPVMYAEK.F		R.ETVQMPVMYAEK.F
430	444	2	1691.8	1.8	1	58.1	22.1	95.00%	S.DLASLCSEAAMQQIR.E	Carbamidomethyl (+57)	K.LADDVDLEQIAAETHGYVGSDLASLCSEAAMQQIR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
74	YHY6_SCHPO	15.92%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
214	225	2	1537.76	3	0	31.7	21.6	95.00%	A.DFPNWYQQVLTK.S		K.DADFPNWYQQVLTK.S
161	187	3	2608.39	2.9	1	26.8	14.5	95.00%	K.SVGVNPIIVDFSAPGSATAPSKPAAQK.K		K.SVGVNPIIVDFSAPGSATAPSKPAAQK.K
147	160	2	1522.84	2.9	0	35	15.2	95.00%	K.TVFVSPAAVQTYLK.S		K.TVFVSPAAVQTYLK.S
335	343	2	1114.59	4.7	0	24.2	20.9	91.20%	K.LNQWNSVVR.W		K.LNQWNSVVR.W
387	398	2	1343.81	4.3	1	30.5	9.03	95.00%	R.IYTDLLAVPVIK.G		R.IYTDLLAVPVIK.G
426	441	3	1703.81	4.5	0	20.8	22.7	95.00%	R.GIQGATSHCLGQNFSK.M	Carbamidomethyl (+57)	R.GIQGATSHCLGQNFSK.M
60	83	3	2367.33	2.5	1	29.1	9.54	95.00%	K.SQTVVPIILAALETTSTPSGIAAK.A		K.SQTVVPIILAALETTSTPSGIAAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
75	RS6B_SCHPO	18.41%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
39	51	2	1414.68	2.5	1	51.3	23.2	95.00%	G.DSVGPEFAGYVFK.I		R.MGQEVPGDSVGPEFAGYVFK.I
99	115	2	1739.01	3.8	1	65.7	11.1	95.00%	R.GCIVGQDLAVLALAIVK.Q	Carbamidomethyl (+57)	R.GCIVGQDLAVLALAIVK.Q
59	72	3	1625.86	4.7	0	32.2	19.1	95.00%	K.QGFPMFQGVLLPHR.V		K.QGFPMFQGVLLPHR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
76	EF1G_SCHPO	15.40%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
290	298	2	1136.52	2.1	1	34.7	23	95.00%	F.DPENYSVWK.V		R.SGALPWFFEHFDPENYSVWK.V

93	115	3	2635.36	2.4	1	73.3	15.7	95.00%	K.VLQYCSFTNSELPGAFRPIIAPR.V	Carbamidomethyl (+57)	K.VLQYCSFTNSELPGAFRPIIAPR.V
207	216	2	1182.71	4	1	27.1	14.6	95.00%	K.FIDQPLPIIK.A		K.FIDQPLPIIK.A
367	375	2	1103.5	2.9	0	23.9	23.3	90.60%	P.DWGSYTFTK.L		K.GHDYVPAFDVAPDWGSYTFTK.L
128	139	2	1303.72	4.6	1	40.7	18.6	95.00%	K.EAETAIALIFAR.F		K.EAETAIALIFAR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
77	LYS12_SCHPO	15.75%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
197	208	2	1324.65	5.3	1	41.8	23	95.00%	K.SNVMSVTDGLFR.E		K.SNVMSVTDGLFR.E
298	307	2	1044.58	4.6	0	32.2	20.9	95.00%	R.GIANPVATFR.S		R.GIANPVATFR.S
279	292	2	1485.66	1.2	1	52.4	23.9	95.00%	G.DNFVMSEPVHGSAP.D		R.EPECFDVVVAPNLYGDILSDGAASLIGSLGLVPSANVGDNFVMSEPVHGSAPDIAGR.G
188	196	3	1047.69	4.7	0	25.1	3.01	95.00%	K.KPLVTIIHK.S		K.KPLVTIIHK.S
86	97	2	1231.7	4.7	0	25.9	16.7	94.00%	K.VAGYSSPIVALR.K		K.VAGYSSPIVALR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
78	SPI1_SCHPO	18.52%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
110	122	2	1514.77	4.6	1	58.5	21.8	95.00%	R.VCENIPIVLCGNK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VCENIPIVLCGNK.V
189	201	2	1607.73	2.2	1	55.2	24	95.00%	V.DQQLLAQYQQEMN.E		K.LVGNPNLEFVASPALAPPEVQVDQQLLAQYQQEMNEAAAMPLPDEDDADL.-
152	165	2	1783.91	1.5	1	36.5	20.4	95.00%	K.SNYNFEKPFLWLAR.K		K.SNYNFEKPFLWLAR.K
189	198	2	1233.6	2.8	0	38.1	23.1	95.00%	V.DQQLLAQYQQ.E		K.LVGNPNLEFVASPALAPPEVQVDQQLLAQYQQEMNEAAAMPLPDEDDADL.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
79	BCA1_SCHPO	13.68%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
315	331	2	1670.97	4.2	1	59.5	12.3	95.00%	R.LLEVFGAGTAALVSPVK.A		R.LLEVFGAGTAALVSPVK.A
262	278	2	1795	4.2	1	43.3	12.3	95.00%	K.EIITAPLDGMILPGVTR.D		K.EIITAPLDGMILPGVTR.D
363	380	2	2024	1.4	1	32	21	95.00%	L.DIQYGKEPNNPWSVPALP.-		K.WILDIQYGKEPNNPWSVPALP.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
80	VATA_SCHPO	7.11%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
227	240	2	1539.8	2.3	0	53.6	19.8	95.00%	A.DNLTANQPLLTGQR.V		R.AARPVADNLTANQPLLTGQR.V
128	136	2	1002.51	5	1	25.2	22.2	93.00%	R.GINTESLNR.E		R.GINTESLNR.E
317	331	2	1544.81	4.6	0	49.4	20.9	95.00%	R.TTLVANTSNMPVAAR.E		R.TTLVANTSNMPVAAR.E
221	240	3	2105.14	4.1	1	35.3	16	95.00%	R.AARPVADNLTANQPLLTGQR.V		R.AARPVADNLTANQPLLTGQR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
81	MMF1_SCHPO	25.31%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
94	105	2	1246.64	3	1	46.5	22	95.00%	Q.EVLTEAGSSLNK.I		R.QCLLNLQEVLTEAGSSLNK.I
59	75	2	1747.86	2.8	0	34.8	21.7	95.00%	K.ANGVIYCSGQIPVANGK.V	Carbamidomethyl (+57)/ Deamidation (+1)	K.ANGVIYCSGQIPVANGK.V
47	58	2	1247.66	5.3	0	27.4	19.6	95.00%	K.LSSAGPYNQAIK.A		K.LSSAGPYNQAIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
82	PMP20_SCHPO	23.08%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
110	119	2	997.56	2.8	0	42.4	16.4	95.00%	F.DASGLLGPLR.S		K.AFDAGFDASGLLGPLR.S

30	55	2	2747.41	2.2	1	52.6	17.2	95.00%	K.FIIVGVPGAFTPPCSSQVPGYIANEK.Q	Carbamidomethyl (+57)	K.FIIVGVPGAFTPPCSSQVPGYIANEK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
83	CARB_SCHPO	6.03%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
968	975	2	1019.52	4.9	0	24.9	23	92.50%	K.VPQFSWTR.L		K.VPQFSWTR.L
932	943	2	1304.72	5.6	1	35.2	18.1	95.00%	K.TLGVNFIDVATR.S		K.TLGVNFIDVATR.S
315	322	2	808.41	1.8	0	28.8	20.6	95.00%	F.DPLGIHTG.D		R.DAANNCITVCNMENFDPLGIHTGDSIVVAPSQTLSDEEYHMLR.T
402	417	3	1672.96	2.4	1	30.2	12	95.00%	K.IALGHTLPELPNAVTK.T		K.IALGHTLPELPNAVTK.T
773	798	3	2736.49	2.9	0	51	13.2	95.00%	K.FANAVGYPVLVRPSYVLSGAAMSVIR.D		K.FANAVGYPVLVRPSYVLSGAAMSVIR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
84	THI4_SCHPO	10.23%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
328	338	2	1056.56	2.8	0	25.1	20.2	92.80%	L.DPVAVGATTAR.S		K.TYIHAAQVNNDLARPVILDPVAVGATTAR.S
373	385	2	1353.71	4.1	1	37.5	19.8	95.00%	R.GVDSISQHTLAAR.I		R.GVDSISQHTLAAR.I
249	265	4	1917.09	3.2	1	33.8	10.4	95.00%	K.LKDFTPLIHHLTNAVAK.N		K.LKDFTPLIHHLTNAVAK.N
237	248	2	1322.76	4.7	0	31.5	13.2	95.00%	K.DLLNQIPAALQK.L		K.DLLNQIPAALQK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
85	IF5A1_SCHPO	13.38%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	81	2	1018.39	3.7	0	28.2	22.2	95.00%	E.DMSPSTHNM.D		K.YEDMSPSTHNMDVPVVK.R
58	69	2	1352.76	4.3	1	43.7	15.6	95.00%	K.VHIVALDIFNGR.K		K.VHIVALDIFNGR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
86	RL13_SCHPO	32.21%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
172	183	2	1398.66	5.4	1	54	23.8	95.00%	K.NFNAFSTLSNER.A		K.NFNAFSTLSNER.A
118	128	3	1326.79	4.7	0	51.2	13.8	95.00%	K.VYLAHLIVFPR.K		K.VYLAHLIVFPR.K
46	64	4	2080.27	3.1	1	20	0	95.00%	K.IAPRPVEAIRPAVKPPTIR.Y		K.IAPRPVEAIRPAVKPPTIR.Y
89	100	2	1263.7	3.9	1	28.9	18.6	95.00%	R.VASTIGIPVDHR.R		R.VASTIGIPVDHR.R
148	160	2	1324.73	2.9	1	58.9	16	95.00%	T.DVAAVLPITQEAV.E		K.GDATDVSGAEQTDVAAVLPITQEAVEEAKPITEEAK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
87	ACL1_SCHPO	9.11%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
369	381	2	1420.73	4.5	1	44	21.2	95.00%	R.GSELTYNNVPISK.V		R.GSELTYNNVPISK.V
171	182	3	1338.74	4.8	0	23.6	16.2	95.00%	K.LYRPGSVAYVSK.S		K.LYRPGSVAYVSK.S
156	170	2	1506.72	3.3	1	45.7	23.6	95.00%	K.IGNTGGMMDNIVASK.L		K.IGNTGGMMDNIVASK.L
328	343	2	1638.94	2.2	1	27.8	12.6	95.00%	K.GVIVPQPEVAPPNIPL.D		K.GVIVPQPEVAPPNIPLDYAWAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
88	ACON_SCHPO	4.88%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
532	549	2	1853.89	4.6	1	68.9	22	95.00%	K.GYDPGSNTYVAPSSVNVK.D		K.GYDPGSNTYVAPSSVNVK.D
392	402	2	1203.6	5.2	1	35.2	22.5	95.00%	R.AASICQQAIDK.G	Carbamidomethyl (+57)	R.AASICQQAIDK.G
462	470	2	1052.53	5	0	36.5	22.4	95.00%	K.NSIVTSYNR.N		K.NSIVTSYNR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
89	AROG_SCHPO	11.83%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

210	226	3	1718.88	2.1	0	21.2	20.4	95.00%	I.DAIGATAHPHTMLGVTK.Q		K.NGTDGTVGVAIDAIGATAHPHTMLGVTK.Q
144	157	2	1521.74	3.8	1	29.4	22.4	95.00%	C.DVTNFGIPLASEML.D	Oxidation (+16)	R.QMYCDVTNFGIPLASEMLDNISPQFFADLLSFGAIGAR.T
186	198	2	1364.74	2.5	0	62.4	18.8	95.00%	R.ELASALSFPVGFK.N		R.ELASALSFPVGFK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
90	GCSP_SCHPO	10.91%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
953	965	2	1458.76	1.1	0	43.1	20.8	95.00%	K.DNNLLVNAPHPQK.D		K.DNNLLVNAPHPQK.D
657	684	3	2835.48	2.1	0	27.9	15.8	95.00%	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C	Carbamidomethyl (+57)	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C
770	788	3	1908.94	2.5	0	21.6	21.9	95.00%	K.TFCIPHGGGGPGVGPICVK.K	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.TFCIPHGGGGPGVGPICVK.K
379	412	3	3679.8	2.3	1	51.4	16.5	95.00%	K.ATSNICTAQALLANMSAFYAIYHGPNGLQEIANR.I	Carbamidomethyl (+57)	K.ATSNICTAQALLANMSAFYAIYHGPNGLQEIANR.I
560	576	2	1831.87	4	0	34.6	23.1	95.00%	K.DLSLAHAMTPLGSCTMK.L	Carbamidomethyl (+57)	K.DLSLAHAMTPLGSCTMK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
91	SODC_SCHPO	24.03%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
98	116	2	1984.04	4.4	1	72.6	17.4	95.00%	K.TTFSDSVISLFGANSIIGR.T		K.TTFSDSVISLFGANSIIGR.T
102	116	2	1547.83	2.1	0	84.5	18.5	95.00%	S.DSVISLFGANSIIGR.T		K.TTFSDSVISLFGANSIIGR.T
53	70	2	1902.78	0.83	1	40.8	23.8	95.00%	G.DNTNGCTSAGPHFNPEGK.T	Deamidation (+1)/ Carbamidomethyl (+57)	R.GFHIHQFGDNTNGCTSAGPHFNPEGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
92	RL3A_SCHPO	13.66%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
11	19	2	982.54	4.3	0	27.2	19	95.00%	R.HGSLGFLPR.K		R.HGSLGFLPR.K
320	334	2	1601.83	3.3	1	29.9	20.5	95.00%	N.DFVMLNGATPGPVKR.V	Deamidation (+1)	R.YGVVENDFVMLNGATPGPVKR.V
101	111	2	1242.63	3.7	1	33.8	21.9	95.00%	R.SLTTVWAEHLS.E		R.SLTTVWAEHLSEEVK.R
249	266	3	2035.03	4.4	0	29.3	20.6	95.00%	K.VACIGAWHPANVQWTVAR.A	Carbamidomethyl (+57)	K.VACIGAWHPANVQWTVAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
93	THRC_SCHPO	10.51%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
265	282	2	1945.01	4.9	1	46.3	19.4	95.00%	R.FIVPTGNFGDILAGYYAK.R		R.FIVPTGNFGDILAGYYAK.R
489	498	2	1135.57	2.9	0	30	22.4	95.00%	R.TCIFSGKPNI.D	Carbamidomethyl (+57)	R.TCIFSGKPNIDILK.Q
313	327	2	1443.73	4.4	1	39.8	22.1	95.00%	K.ADSTQVSPSGPISAK.E		K.ADSTQVSPSGPISAK.E
377	387	2	1184.64	2.5	1	26.1	18.9	94.20%	R.DGTVTVRPEVL.E		R.DGTVTVRPEVLEAAR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
94	FAS1_SCHPO	3.47%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
415	431	3	1929.06	4.4	0	19.3	14.8	92.60%	R.FLSISVPFHSPYLAPVR.S		R.FLSISVPFHSPYLAPVR.S
1870	1881	2	1266.57	5.2	1	37.8	24.2	95.00%	R.SDYGMVAANPSR.V		R.SDYGMVAANPSR.V
1778	1806	3	3141.54	1.9	1	40.3	18.6	95.00%	K.DSTSFSFTHPSGLLSATQFTQPALTLMEK.S		K.DSTSFSFTHPSGLLSATQFTQPALTLMEK.S
781	794	2	1545.81	3.9	1	42.1	20.3	95.00%	K.LPPMPFDGILFGSR.L		K.LPPMPFDGILFGSR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
95	STI1_SCHPO	6.77%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
549	560	2	1269.65	2.9	0	64.8	21.2	95.00%	Q.DPAMQAILGQAR.E		K.DPEVLGILQDPAMQAILGQAR.E
112	132	2	2007.97	4.2	1	89.9	21.8	95.00%	K.SVEAAQTQAASGAGGFNPFAK.L		K.SVEAAQTQAASGAGGFNPFAK.L

371	377	2	800.44	3.8	1	29.8	23	95.00%	R.TPDILSR.L		R.TPDILSR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
96	SCE3_SCHPO	8.51%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
250	271	3	2195.07	4.8	1	32.4	21.2	95.00%	R.SSSNVNTEATPSATTTTSSKPK.R		R.SSSNVNTEATPSATTTTSSKPK.R
112	122	2	1226.6	2.9	1	37.1	23.4	95.00%	G.DFFGEGVTSIR.L		R.DAIPIPSEPPFTAHVGNLSFDLTENDLGDFFGEGVTSIR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
97	ASNS_SCHPO	3.59%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
156	165	2	1143.55	3.3	1	27.5	22.9	95.00%	P.DTAYFASELK.A		R.DPIGITTLYQGFSSDSPDTAYFASELK.A
399	408	2	1120.54	4.9	1	26.3	21.9	94.40%	K.STMAWGLEAR.V		K.STMAWGLEAR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
98	DHOM_SCHPO	16.76%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	138	2	1568.79	4.5	1	56.7	21.1	95.00%	K.AFSASNDVYQNIIK.A		K.AFSASNDVYQNIIK.A
57	67	2	1391.68	4.7	1	33.1	22.6	95.00%	K.DYQPINLSEWK.N		K.DYQPINLSEWK.N
313	325	2	1435.64	3.8	1	44.6	23.9	95.00%	K.YDASHPFANLQSS.D		K.YDASHPFANLQSSDNIISFTTK.R
238	252	2	1526.81	-0.67	1	49.7	20.3	95.00%	R.IAGVHVESASSFPVK.S		R.IAGVHVESASSFPVK.S
266	275	2	1135.56	3.3	1	24.8	22.6	92.40%	A.EEFLAGLPNF.D		K.SAVNAEEFLAGLPNFDSEFASMR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
99	PYC_SCHPO	3.38%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
917	929	2	1447.76	4.7	1	42.2	20.4	95.00%	K.VVGDLAQFMVQNK.L		K.VVGDLAQFMVQNK.L
839	848	2	1297.58	4.8	1	38.2	24	95.00%	R.EIDSYWAQMR.L		R.EIDSYWAQMR.L
107	123	2	1745.84	3.6	1	41.5	22.1	95.00%	R.TGANLVHPGYGFLSENA.E		R.TGANLVHPGYGFLSENAEFAR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
100	RS11_SCHPO	15.13%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	64	2	1161.6	4.7	0	33.4	21.5	95.00%	K.CPFVGQVSIR.G	Carbamidomethyl (+57)	K.CPFVGQVSIR.G
118	130	2	1457.77	2.9	0	55.2	19.7	95.00%	G.DVVTVGQCRPLSK.T	Carbamidomethyl (+57)	R.INEGDVVTVGQCRPLSK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
101	RS8A_SCHPO	21.50%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
165	178	2	1475.79	4.1	0	33.2	18.9	95.00%	R.LYAVVSSRPGQSGR.C		R.LYAVVSSRPGQSGR.C
78	92	2	1751.94	3.2	1	41.3	18.1	95.00%	R.IIQVAYHPSNNELVR.T		R.IIQVAYHPSNNELVR.T
111	124	3	1682.82	4.5	1	23.1	22.3	95.00%	R.VWYETHYGILMGSK.G		R.VWYETHYGILMGSK.G
78	88	2	1254.64	2.5	0	44.3	21.8	95.00%	R.IIQVAYHPSNN.E		R.IIQVAYHPSNNELVR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
102	RS10B_SCHPO	23.13%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	44	3	1428.81	3.2	1	31	16.5	95.00%	K.HPEVGVPNLQVIK.A		K.HPEVGVPNLQVIK.A
10	24	3	1621.94	4.8	0	31.6	12.8	95.00%	K.AIHQALFQQGVLVAK.K		K.AIHQALFQQGVLVAK.K
26	31	2	732.38	5.5	0	30.1	22.2	95.00%	K.DFNLPK.H		K.DFNLPK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
103	PURA_SCHPO	8.53%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
268	276	2	899.55	4.9	0	44.5	18.9	95.00%	R.IANSIGVVK.A		R.IANSIGVVK.A
413	427	2	1514.86	2.3	0	30.4	14.1	95.00%	K.FVGVPITFIGVGPGR.D		K.FVGVPITFIGVGPGR.D
64	76	2	1435.79	2.1	0	26.2	16.8	94.30%	Y.DFHILPSGLVNPK.C		R.CQGGNNAGHTIVANGVTYDFHILPSGLVNPK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
104	RS22_SCHPO	23.85%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
9	19	2	1316.62	3	1	40	23.4	95.00%	A.DCLNNIVNAER.R	Carbamidomethyl (+57)	R.QSVLADCLNNIVNAER.R
98	108	2	1171.7	4.9	0	29.1	13.4	95.00%	R.QVGVIVLTTSR.G		R.QVGVIVLTTSR.G
89	97	2	1111.62	5.6	0	31.9	16.8	95.00%	K.WVNQLLPSR.Q		K.WVNQLLPSR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
105	SERC_SCHPO	11.31%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
216	228	2	1299.74	5	0	37	14.8	95.00%	K.NAGPAGITVVFVR.D		K.NAGPAGITVVFVR.D
229	242	3	1532.84	5.6	1	18.3	16.5	90.20%	R.DSVLARPTPAELHK.L		R.DSVLARPTPAELHK.L
189	199	2	1282.6	4.3	1	67	23.4	95.00%	R.VCDVSSNFISR.K	Carbamidomethyl (+57)	R.VCDVSSNFISR.K
324	329	2	766.38	5.3	0	26.2	21.3	94.30%	R.MNVTFR.I		R.MNVTFR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
106	GCST_SCHPO	17.83%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
266	281	2	1688.87	1.6	1	39.7	20.6	95.00%	D.DTTSPVEGSLSWIIGK.R		R.LEAGMCLYGSDIDDTTSPVEGSLSWIIGK.R
34	51	2	1940.98	2.2	0	51.8	19.6	95.00%	K.EGATIVPFAGFSMPVQYK.G		K.EGATIVPFAGFSMPVQYK.G
165	180	2	1623.93	4	1	75.8	11.5	95.00%	R.ALIAIQGPETASVVQK.L		R.ALIAIQGPETASVVQK.L
326	344	2	1886.91	3.7	1	93.3	21.8	95.00%	V.DGVEVGQVTSGCPSPTLGK.N	Carbamidomethyl (+57)	R.HGSAVEVDGVEVGQVTSGCPSPTLGK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
107	RL10A_SCHPO	13.12%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	128	3	1265.71	4.6	0	30	15.9	95.00%	R.HAFGKPNGLVAR.V		R.HAFGKPNGLVAR.V
129	139	2	1228.7	4.7	0	40	16.1	95.00%	R.VNIGQILMSVR.T		R.VNIGQILMSVR.T
33	38	2	719.4	4.8	1	27.1	17.8	95.00%	R.IFDLGR.K		R.IFDLGR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
108	PPA2_SCHPO	6.05%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
356	365	2	1118.56	2.3	1	25.8	22.3	93.80%	P.DITPEHPLPT.D		K.VFLAFTHDSQIIPVEAALGFFPDITPEHPLPTDK.N
44	61	2	2044.91	2.2	1	68.4	23.9	95.00%	H.EPYFNGPTTSFPESCAIK.Q	Deamidation (+1)/ Carbamidomethyl (+57)	K.DHLGTISVYHEPYFNGPTTSFPESCAIK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
109	SYEC_SCHPO	5.31%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
394	404	2	1196.62	4	1	30.5	21.1	95.00%	V.DSLEGVTHALR.T		R.AYPTYDFACPIVDSLEGVTHALR.T
652	666	2	1734.83	1.5	1	30.9	23.1	95.00%	K.DFLTPQTEFHSPVFA.D		K.DFLTPQTEFHSPVFADVGIK.N
66	77	2	1393.77	4.3	0	31.9	16.8	95.00%	K.LALQTFSQVYPK.L		K.LALQTFSQVYPK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
110	LEU1_SCHPO	10.96%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
464	479	2	1742.82	4.9	1	69.1	23.3	95.00%	R.FSVNDYTLSSNGPQSK.C		R.FSVNDYTLSSNGPQSK.C
388	398	2	1249.63	2.4	1	35.9	22	95.00%	H.DVNSEYAAIIR.V		K.VPYLPLDPHDVNSEYAAIIR.V

341	362	3	2346.15	2.9	1	44.7	21.3	95.00%	R.HPYAGNLVFTAFSGSHQDAISK.G		R.HPYAGNLVFTAFSGSHQDAISK.G
137	151	3	1761.87	4	0	33.2	22.3	95.00%	K.NATVHLYNACSPLFR.E	Carbamidomethyl (+57)	K.NATVHLYNACSPLFR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
111	RL30A_SCHPO	28.44%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
71	89	2	1997.95	6	1	62.5	22	95.00%	K.ANVHHYAGTNIDLGTACGK.L	Carbamidomethyl (+57)	K.ANVHHYAGTNIDLGTACGK.L
47	58	2	1335.77	2.6	0	27.1	13.2	95.00%	K.LILIAGNCPPLR.K	Carbamidomethyl (+57)	K.LILIAGNCPPLR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
112	ASSY_SCHPO	9.51%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
198	205	2	871.41	1.9	0	31.4	22.4	95.00%	E.DPSMTPPK.D		K.KPWSMDENIVHCSYEAGILEDPSMTPPK.D
333	350	2	1885	3.5	1	87.2	17.3	95.00%	R.MLLAANNVSQEVVNGVVK.L	Deamidation (+1)	R.MLLAANNVSQEVVNGVVK.L
320	332	2	1601.77	4.2	0	39.6	23.3	95.00%	K.ILYNGQFFSPCTR.M	Carbamidomethyl (+57)	K.ILYNGQFFSPCTR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
113	RS14_SCHPO	16.55%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
95	105	2	1037.57	5.3	0	47.1	19.2	95.00%	K.TPGPGAQAALR.A		K.TPGPGAQAALR.A
73	84	3	1367.77	4	1	24.2	16.5	95.00%	K.CKEVGITALHIK.I	Carbamidomethyl (+57)	K.CKEVGITALHIK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
114	SYDC_SCHPO	4.14%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
281	294	2	1356.6	4.8	1	27.5	24	95.00%	K.MSGASSEGGSNVFK.I		K.MSGASSEGGSNVFK.I
490	499	2	1300.55	3.9	1	26.9	24.1	95.00%	R.YSNSYDFFMK.G		R.YSNSYDFFMK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
115	GLT1_SCHPO	2.51%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1690	1707	2	2063.08	4.1	1	61.9	18.1	95.00%	K.EALTQLLLTNNFPEFTGR.V		K.EALTQLLLTNNFPEFTGR.V
1787	1802	3	1728.9	3	1	30.5	19	95.00%	R.ADRPGGLLQYGIPNMK.L		R.ADRPGGLLQYGIPNMK.L
1758	1776	2	1792.99	3.3	1	78.8	15.4	95.00%	R.VAIIGSGPAGLAAADQLNR.A		R.VAIIGSGPAGLAAADQLNR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
116	RL12_SCHPO	34.55%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
68	83	2	1538.91	3.4	0	50.5	11.8	95.00%	R.QAAVSVVPSASALVIK.A		R.QAAVSVVPSASALVIK.A
97	106	2	996.5	3.3	0	24.1	21.3	91.10%	K.NVAHSGNVSL.D		K.NVAHSGNVSLDEIIEVAR.T
17	31	2	1312.7	3.6	1	46	18.2	95.00%	R.AVGGEVAGGSTLAPK.I		R.AVGGEVAGGSTLAPK.I
131	146	2	1652.81	4	1	45.9	21.7	95.00%	K.EILGTAFSVGCTVDGK.N	Carbamidomethyl (+57)	K.EILGTAFSVGCTVDGK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
117	NACA_SCHPO	13.87%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	75	2	1164.62	5.8	0	59.3	21.2	95.00%	K.SSNNAYIVLGK.V		K.SSNNAYIVLGK.V
52	64	2	1540.93	4.4	1	50.2	4.77	95.00%	K.NILLIINEPIVYK.S		K.NILLIINEPIVYK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
118	PGM_SCHPO	4.87%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
253	260	2	920.46	2.6	0	25.2	23.3	93.00%	P.DPNLTYAK.S		K.ELGMPSSVCQNCKPLPDFGGGHPDPNLTYAK.S
350	358	2	1160.54	5.2	1	29	23.3	95.00%	K.FFCNLFDAK.R	Carbamidomethyl (+57)	K.FFCNLFDAK.R
297	306	2	1032.54	2.3	0	40.3	21.5	95.00%	S.DSVAIIAHHA.E		R.NMIYGANAFVTPSDSVAIIAHHAELIPYFR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
119	PUR4_SCHPO	3.85%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
507	522	2	1533.78	3.2	1	63.4	21.1	95.00%	H.DVGAGGVSNALPELVH.D		R.AQMVIDACTTMDENIIQSIHDVGAGGVSNALPELVHDAGLGAR.F
323	334	2	1146.56	3.3	1	33.8	22.9	95.00%	R.DEGAVGQGSLSK.A		R.DEGAVGQGSLSK.A
498	506	2	1067.53	2.2	1	30.2	22.3	95.00%	M.DENIIQSIH.D		R.AQMVIDACTTMDENIIQSIHDVGAGGVSNALPELVHDAGLGAR.F
412	425	3	1426.76	5.3	0	35.9	20.9	95.00%	R.GYHKPIMAAGGIGR.I		R.GYHKPIMAAGGIGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
120	PDI1_SCHPO	7.11%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	136	3	1350.87	5.1	1	30.4	0	95.00%	R.KQLLPTVKPISK.D		R.KQLLPTVKPISK.D
85	93	2	1141.51	3.5	1	30.7	24	95.00%	G.DLCSEYSIR.G	Carbamidomethyl (+57)	K.DGISLVEVDCTEEGDLCSEYSIR.G
188	201	2	1436.77	4.3	0	45.1	18.3	95.00%	K.SLGSNFPGIVAFTK.D		K.SLGSNFPGIVAFTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
121	SYTC_SCHPO	3.41%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
248	258	2	1187.55	4.2	1	47.1	24.1	95.00%	K.NSSSYFLGDAK.N		K.NSSSYFLGDAK.N
227	239	3	1445.69	3.9	0	19.9	22.8	93.90%	I.DLCTGPHVPHTGR.I	Carbamidomethyl (+57)	R.CGPLIDLCTGPHVPHTGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
122	IMDH_SCHPO	4.96%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
303	313	2	1155.67	4.5	1	51.3	17.4	95.00%	K.IDVIAGNVVTR.E		K.IDVIAGNVVTR.E
419	433	2	1421.67	3.9	1	52.2	23.9	95.00%	R.GMGSIAAMEGTGVNK.N		R.GMGSIAAMEGTGVNK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
123	PMM_SCHPO	9.34%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
19	28	2	1043.53	3.1	1	40	21.2	95.00%	F.DVDGTLTPAR.L		K.TLVLFDVDGTLTPAR.L
45	58	2	1347.75	4.4	1	41.6	18.1	95.00%	K.VVAIGFVGGSDLSK.Q		K.VVAIGFVGGSDLSK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
124	SPEE_SCHPO	8.39%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	12	2	1291.72	4.1	1	43.5	17.5	95.00%	M.SVQELSHPLIK.D	Acetyl (+42)	-.MSVQELSHPLIK.D
18	31	2	1631.79	4.6	0	31.2	22.5	95.00%	R.EINNMWPGQAMTLK.V		R.EINNMWPGQAMTLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
125	RL27A_SCHPO	19.12%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	48	3	1461.76	5.9	1	42.8	20.6	95.00%	K.SHPFGHAVVAGVER.Y		K.SHPFGHAVVAGVER.Y
23	34	2	1269.74	4.4	1	65.4	15.8	95.00%	K.VVILQAIDQGSK.S		K.VVILQAIDQGSK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
126	TAL1_SCHPO	5.59%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
27	44	3	1917.03	4	1	42	18.3	95.00%	K.YKPQDATTNPSLILAASK.K		K.YKPQDATTNPSLILAASK.K
31	44	2	1400.75	2.6	0	60.7	19	95.00%	Q.DATTNPSLILAASK.K		K.YKPQDATTNPSLILAASK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
127	SLBR2_SCHPO	8.83%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
134	143	2	1115.56	4.3	1	27.1	22.4	95.00%	R.NIESSVQPSR.E		R.NIESSVQPSR.E

149	157	2	1075.63	4.5	1	33	16.1	95.00%	K.LLDQIYALK.H			K.LLDQIYALK.H
294	305	2	1374.72	1.9	1	23.6	20.5	90.00%	G.EPVPVEQVTHLQ.D			R.SWNEYEAQGEPVPVEQVTHLQD DVQSDTSEIIENEPGMHPHVHAER. M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
128	AATR1_SCHPO	9.07%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
305	317	2	1562.83	3.7	1	52.6	18.7	95.00%	R.VGWFTAQPLFIER.G		R.VGWFTAQPLFIER.G
38	54	2	1856.03	4.5	1	36.8	14.3	95.00%	K.IISLAGGLPNPEYFPIR.E		K.IISLAGGLPNPEYFPIR.E
7	19	3	1436.71	5.4	1	43.2	22.8	95.00%	K.DLSHHLSVESASR.K		K.DLSHHLSVESASR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
129	HMCS_SCHPO	9.17%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
155	183	3	2859.52	1.6	1	43.6	14.1	95.00%	K.GNARPTGGAGCVALLVGPNAPIV FEPGLR.G	Carbamidomethyl (+57)	K.GNARPTGGAGCVALLVGPNAPIV FEPGLR.G
217	228	2	1325.64	3.7	1	38.4	23.7	95.00%	K.ALDGAYANYNVR.D		K.ALDGAYANYNVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
130	DHE4_SCHPO	4.66%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
356	367	2	1231.57	4.5	1	27.7	23.5	95.00%	R.ASGEGCWLAPGK.A	Carbamidomethyl (+57)	R.ASGEGCWLAPGK.A
93	101	2	1127.61	5.6	1	29.2	20.5	95.00%	K.FLGFEQIFK.N		K.FLGFEQIFK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
131	SYRC_SCHPO	6.80%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
163	180	2	1987.02	4.1	1	33.9	18.6	95.00%	R.STIIGSFLANLHESQGWK.V		R.STIIGSFLANLHESQGWK.V
480	489	2	1284.6	5.9	1	39.4	23	95.00%	R.INNYAFDWSR.M		R.INNYAFDWSR.M
11	24	2	1544.86	4.5	1	46.7	15.6	95.00%	K.SLSTLGLQDLPVFR.E		K.SLSTLGLQDLPVFR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
132	DAK1_SCHPO	5.86%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
45	66	3	2123.05	5.3	1	21	20.2	95.00%	K.NVSVISGGGAGHEPTHSSFVGK. G		K.NVSVISGGGAGHEPTHSSFVGK. G
388	399	2	1358.73	4.4	1	25.9	20.7	94.00%	R.QAIVNSMENLIK.A		R.QAIVNSMENLIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
133	RS4B_SCHPO	12.60%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
12	22	3	1285.7	4.9	1	18.7	18.9	91.30%	R.VAAPHHWLLDK.L		R.VAAPHHWLLDK.L
222	233	2	1232.68	5.6	1	42.4	19.2	95.00%	R.LSNVFVIGEAGK.S		R.LSNVFVIGEAGK.S
40	49	2	1258.72	4.7	0	26.1	17.2	94.20%	R.ECLPLIVFLR.N	Carbamidomethyl (+57)	R.ECLPLIVFLR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
134	RS2_SCHPO	19.37%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
64	74	2	1441.73	5.7	1	25.1	21.5	92.80%	K.EYQIVDYFLPR.L		K.EYQIVDYFLPR.L
174	185	3	1138.69	4.8	1	25.2	11.8	95.00%	R.GAGLVAAPVTKR.F		R.GAGLVAAPVTKR.F
54	63	2	1237.7	2.7	0	34.7	14.6	95.00%	E.EIYLYSLPIK.E		K.SIEEIYLYSLPIK.E
141	156	3	1696.87	4.8	1	37.6	20.8	95.00%	R.GYWGTALGDPHTVPVK.V		R.GYWGTALGDPHTVPVK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
135	SYG_SCHPO	6.90%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
216	232	3	1983	3.2	1	35.8	19.5	95.00%	K.GYLRPETAQGQFLNFSR.L		K.GYLRPETAQGQFLNFSR.L
492	506	2	1649.85	4.8	1	35.7	20.7	95.00%	R.TYTPNVIEPSFGLGR.I		R.TYTPNVIEPSFGLGR.I

526	538	2	1298.77	3.9	0	28.2	14.3	95.00%	R.GVLSFPASIAPIK.A		R.GVLSFPASIAPIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
136	RL28A_SCHPO	18.24%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
94	110	2	1787.95	2.8	1	56	18.9	95.00%	K.NTEVAPVINVLQSGYGK.V		K.NTEVAPVINVLQSGYGK.V
46	55	3	1210.58	1.4	1	19.2	23.3	92.50%	F.DKYHPGYFGK.V		R.SHFDKYHPGYFGK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
137	TBB_SCHPO	11.83%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
203	216	2	1521.77	2.9	1	62.3	21.1	95.00%	I.DNEALSSIFANTLK.I		K.SSDTVVEPYNATLSMHQLVENSDETFCIDNEALSSIFANTLK.I
128	154	3	2645.36	2.8	0	44.6	17.7	95.00%	C.DALQGFQLTHSLGGGTGSGMGTLLLSK.I		R.EAEACDALQGFQLTHSLGGGTGSGMGTLLLSK.I
163	174	2	1249.62	3.9	0	41.3	22	95.00%	R.MMATFSVAPAPK.S		R.MMATFSVAPAPK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
138	SYLC_SCHPO	3.42%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
843	852	2	1272.56	5	1	24.8	23.7	92.40%	K.SCFYDLQNAR.D	Carbamidomethyl (+57)	K.SCFYDLQNAR.D
382	398	3	1730.98	4.6	1	32.6	13.8	95.00%	K.GQDLIGALVNAPLSVHK.Q		K.GQDLIGALVNAPLSVHK.Q
777	787	2	1185.64	2.4	1	30.6	19.3	95.00%	F.EEALANSAILR.L		R.LALADAGDTVDDANFEEALANSAILR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
139	YHZ8_SCHPO	31.31%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
154	164	2	1234.62	2.9	1	42.7	22.2	95.00%	L.DDPSLYAVVTR.Y		K.ADTSLIIHSLDDPSLYAVVTR.Y
75	103	3	3217.69	3	1	57.2	13.8	95.00%	K.TSNPFLAFANYLTSTHAPLAEPLQLLNFK.V		K.TSNPFLAFANYLTSTHAPLAEPLQLLNFK.V
2	13	2	1361.7	3.8	0	57.2	21.5	95.00%	M.SFPASTHVYIAK.I	Acetyl (+42)	-.MSFPASTHVYIAK.I
144	153	2	1068.58	2.8	1	47.3	17.4	95.00%	K.ADTSLIIHSL.D		K.ADTSLIIHSLDDPSLYAVVTR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
140	RS13_SCHPO	15.23%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
44	55	2	1244.66	3.8	0	40.8	20.8	95.00%	K.GMSPSQIGVTLR.D		K.GMSPSQIGVTLR.D
10	20	2	1132.63	4.4	0	38.6	18.7	95.00%	K.GIASSALPYVR.S		K.GIASSALPYVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
141	DYR_SCHPO	9.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
164	183	3	2062.15	3.7	1	25.4	10.4	95.00%	K.LTTPSLHIAGTSDTLVPLAR.S		K.LTTPSLHIAGTSDTLVPLAR.S
191	212	3	2537.31	3.6	1	37.3	18.1	95.00%	R.CENAHVLLHPGQHIVPQQAVYK.T	Carbamidomethyl (+57)	R.CENAHVLLHPGQHIVPQQAVYK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
142	YHEF_SCHPO	14.29%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
90	104	2	1731.88	2.7	0	53.2	20.6	95.00%	N.DTANFTPLTFTTYLK.T		R.LFTIAENDTANFTPLTFTTYLKTCNPQSIENAMIPFVNTVTSEISFDAWAYTAQNSSR.I
30	41	3	1413.76	4.8	1	20.9	18.8	95.00%	R.LRGPHCGTYLLK.V	Carbamidomethyl (+57)	R.LRGPHCGTYLLKVVGTNATYVGEK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
143	ADK_SCHPO	13.24%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

253	267	2	1483.87	4.5	1	69.4	13.8	95.00%	R.VVVITQGADATIVAK.D		R.VVVITQGADATIVAK.D
126	138	2	1424.68	5.2	0	51	22.3	95.00%	R.SLCTNLGAANNYK.L	Carbamidomethyl (+57)	R.SLCTNLGAANNYK.L
48	64	2	1812.76	4.2	0	83.7	23.8	95.00%	K.EPCVSYSAGGAAQNSCR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.EPCVSYSAGGAAQNSCR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
144	Q9P7B4_SCHPO	13.13%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
234	256	3	2522.27	2.7	1	34.8	18.7	95.00%	R.ENVVIADTLVFPSHQGGANHVYR.K		R.ENVVIADTLVFPSHQGGANHVYR.K
163	173	2	1163.64	5.6	0	26.5	18.9	94.70%	K.SALAQFTSALR.K		K.SALAQFTSALR.K
240	256	3	1896.93	3	0	19.6	21.4	93.40%	A.DTLVFPSHQGGANHVYR.K		R.ENVVIADTLVFPSHQGGANHVYR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
145	RL23_SCHPO	25.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
15	34	2	2090	3.5	1	65.5	21.8	95.00%	R.MTLGLPVQAIMNCADNSGAK.N	Carbamidomethyl (+57)	R.MTLGLPVQAIMNCADNSGAK.N
15	28	2	1517.74	2.3	0	36.9	22.4	95.00%	R.MTLGLPVQAIMNCA.D	Carbamidomethyl (+57)	R.MTLGLPVQAIMNCADNSGAK.N
51	65	2	1531.78	3.4	1	55.2	21.1	95.00%	R.LPAASCGDMVLATVK.K	Carbamidomethyl (+57)	R.LPAASCGDMVLATVK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
146	ACL2_SCHPO	9.55%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
326	334	2	985.56	4.7	1	36	19.5	95.00%	K.LTILNAEGR.V		K.LTILNAEGR.V
382	389	2	947.52	4.5	1	26.9	20.9	95.00%	K.TVLDLMTR.G		K.TVLDLMTR.G
32	61	3	3211.76	3.3	1	47.1	14.5	95.00%	K.TVSATPAVQLAQIQFPLPTLVIPAESTTYR.E		K.TVSATPAVQLAQIQFPLPTLVIPAESTTYR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
147	RLA2_SCHPO	23.64%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
62	87	2	2091.06	1.7	1	82	20.2	95.00%	K.LATVPTGGAASAAPAAAAGGAAPAAE.E		K.LATVPTGGAASAAPAAAAGGAAPAAEEAAK.E
62	86	2	1962.02	3.1	0	70.5	18.6	95.00%	K.LATVPTGGAASAAPAAAAGGAAPAA.E		K.LATVPTGGAASAAPAAAAGGAAPAAEEAAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
148	Q76N21_SCHPO	13.61%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
13	22	2	1195.61	4.9	0	30.3	22.2	95.00%	R.FVTCQIVSSR.V	Carbamidomethyl (+57)	K.SSPYFSRYQTKYRR.R
26	35	2	1098.51	2.4	0	27.6	23.8	95.00%	G.DYVLAHAHSS.E		R.EGKTDYYARKR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
149	RLA1_SCHPO	47.71%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	16	2	1537.79	2.7	1	52.3	21.1	95.00%	M.SASELATSYSALILA.D	Acetyl (+42)	-.MSASELATSYSALILADEGIEITSDK.L
57	81	2	2089.12	2.1	0	54.1	15.1	95.00%	K.ELLLNIGSGAGAAPVAGGAAAPAAA.D		K.ELLLNIGSGAGAAPVAGGAAAPAAADGEAPAEEK.E
37	48	2	1388.74	2.8	1	39.5	19.7	95.00%	V.DVEPIWATIFAK.A		K.AANVDVEPIWATIFAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
150	CYSK1_SCHPO	15.95%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
74	94	3	1964.05	2.4	1	19.5	16.4	93.10%	R.GGTIVEGTAGNTGIGLAHIAR.A		R.GGTIVEGTAGNTGIGLAHIAR.A
10	23	2	1341.78	3	0	85.5	14.1	95.00%	K.VPGIVSGFIGAIGR.T		K.VPGIVSGFIGAIGR.T

180	200	2	2019.93	5.1	1	71.4	23.7	95.00%	K.GTVDGFTCSTGTGGTFAGVTK.Y	Carbamidomethyl (+57)	K.GTVDGFTCSTGTGGTFAGVTK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
151	RLA0_SCHPO	15.06%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
133	144	2	1308.71	5.2	0	29.1	16.9	95.00%	K.TSFFQALGIPTK.I		K.TSFFQALGIPTK.I
118	132	2	1517.72	2	1	30	23.7	95.00%	L.DVFVPAGNTGMEPGK.T		R.ETIIANVIAAPARPNAIAPLDVFVPAGNTGMEPGK.T
98	117	2	2014.16	2.9	0	26.1	9.54	94.20%	R.ETIIANVIAAPARPNAIAPL.D		R.ETIIANVIAAPARPNAIAPLDVFVPAGNTGMEPGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
152	RHP23_SCHPO	9.51%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
244	251	2	931.48	2.6	1	31.3	23.5	95.00%	G.DDPLGFLR.S		R.EESAAALAAQQQQSEALAPTSTGQPANLFEQAALSENENQEQPSNTVGDDPLGFLR.S
137	147	2	1114.58	2.2	0	44	20.9	95.00%	I.DANTLAVGAQR.N		K.VEAPSSTVAESTSTTQTVAAAAPSNPDTTATSEAPIDANTLAVGAQR.N
84	99	2	1518.78	4.7	1	24.2	21.4	91.30%	K.SAASPAPNPPASVPEK.K		K.SAASPAPNPPASVPEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
153	RL2_SCHPO	8.70%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
128	138	2	1144.59	4.4	0	35.6	22.3	95.00%	R.SSGNYVIIVGH.D		R.SSGNYVIIVGHDVDTGK.T
163	173	2	940.55	4.3	0	54.6	13.2	95.00%	R.GVVGIVAGGGR.I		R.GVVGIVAGGGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
154	ODPB_SCHPO	7.65%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
225	234	2	1105.62	3.5	0	44.6	18.2	95.00%	E.DFVLPFGLAK.V		K.EALSEDFVLPFGLAK.V
335	352	2	1879.88	1.7	1	25.3	22.7	93.00%	A.DVPMPYSHPVEAASVPNA.D		R.VSMADVPMPYSHPVEAASVPNADVVVAAAK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
155	ARO1_SCHPO	2.86%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
643	660	2	1749.92	2.5	0	67	17.7	95.00%	S.DASSATYPLAIAAITGTK.C		K.YQNPPHYEIESDASSATYPLAIAAITGTK.C
162	172	2	1299.72	4.7	0	45.2	19.1	95.00%	K.NLVGAFWQPLR.V		K.NLVGAFWQPLR.V
1232	1247	2	1833.96	4.6	1	44.8	18.5	95.00%	R.ITNSMDIPLILFNMGR.F		R.ITNSMDIPLILFNMGR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
156	APE1_SCHPO	2.61%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	149	2	1467.71	4.6	1	42.2	22.8	95.00%	K.YLATTQMEPTSAR.R		K.YLATTQMEPTSAR.R
498	507	2	1204.65	2.2	0	25.3	19.6	93.10%	E.DTVIYWAPLK.L		R.FLSTGDVKPEEDTVIYWAPLK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
157	RS21_SCHPO	25.29%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
76	87	2	1421.7	2.8	1	38.7	23.2	95.00%	Q.DGLLEGVWSYQR.-		R.LTTQDGLLEGVWSYQR.-
51	60	2	1113.59	4.5	0	33.8	20.8	95.00%	K.TTYAISGFVR.S		K.TTYAISGFVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
158	YCO6_SCHPO	7.89%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

15	36	3	2140.01	5.3	0	26.3	21.7	95.00%	K.MSAAPTPHNTPSGTSAPNFGAK.A			K.MSAAPTPHNTPSGTSAPNFGAK.A
186	194	2	939.47	2.5	1	27.9	21.7	95.00%	E.DEGALSHLV.D			K.NVLSLSEMITPEDEGALSHLVDIR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
159	WOS2_SCHPO	13.98%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
150	164	2	1425.62	1.8	1	76.4	24.3	95.00%	M.DFSQFGNLGGAGAGE.D		R.WVDEDEQEAQPEVSPFGAGGMPDLSALGGMGGMDFSQFGNLGGAGAGEDASDSEPELEEEEEVGSNEK.K
139	149	2	1023.44	1.8	0	28.5	22.5	95.00%	P.DLSALGGMGGM.D	Oxidation (+16)	R.WVDEDEQEAQPEVSPFGAGGMPDLSALGGMGGMDFSQFGNLGGAGAGEDASDSEPELEEEEEVGSNEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
160	RL31_SCHPO	21.24%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
91	105	2	1650.87	4.2	1	39.3	18.9	95.00%	K.ALYTYVQAVDVANPK.M		K.ALYTYVQAVDVANPK.M
7	15	2	986.56	5	0	39.5	20.5	95.00%	K.SAINQVVTR.D		K.SAINQVVTR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
161	PABP_SCHPO	2.91%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
258	266	2	1068.57	4.8	0	26.6	19.8	94.80%	K.ANFTNVYIK.N		K.ANFTNVYIK.N
447	456	2	1142.61	4.9	1	33.9	20.4	95.00%	R.SQLEAQIQAR.N		R.SQLEAQIQAR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
162	PNPP_SCHPO	9.06%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
196	213	2	1882	2.6	0	78.3	17.3	95.00%	K.FLPGSGAISYPLIFSTGR.Q		K.FLPGSGAISYPLIFSTGR.Q
285	293	2	1086.53	2.8	1	25.4	21.8	93.20%	P.DYYVESLAK.L		K.DAPVVPDYYVESLAK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
163	LYS4_SCHPO	4.30%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
149	159	2	1179.57	4.4	1	26	23.1	94.10%	K.GQGIDFYPAGR.G		K.GQGIDFYPAGR.G
470	489	2	1872.04	4.8	0	47.2	14.6	95.00%	R.EALAYLASPAVVAASAIAGK.I		R.EALAYLASPAVVAASAIAGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
164	KAPS_SCHPO	13.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	14	2	1413.73	4.2	0	23.6	20.3	90.10%	M.ATNITFHPGSVTK.E	Acetyl (+42)	-.MATNITFHPGSVTK.E
39	52	2	1664.86	3.8	1	65.6	20.5	95.00%	K.STIACALEQYLLQR.G	Carbamidomethyl (+57)	K.STIACALEQYLLQR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
165	RL24A_SCHPO	12.75%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
81	91	2	1097.65	4.7	1	29.4	15.7	95.00%	R.GIVGANLDVIK.E		R.GIVGANLDVIK.E
36	43	2	978.52	4.9	1	29.5	21.8	95.00%	K.SESLFLQR.K		K.SESLFLQR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
166	DLDH_SCHPO	5.87%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
113	128	2	1663.83	1.7	1	25	21.8	92.70%	R.GIDVSGVSVNLSQMMK.A		R.GIDVSGVSVNLSQMMK.A
155	168	2	1448.76	3.8	1	31.8	20.2	95.00%	K.GTGSFIDPQTLSVK.G		K.GTGSFIDPQTLSVK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
167	PPID_SCHPO	5.90%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
214	226	2	1432.74	4.4	1	72	20.6	95.00%	K.QFAQQNLDTAVAK.W		K.QFAQQNLDTAVAK.W
170	177	2	896.46	1.9	1	33.6	19.1	95.00%	K.DQIEAPKP.D		K.DQIEAPKPDVTGDSLEEFPDDYEGDK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
168	EIF3E_SCHPO	6.19%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
267	284	3	2029.08	4.4	0	22.1	17.1	95.00%	R.YLTVAVVTNQNNANQKPR.N		R.YLTVAVVTNQNNANQKPR.N
395	407	2	1184.58	1.9	0	45.6	23.1	95.00%	R.NNPSVAAASNVAA.D		R.NNPSVAAASNVAADQSTEDESIESTSTNVVADDLITEAETATEAEEPEPEVQFGFK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
169	AROC_SCHPO	6.33%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
229	240	2	1276.65	1.5	0	36.9	21.6	95.00%	H.DSIGGTVTCVIR.N	Carbamidomethyl (+57)	R.DNHDSIGGTVTCVIR.N
328	340	2	1331.68	5.2	1	55.6	21.4	95.00%	K.SPATIGVEQSTSR.Y		K.SPATIGVEQSTSR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
170	CH10_SCHPO	22.12%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	84	2	1230.7	4	0	31.7	17.3	95.00%	R.VLLPAYGGSNIK.V		R.VLLPAYGGSNIK.V
62	72	2	1111.6	4.5	1	30.9	17.7	95.00%	K.LAQPSVAVGDR.V		K.LAQPSVAVGDR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
171	ARPC1_SCHPO	10.34%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	23	4	2564.32	3.3	1	37.1	17.6	95.00%	M.ATSQVLHILPKPSYEHAFNSQR.T	Acetyl (+42)	-.MATSQVLHILPKPSYEHAFNSQR.T
226	242	2	1813.89	1.9	1	36.8	21.3	95.00%	H.DSSVTIAYPSAPEQPPR.A		R.LPFNTVCAEYPSGGWVHAVGFSPSGNALAYAGHDSSVTIAYPSAPEQPPR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
172	RLA6_SCHPO	23.64%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
62	86	2	1932.01	2.9	0	57.8	18.5	95.00%	K.LATVPSGGAAAAAAPAAAGGAAPAA.E		K.LATVPSGGAAAAAAPAAAGGAAPAAEEAAK.E
62	87	2	2061.06	3	1	59.1	19.7	95.00%	K.LATVPSGGAAAAAAPAAAGGAAPAAE.E		K.LATVPSGGAAAAAAPAAAGGAAPAAEEAAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
173	BUT2_SCHPO	6.92%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
338	349	2	1493.65	4.2	1	37.5	23.5	95.00%	R.GCEYTQNIPCPR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GCEYTQNIPCPR.A
200	214	2	1679.86	4.8	1	44.1	20.2	95.00%	R.YYGNTEALSSLPLPR.N		R.YYGNTEALSSLPLPR.N

Supplementary Table S2: All "Scaffold" validated proteins and peptides identified from solprotSP (*S.pombe*) and from SCVMprot (*S.cerevisiae*) samples

S.pombe **- Asp-N digest of large tryptic peptides (replicate C)**

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
1	ENO11_SCHPO	45.56%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
361	374	3	1608.73	4.7	1	47.1	24	95.00%	R.MSYEAGWGVMVSHR.S		R.MSYEAGWGVMVSHR.S
185	194	2	1204.59	5.4	1	34	22.9	95.00%	R.WGAETYHTLK.S		R.WGAETYHTLK.S
346	360	2	1586.83	2.6	1	90.9	20.5	95.00%	K.VNQIGSVTESLNAVR.M	Deamidation (+1)	K.VNQIGSVTESLNAVR.M
302	310	2	1160.51	3.3	0	24.3	24.6	90.90%	D.DWSAWTHMK.A		K.YPIVSIEDPFDQDDWSAWTHMK.A
364	374	2	1227.59	2.9	0	36.2	23.7	95.00%	Y.EAGWGVMVSHR.S		R.MSYEAGWGVMVSHR.S
65	79	2	1477.87	4	0	73.7	9.03	95.00%	K.AVGNVNNIIAPAVVK.A		K.AVGNVNNIIAPAVVK.A
106	120	2	1560.82	4.2	0	61.3	19.3	95.00%	K.LGANAILGVSMAICR.A	Oxidation (+16)/ Carbamidomethyl (+57)	K.LGANAILGVSMAICR.A
33	47	2	1470.78	3.5	1	47.6	19	95.00%	R.AIVPSGASTGIWEAL.E		R.AIVPSGASTGIWEALEMR.D
23	32	2	1141.58	3.4	1	44.1	21.6	95.00%	V.DLTTETGIHR.A		R.GNPTVEVDLTTETGIHR.A
380	396	2	1755.96	4.2	0	68.2	15.8	95.00%	A.DTFISHLTVGIGAGQLK.S		R.SGETADTFISHLTVGIGAGQLK.S
168	180	2	1411.67	2.9	0	29.4	23.4	95.00%	Q.EFMILPTGAPSFS.E	Oxidation (+16)	K.GPYVLPVPSFNVLNGGSHAGGDLAFQEFMILPTGAPSFSEAMR.W
301	310	2	1275.54	2.4	1	46	24.5	95.00%	Q.DDWSAWTHMK.A		K.YPIVSIEDPFDQDDWSAWTHMK.A
142	162	2	2039.02	2	0	53.6	21	95.00%	K.GPYVLPVPSFNVLNGGSHAGG.D	Deamidation (+1)	K.GPYVLPVPSFNVLNGGSHAGGDLAFQEFMILPTGAPSFSEAMR.W
338	345	2	901.51	4.7	0	31.4	20.4	95.00%	K.CANALLLK.V	Carbamidomethyl (+57)	K.CANALLLK.V
409	414	2	806.43	5.7	1	29.4	22.3	95.00%	K.YNELLR.I		K.YNELLR.I
217	225	2	1013.51	3.4	1	29.2	21.1	95.00%	P.DLQTPQEAL.D		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
168	184	2	1898.89	1.9	1	50.6	22.9	95.00%	Q.EFMILPTGAPSFSEAMR.W	Oxidation (+16)	K.GPYVLPVPSFNVLNGGSHAGGDLAFQEFMILPTGAPSFSEAMR.W
226	234	2	1013.58	2.9	1	38.7	19	95.00%	L.DLIVEAINK.A		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
320	328	2	1003.52	3.5	1	47.8	21.9	95.00%	G.DDLTVTNVK.R		K.AETDFQIVGDDLTVTNVK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
2	G3P1_SCHPO	34.52%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	126	2	813.5	2.9	0	28.8	16.7	95.00%	R.VIISAPSK.D		R.VIISAPSK.D
39	48	2	1309.58	2.8	1	41.6	23.9	95.00%	I.DLEYMAYMFK.Y		K.TIQVVAINDPFIDLEYMAYMFK.Y
118	126	2	969.6	2.8	1	34	12.6	95.00%	K.RVIISAPSK.D		K.RVIISAPSK.D
296	309	2	1459.77	2.3	0	63.7	19.7	95.00%	F.DASAGIQLSPQFVK.L		K.GVLGYTEDAVVSTDFCGDNHSSIFDASAGIQLSPQFVK.L
249	256	2	934.48	3.6	1	26.5	22.7	94.30%	K.LAKPTNYE.D		K.LAKPTNYEDIK.A
146	162	2	1818.91	4.5	0	75	21.9	95.00%	K.VISNASCTTNCLAPLAK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.VISNASCTTNCLAPLAK.V
324	334	2	1148.65	6.2	1	55.4	16.7	95.00%	R.VVDLVAYTAAK.D		R.VVDLVAYTAAK.D
84	92	2	963.47	2.5	1	54.8	22.9	95.00%	A.DIKWSTSGA.D		R.DPADIKWSTSGADYVIESTGVFTTQETASAHLK.G
172	186	2	1587.8	1.5	0	92.5	21.3	95.00%	E.EGLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK.T
6	13	2	819.43	6.2	0	38.4	21.6	95.00%	K.VGINGFGR.I	Deamidation (+1)	K.VGINGFGR.I
201	215	2	1343.71	4.7	0	69.9	20	95.00%	R.GASANIIPSSTGAAK.A		R.GASANIIPSSTGAAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
3	PGK_SCHPO	33.82%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	169	2	873.41	4	0	24.7	22.5	91.70%	N.DAFGTAHR.A		K.SLTSLGDIFVNDAFGTAHR.A
57	71	2	1591.87	2.9	0	46.2	17.9	95.00%	K.AVILMSHLGRPNGAR.V	Deamidation (+1)	K.AVILMSHLGRPNGAR.V
40	48	2	910.59	3.6	0	25.3	6.02	92.70%	R.IVGALPTIK.Y		R.IVGALPTIK.Y
384	400	2	1625.83	3.6	1	42.1	20.5	95.00%	E.DALSHVSTGGGASLELL.E		K.EDALSHVSTGGGASLELLEGK.A
276	286	2	1235.65	3.2	1	28.7	21.1	95.00%	V.EVFLPVDFVTA.D		K.NNVEVFLPVDFVTADK.F
383	397	2	1399.66	2.7	1	59.7	24	95.00%	K.EDALSHVSTGGGASL.E		K.EDALSHVSTGGGASLELLEGK.A
384	397	2	1270.62	2.7	0	66.9	22.7	95.00%	E.DALSHVSTGGGASL.E		K.EDALSHVSTGGGASLELLEGK.A
359	371	2	1231.59	2.3	1	29	22.5	95.00%	K.TCEAGNVVIVGGG.D	Carbamidomethyl (+57)	K.TCEAGNVVIVGGGDTATVAK.K
404	414	2	1040.63	5.6	0	39.4	15.9	95.00%	K.ALPGVVALSSK.-		K.ALPGVVALSSK.-
321	329	2	994.54	5.5	1	50.2	20.3	95.00%	K.FAEVITTSK.T		K.FAEVITTSK.T
75	86	3	1304.74	4.3	1	59.4	14.8	95.00%	K.YSLKPVAAELSK.L		K.YSLKPVAAELSK.L
197	213	2	1737	3.5	1	54.4	10.8	95.00%	K.ALENPARPFLAILGGAK.V		K.ALENPARPFLAILGGAK.V
170	181	2	1267.64	4	1	58.7	22.2	95.00%	R.AHSSMVGVDLPR.V		R.AHSSMVGVDLPR.V
157	169	2	1461.7	2.8	1	26.7	23.4	94.50%	G.DIFVNDAFGTAHR.A		K.SLTSLGDIFVNDAFGTAHR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
4	METE_SCHPO	40.97%	100%	28

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
561	571	2	1184.7	5.1	0	40.5	15.3	95.00%	K.GMLTAPITILR.W		K.GMLTAPITILR.W
434	449	2	1746.96	3.1	0	63.9	14.3	95.00%	K.LPLFPTTTIGSFPQTK.E		K.LPLFPTTTIGSFPQTK.E
671	679	2	989.51	2.1	1	26.5	23	94.30%	A.DVVSIENSK.S		R.LDADVVSIENSK.S
4	11	2	845.48	4.8	0	33.3	20.6	95.00%	K.SAVLGFPR.I		K.SAVLGFPR.I
325	343	2	1947.01	2.9	1	54.1	19.6	95.00%	R.VQVASSSSILHIPHSLSGE.D		R.VQVASSSSILHIPHSLSGEDQINPEIK.R
71	82	2	1414.7	2.3	0	42.5	22.2	95.00%	M.DHSFSFNVIPPR.Y		K.AQGVDIIPSNDFSLYDQIMDHSFSFNVIPPR.Y
707	714	2	901.49	4.3	1	27.7	23.1	95.00%	R.VPPVSEFK.E		R.VPPVSEFK.E
684	690	2	813.51	5.6	0	34.2	16.9	95.00%	K.LLNVLSR.Y		K.LLNVLSR.Y
691	706	2	1818.88	3.8	1	84	21.9	95.00%	R.YTSCIGPGLFDIHSPR.V	Carbamidomethyl (+57)	R.YTSCIGPGLFDIHSPR.V
344	351	2	955.5	2.7	1	28	20.5	95.00%	E.DQINPEIK.R		R.VQVASSSSILHIPHSLSGEDQINPEIK.R
243	260	2	1982.08	3.5	1	54.1	14.3	95.00%	K.LILTTYFGSLQSNADVLK.G		K.LILTTYFGSLQSNADVLK.G
261	269	2	861.51	2.9	0	32.6	16	95.00%	K.GLPIAGVHV.D		K.GLPIAGVHVDVVR.A
727	738	2	1466.7	4.2	1	48	23	95.00%	K.DHLWLNPDCGLK.T	Carbamidomethyl (+57)	K.DHLWLNPDCGLK.T
428	449	3	2402.33	2.5	1	66.9	12	95.00%	K.QQASLKLPLFPTTTIGSFPQTK.E		K.QQASLKLPLFPTTTIGSFPQTK.E
261	273	2	1330.78	4	1	55.7	11.5	95.00%	K.GLPIAGVHVDVVR.A		K.GLPIAGVHVDVVR.A
500	508	2	1143.5	2.2	1	40	23.7	95.00%	N.DMVQYFGER.M		R.NDMVQYFGER.M
645	656	2	1508.6	2.2	1	30.4	22.9	95.00%	Q.DDTQIHSHFCYS.D	Carbamidomethyl (+57)	R.LATAAVQDDTQIHSHFCYSDFNDIFDAIQR.L
281	299	2	1881.08	4.8	1	87.4	8.45	95.00%	R.ALAVLGENQIISVGVVSGR.N		R.ALAVLGENQIISVGVVSGR.N
92	99	2	959.42	3	0	40.1	23.1	95.00%	L.DTYFAMGR.G		R.LSGLSSLDTYFAMGR.G
361	369	2	1017.56	4.9	1	30.5	20.9	95.00%	K.CAELAILTK.A	Carbamidomethyl (+57)	K.CAELAILTK.A
547	560	2	1596.79	3.6	0	50.8	22.2	95.00%	K.ESQYAQSITSKPMK.G		K.ESQYAQSITSKPMK.G
536	546	2	1275.67	2.5	0	37.4	20.6	95.00%	G.DVYRPAPMTVK.E		R.CVRPPIIVGDVYRPAPMTVK.E
527	546	3	2267.24	3.3	1	44.5	14.3	95.00%	R.CVRPPIIVGDVYRPAPMTVK.E	Carbamidomethyl (+57)	R.CVRPPIIVGDVYRPAPMTVK.E
631	637	2	877.45	5.9	1	49	22.6	95.00%	K.WAIDAFR.L		K.WAIDAFR.L
85	99	2	1616.79	4.1	1	63.5	22.5	95.00%	R.LSGLSSLDTYFAMGR.G		R.LSGLSSLDTYFAMGR.G
221	231	2	1275.68	3.6	1	44.8	20.7	95.00%	L.DLPQEILASYK.E		K.LTEAGAEYIQIDEPILTLDLPQEILASYK.E
581	593	2	1397.77	2.7	0	68	17.6	95.00%	H.DSVQAQQIALGLR.D		R.DDVHDSVQAQQIALGLR.D
156	176	3	2256.33	3.9	0	51.3	6.02	95.00%	K.EAGIITRPVLVGPVTYLFIAK.A		K.EAGIITRPVLVGPVTYLFIAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
5	EF1A1_SCHPO	38.91%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
402	414	2	1495.69	2.1	1	24.6	23.3	91.50%	K.MVPSKPMCVEAFT.D	Carbamidomethyl (+57)	K.MVPSKPMCVEAFTDYAPLGR.F
197	214	2	2238	3.5	1	74.4	22.9	95.00%	G.DNMIEPTTNMPWYQGWQK.E		K.TVPFVPVSGFQGDNMIEPTTNMPWYQGWQK.E
147	154	2	883.55	5.8	0	26.4	15.7	94.10%	K.QLIVAVNK.M		K.QLIVAVNK.M
254	264	2	1024.61	4.2	0	65.4	14	95.00%	K.IGGIGTVPVGR.V		K.IGGIGTVPVGR.V
101	109	2	921.43	3.2	0	35.5	23.2	95.00%	K.NMITGTSQA.D		K.NMITGTSQADCAVLIIGGGTGEFEAGISK.D
6	20	2	1529.84	4.6	1	62.9	17.6	95.00%	K.GHINVVVIGHVDSGK.S		K.GHINVVVIGHVDSGK.S
304	311	2	891.45	2.4	0	34.6	22.2	95.00%	G.DNVGFNVK.N		K.SVEMHHESLDAGLPGDNVGFNVK.N
155	164	2	1151.51	6.4	1	75.8	23.4	95.00%	K.MDTTGWSQAR.F		K.MDTTGWSQAR.F
241	249	2	1078.65	2.1	1	31.6	11.5	95.00%	T.DKPLRLPLQ.D		K.TLLEAIDSIEPPARPTDKPLRLPLQDVYK.I
85	96	2	1340.69	4.4	1	66.1	20.6	95.00%	K.YNVTVIDAPGHR.D		K.YNVTVIDAPGHR.D
246	253	2	974.55	4.1	1	32.1	20.3	95.00%	R.LPLQDVYK.I		R.LPLQDVYK.I
265	285	2	2087.14	1.7	1	38.3	14.8	95.00%	R.VETGVIKPGMIVTFAPAGVTT.E		R.VETGVIKPGMIVTFAPAGVTTEVK.S
135	146	2	1313.74	3.9	0	45.8	17.5	95.00%	R.EHALLAYTLGVK.Q		R.EHALLAYTLGVK.Q
185	196	2	1233.64	3.2	0	27	22	94.90%	K.TVPFVPVSGFQG.D		K.TVPFVPVSGFQGDNMIEPTTNMPWYQGWQK.E
56	62	2	893.47	4.6	1	24.5	22.3	91.40%	K.YAWVLDK.L		K.YAWVLDK.L
231	240	2	1081.54	3.4	1	35.3	22.8	95.00%	I.DSIEPPARPT.D		K.TLLEAIDSIEPPARPTDKPLR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
6	ALF_SCHPO	56.70%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
351	358	2	971.46	3.5	0	31.8	22.7	95.00%	E.DFYTVNTL.-		R.VLTALEDFYTVNTL.-
256	272	2	1779.86	2.9	0	52.1	22	95.00%	N.DKPVFFVFHGGSGSSVN.E		K.TTNDKPVFFVFHGGSGSSVNEFR.T
26	50	2	2496.31	4.1	1	69.4	15.4	95.00%	R.EHGFAIPAINVTSSSTAIAALEAAR.E		R.EHGFAIPAINVTSSSTAIAALEAAR.E
207	234	4	2951.53	3.2	0	31.9	16.8	95.00%	R.ELSSVTPYFSIAAAFGNVHGVYKPGNVK.L		R.ELSSVTPYFSIAAAFGNVHGVYKPGNVK.L
290	300	2	1283.62	3.1	1	74.2	22.3	95.00%	T.DTQFAYVEGVR.D		K.VNIDTDTQFAYVEGVR.D
131	142	2	1382.67	3.2	1	44.6	22.9	95.00%	K.IHGEPLFSSHML.D	Oxidation (+16)	K.IHGEPLFSSHMLDLSEEPK.K
113	118	2	786.45	2.4	1	27.2	21.7	95.00%	K.KLLPWM.D		K.KLLPWMDGMFEADEAYFK.I
94	112	2	2098.02	4.1	1	63.5	21.8	95.00%	R.SIAPFFGVPVVMHSDHCAK.K	Carbamidomethyl (+57)	R.SIAPFFGVPVVMHSDHCAK.K
26	46	2	2069.08	2	0	36.4	18.3	95.00%	R.EHGFAIPAINVTSSSTAIAAL.E		R.EHGFAIPAINVTSSSTAIAALEAAR.E
5	19	2	1539.86	3	1	54.5	16.3	95.00%	L.DIVPTGVITGDNVLK.L		-.MGILDIVPTGVITGDNVLK.L
94	107	2	1486.77	2.9	0	60	20	95.00%	R.SIAPFFGVPVVMHS.D		R.SIAPFFGVPVVMHSDHCAK.K
308	320	2	1378.61	3.2	1	27.3	24.4	95.00%	K.DYLMTPVGNPEGA.D	Oxidation (+16)	K.DYLMTPVGNPEGADKPNK.K
256	275	3	2212.08	2.8	1	29.6	21.4	95.00%	N.DKPVFFVFHGGSGSSVNEFR.T		K.TTNDKPVFFVFHGGSGSSVNEFR.T
235	248	2	1564.88	3.1	0	64.7	14	95.00%	K.LQPALLGQHQAYVK.E		K.LQPALLGQHQAYVK.E
54	71	2	1843.96	3.6	0	105	18.8	95.00%	R.SPIILQTSNGGAHFFAGK.E		R.SPIILQTSNGGAHFFAGK.E
80	93	2	1399.76	5.1	0	89.1	17.4	95.00%	K.ASIAGSIAAAHYIR.S		K.ASIAGSIAAAHYIR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
7	KPYK_SCHPO	31.04%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
487	497	2	1053.66	5.9	0	39.5	11.1	95.00%	K.IIVLQGAVGGK.G		K.IIVLQGAVGGK.G
215	223	2	1114.55	3.8	0	43.6	23	95.00%	V.DMIFASFIR.R	Oxidation (+16)	K.NGVDMIFASFIR.R
422	433	3	1430.81	4.6	0	41.1	14.9	95.00%	K.YRPSIPIVMVTR.C		K.YRPSIPIVMVTR.C

334	344	2	1192.6	2.4	1	50.2	22.5	95.00%	A.DLVMLSGETTK.G			R.AEVSDVGNAVLDGADLVMLSGETTK.G
77	93	2	1741.97	3.8	1	39.2	15.4	95.00%	K.ASATNPLFPLAIALDTK.G			K.ASATNPLFPLAIALDTK.G
309	319	2	1350.64	2.3	0	32.3	23	95.00%	L.ESMTYNPRPTR.A			K.CNIAGKPVACATQMLESMTYNPRPTR.A
57	71	2	1797.78	2.7	1	42.2	24.1	95.00%	R.MNFSHGSYEYHQSVI.D			R.MNFSHGSYEYHQSVIDNAR.K
28	37	2	1088.6	5	0	46.3	19.4	95.00%	R.TSIICTIGPK.S	Carbamidomethyl (+57)		R.TSIICTIGPK.S
468	477	2	1186.55	5.3	0	54.8	23	95.00%	R.VAYGCQQAYK.M	Carbamidomethyl (+57)		R.VAYGCQQAYK.M
294	319	4	2965.41	3.2	1	53	20.4	95.00%	K.CNIAGKPVACATQMLESMTYNPRPTR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)		K.CNIAGKPVACATQMLESMTYNPRPTR.A
294	308	2	1632.78	2.2	0	36	22.4	95.00%	K.CNIAGKPVACATQML.E	Carbamidomethyl (+57)/ Carbamidomethyl (+57)		K.CNIAGKPVACATQMLESMTYNPRPTR.A
405	417	2	1287.72	5.7	0	62	17.6	95.00%	K.AIVVLSTSGNTAR.L			K.AIVVLSTSGNTAR.L
248	257	2	1161.55	3.4	1	25.2	23.1	92.60%	K.IENQQGVNNF.D			K.IENQQGVNNFDSILDVTDGIMVAR.G
212	223	2	1368.69	4.2	1	39.8	21.8	95.00%	K.NGVDMIFASFIR.R			K.NGVDMIFASFIR.R
76	90	2	1525.89	2.7	1	36.5	14.1	95.00%	R.KASATNPLFPLAIAL.D			R.KASATNPLFPLAIALDTK.G
47	56	3	1143.62	4.2	1	26	21.5	95.00%	K.LRDAGMNIVR.M			K.LRDAGMNIVR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
8	PDC2_SCHPO	31.82%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
238	253	2	1690.85	3.2	1	79.1	21.7	95.00%	K.LAEALNCAAFIMPAAK.G	Deamidation (+1)/ Carbamidomethyl (+57)	K.LAEALNCAAFIMPAAK.G
228	237	2	949.49	5	1	30.2	22.7	95.00%	R.AAGAESAFVK.L		R.AAGAESAFVK.L
304	328	2	2694.37	3	1	65.1	18.3	95.00%	R.AAPNPNILLNSDYTSVSIPGYVFSR.V		R.AAPNPNILLNSDYTSVSIPGYVFSR.V
215	225	3	1192.76	4.9	1	19	7.78	92.00%	K.KEKPILLAGPK.L		K.KEKPILLAGPK.L
111	125	3	1623.82	3.5	0	24	22	95.00%	N.DLSSGHLLHHTLGTH.D		R.SNGIACAVVTYSVGALTAFDGIGGAYAENLPVILVSGSPNTNDLSSGHLLHHTLGTHDFEYQMEIAK.K
96	110	2	1552.81	2.6	0	30.1	19.7	95.00%	A.ENLPVILVSGSPNTN.D		R.SNGIACAVVTYSVGALTAFDGIGGAYAENLPVILVSGSPNTNDLSSGHLLHHTLGTHDFEYQMEIAK.K
446	461	2	1808.88	1.9	1	75.4	22.3	95.00%	G.DGSFQLTGQEISQMIR.H		R.TIVMVGDGSFQLTGQEISQMIR.H
315	328	2	1589.78	2.2	0	51.2	22.4	95.00%	S.DYTSVSIPGYVFSR.V		R.AAPNPNILLNSDYTSVSIPGYVFSR.V
137	146	2	1101.64	5.4	1	51.2	17.3	95.00%	K.LTCAAVAIKR.A	Carbamidomethyl (+57)	K.LTCAAVAIKR.A
19	25	2	770.49	4.3	1	34.4	15.4	95.00%	R.LVEIGIK.N		R.LVEIGIK.N
462	474	3	1575.97	4.8	1	29.2	3.01	95.00%	R.HKLPVLIFLLNNR.G		R.HKLPVLIFLLNNR.G
26	37	2	1429.72	4.2	1	38.3	21.6	95.00%	K.NHFVVPGDYNLR.L		K.NHFVVPGDYNLR.L
304	314	2	1122.61	2.9	0	32.8	18.9	95.00%	R.AAPNPNILLNS.D		R.AAPNPNILLNSDYTSVSIPGYVFSR.V
464	474	2	1310.81	4.6	0	66.2	6.02	95.00%	K.LPVLIFLLNNR.G		K.LPVLIFLLNNR.G
136	145	2	1073.63	3.9	1	39.6	14	95.00%	K.KLTCAAVAIK.R	Carbamidomethyl (+57)	K.KLTCAAVAIK.R
56	68	2	1470.66	2.4	1	47.9	23.2	95.00%	N.ELNCAFAAEGYAR.S	Carbamidomethyl (+57)	R.LLDFLEYYPGLSEIGCCNELNCAFAAEGYAR.S
4	18	2	1657.77	2.9	1	66.4	23.8	95.00%	K.DAESTMTVGTYLAQR.L	Oxidation (+16)	K.DAESTMTVGTYLAQR.L
396	405	2	1225.55	6.5	0	39.7	24.4	95.00%	G.DSWFNGLQMK.L	Deamidation (+1)	R.QIQGLVDSNTTLYAETGDSWFNGLQMK.L
216	225	3	1064.66	3.8	0	29.3	12	95.00%	K.EKPILLAGPK.L		K.EKPILLAGPK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
9	ADH4_SCHPO	36.02%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
375	385	3	1245.76	3.9	1	37.6	3.01	95.00%	K.IRPHLVDLGVK.E		K.IRPHLVDLGVK.E

219	236	2	1882.84	3.3	1	37	23.1	95.00%	N.DPETMYGLPPSLTAATGM.D	Oxidation (+16)/ Oxidation (+16)	K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
208	218	2	1253.65	2.3	1	41.8	20.3	95.00%	I.DKHTMPILSVN.D		K.MAIIDKHTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
399	411	2	1380.61	2.3	0	58.1	23.7	95.00%	K.DACGATNPIQPTH.D	Carbamidomethyl (+57)	K.DACGATNPIQPTHDEVK.A
76	87	2	1282.76	5.2	1	44.2	12.8	95.00%	K.NTLIVTDPGIIK.V		K.NTLIVTDPGIIK.V
366	374	2	1027.63	6.6	1	37.3	15.2	95.00%	R.ISQLVLEVK.I		R.ISQLVLEVK.I
149	159	2	1014.58	4.8	0	36.7	19.8	95.00%	K.GIALLATNGGK.I	Deamidation (+1)	K.GIALLATNGGK.I
109	128	2	2077.09	2.3	1	57.4	17.6	95.00%	Y.DGVQPNPTVGNVNQGLEIVK.K		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K
169	191	2	2386.26	3.6	1	87.6	17.2	95.00%	K.SSKPQLPLIAINTTAGTASEMTR.F		K.SSKPQLPLIAINTTAGTASEMTR.F
133	144	2	1116.49	3	0	53.5	24.3	95.00%	C.DSMVSIGGGSAH.D		K.ENCDSMVSIGGGSAHDCAK.G
244	255	2	1235.61	1.8	0	45.5	22.5	95.00%	V.EAYVSTAANPIT.D		K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
169	187	2	1869.03	3.4	0	65.9	14.8	95.00%	K.SSKPQLPLIAINTTAGTAS.E		K.SSKPQLPLIAINTTAGTASEMTR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
10	PMGY_SCHPO	40.28%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
23	30	2	977.54	2.9	0	33.1	20.8	95.00%	K.LNLFTGWK.D		K.LNLFTGWK.D
111	120	2	1271.65	5.7	1	79.8	21.7	95.00%	K.WGAEQVQIWR.R		K.WGAEQVQIWR.R
2	14	2	1439.81	5.3	1	52	15.8	95.00%	M.TTEAAPNLLVLTR.H	Acetyl (+42)	-.MTTEAAPNLLVLTR.H
158	168	2	1149.67	4.5	0	26.5	13.8	94.30%	K.VLIAAHGNSLR.A		K.VLIAAHGNSLR.A
95	104	2	1169.58	4.8	1	46.4	21.9	95.00%	R.YYGDLQGLNK.D		R.YYGDLQGLNK.D
31	40	2	1029.54	2.7	1	36.8	22	95.00%	K.DPALSETGIK.E		K.DPALSETGIK.E
57	66	2	1120.59	3.1	0	57.3	20.1	95.00%	F.DIAFTSALQR.A		K.FDIAFTSALQR.A
1	14	2	1528.83	3.1	1	54.5	17.2	95.00%	-.MTTEAAPNLLVLTR.H		-.MTTEAAPNLLVLTR.H
186	197	2	1310.73	4	0	47.4	17.6	95.00%	R.ELATGVPIVYHL.D		R.ELATGVPIVYHLDK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
11	THI2_SCHPO	18.29%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	15	2	1400.77	3.8	0	74.5	18.3	95.00%	M.APATAVVTPQTAFK.T		-.MAPATAVVTPQTAFK.T
233	242	2	1096.5	3	0	33.7	23.5	95.00%	H.DGPFGAFCVK.R	Carbamidomethyl (+57)	R.IAGVVTNWTLVSLNHGLQSCMDPNTINAHLVVSATGHDGPFGAFCVK.R
46	55	2	1167.56	3.7	1	53.7	22.9	95.00%	L.DESFSFAPIR.E		K.AYPTYSLDESFSFAPIR.E
295	308	2	1459.67	4	0	71.7	23.6	95.00%	R.MGPTFGGMMFSGIK.A		R.MGPTFGGMMFSGIK.A
243	254	2	1307.73	2.4	1	33.5	14.6	95.00%	K.RLASAQLVSNLH.D		K.RLASAQLVSNLHDMRPLDMNR.A
244	254	2	1151.63	2.9	0	63.3	17.3	95.00%	R.LASAQLVSNLH.D		R.LASAQLVSNLHDMRPLDMNR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
12	GLYD_SCHPO	37.69%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
146	159	2	1649.78	3.9	1	75	23.1	95.00%	K.ISAVSTYFESMPYR.V		K.ISAVSTYFESMPYR.V
183	193	2	1209.62	4.5	0	57.8	21.2	95.00%	K.ILVAGTSAYCR.L	Carbamidomethyl (+57)	K.ILVAGTSAYCR.L
361	371	2	1254.76	3.2	1	88.8	9.03	95.00%	R.VLELINIVTNK.N		R.VLELINIVTNK.N
97	123	3	2996.43	3.4	0	55	19.8	95.00%	K.WGVNVQCLSGSPANMQVYQAIMPPHGR.L	Carbamidomethyl (+57)	K.WGVNVQCLSGSPANMQVYQAIMPPHGR.L
5	15	2	1289.66	2.4	1	41.2	21.8	95.00%	N.DSIMLTPLKEQ.D	Oxidation (+16)	-.MSSNDSIMLTPLKEQDPTVAEIMR.H
86	96	2	1129.62	5.1	1	54.8	20.3	95.00%	R.ALAAFNLDPAK.W		R.ALAAFNLDPAK.W

59	67	2	998.45	5.1	1	32.9	23.5	95.00%	K.YSEGYPGAR.Y	K.YSEGYPGAR.Y
277	302	3	2725.45	2.8	0	25.2	14.6	95.00%	K.INFSVFPGHQGGPHNHTITALAVALK.Q	K.INFSVFPGHQGGPHNHTITALAVALK.Q
453	464	2	1305.63	2.9	1	25.8	22.9	93.40%	K.EVAEWASSFPLA.D	K.EVAEWASSFPLADK.W
413	422	2	1075.61	4.3	0	49.9	17.5	95.00%	R.ALTFAANLQK.E	R.ALTFAANLQK.E
250	256	2	840.44	5.4	0	24.1	19.8	90.60%	R.GAMIFFR.R	R.GAMIFFR.R
46	58	2	1321.64	4.2	1	41.4	23.4	95.00%	R.AVMDALGSVMSNK.Y	R.AVMDALGSVMSNK.Y
128	141	2	1467.68	1.6	0	36.2	23.7	95.00%	L.DLPSGGHLSHGYQT.D	R.LMGLDLPSGGHLSHGYQTDTK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
13	TPIS_SCHPO	48.59%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
206	222	2	1841.9	2.2	1	42.9	22	95.00%	R.VIYGGSVNGGNCKEFLK.F	Deamidation (+1)/ Carbamidomethyl (+57)	R.VIYGGSVNGGNCKEFLK.F
160	174	2	1615.9	3.1	1	74.6	15.1	95.00%	K.IVIAYEPVWAIGTGK.T		K.IVIAYEPVWAIGTGK.T
227	249	3	2449.28	2.9	1	19	17	92.20%	I.DGFLVGGASLKPEFHNIVNVHSL.-		K.FHDIDGFLVGGASLKPEFHNIVNVHSL.-
71	84	2	1423.66	2	1	66.7	24	95.00%	K.NGAYTGENSAQSLI.D		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R
135	145	2	1242.66	4.7	1	39.7	19.3	95.00%	R.EANETINVVVR.Q		R.EANETINVVVR.Q
85	98	2	1519.73	1.8	1	59.1	22.4	95.00%	I.DAGITYTLTGHSER.R		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R
36	52	2	2055.04	2.2	1	49.3	19.2	95.00%	G.DVETVIFPQNMYLITTR.Q	Oxidation (+16)	K.LNVGDVETVIFPQNMYLITTR.Q
196	205	2	971.55	5.3	1	76.1	20.9	95.00%	K.LGASVAEGLR.V		K.LGASVAEGLR.V
206	218	2	1324.61	4.4	0	76.9	23.5	95.00%	R.VIYGGSVNGGNCK.E	Deamidation (+1)/ Carbamidomethyl (+57)	R.VIYGGSVNGGNCK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
14	SAHH_SCHPO	25.17%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
246	255	2	1042.52	3	0	34.2	22.5	95.00%	V.DPINALQAAM.D		R.VIVTEVDPINALQAAMDGFEVTTMEEAVK.E
25	35	2	1227.63	2.9	1	29.2	20.9	95.00%	A.ENEMPGLIAVR.E		K.ELEIAENEMPGLIAVR.E
8	18	2	1118.61	3.2	1	77.1	19.2	95.00%	K.VADISLAAFGR.K		K.VADISLAAFGR.K
216	227	2	1117.62	4.3	1	46.5	19.6	95.00%	K.VAVVAGFGDVGK.G		K.VAVVAGFGDVGK.G
269	280	2	1367.65	2.9	0	44.9	23.1	95.00%	K.EGQIFVTTTGCR.D	Carbamidomethyl (+57)	K.EGQIFVTTTGCR.D
119	130	2	1302.7	3	0	43	19.3	95.00%	K.SFPSGKPLNMIL.D		K.SFPSGKPLNMILDDGGDLTALVHER.H
176	187	2	1255.68	4.6	1	42.1	18.7	95.00%	K.VPAINVNDSVTK.S		K.VPAINVNDSVTK.S
336	344	2	1006.6	5	1	31.2	12.6	95.00%	R.HIILLADGR.L		R.HIILLADGR.L
318	328	2	1281.71	3.7	1	30.2	18.2	95.00%	K.DVVNIKPQVDR.Y		K.DVVNIKPQVDR.Y
318	326	2	1010.58	3.8	0	27.1	16.1	95.00%	K.DVVNIKPQV.D		K.DVVNIKPQVDR.Y
135	143	2	1052.56	2.2	1	47.5	19.4	95.00%	G.DLTALVHER.H		K.SFPSGKPLNMILDDGGDLTALVHER.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
15	THI3_SCHPO	33.24%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
47	56	2	959.53	3	0	72.6	20.5	95.00%	S.DVTALIGSGK.V		R.EGIEVAILEPTNPSDVTALIGSGK.V
74	95	2	2353.27	3.5	1	91.4	15.3	95.00%	R.GYPVTSFGSLLNEPFTGLITLK.G		R.GYPVTSFGSLLNEPFTGLITLK.G
128	139	2	1325.67	4.2	1	42.4	21.6	95.00%	K.FGLSPSDYTAIR.C		K.FGLSPSDYTAIR.C
74	85	2	1253.63	3	0	67.2	21.9	95.00%	R.GYPVTSFGSLLN.E		R.GYPVTSFGSLLNEPFTGLITLK.G
6	27	2	2631.39	2.4	1	78.6	14.8	95.00%	K.ITFLTNWEATPYHLPIFLAQTR.G		K.ITFLTNWEATPYHLPIFLAQTR.G
63	71	2	954.54	4.5	0	51.1	15.9	95.00%	K.AMIHTLAAK.A		K.AMIHTLAAK.A
110	118	2	968.5	4.9	1	27.7	21.8	95.00%	R.IGYVGEFGK.I		R.IGYVGEFGK.I

330	339	2	992.51	5.7	0	44.3	22.7	95.00%	K.GGVFSGNSLR.Y		K.GGVFSGNSLR.Y
284	290	2	795.5	2.5	1	27.4	10	95.00%	K.RLGIIPQ.D		K.RLGIIPQDFEPNCTNGYLTWELDPDEK.D
260	273	2	1711.79	4.7	1	88.7	23.2	95.00%	R.CFAYFSHDISNVPR.D	Carbamidomethyl (+57)	R.CFAYFSHDISNVPR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
16	METK_SCHPO	40.05%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
147	155	2	931.5	4.5	0	58	23.4	95.00%	K.LNAAMSVAR.R		K.LNAAMSVAR.R
121	130	2	1101.48	2.9	0	39.3	24.3	95.00%	G.DQGIMFGYAT.D		K.ALEELGAGDQGIMFGYATDETPEK.L
137	146	3	1117.73	2.5	0	24.3	3.01	95.00%	K.LPLTILLAHK.L		K.LPLTILLAHK.L
256	272	2	1623.71	3.2	0	78.3	24.1	95.00%	V.DTYGGWGAHGGGAFSGK.D		K.IIVDTYGGWGAHGGGAFSGK.D
237	251	2	1429.74	3.6	1	73.6	20.9	95.00%	R.FVVGGPQGDAGLTGR.K		R.FVVGGPQGDAGLTGR.K
339	349	2	1256.73	4.3	1	36.5	14.8	95.00%	K.NFDLRPGVLVK.S		K.NFDLRPGVLVK.S
227	236	3	1156.6	4.8	0	18.7	20.6	91.40%	K.TVYHIQPSGR.F		K.TVYHIQPSGR.F
291	299	2	856.52	4.2	0	28.1	17.2	95.00%	K.SLVAAGLAR.R		K.SLVAAGLAR.R
253	272	2	1948.95	4	1	80.8	22.4	95.00%	K.IIVDTYGGWGAHGGGAFSGK.D		K.IIVDTYGGWGAHGGGAFSGK.D
369	378	2	1241.61	2.1	1	30.2	22.8	95.00%	T.DQSKPWEQPK.E		K.LQTPFYLSTASYGHFTDQSKPWEQPK.E
90	102	3	1457.72	2.4	1	33.8	22	95.00%	K.TCNVLVAIEQQSP.D	Carbamidomethyl (+57)	K.TCNVLVAIEQQSPDIAQGLHYEK.A
353	368	2	1831.88	2.3	0	64	22.7	95.00%	K.LQTPFYLSTASYGHFT.D		K.LQTPFYLSTASYGHFTDQSKPWEQPK.E
188	197	2	1039.53	4.6	0	40	20.3	95.00%	V.DTIVVSAQHA.D		R.VDTIVVSAQHADSISTEDLR.S
103	112	2	1172.59	2.8	1	40.8	21.9	95.00%	P.DIAQGLHYEK.A		K.TCNVLVAIEQQSPDIAQGLHYEK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
17	A1EGU1_SCHPO	23.72%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
457	479	2	2580.33	3.2	0	81	18.2	95.00%	K.YVISQCNNALLYPALGVACVLSR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.YVISQCNNALLYPALGVACVLSR.C
372	396	3	2593.42	3.1	1	37.3	11.1	95.00%	G.DINLESAIALVKPTILLGCSGQPGK.F	Carbamidomethyl (+57)	K.EVPSGDINLESAIALVKPTILLGCSGQPGK.F
439	452	2	1418.83	4.1	0	43.8	10	95.00%	K.ALIATGSPLPPLNR.N		K.ALIATGSPLPPLNR.N
490	500	2	1070.58	4.5	1	54.7	19.7	95.00%	K.AASDALATVPR.S		K.AASDALATVPR.S
15	23	2	955.55	4.9	0	32.8	16.9	95.00%	K.GVTLLNSPR.Y		K.GVTLLNSPR.Y
332	339	2	964.49	5	1	34.3	21.6	95.00%	R.GNLFMIDR.C		R.GNLFMIDR.C
456	479	3	2708.42	2.8	1	38.9	14.9	95.00%	K.KYVISQCNNALLYPALGVACVLSR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.KYVISQCNNALLYPALGVACVLSR.C
44	55	2	1363.78	3.1	1	51.6	15.6	95.00%	R.LPPIVETLQQQV.D		R.LPPIVETLQQQVDR.C
178	191	2	1553.75	3.5	1	59.3	23	95.00%	K.GHLMTLCAGLDPNR.F	Carbamidomethyl (+57)	K.GHLMTLCAGLDPNR.F
408	424	2	1964.06	3.3	1	35.8	14.9	95.00%	K.HVERPIIFPISNPTTLM.E		K.HVERPIIFPISNPTTLMEAKPDQIDK.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
18	HSP90_SCHPO	13.78%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
368	375	2	926.52	3.4	0	34	18.1	95.00%	E.DLPLNLSR.E		K.GVVDSEDLPLNLSR.E
465	474	2	1170.6	4.5	1	29.7	21.9	95.00%	K.NIYFITGESK.Q		K.NIYFITGESK.Q
567	587	2	2339.12	5.7	1	92.3	21.4	95.00%	K.IVGSPCLLTTGQYGWSANMER.I	Carbamidomethyl (+57)	K.IVGSPCLLTTGQYGWSANMER.I
351	361	2	1343.75	2.4	1	26	16.6	93.60%	E.ELIPEWLGFIK.G		R.VFITDDCEELIPEWLGFIK.G
596	606	2	1234.5	4.9	0	67.2	23.7	95.00%	R.DTSMSAYMSSR.K		R.DTSMSAYMSSR.K
88	99	2	1282.73	5.3	1	55.5	15.2	95.00%	K.NDLINNLGVIAK.S		K.NDLINNLGVIAK.S
198	212	2	1787.96	4.4	1	31.7	18.3	95.00%	K.HSEFISYPIQLVVTR.E		K.HSEFISYPIQLVVTR.E
655	663	2	1021.45	3.4	1	48	23.1	95.00%	L.DDPSAYAQR.I		K.DLATILYETALLSSGFTLDDPSAYAQR.I

89	99	2	1168.69	3.1	0	25.9	14.5	93.60%	N.DLINNLGVIAK.S		K.NDLINNLGVIAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
19	HSP72_SCHPO	15.61%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
327	340	2	1400.77	3.9	1	39.7	18.9	95.00%	K.ASVNEIVLVGGSTR.I		K.ASVNEIVLVGGSTR.I
55	66	2	1384.66	3.1	0	39.6	23.2	95.00%	K.NQVAMNPHNTIF.D		K.NQVAMNPHNTIFDAK.R
538	548	2	1351.66	4.4	1	37.5	22.2	95.00%	K.NHLESYAYSLR.N		K.NHLESYAYSLR.N
350	359	2	1241.54	3.5	1	26.4	23.7	94.20%	S.DFFNGKEPCK.S	Deamidation (+1)/ Carbamidomethyl (+57)	K.LVSDFFNGKEPCK.S
450	457	2	965.47	3.7	1	24.3	22.6	91.00%	K.DCNLLGKF.E	Carbamidomethyl (+57)	K.DCNLLGKFELSGIPPAPR.G
158	169	2	1210.71	2.5	0	47.6	13.8	95.00%	K.DAGLIAGLNVLR.I		K.DAGLIAGLNVLR.I
55	69	2	1698.82	4.2	1	74.8	21.8	95.00%	K.NQVAMNPHNTIFDAK.R		K.NQVAMNPHNTIFDAK.R
457	467	2	1182.65	4.4	1	28.3	17.7	95.00%	K.FELSGIPPAPR.G		K.FELSGIPPAPR.G
235	244	2	1273.69	4.3	1	25.1	19.5	92.40%	R.LVNHFIQEFK.R		R.LVNHFIQEFK.R
96	106	2	1274.69	4.5	1	24.7	19.8	91.60%	K.DGKPVLQVEYK.G		K.DGKPVLQVEYK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
20	ILV5_SCHPO	25.50%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
317	328	2	1392.58	2.3	0	66.4	24.6	95.00%	L.DYMFAACSTTAR.R	Carbamidomethyl (+57)	K.YGLDYMFAACSTTAR.R
84	104	2	2141.07	2.7	1	91.6	20.6	95.00%	K.NDTLAIIGYGSQGHGQGLNAR.D		K.NDTLAIIGYGSQGHGQGLNAR.D
330	337	2	914.47	6	1	41.2	21.2	95.00%	R.GAIDWTPR.F		R.GAIDWTPR.F
314	328	2	1725.76	3.8	1	69	24.2	95.00%	K.YGLDYMFAACSTTAR.R	Carbamidomethyl (+57)	K.YGLDYMFAACSTTAR.R
173	189	3	2017.04	2.6	1	19	19.9	92.00%	K.TLYFSHGFSVIFKDQTK.I		K.TLYFSHGFSVIFKDQTK.I
301	313	2	1447.76	2.8	1	35.6	20.3	95.00%	V.EEATQSLYPLIGK.Y		R.GHSPAEAFNETVEEATQSLYPLIGK.Y
362	372	2	1312.61	4.6	1	61.6	23.6	95.00%	R.SLEYNSAPNYR.E		R.SLEYNSAPNYR.E
154	163	2	1145.54	3.3	1	26.4	23.5	94.10%	S.DAAQTETWPK.I		K.GSIIMNLLSDAAQTETWPK.I
85	104	3	2027.02	2.2	0	63.6	19.1	95.00%	N.DTLAIIGYGSQGHGQGLNAR.D		K.NDTLAIIGYGSQGHGQGLNAR.D
197	204	2	853.53	2.8	0	34.8	9.54	95.00%	V.DVILVAPK.G		K.DVDVILVAPK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
21	K6PF_SCHPO	16.24%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
613	628	3	1700.87	4.5	1	49.7	19.8	95.00%	R.GHTPLAIDNGFSGFLR.H		R.GHTPLAIDNGFSGFLR.H
510	522	2	1357.66	2	0	64.3	22.6	95.00%	P.DTPSPMIAINGNK.I	Deamidation (+1)	R.MLATLQGVDAVDAVLASTPDTPSPMIAINGNK.I
586	603	3	1720.91	2.8	0	71.2	19.1	95.00%	R.VAIIHVGAPAGGMNSATR.A		R.VAIIHVGAPAGGMNSATR.A
369	380	2	1259.62	4	0	54.5	23.3	95.00%	V.DSISSTAISHSR.A		R.ICEAVDSISSTAISHSR.A
882	896	2	1511.8	2.6	1	53	19	95.00%	N.DLGNDPSSAVVIGIR.G		R.ANDLGNDPSSAVVIGIR.G
844	859	2	1589.77	1.8	0	27.2	22.6	95.00%	R.TAVPGHVQQGGNPTPM.D		R.TAVPGHVQQGGNPTPMDR.A
620	628	2	1012.47	4.1	0	27.6	23.5	95.00%	I.DNGFSGFLR.H	Deamidation (+1)	R.GHTPLAIDNGFSGFLR.H
573	580	2	957.46	2.9	1	39.5	22.4	95.00%	E.DESHFVPK.D		R.DPEFADYLHTWEGTTFIEDESHFVPK.D
798	806	2	934.49	4	1	31.5	20.6	95.00%	K.ATFALEAGR.N		K.ATFALEAGR.N
254	267	2	1400.75	3.4	1	49.7	19.2	95.00%	R.GWLAEGGTLIGTAR.C		R.GWLAEGGTLIGTAR.C
844	861	2	1860.9	4.7	1	42.3	22.5	95.00%	R.TAVPGHVQQGGNPTPMDR.A		R.TAVPGHVQQGGNPTPMDR.A
927	938	2	1323.7	4.7	0	53.3	19.7	95.00%	R.DMHNLVNILAGK.T		R.DMHNLVNILAGK.T
197	214	2	1760.86	4.1	1	84.8	21.3	95.00%	K.IAVMTSGGDSPGMNAVVR.A		K.IAVMTSGGDSPGMNAVVR.A
205	214	2	1044.51	3.8	0	32.3	23.1	95.00%	G.DSPGMNAVVR.A		K.IAVMTSGGDSPGMNAVVR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
22	EF2_SCHPO	12.59%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
272	283	2	1498.77	4.2	1	53.9	20.9	95.00%	R.AFNMFILDPIYR.I		R.AFNMFILDPIYR.I
466	479	2	1474.71	3.7	1	72.8	22.2	95.00%	K.SGTLTTSEVAHNMK.V		K.SGTLTTSEVAHNMK.V

565	578	2	1451.69	4.3	1	44.5	23.1	95.00%	R.ESVSEPSSMTALSK.S		R.ESVSEPSSMTALSK.S
284	292	2	1051.52	4.5	1	27.5	22.9	95.00%	R.IFDAVMNSR.K		R.IFDAVMNSR.K
810	820	2	1200.59	3.6	0	53.9	22.9	95.00%	L.DPTSKPGQIVC.E	Carbamidomethyl (+57)	R.QATAGQAFPQLVFDHWSPMSG DPLDPTSKPGQIVCEAR.K
244	253	2	1266.61	5.9	1	30	23.2	95.00%	R.LWGENYFNPK.T		R.LWGENYFNPK.T
371	384	2	1594.76	4.1	1	55	22.8	95.00%	R.NCDANAPLMIYVSK.M	Carbamidomethyl (+57)	R.NCDANAPLMIYVSK.M
810	823	2	1556.77	2.1	1	37.7	22.2	95.00%	L.DPTSKPGQIVCEAR.K	Carbamidomethyl (+57)	R.QATAGQAFPQLVFDHWSPMSG DPLDPTSKPGQIVCEAR.K
460	465	2	748.41	2.6	0	24.6	20.2	91.50%	V.DQFLVK.S		R.IEPIEDCPAGNIIGLVGVDQFLVK. S
786	798	2	1376.71	3.7	0	35.5	21.3	95.00%	R.QATAGQAFPQLVF.D		R.QATAGQAFPQLVFDHWSPMSG DPLDPTSKPGQIVCEAR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
23	6PGD_SCHPO	21.54%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
156	166	3	1228.76	4.8	0	32.1	7.78	95.00%	R.IKPIFQTLAAK.A		R.IKPIFQTLAAK.A
140	155	2	1669.81	4.7	0	28.8	22.4	95.00%	R.YGPSLMPGGNPAAWPR.I		R.YGPSLMPGGNPAAWPR.I
99	110	2	1285.6	2.9	1	34.8	23.8	95.00%	G.DIIVDGGNSHYP.D		K.GDIIVDGGNSHYPDTTR.R
73	79	2	843.53	4.4	0	24.3	11.1	91.00%	R.VCILLVK.A	Carbamidomethyl (+57)	R.VCILLVK.A
437	449	2	1379.79	4.1	0	52	13.8	95.00%	R.SAVLPANLLQAQR.D		R.SAVLPANLLQAQR.D
276	291	2	1735.89	3.3	1	65.2	20.5	95.00%	L.EMGTPVSLITEAVFAR.C	Oxidation (+16)	K.WTAQNALEMGTPVSLITEAVFAR. C
450	458	2	1112.51	4.7	0	24.9	23.9	92.10%	R.DYFGAHTFR.V		R.DYFGAHTFR.V
175	187	2	1444.68	2.8	1	46.2	23.6	95.00%	C.DWVGEQGAGHYVK.M		K.AGNNEPCCDWVGEQGAGHYVK. M
29	37	2	1175.49	3.9	0	36.7	24.4	95.00%	K.GFTVCCYNR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GFTVCCYNR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
24	EF3_SCHPO	10.41%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
757	765	2	1178.58	7.8	1	24.9	22.3	92.00%	K.TPSEYIQWR.F		K.TPSEYIQWR.F
539	554	2	1731.86	2.6	1	30.5	21.9	95.00%	T.DELINMPIGSLSGGWK.M	Oxidation (+16)	K.ENSFTDELINMPIGSLSGGWK.M
675	691	3	1960.95	2.4	0	23	22	95.00%	K.VQHMSFQYPGTSKPQLN.D		K.VQHMSFQYPGTSKPQLNDISFQV SLSSR.I
434	447	2	1646.71	2.9	1	60.9	23.5	95.00%	E.DLCNCEFSLAYGAK.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.IPGGASHAEEEEEGEDLCNCEFS LAYGAK.I
479	493	2	1636.88	3.9	1	73.9	18.3	95.00%	R.AIVNGQVEGFPTHLR.T		R.AIVNGQVEGFPTHLR.T
133	147	2	1550.87	3.9	1	70.6	14.1	95.00%	K.AIVPSVLESIHTTGK.W		K.AIVPSVLESIHTTGK.W
284	294	2	1209.68	3.5	0	41.1	16.3	95.00%	E.DPQVVAPFLPK.L		K.LVEDPQVVAPFLPK.L
48	59	2	1248.64	3.3	0	58	21.8	95.00%	Q.DAPSQVFSAISK.Q		K.ALASFVNGPIEEQDAPSQVFSAIS K.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
25	TSA1_SCHPO	30.73%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	147	2	1224.69	4.4	1	43.5	16.5	95.00%	R.QITINDLPVGR.S		R.QITINDLPVGR.S
89	102	2	1350.79	2.8	1	34.7	11.1	95.00%	R.KEGGLGGINIPLLA.D		R.KEGGLGGINIPLLADPSHK.V
75	88	2	1648.79	2.2	1	61.4	22.9	95.00%	T.DSEYSHLAFINTPR.K		R.NAQVILTSTDSEYSHLAFINTPR.K
125	132	2	901.53	4.7	1	35.7	19.4	95.00%	R.GLFLIDPK.G		R.GLFLIDPK.G
90	102	2	1222.7	3.7	0	24.2	15.1	90.80%	K.EGGLGGINIPLLA.D		K.EGGLGGINIPLLADPSHK.V
2	13	2	1341.74	4.1	1	36.9	18	95.00%	M.SLQIGKPAPDFK.G	Acetyl (+42)	-.MSLQIGKPAPDFK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
26	TKT_SCHPO	17.96%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

238	252	2	1719.86	5	1	57.2	21.1	95.00%	R.EAMSCTDKPTLINLK.T	Carbamidomethyl (+57)	R.EAMSCTDKPTLINLK.T
8	18	2	1243.68	3	1	27.7	18.6	95.00%	T.DIDTLAINTIR.T		-.MTSSSYTDIDTLAINTIR.T
506	520	2	1548.66	2.6	1	47.1	24.5	95.00%	A.DGNETSAAYYSALTS.D		R.AMPNINCWRPADGNETSAAYYSALTSDSTPSILALTR.Q
653	663	2	1249.63	3.9	0	24.8	22	91.90%	K.FHFTTSGVAQR.A		K.FHFTTSGVAQR.A
480	494	3	1751.84	2.8	1	28.8	21.6	95.00%	E.DGPTHQPIETFAHFR.A		R.VIYVATHDSIGLGEDGPTHQPIETFAHFR.A
182	193	2	1385.74	4.7	1	41.9	19.8	95.00%	K.LSNLIAVWDNNK.I		K.LSNLIAVWDNNK.I
521	531	2	1172.64	3.2	0	50.3	20.3	95.00%	S.DSTPSILALTR.Q		R.AMPNINCWRPADGNETSAAYYSALTSDSTPSILALTR.Q
291	303	2	1603.8	4	1	26.8	22.2	94.60%	K.TFQVPPEVYAYYK.E		K.TFQVPPEVYAYYK.E
30	49	3	1972.02	2.7	0	31.9	18.4	95.00%	K.SGHPGAPMGLAPAAHVLFSR.I		K.SGHPGAPMGLAPAAHVLFSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
27	HSP75_SCHPO	15.99%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	173	2	1168.66	5	0	34.3	16.6	95.00%	K.DAGAIAGLNVLR.I		K.DAGAIAGLNVLR.I
335	344	2	1015.57	3.6	0	48	19.7	95.00%	H.DIVLVGGSTR.I		K.ADVHDIVLVGGSTR.I
501	517	2	1779.92	3.1	1	72.7	19.3	95.00%	R.SAHIEITNSVGHLSSTK.I		R.SAHIEITNSVGHLSSTK.I
144	157	2	1552.8	4.6	1	33.7	20.7	95.00%	K.AVITVPAYFSDSQR.A		K.AVITVPAYFSDSQR.A
457	472	2	1780.92	2.6	1	46.3	19.1	95.00%	N.EPLGEFQLTGIPPMPR.G		R.VNCAENEPLGEFQLTGIPPMPR.G
115	128	2	1565.81	1.4	1	60	19.1	95.00%	K.QFTAQEISAMVLTK.M		K.QFTAQEISAMVLTK.M
436	450	2	1753.83	2.6	1	57.1	22.6	95.00%	A.DNQTTVTFPVYQGER.V		R.TFTTVADNQTTVTFPVYQGER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
28	ACT_SCHPO	22.67%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
244	254	2	1200.62	4.1	1	46.6	21.1	95.00%	P.DGQVITIGNER.F		K.SYELPDGQVITIGNER.F
85	95	3	1514.75	5.5	1	36	22.5	95.00%	K.IWHHTFYNELR.V		K.IWHHTFYNELR.V
69	79	2	1340.66	2.7	1	31.6	22.5	95.00%	K.YPIEHGIVNNW.D		K.YPIEHGIVNNWDDMEK.I
292	312	2	2216.04	5	1	63.1	21.7	95.00%	K.DLYGNVVMSGGTTMYPGIADR.M		K.DLYGNVVMSGGTTMYPGIADR.M
197	206	2	1131.53	5.1	1	41.4	23.9	95.00%	R.GYTFSTTAER.E		R.GYTFSTTAER.E
157	177	3	2339.18	2.4	1	72.1	18.3	95.00%	G.DGVTHTVPIYEGYALPHAIMR.L		R.TTGIVLDSGDGVTHTVPIYEGYALPHAIMR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
29	GPD1_SCHPO	31.17%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
220	232	2	1184.64	3.4	1	57.5	19.2	95.00%	V.DDVAGVALGGALK.N		R.EQIAAVFDRPYFSVVSVDDVAGVALGGALK.N
2	20	2	1989	3.8	1	99.4	20.8	95.00%	M.SGYGQQGVSAANIDSIRPK.K	Acetyl (+42)	-.MSGYGQQGVSAANIDSIRPK.K
287	296	2	1076.53	2.4	0	49.3	22.4	95.00%	A.DLVTSCLGGR.N	Carbamidomethyl (+57)	R.TMVEQSCGIADLVTSCLGGR.N
127	144	2	1913.03	2.5	0	64.7	15.6	95.00%	C.DQMVGLIRPGAVGISCIK.G	Carbamidomethyl (+57)	R.VCDQMVGLIRPGAVGISCIK.G
23	39	2	1628.89	2.5	0	23.8	17.6	90.00%	R.LSIGVVGSGNWGTAIAK.I		R.LSIGVVGSGNWGTAIAK.I
125	144	3	2172.13	3.1	1	41.2	19.2	95.00%	R.VCDQMVGLIRPGAVGISCIK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VCDQMVGLIRPGAVGISCIK.G
111	124	2	1710.95	3	1	39.8	14.3	95.00%	A.DILVFVVPHQFIER.V		R.ADILVFVVPHQFIER.V
317	331	2	1484.82	2.8	0	73.2	17.5	95.00%	K.ELLGGQLLQGAATSK.D		K.ELLGGQLLQGAATSK.D
210	219	2	1167.6	2.8	0	30	21.8	95.00%	F.DRPYFSVVSV.D		R.EQIAAVFDRPYFSVVSVDDVAGVALGGALK.N
315	331	3	1741.96	2.5	1	34.1	16	95.00%	L.EKELLGGQLLQGAATSK.D		K.SLETLEKELLGGQLLQGAATSK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
30	PUR9_SCHPO	22.05%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

235	244	2	1141.62	2.6	0	31.1	18.5	95.00%	M.DALNSWPLVK.E			K.VLCGSPGYINLMDALNSWPLVK.E
121	129	2	942.55	2.3	0	38.6	18.9	95.00%	I.DIGGVTLLR.A			R.ETIAKPNVTIPEAVEEIDIGGVTLLR.A
284	297	2	1626.78	2.4	1	47.9	22.8	95.00%	S.DITEFTPLACAYAR.A	Carbamidomethyl (+57)		K.VYFVSDITEFTPLACAYAR.A
46	60	2	1527.79	2.7	1	59.1	20.8	95.00%	A.DVSSITNAPEILGGR.V			R.ESGMEVADVSSITNAPEILGGR.V
551	565	2	1519.75	4.1	1	63.8	21.9	95.00%	K.YVAAPGGSVMDQAVR.D			K.YVAAPGGSVMDQAVR.D
223	244	2	2446.25	3.4	1	45.9	18.8	95.00%	K.VLCGSPGYINLMDALNSWPLVK.E	Carbamidomethyl (+57)		K.VLCGSPGYINLMDALNSWPLVK.E
93	103	2	1394.71	2.7	0	27.2	22	95.00%	I.DIVVCNLYPFR.E	Carbamidomethyl (+57)		K.IDIVVCNLYPFR.E
354	362	2	1152.54	4.8	1	28.8	23.9	95.00%	K.YCVLQMDPK.Y	Carbamidomethyl (+57)		K.YCVLQMDPK.Y
248	259	2	1216.65	4.7	0	30.2	20.5	95.00%	R.ENIGIPAAASFK.H			R.ENIGIPAAASFK.H
201	222	3	2414.16	4	1	23.8	20	95.00%	R.YGANPHQSPAQAFMEQGPLPFK.V			R.YGANPHQSPAQAFMEQGPLPFK.V
201	214	2	1517.68	2.6	0	34.7	24	95.00%	R.YGANPHQSPAQAFM.E			R.YGANPHQSPAQAFMEQGPLPFK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
31	HXK2_SCHPO	18.02%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
434	449	2	1529.79	4.8	0	96.2	20.7	95.00%	K.DGSGIGAALCALQAVK.E	Carbamidomethyl (+57)	K.DGSGIGAALCALQAVK.E
197	205	2	960.53	1.3	0	32.4	20.2	95.00%	N.DTVGTLVTR.A		R.IEAVINDTVGTLVTR.A
76	86	2	1287.67	3.9	1	30.3	21.5	95.00%	R.VCWIQLLGDGK.Y	Carbamidomethyl (+57)	R.VCWIQLLGDGK.Y
286	296	2	1240.63	5.9	1	25.6	20.9	93.10%	R.VGGMYLGELFR.R		R.VGGMYLGELFR.R
257	265	2	1121.5	3.9	0	25.2	22.7	92.50%	T.DFSCLHSTR.Y	Carbamidomethyl (+57)	K.CTGDHMLINMEWGATDFSCLHSTR.Y
374	388	2	1564.83	4.1	0	56.1	18.1	95.00%	R.MSAVPIASLYLSTGR.A		R.MSAVPIASLYLSTGR.A
1	11	2	1334.67	4.1	1	29.9	22.5	95.00%	-.MEANFQQAVKK.L	Acetyl (+42)	-.MEANFQQAVKK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
32	G6PI_SCHPO	22.36%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
217	228	2	1343.61	5.2	1	37.3	24.3	95.00%	K.TFTTAETCTNAK.S	Carbamidomethyl (+57)	K.TFTTAETCTNAK.S
372	382	2	1171.52	5.1	1	67.7	24.3	95.00%	R.SGDMVNYTTGK.I		R.SGDMVNYTTGK.I
464	477	2	1502.83	4	0	36.9	16.5	95.00%	K.TFVGNRPSNSIIAK.K		K.TFVGNRPSNSIIAK.K
79	86	2	886.45	2.7	1	38.1	21.4	95.00%	K.EANVEGLR.D		K.EANVEGLR.D
2	24	2	2548.27	3.8	1	60.7	19.4	95.00%	M.SFSLASTLPAWQAVQTHYESVGK.H	Acetyl (+42)	-.MSFSLASTLPAWQAVQTHYESVGK.H
118	128	2	1170.59	4.1	1	35.5	21.4	95.00%	K.VNGQDVMPGVR.K		K.VNGQDVMPGVR.K
429	445	2	1870.94	4.8	1	69.7	21.6	95.00%	R.MLFSNFAAQTEALMLGK.T		R.MLFSNFAAQTEALMLGK.T
536	547	2	1308.66	3	0	35.3	22.4	95.00%	H.DSSTNGLINLFK.N	Deamidation (+1)	K.GDVENHDSSTNGLINLFK.N
353	367	2	1712.81	2.6	1	74.2	23.3	95.00%	R.FPAYLQQLSMESNGK.A	Deamidation (+1)	R.FPAYLQQLSMESNGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
33	HSP60_SCHPO	18.04%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	148	2	1316.6	4	1	27.4	24.3	95.00%	R.NVAAGCNPMDLR.R	Carbamidomethyl (+57)	R.NVAAGCNPMDLR.R
437	453	2	1588.85	4.6	1	29.9	18.9	95.00%	K.AAVSEGVLPGAGTSFVK.A		K.AAVSEGVLPGAGTSFVK.A
343	359	3	1806.87	3.6	1	25.8	22	95.00%	K.AQPHHLGSCGSVTVTKE.D	Carbamidomethyl (+57)	K.AQPHHLGSCGSVTVTKEDTIIMK.G
263	275	2	1452.8	3	1	33.8	17.1	95.00%	Q.DILPSLELAAQQR.R		K.VSAVQDILPSLELAAQQR.R
68	79	2	1313.7	4.3	1	39.3	18.6	95.00%	R.NVLIDQPFGSPK.I		R.NVLIDQPFGSPK.I
229	240	2	1401.72	4.3	1	35	20.5	95.00%	R.GYISPYFITDVK.S		R.GYISPYFITDVK.S
186	195	2	1095.6	2.7	1	32.6	18.9	95.00%	G.DTHIGELLAK.A		R.DITTSEEISQVATISANGDTHIGELLAK.A
45	56	2	1215.69	4.9	1	52.6	16.7	95.00%	R.ASLLTGVDTLAR.A		R.ASLLTGVDTLAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
34	SERA_SCHPO	21.89%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
58	73	2	1768.01	2.1	1	94.3	11.5	95.00%	K.ILLLENVNQSALSNLK.D		K.ILLLENVNQSALSNLK.D
275	284	2	1108.56	4.3	0	25.6	22.9	93.10%	K.EGSYLINASR.G		K.EGSYLINASR.G
440	452	2	1454.68	1.5	1	44.2	23.6	95.00%	S.DCTPGSLEALHQK.L	Carbamidomethyl (+57)	R.GDIAYLVADISDCTPGSLEALHQK.L
324	337	2	1676.75	3.1	1	54.5	24	95.00%	V.DSLNSWTSELTHCK.N	Carbamidomethyl (+57)	K.FVDSLNSWTSELTHCK.N
308	319	2	1233.56	3.5	1	29	23	95.00%	I.DVYPSEPAGNGK.D	Deamidation (+1)	K.IAGAAIDVYPSEPAGNGK.D
338	350	2	1350.72	3	1	37.8	20.1	95.00%	K.NIILTPHIGGSTE.E		K.NIILTPHIGGSTEEAQYNIGIEVSEALTR.Y
142	154	2	1394.7	4.8	0	57.8	21.7	95.00%	R.GIAVFNSPYANSR.S		R.GIAVFNSPYANSR.S
237	247	3	1291.73	4.7	1	20.7	16	95.00%	K.QLSSLPELLHR.A		K.QLSSLPELLHR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
35	IPYR_SCHPO	9.69%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
104	113	3	1134.57	1.6	1	20.7	21.8	95.00%	E.DPNVVHPETK.A		R.NCFPHHGYIWNYGAFPQTYEDPNVVHPETK.A
186	192	2	922.44	6	1	35.4	23.7	95.00%	R.ATNEWFR.I		R.ATNEWFR.I
43	53	2	1283.73	4	1	66.7	15.1	95.00%	K.TILNMVVEIPR.W		K.TILNMVVEIPR.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
36	LYS9_SCHPO	21.56%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
204	223	3	2455.17	2.8	0	33.8	21.5	95.00%	M.ETAKPYFIYPGYAFVCYPNR.D	Carbamidomethyl (+57)	K.DLMETAKPYFIYPGYAFVCYPNR.D
177	183	2	740.49	4.7	0	33.1	10.4	95.00%	R.GVLLALR.N		R.GVLLALR.N
171	176	2	768.36	6.1	0	24.6	23.1	91.50%	K.FSWSSR.G		K.FSWSSR.G
38	49	2	1259.66	4.1	1	41.7	20	95.00%	K.AEAFINGIPNSK.A		K.AEAFINGIPNSK.A
2	22	3	2269.25	3.1	1	39	13.2	95.00%	M.PSILLLGSGFVAHPTLEYLSR.R		-.MPSILLLGSGFVAHPTLEYLSR.R
411	423	2	1265.66	2.4	0	31.7	20.4	95.00%	L.DGVINTPGVLAPN.D		K.LVGVPCGVATQQILDGVINTPGVLAPNDMK.L
379	396	2	1989.93	4.3	1	76.6	22.3	95.00%	R.TCTLLDYGVPNGYTSMAK.L	Carbamidomethyl (+57)	R.TCTLLDYGVPNGYTSMAK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
37	C1TC_SCHPO	12.70%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
689	707	3	1923.15	3.9	1	37.5	6.02	95.00%	R.TSGLKPDAIVIVATVQALK.L		R.TSGLKPDAIVIVATVQALK.L
2	12	2	1184.68	4.9	1	55.8	16.5	95.00%	M.ALLLEGTSLAR.K	Acetyl (+42)	-.MALLLEGTSLAR.K
121	130	2	1139.5	3.1	1	24.4	23.3	91.20%	V.DGFCETNLGK.L	Carbamidomethyl (+57)	K.DVDGFCETNLGK.L
170	183	2	1555.88	3.9	1	30.1	13.4	95.00%	R.SNIVGRPMSILLEK.A		R.SNIVGRPMSILLEK.A
764	773	2	1100.55	2.3	1	40.8	21.8	95.00%	S.DSPNEISAIR.E		K.FSSDSPNEISAIR.E
381	396	2	1629.9	3.4	1	106	16.4	95.00%	K.STLTAGLVQALSNLDK.L		K.STLTAGLVQALSNLDK.L
349	356	2	983.58	5.3	1	46.2	15.8	95.00%	K.VNLEILQR.L		K.VNLEILQR.L
259	289	3	3121.66	4	1	20.6	12.6	95.00%	K.EVASAITPVPGSVGPMTVAMLLQNVVESAVR.F		K.EVASAITPVPGSVGPMTVAMLLQNVVESAVR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
38	RL4A_SCHPO	22.31%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
122	140	2	1845.04	4.3	0	48.1	10	95.00%	R.YAISSAVAASGVPSLLLAR.G		R.YAISSAVAASGVPSLLLAR.G
2	13	2	1304.71	4.5	0	25.5	18.4	93.00%	M.AAARPTVSIYSK.D	Acetyl (+42)	-.MAAARPTVSIYSK.D
235	248	3	1457.85	3.8	0	49.3	13.4	95.00%	R.LNLLQLAPGGHLGR.F		R.LNLLQLAPGGHLGR.F
234	248	3	1613.95	3.4	1	23.9	6.02	95.00%	R.RLNLLQLAPGGHLGR.F		R.RLNLLQLAPGGHLGR.F
14	29	2	1695.88	3	1	45.9	19.3	95.00%	K.DGSVSSETIALPFVFK.A		K.DGSVSSETIALPFVFK.A
156	163	2	921.46	3	0	24.8	22.7	91.90%	D.DAVQSFQK.T		R.IEEIPEVPLVVDDAVQSFQK.T
87	97	2	1197.51	4.4	0	32.6	24.2	95.00%	R.SGQAAFGNMCR.S	Carbamidomethyl (+57)	R.SGQAAFGNMCR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
39	MET3_SCHPO	15.31%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
217	229	3	1346.78	2.1	0	24.7	14.1	95.00%	R.VLIHPVVGMTKPG.D		R.VLIHPVVGMTKPGDIDHFTR.V
350	359	2	1102.6	3.9	1	29.9	20.4	95.00%	R.TLNISGTELR.R		R.TLNISGTELR.R
59	68	2	1233.64	5.6	1	40.5	21.9	95.00%	K.DYLNVVENLR.L		K.DYLNVVENLR.L
254	262	2	1012.62	5.1	0	33.5	13	95.00%	K.LSLLPLAMR.M		K.LSLLPLAMR.M
307	317	2	1326.61	3	1	64.1	24.4	95.00%	Y.DAQYLVEQYAQ.E		K.NSQGEDFYGPYDAQYLVEQYAQEIGITIVPFQMMTYLPDEDIYKPVDK.V
73	81	2	1027.6	3.6	0	25.1	17.9	92.40%	G.EVFPIPITL.D		R.LSTGEVFPIPITLDLNESQADSLK.A
458	470	3	1481.83	3.2	1	27.9	15.4	95.00%	K.VPAEWTTVNIKPK.D		K.VPAEWTTVNIKPK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
40	HSP7M_SCHPO	12.02%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
204	215	2	1124.67	4.6	0	48.3	13.8	95.00%	K.AAGAIAGLNVLR.V		K.AAGAIAGLNVLR.V
474	482	2	987.5	3.8	1	30.5	20.7	95.00%	A.DGQTAVEIR.V		K.SQVFSTAADGQTAVEIR.V
105	118	2	1578.81	4.5	1	81.4	20.5	95.00%	R.QAVINPENTFFATK.R		R.QAVINPENTFFATK.R
185	199	2	1679.83	4.3	1	62.1	22	95.00%	K.NAVVTVPAYFNDSQR.Q		K.NAVVTVPAYFNDSQR.Q
496	510	2	1538.89	4.2	0	77.2	13	95.00%	K.LIGNFQLTGIAPAPK.G		K.LIGNFQLTGIAPAPK.G
157	170	2	1496.8	5.1	0	59.3	18.7	95.00%	K.TYSPSQIGGFILSK.M		K.TYSPSQIGGFILSK.M
155	170	2	1681.91	4.3	1	28.5	17.2	95.00%	R.GKTYSPSQIGGFILSK.M		R.GKTYSPSQIGGFILSK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
41	CYSD_SCHPO	26.57%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
47	59	2	1541.79	2.8	1	43.4	20.6	95.00%	R.LFGLQEPGYIYSR.M		R.LFGLQEPGYIYSR.M
27	39	2	1486.79	3.4	0	62.2	19	95.00%	R.AVPIYATTSYVFR.D		R.AVPIYATTSYVFR.D
184	201	2	1844.89	3.2	1	58.4	21.9	95.00%	V.DNTFGGGGYLVRPIDHGA.D		R.IAEVAHAAGVPLMVDNTFGGGGYLVRPIDHGADIVTHSATK.W
72	100	3	2787.49	3.3	1	49.9	14.5	95.00%	R.IAALEHGAAAIATSSGTSALFMALTTLAK.A		R.IAALEHGAAAIATSSGTSALFMALTTLAK.A
151	165	2	1651.8	3.9	1	30.6	22.9	95.00%	K.AVYVESIGNPMYNVP.D		K.AVYVESIGNPMYNVPDFER.I
366	377	2	1185.64	4.4	1	34.5	19.6	95.00%	K.LASQLANVGDAK.T		K.LASQLANVGDAK.T
170	183	2	1376.75	2.3	1	35.2	17.6	95.00%	R.IAEVAHAAGVPLMV.D		R.IAEVAHAAGVPLMVDNTFGGGGYLVRPIDHGADIVTHSATK.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
42	THIL_SCHPO	26.08%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
291	301	2	1160.65	4.8	0	33.2	17.2	95.00%	R.FTTSPSLAIPK.A		R.FTTSPSLAIPK.A
51	69	2	2016.97	2.3	1	93.2	20.9	95.00%	V.DEVFMGNVVSANLGQNPAR.Q		R.VNIKPSDVDEVFMGNVVSANLGQNPAR.Q
14	30	2	1654.81	3.1	0	97	21.8	95.00%	R.TPMGSFGGSFASLPATK.L		R.TPMGSFGGSFASLPATK.L
267	277	3	1194.77	2.2	1	21.4	6.02	95.00%	K.VKELGLKPLAK.I		K.VKELGLKPLAK.I
360	371	2	1405.81	4.5	0	73.2	14.9	95.00%	R.IICTLAYILAQK.D	Carbamidomethyl (+57)	R.IICTLAYILAQK.D
254	266	2	1232.65	3	0	61.5	20.7	95.00%	N.DGASALVLMSAAK.V		K.SNGTVTAANASTLNDGASALVLMSAAK.V
340	359	3	1865.93	4.8	0	31	21.8	95.00%	R.VNINGGGVAMGHPLGSSGSR.I		R.VNINGGGVAMGHPLGSSGSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
43	YL8C_SCHPO	15.18%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
47	60	2	1575.87	3.5	1	43.3	15.8	95.00%	R.EKYPNFPIVLATGK.Q		R.EKYPNFPIVLATGK.Q
217	232	2	1745.96	3.4	1	53.7	14.9	95.00%	K.GTALQYITSNILPEVK.N		K.GTALQYITSNILPEVK.N
49	60	2	1318.74	5.4	0	24.4	17.3	91.10%	K.YPNFPIVLATGK.Q		K.YPNFPIVLATGK.Q

75	90	2	1775.83	2.2	0	60.7	23.3	95.00%	L.DAFPAAHVNGCVLYNK.G	Deamidation (+1)/ Carbamidomethyl (+57)	R.IPLDLDAFPAAHVNGCVLYNK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
44	PUT2_SCHPO	15.33%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
368	384	2	1889.95	2.4	0	63	20.9	95.00%	T.DFANFVGPVIHQASFNK.L		K.VGAPLTDFANFVGPVIHQASFNK.L
362	384	3	2428.26	3.2	1	27	17	95.00%	K.VGAPLTDFANFVGPVIHQASFNK.L		K.VGAPLTDFANFVGPVIHQASFNK.L
254	274	3	2393.15	4.4	1	52.3	20.9	95.00%	K.VCFNHPEFAGLHFTGSTAVFR.S	Carbamidomethyl (+57)	K.VCFNHPEFAGLHFTGSTAVFR.S
275	288	2	1444.74	4.6	1	37.7	21.6	95.00%	R.SLWGTIGENVANGK.Y		R.SLWGTIGENVANGK.Y
495	509	2	1504.71	3.5	1	49.3	22.5	95.00%	K.CTGAVVGEQPFGGAR.A	Carbamidomethyl (+57)	K.CTGAVVGEQPFGGAR.A
484	494	2	1225.58	4.6	1	28	23.5	95.00%	R.NAAGNFYINDK.C		R.NAAGNFYINDK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
45	PDX1_SCHPO	14.53%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
71	83	2	1355.75	4.3	0	66.7	18.3	95.00%	K.EIQAAVSIPVMAK.V		K.EIQAAVSIPVMAK.V
121	132	3	1383.7	4.4	1	31	21.8	95.00%	K.SKFTVPFVCGSR.N	Carbamidomethyl (+57)	K.SKFTVPFVCGSR.N
271	280	2	1016.51	4	0	29.6	23.5	95.00%	S.ENLGAAMVGR.S		K.ILAEVSENLGAAMVGR.S
13	20	2	830.47	4.2	0	38.8	20.6	95.00%	K.AGLAQMLK.G		K.AGLAQMLK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
46	HSP7F_SCHPO	11.25%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
174	189	2	1665.85	4	1	78.4	20.7	95.00%	R.LMNDNAAAALTYGITK.T		R.LMNDNAAAALTYGITK.T
422	434	2	1403.7	2.9	1	60.3	22.3	95.00%	L.EVFSEGNPIPSTK.I		R.EFHVHDVTTYPITFSWEPIPENPEEDSSLEVFSEGNPIPSTK.I
5	16	2	1249.64	6.5	1	29.4	21.8	95.00%	R.TNVVGIDFGNSK.T		R.TNVVGIDFGNSK.T
38	48	2	1194.59	3.8	1	34	23	95.00%	R.STPSLVSYGER.S		R.STPSLVSYGER.S
377	390	2	1549.78	2.9	0	54	21.2	95.00%	R.GCALSCAILSPVFR.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GCALSCAILSPVFR.V
177	189	2	1307.68	3	0	38.5	21.4	95.00%	N.DNAAAALTYGITK.T		R.LMNDNAAAALTYGITK.T
159	173	2	1534.89	4	1	42.9	9.54	95.00%	R.ALLEAANIAGLNPLR.L		R.ALLEAANIAGLNPLR.L
162	173	2	1237.68	2.3	0	26.6	16.7	94.40%	L.EAANIAGLNPLR.L		R.ALLEAANIAGLNPLR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
47	ECM17_SCHPO	4.48%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1031	1044	2	1572.69	3.1	1	69.6	23.6	95.00%	R.NVTCSSTPNNETIH.D	Carbamidomethyl (+57)	R.NVTCSSTPNNETIHDQLFAVSK.Q
1088	1100	2	1518.78	3.3	1	27.7	21.1	95.00%	Q.DVEPLYGPTYLPR.K		K.VAGEAVQDVEPLYGPTYLPR.K
314	325	2	1337.8	4.6	1	39.3	10.8	95.00%	R.LTVLEPITSLPR.K		R.LTVLEPITSLPR.K
1053	1066	2	1588.78	1.7	1	44.7	22.7	95.00%	K.QISNELLPTTSSYH.E		K.QISNELLPTTSSYHEIWIEDPETVEK.R
369	381	2	1372.71	2.9	0	42.1	21.1	95.00%	R.DNLSGALKPSLVC.D	Carbamidomethyl (+57)	R.DNLSGALKPSLVCDFTDGVSQVFVPTPPSIEEAYHK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
48	FAS2_SCHPO	1.57%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
774	793	3	2133.1	3	0	30.4	18.2	95.00%	M.DTRPAQVILPLSPNHGTFGN.D		R.GMDTRPAQVILPLSPNHGTFGNDGLYSESK.L
1393	1401	2	994.61	4.5	1	27.6	10.4	95.00%	K.TPLPIVDLK.F		K.TPLPIVDLK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
49	HOSM_SCHPO	13.88%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	204	2	1315.66	4	1	40.8	22.3	95.00%	R.VGIADTVGCATPR.Q	Carbamidomethyl (+57)	R.VGIADTVGCATPR.Q
248	257	2	1059.56	2.8	1	46.1	21.1	95.00%	I.DTSILGIGER.N		R.GVVSCDIECHFHNDTGMAIANAY CALEAGATHIDTSILGIGER.N
258	269	2	1195.7	3.5	0	24.6	13.2	91.60%	R.NGITPLGALLAR.M	Deamidation (+1)	R.NGITPLGALLAR.M
146	156	2	1221.63	3.5	1	44.8	22.3	95.00%	I.DSATEVINFVK.S		K.DMTYIIDSATEVINFVK.S
32	43	2	1391.75	4.9	1	68.1	19.7	95.00%	R.VNNFSIIESTLR.E		R.VNNFSIIESTLR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
50	CYPH_SCHPO	43.83%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
83	89	2	835.41	2.8	1	29.2	22.3	95.00%	P.DENFALK.H		K.FPDENFALK.H
90	123	3	3611.83	4	1	56	16.4	95.00%	K.HNKPGLLSMANAGPNTNGSQFFI TTVVTPWLDGK.H		K.HNKPGLLSMANAGPNTNGSQFFI TTVVTPWLDGK.H
2	17	2	1835.87	3.9	1	50	22.6	95.00%	M.SNCFFDVIANGQPLGR.I	Acetyl (+42)/ Carbamidomethyl (+57)	-.MSNCFFDVIANGQPLGR.I
54	63	2	1104.57	3.1	0	30.7	21.8	95.00%	R.VIPQFMLQGG.D	Oxidation (+16)	R.VIPQFMLQGGDFTR.G
54	67	2	1607.82	4.3	1	67.2	20.8	95.00%	R.VIPQFMLQGGDFTR.G		R.VIPQFMLQGGDFTR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
51	ADH_SCHPO	23.71%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
236	253	2	1681.87	4.1	0	56	18.3	95.00%	K.AATNGGAHGTLVLSTSPK.S	Deamidation (+1)	K.AATNGGAHGTLVLSTSPK.S
254	278	3	2513.21	3.1	1	41.5	20.2	95.00%	K.SYEQAAGFARPGSTMVTVSMPA GAK.L		K.SYEQAAGFARPGSTMVTVSMPA GAK.L
170	194	3	2506.29	3.6	1	33.6	16.1	95.00%	K.VGPGEWICIPGAGGGLGHLAVQY AK.A	Carbamidomethyl (+57)	K.VGPGEWICIPGAGGGLGHLAVQY AK.A
63	77	3	1462.8	3.2	1	21.3	17.3	95.00%	K.MPLIGGHEGAGVVVK.V		K.MPLIGGHEGAGVVVK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
52	OAT_SCHPO	6.62%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
386	398	3	1374.82	4.6	0	23.2	12.3	95.00%	R.GVLAKPTHGNIIR.F		R.GVLAKPTHGNIIR.F
276	291	2	1561.85	3.3	0	56	17.1	95.00%	K.AISGGVYPVSAVLSSR.E		K.AISGGVYPVSAVLSSR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
53	PPA1_SCHPO	15.45%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
413	427	2	1802.8	2	1	48.5	23.8	95.00%	S.DGMCELYAYLNSPVR.V	Oxidation (+16)/ Carbamidomethyl (+57)	R.HLVNEEVFPLSDCGFGPSNTSD GMCELYAYLNSPVR.V
40	59	3	2404.13	2.5	1	63.3	22.4	95.00%	R.SPYHKPYFYGPSIDFPTTCK.I	Carbamidomethyl (+57)	R.SPYHKPYFYGPSIDFPTTCK.I
417	427	2	1323.69	2.4	0	50.4	21	95.00%	C.ELYAYLNSPVR.V		R.HLVNEEVFPLSDCGFGPSNTSD GMCELYAYLNSPVR.V
73	92	2	2047	4	1	99.4	21.6	95.00%	R.NPTGGNAAFDAVGIANFQQR.L		R.NPTGGNAAFDAVGIANFQQR.L
331	345	2	1606.83	2.8	1	34.1	20	95.00%	H.DANIIPVETALGFFT.D		R.SVENNTQQVFFAFTHDANIIPVET ALGFFTDNTPENPLPTSYQVHSHS MK.A
40	52	2	1554.75	1.7	0	29.7	22.9	95.00%	R.SPYHKPYFYGPSI.D		R.SPYHKPYFYGPSIDFPTTCK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
54	DHAS_SCHPO	22.13%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
231	244	2	1569.8	2.2	1	48.8	20.9	95.00%	T.DNVVSAQCNRVPVI.D	Carbamidomethyl (+57)	K.ILGSVNSTISGYELTDNVVSAQCN RVPVIDGHLMCISVK.F
307	318	2	1278.6	4.8	1	24.6	23.5	91.50%	R.NNENGYAVSVGR.I		R.NNENGYAVSVGR.I
31	39	2	856.52	4.9	0	28.2	17.2	95.00%	K.IAVLGASAR.S		K.IAVLGASAR.S
143	161	2	2003.03	3.7	0	71.8	19.5	95.00%	R.GCIITNSNCSTAAVVVPLK.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GCIITNSNCSTAAVVVPLK.A
267	278	2	1375.7	3.8	1	37.2	21.5	95.00%	R.EVLANYVSEPQK.L		R.EVLANYVSEPQK.L

6	18	2	1227.7	3.7	0	35.6	17.3	95.00%	K.VGILGATGTVGQR.F		K.VGILGATGTVGQR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
55	EF1B_SCHPO	13.08%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
59	73	2	1561.84	4.2	1	60.9	18.5	95.00%	K.QIATYDLATLPGTAK.E		K.QIATYDLATLPGTAK.E
153	165	2	1432.74	3.9	1	44.3	21.2	95.00%	R.SIQMDGLVWGLSK.L		R.SIQMDGLVWGLSK.L
157	165	2	973.53	3.5	0	29.6	22.1	95.00%	M.DGLVWGLSK.L		R.SIQMDGLVWGLSK.L
64	73	2	985.55	3.6	0	31.2	21	95.00%	Y.DLATLPGTAK.E		K.QIATYDLATLPGTAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
56	LEUC_SCHPO	9.37%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
633	649	2	2002.01	4.5	1	59.4	21.1	95.00%	R.VIIAPSFADIFFNNCFK.N	Carbamidomethyl (+57)	R.VIIAPSFADIFFNNCFK.N
603	619	3	1826.86	5.3	1	37.3	22.8	95.00%	R.HATVLVAHDNFGCGSSR.E	Carbamidomethyl (+57)	R.HATVLVAHDNFGCGSSR.E
477	493	2	1810.88	4.1	1	36.5	21.8	95.00%	R.EFFGDVSNGSPSIITNK.N		R.EFFGDVSNGSPSIITNK.N
520	539	2	1786.91	2.7	0	83.5	20.7	95.00%	A.DGIATNVAGSVSSGSAGIPK.F		K.NYDPSHDVEGDIGLSVDDATDAVTDADGIATNVAGSVSSGSAGIPK.F
481	493	2	1331.66	3.1	0	52.7	22	95.00%	G.DVSNGSPSIITNK.N	Deamidation (+1)	R.EFFGDVSNGSPSIITNK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
57	GLNA_SCHPO	11.70%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
247	260	2	1546.65	1.9	0	49.6	24.1	95.00%	G.DWNGAGCHTNVSTK.D	Deamidation (+1)/ Carbamidomethyl (+57)	K.ISFHPKPILGDWNGAGCHTNVSTK.D
153	170	2	1809.83	4.4	0	40.7	23.3	95.00%	K.GGFPGPQGPFYCGVGTGR.V	Carbamidomethyl (+57)	K.GGFPGPQGPFYCGVGTGR.V
237	246	2	1107.65	2.3	0	25.7	14.1	93.30%	K.ISFHPKPILG.D		K.ISFHPKPILGDWNGAGCHTNVSTK.D
237	260	4	2635.31	3.2	1	28.9	19.4	95.00%	K.ISFHPKPILGDWNGAGCHTNVSTK.D	Carbamidomethyl (+57)	K.ISFHPKPILGDWNGAGCHTNVSTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
58	YHY6_SCHPO	16.76%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
214	225	2	1537.76	2.2	0	44.8	21.5	95.00%	A.DFPNWYQQVLTK.S		K.DADFPNWYQQVLTK.S
161	187	3	2608.39	2.9	1	26.8	14.5	95.00%	K.SVGVNPIIVDFSAPGSATAPSKPAAQK.K		K.SVGVNPIIVDFSAPGSATAPSKPAAQK.K
304	313	2	1097.58	2.9	1	25.9	20.1	93.50%	L.DEPIAIRPTS.E		R.AGTSELDEPIAIRPTSETVMYPYYAK.W
147	160	2	1522.84	2.4	0	39.3	15.4	95.00%	K.TVFVSPAAVQTYLK.S		K.TVFVSPAAVQTYLK.S
335	343	2	1114.59	4.7	0	24.2	20.9	90.70%	K.LNQWNSVVR.W		K.LNQWNSVVR.W
492	511	3	2075.19	3.5	0	31.4	8.45	95.00%	K.LPPAIALVQSVVVPCGITNK.T	Carbamidomethyl (+57)	K.LPPAIALVQSVVVPCGITNK.T
387	398	2	1343.81	4.3	1	30.5	9.03	95.00%	R.IYTDLLAVPVIK.G		R.IYTDLLAVPVIK.G
426	441	3	1703.81	4.5	0	20.8	22.7	95.00%	R.GIQGATSHCLGQNFSK.M	Carbamidomethyl (+57)	R.GIQGATSHCLGQNFSK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
59	HXK1_SCHPO	9.09%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
36	47	2	1482.79	3.1	1	33.7	18.7	95.00%	E.EQFTIPTELLHR.V		K.TLQDHLDELEEQFTIPTELLHR.V
304	315	2	1380.7	5.1	1	25.3	22.1	92.60%	K.MIAGCYLGDILR.R	Carbamidomethyl (+57)	K.MIAGCYLGDILR.R
274	282	2	1076.58	2.5	0	54.4	20	95.00%	F.DNQHVVLPR.T		K.YDFPEDMNMIINCEWCDFDNQHVVLPR.T
2	12	3	1409.65	4.4	1	25.1	23.1	95.00%	M.SLHDAYHWPSR.T	Acetyl (+42)	-.MSLHDAYHWPSR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
60	RS18_SCHPO	29.61%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	78	2	1386.79	4	0	45.2	15.2	95.00%	R.IVTIIQNPSQFK.I		R.IVTIIQNPSQFK.I

2	14	2	1578.86	4.3	1	26.6	17.2	94.40%	M.SLVVPDNFQHILR.L	Acetyl (+42)	-.MSLVVPDNFQHILR.L
79	86	2	1031.56	6	0	52.6	20.6	95.00%	K.IPSWFLNR.Q		K.IPSWFLNR.Q
95	106	2	1334.69	4.9	1	24.9	20.8	92.00%	K.SFQLLANNVDSK.L		K.SFQLLANNVDSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
61	ILV3_SCHPO	11.20%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
354	366	2	1328.77	2.5	0	40.6	14	95.00%	E.DLFAIGGIPSVLK.Y		K.YVMEDLFAIGGIPSVLK.Y
539	547	2	999.56	4.1	1	31.4	20.3	95.00%	G.DVIEINAVK.N		R.FSGGSHGFLIGHVDPEAQVGGPIALVQDGDVIEINAVK.N
40	48	2	994.5	5.2	1	30.6	23.7	95.00%	K.YSETITGPK.S		K.YSETITGPK.S
246	265	2	2011.93	3.1	1	81.2	23.1	95.00%	A.EAMGMTLPGSSSYLAGSPEK.F		R.HACPGGGACGGMYTANTMASCAEAMGMTLPGSSSYLAGSPEK.F
197	212	2	1760.87	3.5	1	49.8	21.2	95.00%	I.DIVSAFQSYGEFITGK.I		R.AGHSPCQNNAPIDIVSAFQSYGEFITGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
62	YF19_SCHPO	16.90%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
195	208	2	1516.82	3	1	47.4	17.8	95.00%	K.TAELTPLSALCLTK.F	Carbamidomethyl (+57)	K.TAELTPLSALCLTK.F
18	32	2	1741.92	2.5	0	32.9	18.9	95.00%	K.TYIQPVGLFINNQHV.D		K.TYIQPVGLFINNQHVDSVHGGR.V
422	443	3	2229.12	4.1	0	21.2	19.3	95.00%	R.GNNSTYGLAAGVHTNNITNAIK.V		R.GNNSTYGLAAGVHTNNITNAIK.V
71	80	2	1161.56	3.7	1	28.3	23.5	95.00%	R.AAFQTDAPWR.K		R.AAFQTDAPWR.K
340	349	2	1079.53	3.9	0	35.8	23	95.00%	E.DTFQGAQVSK.Q		K.VGDPFAEDTFQGAQVSK.Q
181	194	2	1439.82	1.1	0	51.4	14.1	95.00%	K.IAPAVACGNTIILK.T	Carbamidomethyl (+57)	K.IAPAVACGNTIILK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
63	UGPA1_SCHPO	16.60%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
22	34	2	1309.62	2.4	0	55.9	23.1	95.00%	F.DNTATSIAASTMK.N		K.SQSAFAFDNTATSIAASTMK.N
493	506	2	1624.79	1.9	1	58.1	23.1	95.00%	L.ENCVITGNLNILEH.-	Carbamidomethyl (+57)	R.IDIPNGSVLENCVITGNLNILEH.-
1	10	2	1166.63	4.6	1	24.9	19.3	92.00%	-.MDLAPRPLGR.Q	Acetyl (+42)	-.MDLAPRPLGR.Q
185	194	2	1205.65	4.7	1	32.1	19.4	95.00%	K.IDILTFNQSR.Y		K.IDILTFNQSR.Y
94	104	2	1118.56	2.6	1	59.2	21.8	95.00%	Y.DTITEAGGLSR.D		R.GSEINWDLVESPKPEQVVEYDTITEAGGLSR.D
115	129	2	1460.72	4.2	0	48.3	22.8	95.00%	K.LNGGLGTTMGCVGPK.S	Carbamidomethyl (+57)	K.LNGGLGTTMGCVGPK.S
35	45	2	1224.65	2.3	1	25.4	20.2	92.80%	K.NELNHLASTVK.D		K.NELNHLASTVK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
64	GBLP_SCHPO	18.47%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
48	57	2	1135.53	4.7	1	43.2	22.9	95.00%	R.DDVNYGVAQR.R		R.DDVNYGVAQR.R
186	212	3	2736.26	2.6	1	43.2	22.2	95.00%	R.TSHYGHTGYVSAVTISPDGSLCASGGR.D	Carbamidomethyl (+57)	R.TSHYGHTGYVSAVTISPDGSLCASGGR.D
234	245	2	1314.71	3.1	0	32.5	19.4	95.00%	K.ANINALVFSPNR.Y		K.ANINALVFSPNR.Y
39	47	2	1112.68	5.9	0	27.8	13	95.00%	K.SIILWNLVR.D		K.SIILWNLVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
65	DHOM_SCHPO	23.94%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
150	164	2	1454.84	3.1	0	37.3	14.3	95.00%	H.EASVGAGLPIISTLK.E		K.ESGALLMHEASVGAGLPIISTLK.E
125	138	2	1568.79	4.5	1	56.7	21.1	95.00%	K.AFSASNDVYQNIIK.A		K.AFSASNDVYQNIIK.A
57	67	2	1391.68	4.7	1	33.1	22.6	95.00%	K.DYQPINLSEWK.N		K.DYQPINLSEWK.N
313	325	2	1435.64	3.8	1	43.6	23.9	95.00%	K.YDASHPFANLQSS.D		K.YDASHPFANLQSSDNIISFTTK.R

238	252	2	1526.81	1	1	42.7	19.8	95.00%	R.IAGVHVESASSFPVK.S		R.IAGVHVESASSFPVK.S
142	164	3	2293.24	2.5	1	28.4	14	95.00%	K.ESGALLMHEASVGAGLPIISTLK.E		K.ESGALLMHEASVGAGLPIISTLK.E
97	110	2	1493.7	2.3	1	57.5	23.2	95.00%	V.DNTASEAIAQSYPK.F		K.SPLPAILVDNTASEAIAQSYPK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
66	EF1G_SCHPO	15.40%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
290	298	2	1136.52	3	1	32.2	23.1	95.00%	F.DPENYSVWK.V		R.SGALPWFFEHFDPENYSVWK.V
93	115	3	2635.36	2.4	1	46.5	15.7	95.00%	K.VLQYCSFTNSELPGAFRPIIAPR.V	Carbamidomethyl (+57)	K.VLQYCSFTNSELPGAFRPIIAPR.V
207	216	2	1182.71	4	1	27.1	14.6	95.00%	K.FIDQPLPIIK.A		K.FIDQPLPIIK.A
367	375	2	1103.5	3.1	0	28.9	23.3	95.00%	P.DWGSYTFTK.L		K.GHDYVPAFDVAPDWGSYTFTK.L
128	139	2	1303.72	4.6	1	40.7	18.6	95.00%	K.EAETAIALIFAR.F		K.EAETAIALIFAR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
67	IF4A_SCHPO	9.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
58	69	2	1173.61	5	0	69	21.8	95.00%	R.DVLAQAQSGTGK.T		R.DVLAQAQSGTGK.T
33	48	2	1854.94	2.2	1	38.6	20.3	95.00%	R.GIYAYGFERPSAIQQR.A		R.GIYAYGFERPSAIQQR.A
298	305	2	1047.49	4.2	1	24.7	22.7	91.70%	R.DTLMHEFR.T		R.DTLMHEFR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
68	PYR1_SCHPO	3.21%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
709	720	2	1229.65	2.3	0	35.7	19.5	95.00%	G.DSIVVAPSQTLT.D		R.DAFDNCITVCNMENFDPLGIHTG DSIVVAPSQTLTDEDYNMLR.T
202	216	2	1513.77	2.2	1	44.7	21.6	95.00%	K.DESPINPSSITGLGK.D		K.DESPINPSSITGLGK.D
1771	1784	2	1494.85	4.1	1	35.2	12.3	95.00%	R.EAIPLLLTAVNEGR.L		R.EAIPLLLTAVNEGR.L
701	708	2	808.41	1.3	0	41.7	20.9	95.00%	F.DPLGIHTG.D		R.DAFDNCITVCNMENFDPLGIHTG DSIVVAPSQTLTDEDYNMLR.T
1897	1906	2	1089.51	2.8	1	32.3	22.6	95.00%	A.EAFGQAPENK.A		K.VSALMSPGLPHAAPSLAEAFGQA PENK.A
1758	1770	2	1371.7	4.4	0	56.2	21.7	95.00%	K.FVGNTAFTGFGVR.E		K.FVGNTAFTGFGVR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
69	RAD24_SCHPO	15.19%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
109	120	2	1236.65	4.7	1	29.1	20.3	95.00%	K.HLIPNAASAESK.V		K.HLIPNAASAESK.V
164	172	2	1032.58	3.9	0	37	17.8	95.00%	A.ELAPTHPIR.L		K.AASEIATAELAPTHPIR.L
76	85	2	1071.6	3.6	1	23.8	19.7	90.10%	K.GNTAQVELIK.E		K.GNTAQVELIK.E
218	227	2	1188.66	2.8	0	53.8	18	95.00%	K.DSTLIMQLLR.D		K.DSTLIMQLLR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
70	RL8_SCHPO	15.06%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
24	32	2	1084.62	4.7	0	29.3	18.8	95.00%	K.NPLFVSRPR.S		K.NPLFVSRPR.S
33	43	2	1188.62	4.1	1	26.8	21.3	94.60%	R.SFGIGQDIQPK.R		R.SFGIGQDIQPK.R
134	146	2	1425.8	4.3	1	45.6	14.5	95.00%	K.YGLNHVVALIEAK.K		K.YGLNHVVALIEAK.K
52	57	2	862.44	5.9	1	26.5	22.3	94.30%	K.WPEYIR.L		K.WPEYIR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
71	VIPI_SCHPO	18.68%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	68	2	1496.86	4.3	1	41.7	13.6	95.00%	K.TALLLQDALLGQNK.I		K.TALLLQDALLGQNK.I
101	110	2	1087.63	5.8	1	34.3	16.6	95.00%	R.SAIISELLSR.G		R.SAIISELLSR.G

122	134	2	1410.71	4.2	1	61.1	21.6	95.00%	K.SIQLDQSYGVSSK.F		K.SIQLDQSYGVSSK.F
137	147	2	1100.62	4.3	1	27.7	18.8	95.00%	K.GILESALSGVR.S		K.GILESALSGVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
72	MMF1_SCHPO	30.25%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
94	105	2	1246.64	3.1	1	54.6	22	95.00%	Q.EVLTEAGSSLNK.I		R.QCLLNLQEVLTEAGSSLNK.I
59	75	2	1747.86	2.8	0	34.8	21.7	95.00%	K.ANGVIYCSGQIPVANGK.V	Carbamidomethyl (+57)/ Deamidation (+1)	K.ANGVIYCSGQIPVANGK.V
117	124	2	878.42	3.4	1	31	22.8	95.00%	M.DDFAAVNK.V		K.VNIFLADMDDFAAVNK.V
47	58	2	1247.66	5.3	0	27.4	19.6	95.00%	K.LSSAGPYNQAIK.A		K.LSSAGPYNQAIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
73	RS6B_SCHPO	18.41%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
39	51	2	1414.68	3.6	1	57.7	23.1	95.00%	G.DSVGPEFAGYVFK.I		R.MGQEVPGDSVGPEFAGYVFK.I
99	115	2	1739.01	3.8	1	65.7	11.1	95.00%	R.GCIVGQDLAVLALAIVK.Q	Carbamidomethyl (+57)	R.GCIVGQDLAVLALAIVK.Q
59	72	3	1625.86	4.7	0	32.2	19.1	95.00%	K.QGFPMFQGVLLPHR.V		K.QGFPMFQGVLLPHR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
74	RS7_SCHPO	16.92%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
59	70	2	1322.84	4	0	46.5	4.77	95.00%	K.AIVVFVPQPLLK.A		K.AIVVFVPQPLLK.A
119	129	2	1180.65	2.5	1	24.4	17.5	91.10%	R.TLTAVHNAILE.D		R.TLTAVHNAILEDIVFPTEIIGK.R
168	177	3	1123.57	4.2	0	19.7	22.8	93.50%	K.LGSFSSVYHK.L		K.LGSFSSVYHK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
75	TRP_SCHPO	11.76%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
382	393	2	1355.77	4.5	0	47.2	17.2	95.00%	K.INNCIGQILLAK.R	Carbamidomethyl (+57)	K.INNCIGQILLAK.R
400	419	3	1938.01	4.3	1	37.5	19.2	95.00%	R.IIAETGAGQHGVATAICAAK.F	Carbamidomethyl (+57)	R.IIAETGAGQHGVATAICAAK.F
445	461	2	1739.98	3.3	1	60.3	14	95.00%	R.LLGAEVVPVTSGTQTLR.D		R.LLGAEVVPVTSGTQTLR.D
590	598	2	899.44	1.9	0	26.1	21.3	93.80%	Q.DTHSISAGL.D		R.EDGQIQDTHSISAGLDYPGVGPELSELK.Y
91	114	2	2617.33	5.8	1	82.3	18.2	95.00%	R.DAGVTIPIILMGYYNPIFSYGDAK.T		R.DAGVTIPIILMGYYNPIFSYGDAK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
76	THI4_SCHPO	8.11%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
373	385	2	1353.71	4.1	1	37.5	19.8	95.00%	R.GVDSISQHTLAAR.I		R.GVDSISQHTLAAR.I
249	265	4	1917.09	3.2	1	33.8	10.4	95.00%	K.LKDFTPLIHHLTNAVAK.N		K.LKDFTPLIHHLTNAVAK.N
237	248	2	1322.76	4.7	0	31.5	13.2	95.00%	K.DLLNQIPAALQK.L		K.DLLNQIPAALQK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
77	ACON_SCHPO	6.68%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
532	549	2	1853.89	4.6	1	68.9	22	95.00%	K.GYDPGSNTYVAPSSVNVK.D		K.GYDPGSNTYVAPSSVNVK.D
392	402	2	1203.6	5.2	1	35.2	22.5	95.00%	R.AASICQQAIDK.G	Carbamidomethyl (+57)	R.AASICQQAIDK.G
476	489	2	1440.67	3	1	25.7	23.5	93.30%	R.NDANPATHAFVTSP.D		R.NDANPATHAFVTSPDIVTAMVFSGDMNFNPLTDTLK.D
462	470	2	1052.53	5	0	36.5	22.4	95.00%	K.NSIVTSYNR.N		K.NSIVTSYNR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
78	LYS12_SCHPO	15.75%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
197	208	2	1324.65	5.3	1	41.8	23	95.00%	K.SNVMSVTDGLFR.E		K.SNVMSVTDGLFR.E
298	307	2	1044.58	4.6	0	32.2	20.9	95.00%	R.GIANPVATFR.S		R.GIANPVATFR.S

279	292	2	1485.66	2.7	1	42.2	23.7	95.00%	G.DNFVMSEPVHGSAP.D		R.EPECFDVVVAPNLYGDILSDGAASLIGSLGLVPSANVGDNFVMSEPVHGSAPDIAGR.G
188	196	3	1047.69	4.7	0	25.1	3.01	95.00%	K.KPLVTIIHK.S		K.KPLVTIIHK.S
86	97	2	1231.7	4.7	0	25.9	16.7	93.60%	K.VAGYSSPIVALR.K		K.VAGYSSPIVALR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
79	SODC_SCHPO	24.03%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
98	116	2	1984.04	4.4	1	72.6	17.4	95.00%	K.TTFSDSVISLFGANSIIGR.T		K.TTFSDSVISLFGANSIIGR.T
102	116	2	1547.83	2.6	0	57	18.6	95.00%	S.DSVISLFGANSIIGR.T		K.TTFSDSVISLFGANSIIGR.T
53	70	2	1902.78	0.41	1	63.8	23.9	95.00%	G.DNTNGCTSAGPHFNPEGK.T	Deamidation (+1)/ Carbamidomethyl (+57)	R.GFHIHQFGDNTNGCTSAGPHFNPEGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
80	CDC48_SCHPO	5.03%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
550	563	2	1522.75	3.6	1	43.8	21.7	95.00%	K.AIANECSANFISVK.G	Carbamidomethyl (+57)	K.AIANECSANFISVK.G
511	522	2	1424.67	4.6	1	24.4	23	91.10%	R.ETVQMPVMYAEK.F		R.ETVQMPVMYAEK.F
430	444	2	1691.8	3.2	1	43	22.1	95.00%	S.DLASLCSEAAMQQIR.E	Carbamidomethyl (+57)	K.LADDVDLEQIAAETHGYVGSDLASLCSEAAMQQIR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
81	VATA_SCHPO	9.37%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
227	240	2	1539.81	3.3	0	65.6	19.8	95.00%	A.DNLTANQPLLTGQR.V		R.AARPVADNLTANQPLLTGQR.V
128	136	2	1002.51	5	1	25.2	22.2	92.50%	R.GINTESLNR.E		R.GINTESLNR.E
317	331	2	1544.81	4.6	0	49.4	20.9	95.00%	R.TTLVANTSNMPVAAR.E		R.TTLVANTSNMPVAAR.E
221	240	3	2105.14	4.1	1	35.3	16	95.00%	R.AARPVADNLTANQPLLTGQR.V		R.AARPVADNLTANQPLLTGQR.V
182	195	2	1466.71	0.88	1	40.5	23	95.00%	R.GTVTYIAEAGSYHV.D		R.GTVTYIAEAGSYHVDEK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
82	RS23_SCHPO	16.08%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
98	107	2	1091.56	2.4	1	57.5	22.2	95.00%	N.DEVLLSGFGR.K		K.VTAFVPHDGCLNFVDENDEVLLSGFGR.K
125	137	2	1326.74	4.4	1	55.5	17.2	95.00%	K.VAGVGLSALFHEK.K		K.VAGVGLSALFHEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
83	RS10B_SCHPO	23.13%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	44	2	1428.81	2.4	1	33.6	16.3	95.00%	K.HPEVGVPNLQVIK.A		K.HPEVGVPNLQVIK.A
10	24	2	1621.94	2.9	0	74.4	14.1	95.00%	K.AIHQALFQQGVLVAK.K		K.AIHQALFQQGVLVAK.K
26	31	2	732.38	5.5	0	30.1	22.2	95.00%	K.DFNLPK.H		K.DFNLPK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
84	RL15A_SCHPO	19.90%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
115	128	2	1699.83	4.1	1	73.6	22.2	95.00%	R.VLNSYWVNQDATYK.F		R.VLNSYWVNQDATYK.F
78	93	3	1761.93	3.4	0	25	18.6	95.00%	K.GQTYGKPVHQGVNHLK.Y		K.GQTYGKPVHQGVNHLK.Y
148	157	3	1218.69	4.4	0	24.4	16.8	95.00%	R.INWIVNPVHK.H		R.INWIVNPVHK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
85	CARB_SCHPO	6.03%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
968	975	2	1019.52	4.9	0	24.9	23	92.10%	K.VPQFSWTR.L		K.VPQFSWTR.L
932	943	2	1304.72	5.6	1	35.2	18.1	95.00%	K.TLGVNFIDVATR.S		K.TLGVNFIDVATR.S
315	322	2	808.41	1.3	0	41.7	20.9	95.00%	F.DPLGIHTG.D		R.DAANNCITVCNMENFDPLGIHTGDSIVVAPSQTLSDEEYHMLR.T

402	417	3	1672.96	3.1	1	32.7	12.3	95.00%	K.IALGHTLPELPNAVTK.T			K.IALGHTLPELPNAVTK.T
773	798	3	2736.49	2.9	0	51	13.2	95.00%	K.FANAVGYPVLVRPSYVLSGAAMSVIR.D			K.FANAVGYPVLVRPSYVLSGAAMSVIR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
86	AROG_SCHPO	11.02%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
66	76	2	1192.67	4.5	0	30.8	17.2	95.00%	R.IIVVVGPCSIH.D	Carbamidomethyl (+57)	R.IIVVVGPCSIHDPK.L
210	226	2	1718.88	2.3	0	70.8	20.3	95.00%	I.DAIGATAHPHTMLGVTK.Q		K.NGTDGTVGVAIDAIGATAHPHTMLGVTK.Q
186	198	2	1364.74	3.5	0	64.5	19	95.00%	R.ELASALSFPVGFK.N		R.ELASALSFPVGFK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
87	GCSP_SCHPO	9.24%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
953	965	2	1458.76	1.1	0	43.1	20.8	95.00%	K.DNNLLVNAPHPQK.D		K.DNNLLVNAPHPQK.D
657	684	3	2835.49	2.9	0	30.5	14.9	95.00%	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C	Carbamidomethyl (+57)	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C
770	788	3	1908.94	3.3	0	26.9	21.8	95.00%	K.TFCIPHGGGGPGVGPICVK.K	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.TFCIPHGGGGPGVGPICVK.K
379	412	3	3679.8	2.3	1	51.4	16.5	95.00%	K.ATSNICTAQALLANMSAFYAIYHGPNGLQEIANR.I	Carbamidomethyl (+57)	K.ATSNICTAQALLANMSAFYAIYHGPNGLQEIANR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
88	RL13_SCHPO	32.21%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
172	183	2	1398.66	5.4	1	54	23.8	95.00%	K.NFNAFSTLSNER.A		K.NFNAFSTLSNER.A
118	128	3	1326.79	4.7	0	51.2	13.8	95.00%	K.VYLAHLIVFPR.K		K.VYLAHLIVFPR.K
46	64	4	2080.27	3.1	1	20	0	95.00%	K.IAPRPVEAIRPAVKPPTIR.Y		K.IAPRPVEAIRPAVKPPTIR.Y
89	100	2	1263.7	3.9	1	28.9	18.6	95.00%	R.VASTIGIPVDHR.R		R.VASTIGIPVDHR.R
148	160	2	1324.73	3.5	1	59.1	16	95.00%	T.DVAAVLPITQEAV.E		K.GDATDVSGAEQTDVAAVLPITQEAVEEAKPITEEAK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
89	FAS1_SCHPO	3.47%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
415	431	3	1929.06	4.4	0	19.3	14.8	92.70%	R.FLSISVPFHSPYLAPVR.S		R.FLSISVPFHSPYLAPVR.S
1870	1881	2	1266.57	5.2	1	37.8	24.2	95.00%	R.SDYGMVAANPSR.V		R.SDYGMVAANPSR.V
1778	1806	3	3141.54	1.9	1	40.3	18.6	95.00%	K.DSTSFSFTHPSGLLSATQFTQPALTLMEK.S		K.DSTSFSFTHPSGLLSATQFTQPALTLMEK.S
781	794	2	1545.81	3.9	1	42.1	20.3	95.00%	K.LPPMPFDGILFGSR.L		K.LPPMPFDGILFGSR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
90	SPI1_SCHPO	18.52%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
110	122	2	1514.77	4.6	1	58.5	21.8	95.00%	R.VCENIPIVLCGNK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VCENIPIVLCGNK.V
189	201	2	1607.73	3.1	1	54.8	24	95.00%	V.DQQLLAQYQQEMN.E		K.LVGNPNLEFVASPALAPPEVQVDQQLLAQYQQEMNEAAAMPLPDEDDADL.-
152	165	3	1783.91	4.6	1	29.2	20.3	95.00%	K.SNYNFEKPFLWLAR.K		K.SNYNFEKPFLWLAR.K
189	198	2	1233.6	2.7	0	34.3	23.1	95.00%	V.DQQLLAQYQQ.E		K.LVGNPNLEFVASPALAPPEVQVDQQLLAQYQQEMNEAAAMPLPDEDDADL.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
91	PYC_SCHPO	3.38%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
917	929	2	1447.76	4.7	1	42.2	20.4	95.00%	K.VVGDLAQFMVQNK.L		K.VVGDLAQFMVQNK.L

839	848	2	1297.58	4.8	1	38.2	24	95.00%	R.EIDSYWAQMR.L		R.EIDSYWAQMR.L
107	123	2	1745.84	4.2	1	40	22.3	95.00%	R.TGANLVHPGYGFLSENA.E		R.TGANLVHPGYGFLSENAEFAR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
92	RS22_SCHPO	23.85%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
9	19	2	1316.62	3.4	1	43.7	23.2	95.00%	A.DCLNNIVNAER.R	Carbamidomethyl (+57)	R.QSVLADCLNNIVNAER.R
98	108	2	1171.7	4.9	0	29.1	13.4	95.00%	R.QVGVIVLTTSR.G		R.QVGVIVLTTSR.G
89	97	2	1111.62	5.6	0	31.9	16.8	95.00%	K.WVNQLLPSR.Q		K.WVNQLLPSR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
93	BCA1_SCHPO	13.68%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
315	331	2	1670.97	3.2	1	71.8	12	95.00%	R.LLEVFGAGTAALVSPVK.A		R.LLEVFGAGTAALVSPVK.A
262	278	2	1795	4.2	1	43.3	12.3	95.00%	K.EIITAPLDGMILPGVTR.D		K.EIITAPLDGMILPGVTR.D
363	380	2	2024.01	2.4	1	43	21	95.00%	L.DIQYGKEPNNPWSVPALP.-		K.WILDIQYGKEPNNPWSVPALP.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
94	RL10A_SCHPO	13.12%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	128	3	1265.71	4.6	0	30	15.9	95.00%	R.HAFGKPNGLVAR.V		R.HAFGKPNGLVAR.V
129	139	2	1228.7	4.7	0	40	16.1	95.00%	R.VNIGQILMSVR.T		R.VNIGQILMSVR.T
33	38	2	719.4	4.8	1	27.1	17.8	94.90%	R.IFDLGR.K		R.IFDLGR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
95	RS8A_SCHPO	21.50%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
165	178	2	1475.79	4.1	0	33.2	18.9	95.00%	R.LYAVVSSRPGQSGR.C		R.LYAVVSSRPGQSGR.C
78	92	2	1751.94	3.5	1	37.5	18.1	95.00%	R.IIQVAYHPSNNELVR.T		R.IIQVAYHPSNNELVR.T
111	124	3	1682.82	4.5	1	23.1	22.3	95.00%	R.VWYETHYGILMGSK.G		R.VWYETHYGILMGSK.G
78	88	2	1254.64	3.2	0	31.5	21.8	95.00%	R.IIQVAYHPSNN.E		R.IIQVAYHPSNNELVR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
96	PMP20_SCHPO	23.08%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
110	119	2	997.56	3	0	59.2	16.4	95.00%	F.DASGLLGPLR.S		K.AFDAGFDASGLLGPLR.S
30	55	2	2747.41	3.6	1	43.7	17	95.00%	K.FIIVGVPGAFTPPCSSQVPGYIANEK.Q	Carbamidomethyl (+57)	K.FIIVGVPGAFTPPCSSQVPGYIANEK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
97	PURA_SCHPO	8.53%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
268	276	2	899.55	4.9	0	44.5	18.9	95.00%	R.IANSIGVVK.A		R.IANSIGVVK.A
413	427	2	1514.86	2.3	0	28.1	14.1	95.00%	K.FVGVPITFIGVGPGR.D		K.FVGVPITFIGVGPGR.D
64	76	3	1435.79	2.6	0	36.2	16.8	95.00%	Y.DFHILPSGLVNPK.C		R.CQGGNNAGHTIVANGVTYDFHILPSGLVNPK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
98	RL3A_SCHPO	13.66%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
11	19	2	982.54	4.3	0	27.2	19	95.00%	R.HGSLGFLPR.K		R.HGSLGFLPR.K
320	334	3	1601.83	2.4	1	36.5	20.5	95.00%	N.DFVMLNGATPGPVKR.V	Deamidation (+1)	R.YGVVENDFVMLNGATPGPVKR.V
101	111	2	1242.63	3.4	1	34	22	95.00%	R.SLTTVWAEHLS.E		R.SLTTVWAEHLSEEVK.R
249	266	3	2035.03	4.4	0	29.3	20.6	95.00%	K.VACIGAWHPANVQWTVAR.A	Carbamidomethyl (+57)	K.VACIGAWHPANVQWTVAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
99	GCST_SCHPO	13.70%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
34	51	2	1940.98	3.4	0	52	19.7	95.00%	K.EGATIVPFAGFSMPVQYK.G		K.EGATIVPFAGFSMPVQYK.G
165	180	2	1623.93	4	1	75.8	11.5	95.00%	R.ALIAIQGPETASVVQK.L		R.ALIAIQGPETASVVQK.L
326	344	2	1886.91	2.9	1	81.9	21.9	95.00%	V.DGVEVGQVTSGCPSPTLGK.N	Carbamidomethyl (+57)	R.HGSAVEVDGVEVGQVTSGCPSPTLGK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
100	SERC_SCHPO	11.31%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
216	228	2	1299.74	5	0	37	14.8	95.00%	K.NAGPAGITVVFVR.D		K.NAGPAGITVVFVR.D
229	242	3	1532.84	5.6	1	18.3	16.5	90.30%	R.DSVLARPTPAELHK.L		R.DSVLARPTPAELHK.L
189	199	2	1282.6	4.3	1	67	23.4	95.00%	R.VCDVSSNFISR.K	Carbamidomethyl (+57)	R.VCDVSSNFISR.K
324	329	2	766.38	5.3	0	26.2	21.3	93.90%	R.MNVTFR.I		R.MNVTFR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
101	GLT1_SCHPO	2.51%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1690	1707	2	2063.08	4.1	1	61.9	18.1	95.00%	K.EALTQLLLTNNFPEFTGR.V		K.EALTQLLLTNNFPEFTGR.V
1787	1802	3	1728.9	3.5	1	28.5	19.3	95.00%	R.ADRPGGLLQYGIPNMK.L		R.ADRPGGLLQYGIPNMK.L
1758	1776	2	1792.99	3.3	1	78.8	15.4	95.00%	R.VAIIGSGPAGLAAADQLNR.A		R.VAIIGSGPAGLAAADQLNR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
102	RS11_SCHPO	15.13%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	64	2	1161.6	4.7	0	33.4	21.5	95.00%	K.CPFVGQVSIR.G	Carbamidomethyl (+57)	K.CPFVGQVSIR.G
118	130	2	1457.77	2.5	0	62.4	19.9	95.00%	G.DVVTVGQCRPLSK.T	Carbamidomethyl (+57)	R.INEGDVVTVGQCRPLSK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
103	LEU1_SCHPO	10.96%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
464	479	2	1742.82	4.9	1	69.1	23.3	95.00%	R.FSVNDYTLSSNGPQSK.C		R.FSVNDYTLSSNGPQSK.C
388	398	2	1249.63	2.9	1	28.5	22	95.00%	H.DVNSEYAAIIR.V		K.VPYLPLDPHDVNSEYAAIIR.V
341	362	3	2346.15	2.9	1	44.7	21.3	95.00%	R.HPYAGNLVFTAFSGSHQDAISK.G		R.HPYAGNLVFTAFSGSHQDAISK.G
137	151	3	1761.87	4	0	33.2	22.3	95.00%	K.NATVHLYNACSPLFR.E	Carbamidomethyl (+57)	K.NATVHLYNACSPLFR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
104	SCE3_SCHPO	8.51%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
250	271	3	2195.06	2.9	1	28.5	21.6	95.00%	R.SSSNVNTEATPSATTTTSSKPK.R		R.SSSNVNTEATPSATTTTSSKPK.R
112	122	2	1226.6	4	1	35.6	23	95.00%	G.DFFGEGVTSIR.L		R.DAIPIPSEPPFTAHVGNLSFDLTENDLGDFFGEGVTSIR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
105	DHE4_SCHPO	6.87%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
430	439	2	1004.53	3.4	0	38.6	21.3	95.00%	V.DGANIAGFLK.V		K.YCDSGSNNIPSLVDGANIAGFLK.V
356	367	2	1231.57	4.5	1	27.7	23.5	95.00%	R.ASGEGCWLAPGK.A	Carbamidomethyl (+57)	R.ASGEGCWLAPGK.A
93	101	2	1127.61	5.6	1	29.2	20.5	95.00%	K.FLGFEQIFK.N		K.FLGFEQIFK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
106	AATR1_SCHPO	9.07%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
305	317	2	1562.83	3.3	1	54.7	18.5	95.00%	R.VGWFTAQPLFIER.G		R.VGWFTAQPLFIER.G
38	54	2	1856.03	4.5	1	36.8	14.3	95.00%	K.IISLAGGLPNPEYFPIR.E		K.IISLAGGLPNPEYFPIR.E
7	19	3	1436.71	5.4	1	43.2	22.8	95.00%	K.DLSHHLSVESASR.K		K.DLSHHLSVESASR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
107	O59743_SCHPO	9.92%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
108	120	2	1495.81	2	1	25.3	17.9	92.70%	K.LKPVPTSWEQALQ.D		K.LKPVPTSWEQALQDNKPEEYYHLSAPDCK.S
1	11	2	1319.72	4	1	28	20	95.00%	-.MDPYTVAIIKK.L	Acetyl (+42)	-.MDPYTVAIIKK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
108	STI1_SCHPO	6.77%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
100	111	2	1270.65	2.3	0	32.9	21.1	95.00%	H.DANNAQLLNGLK.S	Deamidation (+1)	K.HDANNAQLLNGLK.S
112	132	2	2007.97	4.2	1	89.9	21.8	95.00%	K.SVEAAQTQAASGAGGFNPFAK.L		K.SVEAAQTQAASGAGGFNPFAK.L
371	377	2	800.44	3.8	1	29.8	23	95.00%	R.TPDILSR.L		R.TPDILSR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
109	SYEC_SCHPO	5.31%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
394	404	2	1196.62	2.5	1	40.8	21.4	95.00%	V.DSLEGVTHALR.T		R.AYPTYDFACPIVDSLEGVTHALR.T
652	666	2	1734.83	2.9	1	42.6	23	95.00%	K.DFLTPQTEFHSPVFA.D		K.DFLTPQTEFHSPVFADVGIK.N
66	77	2	1393.77	4.3	0	31.9	16.8	95.00%	K.LALQTFSQVYPK.L		K.LALQTFSQVYPK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
110	RL12_SCHPO	34.55%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
68	83	2	1538.91	3.4	0	50.5	11.8	95.00%	R.QAAVSVVPSASALVIK.A		R.QAAVSVVPSASALVIK.A
97	106	2	996.5	3.9	0	26.4	21.3	94.20%	K.NVAHSGNVSL.D		K.NVAHSGNVSLDEIIEVAR.T
17	31	2	1312.7	3.6	1	46	18.2	95.00%	R.AVGGEVAGGSTLAPK.I		R.AVGGEVAGGSTLAPK.I
131	146	2	1652.81	4	1	45.9	21.7	95.00%	K.EILGTAFSVGCTVDGK.N	Carbamidomethyl (+57)	K.EILGTAFSVGCTVDGK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
111	SPEE_SCHPO	8.39%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	12	2	1291.72	4.1	1	43.5	17.5	95.00%	M.SVQELSHPLIK.D	Acetyl (+42)	-.MSVQELSHPLIK.D
18	31	2	1631.79	4.6	0	31.2	22.5	95.00%	R.EINNMWPGQAMTLK.V		R.EINNMWPGQAMTLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
112	ACL1_SCHPO	6.50%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
369	381	2	1420.73	4.5	1	44	21.2	95.00%	R.GSELTYNNVPISK.V		R.GSELTYNNVPISK.V
171	182	3	1338.74	4.8	0	23.6	16.2	95.00%	K.LYRPGSVAYVSK.S		K.LYRPGSVAYVSK.S
156	170	2	1506.72	3.3	1	45.7	23.6	95.00%	K.IGNTGGMMDNIVASK.L		K.IGNTGGMMDNIVASK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
113	RS4B_SCHPO	12.60%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
12	22	3	1285.7	4.9	1	18.7	18.9	91.40%	R.VAAPHHWLLDK.L		R.VAAPHHWLLDK.L
222	233	2	1232.68	5.6	1	42.4	19.2	95.00%	R.LSNVFVIGEAGK.S		R.LSNVFVIGEAGK.S
40	49	2	1258.72	4.7	0	26.1	17.2	93.80%	R.ECLPLIVFLR.N	Carbamidomethyl (+57)	R.ECLPLIVFLR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
114	NACA_SCHPO	13.87%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	75	2	1164.62	5.8	0	59.3	21.2	95.00%	K.SSNNAYIVLGK.V		K.SSNNAYIVLGK.V
52	64	2	1540.93	4.4	1	50.2	4.77	95.00%	K.NILLIINEPIVYK.S		K.NILLIINEPIVYK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
115	SLBR2_SCHPO	8.83%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
134	143	2	1115.56	4.3	1	27.1	22.4	94.90%	R.NIESSVQPSR.E		R.NIESSVQPSR.E
149	157	2	1075.63	4.5	1	33	16.1	95.00%	K.LLDQIYALK.H		K.LLDQIYALK.H
294	305	2	1374.72	3.8	1	35.8	20.5	95.00%	G.EPVPVEQVTHLQ.D		R.SWNEYEAQGEPVPVEQVTHLQD DVQSDTSEIIENEPGMHPHVHAER. M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
116	PMM_SCHPO	9.34%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
19	28	2	1043.53	3.7	1	36.5	21	95.00%	F.DVDGTLTPAR.L		K.TLVLFDVDGTLTPAR.L
45	58	2	1347.75	4.4	1	41.6	18.1	95.00%	K.VVAIGFVGGSDLSK.Q		K.VVAIGFVGGSDLSK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
117	PGM_SCHPO	3.43%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
350	358	2	1160.54	5.2	1	29	23.3	95.00%	K.FFCNLFDAK.R	Carbamidomethyl (+57)	K.FFCNLFDAK.R
297	306	2	1032.54	2.3	0	29.6	21.5	95.00%	S.DSVAIIAHHA.E		R.NMIYGANAFVTPSDSVAIIAHHAE LIPYFR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
118	RS5B_SCHPO	14.78%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
38	54	3	1809.91	3.5	0	44.8	20.8	95.00%	V.DYITIGNGQPLPHTAGR.F	Deamidation (+1)	K.DISLVDYITIGNGQPLPHTAGR.F
146	158	2	1338.8	3.4	0	40.2	11.1	95.00%	R.VNQALALITIGAR.E		R.VNQALALITIGAR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
119	SYTC_SCHPO	3.41%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
248	258	2	1187.55	4.2	1	47.1	24.1	95.00%	K.NSSSYFLGDAK.N		K.NSSSYFLGDAK.N
227	239	3	1445.69	3.3	0	20.5	22.9	94.80%	I.DLCTGPHVPHTGR.I	Carbamidomethyl (+57)	R.CGPLIDLCTGPHVPHTGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
120	RS14_SCHPO	16.55%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
95	105	2	1037.57	5.3	0	47.1	19.2	95.00%	K.TPGPGAQAALR.A		K.TPGPGAQAALR.A
73	84	3	1367.77	4	1	24.2	16.5	95.00%	K.CKEVGITALHIK.I	Carbamidomethyl (+57)	K.CKEVGITALHIK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
121	PDI1_SCHPO	5.28%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	136	3	1350.87	5.1	1	30.4	0	95.00%	R.KQLLPTVKPISK.D		R.KQLLPTVKPISK.D
188	201	2	1436.77	4.3	0	45.1	18.3	95.00%	K.SLGSNFPGIVAFTK.D		K.SLGSNFPGIVAFTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
122	THRC_SCHPO	6.42%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
265	282	2	1945.01	4.9	1	46.3	19.4	95.00%	R.FIVPTGNFGDILAGYYAK.R		R.FIVPTGNFGDILAGYYAK.R
313	327	2	1443.73	4.4	1	39.8	22.1	95.00%	K.ADSTQVSPSGPISAK.E		K.ADSTQVSPSGPISAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
123	RL30A_SCHPO	28.44%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
71	89	2	1997.95	6	1	62.5	22	95.00%	K.ANVHHYAGTNIDLGTACGK.L	Carbamidomethyl (+57)	K.ANVHHYAGTNIDLGTACGK.L
47	58	2	1335.77	3.1	0	24.1	13.8	90.60%	K.LILIAGNCPPLR.K	Carbamidomethyl (+57)	K.LILIAGNCPPLR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
124	YHZ8_SCHPO	31.31%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

154	164	2	1234.62	2.4	1	46.5	22.2	95.00%	L.DDPSLYAVVTR.Y			K.ADTSLIIHSLDDPSLYAVVTR.Y
75	103	3	3217.69	3	1	57.2	13.8	95.00%	K.TSNPFLAFANYLTSTHAPLAEPLQLLNFK.V			K.TSNPFLAFANYLTSTHAPLAEPLQLLNFK.V
2	13	2	1361.7	3.8	0	57.2	21.5	95.00%	M.SFPASTHVYIAK.I	Acetyl (+42)		-.MSFPASTHVYIAK.I
144	153	2	1068.58	3	1	29.7	17.4	95.00%	K.ADTSLIIHSL.D			K.ADTSLIIHSLDDPSLYAVVTR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
125	TAL1_SCHPO	5.59%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
27	44	3	1917.03	4	1	42	18.3	95.00%	K.YKPQDATTNPSLILAASK.K		K.YKPQDATTNPSLILAASK.K
31	44	2	1400.76	3.1	0	64.4	18.6	95.00%	Q.DATTNPSLILAASK.K		K.YKPQDATTNPSLILAASK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
126	RL23_SCHPO	25.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
15	34	2	2090	3.5	1	65.5	21.8	95.00%	R.MTLGLPVQAIMNCADNSGAK.N	Carbamidomethyl (+57)	R.MTLGLPVQAIMNCADNSGAK.N
15	28	2	1517.75	2.9	0	46.2	21.9	95.00%	R.MTLGLPVQAIMNCA.D	Carbamidomethyl (+57)	R.MTLGLPVQAIMNCADNSGAK.N
51	65	2	1531.78	3.4	1	55.2	21.1	95.00%	R.LPAASCGDMVLATVK.K	Carbamidomethyl (+57)	R.LPAASCGDMVLATVK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
127	HMCS_SCHPO	9.17%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
155	183	3	2859.53	3.9	1	40.5	14.5	95.00%	K.GNARPTGGAGCVALLVGPNAPIVFEPGLR.G	Carbamidomethyl (+57)	K.GNARPTGGAGCVALLVGPNAPIVFEPGLR.G
217	228	2	1325.64	3.7	1	38.4	23.7	95.00%	K.ALDGAYANYNVR.D		K.ALDGAYANYNVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
128	RL27A_SCHPO	19.12%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	48	3	1461.76	5.9	1	42.8	20.6	95.00%	K.SHPFGHAVVAGVER.Y		K.SHPFGHAVVAGVER.Y
23	34	2	1269.74	4.4	1	65.4	15.8	95.00%	K.VVILQAIDQGSK.S		K.VVILQAIDQGSK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
129	SYDC_SCHPO	4.14%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
281	294	2	1356.6	4.8	1	27.5	24	95.00%	K.MSGASSEGGSNVFK.I		K.MSGASSEGGSNVFK.I
490	499	2	1300.55	3.9	1	26.9	24.1	94.70%	R.YSNSYDFFMK.G		R.YSNSYDFFMK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
130	DAK1_SCHPO	5.86%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
45	66	3	2123.05	5.3	1	21	20.2	95.00%	K.NVSVISGGGAGHEPTHSSFVGK.G		K.NVSVISGGGAGHEPTHSSFVGK.G
388	399	2	1358.73	4.4	1	25.9	20.7	93.60%	R.QAIVNSMENLIK.A		R.QAIVNSMENLIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
131	ASSY_SCHPO	9.51%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
198	205	2	871.41	2.6	0	28	22.5	95.00%	E.DPSMTPPK.D		K.KPWSMDENIVHCSYEAGILEDPSMTPPK.D
333	350	2	1885	3.4	1	90.4	17.3	95.00%	R.MLLAANNVSQEVVNGVVK.L	Deamidation (+1)	R.MLLAANNVSQEVVNGVVK.L
320	332	2	1601.77	4.2	0	39.6	23.3	95.00%	K.ILYNGQFFSPCTR.M	Carbamidomethyl (+57)	K.ILYNGQFFSPCTR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
132	RS2_SCHPO	19.37%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
64	74	2	1441.73	5.7	1	25.1	21.5	92.30%	K.EYQIVDYFLPR.L		K.EYQIVDYFLPR.L
174	185	3	1138.69	4.8	1	25.2	11.8	95.00%	R.GAGLVAAPVTKR.F		R.GAGLVAAPVTKR.F
54	63	2	1237.7	3.6	0	33.8	14.6	95.00%	E.EIYLYSLPIK.E		K.SIEEIYLYSLPIK.E

141		156	3	1696.87	4.8	1	37.6	20.8	95.00%	R.GYWGTALGDPHTVPVK.V		R.GYWGTALGDPHTVPVK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
133	PPA2_SCHPO	6.05%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
356	365	2	1118.56	3.2	1	32.4	22.4	95.00%	P.DITPEHPLPT.D		K.VFLAFTHDSQIIPVEAALGFFPDITPEHPLPTDK.N
44	61	2	2043.93	3.2	1	52.9	23.3	95.00%	H.EPYFNGPTTSFPESCAIK.Q	Carbamidomethyl (+57)	K.DHLGTISVYHEPYFNGPTTSFPESCAIK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
134	SYG_SCHPO	6.90%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
216	232	3	1983	3.5	1	45.9	19.8	95.00%	K.GYLRPETAQGQFLNFSR.L		K.GYLRPETAQGQFLNFSR.L
492	506	2	1649.85	4.8	1	35.7	20.7	95.00%	R.TYTPNVIEPSFGLGR.I		R.TYTPNVIEPSFGLGR.I
526	538	2	1298.77	3.9	0	28.2	14.3	95.00%	R.GVLSFPASIAPIK.A		R.GVLSFPASIAPIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
135	PABP_SCHPO	7.04%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
258	266	2	1068.57	4.8	0	26.6	19.8	94.40%	K.ANFTNVYIK.N		K.ANFTNVYIK.N
447	456	2	1142.61	4.9	1	33.9	20.4	95.00%	R.SQLEAQIQAR.N		R.SQLEAQIQAR.N
428	441	3	1529.88	3.3	0	37.6	12.8	95.00%	R.MLAGKPLYVALAQR.K		R.MLAGKPLYVALAQR.K
98	110	2	1401.76	2.1	0	35.5	18.8	95.00%	F.ELFNSIGPVASIR.V		K.AEEPEAAAEPSESTSTPTNASSVATPSGTAPTSASLYVGELDPSVTEAMLFELFNSIGPVASIR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
136	IMDH_SCHPO	7.25%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
303	313	2	1155.67	4.5	1	51.3	17.4	95.00%	K.IDVIAGNVVTR.E		K.IDVIAGNVVTR.E
124	135	2	1281.64	2.8	0	25.9	22.5	93.50%	L.DPVVFSPQHTVG.D		K.YENGFILDPVVFSPQHTVGDVLK.I
419	433	2	1421.67	3.9	1	52.2	23.9	95.00%	R.GMGSIAAMEGTGVNK.N		R.GMGSIAAMEGTGVNK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
137	DYR_SCHPO	9.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
164	183	3	2062.15	3.7	1	25.4	10.4	95.00%	K.LTTPSLHIAGTSDTLVPLAR.S		K.LTTPSLHIAGTSDTLVPLAR.S
191	212	3	2537.31	3.6	1	37.3	18.1	95.00%	R.CENAHVLLHPGQHIVPQQAVYK.T	Carbamidomethyl (+57)	R.CENAHVLLHPGQHIVPQQAVYK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
138	PUR4_SCHPO	1.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
323	334	2	1146.56	3	1	31.6	22.4	95.00%	R.DEGAVGQGSLSK.A		R.DEGAVGQGSLSK.A
412	425	3	1426.76	5.3	0	35.9	20.9	95.00%	R.GYHKPIMAAGGIGR.I		R.GYHKPIMAAGGIGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
139	YHEF_SCHPO	14.29%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
90	104	2	1731.88	2.4	0	53.3	20.6	95.00%	N.DTANFTPLTFTTYLK.T		R.LFTIAENDTANFTPLTFTTYLKTCNPQSIENAMIPFVNTVTSEISFDAWAYTAQNSSR.I
30	41	3	1413.76	4.8	1	20.9	18.8	95.00%	R.LRGPHCGTYLLK.V	Carbamidomethyl (+57)	R.LRGPHCGTYLLKVVGTNATYVGEK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
140	RL7C_SCHPO	11.55%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
173	183	2	1113.61	2.8	1	61	19.2	95.00%	S.DNAIIEAALGK.Y		R.IALSDNAIIEAALGK.Y
133	150	2	2092.1	3.7	1	56.5	16.3	95.00%	K.EMLQVVEPYVTYGIPNLK.T		K.EMLQVVEPYVTYGIPNLK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
141	ATPB_SCHPO	5.71%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
124	140	2	1622.87	2.6	0	39	17.3	95.00%	I.DTGSPISIPVGPGTLGR.I		R.GTAVIDTGSPISIPVGPGTLGR.I
210	222	2	1501.86	3.4	1	36	14.8	95.00%	K.TVFIQELINNIAK.A		K.TVFIQELINNIAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
142	RS13_SCHPO	15.23%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
44	55	2	1244.66	3.8	0	40.8	20.8	95.00%	K.GMSPSQIGVTLR.D		K.GMSPSQIGVTLR.D
10	20	2	1132.63	4.4	0	38.6	18.7	95.00%	K.GIASSALPYVR.S		K.GIASSALPYVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
143	SYLC_SCHPO	3.42%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
843	852	2	1272.56	5	1	24.8	23.7	91.90%	K.SCFYDLQNAR.D	Carbamidomethyl (+57)	K.SCFYDLQNAR.D
382	398	3	1730.98	4.6	1	32.6	13.8	95.00%	K.GQDLIGALVNAPLSVHK.Q		K.GQDLIGALVNAPLSVHK.Q
777	787	2	1185.64	2.9	1	36.9	20.1	95.00%	F.EEALANSAILR.L		R.LALADAGDTVDDANFEEALANSAILR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
144	VATB_SCHPO	4.57%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
439	449	2	1284.62	4.2	1	36.9	23.4	95.00%	K.TFISQGAYENR.T		K.TFISQGAYENR.T
166	177	2	1235.67	1	0	34.4	19	95.00%	K.IPIFSAAGLPHN.E		K.IPIFSAAGLPHNEIAAQICR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
145	SYRC_SCHPO	6.80%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
163	180	2	1987.02	4.1	1	33.9	18.6	95.00%	R.STIIGSFLANLHESQGWK.V		R.STIIGSFLANLHESQGWK.V
480	489	2	1284.6	5.9	1	39.4	23	95.00%	R.INNYAFDWSR.M		R.INNYAFDWSR.M
11	24	2	1544.86	4.5	1	46.7	15.6	95.00%	K.SLSTLGLQDLPVFR.E		K.SLSTLGLQDLPVFR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
146	Q76N21_SCHPO	13.61%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
13	22	2	1195.61	4.9	0	30.3	22.2	95.00%	R.FVTCQIVSSR.V	Carbamidomethyl (+57)	K.SSPYFSRYQTKYRR.R
26	35	2	1098.51	4.8	0	36.2	23	95.00%	G.DYVLAHAHSS.E		R.EGKTDYYARKR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
147	RL31_SCHPO	23.01%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
91	105	2	1650.87	4.2	1	39.3	18.9	95.00%	K.ALYTYVQAVDVANPK.M		K.ALYTYVQAVDVANPK.M
89	99	2	1269.67	3.7	1	41.6	20.9	95.00%	D.DKALYTYVQAV.D		R.SDEDDKALYTYVQAVDVANPK.M
7	15	2	986.56	5	0	39.5	20.5	95.00%	K.SAINQVVTR.D		K.SAINQVVTR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
148	TBB_SCHPO	8.71%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
128	154	3	2645.36	2.9	0	40.6	17.7	95.00%	C.DALQGFQLTHSLGGGTGSGMGTLLLSK.I		R.EAEACDALQGFQLTHSLGGGTGSGMGTLLLSK.I
163	174	2	1249.62	3.9	0	41.3	22	95.00%	R.MMATFSVAPAPK.S		R.MMATFSVAPAPK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
149	LYS4_SCHPO	6.24%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
149	159	2	1179.57	4.4	1	26	23.1	93.70%	K.GQGIDFYPAGR.G		K.GQGIDFYPAGR.G
693	706	2	1517.83	3.4	1	31.4	18.3	95.00%	K.IGELGNSVQSLFVR.G		K.IGELGNSVQSLFVR.G
470	489	2	1872.04	4.8	0	47.2	14.6	95.00%	R.EALAYLASPAVVAASAIAGK.I		R.EALAYLASPAVVAASAIAGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
150	ARGD_SCHPO	8.39%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
263	271	2	1046.48	2.4	1	33.8	23.6	95.00%	Y.DEIQCGLGR.S	Carbamidomethyl (+57)	K.VGASLIYDEIQCGLGR.S
283	310	3	2746.56	2.7	1	43.2	10.4	95.00%	K.DVASPDIITVAKPLANGLPIGATIVSSK.I		K.DVASPDIITVAKPLANGLPIGATIVSSK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
151	Q9P7B4_SCHPO	13.13%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
234	256	3	2522.27	2.7	1	34.8	18.7	95.00%	R.ENVVIADTLVFPSHQGGANHVYR.K		R.ENVVIADTLVFPSHQGGANHVYR.K
163	173	2	1163.64	5.6	0	26.5	18.9	94.30%	K.SALAQFTSALR.K		K.SALAQFTSALR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
152	ACL2_SCHPO	9.55%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
326	334	2	985.56	4.7	1	36	19.5	95.00%	K.LTILNAEGR.V		K.LTILNAEGR.V
382	389	2	947.52	4.5	1	26.9	20.9	94.70%	K.TVLDLMTR.G		K.TVLDLMTR.G
32	61	3	3211.76	3.3	1	47.1	14.5	95.00%	K.TVSATPAVQLAQIQFPLPTLVIPAESTTYR.E		K.TVSATPAVQLAQIQFPLPTLVIPAESTTYR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
153	RL2_SCHPO	8.70%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
128	138	2	1144.59	4.4	0	37.1	22.3	95.00%	R.SSGNYVIIVGH.D		R.SSGNYVIIVGHDVDTGK.T
163	173	2	940.55	4.3	0	54.6	13.2	95.00%	R.GVVGIVAGGGR.I		R.GVVGIVAGGGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
154	RHP23_SCHPO	9.51%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
244	251	2	931.48	2.9	1	28	23.4	95.00%	G.DDPLGFLR.S		R.EESAAALAAQQQQSEALAPTSTGQPANLFEQAALSENENQEQPSNTVGDDPLGFLR.S
137	147	2	1114.58	3.7	0	51.6	21.6	95.00%	I.DANTLAVGAQR.N		K.VEAPSSTVAESTSTTQTVAAAAPSNPDTTATSEAPIDANTLAVGAQR.N
84	99	2	1518.78	4.7	1	24.2	21.4	90.80%	K.SAASPAPNPPASVPEK.K		K.SAASPAPNPPASVPEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
155	RS21_SCHPO	25.29%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
76	87	2	1421.7	3.2	1	39.8	22.9	95.00%	Q.DGLLEGVWSYQR.-		R.LTTQDGLLEGVWSYQR.-
51	60	2	1113.59	4.5	0	33.8	20.8	95.00%	K.TTYAISGFVR.S		K.TTYAISGFVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
156	ADK_SCHPO	8.24%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
253	267	2	1483.87	4.5	1	69.4	13.8	95.00%	R.VVVITQGADATIVAK.D		R.VVVITQGADATIVAK.D
126	138	2	1424.68	5.2	0	51	22.3	95.00%	R.SLCTNLGAANNYK.L	Carbamidomethyl (+57)	R.SLCTNLGAANNYK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
157	AROC_SCHPO	6.33%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
229	240	2	1276.65	2.9	0	50.3	21.6	95.00%	H.DSIGGTVTCVIR.N	Carbamidomethyl (+57)	R.DNHDSIGGTVTCVIR.N
328	340	2	1331.68	5.2	1	55.6	21.4	95.00%	K.SPATIGVEQSTSR.Y		K.SPATIGVEQSTSR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
158	ARO1_SCHPO	2.86%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
643	660	2	1749.92	3	0	66.5	17.6	95.00%	S.DASSATYPLAIAAITGTK.C		K.YQNPPHYEIESDASSATYPLAIAAITGTK.C
162	172	2	1299.72	4.7	0	45.2	19.1	95.00%	K.NLVGAFWQPLR.V		K.NLVGAFWQPLR.V
1232	1247	2	1833.96	4.6	1	44.8	18.5	95.00%	R.ITNSMDIPLILFNMGR.F		R.ITNSMDIPLILFNMGR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
159	WOS2_SCHPO	21.51%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	15	2	1695.9	2.7	1	24.3	18.5	91.10%	M.SLNTQIPEVLWAQR.S	Acetyl (+42)	-.MSLNTQIPEVLWAQR.S
150	164	2	1425.62	1.5	1	65.5	24.1	95.00%	M.DFSQFGNLGGAGAGE.D		R.WVDEDEQEAQPEVSPFGAGGMPDLSALGGMGGMDFSQFGNLGGAGAGEDASDSEPELEEEEEVGSNEK.K
139	149	2	1023.44	2.6	0	42.2	22.3	95.00%	P.DLSALGGMGGM.D	Oxidation (+16)	R.WVDEDEQEAQPEVSPFGAGGMPDLSALGGMGGMDFSQFGNLGGAGAGEDASDSEPELEEEEEVGSNEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
160	RLA0_SCHPO	10.26%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
133	144	2	1308.71	5.2	0	29.1	16.9	95.00%	K.TSFFQALGIPTK.I		K.TSFFQALGIPTK.I
98	117	2	2014.16	1.9	0	28.4	9.54	95.00%	R.ETIIANVIAAPARPNAIAPL.D		R.ETIIANVIAAPARPNAIAPLDVFVPAGNTGMEPGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
161	CH10_SCHPO	22.12%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	84	2	1230.7	4	0	31.7	17.3	95.00%	R.VLLPAYGGSNIK.V		R.VLLPAYGGSNIK.V
62	72	2	1111.6	4.5	1	30.9	17.7	95.00%	K.LAQPSVAVGDR.V		K.LAQPSVAVGDR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
162	KAPS_SCHPO	6.93%	99%	1

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
39	52	2	1664.86	3.8	1	65.6	20.5	95.00%	K.STIACALEQYLLQR.G	Carbamidomethyl (+57)	K.STIACALEQYLLQR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
163	RL24A_SCHPO	12.75%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
81	91	2	1097.65	4.7	1	29.4	15.7	95.00%	R.GIVGANLDVIK.E		R.GIVGANLDVIK.E
36	43	2	978.52	4.9	1	29.5	21.8	95.00%	K.SESLFLQR.K		K.SESLFLQR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
164	DLDH_SCHPO	5.87%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
113	128	2	1663.83	1.7	1	25	21.8	92.20%	R.GIDVSGVSVNLSQMMK.A		R.GIDVSGVSVNLSQMMK.A
155	168	2	1448.76	3.8	1	31.8	20.2	95.00%	K.GTGSFIDPQTLSVK.G		K.GTGSFIDPQTLSVK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
165	LYS2_SCHPO	1.27%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
33	41	3	1075.55	3.7	0	19.1	22.4	92.40%	T.DYSRPVPSR.L		K.SQTISHLPTDYSRPVPSR.L

143	151	2	1046.58	3.7	0	29.9	19.7	95.00%	S.DLINFLNAK.L		K.EGSSDAVDFSDLINFLNAK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
166	RLA2_SCHPO	23.64%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
62	87	3	2091.06	2.1	1	38.1	20.3	95.00%	K.LATVPTGGAASAAPAAAAGGAAPAAE.E		K.LATVPTGGAASAAPAAAAGGAAPAAEEAAK.E
62	86	2	1962.03	4.4	0	77	18.6	95.00%	K.LATVPTGGAASAAPAAAAGGAAPAA.E		K.LATVPTGGAASAAPAAAAGGAAPAAEEAAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
167	Q9USR1_SCHPO	8.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
232	241	2	1166.63	3.1	1	31.1	18.9	95.00%	Q.DDQPTIIPLR.F		K.LYINQPNNLSFEDAESFTPTQVIEDIVYEQDDQPTIIPLR.F
109	124	2	1403.73	4.8	0	51.6	20.2	95.00%	K.ATGTGALASSSSAPVK.G		K.ATGTGALASSSSAPVK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
168	BUT2_SCHPO	6.92%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
338	349	2	1493.65	4.2	1	37.5	23.5	95.00%	R.GCEYTQNIPCPR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GCEYTQNIPCPR.A
200	214	2	1679.86	3.5	1	64.5	20.3	95.00%	R.YYGNTEALSSLPLPR.N		R.YYGNTEALSSLPLPR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
169	CYSK1_SCHPO	9.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
10	23	2	1341.78	3.9	0	59.1	14.1	95.00%	K.VPGIVSGFIGAIGR.T		K.VPGIVSGFIGAIGR.T
180	200	2	2019.93	5.1	1	71.4	23.7	95.00%	K.GTVDGFTCSTGTGGTFAGVTK.Y	Carbamidomethyl (+57)	K.GTVDGFTCSTGTGGTFAGVTK.Y

Supplementary Table S2: All "Scaffold" validated proteins and peptides identified from solprotSP (*S.pombe*) and from SCVMprot (*S.cerevisiae*) samples

***S.pombe* - Formic acid digest of large tryptic peptides (replicate A)**

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
1	ENO11_SCHPO	62.87%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
361	374	3	1608.73	4.7	0	47.1	26.5	95.00%	R.MSYEAGWGVMVSHR.S		R.MSYEAGWGVMVSHR.S
185	194	2	1204.59	5.4	0	34	24.9	95.00%	R.WGAETYHTLK.S		R.WGAETYHTLK.S
346	360	2	1585.85	6	0	90.8	21.2	95.00%	K.VNQIGSVTESLNAVR.M		K.VNQIGSVTESLNAVR.M
302	310	2	1160.51	2	1	26.8	26.3	91.20%	D.DWSAWTHMK.A		K.YPIVSIEDPFDQDDWSAWTHMK.A
65	79	2	1477.87	4	0	73.7	11.8	95.00%	K.AVGNVNNIIAPAVVK.A		K.AVGNVNNIIAPAVVK.A
247	257	2	1200.57	2.5	1	47.3	24.9	95.00%	D.VASSEFYVDGK.Y		K.IGLDVASSEFYVDGK.Y
142	163	2	2153.06	3.3	1	30.4	23.7	95.00%	K.GPYVLPVPSFNVLNGGSHAGGD.L		K.GPYVLPVPSFNVLNGGSHAGGDLAFQEFMILPTGAPSFSEAMR.W
106	120	2	1560.82	4.2	0	61.3	22.6	95.00%	K.LGANAILGVSMAICR.A	Oxidation (+16)/ Carbamidomethyl (+57)	K.LGANAILGVSMAICR.A
288	296	2	1062.56	2.6	2	39.1	23.1	95.00%	K.KYPIVSIED.P		K.KYPIVSIEDPFDQDDWSAWTHMK.A
273	287	2	1812.96	4.5	1	75.4	20.8	95.00%	K.LTYQQLTDLYVELSK.K		K.LTYQQLTDLYVELSK.K
227	234	2	898.55	2.6	0	33.1	20	95.00%	D.LIVEAINK.A		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
16	32	2	1837.92	2.6	1	95.4	23.4	95.00%	R.GNPTVEVDLTTETGIHR.A		R.GNPTVEVDLTTETGIHR.A
33	50	2	1886.97	4.8	0	105	23.5	95.00%	R.AIVPSGASTGIWEALEMR.D		R.AIVPSGASTGIWEALEMR.D
338	345	2	901.51	4.7	0	31.4	21.3	95.00%	K.CANALLLK.V	Carbamidomethyl (+57)	K.CANALLLK.V
409	414	2	806.43	5.7	0	29.4	23.6	95.00%	K.YNELLR.I		K.YNELLR.I
218	234	2	1894.04	1.3	1	47.4	15.4	95.00%	D.LQTPQEALDLIVEAINK.A		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
201	217	2	1564.67	3.1	1	30.7	27.1	95.00%	R.YGSSAGNVGDEGGIAPD.L		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
311	320	2	1093.5	2.4	1	38.2	24.8	95.00%	K.AETDFQIVGD.D		K.AETDFQIVGDDLTVTNVK.R
415	432	2	1815.87	2.3	0	95.7	25.6	95.00%	R.IEEELGSEGVYAGAHAGK.Y		R.IEEELGSEGVYAGAHAGK.Y
375	396	2	2201.14	2.9	1	122	20.8	95.00%	R.SGETADTFISHLTVGIGAGQLK.S		R.SGETADTFISHLTVGIGAGQLK.S
89	96	2	905.49	4.7	1	57.4	23.1	95.00%	K.AADEFLLK.L		K.AADEFLLK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
2	G3P1_SCHPO	60.12%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
249	259	3	1290.69	4.5	1	28.4	22.9	95.00%	K.LAKPTNYEDIK.A		K.LAKPTNYEDIK.A
167	186	2	2135.06	2	0	93	23.9	95.00%	D.TFGIEEGLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK.T
94	113	2	2181.1	1.8	0	78.4	23.3	95.00%	D.YVIESTGVFTTQETASAHLK.G		K.WSTSGADYVIESTGVFTTQETASAHLK.G
127	139	2	1449.69	3.7	1	45.1	25.6	95.00%	K.DAPMYVVGVNEEK.F		K.DAPMYVVGVNEEK.F
128	145	2	2036.99	1.8	1	84.8	25.3	95.00%	D.APMYVVGVNEEKFNPSEK.V		K.DAPMYVVGVNEEKFNPSEK.V
297	309	2	1345.73	1.5	0	50.2	22	95.00%	D.ASAGIQLSPQFVK.L	Deamidation (+1)	K.GVLGYTEDAVVSTDFCGDNHSSIFDASAGIQLSPQFVK.L
128	139	2	1334.66	2.1	0	43	24.6	95.00%	D.APMYVVGVNEEK.F		K.DAPMYVVGVNEEK.F
87	113	2	2885.38	3.9	1	116	24.8	95.00%	K.WSTSGADYVIESTGVFTTQETASAHLK.G		K.WSTSGADYVIESTGVFTTQETASAHLK.G
146	162	2	1818.91	4.5	0	75	24.4	95.00%	K.VISNASCTTNCLAPLAK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.VISNASCTTNCLAPLAK.V
286	296	2	1297.51	2	1	25.8	25.5	90.90%	D.FCGDNHSSIFD.A	Carbamidomethyl (+57)	K.GVLGYTEDAVVSTDFCGDNHSSIFDASAGIQLSPQFVK.L
324	334	2	1148.65	6.2	1	55.4	18.2	95.00%	R.VVDLVAYTAAK.D		R.VVDLVAYTAAK.D

163	186	2	2576.29	3.1	1	106	23.6	95.00%	K.VINDTFGIEEGLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK.T
240	248	2	958.57	1.8	1	26.8	17.6	93.30%	D.VSVVDLTVK.L		R.VPTPDVSVVDLTVK.L
36	48	2	1682.77	1.3	1	77.9	26.2	95.00%	D.PFIDLEYMAYMFK.Y	Oxidation (+16)	K.TIQVVAINDPFIDLEYMAYMFK.Y
119	127	2	928.52	1.9	2	36	21.1	95.00%	R.VIISAPSKD.A		R.VIISAPSKDAPMYVVGVNEEK.F
6	13	2	819.43	6.2	0	38.4	22.9	95.00%	K.VGINGFGR.I	Deamidation (+1)	K.VGINGFGR.I
264	279	2	1639.75	3.2	2	26.9	26.6	90.70%	K.AASEGPMKGVLGYTED.A	Oxidation (+16)	K.AASEGPMKGVLGYTEDAVVSTDFCGDNHSSIFDASAGIQLSPQFVK.L
201	215	2	1343.71	4.7	0	69.9	22.6	95.00%	R.GASANIIPSSTGAAK.A		R.GASANIIPSSTGAAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
3	PGK_SCHPO	47.83%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
359	378	2	1917.95	4	1	118	24.2	95.00%	K.TCEAGNVVIVGGGDTATVAK.K	Carbamidomethyl (+57)	K.TCEAGNVVIVGGGDTATVAK.K
151	162	2	1279.63	2.1	1	32.8	25.4	95.00%	K.SLTSLGDIFVND.A		K.SLTSLGDIFVNDAFGTAHR.A
123	132	3	1145.54	4.7	0	33.9	25.7	95.00%	R.FHIEEEGSAK.V		R.FHIEEEGSAK.V
57	71	2	1591.87	2.9	0	46.2	20	95.00%	K.AVILMSHLGRPNGAR.V	Deamidation (+1)	K.AVILMSHLGRPNGAR.V
112	122	2	1211.69	4.5	0	57.3	18.4	95.00%	K.GGEVILLENLR.F		K.GGEVILLENLR.F
40	48	2	910.59	3.6	0	25.3	12.6	90.90%	R.IVGALPTIK.Y		R.IVGALPTIK.Y
330	347	2	2010.99	3.7	1	68.6	24.5	95.00%	K.TIVWNGPAGVFEFDNFAK.G		K.TIVWNGPAGVFEFDNFAK.G
404	414	2	1040.63	5.6	0	39.4	18	95.00%	K.ALPGVVALSSK.-		K.ALPGVVALSSK.-
158	169	2	1346.68	1.4	1	62	24.7	95.00%	D.IFVNDAFGTAHR.A		K.SLTSLGDIFVNDAFGTAHR.A
383	403	2	2069.04	3.6	1	81.1	23.7	95.00%	K.EDALSHVSTGGGASLELLEGK.A		K.EDALSHVSTGGGASLELLEGK.A
321	329	2	994.54	5.5	0	50.2	20.8	95.00%	K.FAEVITTSK.T		K.FAEVITTSK.T
75	86	3	1304.74	4.3	0	59.4	17.9	95.00%	K.YSLKPVAAELSK.L		K.YSLKPVAAELSK.L
385	403	2	1824.96	1.7	0	83.2	21	95.00%	D.ALSHVSTGGGASLELLEGK.A		K.EDALSHVSTGGGASLELLEGK.A
295	306	2	1144.53	2.5	1	43.3	26	95.00%	K.VGSATAEEGIPD.G		K.VGSATAEEGIPDGWMGLDCGPK.S
197	213	2	1764.99	2	0	55.3	15.2	95.00%	K.ALENPARPFLAILGGAK.V	N-Formyl (+28)	K.ALENPARPFLAILGGAK.V
123	134	2	1359.63	2.7	2	35.7	25.9	95.00%	R.FHIEEEGSAKVD.G		R.FHIEEEGSAKVDGK.K
170	181	2	1267.64	4	1	58.7	23.1	95.00%	R.AHSSMVGVDLPR.V		R.AHSSMVGVDLPR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
4	METE_SCHPO	42.02%	100%	28

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
561	571	2	1184.7	5.1	0	40.5	17.5	95.00%	K.GMLTAPITILR.W		K.GMLTAPITILR.W
434	449	2	1746.97	7	0	46.9	17.6	95.00%	K.LPLFPTTTIGSFPQTK.E		K.LPLFPTTTIGSFPQTK.E
4	11	2	845.48	4.8	0	33.3	22.1	95.00%	K.SAVLGFPR.I		K.SAVLGFPR.I
707	714	2	901.49	4.3	0	27.7	24.5	94.40%	R.VPPVSEFK.E		R.VPPVSEFK.E
684	690	2	813.51	5.6	0	34.2	19.1	95.00%	K.LLNVLSR.Y		K.LLNVLSR.Y
691	706	2	1818.88	3.8	1	84	25	95.00%	R.YTSCIGPGLFDIHSPR.V	Carbamidomethyl (+57)	R.YTSCIGPGLFDIHSPR.V
393	404	2	1284.67	4.4	0	68.2	21.6	95.00%	R.AESPITNVEAVR.E		R.AESPITNVEAVR.E
707	716	3	1186.64	4.9	1	25.6	21.3	95.00%	R.VPPVSEFKER.I		R.VPPVSEFKER.I
391	404	2	1511.81	2.7	1	45.9	20.9	95.00%	K.ARAESPITNVEAVR.E		K.ARAESPITNVEAVR.E
499	508	2	1257.55	4.4	1	53.6	25.7	95.00%	R.NDMVQYFGER.M		R.NDMVQYFGER.M
243	260	2	1982.08	3.5	1	54.1	17.6	95.00%	K.LILTTYFGSLQSNADVLK.G		K.LILTTYFGSLQSNADVLK.G
428	449	3	2402.33	4.8	1	46	14.5	95.00%	K.QQASLKLPLFPTTTIGSFPQTK.E		K.QQASLKLPLFPTTTIGSFPQTK.E
325	351	3	2884.5	3.5	1	47.3	18.5	95.00%	R.VQVASSSSILHIPHSLSGEDQINPEIK.R		R.VQVASSSSILHIPHSLSGEDQINPEIK.R
261	273	2	1330.78	4	1	55.7	13.6	95.00%	K.GLPIAGVHVDVVR.A		K.GLPIAGVHVDVVR.A
281	299	2	1881.08	4.8	0	87.4	11.1	95.00%	R.ALAVLGENQIISVGVVSGR.N		R.ALAVLGENQIISVGVVSGR.N
147	155	2	1034.53	5.7	1	36.8	24.6	95.00%	K.ALDEFLEAK.E		K.ALDEFLEAK.E

325	344	2	2062.04	2.1	1	85.7	23.7	95.00%	R.VQVASSSSILHIPHSLSGED.Q		R.VQVASSSSILHIPHSLSGEDQINPEIK.R
670	679	2	1060.54	3.2	1	27.8	23.9	94.50%	D.ADVVSIENSK.S		R.LDADVVSIENSK.S
361	369	2	1017.56	4.9	0	30.5	21.5	95.00%	K.CAELAILTK.A	Carbamidomethyl (+57)	K.CAELAILTK.A
461	473	2	1539.76	4.1	1	67.2	24.3	95.00%	K.GLISQEEYDAFIR.K		K.GLISQEEYDAFIR.K
547	560	2	1596.79	3.6	0	50.8	24.1	95.00%	K.ESQYAQSITSKPMK.G		K.ESQYAQSITSKPMK.G
606	615	2	1199.6	4.3	1	55.1	24.2	95.00%	K.VIQCDEPALR.E	Carbamidomethyl (+57)	K.VIQCDEPALR.E
527	546	3	2267.24	3.3	1	44.5	16.3	95.00%	R.CVRPPIIVGDVYRPAPMTVK.E	Carbamidomethyl (+57)	R.CVRPPIIVGDVYRPAPMTVK.E
631	637	2	877.45	5.9	1	49	23.7	95.00%	K.WAIDAFR.L		K.WAIDAFR.L
85	99	2	1616.79	4.1	1	63.5	25.3	95.00%	R.LSGLSSLDTYFAMGR.G		R.LSGLSSLDTYFAMGR.G
156	176	3	2256.33	3.9	0	51.3	4.77	95.00%	K.EAGIITRPVLVGPVTYLFIAK.A		K.EAGIITRPVLVGPVTYLFIAK.A
661	667	2	861.47	2.2	1	29	20.8	95.00%	D.IFDAIQR.L		R.LATAAVQDDTQIHSHFCYSDFNDIFDAIQR.L
30	40	2	1132.6	4.2	0	58.1	22.9	95.00%	K.TSAEELLATAK.Q		K.TSAEELLATAK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
5	EF1A1_SCHPO	46.09%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
265	288	2	2443.35	2.2	0	46.5	15.3	95.00%	R.VETGVIKPGMIVTFAPAGVTTEVK.S		R.VETGVIKPGMIVTFAPAGVTTEVK.S
402	421	2	2268.08	4	1	67.5	25.3	95.00%	K.MVPSKPMCVEAFTDYAPLGR.F	Carbamidomethyl (+57)	K.MVPSKPMCVEAFTDYAPLGR.F
147	154	2	883.55	5.8	0	26.4	17.9	92.60%	K.QLIVAVNK.M		K.QLIVAVNK.M
289	298	2	1182.5	3.1	1	37	25.6	95.00%	K.SVEMHHESLD.A		K.SVEMHHESLDAGLPGDNVGFNVK.N
254	264	2	1024.61	4.2	0	65.4	14.1	95.00%	K.IGGIGTVPVGR.V		K.IGGIGTVPVGR.V
6	20	2	1529.84	4.6	1	62.9	19.8	95.00%	K.GHINVVVIGHVDSGK.S		K.GHINVVVIGHVDSGK.S
232	241	2	1081.54	3.6	1	35.7	24.1	95.00%	D.SIEPPARPTD.K		K.TLLEAIDSIEPPARPTDKPLR.L
185	214	3	3453.63	3.7	1	49.2	24.8	95.00%	K.TVPFVPVSGFQGDNMIEPTTNMPWYQGWQK.E		K.TVPFVPVSGFQGDNMIEPTTNMPWYQGWQK.E
155	164	2	1151.51	6.4	1	75.8	24.9	95.00%	K.MDTTGWSQAR.F		K.MDTTGWSQAR.F
198	214	2	2122.97	2.3	0	49.5	27	95.00%	D.NMIEPTTNMPWYQGWQK.E		K.TVPFVPVSGFQGDNMIEPTTNMPWYQGWQK.E
225	241	2	1836.95	3.4	1	25.2	22.1	90.70%	K.TLLEAIDSIEPPARPTD.K		K.TLLEAIDSIEPPARPTDKPLR.L
85	96	2	1340.69	4.4	1	66.1	22.7	95.00%	K.YNVTVIDAPGHR.D		K.YNVTVIDAPGHR.D
246	253	2	974.55	4.1	1	32.1	21	95.00%	R.LPLQDVYK.I		R.LPLQDVYK.I
135	146	2	1341.73	3.6	0	46.5	20.9	95.00%	R.EHALLAYTLGVK.Q	N-Formyl (+28)	R.EHALLAYTLGVK.Q
370	376	2	848.47	4.7	0	25.9	22.8	91.90%	K.FAELIEK.I		K.FAELIEK.I
223	231	2	958.54	3.2	2	44.1	22.6	95.00%	K.GKTLLEAID.S		K.GKTLLEAIDSIEPPARPTDKPLR.L
299	311	2	1286.66	1.7	1	45.7	23.3	95.00%	D.AGLPGDNVGFNVK.N		K.SVEMHHESLDAGLPGDNVGFNVK.N
165	177	2	1582.83	3.8	1	66.1	21	95.00%	R.FEEIVKETSNFIK.K		R.FEEIVKETSNFIK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
6	KPYK_SCHPO	62.67%	100%	27

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
332	344	2	1336.66	2.5	1	90.8	24.7	95.00%	D.GADLVMLSGETTK.G	Oxidation (+16)	R.AEVSDVGNAVLDGADLVMLSGETTK.G
108	121	2	1596.72	1.6	1	32	26.6	95.00%	D.YPISSGHEMIFTTD.D		R.TGLTVGGTDYPISSGHEMIFTTDDAYAEK.C
487	497	2	1053.66	5.9	0	39.5	11.1	95.00%	K.IIVLQGAVGGK.G		K.IIVLQGAVGGK.G
233	243	2	1214.66	3.9	1	28.5	22.1	95.00%	R.EVLGEEGKNIK.I		R.EVLGEEGKNIK.I
108	122	2	1711.74	1.7	1	29.9	27.1	94.50%	D.YPISSGHEMIFTTDD.A		R.TGLTVGGTDYPISSGHEMIFTTDDAYAEK.C
422	433	3	1430.81	4.6	0	41.1	17.2	95.00%	K.YRPSIPIVMVTR.C		K.YRPSIPIVMVTR.C
10	26	2	1880.98	3.7	1	90.9	21.6	95.00%	K.QWVAGLNSELDIPAVNR.R		K.QWVAGLNSELDIPAVNR.R
155	164	2	1105.64	2.5	0	35.4	16.1	95.00%	D.GILSFTVIEK.V		R.IIYVDDGILSFTVIEK.V
446	459	2	1607.81	1.6	2	43.4	23.7	95.00%	R.GVYPVIYEKEPLSD.W		R.GVYPVIYEKEPLSDWQK.D

320	331	2	1187.57	2.8	1	27.8	25.9	93.40%	R.AEVSDVGNAVLD.G		R.AEVSDVGNAVLDGADLVMLSGETTK.G
76	91	2	1640.92	2.4	2	37.3	17.8	95.00%	R.KASATNPLFPLAIALD.T		R.KASATNPLFPLAIALDTK.G
77	93	2	1741.97	3.8	1	39.2	17.8	95.00%	K.ASATNPLFPLAIALDTK.G		K.ASATNPLFPLAIALDTK.G
225	232	2	951.52	5	1	30.1	21.1	95.00%	R.AEDVIHIR.E		R.AEDVIHIR.E
248	258	2	1276.57	2.3	1	26.2	26	90.80%	K.IENQQGVNNFD.S		K.IENQQGVNNFDSILDVTDGIMVAR.G
57	75	3	2253.99	2.7	1	51	27.1	95.00%	R.MNFSHGSYEYHQSVIDNAR.K		R.MNFSHGSYEYHQSVIDNAR.K
381	402	2	2261.09	2.1	1	47.3	25.1	95.00%	R.RPLECATETTAVAAIGASIESD.A	Carbamidomethyl (+57)	R.RPLECATETTAVAAIGASIESDAK.A
28	37	2	1088.6	5	0	46.3	21.4	95.00%	R.TSIICTIGPK.S	Carbamidomethyl (+57)	R.TSIICTIGPK.S
274	288	2	1598.91	1.2	0	58.9	16.6	95.00%	D.LGIEIPASQVFVAQK.M		R.GDLGIEIPASQVFVAQK.M
468	477	2	1186.55	5.3	0	54.8	24.7	95.00%	R.VAYGCQQAYK.M	Carbamidomethyl (+57)	R.VAYGCQQAYK.M
345	360	2	1743.82	5.3	0	80.9	25.5	95.00%	K.GSYPVEAVTYMAETAR.V		K.GSYPVEAVTYMAETAR.V
335	344	2	1077.58	2.1	0	27.4	23.3	94.10%	D.LVMLSGETTK.G		R.AEVSDVGNAVLDGADLVMLSGETTK.G
272	288	2	1770.96	3.8	1	69.1	19.7	95.00%	R.GDLGIEIPASQVFVAQK.M		R.GDLGIEIPASQVFVAQK.M
361	380	2	2229.12	2.4	0	103	23.1	95.00%	R.VAEASIPYGSLYQEMFGLVR.R		R.VAEASIPYGSLYQEMFGLVR.R
294	319	4	2966.39	0.4	0	63.5	25.5	95.00%	K.CNIAGKPVACATQMLESMTYNPRPTR.A	Carbamidomethyl (+57)/ Deamidation (+1)/ Carbamidomethyl (+57)	K.CNIAGKPVACATQMLESMTYNPRPTR.A
405	417	2	1287.72	5.7	0	62	19	95.00%	K.AIVVLSTSGNTAR.L		K.AIVVLSTSGNTAR.L
212	223	2	1384.68	2.5	1	62.5	24.4	95.00%	K.NGVDMIFASFIR.R	Oxidation (+16)	K.NGVDMIFASFIR.R
381	404	2	2460.23	3.5	1	76.2	23.7	95.00%	R.RPLECATETTAVAAIGASIESDAK.A	Carbamidomethyl (+57)	R.RPLECATETTAVAAIGASIESDAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
7	ALF_SCHPO	63.97%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
257	275	3	2097.05	1.9	0	50.1	23.9	95.00%	D.KPVFFVFHGGSGSSVNEFR.T		K.TTNDKPVFFVFHGGSGSSVNEFR.T
26	50	2	2496.31	4.1	0	69.4	19.9	95.00%	R.EHGFAIPAINVTSSSTAIAALEAAR.E		R.EHGFAIPAINVTSSSTAIAALEAAR.E
309	325	2	1829.9	2.1	1	53.9	24.7	95.00%	D.YLMTPVGNPEGADKPNK.K		K.DYLMTPVGNPEGADKPNK.K
207	234	4	2951.52	1.9	0	40.3	20.8	95.00%	R.ELSSVTPYFSIAAAFGNVHGVYKPGNVK.L		R.ELSSVTPYFSIAAAFGNVHGVYKPGNVK.L
291	301	2	1283.62	1.9	2	26.4	24.3	92.60%	D.TQFAYVEGVRD.Y		K.VNIDTDTQFAYVEGVRDYVLK.Y
253	275	2	2528.21	2	1	93.7	25.2	95.00%	K.TTNDKPVFFVFHGGSGSSVNEFR.T		K.TTNDKPVFFVFHGGSGSSVNEFR.T
94	112	2	2098.02	4.1	1	63.5	24.9	95.00%	R.SIAPFFGVPVVMHSDHCAK.K	Carbamidomethyl (+57)	R.SIAPFFGVPVVMHSDHCAK.K
345	358	2	1597.83	4.2	1	60.4	23	95.00%	R.VLTALEDFYTVNTL.-		R.VLTALEDFYTVNTL.-
6	19	2	1424.83	2.3	1	46.6	15.2	95.00%	D.IVPTGVITGDNVLK.L		-.MGILDIVPTGVITGDNVLK.L
289	300	2	1384.67	2.2	1	49.5	25.8	95.00%	D.TDTQFAYVEGVR.D		K.VNIDTDTQFAYVEGVR.D
94	108	2	1601.79	2.2	1	57.9	24.5	95.00%	R.SIAPFFGVPVVMHSD.H		R.SIAPFFGVPVVMHSDHCAK.K
291	300	2	1168.59	2.2	0	52.4	22.9	95.00%	D.TQFAYVEGVR.D		K.VNIDTDTQFAYVEGVR.D
120	130	2	1322.55	2.5	1	42	25.6	95.00%	D.GMFEADEAYFK.I	Oxidation (+16)	K.LLPWMDGMFEADEAYFK.I
235	248	2	1564.88	4	0	58.4	15.7	95.00%	K.LQPALLGQHQAYVK.E		K.LQPALLGQHQAYVK.E
54	71	2	1844.94	0.087	0	95.6	23.4	95.00%	R.SPIILQTSNGGAHFFAGK.E	Deamidation (+1)	R.SPIILQTSNGGAHFFAGK.E
131	149	3	2165.05	0.18	1	36.6	24	95.00%	K.IHGEPLFSSHMLDLSEEPK.K		K.IHGEPLFSSHMLDLSEEPK.K
80	93	2	1399.76	5.1	0	89.1	19.9	95.00%	K.ASIAGSIAAAHYIR.S		K.ASIAGSIAAAHYIR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
8	PDC2_SCHPO	51.68%	100%	29

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
5	18	2	1542.74	2.4	0	67.9	25.1	95.00%	D.AESTMTVGTYLAQR.L	Oxidation (+16)	K.DAESTMTVGTYLAQR.L
254	278	3	2854.28	3.1	1	62.6	27	95.00%	K.GFYSEEHKNYAGVYWGEVSSSETTK.A		K.GFYSEEHKNYAGVYWGEVSSSETTK.A
204	214	2	1130.62	4.6	1	53.5	21.3	95.00%	K.ATDIAAELISK.K		K.ATDIAAELISK.K

440	461	2	2409.21	3.3	1	90.9	22.6	95.00%	R.TIVMVGDGSFQLTGQEISQMIR.H		R.TIVMVGDGSFQLTGQEISQMIR.H
546	555	2	1235.55	2.3	1	47.1	25.9	95.00%	D.CTQELVDWGK.A	Carbamidomethyl (+57)/ Deamidation (+1)	K.EGPTLIECAIDTDDCTQELVDWGK.A
238	253	2	1689.86	1.9	0	61.4	23.8	95.00%	K.LAEALNCAAFIMPAAK.G	Carbamidomethyl (+57)	K.LAEALNCAAFIMPAAK.G
516	525	2	1047.55	4.8	0	31.2	23.2	95.00%	K.TGEELTSAIK.V		K.TGEELTSAIK.V
228	237	2	949.49	5	0	30.2	23.3	95.00%	R.AAGAESAFVK.L		R.AAGAESAFVK.L
304	328	2	2694.37	3	1	65.1	21.3	95.00%	R.AAPNPNILLNSDYTSVSIPGYVFSR.V		R.AAPNPNILLNSDYTSVSIPGYVFSR.V
329	340	2	1425.76	4.3	0	95.2	21.9	95.00%	R.VYMAEFLELLAK.K		R.VYMAEFLELLAK.K
386	405	2	2262.03	2.2	1	73.1	26.8	95.00%	D.SNTTLYAETGDSWFNGLQMK.L		R.QIQGLVDSNTTLYAETGDSWFNGLQMK.L
447	461	2	1693.85	2.5	0	58.8	23.8	95.00%	D.GSFQLTGQEISQMIR.H		R.TIVMVGDGSFQLTGQEISQMIR.H
160	198	4	4251.22	3.6	1	16.7	18.8	90.40%	R.QAILQHKPVYIEIPTNMANQPCPVPGPISAVISPEISDK.E	Carbamidomethyl (+57)	R.QAILQHKPVYIEIPTNMANQPCPVPGPISAVISPEISDK.E
495	508	2	1529.69	2.2	0	66.7	26	95.00%	D.FAAFCESLNGETGK.A	Carbamidomethyl (+57)	R.IQNWDFAAFCESLNGETGK.A
397	405	2	1109.54	3.4	0	26.7	24.8	93.20%	D.SWFNGLQMK.L		R.QIQGLVDSNTTLYAETGDSWFNGLQMK.L
316	328	2	1474.75	2.4	0	39.8	23.6	95.00%	D.YTSVSIPGYVFSR.V		R.AAPNPNILLNSDYTSVSIPGYVFSR.V
369	378	2	1157.64	5	1	28	22.4	94.70%	K.AALNRVEVMR.Q		K.AALNRVEVMR.Q
137	146	2	1101.64	5.4	1	51.2	18.6	95.00%	K.LTCAAVAIKR.A	Carbamidomethyl (+57)	K.LTCAAVAIKR.A
19	25	2	770.49	4.3	0	34.4	18.1	95.00%	R.LVEIGIK.N		R.LVEIGIK.N
462	474	3	1603.96	1.9	1	30.1	9.54	95.00%	R.HKLPVLIFLLNNR.G	N-Formyl (+28)	R.HKLPVLIFLLNNR.G
26	37	2	1429.72	4.2	1	38.3	24.4	95.00%	K.NHFVVPGDYNLR.L		K.NHFVVPGDYNLR.L
262	278	2	1876.86	4.2	0	98.1	26.4	95.00%	K.NYAGVYWGEVSSSETTK.A		K.NYAGVYWGEVSSSETTK.A
150	159	2	1137.6	2.2	1	36.7	22.2	95.00%	D.APVMIDHAIR.Q	Oxidation (+16)	R.AEDAPVMIDHAIR.Q
490	508	2	2185.98	2.5	1	88.1	26.9	95.00%	R.IQNWDFAAFCESLNGETGK.A	Carbamidomethyl (+57)	R.IQNWDFAAFCESLNGETGK.A
464	474	2	1310.81	4.6	0	66.2	10.4	95.00%	K.LPVLIFLLNNR.G		K.LPVLIFLLNNR.G
136	145	2	1073.63	3.9	1	39.6	15.9	95.00%	K.KLTCAAVAIK.R	Carbamidomethyl (+57)	K.KLTCAAVAIK.R
4	18	2	1641.77	4.2	1	65.2	26	95.00%	K.DAESTMTVGTYLAQR.L		K.DAESTMTVGTYLAQR.L
304	315	2	1237.63	1.7	1	34.5	23.1	95.00%	R.AAPNPNILLNSD.Y		R.AAPNPNILLNSDYTSVSIPGYVFSR.V
216	225	3	1064.66	3.8	0	29.3	12	95.00%	K.EKPILLAGPK.L		K.EKPILLAGPK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
9	ADH4_SCHPO	50.24%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
238	261	3	2472.24	2.6	1	40.4	22.9	95.00%	D.ALTHAVEAYVSTAANPITDACAVK.C	Carbamidomethyl (+57)	K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
110	128	2	1962.06	1.8	0	59.1	19.9	95.00%	D.GVQPNPTVGNVNQGLEIVK.K		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K
110	129	2	2090.15	2.3	1	70.6	16.4	95.00%	D.GVQPNPTVGNVNQGLEIVKK.E		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVKK.E
375	385	3	1245.76	3.9	1	37.6	9.54	95.00%	K.IRPHLVDLGVK.E		K.IRPHLVDLGVK.E
76	87	2	1282.76	5.2	1	44.2	15.1	95.00%	K.NTLIVTDPGIIK.V		K.NTLIVTDPGIIK.V
366	374	2	1027.63	6.6	0	37.3	16.2	95.00%	R.ISQLVLEVK.I		R.ISQLVLEVK.I
149	159	2	1014.58	4.8	0	36.7	21.2	95.00%	K.GIALLATNGGK.I	Deamidation (+1)	K.GIALLATNGGK.I
210	219	2	1141.55	3.3	1	28.9	25.2	95.00%	K.HTMPILSVND.P	Oxidation (+16)	K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
348	365	4	2038.96	2.2	1	20.4	26	95.00%	D.IAFHLGCEEHTAEAALDR.I	Carbamidomethyl (+57)	R.LGDIAFHLGCEEHTAEAALDR.I
400	412	2	1380.61	2.6	1	28.4	26.3	93.60%	D.ACGATNPIQPTHD.E	Carbamidomethyl (+57)	K.DACGATNPIQPTHDEVK.A
399	412	2	1495.64	2	1	41.7	26.7	95.00%	K.DACGATNPIQPTHD.E	Carbamidomethyl (+57)	K.DACGATNPIQPTHDEVK.A
96	128	3	3573.88	3.6	1	56.5	18.9	95.00%	K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K

209	219	2	1253.65	3.1	2	30.9	22.1	95.00%	D.KHTMPILSVND.P		K.MAIIDKHTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
220	237	2	1882.84	3.7	1	41.5	27	95.00%	D.PETMYGLPPSLTAATGMD.A	Oxidation (+16)/ Oxidation (+16)	K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
169	191	2	2386.26	3.6	0	102	19.2	95.00%	K.SSKPQLPLIAINTTAGTASEMTR.F		K.SSKPQLPLIAINTTAGTASEMTR.F
238	256	2	1942.97	2.9	1	49.1	23.9	95.00%	D.ALTHAVEAYVSTAANPITD.A		K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
192	200	2	1078.57	4	0	35.5	22.9	95.00%	R.FAIITEETR.H		R.FAIITEETR.H
134	148	2	1475.65	2.3	1	43.8	26.6	95.00%	D.SMVSIGGGSAHDCAK.G	Carbamidomethyl (+57)	K.ENCDSMVSIGGGSAHDCAK.G
400	415	2	1736.82	1.6	1	30.9	25.9	95.00%	D.ACGATNPIQPTHDEVK.A	Carbamidomethyl (+57)	K.DACGATNPIQPTHDEVK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
10	TPIS_SCHPO	64.26%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
71	98	3	2925.39	4	1	98.2	25	95.00%	K.NGAYTGENSAQSLIDAGITYTLTGHSER.R		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R
206	222	2	1841.9	2.2	1	42.9	25	95.00%	R.VIYGGSVNGGNCKEFLK.F	Deamidation (+1)/ Carbamidomethyl (+57)	R.VIYGGSVNGGNCKEFLK.F
160	174	2	1615.9	2.4	0	77.1	16.9	95.00%	K.IVIAYEPVWAIGTGK.T		K.IVIAYEPVWAIGTGK.T
175	189	2	1678.84	4.6	0	84.5	24.1	95.00%	K.TATPEQAQEVHAEIR.K		K.TATPEQAQEVHAEIR.K
135	145	2	1242.66	4.7	0	39.7	21.6	95.00%	R.EANETINVVVR.Q		R.EANETINVVVR.Q
115	134	3	2176.12	2.2	0	34.6	21.8	95.00%	K.FALEQGLTVVACIGETLAER.E	Carbamidomethyl (+57)	K.FALEQGLTVVACIGETLAER.E
175	190	2	1807.9	-1.2	1	63.8	24.3	95.00%	K.TATPEQAQEVHAEIRK.W	Deamidation (+1)	K.TATPEQAQEVHAEIRK.W
32	52	2	2422.27	3.5	1	66.1	19.4	95.00%	K.LNVGDVETVIFPQNMYLITTR.Q		K.LNVGDVETVIFPQNMYLITTR.Q
228	249	3	2334.25	1.2	0	27.1	17.9	95.00%	D.GFLVGGASLKPEFHNIVNVHSL.-		K.FHDIDGFLVGGASLKPEFHNIVNVHSL.-
71	85	2	1538.69	2.4	1	52.7	26.6	95.00%	K.NGAYTGENSAQSLID.A		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R
86	98	2	1404.7	1.6	0	51.7	24.8	95.00%	D.AGITYTLTGHSER.R		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R
196	205	2	971.55	5.3	0	76.1	21.9	95.00%	K.LGASVAEGLR.V		K.LGASVAEGLR.V
37	52	2	1940.01	1.4	0	31.7	21	95.00%	D.VETVIFPQNMYLITTR.Q	Oxidation (+16)	K.LNVGDVETVIFPQNMYLITTR.Q
206	218	2	1324.61	4.4	0	76.9	25.9	95.00%	R.VIYGGSVNGGNCK.E	Deamidation (+1)/ Carbamidomethyl (+57)	R.VIYGGSVNGGNCK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
11	PMGY_SCHPO	67.77%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
122	134	2	1389.68	1.8	1	31.1	24.9	95.00%	R.SYDIAPPNGESLK.D		R.SYDIAPPNGESLK.D
23	30	2	977.53	1.3	0	29.5	21.6	95.00%	K.LNLFTGWK.D		K.LNLFTGWK.D
32	43	2	1242.68	2.1	1	49.4	20.7	95.00%	D.PALSETGIKEAK.L		K.DPALSETGIKEAK.L
111	120	2	1271.65	5.7	0	79.8	23.2	95.00%	K.WGAEQVQIWR.R		K.WGAEQVQIWR.R
70	90	2	2429.25	3.7	1	89.6	21.4	95.00%	K.TCQIILEEVGEPNLETIKSEK.L	Carbamidomethyl (+57)	K.TCQIILEEVGEPNLETIKSEK.L
23	31	2	1092.56	1.5	2	27.9	23.2	94.60%	K.LNLFTGWKD.P		K.LNLFTGWKDPALSETGIK.E
186	199	2	1553.85	2.8	1	52.2	18.1	95.00%	R.ELATGVPIVYHLDK.D		R.ELATGVPIVYHLDK.D
146	157	2	1320.78	4.4	1	36.9	13.8	95.00%	K.STIVPHILKGEK.V		K.STIVPHILKGEK.V
2	14	2	1439.81	5.3	0	52	17.6	95.00%	M.TTEAAPNLLVLTR.H	Acetyl (+42)	-.MTTEAAPNLLVLTR.H
158	168	2	1149.67	4.5	0	26.5	14	92.90%	K.VLIAAHGNSLR.A		K.VLIAAHGNSLR.A
95	104	2	1169.58	4.8	1	46.4	23.7	95.00%	R.YYGDLQGLNK.D		R.YYGDLQGLNK.D
58	66	2	1005.56	2.3	0	65.9	18.3	95.00%	D.IAFTSALQR.A		K.FDIAFTSALQR.A
70	87	2	2085.08	4.2	0	96.7	21.2	95.00%	K.TCQIILEEVGEPNLETIK.S	Carbamidomethyl (+57)	K.TCQIILEEVGEPNLETIK.S
1	14	2	1528.84	4.4	0	53	20	95.00%	-.MTTEAAPNLLVLTR.H		-.MTTEAAPNLLVLTR.H
15	30	3	1944.95	0.62	1	26.4	25.3	95.00%	R.HGESEWNKLNLFTGWK.D		R.HGESEWNKLNLFTGWK.D
32	40	2	914.51	1.5	0	50.8	22.1	95.00%	D.PALSETGIK.E		K.DPALSETGIK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
12	GLYD_SCHPO	49.25%	100%	20

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
146	159	2	1649.78	3.9	0	75	26	95.00%	K.ISAVSTYFESMPYR.V		K.ISAVSTYFESMPYR.V
183	193	2	1209.62	4.5	0	57.8	22.4	95.00%	K.ILVAGTSAYCR.L	Carbamidomethyl (+57)	K.ILVAGTSAYCR.L
171	182	3	1483.76	2.4	1	21.8	23	92.20%	D.MLEHDAQLFRPK.I		R.VDPNTGLIDYDMLEHDAQLFRPK.I
361	371	2	1254.76	2.4	0	49.7	13	95.00%	R.VLELINIVTNK.N		R.VLELINIVTNK.N
145	159	2	1777.87	2.1	1	88.3	24.9	95.00%	K.KISAVSTYFESMPYR.V		K.KISAVSTYFESMPYR.V
17	24	2	915.49	4.6	0	43.4	24.3	95.00%	D.PTVAEIMR.H		K.EQDPTVAEIMR.H
97	123	3	2997.42	4.8	0	58.3	25.4	95.00%	K.WGVNVQCLSGSPANMQVYQAIMPPHGR.L	Carbamidomethyl (+57)/ Deamidation (+1)	K.WGVNVQCLSGSPANMQVYQAIMPPHGR.L
74	85	2	1550.75	4.7	1	96.3	25.4	95.00%	K.FIDQIETLCQER.A	Carbamidomethyl (+57)	K.FIDQIETLCQER.A
86	96	2	1129.62	5.1	1	54.8	22.1	95.00%	R.ALAAFNLDPAK.W		R.ALAAFNLDPAK.W
59	67	2	998.45	5.1	0	32.9	23.9	95.00%	K.YSEGYPGAR.Y		K.YSEGYPGAR.Y
277	302	3	2725.45	2.8	0	25.2	18	95.00%	K.INFSVFPGHQGGPHNHTITALAVALK.Q		K.INFSVFPGHQGGPHNHTITALAVALK.Q
303	318	3	1967.95	5.1	1	36.3	25.2	95.00%	K.QCQEPAYKEYQAQVVK.N	Carbamidomethyl (+57)	K.QCQEPAYKEYQAQVVK.N
129	142	2	1467.68	2.5	1	30.4	26	95.00%	D.LPSGGHLSHGYQTD.T		R.LMGLDLPSGGHLSHGYQTDTK.K
413	422	2	1075.61	4.3	0	49.9	20.1	95.00%	R.ALTFAANLQK.E		R.ALTFAANLQK.E
46	58	2	1321.64	4.2	1	41.4	25.2	95.00%	R.AVMDALGSVMSNK.Y		R.AVMDALGSVMSNK.Y
438	452	2	1729.9	3.9	0	75.9	23.1	95.00%	K.LGEGEQYPELVQLQK.E		K.LGEGEQYPELVQLQK.E
6	16	2	1273.66	2	2	45.3	23.1	95.00%	D.SIMLTPLKEQD.P		-.MSSNDSIMLTPLKEQDPTVAEIMR.H
124	142	2	1996.93	0.2	1	43	26.1	95.00%	R.LMGLDLPSGGHLSHGYQTD.T		R.LMGLDLPSGGHLSHGYQTDTK.K
436	452	2	1929.02	1.8	1	61.3	19.7	95.00%	K.AKLGEGEQYPELVQLQK.E		K.AKLGEGEQYPELVQLQK.E
146	161	2	1879.87	2.9	2	39.7	26	95.00%	K.ISAVSTYFESMPYRVD.P	Oxidation (+16)	K.ISAVSTYFESMPYRVDPNTGLIDYDMLEHDAQLFRPK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
13	THI3_SCHPO	57.51%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
234	245	3	1551.81	2.3	1	22.6	21.9	93.60%	D.PVQTYKEYIHFK.R		K.DPVQTYKEYIHFK.R
155	169	2	1717.82	1.9	0	70	25.5	95.00%	D.GGIGIECMQQVELER.W	Carbamidomethyl (+57)	R.CGMNIAPAIINGEIDGGIGIECMQQVELER.W
74	95	2	2353.27	3.5	0	91.4	18.2	95.00%	R.GYPVTSFGSLLNEPFTGLITLK.G		R.GYPVTSFGSLLNEPFTGLITLK.G
316	327	2	1385.71	3.6	1	53.6	23.6	95.00%	K.QEAIAEIQDEIK.Q		K.QEAIAEIQDEIK.Q
312	324	2	1444.69	0.67	2	41.8	25.6	95.00%	D.PMGKQEAIAEIQD.E	Oxidation (+16)	K.DPMGKQEAIAEIQDEIK.Q
222	232	3	1198.64	1.7	1	32.9	21.4	95.00%	R.AIHSATLDMLK.D		R.AIHSATLDMLK.D
128	139	2	1325.67	4.2	1	42.4	23.3	95.00%	K.FGLSPSDYTAIR.C		K.FGLSPSDYTAIR.C
6	27	2	2631.39	2.4	0	78.6	19	95.00%	K.ITFLTNWEATPYHLPIFLAQTR.G		K.ITFLTNWEATPYHLPIFLAQTR.G
63	71	2	954.54	4.5	0	51.1	16.9	95.00%	K.AMIHTLAAK.A		K.AMIHTLAAK.A
110	118	2	968.5	4.9	0	27.7	22.1	94.40%	R.IGYVGEFGK.I		R.IGYVGEFGK.I
330	339	2	992.51	5.7	0	44.3	23.6	95.00%	K.GGVFSGNSLR.Y		K.GGVFSGNSLR.Y
189	211	3	2788.29	2.8	1	29.7	26	95.00%	R.LANLGCCCFCTILYIAHDEFIAK.H	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.LANLGCCCFCTILYIAHDEFIAK.H
33	56	2	2409.27	3	1	74.8	19.3	95.00%	R.EGIEVAILEPTNPSDVTALIGSGK.V		R.EGIEVAILEPTNPSDVTALIGSGK.V
260	273	2	1711.79	4.7	1	88.7	26.2	95.00%	R.CFAYFSHDISNVPR.D	Carbamidomethyl (+57)	R.CFAYFSHDISNVPR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
14	SAHH_SCHPO	35.10%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

257	268	2	1355.63	2.3	0	62	25.4	95.00%	D.GFEVTTMEEAVK.E	Oxidation (+16)	R.VIVTEVDPINALQAAMDGFEVTTMEEAVK.E
174	183	2	1081.62	2.2	2	59.2	18.7	95.00%	K.LKVPAINVND.S		K.LKVPAINVNDSVTK.S
20	35	2	1798.92	1.6	0	72	22.8	95.00%	K.ELEIAENEMPGLIAVR.E	Oxidation (+16)	K.ELEIAENEMPGLIAVR.E
8	18	2	1118.61	3.2	1	77.1	20.1	95.00%	K.VADISLAAFGR.K		K.VADISLAAFGR.K
216	227	2	1117.62	4.3	1	46.5	20.9	95.00%	K.VAVVAGFGDVGK.G		K.VAVVAGFGDVGK.G
269	280	2	1367.66	4	0	40.1	24.9	95.00%	K.EGQIFVTTTGCR.D	Carbamidomethyl (+57)	K.EGQIFVTTTGCR.D
153	167	2	1647.81	1.5	0	74.8	24.8	95.00%	R.GISEETTTGVHNLYK.M		R.GISEETTTGVHNLYK.M
19	35	2	1911.02	1.2	1	91	20.5	95.00%	R.KELEIAENEMPGLIAVR.E		R.KELEIAENEMPGLIAVR.E
247	268	2	2364.14	3	1	97.9	25.1	95.00%	D.PINALQAAMDGFEVTTMEEAVK.E		R.VIVTEVDPINALQAAMDGFEVTTMEEAVK.E
176	187	2	1255.68	4.6	1	42.1	21.1	95.00%	K.VPAINVNDSVTK.S		K.VPAINVNDSVTK.S
336	344	2	1006.6	5	1	31.2	14.9	95.00%	R.HIILLADGR.L		R.HIILLADGR.L
103	118	2	2053.94	4.3	0	72.2	26	95.00%	K.GETEEEYLWCIEQQLK.S	Carbamidomethyl (+57)	K.GETEEEYLWCIEQQLK.S
136	143	2	937.54	2.4	0	25	15.9	90.30%	D.LTALVHER.H		K.SFPSGKPLNMILDDGGDLTALVHER.H
133	143	2	1166.61	1.9	1	32.3	22.5	95.00%	D.GGDLTALVHER.H		K.SFPSGKPLNMILDDGGDLTALVHER.H
377	389	2	1455.76	3.1	0	26.8	22.5	93.20%	D.NTSYPLGVHMLPK.K		R.LVNLGCATGHPSFVMSCSFTNQVLAQIALWTDNTSYPLGVHMLPK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
15	THI2_SCHPO	45.43%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
234	242	2	981.48	2.7	0	34	23.4	95.00%	D.GPFGAFCVK.R	Carbamidomethyl (+57)	R.IAGVVTNWTLVSLNHGLQSCMDPNTINAHLVVSATGHDGPFGAFCVK.R
175	187	2	1431.8	2.4	1	59.1	18.7	95.00%	K.LFNATAVEDLIVK.E		K.LFNATAVEDLIVK.E
2	15	2	1400.77	3.8	0	74.5	20	95.00%	M.APATAVVTPQTAFK.T		-.MAPATAVVTPQTAFK.T
131	146	2	1818.91	2.1	1	34.3	24.6	95.00%	R.KPADLFLNEIGVPYED.E		R.KPADLFLNEIGVPYEDEGDYVVVK.H
39	55	2	1962.95	4.7	1	48.4	25.1	95.00%	K.AYPTYSLDESFSFAPIR.E		K.AYPTYSLDESFSFAPIR.E
244	255	2	1266.66	2.2	1	59.2	22.4	95.00%	R.LASAQLVSNLHD.M		R.LASAQLVSNLHDMRPLDMNR.A
218	233	2	1644.83	3	1	48.5	24.7	95.00%	D.PNTINAHLVVSATGHD.G		R.IAGVVTNWTLVSLNHGLQSCMDPNTINAHLVVSATGHDGPFGAFCVK.R
295	308	2	1459.67	4	0	71.7	26.5	95.00%	R.MGPTFGGMMFSGIK.A		R.MGPTFGGMMFSGIK.A
309	320	2	1332.68	5.8	1	60	23.7	95.00%	K.AAQEALAIFDER.K		K.AAQEALAIFDER.K
274	294	2	2254.05	3.3	1	79.8	26.6	95.00%	R.EVFPGMIVGGMELSEFDGANR.M		R.EVFPGMIVGGMELSEFDGANR.M
244	260	3	1878.97	1.8	1	30.6	22.8	95.00%	R.LASAQLVSNLHDMRPLD.M		R.LASAQLVSNLHDMRPLDMNR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
16	METK_SCHPO	48.95%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
90	103	2	1572.75	1.9	1	25.2	25.3	90.00%	K.TCNVLVAIEQQSPD.I	Carbamidomethyl (+57)	K.TCNVLVAIEQQSPDIAQGLHYEK.A
147	155	2	931.5	4.5	0	58	24	95.00%	K.LNAAMSVAR.R		K.LNAAMSVAR.R
2	18	2	1820.82	0.97	1	79.8	26.6	95.00%	M.AQTFLFTSESVGEGHPD.K		-.MAQTFLFTSESVGEGHPDK.I
237	251	2	1429.74	3.6	1	73.6	22.8	95.00%	R.FVVGGPQGDAGLTGR.K		R.FVVGGPQGDAGLTGR.K
339	349	2	1256.73	4.3	1	36.5	16.5	95.00%	K.NFDLRPGVLVK.S		K.NFDLRPGVLVK.S
90	112	3	2612.3	3.4	1	62.4	23.8	95.00%	K.TCNVLVAIEQQSPDIAQGLHYEK.A	Carbamidomethyl (+57)	K.TCNVLVAIEQQSPDIAQGLHYEK.A
328	338	2	1257.74	4.7	1	49.3	16.3	95.00%	K.TSAELVEIIRK.N		K.TSAELVEIIRK.N
353	378	3	3055.48	3	1	68	23.9	95.00%	K.LQTPFYLSTASYGHFTDQSKPWEQPK.E		K.LQTPFYLSTASYGHFTDQSKPWEQPK.E
291	299	2	856.52	4.2	0	28.1	19.7	94.80%	K.SLVAAGLAR.R		K.SLVAAGLAR.R
213	226	3	1572.93	4.6	1	37.1	12	95.00%	K.IIKPTVPAHLLDEK.T		K.IIKPTVPAHLLDEK.T

253	272	2	1948.95	4	1	80.8	25.2	95.00%	K.IIVDTYGGWGAHGGGAFSGK.D		K.IIVDTYGGWGAHGGGAFSGK.D
132	146	3	1702.01	2.5	1	32.5	12.3	95.00%	D.ETPEKLPLTILLAHK.L		K.ALEELGAGDQGIMFGYATDETPEKLPLTILLAHK.L
169	185	2	1946.97	4.5	0	49.1	24.4	95.00%	K.TQVTIEYEEENGAVIPR.R		K.TQVTIEYEEENGAVIPR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
17	HSP72_SCHPO	33.38%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
327	340	2	1400.77	3.9	0	39.7	20.8	95.00%	K.ASVNEIVLVGGSTR.I		K.ASVNEIVLVGGSTR.I
432	445	2	1584.83	3.7	0	35.6	22.2	95.00%	D.NQPGVLIQVFEGER.A		K.SEIFSTYSDNQPGVLIQVFEGER.A
170	184	2	1530.8	2.3	1	48.1	22.2	95.00%	R.IINEPTAAAIAYGLD.R		R.IINEPTAAAIAYGLDR.S
111	124	2	1611.79	1.5	0	77.8	24.5	95.00%	K.TFTPEEISSMVLMK.M		K.TFTPEEISSMVLMK.M
594	607	2	1556.83	4.2	1	73.7	21.3	95.00%	K.QKELESVANPIMAK.I		K.QKELESVANPIMAK.I
538	548	2	1351.66	4.4	0	37.5	24.8	95.00%	K.NHLESYAYSLR.N		K.NHLESYAYSLR.N
326	340	2	1528.86	2.3	1	50.7	18.3	95.00%	D.KASVNEIVLVGGSTR.I		K.VDKASVNEIVLVGGSTR.I
125	136	2	1324.65	4.5	1	66.6	24.8	95.00%	K.MRETAEAYLGGK.V		K.MRETAEAYLGGK.V
170	185	2	1686.9	4	1	94.1	20	95.00%	R.IINEPTAAAIAYGLDR.S		R.IINEPTAAAIAYGLDR.S
298	306	2	1109.48	3.1	2	26.8	25.3	92.80%	R.ARFEELCAD.L	Carbamidomethyl (+57)	R.ARFEELCADLFR.K
55	69	2	1698.82	4.2	1	74.8	25.4	95.00%	K.NQVAMNPHNTIFDAK.R		K.NQVAMNPHNTIFDAK.R
457	467	2	1182.65	4.4	0	28.3	19.9	95.00%	K.FELSGIPPAPR.G		K.FELSGIPPAPR.G
235	244	2	1273.69	4.3	0	25.1	21.4	90.50%	R.LVNHFIQEFK.R		R.LVNHFIQEFK.R
35	47	2	1486.7	4.2	1	60.5	25.7	95.00%	R.TTPSYVAFTDTER.L		R.TTPSYVAFTDTER.L
608	647	3	3515.61	5.3	1	39.6	25.6	95.00%	K.IYQAGGAPGGMPGAAPGAAPGAAPGAAPGGDNGPEVEEVD.-	Oxidation (+16)	K.IYQAGGAPGGMPGAAPGAAPGAAPGAAPGGDNGPEVEEVD.-
24	34	2	1227.63	5.8	1	33.2	23.4	95.00%	R.VEIIANDQGNR.T		R.VEIIANDQGNR.T
159	169	2	1095.68	3.4	0	35.3	11.5	95.00%	D.AGLIAGLNVLR.I		K.DAGLIAGLNVLR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
18	HSP90_SCHPO	21.88%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
275	289	2	1790.84	2.4	1	68.5	26.2	95.00%	R.NPSEVTKEEYASFYK.S		R.NPSEVTKEEYASFYK.S
523	533	2	1290.59	2.5	1	30.2	25.7	95.00%	D.GLELEETDEEK.A		K.DGLELEETDEEK.A
465	474	2	1170.6	4.5	0	29.7	22.3	95.00%	K.NIYFITGESK.Q		K.NIYFITGESK.Q
567	587	2	2339.11	2.3	0	98.6	25.3	95.00%	K.IVGSPCLLTTGQYGWSANMER.I	Carbamidomethyl (+57)	K.IVGSPCLLTTGQYGWSANMER.I
369	375	2	811.49	2.2	0	30.9	18.1	95.00%	D.LPLNLSR.E		K.GVVDSEDLPLNLSR.E
596	606	2	1234.5	4.9	1	67.2	25.9	95.00%	R.DTSMSAYMSSR.K		R.DTSMSAYMSSR.K
475	487	2	1548.8	4.5	0	76.3	22.9	95.00%	K.QAVENSPFLEIFR.A		K.QAVENSPFLEIFR.A
88	99	2	1282.73	5.3	1	55.5	17.6	95.00%	K.NDLINNLGVIAK.S		K.NDLINNLGVIAK.S
255	267	2	1520.76	4.6	1	46.2	24.1	95.00%	K.VKETTTETEELNK.T		K.VKETTTETEELNK.T
198	212	2	1815.96	2.7	0	51.3	21.9	95.00%	K.HSEFISYPIQLVVTR.E	N-Formyl (+28)	K.HSEFISYPIQLVVTR.E
422	436	2	1574.86	4	1	34.5	19.4	95.00%	K.LGIHEDAANRPALAK.L		K.LGIHEDAANRPALAK.L
499	509	2	1275.67	2	1	48.2	22.2	95.00%	D.PIDEYAVTQLK.E		K.FDVLFMVDPIDEYAVTQLK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
19	K6PF_SCHPO	29.30%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
364	380	3	1831.88	4.2	1	50.7	25.7	95.00%	R.ICEAVDSISSTAISHSR.A	Carbamidomethyl (+57)	R.ICEAVDSISSTAISHSR.A
613	628	3	1700.87	4.5	1	49.7	22.8	95.00%	R.GHTPLAIDNGFSGFLR.H		R.GHTPLAIDNGFSGFLR.H
822	839	4	2058.08	3.2	1	52.7	20.5	95.00%	K.VYTTEVIGNIISEEAHKR.F		K.VYTTEVIGNIISEEAHKR.F
419	431	2	1592.73	4.2	1	27.5	26.3	92.40%	K.WQDELCNSLSSVR.K	Carbamidomethyl (+57)	K.WQDELCNSLSSVR.K
21	31	2	1419.67	1.5	1	46.1	25.5	95.00%	D.TYNQTLDFYQK.L		-.MSGETVHGISCYSVVANTEDTYNQTLDFYQK.L
138	148	2	1187.63	2	1	38.8	22.8	95.00%	D.PLGNLIGFSDR.Y		K.KPDEVYVEDPLGNLIGFSDR.Y
586	603	3	1720.91	1.8	0	65	21.8	95.00%	R.VAIIHVGAPAGGMNSATR.A		R.VAIIHVGAPAGGMNSATR.A
503	522	2	1996.03	1.2	1	51.6	22.3	95.00%	D.AVLASTPDTPSPMIAINGNK.I		R.MLATLQGVDAVDAVLASTPDTPSPMIAINGNK.I

511	522	2	1241.65	2.5	0	41.1	22.7	95.00%	D.TPSPMIAINGNK.I		R.MLATLQGVDAVDAVLASTPDTPSPMIAINGNK.I
160	183	3	2416.24	3.9	1	44	20.9	95.00%	K.SEESGAASNLESGLATPVVETLKK.A		K.SEESGAASNLESGLATPVVETLKK.A
908	918	2	1362.61	2.1	0	40.6	25.7	95.00%	D.VENNETEIEMR.R		R.GTGVSFSSVADVENNETEIEMR.R
798	806	2	934.49	4	0	31.5	22.6	95.00%	K.ATFALEAGR.N		K.ATFALEAGR.N
299	308	2	1035.54	1.5	1	62.5	22.5	95.00%	D.GSLTGADIFR.S		K.NLISAGIDSIIVCGGDGSLTGADIFR.S
254	267	2	1400.75	3.4	0	49.7	22	95.00%	R.GWLAEGGTLIGTAR.C		R.GWLAEGGTLIGTAR.C
844	861	2	1860.9	4.7	1	42.3	25.5	95.00%	R.TAVPGHVQQGGNPTPMDR.A		R.TAVPGHVQQGGNPTPMDR.A
783	790	2	903.49	1.2	1	33.5	23.2	95.00%	D.GISLDMLR.K		R.SGYIATVGGLITGASAIYTPEDGISLDMLR.K
927	938	2	1323.7	4.7	1	53.3	21.2	95.00%	R.DMHNLVNILAGK.T		R.DMHNLVNILAGK.T
77	94	2	1954.97	4.6	1	62	23.7	95.00%	R.LVPGELSLSPAAEDSEWR.G		R.LVPGELSLSPAAEDSEWR.G
197	214	2	1760.86	4.1	1	84.8	25	95.00%	K.IAVMTSGGDSPGMNAVVR.A		K.IAVMTSGGDSPGMNAVVR.A
822	838	2	1901.98	3.2	0	56.8	22.6	95.00%	K.VYTTEVIGNIISEEAHK.R		K.VYTTEVIGNIISEEAHK.R
887	896	2	997.59	2.4	0	75.8	17.2	95.00%	D.PSSAVVIGIR.G		R.ANDLGNDPSSAVVIGIR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
20	A1EGU1_SCHPO	27.26%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
408	429	3	2504.31	0.59	1	22	20.6	92.60%	K.HVERPIIFPISNPTTLMEAKPD.Q		K.HVERPIIFPISNPTTLMEAKPDQIDK.W
457	479	2	2580.33	2.4	0	74	21.5	95.00%	K.YVISQCNNALLYPALGVACVLSR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.YVISQCNNALLYPALGVACVLSR.C
44	57	2	1634.91	4.4	1	89.1	17.2	95.00%	R.LPPIVETLQQQVDR.C		R.LPPIVETLQQQVDR.C
373	396	3	2478.39	1.4	0	28.1	13.2	95.00%	D.INLESAIALVKPTILLGCSGQPGK.F	Carbamidomethyl (+57)	K.EVPSGDINLESAIALVKPTILLGCSGQPGK.F
439	452	2	1418.83	2	0	52.7	10.4	95.00%	K.ALIATGSPLPPLNR.N		K.ALIATGSPLPPLNR.N
367	396	3	3062.64	3.1	1	30.5	17.2	95.00%	K.EVPSGDINLESAIALVKPTILLGCSGQPGK.F	Carbamidomethyl (+57)	K.EVPSGDINLESAIALVKPTILLGCSGQPGK.F
490	500	2	1070.58	4.5	1	54.7	21.7	95.00%	K.AASDALATVPR.S		K.AASDALATVPR.S
15	23	2	955.55	4.9	0	32.8	19.7	95.00%	K.GVTLLNSPR.Y		K.GVTLLNSPR.Y
548	555	2	1085.63	3.7	1	31.8	19.3	95.00%	K.LKEWIIER.E		K.LKEWIIER.E
332	339	2	964.49	5	1	34.3	22.8	95.00%	R.GNLFMIDR.C		R.GNLFMIDR.C
456	479	3	2708.42	2.3	1	27.2	18.6	95.00%	K.KYVISQCNNALLYPALGVACVLSR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.KYVISQCNNALLYPALGVACVLSR.C
178	191	2	1553.75	3.5	1	59.3	25.4	95.00%	K.GHLMTLCAGLDPNR.F	Carbamidomethyl (+57)	K.GHLMTLCAGLDPNR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
21	EF3_SCHPO	26.36%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
333	350	2	1970.01	4.8	0	86.5	22.4	95.00%	K.IPEVSTAANPEVCLETLK.A	Carbamidomethyl (+57)	K.IPEVSTAANPEVCLETLK.A
35	59	2	2604.32	3.9	1	66.4	22.4	95.00%	K.ALASFVNGPIEEQDAPSQVFSAISK.Q		K.ALASFVNGPIEEQDAPSQVFSAISK.Q
351	367	2	1809.03	4.2	1	72.9	15.3	95.00%	K.AVLGEIKVPTNEEVIAK.Y		K.AVLGEIKVPTNEEVIAK.Y
961	994	3	3666.67	2.8	0	62.6	25.7	95.00%	R.EFTEGLTEEVWAVNNGHMTPSGHNWVSGQGSGPR.I		R.EFTEGLTEEVWAVNNGHMTPSGHNWVSGQGSGPR.I
281	294	2	1550.88	4.1	1	60.5	15.8	95.00%	K.LVEDPQVVAPFLPK.L		K.LVEDPQVVAPFLPK.L
757	765	2	1178.58	7.8	0	24.9	24.4	90.10%	K.TPSEYIQWR.F		K.TPSEYIQWR.F
89	103	2	1652.98	2.3	0	39.4	6.99	95.00%	D.VEPYLVELLPAVIAK.V		K.GLEAVANHGSVAADVEPYLVELLPAVIAK.V
479	493	2	1636.88	3.9	0	73.9	21.1	95.00%	R.AIVNGQVEGFPTHLR.T		R.AIVNGQVEGFPTHLR.T
419	447	3	3168.34	2.9	1	77.1	27.1	95.00%	K.IPGGASHAEEEEEGEDLCNCEFSLAYGAK.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.IPGGASHAEEEEEGEDLCNCEFSLAYGAK.I
75	103	3	2944.6	3.2	1	47.9	16	95.00%	K.GLEAVANHGSVAADVEPYLVELLPAVIAK.V		K.GLEAVANHGSVAADVEPYLVELLPAVIAK.V
133	147	2	1550.87	3.9	0	70.6	16.1	95.00%	K.AIVPSVLESIHTTGK.W		K.AIVPSVLESIHTTGK.W

881	900	3	2293.11	2.6	1	44.8	25.5	95.00%	K.EIEEHCSLLGLDAELVSHSR.I	Carbamidomethyl (+57)	K.EIEEHCSLLGLDAELVSHSR.I
739	755	4	1846.91	1.6	1	19	25.1	95.00%	R.IAYVAQAAFTHLGHHPD.K		R.IAYVAQAAFTHLGHHPDK.T
606	621	3	1882.97	3.1	1	22.5	22	93.40%	D.SGFLDHVVQAIIHYER.F		K.DVSSIIVSHDSGFLDHVVQAIIHYER.F
358	367	2	1098.6	4.8	0	47.3	21.4	95.00%	K.VPTNEEVIAK.Y		K.VPTNEEVIAK.Y
675	692	3	2075.98	3.2	1	36.1	26.1	95.00%	K.VQHMSFQYPGTSKPQLND.I		K.VQHMSFQYPGTSKPQLNDISFQVSLSSR.I
35	48	2	1488.71	1.4	1	45	25.2	95.00%	K.ALASFVNGPIEEQD.A		K.ALASFVNGPIEEQDAPSQVFSAISK.Q
49	59	2	1133.61	2.3	0	31.1	21.9	95.00%	D.APSQVFSAISK.Q		K.ALASFVNGPIEEQDAPSQVFSAISK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
22	6PGD_SCHPO	30.49%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
386	403	2	2088.07	2.5	0	53.7	22.3	95.00%	D.PNLESILFHPFFTNGVEK.A		R.EDPNLESILFHPFFTNGVEK.A
156	166	3	1228.76	4.8	0	32.1	8.45	95.00%	R.IKPIFQTLAAK.A		R.IKPIFQTLAAK.A
42	51	2	1134.56	4.5	1	47.7	24.6	95.00%	R.VDEFLANEAK.G		R.VDEFLANEAK.G
123	139	2	1590.81	3.9	0	62.7	23.7	95.00%	K.GILFVGSGVSGGEEGAR.Y		K.GILFVGSGVSGGEEGAR.Y
140	155	2	1669.81	4.7	0	28.8	25.5	95.00%	R.YGPSLMPGGNPAAWPR.I		R.YGPSLMPGGNPAAWPR.I
269	291	2	2504.28	3.2	0	92.8	22.1	95.00%	K.WTAQNALEMGTPVSLITEAVFAR.C		K.WTAQNALEMGTPVSLITEAVFAR.C
437	449	2	1379.79	4.1	0	52	15.2	95.00%	R.SAVLPANLLQAQR.D		R.SAVLPANLLQAQR.D
80	97	2	1925.1	4.4	1	58.2	14.1	95.00%	K.AGKPVDYLIEGLAPLLEK.G		K.AGKPVDYLIEGLAPLLEK.G
54	67	2	1501.78	2.8	0	63.1	22.4	95.00%	K.SIVGAHSLEEFVSK.L		K.SIVGAHSLEEFVSK.L
86	97	2	1357.79	2	0	38.5	16.9	95.00%	D.YLIEGLAPLLEK.G		K.AGKPVDYLIEGLAPLLEK.G
29	37	2	1175.49	3.9	0	36.7	25.7	95.00%	K.GFTVCCYNR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GFTVCCYNR.T
122	139	2	1718.9	2.3	1	103	22.3	95.00%	K.KGILFVGSGVSGGEEGAR.Y		K.KGILFVGSGVSGGEEGAR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
23	EF2_SCHPO	19.95%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
272	283	2	1498.77	4.2	1	53.9	23.1	95.00%	R.AFNMFILDPIYR.I		R.AFNMFILDPIYR.I
466	479	2	1474.71	3.7	0	72.8	24.8	95.00%	K.SGTLTTSEVAHNMK.V		K.SGTLTTSEVAHNMK.V
811	823	3	1441.74	2.3	0	43.5	23.2	95.00%	D.PTSKPGQIVCEAR.K	Carbamidomethyl (+57)	R.QATAGQAFPQLVFDHWSPMSGDPLDPTSKPGQIVCEAR.K
565	578	2	1451.69	4.3	0	44.5	25.6	95.00%	R.ESVSEPSSMTALSK.S		R.ESVSEPSSMTALSK.S
284	292	2	1051.52	4.5	1	27.5	23.6	94.20%	R.IFDAVMNSR.K		R.IFDAVMNSR.K
244	253	2	1266.61	5.9	0	30	24.9	95.00%	R.LWGENYFNPK.T		R.LWGENYFNPK.T
770	785	2	1798.9	4	0	39.1	23.6	95.00%	K.AYLPVNESFGFTGELR.Q		K.AYLPVNESFGFTGELR.Q
111	120	2	1079.56	2.7	0	29.3	23	95.00%	D.FSSEVTAALR.V		K.EPADGTDFLVNLIDSPGHVDFSSEVTAALR.V
371	384	2	1594.76	4.1	1	55	25.8	95.00%	R.NCDANAPLMIYVSK.M	Carbamidomethyl (+57)	R.NCDANAPLMIYVSK.M
327	346	2	2192.18	2.4	1	55.9	18.3	95.00%	K.FLPAADALMEMIVLHLPSPK.T		K.FLPAADALMEMIVLHLPSPK.T
640	651	2	1231.64	3.2	1	28.1	22.6	94.80%	D.TTGANVVVDQTK.A		K.IWCFGPDTTGANVVVDQTK.A
586	609	3	2657.29	3.5	0	32.6	24.6	95.00%	R.IFMTAEPMSEELSVAIETGHVNPR.D		R.IFMTAEPMSEELSVAIETGHVNPR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
24	ILV5_SCHPO	29.46%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
198	204	2	738.5	2.1	0	36.2	11.5	95.00%	D.VILVAPK.G		K.DVDVILVAPK.G
84	104	2	2141.07	4.6	1	90.4	23.6	95.00%	K.NDTLAIIGYGSQGHGQGLNAR.D		K.NDTLAIIGYGSQGHGQGLNAR.D
330	337	2	914.47	6	1	41.2	22.8	95.00%	R.GAIDWTPR.F		R.GAIDWTPR.F
314	328	2	1725.75	2.3	1	70.8	27.5	95.00%	K.YGLDYMFAACSTTAR.R	Carbamidomethyl (+57)	K.YGLDYMFAACSTTAR.R
145	163	2	2074.05	4.2	1	75.2	22.9	95.00%	K.GSIIMNLLSDAAQTETWPK.I		K.GSIIMNLLSDAAQTETWPK.I
362	372	2	1312.61	4.6	0	61.6	25.4	95.00%	R.SLEYNSAPNYR.E		R.SLEYNSAPNYR.E

289	313	2	2687.32	3.5	0	76.3	24.4	95.00%	R.GHSPAEAFNETVEEATQSLYPLIGK.Y		R.GHSPAEAFNETVEEATQSLYPLIGK.Y
318	328	2	1277.56	2.4	0	37.9	25.7	95.00%	D.YMFAACSTTAR.R	Carbamidomethyl (+57)	K.YGLDYMFAACSTTAR.R
123	133	2	1198.6	4.3	1	28.6	23.2	95.00%	K.QAIEDGWVPGK.T		K.QAIEDGWVPGK.T
196	204	2	952.6	2.7	1	61.8	13.6	95.00%	D.VDVILVAPK.G		K.DVDVILVAPK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
25	ACT_SCHPO	37.07%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
223	238	2	1794.87	2.2	0	79.4	25.2	95.00%	D.FEQELQTAAQSSSLEK.S		K.LCYVALDFEQELQTAAQSSSLEK.S
245	254	2	1085.58	0.91	0	53.9	21.9	95.00%	D.GQVITIGNER.F		K.SYELPDGQVITIGNER.F
1	18	2	2007.9	4	1	79.9	26.2	95.00%	-.MEEEIAALVIDNGSGMCK.A	Acetyl (+42)/ Carbamidomethyl (+57)	-.MEEEIAALVIDNGSGMCK.A
255	284	3	3274.66	3.2	1	82.1	20.8	95.00%	R.FRAPEALFQPSALGLENAGIHEATYNSIMK.C		R.FRAPEALFQPSALGLENAGIHEATYNSIMK.C
85	95	3	1514.75	5.5	0	36	24.5	95.00%	K.IWHHTFYNELR.V		K.IWHHTFYNELR.V
96	113	2	2014.03	3.9	0	59.4	23.1	95.00%	R.VAPEEHPCLLTEAPLNPK.S	Carbamidomethyl (+57)	R.VAPEEHPCLLTEAPLNPK.S
197	206	2	1131.53	5.1	0	41.4	25.5	95.00%	R.GYTFSTTAER.E		R.GYTFSTTAER.E
239	254	2	1789.89	5.1	1	75.2	24.6	95.00%	K.SYELPDGQVITIGNER.F		K.SYELPDGQVITIGNER.F
216	238	2	2629.27	3.5	1	106	24.9	95.00%	K.LCYVALDFEQELQTAAQSSSLEK.S	Carbamidomethyl (+57)	K.LCYVALDFEQELQTAAQSSSLEK.S
360	372	2	1511.7	3.8	1	34.6	25.7	95.00%	K.QEYDESGPGIVYR.K		K.QEYDESGPGIVYR.K
257	284	3	2971.48	1.9	0	49.3	22.1	95.00%	R.APEALFQPSALGLENAGIHEATYNSIMK.C		R.APEALFQPSALGLENAGIHEATYNSIMK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
26	TKT_SCHPO	34.16%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
306	318	2	1423.73	4.8	1	73.3	23.1	95.00%	R.VAIASSAEEEYKK.M		R.VAIASSAEEEYKK.M
325	336	2	1449.68	6.5	1	28.4	25.4	94.70%	K.QSYPDLSNQLER.I	Deamidation (+1)	K.QSYPDLSNQLER.I
238	252	2	1719.86	5	1	57.2	24.7	95.00%	R.EAMSCTDKPTLINLK.T	Carbamidomethyl (+57)	R.EAMSCTDKPTLINLK.T
395	407	2	1418.65	3.9	1	52.7	25.9	95.00%	R.WEGAADFQPPSSK.L		R.WEGAADFQPPSSK.L
653	663	3	1249.63	4.3	0	20.8	24.3	90.40%	K.FHFTTSGVAQR.A		K.FHFTTSGVAQR.A
481	494	3	1636.81	2	0	62.2	24.5	95.00%	D.GPTHQPIETFAHFR.A		R.VIYVATHDSIGLGEDGPTHQPIETFAHFR.A
182	193	2	1385.74	4.7	1	41.9	21.6	95.00%	K.LSNLIAVWDNNK.I		K.LSNLIAVWDNNK.I
532	547	2	1810.95	4.2	0	72.5	21.2	95.00%	R.QNLPQLENSTIENALK.G		R.QNLPQLENSTIENALK.G
589	606	2	2252.07	4.5	0	58.5	26.1	95.00%	R.VVSLPCWEVFEQQPESYR.L	Carbamidomethyl (+57)	R.VVSLPCWEVFEQQPESYR.L
630	648	3	2046.93	3.6	1	34	26.8	95.00%	R.YVHEAFGMHTFGDSGPAPK.L		R.YVHEAFGMHTFGDSGPAPK.L
163	181	3	2001.93	2.5	0	25.2	26.5	94.90%	D.GCLQEGVSSEACSLAGHLK.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.AHSAAVYNKPGFDLFSNYTFCFLGDGCLQEGVSSEACSLAGHLK.L
253	281	3	3132.54	2.9	1	59.8	23.5	95.00%	K.TTIGYGSELQGTHSVHGSPLKPEDCVHVK.K	Carbamidomethyl (+57)	K.TTIGYGSELQGTHSVHGSPLKPEDCVHVK.K
291	303	2	1603.8	4	0	26.8	24.3	93.20%	K.TFQVPPEVYAYYK.E		K.TFQVPPEVYAYYK.E
522	531	2	1057.62	3.4	0	25.9	18.9	92.00%	D.STPSILALTR.Q		R.AMPNINCWRPADGNETSAAYYSALTSDSTPSILALTR.Q
30	49	3	1972.01	1.5	0	55.8	22.3	95.00%	K.SGHPGAPMGLAPAAHVLFSR.I		K.SGHPGAPMGLAPAAHVLFSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
27	HSP75_SCHPO	30.18%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	173	2	1168.66	5	1	34.3	18.9	95.00%	K.DAGAIAGLNVLR.I		K.DAGAIAGLNVLR.I
174	188	2	1530.8	2.3	1	48.1	22.2	95.00%	R.IINEPTAAAIAYGLD.A		R.IINEPTAAAIAYGLDAK.S
501	517	2	1779.92	3.1	0	63.6	22.5	95.00%	R.SAHIEITNSVGHLSSTK.I		R.SAHIEITNSVGHLSSTK.I
451	472	2	2468.2	5.8	0	62.2	24.8	95.00%	R.VNCAENEPLGEFQLTGIPPMPR.G	Carbamidomethyl (+57)	R.VNCAENEPLGEFQLTGIPPMPR.G

437	450	2	1638.8	2.3	0	48.1	24.5	95.00%	D.NQTTVTFPVYQGER.V		R.TFTTVADNQTTVTFPVYQGER.V
144	157	2	1552.8	4.6	1	33.7	23	95.00%	K.AVITVPAYFSDSQR.A		K.AVITVPAYFSDSQR.A
115	128	2	1565.81	1.4	0	60	22.4	95.00%	K.QFTAQEISAMVLTK.M		K.QFTAQEISAMVLTK.M
543	564	2	2513.21	3.3	0	64.4	25	95.00%	K.SQLESYISNIETTISEPNVMMK.L		K.SQLESYISNIETTISEPNVMMK.L
174	190	2	1729.93	3.9	1	82.9	19.8	95.00%	R.IINEPTAAAIAYGLDAK.S		R.IINEPTAAAIAYGLDAK.S
288	301	2	1482.73	1.3	1	91.2	25	95.00%	D.SLSNGIDFSSSITR.A		R.ALSSVTQTTVEVDSLSNGIDFSSSITR.A
39	51	2	1484.72	4.2	0	50.9	25.5	95.00%	R.TTPSFVAFTETER.L		R.TTPSFVAFTETER.L
114	128	2	1693.91	2.8	1	85.5	19.7	95.00%	K.KQFTAQEISAMVLTK.M		K.KQFTAQEISAMVLTK.M
430	450	2	2374.16	5.6	1	61.9	24.3	95.00%	R.TFTTVADNQTTVTFPVYQGER.V		R.TFTTVADNQTTVTFPVYQGER.V
96	113	2	1987.03	4.2	1	58.5	20.8	95.00%	K.VIDNNGIPTIEVNYLGEK.K		K.VIDNNGIPTIEVNYLGEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
28	G6PI_SCHPO	32.73%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
217	228	2	1343.61	5.2	0	37.3	25.9	95.00%	K.TFTTAETCTNAK.S	Carbamidomethyl (+57)	K.TFTTAETCTNAK.S
206	216	2	1218.69	2.4	0	60	18.6	95.00%	D.PETTLFLIASK.T		K.CDPETTLFLIASK.T
372	382	2	1171.52	5.1	1	67.7	25.4	95.00%	R.SGDMVNYTTGK.I		R.SGDMVNYTTGK.I
406	422	2	1903.01	2.1	1	27	20.6	93.60%	K.LIPADFLIPIESHNPID.N		K.LIPADFLIPIESHNPIDNNK.H
464	477	2	1502.83	4	0	36.9	18.9	95.00%	K.TFVGNRPSNSIIAK.K		K.TFVGNRPSNSIIAK.K
63	75	2	1499.85	3.9	0	37.5	16.9	95.00%	K.NLITEETVELLVK.L		K.NLITEETVELLVK.L
42	53	2	1432.65	2	2	32.3	26.3	95.00%	K.FSFTFNGLKEED.G		K.FSFTFNGLKEEDGPILFDFSK.N
2	24	2	2548.27	3.8	0	60.7	22.8	95.00%	M.SFSLASTLPAWQAVQTHYESVGK.H	Acetyl (+42)	-.MSFSLASTLPAWQAVQTHYESVGK.H
118	128	2	1170.59	4.1	1	35.5	22.8	95.00%	K.VNGQDVMPGVR.K		K.VNGQDVMPGVR.K
204	216	2	1493.75	4.3	1	51.5	24.3	95.00%	K.CDPETTLFLIASK.T	Carbamidomethyl (+57)	K.CDPETTLFLIASK.T
521	531	2	1186.62	1.8	2	26.8	22.4	93.30%	K.NVLAQLETKGD.V		K.NVLAQLETKGDVENHDSSTNGLINLFK.N
429	445	2	1870.94	4.8	0	69.7	24.3	95.00%	R.MLFSNFAAQTEALMLGK.T		R.MLFSNFAAQTEALMLGK.T
353	367	2	1711.83	4.2	0	71.8	24.8	95.00%	R.FPAYLQQLSMESNGK.A		R.FPAYLQQLSMESNGK.A
537	547	2	1192.65	2	0	31.6	20	95.00%	D.SSTNGLINLFK.N		K.GDVENHDSSTNGLINLFK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
29	TSA1_SCHPO	45.83%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	147	2	1224.69	4.4	1	43.5	18.1	95.00%	R.QITINDLPVGR.S		R.QITINDLPVGR.S
155	175	3	2525.19	2.2	1	43.3	25.6	95.00%	R.LLDAFQFVEEHGEVCPANWHK.G	Carbamidomethyl (+57)	R.LLDAFQFVEEHGEVCPANWHK.G
158	175	3	2183.99	1.8	0	27.2	27.2	95.00%	D.AFQFVEEHGEVCPANWHK.G	Carbamidomethyl (+57)	R.LLDAFQFVEEHGEVCPANWHK.G
125	132	2	901.53	4.7	1	35.7	20.3	95.00%	R.GLFLIDPK.G		R.GLFLIDPK.G
66	88	2	2576.29	0.89	1	97.3	23.4	95.00%	R.NAQVILTSTDSEYSHLAFINTPR.K		R.NAQVILTSTDSEYSHLAFINTPR.K
14	26	2	1333.69	3.6	0	40.1	22.9	95.00%	K.GTAVVNGAFEEIK.L		K.GTAVVNGAFEEIK.L
76	88	2	1533.76	0.96	0	58.3	24.6	95.00%	D.SEYSHLAFINTPR.K		R.NAQVILTSTDSEYSHLAFINTPR.K
2	13	2	1341.74	4.1	1	36.9	20.8	95.00%	M.SLQIGKPAPDFK.G	Acetyl (+42)	-.MSLQIGKPAPDFK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
30	GPD1_SCHPO	42.34%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
222	232	2	954.59	2.2	0	37.6	16.4	95.00%	D.VAGVALGGALK.N		R.EQIAAVFDRPYFSVVSVDDVAGVALGGALK.N
164	182	2	1962	2.4	0	70.2	22.6	95.00%	K.LGIYCGVLSGANVANEVAR.E	Carbamidomethyl (+57)	K.LGIYCGVLSGANVANEVAR.E
2	20	2	1989.98	0.66	1	99.5	24.1	95.00%	M.SGYGQQGVSAANIDSIRPK.K	Acetyl (+42)/ Deamidation (+1)	-.MSGYGQQGVSAANIDSIRPK.K
87	104	2	2008.06	5	1	48.8	20.1	95.00%	K.YLPGIECPPNVIAVPDVR.E	Carbamidomethyl (+57)	K.YLPGIECPPNVIAVPDVR.E

310	331	3	2285.25	1.5	1	28.8	16	95.00%	K.SLETLEKELLGGQLLQGAATSK.D		K.SLETLEKELLGGQLLQGAATSK.D
277	296	2	2153	2.6	1	93.7	26.1	95.00%	R.TMVEQSCGIADLVTSCLGGR.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.TMVEQSCGIADLVTSCLGGR.N
183	202	2	2362.1	3.9	1	116	26.4	95.00%	R.EQFCETTIGFNPPNEVDIPR.E	Carbamidomethyl (+57)	R.EQFCETTIGFNPPNEVDIPR.E
73	86	2	1656.85	2.8	1	62.4	23.2	95.00%	R.KLTEVFNEAHENVK.Y		R.KLTEVFNEAHENVK.Y
74	86	2	1528.76	4.4	0	69.8	24.9	95.00%	K.LTEVFNEAHENVK.Y		K.LTEVFNEAHENVK.Y
125	144	3	2172.13	2.1	1	39.5	21.9	95.00%	R.VCDQMVGLIRPGAVGISCIK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VCDQMVGLIRPGAVGISCIK.G
317	331	2	1484.83	3.6	0	57.3	19.2	95.00%	K.ELLGGQLLQGAATSK.D		K.ELLGGQLLQGAATSK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
31	HSP60_SCHPO	27.15%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
112	128	2	1705.86	4.1	1	84.3	24	95.00%	K.TNEVAGDGTTTATVLTR.A		K.TNEVAGDGTTTATVLTR.A
137	148	2	1316.6	4	1	27.4	26.3	92.20%	R.NVAAGCNPMDLR.R	Carbamidomethyl (+57)	R.NVAAGCNPMDLR.R
437	453	2	1588.85	1.9	0	37.3	21.6	95.00%	K.AAVSEGVLPGAGTSFVK.A		K.AAVSEGVLPGAGTSFVK.A
244	256	2	1529.84	4	0	44.5	19.2	95.00%	K.VEFENPLILLSEK.K		K.VEFENPLILLSEK.K
478	500	3	2377.34	1	0	28.1	14.8	95.00%	K.AITRPAQTILENAGLEGNLIVGK.L		K.AITRPAQTILENAGLEGNLIVGK.L
241	256	2	1873.03	4.6	1	56.5	17.4	95.00%	K.SQKVEFENPLILLSEK.K		K.SQKVEFENPLILLSEK.K
68	79	2	1313.7	4.3	1	39.3	21.4	95.00%	R.NVLIDQPFGSPK.I		R.NVLIDQPFGSPK.I
276	284	2	1024.59	2.1	1	27.5	17.2	94.20%	R.RPLVIIAED.V		R.RPLVIIAEDVDGEALAACILNK.L
387	396	2	1249.62	3.3	1	31.2	24.4	95.00%	D.PNLTEYEKEK.L		R.GVMADPNLTEYEKEK.L
258	275	2	1937.07	4.4	1	74.7	17.7	95.00%	K.VSAVQDILPSLELAAQQR.R		K.VSAVQDILPSLELAAQQR.R
229	240	2	1401.72	4.3	1	35	22.8	95.00%	R.GYISPYFITDVK.S		R.GYISPYFITDVK.S
45	56	2	1215.69	4.9	1	52.6	18.6	95.00%	R.ASLLTGVDTLAR.A		R.ASLLTGVDTLAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
32	IPYR_SCHPO	45.67%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
257	280	3	2423.28	2.5	1	21.1	20	90.90%	D.PSVSSTIPPAQELAPAPVDPSVHK.W		K.SDFSLVNVSVTGSVANDPSVSSTIPPAQELAPAPVDPSVHK.W
257	275	2	1874.97	1.6	1	25.5	22.5	91.20%	D.PSVSSTIPPAQELAPAPVD.P		K.SDFSLVNVSVTGSVANDPSVSSTIPPAQELAPAPVDPSVHK.W
186	192	2	922.44	6	0	35.4	25.3	95.00%	R.ATNEWFR.I		R.ATNEWFR.I
84	113	4	3616.64	3.2	1	34.2	25.8	95.00%	R.NCFPHHGYIWNYGAFPQTYEDPNVVHPETK.A	Carbamidomethyl (+57)	R.NCFPHHGYIWNYGAFPQTYEDPNVVHPETK.A
24	42	2	2112.04	4.6	1	50.5	24.5	95.00%	K.NGTPISSWHDIPLYANAEK.T		K.NGTPISSWHDIPLYANAEK.T
8	23	2	1839.93	4.1	1	74	23.1	95.00%	R.EVGALNTLDYQVYVEK.N		R.EVGALNTLDYQVYVEK.N
199	212	2	1556.7	1.5	0	54.6	26.6	95.00%	D.GKPENSFAFSGECK.N	Carbamidomethyl (+57)	K.IPDGKPENSFAFSGECK.N
120	130	2	1257.61	2	1	80.5	25	95.00%	D.PLDVCEIGEAR.G	Carbamidomethyl (+57)	K.GDSDPLDVCEIGEAR.G
43	53	2	1283.73	4	0	66.7	18.6	95.00%	K.TILNMVVEIPR.W		K.TILNMVVEIPR.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
33	PUR9_SCHPO	27.69%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
551	565	2	1519.75	4.1	1	63.8	24.3	95.00%	K.YVAAPGGSVMDQAVR.D		K.YVAAPGGSVMDQAVR.D
122	129	2	827.52	0.94	0	30.7	17.2	95.00%	D.IGGVTLLR.A		R.ETIAKPNVTIPEAVEEIDIGGVTLLR.A
223	244	2	2446.25	3.4	1	45.9	21.1	95.00%	K.VLCGSPGYINLMDALNSWPLVK.E	Carbamidomethyl (+57)	K.VLCGSPGYINLMDALNSWPLVK.E
39	60	2	2231.08	4.2	1	97.7	25.2	95.00%	R.ESGMEVADVSSITNAPEILGGR.V		R.ESGMEVADVSSITNAPEILGGR.V
566	581	2	1881.9	4.3	1	55.8	25.4	95.00%	R.DTANEFNMVFSEIPLR.L		R.DTANEFNMVFSEIPLR.L
47	60	2	1412.77	1.8	0	32.2	21.4	95.00%	D.VSSITNAPEILGGR.V		R.ESGMEVADVSSITNAPEILGGR.V
354	362	2	1152.54	4.8	1	28.8	25.9	94.60%	K.YCVLQMDPK.Y	Carbamidomethyl (+57)	K.YCVLQMDPK.Y
248	259	2	1216.65	4.7	0	30.2	22.4	95.00%	R.ENIGIPAAASFK.H		R.ENIGIPAAASFK.H

104	129	3	2776.53	2.1	1	22.6	14.6	93.50%	R.ETIAKPNVTIPEAVEEIDIGGVTLLR.A		R.ETIAKPNVTIPEAVEEIDIGGVTLLR.A
260	277	2	1745.94	2.2	1	41.4	20.3	95.00%	K.HVSPAGAAVGLPLSDVEK.K		K.HVSPAGAAVGLPLSDVEK.K
201	222	3	2414.15	2	0	32.2	24.8	95.00%	R.YGANPHQSPAQAFMEQGPLPFK.V		R.YGANPHQSPAQAFMEQGPLPFK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
34	PDX1_SCHPO	29.73%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	49	2	1547.75	2.8	0	63.2	25.3	95.00%	R.IAEAAGACAVMALER.V	Carbamidomethyl (+57)/ Oxidation (+16)	R.IAEAAGACAVMALER.V
265	280	2	1628.86	4	0	87.2	21.6	95.00%	K.ILAEVSENLGAAMVGR.S		K.ILAEVSENLGAAMVGR.S
71	83	2	1355.75	4.3	0	66.7	21	95.00%	K.EIQAAVSIPVMAK.V		K.EIQAAVSIPVMAK.V
21	34	2	1457.74	4	1	89.6	23.5	95.00%	K.GGVIMDVVNAEQAR.I		K.GGVIMDVVNAEQAR.I
121	132	3	1383.7	4.4	1	31	24.4	95.00%	K.SKFTVPFVCGSR.N	Carbamidomethyl (+57)	K.SKFTVPFVCGSR.N
140	149	2	1102.6	4.8	1	28.6	22.3	95.00%	R.RISEGAAMIR.T		R.RISEGAAMIR.T
13	20	2	830.47	4.2	0	38.8	20.2	95.00%	K.AGLAQMLK.G		K.AGLAQMLK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
35	HXK2_SCHPO	22.86%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
12	24	2	1581.77	4.1	1	62.3	24.9	95.00%	K.LVNDFEYPTESLR.E		K.LVNDFEYPTESLR.E
435	449	2	1414.76	2.4	0	41.4	21.5	95.00%	D.GSGIGAALCALQAVK.E	Carbamidomethyl (+57)	K.DGSGIGAALCALQAVK.E
434	449	2	1529.79	4.8	1	96.2	22.6	95.00%	K.DGSGIGAALCALQAVK.E	Carbamidomethyl (+57)	K.DGSGIGAALCALQAVK.E
76	86	2	1287.67	3.9	1	30.3	24.2	95.00%	R.VCWIQLLGDGK.Y	Carbamidomethyl (+57)	R.VCWIQLLGDGK.Y
286	296	2	1240.63	5.9	0	25.6	22.5	91.40%	R.VGGMYLGELFR.R		R.VGGMYLGELFR.R
64	75	2	1322.7	1.9	1	36.1	21	95.00%	D.FLALDFGGTNLR.V		K.NGEVLAMAPAFISTLPTGAETGDFLALDFGGTNLR.V
374	388	2	1564.83	4.1	0	56.1	21.3	95.00%	R.MSAVPIASLYLSTGR.A		R.MSAVPIASLYLSTGR.A
1	11	2	1334.67	4.1	1	29.9	24.5	95.00%	-.MEANFQQAVKK.L	Acetyl (+42)	-.MEANFQQAVKK.L
399	413	3	1798.89	1.5	1	29.3	24.3	95.00%	D.GSLVEHYPHFVDMLR.E		K.SDVGVDGSLVEHYPHFVDMLR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
36	LYS9_SCHPO	30.44%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
177	183	2	740.49	4.7	0	33.1	14.9	95.00%	R.GVLLALR.N		R.GVLLALR.N
412	426	2	1524.8	1.3	1	40	21.5	95.00%	D.GVINTPGVLAPNDMK.L		K.LVGVPCGVATQQILDGVINTPGVLAPNDMK.L
38	49	2	1259.66	4.1	0	41.7	22.6	95.00%	K.AEAFINGIPNSK.A		K.AEAFINGIPNSK.A
149	170	2	2385.11	5.2	1	60.2	26.6	95.00%	K.SFLSYCGGLPAPEDSNNPLGYK.F	Carbamidomethyl (+57)	K.SFLSYCGGLPAPEDSNNPLGYK.F
2	22	3	2269.25	3.1	0	39	16	95.00%	M.PSILLLGSGFVAHPTLEYLSR.R		-.MPSILLLGSGFVAHPTLEYLSR.R
379	396	2	1989.93	4.3	1	76.6	26.4	95.00%	R.TCTLLDYGVPNGYTSMAK.L	Carbamidomethyl (+57)	R.TCTLLDYGVPNGYTSMAK.L
126	135	2	1125.62	2.8	1	29.3	20.3	95.00%	D.PGIDHLYAIK.T		K.AGSICMNEIGVDPGIDHLYAIK.T
104	113	2	1103.56	4	0	29.1	23.4	95.00%	K.MAELEEAAIK.A		K.MAELEEAAIK.A
64	85	3	2488.28	3.3	1	39.1	21.4	95.00%	K.AVSEHDLTISLIPYTYHATVMK.A		K.AVSEHDLTISLIPYTYHATVMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
37	C1TC_SCHPO	14.30%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
689	707	3	1923.15	3.9	1	37.5	6.99	95.00%	R.TSGLKPDAIVIVATVQALK.L		R.TSGLKPDAIVIVATVQALK.L
765	783	2	1913.94	1.2	2	39.7	24.3	95.00%	D.SPNEISAIREEALAAGATD.A		K.FSSDSPNEISAIREEALAAGATDAVDSNHWAEGGK.G
2	12	2	1184.68	4.9	0	55.8	19.1	95.00%	M.ALLLEGTSLAR.K	Acetyl (+42)	-.MALLLEGTSLAR.K
122	130	2	1024.47	3.8	0	30	25.4	95.00%	D.GFCETNLGK.L	Carbamidomethyl (+57)	K.DVDGFCETNLGK.L
497	509	3	1601.76	2.4	1	21.6	25.9	90.00%	D.KTNPEELTEEEQR.K		K.LGIDKTNPEELTEEEQR.K

536	546	2	1228.67	4.9	1	27.4	22	94.00%	R.KITIGENPTEK.G		R.KITIGENPTEK.G
324	336	2	1299.71	5.1	1	59.2	21.1	95.00%	K.NIGDLASEIGIAK.S		K.NIGDLASEIGIAK.S
381	396	2	1629.9	3.4	1	106	18.5	95.00%	K.STLTAGLVQALSNLDK.L		K.STLTAGLVQALSNLDK.L
349	356	2	983.58	5.3	0	46.2	18.5	95.00%	K.VNLEILQR.L		K.VNLEILQR.L
835	849	2	1592.78	4.3	1	53.3	25.6	95.00%	K.EMYGADGIELSPLAK.E		K.EMYGADGIELSPLAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
38	PUT2_SCHPO	27.01%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
388	405	2	1773.91	3.9	1	102	23.5	95.00%	K.VLESAASDSEIEVLAGGK.A		K.VLESAASDSEIEVLAGGK.A
362	384	3	2429.26	9.7	1	29.5	20.7	95.00%	K.VGAPLTDFANFVGPVIHQASFNK.L	Deamidation (+1)	K.VGAPLTDFANFVGPVIHQASFNK.L
82	92	2	1222.64	4.6	1	32.1	22.7	95.00%	K.HVEDAIEAALR.G		K.HVEDAIEAALR.G
254	274	3	2393.15	4.4	0	52.3	25.4	95.00%	K.VCFNHPEFAGLHFTGSTAVFR.S	Carbamidomethyl (+57)	K.VCFNHPEFAGLHFTGSTAVFR.S
275	288	2	1444.74	4.6	0	37.7	23.9	95.00%	R.SLWGTIGENVANGK.Y		R.SLWGTIGENVANGK.Y
233	253	2	2068.09	4.4	1	68.9	20.3	95.00%	R.EAGLPAGALQFIPGDAVEVSK.V		R.EAGLPAGALQFIPGDAVEVSK.V
409	422	2	1551.82	1.8	0	50.7	21.6	95.00%	D.SEGFFVEPTVLLSK.N		K.ADDSEGFFVEPTVLLSK.N
495	509	2	1504.71	3.5	0	49.3	25.6	95.00%	K.CTGAVVGEQPFGGAR.A	Carbamidomethyl (+57)	K.CTGAVVGEQPFGGAR.A
484	494	2	1225.58	4.6	1	28	25.4	94.20%	R.NAAGNFYINDK.C		R.NAAGNFYINDK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
39	SERA_SCHPO	27.04%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
275	284	2	1108.56	4.3	0	25.6	24.4	91.40%	K.EGSYLINASR.G		K.EGSYLINASR.G
58	74	2	1883.04	2.1	2	76.6	16.8	95.00%	K.ILLLENVNQSALSNLKD.E		K.ILLLENVNQSALSNLKDEGYQVEFLK.T
367	385	2	2078.05	3.9	0	76.6	23.3	95.00%	R.YINEGNSIGAVNFPEVSLR.S		R.YINEGNSIGAVNFPEVSLR.S
410	421	2	1468.77	4	1	31.9	21.3	95.00%	R.QVNELFIDHNIK.S		R.QVNELFIDHNIK.S
302	319	2	1728.88	4.5	1	48	23	95.00%	K.IAGAAIDVYPSEPAGNGK.D		K.IAGAAIDVYPSEPAGNGK.D
47	57	3	1247.68	3.8	1	25.6	20.9	95.00%	R.TLKPFASEDIK.I		R.TLKPFASEDIK.I
248	262	2	1596.82	4.1	1	50.8	22.4	95.00%	R.ADFVSLHVPASPETK.N		R.ADFVSLHVPASPETK.N
142	154	2	1394.7	4.8	0	57.8	23.5	95.00%	R.GIAVFNSPYANSR.S		R.GIAVFNSPYANSR.S
237	247	3	1291.73	4.7	0	20.7	16.7	90.10%	K.QLSSLPELLHR.A		K.QLSSLPELLHR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
40	PPA1_SCHPO	24.28%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
414	427	2	1687.77	2.1	0	38.7	26.6	95.00%	D.GMCELYAYLNSPVR.V	Oxidation (+16)/ Carbamidomethyl (+57)	R.HLVNEEVFPLSDCGFGPSNTSDGMCELYAYLNSPVR.V
332	365	4	3754.84	3.4	1	17.9	22.1	93.50%	D.ANIIPVETALGFFTDNTPENPLPTSYQVHSHSMK.A		R.SVENNTQQVFFAFTHDANIIPVETALGFFTDNTPENPLPTSYQVHSHSMK.A
40	59	3	2404.12	1.5	1	68.9	26.1	95.00%	R.SPYHKPYFYGPSIDFPTTCK.I	Carbamidomethyl (+57)	R.SPYHKPYFYGPSIDFPTTCK.I
73	92	2	2046.99	3	1	106	24.8	95.00%	R.NPTGGNAAFDAVGIANFQQR.L		R.NPTGGNAAFDAVGIANFQQR.L
366	387	2	2501.19	3.5	1	42.6	25.4	95.00%	K.ASEFVPFAGNLITELFQCEDSK.Y	Carbamidomethyl (+57)	K.ASEFVPFAGNLITELFQCEDSK.Y
83	92	2	1102.59	2.8	0	44	23.1	95.00%	D.AVGIANFQQR.L		R.NPTGGNAAFDAVGIANFQQR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
41	CYPH_SCHPO	48.77%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
124	138	2	1644.83	4.4	1	86.7	24.7	95.00%	K.HVVFGEVTEGMDVVK.K		K.HVVFGEVTEGMDVVK.K
90	123	3	3611.83	4	1	56	19.8	95.00%	K.HNKPGLLSMANAGPNTNGSQFFITTVVTPWLDGK.H		K.HNKPGLLSMANAGPNTNGSQFFITTVVTPWLDGK.H
2	17	2	1835.87	3.9	1	50	25.9	95.00%	M.SNCFFDVIANGQPLGR.I	Acetyl (+42)/ Carbamidomethyl (+57)	-.MSNCFFDVIANGQPLGR.I
8	17	2	1023.59	2.5	0	27.5	15.4	94.20%	D.VIANGQPLGR.I		-.MSNCFFDVIANGQPLGR.I

54	67	2	1607.82	4.3	1	67.2	23.4	95.00%	R.VIPQFMLQGGDFTR.G		R.VIPQFMLQGGDFTR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
42	RS18_SCHPO	36.84%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	78	2	1386.79	4	0	45.2	17	95.00%	R.IVTIIQNPSQFK.I		R.IVTIIQNPSQFK.I
2	14	2	1578.86	2.1	1	27.7	20	94.40%	M.SLVVPDNFQHILR.L	Acetyl (+42)	-.MSLVVPDNFQHILR.L
56	66	2	1246.61	4	0	41.5	24.8	95.00%	R.AGELTTEELER.I		R.AGELTTEELER.I
79	86	2	1031.56	6	0	52.6	22.1	95.00%	K.IPSWFLNR.Q		K.IPSWFLNR.Q
95	106	2	1334.69	4.9	1	24.9	22.6	90.10%	K.SFQLLANNVDSK.L		K.SFQLLANNVDSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
43	OAT_SCHPO	25.34%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
386	398	3	1374.81	1.5	0	27.1	15.4	95.00%	R.GVLAKPTHGNIIR.F		R.GVLAKPTHGNIIR.F
70	80	2	1268.71	4.2	0	28.4	18.1	95.00%	K.IIEALVEQAQR.V		K.IIEALVEQAQR.V
2	37	4	4216	4.3	0	58.2	22.8	95.00%	M.SAESLLHNTFSTEQIEVLENEYAAHNYHPLPVCFSK.A	Acetyl (+42)/ Carbamidomethyl (+57)	-.MSAESLLHNTFSTEQIEVLENEYAAHNYHPLPVCFSK.A
276	291	2	1561.85	4	0	53	18.6	95.00%	K.AISGGVYPVSAVLSSR.E		K.AISGGVYPVSAVLSSR.E
238	254	2	1838.97	4.4	1	78.8	21.3	95.00%	K.AHNVLFIADEVQTGVAR.T		K.AHNVLFIADEVQTGVAR.T
258	275	3	2051.1	4.3	1	30.2	19.6	95.00%	K.MLCIEHSNVKPDVVILGK.A	Carbamidomethyl (+57)	K.MLCIEHSNVKPDVVILGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
44	MET3_SCHPO	17.96%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
364	382	2	2159.15	2.7	0	56.8	19.6	95.00%	R.VGANIPEWFSYPEVVAILR.Q		R.VGANIPEWFSYPEVVAILR.Q
427	440	2	1651.86	4	1	77.5	20.8	95.00%	R.LDAISVFYAQELQR.A		R.LDAISVFYAQELQR.A
83	92	2	1103.55	2.6	1	26.2	23.8	92.40%	D.LNESQADSLK.A		R.LSTGEVFPIPITLDLNESQADSLK.A
350	359	2	1102.6	3.9	0	29.9	20.9	95.00%	R.TLNISGTELR.R		R.TLNISGTELR.R
59	68	2	1233.64	5.6	1	40.5	22.8	95.00%	K.DYLNVVENLR.L		K.DYLNVVENLR.L
254	262	2	1012.62	5.1	0	33.5	14.1	95.00%	K.LSLLPLAMR.M		K.LSLLPLAMR.M
14	29	2	1808.97	2.9	1	47.5	19.4	95.00%	D.APLREQLEQEATSLPK.I		R.DAPLREQLEQEATSLPK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
45	YL8C_SCHPO	21.12%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
93	112	3	2269.21	3.4	1	35.2	18.3	95.00%	K.IVYADHLKPEVVMEVVEATK.G		K.IVYADHLKPEVVMEVVEATK.G
47	60	2	1575.87	2.5	1	38.9	18.9	95.00%	R.EKYPNFPIVLATGK.Q		R.EKYPNFPIVLATGK.Q
217	232	2	1745.96	4.4	0	53	18.2	95.00%	K.GTALQYITSNILPEVK.N		K.GTALQYITSNILPEVK.N
275	288	2	1456.72	1.8	0	84.6	24.9	95.00%	R.VGNEEGAVGEVLER.I		R.VGNEEGAVGEVLER.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
46	RL4A_SCHPO	27.55%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
122	140	2	1845.04	4.3	0	48.1	14.8	95.00%	R.YAISSAVAASGVPSLLLAR.G		R.YAISSAVAASGVPSLLLAR.G
2	13	2	1304.71	4.5	0	25.5	21.1	91.30%	M.AAARPTVSIYSK.D	Acetyl (+42)	-.MAAARPTVSIYSK.D
15	29	2	1580.85	2	0	39.5	19.8	95.00%	D.GSVSSETIALPFVFK.A		K.DGSVSSETIALPFVFK.A
235	248	3	1457.85	2.5	0	30.8	14.8	95.00%	R.LNLLQLAPGGHLGR.F		R.LNLLQLAPGGHLGR.F
292	303	2	1357.75	4	1	43.8	19.5	95.00%	R.LINSDEIQSIVK.A		R.LINSDEIQSIVK.A
14	29	2	1695.88	4.2	1	38.3	22	95.00%	K.DGSVSSETIALPFVFK.A		K.DGSVSSETIALPFVFK.A
276	291	2	1864.94	1.8	1	39.8	23.9	95.00%	K.NYFLPENIISNADVTR.L		K.NYFLPENIISNADVTR.L
87	97	2	1197.51	4.4	0	32.6	26.5	95.00%	R.SGQAAFGNMCR.S	Carbamidomethyl (+57)	R.SGQAAFGNMCR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
47	THIL_SCHPO	25.06%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

288	301	3	1542.85	3.8	1	24.7	20	95.00%	D.PERFTTSPSLAIPK.A		K.IIGWGEAAQDPERFTTSPSLAIPK.A
196	210	2	1667.89	1.4	0	29.6	20.2	95.00%	K.AFEQEIVPVEVPVGR.G		K.AFEQEIVPVEVPVGR.G
291	301	2	1160.65	4.8	0	33.2	20	95.00%	R.FTTSPSLAIPK.A		R.FTTSPSLAIPK.A
14	30	2	1654.81	2.3	0	83.9	24.5	95.00%	R.TPMGSFGGSFASLPATK.L		R.TPMGSFGGSFASLPATK.L
267	277	3	1194.77	2.2	1	21.9	7.78	92.40%	K.VKELGLKPLAK.I		K.VKELGLKPLAK.I
360	371	2	1405.81	4.5	0	73.2	16.5	95.00%	R.IICTLAYILAQK.D	Carbamidomethyl (+57)	R.IICTLAYILAQK.D
278	290	2	1440.71	4.1	1	44.3	24.4	95.00%	K.IIGWGEAAQDPER.F		K.IIGWGEAAQDPER.F
340	359	3	1865.93	4.8	0	31	24.1	95.00%	R.VNINGGGVAMGHPLGSSGSR.I		R.VNINGGGVAMGHPLGSSGSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
48	HSP7F_SCHPO	12.78%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
174	189	2	1665.84	2.7	1	88.3	23.5	95.00%	R.LMNDNAAAALTYGITK.T		R.LMNDNAAAALTYGITK.T
581	591	2	1385.65	4	1	31.1	26.1	95.00%	K.NALEEYIYDTR.A		K.NALEEYIYDTR.A
5	16	2	1249.64	6.5	1	29.4	23.5	95.00%	R.TNVVGIDFGNSK.T		R.TNVVGIDFGNSK.T
38	48	2	1194.59	3.8	0	34	24	95.00%	R.STPSLVSYGER.S		R.STPSLVSYGER.S
159	173	2	1534.89	2.3	0	57.8	14.8	95.00%	R.ALLEAANIAGLNPLR.L		R.ALLEAANIAGLNPLR.L
96	106	2	1134.6	4	1	31.7	23.2	95.00%	K.LTEVDGFVGAK.V		K.LTEVDGFVGAK.V
419	434	2	1690.85	2.4	0	54.4	24	95.00%	D.SSLEVFSEGNPIPSTK.I		R.EFHVHDVTTYPITFSWEPIPENPEEDSSLEVFSEGNPIPSTK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
49	RAD24_SCHPO	41.11%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
109	120	2	1236.65	4.7	0	29.1	21.9	95.00%	K.HLIPNAASAESK.V		K.HLIPNAASAESK.V
31	44	2	1562.75	4.1	1	82.9	25.3	95.00%	K.SVASTDQELTVEER.N		K.SVASTDQELTVEER.N
97	108	2	1431.77	2.1	1	35.3	21.6	95.00%	D.TICQDILTVLEK.H	Carbamidomethyl (+57)	K.IEQELDTICQDILTVLEK.H
219	227	2	1073.63	2.4	0	41	16.5	95.00%	D.STLIMQLLR.D		K.DSTLIMQLLR.D
237	267	3	2987.31	2.4	0	41.7	27	95.00%	D.AEYSAAAAGGNTEGAQENAPSNAPEGEAEPK.A		R.DNLTLWTSDAEYSAAAAGGNTEGAQENAPSNAPEGEAEPK.A
15	30	3	1896.88	2.3	1	34.6	26.3	95.00%	K.LAEQAERYEGMVENMK.S		K.LAEQAERYEGMVENMK.S
156	172	2	1746.93	2.2	0	80.2	21.1	95.00%	K.AASEIATAELAPTHPIR.L		K.AASEIATAELAPTHPIR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
50	VIPI_SCHPO	34.63%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	68	2	1496.86	4.3	1	41.7	15.9	95.00%	K.TALLLQDALLGQNK.I		K.TALLLQDALLGQNK.I
101	110	2	1087.63	5.8	0	34.3	17.8	95.00%	R.SAIISELLSR.G		R.SAIISELLSR.G
225	254	3	2955.4	2.9	1	65.6	25.4	95.00%	K.NQAEGTASPASSTPTAPAEKEPTAPTTESK.T		K.NQAEGTASPASSTPTAPAEKEPTAPTTESK.T
122	134	2	1410.71	4.2	1	61.1	24.3	95.00%	K.SIQLDQSYGVSSK.F		K.SIQLDQSYGVSSK.F
111	121	2	1260.64	3.7	1	31.8	23.4	95.00%	R.GYHLSDVTLEK.S		R.GYHLSDVTLEK.S
137	147	2	1100.62	4.3	0	27.7	20.7	94.40%	K.GILESALSGVR.S		K.GILESALSGVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
51	FAS2_SCHPO	4.61%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
488	502	3	1650.8	4.5	1	35.5	24.9	95.00%	K.NVNHPTAPSTTIDER.G		K.NVNHPTAPSTTIDER.G
114	146	3	3020.56	3.1	1	35.9	21	95.00%	K.VETAAAAAPAATPAPAPAQTSAPAAALPDEPPK.A		K.VETAAAAAPAATPAPAPAQTSAPAAALPDEPPK.A
517	527	2	1319.7	5.4	1	32	22.4	95.00%	R.KLTHYVTEMAK.G		R.KLTHYVTEMAK.G
1393	1401	2	994.61	4.5	1	27.6	13.4	94.30%	K.TPLPIVDLK.F		K.TPLPIVDLK.F
28	44	2	1939.01	4.4	1	67.5	21.2	95.00%	R.WIETQDVILSPPVSAER.I		R.WIETQDVILSPPVSAER.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
52	ADH_SCHPO	27.14%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
304	313	2	1165.6	2.2	0	29.8	23.2	95.00%	D.SIEALEYVSR.G		R.IDSIEALEYVSR.G

109	125	2	1931.9	3.4	1	41.4	26.4	95.00%	K.AEETICPHIQLSGYTVD.G	Carbamidomethyl (+57)	K.AEETICPHIQLSGYTVDGTFQHYCIANATHATIIPESVPLEVAAPIMCAGITCYR.A
236	253	2	1681.87	4.1	0	56	21.7	95.00%	K.AATNGGAHGTLVLSTSPK.S	Deamidation (+1)	K.AATNGGAHGTLVLSTSPK.S
254	278	3	2513.21	3.1	0	41.5	25	95.00%	K.SYEQAAGFARPGSTMVTVSMPAGAK.L		K.SYEQAAGFARPGSTMVTVSMPAGAK.L
170	194	3	2506.29	3.6	0	33.6	21.1	95.00%	K.VGPGEWICIPGAGGGLGHLAVQYAK.A	Carbamidomethyl (+57)	K.VGPGEWICIPGAGGGLGHLAVQYAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
53	LEUC_SCHPO	16.36%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
521	539	2	1671.88	2.7	0	95.9	21.6	95.00%	D.GIATNVAGSVSSGSAGIPK.F		K.NYDPSHDVEGDIGLSVDDATDAVTDADGIATNVAGSVSSGSAGIPK.F
633	649	2	2002.01	4.5	1	59.4	24.1	95.00%	R.VIIAPSFADIFFNNCFK.N	Carbamidomethyl (+57)	R.VIIAPSFADIFFNNCFK.N
417	436	3	2355.02	4.1	1	24.9	26.8	94.10%	R.EAGCSMCLGMNPDQLKPYER.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.EAGCSMCLGMNPDQLKPYER.C
36	51	3	1860.96	4.5	0	30.3	22.7	95.00%	R.HLIHEVTSPQAFEGLR.T	N-Formyl (+28)	R.HLIHEVTSPQAFEGLR.T
603	619	3	1826.85	2.3	1	42	26.4	95.00%	R.HATVLVAHDNFGCGSSR.E	Carbamidomethyl (+57)	R.HATVLVAHDNFGCGSSR.E
477	493	2	1810.88	4.1	1	36.5	25.2	95.00%	R.EFFGDVSNGSPSIITNK.N		R.EFFGDVSNGSPSIITNK.N
650	667	2	2027	4	1	40.9	24.8	95.00%	K.NGMLPIPTPIEQVNDMMK.A		K.NGMLPIPTPIEQVNDMMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
54	GBLP_SCHPO	31.85%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
295	308	2	1606.81	1.8	1	50.7	23.6	95.00%	D.GQTLFSGWTDNLIR.V		K.SSEPECISLTWSPDGQTLFSGWTDNLIR.V
186	212	3	2736.26	2.6	1	43.2	26.8	95.00%	R.TSHYGHTGYVSAVTISPDGSLCASGGR.D	Carbamidomethyl (+57)	R.TSHYGHTGYVSAVTISPDGSLCASGGR.D
234	245	2	1314.71	3.1	0	32.5	21.9	95.00%	K.ANINALVFSPNR.Y		K.ANINALVFSPNR.Y
176	185	2	1264.65	5.4	1	30.1	23.2	95.00%	K.VWDLETFSLR.T		K.VWDLETFSLR.T
39	47	2	1112.68	5.9	0	27.8	14.1	94.50%	K.SIILWNLVR.D		K.SIILWNLVR.D
9	36	3	2894.45	2.9	1	38.1	22.8	95.00%	R.ATLEGHSGWVTSLSTAPENPDILLSGSR.D		R.ATLEGHSGWVTSLSTAPENPDILLSGSR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
55	CYSD_SCHPO	31.93%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	26	3	2735.28	1.6	1	52.6	26.3	95.00%	M.PVESEHFETLQLHAGQEPDAATSSR.A		-.MPVESEHFETLQLHAGQEPDAATSSR.A
47	59	2	1541.79	1.6	0	31.1	23.2	95.00%	R.LFGLQEPGYIYSR.M		R.LFGLQEPGYIYSR.M
27	39	2	1486.79	2.3	0	63.8	22	95.00%	R.AVPIYATTSYVFR.D		R.AVPIYATTSYVFR.D
72	100	3	2787.49	3.3	0	49.9	17.9	95.00%	R.IAALEHGAAAIATSSGTSALFMALTTLAK.A		R.IAALEHGAAAIATSSGTSALFMALTTLAK.A
366	377	2	1185.64	4.4	1	34.5	21.5	95.00%	K.LASQLANVGDAK.T		K.LASQLANVGDAK.T
151	169	2	2199.04	3.1	1	59.5	26	95.00%	K.AVYVESIGNPMYNVPDFER.I		K.AVYVESIGNPMYNVPDFER.I
378	403	3	2798.48	2.5	1	42.6	18.6	95.00%	K.TLVIAPAYTTHLQLTDEEQISAGVTK.D		K.TLVIAPAYTTHLQLTDEEQISAGVTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
56	HOSM_SCHPO	20.33%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	204	2	1315.66	4	1	40.8	24.8	95.00%	R.VGIADTVGCATPR.Q	Carbamidomethyl (+57)	R.VGIADTVGCATPR.Q
2	31	3	3218.5	4.8	1	47.5	24.7	95.00%	M.SVSEANGTETIKPPMNGNPYGPNPSDFLSR.V	Acetyl (+42)/ Deamidation (+1)	-.MSVSEANGTETIKPPMNGNPYGPNPSDFLSR.V

72	85	2	1578.79	2	0	50.3	24.9	95.00%	D.YIELTSPVASEQSR.Q		K.ALDNFGVDYIELTSPVASEQSR.Q
324	339	2	1772.92	1.7	1	26.3	22.1	92.60%	K.AILANPSTYEILKPED.F		K.AILANPSTYEILKPEDFGMSR.Y
32	43	2	1391.75	4.9	0	68.1	21.5	95.00%	R.VNNFSIIESTLR.E		R.VNNFSIIESTLR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
57	CARB_SCHPO	9.66%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
968	975	2	1019.52	4.9	0	24.9	23.5	90.20%	K.VPQFSWTR.L		K.VPQFSWTR.L
932	943	2	1304.72	5.6	1	35.2	20.9	95.00%	K.TLGVNFIDVATR.S		K.TLGVNFIDVATR.S
1056	1070	2	1655.92	2.2	0	35.9	17.2	95.00%	K.LLQPTSAEVVEFPVK.D		K.LLQPTSAEVVEFPVK.D
773	798	3	2736.49	2.9	0	51	15.6	95.00%	K.FANAVGYPVLVRPSYVLSGAAMSVIR.D		K.FANAVGYPVLVRPSYVLSGAAMSVIR.D
418	433	2	1784.89	2.2	1	43.4	24	95.00%	K.TTTANFEPSLDYVVTK.I		K.TTTANFEPSLDYVVTK.I
575	584	2	1057.58	4.7	1	32.1	22	95.00%	K.LVGASELDVR.A		K.LVGASELDVR.A
249	273	3	2529.22	2.7	1	48.7	24.6	95.00%	R.SAYSLGGLGSGFANNKEELQSMAAK.S		R.SAYSLGGLGSGFANNKEELQSMAAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
58	ECM17_SCHPO	4.62%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
493	502	3	1154.69	1.6	1	30.2	14.5	95.00%	D.PELVISELKK.D		K.NSSVSSESLEVLSNWIVSVDNLESPVDPELVISELKK.D
314	325	2	1337.79	2.1	0	51.5	13.6	95.00%	R.LTVLEPITSLPR.K		R.LTVLEPITSLPR.K
77	90	2	1484.78	2.6	0	37.3	22.5	95.00%	D.AILAEEEVASTQPK.Q		K.SHADPFAHIADAILAEEEVASTQPK.Q
801	810	2	1058.57	5.4	1	27.5	23.1	94.10%	K.GADLNLSELK.Y		K.GADLNLSELK.Y
1031	1045	2	1687.72	2.6	1	36	26.3	95.00%	R.NVTCSSTPNNETIHD.Q	Carbamidomethyl (+57)	R.NVTCSSTPNNETIHDQLFAVSK.Q
70	90	3	2236.14	1.7	1	24.3	22.5	95.00%	D.PFAHIADAILAEEEVASTQPK.Q		K.SHADPFAHIADAILAEEEVASTQPK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
59	RS7_SCHPO	25.13%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	140	3	2393.33	2.1	1	51.3	14	95.00%	R.TLTAVHNAILEDIVFPTEIIGK.R		R.TLTAVHNAILEDIVFPTEIIGK.R
59	70	2	1322.84	4	0	46.5	9.54	95.00%	K.AIVVFVPQPLLK.A		K.AIVVFVPQPLLK.A
20	34	2	1724.87	2.1	1	81.6	24.4	95.00%	D.LLVAQCLYDLESSSK.D	Carbamidomethyl (+57)	R.SSSQPTETDLLVAQCLYDLESSSK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
60	HSP7M_SCHPO	12.76%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
204	215	2	1124.67	4.6	0	48.3	15.3	95.00%	K.AAGAIAGLNVLR.V		K.AAGAIAGLNVLR.V
105	118	2	1578.81	4.5	0	81.4	23.3	95.00%	R.QAVINPENTFFATK.R		R.QAVINPENTFFATK.R
185	199	2	1679.83	4.3	1	62.1	24.4	95.00%	K.NAVVTVPAYFNDSQR.Q		K.NAVVTVPAYFNDSQR.Q
496	510	2	1538.89	4.2	0	77.2	14.9	95.00%	K.LIGNFQLTGIAPAPK.G		K.LIGNFQLTGIAPAPK.G
157	170	2	1496.8	5.1	0	59.3	21.8	95.00%	K.TYSPSQIGGFILSK.M		K.TYSPSQIGGFILSK.M
216	231	2	1630.86	3.8	1	78.5	21.6	95.00%	R.VVNEPTAAALAYGLDK.K		R.VVNEPTAAALAYGLDK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
61	RL8_SCHPO	19.69%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
24	32	2	1084.62	4.7	0	29.3	20.4	95.00%	K.NPLFVSRPR.S		K.NPLFVSRPR.S
33	43	2	1188.62	4.1	1	26.8	23.1	93.20%	R.SFGIGQDIQPK.R		R.SFGIGQDIQPK.R
109	120	2	1171.61	4.7	0	55.2	23.5	95.00%	R.LVAEAEAVANGK.S	Deamidation (+1)	R.LVAEAEAVANGK.S
134	146	2	1425.8	2.1	0	58.9	17.6	95.00%	K.YGLNHVVALIEAK.K		K.YGLNHVVALIEAK.K
52	57	2	862.44	5.9	0	26.5	23.1	92.90%	K.WPEYIR.L		K.WPEYIR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
62	UGPA1_SCHPO	12.45%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	10	2	1166.63	4.6	1	24.9	20.4	90.10%	-.MDLAPRPLGR.Q	Acetyl (+42)	-.MDLAPRPLGR.Q
185	194	2	1205.65	4.7	1	32.1	21.4	95.00%	K.IDILTFNQSR.Y		K.IDILTFNQSR.Y
299	314	3	1876.01	2.3	0	33.2	18.9	95.00%	R.LLEIAQVPPQHVEEFK.S		R.LLEIAQVPPQHVEEFK.S
115	129	2	1460.72	4.2	0	48.3	24.8	95.00%	K.LNGGLGTTMGCVGPK.S	Carbamidomethyl (+57)	K.LNGGLGTTMGCVGPK.S
35	46	2	1339.68	2.5	2	43.8	23.5	95.00%	K.NELNHLASTVKD.P		K.NELNHLASTVKDPLAK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
63	YHY6_SCHPO	13.83%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
678	698	2	2257.13	4.5	1	51.2	23.8	95.00%	K.SLCIPLEQPSGEDAIIEGTTK.C	Carbamidomethyl (+57)	K.SLCIPLEQPSGEDAIIEGTTK.C
161	187	3	2608.39	2.9	1	26.8	18.5	95.00%	K.SVGVNPIIVDFSAPGSATAPSKPAAQK.K		K.SVGVNPIIVDFSAPGSATAPSKPAAQK.K
298	323	3	2901.42	3	1	27.8	23.9	95.00%	R.AGTSELDEPIAIRPTSETVMYPYYAK.W		R.AGTSELDEPIAIRPTSETVMYPYYAK.W
450	462	3	1364.71	3.4	0	39.2	23.1	95.00%	D.PNAEIGPTGERPK.L		K.MFNIVVEDPNAEIGPTGERPK.L
387	398	2	1343.81	4.3	1	30.5	10.4	95.00%	R.IYTDLLAVPVIK.G		R.IYTDLLAVPVIK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
64	BCA1_SCHPO	22.63%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
315	331	2	1670.97	4.2	0	59.5	11.5	95.00%	R.LLEVFGAGTAALVSPVK.A		R.LLEVFGAGTAALVSPVK.A
122	130	2	1010.58	2.4	0	68.3	17.6	95.00%	D.PAELAEIIR.K		R.ISLPSFDPAELAEIIR.K
37	49	3	1581.74	4.5	1	25.4	25.9	95.00%	K.FGENFTDHMLIMK.W		K.FGENFTDHMLIMK.W
262	278	2	1795	4.2	1	43.3	16.4	95.00%	K.EIITAPLDGMILPGVTR.D		K.EIITAPLDGMILPGVTR.D
337	359	2	2462.16	4.4	0	42.7	26	95.00%	K.GTEYEIPMPEGQEAGPITSEISK.W		K.GTEYEIPMPEGQEAGPITSEISK.W
115	130	2	1769.96	3.9	1	43.7	19.2	95.00%	R.ISLPSFDPAELAEIIR.K		R.ISLPSFDPAELAEIIR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
65	ILV3_SCHPO	17.73%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
266	278	3	1408.68	4.8	1	24.2	25.3	95.00%	K.FAECEAAGSAIKR.L	Carbamidomethyl (+57)	K.FAECEAAGSAIKR.L
49	68	2	2142.97	5.2	1	90.3	27.1	95.00%	K.SQGASQAMLYATGLNEEDMK.K		K.SQGASQAMLYATGLNEEDMK.K
538	547	2	1056.58	2.3	1	38.7	22	95.00%	D.GDVIEINAVK.N		R.FSGGSHGFLIGHVDPEAQVGGPIALVQDGDVIEINAVK.N
402	417	4	1843.09	3.6	1	32.1	6.02	95.00%	K.IIRPLSNPIKTEGHLR.V		K.IIRPLSNPIKTEGHLR.V
117	126	2	1009.47	1.8	0	34	25	95.00%	D.GISMGTTGMR.Y		K.AGLTGFQFNTIGVSDGISMGTTGMR.Y
40	48	2	994.5	5.2	0	30.6	24.7	95.00%	K.YSETITGPK.S		K.YSETITGPK.S
185	212	3	3007.42	3.5	1	69.2	25.4	95.00%	R.AGHSPCQNNAPIDIVSAFQSYGEFITGK.I	Carbamidomethyl (+57)	R.AGHSPCQNNAPIDIVSAFQSYGEFITGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
66	HMCS_SCHPO	19.02%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
155	183	3	2859.53	3.9	0	40.5	17.9	95.00%	K.GNARPTGGAGCVALLVGPNAPIVFEPGLR.G	Carbamidomethyl (+57)	K.GNARPTGGAGCVALLVGPNAPIVFEPGLR.G
269	282	2	1454.7	2.5	0	49.6	25.1	95.00%	D.SAAEPSNPELEGVR.E		R.LLYTDSAAEPSNPELEGVR.E
264	282	2	2060.02	4.4	1	63.4	24.8	95.00%	R.LLYTDSAAEPSNPELEGVR.E		R.LLYTDSAAEPSNPELEGVR.E
393	407	2	1858.89	1.7	0	28.1	25.6	94.20%	R.HCLTPTQYEEAIELR.H	Carbamidomethyl (+57)	R.HCLTPTQYEEAIELR.H
207	216	2	1238.58	3.1	0	28.7	25.7	94.70%	D.GHFSLECYVK.A	Carbamidomethyl (+57)	R.GTYMQHAYDFYKPDLTSEYPYVDGHFSLECYVK.A
217	228	2	1325.64	3.7	1	38.4	25.4	95.00%	K.ALDGAYANYNVR.D		K.ALDGAYANYNVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
67	YF19_SCHPO	17.30%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
195	208	2	1516.82	2.3	0	35.8	19.6	95.00%	K.TAELTPLSALCLTK.F	Carbamidomethyl (+57)	K.TAELTPLSALCLTK.F
5	17	2	1406.78	4.6	1	33	18.1	95.00%	K.LVDHVEITVPTGK.T		K.LVDHVEITVPTGK.T
422	443	3	2229.12	4.1	0	21.2	22.8	91.10%	R.GNNSTYGLAAGVHTNNITNAIK.V		R.GNNSTYGLAAGVHTNNITNAIK.V
71	80	2	1161.56	3.7	1	28.3	25.2	94.80%	R.AAFQTDAPWR.K		R.AAFQTDAPWR.K
336	349	2	1523.73	2.5	1	102	25.4	95.00%	D.PFAEDTFQGAQVSK.Q		K.VGDPFAEDTFQGAQVSK.Q
181	194	2	1439.82	3.6	0	42.9	16.5	95.00%	K.IAPAVACGNTIILK.T	Carbamidomethyl (+57)	K.IAPAVACGNTIILK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
68	HXK1_SCHPO	9.50%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
304	315	2	1380.7	5.1	1	25.3	23.4	90.80%	K.MIAGCYLGDILR.R	Carbamidomethyl (+57)	K.MIAGCYLGDILR.R
2	12	3	1409.65	4.4	1	25.1	25.7	95.00%	M.SLHDAYHWPSR.T	Acetyl (+42)	-.MSLHDAYHWPSR.T
455	469	2	1328.73	2.7	0	59.4	20.4	95.00%	D.GSGVGAALVSALEAK.G		K.VVTIPAEDGSGVGAALVSALEAK.G
447	469	2	2153.17	3.4	1	105	18.3	95.00%	K.VVTIPAEDGSGVGAALVSALEAK.G		K.VVTIPAEDGSGVGAALVSALEAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
69	GLNA_SCHPO	20.61%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
153	170	2	1809.83	4.4	0	40.7	26.4	95.00%	K.GGFPGPQGPFYCGVGTGR.V	Carbamidomethyl (+57)	K.GGFPGPQGPFYCGVGTGR.V
345	359	2	1749.87	2.6	0	59.7	24.7	95.00%	D.PYLVTGIITETMFEH.-		R.RPASSIDPYLVTGIITETMFEH.-
237	260	4	2635.31	3.2	1	28.9	24	95.00%	K.ISFHPKPILGDWNGAGCHTNVSTK.D	Carbamidomethyl (+57)	K.ISFHPKPILGDWNGAGCHTNVSTK.D
50	59	3	1113.62	2.8	1	22.6	21.1	93.60%	D.AKPSSIDQLR.V		K.TMTLDAKPSSIDQLR.V
338	359	3	2476.24	4.1	1	26.8	22.9	95.00%	R.RPASSIDPYLVTGIITETMFEH.-		R.RPASSIDPYLVTGIITETMFEH.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
70	EF1G_SCHPO	13.94%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
93	115	3	2635.36	1	0	44	20.6	95.00%	K.VLQYCSFTNSELPGAFRPIIAPR.V	Carbamidomethyl (+57)	K.VLQYCSFTNSELPGAFRPIIAPR.V
207	216	2	1182.71	4	1	27.1	16.6	93.70%	K.FIDQPLPIIK.A		K.FIDQPLPIIK.A
128	139	2	1303.72	4.6	0	40.7	20.3	95.00%	K.EAETAIALIFAR.F		K.EAETAIALIFAR.F
116	127	2	1294.63	4.3	1	26.2	24.9	92.40%	R.VFGAPYDEQAAK.E		R.VFGAPYDEQAAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
71	RS6B_SCHPO	27.20%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	115	2	1739.01	3.8	1	65.7	12	95.00%	R.GCIVGQDLAVLALAIVK.Q	Carbamidomethyl (+57)	R.GCIVGQDLAVLALAIVK.Q
32	51	2	2112.99	2.2	1	56.6	26.2	95.00%	R.MGQEVPGDSVGPEFAGYVFK.I		R.MGQEVPGDSVGPEFAGYVFK.I
59	72	3	1625.86	4.7	0	32.2	21.7	95.00%	K.QGFPMFQGVLLPHR.V		K.QGFPMFQGVLLPHR.V
40	51	2	1299.65	2.5	0	27.8	23.9	94.50%	D.SVGPEFAGYVFK.I		R.MGQEVPGDSVGPEFAGYVFK.I
204	217	2	1606.78	4.3	1	54.8	25.1	95.00%	K.NREEAAEFAQLMAK.R		K.NREEAAEFAQLMAK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
72	FAS1_SCHPO	6.75%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1117	1130	2	1421.7	4.7	0	59.8	25.1	95.00%	K.SLESVSVTEEAGSK.V		K.SLESVSVTEEAGSK.V
1870	1881	2	1266.57	5.2	1	37.8	26	95.00%	R.SDYGMVAANPSR.V		R.SDYGMVAANPSR.V
210	224	3	1723.91	5.4	1	36.5	20.9	95.00%	K.GLNVLDWLAGERPER.D		K.GLNVLDWLAGERPER.D
828	846	3	1903.04	1.5	0	36.5	17.6	95.00%	D.GPTGGIVTVLSELGEPIHK.L		K.TYDGPTGGIVTVLSELGEPIHK.L
2	12	2	1294.67	5.2	0	53.5	22.4	95.00%	M.VEAEQVHQSLR.S		-.MVEAEQVHQSLR.S

1778	1806	3	3141.54	1.9	1	40.3	23.1	95.00%	K.DSTSFSFTHPSGLLSATQFTQPALTLMEK.S		K.DSTSFSFTHPSGLLSATQFTQPALTLMEK.S
781	794	2	1545.81	3.9	1	42.1	22.2	95.00%	K.LPPMPFDGILFGSR.L		K.LPPMPFDGILFGSR.L
1422	1447	3	2983.4	3.2	1	29.8	25.7	95.00%	R.GTFTDFENTFEHTQETPMQLTLATPK.D		R.GTFTDFENTFEHTQETPMQLTLATPK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
73	ACON_SCHPO	13.24%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
723	741	3	1933.07	2.2	1	21.9	16.2	92.40%	D.GLTTFAPGKPLTLVVHPAD.G		K.ISPFDTVDIDGLTTFAPGKPLTLVVHPADGSAEWSTK.L
532	549	2	1853.89	4.6	1	68.9	25.7	95.00%	K.GYDPGSNTYVAPSSVNVK.D		K.GYDPGSNTYVAPSSVNVK.D
375	391	2	1874.82	2.7	1	59	27.2	95.00%	K.VGLIGSCTNSSYEDMSR.A	Carbamidomethyl (+57)	K.VGLIGSCTNSSYEDMSR.A
392	402	2	1203.6	5.2	1	35.2	24.8	95.00%	R.AASICQQAIDK.G	Carbamidomethyl (+57)	R.AASICQQAIDK.G
652	666	2	1665.78	3.4	0	67.3	26.5	95.00%	R.WVTLGEQNFGEGSSR.E		R.WVTLGEQNFGEGSSR.E
518	531	2	1474.79	2.8	1	27.8	21.1	94.50%	D.FKFEPPTGAGLPSK.G		K.DGNDFKFEPPTGAGLPSK.G
462	470	2	1052.53	5	0	36.5	24	95.00%	K.NSIVTSYNR.N		K.NSIVTSYNR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
74	TRP_SCHPO	15.49%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
382	393	2	1355.77	4.5	0	47.2	19	95.00%	K.INNCIGQILLAK.R	Carbamidomethyl (+57)	K.INNCIGQILLAK.R
247	261	2	1623.75	3.4	0	47.6	26.4	95.00%	K.AEPGTAATVVEEYCK.Y	Carbamidomethyl (+57)	K.AEPGTAATVVEEYCK.Y
400	419	3	1938.01	4.3	0	37.5	21.1	95.00%	R.IIAETGAGQHGVATAICAAK.F	Carbamidomethyl (+57)	R.IIAETGAGQHGVATAICAAK.F
275	302	3	2928.48	4.6	0	34.9	22	95.00%	K.QFQSGGSVATAPPAAVVEPINEMYLPQK.Y		K.QFQSGGSVATAPPAAVVEPINEMYLPQK.Y
616	631	2	1825.87	3	1	57.5	26.1	95.00%	R.AEFIAVTDAQCLEGFR.A	Carbamidomethyl (+57)	R.AEFIAVTDAQCLEGFR.A
445	461	2	1739.99	4	0	48.6	15.1	95.00%	R.LLGAEVVPVTSGTQTLR.D		R.LLGAEVVPVTSGTQTLR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
75	RS8A_SCHPO	35.50%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
60	74	2	1568.72	4.4	1	94.1	26	95.00%	R.LDSGNFSWGSEGVSK.K		R.LDSGNFSWGSEGVSK.K
165	178	2	1475.79	4.1	0	33.2	20.9	95.00%	R.LYAVVSSRPGQSGR.C		R.LYAVVSSRPGQSGR.C
154	164	2	1149.58	3.1	0	47.9	23.8	95.00%	D.SALETQFAAGR.L		K.VDSALETQFAAGR.L
152	164	2	1363.68	4.8	1	51.3	24.1	95.00%	K.VDSALETQFAAGR.L		K.VDSALETQFAAGR.L
78	92	2	1751.94	2	0	39.8	20.7	95.00%	R.IIQVAYHPSNNELVR.T		R.IIQVAYHPSNNELVR.T
111	124	3	1682.82	4.5	0	23.1	24.8	94.20%	R.VWYETHYGILMGSK.G		R.VWYETHYGILMGSK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
76	DHAS_SCHPO	18.21%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
31	39	2	856.52	4.9	0	28.2	19.7	94.90%	K.IAVLGASAR.S		K.IAVLGASAR.S
19	30	3	1445.76	4.9	1	23.3	22.5	94.40%	R.FITLLSDHPEFK.I		R.FITLLSDHPEFK.I
143	161	2	2003.03	3.7	0	71.4	22.5	95.00%	R.GCIITNSNCSTAAVVVPLK.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GCIITNSNCSTAAVVVPLK.A
267	278	2	1375.7	3.8	0	37.2	23.7	95.00%	R.EVLANYVSEPQK.L		R.EVLANYVSEPQK.L
6	18	2	1227.7	3.7	0	35.6	19.6	95.00%	K.VGILGATGTVGQR.F		K.VGILGATGTVGQR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
77	EF1B_SCHPO	21.03%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
59	73	2	1561.84	4.2	1	60.9	20.6	95.00%	K.QIATYDLATLPGTAK.E		K.QIATYDLATLPGTAK.E
153	165	2	1432.74	3.9	1	44.3	23.7	95.00%	R.SIQMDGLVWGLSK.L		R.SIQMDGLVWGLSK.L
23	39	2	1885.92	2.7	1	55.5	25	95.00%	K.SFIEGYEPSQADAVVFK.A		K.SFIEGYEPSQADAVVFK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
78	IMDH_SCHPO	10.50%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

125	139	2	1621.89	1.3	1	54.6	18.6	95.00%	D.PVVFSPQHTVGDVLK.I		K.YENGFILDPVVFSPQHTVGDVLK.I
303	313	2	1155.67	4.5	1	51.3	18.8	95.00%	K.IDVIAGNVVTR.E		K.IDVIAGNVVTR.E
2	15	2	1636.88	4	0	27	20.6	93.50%	M.SAFKPYTEALEVLK.K	Acetyl (+42)	-.MSAFKPYTEALEVLK.K
125	136	2	1281.64	2.5	1	35.5	23.8	95.00%	D.PVVFSPQHTVGD.V		K.YENGFILDPVVFSPQHTVGDVLK.I
419	433	2	1421.67	3.9	0	52.2	26	95.00%	R.GMGSIAAMEGTGVNK.N		R.GMGSIAAMEGTGVNK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
79	CDC48_SCHPO	3.31%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
550	563	2	1522.75	3.6	0	43.8	24.4	95.00%	K.AIANECSANFISVK.G	Carbamidomethyl (+57)	K.AIANECSANFISVK.G
774	786	3	1606.82	1.9	1	30.9	23.1	95.00%	R.RYEAYAHQLLTSR.G		R.RYEAYAHQLLTSR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
80	IF5A1_SCHPO	33.76%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	111	2	1413.68	1.7	1	46.2	24.9	95.00%	D.GYLNLMTTDGTTK.D		R.DEYQLVNIDDGYLNLMTTDGTTK.D
2	28	3	2979.31	4	1	77.3	26.7	95.00%	M.AEEEHVDFEGGEAGASLTFPMQCSALR.K	Acetyl (+42)/ Carbamidomethyl (+57)	-.MAEEEHVDFEGGEAGASLTFPMQCSALR.K
9	28	2	2127.98	2.6	0	60.6	26.7	95.00%	D.FEGGEAGASLTFPMQCSALR.K	Carbamidomethyl (+57)	-.MAEEEHVDFEGGEAGASLTFPMQCSALR.K
9	29	3	2256.07	1.5	1	27	26.1	95.00%	D.FEGGEAGASLTFPMQCSALRK.N	Carbamidomethyl (+57)	-.MAEEEHVDFEGGEAGASLTFPMQCSALRK.N
58	69	2	1352.76	2.3	1	49.5	17.8	95.00%	K.VHIVALDIFNGR.K		K.VHIVALDIFNGR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
81	TAL1_SCHPO	13.35%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
27	44	3	1917.03	4	1	42	20.6	95.00%	K.YKPQDATTNPSLILAASK.K		K.YKPQDATTNPSLILAASK.K
288	297	2	1165.55	2	1	33.1	25.7	95.00%	D.FNNDEMAVVK.L		R.FDFNNDEMAVVK.L
32	44	2	1285.73	1.5	0	51.8	19	95.00%	D.ATTNPSLILAASK.K		K.YKPQDATTNPSLILAASK.K
200	214	3	1713.91	2.5	1	25.4	20.5	95.00%	D.PGVVSVSNIFNYYKK.F		R.DYTAQEDPGVVSVSNIFNYYKK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
82	DHE4_SCHPO	15.30%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
334	353	2	2102.95	2.3	0	116	26.6	95.00%	R.YVAEGSNMGSSAEAVEVFEK.S		R.YVAEGSNMGSSAEAVEVFEK.S
25	34	3	1266.71	4.3	1	33.7	18.2	95.00%	K.LFEVHPELKR.V		K.LFEVHPELKR.V
356	367	2	1231.57	4.5	0	27.7	25.3	94.00%	R.ASGEGCWLAPGK.A	Carbamidomethyl (+57)	R.ASGEGCWLAPGK.A
93	101	2	1127.61	5.6	0	29.2	22.5	95.00%	K.FLGFEQIFK.N		K.FLGFEQIFK.N
399	416	2	1950.98	3	1	88.5	23	95.00%	K.LAGIMQNIFEQSTDVASK.Y		K.LAGIMQNIFEQSTDVASK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
83	NACA_SCHPO	29.48%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	75	2	1164.62	5.8	0	59.3	21.7	95.00%	K.SSNNAYIVLGK.V		K.SSNNAYIVLGK.V
11	26	2	1637.87	4.6	0	55.2	20.5	95.00%	K.ISELPAGSTTVVHAEK.A		K.ISELPAGSTTVVHAEK.A
52	64	2	1540.93	4.4	0	50.2	10.8	95.00%	K.NILLIINEPIVYK.S		K.NILLIINEPIVYK.S
76	86	2	1189.58	4.9	1	47.2	25.4	95.00%	K.VTVEDMAAQAR.A		K.VTVEDMAAQAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
84	GLT1_SCHPO	5.59%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
624	638	2	1701.91	4.2	0	45.5	21	95.00%	R.MPTPILTVEEFNALK.N		R.MPTPILTVEEFNALK.N
1690	1707	2	2063.08	4.1	0	61.9	21.1	95.00%	K.EALTQLLLTNNFPEFTGR.V		K.EALTQLLLTNNFPEFTGR.V
1442	1464	3	2335.04	4.9	1	32.4	27	95.00%	R.NSGAIAVVEGVGDHGCEYMTGGR.V	Carbamidomethyl (+57)	R.NSGAIAVVEGVGDHGCEYMTGGR.V
1845	1856	2	1155.67	3.4	0	41.7	18.9	95.00%	D.AVVLASGSTVPR.D		K.VYDAVVLASGSTVPR.D
1022	1038	3	1639.81	4.9	0	25.7	24.5	95.00%	K.MAQGAKPGEGGELPGNK.V		K.MAQGAKPGEGGELPGNK.V
672	685	2	1555.69	5.3	1	68	26	95.00%	R.ICSEADTAVNEGYK.A	Carbamidomethyl (+57)	R.ICSEADTAVNEGYK.A
1758	1776	2	1792.99	3.3	1	78.8	17.7	95.00%	R.VAIIGSGPAGLAAADQLNR.A		R.VAIIGSGPAGLAAADQLNR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
85	RS5B_SCHPO	20.20%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
20	32	2	1552.83	1.3	1	33.9	20	95.00%	K.LFNKFPFEGVEVK.D		K.LFNKFPFEGVEVK.D
146	158	2	1338.8	1.8	0	41.3	13.6	95.00%	R.VNQALALITIGAR.E		R.VNQALALITIGAR.E
167	181	2	1646.82	2.4	0	77.7	24	95.00%	K.SISECLAEEIINAAK.G	Carbamidomethyl (+57)	K.SISECLAEEIINAAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
86	STI1_SCHPO	14.55%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
146	164	2	1935.97	6.4	1	78.1	23.7	95.00%	K.LASNPETASLLADSAFMAK.L		K.LASNPETASLLADSAFMAK.L
112	132	2	2007.97	4.2	0	89.9	25.6	95.00%	K.SVEAAQTQAASGAGGFNPFAK.L		K.SVEAAQTQAASGAGGFNPFAK.L
168	183	2	1781.88	4.3	1	66.6	24.7	95.00%	K.IQQNPGSIMAELNDPR.M		K.IQQNPGSIMAELNDPR.M
550	560	2	1154.62	1.1	0	32.3	21	95.00%	D.PAMQAILGQAR.E		K.DPEVLGILQDPAMQAILGQAR.E
247	258	2	1318.67	3.8	1	41.6	24.4	95.00%	D.KTAEELEEAATK.E		K.EEFAPSSSTPSADSAKPETTNPPPQPQASEPMEEDKTAEELEEAATK.E
371	377	2	800.44	3.8	1	29.8	25.5	95.00%	R.TPDILSR.L		R.TPDILSR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
87	RS23_SCHPO	14.69%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
81	88	2	884.44	1.8	1	27.5	21.3	94.10%	K.VTAFVPHD.G		K.VTAFVPHDGCLNFVDENDEVLLSGFGR.K
125	137	2	1326.74	4.4	0	55.5	19.2	95.00%	K.VAGVGLSALFHEK.K		K.VAGVGLSALFHEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
88	RL27A_SCHPO	22.06%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	48	3	1461.76	5.9	0	42.8	22.9	95.00%	K.SHPFGHAVVAGVER.Y		K.SHPFGHAVVAGVER.Y
23	34	2	1269.74	4.4	1	65.4	16.3	95.00%	K.VVILQAIDQGSK.S		K.VVILQAIDQGSK.S
35	52	4	1963.05	4.3	1	23.2	19.5	95.00%	K.SHPFGHAVVAGVERYPLK.V		K.SHPFGHAVVAGVERYPLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
89	O59743_SCHPO	21.49%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
12	24	2	1387.72	2.3	0	75.5	23.1	95.00%	K.LGIEEQVETAATK.S		K.LGIEEQVETAATK.S
122	136	3	1849.84	2.6	1	26.5	26.5	95.00%	D.NKPEEYYHLSAPDCK.S	Carbamidomethyl (+57)	K.LKPVPTSWEQALQDNKPEEYYHLSAPDCK.S
75	97	3	2588.33	2.8	1	31.8	20.9	95.00%	K.EALDLFLGAYNVITPELAHFEAR.C		K.EALDLFLGAYNVITPELAHFEAR.C
11	24	2	1515.82	4.5	1	53.1	19.8	95.00%	K.KLGIEEQVETAATK.S		K.KLGIEEQVETAATK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
90	GCST_SCHPO	15.25%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
81	97	2	1779.9	3.9	0	64.1	24	95.00%	R.GENATAYLESITPSSLK.E		R.GENATAYLESITPSSLK.E

327	344	2	1771.88	3.2	0	76.3	23.8	95.00%	D.GVEVGQVTSGCPSPTLGK.N	Carbamidomethyl (+57)	R.HGSAVEVDGVEVGQVTSGCPSPTLGK.N
319	344	3	2566.25	4.5	1	41.9	24.8	95.00%	R.HGSAVEVDGVEVGQVTSGCPSPTLGK.N	Carbamidomethyl (+57)	R.HGSAVEVDGVEVGQVTSGCPSPTLGK.N
165	180	2	1623.93	4	0	75.8	14.1	95.00%	R.ALIAIQGPETASVVQK.L		R.ALIAIQGPETASVVQK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
91	SERC_SCHPO	16.20%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
330	345	2	1860.9	1.1	0	26.9	25.3	92.90%	R.IEPQELESEFLAEAEK.H		R.IEPQELESEFLAEAEK.H
330	352	5	2716.42	3.7	1	22	19.4	95.00%	R.IEPQELESEFLAEAEKHHLVQLK.G		R.IEPQELESEFLAEAEKHHLVQLK.G
376	385	2	1147.65	4.7	1	32.8	17.6	95.00%	R.LIDLLESFAK.A		R.LIDLLESFAK.A
216	228	2	1299.74	5	0	37	17.9	95.00%	K.NAGPAGITVVFVR.D		K.NAGPAGITVVFVR.D
189	199	2	1282.6	4.3	1	67	25	95.00%	R.VCDVSSNFISR.K	Carbamidomethyl (+57)	R.VCDVSSNFISR.K
324	329	2	766.38	5.3	0	26.2	21.6	92.40%	R.MNVTFR.I		R.MNVTFR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
92	RL10A_SCHPO	26.24%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	128	3	1265.71	4.6	0	30	18.7	95.00%	R.HAFGKPNGLVAR.V		R.HAFGKPNGLVAR.V
129	139	2	1228.7	4.7	0	40	19.2	95.00%	R.VNIGQILMSVR.T		R.VNIGQILMSVR.T
41	69	3	3260.58	4	1	68.1	23.4	95.00%	R.AGVDEFPLCIHLVSNEYEQITSEALEAAR.I	Carbamidomethyl (+57)	R.AGVDEFPLCIHLVSNEYEQITSEALEAAR.I
33	38	2	719.4	4.8	1	27.1	21.6	93.60%	R.IFDLGR.K		R.IFDLGR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
93	TRXB_SCHPO	24.84%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
78	89	2	1323.7	3.1	0	38.3	21.6	95.00%	R.FGTEIITETVSK.L		R.FGTEIITETVSK.L
114	124	2	1044.6	2.4	0	38.5	19	95.00%	D.SVILATGASAR.R		K.YWLEGAEEEEPHTADSVILATGASAR.R
61	72	2	1321.67	2.2	0	49	25	95.00%	D.GINGTTLTENFR.A		R.GELKPVMYEGMLANGIAAGGQLTTTTDVENFPGFPDGINGTTLTENFR.A
165	175	2	1193.6	2.5	0	25	24.6	90.30%	D.SAAEEAQFLTK.Y		R.NKPLAVVGGGDSAAEEAQFLTK.Y
6	24	3	1865.06	1.9	0	21	14.6	90.70%	K.VVIIGSGPAGHTAAIYLAR.G		K.VVIIGSGPAGHTAAIYLAR.G
99	124	3	2801.32	3.2	1	61.8	26.1	95.00%	K.YWLEGAEEEEPHTADSVILATGASAR.R		K.YWLEGAEEEEPHTADSVILATGASAR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
94	PYC_SCHPO	5.74%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
829	838	2	1275.63	4.5	1	27.7	24.3	94.40%	K.QLEFDNNQLR.E		K.QLEFDNNQLR.E
1111	1129	3	1901.98	2.3	0	51.2	22.2	95.00%	D.PGNPGHVAAPMSGTIVEIR.V		R.ADPGNPGHVAAPMSGTIVEIR.V
1109	1129	3	2088.05	4.4	1	38.2	23	95.00%	R.ADPGNPGHVAAPMSGTIVEIR.V		R.ADPGNPGHVAAPMSGTIVEIR.V
917	929	2	1447.76	4.7	1	42.2	23	95.00%	K.VVGDLAQFMVQNK.L		K.VVGDLAQFMVQNK.L
302	315	2	1628.75	2	1	37.3	26.1	95.00%	K.YCNAGTAEFLLDQK.G	Carbamidomethyl (+57)	K.YCNAGTAEFLLDQK.G
839	848	2	1297.58	4.8	1	38.2	25.9	95.00%	R.EIDSYWAQMR.L		R.EIDSYWAQMR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
95	LYS12_SCHPO	20.44%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
197	208	2	1324.65	5.3	1	41.8	25.1	95.00%	K.SNVMSVTDGLFR.E		K.SNVMSVTDGLFR.E
298	307	2	1044.58	4.6	0	32.2	21.9	95.00%	R.GIANPVATFR.S		R.GIANPVATFR.S
188	196	3	1047.69	4.7	0	25.1	3.01	95.00%	K.KPLVTIIHK.S		K.KPLVTIIHK.S

127	138	2	1568.72	4	1	44	26.2	95.00%	R.ENTECLYVKEER.M	Carbamidomethyl (+57)	R.ENTECLYVKEER.M
86	97	2	1231.7	4.7	0	25.9	18.9	92.00%	K.VAGYSSPIVALR.K		K.VAGYSSPIVALR.K
67	85	3	2071.06	4.3	1	52.5	22	95.00%	R.LKTECNAALFGAVQSPTHK.V	Carbamidomethyl (+57)	R.LKTECNAALFGAVQSPTHK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
96	THRC_SCHPO	10.70%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
265	282	2	1945.01	4.9	1	46.3	22	95.00%	R.FIVPTGNFGDILAGYYAK.R		R.FIVPTGNFGDILAGYYAK.R
421	432	3	1235.66	1.9	0	34.3	21.3	95.00%	D.PHTAVGVETGLR.C		K.IYESDHYIIDPHTAVGVETGLR.C
157	166	2	1007.54	3	0	34	20.8	95.00%	D.TGSAAIYGLR.G		R.DHLTVVGATSGDTGSAAIYGLR.G
313	327	2	1443.73	4.4	1	39.8	24.3	95.00%	K.ADSTQVSPSGPISAK.E		K.ADSTQVSPSGPISAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
97	GCSP_SCHPO	17.11%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
953	965	2	1458.76	1.1	1	43.1	23.1	95.00%	K.DNNLLVNAPHPQK.D		K.DNNLLVNAPHPQK.D
743	754	2	1264.58	2.6	0	36.2	25.6	95.00%	D.GANMNAMVGLCK.A	Carbamidomethyl (+57)	K.EALEVIHEHGGQVYFDGANMNAMVGLCK.A
657	684	3	2835.49	3.7	0	27.8	19	95.00%	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C	Carbamidomethyl (+57)	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C
770	788	3	1908.94	2.5	0	20.7	24.6	90.20%	K.TFCIPHGGGGPGVGPICVK.K	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.TFCIPHGGGGPGVGPICVK.K
379	412	3	3679.8	2.3	0	51.4	21.3	95.00%	K.ATSNICTAQALLANMSAFYAIYHGPNGLQEIANR.I	Carbamidomethyl (+57)	K.ATSNICTAQALLANMSAFYAIYHGPNGLQEIANR.I
577	604	3	3166.6	3.7	0	40.5	20.4	95.00%	K.LNAVTEMMPITNPLFANIHPYVPEEQAK.G		K.LNAVTEMMPITNPLFANIHPYVPEEQAK.G
87	126	3	4380.08	3.8	1	62.7	22.9	95.00%	R.TPESQLMAFGSVNPNEKNPPVNYSESEFTTLANNVANQNK.L		R.TPESQLMAFGSVNPNEKNPPVNYSESEFTTLANNVANQNK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
98	RS3B_SCHPO	11.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
228	241	2	1524.79	4.4	1	71.2	22.7	95.00%	K.LLELHGESQDVGTK.V		K.LLELHGESQDVGTK.V
200	213	2	1513.87	4.8	0	38.9	14.8	95.00%	R.ATGSIFPLQNVLVR.K		R.ATGSIFPLQNVLVR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
99	RL13_SCHPO	25.96%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
172	183	2	1398.66	5.4	0	54	25.5	95.00%	K.NFNAFSTLSNER.A		K.NFNAFSTLSNER.A
118	128	2	1326.78	2.2	0	53.8	15.4	95.00%	K.VYLAHLIVFPR.K		K.VYLAHLIVFPR.K
46	64	4	2080.27	3.1	0	20	4.77	95.00%	K.IAPRPVEAIRPAVKPPTIR.Y		K.IAPRPVEAIRPAVKPPTIR.Y
89	100	2	1263.7	3.9	1	28.9	19.9	95.00%	R.VASTIGIPVDHR.R		R.VASTIGIPVDHR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
100	RL15A_SCHPO	19.90%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
115	128	2	1699.83	4.1	1	73.6	25.6	95.00%	R.VLNSYWVNQDATYK.F		R.VLNSYWVNQDATYK.F
78	93	3	1761.94	4.8	0	23.7	20.7	95.00%	K.GQTYGKPVHQGVNHLK.Y		K.GQTYGKPVHQGVNHLK.Y
148	157	3	1218.69	4.4	0	24.4	18.5	95.00%	R.INWIVNPVHK.H		R.INWIVNPVHK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
101	ACL1_SCHPO	8.94%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
369	381	2	1420.73	4.5	0	44	23.3	95.00%	R.GSELTYNNVPISK.V		R.GSELTYNNVPISK.V
171	182	3	1338.74	4.8	0	23.6	19.4	94.90%	K.LYRPGSVAYVSK.S		K.LYRPGSVAYVSK.S
313	326	2	1570.9	3.9	0	58.3	15.2	95.00%	K.LPALLQEVYEGLVK.K		K.LPALLQEVYEGLVK.K
156	170	2	1506.72	3.3	1	45.7	25.6	95.00%	K.IGNTGGMMDNIVASK.L		K.IGNTGGMMDNIVASK.L
313	327	3	1699	4	1	30.3	10.4	95.00%	K.LPALLQEVYEGLVKK.G		K.LPALLQEVYEGLVKK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
102	VATA_SCHPO	18.74%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
89	114	4	2751.53	2.9	1	22.2	11.5	95.00%	R.TGKPLSVELGPGLAETIYDGIQRPLK.Q		R.TGKPLSVELGPGLAETIYDGIQRPLK.Q
465	476	2	1580.77	4.7	0	39.5	25.5	95.00%	K.YINALQPWYEER.V		K.YINALQPWYEER.V
128	136	2	1002.51	5	0	25.2	23.9	90.80%	R.GINTESLNR.E		R.GINTESLNR.E
373	389	2	1752.85	8	1	36.9	25.3	95.00%	R.LAEMPADSGYPAYLGAK.L		R.LAEMPADSGYPAYLGAK.L
317	331	2	1544.81	4.6	0	49.4	22.6	95.00%	R.TTLVANTSNMPVAAR.E		R.TTLVANTSNMPVAAR.E
182	198	2	1838.88	4.6	1	73	26	95.00%	R.GTVTYIAEAGSYHVDEK.L		R.GTVTYIAEAGSYHVDEK.L
221	240	3	2105.14	4.1	1	35.3	17.6	95.00%	R.AARPVADNLTANQPLLTGQR.V		R.AARPVADNLTANQPLLTGQR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
103	TRX1_SCHPO	29.13%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
40	54	2	1796.83	4.6	1	68.4	26.5	95.00%	K.FEQFSNTYSDATFIK.V		K.FEQFSNTYSDATFIK.V
80	94	2	1567.82	2.3	1	79.5	22.1	95.00%	K.NGEKIEEIVGANPAK.L		K.NGEKIEEIVGANPAK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
104	DAK1_SCHPO	7.93%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
45	66	3	2123.05	5.3	0	21	24	90.80%	K.NVSVISGGGAGHEPTHSSFVGK.G		K.NVSVISGGGAGHEPTHSSFVGK.G
527	538	2	1301.63	4.7	1	60.8	25	95.00%	K.TNDLNAAVEEAR.K		K.TNDLNAAVEEAR.K
388	399	2	1358.73	4.4	0	25.9	21.4	92.00%	R.QAIVNSMENLIK.A		R.QAIVNSMENLIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
105	THI4_SCHPO	11.00%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
373	385	2	1353.71	4.1	1	37.5	22.1	95.00%	R.GVDSISQHTLAAR.I		R.GVDSISQHTLAAR.I
125	140	2	1686.81	1.7	1	71.1	25.4	95.00%	D.GADYVGIGSIYETNTK.D		K.AAADGADYVGIGSIYETNTK.D
27	42	3	1733.95	4.6	0	28	18.1	95.00%	R.QVEEGILGGVTLVQHR.E		R.QVEEGILGGVTLVQHR.E
237	248	2	1322.76	4.7	1	31.5	14.8	95.00%	K.DLLNQIPAALQK.L		K.DLLNQIPAALQK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
106	YA03_SCHPO	19.18%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	47	2	1743.88	2	0	107	23.9	95.00%	D.PVLTSEGIEQCEALAK.E	Carbamidomethyl (+57)	R.DPVLTSEGIEQCEALAK.E
147	172	3	2896.59	3.1	1	53.2	15.4	95.00%	R.SKEALEYLAALPQQQIAVITHSAFIR.F		R.SKEALEYLAALPQQQIAVITHSAFIR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
107	IF4A_SCHPO	12.50%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
58	69	2	1173.61	5	1	69	24.1	95.00%	R.DVLAQAQSGTGK.T		R.DVLAQAQSGTGK.T
33	48	2	1854.94	3.8	0	30.4	23.4	95.00%	R.GIYAYGFERPSAIQQR.A		R.GIYAYGFERPSAIQQR.A
372	392	2	2549.19	2.9	1	26.7	26.1	91.40%	R.EIEQFYNTHIEEMPMNIADLI.-		R.EIEQFYNTHIEEMPMNIADLI.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
108	MMF1_SCHPO	37.65%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
59	75	2	1747.86	2.8	0	34.8	25	95.00%	K.ANGVIYCSGQIPVANGK.V	Carbamidomethyl (+57)/ Deamidation (+1)	K.ANGVIYCSGQIPVANGK.V
87	105	2	2116.09	4.6	0	131	22.6	95.00%	R.QCLLNLQEVLTEAGSSLNK.I	Carbamidomethyl (+57)	R.QCLLNLQEVLTEAGSSLNK.I
125	137	2	1483.81	3.9	1	42.4	19.2	95.00%	K.VYTEVLPDPKPAR.S		K.VYTEVLPDPKPAR.S
47	58	2	1247.66	5.3	0	27.4	22.3	94.00%	K.LSSAGPYNQAIK.A		K.LSSAGPYNQAIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
109	RS22_SCHPO	27.69%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
98	108	2	1171.7	4.9	0	29.1	14.5	95.00%	R.QVGVIVLTTSR.G		R.QVGVIVLTTSR.G
4	19	2	1814.9	4.5	1	77.6	24	95.00%	R.QSVLADCLNNIVNAER.R	Carbamidomethyl (+57)	R.QSVLADCLNNIVNAER.R
89	97	2	1111.62	5.6	0	31.9	19.5	95.00%	K.WVNQLLPSR.Q		K.WVNQLLPSR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
110	SYDC_SCHPO	6.03%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
281	294	2	1356.6	4.8	0	27.5	25.6	93.40%	K.MSGASSEGGSNVFK.I		K.MSGASSEGGSNVFK.I
200	210	2	1229.65	4.9	1	29.1	22.8	95.00%	K.NLPFLVEDAGR.S		K.NLPFLVEDAGR.S
490	499	2	1300.55	3.9	1	26.9	26.1	91.70%	R.YSNSYDFFMK.G		R.YSNSYDFFMK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
111	SODC_SCHPO	37.66%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
98	116	2	1984.04	4.4	1	72.6	21.6	95.00%	K.TTFSDSVISLFGANSIIGR.T		K.TTFSDSVISLFGANSIIGR.T
85	97	2	1357.69	2.6	1	49.8	23.8	95.00%	D.LGNLESDAQGNIK.T		R.HVGDLGNLESDAQGNIK.T
45	70	3	2825.25	4.3	1	41.5	27	95.00%	R.GFHIHQFGDNTNGCTSAGPHFNPEGK.T	Carbamidomethyl (+57)	R.GFHIHQFGDNTNGCTSAGPHFNPEGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
112	RS4B_SCHPO	11.83%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
222	233	2	1232.68	5.6	0	42.4	20.7	95.00%	R.LSNVFVIGEAGK.S		R.LSNVFVIGEAGK.S
246	252	2	846.45	4.8	0	45.4	23.4	95.00%	K.LSITEER.D		K.LSITEER.D
38	49	3	1485.85	2	1	38.5	16	95.00%	K.ARECLPLIVFLR.N	Carbamidomethyl (+57)	K.ARECLPLIVFLR.N
40	49	2	1258.72	4.7	0	26.1	18.5	92.30%	R.ECLPLIVFLR.N	Carbamidomethyl (+57)	R.ECLPLIVFLR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
113	LEU1_SCHPO	14.38%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
82	99	2	1998.98	4.3	1	62	25	95.00%	K.EIEVGFPSASQTDFAFVR.H		K.EIEVGFPSASQTDFAFVR.H
464	479	2	1742.82	4.9	1	69.1	25.9	95.00%	R.FSVNDYTLSSNGPQSK.C		R.FSVNDYTLSSNGPQSK.C
341	362	3	2346.15	2.9	1	44.7	24.6	95.00%	R.HPYAGNLVFTAFSGSHQDAISK.G		R.HPYAGNLVFTAFSGSHQDAISK.G
137	151	3	1761.87	4	0	33.2	25	95.00%	K.NATVHLYNACSPLFR.E	Carbamidomethyl (+57)	K.NATVHLYNACSPLFR.E
386	398	3	1483.75	2.6	1	42.9	24	95.00%	D.PHDVNSEYAAIIR.V		K.VPYLPLDPHDVNSEYAAIIR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
114	COFI_SCHPO	32.12%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
81	94	2	1584.9	4.1	1	54.1	16.2	95.00%	K.IIFISWSPDVAPIK.S		K.IIFISWSPDVAPIK.S
8	20	2	1548.76	4.6	0	71.2	25.7	95.00%	K.VSPECLEAFQELK.L	Carbamidomethyl (+57)	K.VSPECLEAFQELK.L
117	133	2	1941.96	0.3	1	85.2	24.4	95.00%	D.IQATDFSEVAYETVLEK.V		R.AFTGIGTDIQATDFSEVAYETVLEK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
115	PMP20_SCHPO	28.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
30	55	2	2747.41	3.6	0	38	21	95.00%	K.FIIVGVPGAFTPPCSSQVPGYIANEK.Q	Carbamidomethyl (+57)	K.FIIVGVPGAFTPPCSSQVPGYIANEK.Q
11	29	3	2215.13	4.2	0	34.9	22.6	95.00%	K.VTLWENKPEEVVEFPSQGK.F		K.VTLWENKPEEVVEFPSQGK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
116	PMM_SCHPO	11.28%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
29	43	2	1728.91	0.98	0	60.5	21.9	95.00%	R.LSVSPEMLETLQNLR.K		R.LSVSPEMLETLQNLR.K
45	58	2	1347.75	4.4	1	41.6	20	95.00%	K.VVAIGFVGGSDLSK.Q		K.VVAIGFVGGSDLSK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
117	ASNS_SCHPO	5.39%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
516	523	2	1035.55	6.3	1	30	21.3	95.00%	K.LFDEIFPR.Q		K.LFDEIFPR.Q
154	165	2	1327.63	2.4	1	84.7	25.3	95.00%	D.SPDTAYFASELK.A		R.DPIGITTLYQGFSSDSPDTAYFASELK.A
399	408	2	1120.54	4.9	0	26.3	24	92.60%	K.STMAWGLEAR.V		K.STMAWGLEAR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
118	DHOM_SCHPO	24.20%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	138	2	1568.79	4.5	1	56.7	23.6	95.00%	K.AFSASNDVYQNIIK.A		K.AFSASNDVYQNIIK.A
57	67	2	1391.68	4.7	1	33.1	24.9	95.00%	K.DYQPINLSEWK.N		K.DYQPINLSEWK.N
238	252	2	1526.81	1.7	0	45.7	21.5	95.00%	R.IAGVHVESASSFPVK.S		R.IAGVHVESASSFPVK.S
28	56	3	3047.4	3	0	33.8	26.2	95.00%	K.GFNENASTNGTTSFNVVAISSMEGHYVSK.D		K.GFNENASTNGTTSFNVVAISSMEGHYVSK.D
89	110	2	2284.21	4.5	1	95.1	20	95.00%	K.SPLPAILVDNTASEAIAQSYPK.F		K.SPLPAILVDNTASEAIAQSYPK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
119	RL3A_SCHPO	14.69%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
207	222	2	1837.89	2.4	1	78.1	25.4	95.00%	K.STFEQNEMIDVIGVTR.G		K.STFEQNEMIDVIGVTR.G
11	19	2	982.54	4.3	0	27.2	20.1	93.80%	R.HGSLGFLPR.K		R.HGSLGFLPR.K
249	266	3	2035.03	4.4	0	29.3	23.6	95.00%	K.VACIGAWHPANVQWTVAR.A	Carbamidomethyl (+57)	K.VACIGAWHPANVQWTVAR.A
37	50	3	1530.86	1.4	0	36.9	17.6	95.00%	D.ASKPVHLTAFLGYK.A		K.DDASKPVHLTAFLGYK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
120	P25_SCHPO	17.82%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
36	52	2	1976.06	4.7	0	48.2	18.8	95.00%	K.AVIYQFPETLSPEILEK.M		K.AVIYQFPETLSPEILEK.M
2	20	2	2064.09	2.1	0	78.9	19.9	95.00%	M.STANTVAIVIYSTYGHVVK.L	Acetyl (+42)	-.MSTANTVAIVIYSTYGHVVK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
121	RS11_SCHPO	17.76%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	64	2	1161.6	4.7	0	33.4	23.4	95.00%	K.CPFVGQVSIR.G	Carbamidomethyl (+57)	K.CPFVGQVSIR.G
114	130	2	1870.97	4.9	1	41.5	23.3	95.00%	R.INEGDVVTVGQCRPLSK.T	Carbamidomethyl (+57)	R.INEGDVVTVGQCRPLSK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
122	ATPB_SCHPO	7.43%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
167	185	2	2076.03	2.3	0	98.5	24.2	95.00%	D.APSFEEQSTTPEILETGIK.V		K.YSPIHADAPSFEEQSTTPEILETGIK.V
160	185	3	2859.39	2.5	1	29.4	24.2	95.00%	K.YSPIHADAPSFEEQSTTPEILETGIK.V		K.YSPIHADAPSFEEQSTTPEILETGIK.V
210	222	2	1501.86	3.1	0	52.4	15.2	95.00%	K.TVFIQELINNIAK.A		K.TVFIQELINNIAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
123	YHEF_SCHPO	20.20%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
54	65	2	1279.67	5.1	1	47	22.3	95.00%	K.SFIGLDALTESK.G		K.SFIGLDALTESKGEFFQR.M
30	41	3	1413.76	4.8	1	20.9	21.9	90.40%	R.LRGPHCGTYLLK.V	Carbamidomethyl (+57)	R.LRGPHCGTYLLKVVGTNATYVGEK.S
91	104	2	1616.85	2.8	0	41.2	22.4	95.00%	D.TANFTPLTFTTYLK.T		R.LFTIAENDTANFTPLTFTTYLKTCNPQSIENAMIPFVNTVTSEISFDAWAYTAQNSSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
124	YHZ8_SCHPO	25.25%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
75	103	3	3217.69	3	0	57.2	18.5	95.00%	K.TSNPFLAFANYLTSTHAPLAEPLQLLNFK.V		K.TSNPFLAFANYLTSTHAPLAEPLQLLNFK.V
2	13	2	1361.7	3.8	0	57.2	23	95.00%	M.SFPASTHVYIAK.I	Acetyl (+42)	-.MSFPASTHVYIAK.I
156	164	2	1004.57	2.4	0	47.9	20	95.00%	D.PSLYAVVTR.Y		K.ADTSLIIHSLDDPSLYAVVTR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
125	AATR1_SCHPO	9.07%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
305	317	2	1562.83	3.7	0	52.6	20.9	95.00%	R.VGWFTAQPLFIER.G		R.VGWFTAQPLFIER.G
38	54	2	1856.03	4.5	0	36.8	17	95.00%	K.IISLAGGLPNPEYFPIR.E		K.IISLAGGLPNPEYFPIR.E
7	19	3	1436.71	5.4	1	43.2	25.1	95.00%	K.DLSHHLSVESASR.K		K.DLSHHLSVESASR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
126	RL36A_SCHPO	24.24%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	11	2	966.59	4.6	0	38.2	14.5	95.00%	M.APGLVVGLNK.G		-.MAPGLVVGLNK.G
83	96	2	1545.84	4.6	1	75.1	19.7	95.00%	K.GKIEELTSVIQSSR.L		K.GKIEELTSVIQSSR.L
85	96	2	1360.73	3.8	0	56.4	21.8	95.00%	K.IEELTSVIQSSR.L		K.IEELTSVIQSSR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
127	PYR1_SCHPO	2.85%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1880	1906	3	2689.36	3.3	0	28.6	22.3	95.00%	K.VSALMSPGLPHAAPSLAEAFGQAPENK.A		K.VSALMSPGLPHAAPSLAEAFGQAPENK.A
1771	1784	2	1494.85	4.1	0	35.2	15.7	95.00%	R.EAIPLLLTAVNEGR.L		R.EAIPLLLTAVNEGR.L
457	466	2	1084.56	6.1	0	38.9	22.8	95.00%	K.LPGGTIEENR.S		K.LPGGTIEENR.S
1758	1770	2	1371.7	4.4	0	56.2	24	95.00%	K.FVGNTAFTGFGVR.E		K.FVGNTAFTGFGVR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
128	ADK_SCHPO	21.18%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
253	267	2	1483.87	4.5	1	69.4	14.9	95.00%	R.VVVITQGADATIVAK.D		R.VVVITQGADATIVAK.D
86	96	2	1295.61	3.7	1	43.7	25.7	95.00%	K.FADMLLESNEK.A		K.FADMLLESNEK.A
230	245	2	1688.89	3.8	1	56.9	21.8	95.00%	K.STDVQEIALALSSVEK.V		K.STDVQEIALALSSVEK.V
126	138	2	1424.68	5.2	0	51	25.2	95.00%	R.SLCTNLGAANNYK.L	Carbamidomethyl (+57)	R.SLCTNLGAANNYK.L
107	123	2	1770.9	2.2	0	82.8	23.2	95.00%	D.PTTPTGVCAVVLSNNNK.N	Carbamidomethyl (+57)	R.SEFSVDPTTPTGVCAVVLSNNNK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
129	RS2_SCHPO	26.48%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
64	74	2	1441.73	5.7	1	25.1	23.5	90.50%	K.EYQIVDYFLPR.L		K.EYQIVDYFLPR.L
51	63	2	1566.86	4.2	0	34.6	18.6	95.00%	K.SIEEIYLYSLPIK.E		K.SIEEIYLYSLPIK.E
174	185	3	1138.69	4.8	1	25.2	12.6	95.00%	R.GAGLVAAPVTKR.F		R.GAGLVAAPVTKR.F
186	200	2	1799.86	4.8	1	102	25.8	95.00%	R.FLQLAGIEDCYTQSR.G	Carbamidomethyl (+57)	R.FLQLAGIEDCYTQSR.G
141	156	3	1696.87	4.8	1	37.6	23.6	95.00%	R.GYWGTALGDPHTVPVK.V		R.GYWGTALGDPHTVPVK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
130	YDG7_SCHPO	12.15%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
7	23	3	1939.91	3.9	1	22.9	26.2	92.10%	K.YFENAQNVHFTLADGSK.I		K.YFENAQNVHFTLADGSK.I
183	204	3	2603.37	3.4	0	27.8	19.3	95.00%	K.VKPAVHQMELHPFLPQTEFVEK.H		K.VKPAVHQMELHPFLPQTEFVEK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
131	RS0B_SCHPO	12.89%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	88	4	2453.26	4	1	67.3	21.4	95.00%	R.VIATIENPADVCVISSRPYGHR.A	Carbamidomethyl (+57)	R.VIATIENPADVCVISSRPYGHR.A
2	16	2	1599.78	1.6	1	33.2	24.9	95.00%	M.AESIARPSVLNATDD.D	Acetyl (+42)	-.MAESIARPSVLNATDDDIK.N
2	15	2	1484.75	2.1	1	47.3	23.9	95.00%	M.AESIARPSVLNATD.D	Acetyl (+42)	-.MAESIARPSVLNATDDDIK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
132	SYKC_SCHPO	6.09%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
570	591	3	2490.33	2.8	1	30.8	18.1	95.00%	R.EVLLFPHMKPEVQAAEPTVVKE.-		R.EVLLFPHMKPEVQAAEPTVVKE.-
15	28	2	1454.8	4	1	41.2	19.6	95.00%	K.ALVLDPVTGEQVSK.T		K.ALVLDPVTGEQVSK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
133	PUR8_SCHPO	11.00%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
268	292	3	2694.37	3.3	1	34.7	21.9	95.00%	R.LLANLKEVEEPFEAGQIGSSAMAYK.R		R.LLANLKEVEEPFEAGQIGSSAMAYK.R
450	460	2	1248.61	5.4	0	26.4	24.3	92.80%	R.APEQTESFVNK.D		R.APEQTESFVNK.D
372	388	2	1909.94	4.9	0	55.7	24.8	95.00%	R.AELPFMATENIIMAMTK.H		R.AELPFMATENIIMAMTK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
134	RL6_SCHPO	22.05%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	64	2	1497.84	5	0	33.1	18.6	95.00%	R.ASLAPGTVCILLAGR.F	Carbamidomethyl (+57)	R.ASLAPGTVCILLAGR.F
70	87	2	1959.1	3.1	1	33.6	14.3	95.00%	R.VVVLSQLEDTLVVTGPYK.V		R.VVVLSQLEDTLVVTGPYK.V
109	118	2	1031.56	5.5	1	31.2	22.7	95.00%	K.IDVSGVSVEK.F		K.IDVSGVSVEK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
135	SYRC_SCHPO	9.39%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
452	467	2	1759.87	3.7	1	55	24.7	95.00%	K.YAQVENPEEVADIVGK.T		K.YAQVENPEEVADIVGK.T
163	180	2	1987.02	4.1	0	33.9	21.3	95.00%	R.STIIGSFLANLHESQGWK.V		R.STIIGSFLANLHESQGWK.V
480	489	2	1284.6	5.9	1	39.4	25.3	95.00%	R.INNYAFDWSR.M		R.INNYAFDWSR.M
11	24	2	1544.86	4.5	1	46.7	17.6	95.00%	K.SLSTLGLQDLPVFR.E		K.SLSTLGLQDLPVFR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
136	RS17A_SCHPO	16.03%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	59	3	1133.6	4.6	0	24.5	22.7	95.00%	K.IAGYTTHLMK.R		K.IAGYTTHLMK.R
34	44	2	1156.68	4.8	1	51	17.6	95.00%	R.IVDEVAIIASK.R		R.IVDEVAIIASK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
137	RL19A_SCHPO	20.73%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
118	128	3	1386.74	5	0	32.3	21.9	95.00%	K.HLYHTLYLEAK.G		K.HLYHTLYLEAK.G
26	38	2	1429.68	2.5	0	76.2	25.5	95.00%	D.PNEISEISNANSR.Q		K.VWMDPNEISEISNANSR.Q
182	193	2	1422.69	3.6	1	31.8	25	95.00%	R.EQLYTAAEKIEE.-		R.EQLYTAAEKIEE.-
22	38	2	1960.9	4.1	1	66.6	26.4	95.00%	K.VWMDPNEISEISNANSR.Q		K.VWMDPNEISEISNANSR.Q
182	193	2	1422.69	3.6	1	31.8	25	95.00%	R.EQIYTAAEKIEE.-		R.EQLYTAAEKIEE.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
138	ARGD_SCHPO	8.62%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
311	332	3	2276.09	4.8	0	39.5	25.7	95.00%	K.IAAEIHPGEHGSTFGGNPVACR.V	Carbamidomethyl (+57)	K.IAAEIHPGEHGSTFGGNPVACR.V
139	154	2	1784.85	4.1	0	92.8	25.5	95.00%	K.IFFANCGTEANETALK.F	Carbamidomethyl (+57)	K.IFFANCGTEANETALK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

139	RL23_SCHPO	27.34%	100%	3	

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
15	34	2	2090	2.5	1	68.6	25.9	95.00%	R.MTLGLPVQAIMNCADNSGAK.N	Carbamidomethyl (+57)	R.MTLGLPVQAIMNCADNSGAK.N
48	58	2	1172.57	3.5	2	29	24.8	95.00%	R.LNRLPAASCGD.M	Carbamidomethyl (+57)	R.LNRLPAASCGDMVLATVK.K
51	65	2	1531.78	3.4	1	55.2	23.6	95.00%	R.LPAASCGDMVLATVK.K	Carbamidomethyl (+57)	R.LPAASCGDMVLATVK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
140	SCE3_SCHPO	17.01%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
46	66	2	2113.97	4.9	1	94.2	27	95.00%	R.ATPSSADAGYNAPSSTFESVR.S		R.ATPSSADAGYNAPSSTFESVR.S
359	381	2	2403.05	5.1	1	111	27.3	95.00%	K.TPATEDAPATNAGEAEEEEGWTK.I		K.TPATEDAPATNAGEAEEEEGWTK.I
365	381	2	1788.79	3.2	0	87.5	27.1	95.00%	D.APATNAGEAEEEEGWTK.I		K.TPATEDAPATNAGEAEEEEGWTK.I
250	271	3	2195.06	2.9	0	28.5	24.8	95.00%	R.SSSNVNTEATPSATTTTSSKPK.R		R.SSSNVNTEATPSATTTTSSKPK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
141	SYG_SCHPO	8.74%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
187	198	2	1297.63	5.4	0	37	24.5	95.00%	R.NPATNGELETPR.Q		R.NPATNGELETPR.Q
216	232	3	1983.01	5	0	28	22.9	95.00%	K.GYLRPETAQGQFLNFSR.L		K.GYLRPETAQGQFLNFSR.L
492	506	2	1649.85	4.8	0	35.7	23.2	95.00%	R.TYTPNVIEPSFGLGR.I		R.TYTPNVIEPSFGLGR.I
526	538	2	1298.77	3.9	0	28.2	15.8	94.90%	R.GVLSFPASIAPIK.A		R.GVLSFPASIAPIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
142	THI22_SCHPO	4.90%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
138	151	2	1403.74	2.2	1	63.8	22.5	95.00%	D.PVMVATSGDSLVTK.D		K.LVVDPVMVATSGDSLVTK.D
423	435	2	1516.6	5.3	0	56.7	26	95.00%	K.SCEESPACTAYSR.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.SCEESPACTAYSR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
143	Q1L854_SCHPO	12.54%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
14	27	2	1459.74	0.25	0	37.1	23.5	95.00%	D.LLGEETPAATTTEK.K		K.NLFDLLGEETPAATTTEK.K
271	282	2	1286.6	2.6	1	34.3	25.7	95.00%	K.TQQAPPTLSETD.F		K.TQQAPPTLSETDFPALA.-
10	27	2	1948.97	3.6	1	75.2	24.6	95.00%	K.NLFDLLGEETPAATTTEK.K		K.NLFDLLGEETPAATTTEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
144	NACB_SCHPO	26.49%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
95	116	2	2320.31	3	0	52.8	12.8	95.00%	K.TLSEILPGILNNLGPESLTALR.Q		K.TLSEILPGILNNLGPESLTALR.Q
73	90	3	1884.97	4	0	45.6	23.1	95.00%	R.APTVHSSLPNETTAIYGK.A		R.APTVHSSLPNETTAIYGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
145	ACL2_SCHPO	17.07%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
255	266	2	1367.61	3.7	1	48.5	26.1	95.00%	K.LDQTAEFECGAK.W	Carbamidomethyl (+57)	K.LDQTAEFECGAK.W
326	334	2	985.56	4.7	0	36	20.4	95.00%	K.LTILNAEGR.V		K.LTILNAEGR.V
280	304	3	2540.18	1.5	1	23	26.5	91.70%	K.TSGEESGAINADHGPPMVFPAPFGR.E		K.TSGEESGAINADHGPPMVFPAPFGR.E
382	389	2	947.52	4.5	1	26.9	22.7	93.40%	K.TVLDLMTR.G		K.TVLDLMTR.G
32	61	3	3211.76	3.3	0	47.1	15.6	95.00%	K.TVSATPAVQLAQIQFPLPTLVIPAESTTYR.E		K.TVSATPAVQLAQIQFPLPTLVIPAESTTYR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
146	RS14_SCHPO	16.55%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
95	105	2	1037.57	5.3	0	47.1	19.9	95.00%	K.TPGPGAQAALR.A		K.TPGPGAQAALR.A
73	84	3	1367.77	4	1	24.2	19.1	95.00%	K.CKEVGITALHIK.I	Carbamidomethyl (+57)	K.CKEVGITALHIK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
147	PURA_SCHPO	14.29%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
206	224	3	2169.16	3.6	1	37.8	18.5	95.00%	R.LKPFVIDAVAFMYEALQSK.K		R.LKPFVIDAVAFMYEALQSK.K
282	304	3	2420.22	4.2	1	27.4	22.7	95.00%	R.VGAGPFPTEQLNEIGDHLQSVGR.E		R.VGAGPFPTEQLNEIGDHLQSVGR.E
268	276	2	899.55	4.9	0	44.5	20.5	95.00%	R.IANSIGVVK.A		R.IANSIGVVK.A
126	136	2	1129.57	4.6	1	38.6	23.2	95.00%	R.ADALNEAELGK.Q		R.ADALNEAELGK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
148	TBB_SCHPO	12.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
123	154	3	3205.55	2.6	1	82.9	24	95.00%	R.EAEACDALQGFQLTHSLGGGTGSGMGTLLLSK.I	Carbamidomethyl (+57)	R.EAEACDALQGFQLTHSLGGGTGSGMGTLLLSK.I
163	174	2	1249.62	3.9	0	41.3	24.3	95.00%	R.MMATFSVAPAPK.S		R.MMATFSVAPAPK.S
204	216	2	1406.74	3	0	55.3	21.5	95.00%	D.NEALSSIFANTLK.I		K.SSDTVVEPYNATLSMHQLVENSDETFCIDNEALSSIFANTLK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
149	RL12_SCHPO	39.39%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
68	83	2	1538.91	3.4	0	50.5	14.3	95.00%	R.QAAVSVVPSASALVIK.A		R.QAAVSVVPSASALVIK.A
97	114	3	1921.99	2.3	1	29.5	21.9	95.00%	K.NVAHSGNVSLDEIIEVAR.T		K.NVAHSGNVSLDEIIEVAR.T
17	31	2	1312.7	3.6	0	46	21.2	95.00%	R.AVGGEVAGGSTLAPK.I		R.AVGGEVAGGSTLAPK.I
131	146	2	1652.81	4	1	45.9	24.3	95.00%	K.EILGTAFSVGCTVDGK.N	Carbamidomethyl (+57)	K.EILGTAFSVGCTVDGK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
150	RS15B_SCHPO	39.61%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
74	86	2	1382.75	4.3	0	32.6	21.1	95.00%	K.SEAPLNEKPATVK.T		K.SEAPLNEKPATVK.T
110	136	4	3209.67	3.6	0	17.8	19.7	93.40%	K.LFNQVEIRPEMIGHYLGEFSITYKPTK.H		K.LFNQVEIRPEMIGHYLGEFSITYKPTK.H
72	86	4	1581.88	2.1	1	18.7	19	95.00%	K.AKSEAPLNEKPATVK.T		K.AKSEAPLNEKPATVK.T
91	109	2	2033.08	3.1	0	80.9	20.6	95.00%	R.NMIILPEMVGSVVGIYNGK.L		R.NMIILPEMVGSVVGIYNGK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
151	PROF_SCHPO	26.77%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
54	68	2	1515.82	2.8	0	45.9	20.8	95.00%	D.PPSMFGTGIILAGQK.Y		R.AGDSVWAASAGFNLSPQEIQGLAAGFQDPPSMFGTGIILAGQK.Y
95	113	3	2098.08	3.5	0	24.5	21.1	95.00%	K.LCILVSHYPETTLPGEAAK.I	Carbamidomethyl (+57)	K.LCILVSHYPETTLPGEAAK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
152	DYR_SCHPO	13.02%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
164	183	3	2062.15	3.7	1	25.4	14.1	95.00%	K.LTTPSLHIAGTSDTLVPLAR.S		K.LTTPSLHIAGTSDTLVPLAR.S
34	51	2	1958.89	2	1	49.4	27.2	95.00%	K.YAELHFPTGPVVADEEAD.P		K.YAELHFPTGPVVADEEADPNDEEEK.K
191	212	3	2537.31	3.6	0	37.3	21	95.00%	R.CENAHVLLHPGQHIVPQQAVYK.T	Carbamidomethyl (+57)	R.CENAHVLLHPGQHIVPQQAVYK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
153	SLBR2_SCHPO	13.11%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
134	143	2	1115.56	4.3	0	27.1	23.5	93.70%	R.NIESSVQPSR.E		R.NIESSVQPSR.E

166	192	3	3060.53	3.6	1	43.6	22.2	95.00%	R.LVTMEQELVREEAACLVAEAQLSNTTR.E	Carbamidomethyl (+57)	R.LVTMEQELVREEAACLVAEAQLSNTTR.E
149	157	2	1075.63	4.5	1	33	17.2	95.00%	K.LLDQIYALK.H		K.LLDQIYALK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
154	SYTC_SCHPO	4.27%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
248	258	2	1187.55	4.2	1	47.1	26.3	95.00%	K.NSSSYFLGDAK.N		K.NSSSYFLGDAK.N
8	26	3	2136.14	4.2	1	27.4	18.9	95.00%	K.GVQASLDNLSLEIPFIQHR.L		K.GVQASLDNLSLEIPFIQHR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
155	RL31_SCHPO	21.24%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
91	105	2	1650.87	4.2	1	39.3	21	95.00%	K.ALYTYVQAVDVANPK.M		K.ALYTYVQAVDVANPK.M
7	15	2	986.56	5	0	39.5	21.7	95.00%	K.SAINQVVTR.D		K.SAINQVVTR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
156	RS21_SCHPO	29.89%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
77	87	2	1306.67	2.3	0	35.2	23.6	95.00%	D.GLLEGVWSYQR.-		R.LTTQDGLLEGVWSYQR.-
51	60	2	1113.59	4.5	0	33.8	22.6	95.00%	K.TTYAISGFVR.S		K.TTYAISGFVR.S
72	87	2	1864.94	4.3	1	65.3	23.7	95.00%	R.LTTQDGLLEGVWSYQR.-		R.LTTQDGLLEGVWSYQR.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
157	RS10B_SCHPO	34.01%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	44	3	1428.82	4.9	0	23.6	17.2	94.90%	K.HPEVGVPNLQVIK.A		K.HPEVGVPNLQVIK.A
10	24	3	1621.94	4.8	0	31.6	13	95.00%	K.AIHQALFQQGVLVAK.K		K.AIHQALFQQGVLVAK.K
78	93	4	1859.01	4	1	23	18.8	95.00%	R.EYLHLPAEVVPATHKR.Q		R.EYLHLPAEVVPATHKR.Q
26	31	2	732.38	5.5	1	30.1	22.5	95.00%	K.DFNLPK.H		K.DFNLPK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
158	SPEE_SCHPO	8.39%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	12	2	1291.72	4.1	0	43.5	18.5	95.00%	M.SVQELSHPLIK.D	Acetyl (+42)	-.MSVQELSHPLIK.D
18	31	2	1631.79	4.6	0	31.2	25.2	95.00%	R.EINNMWPGQAMTLK.V		R.EINNMWPGQAMTLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
159	RS13_SCHPO	15.23%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
44	55	2	1244.66	3.8	0	40.8	22.5	95.00%	K.GMSPSQIGVTLR.D		K.GMSPSQIGVTLR.D
10	20	2	1132.63	4.4	0	38.6	20.1	95.00%	K.GIASSALPYVR.S		K.GIASSALPYVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
160	RS12A_SCHPO	31.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	111	2	1486.76	2.4	1	27.9	23.3	94.60%	K.VLGEWAGLCVLDR.D	Carbamidomethyl (+57)	K.VLGEWAGLCVLDR.D
79	93	2	1671.88	4.1	0	73.8	21.7	95.00%	K.LVEALCAESETPLIK.V	Carbamidomethyl (+57)	K.LVEALCAESETPLIK.V
61	78	3	2208.97	4.2	1	36.3	27	95.00%	R.QAHLCVLCESCDQEAYVK.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.QAHLCVLCESCDQEAYVK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
161	YDMC_SCHPO	4.59%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
370	385	2	1877	4	0	39.4	20	95.00%	K.LTSLMESIFPEQTIIR.S		K.LTSLMESIFPEQTIIR.S
82	91	2	1136.53	5	1	33.4	25.5	95.00%	R.NADNSVTNFR.D		R.NADNSVTNFR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
162	PGM_SCHPO	10.65%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
423	435	2	1529.66	4.3	1	62.5	26.4	95.00%	R.YDYEELENEAAGK.V		R.YDYEELENEAAGK.V
350	358	2	1160.54	5.2	1	29	25.3	95.00%	K.FFCNLFDAK.R	Carbamidomethyl (+57)	K.FFCNLFDAK.R
127	142	2	1631.79	4.4	0	81.8	25.3	95.00%	K.YNLGNGGPAPESVTEK.I		K.YNLGNGGPAPESVTEK.I
1	21	3	2330.21	3.2	0	23.9	20.7	95.00%	-.MIETIPTKPYEGQRPGTSGLR.K		-.MIETIPTKPYEGQRPGTSGLR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
163	RL14_SCHPO	14.93%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
53	64	3	1345.75	2.2	0	23.6	20.3	94.90%	R.YGSVVLTHIVMK.L		R.YGSVVLTHIVMK.L
87	94	2	905.44	5.7	0	30.4	23.9	95.00%	K.WASSAWAK.K		K.WASSAWAK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
164	RAD25_SCHPO	14.44%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
63	74	2	1417.75	4.9	1	43.2	22.3	95.00%	R.IISSIEQKEESR.G		R.IISSIEQKEESR.G
218	226	2	1073.63	2.4	0	41	16.5	95.00%	D.STLIMQLLR.D		K.DSTLIMQLLR.D
244	261	3	1846.84	4.4	0	24	26	94.10%	K.EEAPAAAAASENEHPEPK.E		K.EEAPAAAAASENEHPEPK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
165	RANG_SCHPO	10.23%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
188	198	2	1253.61	5.8	0	35.7	24.3	95.00%	R.FANSENANLFK.E		R.FANSENANLFK.E
88	98	2	1353.6	4	0	43.5	25.9	95.00%	K.TNEEEETVEFK.M		K.TNEEEETVEFK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
166	KAPS_SCHPO	22.77%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
157	188	3	3532.7	3.1	0	32.4	23.2	95.00%	K.EFTGISAPYEAPISPEIVVSSHTQSIEECVEK.I	Carbamidomethyl (+57)	K.EFTGISAPYEAPISPEIVVSSHTQSIEECVEK.I
39	52	2	1664.86	3.8	0	65.6	22.9	95.00%	K.STIACALEQYLLQR.G	Carbamidomethyl (+57)	K.STIACALEQYLLQR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
167	PABP_SCHPO	8.42%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
258	266	2	1068.57	4.8	0	26.6	21.3	93.00%	K.ANFTNVYIK.N		K.ANFTNVYIK.N
447	456	2	1142.61	4.9	0	33.9	22.1	95.00%	R.SQLEAQIQAR.N		R.SQLEAQIQAR.N
536	571	3	3524.72	4.6	0	28.7	23.2	95.00%	R.GPVPAQGRPMMMPGSVPSAGPAEAEAVPAVPGMPER.F		R.GPVPAQGRPMMMPGSVPSAGPAEAEAVPAVPGMPER.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
168	VATB_SCHPO	8.35%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
415	427	2	1417.68	4.9	1	78	25.4	95.00%	K.SVVGEEALSQEDR.L		K.SVVGEEALSQEDR.L
439	449	2	1284.62	4.2	0	36.9	25.1	95.00%	K.TFISQGAYENR.T		K.TFISQGAYENR.T
42	59	3	2083.09	4.5	1	23.6	21.7	94.90%	R.RPQYNEIVNLNLPDGSVR.S		R.RPQYNEIVNLNLPDGSVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
169	PDI1_SCHPO	5.28%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	136	3	1350.87	5.1	1	30.4	6.02	95.00%	R.KQLLPTVKPISK.D		R.KQLLPTVKPISK.D
188	201	2	1436.77	4.3	0	45.1	19.9	95.00%	K.SLGSNFPGIVAFTK.D		K.SLGSNFPGIVAFTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
170	UBC4_SCHPO	14.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
118	128	3	1264.72	1	0	35.7	16.9	95.00%	D.PLVPEIAHVYK.T		K.VLLSICSLLTDPNPDDPLVPEIAHVYK.T

91	101	2	1244.65	4.6	1	28.4	23.2	95.00%	R.DQWSPALTISK.V		R.DQWSPALTISK.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
171	Q9P7B4_SCHPO	19.69%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
234	256	3	2522.27	2.7	1	34.8	22.5	95.00%	R.ENVVIADTLVFPSHQGGANHVYR.K		R.ENVVIADTLVFPSHQGGANHVYR.K
163	173	2	1163.64	5.6	0	26.5	19	92.90%	K.SALAQFTSALR.K		K.SALAQFTSALR.K
183	199	2	1918.98	6.8	1	60.8	22.6	95.00%	R.IMEVDPGLVETEFSVVR.F		R.IMEVDPGLVETEFSVVR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
172	SPI1_SCHPO	12.50%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
110	122	2	1514.77	4.6	0	58.5	24	95.00%	R.VCENIPIVLCGNK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VCENIPIVLCGNK.V
152	165	3	1783.91	4.6	0	29.2	23.2	95.00%	K.SNYNFEKPFLWLAR.K		K.SNYNFEKPFLWLAR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
173	TCTP_SCHPO	20.24%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
54	73	2	2271.03	1.9	0	79	27	95.00%	D.AEENAEEGTETVNNLVYSFR.L		K.QGGDVDIGANPSAEDAEENAEEGTETVNNLVYSFR.L
99	112	2	1670.87	2.4	1	28.5	22.9	95.00%	R.LQESNPERVPVFEK.N		R.LQESNPERVPVFEK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
174	ASSY_SCHPO	7.56%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
333	350	2	1884.02	1.9	0	74.3	19.7	95.00%	R.MLLAANNVSQEVVNGVVK.L		R.MLLAANNVSQEVVNGVVK.L
320	332	2	1601.77	4.2	0	39.6	25.7	95.00%	K.ILYNGQFFSPCTR.M	Carbamidomethyl (+57)	K.ILYNGQFFSPCTR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
175	YEI3_SCHPO	13.01%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
98	114	2	1641.86	2.5	0	46.1	22.2	95.00%	K.GASTGVGLGNAFLSHVR.A		K.GASTGVGLGNAFLSHVR.A
43	62	2	2148.05	4.6	1	58.6	24.9	95.00%	K.SVLGNPANYPYATIDPEEAK.V		K.SVLGNPANYPYATIDPEEAK.V
329	342	2	1482.75	2.8	1	41.2	24.6	95.00%	K.APQAAGVIHTDFEK.A		K.APQAAGVIHTDFEK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
176	RL2_SCHPO	15.02%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
92	118	3	2780.44	3.2	0	52	20	95.00%	K.NAALTVGNVLPVGEMPEGTIISNVEEK.A		K.NAALTVGNVLPVGEMPEGTIISNVEEK.A
163	173	2	940.55	4.3	0	54.6	16.4	95.00%	R.GVVGIVAGGGR.I		R.GVVGIVAGGGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
177	SRP2_SCHPO	3.84%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
170	183	2	1490.74	2.3	1	27.9	24.5	94.60%	D.PDAANEPLPEVPSR.F		R.EDPDAANEPLPEVPSR.F
172	183	2	1278.66	2.3	0	25.7	23.5	91.60%	D.AANEPLPEVPSR.F		R.EDPDAANEPLPEVPSR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
178	RL11_SCHPO	14.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
36	49	2	1531.83	4.2	0	63.5	20	95.00%	K.VLEQLSGQTPVFSK.A		K.VLEQLSGQTPVFSK.A
154	164	2	1349.67	4.1	1	39.8	24.4	95.00%	K.INAEDTINWFK.Q		K.INAEDTINWFK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
179	CH10_SCHPO	22.12%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

73	84	2	1230.7	4	0	31.7	16.6	95.00%	R.VLLPAYGGSNIK.V		R.VLLPAYGGSNIK.V
62	72	2	1111.6	4.5	1	30.9	20.3	95.00%	K.LAQPSVAVGDR.V		K.LAQPSVAVGDR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
180	YBS7_SCHPO	7.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
442	471	4	3134.5	-0.033	1	26.4	24.5	95.00%	K.EQPPNKAEPAVPTEASSTKPSEAAEESTPR.F		K.EQPPNKAEPAVPTEASSTKPSEAAEESTPR.F
128	146	2	1760.86	5.1	0	31.6	25.1	95.00%	R.TSGSSTGLSNAPPSANVSK.A		R.TSGSSTGLSNAPPSANVSK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
181	PLR1_SCHPO	8.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	66	2	1195.66	1.6	1	49.6	19.1	95.00%	D.PPTSNLDLLAR.Y		K.QTPDEEAFEVMNYALSQGSNYWDAGEFYGVDPPTSNLDLLAR.Y
147	162	3	1747.92	2.1	1	23.1	21.8	94.30%	K.ISCVGLSEVSAETIKR.A	Carbamidomethyl (+57)	K.ISCVGLSEVSAETIKR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
182	RS3_SCHPO	10.04%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
97	108	2	1362.64	3.8	0	61	25.7	95.00%	R.GLCAVAQCESLR.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GLCAVAQCESLR.Y
30	42	2	1513.64	4.2	0	70.9	26.3	95.00%	R.ELSEEGYSGCEVR.V	Carbamidomethyl (+57)	R.ELSEEGYSGCEVR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
183	YBLH_SCHPO	6.75%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
419	432	2	1450.81	3.1	2	60	17.8	95.00%	D.PETNLIAGLAPLKD.T		R.APEPDPETNLIAGLAPLKDTPVMVMGVESDNLMPVECQR.E
57	76	2	1959.98	0.61	0	51.8	23.7	95.00%	D.PSASITSPSLSSGPEPVYGK.I		K.QQACPNSVDPSASITSPSLSSGPEPVYGK.I
419	431	2	1335.78	2.8	0	44.5	13.6	95.00%	D.PETNLIAGLAPLK.D		R.APEPDPETNLIAGLAPLK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
184	G6PD_SCHPO	8.20%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
468	478	3	1340.68	1.3	1	22.4	23.5	93.20%	D.GPECLYSFLKK.F	Carbamidomethyl (+57)	K.YMEEEKPVPEPYEYGSDGPECLYSFLKK.F
28	40	2	1470.76	2.9	0	30.9	23.3	95.00%	K.TFPALFSLFSEGR.L		K.TFPALFSLFSEGR.L
451	467	2	2060.86	1.5	1	45.1	27.1	95.00%	K.YMEEEKPVPEPYEYGSD.G		K.YMEEEKPVPEPYEYGSDGPECLYSFLK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
185	SODM_SCHPO	20.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	173	2	1303.7	4.2	1	48.8	21.3	95.00%	R.ITTTANQDTIVK.S		R.ITTTANQDTIVK.S
26	48	2	2502.32	2.9	0	32.8	19.3	95.00%	K.ATLPPLPYAYNALEPALSETIMK.L		K.ATLPPLPYAYNALEPALSETIMK.L
127	135	2	1108.52	5	1	34	25.8	95.00%	K.WGSLEDFQK.E		K.WGSLEDFQK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
186	RL24A_SCHPO	20.81%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	12	2	1357.64	4.1	1	34.6	25.3	95.00%	-.MKVEVCSFSGSK.V	Carbamidomethyl (+57)	-.MKVEVCSFSGSK.V
81	91	2	1097.65	4.7	1	29.4	18.1	95.00%	R.GIVGANLDVIK.E		R.GIVGANLDVIK.E
36	43	2	978.52	4.9	0	29.5	22.9	95.00%	K.SESLFLQR.K		K.SESLFLQR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
187	MPG1_SCHPO	11.02%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
270	287	2	1776	4.2	1	35.2	16.3	95.00%	K.IGPNVVIGPNVTIGDGVR.L		K.IGPNVVIGPNVTIGDGVR.L
138	159	4	2530.28	3.4	1	22.1	22.9	95.00%	K.VEEPSKYGVVVHYPNSESLIER.F		K.VEEPSKYGVVVHYPNSESLIER.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
188	DLDH_SCHPO	5.87%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
113	128	2	1663.83	1.7	1	25	24.3	90.40%	R.GIDVSGVSVNLSQMMK.A		R.GIDVSGVSVNLSQMMK.A
155	168	2	1448.76	3.8	1	31.8	22.6	95.00%	K.GTGSFIDPQTLSVK.G		K.GTGSFIDPQTLSVK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
189	YET4_SCHPO	13.60%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
190	216	3	2686.32	5.5	1	58	24	95.00%	R.NDEQLGNSPASITSKPATTSAAQPSSK.V		R.NDEQLGNSPASITSKPATTSAAQPSSK.V
419	462	4	4557.19	2.7	1	18.1	22.3	94.10%	K.NEVNVPSTIPTESENPVAVGGTTAEHPVQEAVTAPTETAHDFSK.E		K.NEVNVPSTIPTESENPVAVGGTTAEHPVQEAVTAPTETAHDFSK.E
487	503	3	1712.87	4.4	0	27.8	23.7	95.00%	R.KPSSTGQEPTTPSTPAK.S		R.KPSSTGQEPTTPSTPAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
190	APE1_SCHPO	3.40%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
253	269	2	1912.97	5	1	42.1	23.6	95.00%	K.TLDFFSGVFGEPYPLPK.C		K.TLDFFSGVFGEPYPLPK.C
137	149	2	1467.71	4.6	0	42.2	24.5	95.00%	K.YLATTQMEPTSAR.R		K.YLATTQMEPTSAR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
191	CYSK1_SCHPO	13.11%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
217	227	3	1196.66	2.4	0	24.5	20.5	95.00%	D.PPGSVLYSHIK.T		R.VASFVADPPGSVLYSHIK.T
10	23	2	1341.78	3.9	0	59.1	15.9	95.00%	K.VPGIVSGFIGAIGR.T		K.VPGIVSGFIGAIGR.T
180	200	2	2019.93	5.1	1	71.4	26.6	95.00%	K.GTVDGFTCSTGTGGTFAGVTK.Y	Carbamidomethyl (+57)	K.GTVDGFTCSTGTGGTFAGVTK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
192	CPGL_SCHPO	4.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
40	53	2	1599.79	4.2	1	88.3	24.6	95.00%	K.VVEMADFVVSEFTK.L		K.VVEMADFVVSEFTK.L
113	121	2	1033.55	1.4	1	36.7	21.9	95.00%	D.PFTLTVDNK.G		K.TVLIYNHFDVQPASLEDGWSTDPFTLTVDNK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
193	RL7B_SCHPO	14.00%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	21	2	2002.11	4.4	0	37	16	95.00%	M.VASSTVPSVASIFAPESLLK.K		-.MVASSTVPSVASIFAPESLLK.K
168	182	2	1523.86	4.4	1	56.2	15.9	95.00%	R.IPLSDNAIIEAALGK.Y		R.IPLSDNAIIEAALGK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
194	TBA2_SCHPO	8.46%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
281	304	3	2899.3	3.7	0	55.7	27.3	95.00%	K.AFHESNSVQEITNQCFEPYNQMVK.C	Carbamidomethyl (+57)	K.AFHESNSVQEITNQCFEPYNQMVK.C
47	60	2	1448.66	2.5	0	38.6	26	95.00%	D.GGFSTFFSETGQGK.Y		R.EIISIHVGQAGTQIGNACWELYCLEHGIQPNGYMNPETASQNSDGGFSTFFSETGQGK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
195	PPID_SCHPO	7.87%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

155	169	2	1686.83	0.8	0	59.9	24.5	95.00%	D.PVVPVVIEECGTCTK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.NDDPVVPVVIEECGTCTK.D
214	226	2	1432.74	4.4	1	72	23.8	95.00%	K.QFAQQNLDTAVAK.W		K.QFAQQNLDTAVAK.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
196	ODPB_SCHPO	8.20%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
199	213	2	1682.93	2.1	0	47.6	17.2	95.00%	D.PNPVVVLENEILYGK.T		R.DPNPVVVLENEILYGK.T
220	234	2	1634.86	4.6	1	26.5	21.8	92.90%	K.EALSEDFVLPFGLAK.V		K.EALSEDFVLPFGLAK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
197	ARO1_SCHPO	3.43%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
677	703	3	2950.41	2.7	1	45.4	24.5	95.00%	R.FACDVLRPMGCTVEQTATSTTV QGPPK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.FACDVLRPMGCTVEQTATSTTV QGPPK.G
162	172	2	1299.72	4.7	0	45.2	20.8	95.00%	K.NLVGAFWQPLR.V		K.NLVGAFWQPLR.V
1232	1247	2	1833.96	4.6	1	44.8	21.9	95.00%	R.ITNSMDIPLILFNMGR.F		R.ITNSMDIPLILFNMGR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
198	GPD2_SCHPO	10.46%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	88	4	2626.25	3.3	1	19.3	25.2	95.00%	K.IQHEGKECNLTEVFNTTHENVK.Y	Carbamidomethyl (+57)	K.IQHEGKECNLTEVFNTTHENVK.Y
311	327	3	1907.98	3	1	33.8	22.2	95.00%	K.TGKPMHVVEQELLDGQK.L		K.TGKPMHVVEQELLDGQK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
199	LYS4_SCHPO	4.30%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
149	159	2	1179.57	4.4	1	26	24.9	92.10%	K.GQGIDFYPAGR.G		K.GQGIDFYPAGR.G
470	489	2	1872.04	4.8	0	47.2	15.2	95.00%	R.EALAYLASPAVVAASAIAGK.I		R.EALAYLASPAVVAASAIAGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
200	RL35_SCHPO	19.67%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
11	24	2	1684.85	4.2	0	72	23.8	95.00%	K.QSQENLAEQLQELR.Q		K.QSQENLAEQLQELR.Q
56	65	2	1157.65	4.3	0	33.6	20.5	95.00%	R.ILTVINESNR.L		R.ILTVINESNR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
201	RLA0_SCHPO	15.06%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
133	144	2	1308.71	5.2	0	29.1	19.5	95.00%	K.TSFFQALGIPTK.I		K.TSFFQALGIPTK.I
98	132	3	3513.88	2.7	1	45.6	17.3	95.00%	R.ETIIANVIAAPARPNAIAPLDVFVP AGNTGMEPGK.T		R.ETIIANVIAAPARPNAIAPLDVFVP AGNTGMEPGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
202	MUG64_SCHPO	11.19%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
224	238	3	1767.86	4.9	1	44.3	25.1	95.00%	K.LDVESAKPENLEHCK.S	Carbamidomethyl (+57)	K.LDVESAKPENLEHCK.S
108	125	2	1851.02	3.8	0	41.3	17.2	95.00%	R.NLGNLTPLEQTPLASVGK.N		R.NLGNLTPLEQTPLASVGK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
203	P5CR_SCHPO	15.25%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
116	129	2	1566.76	5	1	85.9	25.3	95.00%	K.TISSLQSMLDESTR.V		K.TISSLQSMLDESTR.V
70	98	3	3111.57	2.6	1	41.3	22.4	95.00%	K.ENAEMAAISNVLLLSCKPQAAED VLNSPK.M	Carbamidomethyl (+57)	K.ENAEMAAISNVLLLSCKPQAAED VLNSPK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
204	ACAC_SCHPO	1.49%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1972	1994	3	2667.36	3.2	1	27.8	21.1	95.00%	K.TAQAINDFNHGEQLPLFILANWR.G		K.TAQAINDFNHGEQLPLFILANWR.G
197	207	2	1131.63	6.1	0	34.7	18.8	95.00%	K.ISSTIVAQSAR.V		K.ISSTIVAQSAR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
205	EIF3E_SCHPO	6.59%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
267	284	3	2029.08	4.4	0	22.1	19.4	92.80%	R.YLTVAVVTNQNNANQKPR.N		R.YLTVAVVTNQNNANQKPR.N
477	491	2	1679.84	3.6	0	46.3	24.2	95.00%	K.SLSFESQNLEQSLAK.S		K.SLSFESQNLEQSLAK.S

Supplementary Table S2: All "Scaffold" validated proteins and peptides identified from solprotSP (*S.pombe*) and from SCVMprot (*S.cerevisiae*) samples

***S.pombe* - Formic acid digest of large tryptic peptides (replicate B)**

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
1	G3P1_SCHPO	50.00%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
249	259	3	1290.69	4.5	1	28.4	22.9	95.00%	K.LAKPTNYEDIK.A		K.LAKPTNYEDIK.A
167	186	2	2135.06	2	0	104	23.9	95.00%	D.TFGIEEGLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK.T
94	113	2	2181.1	2.7	0	82.2	23.3	95.00%	D.YVIESTGVFTTQETASAHLK.G		K.WSTSGADYVIESTGVFTTQETASAHLK.G
127	139	2	1449.69	3.7	1	45.1	25.6	95.00%	K.DAPMYVVGVNEEK.F		K.DAPMYVVGVNEEK.F
128	145	2	2036.99	2.8	1	85.2	25.1	95.00%	D.APMYVVGVNEEKFNPSEK.V		K.DAPMYVVGVNEEKFNPSEK.V
297	309	2	1344.74	3.3	0	59.5	20.4	95.00%	D.ASAGIQLSPQFVK.L		K.GVLGYTEDAVVSTDFCGDNHSSIFDASAGIQLSPQFVK.L
128	139	2	1334.66	2.1	0	54.2	24.6	95.00%	D.APMYVVGVNEEK.F		K.DAPMYVVGVNEEK.F
87	113	2	2885.38	3.9	1	116	24.8	95.00%	K.WSTSGADYVIESTGVFTTQETASAHLK.G		K.WSTSGADYVIESTGVFTTQETASAHLK.G
146	162	2	1818.91	4.5	0	75	24.4	95.00%	K.VISNASCTTNCLAPLAK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.VISNASCTTNCLAPLAK.V
324	334	2	1148.65	6.2	1	55.4	18.2	95.00%	R.VVDLVAYTAAK.D		R.VVDLVAYTAAK.D
163	186	2	2576.28	1.5	1	96.4	23.6	95.00%	K.VINDTFGIEEGLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK.T
85	93	2	963.47	2.5	2	27.4	24.1	94.20%	D.IKWSTSGAD.Y		R.DPADIKWSTSGADYVIESTGVFTTQETASAHLK.G
119	127	2	928.53	2.3	2	36.7	23.1	95.00%	R.VIISAPSKD.A		R.VIISAPSKDAPMYVVGVNEEK.F
36	48	2	1682.78	3	1	69.5	26.1	95.00%	D.PFIDLEYMAYMFK.Y	Oxidation (+16)	K.TIQVVAINDPFIDLEYMAYMFK.Y
6	13	2	819.43	6.2	0	38.4	22.9	95.00%	K.VGINGFGR.I	Deamidation (+1)	K.VGINGFGR.I
201	215	2	1343.71	4.7	0	69.9	22.6	95.00%	R.GASANIIPSSTGAAK.A		R.GASANIIPSSTGAAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
2	ENO11_SCHPO	53.76%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
361	374	3	1608.73	4.7	0	47.1	26.5	95.00%	R.MSYEAGWGVMVSHR.S		R.MSYEAGWGVMVSHR.S
218	226	2	1013.51	2.1	1	26.5	23.3	93.00%	D.LQTPQEALD.L		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
185	194	2	1204.59	5.4	0	34	24.9	95.00%	R.WGAETYHTLK.S		R.WGAETYHTLK.S
346	360	2	1585.85	6	0	90.8	21.2	95.00%	K.VNQIGSVTESLNAVR.M		K.VNQIGSVTESLNAVR.M
381	396	3	1640.93	1.7	0	25.2	16.3	95.00%	D.TFISHLTVGIGAGQLK.S		R.SGETADTFISHLTVGIGAGQLK.S
65	79	2	1477.87	4	0	73.7	11.8	95.00%	K.AVGNVNNIIAPAVVK.A		K.AVGNVNNIIAPAVVK.A
247	257	2	1200.57	3	1	52.6	25	95.00%	D.VASSEFYVDGK.Y		K.IGLDVASSEFYVDGK.Y
106	120	2	1560.82	4.2	0	61.3	22.6	95.00%	K.LGANAILGVSMAICR.A	Oxidation (+16)/ Carbamidomethyl (+57)	K.LGANAILGVSMAICR.A
303	310	2	1045.48	2	0	26.7	25.8	92.10%	D.WSAWTHMK.A		K.YPIVSIEDPFDQDDWSAWTHMK.A
288	296	2	1062.56	2.4	2	38.5	23.1	95.00%	K.KYPIVSIED.P		K.KYPIVSIEDPFDQDDWSAWTHMK.A
273	287	2	1812.96	4.5	1	75.4	20.8	95.00%	K.LTYQQLTDLYVELSK.K		K.LTYQQLTDLYVELSK.K
227	234	2	898.55	2.4	0	35	20	95.00%	D.LIVEAINK.A		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
16	32	2	1837.92	4	1	84.2	23.4	95.00%	R.GNPTVEVDLTTETGIHR.A		R.GNPTVEVDLTTETGIHR.A
33	50	2	1886.97	4.8	0	105	23.5	95.00%	R.AIVPSGASTGIWEALEMR.D		R.AIVPSGASTGIWEALEMR.D
338	345	2	901.51	4.7	0	31.4	21.3	95.00%	K.CANALLLK.V	Carbamidomethyl (+57)	K.CANALLLK.V
409	414	2	806.43	5.7	0	29.4	23.6	95.00%	K.YNELLR.I		K.YNELLR.I

218	234	2	1895.03	0.93	1	67.4	18.2	95.00%	D.LQTPQEALDLIVEAINK.A	Deamidation (+1)	R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
415	432	2	1815.87	2.5	0	84.3	25.6	95.00%	R.IEEELGSEGVYAGAHAGK.Y		R.IEEELGSEGVYAGAHAGK.Y
311	320	2	1093.5	2.1	1	34.4	25	95.00%	K.AETDFQIVGD.D		K.AETDFQIVGDDLTVTNVK.R
375	396	2	2201.14	2.9	1	122	20.8	95.00%	R.SGETADTFISHLTVGIGAGQLK.S		R.SGETADTFISHLTVGIGAGQLK.S
89	96	2	905.49	4.7	1	57.4	23.1	95.00%	K.AADEFLLK.L		K.AADEFLLK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
3	PGK_SCHPO	47.34%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
359	378	2	1917.95	4	1	118	24.2	95.00%	K.TCEAGNVVIVGGGDTATVAK.K	Carbamidomethyl (+57)	K.TCEAGNVVIVGGGDTATVAK.K
151	162	2	1279.63	2.4	1	32.6	25.2	95.00%	K.SLTSLGDIFVND.A		K.SLTSLGDIFVNDAFGTAHR.A
307	316	2	1119.49	3	1	39.3	25.1	95.00%	D.GWMGLDCGPK.S	Carbamidomethyl (+57)	K.VGSATAEEGIPDGWMGLDCGPK.S
123	132	3	1145.54	4.7	0	33.9	25.7	95.00%	R.FHIEEEGSAK.V		R.FHIEEEGSAK.V
57	71	2	1591.87	2.9	0	46.2	20	95.00%	K.AVILMSHLGRPNGAR.V	Deamidation (+1)	K.AVILMSHLGRPNGAR.V
112	122	2	1211.69	4.5	0	57.3	18.4	95.00%	K.GGEVILLENLR.F		K.GGEVILLENLR.F
40	48	2	910.59	3.6	0	25.3	12.6	91.10%	R.IVGALPTIK.Y		R.IVGALPTIK.Y
330	347	2	2010.99	4.7	1	67	24.2	95.00%	K.TIVWNGPAGVFEFDNFAK.G		K.TIVWNGPAGVFEFDNFAK.G
359	372	2	1346.62	2.7	1	25.6	25.6	90.50%	K.TCEAGNVVIVGGGD.T	Carbamidomethyl (+57)	K.TCEAGNVVIVGGGDTATVAK.K
404	414	2	1040.63	5.6	0	39.4	18	95.00%	K.ALPGVVALSSK.-		K.ALPGVVALSSK.-
158	169	2	1346.68	2.4	1	76.5	24.6	95.00%	D.IFVNDAFGTAHR.A		K.SLTSLGDIFVNDAFGTAHR.A
383	403	2	2069.04	3.6	1	81.1	23.7	95.00%	K.EDALSHVSTGGGASLELLEGK.A		K.EDALSHVSTGGGASLELLEGK.A
321	329	2	994.54	5.5	0	50.2	20.8	95.00%	K.FAEVITTSK.T		K.FAEVITTSK.T
75	86	3	1304.74	4.3	0	59.4	17.9	95.00%	K.YSLKPVAAELSK.L		K.YSLKPVAAELSK.L
385	403	2	1824.96	2.1	0	93.3	21	95.00%	D.ALSHVSTGGGASLELLEGK.A		K.EDALSHVSTGGGASLELLEGK.A
197	213	2	1737	3.5	0	54.1	13.4	95.00%	K.ALENPARPFLAILGGAK.V		K.ALENPARPFLAILGGAK.V
123	134	2	1359.63	2	2	29.9	26.1	95.00%	R.FHIEEEGSAKVD.G		R.FHIEEEGSAKVDGK.K
170	181	2	1267.64	4	1	58.7	23.1	95.00%	R.AHSSMVGVDLPR.V		R.AHSSMVGVDLPR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
4	METE_SCHPO	43.98%	100%	29

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
561	571	2	1184.7	5.1	0	40.5	17.5	95.00%	K.GMLTAPITILR.W		K.GMLTAPITILR.W
434	449	2	1746.97	7	0	46.9	17.6	95.00%	K.LPLFPTTTIGSFPQTK.E		K.LPLFPTTTIGSFPQTK.E
4	11	2	845.48	4.8	0	33.3	22.1	95.00%	K.SAVLGFPR.I		K.SAVLGFPR.I
707	714	2	901.49	4.3	0	27.7	24.5	94.50%	R.VPPVSEFK.E		R.VPPVSEFK.E
684	690	2	813.51	5.6	0	34.2	19.1	95.00%	K.LLNVLSR.Y		K.LLNVLSR.Y
691	706	2	1818.88	3.8	1	84	25	95.00%	R.YTSCIGPGLFDIHSPR.V	Carbamidomethyl (+57)	R.YTSCIGPGLFDIHSPR.V
393	404	2	1284.67	4.4	0	68.2	21.6	95.00%	R.AESPITNVEAVR.E		R.AESPITNVEAVR.E
707	716	3	1186.64	4.9	1	25.6	21.3	95.00%	R.VPPVSEFKER.I		R.VPPVSEFKER.I
125	139	2	1821.82	1.6	1	33.2	26.8	95.00%	D.SNYHFLRPEVSEETD.F		K.WFDSNYHFLRPEVSEETDFK.L
391	404	2	1511.81	4	1	42.1	21	95.00%	K.ARAESPITNVEAVR.E		K.ARAESPITNVEAVR.E
499	508	2	1257.55	4.4	1	53.6	25.7	95.00%	R.NDMVQYFGER.M		R.NDMVQYFGER.M
243	260	2	1982.08	3.5	1	54.1	17.6	95.00%	K.LILTTYFGSLQSNADVLK.G		K.LILTTYFGSLQSNADVLK.G
428	449	3	2402.33	4.8	1	46	14.5	95.00%	K.QQASLKLPLFPTTTIGSFPQTK.E		K.QQASLKLPLFPTTTIGSFPQTK.E
325	351	3	2884.5	3.5	1	47.3	18.5	95.00%	R.VQVASSSSILHIPHSLSGEDQINPEIK.R		R.VQVASSSSILHIPHSLSGEDQINPEIK.R
261	273	2	1330.78	2.4	1	55.8	14.8	95.00%	K.GLPIAGVHVDVVR.A		K.GLPIAGVHVDVVR.A
281	299	2	1881.08	4.8	0	87.4	11.1	95.00%	R.ALAVLGENQIISVGVVSGR.N		R.ALAVLGENQIISVGVVSGR.N
147	155	2	1034.53	5.7	1	36.8	24.6	95.00%	K.ALDEFLEAK.E		K.ALDEFLEAK.E
595	601	2	844.46	1.7	1	26	24.1	92.30%	D.EVLDLEK.A		R.DEVLDLEK.A
325	344	2	2062.04	2.1	1	99.2	23.7	95.00%	R.VQVASSSSILHIPHSLSGED.Q		R.VQVASSSSILHIPHSLSGEDQINPEIK.R
670	679	2	1060.54	3.4	1	31	23.9	95.00%	D.ADVVSIENSK.S		R.LDADVVSIENSK.S

361	369	2	1017.56	4.9	0	30.5	21.5	95.00%	K.CAELAILTK.A	Carbamidomethyl (+57)	K.CAELAILTK.A
461	473	2	1539.76	4.1	1	67.2	24.3	95.00%	K.GLISQEEYDAFIR.K		K.GLISQEEYDAFIR.K
547	560	2	1596.79	3.6	0	50.8	24.1	95.00%	K.ESQYAQSITSKPMK.G		K.ESQYAQSITSKPMK.G
606	615	2	1199.6	4.3	1	55.1	24.2	95.00%	K.VIQCDEPALR.E	Carbamidomethyl (+57)	K.VIQCDEPALR.E
527	546	3	2267.24	3.3	1	44.5	16.3	95.00%	R.CVRPPIIVGDVYRPAPMTVK.E	Carbamidomethyl (+57)	R.CVRPPIIVGDVYRPAPMTVK.E
631	637	2	877.45	5.9	1	49	23.7	95.00%	K.WAIDAFR.L		K.WAIDAFR.L
85	99	2	1632.78	1.8	1	68.9	24.9	95.00%	R.LSGLSSLDTYFAMGR.G	Oxidation (+16)	R.LSGLSSLDTYFAMGR.G
156	176	3	2256.33	3.9	0	51.3	4.77	95.00%	K.EAGIITRPVLVGPVTYLFIAK.A		K.EAGIITRPVLVGPVTYLFIAK.A
30	40	2	1132.6	4.2	0	58.1	22.9	95.00%	K.TSAEELLATAK.Q		K.TSAEELLATAK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
5	EF1A1_SCHPO	46.09%	100%	20

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
265	288	3	2443.35	2.4	0	50.1	15.3	95.00%	R.VETGVIKPGMIVTFAPAGVTTEVK.S		R.VETGVIKPGMIVTFAPAGVTTEVK.S
402	421	2	2268.08	3.1	1	85.2	25.3	95.00%	K.MVPSKPMCVEAFTDYAPLGR.F	Carbamidomethyl (+57)	K.MVPSKPMCVEAFTDYAPLGR.F
289	304	2	1692.74	1.8	1	30.3	26.6	95.00%	K.SVEMHHESLDAGLPGD.N		K.SVEMHHESLDAGLPGDNVGFNVK.N
147	154	2	883.55	5.8	0	26.4	17.9	92.80%	K.QLIVAVNK.M		K.QLIVAVNK.M
289	298	2	1182.5	1.9	1	25.8	25.6	90.90%	K.SVEMHHESLD.A		K.SVEMHHESLDAGLPGDNVGFNVK.N
254	264	2	1024.61	4.2	0	65.4	14.1	95.00%	K.IGGIGTVPVGR.V		K.IGGIGTVPVGR.V
6	20	2	1529.84	3.1	1	64.2	19.9	95.00%	K.GHINVVVIGHVDSGK.S		K.GHINVVVIGHVDSGK.S
232	241	2	1081.54	3	1	33.4	24.1	95.00%	D.SIEPPARPTD.K		K.TLLEAIDSIEPPARPTDKPLR.L
185	214	3	3453.63	3.7	1	49.2	24.8	95.00%	K.TVPFVPVSGFQGDNMIEPTTNMPWYQGWQK.E		K.TVPFVPVSGFQGDNMIEPTTNMPWYQGWQK.E
155	164	2	1151.51	6.4	1	75.8	24.9	95.00%	K.MDTTGWSQAR.F		K.MDTTGWSQAR.F
198	214	2	2123.94	-2.5	0	53.9	27.2	95.00%	D.NMIEPTTNMPWYQGWQK.E	Deamidation (+1)	K.TVPFVPVSGFQGDNMIEPTTNMPWYQGWQK.E
225	241	2	1836.95	3.5	1	29.1	22.1	95.00%	K.TLLEAIDSIEPPARPTD.K		K.TLLEAIDSIEPPARPTDKPLR.L
85	96	2	1340.69	4.4	1	66.1	22.7	95.00%	K.YNVTVIDAPGHR.D		K.YNVTVIDAPGHR.D
246	253	2	974.55	4.1	1	32.1	21	95.00%	R.LPLQDVYK.I		R.LPLQDVYK.I
135	146	2	1313.74	3.9	0	45.8	19.1	95.00%	R.EHALLAYTLGVK.Q		R.EHALLAYTLGVK.Q
370	376	2	848.47	4.7	0	25.9	22.8	92.10%	K.FAELIEK.I		K.FAELIEK.I
223	231	2	958.54	2.6	2	31.6	23.4	95.00%	K.GKTLLEAID.S		K.GKTLLEAIDSIEPPARPTDKPLR.L
299	311	2	1286.67	2.3	1	43	23.4	95.00%	D.AGLPGDNVGFNVK.N		K.SVEMHHESLDAGLPGDNVGFNVK.N
165	177	2	1582.83	3.8	1	66.1	21	95.00%	R.FEEIVKETSNFIK.K		R.FEEIVKETSNFIK.K
402	415	2	1610.72	1.2	1	36.9	27.1	95.00%	K.MVPSKPMCVEAFTD.Y	Carbamidomethyl (+57)	K.MVPSKPMCVEAFTDYAPLGR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
6	KPYK_SCHPO	61.69%	100%	26

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
332	344	2	1336.66	2.4	1	89.5	25.1	95.00%	D.GADLVMLSGETTK.G	Oxidation (+16)	R.AEVSDVGNAVLDGADLVMLSGETTK.G
108	121	2	1596.72	2.7	1	30.3	26.6	95.00%	D.YPISSGHEMIFTTD.D		R.TGLTVGGTDYPISSGHEMIFTTDDAYAEK.C
487	497	2	1053.66	5.9	0	39.5	11.1	95.00%	K.IIVLQGAVGGK.G		K.IIVLQGAVGGK.G
233	243	2	1214.66	3.9	1	28.5	22.1	95.00%	R.EVLGEEGKNIK.I		R.EVLGEEGKNIK.I
108	122	2	1711.74	1.7	1	30	27.1	94.80%	D.YPISSGHEMIFTTDD.A		R.TGLTVGGTDYPISSGHEMIFTTDDAYAEK.C
422	433	3	1430.81	4.6	0	41.1	17.2	95.00%	K.YRPSIPIVMVTR.C		K.YRPSIPIVMVTR.C
10	26	2	1880.98	3.7	1	90.9	21.6	95.00%	K.QWVAGLNSELDIPAVNR.R		K.QWVAGLNSELDIPAVNR.R
155	164	2	1105.64	2.5	0	36.8	16.1	95.00%	D.GILSFTVIEK.V		R.IIYVDDGILSFTVIEK.V
446	459	2	1607.81	2	2	41.2	23.6	95.00%	R.GVYPVIYEKEPLSD.W		R.GVYPVIYEKEPLSDWQK.D
76	91	2	1640.92	3.9	2	43.1	17.2	95.00%	R.KASATNPLFPLAIALD.T		R.KASATNPLFPLAIALDTK.G

77	93	2	1741.97	2.2	1	41.6	18	95.00%	K.ASATNPLFPLAIALDTK.G		K.ASATNPLFPLAIALDTK.G
225	232	2	951.52	5	1	30.1	21.1	95.00%	R.AEDVIHIR.E		R.AEDVIHIR.E
57	75	3	2253.99	2.7	1	54.8	27.1	95.00%	R.MNFSHGSYEYHQSVIDNAR.K		R.MNFSHGSYEYHQSVIDNAR.K
28	37	2	1088.6	5	0	46.3	21.4	95.00%	R.TSIICTIGPK.S	Carbamidomethyl (+57)	R.TSIICTIGPK.S
274	288	2	1598.91	1.8	0	60.6	16.4	95.00%	D.LGIEIPASQVFVAQK.M		R.GDLGIEIPASQVFVAQK.M
263	271	2	960.51	2.2	1	35.4	23.2	95.00%	D.VTDGIMVAR.G		K.IENQQGVNNFDSILDVTDGIMVAR.G
468	477	2	1186.55	5.3	0	54.8	24.7	95.00%	R.VAYGCQQAYK.M	Carbamidomethyl (+57)	R.VAYGCQQAYK.M
345	360	2	1743.82	5.3	0	80.9	25.5	95.00%	K.GSYPVEAVTYMAETAR.V		K.GSYPVEAVTYMAETAR.V
335	344	2	1077.58	2.5	0	29.8	23.3	95.00%	D.LVMLSGETTK.G		R.AEVSDVGNAVLDGADLVMLSGETTK.G
272	288	2	1770.96	3.8	1	69.1	19.7	95.00%	R.GDLGIEIPASQVFVAQK.M		R.GDLGIEIPASQVFVAQK.M
361	380	2	2229.12	4.2	0	78.6	22.9	95.00%	R.VAEASIPYGSLYQEMFGLVR.R		R.VAEASIPYGSLYQEMFGLVR.R
294	319	4	2982.39	2.1	0	71.8	25.9	95.00%	K.CNIAGKPVACATQMLESMTYNPRPTR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Oxidation (+16)/ Deamidation (+1)	K.CNIAGKPVACATQMLESMTYNPRPTR.A
405	417	2	1287.72	5.7	0	62	19	95.00%	K.AIVVLSTSGNTAR.L		K.AIVVLSTSGNTAR.L
99	121	2	2398.11	2.2	1	39.9	26.7	95.00%	R.TGLTVGGTDYPISSGHEMIFTTD.D		R.TGLTVGGTDYPISSGHEMIFTTDDAYAEK.C
212	223	2	1384.68	2.2	1	50.1	24.5	95.00%	K.NGVDMIFASFIR.R	Oxidation (+16)	K.NGVDMIFASFIR.R
381	404	2	2460.23	3.5	1	76.2	23.7	95.00%	R.RPLECATETTAVAAIGASIESDAK.A	Carbamidomethyl (+57)	R.RPLECATETTAVAAIGASIESDAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
7	ALF_SCHPO	63.97%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
257	275	3	2097.05	1.8	0	61.9	23.9	95.00%	D.KPVFFVFHGGSGSSVNEFR.T		K.TTNDKPVFFVFHGGSGSSVNEFR.T
26	50	2	2496.31	4.1	0	69.4	19.9	95.00%	R.EHGFAIPAINVTSSSTAIAALEAAR.E		R.EHGFAIPAINVTSSSTAIAALEAAR.E
309	325	2	1829.9	2.5	1	66.8	24.6	95.00%	D.YLMTPVGNPEGADKPNK.K		K.DYLMTPVGNPEGADKPNK.K
207	234	4	2951.53	3.2	0	31.9	20.6	95.00%	R.ELSSVTPYFSIAAAFGNVHGVYKPGNVK.L		R.ELSSVTPYFSIAAAFGNVHGVYKPGNVK.L
291	301	2	1283.62	2.2	2	29.4	24.3	95.00%	D.TQFAYVEGVRD.Y		K.VNIDTDTQFAYVEGVRDYVLK.Y
253	275	2	2528.21	2	1	93.7	25.2	95.00%	K.TTNDKPVFFVFHGGSGSSVNEFR.T		K.TTNDKPVFFVFHGGSGSSVNEFR.T
94	112	2	2098.02	4.1	1	63.5	24.9	95.00%	R.SIAPFFGVPVVMHSDHCAK.K	Carbamidomethyl (+57)	R.SIAPFFGVPVVMHSDHCAK.K
345	358	2	1597.83	4.2	1	60.4	23	95.00%	R.VLTALEDFYTVNTL.-		R.VLTALEDFYTVNTL.-
131	143	3	1481.7	2.6	1	21.3	25.3	90.50%	K.IHGEPLFSSHMLD.L		K.IHGEPLFSSHMLDLSEEPK.K
6	19	2	1424.83	2.4	1	51.5	15.2	95.00%	D.IVPTGVITGDNVLK.L		-.MGILDIVPTGVITGDNVLK.L
289	300	2	1384.67	2.7	1	75.2	25.7	95.00%	D.TDTQFAYVEGVR.D		K.VNIDTDTQFAYVEGVR.D
94	108	2	1601.79	2	1	60	24.4	95.00%	R.SIAPFFGVPVVMHSD.H		R.SIAPFFGVPVVMHSDHCAK.K
291	300	2	1168.59	2.7	0	39.9	23.3	95.00%	D.TQFAYVEGVR.D		K.VNIDTDTQFAYVEGVR.D
120	130	2	1306.56	2	1	41.4	25.8	95.00%	D.GMFEADEAYFK.I		K.LLPWMDGMFEADEAYFK.I
235	248	2	1564.88	4	0	58.4	15.7	95.00%	K.LQPALLGQHQAYVK.E		K.LQPALLGQHQAYVK.E
54	71	2	1843.96	1.9	0	95.7	22.6	95.00%	R.SPIILQTSNGGAHFFAGK.E		R.SPIILQTSNGGAHFFAGK.E
131	149	3	2165.05	3.2	1	36.1	24	95.00%	K.IHGEPLFSSHMLDLSEEPK.K		K.IHGEPLFSSHMLDLSEEPK.K
80	93	2	1399.76	5.1	0	89.1	19.9	95.00%	K.ASIAGSIAAAHYIR.S		K.ASIAGSIAAAHYIR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
8	PDC2_SCHPO	50.00%	100%	28

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
5	18	2	1526.74	2	0	61.8	25.2	95.00%	D.AESTMTVGTYLAQR.L		K.DAESTMTVGTYLAQR.L
254	278	3	2854.28	2.3	1	77	27.1	95.00%	K.GFYSEEHKNYAGVYWGEVSSSETTK.A		K.GFYSEEHKNYAGVYWGEVSSSETTK.A
204	214	2	1130.62	4.6	1	53.5	21.3	95.00%	K.ATDIAAELISK.K		K.ATDIAAELISK.K
440	461	2	2409.21	3.3	1	90.9	22.6	95.00%	R.TIVMVGDGSFQLTGQEISQMIR.H		R.TIVMVGDGSFQLTGQEISQMIR.H

546	555	2	1235.55	2.3	1	38.3	25.9	95.00%	D.CTQELVDWGK.A	Carbamidomethyl (+57)/ Deamidation (+1)	K.EGPTLIECAIDTDDCTQELVDWGK.A
238	253	2	1689.86	2.5	0	64.5	23.7	95.00%	K.LAEALNCAAFIMPAAK.G	Carbamidomethyl (+57)	K.LAEALNCAAFIMPAAK.G
516	525	2	1047.55	4.8	0	31.2	23.2	95.00%	K.TGEELTSAIK.V		K.TGEELTSAIK.V
228	237	2	949.49	5	0	30.2	23.3	95.00%	R.AAGAESAFVK.L		R.AAGAESAFVK.L
304	328	2	2694.38	3.7	1	84	21.2	95.00%	R.AAPNPNILLNSDYTSVSIPGYVFSR.V		R.AAPNPNILLNSDYTSVSIPGYVFSR.V
215	225	3	1192.76	1.6	1	29.2	9.03	95.00%	K.KEKPILLAGPK.L		K.KEKPILLAGPK.L
329	340	2	1425.76	4.3	0	95.2	21.9	95.00%	R.VYMAEFLELLAK.K		R.VYMAEFLELLAK.K
447	461	2	1693.85	2.4	0	65.8	23.8	95.00%	D.GSFQLTGQEISQMIR.H		R.TIVMVGDGSFQLTGQEISQMIR.H
127	135	2	1157.55	2.3	0	35.5	26.3	95.00%	D.FEYQMEIAK.K		R.SNGIACAVVTYSVGALTAFDGIGGAYAENLPVILVSGSPNTNDLSSGHLLHHTLGTHDFEYQMEIAK.K
160	198	4	4251.22	3.6	1	16.7	18.8	90.80%	R.QAILQHKPVYIEIPTNMANQPCPVPGPISAVISPEISDK.E	Carbamidomethyl (+57)	R.QAILQHKPVYIEIPTNMANQPCPVPGPISAVISPEISDK.E
495	508	2	1529.69	2.2	0	65.3	26	95.00%	D.FAAFCESLNGETGK.A	Carbamidomethyl (+57)	R.IQNWDFAAFCESLNGETGK.A
316	328	2	1474.75	3	0	33.5	23.4	95.00%	D.YTSVSIPGYVFSR.V		R.AAPNPNILLNSDYTSVSIPGYVFSR.V
369	378	2	1157.64	5	1	28	22.4	94.90%	K.AALNRVEVMR.Q		K.AALNRVEVMR.Q
137	146	2	1101.64	5.4	1	51.2	18.6	95.00%	K.LTCAAVAIKR.A	Carbamidomethyl (+57)	K.LTCAAVAIKR.A
19	25	2	770.49	4.3	0	34.4	18.1	95.00%	R.LVEIGIK.N		R.LVEIGIK.N
462	474	3	1575.97	4.8	1	29.2	6.02	95.00%	R.HKLPVLIFLLNNR.G		R.HKLPVLIFLLNNR.G
26	37	2	1429.72	4.2	1	38.3	24.4	95.00%	K.NHFVVPGDYNLR.L		K.NHFVVPGDYNLR.L
262	278	2	1876.86	4.2	0	98.1	26.4	95.00%	K.NYAGVYWGEVSSSETTK.A		K.NYAGVYWGEVSSSETTK.A
150	159	2	1121.6	2.8	1	39	21.4	95.00%	D.APVMIDHAIR.Q		R.AEDAPVMIDHAIR.Q
490	508	2	2186.97	4.3	1	85.4	27	95.00%	R.IQNWDFAAFCESLNGETGK.A	Carbamidomethyl (+57)/ Deamidation (+1)	R.IQNWDFAAFCESLNGETGK.A
464	474	2	1310.81	4.6	0	66.2	10.4	95.00%	K.LPVLIFLLNNR.G		K.LPVLIFLLNNR.G
136	145	2	1073.63	3.9	1	39.6	15.9	95.00%	K.KLTCAAVAIK.R	Carbamidomethyl (+57)	K.KLTCAAVAIK.R
4	18	2	1641.77	4.2	1	65.2	26	95.00%	K.DAESTMTVGTYLAQR.L		K.DAESTMTVGTYLAQR.L
216	225	3	1064.66	3.8	0	29.3	12	95.00%	K.EKPILLAGPK.L		K.EKPILLAGPK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
9	ADH4_SCHPO	49.29%	100%	20

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
110	129	2	2090.16	3.2	1	45	16.3	95.00%	D.GVQPNPTVGNVNQGLEIVKK.E		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVKK.E
110	128	2	1962.06	1.9	0	62	19.9	95.00%	D.GVQPNPTVGNVNQGLEIVK.K		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K
375	385	3	1245.76	2	1	42.5	10	95.00%	K.IRPHLVDLGVK.E		K.IRPHLVDLGVK.E
76	87	2	1282.76	5.2	1	44.2	15.1	95.00%	K.NTLIVTDPGIIK.V		K.NTLIVTDPGIIK.V
366	374	2	1027.63	6.6	0	37.3	16.2	95.00%	R.ISQLVLEVK.I		R.ISQLVLEVK.I
348	364	2	1882.86	2.2	1	41.2	26.8	95.00%	D.IAFHLGCEEHTAEAALD.R	Carbamidomethyl (+57)	R.LGDIAFHLGCEEHTAEAALDR.I
149	159	2	1014.58	4.8	0	36.7	21.2	95.00%	K.GIALLATNGGK.I	Deamidation (+1)	K.GIALLATNGGK.I
210	219	2	1125.55	2.7	1	30.7	24.6	95.00%	K.HTMPILSVND.P		K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
348	365	4	2038.96	2	1	33.6	26.1	95.00%	D.IAFHLGCEEHTAEAALDR.I	Carbamidomethyl (+57)	R.LGDIAFHLGCEEHTAEAALDR.I
400	412	2	1381.59	-0.0025	1	39.3	26.3	95.00%	D.ACGATNPIQPTHD.E	Carbamidomethyl (+57)/ Deamidation (+1)	K.DACGATNPIQPTHDEVK.A
399	412	2	1495.64	3.2	1	28.5	26.6	93.50%	K.DACGATNPIQPTHD.E	Carbamidomethyl (+57)	K.DACGATNPIQPTHDEVK.A
96	128	3	3573.88	3.6	1	56.5	18.9	95.00%	K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K
209	219	2	1253.65	3.4	2	37.5	22.1	95.00%	D.KHTMPILSVND.P		K.MAIIDKHTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C

220	237	2	1882.84	3.1	1	43.4	27.1	95.00%	D.PETMYGLPPSLTAATGMD.A	Oxidation (+16)/ Oxidation (+16)	K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
168	191	3	2514.36	4	1	55.3	17.6	95.00%	D.KSSKPQLPLIAINTTAGTASEMTR.F		K.IADYEGVDKSSKPQLPLIAINTTAGTASEMTR.F
169	191	2	2386.26	3.6	0	87.6	19.2	95.00%	K.SSKPQLPLIAINTTAGTASEMTR.F		K.SSKPQLPLIAINTTAGTASEMTR.F
238	256	2	1942.97	2.6	1	44.9	23.9	95.00%	D.ALTHAVEAYVSTAANPITD.A		K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
192	200	2	1078.57	4	0	35.5	22.9	95.00%	R.FAIITEETR.H		R.FAIITEETR.H
134	148	2	1475.65	3	1	61.2	26.6	95.00%	D.SMVSIGGGSAHDCAK.G	Carbamidomethyl (+57)	K.ENCDSMVSIGGGSAHDCAK.G
400	415	2	1736.82	3.5	1	26.5	25.9	91.50%	D.ACGATNPIQPTHDEVK.A	Carbamidomethyl (+57)	K.DACGATNPIQPTHDEVK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
10	PMGY_SCHPO	67.30%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
122	134	2	1389.68	2.2	1	33.5	24.8	95.00%	R.SYDIAPPNGESLK.D		R.SYDIAPPNGESLK.D
23	30	2	977.54	3.1	0	32.1	21.6	95.00%	K.LNLFTGWK.D		K.LNLFTGWK.D
32	43	3	1242.68	1.8	1	58.8	20.5	95.00%	D.PALSETGIKEAK.L		K.DPALSETGIKEAK.L
111	120	2	1271.65	5.7	0	79.8	23.2	95.00%	K.WGAEQVQIWR.R		K.WGAEQVQIWR.R
70	90	2	2429.25	3.7	1	89.6	21.4	95.00%	K.TCQIILEEVGEPNLETIKSEK.L	Carbamidomethyl (+57)	K.TCQIILEEVGEPNLETIKSEK.L
186	199	2	1553.85	1.9	1	46.2	18.5	95.00%	R.ELATGVPIVYHLDK.D		R.ELATGVPIVYHLDK.D
146	157	2	1320.78	4.4	1	36.9	13.8	95.00%	K.STIVPHILKGEK.V		K.STIVPHILKGEK.V
2	14	2	1439.81	5.3	0	52	17.6	95.00%	M.TTEAAPNLLVLTR.H	Acetyl (+42)	-.MTTEAAPNLLVLTR.H
158	168	2	1149.67	4.5	0	26.5	14	93.00%	K.VLIAAHGNSLR.A		K.VLIAAHGNSLR.A
95	104	2	1169.58	4.8	1	46.4	23.7	95.00%	R.YYGDLQGLNK.D		R.YYGDLQGLNK.D
58	66	2	1005.56	3.1	0	63.4	18.3	95.00%	D.IAFTSALQR.A		K.FDIAFTSALQR.A
70	87	2	2085.08	4.2	0	96.7	21.2	95.00%	K.TCQIILEEVGEPNLETIK.S	Carbamidomethyl (+57)	K.TCQIILEEVGEPNLETIK.S
1	14	2	1528.84	4.4	0	53	20	95.00%	-.MTTEAAPNLLVLTR.H		-.MTTEAAPNLLVLTR.H
15	30	3	1944.95	1.4	1	42.7	25.2	95.00%	R.HGESEWNKLNLFTGWK.D		R.HGESEWNKLNLFTGWK.D
32	40	2	914.51	2.4	0	53.6	24.5	95.00%	D.PALSETGIK.E		K.DPALSETGIK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
11	TPIS_SCHPO	64.26%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
71	98	3	2925.39	4	1	98.2	25	95.00%	K.NGAYTGENSAQSLIDAGITYTLTGHSER.R		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R
206	222	2	1841.9	2.2	1	42.9	25	95.00%	R.VIYGGSVNGGNCKEFLK.F	Deamidation (+1)/ Carbamidomethyl (+57)	R.VIYGGSVNGGNCKEFLK.F
160	174	2	1615.9	2.5	0	83.7	16.5	95.00%	K.IVIAYEPVWAIGTGK.T		K.IVIAYEPVWAIGTGK.T
175	189	2	1678.84	4.6	0	84.5	24.1	95.00%	K.TATPEQAQEVHAEIR.K		K.TATPEQAQEVHAEIR.K
135	145	2	1242.66	4.7	0	39.7	21.6	95.00%	R.EANETINVVVR.Q		R.EANETINVVVR.Q
115	134	3	2176.12	2.2	0	34.6	21.8	95.00%	K.FALEQGLTVVACIGETLAER.E	Carbamidomethyl (+57)	K.FALEQGLTVVACIGETLAER.E
175	190	2	1806.93	4.5	1	52	22.5	95.00%	K.TATPEQAQEVHAEIRK.W		K.TATPEQAQEVHAEIRK.W
32	52	2	2422.27	3.5	1	66.1	19.4	95.00%	K.LNVGDVETVIFPQNMYLITTR.Q		K.LNVGDVETVIFPQNMYLITTR.Q
228	249	3	2334.25	2	0	38.5	17.9	95.00%	D.GFLVGGASLKPEFHNIVNVHSL.-		K.FHDIDGFLVGGASLKPEFHNIVNVHSL.-
71	85	2	1538.69	2	1	46.5	26.8	95.00%	K.NGAYTGENSAQSLID.A		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R
86	98	2	1404.7	1.8	0	46.2	24.8	95.00%	D.AGITYTLTGHSER.R		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R
196	205	2	971.55	5.3	0	76.1	21.9	95.00%	K.LGASVAEGLR.V		K.LGASVAEGLR.V
37	52	2	1924.02	2	0	54.2	20.5	95.00%	D.VETVIFPQNMYLITTR.Q		K.LNVGDVETVIFPQNMYLITTR.Q
206	218	2	1324.61	4.4	0	76.9	25.9	95.00%	R.VIYGGSVNGGNCK.E	Deamidation (+1)/ Carbamidomethyl (+57)	R.VIYGGSVNGGNCK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
12	GLYD_SCHPO	45.18%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
146	159	2	1649.78	3.9	0	75	26	95.00%	K.ISAVSTYFESMPYR.V		K.ISAVSTYFESMPYR.V
183	193	2	1209.62	4.5	0	57.8	22.4	95.00%	K.ILVAGTSAYCR.L	Carbamidomethyl (+57)	K.ILVAGTSAYCR.L
171	182	3	1483.76	2.4	1	26.6	23	95.00%	D.MLEHDAQLFRPK.I		R.VDPNTGLIDYDMLEHDAQLFRPK.I
361	371	2	1254.76	2.7	0	53.2	13	95.00%	R.VLELINIVTNK.N		R.VLELINIVTNK.N
145	159	2	1777.88	2.6	1	110	24.9	95.00%	K.KISAVSTYFESMPYR.V		K.KISAVSTYFESMPYR.V
17	24	2	915.49	2.2	0	45.1	24.2	95.00%	D.PTVAEIMR.H		K.EQDPTVAEIMR.H
97	123	3	2996.43	3.4	0	55	24.8	95.00%	K.WGVNVQCLSGSPANMQVYQAIMPPHGR.L	Carbamidomethyl (+57)	K.WGVNVQCLSGSPANMQVYQAIMPPHGR.L
74	85	2	1550.75	4.7	1	96.3	25.4	95.00%	K.FIDQIETLCQER.A	Carbamidomethyl (+57)	K.FIDQIETLCQER.A
86	96	2	1129.62	5.1	1	54.8	22.1	95.00%	R.ALAAFNLDPAK.W		R.ALAAFNLDPAK.W
59	67	2	998.45	5.1	0	32.9	23.9	95.00%	K.YSEGYPGAR.Y		K.YSEGYPGAR.Y
277	302	3	2725.45	2.8	0	25.2	18	95.00%	K.INFSVFPGHQGGPHNHTITALAVALK.Q		K.INFSVFPGHQGGPHNHTITALAVALK.Q
303	318	3	1967.95	5.1	1	36.3	25.2	95.00%	K.QCQEPAYKEYQAQVVK.N	Carbamidomethyl (+57)	K.QCQEPAYKEYQAQVVK.N
413	422	2	1075.61	4.3	0	49.9	20.1	95.00%	R.ALTFAANLQK.E		R.ALTFAANLQK.E
438	452	2	1729.9	3.9	0	75.9	23.1	95.00%	K.LGEGEQYPELVQLQK.E		K.LGEGEQYPELVQLQK.E
46	58	2	1321.64	4.2	1	41.4	25.2	95.00%	R.AVMDALGSVMSNK.Y		R.AVMDALGSVMSNK.Y
6	16	2	1273.66	1.9	2	41	23.3	95.00%	D.SIMLTPLKEQD.P		-.MSSNDSIMLTPLKEQDPTVAEIMR.H
436	452	2	1929.03	2.2	1	73.3	19.5	95.00%	K.AKLGEGEQYPELVQLQK.E		K.AKLGEGEQYPELVQLQK.E
146	161	2	1879.87	3.2	2	43.3	26	95.00%	K.ISAVSTYFESMPYRVD.P	Oxidation (+16)	K.ISAVSTYFESMPYRVDPNTGLIDYDMLEHDAQLFRPK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
13	SAHH_SCHPO	32.79%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
257	268	2	1355.63	2.5	0	65.8	25.4	95.00%	D.GFEVTTMEEAVK.E	Oxidation (+16)	R.VIVTEVDPINALQAAMDGFEVTTMEEAVK.E
174	183	2	1081.62	2.8	2	43	18.6	95.00%	K.LKVPAINVND.S		K.LKVPAINVNDSVTK.S
20	35	2	1782.92	2.2	0	66	22.1	95.00%	K.ELEIAENEMPGLIAVR.E		K.ELEIAENEMPGLIAVR.E
8	18	2	1118.61	3.2	1	77.1	20.1	95.00%	K.VADISLAAFGR.K		K.VADISLAAFGR.K
216	227	2	1117.62	4.3	1	46.5	20.9	95.00%	K.VAVVAGFGDVGK.G		K.VAVVAGFGDVGK.G
269	280	2	1367.66	4	0	40.1	24.9	95.00%	K.EGQIFVTTTGCR.D	Carbamidomethyl (+57)	K.EGQIFVTTTGCR.D
153	167	2	1647.81	2.1	0	75	24.7	95.00%	R.GISEETTTGVHNLYK.M		R.GISEETTTGVHNLYK.M
19	35	2	1911.02	2	1	87.5	20.5	95.00%	R.KELEIAENEMPGLIAVR.E		R.KELEIAENEMPGLIAVR.E
176	187	2	1255.68	4.6	1	42.1	21.1	95.00%	K.VPAINVNDSVTK.S		K.VPAINVNDSVTK.S
336	344	2	1006.6	5	1	31.2	14.9	95.00%	R.HIILLADGR.L		R.HIILLADGR.L
103	118	2	2053.94	4.3	0	72.2	26	95.00%	K.GETEEEYLWCIEQQLK.S	Carbamidomethyl (+57)	K.GETEEEYLWCIEQQLK.S
136	143	2	937.54	2.6	0	31.6	15.9	95.00%	D.LTALVHER.H		K.SFPSGKPLNMILDDGGDLTALVHER.H
133	143	2	1166.61	2.8	1	43.8	22.4	95.00%	D.GGDLTALVHER.H		K.SFPSGKPLNMILDDGGDLTALVHER.H
377	389	2	1455.76	3.2	0	26.5	22.7	93.00%	D.NTSYPLGVHMLPK.K		R.LVNLGCATGHPSFVMSCSFTNQVLAQIALWTDNTSYPLGVHMLPK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
14	THI3_SCHPO	57.51%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
234	245	4	1551.81	2	1	24.2	22	95.00%	D.PVQTYKEYIHFK.R		K.DPVQTYKEYIHFK.R
155	169	2	1717.82	2.3	0	98.8	25.4	95.00%	D.GGIGIECMQQVELER.W	Carbamidomethyl (+57)	R.CGMNIAPAIINGEIDGGIGIECMQQVELER.W
74	95	2	2353.27	3.5	0	91.4	18.2	95.00%	R.GYPVTSFGSLLNEPFTGLITLK.G		R.GYPVTSFGSLLNEPFTGLITLK.G
316	327	2	1385.71	3.6	1	53.6	23.6	95.00%	K.QEAIAEIQDEIK.Q		K.QEAIAEIQDEIK.Q
312	324	2	1444.69	1.4	2	34.3	25.6	95.00%	D.PMGKQEAIAEIQD.E	Oxidation (+16)	K.DPMGKQEAIAEIQDEIK.Q

222	232	3	1198.64	2.2	1	34.4	21.4	95.00%	R.AIHSATLDMLK.D		R.AIHSATLDMLK.D
128	139	2	1325.67	4.2	1	42.4	23.3	95.00%	K.FGLSPSDYTAIR.C		K.FGLSPSDYTAIR.C
6	27	2	2631.39	2.4	0	78.6	19	95.00%	K.ITFLTNWEATPYHLPIFLAQTR.G		K.ITFLTNWEATPYHLPIFLAQTR.G
63	71	2	954.54	4.5	0	51.1	16.9	95.00%	K.AMIHTLAAK.A		K.AMIHTLAAK.A
110	118	2	968.5	4.9	0	27.7	22.1	94.50%	R.IGYVGEFGK.I		R.IGYVGEFGK.I
330	339	2	992.51	5.7	0	44.3	23.6	95.00%	K.GGVFSGNSLR.Y		K.GGVFSGNSLR.Y
189	211	3	2788.29	2.8	1	29.7	26	95.00%	R.LANLGCCCFCTILYIAHDEFIAK.H	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.LANLGCCCFCTILYIAHDEFIAK.H
33	56	2	2409.27	3	1	74.8	19.3	95.00%	R.EGIEVAILEPTNPSDVTALIGSGK.V		R.EGIEVAILEPTNPSDVTALIGSGK.V
260	273	2	1711.79	4.7	1	88.7	26.2	95.00%	R.CFAYFSHDISNVPR.D	Carbamidomethyl (+57)	R.CFAYFSHDISNVPR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
15	THI2_SCHPO	45.73%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
234	242	2	981.48	2.7	0	34	23.4	95.00%	D.GPFGAFCVK.R	Carbamidomethyl (+57)	R.IAGVVTNWTLVSLNHGLQSCMDPNTINAHLVVSATGHDGPFGAFCVK.R
243	255	2	1422.76	1.9	2	35	20.7	95.00%	K.RLASAQLVSNLHD.M		K.RLASAQLVSNLHDMRPLDMNR.A
175	187	2	1431.8	1.8	1	64.3	18.7	95.00%	K.LFNATAVEDLIVK.E		K.LFNATAVEDLIVK.E
2	15	2	1400.77	3.8	0	74.5	20	95.00%	M.APATAVVTPQTAFK.T		-.MAPATAVVTPQTAFK.T
131	146	2	1818.91	1.3	1	40.5	24.5	95.00%	R.KPADLFLNEIGVPYED.E		R.KPADLFLNEIGVPYEDEGDYVVVK.H
39	55	2	1962.95	4.7	1	48.4	25.1	95.00%	K.AYPTYSLDESFSFAPIR.E		K.AYPTYSLDESFSFAPIR.E
244	255	2	1267.65	3.8	1	65.6	22.6	95.00%	R.LASAQLVSNLHD.M	Deamidation (+1)	R.LASAQLVSNLHDMRPLDMNR.A
218	233	3	1644.83	3.7	1	39.7	24.5	95.00%	D.PNTINAHLVVSATGHD.G		R.IAGVVTNWTLVSLNHGLQSCMDPNTINAHLVVSATGHDGPFGAFCVK.R
295	308	2	1459.67	4	0	71.7	26.5	95.00%	R.MGPTFGGMMFSGIK.A		R.MGPTFGGMMFSGIK.A
309	320	2	1332.68	5.8	1	60	23.7	95.00%	K.AAQEALAIFDER.K		K.AAQEALAIFDER.K
274	294	2	2254.05	3.3	1	79.8	26.6	95.00%	R.EVFPGMIVGGMELSEFDGANR.M		R.EVFPGMIVGGMELSEFDGANR.M
244	260	2	1878.97	1.9	1	72.4	22.8	95.00%	R.LASAQLVSNLHDMRPLD.M		R.LASAQLVSNLHDMRPLDMNR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
16	METK_SCHPO	48.95%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
90	103	2	1572.75	1.5	1	43.3	25.6	95.00%	K.TCNVLVAIEQQSPD.I	Carbamidomethyl (+57)	K.TCNVLVAIEQQSPDIAQGLHYEK.A
147	155	2	931.5	4.5	0	58	24	95.00%	K.LNAAMSVAR.R		K.LNAAMSVAR.R
2	18	2	1820.82	1.6	1	75.3	26.5	95.00%	M.AQTFLFTSESVGEGHPD.K		-.MAQTFLFTSESVGEGHPDK.I
137	146	2	1117.72	1.9	0	27.1	3.01	93.80%	K.LPLTILLAHK.L		K.LPLTILLAHK.L
237	251	2	1429.74	3.6	1	73.6	22.8	95.00%	R.FVVGGPQGDAGLTGR.K		R.FVVGGPQGDAGLTGR.K
339	349	2	1256.73	4.3	1	36.5	16.5	95.00%	K.NFDLRPGVLVK.S		K.NFDLRPGVLVK.S
90	112	3	2612.3	3.4	1	62.4	23.8	95.00%	K.TCNVLVAIEQQSPDIAQGLHYEK.A	Carbamidomethyl (+57)	K.TCNVLVAIEQQSPDIAQGLHYEK.A
328	338	2	1257.74	4.7	1	49.3	16.3	95.00%	K.TSAELVEIIRK.N		K.TSAELVEIIRK.N
353	378	3	3055.48	3	1	70.7	23.9	95.00%	K.LQTPFYLSTASYGHFTDQSKPWEQPK.E		K.LQTPFYLSTASYGHFTDQSKPWEQPK.E
291	299	2	856.52	4.2	0	28.1	19.7	94.90%	K.SLVAAGLAR.R		K.SLVAAGLAR.R
213	226	3	1572.93	4.6	1	37.1	12	95.00%	K.IIKPTVPAHLLDEK.T		K.IIKPTVPAHLLDEK.T
253	272	2	1948.95	4	1	80.8	25.2	95.00%	K.IIVDTYGGWGAHGGGAFSGK.D		K.IIVDTYGGWGAHGGGAFSGK.D
132	146	3	1702.01	2.5	1	31.6	12.3	95.00%	D.ETPEKLPLTILLAHK.L		K.ALEELGAGDQGIMFGYATDETPEKLPLTILLAHK.L
169	185	2	1946.97	4.5	0	49.1	24.4	95.00%	K.TQVTIEYEEENGAVIPR.R		K.TQVTIEYEEENGAVIPR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
17	HSP72_SCHPO	34.47%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
327	340	2	1400.77	3.9	0	39.7	20.8	95.00%	K.ASVNEIVLVGGSTR.I		K.ASVNEIVLVGGSTR.I
432	445	2	1584.83	2.6	0	72.9	22.5	95.00%	D.NQPGVLIQVFEGER.A		K.SEIFSTYSDNQPGVLIQVFEGER.A
170	184	2	1530.8	2.5	1	38.8	22.1	95.00%	R.IINEPTAAAIAYGLD.R		R.IINEPTAAAIAYGLDR.S
111	124	2	1611.8	4	0	69	24	95.00%	K.TFTPEEISSMVLMK.M		K.TFTPEEISSMVLMK.M
97	110	2	1574.88	6.7	1	31.9	17.7	95.00%	D.GKPVLQVEYKGETK.T		K.DGKPVLQVEYKGETK.T
140	153	2	1565.79	2.9	1	26.5	23.9	93.00%	D.AVVTVPAYFNDSQR.Q		K.VTDAVVTVPAYFNDSQR.Q
594	607	2	1556.83	4.2	1	73.7	21.3	95.00%	K.QKELESVANPIMAK.I		K.QKELESVANPIMAK.I
538	548	2	1351.66	4.4	0	37.5	24.8	95.00%	K.NHLESYAYSLR.N		K.NHLESYAYSLR.N
125	136	2	1324.65	4.5	1	66.6	24.8	95.00%	K.MRETAEAYLGGK.V		K.MRETAEAYLGGK.V
170	185	2	1686.9	2.5	1	94.2	20.4	95.00%	R.IINEPTAAAIAYGLDR.S		R.IINEPTAAAIAYGLDR.S
55	69	2	1698.82	4.2	1	74.8	25.4	95.00%	K.NQVAMNPHNTIFDAK.R		K.NQVAMNPHNTIFDAK.R
457	467	2	1182.65	4.4	0	28.3	19.9	95.00%	K.FELSGIPPAPR.G		K.FELSGIPPAPR.G
235	244	2	1273.69	4.3	0	25.1	21.4	90.70%	R.LVNHFIQEFK.R		R.LVNHFIQEFK.R
35	47	2	1486.7	4.2	1	60.5	25.7	95.00%	R.TTPSYVAFTDTER.L		R.TTPSYVAFTDTER.L
608	647	3	3515.61	5.3	1	39.6	25.6	95.00%	K.IYQAGGAPGGMPGAAPGAAPGAAPGAAPGGDNGPEVEEVD.-	Oxidation (+16)	K.IYQAGGAPGGMPGAAPGAAPGAAPGAAPGGDNGPEVEEVD.-
24	34	2	1227.63	5.8	1	33.2	23.4	95.00%	R.VEIIANDQGNR.T		R.VEIIANDQGNR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
18	A1EGU1_SCHPO	28.67%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
408	429	3	2504.32	2	1	43	20.3	95.00%	K.HVERPIIFPISNPTTLMEAKPD.Q		K.HVERPIIFPISNPTTLMEAKPDQIDK.W
457	479	2	2580.33	2.4	0	74	21.5	95.00%	K.YVISQCNNALLYPALGVACVLSR.C	Carbamidomethyl (+57)/Carbamidomethyl (+57)	K.YVISQCNNALLYPALGVACVLSR.C
44	57	2	1634.91	4.4	1	89.1	17.2	95.00%	R.LPPIVETLQQQVDR.C		R.LPPIVETLQQQVDR.C
373	396	3	2478.4	3	0	37.3	13.2	95.00%	D.INLESAIALVKPTILLGCSGQPGK.F	Carbamidomethyl (+57)	K.EVPSGDINLESAIALVKPTILLGCSGQPGK.F
439	452	2	1418.83	2.3	0	43.9	10.4	95.00%	K.ALIATGSPLPPLNR.N		K.ALIATGSPLPPLNR.N
367	396	3	3062.64	3.1	1	30.5	17.2	95.00%	K.EVPSGDINLESAIALVKPTILLGCSGQPGK.F	Carbamidomethyl (+57)	K.EVPSGDINLESAIALVKPTILLGCSGQPGK.F
490	500	2	1070.58	4.5	1	54.7	21.7	95.00%	K.AASDALATVPR.S		K.AASDALATVPR.S
15	23	2	955.55	4.9	0	32.8	19.7	95.00%	K.GVTLLNSPR.Y		K.GVTLLNSPR.Y
548	555	2	1085.63	3.7	1	31.8	19.3	95.00%	K.LKEWIIER.E		K.LKEWIIER.E
332	339	2	964.49	5	1	34.3	22.8	95.00%	R.GNLFMIDR.C		R.GNLFMIDR.C
258	265	2	1027.51	3.1	1	29	22.7	95.00%	R.ILDHYRPD.I		R.ILDHYRPDIACFNDDIQGTGAVALAAIIGALHVTK.S
456	479	3	2708.42	2.3	1	27.2	18.6	95.00%	K.KYVISQCNNALLYPALGVACVLSR.C	Carbamidomethyl (+57)/Carbamidomethyl (+57)	K.KYVISQCNNALLYPALGVACVLSR.C
178	191	2	1553.75	3.5	1	59.3	25.4	95.00%	K.GHLMTLCAGLDPNR.F	Carbamidomethyl (+57)	K.GHLMTLCAGLDPNR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
19	HSP90_SCHPO	21.88%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
275	289	2	1790.84	4	1	67.8	26.1	95.00%	R.NPSEVTKEEYASFYK.S		R.NPSEVTKEEYASFYK.S
465	474	2	1170.6	4.5	0	29.7	22.3	95.00%	K.NIYFITGESK.Q		K.NIYFITGESK.Q
567	587	2	2339.12	5.7	0	92.3	25.1	95.00%	K.IVGSPCLLTTGQYGWSANMER.I	Carbamidomethyl (+57)	K.IVGSPCLLTTGQYGWSANMER.I
369	375	2	811.49	2.4	0	27.6	18.1	94.40%	D.LPLNLSR.E		K.GVVDSEDLPLNLSR.E
596	606	2	1234.5	4.9	1	67.2	25.9	95.00%	R.DTSMSAYMSSR.K		R.DTSMSAYMSSR.K
475	487	2	1548.8	4.5	0	76.3	22.9	95.00%	K.QAVENSPFLEIFR.A		K.QAVENSPFLEIFR.A
88	99	2	1282.73	5.3	1	55.5	17.6	95.00%	K.NDLINNLGVIAK.S		K.NDLINNLGVIAK.S
255	267	2	1520.76	4.6	1	46.2	24.1	95.00%	K.VKETTTETEELNK.T		K.VKETTTETEELNK.T
198	212	2	1787.96	2.7	0	47	20.1	95.00%	K.HSEFISYPIQLVVTR.E		K.HSEFISYPIQLVVTR.E
197	212	3	1916.05	1.4	1	31.9	18.4	95.00%	K.KHSEFISYPIQLVVTR.E		K.KHSEFISYPIQLVVTR.E

422	436	2	1574.86	4	1	34.5	19.4	95.00%	K.LGIHEDAANRPALAK.L			K.LGIHEDAANRPALAK.L
180	189	2	1293.62	4.9	1	25.4	25.6	90.10%	K.EDQLQYLEEK.T			K.EDQLQYLEEK.T
499	509	2	1275.67	2	1	57	22.2	95.00%	D.PIDEYAVTQLK.E			K.FDVLFMVDPIDEYAVTQLK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
20	K6PF_SCHPO	26.54%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
364	380	3	1831.88	4.2	1	50.7	25.7	95.00%	R.ICEAVDSISSTAISHSR.A	Carbamidomethyl (+57)	R.ICEAVDSISSTAISHSR.A
613	628	3	1700.87	4.5	1	49.7	22.8	95.00%	R.GHTPLAIDNGFSGFLR.H		R.GHTPLAIDNGFSGFLR.H
822	839	4	2058.08	3.2	1	52.7	20.5	95.00%	K.VYTTEVIGNIISEEAHKR.F		K.VYTTEVIGNIISEEAHKR.F
419	431	2	1592.73	4.2	1	27.5	26.3	92.60%	K.WQDELCNSLSSVR.K	Carbamidomethyl (+57)	K.WQDELCNSLSSVR.K
21	31	2	1419.67	2.3	1	32.2	25.3	95.00%	D.TYNQTLDFYQK.L		-.MSGETVHGISCYSVVANTEDTYNQTLDFYQK.L
138	148	2	1187.63	3	1	40.7	23	95.00%	D.PLGNLIGFSDR.Y		K.KPDEVYVEDPLGNLIGFSDR.Y
586	603	3	1720.91	2.2	0	76.7	21.9	95.00%	R.VAIIHVGAPAGGMNSATR.A		R.VAIIHVGAPAGGMNSATR.A
511	522	2	1241.65	2.3	0	41.4	22.7	95.00%	D.TPSPMIAINGNK.I		R.MLATLQGVDAVDAVLASTPDTPSPMIAINGNK.I
160	183	3	2416.24	3.9	1	44	20.9	95.00%	K.SEESGAASNLESGLATPVVETLKK.A		K.SEESGAASNLESGLATPVVETLKK.A
908	918	2	1362.61	2.7	0	34.2	25.6	95.00%	D.VENNETEIEMR.R		R.GTGVSFSSVADVENNETEIEMR.R
798	806	2	934.49	4	0	31.5	22.6	95.00%	K.ATFALEAGR.N		K.ATFALEAGR.N
254	267	2	1400.75	3.4	0	49.7	22	95.00%	R.GWLAEGGTLIGTAR.C		R.GWLAEGGTLIGTAR.C
844	861	2	1860.9	4.7	1	42.3	25.5	95.00%	R.TAVPGHVQQGGNPTPMDR.A		R.TAVPGHVQQGGNPTPMDR.A
927	938	2	1323.7	4.7	1	53.3	21.2	95.00%	R.DMHNLVNILAGK.T		R.DMHNLVNILAGK.T
77	94	2	1954.97	2.8	1	65.9	24.1	95.00%	R.LVPGELSLSPAAEDSEWR.G		R.LVPGELSLSPAAEDSEWR.G
197	214	2	1760.86	4.1	1	84.8	25	95.00%	K.IAVMTSGGDSPGMNAVVR.A		K.IAVMTSGGDSPGMNAVVR.A
822	838	2	1901.98	2.8	0	58.1	22.5	95.00%	K.VYTTEVIGNIISEEAHK.R		K.VYTTEVIGNIISEEAHK.R
887	896	2	997.6	3	0	78.5	17.2	95.00%	D.PSSAVVIGIR.G		R.ANDLGNDPSSAVVIGIR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
21	EF3_SCHPO	23.40%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
333	350	2	1970.01	4.8	0	86.5	22.4	95.00%	K.IPEVSTAANPEVCLETLK.A	Carbamidomethyl (+57)	K.IPEVSTAANPEVCLETLK.A
35	59	2	2604.32	3.9	1	66.4	22.4	95.00%	K.ALASFVNGPIEEQDAPSQVFSAISK.Q		K.ALASFVNGPIEEQDAPSQVFSAISK.Q
351	367	2	1809.03	4.2	1	72.9	15.3	95.00%	K.AVLGEIKVPTNEEVIAK.Y		K.AVLGEIKVPTNEEVIAK.Y
961	994	3	3666.67	2.8	0	62.6	25.7	95.00%	R.EFTEGLTEEVWAVNNGHMTPSGHNWVSGQGSGPR.I		R.EFTEGLTEEVWAVNNGHMTPSGHNWVSGQGSGPR.I
281	294	2	1550.88	4.1	1	60.5	15.8	95.00%	K.LVEDPQVVAPFLPK.L		K.LVEDPQVVAPFLPK.L
757	765	2	1178.58	7.8	0	24.9	24.4	90.20%	K.TPSEYIQWR.F		K.TPSEYIQWR.F
89	103	2	1652.98	2.8	0	41.3	6.99	95.00%	D.VEPYLVELLPAVIAK.V		K.GLEAVANHGSVAADVEPYLVELLPAVIAK.V
479	493	2	1636.88	3.9	0	73.9	21.1	95.00%	R.AIVNGQVEGFPTHLR.T		R.AIVNGQVEGFPTHLR.T
285	294	2	1094.65	2.1	0	30.4	13.2	95.00%	D.PQVVAPFLPK.L		K.LVEDPQVVAPFLPK.L
719	738	3	2327.16	1.7	0	34.2	23.1	95.00%	K.VLTGELLPTVGEIYQHENCR.I	Carbamidomethyl (+57)	K.VLTGELLPTVGEIYQHENCR.I
419	447	3	3168.34	2.9	1	77.1	27.1	95.00%	K.IPGGASHAEEEEEGEDLCNCEFSLAYGAK.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.IPGGASHAEEEEEGEDLCNCEFSLAYGAK.I
75	103	3	2944.6	3.2	1	47.9	16	95.00%	K.GLEAVANHGSVAADVEPYLVELLPAVIAK.V		K.GLEAVANHGSVAADVEPYLVELLPAVIAK.V
133	147	2	1550.87	3.9	0	70.6	16.1	95.00%	K.AIVPSVLESIHTTGK.W		K.AIVPSVLESIHTTGK.W
881	900	3	2293.11	2.6	1	44.8	25.5	95.00%	K.EIEEHCSLLGLDAELVSHSR.I	Carbamidomethyl (+57)	K.EIEEHCSLLGLDAELVSHSR.I
358	367	2	1098.6	4.8	0	47.3	21.4	95.00%	K.VPTNEEVIAK.Y		K.VPTNEEVIAK.Y
35	48	2	1488.71	2.2	1	41.8	25.1	95.00%	K.ALASFVNGPIEEQD.A		K.ALASFVNGPIEEQDAPSQVFSAISK.Q
49	59	2	1134.59	2.4	0	46.7	22.9	95.00%	D.APSQVFSAISK.Q	Deamidation (+1)	K.ALASFVNGPIEEQDAPSQVFSAISK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
22	6PGD_SCHPO	32.52%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
386	403	2	2088.08	3.5	0	48.8	22.1	95.00%	D.PNLESILFHPFFTNGVEK.A		R.EDPNLESILFHPFFTNGVEK.A
156	166	3	1228.76	1.9	0	35.8	8.45	95.00%	R.IKPIFQTLAAK.A		R.IKPIFQTLAAK.A
42	51	2	1134.56	4.5	1	47.7	24.6	95.00%	R.VDEFLANEAK.G		R.VDEFLANEAK.G
123	139	2	1590.81	3.9	0	62.7	23.7	95.00%	K.GILFVGSGVSGGEEGAR.Y		K.GILFVGSGVSGGEEGAR.Y
140	155	2	1669.81	4.7	0	28.8	25.5	95.00%	R.YGPSLMPGGNPAAWPR.I		R.YGPSLMPGGNPAAWPR.I
269	291	2	2504.28	3.2	0	92.8	22.1	95.00%	K.WTAQNALEMGTPVSLITEAVFAR.C		K.WTAQNALEMGTPVSLITEAVFAR.C
437	449	2	1379.79	4.1	0	52	15.2	95.00%	R.SAVLPANLLQAQR.D		R.SAVLPANLLQAQR.D
80	97	2	1925.1	4.4	1	58.2	14.1	95.00%	K.AGKPVDYLIEGLAPLLEK.G		K.AGKPVDYLIEGLAPLLEK.G
188	197	2	1133.48	2.1	1	27.8	26	93.40%	K.MVHNGIEYGD.M		K.MVHNGIEYGDMQLICETYDIMK.R
54	67	2	1501.78	2.5	0	61.6	22.5	95.00%	K.SIVGAHSLEEFVSK.L		K.SIVGAHSLEEFVSK.L
86	97	2	1357.79	2.3	0	28.6	16.3	95.00%	D.YLIEGLAPLLEK.G		K.AGKPVDYLIEGLAPLLEK.G
29	37	2	1175.49	3.9	0	36.7	25.7	95.00%	K.GFTVCCYNR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GFTVCCYNR.T
122	139	2	1718.9	2.3	1	78.6	22.3	95.00%	K.KGILFVGSGVSGGEEGAR.Y		K.KGILFVGSGVSGGEEGAR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
23	ILV5_SCHPO	29.46%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
198	204	2	738.5	2.1	0	34	11.5	95.00%	D.VILVAPK.G		K.DVDVILVAPK.G
84	104	2	2141.07	2.7	1	91.2	23.9	95.00%	K.NDTLAIIGYGSQGHGQGLNAR.D		K.NDTLAIIGYGSQGHGQGLNAR.D
330	337	2	914.47	6	1	41.2	22.8	95.00%	R.GAIDWTPR.F		R.GAIDWTPR.F
314	328	2	1725.76	3.8	1	69	27.3	95.00%	K.YGLDYMFAACSTTAR.R	Carbamidomethyl (+57)	K.YGLDYMFAACSTTAR.R
145	163	2	2074.05	4.2	1	75.2	22.9	95.00%	K.GSIIMNLLSDAAQTETWPK.I		K.GSIIMNLLSDAAQTETWPK.I
86	104	3	1912	2.4	0	36.6	21.8	95.00%	D.TLAIIGYGSQGHGQGLNAR.D		K.NDTLAIIGYGSQGHGQGLNAR.D
362	372	2	1312.61	4.6	0	61.6	25.4	95.00%	R.SLEYNSAPNYR.E		R.SLEYNSAPNYR.E
289	313	2	2687.32	3.5	0	76.3	24.4	95.00%	R.GHSPAEAFNETVEEATQSLYPLIGK.Y		R.GHSPAEAFNETVEEATQSLYPLIGK.Y
318	328	2	1277.56	2.5	0	30.6	25.7	95.00%	D.YMFAACSTTAR.R	Carbamidomethyl (+57)	K.YGLDYMFAACSTTAR.R
123	133	2	1198.6	4.3	1	28.6	23.2	95.00%	K.QAIEDGWVPGK.T		K.QAIEDGWVPGK.T
196	204	2	952.6	2.9	1	40.3	13.6	95.00%	D.VDVILVAPK.G		K.DVDVILVAPK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
24	EF2_SCHPO	18.65%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
272	283	2	1498.77	4.2	1	53.9	23.1	95.00%	R.AFNMFILDPIYR.I		R.AFNMFILDPIYR.I
466	479	2	1474.71	3.7	0	72.8	24.8	95.00%	K.SGTLTTSEVAHNMK.V		K.SGTLTTSEVAHNMK.V
811	823	3	1441.74	2.3	0	71.3	23.2	95.00%	D.PTSKPGQIVCEAR.K	Carbamidomethyl (+57)	R.QATAGQAFPQLVFDHWSPMSGDPLDPTSKPGQIVCEAR.K
565	578	2	1451.69	4.3	0	44.5	25.6	95.00%	R.ESVSEPSSMTALSK.S		R.ESVSEPSSMTALSK.S
284	292	2	1051.52	4.5	1	27.5	23.6	94.30%	R.IFDAVMNSR.K		R.IFDAVMNSR.K
244	253	2	1266.61	5.9	0	30	24.9	95.00%	R.LWGENYFNPK.T		R.LWGENYFNPK.T
770	785	2	1798.9	4	0	39.1	23.6	95.00%	K.AYLPVNESFGFTGELR.Q		K.AYLPVNESFGFTGELR.Q
151	161	3	1236.76	2.4	2	21	9.54	90.50%	R.IRPVVVVNKVD.R		R.IRPVVVVNKVDR.A
371	384	2	1594.76	4.1	1	55	25.8	95.00%	R.NCDANAPLMIYVSK.M	Carbamidomethyl (+57)	R.NCDANAPLMIYVSK.M
327	346	2	2192.18	2.4	1	55.9	18.3	95.00%	K.FLPAADALMEMIVLHLPSPK.T		K.FLPAADALMEMIVLHLPSPK.T
586	609	3	2657.29	3.5	0	32.6	24.6	95.00%	R.IFMTAEPMSEELSVAIETGHVNPR.D		R.IFMTAEPMSEELSVAIETGHVNPR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
25	ACT_SCHPO	42.40%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

158	177	3	2224.15	3.5	0	29.3	20.7	95.00%	D.GVTHTVPIYEGYALPHAIMR.L		R.TTGIVLDSGDGVTHTVPIYEGYALPHAIMR.L
223	238	2	1794.87	2.1	0	84.7	25.2	95.00%	D.FEQELQTAAQSSSLEK.S		K.LCYVALDFEQELQTAAQSSSLEK.S
245	254	2	1085.59	3.1	0	42.7	23.1	95.00%	D.GQVITIGNER.F		K.SYELPDGQVITIGNER.F
1	18	2	2007.9	4	1	79.9	26.2	95.00%	-.MEEEIAALVIDNGSGMCK.A	Acetyl (+42)/ Carbamidomethyl (+57)	-.MEEEIAALVIDNGSGMCK.A
255	284	3	3274.66	3.2	1	82.1	20.8	95.00%	R.FRAPEALFQPSALGLENAGIHEATYNSIMK.C		R.FRAPEALFQPSALGLENAGIHEATYNSIMK.C
85	95	3	1514.75	5.5	0	36	24.5	95.00%	K.IWHHTFYNELR.V		K.IWHHTFYNELR.V
96	113	2	2014.03	3.9	0	59.4	23.1	95.00%	R.VAPEEHPCLLTEAPLNPK.S	Carbamidomethyl (+57)	R.VAPEEHPCLLTEAPLNPK.S
197	206	2	1131.53	5.1	0	41.4	25.5	95.00%	R.GYTFSTTAER.E		R.GYTFSTTAER.E
239	254	2	1789.89	5.1	1	75.2	24.6	95.00%	K.SYELPDGQVITIGNER.F		K.SYELPDGQVITIGNER.F
216	238	2	2629.27	3.5	1	106	24.9	95.00%	K.LCYVALDFEQELQTAAQSSSLEK.S	Carbamidomethyl (+57)	K.LCYVALDFEQELQTAAQSSSLEK.S
360	372	2	1511.7	3.8	1	34.6	25.7	95.00%	K.QEYDESGPGIVYR.K		K.QEYDESGPGIVYR.K
257	284	3	2971.48	3	0	43.9	22	95.00%	R.APEALFQPSALGLENAGIHEATYNSIMK.C		R.APEALFQPSALGLENAGIHEATYNSIMK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
26	HSP75_SCHPO	35.24%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	173	2	1168.66	5	1	34.3	18.9	95.00%	K.DAGAIAGLNVLR.I		K.DAGAIAGLNVLR.I
364	385	2	2201.14	3	1	48.1	20.8	95.00%	K.SINPDEAVAYGAAVQAAVLTNK.A		K.SINPDEAVAYGAAVQAAVLTNK.A
174	188	2	1530.8	2.5	1	38.8	22.1	95.00%	R.IINEPTAAAIAYGLD.A		R.IINEPTAAAIAYGLDAK.S
501	517	3	1779.92	5.5	0	60.6	22	95.00%	R.SAHIEITNSVGHLSSTK.I		R.SAHIEITNSVGHLSSTK.I
451	472	2	2468.2	5.8	0	62.2	24.8	95.00%	R.VNCAENEPLGEFQLTGIPPMPR.G	Carbamidomethyl (+57)	R.VNCAENEPLGEFQLTGIPPMPR.G
437	450	2	1638.8	2.8	0	52.1	24.4	95.00%	D.NQTTVTFPVYQGER.V		R.TFTTVADNQTTVTFPVYQGER.V
144	157	2	1552.8	4.6	1	33.7	23	95.00%	K.AVITVPAYFSDSQR.A		K.AVITVPAYFSDSQR.A
336	344	2	900.54	2.8	0	31	17.4	95.00%	D.IVLVGGSTR.I		K.ADVHDIVLVGGSTR.I
115	128	2	1565.81	1.4	0	60	22.4	95.00%	K.QFTAQEISAMVLTK.M		K.QFTAQEISAMVLTK.M
543	564	2	2513.21	3.3	0	64.4	25	95.00%	K.SQLESYISNIETTISEPNVMMK.L		K.SQLESYISNIETTISEPNVMMK.L
174	190	2	1729.93	3.9	1	82.9	19.8	95.00%	R.IINEPTAAAIAYGLDAK.S		R.IINEPTAAAIAYGLDAK.S
288	301	2	1482.73	2.1	1	61.4	25.5	95.00%	D.SLSNGIDFSSSITR.A		R.ALSSVTQTTVEVDSLSNGIDFSSSITR.A
114	128	2	1693.91	2.2	1	48	19.4	95.00%	K.KQFTAQEISAMVLTK.M		K.KQFTAQEISAMVLTK.M
39	51	2	1484.72	4.2	0	50.9	25.5	95.00%	R.TTPSFVAFTETER.L		R.TTPSFVAFTETER.L
430	450	2	2374.16	5.6	1	61.9	24.3	95.00%	R.TFTTVADNQTTVTFPVYQGER.V		R.TFTTVADNQTTVTFPVYQGER.V
96	113	2	1987.03	4.2	1	58.5	20.8	95.00%	K.VIDNNGIPTIEVNYLGEK.K		K.VIDNNGIPTIEVNYLGEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
27	TSA1_SCHPO	45.83%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	147	2	1224.69	4.4	1	43.5	18.1	95.00%	R.QITINDLPVGR.S		R.QITINDLPVGR.S
155	175	3	2525.19	3.9	1	36.8	25.5	95.00%	R.LLDAFQFVEEHGEVCPANWHK.G	Carbamidomethyl (+57)	R.LLDAFQFVEEHGEVCPANWHK.G
158	175	3	2183.99	1.8	0	30.8	27.2	95.00%	D.AFQFVEEHGEVCPANWHK.G	Carbamidomethyl (+57)	R.LLDAFQFVEEHGEVCPANWHK.G
125	132	2	901.53	4.7	1	35.7	20.3	95.00%	R.GLFLIDPK.G		R.GLFLIDPK.G
66	88	2	2576.29	0.89	1	97.3	23.4	95.00%	R.NAQVILTSTDSEYSHLAFINTPR.K		R.NAQVILTSTDSEYSHLAFINTPR.K
14	26	2	1333.69	3.6	0	40.1	22.9	95.00%	K.GTAVVNGAFEEIK.L		K.GTAVVNGAFEEIK.L
76	88	2	1533.76	1.6	0	47	24.5	95.00%	D.SEYSHLAFINTPR.K		R.NAQVILTSTDSEYSHLAFINTPR.K
2	13	2	1341.74	4.1	1	36.9	20.8	95.00%	M.SLQIGKPAPDFK.G	Acetyl (+42)	-.MSLQIGKPAPDFK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
28	TKT_SCHPO	33.58%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
306	318	2	1423.73	4.8	1	73.3	23.1	95.00%	R.VAIASSAEEEYKK.M		R.VAIASSAEEEYKK.M
325	336	2	1449.68	6.5	1	28.4	25.4	94.80%	K.QSYPDLSNQLER.I	Deamidation (+1)	K.QSYPDLSNQLER.I
238	252	2	1719.86	5	1	57.2	24.7	95.00%	R.EAMSCTDKPTLINLK.T	Carbamidomethyl (+57)	R.EAMSCTDKPTLINLK.T
395	407	2	1418.65	3.9	1	52.7	25.9	95.00%	R.WEGAADFQPPSSK.L		R.WEGAADFQPPSSK.L
653	663	2	1249.63	3.9	0	24.8	24.4	90.10%	K.FHFTTSGVAQR.A		K.FHFTTSGVAQR.A
481	494	3	1636.81	2.2	0	41.2	24.5	95.00%	D.GPTHQPIETFAHFR.A		R.VIYVATHDSIGLGEDGPTHQPIETFAHFR.A
182	193	2	1385.74	4.7	1	41.9	21.6	95.00%	K.LSNLIAVWDNNK.I		K.LSNLIAVWDNNK.I
532	547	2	1810.95	4.2	0	72.5	21.2	95.00%	R.QNLPQLENSTIENALK.G		R.QNLPQLENSTIENALK.G
507	531	2	2588.27	2.6	1	78.8	24.1	95.00%	D.GNETSAAYYSALTSDSTPSILALTR.Q		R.AMPNINCWRPADGNETSAAYYSALTSDSTPSILALTR.Q
589	606	2	2252.07	4.5	0	58.5	26.1	95.00%	R.VVSLPCWEVFEQQPESYR.L	Carbamidomethyl (+57)	R.VVSLPCWEVFEQQPESYR.L
630	648	3	2046.93	3.6	1	34	26.8	95.00%	R.YVHEAFGMHTFGDSGPAPK.L		R.YVHEAFGMHTFGDSGPAPK.L
253	281	3	3132.54	2.9	1	59.8	23.5	95.00%	K.TTIGYGSELQGTHSVHGSPLKPEDCVHVK.K	Carbamidomethyl (+57)	K.TTIGYGSELQGTHSVHGSPLKPEDCVHVK.K
253	276	3	2509.21	1.5	1	25.2	24.6	95.00%	K.TTIGYGSELQGTHSVHGSPLKPED.C		K.TTIGYGSELQGTHSVHGSPLKPEDCVHVK.K
291	303	2	1603.8	4	0	26.8	24.3	93.40%	K.TFQVPPEVYAYYK.E		K.TFQVPPEVYAYYK.E
522	531	2	1057.62	2.6	0	34.4	18.9	95.00%	D.STPSILALTR.Q		R.AMPNINCWRPADGNETSAAYYSALTSDSTPSILALTR.Q
30	49	3	1972.01	1.6	0	48.6	22.1	95.00%	K.SGHPGAPMGLAPAAHVLFSR.I		K.SGHPGAPMGLAPAAHVLFSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
29	IPYR_SCHPO	45.67%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
257	280	3	2423.28	2.2	1	21.9	20.1	92.30%	D.PSVSSTIPPAQELAPAPVDPSVHK.W		K.SDFSLVNVSVTGSVANDPSVSSTIPPAQELAPAPVDPSVHK.W
257	275	2	1874.97	2.6	1	33.7	22.3	95.00%	D.PSVSSTIPPAQELAPAPVD.P		K.SDFSLVNVSVTGSVANDPSVSSTIPPAQELAPAPVDPSVHK.W
186	192	2	922.44	6	0	35.4	25.3	95.00%	R.ATNEWFR.I		R.ATNEWFR.I
105	113	2	1047.54	2.5	0	25.2	23.3	90.80%	D.PNVVHPETK.A	N-Formyl (+28)	R.NCFPHHGYIWNYGAFPQTYEDPNVVHPETK.A
84	113	4	3616.64	3.2	1	34.2	25.8	95.00%	R.NCFPHHGYIWNYGAFPQTYEDPNVVHPETK.A	Carbamidomethyl (+57)	R.NCFPHHGYIWNYGAFPQTYEDPNVVHPETK.A
24	42	2	2112.04	4.6	1	50.5	24.5	95.00%	K.NGTPISSWHDIPLYANAEK.T		K.NGTPISSWHDIPLYANAEK.T
8	23	2	1839.93	4.1	1	74	23.1	95.00%	R.EVGALNTLDYQVYVEK.N		R.EVGALNTLDYQVYVEK.N
199	212	2	1556.7	2.7	0	51.4	26.7	95.00%	D.GKPENSFAFSGECK.N	Carbamidomethyl (+57)	K.IPDGKPENSFAFSGECK.N
120	130	2	1257.61	2.1	1	54.4	25	95.00%	D.PLDVCEIGEAR.G	Carbamidomethyl (+57)	K.GDSDPLDVCEIGEAR.G
43	53	2	1283.73	4	0	66.7	18.6	95.00%	K.TILNMVVEIPR.W		K.TILNMVVEIPR.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
30	GPD1_SCHPO	39.48%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
164	182	2	1962	2.7	0	73.2	22.5	95.00%	K.LGIYCGVLSGANVANEVAR.E	Carbamidomethyl (+57)	K.LGIYCGVLSGANVANEVAR.E
2	20	2	1989	3.8	1	99.4	23.8	95.00%	M.SGYGQQGVSAANIDSIRPK.K	Acetyl (+42)	-.MSGYGQQGVSAANIDSIRPK.K
87	104	2	2008.05	3	1	50.1	20.6	95.00%	K.YLPGIECPPNVIAVPDVR.E	Carbamidomethyl (+57)	K.YLPGIECPPNVIAVPDVR.E
310	331	3	2285.26	3	1	24.3	15.7	95.00%	K.SLETLEKELLGGQLLQGAATSK.D		K.SLETLEKELLGGQLLQGAATSK.D
277	296	2	2153	2.6	1	93.7	26.1	95.00%	R.TMVEQSCGIADLVTSCLGGR.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.TMVEQSCGIADLVTSCLGGR.N
183	202	2	2362.1	3.9	1	116	26.4	95.00%	R.EQFCETTIGFNPPNEVDIPR.E	Carbamidomethyl (+57)	R.EQFCETTIGFNPPNEVDIPR.E
288	296	2	961.5	2.9	0	29.3	22.3	95.00%	D.LVTSCLGGR.N	Carbamidomethyl (+57)	R.TMVEQSCGIADLVTSCLGGR.N
73	86	2	1656.85	3.7	1	59.4	23	95.00%	R.KLTEVFNEAHENVK.Y		R.KLTEVFNEAHENVK.Y
74	86	2	1528.76	4.4	0	69.8	24.9	95.00%	K.LTEVFNEAHENVK.Y		K.LTEVFNEAHENVK.Y

125	144	3	2172.13	2.4	1	35.7	21.9	95.00%	R.VCDQMVGLIRPGAVGISCIK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VCDQMVGLIRPGAVGISCIK.G
317	331	2	1484.83	3.6	0	57.3	19.2	95.00%	K.ELLGGQLLQGAATSK.D		K.ELLGGQLLQGAATSK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
31	G6PI_SCHPO	32.36%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
217	228	2	1343.61	5.2	0	37.3	25.9	95.00%	K.TFTTAETCTNAK.S	Carbamidomethyl (+57)	K.TFTTAETCTNAK.S
206	216	2	1218.69	2	0	65.3	18.5	95.00%	D.PETTLFLIASK.T		K.CDPETTLFLIASK.T
372	382	2	1171.52	5.1	1	67.7	25.4	95.00%	R.SGDMVNYTTGK.I		R.SGDMVNYTTGK.I
406	422	2	1903.02	2.9	1	28.1	20.4	95.00%	K.LIPADFLIPIESHNPID.N		K.LIPADFLIPIESHNPIDNNK.H
464	477	2	1502.83	4	0	36.9	18.9	95.00%	K.TFVGNRPSNSIIAK.K		K.TFVGNRPSNSIIAK.K
63	75	2	1499.85	3.9	0	37.5	16.9	95.00%	K.NLITEETVELLVK.L		K.NLITEETVELLVK.L
42	53	2	1432.66	3.1	2	27.2	26.3	92.10%	K.FSFTFNGLKEED.G		K.FSFTFNGLKEEDGPILFDFSK.N
2	24	2	2548.27	3.8	0	60.7	22.8	95.00%	M.SFSLASTLPAWQAVQTHYESVGK.H	Acetyl (+42)	- .MSFSLASTLPAWQAVQTHYESVGK.H
118	128	2	1170.59	4.1	1	35.5	22.8	95.00%	K.VNGQDVMPGVR.K		K.VNGQDVMPGVR.K
204	216	2	1493.75	4.3	1	51.5	24.3	95.00%	K.CDPETTLFLIASK.T	Carbamidomethyl (+57)	K.CDPETTLFLIASK.T
521	531	2	1186.62	2.1	2	34.2	22.4	95.00%	K.NVLAQLETKGD.V		K.NVLAQLETKGDVENHDSSTNGLINLFK.N
54	62	2	1022.55	2.5	1	39.2	22.2	95.00%	D.GPILFDFSK.N		K.EEDGPILFDFSK.N
429	445	2	1870.94	4.8	0	69.7	24.3	95.00%	R.MLFSNFAAQTEALMLGK.T		R.MLFSNFAAQTEALMLGK.T
353	367	2	1711.83	4.2	0	71.8	24.8	95.00%	R.FPAYLQQLSMESNGK.A		R.FPAYLQQLSMESNGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
32	HSP60_SCHPO	25.60%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
112	128	2	1705.86	4.1	1	84.3	24	95.00%	K.TNEVAGDGTTTATVLTR.A		K.TNEVAGDGTTTATVLTR.A
137	148	2	1316.6	4	1	27.4	26.3	92.30%	R.NVAAGCNPMDLR.R	Carbamidomethyl (+57)	R.NVAAGCNPMDLR.R
437	453	2	1588.85	2.3	0	45.3	21.6	95.00%	K.AAVSEGVLPGAGTSFVK.A		K.AAVSEGVLPGAGTSFVK.A
244	256	2	1529.84	3.1	0	55.3	19.5	95.00%	K.VEFENPLILLSEK.K		K.VEFENPLILLSEK.K
478	500	3	2377.34	2.9	0	22.4	14.5	93.10%	K.AITRPAQTILENAGLEGNLIVGK.L		K.AITRPAQTILENAGLEGNLIVGK.L
241	256	2	1873.03	3.8	1	66.7	17.4	95.00%	K.SQKVEFENPLILLSEK.K		K.SQKVEFENPLILLSEK.K
68	79	2	1313.7	4.3	1	39.3	21.4	95.00%	R.NVLIDQPFGSPK.I		R.NVLIDQPFGSPK.I
387	396	2	1249.62	3.1	1	48.7	24.5	95.00%	D.PNLTEYEKEK.L		R.GVMADPNLTEYEKEK.L
258	275	2	1937.07	4.4	1	74.7	17.7	95.00%	K.VSAVQDILPSLELAAQQR.R		K.VSAVQDILPSLELAAQQR.R
229	240	2	1401.72	4.3	1	35	22.8	95.00%	R.GYISPYFITDVK.S		R.GYISPYFITDVK.S
45	56	2	1215.69	4.9	1	52.6	18.6	95.00%	R.ASLLTGVDTLAR.A		R.ASLLTGVDTLAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
33	PUT2_SCHPO	32.66%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
388	405	2	1773.91	3.9	1	102	23.5	95.00%	K.VLESAASDSEIEVLAGGK.A		K.VLESAASDSEIEVLAGGK.A
362	384	3	2429.24	-0.26	1	27.4	21.1	95.00%	K.VGAPLTDFANFVGPVIHQASFNK.L	Deamidation (+1)	K.VGAPLTDFANFVGPVIHQASFNK.L
82	92	2	1222.64	4.6	1	32.1	22.7	95.00%	K.HVEDAIEAALR.G		K.HVEDAIEAALR.G
254	274	3	2393.15	4.4	0	52.3	25.4	95.00%	K.VCFNHPEFAGLHFTGSTAVFR.S	Carbamidomethyl (+57)	K.VCFNHPEFAGLHFTGSTAVFR.S
275	288	2	1444.74	4.6	0	37.7	23.9	95.00%	R.SLWGTIGENVANGK.Y		R.SLWGTIGENVANGK.Y
51	63	3	1459.73	4.3	1	22.8	23.7	93.70%	D.GKEVETNTIGEQR.C		K.ELEAELPVTIPVIIDGKEVETNTIGEQR.C
33	50	2	2012.12	3.5	2	33.2	17.4	95.00%	K.AYKELEAELPVTIPVIID.G		K.AYKELEAELPVTIPVIIDGK.E
233	253	2	2068.09	4.4	1	68.9	20.3	95.00%	R.EAGLPAGALQFIPGDAVEVSK.V		R.EAGLPAGALQFIPGDAVEVSK.V
409	422	2	1551.82	1.8	0	31.9	21.6	95.00%	D.SEGFFVEPTVLLSK.N		K.ADDSEGFFVEPTVLLSK.N
495	509	2	1504.71	3.5	0	49.3	25.6	95.00%	K.CTGAVVGEQPFGGAR.A	Carbamidomethyl (+57)	K.CTGAVVGEQPFGGAR.A
484	494	2	1225.58	4.6	1	28	25.4	94.40%	R.NAAGNFYINDK.C		R.NAAGNFYINDK.C

396	405	2	1001.54	3	0	26.5	23.6	93.00%	D.SEIEVLAGGK.A		K.VLESAASDSEIEVLAGGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
34	PUR9_SCHPO	24.62%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
551	565	2	1519.75	4.1	1	63.8	24.3	95.00%	K.YVAAPGGSVMDQAVR.D		K.YVAAPGGSVMDQAVR.D
122	129	2	827.52	2.1	0	34.9	17.2	95.00%	D.IGGVTLLR.A		R.ETIAKPNVTIPEAVEEIDIGGVTLLR.A
223	244	2	2446.25	3.4	1	45.9	21.1	95.00%	K.VLCGSPGYINLMDALNSWPLVK.E	Carbamidomethyl (+57)	K.VLCGSPGYINLMDALNSWPLVK.E
39	60	2	2231.08	4.2	1	97.7	25.2	95.00%	R.ESGMEVADVSSITNAPEILGGR.V		R.ESGMEVADVSSITNAPEILGGR.V
566	581	2	1881.9	4.3	1	55.8	25.4	95.00%	R.DTANEFNMVFSEIPLR.L		R.DTANEFNMVFSEIPLR.L
47	60	2	1412.77	2.5	0	38.4	20.4	95.00%	D.VSSITNAPEILGGR.V		R.ESGMEVADVSSITNAPEILGGR.V
354	362	2	1152.54	4.8	1	28.8	25.9	94.80%	K.YCVLQMDPK.Y	Carbamidomethyl (+57)	K.YCVLQMDPK.Y
248	259	2	1216.65	4.7	0	30.2	22.4	95.00%	R.ENIGIPAAASFK.H		R.ENIGIPAAASFK.H
104	129	3	2776.53	2.1	1	22.6	14.6	93.30%	R.ETIAKPNVTIPEAVEEIDIGGVTLLR.A		R.ETIAKPNVTIPEAVEEIDIGGVTLLR.A
201	222	3	2414.15	2.2	0	46.3	24.8	95.00%	R.YGANPHQSPAQAFMEQGPLPFK.V		R.YGANPHQSPAQAFMEQGPLPFK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
35	SERA_SCHPO	27.90%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
438	452	2	1654.8	2.4	1	44.3	24.7	95.00%	D.ISDCTPGSLEALHQK.L	Carbamidomethyl (+57)	R.GDIAYLVADISDCTPGSLEALHQK.L
58	73	2	1768.01	2.5	0	67.1	14	95.00%	K.ILLLENVNQSALSNLK.D		K.ILLLENVNQSALSNLK.D
275	284	2	1108.56	4.3	0	25.6	24.4	91.60%	K.EGSYLINASR.G		K.EGSYLINASR.G
58	74	2	1883.04	1.7	2	64.8	16.7	95.00%	K.ILLLENVNQSALSNLKD.E		K.ILLLENVNQSALSNLKDEGYQVEFLK.T
367	385	2	2078.05	3	0	87.6	23.5	95.00%	R.YINEGNSIGAVNFPEVSLR.S		R.YINEGNSIGAVNFPEVSLR.S
410	421	2	1468.77	4	1	31.9	21.3	95.00%	R.QVNELFIDHNIK.S		R.QVNELFIDHNIK.S
302	319	2	1728.88	4.5	1	48	23	95.00%	K.IAGAAIDVYPSEPAGNGK.D		K.IAGAAIDVYPSEPAGNGK.D
47	57	3	1247.68	3.8	1	25.6	20.9	95.00%	R.TLKPFASEDIK.I		R.TLKPFASEDIK.I
248	262	2	1596.82	4.1	1	50.8	22.4	95.00%	R.ADFVSLHVPASPETK.N		R.ADFVSLHVPASPETK.N
142	154	2	1394.7	4.8	0	57.8	23.5	95.00%	R.GIAVFNSPYANSR.S		R.GIAVFNSPYANSR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
36	HXK2_SCHPO	25.05%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
12	24	2	1581.77	4.1	1	62.3	24.9	95.00%	K.LVNDFEYPTESLR.E		K.LVNDFEYPTESLR.E
435	449	2	1414.76	2	0	40.6	21.4	95.00%	D.GSGIGAALCALQAVK.E	Carbamidomethyl (+57)	K.DGSGIGAALCALQAVK.E
434	449	2	1529.79	4.8	1	96.2	22.6	95.00%	K.DGSGIGAALCALQAVK.E	Carbamidomethyl (+57)	K.DGSGIGAALCALQAVK.E
191	205	2	1599.89	1.9	1	66.6	18.6	95.00%	R.IEAVINDTVGTLVTR.A		R.IEAVINDTVGTLVTR.A
76	86	2	1287.67	3.9	1	30.3	24.2	95.00%	R.VCWIQLLGDGK.Y	Carbamidomethyl (+57)	R.VCWIQLLGDGK.Y
286	296	2	1240.63	5.9	0	25.6	22.5	91.60%	R.VGGMYLGELFR.R		R.VGGMYLGELFR.R
64	75	2	1322.7	2.1	1	49.3	21	95.00%	D.FLALDFGGTNLR.V		K.NGEVLAMAPAFISTLPTGAETGDFLALDFGGTNLR.V
374	388	2	1564.83	4.1	0	56.1	21.3	95.00%	R.MSAVPIASLYLSTGR.A		R.MSAVPIASLYLSTGR.A
174	183	2	1186.61	2.2	0	25.7	24.2	91.80%	D.FAQFLTEGFK.A		K.DFAQFLTEGFK.A
1	11	2	1334.67	4.1	1	29.9	24.5	95.00%	-.MEANFQQAVKK.L	Acetyl (+42)	-.MEANFQQAVKK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
37	LYS9_SCHPO	33.78%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
177	183	2	740.49	4.7	0	33.1	14.9	95.00%	R.GVLLALR.N		R.GVLLALR.N
412	426	2	1524.8	1.8	1	42.9	21.6	95.00%	D.GVINTPGVLAPNDMK.L		K.LVGVPCGVATQQILDGVINTPGVLAPNDMK.L

38	49	2	1259.66	4.1	0	41.7	22.6	95.00%	K.AEAFINGIPNSK.A		K.AEAFINGIPNSK.A
149	170	2	2385.11	5.2	1	60.2	26.6	95.00%	K.SFLSYCGGLPAPEDSNNPLGYK.F	Carbamidomethyl (+57)	K.SFLSYCGGLPAPEDSNNPLGYK.F
2	22	3	2269.25	3.1	0	39	16	95.00%	M.PSILLLGSGFVAHPTLEYLSR.R		-.MPSILLLGSGFVAHPTLEYLSR.R
379	396	2	1989.93	4.3	1	76.6	26.4	95.00%	R.TCTLLDYGVPNGYTSMAK.L	Carbamidomethyl (+57)	R.TCTLLDYGVPNGYTSMAK.L
126	135	2	1125.62	2.8	1	28.9	20.3	95.00%	D.PGIDHLYAIK.T		K.AGSICMNEIGVDPGIDHLYAIK.T
104	113	2	1103.56	4	0	29.1	23.4	95.00%	K.MAELEEAAIK.A		K.MAELEEAAIK.A
397	411	2	1568.83	1.9	1	30.1	21.6	95.00%	K.LVGVPCGVATQQILD.G	Carbamidomethyl (+57)	K.LVGVPCGVATQQILDGVINTPGVLAPNDMK.L
64	85	3	2488.28	3.3	1	39.1	21.4	95.00%	K.AVSEHDLTISLIPYTYHATVMK.A		K.AVSEHDLTISLIPYTYHATVMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
38	PDX1_SCHPO	29.73%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	49	2	1547.75	2.7	0	74.2	25.3	95.00%	R.IAEAAGACAVMALER.V	Carbamidomethyl (+57)/ Oxidation (+16)	R.IAEAAGACAVMALER.V
265	280	2	1628.86	4	0	87.2	21.6	95.00%	K.ILAEVSENLGAAMVGR.S		K.ILAEVSENLGAAMVGR.S
71	83	2	1355.75	4.3	0	66.7	21	95.00%	K.EIQAAVSIPVMAK.V		K.EIQAAVSIPVMAK.V
21	34	2	1457.74	4	1	89.6	23.5	95.00%	K.GGVIMDVVNAEQAR.I		K.GGVIMDVVNAEQAR.I
121	132	3	1383.7	4.4	1	31	24.4	95.00%	K.SKFTVPFVCGSR.N	Carbamidomethyl (+57)	K.SKFTVPFVCGSR.N
140	149	2	1102.6	4.8	1	28.6	22.3	95.00%	R.RISEGAAMIR.T		R.RISEGAAMIR.T
13	20	2	830.47	4.2	0	38.8	20.2	95.00%	K.AGLAQMLK.G		K.AGLAQMLK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
39	C1TC_SCHPO	13.13%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
689	707	3	1923.15	3.9	1	37.5	6.99	95.00%	R.TSGLKPDAIVIVATVQALK.L		R.TSGLKPDAIVIVATVQALK.L
765	783	2	1913.94	1.8	2	51	24.4	95.00%	D.SPNEISAIREEALAAGATD.A		K.FSSDSPNEISAIREEALAAGATDAVDSNHWAEGGK.G
2	12	2	1184.68	4.9	0	55.8	19.1	95.00%	M.ALLLEGTSLAR.K	Acetyl (+42)	-.MALLLEGTSLAR.K
122	130	2	1024.47	3.6	0	26.7	25.4	92.70%	D.GFCETNLGK.L	Carbamidomethyl (+57)	K.DVDGFCETNLGK.L
120	130	2	1238.56	3.6	1	42.1	25.8	95.00%	D.VDGFCETNLGK.L	Carbamidomethyl (+57)	K.DVDGFCETNLGK.L
536	546	2	1228.67	4.9	1	27.4	22	94.20%	R.KITIGENPTEK.G		R.KITIGENPTEK.G
324	336	2	1299.71	5.1	1	59.2	21.1	95.00%	K.NIGDLASEIGIAK.S		K.NIGDLASEIGIAK.S
381	396	2	1629.9	3.4	1	106	18.5	95.00%	K.STLTAGLVQALSNLDK.L		K.STLTAGLVQALSNLDK.L
349	356	2	983.58	5.3	0	46.2	18.5	95.00%	K.VNLEILQR.L		K.VNLEILQR.L
835	849	2	1592.78	4.3	1	53.3	25.6	95.00%	K.EMYGADGIELSPLAK.E		K.EMYGADGIELSPLAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
40	THIL_SCHPO	30.38%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
196	210	2	1667.89	1.4	0	31.1	20.2	95.00%	K.AFEQEIVPVEVPVGR.G		K.AFEQEIVPVEVPVGR.G
291	301	2	1160.65	4.8	0	33.2	20	95.00%	R.FTTSPSLAIPK.A		R.FTTSPSLAIPK.A
14	30	2	1654.81	3.8	0	74.4	24.4	95.00%	R.TPMGSFGGSFASLPATK.L		R.TPMGSFGGSFASLPATK.L
156	173	2	1912.84	3	1	41	27.2	95.00%	D.GLPMGNAAELCAEEHSID.R	Carbamidomethyl (+57)	R.DGLSDAYDGLPMGNAAELCAEEHSIDR.A
267	277	3	1194.77	2.9	1	21.4	8.45	91.20%	K.VKELGLKPLAK.I		K.VKELGLKPLAK.I
360	371	2	1405.81	4.5	0	73.2	16.5	95.00%	R.IICTLAYILAQK.D	Carbamidomethyl (+57)	R.IICTLAYILAQK.D
337	359	4	2248.12	2.3	1	21.1	24	95.00%	D.PERVNINGGGVAMGHPLGSSGSR.I		K.ILGLDPERVNINGGGVAMGHPLGSSGSR.I
278	290	2	1440.71	4.1	1	44.3	24.4	95.00%	K.IIGWGEAAQDPER.F		K.IIGWGEAAQDPER.F
340	359	2	1865.92	3.4	0	43.9	24.1	95.00%	R.VNINGGGVAMGHPLGSSGSR.I		R.VNINGGGVAMGHPLGSSGSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
41	PPA1_SCHPO	16.78%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

414	427	2	1671.78	2	0	52.9	26.6	95.00%	D.GMCELYAYLNSPVR.V	Carbamidomethyl (+57)	R.HLVNEEVFPLSDCGFGPSNTSDGMCELYAYLNSPVR.V
40	59	3	2404.13	2.5	1	63.3	26.2	95.00%	R.SPYHKPYFYGPSIDFPTTCK.I	Carbamidomethyl (+57)	R.SPYHKPYFYGPSIDFPTTCK.I
73	92	2	2046.99	3	1	106	24.8	95.00%	R.NPTGGNAAFDAVGIANFQQR.L		R.NPTGGNAAFDAVGIANFQQR.L
366	387	2	2501.19	3.5	1	42.6	25.4	95.00%	K.ASEFVPFAGNLITELFQCEDSK.Y	Carbamidomethyl (+57)	K.ASEFVPFAGNLITELFQCEDSK.Y
83	92	2	1102.59	2.8	0	33.6	23.1	95.00%	D.AVGIANFQQR.L		R.NPTGGNAAFDAVGIANFQQR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
42	MET3_SCHPO	21.43%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
364	382	2	2159.15	2.7	0	56.8	19.6	95.00%	R.VGANIPEWFSYPEVVAILR.Q		R.VGANIPEWFSYPEVVAILR.Q
427	440	2	1651.86	4	1	77.5	20.8	95.00%	R.LDAISVFYAQELQR.A		R.LDAISVFYAQELQR.A
83	92	2	1103.55	3.3	1	32	23.8	95.00%	D.LNESQADSLK.A		R.LSTGEVFPIPITLDLNESQADSLK.A
350	359	2	1102.6	3.9	0	29.9	20.9	95.00%	R.TLNISGTELR.R		R.TLNISGTELR.R
454	470	3	1867.06	1.3	1	32.5	13.6	95.00%	D.ASVKVPAEWTTVNIKPK.D		R.AGAAVVVSLADADASVKVPAEWTTVNIKPK.D
59	68	2	1233.64	5.6	1	40.5	22.8	95.00%	K.DYLNVVENLR.L		K.DYLNVVENLR.L
254	262	2	1012.62	5.1	0	33.5	14.1	95.00%	K.LSLLPLAMR.M		K.LSLLPLAMR.M
14	29	2	1808.97	2.5	1	43.5	19.4	95.00%	D.APLREQLEQEATSLPK.I		R.DAPLREQLEQEATSLPK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
43	CYPH_SCHPO	48.77%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
124	138	2	1644.83	4.4	1	86.7	24.7	95.00%	K.HVVFGEVTEGMDVVK.K		K.HVVFGEVTEGMDVVK.K
90	123	3	3611.83	4	1	56	19.8	95.00%	K.HNKPGLLSMANAGPNTNGSQFFITTVVTPWLDGK.H		K.HNKPGLLSMANAGPNTNGSQFFITTVVTPWLDGK.H
2	17	2	1835.87	3.9	1	50	25.9	95.00%	M.SNCFFDVIANGQPLGR.I	Acetyl (+42)/ Carbamidomethyl (+57)	-.MSNCFFDVIANGQPLGR.I
54	67	2	1607.82	4.3	1	67.2	23.4	95.00%	R.VIPQFMLQGGDFTR.G		R.VIPQFMLQGGDFTR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
44	RS18_SCHPO	36.84%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	78	2	1386.79	4	0	45.2	17	95.00%	R.IVTIIQNPSQFK.I		R.IVTIIQNPSQFK.I
2	14	2	1578.86	2	1	34.1	20	95.00%	M.SLVVPDNFQHILR.L	Acetyl (+42)	-.MSLVVPDNFQHILR.L
56	66	2	1246.61	4	0	41.5	24.8	95.00%	R.AGELTTEELER.I		R.AGELTTEELER.I
79	86	2	1031.56	6	0	52.6	22.1	95.00%	K.IPSWFLNR.Q		K.IPSWFLNR.Q
95	106	2	1334.69	4.9	1	24.9	22.6	90.30%	K.SFQLLANNVDSK.L		K.SFQLLANNVDSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
45	ADH_SCHPO	26.57%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
304	313	2	1165.6	2.4	0	39.7	23.2	95.00%	D.SIEALEYVSR.G		R.IDSIEALEYVSR.G
236	253	2	1681.87	4.1	0	56	21.7	95.00%	K.AATNGGAHGTLVLSTSPK.S	Deamidation (+1)	K.AATNGGAHGTLVLSTSPK.S
254	278	3	2513.21	3.1	0	41.5	25	95.00%	K.SYEQAAGFARPGSTMVTVSMPAGAK.L		K.SYEQAAGFARPGSTMVTVSMPAGAK.L
170	194	3	2506.28	2.2	0	41	21	95.00%	K.VGPGEWICIPGAGGGLGHLAVQYAK.A	Carbamidomethyl (+57)	K.VGPGEWICIPGAGGGLGHLAVQYAK.A
63	77	2	1462.8	1.8	0	42.9	19.4	95.00%	K.MPLIGGHEGAGVVVK.V		K.MPLIGGHEGAGVVVK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
46	FAS2_SCHPO	5.43%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
488	502	3	1650.8	4.5	1	35.5	24.9	95.00%	K.NVNHPTAPSTTIDER.G		K.NVNHPTAPSTTIDER.G
614	628	2	1552.8	3.6	1	42.8	22	95.00%	K.SLTGTYLDVLESGAK.N		K.SLTGTYLDVLESGAK.N
114	146	3	3020.56	3.1	1	35.9	21	95.00%	K.VETAAAAAPAATPAPAPAQTSAPAAALPDEPPK.A		K.VETAAAAAPAATPAPAPAQTSAPAAALPDEPPK.A

517	527	2	1319.7	5.4	1	32	22.4	95.00%	R.KLTHYVTEMAK.G		R.KLTHYVTEMAK.G
1393	1401	2	994.61	4.5	1	27.6	13.4	94.40%	K.TPLPIVDLK.F		K.TPLPIVDLK.F
28	44	2	1939.01	4.4	1	67.5	21.2	95.00%	R.WIETQDVILSPPVSAER.I		R.WIETQDVILSPPVSAER.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
47	RAD24_SCHPO	36.67%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
109	120	2	1236.65	4.7	0	29.1	21.9	95.00%	K.HLIPNAASAESK.V		K.HLIPNAASAESK.V
31	44	2	1562.75	4.1	1	82.9	25.3	95.00%	K.SVASTDQELTVEER.N		K.SVASTDQELTVEER.N
219	227	2	1073.63	2.8	0	43.9	16.5	95.00%	D.STLIMQLLR.D		K.DSTLIMQLLR.D
237	267	3	2987.31	3.8	0	51	27	95.00%	D.AEYSAAAAGGNTEGAQENAPSNAPEGEAEPK.A		R.DNLTLWTSDAEYSAAAAGGNTEGAQENAPSNAPEGEAEPK.A
15	30	3	1896.88	4.4	1	24.8	26.4	94.40%	K.LAEQAERYEGMVENMK.S		K.LAEQAERYEGMVENMK.S
156	172	3	1746.93	2.9	0	66	21.1	95.00%	K.AASEIATAELAPTHPIR.L		K.AASEIATAELAPTHPIR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
48	RL4A_SCHPO	27.55%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
122	140	2	1845.04	4.3	0	48.1	14.8	95.00%	R.YAISSAVAASGVPSLLLAR.G		R.YAISSAVAASGVPSLLLAR.G
2	13	2	1304.71	4.5	0	25.5	21.1	91.50%	M.AAARPTVSIYSK.D	Acetyl (+42)	-.MAAARPTVSIYSK.D
15	29	2	1580.85	0.11	0	42	20.3	95.00%	D.GSVSSETIALPFVFK.A		K.DGSVSSETIALPFVFK.A
235	248	3	1457.85	2.1	0	29.4	14.8	95.00%	R.LNLLQLAPGGHLGR.F		R.LNLLQLAPGGHLGR.F
292	303	2	1357.75	4	1	43.8	19.5	95.00%	R.LINSDEIQSIVK.A		R.LINSDEIQSIVK.A
14	29	2	1695.88	4.2	1	38.3	22	95.00%	K.DGSVSSETIALPFVFK.A		K.DGSVSSETIALPFVFK.A
276	291	2	1864.94	2.5	1	77.2	23.8	95.00%	K.NYFLPENIISNADVTR.L		K.NYFLPENIISNADVTR.L
87	97	2	1197.51	4.4	0	32.6	26.5	95.00%	R.SGQAAFGNMCR.S	Carbamidomethyl (+57)	R.SGQAAFGNMCR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
49	YL8C_SCHPO	21.12%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
93	112	3	2269.21	2.4	1	44.9	18.3	95.00%	K.IVYADHLKPEVVMEVVEATK.G		K.IVYADHLKPEVVMEVVEATK.G
47	60	2	1575.87	2.1	1	38.2	19	95.00%	R.EKYPNFPIVLATGK.Q		R.EKYPNFPIVLATGK.Q
217	232	2	1745.96	4.4	0	53	18.2	95.00%	K.GTALQYITSNILPEVK.N		K.GTALQYITSNILPEVK.N
275	288	2	1456.72	2.4	0	76.5	24.7	95.00%	R.VGNEEGAVGEVLER.I		R.VGNEEGAVGEVLER.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
50	HSP7M_SCHPO	13.80%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
204	215	2	1124.67	4.6	0	48.3	15.3	95.00%	K.AAGAIAGLNVLR.V		K.AAGAIAGLNVLR.V
105	118	2	1578.81	4.5	0	81.4	23.3	95.00%	R.QAVINPENTFFATK.R		R.QAVINPENTFFATK.R
185	199	2	1679.83	4.3	1	62.1	24.4	95.00%	K.NAVVTVPAYFNDSQR.Q		K.NAVVTVPAYFNDSQR.Q
496	510	2	1538.89	4.2	0	77.2	14.9	95.00%	K.LIGNFQLTGIAPAPK.G		K.LIGNFQLTGIAPAPK.G
157	170	2	1496.8	5.1	0	59.3	21.8	95.00%	K.TYSPSQIGGFILSK.M		K.TYSPSQIGGFILSK.M
275	281	2	818.47	2.7	1	26.1	19.6	92.40%	D.FDVALVR.H		R.STNGDTHLGGEDFDVALVR.H
216	231	2	1630.86	3.8	1	78.5	21.6	95.00%	R.VVNEPTAAALAYGLDK.K		R.VVNEPTAAALAYGLDK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
51	CARB_SCHPO	9.74%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
968	975	2	1019.52	4.9	0	24.9	23.5	90.40%	K.VPQFSWTR.L		K.VPQFSWTR.L
932	943	2	1304.72	5.6	1	35.2	20.9	95.00%	K.TLGVNFIDVATR.S		K.TLGVNFIDVATR.S
402	417	3	1672.96	2.6	0	21.3	14.6	91.10%	K.IALGHTLPELPNAVTK.T		K.IALGHTLPELPNAVTK.T
773	798	3	2736.49	2.9	0	51	15.6	95.00%	K.FANAVGYPVLVRPSYVLSGAAMSVIR.D		K.FANAVGYPVLVRPSYVLSGAAMSVIR.D
418	433	2	1784.89	2.6	1	45.5	24.1	95.00%	K.TTTANFEPSLDYVVTK.I		K.TTTANFEPSLDYVVTK.I
575	584	2	1057.58	4.7	1	32.1	22	95.00%	K.LVGASELDVR.A		K.LVGASELDVR.A
249	273	3	2529.22	2.7	1	48.7	24.6	95.00%	R.SAYSLGGLGSGFANNKEELQSMAAK.S		R.SAYSLGGLGSGFANNKEELQSMAAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
52	ECM17_SCHPO	4.14%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
493	502	3	1154.69	2.2	1	31.2	14.5	95.00%	D.PELVISELKK.D		K.NSSVSSESLEVLSNWIVSVDNLESPVDPELVISELKK.D
314	325	2	1337.79	2.1	0	41.1	13.6	95.00%	R.LTVLEPITSLPR.K		R.LTVLEPITSLPR.K
77	90	2	1484.78	3	0	51	22.6	95.00%	D.AILAEEEVASTQPK.Q		K.SHADPFAHIADAILAEEEVASTQPK.Q
801	810	2	1058.57	5.4	1	27.5	23.1	94.20%	K.GADLNLSELK.Y		K.GADLNLSELK.Y
1031	1045	2	1687.72	4	1	52.6	26.5	95.00%	R.NVTCSSTPNNETIHD.Q	Carbamidomethyl (+57)	R.NVTCSSTPNNETIHDQLFAVSK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
53	OAT_SCHPO	25.34%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
386	398	3	1374.82	4.6	0	23.2	13.4	94.20%	R.GVLAKPTHGNIIR.F		R.GVLAKPTHGNIIR.F
70	80	2	1268.71	4.2	0	28.4	18.1	95.00%	K.IIEALVEQAQR.V		K.IIEALVEQAQR.V
2	37	4	4216	4.3	0	58.2	22.8	95.00%	M.SAESLLHNTFSTEQIEVLENEYAAHNYHPLPVCFSK.A	Acetyl (+42)/ Carbamidomethyl (+57)	-.MSAESLLHNTFSTEQIEVLENEYAAHNYHPLPVCFSK.A
276	291	2	1561.85	1.7	0	54.1	20.1	95.00%	K.AISGGVYPVSAVLSSR.E		K.AISGGVYPVSAVLSSR.E
238	254	2	1838.97	4.4	1	78.8	21.3	95.00%	K.AHNVLFIADEVQTGVAR.T		K.AHNVLFIADEVQTGVAR.T
258	275	3	2051.1	4.3	1	30.2	19.6	95.00%	K.MLCIEHSNVKPDVVILGK.A	Carbamidomethyl (+57)	K.MLCIEHSNVKPDVVILGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
54	HOSM_SCHPO	20.33%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	204	2	1315.66	4	1	40.8	24.8	95.00%	R.VGIADTVGCATPR.Q	Carbamidomethyl (+57)	R.VGIADTVGCATPR.Q
2	31	3	3218.5	4.8	1	47.5	24.7	95.00%	M.SVSEANGTETIKPPMNGNPYGPNPSDFLSR.V	Acetyl (+42)/ Deamidation (+1)	-.MSVSEANGTETIKPPMNGNPYGPNPSDFLSR.V
72	85	2	1578.79	2.6	0	49.8	24.8	95.00%	D.YIELTSPVASEQSR.Q		K.ALDNFGVDYIELTSPVASEQSR.Q
324	339	2	1772.92	2	1	31.8	22	95.00%	K.AILANPSTYEILKPED.F		K.AILANPSTYEILKPEDFGMSR.Y
32	43	2	1391.75	4.9	0	68.1	21.5	95.00%	R.VNNFSIIESTLR.E		R.VNNFSIIESTLR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
55	GBLP_SCHPO	35.99%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
295	308	2	1606.81	2.3	1	46.3	23.6	95.00%	D.GQTLFSGWTDNLIR.V		K.SSEPECISLTWSPDGQTLFSGWTDNLIR.V
186	212	3	2736.26	2.6	1	43.2	26.8	95.00%	R.TSHYGHTGYVSAVTISPDGSLCASGGR.D	Carbamidomethyl (+57)	R.TSHYGHTGYVSAVTISPDGSLCASGGR.D
234	245	2	1314.71	3.1	0	32.5	21.9	95.00%	K.ANINALVFSPNR.Y		K.ANINALVFSPNR.Y
176	185	2	1264.65	5.4	1	30.1	23.2	95.00%	K.VWDLETFSLR.T		K.VWDLETFSLR.T
39	47	2	1112.68	5.9	0	27.8	14.1	94.60%	K.SIILWNLVR.D		K.SIILWNLVR.D
221	233	2	1503.76	3.2	0	35.7	23.9	95.00%	D.LNESTHLYSLEAK.A		R.DGTLMLWDLNESTHLYSLEAK.A
9	36	3	2894.45	2.9	1	38.1	22.8	95.00%	R.ATLEGHSGWVTSLSTAPENPDILLSGSR.D		R.ATLEGHSGWVTSLSTAPENPDILLSGSR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
56	CYSD_SCHPO	31.93%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	26	3	2735.29	3.8	1	45.2	26.1	95.00%	M.PVESEHFETLQLHAGQEPDAATSSR.A		-.MPVESEHFETLQLHAGQEPDAATSSR.A
47	59	2	1541.79	1.7	0	40.6	23.2	95.00%	R.LFGLQEPGYIYSR.M		R.LFGLQEPGYIYSR.M
27	39	2	1486.79	3	0	48.8	21.9	95.00%	R.AVPIYATTSYVFR.D		R.AVPIYATTSYVFR.D

72	100	3	2787.49	3.3	0	49.9	17.9	95.00%	R.IAALEHGAAAIATSSGTSALFMALTTLAK.A			R.IAALEHGAAAIATSSGTSALFMALTTLAK.A
366	377	2	1185.64	4.4	1	34.5	21.5	95.00%	K.LASQLANVGDAK.T			K.LASQLANVGDAK.T
151	169	2	2199.03	1.3	1	62.5	26.2	95.00%	K.AVYVESIGNPMYNVPDFER.I			K.AVYVESIGNPMYNVPDFER.I
378	403	3	2798.48	2.5	1	42.6	18.6	95.00%	K.TLVIAPAYTTHLQLTDEEQISAGVTK.D			K.TLVIAPAYTTHLQLTDEEQISAGVTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
57	VIPI_SCHPO	34.63%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	68	2	1496.86	4.3	1	41.7	15.9	95.00%	K.TALLLQDALLGQNK.I		K.TALLLQDALLGQNK.I
101	110	2	1087.63	5.8	0	34.3	17.8	95.00%	R.SAIISELLSR.G		R.SAIISELLSR.G
225	254	3	2955.4	2.7	1	57.6	25.4	95.00%	K.NQAEGTASPASSTPTAPAEKEPTAPTTESK.T		K.NQAEGTASPASSTPTAPAEKEPTAPTTESK.T
122	134	2	1410.71	4.2	1	61.1	24.3	95.00%	K.SIQLDQSYGVSSK.F		K.SIQLDQSYGVSSK.F
111	121	2	1260.64	3.7	1	31.8	23.4	95.00%	R.GYHLSDVTLEK.S		R.GYHLSDVTLEK.S
137	147	2	1100.62	4.3	0	27.7	20.7	94.50%	K.GILESALSGVR.S		K.GILESALSGVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
58	HSP7F_SCHPO	12.78%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
174	189	2	1665.84	2.2	1	79.5	23.5	95.00%	R.LMNDNAAAALTYGITK.T		R.LMNDNAAAALTYGITK.T
581	591	2	1385.65	4	1	31.1	26.1	95.00%	K.NALEEYIYDTR.A		K.NALEEYIYDTR.A
5	16	2	1249.64	6.5	1	29.4	23.5	95.00%	R.TNVVGIDFGNSK.T		R.TNVVGIDFGNSK.T
38	48	2	1194.59	3.8	0	34	24	95.00%	R.STPSLVSYGER.S		R.STPSLVSYGER.S
159	173	2	1534.89	4	0	42.9	13.2	95.00%	R.ALLEAANIAGLNPLR.L		R.ALLEAANIAGLNPLR.L
96	106	2	1134.6	4	1	31.7	23.2	95.00%	K.LTEVDGFVGAK.V		K.LTEVDGFVGAK.V
419	434	2	1690.85	2.6	0	62.7	24	95.00%	D.SSLEVFSEGNPIPSTK.I		R.EFHVHDVTTYPITFSWEPIPENPEEDSSLEVFSEGNPIPSTK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
59	RS7_SCHPO	25.64%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
131	141	3	1271.76	2.6	1	22.1	13.2	92.50%	D.IVFPTEIIGKR.T		R.TLTAVHNAILEDIVFPTEIIGKR.T
119	140	3	2393.33	3.6	1	40.9	13.6	95.00%	R.TLTAVHNAILEDIVFPTEIIGK.R		R.TLTAVHNAILEDIVFPTEIIGK.R
59	70	2	1322.84	4	0	46.5	9.54	95.00%	K.AIVVFVPQPLLK.A		K.AIVVFVPQPLLK.A
20	34	2	1724.87	2.2	1	78.2	24.4	95.00%	D.LLVAQCLYDLESSSK.D	Carbamidomethyl (+57)	R.SSSQPTETDLLVAQCLYDLESSSK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
60	LEUC_SCHPO	14.25%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
521	539	2	1671.88	1.9	0	96.7	21.7	95.00%	D.GIATNVAGSVSSGSAGIPK.F		K.NYDPSHDVEGDIGLSVDDATDAVTDADGIATNVAGSVSSGSAGIPK.F
633	649	2	2002.01	4.5	1	59.4	24.1	95.00%	R.VIIAPSFADIFFNNCFK.N	Carbamidomethyl (+57)	R.VIIAPSFADIFFNNCFK.N
417	436	3	2355.02	4.1	1	24.9	26.8	93.90%	R.EAGCSMCLGMNPDQLKPYER.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.EAGCSMCLGMNPDQLKPYER.C
603	619	3	1826.85	2.8	1	41.7	26.5	95.00%	R.HATVLVAHDNFGCGSSR.E	Carbamidomethyl (+57)	R.HATVLVAHDNFGCGSSR.E
477	493	2	1810.88	4.1	1	36.5	25.2	95.00%	R.EFFGDVSNGSPSIITNK.N		R.EFFGDVSNGSPSIITNK.N
482	493	2	1215.65	3.5	0	26.1	21.9	92.40%	D.VSNGSPSIITNK.N		R.EFFGDVSNGSPSIITNK.N
650	667	2	2027	4	1	40.9	24.8	95.00%	K.NGMLPIPTPIEQVNDMMK.A		K.NGMLPIPTPIEQVNDMMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
61	ILV3_SCHPO	16.05%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
266	278	3	1408.68	4.8	1	24.2	25.3	95.00%	K.FAECEAAGSAIKR.L	Carbamidomethyl (+57)	K.FAECEAAGSAIKR.L
49	68	2	2142.97	5.2	1	90.3	27.1	95.00%	K.SQGASQAMLYATGLNEEDMK.K		K.SQGASQAMLYATGLNEEDMK.K

538	547	2	1056.58	3	1	38.4	22	95.00%	D.GDVIEINAVK.N			R.FSGGSHGFLIGHVDPEAQVGGPIALVQDGDVIEINAVK.N
402	417	4	1843.09	3.6	1	32.1	6.02	95.00%	K.IIRPLSNPIKTEGHLR.V			K.IIRPLSNPIKTEGHLR.V
198	212	2	1645.84	2.5	0	33.7	22.5	95.00%	D.IVSAFQSYGEFITGK.I			R.AGHSPCQNNAPIDIVSAFQSYGEFITGK.I
40	48	2	994.5	5.2	0	30.6	24.7	95.00%	K.YSETITGPK.S			K.YSETITGPK.S
185	212	3	3007.42	3.5	1	69.2	25.4	95.00%	R.AGHSPCQNNAPIDIVSAFQSYGEFITGK.I	Carbamidomethyl (+57)		R.AGHSPCQNNAPIDIVSAFQSYGEFITGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
62	UGPA1_SCHPO	14.43%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	10	2	1166.63	4.6	1	24.9	20.4	90.30%	-.MDLAPRPLGR.Q	Acetyl (+42)	-.MDLAPRPLGR.Q
185	194	2	1205.65	4.7	1	32.1	21.4	95.00%	K.IDILTFNQSR.Y		K.IDILTFNQSR.Y
299	314	3	1876.02	4.4	0	30	18.4	95.00%	R.LLEIAQVPPQHVEEFK.S		R.LLEIAQVPPQHVEEFK.S
115	129	2	1460.72	4.2	0	48.3	24.8	95.00%	K.LNGGLGTTMGCVGPK.S	Carbamidomethyl (+57)	K.LNGGLGTTMGCVGPK.S
35	46	2	1339.68	2.5	2	36.4	23.5	95.00%	K.NELNHLASTVKD.P		K.NELNHLASTVKDPLAK.K
95	104	2	1003.53	2.3	0	36.7	22.9	95.00%	D.TITEAGGLSR.D		R.GSEINWDLVESPKPEQVVEYDTITEAGGLSR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
63	RL8_SCHPO	19.69%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
24	32	2	1084.62	4.7	0	29.3	20.4	95.00%	K.NPLFVSRPR.S		K.NPLFVSRPR.S
33	43	2	1188.62	4.1	1	26.8	23.1	93.30%	R.SFGIGQDIQPK.R		R.SFGIGQDIQPK.R
109	120	2	1171.61	4.7	0	55.2	23.5	95.00%	R.LVAEAEAVANGK.S	Deamidation (+1)	R.LVAEAEAVANGK.S
134	146	2	1425.8	2.8	0	58.2	17.6	95.00%	K.YGLNHVVALIEAK.K		K.YGLNHVVALIEAK.K
52	57	2	862.44	5.9	0	26.5	23.1	93.00%	K.WPEYIR.L		K.WPEYIR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
64	YF19_SCHPO	20.08%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
195	208	2	1516.82	4.7	0	34.9	19.7	95.00%	K.TAELTPLSALCLTK.F	Carbamidomethyl (+57)	K.TAELTPLSALCLTK.F
5	17	2	1406.78	4.6	1	33	18.1	95.00%	K.LVDHVEITVPTGK.T		K.LVDHVEITVPTGK.T
355	368	2	1443.78	2.8	0	40.7	21.4	95.00%	R.IVSYIESGIAHGAK.L		R.IVSYIESGIAHGAK.L
422	443	3	2229.12	4.1	0	21.2	22.8	90.80%	R.GNNSTYGLAAGVHTNNITNAIK.V		R.GNNSTYGLAAGVHTNNITNAIK.V
71	80	2	1161.56	3.7	1	28.3	25.2	94.90%	R.AAFQTDAPWR.K		R.AAFQTDAPWR.K
336	349	2	1523.73	2.1	1	97.1	25.5	95.00%	D.PFAEDTFQGAQVSK.Q		K.VGDPFAEDTFQGAQVSK.Q
181	194	2	1439.82	2.6	0	44	16.5	95.00%	K.IAPAVACGNTIILK.T	Carbamidomethyl (+57)	K.IAPAVACGNTIILK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
65	HXK1_SCHPO	9.50%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
304	315	2	1380.7	5.1	1	25.3	23.4	91.00%	K.MIAGCYLGDILR.R	Carbamidomethyl (+57)	K.MIAGCYLGDILR.R
2	12	3	1409.65	4.4	1	25.1	25.7	95.00%	M.SLHDAYHWPSR.T	Acetyl (+42)	-.MSLHDAYHWPSR.T
455	469	2	1328.73	2.4	0	59.8	20.8	95.00%	D.GSGVGAALVSALEAK.G		K.VVTIPAEDGSGVGAALVSALEAK.G
447	469	2	2153.17	3.4	1	105	18.3	95.00%	K.VVTIPAEDGSGVGAALVSALEAK.G		K.VVTIPAEDGSGVGAALVSALEAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
66	IF5A1_SCHPO	42.68%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
74	87	2	1540.74	2.6	1	36.8	25.9	95.00%	D.MSPSTHNMDVPVVK.R		K.YEDMSPSTHNMDVPVVK.R
99	111	2	1413.68	1.8	1	26.4	24.9	92.90%	D.GYLNLMTTDGTTK.D		R.DEYQLVNIDDGYLNLMTTDGTTK.D

2	28	3	2979.31	4	1	77.3	26.7	95.00%	M.AEEEHVDFEGGEAGASLTFPMQCSALR.K	Acetyl (+42)/ Carbamidomethyl (+57)	-.MAEEEHVDFEGGEAGASLTFPMQCSALR.K
9	28	2	2127.98	2.6	0	46.2	26.7	95.00%	D.FEGGEAGASLTFPMQCSALR.K	Carbamidomethyl (+57)	-.MAEEEHVDFEGGEAGASLTFPMQCSALR.K
9	29	3	2256.07	2.1	1	43	26.1	95.00%	D.FEGGEAGASLTFPMQCSALRK.N	Carbamidomethyl (+57)	-.MAEEEHVDFEGGEAGASLTFPMQCSALRK.N
58	69	2	1352.76	4.3	1	43.7	17	95.00%	K.VHIVALDIFNGR.K		K.VHIVALDIFNGR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
67	YHY6_SCHPO	13.83%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
678	698	2	2257.13	4.5	1	51.2	23.8	95.00%	K.SLCIPLEQPSGEDAIIEGTTK.C	Carbamidomethyl (+57)	K.SLCIPLEQPSGEDAIIEGTTK.C
161	187	3	2608.39	2.9	1	26.8	18.5	95.00%	K.SVGVNPIIVDFSAPGSATAPSKPAAQK.K		K.SVGVNPIIVDFSAPGSATAPSKPAAQK.K
298	323	3	2901.42	3	1	27.8	23.9	95.00%	R.AGTSELDEPIAIRPTSETVMYPYYAK.W		R.AGTSELDEPIAIRPTSETVMYPYYAK.W
450	462	3	1364.71	2.7	0	39.9	23.3	95.00%	D.PNAEIGPTGERPK.L		K.MFNIVVEDPNAEIGPTGERPK.L
387	398	2	1343.81	2.1	1	37.6	10.8	95.00%	R.IYTDLLAVPVIK.G		R.IYTDLLAVPVIK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
68	GLNA_SCHPO	17.83%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
153	170	2	1809.83	4.4	0	40.7	26.4	95.00%	K.GGFPGPQGPFYCGVGTGR.V	Carbamidomethyl (+57)	K.GGFPGPQGPFYCGVGTGR.V
345	359	2	1749.87	2.6	0	54.7	24.7	95.00%	D.PYLVTGIITETMFEH.-		R.RPASSIDPYLVTGIITETMFEH.-
237	260	4	2635.31	3.2	1	28.9	24	95.00%	K.ISFHPKPILGDWNGAGCHTNVSTK.D	Carbamidomethyl (+57)	K.ISFHPKPILGDWNGAGCHTNVSTK.D
338	359	3	2476.24	4.1	1	26.8	22.9	95.00%	R.RPASSIDPYLVTGIITETMFEH.-		R.RPASSIDPYLVTGIITETMFEH.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
69	BCA1_SCHPO	22.89%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
315	331	2	1670.97	4.2	0	59.5	11.5	95.00%	R.LLEVFGAGTAALVSPVK.A		R.LLEVFGAGTAALVSPVK.A
122	130	2	1010.58	1.6	0	64.5	17.6	95.00%	D.PAELAEIIR.K		R.ISLPSFDPAELAEIIR.K
37	49	3	1581.74	4.5	1	25.4	25.9	95.00%	K.FGENFTDHMLIMK.W		K.FGENFTDHMLIMK.W
262	278	2	1795	4.2	1	43.3	16.4	95.00%	K.EIITAPLDGMILPGVTR.D		K.EIITAPLDGMILPGVTR.D
337	359	2	2462.16	4.4	0	42.7	26	95.00%	K.GTEYEIPMPEGQEAGPITSEISK.W		K.GTEYEIPMPEGQEAGPITSEISK.W
115	130	2	1769.96	3.9	1	43.7	19.2	95.00%	R.ISLPSFDPAELAEIIR.K		R.ISLPSFDPAELAEIIR.K
122	131	3	1138.67	0.95	1	31.3	15.3	95.00%	D.PAELAEIIRK.F		R.ISLPSFDPAELAEIIRK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
70	RS6B_SCHPO	27.20%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	115	2	1739.01	3.8	1	65.7	12	95.00%	R.GCIVGQDLAVLALAIVK.Q	Carbamidomethyl (+57)	R.GCIVGQDLAVLALAIVK.Q
32	51	2	2112.99	4.1	1	51.8	26.1	95.00%	R.MGQEVPGDSVGPEFAGYVFK.I		R.MGQEVPGDSVGPEFAGYVFK.I
59	72	3	1625.86	4.7	0	32.2	21.7	95.00%	K.QGFPMFQGVLLPHR.V		K.QGFPMFQGVLLPHR.V
40	51	2	1299.65	2.8	0	41.4	23.9	95.00%	D.SVGPEFAGYVFK.I		R.MGQEVPGDSVGPEFAGYVFK.I
204	217	2	1606.78	4.3	1	54.8	25.1	95.00%	K.NREEAAEFAQLMAK.R		K.NREEAAEFAQLMAK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
71	FAS1_SCHPO	6.75%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1117	1130	2	1421.7	4.7	0	59.8	25.1	95.00%	K.SLESVSVTEEAGSK.V		K.SLESVSVTEEAGSK.V
1870	1881	2	1266.57	5.2	1	37.8	26	95.00%	R.SDYGMVAANPSR.V		R.SDYGMVAANPSR.V

210	224	3	1723.91	5.4	1	36.5	20.9	95.00%	K.GLNVLDWLAGERPER.D		K.GLNVLDWLAGERPER.D
828	846	3	1903.05	1.8	0	33.3	17.6	95.00%	D.GPTGGIVTVLSELGEPIHK.L		K.TYDGPTGGIVTVLSELGEPIHK.L
2	12	2	1294.67	5.2	0	53.5	22.4	95.00%	M.VEAEQVHQSLR.S		-.MVEAEQVHQSLR.S
1778	1806	3	3141.54	1.9	1	40.3	23.1	95.00%	K.DSTSFSFTHPSGLLSATQFTQPALTLMEK.S		K.DSTSFSFTHPSGLLSATQFTQPALTLMEK.S
781	794	2	1545.81	3.9	1	42.1	22.2	95.00%	K.LPPMPFDGILFGSR.L		K.LPPMPFDGILFGSR.L
1422	1447	3	2983.4	3.2	1	29.8	25.7	95.00%	R.GTFTDFENTFEHTQETPMQLTLATPK.D		R.GTFTDFENTFEHTQETPMQLTLATPK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
72	TRP_SCHPO	15.49%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
382	393	2	1355.77	4.5	0	47.2	19	95.00%	K.INNCIGQILLAK.R	Carbamidomethyl (+57)	K.INNCIGQILLAK.R
247	261	2	1623.75	3.4	0	47.6	26.4	95.00%	K.AEPGTAATVVEEYCK.Y	Carbamidomethyl (+57)	K.AEPGTAATVVEEYCK.Y
400	419	3	1938.01	4.3	0	37.5	21.1	95.00%	R.IIAETGAGQHGVATAICAAK.F	Carbamidomethyl (+57)	R.IIAETGAGQHGVATAICAAK.F
275	302	3	2928.48	4.6	0	34.9	22	95.00%	K.QFQSGGSVATAPPAAVVEPINEMYLPQK.Y		K.QFQSGGSVATAPPAAVVEPINEMYLPQK.Y
616	631	2	1825.87	3	1	57.5	26.1	95.00%	R.AEFIAVTDAQCLEGFR.A	Carbamidomethyl (+57)	R.AEFIAVTDAQCLEGFR.A
445	461	2	1739.99	4	0	48.6	15.1	95.00%	R.LLGAEVVPVTSGTQTLR.D		R.LLGAEVVPVTSGTQTLR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
73	CDC48_SCHPO	5.28%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
550	563	2	1522.75	3.6	0	43.8	24.4	95.00%	K.AIANECSANFISVK.G	Carbamidomethyl (+57)	K.AIANECSANFISVK.G
359	374	2	1686.84	2.6	1	52.6	24.2	95.00%	R.SNVVVMAATNRPNSID.P		R.SNVVVMAATNRPNSIDPALR.R
774	786	3	1606.83	2.9	1	38.4	22.8	95.00%	R.RYEAYAHQLLTSR.G		R.RYEAYAHQLLTSR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
74	EF1G_SCHPO	15.89%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
93	115	3	2635.36	1.8	0	49.2	20.6	95.00%	K.VLQYCSFTNSELPGAFRPIIAPR.V	Carbamidomethyl (+57)	K.VLQYCSFTNSELPGAFRPIIAPR.V
207	216	2	1182.71	4	1	27.1	16.6	93.80%	K.FIDQPLPIIK.A		K.FIDQPLPIIK.A
291	298	2	1021.49	2.5	0	25.7	24	91.70%	D.PENYSVWK.V		R.SGALPWFFEHFDPENYSVWK.V
128	139	2	1303.72	4.6	0	40.7	20.3	95.00%	K.EAETAIALIFAR.F		K.EAETAIALIFAR.F
116	127	2	1294.63	4.3	1	26.2	24.9	92.60%	R.VFGAPYDEQAAK.E		R.VFGAPYDEQAAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
75	DHAS_SCHPO	18.21%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
31	39	2	856.52	4.9	0	28.2	19.7	95.00%	K.IAVLGASAR.S		K.IAVLGASAR.S
19	30	3	1445.76	4.9	1	23.3	22.5	94.30%	R.FITLLSDHPEFK.I		R.FITLLSDHPEFK.I
143	161	2	2003.02	2.7	0	76.4	22.4	95.00%	R.GCIITNSNCSTAAVVVPLK.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GCIITNSNCSTAAVVVPLK.A
267	278	2	1375.7	3.8	0	37.2	23.7	95.00%	R.EVLANYVSEPQK.L		R.EVLANYVSEPQK.L
6	18	2	1227.7	3.7	0	35.6	19.6	95.00%	K.VGILGATGTVGQR.F		K.VGILGATGTVGQR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
76	RS3B_SCHPO	11.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
228	241	2	1524.79	4.4	1	71.2	22.7	95.00%	K.LLELHGESQDVGTK.V		K.LLELHGESQDVGTK.V
200	213	2	1513.87	4.8	0	38.9	14.8	95.00%	R.ATGSIFPLQNVLVR.K		R.ATGSIFPLQNVLVR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
77	DHE4_SCHPO	15.30%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

334	353	2	2102.95	2.3	0	116	26.6	95.00%	R.YVAEGSNMGSSAEAVEVFEK.S		R.YVAEGSNMGSSAEAVEVFEK.S
25	34	3	1266.71	4.3	1	33.7	18.2	95.00%	K.LFEVHPELKR.V		K.LFEVHPELKR.V
356	367	2	1231.57	4.5	0	27.7	25.3	94.10%	R.ASGEGCWLAPGK.A	Carbamidomethyl (+57)	R.ASGEGCWLAPGK.A
93	101	2	1127.61	5.6	0	29.2	22.5	95.00%	K.FLGFEQIFK.N		K.FLGFEQIFK.N
399	416	2	1950.98	4.6	1	78.4	22.9	95.00%	K.LAGIMQNIFEQSTDVASK.Y		K.LAGIMQNIFEQSTDVASK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
78	EF1B_SCHPO	21.03%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
59	73	2	1561.84	4.2	1	60.9	20.6	95.00%	K.QIATYDLATLPGTAK.E		K.QIATYDLATLPGTAK.E
153	165	2	1432.74	3.9	1	44.3	23.7	95.00%	R.SIQMDGLVWGLSK.L		R.SIQMDGLVWGLSK.L
23	39	2	1885.91	2.3	1	55.7	24.9	95.00%	K.SFIEGYEPSQADAVVFK.A		K.SFIEGYEPSQADAVVFK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
79	PYC_SCHPO	5.74%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
829	838	2	1275.63	4.5	1	27.7	24.3	94.50%	K.QLEFDNNQLR.E		K.QLEFDNNQLR.E
1111	1129	3	1901.98	2.7	0	41.3	22.2	95.00%	D.PGNPGHVAAPMSGTIVEIR.V		R.ADPGNPGHVAAPMSGTIVEIR.V
1109	1129	3	2088.05	4.4	1	38.2	23	95.00%	R.ADPGNPGHVAAPMSGTIVEIR.V		R.ADPGNPGHVAAPMSGTIVEIR.V
917	929	2	1447.76	4.7	1	42.2	23	95.00%	K.VVGDLAQFMVQNK.L		K.VVGDLAQFMVQNK.L
302	315	2	1628.75	2	1	37.3	26.1	95.00%	K.YCNAGTAEFLLDQK.G	Carbamidomethyl (+57)	K.YCNAGTAEFLLDQK.G
839	848	2	1297.58	4.8	1	38.2	25.9	95.00%	R.EIDSYWAQMR.L		R.EIDSYWAQMR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
80	SERC_SCHPO	16.20%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
330	352	5	2716.42	3.7	1	22	19.4	95.00%	R.IEPQELESEFLAEAEKHHLVQLK.G		R.IEPQELESEFLAEAEKHHLVQLK.G
376	385	2	1147.65	4.7	1	32.8	17.6	95.00%	R.LIDLLESFAK.A		R.LIDLLESFAK.A
216	228	2	1299.74	5	0	37	17.9	95.00%	K.NAGPAGITVVFVR.D		K.NAGPAGITVVFVR.D
189	199	2	1282.6	4.3	1	67	25	95.00%	R.VCDVSSNFISR.K	Carbamidomethyl (+57)	R.VCDVSSNFISR.K
324	329	2	766.38	5.3	0	26.2	21.6	92.50%	R.MNVTFR.I		R.MNVTFR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
81	O59743_SCHPO	21.49%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
12	24	2	1387.72	1.7	0	68.8	23.2	95.00%	K.LGIEEQVETAATK.S		K.LGIEEQVETAATK.S
122	136	3	1849.83	2.1	1	31.6	26.6	95.00%	D.NKPEEYYHLSAPDCK.S	Carbamidomethyl (+57)	K.LKPVPTSWEQALQDNKPEEYYHLSAPDCK.S
75	97	3	2588.33	2.8	1	31.8	20.9	95.00%	K.EALDLFLGAYNVITPELAHFEAR.C		K.EALDLFLGAYNVITPELAHFEAR.C
11	24	2	1515.82	2.4	1	54.4	20.9	95.00%	K.KLGIEEQVETAATK.S		K.KLGIEEQVETAATK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
82	HMCS_SCHPO	13.42%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
155	183	3	2859.53	2.4	0	41.9	18.1	95.00%	K.GNARPTGGAGCVALLVGPNAPIVFEPGLR.G	Carbamidomethyl (+57)	K.GNARPTGGAGCVALLVGPNAPIVFEPGLR.G
269	282	2	1454.7	3.2	0	38.8	25.2	95.00%	D.SAAEPSNPELEGVR.E		R.LLYTDSAAEPSNPELEGVR.E
264	282	2	2060.01	1.5	1	74.2	25	95.00%	R.LLYTDSAAEPSNPELEGVR.E		R.LLYTDSAAEPSNPELEGVR.E
217	228	2	1325.64	3.7	1	38.4	25.4	95.00%	K.ALDGAYANYNVR.D		K.ALDGAYANYNVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
83	NACA_SCHPO	29.48%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	75	2	1164.62	5.8	0	59.3	21.7	95.00%	K.SSNNAYIVLGK.V		K.SSNNAYIVLGK.V

11	26	2	1637.87	3	0	63.3	21	95.00%	K.ISELPAGSTTVVHAEK.A			K.ISELPAGSTTVVHAEK.A
52	64	2	1540.93	4.4	0	50.2	10.8	95.00%	K.NILLIINEPIVYK.S			K.NILLIINEPIVYK.S
76	86	2	1189.58	4.9	1	47.2	25.4	95.00%	K.VTVEDMAAQAR.A			K.VTVEDMAAQAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
84	ACON_SCHPO	9.00%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
532	549	2	1853.89	4.6	1	68.9	25.7	95.00%	K.GYDPGSNTYVAPSSVNVK.D		K.GYDPGSNTYVAPSSVNVK.D
375	391	2	1874.82	2.6	1	58.9	27.2	95.00%	K.VGLIGSCTNSSYEDMSR.A	Carbamidomethyl (+57)	K.VGLIGSCTNSSYEDMSR.A
392	402	2	1203.6	5.2	1	35.2	24.8	95.00%	R.AASICQQAIDK.G	Carbamidomethyl (+57)	R.AASICQQAIDK.G
652	666	2	1665.78	3.4	0	67.3	26.5	95.00%	R.WVTLGEQNFGEGSSR.E		R.WVTLGEQNFGEGSSR.E
462	470	2	1052.53	5	0	36.5	24	95.00%	K.NSIVTSYNR.N		K.NSIVTSYNR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
85	THRC_SCHPO	10.70%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
265	282	2	1945.01	4.9	1	46.3	22	95.00%	R.FIVPTGNFGDILAGYYAK.R		R.FIVPTGNFGDILAGYYAK.R
421	432	2	1235.66	1	0	29.9	20.4	95.00%	D.PHTAVGVETGLR.C		K.IYESDHYIIDPHTAVGVETGLR.C
157	166	2	1007.54	2.4	0	37.5	20.8	95.00%	D.TGSAAIYGLR.G		R.DHLTVVGATSGDTGSAAIYGLR.G
313	327	2	1443.73	4.4	1	39.8	24.3	95.00%	K.ADSTQVSPSGPISAK.E		K.ADSTQVSPSGPISAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
86	VATA_SCHPO	18.74%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
89	114	4	2751.53	2.9	1	22.2	11.5	95.00%	R.TGKPLSVELGPGLAETIYDGIQRPLK.Q		R.TGKPLSVELGPGLAETIYDGIQRPLK.Q
465	476	2	1580.77	4.7	0	39.5	25.5	95.00%	K.YINALQPWYEER.V		K.YINALQPWYEER.V
128	136	2	1002.51	5	0	25.2	23.9	90.90%	R.GINTESLNR.E		R.GINTESLNR.E
373	389	2	1752.85	8	1	36.9	25.3	95.00%	R.LAEMPADSGYPAYLGAK.L		R.LAEMPADSGYPAYLGAK.L
317	331	2	1544.81	4.6	0	49.4	22.6	95.00%	R.TTLVANTSNMPVAAR.E		R.TTLVANTSNMPVAAR.E
182	198	2	1838.88	4.6	1	73	26	95.00%	R.GTVTYIAEAGSYHVDEK.L		R.GTVTYIAEAGSYHVDEK.L
221	240	3	2105.14	4.1	1	35.3	17.6	95.00%	R.AARPVADNLTANQPLLTGQR.V		R.AARPVADNLTANQPLLTGQR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
87	STI1_SCHPO	12.52%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
146	164	2	1935.97	6.4	1	78.1	23.7	95.00%	K.LASNPETASLLADSAFMAK.L		K.LASNPETASLLADSAFMAK.L
112	132	2	2007.97	4.2	0	89.9	25.6	95.00%	K.SVEAAQTQAASGAGGFNPFAK.L		K.SVEAAQTQAASGAGGFNPFAK.L
168	183	2	1781.88	4.3	1	66.6	24.7	95.00%	K.IQQNPGSIMAELNDPR.M		K.IQQNPGSIMAELNDPR.M
550	560	2	1154.63	2.1	0	48.6	21	95.00%	D.PAMQAILGQAR.E		K.DPEVLGILQDPAMQAILGQAR.E
371	377	2	800.44	3.8	1	29.8	25.5	95.00%	R.TPDILSR.L		R.TPDILSR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
88	RS23_SCHPO	14.69%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
81	88	2	884.44	2	1	35.3	21.3	95.00%	K.VTAFVPHD.G		K.VTAFVPHDGCLNFVDENDEVLLSGFGR.K
125	137	2	1326.74	4.4	0	55.5	19.2	95.00%	K.VAGVGLSALFHEK.K		K.VAGVGLSALFHEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
89	IF4A_SCHPO	12.50%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
58	69	2	1173.61	5	1	69	24.1	95.00%	R.DVLAQAQSGTGK.T		R.DVLAQAQSGTGK.T
33	48	2	1854.94	2.4	0	31.2	23.4	95.00%	R.GIYAYGFERPSAIQQR.A		R.GIYAYGFERPSAIQQR.A
372	392	2	2549.19	2.9	1	26.7	26.1	91.60%	R.EIEQFYNTHIEEMPMNIADLI.-		R.EIEQFYNTHIEEMPMNIADLI.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
90	GCST_SCHPO	15.25%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
81	97	2	1779.9	3.9	0	64.1	24	95.00%	R.GENATAYLESITPSSLK.E		R.GENATAYLESITPSSLK.E
327	344	2	1771.88	3.1	0	70.5	23.8	95.00%	D.GVEVGQVTSGCPSPTLGK.N	Carbamidomethyl (+57)	R.HGSAVEVDGVEVGQVTSGCPSPTLGK.N
319	344	3	2566.25	4.5	1	41.9	24.8	95.00%	R.HGSAVEVDGVEVGQVTSGCPSPTLGK.N	Carbamidomethyl (+57)	R.HGSAVEVDGVEVGQVTSGCPSPTLGK.N
165	180	2	1623.93	4	0	75.8	14.1	95.00%	R.ALIAIQGPETASVVQK.L		R.ALIAIQGPETASVVQK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
91	SODC_SCHPO	40.26%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
98	116	2	1984.04	4.4	1	72.6	21.6	95.00%	K.TTFSDSVISLFGANSIIGR.T		K.TTFSDSVISLFGANSIIGR.T
85	97	2	1357.69	2.4	1	59.8	23.9	95.00%	D.LGNLESDAQGNIK.T		R.HVGDLGNLESDAQGNIK.T
81	91	2	1154.52	2.5	1	32.3	25.7	95.00%	R.HVGDLGNLESD.A		R.HVGDLGNLESDAQGNIK.T
45	70	3	2825.25	4.3	1	41.5	27	95.00%	R.GFHIHQFGDNTNGCTSAGPHFNPEGK.T	Carbamidomethyl (+57)	R.GFHIHQFGDNTNGCTSAGPHFNPEGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
92	LYS12_SCHPO	20.44%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
197	208	2	1324.65	5.3	1	41.8	25.1	95.00%	K.SNVMSVTDGLFR.E		K.SNVMSVTDGLFR.E
298	307	2	1044.58	4.6	0	32.2	21.9	95.00%	R.GIANPVATFR.S		R.GIANPVATFR.S
188	196	3	1047.69	4.7	0	25.1	3.01	95.00%	K.KPLVTIIHK.S		K.KPLVTIIHK.S
127	138	2	1568.72	4	1	44	26.2	95.00%	R.ENTECLYVKEER.M	Carbamidomethyl (+57)	R.ENTECLYVKEER.M
86	97	2	1231.7	4.7	0	25.9	18.9	92.10%	K.VAGYSSPIVALR.K		K.VAGYSSPIVALR.K
67	85	3	2071.06	4.3	1	52.5	22	95.00%	R.LKTECNAALFGAVQSPTHK.V	Carbamidomethyl (+57)	R.LKTECNAALFGAVQSPTHK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
93	TAL1_SCHPO	8.70%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
27	44	3	1917.03	2.7	1	51.5	20.4	95.00%	K.YKPQDATTNPSLILAASK.K		K.YKPQDATTNPSLILAASK.K
288	297	2	1165.55	3	1	28.4	25.8	94.50%	D.FNNDEMAVVK.L		R.FDFNNDEMAVVK.L
32	44	2	1285.73	2.5	0	49.7	19	95.00%	D.ATTNPSLILAASK.K		K.YKPQDATTNPSLILAASK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
94	RL13_SCHPO	25.96%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
172	183	2	1398.66	5.4	0	54	25.5	95.00%	K.NFNAFSTLSNER.A		K.NFNAFSTLSNER.A
118	128	3	1326.79	4.7	0	51.2	15.6	95.00%	K.VYLAHLIVFPR.K		K.VYLAHLIVFPR.K
46	64	4	2080.27	3.1	0	20	4.77	95.00%	K.IAPRPVEAIRPAVKPPTIR.Y		K.IAPRPVEAIRPAVKPPTIR.Y
89	100	2	1263.7	3.9	1	28.9	19.9	95.00%	R.VASTIGIPVDHR.R		R.VASTIGIPVDHR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
95	RAD25_SCHPO	17.41%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
63	74	2	1417.75	4.9	1	43.2	22.3	95.00%	R.IISSIEQKEESR.G		R.IISSIEQKEESR.G
218	226	2	1073.63	2.8	0	43.9	16.5	95.00%	D.STLIMQLLR.D		K.DSTLIMQLLR.D
236	261	3	2738.25	2.4	1	37.9	26.6	95.00%	D.AEYNQSAKEEAPAAAAASENEHPEPK.E		R.DNLTLWTSDAEYNQSAKEEAPAAAAASENEHPEPK.E
244	261	3	1846.84	4.4	0	24	26	93.90%	K.EEAPAAAAASENEHPEPK.E		K.EEAPAAAAASENEHPEPK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
96	IMDH_SCHPO	10.50%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	139	2	1621.89	1.9	1	51.2	18.3	95.00%	D.PVVFSPQHTVGDVLK.I		K.YENGFILDPVVFSPQHTVGDVLK.I
303	313	2	1155.67	4.5	1	51.3	18.8	95.00%	K.IDVIAGNVVTR.E		K.IDVIAGNVVTR.E

2	15	2	1636.88	4	0	27	20.6	93.60%	M.SAFKPYTEALEVLK.K	Acetyl (+42)	-.MSAFKPYTEALEVLK.K
125	136	2	1281.64	2.2	1	40.1	24	95.00%	D.PVVFSPQHTVGD.V		K.YENGFILDPVVFSPQHTVGDVLK.I
419	433	2	1421.67	3.9	0	52.2	26	95.00%	R.GMGSIAAMEGTGVNK.N		R.GMGSIAAMEGTGVNK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
97	TRX1_SCHPO	29.13%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
40	54	2	1796.83	4.6	1	68.4	26.5	95.00%	K.FEQFSNTYSDATFIK.V		K.FEQFSNTYSDATFIK.V
80	94	2	1567.82	2.6	1	82.3	22.1	95.00%	K.NGEKIEEIVGANPAK.L		K.NGEKIEEIVGANPAK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
98	PMM_SCHPO	11.28%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
29	43	2	1728.91	2.7	0	58.6	21.7	95.00%	R.LSVSPEMLETLQNLR.K		R.LSVSPEMLETLQNLR.K
45	58	2	1347.75	4.4	1	41.6	20	95.00%	K.VVAIGFVGGSDLSK.Q		K.VVAIGFVGGSDLSK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
99	GLT1_SCHPO	5.59%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
624	638	2	1701.91	4.2	0	45.5	21	95.00%	R.MPTPILTVEEFNALK.N		R.MPTPILTVEEFNALK.N
1690	1707	2	2063.08	4.1	0	61.9	21.1	95.00%	K.EALTQLLLTNNFPEFTGR.V		K.EALTQLLLTNNFPEFTGR.V
1442	1464	3	2335.04	4.9	1	32.4	27	95.00%	R.NSGAIAVVEGVGDHGCEYMTGGR.V	Carbamidomethyl (+57)	R.NSGAIAVVEGVGDHGCEYMTGGR.V
1845	1856	2	1155.67	3.5	0	56	18.9	95.00%	D.AVVLASGSTVPR.D		K.VYDAVVLASGSTVPR.D
1022	1038	3	1639.81	4.9	0	25.7	24.5	95.00%	K.MAQGAKPGEGGELPGNK.V		K.MAQGAKPGEGGELPGNK.V
672	685	2	1555.69	5.3	1	68	26	95.00%	R.ICSEADTAVNEGYK.A	Carbamidomethyl (+57)	R.ICSEADTAVNEGYK.A
1758	1776	2	1792.98	2.4	1	106	17.6	95.00%	R.VAIIGSGPAGLAAADQLNR.A		R.VAIIGSGPAGLAAADQLNR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
100	RS8A_SCHPO	35.50%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
60	74	2	1568.72	4.4	1	94.1	26	95.00%	R.LDSGNFSWGSEGVSK.K		R.LDSGNFSWGSEGVSK.K
165	178	2	1475.79	4.1	0	33.2	20.9	95.00%	R.LYAVVSSRPGQSGR.C		R.LYAVVSSRPGQSGR.C
152	164	2	1363.68	4.8	1	51.3	24.1	95.00%	K.VDSALETQFAAGR.L		K.VDSALETQFAAGR.L
78	92	2	1751.94	4.6	0	25.6	19.9	91.60%	R.IIQVAYHPSNNELVR.T		R.IIQVAYHPSNNELVR.T
111	124	3	1682.82	4.5	0	23.1	24.8	94.00%	R.VWYETHYGILMGSK.G		R.VWYETHYGILMGSK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
101	YA03_SCHPO	19.18%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	47	2	1743.88	2.4	0	95.9	23.8	95.00%	D.PVLTSEGIEQCEALAK.E	Carbamidomethyl (+57)	R.DPVLTSEGIEQCEALAK.E
147	172	3	2896.59	3.1	1	53.2	15.4	95.00%	R.SKEALEYLAALPQQQIAVITHSAFIR.F		R.SKEALEYLAALPQQQIAVITHSAFIR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
102	RL15A_SCHPO	19.90%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
115	128	2	1699.83	4.1	1	73.6	25.6	95.00%	R.VLNSYWVNQDATYK.F		R.VLNSYWVNQDATYK.F
78	93	3	1761.93	3.8	0	27.5	21	95.00%	K.GQTYGKPVHQGVNHLK.Y		K.GQTYGKPVHQGVNHLK.Y
148	157	3	1218.69	4.4	0	24.4	18.5	95.00%	R.INWIVNPVHK.H		R.INWIVNPVHK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
103	MMF1_SCHPO	37.65%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
59	75	2	1747.86	2.8	0	34.8	25	95.00%	K.ANGVIYCSGQIPVANGK.V	Carbamidomethyl (+57)/ Deamidation (+1)	K.ANGVIYCSGQIPVANGK.V
87	105	2	2116.09	4.6	0	131	22.6	95.00%	R.QCLLNLQEVLTEAGSSLNK.I	Carbamidomethyl (+57)	R.QCLLNLQEVLTEAGSSLNK.I
125	137	2	1483.81	3.9	1	42.4	19.2	95.00%	K.VYTEVLPDPKPAR.S		K.VYTEVLPDPKPAR.S

47	58	2	1247.66	5.3	0	27.4	22.3	94.20%	K.LSSAGPYNQAIK.A		K.LSSAGPYNQAIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
104	RL10A_SCHPO	26.24%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	128	3	1265.71	4.6	0	30	18.7	95.00%	R.HAFGKPNGLVAR.V		R.HAFGKPNGLVAR.V
129	139	2	1228.7	4.7	0	40	19.2	95.00%	R.VNIGQILMSVR.T		R.VNIGQILMSVR.T
41	69	3	3260.58	4	1	68.1	23.4	95.00%	R.AGVDEFPLCIHLVSNEYEQITSEALEAAR.I	Carbamidomethyl (+57)	R.AGVDEFPLCIHLVSNEYEQITSEALEAAR.I
33	38	2	719.4	4.8	1	27.1	21.6	93.80%	R.IFDLGR.K		R.IFDLGR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
105	RS22_SCHPO	27.69%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
98	108	2	1171.7	4.9	0	29.1	14.5	95.00%	R.QVGVIVLTTSR.G		R.QVGVIVLTTSR.G
4	19	2	1814.9	4.5	1	77.6	24	95.00%	R.QSVLADCLNNIVNAER.R	Carbamidomethyl (+57)	R.QSVLADCLNNIVNAER.R
89	97	2	1111.62	5.6	0	31.9	19.5	95.00%	K.WVNQLLPSR.Q		K.WVNQLLPSR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
106	PMP20_SCHPO	28.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
30	55	2	2747.41	3.6	0	38	21	95.00%	K.FIIVGVPGAFTPPCSSQVPGYIANEK.Q	Carbamidomethyl (+57)	K.FIIVGVPGAFTPPCSSQVPGYIANEK.Q
11	29	2	2215.12	2.3	0	49.4	22.7	95.00%	K.VTLWENKPEEVVEFPSQGK.F		K.VTLWENKPEEVVEFPSQGK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
107	SYDC_SCHPO	6.03%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
281	294	2	1356.6	4.8	0	27.5	25.6	93.50%	K.MSGASSEGGSNVFK.I		K.MSGASSEGGSNVFK.I
200	210	2	1229.65	4.9	1	29.1	22.8	95.00%	K.NLPFLVEDAGR.S		K.NLPFLVEDAGR.S
490	499	2	1300.55	3.9	1	26.9	26.1	91.90%	R.YSNSYDFFMK.G		R.YSNSYDFFMK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
108	PUR8_SCHPO	11.00%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
268	292	3	2694.37	3.3	1	34.7	21.9	95.00%	R.LLANLKEVEEPFEAGQIGSSAMAYK.R		R.LLANLKEVEEPFEAGQIGSSAMAYK.R
450	460	2	1248.61	5.4	0	26.4	24.3	92.90%	R.APEQTESFVNK.D		R.APEQTESFVNK.D
372	388	2	1909.94	4.9	0	55.7	24.8	95.00%	R.AELPFMATENIIMAMTK.H		R.AELPFMATENIIMAMTK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
109	ADK_SCHPO	21.18%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
253	267	2	1483.87	4.5	1	69.4	14.9	95.00%	R.VVVITQGADATIVAK.D		R.VVVITQGADATIVAK.D
86	96	2	1295.61	3.7	1	43.7	25.7	95.00%	K.FADMLLESNEK.A		K.FADMLLESNEK.A
230	245	2	1688.89	3.8	1	56.9	21.8	95.00%	K.STDVQEIALALSSVEK.V		K.STDVQEIALALSSVEK.V
126	138	2	1424.68	5.2	0	51	25.2	95.00%	R.SLCTNLGAANNYK.L	Carbamidomethyl (+57)	R.SLCTNLGAANNYK.L
107	123	2	1770.9	2.5	0	66.8	23.4	95.00%	D.PTTPTGVCAVVLSNNNK.N	Carbamidomethyl (+57)	R.SEFSVDPTTPTGVCAVVLSNNNK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
110	DHOM_SCHPO	24.20%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	138	2	1568.79	4.5	1	56.7	23.6	95.00%	K.AFSASNDVYQNIIK.A		K.AFSASNDVYQNIIK.A
57	67	2	1391.68	4.7	1	33.1	24.9	95.00%	K.DYQPINLSEWK.N		K.DYQPINLSEWK.N
238	252	2	1526.81	1.4	0	40.2	21.5	95.00%	R.IAGVHVESASSFPVK.S		R.IAGVHVESASSFPVK.S
28	56	3	3047.4	3	0	33.8	26.2	95.00%	K.GFNENASTNGTTSFNVVAISSMEGHYVSK.D		K.GFNENASTNGTTSFNVVAISSMEGHYVSK.D

89	110	2	2284.2	3.6	1	128	20.2	95.00%	K.SPLPAILVDNTASEAIAQSYPK.F			K.SPLPAILVDNTASEAIAQSYPK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
111	LEU1_SCHPO	14.38%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
82	99	2	1998.98	4.3	1	62	25	95.00%	K.EIEVGFPSASQTDFAFVR.H		K.EIEVGFPSASQTDFAFVR.H
464	479	2	1742.82	4.9	1	69.1	25.9	95.00%	R.FSVNDYTLSSNGPQSK.C		R.FSVNDYTLSSNGPQSK.C
389	398	2	1134.61	1.7	0	28.6	21.4	95.00%	D.VNSEYAAIIR.V		K.VPYLPLDPHDVNSEYAAIIR.V
341	362	3	2346.15	2.9	1	44.7	24.6	95.00%	R.HPYAGNLVFTAFSGSHQDAISK.G		R.HPYAGNLVFTAFSGSHQDAISK.G
137	151	3	1761.87	4	0	33.2	25	95.00%	K.NATVHLYNACSPLFR.E	Carbamidomethyl (+57)	K.NATVHLYNACSPLFR.E
386	398	3	1483.75	3.2	1	32.8	23.9	95.00%	D.PHDVNSEYAAIIR.V		K.VPYLPLDPHDVNSEYAAIIR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
112	RS0B_SCHPO	12.54%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	88	4	2453.26	4	1	67.3	21.4	95.00%	R.VIATIENPADVCVISSRPYGHR.A	Carbamidomethyl (+57)	R.VIATIENPADVCVISSRPYGHR.A
2	15	2	1484.75	1.8	1	51	23.9	95.00%	M.AESIARPSVLNATD.D	Acetyl (+42)	-.MAESIARPSVLNATDDDIK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
113	THI4_SCHPO	11.00%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
373	385	2	1353.71	4.1	1	37.5	22.1	95.00%	R.GVDSISQHTLAAR.I		R.GVDSISQHTLAAR.I
125	140	2	1686.81	1.8	1	65.6	25.4	95.00%	D.GADYVGIGSIYETNTK.D		K.AAADGADYVGIGSIYETNTK.D
27	42	3	1733.95	4.6	0	28	18.1	95.00%	R.QVEEGILGGVTLVQHR.E		R.QVEEGILGGVTLVQHR.E
237	248	2	1322.76	4.7	1	31.5	14.8	95.00%	K.DLLNQIPAALQK.L		K.DLLNQIPAALQK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
114	YDG7_SCHPO	12.15%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
7	23	3	1939.91	3.9	1	22.9	26.2	91.90%	K.YFENAQNVHFTLADGSK.I		K.YFENAQNVHFTLADGSK.I
183	204	3	2603.37	3.4	0	27.8	19.3	95.00%	K.VKPAVHQMELHPFLPQTEFVEK.H		K.VKPAVHQMELHPFLPQTEFVEK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
115	RS11_SCHPO	17.76%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	64	2	1161.6	4.7	0	33.4	23.4	95.00%	K.CPFVGQVSIR.G	Carbamidomethyl (+57)	K.CPFVGQVSIR.G
114	130	2	1870.96	2.4	1	48.1	23.4	95.00%	R.INEGDVVTVGQCRPLSK.T	Carbamidomethyl (+57)	R.INEGDVVTVGQCRPLSK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
116	ASNS_SCHPO	5.39%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
516	523	2	1035.55	6.3	1	30	21.3	95.00%	K.LFDEIFPR.Q		K.LFDEIFPR.Q
154	165	2	1327.63	2.4	1	71.1	25.3	95.00%	D.SPDTAYFASELK.A		R.DPIGITTLYQGFSSDSPDTAYFASELK.A
399	408	2	1120.54	4.9	0	26.3	24	92.70%	K.STMAWGLEAR.V		K.STMAWGLEAR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
117	RS5B_SCHPO	13.79%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
20	32	2	1552.83	1.9	1	45.6	20.2	95.00%	K.LFNKFPFEGVEVK.D		K.LFNKFPFEGVEVK.D
167	181	2	1646.82	1.9	0	69.2	24	95.00%	K.SISECLAEEIINAAK.G	Carbamidomethyl (+57)	K.SISECLAEEIINAAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
118	COFI_SCHPO	32.12%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

81	94	2	1584.9	4.1	1	54.1	16.2	95.00%	K.IIFISWSPDVAPIK.S		K.IIFISWSPDVAPIK.S
122	133	2	1413.71	1.9	0	64.6	23.9	95.00%	D.FSEVAYETVLEK.V		R.AFTGIGTDIQATDFSEVAYETVLEK.V
8	20	2	1548.76	4.6	0	71.2	25.7	95.00%	K.VSPECLEAFQELK.L	Carbamidomethyl (+57)	K.VSPECLEAFQELK.L
117	133	2	1941.96	3.2	1	86.4	24.2	95.00%	D.IQATDFSEVAYETVLEK.V		R.AFTGIGTDIQATDFSEVAYETVLEK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
119	P25_SCHPO	17.82%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
36	52	2	1976.06	2.2	0	48.7	19.3	95.00%	K.AVIYQFPETLSPEILEK.M		K.AVIYQFPETLSPEILEK.M
2	20	2	2064.1	3.1	0	107	19.8	95.00%	M.STANTVAIVIYSTYGHVVK.L	Acetyl (+42)	-.MSTANTVAIVIYSTYGHVVK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
120	PYR1_SCHPO	2.85%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1880	1906	3	2689.36	3.3	0	28.6	22.3	95.00%	K.VSALMSPGLPHAAPSLAEAFGQAPENK.A		K.VSALMSPGLPHAAPSLAEAFGQAPENK.A
1771	1784	2	1494.85	4.1	0	35.2	15.7	95.00%	R.EAIPLLLTAVNEGR.L		R.EAIPLLLTAVNEGR.L
457	466	2	1084.56	6.1	0	38.9	22.8	95.00%	K.LPGGTIEENR.S		K.LPGGTIEENR.S
1758	1770	2	1371.7	4.4	0	56.2	24	95.00%	K.FVGNTAFTGFGVR.E		K.FVGNTAFTGFGVR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
121	YHEF_SCHPO	20.20%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
54	65	2	1279.67	5.1	1	47	22.3	95.00%	K.SFIGLDALTESK.G		K.SFIGLDALTESKGEFFQR.M
30	41	3	1413.76	4.8	1	20.9	21.9	90.20%	R.LRGPHCGTYLLK.V	Carbamidomethyl (+57)	R.LRGPHCGTYLLKVVGTNATYVGEK.S
91	104	2	1616.85	2.4	0	39	22.6	95.00%	D.TANFTPLTFTTYLK.T		R.LFTIAENDTANFTPLTFTTYLKTCNPQSIENAMIPFVNTVTSEISFDAWAYTAQNSSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
122	YHZ8_SCHPO	25.25%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
75	103	3	3217.69	3	0	57.2	18.5	95.00%	K.TSNPFLAFANYLTSTHAPLAEPLQLLNFK.V		K.TSNPFLAFANYLTSTHAPLAEPLQLLNFK.V
2	13	2	1361.7	3.8	0	57.2	23	95.00%	M.SFPASTHVYIAK.I	Acetyl (+42)	-.MSFPASTHVYIAK.I
156	164	2	1004.57	2	0	48	20.5	95.00%	D.PSLYAVVTR.Y		K.ADTSLIIHSLDDPSLYAVVTR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
123	RL36A_SCHPO	24.24%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	11	2	966.59	4.6	0	38.2	14.5	95.00%	M.APGLVVGLNK.G		-.MAPGLVVGLNK.G
83	96	2	1545.84	4.6	1	75.1	19.7	95.00%	K.GKIEELTSVIQSSR.L		K.GKIEELTSVIQSSR.L
85	96	2	1360.73	3.8	0	56.4	21.8	95.00%	K.IEELTSVIQSSR.L		K.IEELTSVIQSSR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
124	AATR1_SCHPO	9.07%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
305	317	2	1562.83	2.8	0	53.3	20.8	95.00%	R.VGWFTAQPLFIER.G		R.VGWFTAQPLFIER.G
38	54	2	1856.03	4.5	0	36.8	17	95.00%	K.IISLAGGLPNPEYFPIR.E		K.IISLAGGLPNPEYFPIR.E
7	19	3	1436.71	5.4	1	43.2	25.1	95.00%	K.DLSHHLSVESASR.K		K.DLSHHLSVESASR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
125	RL6_SCHPO	22.05%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	64	2	1497.84	5	0	33.1	18.6	95.00%	R.ASLAPGTVCILLAGR.F	Carbamidomethyl (+57)	R.ASLAPGTVCILLAGR.F
70	87	2	1959.1	3.1	1	33.6	14.3	95.00%	R.VVVLSQLEDTLVVTGPYK.V		R.VVVLSQLEDTLVVTGPYK.V

109	118	2	1031.56	5.5	1	31.2	22.7	95.00%	K.IDVSGVSVEK.F		K.IDVSGVSVEK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
126	RL27A_SCHPO	22.06%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	48	3	1461.76	5.9	0	42.8	22.9	95.00%	K.SHPFGHAVVAGVER.Y		K.SHPFGHAVVAGVER.Y
23	34	2	1269.74	4.4	1	65.4	16.3	95.00%	K.VVILQAIDQGSK.S		K.VVILQAIDQGSK.S
35	52	4	1963.05	4.3	1	23.2	19.5	95.00%	K.SHPFGHAVVAGVERYPLK.V		K.SHPFGHAVVAGVERYPLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
127	RS12A_SCHPO	38.62%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
129	138	2	1080.51	3.3	1	40.8	25.8	95.00%	D.YGEDSAALQK.L		K.VVGCSCVAVTDYGEDSAALQK.L
99	111	2	1486.76	2.4	1	27.9	23.3	94.70%	K.VLGEWAGLCVLDR.D	Carbamidomethyl (+57)	K.VLGEWAGLCVLDR.D
79	93	2	1671.88	4.1	0	73.8	21.7	95.00%	K.LVEALCAESETPLIK.V	Carbamidomethyl (+57)	K.LVEALCAESETPLIK.V
61	78	3	2208.97	4.2	1	36.3	27	95.00%	R.QAHLCVLCESCDQEAYVK.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.QAHLCVLCESCDQEAYVK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
128	GCSP_SCHPO	14.06%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
953	965	2	1458.76	1.1	1	43.1	23.1	95.00%	K.DNNLLVNAPHPQK.D		K.DNNLLVNAPHPQK.D
657	684	3	2835.48	2.2	0	37.9	19.2	95.00%	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C	Carbamidomethyl (+57)	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C
379	412	3	3679.8	2.3	0	51.4	21.3	95.00%	K.ATSNICTAQALLANMSAFYAIYHGPNGLQEIANR.I	Carbamidomethyl (+57)	K.ATSNICTAQALLANMSAFYAIYHGPNGLQEIANR.I
577	604	3	3166.6	3.7	0	40.5	20.4	95.00%	K.LNAVTEMMPITNPLFANIHPYVPEEQAK.G		K.LNAVTEMMPITNPLFANIHPYVPEEQAK.G
87	126	3	4380.08	3.8	1	62.7	22.9	95.00%	R.TPESQLMAFGSVNPNEKNPPVNYSESEFTTLANNVANQNK.L		R.TPESQLMAFGSVNPNEKNPPVNYSESEFTTLANNVANQNK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
129	RS2_SCHPO	26.48%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
64	74	2	1441.73	5.7	1	25.1	23.5	90.70%	K.EYQIVDYFLPR.L		K.EYQIVDYFLPR.L
51	63	2	1566.86	4.2	0	34.6	18.6	95.00%	K.SIEEIYLYSLPIK.E		K.SIEEIYLYSLPIK.E
174	185	3	1138.69	4.8	1	25.2	12.6	95.00%	R.GAGLVAAPVTKR.F		R.GAGLVAAPVTKR.F
186	200	2	1799.86	2.9	1	106	25.9	95.00%	R.FLQLAGIEDCYTQSR.G	Carbamidomethyl (+57)	R.FLQLAGIEDCYTQSR.G
141	156	3	1696.87	4.8	1	37.6	23.6	95.00%	R.GYWGTALGDPHTVPVK.V		R.GYWGTALGDPHTVPVK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
130	ACL1_SCHPO	8.94%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
369	381	2	1420.73	4.5	0	44	23.3	95.00%	R.GSELTYNNVPISK.V		R.GSELTYNNVPISK.V
171	182	3	1338.74	4.8	0	23.6	19.4	94.70%	K.LYRPGSVAYVSK.S		K.LYRPGSVAYVSK.S
313	326	2	1570.9	3.9	0	58.3	15.2	95.00%	K.LPALLQEVYEGLVK.K		K.LPALLQEVYEGLVK.K
156	170	2	1506.72	3.3	1	45.7	25.6	95.00%	K.IGNTGGMMDNIVASK.L		K.IGNTGGMMDNIVASK.L
313	327	3	1699	4	1	30.3	10.4	95.00%	K.LPALLQEVYEGLVKK.G		K.LPALLQEVYEGLVKK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
131	RL3A_SCHPO	14.69%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
207	222	2	1837.9	4.3	1	73.9	25.2	95.00%	K.STFEQNEMIDVIGVTR.G		K.STFEQNEMIDVIGVTR.G
11	19	2	982.54	4.3	0	27.2	20.1	93.90%	R.HGSLGFLPR.K		R.HGSLGFLPR.K
249	266	3	2035.03	4.4	0	29.3	23.6	95.00%	K.VACIGAWHPANVQWTVAR.A	Carbamidomethyl (+57)	K.VACIGAWHPANVQWTVAR.A
37	50	3	1530.86	2.5	0	46	17.2	95.00%	D.ASKPVHLTAFLGYK.A		K.DDASKPVHLTAFLGYK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
132	RANG_SCHPO	16.74%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
188	198	2	1253.61	5.8	0	35.7	24.3	95.00%	R.FANSENANLFK.E		R.FANSENANLFK.E
174	187	2	1505.74	2.4	0	46.3	25.4	95.00%	D.VSEGEPTAETFAIR.F		R.SWVWTVAADVSEGEPTAETFAIR.F
88	98	2	1353.6	4	0	43.5	25.9	95.00%	K.TNEEEETVEFK.M		K.TNEEEETVEFK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
133	SYRC_SCHPO	9.39%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
452	467	2	1759.87	3.7	1	55	24.7	95.00%	K.YAQVENPEEVADIVGK.T		K.YAQVENPEEVADIVGK.T
163	180	2	1987.02	4.1	0	33.9	21.3	95.00%	R.STIIGSFLANLHESQGWK.V		R.STIIGSFLANLHESQGWK.V
480	489	2	1284.6	5.9	1	39.4	25.3	95.00%	R.INNYAFDWSR.M		R.INNYAFDWSR.M
11	24	2	1544.86	4.5	1	46.7	17.6	95.00%	K.SLSTLGLQDLPVFR.E		K.SLSTLGLQDLPVFR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
134	DAK1_SCHPO	7.93%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
45	66	3	2123.05	5.3	0	21	24	90.60%	K.NVSVISGGGAGHEPTHSSFVGK.G		K.NVSVISGGGAGHEPTHSSFVGK.G
527	538	2	1301.63	4.7	1	60.8	25	95.00%	K.TNDLNAAVEEAR.K		K.TNDLNAAVEEAR.K
388	399	2	1358.73	4.4	0	25.9	21.4	92.10%	R.QAIVNSMENLIK.A		R.QAIVNSMENLIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
135	RL19B_SCHPO	20.73%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
118	128	3	1386.74	5	0	32.3	21.9	95.00%	K.HLYHTLYLEAK.G		K.HLYHTLYLEAK.G
26	38	2	1429.68	2.9	0	70.3	25.5	95.00%	D.PNEISEISNANSR.Q		K.VWMDPNEISEISNANSR.Q
22	38	2	1960.9	4.1	1	66.6	26.4	95.00%	K.VWMDPNEISEISNANSR.Q		K.VWMDPNEISEISNANSR.Q
182	193	2	1422.69	3.6	1	31.8	25	95.00%	R.EQIYTAAEKIEE.-		R.EQIYTAAEKIEE.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
136	RS15A_SCHPO	47.06%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	85	2	1396.76	4.6	0	40.4	20	95.00%	K.TEAPLNEKPATVK.T		K.TEAPLNEKPATVK.T
36	48	3	1497.8	2.9	1	22.1	21.2	92.50%	D.LSAEQLVDLFHAR.A		R.GVELEQLLDLSAEQLVDLFHAR.A
109	135	4	3209.67	3.6	0	17.8	19.7	93.80%	K.LFNQVEIRPEMIGHYLGEFSITYKPTK.H		K.LFNQVEIRPEMIGHYLGEFSITYKPTK.H
90	108	2	2033.08	3.1	0	80.9	20.6	95.00%	R.NMIILPEMVGSVVGIYNGK.L		R.NMIILPEMVGSVVGIYNGK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
137	RS17B_SCHPO	15.91%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	59	3	1133.6	4.6	0	24.5	22.7	95.00%	K.IAGYTTHLMK.R		K.IAGYTTHLMK.R
34	44	2	1156.68	4.8	1	51	17.6	95.00%	R.IVDEVAIIASK.R		R.IVDEVAIIASK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
138	RS10B_SCHPO	34.01%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	44	3	1428.82	4.9	0	23.6	17.2	94.70%	K.HPEVGVPNLQVIK.A		K.HPEVGVPNLQVIK.A
10	24	3	1621.94	4.8	0	31.6	13	95.00%	K.AIHQALFQQGVLVAK.K		K.AIHQALFQQGVLVAK.K
78	93	4	1859.01	4	1	23	18.8	95.00%	R.EYLHLPAEVVPATHKR.Q		R.EYLHLPAEVVPATHKR.Q
26	31	2	732.38	5.5	1	30.1	22.5	95.00%	K.DFNLPK.H		K.DFNLPK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
139	RS4B_SCHPO	11.07%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

222	233	2	1232.68	5.6	0	42.4	20.7	95.00%	R.LSNVFVIGEAGK.S		R.LSNVFVIGEAGK.S
246	252	2	846.45	4.8	0	45.4	23.4	95.00%	K.LSITEER.D		K.LSITEER.D
40	49	2	1258.72	4.7	0	26.1	18.5	92.50%	R.ECLPLIVFLR.N	Carbamidomethyl (+57)	R.ECLPLIVFLR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
140	KAD1_SCHPO	25.00%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
196	218	3	2621.39	2.8	1	47.7	18.4	95.00%	K.WAAVDAAQKPEQVWEQIVAILEK.A		K.WAAVDAAQKPEQVWEQIVAILEK.A
27	39	3	1416.72	2.3	1	21.5	23.5	91.50%	K.YGIAHLATGDMLR.S		K.YGIAHLATGDMLR.S
155	164	2	1126.6	2.6	1	32.3	21.8	95.00%	D.DVTGEPLIQR.S		K.DDVTGEPLIQR.S
74	82	2	1115.53	2.2	0	26.4	25.4	92.30%	D.EILNNPECK.N	Carbamidomethyl (+57)	K.DEILNNPECK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
141	SYKC_SCHPO	6.09%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
570	591	3	2490.33	2.8	1	30.8	18.1	95.00%	R.EVLLFPHMKPEVQAAEPTVVKE.-		R.EVLLFPHMKPEVQAAEPTVVKE.-
15	28	2	1454.8	4	1	41.2	19.6	95.00%	K.ALVLDPVTGEQVSK.T		K.ALVLDPVTGEQVSK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
142	ACL2_SCHPO	17.07%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
255	266	2	1367.61	3.7	1	48.5	26.1	95.00%	K.LDQTAEFECGAK.W	Carbamidomethyl (+57)	K.LDQTAEFECGAK.W
326	334	2	985.56	4.7	0	36	20.4	95.00%	K.LTILNAEGR.V		K.LTILNAEGR.V
280	304	3	2540.18	1.5	1	29.4	26.5	95.00%	K.TSGEESGAINADHGPPMVFPAPFGR.E		K.TSGEESGAINADHGPPMVFPAPFGR.E
382	389	2	947.52	4.5	1	26.9	22.7	93.50%	K.TVLDLMTR.G		K.TVLDLMTR.G
32	61	3	3211.76	3.3	0	47.1	15.6	95.00%	K.TVSATPAVQLAQIQFPLPTLVIPAESTTYR.E		K.TVSATPAVQLAQIQFPLPTLVIPAESTTYR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
143	ARGD_SCHPO	14.51%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
104	129	3	2885.5	2.7	0	27.9	19.5	95.00%	K.LVHSSNLFYNEPAIELSNVINNSLAK.N		K.LVHSSNLFYNEPAIELSNVINNSLAK.N
311	332	3	2276.09	4.8	0	39.5	25.7	95.00%	K.IAAEIHPGEHGSTFGGNPVACR.V	Carbamidomethyl (+57)	K.IAAEIHPGEHGSTFGGNPVACR.V
139	154	2	1784.85	4.1	0	92.8	25.5	95.00%	K.IFFANCGTEANETALK.F	Carbamidomethyl (+57)	K.IFFANCGTEANETALK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
144	SCE3_SCHPO	17.01%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
46	66	2	2113.97	4.9	1	94.2	27	95.00%	R.ATPSSADAGYNAPSSTFESVR.S		R.ATPSSADAGYNAPSSTFESVR.S
359	381	2	2403.05	5.1	1	111	27.3	95.00%	K.TPATEDAPATNAGEAEEEEGWTK.I		K.TPATEDAPATNAGEAEEEEGWTK.I
365	381	2	1788.79	2.7	0	90.9	27.2	95.00%	D.APATNAGEAEEEEGWTK.I		K.TPATEDAPATNAGEAEEEEGWTK.I
250	271	3	2195.06	2.9	0	28.5	24.8	95.00%	R.SSSNVNTEATPSATTTTSSKPK.R		R.SSSNVNTEATPSATTTTSSKPK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
145	RL23_SCHPO	25.18%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
15	34	2	2090	3.5	1	65.5	25.8	95.00%	R.MTLGLPVQAIMNCADNSGAK.N	Carbamidomethyl (+57)	R.MTLGLPVQAIMNCADNSGAK.N
51	65	2	1531.78	3.4	1	55.2	23.6	95.00%	R.LPAASCGDMVLATVK.K	Carbamidomethyl (+57)	R.LPAASCGDMVLATVK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
146	TRXB_SCHPO	22.36%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
78	89	2	1323.7	5	0	25.2	21.2	90.90%	R.FGTEIITETVSK.L		R.FGTEIITETVSK.L
154	175	3	2201.14	2.7	1	25.9	20.7	95.00%	R.NKPLAVVGGGDSAAEEAQFLTK.Y		R.NKPLAVVGGGDSAAEEAQFLTK.Y
114	124	2	1044.59	2	0	53.5	19	95.00%	D.SVILATGASAR.R		K.YWLEGAEEEEPHTADSVILATGASAR.R
61	72	2	1321.67	2.8	0	47.5	24.8	95.00%	D.GINGTTLTENFR.A		R.GELKPVMYEGMLANGIAAGGQLTTTTDVENFPGFPDGINGTTLTENFR.A
99	124	3	2801.32	3.2	1	61.8	26.1	95.00%	K.YWLEGAEEEEPHTADSVILATGASAR.R		K.YWLEGAEEEEPHTADSVILATGASAR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
147	THI22_SCHPO	4.90%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
138	151	2	1403.74	3.1	1	61.1	22.2	95.00%	D.PVMVATSGDSLVTK.D		K.LVVDPVMVATSGDSLVTK.D
423	435	2	1516.6	5.3	0	56.7	26	95.00%	K.SCEESPACTAYSR.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.SCEESPACTAYSR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
148	Q1L854_SCHPO	12.54%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
14	27	2	1459.75	2.9	0	36.4	23.7	95.00%	D.LLGEETPAATTTEK.K		K.NLFDLLGEETPAATTTEK.K
271	282	2	1286.6	3.1	1	33.7	26	95.00%	K.TQQAPPTLSETD.F		K.TQQAPPTLSETDFPALA.-
10	27	2	1948.97	3.6	1	75.2	24.6	95.00%	K.NLFDLLGEETPAATTTEK.K		K.NLFDLLGEETPAATTTEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
149	NACB_SCHPO	26.49%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
95	116	2	2320.31	3	0	52.8	12.8	95.00%	K.TLSEILPGILNNLGPESLTALR.Q		K.TLSEILPGILNNLGPESLTALR.Q
73	90	2	1884.96	2.1	0	67.3	23	95.00%	R.APTVHSSLPNETTAIYGK.A		R.APTVHSSLPNETTAIYGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
150	RS14_SCHPO	16.55%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
95	105	2	1037.57	5.3	0	47.1	19.9	95.00%	K.TPGPGAQAALR.A		K.TPGPGAQAALR.A
73	84	3	1367.77	4	1	24.2	19.1	95.00%	K.CKEVGITALHIK.I	Carbamidomethyl (+57)	K.CKEVGITALHIK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
151	RL12_SCHPO	39.39%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
68	83	2	1538.91	3.4	0	50.5	14.3	95.00%	R.QAAVSVVPSASALVIK.A		R.QAAVSVVPSASALVIK.A
97	114	3	1921.99	2.5	1	33.8	21.9	95.00%	K.NVAHSGNVSLDEIIEVAR.T		K.NVAHSGNVSLDEIIEVAR.T
17	31	2	1312.7	3.6	0	46	21.2	95.00%	R.AVGGEVAGGSTLAPK.I		R.AVGGEVAGGSTLAPK.I
131	146	2	1652.81	4	1	45.9	24.3	95.00%	K.EILGTAFSVGCTVDGK.N	Carbamidomethyl (+57)	K.EILGTAFSVGCTVDGK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
152	DYR_SCHPO	13.02%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
164	183	3	2062.15	3.7	1	25.4	14.1	95.00%	K.LTTPSLHIAGTSDTLVPLAR.S		K.LTTPSLHIAGTSDTLVPLAR.S
34	51	2	1958.89	0.85	1	31.2	27.3	95.00%	K.YAELHFPTGPVVADEEAD.P		K.YAELHFPTGPVVADEEADPNDEEEK.K
191	212	3	2537.31	3.6	0	37.3	21	95.00%	R.CENAHVLLHPGQHIVPQQAVYK.T	Carbamidomethyl (+57)	R.CENAHVLLHPGQHIVPQQAVYK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
153	SLBR2_SCHPO	13.11%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

134	143	2	1115.56	4.3	0	27.1	23.5	93.80%	R.NIESSVQPSR.E		R.NIESSVQPSR.E
166	192	3	3060.53	3.6	1	43.6	22.2	95.00%	R.LVTMEQELVREEAACLVAEAQLSNTTR.E	Carbamidomethyl (+57)	R.LVTMEQELVREEAACLVAEAQLSNTTR.E
149	157	2	1075.63	4.5	1	33	17.2	95.00%	K.LLDQIYALK.H		K.LLDQIYALK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
154	SYTC_SCHPO	4.27%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
248	258	2	1187.55	4.2	1	47.1	26.3	95.00%	K.NSSSYFLGDAK.N		K.NSSSYFLGDAK.N
8	26	3	2136.14	4.2	1	27.4	18.9	95.00%	K.GVQASLDNLSLEIPFIQHR.L		K.GVQASLDNLSLEIPFIQHR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
155	RL31_SCHPO	21.24%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
91	105	2	1650.87	4.2	1	39.3	21	95.00%	K.ALYTYVQAVDVANPK.M		K.ALYTYVQAVDVANPK.M
7	15	2	986.56	5	0	39.5	21.7	95.00%	K.SAINQVVTR.D		K.SAINQVVTR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
156	SYG_SCHPO	8.74%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
187	198	2	1297.63	5.4	0	37	24.5	95.00%	R.NPATNGELETPR.Q		R.NPATNGELETPR.Q
216	232	3	1983	2	0	33.7	23.5	95.00%	K.GYLRPETAQGQFLNFSR.L		K.GYLRPETAQGQFLNFSR.L
492	506	2	1649.85	4.8	0	35.7	23.2	95.00%	R.TYTPNVIEPSFGLGR.I		R.TYTPNVIEPSFGLGR.I
526	538	2	1298.77	3.9	0	28.2	15.8	95.00%	R.GVLSFPASIAPIK.A		R.GVLSFPASIAPIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
157	RL11_SCHPO	14.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
36	49	2	1531.83	4.2	0	63.5	20	95.00%	K.VLEQLSGQTPVFSK.A		K.VLEQLSGQTPVFSK.A
154	164	2	1349.67	4.1	1	39.8	24.4	95.00%	K.INAEDTINWFK.Q		K.INAEDTINWFK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
158	RL7C_SCHPO	14.34%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	22	3	2201.2	3.5	1	23.5	16.3	94.50%	M.AVASSTVPSKEQIFAPESLLK.K		-.MAVASSTVPSKEQIFAPESLLK.K
169	183	2	1497.85	4.8	1	75.4	17.8	95.00%	R.IALSDNAIIEAALGK.Y		R.IALSDNAIIEAALGK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
159	SPI1_SCHPO	12.50%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
110	122	2	1514.77	4.6	0	58.5	24	95.00%	R.VCENIPIVLCGNK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VCENIPIVLCGNK.V
152	165	3	1783.91	2.1	0	30.8	22.9	95.00%	K.SNYNFEKPFLWLAR.K		K.SNYNFEKPFLWLAR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
160	SPEE_SCHPO	8.39%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	12	2	1291.72	4.1	0	43.5	18.5	95.00%	M.SVQELSHPLIK.D	Acetyl (+42)	-.MSVQELSHPLIK.D
18	31	2	1631.79	4.6	0	31.2	25.2	95.00%	R.EINNMWPGQAMTLK.V		R.EINNMWPGQAMTLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
161	PABP_SCHPO	8.42%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
258	266	2	1068.57	4.8	0	26.6	21.3	93.10%	K.ANFTNVYIK.N		K.ANFTNVYIK.N
447	456	2	1142.61	4.9	0	33.9	22.1	95.00%	R.SQLEAQIQAR.N		R.SQLEAQIQAR.N
536	571	3	3524.72	4.6	0	28.7	23.2	95.00%	R.GPVPAQGRPMMMPGSVPSAGPAEAEAVPAVPGMPER.F		R.GPVPAQGRPMMMPGSVPSAGPAEAEAVPAVPGMPER.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
162	PURA_SCHPO	14.29%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
206	224	3	2169.16	3.6	1	37.8	18.5	95.00%	R.LKPFVIDAVAFMYEALQSK.K		R.LKPFVIDAVAFMYEALQSK.K
282	304	3	2420.22	4.2	1	27.4	22.7	95.00%	R.VGAGPFPTEQLNEIGDHLQSVGR.E		R.VGAGPFPTEQLNEIGDHLQSVGR.E
268	276	2	899.55	4.9	0	44.5	20.5	95.00%	R.IANSIGVVK.A		R.IANSIGVVK.A
126	136	2	1129.57	4.6	1	38.6	23.2	95.00%	R.ADALNEAELGK.Q		R.ADALNEAELGK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
163	PGM_SCHPO	10.65%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
423	435	2	1529.66	4.3	1	62.5	26.4	95.00%	R.YDYEELENEAAGK.V		R.YDYEELENEAAGK.V
350	358	2	1160.54	5.2	1	29	25.3	95.00%	K.FFCNLFDAK.R	Carbamidomethyl (+57)	K.FFCNLFDAK.R
127	142	2	1631.79	4.4	0	81.8	25.3	95.00%	K.YNLGNGGPAPESVTEK.I		K.YNLGNGGPAPESVTEK.I
1	21	3	2330.21	3.2	0	23.9	20.7	95.00%	-.MIETIPTKPYEGQRPGTSGLR.K		-.MIETIPTKPYEGQRPGTSGLR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
164	RL28A_SCHPO	20.27%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
94	110	2	1787.95	2.3	0	58	20.4	95.00%	K.NTEVAPVINVLQSGYGK.V		K.NTEVAPVINVLQSGYGK.V
115	127	3	1464.85	2.7	1	25.6	14.6	95.00%	K.GRLPETPVIVQTR.Y		K.GRLPETPVIVQTR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
165	RL14_SCHPO	14.93%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
53	64	3	1345.75	2.6	0	26.2	20.3	95.00%	R.YGSVVLTHIVMK.L		R.YGSVVLTHIVMK.L
87	94	2	905.44	5.7	0	30.4	23.9	95.00%	K.WASSAWAK.K		K.WASSAWAK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
166	RS13_SCHPO	15.23%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
44	55	2	1244.66	3.8	0	40.8	22.5	95.00%	K.GMSPSQIGVTLR.D		K.GMSPSQIGVTLR.D
10	20	2	1132.63	4.4	0	38.6	20.1	95.00%	K.GIASSALPYVR.S		K.GIASSALPYVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
167	KAPS_SCHPO	22.77%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
157	188	3	3532.7	3.1	0	32.4	23.2	95.00%	K.EFTGISAPYEAPISPEIVVSSHTQSIEECVEK.I	Carbamidomethyl (+57)	K.EFTGISAPYEAPISPEIVVSSHTQSIEECVEK.I
39	52	2	1664.86	3.8	0	65.6	22.9	95.00%	K.STIACALEQYLLQR.G	Carbamidomethyl (+57)	K.STIACALEQYLLQR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
168	YBS1_SCHPO	6.73%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
240	248	2	959.52	2.1	0	25.7	22.4	91.70%	D.GPFLVASNR.Y		K.FPQPPSAAEVAVVHDGPFLVASNR.Y
162	175	2	1422.8	2	0	35.7	17.1	95.00%	D.PVVVVNVPAGYGPR.H		R.FSIFDAEDTSSDPVVVVNVPAGYGPR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
169	VATB_SCHPO	8.35%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
415	427	2	1417.68	4.9	1	78	25.4	95.00%	K.SVVGEEALSQEDR.L		K.SVVGEEALSQEDR.L
439	449	2	1284.62	4.2	0	36.9	25.1	95.00%	K.TFISQGAYENR.T		K.TFISQGAYENR.T
42	59	3	2083.09	4.5	1	23.6	21.7	94.70%	R.RPQYNEIVNLNLPDGSVR.S		R.RPQYNEIVNLNLPDGSVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
170	RS21_SCHPO	29.89%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
51	60	2	1113.59	4.5	0	33.8	22.6	95.00%	K.TTYAISGFVR.S		K.TTYAISGFVR.S
72	87	2	1864.94	4.3	1	65.3	23.7	95.00%	R.LTTQDGLLEGVWSYQR.-		R.LTTQDGLLEGVWSYQR.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
171	PDI1_SCHPO	5.28%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	136	3	1350.87	5.1	1	30.4	6.02	95.00%	R.KQLLPTVKPISK.D		R.KQLLPTVKPISK.D
188	201	2	1436.77	4.3	0	45.1	19.9	95.00%	K.SLGSNFPGIVAFTK.D		K.SLGSNFPGIVAFTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
172	TBA2_SCHPO	8.46%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
281	304	3	2899.3	3.7	0	55.7	27.3	95.00%	K.AFHESNSVQEITNQCFEPYNQMV K.C	Carbamidomethyl (+57)	K.AFHESNSVQEITNQCFEPYNQMV K.C
47	60	2	1448.66	2.5	0	39.1	26	95.00%	D.GGFSTFFSETGQGK.Y		R.EIISIHVGQAGTQIGNACWELYCL EHGIQPNGYMNPETASQNSDGGF STFFSETGQGK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
173	UBC4_SCHPO	14.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
118	128	3	1264.72	1.3	0	36	16.8	95.00%	D.PLVPEIAHVYK.T		K.VLLSICSLLTDPNPDDPLVPEIAHV YK.T
91	101	2	1244.65	4.6	1	28.4	23.2	95.00%	R.DQWSPALTISK.V		R.DQWSPALTISK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
174	DLDH_SCHPO	5.87%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
113	128	2	1663.83	1.7	1	25	24.3	90.50%	R.GIDVSGVSVNLSQMMK.A		R.GIDVSGVSVNLSQMMK.A
155	168	2	1448.76	3.8	1	31.8	22.6	95.00%	K.GTGSFIDPQTLSVK.G		K.GTGSFIDPQTLSVK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
175	MPG1_SCHPO	11.02%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
270	287	2	1776	4.2	1	35.2	16.3	95.00%	K.IGPNVVIGPNVTIGDGVR.L		K.IGPNVVIGPNVTIGDGVR.L
138	159	4	2530.28	3.4	1	22.1	22.9	95.00%	K.VEEPSKYGVVVHYPNSESLIER.F		K.VEEPSKYGVVVHYPNSESLIER.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
176	Q9P7B4_SCHPO	19.69%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
234	256	3	2522.27	2.7	1	34.8	22.5	95.00%	R.ENVVIADTLVFPSHQGGANHVYR .K		R.ENVVIADTLVFPSHQGGANHVYR .K
163	173	2	1163.64	5.6	0	26.5	19	93.00%	K.SALAQFTSALR.K		K.SALAQFTSALR.K
183	199	2	1918.98	6.8	1	60.8	22.6	95.00%	R.IMEVDPGLVETEFSVVR.F		R.IMEVDPGLVETEFSVVR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
177	TBB_SCHPO	9.82%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
123	154	3	3205.55	2.6	1	82.9	24	95.00%	R.EAEACDALQGFQLTHSLGGGTG SGMGTLLLSK.I	Carbamidomethyl (+57)	R.EAEACDALQGFQLTHSLGGGTG SGMGTLLLSK.I
163	174	2	1249.62	3.9	0	41.3	24.3	95.00%	R.MMATFSVAPAPK.S		R.MMATFSVAPAPK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
178	TCTP_SCHPO	20.24%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

54	73	2	2271.04	2.8	0	92.2	27	95.00%	D.AEENAEEGTETVNNLVYSFR.L		K.QGGDVDIGANPSAEDAEENAEEGTETVNNLVYSFR.L
99	112	2	1670.87	2.7	1	31.5	22.9	95.00%	R.LQESNPERVPVFEK.N		R.LQESNPERVPVFEK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
179	RL2_SCHPO	15.02%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
92	118	3	2780.43	1.8	0	61.4	20.1	95.00%	K.NAALTVGNVLPVGEMPEGTIISNVEEK.A		K.NAALTVGNVLPVGEMPEGTIISNVEEK.A
163	173	2	940.55	4.3	0	54.6	16.4	95.00%	R.GVVGIVAGGGR.I		R.GVVGIVAGGGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
180	APE1_SCHPO	3.40%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
253	269	2	1912.97	5	1	42.1	23.6	95.00%	K.TLDFFSGVFGEPYPLPK.C		K.TLDFFSGVFGEPYPLPK.C
137	149	2	1467.71	4.6	0	42.2	24.5	95.00%	K.YLATTQMEPTSAR.R		K.YLATTQMEPTSAR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
181	RL24A_SCHPO	20.81%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	12	2	1357.64	4.1	1	34.6	25.3	95.00%	-.MKVEVCSFSGSK.V	Carbamidomethyl (+57)	-.MKVEVCSFSGSK.V
81	91	2	1097.65	4.7	1	29.4	18.1	95.00%	R.GIVGANLDVIK.E		R.GIVGANLDVIK.E
36	43	2	978.52	4.9	0	29.5	22.9	95.00%	K.SESLFLQR.K		K.SESLFLQR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
182	CH10_SCHPO	22.12%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	84	2	1230.7	4	0	31.7	16.6	95.00%	R.VLLPAYGGSNIK.V		R.VLLPAYGGSNIK.V
62	72	2	1111.6	4.5	1	30.9	20.3	95.00%	K.LAQPSVAVGDR.V		K.LAQPSVAVGDR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
183	YBS7_SCHPO	7.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
442	471	4	3134.5	-0.033	1	26.4	24.5	95.00%	K.EQPPNKAEPAVPTEASSTKPSEAAEESTPR.F		K.EQPPNKAEPAVPTEASSTKPSEAAEESTPR.F
128	146	2	1760.86	5.1	0	31.6	25.1	95.00%	R.TSGSSTGLSNAPPSANVSK.A		R.TSGSSTGLSNAPPSANVSK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
184	YDMC_SCHPO	4.59%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
370	385	2	1877	4	0	39.4	20	95.00%	K.LTSLMESIFPEQTIIR.S		K.LTSLMESIFPEQTIIR.S
82	91	2	1136.53	5	1	33.4	25.5	95.00%	R.NADNSVTNFR.D		R.NADNSVTNFR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
185	RS3_SCHPO	10.04%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
97	108	2	1362.64	3.8	0	61	25.7	95.00%	R.GLCAVAQCESLR.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GLCAVAQCESLR.Y
30	42	2	1513.64	4.2	0	70.9	26.3	95.00%	R.ELSEEGYSGCEVR.V	Carbamidomethyl (+57)	R.ELSEEGYSGCEVR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
186	G6PD_SCHPO	5.60%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
468	478	3	1340.68	1.7	1	25.4	23.1	95.00%	D.GPECLYSFLKK.F	Carbamidomethyl (+57)	K.YMEEEKPVPEPYEYGSDGPECLYSFLKK.F
451	467	2	2060.86	2.5	1	34.5	27.1	95.00%	K.YMEEEKPVPEPYEYGSD.G		K.YMEEEKPVPEPYEYGSDGPECLYSFLK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
187	ATPB_SCHPO	7.43%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
167	185	2	2076.03	2.3	0	83	24.2	95.00%	D.APSFEEQSTTPEILETGIK.V		K.YSPIHADAPSFEEQSTTPEILETGIK.V
160	185	3	2859.39	2.5	1	29.4	24.2	95.00%	K.YSPIHADAPSFEEQSTTPEILETGIK.V		K.YSPIHADAPSFEEQSTTPEILETGIK.V
210	222	2	1501.86	4.8	0	34.9	15.2	95.00%	K.TVFIQELINNIAK.A		K.TVFIQELINNIAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
188	SODM_SCHPO	20.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	173	2	1303.7	4.2	1	48.8	21.3	95.00%	R.ITTTANQDTIVK.S		R.ITTTANQDTIVK.S
26	48	2	2502.32	2.9	0	32.8	19.3	95.00%	K.ATLPPLPYAYNALEPALSETIMK.L		K.ATLPPLPYAYNALEPALSETIMK.L
127	135	2	1108.52	5	1	34	25.8	95.00%	K.WGSLEDFQK.E		K.WGSLEDFQK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
189	PROF_SCHPO	26.77%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
54	68	2	1515.82	3.2	0	31.2	20.7	95.00%	D.PPSMFGTGIILAGQK.Y		R.AGDSVWAASAGFNLSPQEIQGLAAGFQDPPSMFGTGIILAGQK.Y
95	113	3	2098.08	3.5	0	24.5	21.1	95.00%	K.LCILVSHYPETTLPGEAAK.I	Carbamidomethyl (+57)	K.LCILVSHYPETTLPGEAAK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
190	YET4_SCHPO	13.60%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
190	216	3	2686.32	5.5	1	58	24	95.00%	R.NDEQLGNSPASITSKPATTSAAQPSSK.V		R.NDEQLGNSPASITSKPATTSAAQPSSK.V
419	462	4	4557.19	2.7	1	18.1	22.3	94.50%	K.NEVNVPSTIPTESENPVAVGGTTAEHPVQEAVTAPTETAHDFSK.E		K.NEVNVPSTIPTESENPVAVGGTTAEHPVQEAVTAPTETAHDFSK.E
487	503	3	1712.87	4.4	0	27.8	23.7	95.00%	R.KPSSTGQEPTTPSTPAK.S		R.KPSSTGQEPTTPSTPAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
191	CYSK1_SCHPO	9.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
10	23	2	1341.78	3.9	0	59.1	15.9	95.00%	K.VPGIVSGFIGAIGR.T		K.VPGIVSGFIGAIGR.T
180	200	2	2019.93	5.1	1	71.4	26.6	95.00%	K.GTVDGFTCSTGTGGTFAGVTK.Y	Carbamidomethyl (+57)	K.GTVDGFTCSTGTGGTFAGVTK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
192	MUG64_SCHPO	11.19%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
224	238	3	1767.86	4.9	1	44.3	25.1	95.00%	K.LDVESAKPENLEHCK.S	Carbamidomethyl (+57)	K.LDVESAKPENLEHCK.S
108	125	2	1851.02	3.8	0	41.3	17.2	95.00%	R.NLGNLTPLEQTPLASVGK.N		R.NLGNLTPLEQTPLASVGK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
193	RL7B_SCHPO	14.00%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	21	2	2002.11	4.4	0	37	16	95.00%	M.VASSTVPSVASIFAPESLLK.K		-.MVASSTVPSVASIFAPESLLK.K
168	182	2	1523.86	4.4	1	56.2	15.9	95.00%	R.IPLSDNAIIEAALGK.Y		R.IPLSDNAIIEAALGK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
194	PPID_SCHPO	7.87%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
155	169	2	1686.83	1.2	0	57.2	24.4	95.00%	D.PVVPVVIEECGTCTK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.NDDPVVPVVIEECGTCTK.D
214	226	2	1432.74	4.4	1	72	23.8	95.00%	K.QFAQQNLDTAVAK.W		K.QFAQQNLDTAVAK.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
195	ODPB_SCHPO	8.20%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
199	213	2	1682.93	1.4	0	28.4	17.6	95.00%	D.PNPVVVLENEILYGK.T		R.DPNPVVVLENEILYGK.T
220	234	2	1634.86	4.6	1	26.5	21.8	93.00%	K.EALSEDFVLPFGLAK.V		K.EALSEDFVLPFGLAK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
196	RLA0_SCHPO	15.06%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
133	144	2	1308.71	5.2	0	29.1	19.5	95.00%	K.TSFFQALGIPTK.I		K.TSFFQALGIPTK.I
98	132	3	3513.88	2.7	1	45.6	17.3	95.00%	R.ETIIANVIAAPARPNAIAPLDVFVP AGNTGMEPGK.T		R.ETIIANVIAAPARPNAIAPLDVFVP AGNTGMEPGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
197	ARO1_SCHPO	3.43%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
677	703	3	2950.41	2.7	1	45.4	24.5	95.00%	R.FACDVLRPMGCTVEQTATSTTV QGPPK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.FACDVLRPMGCTVEQTATSTTV QGPPK.G
162	172	2	1299.72	4.7	0	45.2	20.8	95.00%	K.NLVGAFWQPLR.V		K.NLVGAFWQPLR.V
1232	1247	2	1833.96	4.6	1	44.8	21.9	95.00%	R.ITNSMDIPLILFNMGR.F		R.ITNSMDIPLILFNMGR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
198	GPD2_SCHPO	10.46%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	88	4	2626.25	3.3	1	19.3	25.2	95.00%	K.IQHEGKECNLTEVFNTTHENVK.Y	Carbamidomethyl (+57)	K.IQHEGKECNLTEVFNTTHENVK.Y
311	327	3	1907.98	3	1	33.8	22.2	95.00%	K.TGKPMHVVEQELLDGQK.L		K.TGKPMHVVEQELLDGQK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
199	LYS2_SCHPO	1.62%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
308	316	2	1056.53	4.1	0	27.9	24.4	94.80%	D.APVTSYTYR.Q		R.ECIVVTPSVTIDAPVTSYTYR.Q
394	407	2	1489.81	2.4	0	25.3	20.6	91.00%	D.AGVLSPTVVEYVEK.S		R.ALVVLEDAGVLSPTVVEYVEK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
200	YEI3_SCHPO	8.67%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
43	62	2	2148.05	4.6	1	58.6	24.9	95.00%	K.SVLGNPANYPYATIDPEEAK.V		K.SVLGNPANYPYATIDPEEAK.V
329	342	2	1482.75	2.8	1	41.2	24.6	95.00%	K.APQAAGVIHTDFEK.A		K.APQAAGVIHTDFEK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
201	RL35_SCHPO	19.67%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
11	24	2	1684.85	4.2	0	72	23.8	95.00%	K.QSQENLAEQLQELR.Q		K.QSQENLAEQLQELR.Q
56	65	2	1157.65	4.3	0	33.6	20.5	95.00%	R.ILTVINESNR.L		R.ILTVINESNR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
202	P5CR_SCHPO	15.25%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
116	129	2	1566.76	5	1	85.9	25.3	95.00%	K.TISSLQSMLDESTR.V		K.TISSLQSMLDESTR.V
70	98	3	3111.57	2.6	1	41.3	22.4	95.00%	K.ENAEMAAISNVLLLSCKPQAAED VLNSPK.M	Carbamidomethyl (+57)	K.ENAEMAAISNVLLLSCKPQAAED VLNSPK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
203	LYS4_SCHPO	4.30%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
149	159	2	1179.57	4.4	1	26	24.9	92.30%	K.GQGIDFYPAGR.G		K.GQGIDFYPAGR.G
470	489	2	1872.04	4.8	0	47.2	15.2	95.00%	R.EALAYLASPAVVAASAIAGK.I		R.EALAYLASPAVVAASAIAGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
204	ACAC_SCHPO	1.49%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1972	1994	3	2667.36	3.2	1	27.8	21.1	95.00%	K.TAQAINDFNHGEQLPLFILANWR.G		K.TAQAINDFNHGEQLPLFILANWR.G
197	207	2	1131.63	6.1	0	34.7	18.8	95.00%	K.ISSTIVAQSAR.V		K.ISSTIVAQSAR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
205	EIF3E_SCHPO	6.59%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
267	284	3	2029.08	4.4	0	22.1	19.4	92.50%	R.YLTVAVVTNQNNANQKPR.N		R.YLTVAVVTNQNNANQKPR.N
477	491	2	1679.84	3.6	0	46.3	24.2	95.00%	K.SLSFESQNLEQSLAK.S		K.SLSFESQNLEQSLAK.S

Supplementary Table S2: All "Scaffold" validated proteins and peptides identified from solprotSP (*S.pombe*) and from SCVMprot (*S.cerevisiae*) samples

***S.pombe* - Formic acid digest of large tryptic peptides (replicate C)**

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
1	G3P1_SCHPO	55.65%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
249	259	3	1290.69	4.5	1	28.4	22.9	95.00%	K.LAKPTNYEDIK.A		K.LAKPTNYEDIK.A
167	186	2	2135.06	2	0	87.1	23.9	95.00%	D.TFGIEEGLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK.T
118	126	2	997.59	2.6	1	28.5	17.2	95.00%	K.RVIISAPSK.D	N-Formyl (+28)	K.RVIISAPSK.D
94	113	2	2181.1	2.7	0	78.4	23.3	95.00%	D.YVIESTGVFTTQETASAHLK.G		K.WSTSGADYVIESTGVFTTQETASAHLK.G
127	139	2	1449.69	3.7	1	45.1	25.6	95.00%	K.DAPMYVVGVNEEK.F		K.DAPMYVVGVNEEK.F
40	48	2	1194.55	2.1	0	31.9	26.2	95.00%	D.LEYMAYMFK.Y		K.TIQVVAINDPFIDLEYMAYMFK.Y
128	145	2	2036.99	1.8	1	89.1	25.3	95.00%	D.APMYVVGVNEEKFNPSEK.V		K.DAPMYVVGVNEEKFNPSEK.V
297	309	2	1344.74	2.5	0	53.6	20.5	95.00%	D.ASAGIQLSPQFVK.L		K.GVLGYTEDAVVSTDFCGDNHSSIFDASAGIQLSPQFVK.L
128	139	2	1334.66	2.7	0	57.4	24.6	95.00%	D.APMYVVGVNEEK.F		K.DAPMYVVGVNEEK.F
87	113	2	2885.38	3.9	1	116	24.8	95.00%	K.WSTSGADYVIESTGVFTTQETASAHLK.G		K.WSTSGADYVIESTGVFTTQETASAHLK.G
146	162	2	1818.91	4.5	0	75	24.4	95.00%	K.VISNASCTTNCLAPLAK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.VISNASCTTNCLAPLAK.V
286	296	2	1297.51	2.8	1	38.9	25.2	95.00%	D.FCGDNHSSIFD.A	Carbamidomethyl (+57)	K.GVLGYTEDAVVSTDFCGDNHSSIFDASAGIQLSPQFVK.L
324	334	2	1148.65	6.2	1	55.4	18.2	95.00%	R.VVDLVAYTAAK.D		R.VVDLVAYTAAK.D
163	186	2	2576.29	2.3	1	106	23.6	95.00%	K.VINDTFGIEEGLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK.T
240	248	2	958.57	2.4	1	29.2	17.6	95.00%	D.VSVVDLTVK.L		R.VPTPDVSVVDLTVK.L
36	48	2	1682.78	1.7	1	73.9	26.1	95.00%	D.PFIDLEYMAYMFK.Y	Oxidation (+16)	K.TIQVVAINDPFIDLEYMAYMFK.Y
119	127	2	928.53	2.1	2	33.1	23.1	95.00%	R.VIISAPSKD.A		R.VIISAPSKDAPMYVVGVNEEK.F
6	13	2	819.43	6.2	0	38.4	22.9	95.00%	K.VGINGFGR.I	Deamidation (+1)	K.VGINGFGR.I
201	215	2	1343.71	4.7	0	69.9	22.6	95.00%	R.GASANIIPSSTGAAK.A		R.GASANIIPSSTGAAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
2	ENO11_SCHPO	53.76%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
361	374	2	1624.72	3	0	62.3	26.8	95.00%	R.MSYEAGWGVMVSHR.S	Oxidation (+16)	R.MSYEAGWGVMVSHR.S
218	226	2	1013.51	3.6	1	29.6	23.1	95.00%	D.LQTPQEALD.L		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
185	194	2	1204.59	5.4	0	34	24.9	95.00%	R.WGAETYHTLK.S		R.WGAETYHTLK.S
346	360	2	1585.85	6	0	90.8	21.2	95.00%	K.VNQIGSVTESLNAVR.M		K.VNQIGSVTESLNAVR.M
381	396	2	1640.93	1.8	0	48	16.3	95.00%	D.TFISHLTVGIGAGQLK.S		R.SGETADTFISHLTVGIGAGQLK.S
247	257	2	1200.57	2.8	1	43.9	25	95.00%	D.VASSEFYVDGK.Y		K.IGLDVASSEFYVDGK.Y
65	79	2	1477.87	4	0	73.7	11.8	95.00%	K.AVGNVNNIIAPAVVK.A		K.AVGNVNNIIAPAVVK.A
106	120	2	1560.82	4.2	0	61.3	22.6	95.00%	K.LGANAILGVSMAICR.A	Oxidation (+16)/ Carbamidomethyl (+57)	K.LGANAILGVSMAICR.A
303	310	2	1045.48	2.6	0	26.6	25.7	91.90%	D.WSAWTHMK.A		K.YPIVSIEDPFDQDDWSAWTHMK.A
288	296	2	1062.56	2.4	2	37.5	23.1	95.00%	K.KYPIVSIED.P		K.KYPIVSIEDPFDQDDWSAWTHMK.A
273	287	2	1812.96	4.5	1	75.4	20.8	95.00%	K.LTYQQLTDLYVELSK.K		K.LTYQQLTDLYVELSK.K
227	234	2	898.55	2.2	0	35.2	16.9	95.00%	D.LIVEAINK.A		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
16	32	2	1837.92	2.1	1	85.7	23.6	95.00%	R.GNPTVEVDLTTETGIHR.A		R.GNPTVEVDLTTETGIHR.A

33	50	2	1886.97	4.8	0	105	23.5	95.00%	R.AIVPSGASTGIWEALEMR.D		R.AIVPSGASTGIWEALEMR.D
338	345	2	901.51	4.7	0	31.4	21.3	95.00%	K.CANALLLK.V	Carbamidomethyl (+57)	K.CANALLLK.V
409	414	2	806.43	5.7	0	29.4	23.6	95.00%	K.YNELLR.I		K.YNELLR.I
218	234	2	1894.05	2	1	80.8	15.9	95.00%	D.LQTPQEALDLIVEAINK.A		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
415	432	2	1815.87	2.6	0	90.9	25.6	95.00%	R.IEEELGSEGVYAGAHAGK.Y		R.IEEELGSEGVYAGAHAGK.Y
311	320	2	1093.5	3.5	1	61.9	25.2	95.00%	K.AETDFQIVGD.D		K.AETDFQIVGDDLTVTNVK.R
375	396	2	2201.14	2.9	1	122	20.8	95.00%	R.SGETADTFISHLTVGIGAGQLK.S		R.SGETADTFISHLTVGIGAGQLK.S
89	96	2	905.49	4.7	1	57.4	23.1	95.00%	K.AADEFLLK.L		K.AADEFLLK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
3	PGK_SCHPO	44.93%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
359	378	2	1917.95	4	1	118	24.2	95.00%	K.TCEAGNVVIVGGGDTATVAK.K	Carbamidomethyl (+57)	K.TCEAGNVVIVGGGDTATVAK.K
151	162	2	1279.63	2.6	1	27	25.2	93.40%	K.SLTSLGDIFVND.A		K.SLTSLGDIFVNDAFGTAHR.A
123	132	3	1145.54	4.7	0	33.9	25.7	95.00%	R.FHIEEEGSAK.V		R.FHIEEEGSAK.V
57	71	2	1591.87	2.9	0	46.2	20	95.00%	K.AVILMSHLGRPNGAR.V	Deamidation (+1)	K.AVILMSHLGRPNGAR.V
112	122	2	1211.69	4.5	0	57.3	18.4	95.00%	K.GGEVILLENLR.F		K.GGEVILLENLR.F
40	48	2	910.59	3.6	0	25.3	12.6	91.10%	R.IVGALPTIK.Y		R.IVGALPTIK.Y
330	347	2	2010.99	3.7	1	70.7	24.5	95.00%	K.TIVWNGPAGVFEFDNFAK.G		K.TIVWNGPAGVFEFDNFAK.G
158	169	2	1346.68	2.6	1	56.4	24.6	95.00%	D.IFVNDAFGTAHR.A		K.SLTSLGDIFVNDAFGTAHR.A
404	414	2	1040.63	5.6	0	39.4	18	95.00%	K.ALPGVVALSSK.-		K.ALPGVVALSSK.-
383	403	2	2069.04	3.6	1	81.1	23.7	95.00%	K.EDALSHVSTGGGASLELLEGK.A		K.EDALSHVSTGGGASLELLEGK.A
321	329	2	994.54	5.5	0	50.2	20.8	95.00%	K.FAEVITTSK.T		K.FAEVITTSK.T
75	86	3	1304.74	4.3	0	59.4	17.9	95.00%	K.YSLKPVAAELSK.L		K.YSLKPVAAELSK.L
385	403	2	1824.96	2.7	0	85.5	20.9	95.00%	D.ALSHVSTGGGASLELLEGK.A		K.EDALSHVSTGGGASLELLEGK.A
197	213	2	1737	3.8	0	59.4	13.4	95.00%	K.ALENPARPFLAILGGAK.V		K.ALENPARPFLAILGGAK.V
123	134	2	1359.63	2.4	2	39.9	25.9	95.00%	R.FHIEEEGSAKVD.G		R.FHIEEEGSAKVDGK.K
170	181	2	1267.64	4	1	58.7	23.1	95.00%	R.AHSSMVGVDLPR.V		R.AHSSMVGVDLPR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
4	METE_SCHPO	43.98%	100%	31

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
561	571	2	1184.7	5.1	0	40.5	17.5	95.00%	K.GMLTAPITILR.W		K.GMLTAPITILR.W
434	449	2	1746.97	7	0	46.9	17.6	95.00%	K.LPLFPTTTIGSFPQTK.E		K.LPLFPTTTIGSFPQTK.E
4	11	2	845.48	4.8	0	33.3	22.1	95.00%	K.SAVLGFPR.I		K.SAVLGFPR.I
707	714	2	901.49	4.3	0	27.7	24.5	94.50%	R.VPPVSEFK.E		R.VPPVSEFK.E
684	690	2	813.51	5.6	0	34.2	19.1	95.00%	K.LLNVLSR.Y		K.LLNVLSR.Y
691	706	2	1818.88	3.8	1	84	25	95.00%	R.YTSCIGPGLFDIHSPR.V	Carbamidomethyl (+57)	R.YTSCIGPGLFDIHSPR.V
501	508	2	1028.48	2.8	0	29.6	24.1	95.00%	D.MVQYFGER.M		R.NDMVQYFGER.M
393	404	2	1284.67	4.4	0	68.2	21.6	95.00%	R.AESPITNVEAVR.E		R.AESPITNVEAVR.E
707	716	3	1186.64	4.9	1	25.6	21.3	95.00%	R.VPPVSEFKER.I		R.VPPVSEFKER.I
125	139	2	1821.82	2.1	1	28.6	26.8	93.40%	D.SNYHFLRPEVSEETD.F		K.WFDSNYHFLRPEVSEETDFK.L
391	404	2	1511.81	4	1	42.1	21	95.00%	K.ARAESPITNVEAVR.E		K.ARAESPITNVEAVR.E
499	508	2	1257.55	4.4	1	53.6	25.7	95.00%	R.NDMVQYFGER.M		R.NDMVQYFGER.M
243	260	2	1982.08	3.5	1	54.1	17.6	95.00%	K.LILTTYFGSLQSNADVLK.G		K.LILTTYFGSLQSNADVLK.G
428	449	3	2402.33	4.8	1	46	14.5	95.00%	K.QQASLKLPLFPTTTIGSFPQTK.E		K.QQASLKLPLFPTTTIGSFPQTK.E
325	351	3	2884.5	3.5	1	47.3	18.5	95.00%	R.VQVASSSSILHIPHSLSGEDQINPEIK.R		R.VQVASSSSILHIPHSLSGEDQINPEIK.R
261	273	2	1330.77	1.9	1	60.9	14.8	95.00%	K.GLPIAGVHVDVVR.A		K.GLPIAGVHVDVVR.A
281	299	2	1881.08	4.8	0	87.4	11.1	95.00%	R.ALAVLGENQIISVGVVSGR.N		R.ALAVLGENQIISVGVVSGR.N
147	155	2	1034.53	5.7	1	36.8	24.6	95.00%	K.ALDEFLEAK.E		K.ALDEFLEAK.E
595	601	2	844.46	2.7	1	25.8	23.6	91.90%	D.EVLDLEK.A		R.DEVLDLEK.A
325	344	2	2062.04	3.1	1	76.7	23.7	95.00%	R.VQVASSSSILHIPHSLSGED.Q		R.VQVASSSSILHIPHSLSGEDQINPEIK.R

670	679	2	1060.54	3.6	1	31.1	23.9	95.00%	D.ADVVSIENSK.S		R.LDADVVSIENSK.S
361	369	2	1017.56	4.9	0	30.5	21.5	95.00%	K.CAELAILTK.A	Carbamidomethyl (+57)	K.CAELAILTK.A
461	473	2	1539.76	4.1	1	67.2	24.3	95.00%	K.GLISQEEYDAFIR.K		K.GLISQEEYDAFIR.K
547	560	2	1596.79	3.6	0	50.8	24.1	95.00%	K.ESQYAQSITSKPMK.G		K.ESQYAQSITSKPMK.G
606	615	2	1199.6	4.3	1	55.1	24.2	95.00%	K.VIQCDEPALR.E	Carbamidomethyl (+57)	K.VIQCDEPALR.E
527	546	3	2267.24	3.3	1	44.5	16.3	95.00%	R.CVRPPIIVGDVYRPAPMTVK.E	Carbamidomethyl (+57)	R.CVRPPIIVGDVYRPAPMTVK.E
631	637	2	877.45	5.9	1	49	23.7	95.00%	K.WAIDAFR.L		K.WAIDAFR.L
85	99	2	1616.79	4.1	1	63.5	25.3	95.00%	R.LSGLSSLDTYFAMGR.G		R.LSGLSSLDTYFAMGR.G
537	546	3	1160.64	2.6	0	28.4	20.4	95.00%	D.VYRPAPMTVK.E		R.CVRPPIIVGDVYRPAPMTVK.E
156	176	3	2256.33	3.9	0	51.3	4.77	95.00%	K.EAGIITRPVLVGPVTYLFIAK.A		K.EAGIITRPVLVGPVTYLFIAK.A
30	40	2	1132.6	4.2	0	58.1	22.9	95.00%	K.TSAEELLATAK.Q		K.TSAEELLATAK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
5	EF1A1_SCHPO	46.09%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
265	288	2	2443.35	2.2	0	50.7	15.3	95.00%	R.VETGVIKPGMIVTFAPAGVTTEVK.S		R.VETGVIKPGMIVTFAPAGVTTEVK.S
402	421	2	2268.08	3.1	1	68	25.3	95.00%	K.MVPSKPMCVEAFTDYAPLGR.F	Carbamidomethyl (+57)	K.MVPSKPMCVEAFTDYAPLGR.F
147	154	2	883.55	5.8	0	26.4	17.9	92.80%	K.QLIVAVNK.M		K.QLIVAVNK.M
289	298	2	1182.5	2.6	1	30	25.6	95.00%	K.SVEMHHESLD.A		K.SVEMHHESLDAGLPGDNVGFNVK.N
254	264	2	1024.61	4.2	0	65.4	14.1	95.00%	K.IGGIGTVPVGR.V		K.IGGIGTVPVGR.V
6	20	2	1529.84	2.3	1	74	20.3	95.00%	K.GHINVVVIGHVDSGK.S		K.GHINVVVIGHVDSGK.S
232	241	2	1081.54	3.4	1	39.7	24.1	95.00%	D.SIEPPARPTD.K		K.TLLEAIDSIEPPARPTDKPLR.L
185	214	3	3453.63	3.7	1	49.2	24.8	95.00%	K.TVPFVPVSGFQGDNMIEPTTNMPWYQGWQK.E		K.TVPFVPVSGFQGDNMIEPTTNMPWYQGWQK.E
155	164	2	1151.51	6.4	1	75.8	24.9	95.00%	K.MDTTGWSQAR.F		K.MDTTGWSQAR.F
198	214	2	2122.97	2.3	0	60.5	27	95.00%	D.NMIEPTTNMPWYQGWQK.E		K.TVPFVPVSGFQGDNMIEPTTNMPWYQGWQK.E
225	241	2	1836.95	2.5	1	27.6	22.1	94.40%	K.TLLEAIDSIEPPARPTD.K		K.TLLEAIDSIEPPARPTDKPLR.L
85	96	2	1340.69	4.4	1	66.1	22.7	95.00%	K.YNVTVIDAPGHR.D		K.YNVTVIDAPGHR.D
246	253	2	974.55	4.1	1	32.1	21	95.00%	R.LPLQDVYK.I		R.LPLQDVYK.I
135	146	2	1313.74	2.7	0	45.9	19.4	95.00%	R.EHALLAYTLGVK.Q		R.EHALLAYTLGVK.Q
370	376	2	848.47	4.7	0	25.9	22.8	92.00%	K.FAELIEK.I		K.FAELIEK.I
223	231	2	958.54	3.2	2	44.4	22.6	95.00%	K.GKTLLEAID.S		K.GKTLLEAIDSIEPPARPTDKPLR.L
299	311	2	1286.66	1.7	1	36.4	23.3	95.00%	D.AGLPGDNVGFNVK.N		K.SVEMHHESLDAGLPGDNVGFNVK.N
165	177	2	1582.83	3.8	1	66.1	21	95.00%	R.FEEIVKETSNFIK.K		R.FEEIVKETSNFIK.K
402	415	2	1610.72	2.2	1	34.5	27	95.00%	K.MVPSKPMCVEAFTD.Y	Carbamidomethyl (+57)	K.MVPSKPMCVEAFTDYAPLGR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
6	KPYK_SCHPO	66.21%	100%	28

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
332	344	2	1320.66	2.5	1	80	24.3	95.00%	D.GADLVMLSGETTK.G		R.AEVSDVGNAVLDGADLVMLSGETTK.G
108	121	2	1596.72	3.3	1	30.4	26.6	95.00%	D.YPISSGHEMIFTTD.D		R.TGLTVGGTDYPISSGHEMIFTTDDAYAEK.C
487	497	2	1053.66	5.9	0	39.5	11.1	95.00%	K.IIVLQGAVGGK.G		K.IIVLQGAVGGK.G
233	243	2	1214.66	3.9	1	28.5	22.1	95.00%	R.EVLGEEGKNIK.I		R.EVLGEEGKNIK.I
108	122	2	1711.74	2.2	1	30.3	27	95.00%	D.YPISSGHEMIFTTDD.A		R.TGLTVGGTDYPISSGHEMIFTTDDAYAEK.C
422	433	3	1430.81	3.1	0	41.3	17.2	95.00%	K.YRPSIPIVMVTR.C		K.YRPSIPIVMVTR.C
10	26	2	1880.98	3.7	1	90.9	21.6	95.00%	K.QWVAGLNSELDIPAVNR.R		K.QWVAGLNSELDIPAVNR.R
155	164	2	1105.64	2.3	0	37.6	16.1	95.00%	D.GILSFTVIEK.V		R.IIYVDDGILSFTVIEK.V
446	459	2	1607.81	0.86	2	46.6	23.8	95.00%	R.GVYPVIYEKEPLSD.W		R.GVYPVIYEKEPLSDWQK.D

320	331	2	1187.57	3	1	28.8	25	95.00%	R.AEVSDVGNAVLD.G		R.AEVSDVGNAVLDGADLVMLSGETTK.G
76	91	2	1640.92	3.9	2	45.4	17.2	95.00%	R.KASATNPLFPLAIALD.T		R.KASATNPLFPLAIALDTK.G
77	93	2	1741.97	3.8	1	39.2	17.8	95.00%	K.ASATNPLFPLAIALDTK.G		K.ASATNPLFPLAIALDTK.G
225	232	2	951.52	5	1	30.1	21.1	95.00%	R.AEDVIHIR.E		R.AEDVIHIR.E
248	258	2	1277.56	3.4	1	35.6	26.3	95.00%	K.IENQQGVNNFD.S	Deamidation (+1)	K.IENQQGVNNFDSILDVTDGIMVAR.G
57	75	3	2253.99	2.7	1	52.9	27.1	95.00%	R.MNFSHGSYEYHQSVIDNAR.K		R.MNFSHGSYEYHQSVIDNAR.K
28	37	2	1088.6	5	0	46.3	21.4	95.00%	R.TSIICTIGPK.S	Carbamidomethyl (+57)	R.TSIICTIGPK.S
274	288	2	1598.91	2.2	0	48.1	16.4	95.00%	D.LGIEIPASQVFVAQK.M		R.GDLGIEIPASQVFVAQK.M
263	271	2	960.51	3	1	45.6	23.1	95.00%	D.VTDGIMVAR.G		K.IENQQGVNNFDSILDVTDGIMVAR.G
468	477	2	1186.55	5.3	0	54.8	24.7	95.00%	R.VAYGCQQAYK.M	Carbamidomethyl (+57)	R.VAYGCQQAYK.M
345	360	2	1743.82	5.3	0	80.9	25.5	95.00%	K.GSYPVEAVTYMAETAR.V		K.GSYPVEAVTYMAETAR.V
335	344	2	1077.58	2.7	0	30.3	23.3	95.00%	D.LVMLSGETTK.G		R.AEVSDVGNAVLDGADLVMLSGETTK.G
272	288	2	1770.96	3.8	1	69.1	19.7	95.00%	R.GDLGIEIPASQVFVAQK.M		R.GDLGIEIPASQVFVAQK.M
361	380	2	2229.12	2.4	0	84.2	23.1	95.00%	R.VAEASIPYGSLYQEMFGLVR.R		R.VAEASIPYGSLYQEMFGLVR.R
294	319	4	2982.39	2.4	0	57.2	26	95.00%	K.CNIAGKPVACATQMLESMTYNPRPTR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Oxidation (+16)/ Deamidation (+1)	K.CNIAGKPVACATQMLESMTYNPRPTR.A
405	417	2	1287.72	5.7	0	62	19	95.00%	K.AIVVLSTSGNTAR.L		K.AIVVLSTSGNTAR.L
99	121	2	2398.11	3	1	27.8	26.6	92.50%	R.TGLTVGGTDYPISSGHEMIFTTD.D		R.TGLTVGGTDYPISSGHEMIFTTDDAYAEK.C
212	223	2	1384.68	2.5	1	47.3	24.4	95.00%	K.NGVDMIFASFIR.R	Oxidation (+16)	K.NGVDMIFASFIR.R
381	404	2	2460.23	3.5	1	76.2	23.7	95.00%	R.RPLECATETTAVAAIGASIESDAK.A	Carbamidomethyl (+57)	R.RPLECATETTAVAAIGASIESDAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
7	ALF_SCHPO	63.97%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
257	275	2	2097.04	0.13	0	59.8	24	95.00%	D.KPVFFVFHGGSGSSVNEFR.T		K.TTNDKPVFFVFHGGSGSSVNEFR.T
26	50	2	2496.31	4.1	0	69.4	19.9	95.00%	R.EHGFAIPAINVTSSSTAIAALEAAR.E		R.EHGFAIPAINVTSSSTAIAALEAAR.E
309	325	2	1829.91	4	1	61.7	24.7	95.00%	D.YLMTPVGNPEGADKPNK.K		K.DYLMTPVGNPEGADKPNK.K
207	234	4	2951.53	3.2	0	31.9	20.6	95.00%	R.ELSSVTPYFSIAAAFGNVHGVYKPGNVK.L		R.ELSSVTPYFSIAAAFGNVHGVYKPGNVK.L
291	301	2	1283.62	2.6	2	56.4	24.3	95.00%	D.TQFAYVEGVRD.Y		K.VNIDTDTQFAYVEGVRDYVLK.Y
253	275	2	2528.21	2	1	93.7	25.2	95.00%	K.TTNDKPVFFVFHGGSGSSVNEFR.T		K.TTNDKPVFFVFHGGSGSSVNEFR.T
94	112	2	2098.02	3.1	1	64.2	25.1	95.00%	R.SIAPFFGVPVVMHSDHCAK.K	Carbamidomethyl (+57)	R.SIAPFFGVPVVMHSDHCAK.K
345	358	2	1597.83	4.2	1	60.4	23	95.00%	R.VLTALEDFYTVNTL.-		R.VLTALEDFYTVNTL.-
131	143	3	1481.7	3.2	1	21.5	25.6	90.50%	K.IHGEPLFSSHMLD.L		K.IHGEPLFSSHMLDLSEEPK.K
6	19	2	1424.83	2	1	63	15.2	95.00%	D.IVPTGVITGDNVLK.L		-.MGILDIVPTGVITGDNVLK.L
289	300	2	1384.67	2.7	1	78.5	25.7	95.00%	D.TDTQFAYVEGVR.D		K.VNIDTDTQFAYVEGVR.D
94	108	2	1601.8	2.4	1	55.6	24.4	95.00%	R.SIAPFFGVPVVMHSD.H		R.SIAPFFGVPVVMHSDHCAK.K
291	300	2	1168.59	2.7	0	51.7	23.3	95.00%	D.TQFAYVEGVR.D		K.VNIDTDTQFAYVEGVR.D
120	130	2	1306.56	2.4	1	42.4	25.7	95.00%	D.GMFEADEAYFK.I		K.LLPWMDGMFEADEAYFK.I
235	248	2	1564.88	2.5	0	69	16.8	95.00%	K.LQPALLGQHQAYVK.E		K.LQPALLGQHQAYVK.E
54	71	2	1844.94	0.85	0	86	23.4	95.00%	R.SPIILQTSNGGAHFFAGK.E	Deamidation (+1)	R.SPIILQTSNGGAHFFAGK.E
131	149	3	2165.05	3.2	1	36.1	24	95.00%	K.IHGEPLFSSHMLDLSEEPK.K		K.IHGEPLFSSHMLDLSEEPK.K
80	93	2	1399.76	5.1	0	89.1	19.9	95.00%	K.ASIAGSIAAAHYIR.S		K.ASIAGSIAAAHYIR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
8	PDC2_SCHPO	50.00%	100%	29

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
5	18	2	1542.74	2.7	0	55.2	25	95.00%	D.AESTMTVGTYLAQR.L	Oxidation (+16)	K.DAESTMTVGTYLAQR.L

254	278	3	2854.28	2.1	1	68.9	27.1	95.00%	K.GFYSEEHKNYAGVYWGEVSSSETTK.A		K.GFYSEEHKNYAGVYWGEVSSSETTK.A
204	214	2	1130.62	4.6	1	53.5	21.3	95.00%	K.ATDIAAELISK.K		K.ATDIAAELISK.K
440	461	2	2409.21	3.3	1	90.9	22.6	95.00%	R.TIVMVGDGSFQLTGQEISQMIR.H		R.TIVMVGDGSFQLTGQEISQMIR.H
546	555	2	1235.55	1.1	1	38.5	25.7	95.00%	D.CTQELVDWGK.A	Carbamidomethyl (+57)/ Deamidation (+1)	K.EGPTLIECAIDTDDCTQELVDWGK.A
238	253	2	1689.86	2.8	0	62.5	23.6	95.00%	K.LAEALNCAAFIMPAAK.G	Carbamidomethyl (+57)	K.LAEALNCAAFIMPAAK.G
516	525	2	1047.55	4.8	0	31.2	23.2	95.00%	K.TGEELTSAIK.V		K.TGEELTSAIK.V
228	237	2	949.49	5	0	30.2	23.3	95.00%	R.AAGAESAFVK.L		R.AAGAESAFVK.L
304	328	2	2694.37	3	1	65.1	21.3	95.00%	R.AAPNPNILLNSDYTSVSIPGYVFSR.V		R.AAPNPNILLNSDYTSVSIPGYVFSR.V
215	225	3	1192.76	2.3	1	34	9.03	95.00%	K.KEKPILLAGPK.L		K.KEKPILLAGPK.L
329	340	2	1425.76	4.3	0	95.2	21.9	95.00%	R.VYMAEFLELLAK.K		R.VYMAEFLELLAK.K
447	461	2	1693.85	1.5	0	68.8	24.1	95.00%	D.GSFQLTGQEISQMIR.H		R.TIVMVGDGSFQLTGQEISQMIR.H
127	135	2	1157.55	3.4	0	28.7	26.3	94.10%	D.FEYQMEIAK.K		R.SNGIACAVVTYSVGALTAFDGIGGAYAENLPVILVSGSPNTNDLSSGHLLHHTLGTHDFEYQMEIAK.K
160	198	4	4251.22	3.6	1	16.7	18.8	91.70%	R.QAILQHKPVYIEIPTNMANQPCPVPGPISAVISPEISDK.E	Carbamidomethyl (+57)	R.QAILQHKPVYIEIPTNMANQPCPVPGPISAVISPEISDK.E
495	508	2	1529.69	2	0	70.9	25.9	95.00%	D.FAAFCESLNGETGK.A	Carbamidomethyl (+57)	R.IQNWDFAAFCESLNGETGK.A
316	328	2	1474.75	2.1	0	52.9	23.6	95.00%	D.YTSVSIPGYVFSR.V		R.AAPNPNILLNSDYTSVSIPGYVFSR.V
369	378	2	1157.64	5	1	28	22.4	94.80%	K.AALNRVEVMR.Q		K.AALNRVEVMR.Q
137	146	2	1101.64	5.4	1	51.2	18.6	95.00%	K.LTCAAVAIKR.A	Carbamidomethyl (+57)	K.LTCAAVAIKR.A
19	25	2	770.49	4.3	0	34.4	18.1	95.00%	R.LVEIGIK.N		R.LVEIGIK.N
462	474	3	1575.97	4.8	1	29.2	6.02	95.00%	R.HKLPVLIFLLNNR.G		R.HKLPVLIFLLNNR.G
26	37	2	1429.72	4.2	1	38.3	24.4	95.00%	K.NHFVVPGDYNLR.L		K.NHFVVPGDYNLR.L
262	278	2	1876.86	4.2	0	98.1	26.4	95.00%	K.NYAGVYWGEVSSSETTK.A		K.NYAGVYWGEVSSSETTK.A
150	159	2	1121.6	2.5	1	50	21.4	95.00%	D.APVMIDHAIR.Q		R.AEDAPVMIDHAIR.Q
490	508	2	2186.97	4.3	1	85.4	27	95.00%	R.IQNWDFAAFCESLNGETGK.A	Carbamidomethyl (+57)/ Deamidation (+1)	R.IQNWDFAAFCESLNGETGK.A
464	474	2	1310.81	4.6	0	66.2	10.4	95.00%	K.LPVLIFLLNNR.G		K.LPVLIFLLNNR.G
136	145	2	1073.63	3.9	1	39.6	15.9	95.00%	K.KLTCAAVAIK.R	Carbamidomethyl (+57)	K.KLTCAAVAIK.R
4	18	2	1641.77	4.2	1	65.2	26	95.00%	K.DAESTMTVGTYLAQR.L		K.DAESTMTVGTYLAQR.L
304	315	2	1237.63	2.3	1	33.9	23.1	95.00%	R.AAPNPNILLNSD.Y		R.AAPNPNILLNSDYTSVSIPGYVFSR.V
216	225	3	1064.66	3.8	0	29.3	12	95.00%	K.EKPILLAGPK.L		K.EKPILLAGPK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
9	ADH4_SCHPO	48.10%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
110	129	2	2090.15	2.3	1	59.2	16.4	95.00%	D.GVQPNPTVGNVNQGLEIVKK.E		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVKK.E
110	128	2	1962.06	3	0	64.7	19.5	95.00%	D.GVQPNPTVGNVNQGLEIVK.K		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K
375	385	3	1245.76	3.9	1	37.6	9.54	95.00%	K.IRPHLVDLGVK.E		K.IRPHLVDLGVK.E
76	87	2	1282.76	5.2	1	44.2	15.1	95.00%	K.NTLIVTDPGIIK.V		K.NTLIVTDPGIIK.V
366	374	2	1027.63	6.6	0	37.3	16.2	95.00%	R.ISQLVLEVK.I		R.ISQLVLEVK.I
348	364	2	1882.86	3.1	1	41.6	26.7	95.00%	D.IAFHLGCEEHTAEAALD.R	Carbamidomethyl (+57)	R.LGDIAFHLGCEEHTAEAALDR.I
149	159	2	1014.58	4.8	0	36.7	21.2	95.00%	K.GIALLATNGGK.I	Deamidation (+1)	K.GIALLATNGGK.I
210	219	2	1153.55	5	1	37.5	24.2	95.00%	K.HTMPILSVND.P	N-Formyl (+28)	K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
348	365	4	2038.96	2.6	1	22.2	25.9	95.00%	D.IAFHLGCEEHTAEAALDR.I	Carbamidomethyl (+57)	R.LGDIAFHLGCEEHTAEAALDR.I
400	412	2	1380.61	3	1	31.3	26.2	95.00%	D.ACGATNPIQPTHD.E	Carbamidomethyl (+57)	K.DACGATNPIQPTHDEVK.A
96	128	3	3573.88	3.6	1	56.5	18.9	95.00%	K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K

209	219	2	1269.64	3.4	2	28.1	23	95.00%	D.KHTMPILSVND.P	Oxidation (+16)	K.MAIIDKHTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
220	237	2	1882.84	2.4	1	29.1	27.3	93.40%	D.PETMYGLPPSLTAATGMD.A	Oxidation (+16)/ Oxidation (+16)	K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
169	191	2	2386.26	1.9	0	106	19.6	95.00%	K.SSKPQLPLIAINTTAGTASEMTR.F		K.SSKPQLPLIAINTTAGTASEMTR.F
238	256	2	1942.97	3	1	47.3	23.9	95.00%	D.ALTHAVEAYVSTAANPITD.A		K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
192	200	2	1078.57	4	0	35.5	22.9	95.00%	R.FAIITEETR.H		R.FAIITEETR.H
134	148	2	1475.65	3	1	49.8	26.6	95.00%	D.SMVSIGGGSAHDCAK.G	Carbamidomethyl (+57)	K.ENCDSMVSIGGGSAHDCAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
10	PMGY_SCHPO	61.61%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
23	30	2	977.54	3.1	0	31	21.6	95.00%	K.LNLFTGWK.D		K.LNLFTGWK.D
32	43	3	1242.68	2	1	46.1	20	95.00%	D.PALSETGIKEAK.L		K.DPALSETGIKEAK.L
111	120	2	1271.65	5.7	0	79.8	23.2	95.00%	K.WGAEQVQIWR.R		K.WGAEQVQIWR.R
70	90	2	2429.25	3.7	1	89.6	21.4	95.00%	K.TCQIILEEVGEPNLETIKSEK.L	Carbamidomethyl (+57)	K.TCQIILEEVGEPNLETIKSEK.L
23	31	2	1092.56	2.4	2	32.1	23.2	95.00%	K.LNLFTGWKD.P		K.LNLFTGWKDPALSETGIK.E
186	199	2	1553.85	2.9	1	39.8	18.1	95.00%	R.ELATGVPIVYHLDK.D		R.ELATGVPIVYHLDK.D
146	157	2	1320.78	4.4	1	36.9	13.8	95.00%	K.STIVPHILKGEK.V		K.STIVPHILKGEK.V
2	14	2	1439.81	5.3	0	52	17.6	95.00%	M.TTEAAPNLLVLTR.H	Acetyl (+42)	-.MTTEAAPNLLVLTR.H
158	168	2	1149.67	4.5	0	26.5	14	93.00%	K.VLIAAHGNSLR.A		K.VLIAAHGNSLR.A
95	104	2	1169.58	4.8	1	46.4	23.7	95.00%	R.YYGDLQGLNK.D		R.YYGDLQGLNK.D
58	66	2	1005.56	3.1	0	45.4	18.3	95.00%	D.IAFTSALQR.A		K.FDIAFTSALQR.A
70	87	2	2085.07	3.2	0	105	21.4	95.00%	K.TCQIILEEVGEPNLETIK.S	Carbamidomethyl (+57)	K.TCQIILEEVGEPNLETIK.S
1	14	2	1528.84	4.4	0	53	20	95.00%	-.MTTEAAPNLLVLTR.H		-.MTTEAAPNLLVLTR.H
15	30	3	1944.95	2.2	1	29.9	25.1	95.00%	R.HGESEWNKLNLFTGWK.D		R.HGESEWNKLNLFTGWK.D
32	40	2	914.51	2.6	0	48.7	24.5	95.00%	D.PALSETGIK.E		K.DPALSETGIK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
11	TPIS_SCHPO	64.66%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
71	98	3	2925.39	4	1	98.2	25	95.00%	K.NGAYTGENSAQSLIDAGITYTLTGHSER.R		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R
206	222	2	1841.9	2.2	1	42.9	25	95.00%	R.VIYGGSVNGGNCKEFLK.F	Deamidation (+1)/ Carbamidomethyl (+57)	R.VIYGGSVNGGNCKEFLK.F
160	174	2	1615.9	4	0	77.2	16.3	95.00%	K.IVIAYEPVWAIGTGK.T		K.IVIAYEPVWAIGTGK.T
175	189	2	1678.84	4.6	0	84.5	24.1	95.00%	K.TATPEQAQEVHAEIR.K		K.TATPEQAQEVHAEIR.K
86	99	3	1560.81	3.5	1	33.5	22.8	95.00%	D.AGITYTLTGHSERR.T		K.NGAYTGENSAQSLIDAGITYTLTGHSERR.T
135	145	2	1242.66	4.7	0	39.7	21.6	95.00%	R.EANETINVVVR.Q		R.EANETINVVVR.Q
115	134	3	2176.12	2.2	0	34.6	21.8	95.00%	K.FALEQGLTVVACIGETLAER.E	Carbamidomethyl (+57)	K.FALEQGLTVVACIGETLAER.E
175	190	2	1807.91	1.2	1	63.9	23.7	95.00%	K.TATPEQAQEVHAEIRK.W	Deamidation (+1)	K.TATPEQAQEVHAEIRK.W
32	52	2	2422.27	3.5	1	66.1	19.4	95.00%	K.LNVGDVETVIFPQNMYLITTR.Q		K.LNVGDVETVIFPQNMYLITTR.Q
228	249	3	2334.25	2.5	0	40.8	17.9	95.00%	D.GFLVGGASLKPEFHNIVNVHSL.-		K.FHDIDGFLVGGASLKPEFHNIVNVHSL.-
71	85	2	1538.69	2.8	1	52	26.5	95.00%	K.NGAYTGENSAQSLID.A		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R
86	98	2	1404.7	2.4	0	60.5	24.5	95.00%	D.AGITYTLTGHSER.R		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R
196	205	2	971.55	5.3	0	76.1	21.9	95.00%	K.LGASVAEGLR.V		K.LGASVAEGLR.V
37	52	2	1940.01	2	0	43.1	20.8	95.00%	D.VETVIFPQNMYLITTR.Q	Oxidation (+16)	K.LNVGDVETVIFPQNMYLITTR.Q
206	218	2	1324.61	4.4	0	76.9	25.9	95.00%	R.VIYGGSVNGGNCK.E	Deamidation (+1)/ Carbamidomethyl (+57)	R.VIYGGSVNGGNCK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
12	GLYD_SCHPO	51.18%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
341	349	2	1026.56	2.5	1	25.7	20.6	91.70%	D.SHMVLVDVK.S		K.LAADGTDSHMVLVDVK.S
146	159	2	1649.78	3.9	0	75	26	95.00%	K.ISAVSTYFESMPYR.V		K.ISAVSTYFESMPYR.V
183	193	2	1209.62	4.5	0	57.8	22.4	95.00%	K.ILVAGTSAYCR.L	Carbamidomethyl (+57)	K.ILVAGTSAYCR.L
171	182	3	1483.76	2.8	1	25.8	23	95.00%	D.MLEHDAQLFRPK.I		R.VDPNTGLIDYDMLEHDAQLFRPK.I
361	371	2	1254.76	2.7	0	60.5	13	95.00%	R.VLELINIVTNK.N		R.VLELINIVTNK.N
145	159	2	1777.87	1.8	1	111	24.7	95.00%	K.KISAVSTYFESMPYR.V		K.KISAVSTYFESMPYR.V
17	24	2	915.49	4.6	0	43.4	24.3	95.00%	D.PTVAEIMR.H		K.EQDPTVAEIMR.H
97	123	3	2996.43	3.4	0	55	24.8	95.00%	K.WGVNVQCLSGSPANMQVYQAIMPPHGR.L	Carbamidomethyl (+57)	K.WGVNVQCLSGSPANMQVYQAIMPPHGR.L
74	85	2	1550.75	4.7	1	96.3	25.4	95.00%	K.FIDQIETLCQER.A	Carbamidomethyl (+57)	K.FIDQIETLCQER.A
86	96	2	1129.62	5.1	1	54.8	22.1	95.00%	R.ALAAFNLDPAK.W		R.ALAAFNLDPAK.W
59	67	2	998.45	5.1	0	32.9	23.9	95.00%	K.YSEGYPGAR.Y		K.YSEGYPGAR.Y
277	302	3	2725.45	2.8	0	25.2	18	95.00%	K.INFSVFPGHQGGPHNHTITALAVALK.Q		K.INFSVFPGHQGGPHNHTITALAVALK.Q
303	318	3	1967.95	5.1	1	36.3	25.2	95.00%	K.QCQEPAYKEYQAQVVK.N	Carbamidomethyl (+57)	K.QCQEPAYKEYQAQVVK.N
129	142	2	1467.68	2.6	1	26	26.1	90.20%	D.LPSGGHLSHGYQTD.T		R.LMGLDLPSGGHLSHGYQTDTK.K
413	422	2	1075.61	4.3	0	49.9	20.1	95.00%	R.ALTFAANLQK.E		R.ALTFAANLQK.E
46	58	2	1321.64	4.2	1	41.4	25.2	95.00%	R.AVMDALGSVMSNK.Y		R.AVMDALGSVMSNK.Y
438	452	2	1729.9	3.9	0	75.9	23.1	95.00%	K.LGEGEQYPELVQLQK.E		K.LGEGEQYPELVQLQK.E
6	16	2	1273.66	2.2	2	32.2	23.1	95.00%	D.SIMLTPLKEQD.P		-.MSSNDSIMLTPLKEQDPTVAEIMR.H
124	142	2	1996.94	2.9	1	31.4	26.2	95.00%	R.LMGLDLPSGGHLSHGYQTD.T		R.LMGLDLPSGGHLSHGYQTDTK.K
436	452	2	1929.03	2.7	1	61.6	19.5	95.00%	K.AKLGEGEQYPELVQLQK.E		K.AKLGEGEQYPELVQLQK.E
146	161	2	1879.87	4.2	2	74.3	26.1	95.00%	K.ISAVSTYFESMPYRVD.P	Oxidation (+16)	K.ISAVSTYFESMPYRVDPNTGLIDYDMLEHDAQLFRPK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
13	SAHH_SCHPO	35.10%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
257	268	2	1355.63	3	0	52.5	25.2	95.00%	D.GFEVTTMEEAVK.E	Oxidation (+16)	R.VIVTEVDPINALQAAMDGFEVTTMEEAVK.E
174	183	2	1081.62	2.4	2	51.9	18.6	95.00%	K.LKVPAINVND.S		K.LKVPAINVNDSVTK.S
20	35	2	1782.93	3.6	0	76.2	22	95.00%	K.ELEIAENEMPGLIAVR.E		K.ELEIAENEMPGLIAVR.E
8	18	2	1118.61	3.2	1	77.1	20.1	95.00%	K.VADISLAAFGR.K		K.VADISLAAFGR.K
216	227	2	1117.62	4.3	1	46.5	20.9	95.00%	K.VAVVAGFGDVGK.G		K.VAVVAGFGDVGK.G
269	280	2	1367.66	4	0	40.1	24.9	95.00%	K.EGQIFVTTTGCR.D	Carbamidomethyl (+57)	K.EGQIFVTTTGCR.D
153	167	2	1647.82	4.5	0	70.1	24.4	95.00%	R.GISEETTTGVHNLYK.M		R.GISEETTTGVHNLYK.M
19	35	2	1911.02	1.5	1	95.5	20.6	95.00%	R.KELEIAENEMPGLIAVR.E		R.KELEIAENEMPGLIAVR.E
247	268	2	2364.14	1.3	1	96.8	24.9	95.00%	D.PINALQAAMDGFEVTTMEEAVK.E		R.VIVTEVDPINALQAAMDGFEVTTMEEAVK.E
176	187	2	1255.68	4.6	1	42.1	21.1	95.00%	K.VPAINVNDSVTK.S		K.VPAINVNDSVTK.S
336	344	2	1006.6	5	1	31.2	14.9	95.00%	R.HIILLADGR.L		R.HIILLADGR.L
103	118	2	2053.93	1.4	0	82.6	26.4	95.00%	K.GETEEEYLWCIEQQLK.S	Carbamidomethyl (+57)	K.GETEEEYLWCIEQQLK.S
133	143	2	1166.61	3	1	32	22.7	95.00%	D.GGDLTALVHER.H		K.SFPSGKPLNMILDDGGDLTALVHER.H
377	389	2	1455.76	2.7	0	33.2	22.5	95.00%	D.NTSYPLGVHMLPK.K		R.LVNLGCATGHPSFVMSCSFTNQVLAQIALWTDNTSYPLGVHMLPK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
14	THI2_SCHPO	49.39%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

234	242	2	981.48	3	0	28.7	23.4	95.00%	D.GPFGAFCVK.R	Carbamidomethyl (+57)	R.IAGVVTNWTLVSLNHGLQSCMDPNTINAHLVVSATGHDGPFGAFCVK.R
243	255	2	1422.76	2.6	2	30.4	20.4	95.00%	K.RLASAQLVSNLHD.M		K.RLASAQLVSNLHDMRPLDMNR.A
175	187	2	1431.8	2.6	1	65.5	18.5	95.00%	K.LFNATAVEDLIVK.E		K.LFNATAVEDLIVK.E
2	15	2	1400.77	3.8	0	74.5	20	95.00%	M.APATAVVTPQTAFK.T		-.MAPATAVVTPQTAFK.T
131	146	2	1818.91	1.9	1	45	24.6	95.00%	R.KPADLFLNEIGVPYED.E		R.KPADLFLNEIGVPYEDEGDYVVVK.H
39	55	2	1962.95	4.7	1	48.4	25.1	95.00%	K.AYPTYSLDESFSFAPIR.E		K.AYPTYSLDESFSFAPIR.E
155	166	2	1319.67	2.5	0	27.1	24.3	93.80%	K.HAALFTSTVMAR.T	Oxidation (+16)	K.HAALFTSTVMAR.T
244	255	2	1266.66	2	1	69.6	22.5	95.00%	R.LASAQLVSNLHD.M		R.LASAQLVSNLHDMRPLDMNR.A
218	233	2	1644.83	2.3	1	64.3	24.7	95.00%	D.PNTINAHLVVSATGHD.G		R.IAGVVTNWTLVSLNHGLQSCMDPNTINAHLVVSATGHDGPFGAFCVK.R
295	308	2	1459.67	2.7	0	78.3	26.4	95.00%	R.MGPTFGGMMFSGIK.A		R.MGPTFGGMMFSGIK.A
309	320	2	1332.68	5.8	1	60	23.7	95.00%	K.AAQEALAIFDER.K		K.AAQEALAIFDER.K
274	294	2	2254.05	3.3	1	79.8	26.6	95.00%	R.EVFPGMIVGGMELSEFDGANR.M		R.EVFPGMIVGGMELSEFDGANR.M
244	260	3	1878.97	2.9	1	30.2	22.9	95.00%	R.LASAQLVSNLHDMRPLD.M		R.LASAQLVSNLHDMRPLDMNR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
15	THI3_SCHPO	57.51%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
234	245	4	1551.81	2.5	1	22	21.7	95.00%	D.PVQTYKEYIHFK.R		K.DPVQTYKEYIHFK.R
155	169	2	1717.82	2.1	0	67.8	25.5	95.00%	D.GGIGIECMQQVELER.W	Carbamidomethyl (+57)	R.CGMNIAPAIINGEIDGGIGIECMQQVELER.W
74	95	2	2353.27	3.5	0	91.4	18.2	95.00%	R.GYPVTSFGSLLNEPFTGLITLK.G		R.GYPVTSFGSLLNEPFTGLITLK.G
316	327	2	1385.71	3.6	1	53.6	23.6	95.00%	K.QEAIAEIQDEIK.Q		K.QEAIAEIQDEIK.Q
312	324	2	1428.7	2	2	42	24.3	95.00%	D.PMGKQEAIAEIQD.E		K.DPMGKQEAIAEIQDEIK.Q
222	232	3	1198.64	1.4	1	32.7	21.5	95.00%	R.AIHSATLDMLK.D		R.AIHSATLDMLK.D
128	139	2	1325.67	4.2	1	42.4	23.3	95.00%	K.FGLSPSDYTAIR.C		K.FGLSPSDYTAIR.C
6	27	2	2631.39	2.4	0	78.6	19	95.00%	K.ITFLTNWEATPYHLPIFLAQTR.G		K.ITFLTNWEATPYHLPIFLAQTR.G
63	71	2	954.54	4.5	0	51.1	16.9	95.00%	K.AMIHTLAAK.A		K.AMIHTLAAK.A
110	118	2	968.5	4.9	0	27.7	22.1	94.50%	R.IGYVGEFGK.I		R.IGYVGEFGK.I
330	339	2	992.51	5.7	0	44.3	23.6	95.00%	K.GGVFSGNSLR.Y		K.GGVFSGNSLR.Y
189	211	3	2788.29	2.8	1	29.7	26	95.00%	R.LANLGCCCFCTILYIAHDEFIAK.H	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.LANLGCCCFCTILYIAHDEFIAK.H
33	56	2	2409.27	3	1	74.8	19.3	95.00%	R.EGIEVAILEPTNPSDVTALIGSGK.V		R.EGIEVAILEPTNPSDVTALIGSGK.V
260	273	2	1711.79	4.7	1	88.7	26.2	95.00%	R.CFAYFSHDISNVPR.D	Carbamidomethyl (+57)	R.CFAYFSHDISNVPR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
16	METK_SCHPO	51.57%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
90	103	2	1572.75	2.4	1	49.2	25.4	95.00%	K.TCNVLVAIEQQSPD.I	Carbamidomethyl (+57)	K.TCNVLVAIEQQSPDIAQGLHYEK.A
147	155	2	931.5	4.5	0	58	24	95.00%	K.LNAAMSVAR.R		K.LNAAMSVAR.R
2	18	2	1820.82	1.4	1	75.1	26.5	95.00%	M.AQTFLFTSESVGEGHPD.K		-.MAQTFLFTSESVGEGHPDK.I
237	251	2	1429.74	3.6	1	73.6	22.8	95.00%	R.FVVGGPQGDAGLTGR.K		R.FVVGGPQGDAGLTGR.K
339	349	2	1256.73	4.3	1	36.5	16.5	95.00%	K.NFDLRPGVLVK.S		K.NFDLRPGVLVK.S
189	198	2	1039.53	3.1	1	27.7	21.6	94.50%	D.TIVVSAQHAD.S		R.VDTIVVSAQHADSISTEDLR.S
90	112	3	2612.3	3.4	1	62.4	23.8	95.00%	K.TCNVLVAIEQQSPDIAQGLHYEK.A	Carbamidomethyl (+57)	K.TCNVLVAIEQQSPDIAQGLHYEK.A
328	338	2	1257.74	4.7	1	49.3	16.3	95.00%	K.TSAELVEIIRK.N		K.TSAELVEIIRK.N

353	378	3	3055.48	3	1	68	23.9	95.00%	K.LQTPFYLSTASYGHFTDQSKPWEQPK.E		K.LQTPFYLSTASYGHFTDQSKPWEQPK.E
257	272	2	1508.68	2.4	0	56.4	25.7	95.00%	D.TYGGWGAHGGGAFSGK.D		K.IIVDTYGGWGAHGGGAFSGK.D
291	299	2	856.52	4.2	0	28.1	19.7	94.90%	K.SLVAAGLAR.R		K.SLVAAGLAR.R
213	226	3	1572.93	4.6	1	37.1	12	95.00%	K.IIKPTVPAHLLDEK.T		K.IIKPTVPAHLLDEK.T
253	272	2	1948.95	4	1	80.8	25.2	95.00%	K.IIVDTYGGWGAHGGGAFSGK.D		K.IIVDTYGGWGAHGGGAFSGK.D
132	146	3	1702.01	3	1	22.9	12.3	93.90%	D.ETPEKLPLTILLAHK.L		K.ALEELGAGDQGIMFGYATDETPEKLPLTILLAHK.L
169	185	2	1946.97	4.5	0	49.1	24.4	95.00%	K.TQVTIEYEEENGAVIPR.R		K.TQVTIEYEEENGAVIPR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
17	HSP72_SCHPO	35.39%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
327	340	2	1400.77	3.9	0	39.7	20.8	95.00%	K.ASVNEIVLVGGSTR.I		K.ASVNEIVLVGGSTR.I
432	445	2	1584.83	2.6	0	60.4	22.5	95.00%	D.NQPGVLIQVFEGER.A		K.SEIFSTYSDNQPGVLIQVFEGER.A
111	124	2	1611.8	4	0	69	24	95.00%	K.TFTPEEISSMVLMK.M		K.TFTPEEISSMVLMK.M
97	110	2	1574.87	3.8	1	40.6	17.9	95.00%	D.GKPVLQVEYKGETK.T		K.DGKPVLQVEYKGETK.T
594	607	2	1556.83	4.2	1	73.7	21.3	95.00%	K.QKELESVANPIMAK.I		K.QKELESVANPIMAK.I
538	548	2	1351.66	4.4	0	37.5	24.8	95.00%	K.NHLESYAYSLR.N		K.NHLESYAYSLR.N
326	340	2	1528.86	2.3	1	37.6	18.3	95.00%	D.KASVNEIVLVGGSTR.I		K.VDKASVNEIVLVGGSTR.I
125	136	2	1324.65	4.5	1	66.6	24.8	95.00%	K.MRETAEAYLGGK.V		K.MRETAEAYLGGK.V
170	185	2	1686.9	4	1	94.1	20	95.00%	R.IINEPTAAAIAYGLDR.S		R.IINEPTAAAIAYGLDR.S
298	306	2	1109.48	2.7	2	26.1	25.5	91.70%	R.ARFEELCAD.L	Carbamidomethyl (+57)	R.ARFEELCADLFR.K
55	69	2	1698.82	4.2	1	74.8	25.4	95.00%	K.NQVAMNPHNTIFDAK.R		K.NQVAMNPHNTIFDAK.R
457	467	2	1182.65	4.4	0	28.3	19.9	95.00%	K.FELSGIPPAPR.G		K.FELSGIPPAPR.G
235	244	2	1273.69	4.3	0	25.1	21.4	90.60%	R.LVNHFIQEFK.R		R.LVNHFIQEFK.R
35	47	2	1486.7	4.2	1	60.5	25.7	95.00%	R.TTPSYVAFTDTER.L		R.TTPSYVAFTDTER.L
608	647	3	3515.61	5.3	1	39.6	25.6	95.00%	K.IYQAGGAPGGMPGAAPGAAPGAAPGAAPGAAPGGDNGPEVEEVD.-	Oxidation (+16)	K.IYQAGGAPGGMPGAAPGAAPGAAPGAAPGAAPGGDNGPEVEEVD.-
24	34	2	1227.63	5.8	1	33.2	23.4	95.00%	R.VEIIANDQGNR.T		R.VEIIANDQGNR.T
422	431	2	1175.54	2.4	2	29.8	25.6	95.00%	K.KSEIFSTYSD.N		K.KSEIFSTYSDNQPGVLIQVFEGER.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
18	A1EGU1_SCHPO	27.79%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
408	429	3	2504.31	-0.0051	1	41.9	20.8	95.00%	K.HVERPIIFPISNPTTLMEAKPD.Q		K.HVERPIIFPISNPTTLMEAKPDQIDK.W
457	479	2	2580.33	2.4	0	74	21.5	95.00%	K.YVISQCNNALLYPALGVACVLSR.C	Carbamidomethyl (+57)/Carbamidomethyl (+57)	K.YVISQCNNALLYPALGVACVLSR.C
44	57	2	1634.91	4.4	1	89.1	17.2	95.00%	R.LPPIVETLQQQVDR.C		R.LPPIVETLQQQVDR.C
373	396	3	2478.39	2.2	0	37.8	13.4	95.00%	D.INLESAIALVKPTILLGCSGQPGK.F	Carbamidomethyl (+57)	K.EVPSGDINLESAIALVKPTILLGCSGQPGK.F
439	452	2	1418.83	4.1	0	43.8	10.4	95.00%	K.ALIATGSPLPPLNR.N		K.ALIATGSPLPPLNR.N
367	396	3	3062.64	3.1	1	30.5	17.2	95.00%	K.EVPSGDINLESAIALVKPTILLGCSGQPGK.F	Carbamidomethyl (+57)	K.EVPSGDINLESAIALVKPTILLGCSGQPGK.F
490	500	2	1070.58	4.5	1	54.7	21.7	95.00%	K.AASDALATVPR.S		K.AASDALATVPR.S
15	23	2	955.55	4.9	0	32.8	19.7	95.00%	K.GVTLLNSPR.Y		K.GVTLLNSPR.Y
548	555	2	1085.63	3.7	1	31.8	19.3	95.00%	K.LKEWIIER.E		K.LKEWIIER.E
332	339	2	964.49	5	1	34.3	22.8	95.00%	R.GNLFMIDR.C		R.GNLFMIDR.C
456	479	3	2708.42	0.74	1	29.2	18.8	95.00%	K.KYVISQCNNALLYPALGVACVLSR.C	Carbamidomethyl (+57)/Carbamidomethyl (+57)	K.KYVISQCNNALLYPALGVACVLSR.C
178	191	2	1553.75	3.5	1	59.3	25.4	95.00%	K.GHLMTLCAGLDPNR.F	Carbamidomethyl (+57)	K.GHLMTLCAGLDPNR.F
408	432	3	2860.48	-0.14	1	31.8	21.1	95.00%	K.HVERPIIFPISNPTTLMEAKPDQID.K		K.HVERPIIFPISNPTTLMEAKPDQIDK.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
19	HSP90_SCHPO	21.88%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
275	289	2	1790.84	4	1	67.8	26.1	95.00%	R.NPSEVTKEEYASFYK.S		R.NPSEVTKEEYASFYK.S
465	474	2	1170.6	4.5	0	29.7	22.3	95.00%	K.NIYFITGESK.Q		K.NIYFITGESK.Q
567	587	2	2339.12	5.7	0	92.3	25.1	95.00%	K.IVGSPCLLTTGQYGWSANMER.I	Carbamidomethyl (+57)	K.IVGSPCLLTTGQYGWSANMER.I
369	375	2	811.49	1.9	0	27.5	18.1	94.20%	D.LPLNLSR.E		K.GVVDSEDLPLNLSR.E
596	606	2	1234.5	4.9	1	67.2	25.9	95.00%	R.DTSMSAYMSSR.K		R.DTSMSAYMSSR.K
475	487	2	1548.8	4.5	0	76.3	22.9	95.00%	K.QAVENSPFLEIFR.A		K.QAVENSPFLEIFR.A
88	99	2	1282.73	5.3	1	55.5	17.6	95.00%	K.NDLINNLGVIAK.S		K.NDLINNLGVIAK.S
255	267	2	1520.76	4.6	1	46.2	24.1	95.00%	K.VKETTTETEELNK.T		K.VKETTTETEELNK.T
197	212	3	1916.06	1.7	1	25.7	18.3	95.00%	K.KHSEFISYPIQLVVTR.E		K.KHSEFISYPIQLVVTR.E
198	212	2	1787.96	4	0	47.5	20	95.00%	K.HSEFISYPIQLVVTR.E		K.HSEFISYPIQLVVTR.E
422	436	2	1574.86	4	1	34.5	19.4	95.00%	K.LGIHEDAANRPALAK.L		K.LGIHEDAANRPALAK.L
180	189	2	1293.62	4.9	1	25.4	25.6	90.00%	K.EDQLQYLEEK.T		K.EDQLQYLEEK.T
499	509	2	1275.67	2.5	1	54.9	22.1	95.00%	D.PIDEYAVTQLK.E		K.FDVLFMVDPIDEYAVTQLK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
20	K6PF_SCHPO	29.62%	100%	22

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
364	380	3	1831.88	4.2	1	50.7	25.7	95.00%	R.ICEAVDSISSTAISHSR.A	Carbamidomethyl (+57)	R.ICEAVDSISSTAISHSR.A
613	628	3	1700.87	4.5	1	49.7	22.8	95.00%	R.GHTPLAIDNGFSGFLR.H		R.GHTPLAIDNGFSGFLR.H
822	839	4	2058.08	3.2	1	52.7	20.5	95.00%	K.VYTTEVIGNIISEEAHKR.F		K.VYTTEVIGNIISEEAHKR.F
419	431	2	1592.73	4.2	1	27.5	26.3	92.50%	K.WQDELCNSLSSVR.K	Carbamidomethyl (+57)	K.WQDELCNSLSSVR.K
21	31	2	1419.67	2	1	38.5	25.3	95.00%	D.TYNQTLDFYQK.L		-.MSGETVHGISCYSVVANTEDTYNQTLDFYQK.L
138	148	2	1187.63	2.3	1	44.3	22.9	95.00%	D.PLGNLIGFSDR.Y		K.KPDEVYVEDPLGNLIGFSDR.Y
586	603	3	1736.9	2.4	0	64.1	21.6	95.00%	R.VAIIHVGAPAGGMNSATR.A	Oxidation (+16)	R.VAIIHVGAPAGGMNSATR.A
503	522	2	1996.04	2.5	1	40.8	22.4	95.00%	D.AVLASTPDTPSPMIAINGNK.I		R.MLATLQGVDAVDAVLASTPDTPSPMIAINGNK.I
511	522	2	1241.65	2.5	0	27.4	22.7	94.10%	D.TPSPMIAINGNK.I		R.MLATLQGVDAVDAVLASTPDTPSPMIAINGNK.I
160	183	3	2416.24	3.9	1	44	20.9	95.00%	K.SEESGAASNLESGLATPVVETLKK.A		K.SEESGAASNLESGLATPVVETLKK.A
908	918	2	1362.61	4	0	47.2	25.7	95.00%	D.VENNETEIEMR.R		R.GTGVSFSSVADVENNETEIEMR.R
798	806	2	934.49	4	0	31.5	22.6	95.00%	K.ATFALEAGR.N		K.ATFALEAGR.N
523	533	2	1297.76	2.5	1	27.3	16	94.00%	K.INRKPLMEAVK.L		K.INRKPLMEAVK.L
299	308	2	1035.54	2.1	1	61.4	22.4	95.00%	D.GSLTGADIFR.S		K.NLISAGIDSIIVCGGDGSLTGADIFR.S
254	267	2	1400.75	3.4	0	49.7	22	95.00%	R.GWLAEGGTLIGTAR.C		R.GWLAEGGTLIGTAR.C
844	861	2	1860.9	4.7	1	42.3	25.5	95.00%	R.TAVPGHVQQGGNPTPMDR.A		R.TAVPGHVQQGGNPTPMDR.A
927	938	2	1323.7	4.7	1	53.3	21.2	95.00%	R.DMHNLVNILAGK.T		R.DMHNLVNILAGK.T
77	94	2	1954.97	2.7	1	65	24	95.00%	R.LVPGELSLSPAAEDSEWR.G		R.LVPGELSLSPAAEDSEWR.G
197	214	2	1760.86	4.1	1	84.8	25	95.00%	K.IAVMTSGGDSPGMNAVVR.A		K.IAVMTSGGDSPGMNAVVR.A
844	860	2	1704.79	2.2	1	31.8	26.2	95.00%	R.TAVPGHVQQGGNPTPMD.R		R.TAVPGHVQQGGNPTPMDR.A
822	838	2	1901.98	1.1	0	64.8	22.9	95.00%	K.VYTTEVIGNIISEEAHK.R		K.VYTTEVIGNIISEEAHK.R
887	896	2	997.6	3.2	0	55.1	17.2	95.00%	D.PSSAVVIGIR.G		R.ANDLGNDPSSAVVIGIR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
21	EF3_SCHPO	21.49%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
333	350	2	1970.01	4.8	0	86.5	22.4	95.00%	K.IPEVSTAANPEVCLETLK.A	Carbamidomethyl (+57)	K.IPEVSTAANPEVCLETLK.A
35	59	2	2604.32	3.9	1	66.4	22.4	95.00%	K.ALASFVNGPIEEQDAPSQVFSAISK.Q		K.ALASFVNGPIEEQDAPSQVFSAISK.Q
351	367	2	1809.03	4.2	1	72.9	15.3	95.00%	K.AVLGEIKVPTNEEVIAK.Y		K.AVLGEIKVPTNEEVIAK.Y
961	994	3	3666.67	2.8	0	62.6	25.7	95.00%	R.EFTEGLTEEVWAVNNGHMTPSGHNWVSGQGSGPR.I		R.EFTEGLTEEVWAVNNGHMTPSGHNWVSGQGSGPR.I
281	294	2	1550.88	4.1	1	60.5	15.8	95.00%	K.LVEDPQVVAPFLPK.L		K.LVEDPQVVAPFLPK.L

757	765	2	1178.58	7.8	0	24.9	24.4	90.20%	K.TPSEYIQWR.F		K.TPSEYIQWR.F
89	103	2	1652.98	2.5	0	36.7	6.99	95.00%	D.VEPYLVELLPAVIAK.V		K.GLEAVANHGSVAADVEPYLVELLPAVIAK.V
479	493	2	1636.88	3.9	0	73.9	21.1	95.00%	R.AIVNGQVEGFPTHLR.T		R.AIVNGQVEGFPTHLR.T
285	294	2	1095.64	2.8	0	27.2	17	93.90%	D.PQVVAPFLPK.L	Deamidation (+1)	K.LVEDPQVVAPFLPK.L
419	447	3	3168.34	2.9	1	77.1	27.1	95.00%	K.IPGGASHAEEEEEGEDLCNCEFSLAYGAK.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.IPGGASHAEEEEEGEDLCNCEFSLAYGAK.I
75	103	3	2944.6	3.2	1	47.9	16	95.00%	K.GLEAVANHGSVAADVEPYLVELLPAVIAK.V		K.GLEAVANHGSVAADVEPYLVELLPAVIAK.V
133	147	2	1550.87	1.9	0	70.7	16.7	95.00%	K.AIVPSVLESIHTTGK.W		K.AIVPSVLESIHTTGK.W
881	900	3	2293.11	2.6	1	44.8	25.5	95.00%	K.EIEEHCSLLGLDAELVSHSR.I	Carbamidomethyl (+57)	K.EIEEHCSLLGLDAELVSHSR.I
358	367	2	1098.6	4.8	0	47.3	21.4	95.00%	K.VPTNEEVIAK.Y		K.VPTNEEVIAK.Y
35	48	2	1488.71	2.5	1	42.3	25.3	95.00%	K.ALASFVNGPIEEQD.A		K.ALASFVNGPIEEQDAPSQVFSAISK.Q
49	59	2	1133.61	2.5	0	32.7	21.9	95.00%	D.APSQVFSAISK.Q		K.ALASFVNGPIEEQDAPSQVFSAISK.Q
75	88	2	1309.63	3.2	1	25.4	24.9	91.20%	K.GLEAVANHGSVAAD.V		K.GLEAVANHGSVAADVEPYLVELLPAVIAK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
22	6PGD_SCHPO	30.49%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
386	403	3	2088.07	1.7	0	29.6	22.4	95.00%	D.PNLESILFHPFFTNGVEK.A		R.EDPNLESILFHPFFTNGVEK.A
156	166	3	1228.76	4.8	0	32.1	8.45	95.00%	R.IKPIFQTLAAK.A		R.IKPIFQTLAAK.A
42	51	2	1134.56	4.5	1	47.7	24.6	95.00%	R.VDEFLANEAK.G		R.VDEFLANEAK.G
123	139	2	1590.81	3.9	0	62.7	23.7	95.00%	K.GILFVGSGVSGGEEGAR.Y		K.GILFVGSGVSGGEEGAR.Y
140	155	2	1669.81	4.7	0	28.8	25.5	95.00%	R.YGPSLMPGGNPAAWPR.I		R.YGPSLMPGGNPAAWPR.I
269	291	2	2504.28	3.2	0	92.8	22.1	95.00%	K.WTAQNALEMGTPVSLITEAVFAR.C		K.WTAQNALEMGTPVSLITEAVFAR.C
437	449	2	1379.79	4.1	0	52	15.2	95.00%	R.SAVLPANLLQAQR.D		R.SAVLPANLLQAQR.D
80	97	2	1925.1	4.4	1	58.2	14.1	95.00%	K.AGKPVDYLIEGLAPLLEK.G		K.AGKPVDYLIEGLAPLLEK.G
54	67	2	1501.78	2.4	0	63.3	22.6	95.00%	K.SIVGAHSLEEFVSK.L		K.SIVGAHSLEEFVSK.L
86	97	2	1357.79	1.8	0	38.5	16.9	95.00%	D.YLIEGLAPLLEK.G		K.AGKPVDYLIEGLAPLLEK.G
29	37	2	1175.49	3.9	0	36.7	25.7	95.00%	K.GFTVCCYNR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GFTVCCYNR.T
122	139	2	1718.9	1.9	1	90.2	22.2	95.00%	K.KGILFVGSGVSGGEEGAR.Y		K.KGILFVGSGVSGGEEGAR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
23	ILV5_SCHPO	29.46%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
84	104	2	2141.07	4.6	1	90.4	23.6	95.00%	K.NDTLAIIGYGSQGHGQGLNAR.D		K.NDTLAIIGYGSQGHGQGLNAR.D
330	337	2	914.47	6	1	41.2	22.8	95.00%	R.GAIDWTPR.F		R.GAIDWTPR.F
314	328	2	1725.76	3.8	1	69	27.3	95.00%	K.YGLDYMFAACSTTAR.R	Carbamidomethyl (+57)	K.YGLDYMFAACSTTAR.R
145	163	2	2074.05	4.2	1	75.2	22.9	95.00%	K.GSIIMNLLSDAAQTETWPK.I		K.GSIIMNLLSDAAQTETWPK.I
86	104	2	1911.99	1.5	0	55.1	21.8	95.00%	D.TLAIIGYGSQGHGQGLNAR.D		K.NDTLAIIGYGSQGHGQGLNAR.D
362	372	2	1312.61	4.6	0	61.6	25.4	95.00%	R.SLEYNSAPNYR.E		R.SLEYNSAPNYR.E
289	313	2	2687.32	3.5	0	76.3	24.4	95.00%	R.GHSPAEAFNETVEEATQSLYPLIGK.Y		R.GHSPAEAFNETVEEATQSLYPLIGK.Y
318	328	2	1277.56	1.7	0	26.6	25.8	91.90%	D.YMFAACSTTAR.R	Carbamidomethyl (+57)	K.YGLDYMFAACSTTAR.R
123	133	2	1198.6	4.3	1	28.6	23.2	95.00%	K.QAIEDGWVPGK.T		K.QAIEDGWVPGK.T
196	204	2	952.6	2.5	1	51.1	13.6	95.00%	D.VDVILVAPK.G		K.DVDVILVAPK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
24	EF2_SCHPO	20.07%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
272	283	2	1498.77	4.2	1	53.9	23.1	95.00%	R.AFNMFILDPIYR.I		R.AFNMFILDPIYR.I
466	479	2	1474.71	3.7	0	72.8	24.8	95.00%	K.SGTLTTSEVAHNMK.V		K.SGTLTTSEVAHNMK.V

811	823	3	1441.74	1.9	0	40	23	95.00%	D.PTSKPGQIVCEAR.K	Carbamidomethyl (+57)	R.QATAGQAFPQLVFDHWSPMSGDPLDPTSKPGQIVCEAR.K
565	578	2	1451.69	4.3	0	44.5	25.6	95.00%	R.ESVSEPSSMTALSK.S		R.ESVSEPSSMTALSK.S
284	292	2	1051.52	4.5	1	27.5	23.6	94.30%	R.IFDAVMNSR.K		R.IFDAVMNSR.K
244	253	2	1266.61	5.9	0	30	24.9	95.00%	R.LWGENYFNPK.T		R.LWGENYFNPK.T
770	785	2	1798.9	4	0	39.1	23.6	95.00%	K.AYLPVNESFGFTGELR.Q		K.AYLPVNESFGFTGELR.Q
151	161	3	1236.76	1.9	2	28	9.54	95.00%	R.IRPVVVVNKVD.R		R.IRPVVVVNKVDR.A
371	384	2	1594.76	4.1	1	55	25.8	95.00%	R.NCDANAPLMIYVSK.M	Carbamidomethyl (+57)	R.NCDANAPLMIYVSK.M
327	346	2	2192.18	2.4	1	55.9	18.3	95.00%	K.FLPAADALMEMIVLHLPSPK.T		K.FLPAADALMEMIVLHLPSPK.T
640	651	2	1231.65	4	1	32.5	22.5	95.00%	D.TTGANVVVDQTK.A		K.IWCFGPDTTGANVVVDQTK.A
586	609	3	2657.29	3.5	0	32.6	24.6	95.00%	R.IFMTAEPMSEELSVAIETGHVNPR.D		R.IFMTAEPMSEELSVAIETGHVNPR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
25	TKT_SCHPO	32.70%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
306	318	2	1423.73	4.8	1	73.3	23.1	95.00%	R.VAIASSAEEEYKK.M		R.VAIASSAEEEYKK.M
325	336	2	1449.68	6.5	1	28.4	25.4	94.80%	K.QSYPDLSNQLER.I	Deamidation (+1)	K.QSYPDLSNQLER.I
238	252	2	1719.86	5	1	57.2	24.7	95.00%	R.EAMSCTDKPTLINLK.T	Carbamidomethyl (+57)	R.EAMSCTDKPTLINLK.T
395	407	2	1418.65	3.9	1	52.7	25.9	95.00%	R.WEGAADFQPPSSK.L		R.WEGAADFQPPSSK.L
653	663	2	1249.63	3.9	0	24.8	24.4	90.00%	K.FHFTTSGVAQR.A		K.FHFTTSGVAQR.A
481	494	3	1636.81	1.6	0	44.8	24.3	95.00%	D.GPTHQPIETFAHFR.A		R.VIYVATHDSIGLGEDGPTHQPIETFAHFR.A
182	193	2	1385.74	4.7	1	41.9	21.6	95.00%	K.LSNLIAVWDNNK.I		K.LSNLIAVWDNNK.I
532	547	2	1810.95	4.2	0	72.5	21.2	95.00%	R.QNLPQLENSTIENALK.G		R.QNLPQLENSTIENALK.G
589	606	2	2252.07	4.5	0	58.5	26.1	95.00%	R.VVSLPCWEVFEQQPESYR.L	Carbamidomethyl (+57)	R.VVSLPCWEVFEQQPESYR.L
630	648	3	2046.93	3.6	1	34	26.8	95.00%	R.YVHEAFGMHTFGDSGPAPK.L		R.YVHEAFGMHTFGDSGPAPK.L
163	181	3	2001.93	2.7	0	26.7	26.5	95.00%	D.GCLQEGVSSEACSLAGHLK.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.AHSAAVYNKPGFDLFSNYTFCFLGDGCLQEGVSSEACSLAGHLK.L
253	281	3	3132.54	2.9	1	59.8	23.5	95.00%	K.TTIGYGSELQGTHSVHGSPLKPEDCVHVK.K	Carbamidomethyl (+57)	K.TTIGYGSELQGTHSVHGSPLKPEDCVHVK.K
291	303	2	1603.8	4	0	26.8	24.3	93.30%	K.TFQVPPEVYAYYK.E		K.TFQVPPEVYAYYK.E
30	49	3	1972.01	2.1	0	48.7	22.2	95.00%	K.SGHPGAPMGLAPAAHVLFSR.I		K.SGHPGAPMGLAPAAHVLFSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
26	ACT_SCHPO	37.07%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
223	238	2	1794.87	2.4	0	95	25.1	95.00%	D.FEQELQTAAQSSSLEK.S		K.LCYVALDFEQELQTAAQSSSLEK.S
245	254	2	1085.59	2.6	0	33.7	21.9	95.00%	D.GQVITIGNER.F		K.SYELPDGQVITIGNER.F
1	18	2	2007.9	4	1	79.9	26.2	95.00%	-.MEEEIAALVIDNGSGMCK.A	Acetyl (+42)/ Carbamidomethyl (+57)	-.MEEEIAALVIDNGSGMCK.A
255	284	3	3274.66	3.2	1	82.1	20.8	95.00%	R.FRAPEALFQPSALGLENAGIHEATYNSIMK.C		R.FRAPEALFQPSALGLENAGIHEATYNSIMK.C
85	95	3	1514.75	5.5	0	36	24.5	95.00%	K.IWHHTFYNELR.V		K.IWHHTFYNELR.V
96	113	2	2014.03	3.9	0	59.4	23.1	95.00%	R.VAPEEHPCLLTEAPLNPK.S	Carbamidomethyl (+57)	R.VAPEEHPCLLTEAPLNPK.S
197	206	2	1131.53	5.1	0	41.4	25.5	95.00%	R.GYTFSTTAER.E		R.GYTFSTTAER.E
239	254	2	1789.89	5.1	1	75.2	24.6	95.00%	K.SYELPDGQVITIGNER.F		K.SYELPDGQVITIGNER.F
216	238	2	2629.27	3.5	1	106	24.9	95.00%	K.LCYVALDFEQELQTAAQSSSLEK.S	Carbamidomethyl (+57)	K.LCYVALDFEQELQTAAQSSSLEK.S
360	372	2	1511.7	3.8	1	34.6	25.7	95.00%	K.QEYDESGPGIVYR.K		K.QEYDESGPGIVYR.K
257	284	3	2971.48	3	0	43.9	22	95.00%	R.APEALFQPSALGLENAGIHEATYNSIMK.C		R.APEALFQPSALGLENAGIHEATYNSIMK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
27	G6PI_SCHPO	30.18%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
217	228	2	1343.61	5.2	0	37.3	25.9	95.00%	K.TFTTAETCTNAK.S	Carbamidomethyl (+57)	K.TFTTAETCTNAK.S

206	216	2	1218.69	2.5	0	61	18.6	95.00%	D.PETTLFLIASK.T		K.CDPETTLFLIASK.T
372	382	2	1171.52	5.1	1	67.7	25.4	95.00%	R.SGDMVNYTTGK.I		R.SGDMVNYTTGK.I
406	422	2	1903.01	2.4	1	26.4	20.5	92.80%	K.LIPADFLIPIESHNPID.N		K.LIPADFLIPIESHNPIDNNK.H
464	477	2	1502.83	4	0	36.9	18.9	95.00%	K.TFVGNRPSNSIIAK.K		K.TFVGNRPSNSIIAK.K
63	75	2	1499.85	3.9	0	37.5	16.9	95.00%	K.NLITEETVELLVK.L		K.NLITEETVELLVK.L
2	24	2	2548.27	3.8	0	60.7	22.8	95.00%	M.SFSLASTLPAWQAVQTHYESVGK.H	Acetyl (+42)	-.MSFSLASTLPAWQAVQTHYESVGK.H
118	128	2	1170.59	4.1	1	35.5	22.8	95.00%	K.VNGQDVMPGVR.K		K.VNGQDVMPGVR.K
204	216	2	1493.75	4.3	1	51.5	24.3	95.00%	K.CDPETTLFLIASK.T	Carbamidomethyl (+57)	K.CDPETTLFLIASK.T
54	62	2	1022.55	1.7	1	35.3	22.2	95.00%	D.GPILFDFSK.N		K.EEDGPILFDFSK.N
429	445	2	1870.94	4.8	0	69.7	24.3	95.00%	R.MLFSNFAAQTEALMLGK.T		R.MLFSNFAAQTEALMLGK.T
353	367	2	1711.83	4.2	0	71.8	24.8	95.00%	R.FPAYLQQLSMESNGK.A		R.FPAYLQQLSMESNGK.A
537	547	2	1192.65	3.5	0	25.2	20.3	90.80%	D.SSTNGLINLFK.N		K.GDVENHDSSTNGLINLFK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
28	TSA1_SCHPO	45.83%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	147	2	1224.69	4.4	1	43.5	18.1	95.00%	R.QITINDLPVGR.S		R.QITINDLPVGR.S
155	175	3	2525.19	2.7	1	39.8	25.5	95.00%	R.LLDAFQFVEEHGEVCPANWHK.G	Carbamidomethyl (+57)	R.LLDAFQFVEEHGEVCPANWHK.G
158	175	3	2183.99	2.6	0	40.2	27	95.00%	D.AFQFVEEHGEVCPANWHK.G	Carbamidomethyl (+57)	R.LLDAFQFVEEHGEVCPANWHK.G
125	132	2	901.53	4.7	1	35.7	20.3	95.00%	R.GLFLIDPK.G		R.GLFLIDPK.G
66	88	2	2576.29	0.89	1	97.3	23.4	95.00%	R.NAQVILTSTDSEYSHLAFINTPR.K		R.NAQVILTSTDSEYSHLAFINTPR.K
14	26	2	1333.69	3.6	0	40.1	22.9	95.00%	K.GTAVVNGAFEEIK.L		K.GTAVVNGAFEEIK.L
76	88	2	1533.76	2.9	0	70.1	24.1	95.00%	D.SEYSHLAFINTPR.K		R.NAQVILTSTDSEYSHLAFINTPR.K
2	13	2	1341.74	4.1	1	36.9	20.8	95.00%	M.SLQIGKPAPDFK.G	Acetyl (+42)	-.MSLQIGKPAPDFK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
29	HSP75_SCHPO	31.65%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	173	2	1168.66	5	1	34.3	18.9	95.00%	K.DAGAIAGLNVLR.I		K.DAGAIAGLNVLR.I
501	517	3	1779.92	5.5	0	60.6	22	95.00%	R.SAHIEITNSVGHLSSTK.I		R.SAHIEITNSVGHLSSTK.I
451	472	2	2468.2	5.8	0	62.2	24.8	95.00%	R.VNCAENEPLGEFQLTGIPPMPR.G	Carbamidomethyl (+57)	R.VNCAENEPLGEFQLTGIPPMPR.G
437	450	2	1638.8	1.8	0	46.9	24.4	95.00%	D.NQTTVTFPVYQGER.V		R.TFTTVADNQTTVTFPVYQGER.V
144	157	2	1552.8	4.6	1	33.7	23	95.00%	K.AVITVPAYFSDSQR.A		K.AVITVPAYFSDSQR.A
336	344	2	900.54	2.5	0	36	17.6	95.00%	D.IVLVGGSTR.I		K.ADVHDIVLVGGSTR.I
115	128	2	1565.81	1.4	0	60	22.4	95.00%	K.QFTAQEISAMVLTK.M		K.QFTAQEISAMVLTK.M
543	564	2	2513.21	3.3	0	64.4	25	95.00%	K.SQLESYISNIETTISEPNVMMK.L		K.SQLESYISNIETTISEPNVMMK.L
174	190	2	1729.93	3.9	1	82.9	19.8	95.00%	R.IINEPTAAAIAYGLDAK.S		R.IINEPTAAAIAYGLDAK.S
288	301	2	1482.73	2.1	1	73.2	25.5	95.00%	D.SLSNGIDFSSSITR.A		R.ALSSVTQTTVEVDSLSNGIDFSSSITR.A
114	128	2	1693.91	1.9	1	61.9	19.6	95.00%	K.KQFTAQEISAMVLTK.M		K.KQFTAQEISAMVLTK.M
39	51	2	1484.72	4.2	0	50.9	25.5	95.00%	R.TTPSFVAFTETER.L		R.TTPSFVAFTETER.L
430	450	2	2374.16	5.6	1	61.9	24.3	95.00%	R.TFTTVADNQTTVTFPVYQGER.V		R.TFTTVADNQTTVTFPVYQGER.V
96	113	2	1987.03	4.2	1	58.5	20.8	95.00%	K.VIDNNGIPTIEVNYLGEK.K		K.VIDNNGIPTIEVNYLGEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
30	IPYR_SCHPO	43.94%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
257	275	2	1874.97	3.1	1	39.6	22.3	95.00%	D.PSVSSTIPPAQELAPAPVD.P		K.SDFSLVNVSVTGSVANDPSVSSTIPPAQELAPAPVDPSVHK.W
186	192	2	922.44	6	0	35.4	25.3	95.00%	R.ATNEWFR.I		R.ATNEWFR.I

84	113	4	3616.64	3.2	1	34.2	25.8	95.00%	R.NCFPHHGYIWNYGAFPQTYEDPNVVHPETK.A	Carbamidomethyl (+57)	R.NCFPHHGYIWNYGAFPQTYEDPNVVHPETK.A
24	42	2	2112.04	4.6	1	50.5	24.5	95.00%	K.NGTPISSWHDIPLYANAEK.T		K.NGTPISSWHDIPLYANAEK.T
8	23	2	1839.93	4.1	1	74	23.1	95.00%	R.EVGALNTLDYQVYVEK.N		R.EVGALNTLDYQVYVEK.N
199	212	2	1556.7	2.9	0	37.4	26.7	95.00%	D.GKPENSFAFSGECK.N	Carbamidomethyl (+57)	K.IPDGKPENSFAFSGECK.N
120	130	2	1257.61	2.3	1	62.2	25	95.00%	D.PLDVCEIGEAR.G	Carbamidomethyl (+57)	K.GDSDPLDVCEIGEAR.G
43	53	2	1283.73	4	0	66.7	18.6	95.00%	K.TILNMVVEIPR.W		K.TILNMVVEIPR.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
31	GPD1_SCHPO	42.60%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
222	232	2	954.59	2.2	0	30.2	16.4	95.00%	D.VAGVALGGALK.N		R.EQIAAVFDRPYFSVVSVDDVAGVALGGALK.N
164	182	2	1962.01	3.3	0	81.7	22.7	95.00%	K.LGIYCGVLSGANVANEVAR.E	Carbamidomethyl (+57)	K.LGIYCGVLSGANVANEVAR.E
2	20	2	1989	3.8	1	99.4	23.8	95.00%	M.SGYGQQGVSAANIDSIRPK.K	Acetyl (+42)	-.MSGYGQQGVSAANIDSIRPK.K
87	104	2	2008.05	3	1	51.2	20.6	95.00%	K.YLPGIECPPNVIAVPDVR.E	Carbamidomethyl (+57)	K.YLPGIECPPNVIAVPDVR.E
310	331	3	2285.26	3	1	24.3	15.7	95.00%	K.SLETLEKELLGGQLLQGAATSK.D		K.SLETLEKELLGGQLLQGAATSK.D
277	296	2	2153	2.6	1	93.8	26.1	95.00%	R.TMVEQSCGIADLVTSCLGGR.N	Carbamidomethyl (+57)/Carbamidomethyl (+57)	R.TMVEQSCGIADLVTSCLGGR.N
183	202	2	2362.1	3.9	1	116	26.4	95.00%	R.EQFCETTIGFNPPNEVDIPR.E	Carbamidomethyl (+57)	R.EQFCETTIGFNPPNEVDIPR.E
288	296	2	961.5	2.9	0	27.2	22.3	94.00%	D.LVTSCLGGR.N	Carbamidomethyl (+57)	R.TMVEQSCGIADLVTSCLGGR.N
73	86	2	1656.85	1.7	1	64.4	23.1	95.00%	R.KLTEVFNEAHENVK.Y		R.KLTEVFNEAHENVK.Y
74	86	2	1528.76	4.4	0	69.8	24.9	95.00%	K.LTEVFNEAHENVK.Y		K.LTEVFNEAHENVK.Y
125	144	3	2172.13	2.1	1	28.9	21.9	95.00%	R.VCDQMVGLIRPGAVGISCIK.G	Carbamidomethyl (+57)/Carbamidomethyl (+57)	R.VCDQMVGLIRPGAVGISCIK.G
317	331	2	1484.83	3.6	0	57.3	19.2	95.00%	K.ELLGGQLLQGAATSK.D		K.ELLGGQLLQGAATSK.D
221	232	2	1069.62	1.8	1	29.5	19	95.00%	D.DVAGVALGGALK.N		R.EQIAAVFDRPYFSVVSVDDVAGVALGGALK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
32	HSP60_SCHPO	28.69%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
112	128	2	1705.86	4.1	1	84.3	24	95.00%	K.TNEVAGDGTTTATVLTR.A		K.TNEVAGDGTTTATVLTR.A
137	148	2	1316.6	4	1	27.4	26.3	92.30%	R.NVAAGCNPMDLR.R	Carbamidomethyl (+57)	R.NVAAGCNPMDLR.R
437	453	2	1588.85	4.6	0	29.9	21.1	95.00%	K.AAVSEGVLPGAGTSFVK.A		K.AAVSEGVLPGAGTSFVK.A
244	256	2	1529.84	1.9	0	69.9	19.8	95.00%	K.VEFENPLILLSEK.K		K.VEFENPLILLSEK.K
478	500	3	2377.34	2.3	0	32.6	14.6	95.00%	K.AITRPAQTILENAGLEGNLIVGK.L		K.AITRPAQTILENAGLEGNLIVGK.L
241	256	2	1873.03	3	1	68.5	17.8	95.00%	K.SQKVEFENPLILLSEK.K		K.SQKVEFENPLILLSEK.K
68	79	2	1313.7	4.3	1	39.3	21.4	95.00%	R.NVLIDQPFGSPK.I		R.NVLIDQPFGSPK.I
387	396	2	1249.62	3.9	1	34	24.2	95.00%	D.PNLTEYEKEK.L		R.GVMADPNLTEYEKEK.L
258	275	2	1937.07	4.4	1	74.7	17.7	95.00%	K.VSAVQDILPSLELAAQQR.R		K.VSAVQDILPSLELAAQQR.R
229	240	2	1401.72	4.3	1	35	22.8	95.00%	R.GYISPYFITDVK.S		R.GYISPYFITDVK.S
343	360	3	1921.9	2.8	2	32.7	26.3	95.00%	K.AQPHHLGSCGSVTVTKED.T	Carbamidomethyl (+57)	K.AQPHHLGSCGSVTVTKEDTIIMK.G
45	56	2	1215.69	4.9	1	52.6	18.6	95.00%	R.ASLLTGVDTLAR.A		R.ASLLTGVDTLAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
33	PUR9_SCHPO	27.35%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
332	347	2	1697.93	2.3	0	25.7	18.7	91.80%	D.GVIAPGYEPEALELLK.K		R.EVSDGVIAPGYEPEALELLK.K
551	565	2	1519.75	4.1	1	63.8	24.3	95.00%	K.YVAAPGGSVMDQAVR.D		K.YVAAPGGSVMDQAVR.D
122	129	2	827.52	1.9	0	47.5	17.2	95.00%	D.IGGVTLLR.A		R.ETIAKPNVTIPEAVEEIDIGGVTLLR.A
223	244	2	2446.25	3.4	1	45.9	21.1	95.00%	K.VLCGSPGYINLMDALNSWPLVK.E	Carbamidomethyl (+57)	K.VLCGSPGYINLMDALNSWPLVK.E
39	60	2	2231.08	4.2	1	97.7	25.2	95.00%	R.ESGMEVADVSSITNAPEILGGR.V		R.ESGMEVADVSSITNAPEILGGR.V

566	581	2	1881.9	4.3	1	55.8	25.4	95.00%	R.DTANEFNMVFSEIPLR.L		R.DTANEFNMVFSEIPLR.L
354	362	2	1152.54	4.8	1	28.8	25.9	94.70%	K.YCVLQMDPK.Y	Carbamidomethyl (+57)	K.YCVLQMDPK.Y
248	259	2	1216.65	4.7	0	30.2	22.4	95.00%	R.ENIGIPAAASFK.H		R.ENIGIPAAASFK.H
104	129	3	2776.53	2.1	1	22.6	14.6	93.50%	R.ETIAKPNVTIPEAVEEIDIGGVTLLR.A		R.ETIAKPNVTIPEAVEEIDIGGVTLLR.A
201	222	3	2414.15	2.7	0	35.9	24.7	95.00%	R.YGANPHQSPAQAFMEQGPLPFK.V		R.YGANPHQSPAQAFMEQGPLPFK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
34	SERA_SCHPO	30.26%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
438	452	2	1654.8	3	1	83.8	24.6	95.00%	D.ISDCTPGSLEALHQK.L	Carbamidomethyl (+57)	R.GDIAYLVADISDCTPGSLEALHQK.L
58	73	2	1768.01	2.2	0	74.4	14	95.00%	K.ILLLENVNQSALSNLK.D		K.ILLLENVNQSALSNLK.D
275	284	2	1108.56	4.3	0	25.6	24.4	91.50%	K.EGSYLINASR.G		K.EGSYLINASR.G
58	74	2	1883.04	2.5	2	79.6	16.6	95.00%	K.ILLLENVNQSALSNLKD.E		K.ILLLENVNQSALSNLKDEGYQVEFLK.T
367	385	2	2078.05	3	0	83.5	23.5	95.00%	R.YINEGNSIGAVNFPEVSLR.S		R.YINEGNSIGAVNFPEVSLR.S
410	421	2	1468.77	4	1	31.9	21.3	95.00%	R.QVNELFIDHNIK.S		R.QVNELFIDHNIK.S
302	319	2	1728.88	4.5	1	48	23	95.00%	K.IAGAAIDVYPSEPAGNGK.D		K.IAGAAIDVYPSEPAGNGK.D
47	57	3	1247.68	3.8	1	25.6	20.9	95.00%	R.TLKPFASEDIK.I		R.TLKPFASEDIK.I
248	262	2	1596.82	2.4	1	64.5	22.5	95.00%	R.ADFVSLHVPASPETK.N		R.ADFVSLHVPASPETK.N
142	154	2	1394.7	4.8	0	57.8	23.5	95.00%	R.GIAVFNSPYANSR.S		R.GIAVFNSPYANSR.S
237	247	3	1291.73	4.7	0	20.7	16.7	90.10%	K.QLSSLPELLHR.A		K.QLSSLPELLHR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
35	LYS9_SCHPO	30.44%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
177	183	2	740.49	4.7	0	33.1	14.9	95.00%	R.GVLLALR.N		R.GVLLALR.N
412	426	2	1524.8	2.1	1	42.7	21.6	95.00%	D.GVINTPGVLAPNDMK.L		K.LVGVPCGVATQQILDGVINTPGVLAPNDMK.L
38	49	2	1259.66	4.1	0	41.7	22.6	95.00%	K.AEAFINGIPNSK.A		K.AEAFINGIPNSK.A
149	170	2	2385.11	5.2	1	60.2	26.6	95.00%	K.SFLSYCGGLPAPEDSNNPLGYK.F	Carbamidomethyl (+57)	K.SFLSYCGGLPAPEDSNNPLGYK.F
2	22	3	2269.25	3.1	0	39	16	95.00%	M.PSILLLGSGFVAHPTLEYLSR.R		-.MPSILLLGSGFVAHPTLEYLSR.R
379	396	2	1989.93	4.3	1	76.6	26.4	95.00%	R.TCTLLDYGVPNGYTSMAK.L	Carbamidomethyl (+57)	R.TCTLLDYGVPNGYTSMAK.L
126	135	3	1125.62	2.3	1	32.3	20.2	95.00%	D.PGIDHLYAIK.T		K.AGSICMNEIGVDPGIDHLYAIK.T
104	113	2	1103.56	4	0	29.1	23.4	95.00%	K.MAELEEAAIK.A		K.MAELEEAAIK.A
64	85	3	2488.28	3.3	1	39.1	21.4	95.00%	K.AVSEHDLTISLIPYTYHATVMK.A		K.AVSEHDLTISLIPYTYHATVMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
36	HXK2_SCHPO	25.05%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
12	24	2	1581.77	4.1	1	62.3	24.9	95.00%	K.LVNDFEYPTESLR.E		K.LVNDFEYPTESLR.E
435	449	2	1414.76	2.8	0	42.2	21.5	95.00%	D.GSGIGAALCALQAVK.E	Carbamidomethyl (+57)	K.DGSGIGAALCALQAVK.E
434	449	2	1529.79	4.8	1	96.2	22.6	95.00%	K.DGSGIGAALCALQAVK.E	Carbamidomethyl (+57)	K.DGSGIGAALCALQAVK.E
76	86	2	1287.67	3.9	1	30.3	24.2	95.00%	R.VCWIQLLGDGK.Y	Carbamidomethyl (+57)	R.VCWIQLLGDGK.Y
286	296	2	1240.63	5.9	0	25.6	22.5	91.50%	R.VGGMYLGELFR.R		R.VGGMYLGELFR.R
64	75	2	1322.7	2.5	1	39.2	21	95.00%	D.FLALDFGGTNLR.V		K.NGEVLAMAPAFISTLPTGAETGDFLALDFGGTNLR.V
374	388	2	1564.83	4.1	0	56.1	21.3	95.00%	R.MSAVPIASLYLSTGR.A		R.MSAVPIASLYLSTGR.A
174	183	2	1186.6	2.1	0	26.3	24.1	92.70%	D.FAQFLTEGFK.A		K.DFAQFLTEGFK.A
1	11	2	1334.67	4.1	1	29.9	24.5	95.00%	-.MEANFQQAVKK.L	Acetyl (+42)	-.MEANFQQAVKK.L
399	413	3	1798.89	2.8	1	27.7	24.2	95.00%	D.GSLVEHYPHFVDMLR.E		K.SDVGVDGSLVEHYPHFVDMLR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
37	PDX1_SCHPO	29.73%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	49	2	1547.75	1.9	0	83.8	25.4	95.00%	R.IAEAAGACAVMALER.V	Carbamidomethyl (+57)/ Oxidation (+16)	R.IAEAAGACAVMALER.V
265	280	2	1628.86	4	0	87.2	21.6	95.00%	K.ILAEVSENLGAAMVGR.S		K.ILAEVSENLGAAMVGR.S
71	83	2	1355.75	4.3	0	66.7	21	95.00%	K.EIQAAVSIPVMAK.V		K.EIQAAVSIPVMAK.V
21	34	2	1457.74	4	1	89.6	23.5	95.00%	K.GGVIMDVVNAEQAR.I		K.GGVIMDVVNAEQAR.I
121	132	3	1383.7	4.4	1	31	24.4	95.00%	K.SKFTVPFVCGSR.N	Carbamidomethyl (+57)	K.SKFTVPFVCGSR.N
140	149	2	1102.6	4.8	1	28.6	22.3	95.00%	R.RISEGAAMIR.T		R.RISEGAAMIR.T
13	20	2	830.47	4.2	0	38.8	20.2	95.00%	K.AGLAQMLK.G		K.AGLAQMLK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
38	CYPH_SCHPO	48.77%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
124	138	2	1644.83	4.4	1	86.7	24.7	95.00%	K.HVVFGEVTEGMDVVK.K		K.HVVFGEVTEGMDVVK.K
90	123	3	3611.83	4	1	56	19.8	95.00%	K.HNKPGLLSMANAGPNTNGSQFFITTVVTPWLDGK.H		K.HNKPGLLSMANAGPNTNGSQFFITTVVTPWLDGK.H
2	17	2	1835.87	3.9	1	50	25.9	95.00%	M.SNCFFDVIANGQPLGR.I	Acetyl (+42)/ Carbamidomethyl (+57)	-.MSNCFFDVIANGQPLGR.I
54	67	2	1607.82	4.3	1	67.2	23.4	95.00%	R.VIPQFMLQGGDFTR.G		R.VIPQFMLQGGDFTR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
39	C1TC_SCHPO	14.62%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
689	707	3	1923.15	3.9	1	37.5	6.99	95.00%	R.TSGLKPDAIVIVATVQALK.L		R.TSGLKPDAIVIVATVQALK.L
204	219	3	1649.95	2.3	1	30.9	12.3	95.00%	R.TADIVVAAIGIPHFVK.A		R.TADIVVAAIGIPHFVK.A
765	783	2	1913.94	1.8	2	59.6	24.4	95.00%	D.SPNEISAIREEALAAGATD.A		K.FSSDSPNEISAIREEALAAGATDAVDSNHWAEGGK.G
2	12	2	1184.68	4.9	0	55.8	19.1	95.00%	M.ALLLEGTSLAR.K	Acetyl (+42)	-.MALLLEGTSLAR.K
122	130	2	1024.47	4.2	0	27.4	25.4	93.70%	D.GFCETNLGK.L	Carbamidomethyl (+57)	K.DVDGFCETNLGK.L
536	546	2	1228.67	4.9	1	27.4	22	94.10%	R.KITIGENPTEK.G		R.KITIGENPTEK.G
324	336	2	1299.71	5.1	1	59.2	21.1	95.00%	K.NIGDLASEIGIAK.S		K.NIGDLASEIGIAK.S
381	396	2	1629.9	3.4	1	106	18.5	95.00%	K.STLTAGLVQALSNLDK.L		K.STLTAGLVQALSNLDK.L
349	356	2	983.58	5.3	0	46.2	18.5	95.00%	K.VNLEILQR.L		K.VNLEILQR.L
835	849	2	1592.78	4.3	1	53.3	25.6	95.00%	K.EMYGADGIELSPLAK.E		K.EMYGADGIELSPLAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
40	PUT2_SCHPO	27.01%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
388	405	2	1773.91	3.9	1	102	23.5	95.00%	K.VLESAASDSEIEVLAGGK.A		K.VLESAASDSEIEVLAGGK.A
362	384	3	2428.26	3.2	1	27	20.5	95.00%	K.VGAPLTDFANFVGPVIHQASFNK.L		K.VGAPLTDFANFVGPVIHQASFNK.L
82	92	2	1222.64	4.6	1	32.1	22.7	95.00%	K.HVEDAIEAALR.G		K.HVEDAIEAALR.G
254	274	3	2393.15	4.4	0	52.3	25.4	95.00%	K.VCFNHPEFAGLHFTGSTAVFR.S	Carbamidomethyl (+57)	K.VCFNHPEFAGLHFTGSTAVFR.S
275	288	2	1444.74	4.6	0	37.7	23.9	95.00%	R.SLWGTIGENVANGK.Y		R.SLWGTIGENVANGK.Y
233	253	2	2068.09	4.4	1	68.9	20.3	95.00%	R.EAGLPAGALQFIPGDAVEVSK.V		R.EAGLPAGALQFIPGDAVEVSK.V
409	422	2	1551.82	2.5	0	40.7	21.4	95.00%	D.SEGFFVEPTVLLSK.N		K.ADDSEGFFVEPTVLLSK.N
495	509	2	1504.71	3.5	0	49.3	25.6	95.00%	K.CTGAVVGEQPFGGAR.A	Carbamidomethyl (+57)	K.CTGAVVGEQPFGGAR.A
484	494	2	1225.58	4.6	1	28	25.4	94.30%	R.NAAGNFYINDK.C		R.NAAGNFYINDK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
41	THIL_SCHPO	23.04%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
291	301	2	1160.65	4.8	0	33.2	20	95.00%	R.FTTSPSLAIPK.A		R.FTTSPSLAIPK.A
14	30	2	1654.81	2.4	0	81.4	24.5	95.00%	R.TPMGSFGGSFASLPATK.L		R.TPMGSFGGSFASLPATK.L
156	173	2	1912.84	4	1	36.4	27.1	95.00%	D.GLPMGNAAELCAEEHSID.R	Carbamidomethyl (+57)	R.DGLSDAYDGLPMGNAAELCAEEHSIDR.A

360	371	2	1405.81	4.5	0	73.2	16.5	95.00%	R.IICTLAYILAQK.D	Carbamidomethyl (+57)	R.IICTLAYILAQK.D
278	290	2	1440.71	4.1	1	44.3	24.4	95.00%	K.IIGWGEAAQDPER.F		K.IIGWGEAAQDPER.F
340	359	3	1865.93	4.8	0	31	24.1	95.00%	R.VNINGGGVAMGHPLGSSGSR.I		R.VNINGGGVAMGHPLGSSGSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
42	PPA1_SCHPO	26.71%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
414	427	2	1687.77	2.4	0	39.2	26.6	95.00%	D.GMCELYAYLNSPVR.V	Oxidation (+16)/ Carbamidomethyl (+57)	R.HLVNEEVFPLSDCGFGPSNTSD GMCELYAYLNSPVR.V
332	365	4	3754.84	1.3	1	24.5	22.6	95.00%	D.ANIIPVETALGFFTDNTPENPLPT SYQVHSHSMK.A		R.SVENNTQQVFFAFTHDANIIPVET ALGFFTDNTPENPLPTSYQVHSHS MK.A
40	53	2	1669.78	2	1	32.3	26.2	95.00%	R.SPYHKPYFYGPSID.F		R.SPYHKPYFYGPSIDFPTTCK.I
40	59	3	2404.12	1.1	1	74.5	26.1	95.00%	R.SPYHKPYFYGPSIDFPTTCK.I	Carbamidomethyl (+57)	R.SPYHKPYFYGPSIDFPTTCK.I
73	92	2	2046.99	3	1	99.7	24.8	95.00%	R.NPTGGNAAFDAVGIANFQQR.L		R.NPTGGNAAFDAVGIANFQQR.L
366	387	2	2501.19	3.5	1	42.6	25.4	95.00%	K.ASEFVPFAGNLITELFQCEDSK.Y	Carbamidomethyl (+57)	K.ASEFVPFAGNLITELFQCEDSK.Y
214	224	2	1305.64	3.8	1	36.2	24.4	95.00%	D.DFTTPALEAWR.N		R.VVDSALWYGYGMFGEDVHNFTN YILVSENATAGSNSLSSYNACPASD ADDFTTPALEAWR.N
83	92	2	1102.59	2.6	0	33	23.1	95.00%	D.AVGIANFQQR.L		R.NPTGGNAAFDAVGIANFQQR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
43	YL8C_SCHPO	26.07%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
93	112	3	2269.21	3.4	1	35.2	18.3	95.00%	K.IVYADHLKPEVVMEVVEATK.G		K.IVYADHLKPEVVMEVVEATK.G
47	60	2	1575.87	2	1	38.8	19	95.00%	R.EKYPNFPIVLATGK.Q		R.EKYPNFPIVLATGK.Q
217	232	2	1745.96	4.4	0	53	18.2	95.00%	K.GTALQYITSNILPEVK.N		K.GTALQYITSNILPEVK.N
275	288	2	1456.72	3	0	84.8	24.8	95.00%	R.VGNEEGAVGEVLER.I		R.VGNEEGAVGEVLER.I
98	112	3	1707.93	1.8	0	31.2	19.5	95.00%	D.HLKPEVVMEVVEATK.G		K.IVYADHLKPEVVMEVVEATK.G
76	90	2	1659.82	1.3	0	38.7	24.3	95.00%	D.AFPAAHVNGCVLYNK.G	Carbamidomethyl (+57)	R.IPLDLDAFPAAHVNGCVLYNK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
44	RAD24_SCHPO	41.11%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
109	120	2	1236.65	4.7	0	29.1	21.9	95.00%	K.HLIPNAASAESK.V		K.HLIPNAASAESK.V
31	44	2	1562.75	4.1	1	82.9	25.3	95.00%	K.SVASTDQELTVEER.N		K.SVASTDQELTVEER.N
97	108	2	1431.77	1.7	1	36.6	21.6	95.00%	D.TICQDILTVLEK.H	Carbamidomethyl (+57)	K.IEQELDTICQDILTVLEK.H
219	227	2	1073.63	2	0	32.8	16.5	95.00%	D.STLIMQLLR.D		K.DSTLIMQLLR.D
237	267	3	2987.31	3.5	0	56.8	26.9	95.00%	D.AEYSAAAAGGNTEGAQENAPSN APEGEAEPK.A		R.DNLTLWTSDAEYSAAAAGGNTE GAQENAPSNAPEGEAEPK.A
15	30	3	1896.88	2.3	1	29.8	26.3	95.00%	K.LAEQAERYEGMVENMK.S		K.LAEQAERYEGMVENMK.S
156	172	2	1746.93	2.4	0	85.3	21.1	95.00%	K.AASEIATAELAPTHPIR.L		K.AASEIATAELAPTHPIR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
45	RS18_SCHPO	36.84%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	78	2	1386.79	4	0	45.2	17	95.00%	R.IVTIIQNPSQFK.I		R.IVTIIQNPSQFK.I
2	14	2	1578.86	2.4	1	29.1	20	95.00%	M.SLVVPDNFQHILR.L	Acetyl (+42)	-.MSLVVPDNFQHILR.L
56	66	2	1246.61	4	0	41.5	24.8	95.00%	R.AGELTTEELER.I		R.AGELTTEELER.I
79	86	2	1031.56	6	0	52.6	22.1	95.00%	K.IPSWFLNR.Q		K.IPSWFLNR.Q
95	106	2	1334.69	4.9	1	24.9	22.6	90.30%	K.SFQLLANNVDSK.L		K.SFQLLANNVDSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
46	MET3_SCHPO	24.29%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
217	230	3	1461.81	2.5	1	23	19.3	94.10%	R.VLIHPVVGMTKPGD.I		R.VLIHPVVGMTKPGDIDHFTR.V
364	382	2	2159.15	2.7	0	56.8	19.6	95.00%	R.VGANIPEWFSYPEVVAILR.Q		R.VGANIPEWFSYPEVVAILR.Q

427	440	2	1651.86	4	1	77.5	20.8	95.00%	R.LDAISVFYAQELQR.A		R.LDAISVFYAQELQR.A
83	92	2	1103.55	1.9	1	30.3	24.1	95.00%	D.LNESQADSLK.A		R.LSTGEVFPIPITLDLNESQADSLK.A
350	359	2	1102.6	3.9	0	29.9	20.9	95.00%	R.TLNISGTELR.R		R.TLNISGTELR.R
454	470	3	1867.06	1.7	1	25.1	13.6	95.00%	D.ASVKVPAEWTTVNIKPK.D		R.AGAAVVVSLADADASVKVPAEWTTVNIKPK.D
59	68	2	1233.64	5.6	1	40.5	22.8	95.00%	K.DYLNVVENLR.L		K.DYLNVVENLR.L
254	262	2	1012.62	5.1	0	33.5	14.1	95.00%	K.LSLLPLAMR.M		K.LSLLPLAMR.M
14	29	2	1808.97	2	1	41.3	19.5	95.00%	D.APLREQLEQEATSLPK.I		R.DAPLREQLEQEATSLPK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
47	GBLP_SCHPO	39.49%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
295	308	2	1606.81	2.3	1	56	23.6	95.00%	D.GQTLFSGWTDNLIR.V		K.SSEPECISLTWSPDGQTLFSGWTDNLIR.V
108	118	2	1185.64	3.1	1	53.9	21.8	95.00%	D.VLSVSISPDNR.Q		K.GECTHQFVGHTSDVLSVSISPDNR.Q
186	212	3	2736.26	2.6	1	43.2	26.8	95.00%	R.TSHYGHTGYVSAVTISPDGSLCASGGR.D	Carbamidomethyl (+57)	R.TSHYGHTGYVSAVTISPDGSLCASGGR.D
234	245	2	1314.71	3.1	0	32.5	21.9	95.00%	K.ANINALVFSPNR.Y		K.ANINALVFSPNR.Y
176	185	2	1264.65	5.4	1	30.1	23.2	95.00%	K.VWDLETFSLR.T		K.VWDLETFSLR.T
39	47	2	1112.68	5.9	0	27.8	14.1	94.60%	K.SIILWNLVR.D		K.SIILWNLVR.D
221	233	2	1503.76	1.9	0	33.6	23.8	95.00%	D.LNESTHLYSLEAK.A		R.DGTLMLWDLNESTHLYSLEAK.A
9	36	3	2894.45	2.9	1	38.1	22.8	95.00%	R.ATLEGHSGWVTSLSTAPENPDILLSGSR.D		R.ATLEGHSGWVTSLSTAPENPDILLSGSR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
48	RL4A_SCHPO	27.55%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
122	140	2	1845.04	2.8	0	55.4	15.1	95.00%	R.YAISSAVAASGVPSLLLAR.G		R.YAISSAVAASGVPSLLLAR.G
2	13	2	1304.71	4.5	0	25.5	21.1	91.40%	M.AAARPTVSIYSK.D	Acetyl (+42)	-.MAAARPTVSIYSK.D
15	29	2	1580.85	2.6	0	34	19.5	95.00%	D.GSVSSETIALPFVFK.A		K.DGSVSSETIALPFVFK.A
235	248	3	1457.85	2.5	0	34.3	14.8	95.00%	R.LNLLQLAPGGHLGR.F		R.LNLLQLAPGGHLGR.F
292	303	2	1357.75	4	1	43.8	19.5	95.00%	R.LINSDEIQSIVK.A		R.LINSDEIQSIVK.A
14	29	2	1695.88	4.2	1	38.3	22	95.00%	K.DGSVSSETIALPFVFK.A		K.DGSVSSETIALPFVFK.A
276	291	2	1864.94	2.5	1	80.9	23.8	95.00%	K.NYFLPENIISNADVTR.L		K.NYFLPENIISNADVTR.L
87	97	2	1197.51	4.4	0	32.6	26.5	95.00%	R.SGQAAFGNMCR.S	Carbamidomethyl (+57)	R.SGQAAFGNMCR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
49	CARB_SCHPO	11.03%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
968	975	2	1019.52	4.9	0	24.9	23.5	90.30%	K.VPQFSWTR.L		K.VPQFSWTR.L
932	943	2	1304.72	5.6	1	35.2	20.9	95.00%	K.TLGVNFIDVATR.S		K.TLGVNFIDVATR.S
1056	1070	2	1655.92	2.2	0	41.5	17.2	95.00%	K.LLQPTSAEVVEFPVK.D		K.LLQPTSAEVVEFPVK.D
402	417	3	1672.96	2.6	0	22.7	14.6	93.70%	K.IALGHTLPELPNAVTK.T		K.IALGHTLPELPNAVTK.T
773	798	3	2736.49	2.9	0	51	15.6	95.00%	K.FANAVGYPVLVRPSYVLSGAAMSVIR.D		K.FANAVGYPVLVRPSYVLSGAAMSVIR.D
418	433	2	1784.89	1.8	1	49.3	24.2	95.00%	K.TTTANFEPSLDYVVTK.I		K.TTTANFEPSLDYVVTK.I
575	584	2	1057.58	4.7	1	32.1	22	95.00%	K.LVGASELDVR.A		K.LVGASELDVR.A
249	273	3	2529.22	2.7	1	48.7	24.6	95.00%	R.SAYSLGGLGSGFANNKEELQSMAAK.S		R.SAYSLGGLGSGFANNKEELQSMAAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
50	HOSM_SCHPO	23.68%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	204	2	1315.66	4	1	40.8	24.8	95.00%	R.VGIADTVGCATPR.Q	Carbamidomethyl (+57)	R.VGIADTVGCATPR.Q

2	31	3	3218.5	4.8	1	47.5	24.7	95.00%	M.SVSEANGTETIKPPMNGNPYGPNPSDFLSR.V	Acetyl (+42)/ Deamidation (+1)	-.MSVSEANGTETIKPPMNGNPYGPNPSDFLSR.V
249	257	2	944.53	2.1	0	41.8	21.6	95.00%	D.TSILGIGER.N		R.GVVSCDIECHFHNDTGMAIANAYCALEAGATHIDTSILGIGER.N
72	85	2	1578.79	2.5	0	61.7	24.8	95.00%	D.YIELTSPVASEQSR.Q		K.ALDNFGVDYIELTSPVASEQSR.Q
324	339	2	1772.92	1.8	1	33	22.1	95.00%	K.AILANPSTYEILKPED.F		K.AILANPSTYEILKPEDFGMSR.Y
324	344	3	2351.19	2.6	1	25.6	23.4	95.00%	K.AILANPSTYEILKPEDFGMSR.Y		K.AILANPSTYEILKPEDFGMSR.Y
32	43	2	1391.75	4.9	0	68.1	21.5	95.00%	R.VNNFSIIESTLR.E		R.VNNFSIIESTLR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
51	FAS2_SCHPO	4.61%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
488	502	3	1650.8	4.5	1	35.5	24.9	95.00%	K.NVNHPTAPSTTIDER.G		K.NVNHPTAPSTTIDER.G
114	146	3	3020.56	3.1	1	35.9	21	95.00%	K.VETAAAAAPAATPAPAPAQTSAPAAALPDEPPK.A		K.VETAAAAAPAATPAPAPAQTSAPAAALPDEPPK.A
517	527	2	1319.7	5.4	1	32	22.4	95.00%	R.KLTHYVTEMAK.G		R.KLTHYVTEMAK.G
1393	1401	2	994.61	4.5	1	27.6	13.4	94.40%	K.TPLPIVDLK.F		K.TPLPIVDLK.F
28	44	2	1939.01	4.4	1	67.5	21.2	95.00%	R.WIETQDVILSPPVSAER.I		R.WIETQDVILSPPVSAER.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
52	ECM17_SCHPO	4.62%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
493	502	3	1154.69	1.9	1	20.8	14.5	90.40%	D.PELVISELKK.D		K.NSSVSSESLEVLSNWIVSVDNLESPVDPELVISELKK.D
314	325	2	1337.79	2.1	0	44.5	13.6	95.00%	R.LTVLEPITSLPR.K		R.LTVLEPITSLPR.K
77	90	2	1484.78	3	0	48.5	22.6	95.00%	D.AILAEEEVASTQPK.Q		K.SHADPFAHIADAILAEEEVASTQPK.Q
801	810	2	1058.57	5.4	1	27.5	23.1	94.20%	K.GADLNLSELK.Y		K.GADLNLSELK.Y
1031	1045	2	1687.72	2.9	1	44.4	26.3	95.00%	R.NVTCSSTPNNETIHD.Q	Carbamidomethyl (+57)	R.NVTCSSTPNNETIHDQLFAVSK.Q
70	90	3	2236.14	2.2	1	30.6	22.3	95.00%	D.PFAHIADAILAEEEVASTQPK.Q		K.SHADPFAHIADAILAEEEVASTQPK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
53	YHY6_SCHPO	13.83%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
678	698	2	2257.13	4.5	1	51.2	23.8	95.00%	K.SLCIPLEQPSGEDAIIEGTTK.C	Carbamidomethyl (+57)	K.SLCIPLEQPSGEDAIIEGTTK.C
161	187	3	2608.39	0.96	1	27	19	95.00%	K.SVGVNPIIVDFSAPGSATAPSKPAAQK.K		K.SVGVNPIIVDFSAPGSATAPSKPAAQK.K
298	323	3	2901.42	3	1	27.8	23.9	95.00%	R.AGTSELDEPIAIRPTSETVMYPYYAK.W		R.AGTSELDEPIAIRPTSETVMYPYYAK.W
450	462	3	1364.71	2.7	0	38	23.3	95.00%	D.PNAEIGPTGERPK.L		K.MFNIVVEDPNAEIGPTGERPK.L
387	398	2	1343.81	2.7	1	31.1	10.4	95.00%	R.IYTDLLAVPVIK.G		R.IYTDLLAVPVIK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
54	CYSD_SCHPO	34.27%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	26	3	2735.29	3.8	1	45.2	26.1	95.00%	M.PVESEHFETLQLHAGQEPDAATSSR.A		-.MPVESEHFETLQLHAGQEPDAATSSR.A
47	59	2	1541.79	1.7	0	40.9	23.2	95.00%	R.LFGLQEPGYIYSR.M		R.LFGLQEPGYIYSR.M
27	39	2	1486.79	2.2	0	56.5	22	95.00%	R.AVPIYATTSYVFR.D		R.AVPIYATTSYVFR.D
72	100	3	2787.49	3.3	0	49.9	17.9	95.00%	R.IAALEHGAAAIATSSGTSALFMALTTLAK.A		R.IAALEHGAAAIATSSGTSALFMALTTLAK.A
366	377	2	1185.64	4.4	1	34.5	21.5	95.00%	K.LASQLANVGDAK.T		K.LASQLANVGDAK.T
151	169	2	2199.04	3.1	1	69.1	26	95.00%	K.AVYVESIGNPMYNVPDFER.I		K.AVYVESIGNPMYNVPDFER.I

378	403	3	2798.48	2.5	1	42.6	18.6	95.00%	K.TLVIAPAYTTHLQLTDEEQISAGVTK.D		K.TLVIAPAYTTHLQLTDEEQISAGVTK.D
141	150	2	1101.57	3.5	1	30.4	22.8	95.00%	D.LAAQIDENTK.A		K.FVNGDDPNDLAAQIDENTK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
55	RS7_SCHPO	25.13%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	140	3	2393.33	3.6	1	40.9	13.6	95.00%	R.TLTAVHNAILEDIVFPTEIIGK.R		R.TLTAVHNAILEDIVFPTEIIGK.R
59	70	2	1322.84	4	0	46.5	9.54	95.00%	K.AIVVFVPQPLLK.A		K.AIVVFVPQPLLK.A
20	34	2	1724.87	3.4	1	74.9	24.2	95.00%	D.LLVAQCLYDLESSSK.D	Carbamidomethyl (+57)	R.SSSQPTETDLLVAQCLYDLESSSK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
56	VIPI_SCHPO	34.63%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	68	2	1496.86	4.3	1	41.7	15.9	95.00%	K.TALLLQDALLGQNK.I		K.TALLLQDALLGQNK.I
101	110	2	1087.63	5.8	0	34.3	17.8	95.00%	R.SAIISELLSR.G		R.SAIISELLSR.G
225	254	3	2955.41	4.7	1	54.3	25.3	95.00%	K.NQAEGTASPASSTPTAPAEKEPTAPTTESK.T		K.NQAEGTASPASSTPTAPAEKEPTAPTTESK.T
122	134	2	1410.71	4.2	1	61.1	24.3	95.00%	K.SIQLDQSYGVSSK.F		K.SIQLDQSYGVSSK.F
111	121	2	1260.64	3.7	1	31.8	23.4	95.00%	R.GYHLSDVTLEK.S		R.GYHLSDVTLEK.S
137	147	2	1100.62	4.3	0	27.7	20.7	94.50%	K.GILESALSGVR.S		K.GILESALSGVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
57	OAT_SCHPO	25.34%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
386	398	3	1374.82	4.6	0	23.2	13.4	94.40%	R.GVLAKPTHGNIIR.F		R.GVLAKPTHGNIIR.F
70	80	2	1268.71	4.2	0	28.4	18.1	95.00%	K.IIEALVEQAQR.V		K.IIEALVEQAQR.V
2	37	4	4216	4.3	0	58.2	22.8	95.00%	M.SAESLLHNTFSTEQIEVLENEYAAHNYHPLPVCFSK.A	Acetyl (+42)/ Carbamidomethyl (+57)	-.MSAESLLHNTFSTEQIEVLENEYAAHNYHPLPVCFSK.A
276	291	2	1561.85	4	0	53	18.6	95.00%	K.AISGGVYPVSAVLSSR.E		K.AISGGVYPVSAVLSSR.E
238	254	2	1838.97	4.4	1	78.8	21.3	95.00%	K.AHNVLFIADEVQTGVAR.T		K.AHNVLFIADEVQTGVAR.T
258	275	3	2051.1	4.3	1	30.2	19.6	95.00%	K.MLCIEHSNVKPDVVILGK.A	Carbamidomethyl (+57)	K.MLCIEHSNVKPDVVILGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
58	HSP7F_SCHPO	12.78%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
174	189	2	1665.84	2.6	1	90.6	23.5	95.00%	R.LMNDNAAAALTYGITK.T		R.LMNDNAAAALTYGITK.T
581	591	2	1385.65	4	1	31.1	26.1	95.00%	K.NALEEYIYDTR.A		K.NALEEYIYDTR.A
5	16	2	1249.64	6.5	1	29.4	23.5	95.00%	R.TNVVGIDFGNSK.T		R.TNVVGIDFGNSK.T
38	48	2	1194.59	3.8	0	34	24	95.00%	R.STPSLVSYGER.S		R.STPSLVSYGER.S
159	173	2	1534.89	2.2	0	51.3	14.8	95.00%	R.ALLEAANIAGLNPLR.L		R.ALLEAANIAGLNPLR.L
96	106	2	1134.6	4	1	31.7	23.2	95.00%	K.LTEVDGFVGAK.V		K.LTEVDGFVGAK.V
419	434	2	1690.85	2.9	0	64	23.9	95.00%	D.SSLEVFSEGNPIPSTK.I		R.EFHVHDVTTYPITFSWEPIPENPEEDSSLEVFSEGNPIPSTK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
59	LEUC_SCHPO	15.83%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
521	539	2	1671.88	2.5	0	108	21.7	95.00%	D.GIATNVAGSVSSGSAGIPK.F		K.NYDPSHDVEGDIGLSVDDATDAVTDADGIATNVAGSVSSGSAGIPK.F
633	649	2	2002.01	4.5	1	59.4	24.1	95.00%	R.VIIAPSFADIFFNNCFK.N	Carbamidomethyl (+57)	R.VIIAPSFADIFFNNCFK.N
417	436	3	2355.02	4.1	1	24.9	26.8	94.10%	R.EAGCSMCLGMNPDQLKPYER.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.EAGCSMCLGMNPDQLKPYER.C
603	619	3	1826.86	5.3	1	37.3	26.5	95.00%	R.HATVLVAHDNFGCGSSR.E	Carbamidomethyl (+57)	R.HATVLVAHDNFGCGSSR.E
477	493	2	1810.88	4.1	1	36.5	25.2	95.00%	R.EFFGDVSNGSPSIITNK.N		R.EFFGDVSNGSPSIITNK.N
572	583	2	1400.71	1.3	0	33.7	24	95.00%	R.TGLGQFAFYEIR.Y		R.TGLGQFAFYEIR.Y

650	667	2	2027	4	1	40.9	24.8	95.00%	K.NGMLPIPTPIEQVNDMMK.A		K.NGMLPIPTPIEQVNDMMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
60	ADH_SCHPO	28.57%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
109	125	2	1931.9	3.1	1	30.2	26.4	95.00%	K.AEETICPHIQLSGYTVD.G	Carbamidomethyl (+57)	K.AEETICPHIQLSGYTVDGTFQHYCIANATHATIIPESVPLEVAAPIMCAGITCYR.A
236	253	2	1681.87	4.1	0	56	21.7	95.00%	K.AATNGGAHGTLVLSTSPK.S	Deamidation (+1)	K.AATNGGAHGTLVLSTSPK.S
254	278	3	2513.21	3.1	0	41.5	25	95.00%	K.SYEQAAGFARPGSTMVTVSMPAGAK.L		K.SYEQAAGFARPGSTMVTVSMPAGAK.L
170	194	3	2506.29	2.3	0	42.2	21.1	95.00%	K.VGPGEWICIPGAGGGLGHLAVQYAK.A	Carbamidomethyl (+57)	K.VGPGEWICIPGAGGGLGHLAVQYAK.A
63	77	3	1462.8	2.2	0	29	19.4	95.00%	K.MPLIGGHEGAGVVVK.V		K.MPLIGGHEGAGVVVK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
61	HSP7M_SCHPO	12.76%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
204	215	2	1124.67	4.6	0	48.3	15.3	95.00%	K.AAGAIAGLNVLR.V		K.AAGAIAGLNVLR.V
105	118	2	1578.81	4.5	0	81.4	23.3	95.00%	R.QAVINPENTFFATK.R		R.QAVINPENTFFATK.R
185	199	2	1679.83	4.3	1	62.1	24.4	95.00%	K.NAVVTVPAYFNDSQR.Q		K.NAVVTVPAYFNDSQR.Q
496	510	2	1538.89	4.2	0	77.2	14.9	95.00%	K.LIGNFQLTGIAPAPK.G		K.LIGNFQLTGIAPAPK.G
157	170	2	1496.8	5.1	0	59.3	21.8	95.00%	K.TYSPSQIGGFILSK.M		K.TYSPSQIGGFILSK.M
216	231	2	1630.86	3.8	1	78.5	21.6	95.00%	R.VVNEPTAAALAYGLDK.K		R.VVNEPTAAALAYGLDK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
62	ACON_SCHPO	11.31%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
435	452	2	1870.92	1.7	0	33.8	24.5	95.00%	K.AGGIVLANACGPCIGQWK.R	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.AGGIVLANACGPCIGQWK.R
532	549	2	1853.89	4.6	1	68.9	25.7	95.00%	K.GYDPGSNTYVAPSSVNVK.D		K.GYDPGSNTYVAPSSVNVK.D
375	391	2	1874.82	3.1	1	58.4	26.8	95.00%	K.VGLIGSCTNSSYEDMSR.A	Carbamidomethyl (+57)	K.VGLIGSCTNSSYEDMSR.A
392	402	2	1203.6	5.2	1	35.2	24.8	95.00%	R.AASICQQAIDK.G	Carbamidomethyl (+57)	R.AASICQQAIDK.G
652	666	2	1665.78	3.4	0	67.3	26.5	95.00%	R.WVTLGEQNFGEGSSR.E		R.WVTLGEQNFGEGSSR.E
462	470	2	1052.53	5	0	36.5	24	95.00%	K.NSIVTSYNR.N		K.NSIVTSYNR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
63	UGPA1_SCHPO	17.98%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	10	2	1166.63	4.6	1	24.9	20.4	90.20%	-.MDLAPRPLGR.Q	Acetyl (+42)	-.MDLAPRPLGR.Q
185	194	2	1205.65	4.7	1	32.1	21.4	95.00%	K.IDILTFNQSR.Y		K.IDILTFNQSR.Y
299	314	3	1876.02	4.4	0	30	18.4	95.00%	R.LLEIAQVPPQHVEEFK.S		R.LLEIAQVPPQHVEEFK.S
81	104	3	2616.33	2	1	24.3	21.8	95.00%	D.LVESPKPEQVVEYDTITEAGGLSR.D		R.GSEINWDLVESPKPEQVVEYDTITEAGGLSR.D
337	352	3	1863.99	2.4	1	22.3	20	93.10%	R.VVNNHELSMEIIPNKK.T		R.VVNNHELSMEIIPNKK.T
115	129	2	1460.72	4.2	0	48.3	24.8	95.00%	K.LNGGLGTTMGCVGPK.S	Carbamidomethyl (+57)	K.LNGGLGTTMGCVGPK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
64	ILV3_SCHPO	17.73%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
266	278	3	1408.68	4.8	1	24.2	25.3	95.00%	K.FAECEAAGSAIKR.L	Carbamidomethyl (+57)	K.FAECEAAGSAIKR.L
49	68	2	2142.97	5.2	1	90.3	27.1	95.00%	K.SQGASQAMLYATGLNEEDMK.K		K.SQGASQAMLYATGLNEEDMK.K
538	547	2	1056.58	3	1	42.8	22	95.00%	D.GDVIEINAVK.N		R.FSGGSHGFLIGHVDPEAQVGGPIALVQDGDVIEINAVK.N
402	417	4	1843.09	3.6	1	32.1	6.02	95.00%	K.IIRPLSNPIKTEGHLR.V		K.IIRPLSNPIKTEGHLR.V
117	126	2	1009.47	3.4	0	29	24.1	95.00%	D.GISMGTTGMR.Y		K.AGLTGFQFNTIGVSDGISMGTTGMR.Y
40	48	2	994.5	5.2	0	30.6	24.7	95.00%	K.YSETITGPK.S		K.YSETITGPK.S

185	212	3	3007.42	3.5	1	69.2	25.4	95.00%	R.AGHSPCQNNAPIDIVSAFQSYGEFITGK.I	Carbamidomethyl (+57)	R.AGHSPCQNNAPIDIVSAFQSYGEFITGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
65	RL8_SCHPO	19.69%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
24	32	2	1084.62	4.7	0	29.3	20.4	95.00%	K.NPLFVSRPR.S		K.NPLFVSRPR.S
33	43	2	1188.62	4.1	1	26.8	23.1	93.30%	R.SFGIGQDIQPK.R		R.SFGIGQDIQPK.R
109	120	2	1171.61	4.7	0	55.2	23.5	95.00%	R.LVAEAEAVANGK.S	Deamidation (+1)	R.LVAEAEAVANGK.S
134	146	2	1425.8	2.4	0	51	17.6	95.00%	K.YGLNHVVALIEAK.K		K.YGLNHVVALIEAK.K
52	57	2	862.44	5.9	0	26.5	23.1	93.00%	K.WPEYIR.L		K.WPEYIR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
66	HXK1_SCHPO	9.50%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
304	315	2	1380.7	5.1	1	25.3	23.4	91.00%	K.MIAGCYLGDILR.R	Carbamidomethyl (+57)	K.MIAGCYLGDILR.R
2	12	3	1409.65	4.4	1	25.1	25.7	95.00%	M.SLHDAYHWPSR.T	Acetyl (+42)	-.MSLHDAYHWPSR.T
455	469	2	1328.73	2.5	0	53.9	20.4	95.00%	D.GSGVGAALVSALEAK.G		K.VVTIPAEDGSGVGAALVSALEAK.G
447	469	2	2153.17	3.4	1	105	18.3	95.00%	K.VVTIPAEDGSGVGAALVSALEAK.G		K.VVTIPAEDGSGVGAALVSALEAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
67	TRP_SCHPO	15.49%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
382	393	2	1355.77	4.5	0	47.2	19	95.00%	K.INNCIGQILLAK.R	Carbamidomethyl (+57)	K.INNCIGQILLAK.R
247	261	2	1623.75	3.4	0	47.6	26.4	95.00%	K.AEPGTAATVVEEYCK.Y	Carbamidomethyl (+57)	K.AEPGTAATVVEEYCK.Y
400	419	3	1938.01	4.3	0	37.5	21.1	95.00%	R.IIAETGAGQHGVATAICAAK.F	Carbamidomethyl (+57)	R.IIAETGAGQHGVATAICAAK.F
275	302	3	2928.48	4.6	0	34.9	22	95.00%	K.QFQSGGSVATAPPAAVVEPINEMYLPQK.Y		K.QFQSGGSVATAPPAAVVEPINEMYLPQK.Y
616	631	2	1825.87	3	1	57.5	26.1	95.00%	R.AEFIAVTDAQCLEGFR.A	Carbamidomethyl (+57)	R.AEFIAVTDAQCLEGFR.A
445	461	2	1739.99	4	0	48.6	15.1	95.00%	R.LLGAEVVPVTSGTQTLR.D		R.LLGAEVVPVTSGTQTLR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
68	DHAS_SCHPO	18.21%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
31	39	2	856.52	4.9	0	28.2	19.7	95.00%	K.IAVLGASAR.S		K.IAVLGASAR.S
19	30	3	1445.76	4.9	1	23.3	22.5	94.40%	R.FITLLSDHPEFK.I		R.FITLLSDHPEFK.I
143	161	2	2003.02	2.7	0	72.8	22.4	95.00%	R.GCIITNSNCSTAAVVVPLK.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GCIITNSNCSTAAVVVPLK.A
267	278	2	1375.7	3.8	0	37.2	23.7	95.00%	R.EVLANYVSEPQK.L		R.EVLANYVSEPQK.L
6	18	2	1227.7	3.7	0	35.6	19.6	95.00%	K.VGILGATGTVGQR.F		K.VGILGATGTVGQR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
69	FAS1_SCHPO	6.75%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1117	1130	2	1421.7	4.7	0	59.8	25.1	95.00%	K.SLESVSVTEEAGSK.V		K.SLESVSVTEEAGSK.V
1870	1881	2	1266.57	5.2	1	37.8	26	95.00%	R.SDYGMVAANPSR.V		R.SDYGMVAANPSR.V
210	224	3	1723.91	5.4	1	36.5	20.9	95.00%	K.GLNVLDWLAGERPER.D		K.GLNVLDWLAGERPER.D
828	846	3	1903.05	2.3	0	46.8	17.6	95.00%	D.GPTGGIVTVLSELGEPIHK.L		K.TYDGPTGGIVTVLSELGEPIHK.L
2	12	2	1294.67	5.2	0	53.5	22.4	95.00%	M.VEAEQVHQSLR.S		-.MVEAEQVHQSLR.S
1778	1806	3	3141.54	1.9	1	40.3	23.1	95.00%	K.DSTSFSFTHPSGLLSATQFTQPALTLMEK.S		K.DSTSFSFTHPSGLLSATQFTQPALTLMEK.S
781	794	2	1545.81	3.9	1	42.1	22.2	95.00%	K.LPPMPFDGILFGSR.L		K.LPPMPFDGILFGSR.L
1422	1447	3	2983.4	3.2	1	29.8	25.7	95.00%	R.GTFTDFENTFEHTQETPMQLTLATPK.D		R.GTFTDFENTFEHTQETPMQLTLATPK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
70	HMCS_SCHPO	19.02%	100%	6									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
155	183	3	2859.53	3.9	0	40.5	17.9	95.00%	K.GNARPTGGAGCVALLVGPNAPIVFEPGLR.G	Carbamidomethyl (+57)	K.GNARPTGGAGCVALLVGPNAPIVFEPGLR.G		
269	282	2	1454.7	2.8	0	27.2	25.3	93.60%	D.SAAEPSNPELEGVR.E		R.LLYTDSAAEPSNPELEGVR.E		
264	282	2	2060.02	4.4	1	63.4	24.8	95.00%	R.LLYTDSAAEPSNPELEGVR.E		R.LLYTDSAAEPSNPELEGVR.E		
393	407	2	1886.89	2.3	0	35.8	26.2	95.00%	R.HCLTPTQYEEAIELR.H	N-Formyl (+28)/ Carbamidomethyl (+57)	R.HCLTPTQYEEAIELR.H		
207	216	3	1238.58	3	0	24.6	25.7	95.00%	D.GHFSLECYVK.A	Carbamidomethyl (+57)	R.GTYMQHAYDFYKPDLTSEYPYVDGHFSLECYVK.A		
217	228	2	1325.64	3.7	1	38.4	25.4	95.00%	K.ALDGAYANYNVR.D		K.ALDGAYANYNVR.D		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
71	TAL1_SCHPO	13.35%	100%	5									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
27	44	3	1917.03	4	1	42	20.6	95.00%	K.YKPQDATTNPSLILAASK.K		K.YKPQDATTNPSLILAASK.K		
288	297	2	1165.55	2.5	1	35.2	25.7	95.00%	D.FNNDEMAVVK.L		R.FDFNNDEMAVVK.L		
200	213	2	1585.82	2.8	0	45.2	23.2	95.00%	D.PGVVSVSNIFNYYK.K		R.DYTAQEDPGVVSVSNIFNYYK.K		
32	44	2	1285.73	2.2	0	43.9	19.6	95.00%	D.ATTNPSLILAASK.K		K.YKPQDATTNPSLILAASK.K		
200	214	3	1713.91	2.2	1	23.6	20.2	94.80%	D.PGVVSVSNIFNYYKK.F		R.DYTAQEDPGVVSVSNIFNYYKK.F		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
72	O59743_SCHPO	23.14%	100%	4									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
12	24	2	1387.72	2.1	0	69.3	23.1	95.00%	K.LGIEEQVETAATK.S		K.LGIEEQVETAATK.S		
75	97	3	2588.33	2.8	1	31.8	20.9	95.00%	K.EALDLFLGAYNVITPELAHFEAR.C		K.EALDLFLGAYNVITPELAHFEAR.C		
11	24	2	1515.82	4.5	1	53.1	19.8	95.00%	K.KLGIEEQVETAATK.S		K.KLGIEEQVETAATK.S		
25	43	3	1929.02	2.8	1	22.3	20.2	93.00%	K.SPFIEGLANGTAPPGAFKR.W		K.SPFIEGLANGTAPPGAFKR.W		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
73	SERC_SCHPO	19.02%	100%	6									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
330	352	5	2716.42	3.7	1	22	19.4	95.00%	R.IEPQELESEFLAEAEKHHLVQLK.G		R.IEPQELESEFLAEAEKHHLVQLK.G		
311	321	2	1216.68	2.7	0	29.3	19.4	95.00%	D.LYISVVEPAAR.S		K.HDLYISVVEPAAR.S		
376	385	2	1147.65	4.7	1	32.8	17.6	95.00%	R.LIDLLESFAK.A		R.LIDLLESFAK.A		
216	228	2	1299.74	5	0	37	17.9	95.00%	K.NAGPAGITVVFVR.D		K.NAGPAGITVVFVR.D		
189	199	2	1282.6	4.3	1	67	25	95.00%	R.VCDVSSNFISR.K	Carbamidomethyl (+57)	R.VCDVSSNFISR.K		
324	329	2	766.38	5.3	0	26.2	21.6	92.50%	R.MNVTFR.I		R.MNVTFR.I		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
74	YF19_SCHPO	17.30%	100%	6									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
195	208	2	1516.82	4.7	0	34.9	19.7	95.00%	K.TAELTPLSALCLTK.F	Carbamidomethyl (+57)	K.TAELTPLSALCLTK.F		
5	17	2	1406.78	4.6	1	33	18.1	95.00%	K.LVDHVEITVPTGK.T		K.LVDHVEITVPTGK.T		
422	443	3	2229.12	4.1	0	21.2	22.8	91.10%	R.GNNSTYGLAAGVHTNNITNAIK.V		R.GNNSTYGLAAGVHTNNITNAIK.V		
71	80	2	1161.56	3.7	1	28.3	25.2	94.90%	R.AAFQTDAPWR.K		R.AAFQTDAPWR.K		
336	349	2	1523.73	2.3	1	93.4	25.5	95.00%	D.PFAEDTFQGAQVSK.Q		K.VGDPFAEDTFQGAQVSK.Q		
181	194	2	1439.82	3.6	0	42.9	16.5	95.00%	K.IAPAVACGNTIILK.T	Carbamidomethyl (+57)	K.IAPAVACGNTIILK.T		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
75	BCA1_SCHPO	22.63%	100%	6									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
315	331	2	1670.97	4.2	0	59.5	11.5	95.00%	R.LLEVFGAGTAALVSPVK.A		R.LLEVFGAGTAALVSPVK.A		
122	130	2	1010.58	2.8	0	50.5	17.6	95.00%	D.PAELAEIIR.K		R.ISLPSFDPAELAEIIR.K		

37	49	3	1581.74	3.3	1	27.3	26.3	95.00%	K.FGENFTDHMLIMK.W		K.FGENFTDHMLIMK.W
262	278	2	1795	4.2	1	43.3	16.4	95.00%	K.EIITAPLDGMILPGVTR.D		K.EIITAPLDGMILPGVTR.D
337	359	2	2462.16	4.4	0	42.7	26	95.00%	K.GTEYEIPMPEGQEAGPITSEISK.W		K.GTEYEIPMPEGQEAGPITSEISK.W
115	130	2	1769.96	3.9	1	43.7	19.2	95.00%	R.ISLPSFDPAELAEIIR.K		R.ISLPSFDPAELAEIIR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
76	RS6B_SCHPO	27.20%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	115	2	1739.01	3.8	1	65.7	12	95.00%	R.GCIVGQDLAVLALAIVK.Q	Carbamidomethyl (+57)	R.GCIVGQDLAVLALAIVK.Q
32	51	2	2112.99	3.1	1	58.1	26.1	95.00%	R.MGQEVPGDSVGPEFAGYVFK.I		R.MGQEVPGDSVGPEFAGYVFK.I
59	72	3	1625.86	4.7	0	32.2	21.7	95.00%	K.QGFPMFQGVLLPHR.V		K.QGFPMFQGVLLPHR.V
40	51	2	1299.65	1.9	0	31.7	23.9	95.00%	D.SVGPEFAGYVFK.I		R.MGQEVPGDSVGPEFAGYVFK.I
204	217	2	1606.78	4.3	1	54.8	25.1	95.00%	K.NREEAAEFAQLMAK.R		K.NREEAAEFAQLMAK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
77	EF1G_SCHPO	15.89%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
93	115	3	2636.34	0.76	0	70.6	22	95.00%	K.VLQYCSFTNSELPGAFRPIIAPR.V	Carbamidomethyl (+57)/ Deamidation (+1)	K.VLQYCSFTNSELPGAFRPIIAPR.V
207	216	2	1182.71	4	1	27.1	16.6	93.80%	K.FIDQPLPIIK.A		K.FIDQPLPIIK.A
291	298	2	1021.49	3.5	0	27.5	24	94.30%	D.PENYSVWK.V		R.SGALPWFFEHFDPENYSVWK.V
128	139	2	1303.72	4.6	0	40.7	20.3	95.00%	K.EAETAIALIFAR.F		K.EAETAIALIFAR.F
116	127	2	1294.63	4.3	1	26.2	24.9	92.50%	R.VFGAPYDEQAAK.E		R.VFGAPYDEQAAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
78	EF1B_SCHPO	21.03%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
59	73	2	1561.84	4.2	1	60.9	20.6	95.00%	K.QIATYDLATLPGTAK.E		K.QIATYDLATLPGTAK.E
153	165	2	1432.74	3.9	1	44.3	23.7	95.00%	R.SIQMDGLVWGLSK.L		R.SIQMDGLVWGLSK.L
23	39	2	1885.92	2.7	1	60.4	25	95.00%	K.SFIEGYEPSQADAVVFK.A		K.SFIEGYEPSQADAVVFK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
79	RL13_SCHPO	25.96%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
172	183	2	1398.66	5.4	0	54	25.5	95.00%	K.NFNAFSTLSNER.A		K.NFNAFSTLSNER.A
118	128	3	1326.79	4.7	0	51.2	15.6	95.00%	K.VYLAHLIVFPR.K		K.VYLAHLIVFPR.K
46	64	4	2080.27	3.1	0	20	4.77	95.00%	K.IAPRPVEAIRPAVKPPTIR.Y		K.IAPRPVEAIRPAVKPPTIR.Y
89	100	2	1263.7	3.9	1	28.9	19.9	95.00%	R.VASTIGIPVDHR.R		R.VASTIGIPVDHR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
80	RS8A_SCHPO	35.50%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
60	74	2	1568.72	4.4	1	94.1	26	95.00%	R.LDSGNFSWGSEGVSK.K		R.LDSGNFSWGSEGVSK.K
165	178	2	1475.79	4.1	0	33.2	20.9	95.00%	R.LYAVVSSRPGQSGR.C		R.LYAVVSSRPGQSGR.C
152	164	2	1363.68	4.8	1	51.3	24.1	95.00%	K.VDSALETQFAAGR.L		K.VDSALETQFAAGR.L
78	92	2	1751.93	1.7	0	32.4	20.6	95.00%	R.IIQVAYHPSNNELVR.T		R.IIQVAYHPSNNELVR.T
111	124	3	1682.82	4.5	0	23.1	24.8	94.20%	R.VWYETHYGILMGSK.G		R.VWYETHYGILMGSK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
81	COFI_SCHPO	32.12%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
81	94	2	1584.9	4.1	1	54.1	16.2	95.00%	K.IIFISWSPDVAPIK.S		K.IIFISWSPDVAPIK.S
122	133	2	1413.71	2	0	91.9	23.9	95.00%	D.FSEVAYETVLEK.V		R.AFTGIGTDIQATDFSEVAYETVLEK.V
8	20	2	1548.76	4.6	0	71.2	25.7	95.00%	K.VSPECLEAFQELK.L	Carbamidomethyl (+57)	K.VSPECLEAFQELK.L

117	133	2	1941.96	2.2	1	102	24.3	95.00%	D.IQATDFSEVAYETVLEK.V		R.AFTGIGTDIQATDFSEVAYETVLEK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
82	STI1_SCHPO	14.55%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
146	164	2	1935.97	6.4	1	78.1	23.7	95.00%	K.LASNPETASLLADSAFMAK.L		K.LASNPETASLLADSAFMAK.L
112	132	2	2007.97	4.2	0	89.9	25.6	95.00%	K.SVEAAQTQAASGAGGFNPFAK.L		K.SVEAAQTQAASGAGGFNPFAK.L
168	183	2	1781.88	4.3	1	66.6	24.7	95.00%	K.IQQNPGSIMAELNDPR.M		K.IQQNPGSIMAELNDPR.M
550	560	2	1154.63	3	0	52.9	21	95.00%	D.PAMQAILGQAR.E		K.DPEVLGILQDPAMQAILGQAR.E
247	258	2	1318.67	3.5	1	65.1	24.5	95.00%	D.KTAEELEEAATK.E		K.EEFAPSSSTPSADSAKPETTNPPPQPQPQASEPMEEDKTAEELEEAATK.E
371	377	2	800.44	3.8	1	29.8	25.5	95.00%	R.TPDILSR.L		R.TPDILSR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
83	YA03_SCHPO	19.18%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	47	2	1743.88	2.4	0	87.8	23.8	95.00%	D.PVLTSEGIEQCEALAK.E	Carbamidomethyl (+57)	R.DPVLTSEGIEQCEALAK.E
147	172	3	2896.59	3.1	1	53.2	15.4	95.00%	R.SKEALEYLAALPQQQIAVITHSAFIR.F		R.SKEALEYLAALPQQQIAVITHSAFIR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
84	RS3B_SCHPO	11.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
228	241	2	1524.79	4.4	1	71.2	22.7	95.00%	K.LLELHGESQDVGTK.V		K.LLELHGESQDVGTK.V
200	213	2	1513.87	4.8	0	38.9	14.8	95.00%	R.ATGSIFPLQNVLVR.K		R.ATGSIFPLQNVLVR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
85	IF5A1_SCHPO	34.39%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
74	87	2	1540.74	2.1	1	43.5	25.9	95.00%	D.MSPSTHNMDVPVVK.R		K.YEDMSPSTHNMDVPVVK.R
2	28	3	2979.31	4	1	77.3	26.7	95.00%	M.AEEEHVDFEGGEAGASLTFPMQCSALR.K	Acetyl (+42)/ Carbamidomethyl (+57)	-.MAEEEHVDFEGGEAGASLTFPMQCSALR.K
9	29	3	2256.07	1.7	1	43.3	26	95.00%	D.FEGGEAGASLTFPMQCSALRK.N	Carbamidomethyl (+57)	-.MAEEEHVDFEGGEAGASLTFPMQCSALRK.N
58	69	2	1352.76	3	1	46.3	17.3	95.00%	K.VHIVALDIFNGR.K		K.VHIVALDIFNGR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
86	CDC48_SCHPO	3.31%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
550	563	2	1522.75	3.6	0	43.8	24.4	95.00%	K.AIANECSANFISVK.G	Carbamidomethyl (+57)	K.AIANECSANFISVK.G
774	786	3	1606.83	4.7	1	28.9	22.6	95.00%	R.RYEAYAHQLLTSR.G		R.RYEAYAHQLLTSR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
87	DHE4_SCHPO	15.30%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
334	353	2	2102.95	3.3	0	126	26.5	95.00%	R.YVAEGSNMGSSAEAVEVFEK.S		R.YVAEGSNMGSSAEAVEVFEK.S
25	34	3	1266.71	4.3	1	33.7	18.2	95.00%	K.LFEVHPELKR.V		K.LFEVHPELKR.V
356	367	2	1231.57	4.5	0	27.7	25.3	94.10%	R.ASGEGCWLAPGK.A	Carbamidomethyl (+57)	R.ASGEGCWLAPGK.A
93	101	2	1127.61	5.6	0	29.2	22.5	95.00%	K.FLGFEQIFK.N		K.FLGFEQIFK.N
399	416	2	1950.98	4.6	1	78.4	22.9	95.00%	K.LAGIMQNIFEQSTDVASK.Y		K.LAGIMQNIFEQSTDVASK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
88	GLNA_SCHPO	17.83%	100%	4									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
153	170	2	1809.83	4.4	0	40.7	26.4	95.00%	K.GGFPGPQGPFYCGVGTGR.V	Carbamidomethyl (+57)	K.GGFPGPQGPFYCGVGTGR.V		
345	359	2	1749.87	2.9	0	69.6	24.6	95.00%	D.PYLVTGIITETMFEH.-		R.RPASSIDPYLVTGIITETMFEH.-		
237	260	4	2635.31	3.2	1	28.9	24	95.00%	K.ISFHPKPILGDWNGAGCHTNVSTK.D	Carbamidomethyl (+57)	K.ISFHPKPILGDWNGAGCHTNVSTK.D		
338	359	3	2476.24	4.1	1	26.8	22.9	95.00%	R.RPASSIDPYLVTGIITETMFEH.-		R.RPASSIDPYLVTGIITETMFEH.-		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
89	RL10A_SCHPO	26.24%	100%	4									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
117	128	3	1265.71	4.6	0	30	18.7	95.00%	R.HAFGKPNGLVAR.V		R.HAFGKPNGLVAR.V		
129	139	2	1228.7	4.7	0	40	19.2	95.00%	R.VNIGQILMSVR.T		R.VNIGQILMSVR.T		
41	69	3	3260.58	4	1	68.1	23.4	95.00%	R.AGVDEFPLCIHLVSNEYEQITSEALEAAR.I	Carbamidomethyl (+57)	R.AGVDEFPLCIHLVSNEYEQITSEALEAAR.I		
33	38	2	719.4	4.8	1	27.1	21.6	93.70%	R.IFDLGR.K		R.IFDLGR.K		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
90	ACL1_SCHPO	12.03%	100%	6									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
369	381	2	1420.73	4.5	0	44	23.3	95.00%	R.GSELTYNNVPISK.V		R.GSELTYNNVPISK.V		
171	182	3	1338.74	4.8	0	23.6	19.4	94.80%	K.LYRPGSVAYVSK.S		K.LYRPGSVAYVSK.S		
313	326	2	1570.9	3.9	0	58.3	15.2	95.00%	K.LPALLQEVYEGLVK.K		K.LPALLQEVYEGLVK.K		
156	170	2	1506.72	3.3	1	45.7	25.6	95.00%	K.IGNTGGMMDNIVASK.L		K.IGNTGGMMDNIVASK.L		
313	327	3	1699	4	1	30.3	10.4	95.00%	K.LPALLQEVYEGLVKK.G		K.LPALLQEVYEGLVKK.G		
137	155	2	1926.08	3.3	0	40.4	15.8	95.00%	K.NVVIIGPATVGGIKPGCFK.I	Carbamidomethyl (+57)	K.NVVIIGPATVGGIKPGCFK.I		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
91	PYC_SCHPO	5.74%	100%	6									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
829	838	2	1275.63	4.5	1	27.7	24.3	94.50%	K.QLEFDNNQLR.E		K.QLEFDNNQLR.E		
1111	1129	3	1901.98	2.6	0	42.9	22.2	95.00%	D.PGNPGHVAAPMSGTIVEIR.V		R.ADPGNPGHVAAPMSGTIVEIR.V		
1109	1129	3	2088.05	4.4	1	38.2	23	95.00%	R.ADPGNPGHVAAPMSGTIVEIR.V		R.ADPGNPGHVAAPMSGTIVEIR.V		
917	929	2	1447.76	4.7	1	42.2	23	95.00%	K.VVGDLAQFMVQNK.L		K.VVGDLAQFMVQNK.L		
302	315	2	1628.75	2	1	37.3	26.1	95.00%	K.YCNAGTAEFLLDQK.G	Carbamidomethyl (+57)	K.YCNAGTAEFLLDQK.G		
839	848	2	1297.58	4.8	1	38.2	25.9	95.00%	R.EIDSYWAQMR.L		R.EIDSYWAQMR.L		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
92	THRC_SCHPO	10.70%	100%	4									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
265	282	2	1945.01	4.9	1	46.3	22	95.00%	R.FIVPTGNFGDILAGYYAK.R		R.FIVPTGNFGDILAGYYAK.R		
421	432	2	1235.67	2.6	0	41.6	21.1	95.00%	D.PHTAVGVETGLR.C		K.IYESDHYIIDPHTAVGVETGLR.C		
157	166	2	1007.54	3.2	0	33	20.8	95.00%	D.TGSAAIYGLR.G		R.DHLTVVGATSGDTGSAAIYGLR.G		
313	327	2	1443.73	4.4	1	39.8	24.3	95.00%	K.ADSTQVSPSGPISAK.E		K.ADSTQVSPSGPISAK.E		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
93	LYS12_SCHPO	20.44%	100%	6									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
197	208	2	1324.65	5.3	1	41.8	25.1	95.00%	K.SNVMSVTDGLFR.E		K.SNVMSVTDGLFR.E		
298	307	2	1044.58	4.6	0	32.2	21.9	95.00%	R.GIANPVATFR.S		R.GIANPVATFR.S		
188	196	3	1047.69	4.7	0	25.1	3.01	95.00%	K.KPLVTIIHK.S		K.KPLVTIIHK.S		
127	138	2	1568.72	4	1	44	26.2	95.00%	R.ENTECLYVKEER.M	Carbamidomethyl (+57)	R.ENTECLYVKEER.M		
86	97	2	1231.7	4.7	0	25.9	18.9	92.10%	K.VAGYSSPIVALR.K		K.VAGYSSPIVALR.K		
67	85	3	2071.06	4.3	1	52.5	22	95.00%	R.LKTECNAALFGAVQSPTHK.V	Carbamidomethyl (+57)	R.LKTECNAALFGAVQSPTHK.V		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
94	NACA_SCHPO	29.48%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	75	2	1164.62	5.8	0	59.3	21.7	95.00%	K.SSNNAYIVLGK.V		K.SSNNAYIVLGK.V
11	26	2	1637.87	4.6	0	55.2	20.5	95.00%	K.ISELPAGSTTVVHAEK.A		K.ISELPAGSTTVVHAEK.A
52	64	2	1540.93	4.4	0	50.2	10.8	95.00%	K.NILLIINEPIVYK.S		K.NILLIINEPIVYK.S
76	86	2	1189.58	4.9	1	47.2	25.4	95.00%	K.VTVEDMAAQAR.A		K.VTVEDMAAQAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
95	THI4_SCHPO	13.90%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
373	385	2	1353.71	4.1	1	37.5	22.1	95.00%	R.GVDSISQHTLAAR.I		R.GVDSISQHTLAAR.I
125	140	2	1686.81	2.4	1	68.8	25.4	95.00%	D.GADYVGIGSIYETNTK.D		K.AAADGADYVGIGSIYETNTK.D
27	42	3	1733.95	4.6	0	28	18.1	95.00%	R.QVEEGILGGVTLVQHR.E		R.QVEEGILGGVTLVQHR.E
237	248	2	1322.76	4.7	1	31.5	14.8	95.00%	K.DLLNQIPAALQK.L		K.DLLNQIPAALQK.L
106	120	2	1628.86	1.5	0	60	21.6	95.00%	D.AIIGVSTNNIEEIEK.A		K.ILGDDAIIGVSTNNIEEIEK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
96	LEU1_SCHPO	14.38%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
82	99	2	1998.98	4.3	1	62	25	95.00%	K.EIEVGFPSASQTDFAFVR.H		K.EIEVGFPSASQTDFAFVR.H
464	479	2	1742.82	4.9	1	69.1	25.9	95.00%	R.FSVNDYTLSSNGPQSK.C		R.FSVNDYTLSSNGPQSK.C
389	398	2	1134.61	1.9	0	26.2	21.4	92.50%	D.VNSEYAAIIR.V		K.VPYLPLDPHDVNSEYAAIIR.V
341	362	3	2346.15	2.9	1	44.7	24.6	95.00%	R.HPYAGNLVFTAFSGSHQDAISK.G		R.HPYAGNLVFTAFSGSHQDAISK.G
137	151	3	1761.87	4	0	33.2	25	95.00%	K.NATVHLYNACSPLFR.E	Carbamidomethyl (+57)	K.NATVHLYNACSPLFR.E
386	398	3	1483.75	2.4	1	35.3	24.4	95.00%	D.PHDVNSEYAAIIR.V		K.VPYLPLDPHDVNSEYAAIIR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
97	VATA_SCHPO	18.74%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
89	114	4	2751.53	2.9	1	22.2	11.5	95.00%	R.TGKPLSVELGPGLAETIYDGIQRPLK.Q		R.TGKPLSVELGPGLAETIYDGIQRPLK.Q
465	476	2	1580.77	4.7	0	39.5	25.5	95.00%	K.YINALQPWYEER.V		K.YINALQPWYEER.V
128	136	2	1002.51	5	0	25.2	23.9	90.90%	R.GINTESLNR.E		R.GINTESLNR.E
373	389	2	1752.85	8	1	36.9	25.3	95.00%	R.LAEMPADSGYPAYLGAK.L		R.LAEMPADSGYPAYLGAK.L
317	331	2	1544.81	4.6	0	49.4	22.6	95.00%	R.TTLVANTSNMPVAAR.E		R.TTLVANTSNMPVAAR.E
182	198	2	1838.88	4.6	1	73	26	95.00%	R.GTVTYIAEAGSYHVDEK.L		R.GTVTYIAEAGSYHVDEK.L
221	240	3	2105.14	4.1	1	35.3	17.6	95.00%	R.AARPVADNLTANQPLLTGQR.V		R.AARPVADNLTANQPLLTGQR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
98	IMDH_SCHPO	10.50%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	139	2	1621.89	1.9	1	50	18.3	95.00%	D.PVVFSPQHTVGDVLK.I		K.YENGFILDPVVFSPQHTVGDVLK.I
303	313	2	1155.67	4.5	1	51.3	18.8	95.00%	K.IDVIAGNVVTR.E		K.IDVIAGNVVTR.E
2	15	2	1636.88	4	0	27	20.6	93.60%	M.SAFKPYTEALEVLK.K	Acetyl (+42)	-.MSAFKPYTEALEVLK.K
125	136	2	1281.64	2.2	1	32.5	24	95.00%	D.PVVFSPQHTVGD.V		K.YENGFILDPVVFSPQHTVGDVLK.I
419	433	2	1421.67	3.9	0	52.2	26	95.00%	R.GMGSIAAMEGTGVNK.N		R.GMGSIAAMEGTGVNK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
99	DAK1_SCHPO	7.93%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
45	66	3	2123.05	5.3	0	21	24	90.80%	K.NVSVISGGGAGHEPTHSSFVGK.G		K.NVSVISGGGAGHEPTHSSFVGK.G
527	538	2	1301.63	4.7	1	60.8	25	95.00%	K.TNDLNAAVEEAR.K		K.TNDLNAAVEEAR.K
388	399	2	1358.73	4.4	0	25.9	21.4	92.10%	R.QAIVNSMENLIK.A		R.QAIVNSMENLIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

100	RS23_SCHPO	14.69%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
81	88	2	884.44	2.7	1	35.3	21.8	95.00%	K.VTAFVPHD.G		K.VTAFVPHDGCLNFVDENDEVLLSGFGR.K		
125	137	2	1326.74	4.4	0	55.5	19.2	95.00%	K.VAGVGLSALFHEK.K		K.VAGVGLSALFHEK.K		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
101	MMF1_SCHPO	37.65%	100%	4									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
59	75	2	1747.86	2.8	0	34.8	25	95.00%	K.ANGVIYCSGQIPVANGK.V	Carbamidomethyl (+57)/ Deamidation (+1)	K.ANGVIYCSGQIPVANGK.V		
87	105	2	2116.09	4.6	0	131	22.6	95.00%	R.QCLLNLQEVLTEAGSSLNK.I	Carbamidomethyl (+57)	R.QCLLNLQEVLTEAGSSLNK.I		
125	137	2	1483.81	3.9	1	42.4	19.2	95.00%	K.VYTEVLPDPKPAR.S		K.VYTEVLPDPKPAR.S		
47	58	2	1247.66	5.3	0	27.4	22.3	94.10%	K.LSSAGPYNQAIK.A		K.LSSAGPYNQAIK.A		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
102	IF4A_SCHPO	12.50%	100%	3									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
58	69	2	1173.61	5	1	69	24.1	95.00%	R.DVLAQAQSGTGK.T		R.DVLAQAQSGTGK.T		
33	48	2	1854.94	3.8	0	30.4	23.4	95.00%	R.GIYAYGFERPSAIQQR.A		R.GIYAYGFERPSAIQQR.A		
372	392	2	2549.19	2.9	1	26.7	26.1	91.50%	R.EIEQFYNTHIEEMPMNIADLI.-		R.EIEQFYNTHIEEMPMNIADLI.-		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
103	RL15A_SCHPO	19.90%	100%	3									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
115	128	2	1699.83	4.1	1	73.6	25.6	95.00%	R.VLNSYWVNQDATYK.F		R.VLNSYWVNQDATYK.F		
78	93	3	1761.94	4.8	0	23.7	20.7	95.00%	K.GQTYGKPVHQGVNHLK.Y		K.GQTYGKPVHQGVNHLK.Y		
148	157	3	1218.69	4.4	0	24.4	18.5	95.00%	R.INWIVNPVHK.H		R.INWIVNPVHK.H		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
104	RS22_SCHPO	27.69%	100%	3									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
98	108	2	1171.7	4.9	0	29.1	14.5	95.00%	R.QVGVIVLTTSR.G		R.QVGVIVLTTSR.G		
4	19	2	1814.9	4.5	1	77.6	24	95.00%	R.QSVLADCLNNIVNAER.R	Carbamidomethyl (+57)	R.QSVLADCLNNIVNAER.R		
89	97	2	1111.62	5.6	0	31.9	19.5	95.00%	K.WVNQLLPSR.Q		K.WVNQLLPSR.Q		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
105	GCST_SCHPO	15.25%	100%	4									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
81	97	2	1779.9	3.9	0	64.1	24	95.00%	R.GENATAYLESITPSSLK.E		R.GENATAYLESITPSSLK.E		
327	344	2	1771.88	2.7	0	74.4	23.8	95.00%	D.GVEVGQVTSGCPSPTLGK.N	Carbamidomethyl (+57)	R.HGSAVEVDGVEVGQVTSGCPSPTLGK.N		
319	344	3	2566.25	4.5	1	41.9	24.8	95.00%	R.HGSAVEVDGVEVGQVTSGCPSPTLGK.N	Carbamidomethyl (+57)	R.HGSAVEVDGVEVGQVTSGCPSPTLGK.N		
165	180	2	1623.93	4	0	75.8	14.1	95.00%	R.ALIAIQGPETASVVQK.L		R.ALIAIQGPETASVVQK.L		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
106	RS4B_SCHPO	11.07%	100%	3									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
222	233	2	1232.68	5.6	0	42.4	20.7	95.00%	R.LSNVFVIGEAGK.S		R.LSNVFVIGEAGK.S		
246	252	2	846.45	4.8	0	45.4	23.4	95.00%	K.LSITEER.D		K.LSITEER.D		
40	49	2	1258.72	4.7	0	26.1	18.5	92.40%	R.ECLPLIVFLR.N	Carbamidomethyl (+57)	R.ECLPLIVFLR.N		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
107	SODC_SCHPO	36.36%	100%	3									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
98	116	2	1984.04	4.4	1	72.6	21.6	95.00%	K.TTFSDSVISLFGANSIIGR.T		K.TTFSDSVISLFGANSIIGR.T		
81	91	2	1154.52	3.2	1	27.3	25.6	93.20%	R.HVGDLGNLESD.A		R.HVGDLGNLESDAQGNIK.T		

45	70	3	2825.25	4.3	1	41.5	27	95.00%	R.GFHIHQFGDNTNGCTSAGPHFNPEGK.T	Carbamidomethyl (+57)	R.GFHIHQFGDNTNGCTSAGPHFNPEGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
108	RL27A_SCHPO	22.06%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	48	3	1461.76	5.9	0	42.8	22.9	95.00%	K.SHPFGHAVVAGVER.Y		K.SHPFGHAVVAGVER.Y
23	34	2	1269.74	4.4	1	65.4	16.3	95.00%	K.VVILQAIDQGSK.S		K.VVILQAIDQGSK.S
35	52	4	1963.05	4.3	1	23.2	19.5	95.00%	K.SHPFGHAVVAGVERYPLK.V		K.SHPFGHAVVAGVERYPLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
109	YDG7_SCHPO	12.15%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
7	23	3	1939.91	3.9	1	22.9	26.2	92.10%	K.YFENAQNVHFTLADGSK.I		K.YFENAQNVHFTLADGSK.I
183	204	3	2603.37	3.4	0	27.8	19.3	95.00%	K.VKPAVHQMELHPFLPQTEFVEK.H		K.VKPAVHQMELHPFLPQTEFVEK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
110	RS0B_SCHPO	12.54%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	88	4	2453.26	4	1	67.3	21.4	95.00%	R.VIATIENPADVCVISSRPYGHR.A	Carbamidomethyl (+57)	R.VIATIENPADVCVISSRPYGHR.A
2	15	2	1484.75	3.2	1	51	23.7	95.00%	M.AESIARPSVLNATD.D	Acetyl (+42)	-.MAESIARPSVLNATDDDIK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
111	SYDC_SCHPO	6.03%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
281	294	2	1356.6	4.8	0	27.5	25.6	93.50%	K.MSGASSEGGSNVFK.I		K.MSGASSEGGSNVFK.I
200	210	2	1229.65	4.9	1	29.1	22.8	95.00%	K.NLPFLVEDAGR.S		K.NLPFLVEDAGR.S
490	499	2	1300.55	3.9	1	26.9	26.1	91.80%	R.YSNSYDFFMK.G		R.YSNSYDFFMK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
112	PUR8_SCHPO	11.00%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
268	292	3	2694.37	3.3	1	34.7	21.9	95.00%	R.LLANLKEVEEPFEAGQIGSSAMAYK.R		R.LLANLKEVEEPFEAGQIGSSAMAYK.R
450	460	2	1248.61	5.4	0	26.4	24.3	92.90%	R.APEQTESFVNK.D		R.APEQTESFVNK.D
372	388	2	1909.94	4.9	0	55.7	24.8	95.00%	R.AELPFMATENIIMAMTK.H		R.AELPFMATENIIMAMTK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
113	GLT1_SCHPO	5.59%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
624	638	2	1701.91	4.2	0	45.5	21	95.00%	R.MPTPILTVEEFNALK.N		R.MPTPILTVEEFNALK.N
1690	1707	2	2063.08	4.1	0	61.9	21.1	95.00%	K.EALTQLLLTNNFPEFTGR.V		K.EALTQLLLTNNFPEFTGR.V
1442	1464	3	2335.04	4.9	1	32.4	27	95.00%	R.NSGAIAVVEGVGDHGCEYMTGGR.V	Carbamidomethyl (+57)	R.NSGAIAVVEGVGDHGCEYMTGGR.V
1845	1856	2	1155.66	2.3	0	40.2	18.3	95.00%	D.AVVLASGSTVPR.D		K.VYDAVVLASGSTVPR.D
1022	1038	3	1639.81	4.9	0	25.7	24.5	95.00%	K.MAQGAKPGEGGELPGNK.V		K.MAQGAKPGEGGELPGNK.V
672	685	2	1555.69	5.3	1	68	26	95.00%	R.ICSEADTAVNEGYK.A	Carbamidomethyl (+57)	R.ICSEADTAVNEGYK.A
1758	1776	2	1792.99	3.3	1	78.8	17.7	95.00%	R.VAIIGSGPAGLAAADQLNR.A		R.VAIIGSGPAGLAAADQLNR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
114	ADK_SCHPO	21.18%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
253	267	2	1483.87	4.5	1	69.4	14.9	95.00%	R.VVVITQGADATIVAK.D		R.VVVITQGADATIVAK.D
86	96	2	1295.61	3.7	1	43.7	25.7	95.00%	K.FADMLLESNEK.A		K.FADMLLESNEK.A
230	245	2	1688.89	3.8	1	56.9	21.8	95.00%	K.STDVQEIALALSSVEK.V		K.STDVQEIALALSSVEK.V
126	138	2	1424.68	5.2	0	51	25.2	95.00%	R.SLCTNLGAANNYK.L	Carbamidomethyl (+57)	R.SLCTNLGAANNYK.L

107	123	2	1770.9	1.9	0	92.7	23.1	95.00%	D.PTTPTGVCAVVLSNNNK.N	Carbamidomethyl (+57)	R.SEFSVDPTTPTGVCAVVLSNNNK.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
115	ASNS_SCHPO	5.39%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
516	523	2	1035.55	6.3	1	30	21.3	95.00%	K.LFDEIFPR.Q		K.LFDEIFPR.Q
154	165	2	1327.63	2.8	1	61.1	25.2	95.00%	D.SPDTAYFASELK.A		R.DPIGITTLYQGFSSDSPDTAYFASELK.A
399	408	2	1120.54	4.9	0	26.3	24	92.70%	K.STMAWGLEAR.V		K.STMAWGLEAR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
116	PYR1_SCHPO	2.85%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1880	1906	3	2689.36	3.3	0	28.6	22.3	95.00%	K.VSALMSPGLPHAAPSLAEAFGQAPENK.A		K.VSALMSPGLPHAAPSLAEAFGQAPENK.A
1771	1784	2	1494.85	4.1	0	35.2	15.7	95.00%	R.EAIPLLLTAVNEGR.L		R.EAIPLLLTAVNEGR.L
457	466	2	1084.56	6.1	0	38.9	22.8	95.00%	K.LPGGTIEENR.S		K.LPGGTIEENR.S
1758	1770	2	1371.7	4.4	0	56.2	24	95.00%	K.FVGNTAFTGFGVR.E		K.FVGNTAFTGFGVR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
117	PMM_SCHPO	11.28%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
29	43	2	1728.92	4.2	0	56.6	21.1	95.00%	R.LSVSPEMLETLQNLR.K		R.LSVSPEMLETLQNLR.K
45	58	2	1347.75	4.4	1	41.6	20	95.00%	K.VVAIGFVGGSDLSK.Q		K.VVAIGFVGGSDLSK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
118	PMP20_SCHPO	28.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
30	55	3	2747.41	3	0	39.4	21.2	95.00%	K.FIIVGVPGAFTPPCSSQVPGYIANEK.Q	Carbamidomethyl (+57)	K.FIIVGVPGAFTPPCSSQVPGYIANEK.Q
11	29	3	2215.12	2.2	0	40.6	22.7	95.00%	K.VTLWENKPEEVVEFPSQGK.F		K.VTLWENKPEEVVEFPSQGK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
119	RS2_SCHPO	26.48%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
64	74	2	1441.73	5.7	1	25.1	23.5	90.60%	K.EYQIVDYFLPR.L		K.EYQIVDYFLPR.L
51	63	2	1566.86	4.2	0	34.6	18.6	95.00%	K.SIEEIYLYSLPIK.E		K.SIEEIYLYSLPIK.E
174	185	3	1138.69	4.8	1	25.2	12.6	95.00%	R.GAGLVAAPVTKR.F		R.GAGLVAAPVTKR.F
186	200	2	1799.86	4.8	1	102	25.8	95.00%	R.FLQLAGIEDCYTQSR.G	Carbamidomethyl (+57)	R.FLQLAGIEDCYTQSR.G
141	156	3	1696.87	4.8	1	37.6	23.6	95.00%	R.GYWGTALGDPHTVPVK.V		R.GYWGTALGDPHTVPVK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
120	TRX1_SCHPO	29.13%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
40	54	2	1796.83	4.6	1	68.4	26.5	95.00%	K.FEQFSNTYSDATFIK.V		K.FEQFSNTYSDATFIK.V
80	94	2	1567.83	3	1	72.1	21.7	95.00%	K.NGEKIEEIVGANPAK.L		K.NGEKIEEIVGANPAK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
121	SYRC_SCHPO	11.00%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
452	467	2	1759.87	3.7	1	55	24.7	95.00%	K.YAQVENPEEVADIVGK.T		K.YAQVENPEEVADIVGK.T
163	180	2	1987.02	4.1	0	33.9	21.3	95.00%	R.STIIGSFLANLHESQGWK.V		R.STIIGSFLANLHESQGWK.V
480	489	2	1284.6	5.9	1	39.4	25.3	95.00%	R.INNYAFDWSR.M		R.INNYAFDWSR.M
120	129	2	1279.77	2.5	0	29.5	11.1	95.00%	K.LILPIIWEQR.E		K.LILPIIWEQR.E
11	24	2	1544.86	4.5	1	46.7	17.6	95.00%	K.SLSTLGLQDLPVFR.E		K.SLSTLGLQDLPVFR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
122	RL6_SCHPO	22.05%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	64	2	1497.84	5	0	33.1	18.6	95.00%	R.ASLAPGTVCILLAGR.F	Carbamidomethyl (+57)	R.ASLAPGTVCILLAGR.F
70	87	2	1959.1	3.1	1	33.6	14.3	95.00%	R.VVVLSQLEDTLVVTGPYK.V		R.VVVLSQLEDTLVVTGPYK.V
109	118	2	1031.56	5.5	1	31.2	22.7	95.00%	K.IDVSGVSVEK.F		K.IDVSGVSVEK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
123	RS11_SCHPO	17.76%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	64	2	1161.6	4.7	0	33.4	23.4	95.00%	K.CPFVGQVSIR.G	Carbamidomethyl (+57)	K.CPFVGQVSIR.G
114	130	2	1870.96	3.6	1	44.1	23.3	95.00%	R.INEGDVVTVGQCRPLSK.T	Carbamidomethyl (+57)	R.INEGDVVTVGQCRPLSK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
124	YHZ8_SCHPO	25.25%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
75	103	3	3217.69	3	0	57.2	18.5	95.00%	K.TSNPFLAFANYLTSTHAPLAEPLQLLNFK.V		K.TSNPFLAFANYLTSTHAPLAEPLQLLNFK.V
2	13	2	1361.7	3.8	0	57.2	23	95.00%	M.SFPASTHVYIAK.I	Acetyl (+42)	-.MSFPASTHVYIAK.I
156	164	2	1004.57	3.4	0	44.7	20.1	95.00%	D.PSLYAVVTR.Y		K.ADTSLIIHSLDDPSLYAVVTR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
125	AATR1_SCHPO	9.07%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
305	317	2	1562.83	2.8	0	60.9	20.8	95.00%	R.VGWFTAQPLFIER.G		R.VGWFTAQPLFIER.G
38	54	2	1856.03	4.5	0	36.8	17	95.00%	K.IISLAGGLPNPEYFPIR.E		K.IISLAGGLPNPEYFPIR.E
7	19	3	1436.71	5.4	1	43.2	25.1	95.00%	K.DLSHHLSVESASR.K		K.DLSHHLSVESASR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
126	RS5B_SCHPO	13.79%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
20	32	2	1552.83	2.3	1	36.8	20	95.00%	K.LFNKFPFEGVEVK.D		K.LFNKFPFEGVEVK.D
167	181	2	1646.82	3.2	0	74.1	23.9	95.00%	K.SISECLAEEIINAAK.G	Carbamidomethyl (+57)	K.SISECLAEEIINAAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
127	P25_SCHPO	17.82%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
36	52	2	1976.06	3.1	0	52.6	19.4	95.00%	K.AVIYQFPETLSPEILEK.M		K.AVIYQFPETLSPEILEK.M
2	20	2	2064.1	3.1	0	81.2	19.8	95.00%	M.STANTVAIVIYSTYGHVVK.L	Acetyl (+42)	-.MSTANTVAIVIYSTYGHVVK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
128	GCSP_SCHPO	14.06%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
953	965	2	1458.76	1.1	1	43.1	23.1	95.00%	K.DNNLLVNAPHPQK.D		K.DNNLLVNAPHPQK.D
657	684	3	2835.48	2	0	31.8	19.2	95.00%	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C	Carbamidomethyl (+57)	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C
379	412	3	3679.8	2.3	0	51.4	21.3	95.00%	K.ATSNICTAQALLANMSAFYAIYHGPNGLQEIANR.I	Carbamidomethyl (+57)	K.ATSNICTAQALLANMSAFYAIYHGPNGLQEIANR.I
577	604	3	3166.6	3.7	0	40.5	20.4	95.00%	K.LNAVTEMMPITNPLFANIHPYVPEEQAK.G		K.LNAVTEMMPITNPLFANIHPYVPEEQAK.G
87	126	3	4380.08	3.8	1	62.7	22.9	95.00%	R.TPESQLMAFGSVNPNEKNPPVNYSESEFTTLANNVANQNK.L		R.TPESQLMAFGSVNPNEKNPPVNYSESEFTTLANNVANQNK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
129	RL3A_SCHPO	14.69%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
207	222	2	1837.9	4.3	1	73.9	25.2	95.00%	K.STFEQNEMIDVIGVTR.G		K.STFEQNEMIDVIGVTR.G
11	19	2	982.54	4.3	0	27.2	20.1	93.90%	R.HGSLGFLPR.K		R.HGSLGFLPR.K
249	266	3	2035.03	4.4	0	29.3	23.6	95.00%	K.VACIGAWHPANVQWTVAR.A	Carbamidomethyl (+57)	K.VACIGAWHPANVQWTVAR.A
37	50	3	1530.86	2.4	0	26.6	17.2	95.00%	D.ASKPVHLTAFLGYK.A		K.DDASKPVHLTAFLGYK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
130	RS17A_SCHPO	16.03%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	59	3	1133.6	4.6	0	24.5	22.7	95.00%	K.IAGYTTHLMK.R		K.IAGYTTHLMK.R
34	44	2	1156.68	4.8	1	51	17.6	95.00%	R.IVDEVAIIASK.R		R.IVDEVAIIASK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
131	SCE3_SCHPO	17.01%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
46	66	2	2113.97	4.9	1	94.2	27	95.00%	R.ATPSSADAGYNAPSSTFESVR.S		R.ATPSSADAGYNAPSSTFESVR.S
359	381	2	2403.05	5.1	1	111	27.3	95.00%	K.TPATEDAPATNAGEAEEEEGWTK.I		K.TPATEDAPATNAGEAEEEEGWTK.I
365	381	2	1788.79	2.8	0	95.3	27.2	95.00%	D.APATNAGEAEEEEGWTK.I		K.TPATEDAPATNAGEAEEEEGWTK.I
250	271	3	2195.06	2.9	0	28.5	24.8	95.00%	R.SSSNVNTEATPSATTTTSSKPK.R		R.SSSNVNTEATPSATTTTSSKPK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
132	NACB_SCHPO	26.49%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
95	116	2	2320.31	3	0	52.8	12.8	95.00%	K.TLSEILPGILNNLGPESLTALR.Q		K.TLSEILPGILNNLGPESLTALR.Q
73	90	2	1884.96	3.2	0	58.2	23	95.00%	R.APTVHSSLPNETTAIYGK.A		R.APTVHSSLPNETTAIYGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
133	RS10B_SCHPO	34.01%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	44	3	1428.82	4.9	0	23.6	17.2	94.80%	K.HPEVGVPNLQVIK.A		K.HPEVGVPNLQVIK.A
10	24	3	1621.94	4.8	0	31.6	13	95.00%	K.AIHQALFQQGVLVAK.K		K.AIHQALFQQGVLVAK.K
78	93	4	1859.01	4	1	23	18.8	95.00%	R.EYLHLPAEVVPATHKR.Q		R.EYLHLPAEVVPATHKR.Q
26	31	2	732.38	5.5	1	30.1	22.5	95.00%	K.DFNLPK.H		K.DFNLPK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
134	YHEF_SCHPO	20.20%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
54	65	2	1279.67	5.1	1	47	22.3	95.00%	K.SFIGLDALTESK.G		K.SFIGLDALTESKGEFFQR.M
30	41	3	1413.76	4.8	1	20.9	21.9	90.50%	R.LRGPHCGTYLLK.V	Carbamidomethyl (+57)	R.LRGPHCGTYLLKVVGTNATYVGEK.S
91	104	2	1616.85	1.9	0	42	22.8	95.00%	D.TANFTPLTFTTYLK.T		R.LFTIAENDTANFTPLTFTTYLKTCNPQSIENAMIPFVNTVTSEISFDAWAYTAQNSSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
135	THI22_SCHPO	4.90%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
138	151	2	1403.74	2.3	1	61	22.5	95.00%	D.PVMVATSGDSLVTK.D		K.LVVDPVMVATSGDSLVTK.D
423	435	2	1516.6	5.3	0	56.7	26	95.00%	K.SCEESPACTAYSR.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.SCEESPACTAYSR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
136	ARGD_SCHPO	11.11%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
311	332	3	2276.09	4.8	0	39.5	25.7	95.00%	K.IAAEIHPGEHGSTFGGNPVACR.V	Carbamidomethyl (+57)	K.IAAEIHPGEHGSTFGGNPVACR.V
139	154	2	1784.85	4.1	0	92.8	25.5	95.00%	K.IFFANCGTEANETALK.F	Carbamidomethyl (+57)	K.IFFANCGTEANETALK.F
213	223	2	1246.62	1.9	1	27.8	24.3	94.60%	D.PASIEQFVNDK.T		R.GFQPLLPDVVQAVYNDPASIEQFVNDK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
137	SYTC_SCHPO	4.27%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
248	258	2	1187.55	4.2	1	47.1	26.3	95.00%	K.NSSSYFLGDAK.N		K.NSSSYFLGDAK.N		
8	26	3	2136.14	4.2	1	27.4	18.9	95.00%	K.GVQASLDNLSLEIPFIQHR.L		K.GVQASLDNLSLEIPFIQHR.L		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
138	RL36A_SCHPO	24.24%	100%	3									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
2	11	2	966.59	4.6	0	38.2	14.5	95.00%	M.APGLVVGLNK.G		-.MAPGLVVGLNK.G		
83	96	2	1545.84	4.6	1	75.1	19.7	95.00%	K.GKIEELTSVIQSSR.L		K.GKIEELTSVIQSSR.L		
85	96	2	1360.73	3.8	0	56.4	21.8	95.00%	K.IEELTSVIQSSR.L		K.IEELTSVIQSSR.L		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
139	TRXB_SCHPO	18.94%	100%	5									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
78	89	2	1323.7	5	0	25.2	21.2	90.90%	R.FGTEIITETVSK.L		R.FGTEIITETVSK.L		
114	124	2	1044.6	3.3	0	61.7	18.6	95.00%	D.SVILATGASAR.R		K.YWLEGAEEEEPHTADSVILATGASAR.R		
61	72	2	1321.67	2.8	0	47.4	24.8	95.00%	D.GINGTTLTENFR.A		R.GELKPVMYEGMLANGIAAGGQLTTTTDVENFPGFPDGINGTTLTENFR.A		
165	175	2	1193.6	3.3	0	25.5	24.8	91.40%	D.SAAEEAQFLTK.Y		R.NKPLAVVGGGDSAAEEAQFLTK.Y		
99	124	3	2801.32	3.2	1	61.8	26.1	95.00%	K.YWLEGAEEEEPHTADSVILATGASAR.R		K.YWLEGAEEEEPHTADSVILATGASAR.R		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
140	Q1L854_SCHPO	7.32%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
14	27	2	1459.74	2.2	0	64.8	23.5	95.00%	D.LLGEETPAATTTEK.K		K.NLFDLLGEETPAATTTEK.K		
10	27	2	1948.97	3.6	1	75.2	24.6	95.00%	K.NLFDLLGEETPAATTTEK.K		K.NLFDLLGEETPAATTTEK.K		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
141	RANG_SCHPO	16.74%	100%	3									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
188	198	2	1253.61	5.8	0	35.7	24.3	95.00%	R.FANSENANLFK.E		R.FANSENANLFK.E		
174	187	2	1505.74	2.9	0	25.7	25.1	91.40%	D.VSEGEPTAETFAIR.F		R.SWVWTVAADVSEGEPTAETFAIR.F		
88	98	2	1353.6	4	0	43.5	25.9	95.00%	K.TNEEEETVEFK.M		K.TNEEEETVEFK.M		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
142	SLBR2_SCHPO	13.11%	100%	3									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
134	143	2	1115.56	4.3	0	27.1	23.5	93.80%	R.NIESSVQPSR.E		R.NIESSVQPSR.E		
166	192	3	3060.53	3.6	1	43.6	22.2	95.00%	R.LVTMEQELVREEAACLVAEAQLSNTTR.E	Carbamidomethyl (+57)	R.LVTMEQELVREEAACLVAEAQLSNTTR.E		
149	157	2	1075.63	4.5	1	33	17.2	95.00%	K.LLDQIYALK.H		K.LLDQIYALK.H		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
143	RS14_SCHPO	16.55%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
95	105	2	1037.57	5.3	0	47.1	19.9	95.00%	K.TPGPGAQAALR.A		K.TPGPGAQAALR.A		
73	84	3	1367.77	4	1	24.2	19.1	95.00%	K.CKEVGITALHIK.I	Carbamidomethyl (+57)	K.CKEVGITALHIK.I		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
144	PURA_SCHPO	14.29%	100%	4									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
206	224	3	2169.16	3.6	1	37.8	18.5	95.00%	R.LKPFVIDAVAFMYEALQSK.K		R.LKPFVIDAVAFMYEALQSK.K		

282	304	3	2420.22	4.2	1	27.4	22.7	95.00%	R.VGAGPFPTEQLNEIGDHLQSVGR.E		R.VGAGPFPTEQLNEIGDHLQSVGR.E
268	276	2	899.55	4.9	0	44.5	20.5	95.00%	R.IANSIGVVK.A		R.IANSIGVVK.A
126	136	2	1129.57	4.6	1	38.6	23.2	95.00%	R.ADALNEAELGK.Q		R.ADALNEAELGK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
145	RL19A_SCHPO	20.73%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
118	128	3	1386.74	5	0	32.3	21.9	95.00%	K.HLYHTLYLEAK.G		K.HLYHTLYLEAK.G
26	38	2	1429.68	2.8	0	92.7	25.5	95.00%	D.PNEISEISNANSR.Q		K.VWMDPNEISEISNANSR.Q
182	193	2	1422.69	3.6	1	31.8	25	95.00%	R.EQLYTAAEKIEE.-		R.EQLYTAAEKIEE.-
22	38	2	1960.9	4.1	1	66.6	26.4	95.00%	K.VWMDPNEISEISNANSR.Q		K.VWMDPNEISEISNANSR.Q
182	193	2	1422.69	3.6	1	31.8	25	95.00%	R.EQIYTAAEKIEE.-		R.EQLYTAAEKIEE.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
146	TBB_SCHPO	12.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
123	154	3	3205.55	2.6	1	82.9	24	95.00%	R.EAEACDALQGFQLTHSLGGGTGSGMGTLLLSK.I	Carbamidomethyl (+57)	R.EAEACDALQGFQLTHSLGGGTGSGMGTLLLSK.I
163	174	2	1249.62	3.9	0	41.3	24.3	95.00%	R.MMATFSVAPAPK.S		R.MMATFSVAPAPK.S
204	216	2	1406.75	3.6	0	43.4	22.1	95.00%	D.NEALSSIFANTLK.I		K.SSDTVVEPYNATLSMHQLVENSDETFCIDNEALSSIFANTLK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
147	RL12_SCHPO	39.39%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
68	83	2	1538.91	3.4	0	50.5	14.3	95.00%	R.QAAVSVVPSASALVIK.A		R.QAAVSVVPSASALVIK.A
97	114	3	1921.99	3.3	1	30.5	21.6	95.00%	K.NVAHSGNVSLDEIIEVAR.T		K.NVAHSGNVSLDEIIEVAR.T
17	31	2	1312.7	3.6	0	46	21.2	95.00%	R.AVGGEVAGGSTLAPK.I		R.AVGGEVAGGSTLAPK.I
131	146	2	1652.81	4	1	45.9	24.3	95.00%	K.EILGTAFSVGCTVDGK.N	Carbamidomethyl (+57)	K.EILGTAFSVGCTVDGK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
148	UBC4_SCHPO	14.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
118	128	3	1264.72	2.2	0	38.5	17	95.00%	D.PLVPEIAHVYK.T		K.VLLSICSLLTDPNPDDPLVPEIAHVYK.T
91	101	2	1244.65	4.6	1	28.4	23.2	95.00%	R.DQWSPALTISK.V		R.DQWSPALTISK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
149	AROG_SCHPO	16.67%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
22	46	3	2707.5	1.7	1	25.7	15.9	95.00%	R.VLGYNPLVPAALVQQEIPVSETSRK.V		R.VLGYNPLVPAALVQQEIPVSETSRK.V
203	226	3	2316.23	2.3	1	25.4	19.3	95.00%	D.GTVGVAIDAIGATAHPHTMLGVTK.Q		K.NGTDGTVGVAIDAIGATAHPHTMLGVTK.Q
186	198	2	1364.74	4.4	0	39.9	20.8	95.00%	R.ELASALSFPVGFK.N		R.ELASALSFPVGFK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
150	RS15A_SCHPO	39.87%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	85	2	1396.76	4.6	0	40.4	20	95.00%	K.TEAPLNEKPATVK.T		K.TEAPLNEKPATVK.T
71	85	3	1595.9	4.3	1	22.7	17.2	93.70%	K.AKTEAPLNEKPATVK.T		K.AKTEAPLNEKPATVK.T
109	135	4	3209.67	3.6	0	17.8	19.7	94.40%	K.LFNQVEIRPEMIGHYLGEFSITYKPTK.H		K.LFNQVEIRPEMIGHYLGEFSITYKPTK.H
90	108	2	2033.08	3.1	0	80.9	20.6	95.00%	R.NMIILPEMVGSVVGIYNGK.L		R.NMIILPEMVGSVVGIYNGK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
151	DYR_SCHPO	13.02%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

164	183	3	2062.15	3.7	1	25.4	14.1	95.00%	K.LTTPSLHIAGTSDTLVPLAR.S		K.LTTPSLHIAGTSDTLVPLAR.S
34	51	2	1958.89	2.1	1	35.4	27.2	95.00%	K.YAELHFPTGPVVADEEAD.P		K.YAELHFPTGPVVADEEADPNDEEEK.K
191	212	3	2537.31	3.6	0	37.3	21	95.00%	R.CENAHVLLHPGQHIVPQQAVYK.T	Carbamidomethyl (+57)	R.CENAHVLLHPGQHIVPQQAVYK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
152	RL31_SCHPO	21.24%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
91	105	2	1650.87	4.2	1	39.3	21	95.00%	K.ALYTYVQAVDVANPK.M		K.ALYTYVQAVDVANPK.M
7	15	2	986.56	5	0	39.5	21.7	95.00%	K.SAINQVVTR.D		K.SAINQVVTR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
153	DHOM_SCHPO	24.20%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	138	2	1568.79	4.5	1	56.7	23.6	95.00%	K.AFSASNDVYQNIIK.A		K.AFSASNDVYQNIIK.A
57	67	2	1391.68	4.7	1	33.1	24.9	95.00%	K.DYQPINLSEWK.N		K.DYQPINLSEWK.N
238	252	3	1526.81	2.4	0	31	21.4	95.00%	R.IAGVHVESASSFPVK.S		R.IAGVHVESASSFPVK.S
28	56	3	3047.4	3	0	33.8	26.2	95.00%	K.GFNENASTNGTTSFNVVAISSMEGHYVSK.D		K.GFNENASTNGTTSFNVVAISSMEGHYVSK.D
89	110	2	2284.21	4.5	1	95.1	20	95.00%	K.SPLPAILVDNTASEAIAQSYPK.F		K.SPLPAILVDNTASEAIAQSYPK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
154	KAD1_SCHPO	15.00%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
196	218	3	2621.39	2.8	1	47.7	18.4	95.00%	K.WAAVDAAQKPEQVWEQIVAILEK.A		K.WAAVDAAQKPEQVWEQIVAILEK.A
155	164	2	1126.6	2.6	1	24.9	21.8	90.30%	D.DVTGEPLIQR.S		K.DDVTGEPLIQR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
155	PGM_SCHPO	10.65%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
423	435	2	1529.66	4.3	1	62.5	26.4	95.00%	R.YDYEELENEAAGK.V		R.YDYEELENEAAGK.V
350	358	2	1160.54	5.2	1	29	25.3	95.00%	K.FFCNLFDAK.R	Carbamidomethyl (+57)	K.FFCNLFDAK.R
127	142	2	1631.79	4.4	0	81.8	25.3	95.00%	K.YNLGNGGPAPESVTEK.I		K.YNLGNGGPAPESVTEK.I
1	21	3	2330.21	3.2	0	23.9	20.7	95.00%	-.MIETIPTKPYEGQRPGTSGLR.K		-.MIETIPTKPYEGQRPGTSGLR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
156	SPI1_SCHPO	12.50%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
110	122	2	1514.77	4.6	0	58.5	24	95.00%	R.VCENIPIVLCGNK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VCENIPIVLCGNK.V
152	165	3	1783.91	4.6	0	29.2	23.2	95.00%	K.SNYNFEKPFLWLAR.K		K.SNYNFEKPFLWLAR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
157	SPEE_SCHPO	8.39%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	12	2	1291.72	4.1	0	43.5	18.5	95.00%	M.SVQELSHPLIK.D	Acetyl (+42)	-.MSVQELSHPLIK.D
18	31	2	1631.79	4.6	0	31.2	25.2	95.00%	R.EINNMWPGQAMTLK.V		R.EINNMWPGQAMTLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
158	RS13_SCHPO	15.23%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
44	55	2	1244.66	3.8	0	40.8	22.5	95.00%	K.GMSPSQIGVTLR.D		K.GMSPSQIGVTLR.D
10	20	2	1132.63	4.4	0	38.6	20.1	95.00%	K.GIASSALPYVR.S		K.GIASSALPYVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
159	SYKC_SCHPO	6.09%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
570	591	3	2490.33	2.8	1	30.8	18.1	95.00%	R.EVLLFPHMKPEVQAAEPTVVKE.-		R.EVLLFPHMKPEVQAAEPTVVKE.-
15	28	2	1454.8	4	1	41.2	19.6	95.00%	K.ALVLDPVTGEQVSK.T		K.ALVLDPVTGEQVSK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
160	RL23_SCHPO	25.18%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
15	34	2	2090	3.5	1	65.5	25.8	95.00%	R.MTLGLPVQAIMNCADNSGAK.N	Carbamidomethyl (+57)	R.MTLGLPVQAIMNCADNSGAK.N
51	65	2	1531.78	3.4	1	55.2	23.6	95.00%	R.LPAASCGDMVLATVK.K	Carbamidomethyl (+57)	R.LPAASCGDMVLATVK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
161	PABP_SCHPO	8.42%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
258	266	2	1068.57	4.8	0	26.6	21.3	93.10%	K.ANFTNVYIK.N		K.ANFTNVYIK.N
447	456	2	1142.61	4.9	0	33.9	22.1	95.00%	R.SQLEAQIQAR.N		R.SQLEAQIQAR.N
536	571	3	3524.72	4.6	0	28.7	23.2	95.00%	R.GPVPAQGRPMMMPGSVPSAGP AEAEAVPAVPGMPER.F		R.GPVPAQGRPMMMPGSVPSAGP AEAEAVPAVPGMPER.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
162	ASSY_SCHPO	10.98%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
333	350	2	1884.02	2.8	0	58	19.5	95.00%	R.MLLAANNVSQEVVNGVVK.L		R.MLLAANNVSQEVVNGVVK.L
386	399	2	1651.81	2.6	0	29.3	24.8	95.00%	D.PTWTSGFIQIESMR.L		K.LSSMDELGGFDPTWTSGFIQIES MR.L
320	332	2	1601.77	4.2	0	39.6	25.7	95.00%	K.ILYNGQFFSPCTR.M	Carbamidomethyl (+57)	K.ILYNGQFFSPCTR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
163	CYSK1_SCHPO	13.11%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
217	227	3	1196.66	2.9	0	25.3	20.5	95.00%	D.PPGSVLYSHIK.T		R.VASFVADPPGSVLYSHIK.T
10	23	2	1341.78	3.9	0	59.1	15.9	95.00%	K.VPGIVSGFIGAIGR.T		K.VPGIVSGFIGAIGR.T
180	200	2	2019.93	5.1	1	71.4	26.6	95.00%	K.GTVDGFTCSTGTGGTFAGVTK.Y	Carbamidomethyl (+57)	K.GTVDGFTCSTGTGGTFAGVTK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
164	RS12A_SCHPO	31.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	111	2	1486.76	2.4	1	27.9	23.3	94.70%	K.VLGEWAGLCVLDR.D	Carbamidomethyl (+57)	K.VLGEWAGLCVLDR.D
79	93	2	1671.88	4.1	0	73.8	21.7	95.00%	K.LVEALCAESETPLIK.V	Carbamidomethyl (+57)	K.LVEALCAESETPLIK.V
61	78	3	2208.97	4.2	1	36.3	27	95.00%	R.QAHLCVLCESCDQEAYVK.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.QAHLCVLCESCDQEAYVK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
165	RAD25_SCHPO	14.44%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
63	74	2	1417.75	4.9	1	43.2	22.3	95.00%	R.IISSIEQKEESR.G		R.IISSIEQKEESR.G
218	226	2	1073.63	2	0	32.8	16.5	95.00%	D.STLIMQLLR.D		K.DSTLIMQLLR.D
244	261	3	1846.84	4.4	0	24	26	94.10%	K.EEAPAAAAASENEHPEPK.E		K.EEAPAAAAASENEHPEPK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
166	PDI1_SCHPO	5.28%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	136	3	1350.87	5.1	1	30.4	6.02	95.00%	R.KQLLPTVKPISK.D		R.KQLLPTVKPISK.D
188	201	2	1436.77	4.3	0	45.1	19.9	95.00%	K.SLGSNFPGIVAFTK.D		K.SLGSNFPGIVAFTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
167	RS21_SCHPO	29.89%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
77	87	2	1306.67	2.1	0	40.7	23.6	95.00%	D.GLLEGVWSYQR.-		R.LTTQDGLLEGVWSYQR.-
51	60	2	1113.59	4.5	0	33.8	22.6	95.00%	K.TTYAISGFVR.S		K.TTYAISGFVR.S
72	87	2	1864.94	4.3	1	65.3	23.7	95.00%	R.LTTQDGLLEGVWSYQR.-		R.LTTQDGLLEGVWSYQR.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
168	KAPS_SCHPO	22.77%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
157	188	3	3532.7	3.1	0	32.4	23.2	95.00%	K.EFTGISAPYEAPISPEIVVSSHTQSIEECVEK.I	Carbamidomethyl (+57)	K.EFTGISAPYEAPISPEIVVSSHTQSIEECVEK.I
39	52	2	1664.86	3.8	0	65.6	22.9	95.00%	K.STIACALEQYLLQR.G	Carbamidomethyl (+57)	K.STIACALEQYLLQR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
169	ACL2_SCHPO	11.99%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
255	266	2	1367.61	3.7	1	48.5	26.1	95.00%	K.LDQTAEFECGAK.W	Carbamidomethyl (+57)	K.LDQTAEFECGAK.W
326	334	2	985.56	4.7	0	36	20.4	95.00%	K.LTILNAEGR.V		K.LTILNAEGR.V
382	389	2	947.52	4.5	1	26.9	22.7	93.50%	K.TVLDLMTR.G		K.TVLDLMTR.G
32	61	3	3211.76	3.3	0	47.1	15.6	95.00%	K.TVSATPAVQLAQIQFPLPTLVIPAESTTYR.E		K.TVSATPAVQLAQIQFPLPTLVIPAESTTYR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
170	VATB_SCHPO	8.35%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
415	427	2	1417.68	4.9	1	78	25.4	95.00%	K.SVVGEEALSQEDR.L		K.SVVGEEALSQEDR.L
439	449	2	1284.62	4.2	0	36.9	25.1	95.00%	K.TFISQGAYENR.T		K.TFISQGAYENR.T
42	59	3	2083.09	4.5	1	23.6	21.7	94.90%	R.RPQYNEIVNLNLPDGSVR.S		R.RPQYNEIVNLNLPDGSVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
171	RL11_SCHPO	14.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
36	49	2	1531.83	4.2	0	63.5	20	95.00%	K.VLEQLSGQTPVFSK.A		K.VLEQLSGQTPVFSK.A
154	164	2	1349.67	4.1	1	39.8	24.4	95.00%	K.INAEDTINWFK.Q		K.INAEDTINWFK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
172	SYG_SCHPO	8.74%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
187	198	2	1297.63	5.4	0	37	24.5	95.00%	R.NPATNGELETPR.Q		R.NPATNGELETPR.Q
216	232	3	1983.01	5	0	28	22.9	95.00%	K.GYLRPETAQGQFLNFSR.L		K.GYLRPETAQGQFLNFSR.L
492	506	2	1649.85	4.8	0	35.7	23.2	95.00%	R.TYTPNVIEPSFGLGR.I		R.TYTPNVIEPSFGLGR.I
526	538	2	1298.77	3.9	0	28.2	15.8	95.00%	R.GVLSFPASIAPIK.A		R.GVLSFPASIAPIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
173	MPG1_SCHPO	11.02%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
270	287	2	1776	4.2	1	35.2	16.3	95.00%	K.IGPNVVIGPNVTIGDGVR.L		K.IGPNVVIGPNVTIGDGVR.L
138	159	4	2530.28	3.4	1	22.1	22.9	95.00%	K.VEEPSKYGVVVHYPNSESLIER.F		K.VEEPSKYGVVVHYPNSESLIER.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
174	TCTP_SCHPO	20.24%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
54	73	2	2271.03	1.9	0	80.9	27	95.00%	D.AEENAEEGTETVNNLVYSFR.L		K.QGGDVDIGANPSAEDAEENAEEGTETVNNLVYSFR.L
99	112	2	1670.87	2.4	1	43.2	22.9	95.00%	R.LQESNPERVPVFEK.N		R.LQESNPERVPVFEK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
175	YCO6_SCHPO	10.94%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

15	36	3	2140.01	5.3	0	26.3	26.1	95.00%	K.MSAAPTPHNTPSGTSAPNFGAK.A		K.MSAAPTPHNTPSGTSAPNFGAK.A
57	77	3	2234.19	1.5	0	33.5	18.2	95.00%	K.LGSLLHLTSEGVSELPEAVQR.R		K.LGSLLHLTSEGVSELPEAVQR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
176	RL2_SCHPO	15.02%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
92	118	3	2780.44	3.2	0	52	20	95.00%	K.NAALTVGNVLPVGEMPEGTIISNVEEK.A		K.NAALTVGNVLPVGEMPEGTIISNVEEK.A
163	173	2	940.55	4.3	0	54.6	16.4	95.00%	R.GVVGIVAGGGR.I		R.GVVGIVAGGGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
177	SRP2_SCHPO	3.84%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
170	183	2	1490.74	2.3	1	43.5	24.5	95.00%	D.PDAANEPLPEVPSR.F		R.EDPDAANEPLPEVPSR.F
172	183	2	1278.66	2.9	0	38.3	23.3	95.00%	D.AANEPLPEVPSR.F		R.EDPDAANEPLPEVPSR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
178	RL24A_SCHPO	20.81%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	12	2	1357.64	4.1	1	34.6	25.3	95.00%	-.MKVEVCSFSGSK.V	Carbamidomethyl (+57)	-.MKVEVCSFSGSK.V
81	91	2	1097.65	4.7	1	29.4	18.1	95.00%	R.GIVGANLDVIK.E		R.GIVGANLDVIK.E
36	43	2	978.52	4.9	0	29.5	22.9	95.00%	K.SESLFLQR.K		K.SESLFLQR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
179	DLDH_SCHPO	5.87%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
113	128	2	1663.83	1.7	1	25	24.3	90.50%	R.GIDVSGVSVNLSQMMK.A		R.GIDVSGVSVNLSQMMK.A
155	168	2	1448.76	3.8	1	31.8	22.6	95.00%	K.GTGSFIDPQTLSVK.G		K.GTGSFIDPQTLSVK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
180	CH10_SCHPO	22.12%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	84	2	1230.7	4	0	31.7	16.6	95.00%	R.VLLPAYGGSNIK.V		R.VLLPAYGGSNIK.V
62	72	2	1111.6	4.5	1	30.9	20.3	95.00%	K.LAQPSVAVGDR.V		K.LAQPSVAVGDR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
181	YBS7_SCHPO	7.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
442	471	4	3134.5	-0.033	1	26.4	24.5	95.00%	K.EQPPNKAEPAVPTEASSTKPSEAAEESTPR.F		K.EQPPNKAEPAVPTEASSTKPSEAAEESTPR.F
128	146	2	1760.86	5.1	0	31.6	25.1	95.00%	R.TSGSSTGLSNAPPSANVSK.A		R.TSGSSTGLSNAPPSANVSK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
182	YDMC_SCHPO	4.59%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
370	385	2	1877	4	0	39.4	20	95.00%	K.LTSLMESIFPEQTIIR.S		K.LTSLMESIFPEQTIIR.S
82	91	2	1136.53	5	1	33.4	25.5	95.00%	R.NADNSVTNFR.D		R.NADNSVTNFR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
183	CPGL_SCHPO	4.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
40	53	2	1599.79	4.2	1	88.3	24.6	95.00%	K.VVEMADFVVSEFTK.L		K.VVEMADFVVSEFTK.L
113	121	2	1033.55	2.4	1	34.5	22.1	95.00%	D.PFTLTVDNK.G		K.TVLIYNHFDVQPASLEDGWSTDPFTLTVDNK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
184	PLR1_SCHPO	8.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	66	2	1195.66	3	1	60	19.6	95.00%	D.PPTSNLDLLAR.Y		K.QTPDEEAFEVMNYALSQGSNYWDAGEFYGVDPPTSNLDLLAR.Y
147	162	3	1747.92	2.1	1	29.8	21.8	95.00%	K.ISCVGLSEVSAETIKR.A	Carbamidomethyl (+57)	K.ISCVGLSEVSAETIKR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
185	Q9P7B4_SCHPO	19.69%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
234	256	3	2522.27	2.7	1	34.8	22.5	95.00%	R.ENVVIADTLVFPSHQGGANHVYR.K		R.ENVVIADTLVFPSHQGGANHVYR.K
163	173	2	1163.64	5.6	0	26.5	19	93.00%	K.SALAQFTSALR.K		K.SALAQFTSALR.K
183	199	2	1918.98	6.8	1	60.8	22.6	95.00%	R.IMEVDPGLVETEFSVVR.F		R.IMEVDPGLVETEFSVVR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
186	ACAC_SCHPO	1.97%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1972	1994	3	2667.36	3.2	1	27.8	21.1	95.00%	K.TAQAINDFNHGEQLPLFILANWR.G		K.TAQAINDFNHGEQLPLFILANWR.G
197	207	2	1131.63	6.1	0	34.7	18.8	95.00%	K.ISSTIVAQSAR.V		K.ISSTIVAQSAR.V
974	984	3	1193.73	3.7	1	21.6	6.02	92.00%	D.KVIALALSHSR.I		K.DDVDKVIALALSHSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
187	ATPB_SCHPO	7.43%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
167	185	2	2076.03	2.3	0	87.1	24.2	95.00%	D.APSFEEQSTTPEILETGIK.V		K.YSPIHADAPSFEEQSTTPEILETGIK.V
160	185	3	2859.39	2.5	1	29.4	24.2	95.00%	K.YSPIHADAPSFEEQSTTPEILETGIK.V		K.YSPIHADAPSFEEQSTTPEILETGIK.V
210	222	2	1501.86	4.8	0	34.9	15.2	95.00%	K.TVFIQELINNIAK.A		K.TVFIQELINNIAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
188	RPE_SCHPO	11.84%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
6	20	2	1557.85	4.3	1	29.9	20.6	95.00%	K.IAPSLLAGDFANLEK.E		K.IAPSLLAGDFANLEK.E
123	134	2	1369.79	2.3	0	25.6	17.2	91.60%	K.TPVEVILPFVEK.L		K.TPVEVILPFVEK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
189	RL21A_SCHPO	14.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
138	160	3	2554.24	2	1	27.5	24.3	95.00%	K.AHFVSTENNEPVTLHPVAYDTTI.-		K.AHFVSTENNEPVTLHPVAYDTTI.-
138	157	3	2239.06	3.5	1	22.7	26	92.00%	K.AHFVSTENNEPVTLHPVAYD.T		K.AHFVSTENNEPVTLHPVAYDTTI.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
190	YBS1_SCHPO	6.73%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
240	248	2	959.52	2.7	0	26.5	22.4	92.90%	D.GPFLVASNR.Y		K.FPQPPSAAEVAVVHDGPFLVASNR.Y
162	175	2	1422.8	1.7	0	39.8	17.1	95.00%	D.PVVVVNVPAGYGPR.H		R.FSIFDAEDTSSDPVVVVNVPAGYGPR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
191	APE1_SCHPO	3.40%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
253	269	2	1912.97	5	1	42.1	23.6	95.00%	K.TLDFFSGVFGEPYPLPK.C		K.TLDFFSGVFGEPYPLPK.C
137	149	2	1467.71	4.6	0	42.2	24.5	95.00%	K.YLATTQMEPTSAR.R		K.YLATTQMEPTSAR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
192	SODM_SCHPO	20.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	173	2	1303.7	4.2	1	48.8	21.3	95.00%	R.ITTTANQDTIVK.S		R.ITTTANQDTIVK.S
26	48	2	2502.32	2.9	0	32.8	19.3	95.00%	K.ATLPPLPYAYNALEPALSETIMK.L		K.ATLPPLPYAYNALEPALSETIMK.L
127	135	2	1108.52	5	1	34	25.8	95.00%	K.WGSLEDFQK.E		K.WGSLEDFQK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
193	PROF_SCHPO	26.77%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
54	68	2	1515.82	3.2	0	39.2	20.7	95.00%	D.PPSMFGTGIILAGQK.Y		R.AGDSVWAASAGFNLSPQEIQGLAAGFQDPPSMFGTGIILAGQK.Y
95	113	3	2098.08	3.5	0	24.5	21.1	95.00%	K.LCILVSHYPETTLPGEAAK.I	Carbamidomethyl (+57)	K.LCILVSHYPETTLPGEAAK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
194	YET4_SCHPO	13.60%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
190	216	3	2686.32	5.5	1	58	24	95.00%	R.NDEQLGNSPASITSKPATTSAAQPSSK.V		R.NDEQLGNSPASITSKPATTSAAQPSSK.V
419	462	4	4557.19	2.7	1	18.1	22.3	95.00%	K.NEVNVPSTIPTESENPVAVGGTTAEHPVQEAVTAPTETAHDFSK.E		K.NEVNVPSTIPTESENPVAVGGTTAEHPVQEAVTAPTETAHDFSK.E
487	503	3	1712.87	4.4	0	27.8	23.7	95.00%	R.KPSSTGQEPTTPSTPAK.S		R.KPSSTGQEPTTPSTPAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
195	RL7B_SCHPO	14.00%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	21	2	2002.11	3.4	0	39.6	16.1	95.00%	M.VASSTVPSVASIFAPESLLK.K		-.MVASSTVPSVASIFAPESLLK.K
168	182	2	1523.86	4.4	1	56.2	15.9	95.00%	R.IPLSDNAIIEAALGK.Y		R.IPLSDNAIIEAALGK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
196	ODPA_SCHPO	7.33%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
200	229	3	3269.55	4.6	1	77.4	24.9	95.00%	K.YLEKPTTTFALYGDGASNQGQAFEAFNMAK.L		K.YLEKPTTTFALYGDGASNQGQAFEAFNMAK.L
214	229	2	1669.75	1.7	0	43.2	27.1	95.00%	D.GASNQGQAFEAFNMAK.L		K.YLEKPTTTFALYGDGASNQGQAFEAFNMAK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
197	RS3_SCHPO	10.04%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
97	108	2	1362.64	3.8	0	61	25.7	95.00%	R.GLCAVAQCESLR.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GLCAVAQCESLR.Y
30	42	2	1513.64	4.2	0	70.9	26.3	95.00%	R.ELSEEGYSGCEVR.V	Carbamidomethyl (+57)	R.ELSEEGYSGCEVR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
198	YEI3_SCHPO	8.67%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
43	62	2	2148.05	4.6	1	58.6	24.9	95.00%	K.SVLGNPANYPYATIDPEEAK.V		K.SVLGNPANYPYATIDPEEAK.V
329	342	2	1482.75	2.8	1	41.2	24.6	95.00%	K.APQAAGVIHTDFEK.A		K.APQAAGVIHTDFEK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
199	PPID_SCHPO	7.87%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
155	169	2	1686.83	0.8	0	60.8	24.5	95.00%	D.PVVPVVIEECGTCTK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.NDDPVVPVVIEECGTCTK.D
214	226	2	1432.74	4.4	1	72	23.8	95.00%	K.QFAQQNLDTAVAK.W		K.QFAQQNLDTAVAK.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
200	ODPB_SCHPO	8.20%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
199	213	2	1682.93	1.2	0	45.3	17.6	95.00%	D.PNPVVVLENEILYGK.T		R.DPNPVVVLENEILYGK.T
220	234	2	1634.86	4.6	1	26.5	21.8	93.00%	K.EALSEDFVLPFGLAK.V		K.EALSEDFVLPFGLAK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
201	ARO1_SCHPO	3.43%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
677	703	3	2950.41	2.7	1	45.4	24.5	95.00%	R.FACDVLRPMGCTVEQTATSTTV QGPPK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.FACDVLRPMGCTVEQTATSTTV QGPPK.G
162	172	2	1299.72	4.7	0	45.2	20.8	95.00%	K.NLVGAFWQPLR.V		K.NLVGAFWQPLR.V
1232	1247	2	1833.96	4.6	1	44.8	21.9	95.00%	R.ITNSMDIPLILFNMGR.F		R.ITNSMDIPLILFNMGR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
202	GPD2_SCHPO	10.46%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	88	4	2626.25	3.3	1	19.3	25.2	95.00%	K.IQHEGKECNLTEVFNTTHENVK.Y	Carbamidomethyl (+57)	K.IQHEGKECNLTEVFNTTHENVK.Y
311	327	3	1907.98	3	1	33.8	22.2	95.00%	K.TGKPMHVVEQELLDGQK.L		K.TGKPMHVVEQELLDGQK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
203	PPA2_SCHPO	4.10%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
157	167	2	1278.62	3.3	1	27.8	24.9	94.60%	D.VYDINTAAQER.V		R.YYELFDTDVYDINTAAQER.V
136	143	2	961.53	5.4	1	31.9	22.9	95.00%	R.IELFDLGR.Q		R.IELFDLGR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
204	LYS4_SCHPO	4.30%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
149	159	2	1179.57	4.4	1	26	24.9	92.20%	K.GQGIDFYPAGR.G		K.GQGIDFYPAGR.G
470	489	2	1872.04	4.8	0	47.2	15.2	95.00%	R.EALAYLASPAVVAASAIAGK.I		R.EALAYLASPAVVAASAIAGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
205	RLA0_SCHPO	15.06%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
133	144	2	1308.71	5.2	0	29.1	19.5	95.00%	K.TSFFQALGIPTK.I		K.TSFFQALGIPTK.I
98	132	3	3513.88	2.7	1	45.6	17.3	95.00%	R.ETIIANVIAAPARPNAIAPLDVFVP AGNTGMEPGK.T		R.ETIIANVIAAPARPNAIAPLDVFVP AGNTGMEPGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
206	YBLH_SCHPO	2.78%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
419	432	2	1450.81	3	2	50.9	17.7	95.00%	D.PETNLIAGLAPLKD.T		R.APEPDPETNLIAGLAPLKDTPVM VMGVESDNLMPVECQR.E
419	431	2	1335.78	3.4	0	58.7	13.6	95.00%	D.PETNLIAGLAPLK.D		R.APEPDPETNLIAGLAPLK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
207	MUG64_SCHPO	11.19%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
224	238	3	1767.86	4.9	1	44.3	25.1	95.00%	K.LDVESAKPENLEHCK.S	Carbamidomethyl (+57)	K.LDVESAKPENLEHCK.S
108	125	2	1851.02	3.8	0	41.3	17.2	95.00%	R.NLGNLTPLEQTPLASVGK.N		R.NLGNLTPLEQTPLASVGK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
208	RL35_SCHPO	19.67%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
11	24	2	1684.85	4.2	0	72	23.8	95.00%	K.QSQENLAEQLQELR.Q		K.QSQENLAEQLQELR.Q
56	65	2	1157.65	4.3	0	33.6	20.5	95.00%	R.ILTVINESNR.L		R.ILTVINESNR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
209	P5CR_SCHPO	15.25%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
116	129	2	1566.76	5	1	85.9	25.3	95.00%	K.TISSLQSMLDESTR.V		K.TISSLQSMLDESTR.V
70	98	3	3111.57	2.6	1	41.3	22.4	95.00%	K.ENAEMAAISNVLLLSCKPQAAEDVLNSPK.M	Carbamidomethyl (+57)	K.ENAEMAAISNVLLLSCKPQAAEDVLNSPK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
210	EIF3E_SCHPO	6.59%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
267	284	3	2029.08	4.4	0	22.1	19.4	92.80%	R.YLTVAVVTNQNNANQKPR.N		R.YLTVAVVTNQNNANQKPR.N
477	491	2	1679.84	3.6	0	46.3	24.2	95.00%	K.SLSFESQNLEQSLAK.S		K.SLSFESQNLEQSLAK.S

Supplementary Table S2: All "Scaffold" validated proteins and peptides identified from solprotSP (*S.pombe*) and from SCVMprot (*S.cerevisiae*) samples

***S.pombe* - Formic acid digest of large tryptic peptides (replicate D)**

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
1	ENO11_SCHPO	53.99%	100%	20

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
361	374	2	1608.72	-0.75	0	50	26.7	95.00%	R.MSYEAGWGVMVSHR.S		R.MSYEAGWGVMVSHR.S
185	194	2	1204.59	5.4	0	34	24.9	95.00%	R.WGAETYHTLK.S		R.WGAETYHTLK.S
346	360	2	1585.85	6	0	90.8	21.2	95.00%	K.VNQIGSVTESLNAVR.M		K.VNQIGSVTESLNAVR.M
302	310	2	1160.51	-0.1	1	26.8	26	91.90%	D.DWSAWTHMK.A		K.YPIVSIEDPFDQDDWSAWTHMK.A
381	396	3	1640.93	0.8	0	24.1	16.2	95.00%	D.TFISHLTVGIGAGQLK.S		R.SGETADTFISHLTVGIGAGQLK.S
65	79	2	1477.87	4	0	73.7	11.8	95.00%	K.AVGNVNNIIAPAVVK.A		K.AVGNVNNIIAPAVVK.A
247	257	2	1200.57	-0.68	1	53.8	25	95.00%	D.VASSEFYVDGK.Y		K.IGLDVASSEFYVDGK.Y
106	120	2	1560.82	4.2	0	61.3	22.6	95.00%	K.LGANAILGVSMAICR.A	Oxidation (+16)/ Carbamidomethyl (+57)	K.LGANAILGVSMAICR.A
288	296	2	1062.56	-0.015	2	37.5	21.5	95.00%	K.KYPIVSIED.P		K.KYPIVSIEDPFDQDDWSAWTHMK.A
273	287	2	1812.95	0.061	1	77.9	21.8	95.00%	K.LTYQQLTDLYVELSK.K		K.LTYQQLTDLYVELSK.K
227	234	2	898.55	-0.91	0	26.7	16.9	93.20%	D.LIVEAINK.A		R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
16	32	2	1837.91	-1.5	1	94.8	24	95.00%	R.GNPTVEVDLTTETGIHR.A		R.GNPTVEVDLTTETGIHR.A
338	345	2	901.51	4.7	0	31.4	21.3	95.00%	K.CANALLLK.V	Carbamidomethyl (+57)	K.CANALLLK.V
409	414	2	806.43	5.7	0	29.4	23.6	95.00%	K.YNELLR.I		K.YNELLR.I
33	50	2	1886.96	-0.49	0	119	24.2	95.00%	R.AIVPSGASTGIWEALEMR.D		R.AIVPSGASTGIWEALEMR.D
218	234	2	1895.02	-2.7	1	71.7	19.3	95.00%	D.LQTPQEALDLIVEAINK.A	Deamidation (+1)	R.YGSSAGNVGDEGGIAPDLQTPQEALDLIVEAINK.A
311	320	2	1093.49	0.44	1	35.1	24.6	95.00%	K.AETDFQIVGD.D		K.AETDFQIVGDDLTVTNVK.R
415	432	2	1815.86	-0.56	0	86.3	25.8	95.00%	R.IEEELGSEGVYAGAHAGK.Y		R.IEEELGSEGVYAGAHAGK.Y
375	396	2	2201.14	2.9	1	122	20.8	95.00%	R.SGETADTFISHLTVGIGAGQLK.S		R.SGETADTFISHLTVGIGAGQLK.S
89	96	2	905.49	4.7	1	57.4	23.1	95.00%	K.AADEFLLK.L		K.AADEFLLK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
2	G3P1_SCHPO	52.08%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
249	259	3	1290.69	4.5	1	28.4	22.9	95.00%	K.LAKPTNYEDIK.A		K.LAKPTNYEDIK.A
119	126	2	813.5	-1.3	0	28	18.8	94.80%	R.VIISAPSK.D		R.VIISAPSK.D
167	186	2	2135.06	-0.8	0	102	24.2	95.00%	D.TFGIEEGLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK.T
94	113	2	2181.1	0.91	0	61.6	23.4	95.00%	D.YVIESTGVFTTQETASAHLK.G		K.WSTSGADYVIESTGVFTTQETASAHLK.G
127	139	2	1449.69	3.7	1	45.1	25.6	95.00%	K.DAPMYVVGVNEEK.F		K.DAPMYVVGVNEEK.F
128	145	2	2036.99	-0.16	1	81	25.3	95.00%	D.APMYVVGVNEEKFNPSEK.V		K.DAPMYVVGVNEEKFNPSEK.V
297	309	2	1344.74	-0.6	0	58.1	20.6	95.00%	D.ASAGIQLSPQFVK.L		K.GVLGYTEDAVVSTDFCGDNHSSIFDASAGIQLSPQFVK.L
128	139	2	1334.65	-0.46	0	31.9	24.6	95.00%	D.APMYVVGVNEEK.F		K.DAPMYVVGVNEEK.F
87	113	2	2885.38	3.9	1	116	24.8	95.00%	K.WSTSGADYVIESTGVFTTQETASAHLK.G		K.WSTSGADYVIESTGVFTTQETASAHLK.G
146	162	2	1818.91	4.5	0	75	24.4	95.00%	K.VISNASCTTNCLAPLAK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.VISNASCTTNCLAPLAK.V
324	334	2	1148.65	6.2	1	55.4	18.2	95.00%	R.VVDLVAYTAAK.D		R.VVDLVAYTAAK.D
163	186	2	2576.29	4.6	1	94.8	23.7	95.00%	K.VINDTFGIEEGLMTTVHATTATQK.T		K.VINDTFGIEEGLMTTVHATTATQK.T
240	248	2	958.57	-1.2	1	38.7	18.5	95.00%	D.VSVVDLTVK.L		R.VPTPDVSVVDLTVK.L
36	48	2	1682.77	-0.44	1	60.6	26.4	95.00%	D.PFIDLEYMAYMFK.Y	Oxidation (+16)	K.TIQVVAINDPFIDLEYMAYMFK.Y

119	127	2	928.52	-1.7	2	37.8	21.5	95.00%	R.VIISAPSKD.A		R.VIISAPSKDAPMYVVGVNEEK.F
6	13	2	819.43	6.2	0	38.4	22.9	95.00%	K.VGINGFGR.I	Deamidation (+1)	K.VGINGFGR.I
201	215	2	1343.71	4.7	0	69.9	22.6	95.00%	R.GASANIIPSSTGAAK.A		R.GASANIIPSSTGAAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
3	PGK_SCHPO	48.79%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
359	378	2	1917.95	4	1	118	24.2	95.00%	K.TCEAGNVVIVGGGDTATVAK.K	Carbamidomethyl (+57)	K.TCEAGNVVIVGGGDTATVAK.K
307	316	2	1119.48	-2.7	1	40.6	25.4	95.00%	D.GWMGLDCGPK.S	Carbamidomethyl (+57)	K.VGSATAEEGIPDGWMGLDCGPK.S
123	132	3	1145.54	4.7	0	33.9	25.7	95.00%	R.FHIEEEGSAK.V		R.FHIEEEGSAK.V
57	71	2	1591.87	2.9	0	46.2	20	95.00%	K.AVILMSHLGRPNGAR.V	Deamidation (+1)	K.AVILMSHLGRPNGAR.V
112	122	2	1211.69	4.5	0	57.3	18.4	95.00%	K.GGEVILLENLR.F		K.GGEVILLENLR.F
40	48	2	910.59	3.6	0	25.3	12.6	91.00%	R.IVGALPTIK.Y		R.IVGALPTIK.Y
330	347	2	2010.99	4.7	1	67	24.2	95.00%	K.TIVWNGPAGVFEFDNFAK.G		K.TIVWNGPAGVFEFDNFAK.G
359	372	2	1346.61	-0.58	1	34	25.8	95.00%	K.TCEAGNVVIVGGGD.T	Carbamidomethyl (+57)	K.TCEAGNVVIVGGGDTATVAK.K
404	414	2	1040.63	5.6	0	39.4	18	95.00%	K.ALPGVVALSSK.-		K.ALPGVVALSSK.-
158	169	2	1346.67	-1.1	1	59.5	24.5	95.00%	D.IFVNDAFGTAHR.A		K.SLTSLGDIFVNDAFGTAHR.A
383	403	2	2069.04	3.6	1	81.1	23.7	95.00%	K.EDALSHVSTGGGASLELLEGK.A		K.EDALSHVSTGGGASLELLEGK.A
321	329	2	994.54	5.5	0	50.2	20.8	95.00%	K.FAEVITTSK.T		K.FAEVITTSK.T
75	86	3	1304.74	4.3	0	59.4	17.9	95.00%	K.YSLKPVAAELSK.L		K.YSLKPVAAELSK.L
385	403	2	1824.96	0.49	0	71.7	21.4	95.00%	D.ALSHVSTGGGASLELLEGK.A		K.EDALSHVSTGGGASLELLEGK.A
197	213	2	1764.99	-0.6	0	54.5	15.4	95.00%	K.ALENPARPFLAILGGAK.V	N-Formyl (+28)	K.ALENPARPFLAILGGAK.V
273	287	2	1677.83	0.22	1	35.8	25.1	95.00%	K.NNVEVFLPVDFVTAD.K		K.NNVEVFLPVDFVTADK.F
170	181	2	1267.64	4	1	58.7	23.1	95.00%	R.AHSSMVGVDLPR.V		R.AHSSMVGVDLPR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
4	METE_SCHPO	43.32%	100%	31

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
582	594	2	1397.76	-0.29	2	42.2	20.1	95.00%	D.SVQAQQIALGLRD.E		R.DDVHDSVQAQQIALGLRDEVLDLEK.A
561	571	2	1184.7	5.1	0	40.5	17.5	95.00%	K.GMLTAPITILR.W		K.GMLTAPITILR.W
434	449	2	1746.97	7	0	46.9	17.6	95.00%	K.LPLFPTTTIGSFPQTK.E		K.LPLFPTTTIGSFPQTK.E
4	11	2	845.48	4.8	0	33.3	22.1	95.00%	K.SAVLGFPR.I		K.SAVLGFPR.I
707	714	2	901.49	4.3	0	27.7	24.5	94.40%	R.VPPVSEFK.E		R.VPPVSEFK.E
684	690	2	813.51	5.6	0	34.2	19.1	95.00%	K.LLNVLSR.Y		K.LLNVLSR.Y
691	706	2	1818.88	3.8	1	84	25	95.00%	R.YTSCIGPGLFDIHSPR.V	Carbamidomethyl (+57)	R.YTSCIGPGLFDIHSPR.V
393	404	2	1284.67	4.4	0	68.2	21.6	95.00%	R.AESPITNVEAVR.E		R.AESPITNVEAVR.E
707	716	3	1186.64	4.9	1	25.6	21.3	95.00%	R.VPPVSEFKER.I		R.VPPVSEFKER.I
391	404	2	1511.81	4	1	42.1	21	95.00%	K.ARAESPITNVEAVR.E		K.ARAESPITNVEAVR.E
499	508	2	1257.55	4.4	1	53.6	25.7	95.00%	R.NDMVQYFGER.M		R.NDMVQYFGER.M
243	260	2	1982.08	3.5	1	54.1	17.6	95.00%	K.LILTTYFGSLQSNADVLK.G		K.LILTTYFGSLQSNADVLK.G
261	270	2	976.53	-0.33	1	25.5	21.6	91.40%	K.GLPIAGVHVD.V		K.GLPIAGVHVDVVR.A
428	449	3	2402.33	4.8	1	46	14.5	95.00%	K.QQASLKLPLFPTTTIGSFPQTK.E		K.QQASLKLPLFPTTTIGSFPQTK.E
325	351	3	2884.49	-0.44	1	58.6	19.7	95.00%	R.VQVASSSSILHIPHSLSGEDQINPEIK.R		R.VQVASSSSILHIPHSLSGEDQINPEIK.R
261	273	2	1330.77	-1.1	1	60.3	16.8	95.00%	K.GLPIAGVHVDVVR.A		K.GLPIAGVHVDVVR.A
281	299	2	1881.08	4.8	0	87.4	11.1	95.00%	R.ALAVLGENQIISVGVVSGR.N		R.ALAVLGENQIISVGVVSGR.N
147	155	2	1034.53	5.7	1	36.8	24.6	95.00%	K.ALDEFLEAK.E		K.ALDEFLEAK.E
595	601	2	844.45	-1.3	1	28.9	24.2	95.00%	D.EVLDLEK.A		R.DEVLDLEK.A
325	344	2	2062.03	-0.82	1	82.7	24.3	95.00%	R.VQVASSSSILHIPHSLSGED.Q		R.VQVASSSSILHIPHSLSGEDQINPEIK.R
361	369	2	1017.56	4.9	0	30.5	21.5	95.00%	K.CAELAILTK.A	Carbamidomethyl (+57)	K.CAELAILTK.A
461	473	2	1539.76	4.1	1	67.2	24.3	95.00%	K.GLISQEEYDAFIR.K		K.GLISQEEYDAFIR.K
547	560	2	1596.79	3.6	0	50.8	24.1	95.00%	K.ESQYAQSITSKPMK.G		K.ESQYAQSITSKPMK.G

606	615	2	1199.6	4.3	1	55.1	24.2	95.00%	K.VIQCDEPALR.E	Carbamidomethyl (+57)	K.VIQCDEPALR.E
527	546	3	2267.24	3.3	1	44.5	16.3	95.00%	R.CVRPPIIVGDVYRPAPMTVK.E	Carbamidomethyl (+57)	R.CVRPPIIVGDVYRPAPMTVK.E
631	637	2	877.45	5.9	1	49	23.7	95.00%	K.WAIDAFR.L		K.WAIDAFR.L
85	99	2	1616.79	4.1	1	63.5	25.3	95.00%	R.LSGLSSLDTYFAMGR.G		R.LSGLSSLDTYFAMGR.G
537	546	3	1160.64	-1.3	0	26.1	21.3	95.00%	D.VYRPAPMTVK.E		R.CVRPPIIVGDVYRPAPMTVK.E
156	176	2	2284.32	-0.15	0	80.7	8.45	95.00%	K.EAGIITRPVLVGPVTYLFIAK.A	N-Formyl (+28)	K.EAGIITRPVLVGPVTYLFIAK.A
661	667	2	861.47	-1.3	1	30.5	22	95.00%	D.IFDAIQR.L		R.LATAAVQDDTQIHSHFCYSDFNDIFDAIQR.L
30	40	2	1132.6	4.2	0	58.1	22.9	95.00%	K.TSAEELLATAK.Q		K.TSAEELLATAK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
5	KPYK_SCHPO	65.23%	100%	28

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
332	344	2	1320.66	-0.84	1	78.4	24.7	95.00%	D.GADLVMLSGETTK.G		R.AEVSDVGNAVLDGADLVMLSGETTK.G
108	121	2	1596.71	-0.071	1	32.5	26.8	95.00%	D.YPISSGHEMIFTTD.D		R.TGLTVGGTDYPISSGHEMIFTTDDAYAEK.C
487	497	2	1053.66	5.9	0	39.5	11.1	95.00%	K.IIVLQGAVGGK.G		K.IIVLQGAVGGK.G
233	243	2	1214.66	3.9	1	28.5	22.1	95.00%	R.EVLGEEGKNIK.I		R.EVLGEEGKNIK.I
422	433	3	1430.81	0.21	0	57.7	17.3	95.00%	K.YRPSIPIVMVTR.C		K.YRPSIPIVMVTR.C
10	26	2	1880.98	3.7	1	90.9	21.6	95.00%	K.QWVAGLNSELDIPAVNR.R		K.QWVAGLNSELDIPAVNR.R
155	164	2	1105.64	0.16	0	48.9	16.2	95.00%	D.GILSFTVIEK.V		R.IIYVDDGILSFTVIEK.V
446	459	2	1607.81	0.12	2	36.9	24	95.00%	R.GVYPVIYEKEPLSD.W		R.GVYPVIYEKEPLSDWQK.D
216	223	2	983.53	1.6	0	40.9	20.8	95.00%	D.MIFASFIR.R		K.NGVDMIFASFIR.R
195	202	2	871.46	-0.49	2	30.4	23.1	95.00%	D.LPALSEKD.K		K.TDVDLPALSEKDK.A
76	91	2	1640.92	0.65	2	45.6	17.8	95.00%	R.KASATNPLFPLAIALD.T		R.KASATNPLFPLAIALDTK.G
77	93	2	1741.97	3.8	1	39.2	17.8	95.00%	K.ASATNPLFPLAIALDTK.G		K.ASATNPLFPLAIALDTK.G
225	232	2	951.52	5	1	30.1	21.1	95.00%	R.AEDVIHIR.E		R.AEDVIHIR.E
248	258	2	1276.57	-0.79	1	36.6	25.8	95.00%	K.IENQQGVNNFD.S		K.IENQQGVNNFDSILDVTDGIMVAR.G
57	75	3	2253.98	-1.9	1	47.6	27.1	95.00%	R.MNFSHGSYEYHQSVIDNAR.K		R.MNFSHGSYEYHQSVIDNAR.K
381	402	2	2261.08	-0.57	1	63.8	25.6	95.00%	R.RPLECATETTAVAAIGASIESD.A	Carbamidomethyl (+57)	R.RPLECATETTAVAAIGASIESDAK.A
28	37	2	1088.6	5	0	46.3	21.4	95.00%	R.TSIICTIGPK.S	Carbamidomethyl (+57)	R.TSIICTIGPK.S
274	288	2	1598.9	-1.8	0	56.3	17.8	95.00%	D.LGIEIPASQVFVAQK.M		R.GDLGIEIPASQVFVAQK.M
263	271	2	960.51	-0.33	1	29.7	22.8	95.00%	D.VTDGIMVAR.G		K.IENQQGVNNFDSILDVTDGIMVAR.G
468	477	2	1186.55	5.3	0	54.8	24.7	95.00%	R.VAYGCQQAYK.M	Carbamidomethyl (+57)	R.VAYGCQQAYK.M
345	360	2	1743.81	-0.64	0	88	26.1	95.00%	K.GSYPVEAVTYMAETAR.V		K.GSYPVEAVTYMAETAR.V
272	288	2	1770.96	3.8	1	69.1	19.7	95.00%	R.GDLGIEIPASQVFVAQK.M		R.GDLGIEIPASQVFVAQK.M
361	380	2	2229.12	4.2	0	78.6	22.9	95.00%	R.VAEASIPYGSLYQEMFGLVR.R		R.VAEASIPYGSLYQEMFGLVR.R
294	319	4	2982.38	0.62	0	50.4	26.1	95.00%	K.CNIAGKPVACATQMLESMTYNPRPTR.A	Carbamidomethyl (+57)/ Deamidation (+1)/ Carbamidomethyl (+57)/ Oxidation (+16)	K.CNIAGKPVACATQMLESMTYNPRPTR.A
405	417	2	1287.72	5.7	0	62	19	95.00%	K.AIVVLSTSGNTAR.L		K.AIVVLSTSGNTAR.L
99	121	2	2398.1	-0.34	1	28.6	26.8	93.50%	R.TGLTVGGTDYPISSGHEMIFTTD.D		R.TGLTVGGTDYPISSGHEMIFTTDDAYAEK.C
212	223	2	1368.69	-0.021	1	44.4	23.7	95.00%	K.NGVDMIFASFIR.R		K.NGVDMIFASFIR.R
381	404	2	2460.23	3.5	1	76.2	23.7	95.00%	R.RPLECATETTAVAAIGASIESDAK.A	Carbamidomethyl (+57)	R.RPLECATETTAVAAIGASIESDAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
6	EF1A1_SCHPO	43.91%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
265	288	2	2443.34	-0.21	0	50.4	15.1	95.00%	R.VETGVIKPGMIVTFAPAGVTTEVK.S		R.VETGVIKPGMIVTFAPAGVTTEVK.S
402	421	2	2268.08	4	1	67.5	25.3	95.00%	K.MVPSKPMCVEAFTDYAPLGR.F	Carbamidomethyl (+57)	K.MVPSKPMCVEAFTDYAPLGR.F

147	154	2	883.55	5.8	0	26.4	17.9	92.70%	K.QLIVAVNK.M		K.QLIVAVNK.M
254	264	2	1024.61	4.2	0	65.4	14.1	95.00%	K.IGGIGTVPVGR.V		K.IGGIGTVPVGR.V
6	20	2	1529.83	-0.85	1	74.2	20.3	95.00%	K.GHINVVVIGHVDSGK.S		K.GHINVVVIGHVDSGK.S
185	214	3	3453.63	3.7	1	49.2	24.8	95.00%	K.TVPFVPVSGFQGDNMIEPTTNMPWYQGWQK.E		K.TVPFVPVSGFQGDNMIEPTTNMPWYQGWQK.E
155	164	2	1151.51	6.4	1	75.8	24.9	95.00%	K.MDTTGWSQAR.F		K.MDTTGWSQAR.F
198	214	2	2122.96	-0.57	0	58.4	26.9	95.00%	D.NMIEPTTNMPWYQGWQK.E		K.TVPFVPVSGFQGDNMIEPTTNMPWYQGWQK.E
225	241	2	1836.95	-0.45	1	37.5	22.4	95.00%	K.TLLEAIDSIEPPARPTD.K		K.TLLEAIDSIEPPARPTDKPLR.L
85	96	2	1340.69	4.4	1	66.1	22.7	95.00%	K.YNVTVIDAPGHR.D		K.YNVTVIDAPGHR.D
246	253	2	974.55	4.1	1	32.1	21	95.00%	R.LPLQDVYK.I		R.LPLQDVYK.I
135	146	2	1341.73	0.65	0	52.8	20.9	95.00%	R.EHALLAYTLGVK.Q	N-Formyl (+28)	R.EHALLAYTLGVK.Q
370	376	2	848.47	4.7	0	25.9	22.8	92.00%	K.FAELIEK.I		K.FAELIEK.I
223	231	2	958.53	-0.75	2	44.9	22.8	95.00%	K.GKTLLEAID.S		K.GKTLLEAIDSIEPPARPTDKPLR.L
299	311	2	1286.66	-0.49	1	32.5	23.6	95.00%	D.AGLPGDNVGFNVK.N		K.SVEMHHESLDAGLPGDNVGFNVK.N
165	177	2	1582.83	3.8	1	66.1	21	95.00%	R.FEEIVKETSNFIK.K		R.FEEIVKETSNFIK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
7	ALF_SCHPO	63.97%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
257	275	3	2097.04	-1.8	0	29.5	23.9	95.00%	D.KPVFFVFHGGSGSSVNEFR.T		K.TTNDKPVFFVFHGGSGSSVNEFR.T
26	50	2	2496.31	4.1	0	69.4	19.9	95.00%	R.EHGFAIPAINVTSSSTAIAALEAAR.E		R.EHGFAIPAINVTSSSTAIAALEAAR.E
309	325	2	1829.9	0.097	1	49.4	24.9	95.00%	D.YLMTPVGNPEGADKPNK.K		K.DYLMTPVGNPEGADKPNK.K
207	234	4	2951.52	-0.43	0	34.6	21.6	95.00%	R.ELSSVTPYFSIAAAFGNVHGVYKPGNVK.L		R.ELSSVTPYFSIAAAFGNVHGVYKPGNVK.L
291	301	2	1283.61	-0.64	2	43.2	24.1	95.00%	D.TQFAYVEGVRD.Y		K.VNIDTDTQFAYVEGVRDYVLK.Y
253	275	2	2528.21	2	1	93.7	25.2	95.00%	K.TTNDKPVFFVFHGGSGSSVNEFR.T		K.TTNDKPVFFVFHGGSGSSVNEFR.T
94	112	2	2098.02	4.1	1	63.5	24.9	95.00%	R.SIAPFFGVPVVMHSDHCAK.K	Carbamidomethyl (+57)	R.SIAPFFGVPVVMHSDHCAK.K
345	358	2	1597.83	4.2	1	60.4	23	95.00%	R.VLTALEDFYTVNTL.-		R.VLTALEDFYTVNTL.-
131	143	3	1481.7	0.95	1	28.1	25.3	95.00%	K.IHGEPLFSSHMLD.L		K.IHGEPLFSSHMLDLSEEPK.K
6	19	2	1424.82	-1.2	1	63.5	15.7	95.00%	D.IVPTGVITGDNVLK.L		-.MGILDIVPTGVITGDNVLK.L
289	300	2	1384.66	-0.52	1	76	25.9	95.00%	D.TDTQFAYVEGVR.D		K.VNIDTDTQFAYVEGVR.D
94	108	2	1601.79	-0.39	1	63.3	24.6	95.00%	R.SIAPFFGVPVVMHSD.H		R.SIAPFFGVPVVMHSDHCAK.K
291	300	2	1168.59	-0.53	0	55.3	23.2	95.00%	D.TQFAYVEGVR.D		K.VNIDTDTQFAYVEGVR.D
120	130	2	1306.55	-0.48	1	43	25.6	95.00%	D.GMFEADEAYFK.I		K.LLPWMDGMFEADEAYFK.I
235	248	2	1564.87	-0.45	0	62	17.6	95.00%	K.LQPALLGQHQAYVK.E		K.LQPALLGQHQAYVK.E
309	321	2	1362.61	-0.38	1	26.2	25.6	91.60%	D.YLMTPVGNPEGAD.K		K.DYLMTPVGNPEGADKPNK.K
54	71	2	1843.96	-0.77	0	96.1	22.9	95.00%	R.SPIILQTSNGGAHFFAGK.E		R.SPIILQTSNGGAHFFAGK.E
131	149	3	2165.05	3.2	1	36.1	24	95.00%	K.IHGEPLFSSHMLDLSEEPK.K		K.IHGEPLFSSHMLDLSEEPK.K
80	93	2	1399.76	5.1	0	89.1	19.9	95.00%	K.ASIAGSIAAAHYIR.S		K.ASIAGSIAAAHYIR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
8	PDC2_SCHPO	50.17%	100%	28

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
254	278	3	2854.27	0.5	1	63	27.1	95.00%	K.GFYSEEHKNYAGVYWGEVSSSETTK.A		K.GFYSEEHKNYAGVYWGEVSSSETTK.A
204	214	2	1130.62	4.6	1	53.5	21.3	95.00%	K.ATDIAAELISK.K		K.ATDIAAELISK.K
5	18	2	1526.74	-1.2	0	61.8	25.6	95.00%	D.AESTMTVGTYLAQR.L		K.DAESTMTVGTYLAQR.L
440	461	2	2409.21	3.3	1	90.9	22.6	95.00%	R.TIVMVGDGSFQLTGQEISQMIR.H		R.TIVMVGDGSFQLTGQEISQMIR.H
238	253	2	1689.86	-0.3	0	62.3	23.9	95.00%	K.LAEALNCAAFIMPAAK.G	Carbamidomethyl (+57)	K.LAEALNCAAFIMPAAK.G
516	525	2	1047.55	4.8	0	31.2	23.2	95.00%	K.TGEELTSAIK.V		K.TGEELTSAIK.V
228	237	2	949.49	5	0	30.2	23.3	95.00%	R.AAGAESAFVK.L		R.AAGAESAFVK.L

304	328	2	2694.37	3	1	65.1	21.3	95.00%	R.AAPNPNILLNSDYTSVSIPGYVFSR.V		R.AAPNPNILLNSDYTSVSIPGYVFSR.V
215	225	3	1192.75	-0.68	1	28.3	9.54	95.00%	K.KEKPILLAGPK.L		K.KEKPILLAGPK.L
329	340	2	1425.76	4.3	0	95.2	21.9	95.00%	R.VYMAEFLELLAK.K		R.VYMAEFLELLAK.K
386	405	2	2262.03	-0.44	1	81.5	26.7	95.00%	D.SNTTLYAETGDSWFNGLQMK.L		R.QIQGLVDSNTTLYAETGDSWFNGLQMK.L
447	461	2	1693.85	-0.3	0	68.2	24.1	95.00%	D.GSFQLTGQEISQMIR.H		R.TIVMVGDGSFQLTGQEISQMIR.H
160	198	4	4251.22	3.6	1	16.7	18.8	90.90%	R.QAILQHKPVYIEIPTNMANQPCPVPGPISAVISPEISDK.E	Carbamidomethyl (+57)	R.QAILQHKPVYIEIPTNMANQPCPVPGPISAVISPEISDK.E
495	508	2	1529.68	-0.85	0	58.7	26.1	95.00%	D.FAAFCESLNGETGK.A	Carbamidomethyl (+57)	R.IQNWDFAAFCESLNGETGK.A
397	405	2	1109.53	0.35	0	29.6	25.6	95.00%	D.SWFNGLQMK.L		R.QIQGLVDSNTTLYAETGDSWFNGLQMK.L
316	328	2	1474.75	0.2	0	52.1	23.8	95.00%	D.YTSVSIPGYVFSR.V		R.AAPNPNILLNSDYTSVSIPGYVFSR.V
369	378	2	1157.64	5	1	28	22.4	94.80%	K.AALNRVEVMR.Q		K.AALNRVEVMR.Q
137	146	2	1101.64	5.4	1	51.2	18.6	95.00%	K.LTCAAVAIKR.A	Carbamidomethyl (+57)	K.LTCAAVAIKR.A
19	25	2	770.49	4.3	0	34.4	18.1	95.00%	R.LVEIGIK.N		R.LVEIGIK.N
462	474	3	1575.97	4.8	1	29.2	6.02	95.00%	R.HKLPVLIFLLNNR.G		R.HKLPVLIFLLNNR.G
26	37	2	1429.72	4.2	1	38.3	24.4	95.00%	K.NHFVVPGDYNLR.L		K.NHFVVPGDYNLR.L
262	278	2	1876.86	4.2	0	98.1	26.4	95.00%	K.NYAGVYWGEVSSSETTK.A		K.NYAGVYWGEVSSSETTK.A
150	159	3	1137.6	-1.2	1	28.5	22.2	95.00%	D.APVMIDHAIR.Q	Oxidation (+16)	R.AEDAPVMIDHAIR.Q
490	508	2	2186.97	4.3	1	85.4	27	95.00%	R.IQNWDFAAFCESLNGETGK.A	Carbamidomethyl (+57)/ Deamidation (+1)	R.IQNWDFAAFCESLNGETGK.A
464	474	2	1310.81	4.6	0	66.2	10.4	95.00%	K.LPVLIFLLNNR.G		K.LPVLIFLLNNR.G
136	145	2	1073.63	3.9	1	39.6	15.9	95.00%	K.KLTCAAVAIK.R	Carbamidomethyl (+57)	K.KLTCAAVAIK.R
4	18	2	1641.77	4.2	1	65.2	26	95.00%	K.DAESTMTVGTYLAQR.L		K.DAESTMTVGTYLAQR.L
216	225	3	1064.66	3.8	0	29.3	12	95.00%	K.EKPILLAGPK.L		K.EKPILLAGPK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
9	ADH4_SCHPO	36.49%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
345	364	2	2167.98	-0.6	1	36.8	26.9	95.00%	R.LGDIAFHLGCEEHTAEAALD.R	Carbamidomethyl (+57)	R.LGDIAFHLGCEEHTAEAALDR.I
110	128	2	1962.05	-0.82	0	42.9	20.2	95.00%	D.GVQPNPTVGNVNQGLEIVK.K		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K
110	129	3	2090.15	0.0084	1	24.1	16.5	95.00%	D.GVQPNPTVGNVNQGLEIVKK.E		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVKK.E
375	385	3	1245.75	-1.4	1	42.1	11.5	95.00%	K.IRPHLVDLGVK.E		K.IRPHLVDLGVK.E
76	87	2	1282.76	5.2	1	44.2	15.1	95.00%	K.NTLIVTDPGIIK.V		K.NTLIVTDPGIIK.V
366	374	2	1027.63	6.6	0	37.3	16.2	95.00%	R.ISQLVLEVK.I		R.ISQLVLEVK.I
348	364	2	1882.85	-1	1	34.7	26.7	95.00%	D.IAFHLGCEEHTAEAALD.R	Carbamidomethyl (+57)	R.LGDIAFHLGCEEHTAEAALDR.I
149	159	2	1014.58	4.8	0	36.7	21.2	95.00%	K.GIALLATNGGK.I	Deamidation (+1)	K.GIALLATNGGK.I
210	219	2	1153.54	-1.2	1	37.9	25.5	95.00%	K.HTMPILSVND.P	N-Formyl (+28)	K.HTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
348	365	3	2038.95	0.2	1	25.8	26	95.00%	D.IAFHLGCEEHTAEAALDR.I	Carbamidomethyl (+57)	R.LGDIAFHLGCEEHTAEAALDR.I
400	412	2	1380.61	-1.9	1	27.6	26.8	91.90%	D.ACGATNPIQPTHD.E	Carbamidomethyl (+57)	K.DACGATNPIQPTHDEVK.A
96	128	3	3573.88	3.6	1	56.5	18.9	95.00%	K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K		K.ALLEEQSITVHLYDGVQPNPTVGNVNQGLEIVK.K
209	219	2	1253.64	-1.4	2	33.8	22.6	95.00%	D.KHTMPILSVND.P		K.MAIIDKHTMPILSVNDPETMYGLPPSLTAATGMDALTHAVEAYVSTAANPITDACAVK.C
169	191	2	2386.25	0.24	0	89.6	19.8	95.00%	K.SSKPQLPLIAINTTAGTASEMTR.F		K.SSKPQLPLIAINTTAGTASEMTR.F
192	200	2	1078.57	4	0	35.5	22.9	95.00%	R.FAIITEETR.H		R.FAIITEETR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
10	PMGY_SCHPO	61.61%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

23	30	2	977.53	0.49	0	33.7	21.6	95.00%	K.LNLFTGWK.D		K.LNLFTGWK.D
32	43	3	1242.68	-1.9	1	24.9	20.9	95.00%	D.PALSETGIKEAK.L		K.DPALSETGIKEAK.L
111	120	2	1271.65	5.7	0	79.8	23.2	95.00%	K.WGAEQVQIWR.R		K.WGAEQVQIWR.R
70	90	2	2429.25	3.7	1	89.6	21.4	95.00%	K.TCQIILEEVGEPNLETIKSEK.L	Carbamidomethyl (+57)	K.TCQIILEEVGEPNLETIKSEK.L
23	31	2	1092.56	0.98	2	35.9	23.2	95.00%	K.LNLFTGWKD.P		K.LNLFTGWKDPALSETGIK.E
186	199	2	1553.84	-0.59	1	54.3	19.4	95.00%	R.ELATGVPIVYHLDK.D		R.ELATGVPIVYHLDK.D
146	157	2	1320.78	4.4	1	36.9	13.8	95.00%	K.STIVPHILKGEK.V		K.STIVPHILKGEK.V
2	14	2	1439.81	5.3	0	52	17.6	95.00%	M.TTEAAPNLLVLTR.H	Acetyl (+42)	-.MTTEAAPNLLVLTR.H
158	168	2	1149.67	4.5	0	26.5	14	93.00%	K.VLIAAHGNSLR.A		K.VLIAAHGNSLR.A
95	104	2	1169.58	4.8	1	46.4	23.7	95.00%	R.YYGDLQGLNK.D		R.YYGDLQGLNK.D
58	66	2	1005.56	-0.12	0	65.2	18.4	95.00%	D.IAFTSALQR.A		K.FDIAFTSALQR.A
70	87	2	2085.08	4.2	0	96.7	21.2	95.00%	K.TCQIILEEVGEPNLETIK.S	Carbamidomethyl (+57)	K.TCQIILEEVGEPNLETIK.S
1	14	2	1528.84	4.4	0	53	20	95.00%	-.MTTEAAPNLLVLTR.H		-.MTTEAAPNLLVLTR.H
15	30	3	1944.95	-0.31	1	36.6	25.3	95.00%	R.HGESEWNKLNLFTGWK.D		R.HGESEWNKLNLFTGWK.D
32	40	2	914.51	-1.1	0	56.7	22.9	95.00%	D.PALSETGIK.E		K.DPALSETGIK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
11	TPIS_SCHPO	64.26%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
71	98	3	2925.39	4	1	98.2	25	95.00%	K.NGAYTGENSAQSLIDAGITYTLTGHSER.R		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R
206	222	2	1841.9	2.2	1	42.9	25	95.00%	R.VIYGGSVNGGNCKEFLK.F	Deamidation (+1)/ Carbamidomethyl (+57)	R.VIYGGSVNGGNCKEFLK.F
160	174	2	1615.9	-0.071	0	68.9	17.6	95.00%	K.IVIAYEPVWAIGTGK.T		K.IVIAYEPVWAIGTGK.T
175	189	2	1678.84	4.6	0	84.5	24.1	95.00%	K.TATPEQAQEVHAEIR.K		K.TATPEQAQEVHAEIR.K
135	145	2	1242.66	4.7	0	39.7	21.6	95.00%	R.EANETINVVVR.Q		R.EANETINVVVR.Q
115	134	3	2176.12	2.2	0	34.6	21.8	95.00%	K.FALEQGLTVVACIGETLAER.E	Carbamidomethyl (+57)	K.FALEQGLTVVACIGETLAER.E
175	190	2	1806.93	4.5	1	52	22.5	95.00%	K.TATPEQAQEVHAEIRK.W		K.TATPEQAQEVHAEIRK.W
32	52	2	2422.26	-0.58	1	69.1	19.9	95.00%	K.LNVGDVETVIFPQNMYLITTR.Q		K.LNVGDVETVIFPQNMYLITTR.Q
228	249	3	2334.25	-0.56	0	43.7	18.5	95.00%	D.GFLVGGASLKPEFHNIVNVHSL.-		K.FHDIDGFLVGGASLKPEFHNIVNVHSL.-
71	85	2	1538.68	-0.72	1	46.5	26.6	95.00%	K.NGAYTGENSAQSLID.A		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R
86	98	2	1404.7	-2.1	0	58.6	24.4	95.00%	D.AGITYTLTGHSER.R		K.NGAYTGENSAQSLIDAGITYTLTGHSER.R
196	205	2	971.55	5.3	0	76.1	21.9	95.00%	K.LGASVAEGLR.V		K.LGASVAEGLR.V
206	218	2	1324.61	4.4	0	76.9	25.9	95.00%	R.VIYGGSVNGGNCK.E	Deamidation (+1)/ Carbamidomethyl (+57)	R.VIYGGSVNGGNCK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
12	GLYD_SCHPO	50.75%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
341	349	2	1026.55	-0.0082	1	28.5	20.3	95.00%	D.SHMVLVDVK.S		K.LAADGTDSHMVLVDVK.S
146	159	2	1649.78	3.9	0	75	26	95.00%	K.ISAVSTYFESMPYR.V		K.ISAVSTYFESMPYR.V
183	193	2	1209.62	4.5	0	57.8	22.4	95.00%	K.ILVAGTSAYCR.L	Carbamidomethyl (+57)	K.ILVAGTSAYCR.L
171	182	3	1483.76	-0.61	1	25	23.2	95.00%	D.MLEHDAQLFRPK.I		R.VDPNTGLIDYDMLEHDAQLFRPK.I
361	371	2	1254.76	0.31	0	65.7	14.6	95.00%	R.VLELINIVTNK.N		R.VLELINIVTNK.N
145	159	2	1777.87	-0.79	1	82.8	25.1	95.00%	K.KISAVSTYFESMPYR.V		K.KISAVSTYFESMPYR.V
17	24	2	915.49	4.6	0	43.4	24.3	95.00%	D.PTVAEIMR.H		K.EQDPTVAEIMR.H
97	123	3	2996.43	3.4	0	55	24.8	95.00%	K.WGVNVQCLSGSPANMQVYQAIMPPHGR.L	Carbamidomethyl (+57)	K.WGVNVQCLSGSPANMQVYQAIMPPHGR.L
74	85	2	1550.75	4.7	1	96.3	25.4	95.00%	K.FIDQIETLCQER.A	Carbamidomethyl (+57)	K.FIDQIETLCQER.A
86	96	2	1129.62	5.1	1	54.8	22.1	95.00%	R.ALAAFNLDPAK.W		R.ALAAFNLDPAK.W
59	67	2	998.45	5.1	0	32.9	23.9	95.00%	K.YSEGYPGAR.Y		K.YSEGYPGAR.Y
277	302	3	2725.45	2.8	0	25.2	18	95.00%	K.INFSVFPGHQGGPHNHTITALAVALK.Q		K.INFSVFPGHQGGPHNHTITALAVALK.Q
303	318	3	1967.95	5.1	1	36.3	25.2	95.00%	K.QCQEPAYKEYQAQVVK.N	Carbamidomethyl (+57)	K.QCQEPAYKEYQAQVVK.N
413	422	2	1075.61	4.3	0	49.9	20.1	95.00%	R.ALTFAANLQK.E		R.ALTFAANLQK.E

438	452	2	1729.9	3.9	0	75.9	23.1	95.00%	K.LGEGEQYPELVQLQK.E		K.LGEGEQYPELVQLQK.E
46	58	2	1321.64	4.2	1	41.4	25.2	95.00%	R.AVMDALGSVMSNK.Y		R.AVMDALGSVMSNK.Y
6	16	2	1273.66	-0.48	2	34.3	23.4	95.00%	D.SIMLTPLKEQD.P		-.MSSNDSIMLTPLKEQDPTVAEIMR.H
124	142	3	1996.93	-0.24	1	23.4	26.1	92.70%	R.LMGLDLPSGGHLSHGYQTD.T		R.LMGLDLPSGGHLSHGYQTDTK.K
436	452	2	1929.02	0.62	1	43.5	19.7	95.00%	K.AKLGEGEQYPELVQLQK.E		K.AKLGEGEQYPELVQLQK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
13	THI3_SCHPO	54.05%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
155	169	2	1717.81	-0.69	0	49.2	25.7	95.00%	D.GGIGIECMQQVELER.W	Carbamidomethyl (+57)	R.CGMNIAPAIINGEIDGGIGIECMQQVELER.W
74	95	2	2353.26	0.077	0	96.4	18.9	95.00%	R.GYPVTSFGSLLNEPFTGLITLK.G		R.GYPVTSFGSLLNEPFTGLITLK.G
316	327	2	1385.71	3.6	1	53.6	23.6	95.00%	K.QEAIAEIQDEIK.Q		K.QEAIAEIQDEIK.Q
312	324	2	1428.69	-2	2	42.5	24.9	95.00%	D.PMGKQEAIAEIQD.E		K.DPMGKQEAIAEIQDEIK.Q
222	232	3	1198.64	-1.1	1	30.7	21.3	95.00%	R.AIHSATLDMLK.D		R.AIHSATLDMLK.D
128	139	2	1325.67	4.2	1	42.4	23.3	95.00%	K.FGLSPSDYTAIR.C		K.FGLSPSDYTAIR.C
6	27	2	2631.39	2.4	0	78.6	19	95.00%	K.ITFLTNWEATPYHLPIFLAQTR.G		K.ITFLTNWEATPYHLPIFLAQTR.G
63	71	2	954.54	4.5	0	51.1	16.9	95.00%	K.AMIHTLAAK.A		K.AMIHTLAAK.A
110	118	2	968.5	4.9	0	27.7	22.1	94.40%	R.IGYVGEFGK.I		R.IGYVGEFGK.I
330	339	2	992.51	5.7	0	44.3	23.6	95.00%	K.GGVFSGNSLR.Y		K.GGVFSGNSLR.Y
189	211	3	2788.29	2.8	1	29.7	26	95.00%	R.LANLGCCCFCTILYIAHDEFIAK.H	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.LANLGCCCFCTILYIAHDEFIAK.H
33	56	2	2409.27	3	1	74.8	19.3	95.00%	R.EGIEVAILEPTNPSDVTALIGSGK.V		R.EGIEVAILEPTNPSDVTALIGSGK.V
260	273	2	1711.79	4.7	1	88.7	26.2	95.00%	R.CFAYFSHDISNVPR.D	Carbamidomethyl (+57)	R.CFAYFSHDISNVPR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
14	THI2_SCHPO	40.85%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
234	242	2	981.48	0.91	0	44	24.3	95.00%	D.GPFGAFCVK.R	Carbamidomethyl (+57)	R.IAGVVTNWTLVSLNHGLQSCMDPNTINAHLVVSATGHDGPFGAFCVK.R
243	255	3	1422.76	-0.69	2	20.9	20.1	90.10%	K.RLASAQLVSNLHD.M		K.RLASAQLVSNLHDMRPLDMNR.A
175	187	2	1431.8	-0.99	1	75.7	19.2	95.00%	K.LFNATAVEDLIVK.E		K.LFNATAVEDLIVK.E
2	15	2	1400.77	3.8	0	74.5	20	95.00%	M.APATAVVTPQTAFK.T		-.MAPATAVVTPQTAFK.T
131	146	2	1818.9	-0.79	1	37.8	24.5	95.00%	R.KPADLFLNEIGVPYED.E		R.KPADLFLNEIGVPYEDEGDYVVVK.H
39	55	2	1962.95	4.7	1	48.4	25.1	95.00%	K.AYPTYSLDESFSFAPIR.E		K.AYPTYSLDESFSFAPIR.E
244	255	2	1266.66	-0.95	1	81	22.6	95.00%	R.LASAQLVSNLHD.M		R.LASAQLVSNLHDMRPLDMNR.A
295	308	2	1459.67	4	0	71.7	26.5	95.00%	R.MGPTFGGMMFSGIK.A		R.MGPTFGGMMFSGIK.A
309	320	2	1332.68	5.8	1	60	23.7	95.00%	K.AAQEALAIFDER.K		K.AAQEALAIFDER.K
274	294	2	2254.05	3.3	1	79.8	26.6	95.00%	R.EVFPGMIVGGMELSEFDGANR.M		R.EVFPGMIVGGMELSEFDGANR.M
244	260	2	1878.96	-0.49	1	65	23	95.00%	R.LASAQLVSNLHDMRPLD.M		R.LASAQLVSNLHDMRPLDMNR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
15	SAHH_SCHPO	32.10%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
257	268	2	1355.63	-0.69	0	58.5	25.6	95.00%	D.GFEVTTMEEAVK.E	Oxidation (+16)	R.VIVTEVDPINALQAAMDGFEVTTMEEAVK.E
174	183	2	1081.61	-0.2	2	45.3	17.8	95.00%	K.LKVPAINVND.S		K.LKVPAINVNDSVTK.S
20	35	2	1782.93	4.3	0	65	22	95.00%	K.ELEIAENEMPGLIAVR.E		K.ELEIAENEMPGLIAVR.E

8	18	2	1118.61	3.2	1	77.1	20.1	95.00%	K.VADISLAAFGR.K		K.VADISLAAFGR.K
216	227	2	1117.62	4.3	1	46.5	20.9	95.00%	K.VAVVAGFGDVGK.G		K.VAVVAGFGDVGK.G
269	280	2	1367.66	4	0	40.1	24.9	95.00%	K.EGQIFVTTTGCR.D	Carbamidomethyl (+57)	K.EGQIFVTTTGCR.D
153	167	2	1647.82	4.5	0	70.1	24.4	95.00%	R.GISEETTTGVHNLYK.M		R.GISEETTTGVHNLYK.M
19	35	2	1911.01	-0.7	1	81.8	20.6	95.00%	R.KELEIAENEMPGLIAVR.E		R.KELEIAENEMPGLIAVR.E
247	268	3	2364.14	0.42	1	72.3	25.2	95.00%	D.PINALQAAMDGFEVTTMEEAVK.E		R.VIVTEVDPINALQAAMDGFEVTTMEEAVK.E
176	187	2	1255.68	4.6	1	42.1	21.1	95.00%	K.VPAINVNDSVTK.S		K.VPAINVNDSVTK.S
336	344	2	1006.6	5	1	31.2	14.9	95.00%	R.HIILLADGR.L		R.HIILLADGR.L
103	118	2	2053.94	4.3	0	72.2	26	95.00%	K.GETEEEYLWCIEQQLK.S	Carbamidomethyl (+57)	K.GETEEEYLWCIEQQLK.S
133	143	3	1166.6	-0.68	1	43.6	23.2	95.00%	D.GGDLTALVHER.H		K.SFPSGKPLNMILDDGGDLTALVHER.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
16	METK_SCHPO	48.95%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
353	369	2	1946.9	-0.16	1	43.5	26.4	95.00%	K.LQTPFYLSTASYGHFTD.Q		K.LQTPFYLSTASYGHFTDQSKPWEQPK.E
90	103	2	1572.74	-1.6	1	28.9	25.5	95.00%	K.TCNVLVAIEQQSPD.I	Carbamidomethyl (+57)	K.TCNVLVAIEQQSPDIAQGLHYEK.A
147	155	2	931.5	4.5	0	58	24	95.00%	K.LNAAMSVAR.R		K.LNAAMSVAR.R
2	18	2	1820.82	-0.78	1	62.1	26.6	95.00%	M.AQTFLFTSESVGEGHPD.K		-.MAQTFLFTSESVGEGHPDK.I
137	146	2	1117.72	-0.64	0	28.7	3.01	95.00%	K.LPLTILLAHK.L		K.LPLTILLAHK.L
237	251	2	1429.74	3.6	1	73.6	22.8	95.00%	R.FVVGGPQGDAGLTGR.K		R.FVVGGPQGDAGLTGR.K
339	349	2	1256.73	4.3	1	36.5	16.5	95.00%	K.NFDLRPGVLVK.S		K.NFDLRPGVLVK.S
90	112	3	2612.3	3.4	1	62.4	23.8	95.00%	K.TCNVLVAIEQQSPDIAQGLHYEK.A	Carbamidomethyl (+57)	K.TCNVLVAIEQQSPDIAQGLHYEK.A
328	338	2	1257.74	4.7	1	49.3	16.3	95.00%	K.TSAELVEIIRK.N		K.TSAELVEIIRK.N
353	378	3	3055.48	3	1	68	23.9	95.00%	K.LQTPFYLSTASYGHFTDQSKPWEQPK.E		K.LQTPFYLSTASYGHFTDQSKPWEQPK.E
257	272	2	1508.68	-0.012	0	53.7	26.1	95.00%	D.TYGGWGAHGGGAFSGK.D		K.IIVDTYGGWGAHGGGAFSGK.D
291	299	2	856.52	4.2	0	28.1	19.7	94.90%	K.SLVAAGLAR.R		K.SLVAAGLAR.R
213	226	3	1572.93	4.6	1	37.1	12	95.00%	K.IIKPTVPAHLLDEK.T		K.IIKPTVPAHLLDEK.T
253	272	2	1948.95	4	1	80.8	25.2	95.00%	K.IIVDTYGGWGAHGGGAFSGK.D		K.IIVDTYGGWGAHGGGAFSGK.D
132	146	3	1702	0.88	1	24.9	12.6	95.00%	D.ETPEKLPLTILLAHK.L		K.ALEELGAGDQGIMFGYATDETPEKLPLTILLAHK.L
169	185	2	1946.97	4.5	0	49.1	24.4	95.00%	K.TQVTIEYEEENGAVIPR.R		K.TQVTIEYEEENGAVIPR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
17	A1EGU1_SCHPO	30.80%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
408	429	3	2504.31	-0.12	1	46	20.6	95.00%	K.HVERPIIFPISNPTTLMEAKPD.Q		K.HVERPIIFPISNPTTLMEAKPDQIDK.W
457	479	2	2580.33	2.4	0	74	21.5	95.00%	K.YVISQCNNALLYPALGVACVLSR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.YVISQCNNALLYPALGVACVLSR.C
44	57	2	1634.91	4.4	1	89.1	17.2	95.00%	R.LPPIVETLQQQVDR.C		R.LPPIVETLQQQVDR.C
373	396	3	2478.39	-0.43	0	28.9	13.8	95.00%	D.INLESAIALVKPTILLGCSGQPGK.F	Carbamidomethyl (+57)	K.EVPSGDINLESAIALVKPTILLGCSGQPGK.F
439	452	2	1418.82	-0.8	0	59.9	12.3	95.00%	K.ALIATGSPLPPLNR.N		K.ALIATGSPLPPLNR.N
273	292	3	1903.13	1.4	0	21.5	7.78	91.30%	D.IQGTGAVALAAIIGALHVTK.S		R.ILDHYRPDIACFNDDIQGTGAVALAAIIGALHVTK.S
367	396	3	3062.64	3.1	1	30.5	17.2	95.00%	K.EVPSGDINLESAIALVKPTILLGCSGQPGK.F	Carbamidomethyl (+57)	K.EVPSGDINLESAIALVKPTILLGCSGQPGK.F
490	500	2	1070.58	4.5	1	54.7	21.7	95.00%	K.AASDALATVPR.S		K.AASDALATVPR.S
15	23	2	955.55	4.9	0	32.8	19.7	95.00%	K.GVTLLNSPR.Y		K.GVTLLNSPR.Y
548	555	2	1085.63	3.7	1	31.8	19.3	95.00%	K.LKEWIIER.E		K.LKEWIIER.E
332	339	2	964.49	5	1	34.3	22.8	95.00%	R.GNLFMIDR.C		R.GNLFMIDR.C
456	479	3	2708.42	2.3	1	27.2	18.6	95.00%	K.KYVISQCNNALLYPALGVACVLSR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.KYVISQCNNALLYPALGVACVLSR.C

178	191	2	1553.75	3.5	1	59.3	25.4	95.00%	K.GHLMTLCAGLDPNR.F	Carbamidomethyl (+57)	K.GHLMTLCAGLDPNR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
18	HSP72_SCHPO	34.16%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
327	340	2	1400.77	3.9	0	39.7	20.8	95.00%	K.ASVNEIVLVGGSTR.I		K.ASVNEIVLVGGSTR.I
432	445	2	1584.83	0.81	0	41.1	22.4	95.00%	D.NQPGVLIQVFEGER.A		K.SEIFSTYSDNQPGVLIQVFEGER.A
170	184	2	1530.79	-1.6	1	42.6	22.5	95.00%	R.IINEPTAAAIAYGLD.R		R.IINEPTAAAIAYGLDR.S
111	124	2	1611.8	4	0	69	24	95.00%	K.TFTPEEISSMVLMK.M		K.TFTPEEISSMVLMK.M
140	153	2	1565.78	-2.5	1	29.1	24.5	95.00%	D.AVVTVPAYFNDSQR.Q		K.VTDAVVTVPAYFNDSQR.Q
594	607	2	1556.83	4.2	1	73.7	21.3	95.00%	K.QKELESVANPIMAK.I		K.QKELESVANPIMAK.I
538	548	2	1351.66	4.4	0	37.5	24.8	95.00%	K.NHLESYAYSLR.N		K.NHLESYAYSLR.N
326	340	2	1528.86	0.055	1	40.2	18.3	95.00%	D.KASVNEIVLVGGSTR.I		K.VDKASVNEIVLVGGSTR.I
125	136	2	1324.65	4.5	1	66.6	24.8	95.00%	K.MRETAEAYLGGK.V		K.MRETAEAYLGGK.V
170	185	2	1686.9	4	1	94.1	20	95.00%	R.IINEPTAAAIAYGLDR.S		R.IINEPTAAAIAYGLDR.S
55	69	2	1698.82	4.2	1	74.8	25.4	95.00%	K.NQVAMNPHNTIFDAK.R		K.NQVAMNPHNTIFDAK.R
457	467	2	1182.65	4.4	0	28.3	19.9	95.00%	K.FELSGIPPAPR.G		K.FELSGIPPAPR.G
235	244	2	1273.69	4.3	0	25.1	21.4	90.60%	R.LVNHFIQEFK.R		R.LVNHFIQEFK.R
35	47	2	1486.7	4.2	1	60.5	25.7	95.00%	R.TTPSYVAFTDTER.L		R.TTPSYVAFTDTER.L
608	647	3	3515.61	5.3	1	39.6	25.6	95.00%	K.IYQAGGAPGGMPGAAPGAAPGAAPGAPGAAPGGDNGPEVEEVD.-	Oxidation (+16)	K.IYQAGGAPGGMPGAAPGAAPGAAPGAPGAAPGGDNGPEVEEVD.-
24	34	2	1227.63	5.8	1	33.2	23.4	95.00%	R.VEIIANDQGNR.T		R.VEIIANDQGNR.T
159	169	2	1095.68	0.071	0	43.1	10.8	95.00%	D.AGLIAGLNVLR.I		K.DAGLIAGLNVLR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
19	HSP90_SCHPO	20.31%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
275	289	2	1790.84	-0.46	1	73.4	25.9	95.00%	R.NPSEVTKEEYASFYK.S		R.NPSEVTKEEYASFYK.S
465	474	2	1170.6	4.5	0	29.7	22.3	95.00%	K.NIYFITGESK.Q		K.NIYFITGESK.Q
567	587	2	2339.12	5.7	0	92.3	25.1	95.00%	K.IVGSPCLLTTGQYGWSANMER.I	Carbamidomethyl (+57)	K.IVGSPCLLTTGQYGWSANMER.I
369	375	2	811.49	-0.52	0	37	18.1	95.00%	D.LPLNLSR.E		K.GVVDSEDLPLNLSR.E
596	606	2	1234.5	4.9	1	67.2	25.9	95.00%	R.DTSMSAYMSSR.K		R.DTSMSAYMSSR.K
475	487	2	1548.8	4.5	0	76.3	22.9	95.00%	K.QAVENSPFLEIFR.A		K.QAVENSPFLEIFR.A
88	99	2	1282.73	5.3	1	55.5	17.6	95.00%	K.NDLINNLGVIAK.S		K.NDLINNLGVIAK.S
255	267	2	1520.76	4.6	1	46.2	24.1	95.00%	K.VKETTTETEELNK.T		K.VKETTTETEELNK.T
198	212	3	1787.96	0.73	0	55.8	20.3	95.00%	K.HSEFISYPIQLVVTR.E		K.HSEFISYPIQLVVTR.E
422	436	2	1574.86	4	1	34.5	19.4	95.00%	K.LGIHEDAANRPALAK.L		K.LGIHEDAANRPALAK.L
499	509	2	1275.67	-0.17	1	54.3	22.1	95.00%	D.PIDEYAVTQLK.E		K.FDVLFMVDPIDEYAVTQLK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
20	EF3_SCHPO	26.17%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
333	350	2	1970.01	4.8	0	86.5	22.4	95.00%	K.IPEVSTAANPEVCLETLK.A	Carbamidomethyl (+57)	K.IPEVSTAANPEVCLETLK.A
435	447	2	1531.68	-0.75	0	27.7	26.3	92.80%	D.LCNCEFSLAYGAK.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.IPGGASHAEEEEEGEDLCNCEFSLAYGAK.I
35	59	2	2604.32	3.9	1	66.4	22.4	95.00%	K.ALASFVNGPIEEQDAPSQVFSAISK.Q		K.ALASFVNGPIEEQDAPSQVFSAISK.Q
351	367	2	1809.03	4.2	1	72.9	15.3	95.00%	K.AVLGEIKVPTNEEVIAK.Y		K.AVLGEIKVPTNEEVIAK.Y
961	994	3	3666.67	2.8	0	62.6	25.7	95.00%	R.EFTEGLTEEVWAVNNGHMTPSGHNWVSGQGSGPR.I		R.EFTEGLTEEVWAVNNGHMTPSGHNWVSGQGSGPR.I
281	294	2	1550.88	4.1	1	60.5	15.8	95.00%	K.LVEDPQVVAPFLPK.L		K.LVEDPQVVAPFLPK.L
757	765	2	1178.58	7.8	0	24.9	24.4	90.10%	K.TPSEYIQWR.F		K.TPSEYIQWR.F
89	103	2	1652.98	-0.012	0	33.4	8.45	95.00%	D.VEPYLVELLPAVIAK.V		K.GLEAVANHGSVAADVEPYLVELLPAVIAK.V
479	493	2	1636.88	3.9	0	73.9	21.1	95.00%	R.AIVNGQVEGFPTHLR.T		R.AIVNGQVEGFPTHLR.T
285	294	2	1094.65	-1	0	30.2	13.6	95.00%	D.PQVVAPFLPK.L		K.LVEDPQVVAPFLPK.L
719	738	2	2327.16	0.53	0	61.6	23.4	95.00%	K.VLTGELLPTVGEIYQHENCR.I	Carbamidomethyl (+57)	K.VLTGELLPTVGEIYQHENCR.I

756	765	3	1306.67	0.54	1	21.1	23.9	90.50%	D.KTPSEYIQWR.F		R.IAYVAQAAFTHLGHHPDKTPSEYIQWR.F
419	447	3	3168.34	2.9	1	77.1	27.1	95.00%	K.IPGGASHAEEEEEGEDLCNCEFSLAYGAK.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.IPGGASHAEEEEEGEDLCNCEFSLAYGAK.I
75	103	3	2944.6	3.2	1	47.9	16	95.00%	K.GLEAVANHGSVAADVEPYLVELLPAVIAK.V		K.GLEAVANHGSVAADVEPYLVELLPAVIAK.V
133	147	2	1550.87	3.9	0	70.6	16.1	95.00%	K.AIVPSVLESIHTTGK.W		K.AIVPSVLESIHTTGK.W
881	900	3	2293.11	2.6	1	44.8	25.5	95.00%	K.EIEEHCSLLGLDAELVSHSR.I	Carbamidomethyl (+57)	K.EIEEHCSLLGLDAELVSHSR.I
606	621	3	1882.97	-0.84	1	27.9	22.2	95.00%	D.SGFLDHVVQAIIHYER.F		K.DVSSIIVSHDSGFLDHVVQAIIHYER.F
358	367	2	1098.6	4.8	0	47.3	21.4	95.00%	K.VPTNEEVIAK.Y		K.VPTNEEVIAK.Y
331	350	2	2155.12	-0.14	1	46.8	21.5	95.00%	D.GKIPEVSTAANPEVCLETLK.A	Carbamidomethyl (+57)	R.VGNVVDGKIPEVSTAANPEVCLETLK.A
35	48	2	1488.71	-1	1	48.5	25.2	95.00%	K.ALASFVNGPIEEQD.A		K.ALASFVNGPIEEQDAPSQVFSAISK.Q
596	605	2	1070.52	-0.38	1	26.5	23.7	93.00%	K.DVSSIIVSHD.S		K.DVSSIIVSHDSGFLDHVVQAIIHYER.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
21	K6PF_SCHPO	25.37%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
364	380	2	1831.87	-1.7	1	65.1	25.8	95.00%	R.ICEAVDSISSTAISHSR.A	Carbamidomethyl (+57)	R.ICEAVDSISSTAISHSR.A
613	628	3	1700.87	4.5	1	49.7	22.8	95.00%	R.GHTPLAIDNGFSGFLR.H		R.GHTPLAIDNGFSGFLR.H
822	839	4	2058.08	3.2	1	52.7	20.5	95.00%	K.VYTTEVIGNIISEEAHKR.F		K.VYTTEVIGNIISEEAHKR.F
419	431	2	1592.73	4.2	1	27.5	26.3	92.50%	K.WQDELCNSLSSVR.K	Carbamidomethyl (+57)	K.WQDELCNSLSSVR.K
138	148	2	1187.63	-0.7	1	53.8	23.3	95.00%	D.PLGNLIGFSDR.Y		K.KPDEVYVEDPLGNLIGFSDR.Y
586	603	3	1720.9	-0.11	0	59.9	22.1	95.00%	R.VAIIHVGAPAGGMNSATR.A		R.VAIIHVGAPAGGMNSATR.A
511	522	2	1241.64	-1.4	0	33.8	22.9	95.00%	D.TPSPMIAINGNK.I		R.MLATLQGVDAVDAVLASTPDTPSPMIAINGNK.I
160	183	3	2416.24	3.9	1	44	20.9	95.00%	K.SEESGAASNLESGLATPVVETLKK.A		K.SEESGAASNLESGLATPVVETLKK.A
908	918	2	1362.61	-0.39	0	39.5	25.7	95.00%	D.VENNETEIEMR.R		R.GTGVSFSSVADVENNETEIEMR.R
798	806	2	934.49	4	0	31.5	22.6	95.00%	K.ATFALEAGR.N		K.ATFALEAGR.N
254	267	2	1400.75	3.4	0	49.7	22	95.00%	R.GWLAEGGTLIGTAR.C		R.GWLAEGGTLIGTAR.C
844	861	2	1860.9	4.7	1	42.3	25.5	95.00%	R.TAVPGHVQQGGNPTPMDR.A		R.TAVPGHVQQGGNPTPMDR.A
927	938	2	1323.7	4.7	1	53.3	21.2	95.00%	R.DMHNLVNILAGK.T		R.DMHNLVNILAGK.T
77	94	2	1954.97	4.6	1	62	23.7	95.00%	R.LVPGELSLSPAAEDSEWR.G		R.LVPGELSLSPAAEDSEWR.G
197	214	2	1760.86	4.1	1	84.8	25	95.00%	K.IAVMTSGGDSPGMNAVVR.A		K.IAVMTSGGDSPGMNAVVR.A
822	838	2	1901.98	4.1	0	50.4	22.4	95.00%	K.VYTTEVIGNIISEEAHK.R		K.VYTTEVIGNIISEEAHK.R
887	896	2	997.59	-0.019	0	60.2	16.3	95.00%	D.PSSAVVIGIR.G		R.ANDLGNDPSSAVVIGIR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
22	6PGD_SCHPO	30.49%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
386	403	3	2088.07	-0.44	0	27.2	22	95.00%	D.PNLESILFHPFFTNGVEK.A		R.EDPNLESILFHPFFTNGVEK.A
156	166	3	1228.76	4.8	0	32.1	8.45	95.00%	R.IKPIFQTLAAK.A		R.IKPIFQTLAAK.A
42	51	2	1134.56	4.5	1	47.7	24.6	95.00%	R.VDEFLANEAK.G		R.VDEFLANEAK.G
123	139	2	1590.81	3.9	0	62.7	23.7	95.00%	K.GILFVGSGVSGGEEGAR.Y		K.GILFVGSGVSGGEEGAR.Y
140	155	2	1669.81	4.7	0	28.8	25.5	95.00%	R.YGPSLMPGGNPAAWPR.I		R.YGPSLMPGGNPAAWPR.I
269	291	2	2504.28	3.2	0	92.8	22.1	95.00%	K.WTAQNALEMGTPVSLITEAVFAR.C		K.WTAQNALEMGTPVSLITEAVFAR.C
437	449	2	1379.79	4.1	0	52	15.2	95.00%	R.SAVLPANLLQAQR.D		R.SAVLPANLLQAQR.D
80	97	2	1925.1	4.4	1	58.2	14.1	95.00%	K.AGKPVDYLIEGLAPLLEK.G		K.AGKPVDYLIEGLAPLLEK.G
54	67	2	1501.78	-0.55	0	66.1	23	95.00%	K.SIVGAHSLEEFVSK.L		K.SIVGAHSLEEFVSK.L
86	97	2	1357.78	-1.4	0	38.5	17.9	95.00%	D.YLIEGLAPLLEK.G		K.AGKPVDYLIEGLAPLLEK.G
29	37	2	1175.49	3.9	0	36.7	25.7	95.00%	K.GFTVCCYNR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GFTVCCYNR.T
122	139	2	1718.89	-0.89	1	90.2	22.7	95.00%	K.KGILFVGSGVSGGEEGAR.Y		K.KGILFVGSGVSGGEEGAR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
23	ILV5_SCHPO	29.46%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
198	204	2	738.5	-0.3	0	36	11.5	95.00%	D.VILVAPK.G		K.DVDVILVAPK.G
84	104	2	2141.07	4.6	1	90.4	23.6	95.00%	K.NDTLAIIGYGSQGHGQGLNAR.D		K.NDTLAIIGYGSQGHGQGLNAR.D
330	337	2	914.47	6	1	41.2	22.8	95.00%	R.GAIDWTPR.F		R.GAIDWTPR.F
314	328	2	1725.76	3.8	1	69	27.3	95.00%	K.YGLDYMFAACSTTAR.R	Carbamidomethyl (+57)	K.YGLDYMFAACSTTAR.R
145	163	2	2074.05	4.2	1	75.2	22.9	95.00%	K.GSIIMNLLSDAAQTETWPK.I		K.GSIIMNLLSDAAQTETWPK.I
86	104	3	1911.99	-1.2	0	40.3	22.2	95.00%	D.TLAIIGYGSQGHGQGLNAR.D		K.NDTLAIIGYGSQGHGQGLNAR.D
362	372	2	1312.61	4.6	0	61.6	25.4	95.00%	R.SLEYNSAPNYR.E		R.SLEYNSAPNYR.E
289	313	2	2687.32	3.5	0	76.3	24.4	95.00%	R.GHSPAEAFNETVEEATQSLYPLIGK.Y		R.GHSPAEAFNETVEEATQSLYPLIGK.Y
318	328	2	1277.55	-0.77	0	46.2	25.7	95.00%	D.YMFAACSTTAR.R	Carbamidomethyl (+57)	K.YGLDYMFAACSTTAR.R
123	133	2	1198.6	4.3	1	28.6	23.2	95.00%	K.QAIEDGWVPGK.T		K.QAIEDGWVPGK.T
196	204	2	952.6	-0.23	1	58.3	9.54	95.00%	D.VDVILVAPK.G		K.DVDVILVAPK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
24	EF2_SCHPO	18.65%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
272	283	2	1498.77	4.2	1	53.9	23.1	95.00%	R.AFNMFILDPIYR.I		R.AFNMFILDPIYR.I
466	479	2	1474.71	3.7	0	72.8	24.8	95.00%	K.SGTLTTSEVAHNMK.V		K.SGTLTTSEVAHNMK.V
811	823	3	1441.73	-1.8	0	30.7	23.5	95.00%	D.PTSKPGQIVCEAR.K	Carbamidomethyl (+57)	R.QATAGQAFPQLVFDHWSPMSGDPLDPTSKPGQIVCEAR.K
565	578	2	1451.69	4.3	0	44.5	25.6	95.00%	R.ESVSEPSSMTALSK.S		R.ESVSEPSSMTALSK.S
284	292	2	1051.52	4.5	1	27.5	23.6	94.20%	R.IFDAVMNSR.K		R.IFDAVMNSR.K
244	253	2	1266.61	5.9	0	30	24.9	95.00%	R.LWGENYFNPK.T		R.LWGENYFNPK.T
770	785	2	1798.9	4	0	39.1	23.6	95.00%	K.AYLPVNESFGFTGELR.Q		K.AYLPVNESFGFTGELR.Q
686	696	2	1254.66	0.54	1	74.1	22.5	95.00%	R.FNILDVVLHAD.A		R.FNILDVVLHADAIHR.G
371	384	2	1594.76	4.1	1	55	25.8	95.00%	R.NCDANAPLMIYVSK.M	Carbamidomethyl (+57)	R.NCDANAPLMIYVSK.M
327	346	2	2192.18	2.4	1	55.9	18.3	95.00%	K.FLPAADALMEMIVLHLPSPK.T		K.FLPAADALMEMIVLHLPSPK.T
586	609	3	2657.29	3.5	0	32.6	24.6	95.00%	R.IFMTAEPMSEELSVAIETGHVNPR.D		R.IFMTAEPMSEELSVAIETGHVNPR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
25	ACT_SCHPO	42.40%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
158	177	4	2224.15	-0.16	0	21.5	21.3	95.00%	D.GVTHTVPIYEGYALPHAIMR.L		R.TTGIVLDSGDGVTHTVPIYEGYALPHAIMR.L
223	238	2	1794.86	-0.79	0	97.8	25.4	95.00%	D.FEQELQTAAQSSSLEK.S		K.LCYVALDFEQELQTAAQSSSLEK.S
245	254	2	1085.58	-0.57	0	40.5	23.3	95.00%	D.GQVITIGNER.F		K.SYELPDGQVITIGNER.F
1	18	2	2007.9	4	1	79.9	26.2	95.00%	-.MEEEIAALVIDNGSGMCK.A	Acetyl (+42)/ Carbamidomethyl (+57)	-.MEEEIAALVIDNGSGMCK.A
255	284	3	3274.66	3.2	1	82.1	20.8	95.00%	R.FRAPEALFQPSALGLENAGIHEATYNSIMK.C		R.FRAPEALFQPSALGLENAGIHEATYNSIMK.C
85	95	3	1514.75	5.5	0	36	24.5	95.00%	K.IWHHTFYNELR.V		K.IWHHTFYNELR.V
96	113	2	2014.02	-0.1	0	60.5	23.6	95.00%	R.VAPEEHPCLLTEAPLNPK.S	Carbamidomethyl (+57)	R.VAPEEHPCLLTEAPLNPK.S
197	206	2	1131.53	5.1	0	41.4	25.5	95.00%	R.GYTFSTTAER.E		R.GYTFSTTAER.E
239	254	2	1789.89	5.1	1	75.2	24.6	95.00%	K.SYELPDGQVITIGNER.F		K.SYELPDGQVITIGNER.F
216	238	2	2629.27	3.5	1	106	24.9	95.00%	K.LCYVALDFEQELQTAAQSSSLEK.S	Carbamidomethyl (+57)	K.LCYVALDFEQELQTAAQSSSLEK.S
360	372	2	1511.7	3.8	1	34.6	25.7	95.00%	K.QEYDESGPGIVYR.K		K.QEYDESGPGIVYR.K
257	284	3	2971.47	-0.6	0	44.6	22.4	95.00%	R.APEALFQPSALGLENAGIHEATYNSIMK.C		R.APEALFQPSALGLENAGIHEATYNSIMK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
26	HSP75_SCHPO	35.24%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	173	2	1168.66	5	1	34.3	18.9	95.00%	K.DAGAIAGLNVLR.I		K.DAGAIAGLNVLR.I
364	385	2	2201.13	-0.64	1	75.3	21.4	95.00%	K.SINPDEAVAYGAAVQAAVLTNK.A		K.SINPDEAVAYGAAVQAAVLTNK.A
174	188	2	1530.79	-1.6	1	42.6	22.5	95.00%	R.IINEPTAAAIAYGLD.A		R.IINEPTAAAIAYGLDAK.S
501	517	3	1779.92	5.5	0	60.6	22	95.00%	R.SAHIEITNSVGHLSSTK.I		R.SAHIEITNSVGHLSSTK.I
451	472	2	2468.2	5.8	0	62.2	24.8	95.00%	R.VNCAENEPLGEFQLTGIPPMPR.G	Carbamidomethyl (+57)	R.VNCAENEPLGEFQLTGIPPMPR.G
437	450	2	1638.8	-1.2	0	45.4	24.3	95.00%	D.NQTTVTFPVYQGER.V		R.TFTTVADNQTTVTFPVYQGER.V
144	157	2	1552.8	4.6	1	33.7	23	95.00%	K.AVITVPAYFSDSQR.A		K.AVITVPAYFSDSQR.A
336	344	2	900.54	-1	0	37.8	17.5	95.00%	D.IVLVGGSTR.I		K.ADVHDIVLVGGSTR.I
115	128	2	1565.81	1.4	0	60	22.4	95.00%	K.QFTAQEISAMVLTK.M		K.QFTAQEISAMVLTK.M
543	564	2	2513.21	3.3	0	64.4	25	95.00%	K.SQLESYISNIETTISEPNVMMK.L		K.SQLESYISNIETTISEPNVMMK.L
174	190	2	1729.93	3.9	1	82.9	19.8	95.00%	R.IINEPTAAAIAYGLDAK.S		R.IINEPTAAAIAYGLDAK.S
288	301	2	1482.73	-0.82	1	54.3	24.6	95.00%	D.SLSNGIDFSSSITR.A		R.ALSSVTQTTVEVDSLSNGIDFSSSITR.A
39	51	2	1484.72	4.2	0	50.9	25.5	95.00%	R.TTPSFVAFTETER.L		R.TTPSFVAFTETER.L
114	128	2	1693.91	-0.24	1	75.6	19.6	95.00%	K.KQFTAQEISAMVLTK.M		K.KQFTAQEISAMVLTK.M
430	450	2	2374.16	5.6	1	61.9	24.3	95.00%	R.TFTTVADNQTTVTFPVYQGER.V		R.TFTTVADNQTTVTFPVYQGER.V
96	113	2	1987.03	-0.71	1	59.6	21.3	95.00%	K.VIDNNGIPTIEVNYLGEK.K		K.VIDNNGIPTIEVNYLGEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
27	TSA1_SCHPO	45.83%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	147	2	1224.69	4.4	1	43.5	18.1	95.00%	R.QITINDLPVGR.S		R.QITINDLPVGR.S
155	175	3	2525.18	-0.029	1	53.7	25.9	95.00%	R.LLDAFQFVEEHGEVCPANWHK.G	Carbamidomethyl (+57)	R.LLDAFQFVEEHGEVCPANWHK.G
125	132	2	901.53	4.7	1	35.7	20.3	95.00%	R.GLFLIDPK.G		R.GLFLIDPK.G
66	88	2	2576.29	0.89	1	97.3	23.4	95.00%	R.NAQVILTSTDSEYSHLAFINTPR.K		R.NAQVILTSTDSEYSHLAFINTPR.K
14	26	2	1333.69	3.6	0	40.1	22.9	95.00%	K.GTAVVNGAFEEIK.L		K.GTAVVNGAFEEIK.L
76	88	2	1533.76	0.05	0	44.9	24.8	95.00%	D.SEYSHLAFINTPR.K		R.NAQVILTSTDSEYSHLAFINTPR.K
2	13	2	1341.74	4.1	1	36.9	20.8	95.00%	M.SLQIGKPAPDFK.G	Acetyl (+42)	-.MSLQIGKPAPDFK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
28	TKT_SCHPO	33.58%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
306	318	2	1423.73	4.8	1	73.3	23.1	95.00%	R.VAIASSAEEEYKK.M		R.VAIASSAEEEYKK.M
325	336	2	1449.68	6.5	1	28.4	25.4	94.80%	K.QSYPDLSNQLER.I	Deamidation (+1)	K.QSYPDLSNQLER.I
238	252	2	1719.86	5	1	57.2	24.7	95.00%	R.EAMSCTDKPTLINLK.T	Carbamidomethyl (+57)	R.EAMSCTDKPTLINLK.T
395	407	2	1418.65	3.9	1	52.7	25.9	95.00%	R.WEGAADFQPPSSK.L		R.WEGAADFQPPSSK.L
481	494	3	1636.81	0.18	0	33.9	24.5	95.00%	D.GPTHQPIETFAHFR.A		R.VIYVATHDSIGLGEDGPTHQPIETFAHFR.A
653	663	2	1249.63	3.9	0	24.8	24.4	90.00%	K.FHFTTSGVAQR.A		K.FHFTTSGVAQR.A
182	193	2	1385.74	4.7	1	41.9	21.6	95.00%	K.LSNLIAVWDNNK.I		K.LSNLIAVWDNNK.I
532	547	2	1810.95	4.2	0	72.5	21.2	95.00%	R.QNLPQLENSTIENALK.G		R.QNLPQLENSTIENALK.G
507	531	2	2588.26	-0.47	1	112	24.4	95.00%	D.GNETSAAYYSALTSDSTPSILALTR.Q		R.AMPNINCWRPADGNETSAAYYSALTSDSTPSILALTR.Q
589	606	2	2252.07	4.5	0	58.5	26.1	95.00%	R.VVSLPCWEVFEQQPESYR.L	Carbamidomethyl (+57)	R.VVSLPCWEVFEQQPESYR.L
630	648	3	2046.93	3.6	1	34	26.8	95.00%	R.YVHEAFGMHTFGDSGPAPK.L		R.YVHEAFGMHTFGDSGPAPK.L
253	281	3	3132.54	2.9	1	59.8	23.5	95.00%	K.TTIGYGSELQGTHSVHGSPLKPEDCVHVK.K	Carbamidomethyl (+57)	K.TTIGYGSELQGTHSVHGSPLKPEDCVHVK.K
253	276	3	2509.21	-0.87	1	22.3	24.5	92.80%	K.TTIGYGSELQGTHSVHGSPLKPED.C		K.TTIGYGSELQGTHSVHGSPLKPEDCVHVK.K
291	303	2	1603.8	4	0	26.8	24.3	93.30%	K.TFQVPPEVYAYYK.E		K.TFQVPPEVYAYYK.E

522	531	2	1057.61	0.36	0	47.6	18.8	95.00%	D.STPSILALTR.Q		R.AMPNINCWRPADGNETSAAYYSALTSDSTPSILALTR.Q
30	49	3	1972.01	-0.21	0	43.8	22.1	95.00%	K.SGHPGAPMGLAPAAHVLFSR.I		K.SGHPGAPMGLAPAAHVLFSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
29	HSP60_SCHPO	25.77%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
112	128	2	1705.86	4.1	1	84.3	24	95.00%	K.TNEVAGDGTTTATVLTR.A		K.TNEVAGDGTTTATVLTR.A
477	500	3	2505.43	-1.2	1	27.9	10.8	95.00%	R.KAITRPAQTILENAGLEGNLIVGK.L		R.KAITRPAQTILENAGLEGNLIVGK.L
137	148	2	1316.6	4	1	27.4	26.3	92.20%	R.NVAAGCNPMDLR.R	Carbamidomethyl (+57)	R.NVAAGCNPMDLR.R
437	453	2	1588.84	-1.5	0	31.5	21.8	95.00%	K.AAVSEGVLPGAGTSFVK.A		K.AAVSEGVLPGAGTSFVK.A
244	256	2	1529.84	4	0	44.5	19.2	95.00%	K.VEFENPLILLSEK.K		K.VEFENPLILLSEK.K
478	500	3	2377.33	0.63	0	30.2	14.8	95.00%	K.AITRPAQTILENAGLEGNLIVGK.L		K.AITRPAQTILENAGLEGNLIVGK.L
241	256	2	1873.03	4.6	1	56.5	17.4	95.00%	K.SQKVEFENPLILLSEK.K		K.SQKVEFENPLILLSEK.K
68	79	2	1313.7	4.3	1	39.3	21.4	95.00%	R.NVLIDQPFGSPK.I		R.NVLIDQPFGSPK.I
387	396	2	1249.62	-1.9	1	25.5	24.5	91.30%	D.PNLTEYEKEK.L		R.GVMADPNLTEYEKEK.L
258	275	2	1937.07	4.4	1	74.7	17.7	95.00%	K.VSAVQDILPSLELAAQQR.R		K.VSAVQDILPSLELAAQQR.R
229	240	2	1401.72	4.3	1	35	22.8	95.00%	R.GYISPYFITDVK.S		R.GYISPYFITDVK.S
45	56	2	1215.69	4.9	1	52.6	18.6	95.00%	R.ASLLTGVDTLAR.A		R.ASLLTGVDTLAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
30	GPD1_SCHPO	42.34%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
222	232	2	954.59	-0.54	0	29.9	15.3	95.00%	D.VAGVALGGALK.N		R.EQIAAVFDRPYFSVVSVDDVAGVALGGALK.N
164	182	2	1962	1.4	0	77	22.7	95.00%	K.LGIYCGVLSGANVANEVAR.E	Carbamidomethyl (+57)	K.LGIYCGVLSGANVANEVAR.E
2	20	2	1989	3.8	1	99.4	23.8	95.00%	M.SGYGQQGVSAANIDSIRPK.K	Acetyl (+42)	-.MSGYGQQGVSAANIDSIRPK.K
87	104	2	2008.04	-0.99	1	58.9	21.3	95.00%	K.YLPGIECPPNVIAVPDVR.E	Carbamidomethyl (+57)	K.YLPGIECPPNVIAVPDVR.E
310	331	3	2285.25	-0.52	1	28.7	16.2	95.00%	K.SLETLEKELLGGQLLQGAATSK.D		K.SLETLEKELLGGQLLQGAATSK.D
277	296	2	2153	2.6	1	93.7	26.1	95.00%	R.TMVEQSCGIADLVTSCLGGR.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.TMVEQSCGIADLVTSCLGGR.N
183	202	2	2362.1	3.9	1	116	26.4	95.00%	R.EQFCETTIGFNPPNEVDIPR.E	Carbamidomethyl (+57)	R.EQFCETTIGFNPPNEVDIPR.E
73	86	2	1656.85	-0.68	1	48	23.5	95.00%	R.KLTEVFNEAHENVK.Y		R.KLTEVFNEAHENVK.Y
74	86	2	1528.76	4.4	0	69.8	24.9	95.00%	K.LTEVFNEAHENVK.Y		K.LTEVFNEAHENVK.Y
125	144	3	2172.12	0.45	1	35.2	22.2	95.00%	R.VCDQMVGLIRPGAVGISCIK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VCDQMVGLIRPGAVGISCIK.G
317	331	2	1484.83	3.6	0	57.3	19.2	95.00%	K.ELLGGQLLQGAATSK.D		K.ELLGGQLLQGAATSK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
31	IPYR_SCHPO	45.67%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
257	280	3	2423.27	-0.37	1	31.7	20.5	95.00%	D.PSVSSTIPPAQELAPAPVDPSVHK.W		K.SDFSLVNVSVTGSVANDPSVSSTIPPAQELAPAPVDPSVHK.W
186	192	2	922.44	6	0	35.4	25.3	95.00%	R.ATNEWFR.I		R.ATNEWFR.I
84	113	4	3616.64	3.2	1	34.2	25.8	95.00%	R.NCFPHHGYIWNYGAFPQTYEDPNVVHPETK.A	Carbamidomethyl (+57)	R.NCFPHHGYIWNYGAFPQTYEDPNVVHPETK.A
24	42	2	2112.04	4.6	1	50.5	24.5	95.00%	K.NGTPISSWHDIPLYANAEK.T		K.NGTPISSWHDIPLYANAEK.T
8	23	2	1839.93	4.1	1	74	23.1	95.00%	R.EVGALNTLDYQVYVEK.N		R.EVGALNTLDYQVYVEK.N
199	212	2	1556.69	-1	0	60.8	27	95.00%	D.GKPENSFAFSGECK.N	Carbamidomethyl (+57)	K.IPDGKPENSFAFSGECK.N
120	130	2	1257.6	-1.8	1	68.5	25.9	95.00%	D.PLDVCEIGEAR.G	Carbamidomethyl (+57)	K.GDSDPLDVCEIGEAR.G
43	53	2	1283.73	4	0	66.7	18.6	95.00%	K.TILNMVVEIPR.W		K.TILNMVVEIPR.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
32	PUR9_SCHPO	27.35%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
332	347	2	1697.92	-0.13	0	35.4	19.2	95.00%	D.GVIAPGYEPEALELLK.K		R.EVSDGVIAPGYEPEALELLK.K

551	565	2	1519.75	4.1	1	63.8	24.3	95.00%	K.YVAAPGGSVMDQAVR.D		K.YVAAPGGSVMDQAVR.D
122	129	2	827.52	-0.75	0	36	17.2	95.00%	D.IGGVTLLR.A		R.ETIAKPNVTIPEAVEEIDIGGVTLLR.A
223	244	2	2446.24	-1.5	1	52.5	21.5	95.00%	K.VLCGSPGYINLMDALNSWPLVK.E	Carbamidomethyl (+57)	K.VLCGSPGYINLMDALNSWPLVK.E
39	60	2	2231.08	4.2	1	97.7	25.2	95.00%	R.ESGMEVADVSSITNAPEILGGR.V		R.ESGMEVADVSSITNAPEILGGR.V
566	581	2	1881.9	4.3	1	55.8	25.4	95.00%	R.DTANEFNMVFSEIPLR.L		R.DTANEFNMVFSEIPLR.L
47	60	2	1412.76	-0.3	0	52.3	20.6	95.00%	D.VSSITNAPEILGGR.V		R.ESGMEVADVSSITNAPEILGGR.V
354	362	2	1152.54	4.8	1	28.8	25.9	94.70%	K.YCVLQMDPK.Y	Carbamidomethyl (+57)	K.YCVLQMDPK.Y
248	259	2	1216.65	4.7	0	30.2	22.4	95.00%	R.ENIGIPAAASFK.H		R.ENIGIPAAASFK.H
104	129	3	2776.53	2.1	1	22.6	14.6	93.20%	R.ETIAKPNVTIPEAVEEIDIGGVTLLR.A		R.ETIAKPNVTIPEAVEEIDIGGVTLLR.A
201	222	3	2414.15	-1.2	0	30	25.1	95.00%	R.YGANPHQSPAQAFMEQGPLPFK.V		R.YGANPHQSPAQAFMEQGPLPFK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
33	G6PI_SCHPO	29.09%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
217	228	2	1343.61	5.2	0	37.3	25.9	95.00%	K.TFTTAETCTNAK.S	Carbamidomethyl (+57)	K.TFTTAETCTNAK.S
206	216	2	1218.69	-0.27	0	53.7	19.2	95.00%	D.PETTLFLIASK.T		K.CDPETTLFLIASK.T
372	382	2	1171.52	5.1	1	67.7	25.4	95.00%	R.SGDMVNYTTGK.I		R.SGDMVNYTTGK.I
464	477	2	1502.83	4	0	36.9	18.9	95.00%	K.TFVGNRPSNSIIAK.K		K.TFVGNRPSNSIIAK.K
63	75	2	1499.85	3.9	0	37.5	16.9	95.00%	K.NLITEETVELLVK.L		K.NLITEETVELLVK.L
2	24	2	2548.26	-0.14	0	63.7	23.2	95.00%	M.SFSLASTLPAWQAVQTHYESVGK.H	Acetyl (+42)	-.MSFSLASTLPAWQAVQTHYESVGK.H
118	128	2	1170.59	4.1	1	35.5	22.8	95.00%	K.VNGQDVMPGVR.K		K.VNGQDVMPGVR.K
204	216	2	1493.75	4.3	1	51.5	24.3	95.00%	K.CDPETTLFLIASK.T	Carbamidomethyl (+57)	K.CDPETTLFLIASK.T
521	531	2	1186.62	0.41	2	41.5	22.9	95.00%	K.NVLAQLETKGD.V		K.NVLAQLETKGDVENHDSSTNGLINLFK.N
54	62	2	1022.54	-0.62	1	57.5	22.1	95.00%	D.GPILFDFSK.N		K.EEDGPILFDFSK.N
429	445	2	1870.94	4.8	0	69.7	24.3	95.00%	R.MLFSNFAAQTEALMLGK.T		R.MLFSNFAAQTEALMLGK.T
353	367	2	1711.83	4.2	0	71.8	24.8	95.00%	R.FPAYLQQLSMESNGK.A		R.FPAYLQQLSMESNGK.A
537	547	2	1192.64	-0.35	0	50.2	21	95.00%	D.SSTNGLINLFK.N		K.GDVENHDSSTNGLINLFK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
34	PDX1_SCHPO	29.73%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	49	2	1547.74	-1.2	0	73.7	25.2	95.00%	R.IAEAAGACAVMALER.V	Carbamidomethyl (+57)/ Oxidation (+16)	R.IAEAAGACAVMALER.V
265	280	2	1628.86	4	0	87.2	21.6	95.00%	K.ILAEVSENLGAAMVGR.S		K.ILAEVSENLGAAMVGR.S
71	83	2	1355.75	4.3	0	66.7	21	95.00%	K.EIQAAVSIPVMAK.V		K.EIQAAVSIPVMAK.V
21	34	2	1457.74	4	1	89.6	23.5	95.00%	K.GGVIMDVVNAEQAR.I		K.GGVIMDVVNAEQAR.I
121	132	3	1383.7	4.4	1	31	24.4	95.00%	K.SKFTVPFVCGSR.N	Carbamidomethyl (+57)	K.SKFTVPFVCGSR.N
140	149	2	1102.6	4.8	1	28.6	22.3	95.00%	R.RISEGAAMIR.T		R.RISEGAAMIR.T
13	20	2	830.47	4.2	0	38.8	20.2	95.00%	K.AGLAQMLK.G		K.AGLAQMLK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
35	LYS9_SCHPO	30.44%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
177	183	2	740.49	4.7	0	33.1	14.9	95.00%	R.GVLLALR.N		R.GVLLALR.N
412	426	2	1524.8	0.12	1	45.8	22.1	95.00%	D.GVINTPGVLAPNDMK.L		K.LVGVPCGVATQQILDGVINTPGVLAPNDMK.L
38	49	2	1259.66	4.1	0	41.7	22.6	95.00%	K.AEAFINGIPNSK.A		K.AEAFINGIPNSK.A
149	170	2	2385.11	5.2	1	60.2	26.6	95.00%	K.SFLSYCGGLPAPEDSNNPLGYK.F	Carbamidomethyl (+57)	K.SFLSYCGGLPAPEDSNNPLGYK.F

2	22	3	2269.25	3.1	0	39	16	95.00%	M.PSILLLGSGFVAHPTLEYLSR.R		-.MPSILLLGSGFVAHPTLEYLSR.R
379	396	2	1989.93	4.3	1	76.6	26.4	95.00%	R.TCTLLDYGVPNGYTSMAK.L	Carbamidomethyl (+57)	R.TCTLLDYGVPNGYTSMAK.L
126	135	2	1125.62	0.7	1	28.7	20.1	95.00%	D.PGIDHLYAIK.T		K.AGSICMNEIGVDPGIDHLYAIK.T
104	113	2	1103.56	4	0	29.1	23.4	95.00%	K.MAELEEAAIK.A		K.MAELEEAAIK.A
64	85	3	2488.28	3.3	1	39.1	21.4	95.00%	K.AVSEHDLTISLIPYTYHATVMK.A		K.AVSEHDLTISLIPYTYHATVMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
36	SERA_SCHPO	27.90%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
438	452	3	1654.8	-1.5	1	25	25.1	95.00%	D.ISDCTPGSLEALHQK.L	Carbamidomethyl (+57)	R.GDIAYLVADISDCTPGSLEALHQK.L
275	284	2	1108.56	4.3	0	25.6	24.4	91.50%	K.EGSYLINASR.G		K.EGSYLINASR.G
58	74	2	1883.04	-0.057	2	62.8	17.6	95.00%	K.ILLLENVNQSALSNLKD.E		K.ILLLENVNQSALSNLKDEGYQVEFLK.T
367	385	2	2078.04	0.086	0	85.1	24	95.00%	R.YINEGNSIGAVNFPEVSLR.S		R.YINEGNSIGAVNFPEVSLR.S
410	421	2	1468.77	4	1	31.9	21.3	95.00%	R.QVNELFIDHNIK.S		R.QVNELFIDHNIK.S
302	319	2	1728.87	0.91	1	54.5	23.5	95.00%	K.IAGAAIDVYPSEPAGNGK.D		K.IAGAAIDVYPSEPAGNGK.D
47	57	3	1247.68	3.8	1	25.6	20.9	95.00%	R.TLKPFASEDIK.I		R.TLKPFASEDIK.I
248	262	2	1596.82	4.1	1	50.8	22.4	95.00%	R.ADFVSLHVPASPETK.N		R.ADFVSLHVPASPETK.N
142	154	2	1394.7	4.8	0	57.8	23.5	95.00%	R.GIAVFNSPYANSR.S		R.GIAVFNSPYANSR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
37	PUT2_SCHPO	30.29%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
388	405	2	1773.91	3.9	1	102	23.5	95.00%	K.VLESAASDSEIEVLAGGK.A		K.VLESAASDSEIEVLAGGK.A
362	384	3	2428.26	0.86	1	42.9	20.4	95.00%	K.VGAPLTDFANFVGPVIHQASFNK.L		K.VGAPLTDFANFVGPVIHQASFNK.L
82	92	2	1222.64	4.6	1	32.1	22.7	95.00%	K.HVEDAIEAALR.G		K.HVEDAIEAALR.G
254	274	3	2393.15	4.4	0	52.3	25.4	95.00%	K.VCFNHPEFAGLHFTGSTAVFR.S	Carbamidomethyl (+57)	K.VCFNHPEFAGLHFTGSTAVFR.S
275	288	2	1444.74	4.6	0	37.7	23.9	95.00%	R.SLWGTIGENVANGK.Y		R.SLWGTIGENVANGK.Y
33	50	2	2012.11	-1.5	2	37.2	18.2	95.00%	K.AYKELEAELPVTIPVIID.G		K.AYKELEAELPVTIPVIIDGK.E
233	253	2	2068.09	4.4	1	68.9	20.3	95.00%	R.EAGLPAGALQFIPGDAVEVSK.V		R.EAGLPAGALQFIPGDAVEVSK.V
409	422	2	1551.82	0.046	0	33.7	22	95.00%	D.SEGFFVEPTVLLSK.N		K.ADDSEGFFVEPTVLLSK.N
495	509	2	1504.71	3.5	0	49.3	25.6	95.00%	K.CTGAVVGEQPFGGAR.A	Carbamidomethyl (+57)	K.CTGAVVGEQPFGGAR.A
484	494	2	1225.58	4.6	1	28	25.4	94.30%	R.NAAGNFYINDK.C		R.NAAGNFYINDK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
38	HXK2_SCHPO	23.52%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
12	24	2	1581.77	4.1	1	62.3	24.9	95.00%	K.LVNDFEYPTESLR.E		K.LVNDFEYPTESLR.E
435	449	2	1414.76	0.44	0	45.3	22	95.00%	D.GSGIGAALCALQAVK.E	Carbamidomethyl (+57)	K.DGSGIGAALCALQAVK.E
434	449	2	1529.79	4.8	1	96.2	22.6	95.00%	K.DGSGIGAALCALQAVK.E	Carbamidomethyl (+57)	K.DGSGIGAALCALQAVK.E
191	205	2	1599.88	-0.7	1	66.9	18.2	95.00%	R.IEAVINDTVGTLVTR.A		R.IEAVINDTVGTLVTR.A
76	86	2	1287.67	3.9	1	30.3	24.2	95.00%	R.VCWIQLLGDGK.Y	Carbamidomethyl (+57)	R.VCWIQLLGDGK.Y
286	296	2	1240.63	5.9	0	25.6	22.5	91.50%	R.VGGMYLGELFR.R		R.VGGMYLGELFR.R
374	388	2	1564.83	4.1	0	56.1	21.3	95.00%	R.MSAVPIASLYLSTGR.A		R.MSAVPIASLYLSTGR.A
1	11	2	1334.67	4.1	1	29.9	24.5	95.00%	-.MEANFQQAVKK.L	Acetyl (+42)	-.MEANFQQAVKK.L
399	413	3	1798.88	0.84	1	31.2	24.3	95.00%	D.GSLVEHYPHFVDMLR.E		K.SDVGVDGSLVEHYPHFVDMLR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
39	C1TC_SCHPO	12.91%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
689	707	3	1923.15	3.9	1	37.5	6.99	95.00%	R.TSGLKPDAIVIVATVQALK.L		R.TSGLKPDAIVIVATVQALK.L

765	783	2	1913.93	-1.2	2	41.1	24.8	95.00%	D.SPNEISAIREEALAAGATD.A		K.FSSDSPNEISAIREEALAAGATDAVDSNHWAEGGK.G
2	12	2	1184.68	4.9	0	55.8	19.1	95.00%	M.ALLLEGTSLAR.K	Acetyl (+42)	-.MALLLEGTSLAR.K
122	130	2	1024.46	-1.1	0	33.9	25	95.00%	D.GFCETNLGK.L	Carbamidomethyl (+57)	K.DVDGFCETNLGK.L
536	546	2	1228.67	4.9	1	27.4	22	94.10%	R.KITIGENPTEK.G		R.KITIGENPTEK.G
324	336	2	1299.71	5.1	1	59.2	21.1	95.00%	K.NIGDLASEIGIAK.S		K.NIGDLASEIGIAK.S
381	396	2	1629.9	3.4	1	106	18.5	95.00%	K.STLTAGLVQALSNLDK.L		K.STLTAGLVQALSNLDK.L
349	356	2	983.58	5.3	0	46.2	18.5	95.00%	K.VNLEILQR.L		K.VNLEILQR.L
835	849	2	1592.78	4.3	1	53.3	25.6	95.00%	K.EMYGADGIELSPLAK.E		K.EMYGADGIELSPLAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
40	YL8C_SCHPO	21.12%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
93	112	3	2269.21	3.4	1	35.2	18.3	95.00%	K.IVYADHLKPEVVMEVVEATK.G		K.IVYADHLKPEVVMEVVEATK.G
47	60	2	1575.87	4.2	1	37.4	18.7	95.00%	R.EKYPNFPIVLATGK.Q		R.EKYPNFPIVLATGK.Q
217	232	2	1745.96	4.4	0	53	18.2	95.00%	K.GTALQYITSNILPEVK.N		K.GTALQYITSNILPEVK.N
275	288	2	1456.72	4.1	0	65.8	24.9	95.00%	R.VGNEEGAVGEVLER.I		R.VGNEEGAVGEVLER.I
98	112	3	1707.92	0.061	0	24.5	19.7	95.00%	D.HLKPEVVMEVVEATK.G		K.IVYADHLKPEVVMEVVEATK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
41	THIL_SCHPO	26.08%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
291	301	2	1160.65	4.8	0	33.2	20	95.00%	R.FTTSPSLAIPK.A		R.FTTSPSLAIPK.A
14	30	2	1654.8	-1.1	0	75.5	24.8	95.00%	R.TPMGSFGGSFASLPATK.L		R.TPMGSFGGSFASLPATK.L
156	173	2	1912.83	-0.26	1	40.2	27	95.00%	D.GLPMGNAAELCAEEHSID.R	Carbamidomethyl (+57)	R.DGLSDAYDGLPMGNAAELCAEEHSIDR.A
360	371	2	1405.81	4.5	0	73.2	16.5	95.00%	R.IICTLAYILAQK.D	Carbamidomethyl (+57)	R.IICTLAYILAQK.D
255	266	2	1117.62	-0.64	0	42.1	21.5	95.00%	D.GASALVLMSAAK.V		K.SNGTVTAANASTLNDGASALVLMSAAK.V
278	290	2	1440.71	4.1	1	44.3	24.4	95.00%	K.IIGWGEAAQDPER.F		K.IIGWGEAAQDPER.F
340	359	3	1865.93	4.8	0	31	24.1	95.00%	R.VNINGGGVAMGHPLGSSGSR.I		R.VNINGGGVAMGHPLGSSGSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
42	CYSD_SCHPO	31.93%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	26	3	2735.29	3.8	1	45.2	26.1	95.00%	M.PVESEHFETLQLHAGQEPDAATSSR.A		-.MPVESEHFETLQLHAGQEPDAATSSR.A
47	59	2	1541.79	-1.2	0	31	23.6	95.00%	R.LFGLQEPGYIYSR.M		R.LFGLQEPGYIYSR.M
27	39	2	1486.78	0.46	0	70.2	22.4	95.00%	R.AVPIYATTSYVFR.D		R.AVPIYATTSYVFR.D
72	100	3	2787.49	3.3	0	49.9	17.9	95.00%	R.IAALEHGAAAIATSSGTSALFMALTTLAK.A		R.IAALEHGAAAIATSSGTSALFMALTTLAK.A
366	377	2	1185.64	4.4	1	34.5	21.5	95.00%	K.LASQLANVGDAK.T		K.LASQLANVGDAK.T
151	169	2	2199.03	0.36	1	61.8	26.3	95.00%	K.AVYVESIGNPMYNVPDFER.I		K.AVYVESIGNPMYNVPDFER.I
378	403	3	2798.48	2.5	1	42.6	18.6	95.00%	K.TLVIAPAYTTHLQLTDEEQISAGVTK.D		K.TLVIAPAYTTHLQLTDEEQISAGVTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
43	RS18_SCHPO	36.84%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	78	2	1386.79	4	0	45.2	17	95.00%	R.IVTIIQNPSQFK.I		R.IVTIIQNPSQFK.I
2	14	2	1578.86	4.3	1	26.6	19.4	93.00%	M.SLVVPDNFQHILR.L	Acetyl (+42)	-.MSLVVPDNFQHILR.L
56	66	2	1246.61	4	0	41.5	24.8	95.00%	R.AGELTTEELER.I		R.AGELTTEELER.I
79	86	2	1031.56	6	0	52.6	22.1	95.00%	K.IPSWFLNR.Q		K.IPSWFLNR.Q
95	106	2	1334.69	4.9	1	24.9	22.6	90.20%	K.SFQLLANNVDSK.L		K.SFQLLANNVDSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
44	CYPH_SCHPO	48.77%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

124	138	2	1644.83	4.4	1	86.7	24.7	95.00%	K.HVVFGEVTEGMDVVK.K		K.HVVFGEVTEGMDVVK.K
90	123	3	3611.83	4	1	56	19.8	95.00%	K.HNKPGLLSMANAGPNTNGSQFFITTVVTPWLDGK.H		K.HNKPGLLSMANAGPNTNGSQFFITTVVTPWLDGK.H
2	17	2	1835.87	3.9	1	50	25.9	95.00%	M.SNCFFDVIANGQPLGR.I	Acetyl (+42)/ Carbamidomethyl (+57)	-.MSNCFFDVIANGQPLGR.I
54	67	2	1607.82	4.3	1	67.2	23.4	95.00%	R.VIPQFMLQGGDFTR.G		R.VIPQFMLQGGDFTR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
45	PPA1_SCHPO	15.89%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
40	59	3	2404.13	2.5	1	63.3	26.2	95.00%	R.SPYHKPYFYGPSIDFPTTCK.I	Carbamidomethyl (+57)	R.SPYHKPYFYGPSIDFPTTCK.I
73	92	2	2046.99	-0.89	1	108	24.8	95.00%	R.NPTGGNAAFDAVGIANFQQR.L		R.NPTGGNAAFDAVGIANFQQR.L
366	387	2	2501.19	3.5	1	42.6	25.4	95.00%	K.ASEFVPFAGNLITELFQCEDSK.Y	Carbamidomethyl (+57)	K.ASEFVPFAGNLITELFQCEDSK.Y
215	224	2	1190.61	-0.37	0	31.1	24.5	95.00%	D.FTTPALEAWR.N		R.VVDSALWYGYGMFGEDVHNFTNYILVSENATAGSNSLSSYNACPASDADDFTTPALEAWR.N
83	92	2	1102.59	-0.11	0	35.2	22.6	95.00%	D.AVGIANFQQR.L		R.NPTGGNAAFDAVGIANFQQR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
46	MET3_SCHPO	18.78%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
217	230	3	1461.8	0.0069	1	27.2	18.9	95.00%	R.VLIHPVVGMTKPGD.I		R.VLIHPVVGMTKPGDIDHFTR.V
364	382	2	2159.15	2.7	0	56.8	19.6	95.00%	R.VGANIPEWFSYPEVVAILR.Q		R.VGANIPEWFSYPEVVAILR.Q
427	440	2	1651.86	4	1	77.5	20.8	95.00%	R.LDAISVFYAQELQR.A		R.LDAISVFYAQELQR.A
350	359	2	1102.6	3.9	0	29.9	20.9	95.00%	R.TLNISGTELR.R		R.TLNISGTELR.R
59	68	2	1233.64	5.6	1	40.5	22.8	95.00%	K.DYLNVVENLR.L		K.DYLNVVENLR.L
254	262	2	1012.62	5.1	0	33.5	14.1	95.00%	K.LSLLPLAMR.M		K.LSLLPLAMR.M
14	29	3	1808.96	-0.66	1	37.9	20.1	95.00%	D.APLREQLEQEATSLPK.I		R.DAPLREQLEQEATSLPK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
47	VIPI_SCHPO	34.63%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	68	2	1496.86	4.3	1	41.7	15.9	95.00%	K.TALLLQDALLGQNK.I		K.TALLLQDALLGQNK.I
101	110	2	1087.63	5.8	0	34.3	17.8	95.00%	R.SAIISELLSR.G		R.SAIISELLSR.G
225	254	3	2955.41	4.7	1	54.3	25.3	95.00%	K.NQAEGTASPASSTPTAPAEKEPTAPTTESK.T		K.NQAEGTASPASSTPTAPAEKEPTAPTTESK.T
122	134	2	1410.71	4.2	1	61.1	24.3	95.00%	K.SIQLDQSYGVSSK.F		K.SIQLDQSYGVSSK.F
111	121	2	1260.64	3.7	1	31.8	23.4	95.00%	R.GYHLSDVTLEK.S		R.GYHLSDVTLEK.S
137	147	2	1100.62	4.3	0	27.7	20.7	94.50%	K.GILESALSGVR.S		K.GILESALSGVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
48	RL4A_SCHPO	27.55%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
122	140	2	1845.04	4.3	0	48.1	14.8	95.00%	R.YAISSAVAASGVPSLLLAR.G		R.YAISSAVAASGVPSLLLAR.G
2	13	2	1304.71	4.5	0	25.5	21.1	91.40%	M.AAARPTVSIYSK.D	Acetyl (+42)	-.MAAARPTVSIYSK.D
15	29	2	1580.84	-2.4	0	32	20.4	95.00%	D.GSVSSETIALPFVFK.A		K.DGSVSSETIALPFVFK.A
235	248	3	1457.85	0.28	0	50.6	15.8	95.00%	R.LNLLQLAPGGHLGR.F		R.LNLLQLAPGGHLGR.F
292	303	2	1357.75	4	1	43.8	19.5	95.00%	R.LINSDEIQSIVK.A		R.LINSDEIQSIVK.A
14	29	2	1695.88	4.2	1	38.3	22	95.00%	K.DGSVSSETIALPFVFK.A		K.DGSVSSETIALPFVFK.A
276	291	2	1864.94	4.5	1	39	23.7	95.00%	K.NYFLPENIISNADVTR.L		K.NYFLPENIISNADVTR.L
87	97	2	1197.51	4.4	0	32.6	26.5	95.00%	R.SGQAAFGNMCR.S	Carbamidomethyl (+57)	R.SGQAAFGNMCR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
49	ADH_SCHPO	22.29%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
304	313	2	1165.6	-0.36	0	33.2	23	95.00%	D.SIEALEYVSR.G		R.IDSIEALEYVSR.G
236	253	2	1681.87	4.1	0	56	21.7	95.00%	K.AATNGGAHGTLVLSTSPK.S	Deamidation (+1)	K.AATNGGAHGTLVLSTSPK.S

254	278	3	2513.21	3.1	0	41.5	25	95.00%	K.SYEQAAGFARPGSTMVTVSMPAGAK.L		K.SYEQAAGFARPGSTMVTVSMPAGAK.L
170	194	3	2506.28	-0.1	0	45.1	21.5	95.00%	K.VGPGEWICIPGAGGGLGHLAVQYAK.A	Carbamidomethyl (+57)	K.VGPGEWICIPGAGGGLGHLAVQYAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
50	HOSM_SCHPO	23.92%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	204	2	1315.66	4	1	40.8	24.8	95.00%	R.VGIADTVGCATPR.Q	Carbamidomethyl (+57)	R.VGIADTVGCATPR.Q
2	31	3	3218.5	4.8	1	47.5	24.7	95.00%	M.SVSEANGTETIKPPMNGNPYGPNPSDFLSR.V	Acetyl (+42)/ Deamidation (+1)	-.MSVSEANGTETIKPPMNGNPYGPNPSDFLSR.V
72	85	2	1578.79	-0.58	0	57.3	24.6	95.00%	D.YIELTSPVASEQSR.Q		K.ALDNFGVDYIELTSPVASEQSR.Q
324	339	2	1772.92	-0.13	1	27.9	22.2	94.70%	K.AILANPSTYEILKPED.F		K.AILANPSTYEILKPEDFGMSR.Y
324	344	3	2351.18	-0.47	1	23.8	23.8	94.80%	K.AILANPSTYEILKPEDFGMSR.Y		K.AILANPSTYEILKPEDFGMSR.Y
147	156	2	1106.6	0.069	0	32	20.5	95.00%	D.SATEVINFVK.S		K.DMTYIIDSATEVINFVK.S
32	43	2	1391.75	4.9	0	68.1	21.5	95.00%	R.VNNFSIIESTLR.E		R.VNNFSIIESTLR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
51	FAS2_SCHPO	4.61%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
488	502	3	1650.8	4.5	1	35.5	24.9	95.00%	K.NVNHPTAPSTTIDER.G		K.NVNHPTAPSTTIDER.G
114	146	3	3020.56	3.1	1	35.9	21	95.00%	K.VETAAAAAPAATPAPAPAQTSAPAAALPDEPPK.A		K.VETAAAAAPAATPAPAPAQTSAPAAALPDEPPK.A
517	527	2	1319.7	5.4	1	32	22.4	95.00%	R.KLTHYVTEMAK.G		R.KLTHYVTEMAK.G
1393	1401	2	994.61	4.5	1	27.6	13.4	94.30%	K.TPLPIVDLK.F		K.TPLPIVDLK.F
28	44	2	1939.01	4.4	1	67.5	21.2	95.00%	R.WIETQDVILSPPVSAER.I		R.WIETQDVILSPPVSAER.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
52	RAD24_SCHPO	29.63%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
109	120	2	1236.65	4.7	0	29.1	21.9	95.00%	K.HLIPNAASAESK.V		K.HLIPNAASAESK.V
31	44	2	1562.75	4.1	1	82.9	25.3	95.00%	K.SVASTDQELTVEER.N		K.SVASTDQELTVEER.N
97	108	2	1431.76	-0.12	1	44.6	21.8	95.00%	D.TICQDILTVLEK.H	Carbamidomethyl (+57)	K.IEQELDTICQDILTVLEK.H
219	227	2	1073.63	0.55	0	44	16.5	95.00%	D.STLIMQLLR.D		K.DSTLIMQLLR.D
15	30	3	1896.87	-1.3	1	34.7	26.5	95.00%	K.LAEQAERYEGMVENMK.S		K.LAEQAERYEGMVENMK.S
156	172	3	1746.92	-1.3	0	66.4	21.5	95.00%	K.AASEIATAELAPTHPIR.L		K.AASEIATAELAPTHPIR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
53	HSP7M_SCHPO	15.58%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
204	215	2	1124.67	4.6	0	48.3	15.3	95.00%	K.AAGAIAGLNVLR.V		K.AAGAIAGLNVLR.V
370	388	2	2044.06	-0.49	0	32.3	21.9	95.00%	D.ANLQTSEINEVILVGGMTR.M		K.DANLQTSEINEVILVGGMTR.M
105	118	2	1578.81	4.5	0	81.4	23.3	95.00%	R.QAVINPENTFFATK.R		R.QAVINPENTFFATK.R
185	199	2	1679.83	4.3	1	62.1	24.4	95.00%	K.NAVVTVPAYFNDSQR.Q		K.NAVVTVPAYFNDSQR.Q
496	510	2	1538.89	4.2	0	77.2	14.9	95.00%	K.LIGNFQLTGIAPAPK.G		K.LIGNFQLTGIAPAPK.G
157	170	2	1496.8	5.1	0	59.3	21.8	95.00%	K.TYSPSQIGGFILSK.M		K.TYSPSQIGGFILSK.M
216	231	2	1630.86	3.8	1	78.5	21.6	95.00%	R.VVNEPTAAALAYGLDK.K		R.VVNEPTAAALAYGLDK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
54	OAT_SCHPO	25.34%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
386	398	3	1374.82	4.6	0	23.2	13.4	94.10%	R.GVLAKPTHGNIIR.F		R.GVLAKPTHGNIIR.F
70	80	2	1268.71	4.2	0	28.4	18.1	95.00%	K.IIEALVEQAQR.V		K.IIEALVEQAQR.V
2	37	4	4216	4.3	0	58.2	22.8	95.00%	M.SAESLLHNTFSTEQIEVLENEYAAHNYHPLPVCFSK.A	Acetyl (+42)/ Carbamidomethyl (+57)	-.MSAESLLHNTFSTEQIEVLENEYAAHNYHPLPVCFSK.A
276	291	2	1561.85	4	0	53	18.6	95.00%	K.AISGGVYPVSAVLSSR.E		K.AISGGVYPVSAVLSSR.E

238	254	2	1838.97	4.4	1	78.8	21.3	95.00%	K.AHNVLFIADEVQTGVAR.T		K.AHNVLFIADEVQTGVAR.T
258	275	3	2051.1	4.3	1	30.2	19.6	95.00%	K.MLCIEHSNVKPDVVILGK.A	Carbamidomethyl (+57)	K.MLCIEHSNVKPDVVILGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
55	HSP7F_SCHPO	12.78%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
174	189	2	1665.84	-1.7	1	86.5	24.1	95.00%	R.LMNDNAAAALTYGITK.T		R.LMNDNAAAALTYGITK.T
581	591	2	1385.65	4	1	31.1	26.1	95.00%	K.NALEEYIYDTR.A		K.NALEEYIYDTR.A
5	16	2	1249.64	6.5	1	29.4	23.5	95.00%	R.TNVVGIDFGNSK.T		R.TNVVGIDFGNSK.T
38	48	2	1194.59	3.8	0	34	24	95.00%	R.STPSLVSYGER.S		R.STPSLVSYGER.S
159	173	2	1534.88	-0.54	0	47.4	14.6	95.00%	R.ALLEAANIAGLNPLR.L		R.ALLEAANIAGLNPLR.L
96	106	2	1134.6	4	1	31.7	23.2	95.00%	K.LTEVDGFVGAK.V		K.LTEVDGFVGAK.V
419	434	2	1690.84	-0.61	0	65.9	24.2	95.00%	D.SSLEVFSEGNPIPSTK.I		R.EFHVHDVTTYPITFSWEPIPENPEEDSSLEVFSEGNPIPSTK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
56	CARB_SCHPO	8.36%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
968	975	2	1019.52	4.9	0	24.9	23.5	90.20%	K.VPQFSWTR.L		K.VPQFSWTR.L
932	943	2	1304.72	5.6	1	35.2	20.9	95.00%	K.TLGVNFIDVATR.S		K.TLGVNFIDVATR.S
773	798	3	2736.49	2.9	0	51	15.6	95.00%	K.FANAVGYPVLVRPSYVLSGAAMSVIR.D		K.FANAVGYPVLVRPSYVLSGAAMSVIR.D
418	433	2	1784.89	3.2	1	42	23.9	95.00%	K.TTTANFEPSLDYVVTK.I		K.TTTANFEPSLDYVVTK.I
575	584	2	1057.58	4.7	1	32.1	22	95.00%	K.LVGASELDVR.A		K.LVGASELDVR.A
249	273	3	2529.22	2.7	1	48.7	24.6	95.00%	R.SAYSLGGLGSGFANNKEELQSMAAK.S		R.SAYSLGGLGSGFANNKEELQSMAAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
57	GBLP_SCHPO	27.39%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
186	212	3	2736.26	2.6	1	43.2	26.8	95.00%	R.TSHYGHTGYVSAVTISPDGSLCASGGR.D	Carbamidomethyl (+57)	R.TSHYGHTGYVSAVTISPDGSLCASGGR.D
234	245	2	1314.71	3.1	0	32.5	21.9	95.00%	K.ANINALVFSPNR.Y		K.ANINALVFSPNR.Y
176	185	2	1264.65	5.4	1	30.1	23.2	95.00%	K.VWDLETFSLR.T		K.VWDLETFSLR.T
39	47	2	1112.68	5.9	0	27.8	14.1	94.50%	K.SIILWNLVR.D		K.SIILWNLVR.D
9	36	3	2894.44	-0.34	1	38.5	23	95.00%	R.ATLEGHSGWVTSLSTAPENPDILLSGSR.D		R.ATLEGHSGWVTSLSTAPENPDILLSGSR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
58	HXK1_SCHPO	11.36%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
304	315	2	1380.7	5.1	1	25.3	23.4	90.90%	K.MIAGCYLGDILR.R	Carbamidomethyl (+57)	K.MIAGCYLGDILR.R
2	12	3	1409.65	4.4	1	25.1	25.7	95.00%	M.SLHDAYHWPSR.T	Acetyl (+42)	-.MSLHDAYHWPSR.T
455	469	2	1328.73	-0.77	0	57.3	21.1	95.00%	D.GSGVGAALVSALEAK.G		K.VVTIPAEDGSGVGAALVSALEAK.G
418	426	2	1067.54	0.46	0	32.2	22.9	95.00%	D.GSVYNLYPR.F		K.MNKPSMIVGTDGSVYNLYPR.F
447	469	2	2153.17	3.4	1	105	18.3	95.00%	K.VVTIPAEDGSGVGAALVSALEAK.G		K.VVTIPAEDGSGVGAALVSALEAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
59	LEUC_SCHPO	14.25%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
521	539	2	1671.88	0.11	0	87.8	21.6	95.00%	D.GIATNVAGSVSSGSAGIPK.F		K.NYDPSHDVEGDIGLSVDDATDAVTDADGIATNVAGSVSSGSAGIPK.F
633	649	2	2002.01	4.5	1	59.4	24.1	95.00%	R.VIIAPSFADIFFNNCFK.N	Carbamidomethyl (+57)	R.VIIAPSFADIFFNNCFK.N
417	436	3	2355.02	4.1	1	24.9	26.8	93.90%	R.EAGCSMCLGMNPDQLKPYER.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.EAGCSMCLGMNPDQLKPYER.C
603	619	3	1826.86	5.3	1	37.3	26.5	95.00%	R.HATVLVAHDNFGCGSSR.E	Carbamidomethyl (+57)	R.HATVLVAHDNFGCGSSR.E

477	493	2	1810.88	4.1	1	36.5	25.2	95.00%	R.EFFGDVSNGSPSIITNK.N		R.EFFGDVSNGSPSIITNK.N
650	667	2	2027	4	1	40.9	24.8	95.00%	K.NGMLPIPTPIEQVNDMMK.A		K.NGMLPIPTPIEQVNDMMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
60	YHY6_SCHPO	13.83%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
678	698	2	2257.13	4.5	1	51.2	23.8	95.00%	K.SLCIPLEQPSGEDAIIEGTTK.C	Carbamidomethyl (+57)	K.SLCIPLEQPSGEDAIIEGTTK.C
161	187	3	2608.39	2.9	1	26.8	18.5	95.00%	K.SVGVNPIIVDFSAPGSATAPSKPAAQK.K		K.SVGVNPIIVDFSAPGSATAPSKPAAQK.K
298	323	3	2901.41	-0.24	1	40.8	24.4	95.00%	R.AGTSELDEPIAIRPTSETVMYPYYAK.W		R.AGTSELDEPIAIRPTSETVMYPYYAK.W
450	462	3	1364.7	-1.9	0	34.5	23.2	95.00%	D.PNAEIGPTGERPK.L		K.MFNIVVEDPNAEIGPTGERPK.L
387	398	2	1343.81	4.3	1	30.5	10.4	95.00%	R.IYTDLLAVPVIK.G		R.IYTDLLAVPVIK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
61	GLNA_SCHPO	17.83%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
153	170	2	1809.83	4.4	0	40.7	26.4	95.00%	K.GGFPGPQPGPFYCGVGTGR.V	Carbamidomethyl (+57)	K.GGFPGPQPGPFYCGVGTGR.V
345	359	2	1749.87	0.049	0	64.3	24.7	95.00%	D.PYLVTGIITETMFEH.-		R.RPASSIDPYLVTGIITETMFEH.-
237	260	4	2635.31	3.2	1	28.9	24	95.00%	K.ISFHPKPILGDWNGAGCHTNVSTK.D	Carbamidomethyl (+57)	K.ISFHPKPILGDWNGAGCHTNVSTK.D
338	359	3	2476.24	4.1	1	26.8	22.9	95.00%	R.RPASSIDPYLVTGIITETMFEH.-		R.RPASSIDPYLVTGIITETMFEH.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
62	UGPA1_SCHPO	20.36%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	10	2	1166.63	4.6	1	24.9	20.4	90.10%	-.MDLAPRPLGR.Q	Acetyl (+42)	-.MDLAPRPLGR.Q
185	194	2	1205.65	4.7	1	32.1	21.4	95.00%	K.IDILTFNQSR.Y		K.IDILTFNQSR.Y
299	314	3	1876.02	4.4	0	30	18.4	95.00%	R.LLEIAQVPPQHVEEFK.S		R.LLEIAQVPPQHVEEFK.S
23	34	2	1194.59	-1.9	0	38.7	24.2	95.00%	D.NTATSIAASTMK.N		K.SQSAFAFDNTATSIAASTMK.N
81	104	3	2616.33	-0.57	1	30.5	22.1	95.00%	D.LVESPKPEQVVEYDTITEAGGLSR.D		R.GSEINWDLVESPKPEQVVEYDTITEAGGLSR.D
115	129	2	1460.72	4.2	0	48.3	24.8	95.00%	K.LNGGLGTTMGCVGPK.S	Carbamidomethyl (+57)	K.LNGGLGTTMGCVGPK.S
404	419	3	1858.86	-0.9	1	23.3	26.9	91.30%	K.SDLYSINHGQVEMNPR.R		K.SDLYSINHGQVEMNPR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
63	RS7_SCHPO	17.44%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	140	3	2393.32	0.58	1	41.9	14.1	95.00%	R.TLTAVHNAILEDIVFPTEIIGK.R		R.TLTAVHNAILEDIVFPTEIIGK.R
59	70	2	1322.84	4	0	46.5	9.54	95.00%	K.AIVVFVPQPLLK.A		K.AIVVFVPQPLLK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
64	ECM17_SCHPO	3.60%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
493	502	3	1154.69	-0.69	1	33.7	13.4	95.00%	D.PELVISELKK.D		K.NSSVSSESLEVLSNWIVSVDNLESPVDPELVISELKK.D
314	325	2	1337.79	-0.62	0	42.5	13.8	95.00%	R.LTVLEPITSLPR.K		R.LTVLEPITSLPR.K
77	90	2	1484.77	-1.2	0	39.4	22.5	95.00%	D.AILAEEEVASTQPK.Q		K.SHADPFAHIADAILAEEEVASTQPK.Q
801	810	2	1058.57	5.4	1	27.5	23.1	94.20%	K.GADLNLSELK.Y		K.GADLNLSELK.Y
70	90	3	2236.14	0.49	1	24.7	22.4	95.00%	D.PFAHIADAILAEEEVASTQPK.Q		K.SHADPFAHIADAILAEEEVASTQPK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
65	RL8_SCHPO	24.32%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
24	32	2	1084.62	4.7	0	29.3	20.4	95.00%	K.NPLFVSRPR.S		K.NPLFVSRPR.S
33	43	2	1188.62	4.1	1	26.8	23.1	93.30%	R.SFGIGQDIQPK.R		R.SFGIGQDIQPK.R
109	120	2	1171.61	4.7	0	55.2	23.5	95.00%	R.LVAEAEAVANGK.S	Deamidation (+1)	R.LVAEAEAVANGK.S

134	146	2	1425.8	4.3	0	45.6	17.6	95.00%	K.YGLNHVVALIEAK.K		K.YGLNHVVALIEAK.K
69	80	3	1338.8	0.23	1	22.8	13.6	93.60%	R.LKVPPAIAQFQK.T		R.LKVPPAIAQFQK.T
52	57	2	862.44	5.9	0	26.5	23.1	92.90%	K.WPEYIR.L		K.WPEYIR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
66	DHAS_SCHPO	18.21%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
31	39	2	856.52	4.9	0	28.2	19.7	95.00%	K.IAVLGASAR.S		K.IAVLGASAR.S
19	30	3	1445.76	0.55	1	33.5	22.7	95.00%	R.FITLLSDHPEFK.I		R.FITLLSDHPEFK.I
143	161	2	2003.02	-0.32	0	72.3	23.1	95.00%	R.GCIITNSNCSTAAVVVPLK.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GCIITNSNCSTAAVVVPLK.A
267	278	2	1375.7	3.8	0	37.2	23.7	95.00%	R.EVLANYVSEPQK.L		R.EVLANYVSEPQK.L
6	18	2	1227.7	3.7	0	35.6	19.6	95.00%	K.VGILGATGTVGQR.F		K.VGILGATGTVGQR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
67	BCA1_SCHPO	22.63%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
315	331	2	1670.97	4.2	0	59.5	11.5	95.00%	R.LLEVFGAGTAALVSPVK.A		R.LLEVFGAGTAALVSPVK.A
122	130	2	1010.58	-0.13	0	68.1	16.9	95.00%	D.PAELAEIIR.K		R.ISLPSFDPAELAEIIR.K
37	49	3	1581.74	4.5	1	25.4	25.9	95.00%	K.FGENFTDHMLIMK.W		K.FGENFTDHMLIMK.W
262	278	2	1795	4.2	1	43.3	16.4	95.00%	K.EIITAPLDGMILPGVTR.D		K.EIITAPLDGMILPGVTR.D
337	359	2	2462.16	4.4	0	42.7	26	95.00%	K.GTEYEIPMPEGQEAGPITSEISK.W		K.GTEYEIPMPEGQEAGPITSEISK.W
115	130	2	1769.96	3.9	1	43.7	19.2	95.00%	R.ISLPSFDPAELAEIIR.K		R.ISLPSFDPAELAEIIR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
68	TRP_SCHPO	15.49%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
382	393	2	1355.77	4.5	0	47.2	19	95.00%	K.INNCIGQILLAK.R	Carbamidomethyl (+57)	K.INNCIGQILLAK.R
247	261	2	1623.75	3.4	0	47.6	26.4	95.00%	K.AEPGTAATVVEEYCK.Y	Carbamidomethyl (+57)	K.AEPGTAATVVEEYCK.Y
400	419	3	1938.01	4.3	0	37.5	21.1	95.00%	R.IIAETGAGQHGVATAICAAK.F	Carbamidomethyl (+57)	R.IIAETGAGQHGVATAICAAK.F
275	302	3	2928.48	4.6	0	34.9	22	95.00%	K.QFQSGGSVATAPPAAVVEPINEMYLPQK.Y		K.QFQSGGSVATAPPAAVVEPINEMYLPQK.Y
616	631	2	1825.87	3	1	57.5	26.1	95.00%	R.AEFIAVTDAQCLEGFR.A	Carbamidomethyl (+57)	R.AEFIAVTDAQCLEGFR.A
445	461	2	1739.98	-0.64	0	55.6	16.8	95.00%	R.LLGAEVVPVTSGTQTLR.D		R.LLGAEVVPVTSGTQTLR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
69	RS3B_SCHPO	11.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
228	241	2	1524.79	4.4	1	71.2	22.7	95.00%	K.LLELHGESQDVGTK.V		K.LLELHGESQDVGTK.V
200	213	2	1513.86	-0.078	0	43.9	16.1	95.00%	R.ATGSIFPLQNVLVR.K		R.ATGSIFPLQNVLVR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
70	YF19_SCHPO	17.30%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
195	208	2	1516.82	4.7	0	34.9	19.7	95.00%	K.TAELTPLSALCLTK.F	Carbamidomethyl (+57)	K.TAELTPLSALCLTK.F
5	17	2	1406.78	4.6	1	33	18.1	95.00%	K.LVDHVEITVPTGK.T		K.LVDHVEITVPTGK.T
422	443	3	2229.12	4.1	0	21.2	22.8	90.80%	R.GNNSTYGLAAGVHTNNITNAIK.V		R.GNNSTYGLAAGVHTNNITNAIK.V
71	80	2	1161.56	3.7	1	28.3	25.2	94.80%	R.AAFQTDAPWR.K		R.AAFQTDAPWR.K
336	349	2	1523.72	-1	1	96.5	25.7	95.00%	D.PFAEDTFQGAQVSK.Q		K.VGDPFAEDTFQGAQVSK.Q
181	194	2	1439.82	3.6	0	42.9	16.5	95.00%	K.IAPAVACGNTIILK.T	Carbamidomethyl (+57)	K.IAPAVACGNTIILK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
71	RS6B_SCHPO	27.20%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	115	2	1739.01	3.8	1	65.7	12	95.00%	R.GCIVGQDLAVLALAIVK.Q	Carbamidomethyl (+57)	R.GCIVGQDLAVLALAIVK.Q
32	51	2	2112.99	4.1	1	51.8	26.1	95.00%	R.MGQEVPGDSVGPEFAGYVFK.I		R.MGQEVPGDSVGPEFAGYVFK.I

59	72	3	1625.86	4.7	0	32.2	21.7	95.00%	K.QGFPMFQGVLLPHR.V		K.QGFPMFQGVLLPHR.V
40	51	2	1299.65	0.36	0	45.9	24.2	95.00%	D.SVGPEFAGYVFK.I		R.MGQEVPGDSVGPEFAGYVFK.I
204	217	3	1606.78	-0.44	1	55.8	25	95.00%	K.NREEAAEFAQLMAK.R		K.NREEAAEFAQLMAK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
72	O59743_SCHPO	15.29%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
12	24	2	1387.72	-2.6	0	73.1	22.9	95.00%	K.LGIEEQVETAATK.S		K.LGIEEQVETAATK.S
75	97	3	2588.33	2.8	1	31.8	20.9	95.00%	K.EALDLFLGAYNVITPELAHFEAR.C		K.EALDLFLGAYNVITPELAHFEAR.C
11	24	2	1515.82	4.5	1	53.1	19.8	95.00%	K.KLGIEEQVETAATK.S		K.KLGIEEQVETAATK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
73	TAL1_SCHPO	10.25%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
27	44	3	1917.03	4	1	42	20.6	95.00%	K.YKPQDATTNPSLILAASK.K		K.YKPQDATTNPSLILAASK.K
200	213	2	1585.81	0.56	0	38.3	23.5	95.00%	D.PGVVSVSNIFNYYK.K		R.DYTAQEDPGVVSVSNIFNYYK.K
32	44	2	1285.72	-0.48	0	58.5	19.6	95.00%	D.ATTNPSLILAASK.K		K.YKPQDATTNPSLILAASK.K
200	214	3	1713.91	-0.63	1	22.6	20.9	93.30%	D.PGVVSVSNIFNYYKK.F		R.DYTAQEDPGVVSVSNIFNYYKK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
74	EF1B_SCHPO	21.03%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
59	73	2	1561.84	4.2	1	60.9	20.6	95.00%	K.QIATYDLATLPGTAK.E		K.QIATYDLATLPGTAK.E
153	165	2	1432.74	3.9	1	44.3	23.7	95.00%	R.SIQMDGLVWGLSK.L		R.SIQMDGLVWGLSK.L
23	39	2	1885.92	3.6	1	50.9	24.9	95.00%	K.SFIEGYEPSQADAVVFK.A		K.SFIEGYEPSQADAVVFK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
75	ACON_SCHPO	10.41%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
532	549	2	1853.89	4.6	1	68.9	25.7	95.00%	K.GYDPGSNTYVAPSSVNVK.D		K.GYDPGSNTYVAPSSVNVK.D
375	391	2	1874.81	-0.46	1	61.9	27.2	95.00%	K.VGLIGSCTNSSYEDMSR.A	Carbamidomethyl (+57)	K.VGLIGSCTNSSYEDMSR.A
392	402	2	1203.6	5.2	1	35.2	24.8	95.00%	R.AASICQQAIDK.G	Carbamidomethyl (+57)	R.AASICQQAIDK.G
652	666	2	1665.78	3.4	0	67.3	26.5	95.00%	R.WVTLGEQNFGEGSSR.E		R.WVTLGEQNFGEGSSR.E
462	470	2	1052.53	5	0	36.5	24	95.00%	K.NSIVTSYNR.N		K.NSIVTSYNR.N
696	706	2	1201.67	1.1	2	34.1	19.6	95.00%	K.KQGLLPLTFAD.P		K.KQGLLPLTFADPAAYDK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
76	ILV3_SCHPO	16.05%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
266	278	3	1408.68	4.8	1	24.2	25.3	95.00%	K.FAECEAAGSAIKR.L	Carbamidomethyl (+57)	K.FAECEAAGSAIKR.L
49	68	2	2142.97	5.2	1	90.3	27.1	95.00%	K.SQGASQAMLYATGLNEEDMK.K		K.SQGASQAMLYATGLNEEDMK.K
538	547	2	1056.58	0.55	1	26.8	22	93.40%	D.GDVIEINAVK.N		R.FSGGSHGFLIGHVDPEAQVGGPIALVQDGDVIEINAVK.N
402	417	4	1843.09	3.6	1	32.1	6.02	95.00%	K.IIRPLSNPIKTEGHLR.V		K.IIRPLSNPIKTEGHLR.V
40	48	2	994.5	5.2	0	30.6	24.7	95.00%	K.YSETITGPK.S		K.YSETITGPK.S
185	212	3	3007.42	3.5	1	69.2	25.4	95.00%	R.AGHSPCQNNAPIDIVSAFQSYGEFITGK.I	Carbamidomethyl (+57)	R.AGHSPCQNNAPIDIVSAFQSYGEFITGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
77	NACA_SCHPO	29.48%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	75	2	1164.62	5.8	0	59.3	21.7	95.00%	K.SSNNAYIVLGK.V		K.SSNNAYIVLGK.V
11	26	2	1637.87	4.6	0	55.2	20.5	95.00%	K.ISELPAGSTTVVHAEK.A		K.ISELPAGSTTVVHAEK.A
52	64	2	1540.92	-0.0083	0	51.5	13.2	95.00%	K.NILLIINEPIVYK.S		K.NILLIINEPIVYK.S

76	86	2	1189.58	4.9	1	47.2	25.4	95.00%	K.VTVEDMAAQAR.A		K.VTVEDMAAQAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
78	FAS1_SCHPO	6.75%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1117	1130	2	1421.7	4.7	0	59.8	25.1	95.00%	K.SLESVSVTEEAGSK.V		K.SLESVSVTEEAGSK.V
1870	1881	2	1266.57	5.2	1	37.8	26	95.00%	R.SDYGMVAANPSR.V		R.SDYGMVAANPSR.V
210	224	3	1723.91	5.4	1	36.5	20.9	95.00%	K.GLNVLDWLAGERPER.D		K.GLNVLDWLAGERPER.D
828	846	3	1903.04	-0.73	0	51.9	18.2	95.00%	D.GPTGGIVTVLSELGEPIHK.L		K.TYDGPTGGIVTVLSELGEPIHK.L
2	12	2	1294.67	5.2	0	53.5	22.4	95.00%	M.VEAEQVHQSLR.S		-.MVEAEQVHQSLR.S
1778	1806	3	3141.54	1.9	1	40.3	23.1	95.00%	K.DSTSFSFTHPSGLLSATQFTQPALTLMEK.S		K.DSTSFSFTHPSGLLSATQFTQPALTLMEK.S
781	794	2	1545.81	3.9	1	42.1	22.2	95.00%	K.LPPMPFDGILFGSR.L		K.LPPMPFDGILFGSR.L
1422	1447	3	2983.4	3.2	1	29.8	25.7	95.00%	R.GTFTDFENTFEHTQETPMQLTLATPK.D		R.GTFTDFENTFEHTQETPMQLTLATPK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
79	DHE4_SCHPO	17.29%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
334	353	2	2102.96	4.2	0	111	26.3	95.00%	R.YVAEGSNMGSSAEAVEVFEK.S		R.YVAEGSNMGSSAEAVEVFEK.S
25	34	3	1266.71	4.3	1	33.7	18.2	95.00%	K.LFEVHPELKR.V		K.LFEVHPELKR.V
356	367	2	1231.57	4.5	0	27.7	25.3	94.10%	R.ASGEGCWLAPGK.A	Carbamidomethyl (+57)	R.ASGEGCWLAPGK.A
93	101	2	1127.61	5.6	0	29.2	22.5	95.00%	K.FLGFEQIFK.N		K.FLGFEQIFK.N
399	416	2	1950.97	-1	1	87.2	23.7	95.00%	K.LAGIMQNIFEQSTDVASK.Y		K.LAGIMQNIFEQSTDVASK.Y
431	439	2	889.5	-0.48	0	31	20.6	95.00%	D.GANIAGFLK.V		K.YCDSGSNNIPSLVDGANIAGFLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
80	EF1G_SCHPO	13.94%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
93	115	3	2635.35	-1.3	0	59.3	21.2	95.00%	K.VLQYCSFTNSELPGAFRPIIAPR.V	Carbamidomethyl (+57)	K.VLQYCSFTNSELPGAFRPIIAPR.V
207	216	2	1182.71	4	1	27.1	16.6	93.70%	K.FIDQPLPIIK.A		K.FIDQPLPIIK.A
128	139	2	1303.72	4.6	0	40.7	20.3	95.00%	K.EAETAIALIFAR.F		K.EAETAIALIFAR.F
116	127	2	1294.63	4.3	1	26.2	24.9	92.50%	R.VFGAPYDEQAAK.E		R.VFGAPYDEQAAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
81	CDC48_SCHPO	3.31%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
550	563	2	1522.75	3.6	0	43.8	24.4	95.00%	K.AIANECSANFISVK.G	Carbamidomethyl (+57)	K.AIANECSANFISVK.G
774	786	3	1606.83	4.7	1	28.9	22.6	95.00%	R.RYEAYAHQLLTSR.G		R.RYEAYAHQLLTSR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
82	GCST_SCHPO	20.67%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
81	97	2	1779.9	3.9	0	64.1	24	95.00%	R.GENATAYLESITPSSLK.E		R.GENATAYLESITPSSLK.E
327	344	2	1771.88	-0.83	0	70.6	24.1	95.00%	D.GVEVGQVTSGCPSPTLGK.N	Carbamidomethyl (+57)	R.HGSAVEVDGVEVGQVTSGCPSPTLGK.N
319	344	3	2566.25	4.5	1	41.9	24.8	95.00%	R.HGSAVEVDGVEVGQVTSGCPSPTLGK.N	Carbamidomethyl (+57)	R.HGSAVEVDGVEVGQVTSGCPSPTLGK.N
165	180	2	1623.93	4	0	75.8	14.1	95.00%	R.ALIAIQGPETASVVQK.L		R.ALIAIQGPETASVVQK.L
345	365	3	2207.15	0.37	0	29.9	20.8	95.00%	K.NIAMGYISTGLHQVGTPAHIK.V		K.NIAMGYISTGLHQVGTPAHIK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
83	LEU1_SCHPO	14.38%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
82	99	2	1998.98	4.3	1	62	25	95.00%	K.EIEVGFPSASQTDFAFVR.H		K.EIEVGFPSASQTDFAFVR.H

464	479	2	1742.82	4.9	1	69.1	25.9	95.00%	R.FSVNDYTLSSNGPQSK.C		R.FSVNDYTLSSNGPQSK.C
389	398	2	1134.6	-1.2	0	33.8	22.9	95.00%	D.VNSEYAAIIR.V		K.VPYLPLDPHDVNSEYAAIIR.V
341	362	3	2346.15	2.9	1	44.7	24.6	95.00%	R.HPYAGNLVFTAFSGSHQDAISK.G		R.HPYAGNLVFTAFSGSHQDAISK.G
137	151	3	1761.87	4	0	33.2	25	95.00%	K.NATVHLYNACSPLFR.E	Carbamidomethyl (+57)	K.NATVHLYNACSPLFR.E
386	398	3	1483.74	0.54	1	31.2	24.4	95.00%	D.PHDVNSEYAAIIR.V		K.VPYLPLDPHDVNSEYAAIIR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
84	THI4_SCHPO	11.00%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
373	385	2	1353.71	4.1	1	37.5	22.1	95.00%	R.GVDSISQHTLAAR.I		R.GVDSISQHTLAAR.I
125	140	2	1686.81	-1.5	1	53.8	25.6	95.00%	D.GADYVGIGSIYETNTK.D		K.AAADGADYVGIGSIYETNTK.D
27	42	3	1733.95	4.6	0	28	18.1	95.00%	R.QVEEGILGGVTLVQHR.E		R.QVEEGILGGVTLVQHR.E
237	248	2	1322.76	4.7	1	31.5	14.8	95.00%	K.DLLNQIPAALQK.L		K.DLLNQIPAALQK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
85	GCSP_SCHPO	15.34%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
953	965	2	1458.76	1.1	1	43.1	23.1	95.00%	K.DNNLLVNAPHPQK.D		K.DNNLLVNAPHPQK.D
657	684	3	2835.49	3.7	0	27.8	19	95.00%	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C	Carbamidomethyl (+57)	R.NICLIPVSAHGTNPASAAMAGFTVIPVK.C
379	412	3	3679.8	2.3	0	51.4	21.3	95.00%	K.ATSNICTAQALLANMSAFYAIYHGPNGLQEIANR.I	Carbamidomethyl (+57)	K.ATSNICTAQALLANMSAFYAIYHGPNGLQEIANR.I
244	256	2	1497.83	1.4	1	36.3	19.1	95.00%	K.IELDNITPELITK.S		K.IELDNITPELITK.S
577	604	3	3166.6	3.7	0	40.5	20.4	95.00%	K.LNAVTEMMPITNPLFANIHPYVPEEQAK.G		K.LNAVTEMMPITNPLFANIHPYVPEEQAK.G
87	126	3	4380.08	3.8	1	62.7	22.9	95.00%	R.TPESQLMAFGSVNPNEKNPPVNYSESEFTTLANNVANQNK.L		R.TPESQLMAFGSVNPNEKNPPVNYSESEFTTLANNVANQNK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
86	IF5A1_SCHPO	25.48%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	28	3	2979.31	4	1	77.3	26.7	95.00%	M.AEEEHVDFEGGEAGASLTFPMQCSALR.K	Acetyl (+42)/ Carbamidomethyl (+57)	-.MAEEEHVDFEGGEAGASLTFPMQCSALR.K
9	29	3	2256.06	-1.7	1	29.5	26.1	95.00%	D.FEGGEAGASLTFPMQCSALRK.N	Carbamidomethyl (+57)	-.MAEEEHVDFEGGEAGASLTFPMQCSALRK.N
58	69	2	1352.76	0.65	1	49.6	18.5	95.00%	K.VHIVALDIFNGR.K		K.VHIVALDIFNGR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
87	RS8A_SCHPO	35.50%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
60	74	2	1568.72	4.4	1	94.1	26	95.00%	R.LDSGNFSWGSEGVSK.K		R.LDSGNFSWGSEGVSK.K
165	178	2	1475.79	4.1	0	33.2	20.9	95.00%	R.LYAVVSSRPGQSGR.C		R.LYAVVSSRPGQSGR.C
152	164	2	1363.68	4.8	1	51.3	24.1	95.00%	K.VDSALETQFAAGR.L		K.VDSALETQFAAGR.L
78	92	2	1751.93	-1.1	0	33	21.2	95.00%	R.IIQVAYHPSNNELVR.T		R.IIQVAYHPSNNELVR.T
111	124	3	1682.82	4.5	0	23.1	24.8	93.90%	R.VWYETHYGILMGSK.G		R.VWYETHYGILMGSK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
88	SODC_SCHPO	40.26%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
98	116	2	1984.04	4.4	1	72.6	21.6	95.00%	K.TTFSDSVISLFGANSIIGR.T		K.TTFSDSVISLFGANSIIGR.T
85	97	2	1357.68	-0.53	1	38.6	24.3	95.00%	D.LGNLESDAQGNIK.T		R.HVGDLGNLESDAQGNIK.T
81	91	2	1154.52	0.072	1	33.1	25.8	95.00%	R.HVGDLGNLESD.A		R.HVGDLGNLESDAQGNIK.T
45	70	3	2825.25	4.3	1	41.5	27	95.00%	R.GFHIHQFGDNTNGCTSAGPHFNPEGK.T	Carbamidomethyl (+57)	R.GFHIHQFGDNTNGCTSAGPHFNPEGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
89	DAK1_SCHPO	12.24%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
9	18	2	1081.64	0.074	1	31.3	14	95.00%	D.PEVLVLDGLK.S		K.HFINDPEVLVLDGLK.S
45	66	3	2123.04	-1.1	0	25.9	24.5	95.00%	K.NVSVISGGGAGHEPTHSSFVGK.G		K.NVSVISGGGAGHEPTHSSFVGK.G
527	538	2	1301.63	4.7	1	60.8	25	95.00%	K.TNDLNAAVEEAR.K		K.TNDLNAAVEEAR.K
388	399	2	1358.73	4.4	0	25.9	21.4	92.00%	R.QAIVNSMENLIK.A		R.QAIVNSMENLIK.A
566	580	2	1430.81	-0.58	0	60.6	17.2	95.00%	D.AGALGVVAIVEGFTK.-		K.VPDAGALGVVAIVEGFTK.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
90	TRX1_SCHPO	29.13%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
40	54	2	1796.83	-0.29	1	71.2	26.7	95.00%	K.FEQFSNTYSDATFIK.V		K.FEQFSNTYSDATFIK.V
80	94	2	1567.82	-1.2	1	71.1	21.6	95.00%	K.NGEKIEEIVGANPAK.L		K.NGEKIEEIVGANPAK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
91	SERC_SCHPO	23.39%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
157	184	3	3208.47	0.95	1	27.6	26.3	95.00%	D.GETSLVYYCDNETVHGVEFNEPPTNIPK.G	Carbamidomethyl (+57)	K.FTPDGETSLVYYCDNETVHGVEFNEPPTNIPK.G
330	352	5	2716.42	3.7	1	22	19.4	95.00%	R.IEPQELESEFLAEAEKHHLVQLK.G		R.IEPQELESEFLAEAEKHHLVQLK.G
376	385	2	1147.65	4.7	1	32.8	17.6	95.00%	R.LIDLLESFAK.A		R.LIDLLESFAK.A
216	228	2	1299.74	5	0	37	17.9	95.00%	K.NAGPAGITVVFVR.D		K.NAGPAGITVVFVR.D
189	199	2	1282.6	4.3	1	67	25	95.00%	R.VCDVSSNFISR.K	Carbamidomethyl (+57)	R.VCDVSSNFISR.K
324	329	2	766.38	5.3	0	26.2	21.6	92.40%	R.MNVTFR.I		R.MNVTFR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
92	PYR1_SCHPO	3.74%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1880	1906	3	2689.36	3.3	0	28.6	22.3	95.00%	K.VSALMSPGLPHAAPSLAEAFGQAPENK.A		K.VSALMSPGLPHAAPSLAEAFGQAPENK.A
1771	1784	2	1494.85	4.1	0	35.2	15.7	95.00%	R.EAIPLLLTAVNEGR.L		R.EAIPLLLTAVNEGR.L
457	466	2	1084.56	6.1	0	38.9	22.8	95.00%	K.LPGGTIEENR.S		K.LPGGTIEENR.S
35	54	3	2225.01	-0.57	1	32.2	26.8	95.00%	D.PKEPTCSPSPAFYSVNGEMK.D	Carbamidomethyl (+57)	R.THGPKPSENDPKEPTCSPSPAFYSVNGEMK.D
1758	1770	2	1371.7	4.4	0	56.2	24	95.00%	K.FVGNTAFTGFGVR.E		K.FVGNTAFTGFGVR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
93	PMP20_SCHPO	28.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
30	55	2	2747.41	3.6	0	38	21	95.00%	K.FIIVGVPGAFTPPCSSQVPGYIANEK.Q	Carbamidomethyl (+57)	K.FIIVGVPGAFTPPCSSQVPGYIANEK.Q
11	29	3	2215.13	4.2	0	34.9	22.6	95.00%	K.VTLWENKPEEVVEFPSQGK.F		K.VTLWENKPEEVVEFPSQGK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
94	HMCS_SCHPO	13.42%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
155	183	3	2859.52	-0.52	0	52.5	18.3	95.00%	K.GNARPTGGAGCVALLVGPNAPIVFEPGLR.G	Carbamidomethyl (+57)	K.GNARPTGGAGCVALLVGPNAPIVFEPGLR.G
269	282	2	1454.7	-1.3	0	53.3	25.4	95.00%	D.SAAEPSNPELEGVR.E		R.LLYTDSAAEPSNPELEGVR.E
264	282	2	2060.01	-0.45	1	66.3	25.1	95.00%	R.LLYTDSAAEPSNPELEGVR.E		R.LLYTDSAAEPSNPELEGVR.E
217	228	2	1325.64	3.7	1	38.4	25.4	95.00%	K.ALDGAYANYNVR.D		K.ALDGAYANYNVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
95	RL13_SCHPO	25.96%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
172	183	2	1398.66	5.4	0	54	25.5	95.00%	K.NFNAFSTLSNER.A		K.NFNAFSTLSNER.A
118	128	3	1326.79	4.7	0	51.2	15.6	95.00%	K.VYLAHLIVFPR.K		K.VYLAHLIVFPR.K

46	64	4	2080.27	3.1	0	20	4.77	95.00%	K.IAPRPVEAIRPAVKPPTIR.Y		K.IAPRPVEAIRPAVKPPTIR.Y
89	100	2	1263.7	3.9	1	28.9	19.9	95.00%	R.VASTIGIPVDHR.R		R.VASTIGIPVDHR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
96	AROG_SCHPO	9.95%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
203	226	3	2316.22	-1.7	1	29.5	20.3	95.00%	D.GTVGVAIDAIGATAHPHTMLGVTK.Q		K.NGTDGTVGVAIDAIGATAHPHTMLGVTK.Q
186	198	2	1364.74	0.85	0	48.5	21.2	95.00%	R.ELASALSFPVGFK.N		R.ELASALSFPVGFK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
97	GLT1_SCHPO	5.59%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
624	638	2	1701.91	4.2	0	45.5	21	95.00%	R.MPTPILTVEEFNALK.N		R.MPTPILTVEEFNALK.N
1690	1707	2	2063.08	4.1	0	61.9	21.1	95.00%	K.EALTQLLLTNNFPEFTGR.V		K.EALTQLLLTNNFPEFTGR.V
1442	1464	3	2335.04	4.9	1	32.4	27	95.00%	R.NSGAIAVVEGVGDHGCEYMTGGR.V	Carbamidomethyl (+57)	R.NSGAIAVVEGVGDHGCEYMTGGR.V
1845	1856	2	1155.66	-1.1	0	33.2	20	95.00%	D.AVVLASGSTVPR.D		K.VYDAVVLASGSTVPR.D
1022	1038	3	1639.81	4.9	0	25.7	24.5	95.00%	K.MAQGAKPGEGGELPGNK.V		K.MAQGAKPGEGGELPGNK.V
672	685	2	1555.69	5.3	1	68	26	95.00%	R.ICSEADTAVNEGYK.A	Carbamidomethyl (+57)	R.ICSEADTAVNEGYK.A
1758	1776	2	1792.99	3.3	1	78.8	17.7	95.00%	R.VAIIGSGPAGLAAADQLNR.A		R.VAIIGSGPAGLAAADQLNR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
98	VATA_SCHPO	18.74%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
89	114	4	2751.53	2.9	1	22.2	11.5	95.00%	R.TGKPLSVELGPGLAETIYDGIQRPLK.Q		R.TGKPLSVELGPGLAETIYDGIQRPLK.Q
465	476	2	1580.77	4.7	0	39.5	25.5	95.00%	K.YINALQPWYEER.V		K.YINALQPWYEER.V
128	136	2	1002.51	5	0	25.2	23.9	90.80%	R.GINTESLNR.E		R.GINTESLNR.E
373	389	2	1752.85	8	1	36.9	25.3	95.00%	R.LAEMPADSGYPAYLGAK.L		R.LAEMPADSGYPAYLGAK.L
317	331	2	1544.81	4.6	0	49.4	22.6	95.00%	R.TTLVANTSNMPVAAR.E		R.TTLVANTSNMPVAAR.E
182	198	2	1838.88	4.6	1	73	26	95.00%	R.GTVTYIAEAGSYHVDEK.L		R.GTVTYIAEAGSYHVDEK.L
221	240	3	2105.13	-0.47	1	44.3	18.4	95.00%	R.AARPVADNLTANQPLLTGQR.V		R.AARPVADNLTANQPLLTGQR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
99	RL10A_SCHPO	26.24%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	128	3	1265.71	4.6	0	30	18.7	95.00%	R.HAFGKPNGLVAR.V		R.HAFGKPNGLVAR.V
129	139	2	1228.7	4.7	0	40	19.2	95.00%	R.VNIGQILMSVR.T		R.VNIGQILMSVR.T
41	69	3	3260.58	4	1	68.1	23.4	95.00%	R.AGVDEFPLCIHLVSNEYEQITSEALEAAR.I	Carbamidomethyl (+57)	R.AGVDEFPLCIHLVSNEYEQITSEALEAAR.I
33	38	2	719.4	4.8	1	27.1	21.6	93.70%	R.IFDLGR.K		R.IFDLGR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
100	IF4A_SCHPO	12.50%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
58	69	2	1173.61	5	1	69	24.1	95.00%	R.DVLAQAQSGTGK.T		R.DVLAQAQSGTGK.T
33	48	2	1854.94	3.8	0	30.4	23.4	95.00%	R.GIYAYGFERPSAIQQR.A		R.GIYAYGFERPSAIQQR.A
372	392	2	2549.19	2.9	1	26.7	26.1	91.40%	R.EIEQFYNTHIEEMPMNIADLI.-		R.EIEQFYNTHIEEMPMNIADLI.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
101	STI1_SCHPO	12.52%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
146	164	2	1935.97	6.4	1	78.1	23.7	95.00%	K.LASNPETASLLADSAFMAK.L		K.LASNPETASLLADSAFMAK.L
112	132	2	2007.97	4.2	0	89.9	25.6	95.00%	K.SVEAAQTQAASGAGGFNPFAK.L		K.SVEAAQTQAASGAGGFNPFAK.L
168	183	2	1781.88	4.3	1	66.6	24.7	95.00%	K.IQQNPGSIMAELNDPR.M		K.IQQNPGSIMAELNDPR.M
550	560	2	1154.62	-0.79	0	41.8	21.3	95.00%	D.PAMQAILGQAR.E		K.DPEVLGILQDPAMQAILGQAR.E

371	377	2	800.44	3.8	1	29.8	25.5	95.00%	R.TPDILSR.L		R.TPDILSR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
102	RS5B_SCHPO	20.20%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
20	32	3	1552.84	4.7	1	30.8	20.3	95.00%	K.LFNKFPFEGVEVK.D		K.LFNKFPFEGVEVK.D
146	158	2	1338.8	1.3	0	39.9	15.6	95.00%	R.VNQALALITIGAR.E		R.VNQALALITIGAR.E
167	181	2	1646.83	4.1	0	68	23.9	95.00%	K.SISECLAEEIINAAK.G	Carbamidomethyl (+57)	K.SISECLAEEIINAAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
103	RS0B_SCHPO	12.54%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	88	4	2453.25	0.76	1	72.8	22	95.00%	R.VIATIENPADVCVISSRPYGHR.A	Carbamidomethyl (+57)	R.VIATIENPADVCVISSRPYGHR.A
2	15	2	1484.75	-0.47	1	62.7	23.5	95.00%	M.AESIARPSVLNATD.D	Acetyl (+42)	-.MAESIARPSVLNATDDDIK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
104	RS4B_SCHPO	16.79%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
222	233	2	1232.68	5.6	0	42.4	20.7	95.00%	R.LSNVFVIGEAGK.S		R.LSNVFVIGEAGK.S
246	252	2	846.45	4.8	0	45.4	23.4	95.00%	K.LSITEER.D		K.LSITEER.D
38	49	3	1485.85	0.15	1	22.6	15.8	93.30%	K.ARECLPLIVFLR.N	Carbamidomethyl (+57)	K.ARECLPLIVFLR.N
162	174	3	1547.86	-0.39	1	21.8	18.5	91.90%	K.LNLETNKIESFIK.F		K.LNLETNKIESFIK.F
40	49	2	1258.72	4.7	0	26.1	18.5	92.40%	R.ECLPLIVFLR.N	Carbamidomethyl (+57)	R.ECLPLIVFLR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
105	RS11_SCHPO	17.76%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	64	2	1161.6	4.7	0	33.4	23.4	95.00%	K.CPFVGQVSIR.G	Carbamidomethyl (+57)	K.CPFVGQVSIR.G
114	130	2	1870.97	4.9	1	41.5	23.3	95.00%	R.INEGDVVTVGQCRPLSK.T	Carbamidomethyl (+57)	R.INEGDVVTVGQCRPLSK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
106	LYS12_SCHPO	20.44%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
197	208	2	1324.65	5.3	1	41.8	25.1	95.00%	K.SNVMSVTDGLFR.E		K.SNVMSVTDGLFR.E
298	307	2	1044.58	4.6	0	32.2	21.9	95.00%	R.GIANPVATFR.S		R.GIANPVATFR.S
188	196	3	1047.69	4.7	0	25.1	3.01	95.00%	K.KPLVTIIHK.S		K.KPLVTIIHK.S
127	138	2	1568.72	4	1	44	26.2	95.00%	R.ENTECLYVKEER.M	Carbamidomethyl (+57)	R.ENTECLYVKEER.M
86	97	2	1231.7	4.7	0	25.9	18.9	92.00%	K.VAGYSSPIVALR.K		K.VAGYSSPIVALR.K
67	85	3	2071.06	4.3	1	52.5	22	95.00%	R.LKTECNAALFGAVQSPTHK.V	Carbamidomethyl (+57)	R.LKTECNAALFGAVQSPTHK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
107	RL15A_SCHPO	19.90%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
115	128	2	1699.83	4.1	1	73.6	25.6	95.00%	R.VLNSYWVNQDATYK.F		R.VLNSYWVNQDATYK.F
78	93	3	1761.94	4.8	0	23.7	20.7	94.70%	K.GQTYGKPVHQGVNHLK.Y		K.GQTYGKPVHQGVNHLK.Y
148	157	3	1218.69	4.4	0	24.4	18.5	95.00%	R.INWIVNPVHK.H		R.INWIVNPVHK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
108	TRXB_SCHPO	18.94%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
78	89	2	1323.7	5	0	25.2	21.2	90.80%	R.FGTEIITETVSK.L		R.FGTEIITETVSK.L
114	124	2	1044.59	-0.5	0	52.7	19.3	95.00%	D.SVILATGASAR.R		K.YWLEGAEEEEPHTADSVILATGASAR.R
61	72	2	1321.66	-1	0	43.7	24.9	95.00%	D.GINGTTLTENFR.A		R.GELKPVMYEGMLANGIAAGGQLTTTTDVENFPGFPDGINGTTLTENFR.A
165	175	2	1193.59	0.65	0	31.4	24.1	95.00%	D.SAAEEAQFLTK.Y		R.NKPLAVVGGGDSAAEEAQFLTK.Y

99	124	3	2801.32	3.2	1	61.8	26.1	95.00%	K.YWLEGAEEEEPHTADSVILATGASAR.R			K.YWLEGAEEEEPHTADSVILATGASAR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
109	DHOM_SCHPO	20.21%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	138	2	1568.79	4.5	1	56.7	23.6	95.00%	K.AFSASNDVYQNIIK.A		K.AFSASNDVYQNIIK.A
57	67	2	1391.68	4.7	1	33.1	24.9	95.00%	K.DYQPINLSEWK.N		K.DYQPINLSEWK.N
28	56	3	3047.4	3	0	33.8	26.2	95.00%	K.GFNENASTNGTTSFNVVAISSMEGHYVSK.D		K.GFNENASTNGTTSFNVVAISSMEGHYVSK.D
89	110	2	2284.21	4.5	1	95.1	20	95.00%	K.SPLPAILVDNTASEAIAQSYPK.F		K.SPLPAILVDNTASEAIAQSYPK.F
98	110	2	1378.67	-1.3	0	66.7	25.1	95.00%	D.NTASEAIAQSYPK.F		K.SPLPAILVDNTASEAIAQSYPK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
110	PYC_SCHPO	5.74%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
829	838	2	1275.63	4.5	1	27.7	24.3	94.40%	K.QLEFDNNQLR.E		K.QLEFDNNQLR.E
1111	1129	3	1901.98	0.21	0	64.4	22.5	95.00%	D.PGNPGHVAAPMSGTIVEIR.V		R.ADPGNPGHVAAPMSGTIVEIR.V
1109	1129	3	2088.05	4.4	1	38.2	23	95.00%	R.ADPGNPGHVAAPMSGTIVEIR.V		R.ADPGNPGHVAAPMSGTIVEIR.V
917	929	2	1447.76	4.7	1	42.2	23	95.00%	K.VVGDLAQFMVQNK.L		K.VVGDLAQFMVQNK.L
302	315	2	1628.75	2	1	37.3	26.1	95.00%	K.YCNAGTAEFLLDQK.G	Carbamidomethyl (+57)	K.YCNAGTAEFLLDQK.G
839	848	2	1297.58	4.8	1	38.2	25.9	95.00%	R.EIDSYWAQMR.L		R.EIDSYWAQMR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
111	RS22_SCHPO	27.69%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
98	108	2	1171.7	4.9	0	29.1	14.5	95.00%	R.QVGVIVLTTSR.G		R.QVGVIVLTTSR.G
4	19	2	1814.9	4.5	1	77.6	24	95.00%	R.QSVLADCLNNIVNAER.R	Carbamidomethyl (+57)	R.QSVLADCLNNIVNAER.R
89	97	2	1111.62	5.6	0	31.9	19.5	95.00%	K.WVNQLLPSR.Q		K.WVNQLLPSR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
112	ADK_SCHPO	30.00%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
253	267	2	1483.87	4.5	1	69.4	14.9	95.00%	R.VVVITQGADATIVAK.D		R.VVVITQGADATIVAK.D
86	96	2	1295.61	3.7	1	43.7	25.7	95.00%	K.FADMLLESNEK.A		K.FADMLLESNEK.A
230	245	2	1688.89	3.8	1	56.9	21.8	95.00%	K.STDVQEIALALSSVEK.V		K.STDVQEIALALSSVEK.V
126	138	2	1424.68	5.2	0	51	25.2	95.00%	R.SLCTNLGAANNYK.L	Carbamidomethyl (+57)	R.SLCTNLGAANNYK.L
107	123	2	1770.89	-1.7	0	70.2	23.5	95.00%	D.PTTPTGVCAVVLSNNNK.N	Carbamidomethyl (+57)	R.SEFSVDPTTPTGVCAVVLSNNNK.N
35	64	3	3190.45	-0.94	1	48.2	26.4	95.00%	D.AVLASESQMGIYKEPCVSYSAGGAAQNSCR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.SNDAVLASESQMGIYKEPCVSYSAGGAAQNSCR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
113	ACL1_SCHPO	8.94%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
369	381	2	1420.73	4.5	0	44	23.3	95.00%	R.GSELTYNNVPISK.V		R.GSELTYNNVPISK.V
171	182	3	1338.74	4.8	0	23.6	19.4	94.60%	K.LYRPGSVAYVSK.S		K.LYRPGSVAYVSK.S
313	326	2	1570.9	3.9	0	58.3	15.2	95.00%	K.LPALLQEVYEGLVK.K		K.LPALLQEVYEGLVK.K
156	170	2	1506.72	3.3	1	45.7	25.6	95.00%	K.IGNTGGMMDNIVASK.L		K.IGNTGGMMDNIVASK.L
313	327	3	1699	4	1	30.3	10.4	95.00%	K.LPALLQEVYEGLVKK.G		K.LPALLQEVYEGLVKK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
114	MMF1_SCHPO	37.65%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

59	75	2	1747.86	2.8	0	34.8	25	95.00%	K.ANGVIYCSGQIPVANGK.V	Carbamidomethyl (+57)/ Deamidation (+1)	K.ANGVIYCSGQIPVANGK.V	
87	105	2	2116.09	4.6	0	131	22.6	95.00%	R.QCLLNLQEVLTEAGSSLNK.I	Carbamidomethyl (+57)	R.QCLLNLQEVLTEAGSSLNK.I	
125	137	2	1483.81	3.9	1	42.4	19.2	95.00%	K.VYTEVLPDPKPAR.S		K.VYTEVLPDPKPAR.S	
47	58	2	1247.66	5.3	0	27.4	22.3	94.10%	K.LSSAGPYNQAIK.A		K.LSSAGPYNQAIK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
115	COFI_SCHPO	32.12%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
81	94	2	1584.9	4.1	1	54.1	16.2	95.00%	K.IIFISWSPDVAPIK.S		K.IIFISWSPDVAPIK.S
8	20	2	1548.76	4.6	0	71.2	25.7	95.00%	K.VSPECLEAFQELK.L	Carbamidomethyl (+57)	K.VSPECLEAFQELK.L
117	133	2	1941.96	0.4	1	67.2	24.4	95.00%	D.IQATDFSEVAYETVLEK.V		R.AFTGIGTDIQATDFSEVAYETVLEK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
116	RS2_SCHPO	26.48%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
64	74	2	1441.73	5.7	1	25.1	23.5	90.50%	K.EYQIVDYFLPR.L		K.EYQIVDYFLPR.L
51	63	2	1566.86	4.2	0	34.6	18.6	95.00%	K.SIEEIYLYSLPIK.E		K.SIEEIYLYSLPIK.E
174	185	3	1138.69	4.8	1	25.2	12.6	95.00%	R.GAGLVAAPVTKR.F		R.GAGLVAAPVTKR.F
186	200	2	1799.85	0.46	1	104	25.9	95.00%	R.FLQLAGIEDCYTQSR.G	Carbamidomethyl (+57)	R.FLQLAGIEDCYTQSR.G
141	156	3	1696.87	4.8	1	37.6	23.6	95.00%	R.GYWGTALGDPHTVPVK.V		R.GYWGTALGDPHTVPVK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
117	RS23_SCHPO	17.48%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
96	107	2	1334.65	1.3	1	32.5	25.6	95.00%	D.ENDEVLLSGFGR.K		K.VTAFVPHDGCLNFVDENDEVLLSGFGR.K
125	137	2	1326.74	4.4	0	55.5	19.2	95.00%	K.VAGVGLSALFHEK.K		K.VAGVGLSALFHEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
118	IMDH_SCHPO	10.50%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	139	2	1621.88	0.92	1	48	18.6	95.00%	D.PVVFSPQHTVGDVLK.I		K.YENGFILDPVVFSPQHTVGDVLK.I
303	313	2	1155.67	4.5	1	51.3	18.8	95.00%	K.IDVIAGNVVTR.E		K.IDVIAGNVVTR.E
2	15	2	1636.88	4	0	27	20.6	93.50%	M.SAFKPYTEALEVLK.K	Acetyl (+42)	-.MSAFKPYTEALEVLK.K
419	433	2	1421.67	3.9	0	52.2	26	95.00%	R.GMGSIAAMEGTGVNK.N		R.GMGSIAAMEGTGVNK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
119	SYRC_SCHPO	9.39%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
452	467	2	1759.87	3.7	1	55	24.7	95.00%	K.YAQVENPEEVADIVGK.T		K.YAQVENPEEVADIVGK.T
163	180	2	1987.02	4.1	0	33.9	21.3	95.00%	R.STIIGSFLANLHESQGWK.V		R.STIIGSFLANLHESQGWK.V
480	489	2	1284.6	5.9	1	39.4	25.3	95.00%	R.INNYAFDWSR.M		R.INNYAFDWSR.M
11	24	2	1544.86	4.5	1	46.7	17.6	95.00%	K.SLSTLGLQDLPVFR.E		K.SLSTLGLQDLPVFR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
120	RL27A_SCHPO	22.06%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	48	3	1461.76	5.9	0	42.8	22.9	95.00%	K.SHPFGHAVVAGVER.Y		K.SHPFGHAVVAGVER.Y
23	34	2	1269.74	4.4	1	65.4	16.3	95.00%	K.VVILQAIDQGSK.S		K.VVILQAIDQGSK.S
35	52	4	1963.05	4.3	1	23.2	19.5	95.00%	K.SHPFGHAVVAGVERYPLK.V		K.SHPFGHAVVAGVERYPLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
121	SYDC_SCHPO	6.03%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
281	294	2	1356.6	4.8	0	27.5	25.6	93.50%	K.MSGASSEGGSNVFK.I		K.MSGASSEGGSNVFK.I
200	210	2	1229.65	4.9	1	29.1	22.8	95.00%	K.NLPFLVEDAGR.S		K.NLPFLVEDAGR.S

490	499	2	1300.55	3.9	1	26.9	26.1	91.80%	R.YSNSYDFFMK.G		R.YSNSYDFFMK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
122	PUR8_SCHPO	11.00%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
268	292	3	2694.37	3.3	1	34.7	21.9	95.00%	R.LLANLKEVEEPFEAGQIGSSAMAYK.R		R.LLANLKEVEEPFEAGQIGSSAMAYK.R
450	460	2	1248.61	5.4	0	26.4	24.3	92.80%	R.APEQTESFVNK.D		R.APEQTESFVNK.D
372	388	2	1909.94	4.9	0	55.7	24.8	95.00%	R.AELPFMATENIIMAMTK.H		R.AELPFMATENIIMAMTK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
123	YA03_SCHPO	19.18%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	47	2	1743.87	0.064	0	91.4	24	95.00%	D.PVLTSEGIEQCEALAK.E	Carbamidomethyl (+57)	R.DPVLTSEGIEQCEALAK.E
147	172	3	2896.59	3.1	1	53.2	15.4	95.00%	R.SKEALEYLAALPQQQIAVITHSAFIR.F		R.SKEALEYLAALPQQQIAVITHSAFIR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
124	YHEF_SCHPO	20.20%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
54	65	2	1279.67	5.1	1	47	22.3	95.00%	K.SFIGLDALTESK.G		K.SFIGLDALTESKGEFFQR.M
30	41	3	1413.76	4.8	1	20.9	21.9	90.10%	R.LRGPHCGTYLLK.V	Carbamidomethyl (+57)	R.LRGPHCGTYLLKVVGTNATYVGEK.S
91	104	2	1616.85	0.29	0	34.4	23.2	95.00%	D.TANFTPLTFTTYLK.T		R.LFTIAENDTANFTPLTFTTYLKTCNPQSIENAMIPFVNTVTSEISFDAWAYTAQNSSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
125	THRC_SCHPO	10.70%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
265	282	2	1945.01	4.9	1	46.3	22	95.00%	R.FIVPTGNFGDILAGYYAK.R		R.FIVPTGNFGDILAGYYAK.R
421	432	3	1235.66	-0.57	0	37.6	21.7	95.00%	D.PHTAVGVETGLR.C		K.IYESDHYIIDPHTAVGVETGLR.C
157	166	2	1007.54	-0.41	0	31.1	20.3	95.00%	D.TGSAAIYGLR.G		R.DHLTVVGATSGDTGSAAIYGLR.G
313	327	2	1443.73	4.4	1	39.8	24.3	95.00%	K.ADSTQVSPSGPISAK.E		K.ADSTQVSPSGPISAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
126	AATR1_SCHPO	9.07%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
305	317	2	1562.83	1.5	0	56.2	21	95.00%	R.VGWFTAQPLFIER.G		R.VGWFTAQPLFIER.G
38	54	2	1856.03	4.5	0	36.8	17	95.00%	K.IISLAGGLPNPEYFPIR.E		K.IISLAGGLPNPEYFPIR.E
7	19	3	1436.71	5.4	1	43.2	25.1	95.00%	K.DLSHHLSVESASR.K		K.DLSHHLSVESASR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
127	SYG_SCHPO	10.58%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
187	198	2	1297.63	5.4	0	37	24.5	95.00%	R.NPATNGELETPR.Q		R.NPATNGELETPR.Q
216	232	3	1983.01	5	0	28	22.9	95.00%	K.GYLRPETAQGQFLNFSR.L		K.GYLRPETAQGQFLNFSR.L
492	506	2	1649.85	4.8	0	35.7	23.2	95.00%	R.TYTPNVIEPSFGLGR.I		R.TYTPNVIEPSFGLGR.I
105	116	2	1379.7	-1.5	1	42.2	23.9	95.00%	R.ADHLVEEVLEAR.L		R.ADHLVEEVLEAR.L
526	538	2	1298.77	3.9	0	28.2	15.8	95.00%	R.GVLSFPASIAPIK.A		R.GVLSFPASIAPIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
128	YDG7_SCHPO	12.15%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
7	23	3	1939.91	3.9	1	22.9	26.2	91.80%	K.YFENAQNVHFTLADGSK.I		K.YFENAQNVHFTLADGSK.I
183	204	3	2603.37	3.4	0	27.8	19.3	95.00%	K.VKPAVHQMELHPFLPQTEFVEK.H		K.VKPAVHQMELHPFLPQTEFVEK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
129	ASNS_SCHPO	5.39%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
516	523	2	1035.55	6.3	1	30	21.3	95.00%	K.LFDEIFPR.Q		K.LFDEIFPR.Q
154	165	2	1327.63	-0.17	1	69.2	25.8	95.00%	D.SPDTAYFASELK.A		R.DPIGITTLYQGFSSDSPDTAYFASELK.A
399	408	2	1120.54	4.9	0	26.3	24	92.60%	K.STMAWGLEAR.V		K.STMAWGLEAR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
130	SCE3_SCHPO	17.01%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
46	66	2	2113.97	4.9	1	94.2	27	95.00%	R.ATPSSADAGYNAPSSTFESVR.S		R.ATPSSADAGYNAPSSTFESVR.S
359	381	2	2403.05	5.1	1	111	27.3	95.00%	K.TPATEDAPATNAGEAEEEEGWTK.I		K.TPATEDAPATNAGEAEEEEGWTK.I
365	381	2	1788.78	-1.4	0	94.5	27.2	95.00%	D.APATNAGEAEEEEGWTK.I		K.TPATEDAPATNAGEAEEEEGWTK.I
250	271	3	2195.06	2.9	0	28.5	24.8	95.00%	R.SSSNVNTEATPSATTTTSSKPK.R		R.SSSNVNTEATPSATTTTSSKPK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
131	ARGD_SCHPO	14.51%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
104	129	3	2885.49	-0.76	0	29.2	19.8	95.00%	K.LVHSSNLFYNEPAIELSNVINNSLAK.N		K.LVHSSNLFYNEPAIELSNVINNSLAK.N
311	332	3	2276.09	4.8	0	39.5	25.7	95.00%	K.IAAEIHPGEHGSTFGGNPVACR.V	Carbamidomethyl (+57)	K.IAAEIHPGEHGSTFGGNPVACR.V
139	154	2	1784.85	4.1	0	92.8	25.5	95.00%	K.IFFANCGTEANETALK.F	Carbamidomethyl (+57)	K.IFFANCGTEANETALK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
132	RS10A_SCHPO	34.72%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	44	3	1428.82	4.9	0	23.6	17.2	94.60%	K.HPEVGVPNLQVIK.A		K.HPEVGVPNLQVIK.A
78	93	4	1859.01	4	1	23	18.8	95.00%	R.EYLHLPAEVVPATHKR.Q		R.EYLHLPAEVVPATHKR.Q
10	24	3	1580.9	0.45	0	36.5	14.6	95.00%	K.AIHQALFSQGVLVAK.K		K.AIHQALFSQGVLVAK.K
26	31	2	732.38	5.5	1	30.1	22.5	95.00%	K.DFNLPK.H		K.DFNLPK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
133	RL3A_SCHPO	18.81%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
207	222	2	1837.9	4.3	1	73.9	25.2	95.00%	K.STFEQNEMIDVIGVTR.G		K.STFEQNEMIDVIGVTR.G
11	19	2	982.54	4.3	0	27.2	20.1	93.80%	R.HGSLGFLPR.K		R.HGSLGFLPR.K
249	266	3	2035.03	4.4	0	29.3	23.6	95.00%	K.VACIGAWHPANVQWTVAR.A	Carbamidomethyl (+57)	K.VACIGAWHPANVQWTVAR.A
37	50	3	1530.86	0.0027	0	23.1	18.1	94.00%	D.ASKPVHLTAFLGYK.A		K.DDASKPVHLTAFLGYK.A
101	116	3	1883.97	-0.42	1	21.5	22.4	91.50%	R.SLTTVWAEHLSEEVKR.R		R.SLTTVWAEHLSEEVKR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
134	SYKC_SCHPO	6.09%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
570	591	3	2490.33	2.8	1	30.8	18.1	95.00%	R.EVLLFPHMKPEVQAAEPTVVKE.-		R.EVLLFPHMKPEVQAAEPTVVKE.-
15	28	2	1454.8	4	1	41.2	19.6	95.00%	K.ALVLDPVTGEQVSK.T		K.ALVLDPVTGEQVSK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
135	YHZ8_SCHPO	25.25%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
75	103	3	3217.69	3	0	57.2	18.5	95.00%	K.TSNPFLAFANYLTSTHAPLAEPLQLLNFK.V		K.TSNPFLAFANYLTSTHAPLAEPLQLLNFK.V
2	13	2	1361.7	3.8	0	57.2	23	95.00%	M.SFPASTHVYIAK.I	Acetyl (+42)	-.MSFPASTHVYIAK.I

156	164	2	1004.57	-0.21	0	30.7	19.7	95.00%	D.PSLYAVVTR.Y		K.ADTSLIIHSLDDPSLYAVVTR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
136	RS15A_SCHPO	38.56%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	85	2	1396.76	4.6	0	40.4	20	95.00%	K.TEAPLNEKPATVK.T		K.TEAPLNEKPATVK.T
109	135	4	3209.67	3.6	0	17.8	19.7	93.90%	K.LFNQVEIRPEMIGHYLGEFSITYK PTK.H		K.LFNQVEIRPEMIGHYLGEFSITYK PTK.H
90	108	2	2033.08	3.1	0	80.9	20.6	95.00%	R.NMIILPEMVGSVVGIYNGK.L		R.NMIILPEMVGSVVGIYNGK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
137	RL23_SCHPO	25.18%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
15	34	2	2090	0.63	1	77.4	25.8	95.00%	R.MTLGLPVQAIMNCADNSGAK.N	Carbamidomethyl (+57)	R.MTLGLPVQAIMNCADNSGAK.N
51	65	2	1531.78	3.4	1	55.2	23.6	95.00%	R.LPAASCGDMVLATVK.K	Carbamidomethyl (+57)	R.LPAASCGDMVLATVK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
138	SLBR2_SCHPO	13.11%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
134	143	2	1115.56	4.3	0	27.1	23.5	93.70%	R.NIESSVQPSR.E		R.NIESSVQPSR.E
166	192	3	3060.53	3.6	1	43.6	22.2	95.00%	R.LVTMEQELVREEAACLVAEAQLS NTTR.E	Carbamidomethyl (+57)	R.LVTMEQELVREEAACLVAEAQLS NTTR.E
149	157	2	1075.63	4.5	1	33	17.2	95.00%	K.LLDQIYALK.H		K.LLDQIYALK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
139	ASSY_SCHPO	12.20%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
129	147	3	2278.22	0.75	1	25.8	18.9	95.00%	R.FELAYYALKPDVQVIAPWR.L		R.FELAYYALKPDVQVIAPWR.L
333	350	2	1884.01	-0.53	0	51.3	20	95.00%	R.MLLAANNVSQEVVNGVVK.L		R.MLLAANNVSQEVVNGVVK.L
320	332	2	1601.77	4.2	0	39.6	25.7	95.00%	K.ILYNGQFFSPCTR.M	Carbamidomethyl (+57)	K.ILYNGQFFSPCTR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
140	RS21_SCHPO	29.89%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
77	87	2	1306.66	-2	0	40	24.6	95.00%	D.GLLEGVWSYQR.-		R.LTTQDGLLEGVWSYQR.-
51	60	2	1113.59	4.5	0	33.8	22.6	95.00%	K.TTYAISGFVR.S		K.TTYAISGFVR.S
72	87	2	1864.94	4.3	1	65.3	23.7	95.00%	R.LTTQDGLLEGVWSYQR.-		R.LTTQDGLLEGVWSYQR.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
141	RL28A_SCHPO	20.27%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
94	110	2	1787.94	-0.45	0	41.2	20.8	95.00%	K.NTEVAPVINVLQSGYGK.V		K.NTEVAPVINVLQSGYGK.V
115	127	3	1464.84	-0.55	1	37.3	15.7	95.00%	K.GRLPETPVIVQTR.Y		K.GRLPETPVIVQTR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
142	NACB_SCHPO	31.13%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
66	72	2	761.42	-1.3	0	30.6	21	95.00%	D.GGVINFR.A		K.EDGGVINFR.A
95	116	2	2320.31	3	0	52.8	12.8	95.00%	K.TLSEILPGILNNLGPESLTALR.Q		K.TLSEILPGILNNLGPESLTALR.Q
73	90	3	1884.95	-1.7	0	48.6	23.2	95.00%	R.APTVHSSLPNETTAIYGK.A		R.APTVHSSLPNETTAIYGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
143	P25_SCHPO	17.82%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
36	52	2	1976.05	-0.01	0	48.5	19.8	95.00%	K.AVIYQFPETLSPEILEK.M		K.AVIYQFPETLSPEILEK.M
2	20	2	2064.09	2.1	0	77.6	19.9	95.00%	M.STANTVAIVIYSTYGHVVK.L	Acetyl (+42)	-.MSTANTVAIVIYSTYGHVVK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
144	RL6_SCHPO	22.05%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	64	2	1497.84	5	0	33.1	18.6	95.00%	R.ASLAPGTVCILLAGR.F	Carbamidomethyl (+57)	R.ASLAPGTVCILLAGR.F
70	87	2	1959.1	3.1	1	33.6	14.3	95.00%	R.VVVLSQLEDTLVVTGPYK.V		R.VVVLSQLEDTLVVTGPYK.V
109	118	2	1031.56	5.5	1	31.2	22.7	95.00%	K.IDVSGVSVEK.F		K.IDVSGVSVEK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
145	RS17A_SCHPO	16.03%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	59	3	1133.6	4.6	0	24.5	22.7	95.00%	K.IAGYTTHLMK.R		K.IAGYTTHLMK.R
34	44	2	1156.68	4.8	1	51	17.6	95.00%	R.IVDEVAIIASK.R		R.IVDEVAIIASK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
146	KAD1_SCHPO	16.36%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
196	218	3	2621.39	2.8	1	47.7	18.4	95.00%	K.WAAVDAAQKPEQVWEQIVAILEK.A		K.WAAVDAAQKPEQVWEQIVAILEK.A
27	39	3	1416.72	-1.3	1	31.5	24.1	95.00%	K.YGIAHLATGDMLR.S		K.YGIAHLATGDMLR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
147	KAPS_SCHPO	22.77%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
157	188	3	3532.7	3.1	0	32.4	23.2	95.00%	K.EFTGISAPYEAPISPEIVVSSHTQSIEECVEK.I	Carbamidomethyl (+57)	K.EFTGISAPYEAPISPEIVVSSHTQSIEECVEK.I
39	52	2	1664.86	3.8	0	65.6	22.9	95.00%	K.STIACALEQYLLQR.G	Carbamidomethyl (+57)	K.STIACALEQYLLQR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
148	ARO1_SCHPO	4.51%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
677	703	3	2950.41	2.7	1	45.4	24.5	95.00%	R.FACDVLRPMGCTVEQTATSTTVQGPPK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.FACDVLRPMGCTVEQTATSTTVQGPPK.G
644	660	2	1634.89	-0.87	0	27.3	19.7	94.00%	D.ASSATYPLAIAAITGTK.C		K.YQNPPHYEIESDASSATYPLAIAAITGTK.C
162	172	2	1299.72	4.7	0	45.2	20.8	95.00%	K.NLVGAFWQPLR.V		K.NLVGAFWQPLR.V
1232	1247	2	1833.96	4.6	1	44.8	21.9	95.00%	R.ITNSMDIPLILFNMGR.F		R.ITNSMDIPLILFNMGR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
149	PABP_SCHPO	10.57%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
258	266	2	1068.57	4.8	0	26.6	21.3	93.00%	K.ANFTNVYIK.N		K.ANFTNVYIK.N
447	456	2	1142.61	4.9	0	33.9	22.1	95.00%	R.SQLEAQIQAR.N		R.SQLEAQIQAR.N
536	571	3	3524.72	4.6	0	28.7	23.2	95.00%	R.GPVPAQGRPMMMPGSVPSAGPAEAEAVPAVPGMPER.F		R.GPVPAQGRPMMMPGSVPSAGPAEAEAVPAVPGMPER.F
428	441	3	1529.87	-1.4	0	22	16	92.20%	R.MLAGKPLYVALAQR.K		R.MLAGKPLYVALAQR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
150	RL19A_SCHPO	20.73%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
118	128	3	1386.74	5	0	32.3	21.9	95.00%	K.HLYHTLYLEAK.G		K.HLYHTLYLEAK.G
26	38	2	1429.68	-1.3	0	61	25.5	95.00%	D.PNEISEISNANSR.Q		K.VWMDPNEISEISNANSR.Q
182	193	2	1422.69	3.6	1	31.8	25	95.00%	R.EQLYTAAEKIEE.-		R.EQLYTAAEKIEE.-
22	38	2	1960.9	4.1	1	66.6	26.4	95.00%	K.VWMDPNEISEISNANSR.Q		K.VWMDPNEISEISNANSR.Q
182	193	2	1422.69	3.6	1	31.8	25	95.00%	R.EQIYTAAEKIEE.-		R.EQLYTAAEKIEE.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
151	DYR_SCHPO	13.02%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
164	183	3	2062.15	3.7	1	25.4	14.1	95.00%	K.LTTPSLHIAGTSDTLVPLAR.S		K.LTTPSLHIAGTSDTLVPLAR.S
34	51	2	1958.89	-0.37	1	32.4	27.3	95.00%	K.YAELHFPTGPVVADEEAD.P		K.YAELHFPTGPVVADEEADPNDEEEK.K

191	212	3	2537.31	3.6	0	37.3	21	95.00%	R.CENAHVLLHPGQHIVPQQAVYK.T	Carbamidomethyl (+57)	R.CENAHVLLHPGQHIVPQQAVYK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
152	ACL2_SCHPO	11.99%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
255	266	2	1367.61	3.7	1	48.5	26.1	95.00%	K.LDQTAEFECGAK.W	Carbamidomethyl (+57)	K.LDQTAEFECGAK.W
326	334	2	985.56	4.7	0	36	20.4	95.00%	K.LTILNAEGR.V		K.LTILNAEGR.V
382	389	2	947.52	4.5	1	26.9	22.7	93.50%	K.TVLDLMTR.G		K.TVLDLMTR.G
32	61	3	3211.76	3.3	0	47.1	15.6	95.00%	K.TVSATPAVQLAQIQFPLPTLVIPAESTTYR.E		K.TVSATPAVQLAQIQFPLPTLVIPAESTTYR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
153	RL36A_SCHPO	24.24%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	11	2	966.59	4.6	0	38.2	14.5	95.00%	M.APGLVVGLNK.G		-.MAPGLVVGLNK.G
83	96	2	1545.84	4.6	1	75.1	19.7	95.00%	K.GKIEELTSVIQSSR.L		K.GKIEELTSVIQSSR.L
85	96	2	1360.73	3.8	0	56.4	21.8	95.00%	K.IEELTSVIQSSR.L		K.IEELTSVIQSSR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
154	PMM_SCHPO	11.28%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
29	43	2	1728.92	4.2	0	56.6	21.1	95.00%	R.LSVSPEMLETLQNLR.K		R.LSVSPEMLETLQNLR.K
45	58	2	1347.75	4.4	1	41.6	20	95.00%	K.VVAIGFVGGSDLSK.Q		K.VVAIGFVGGSDLSK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
155	PURA_SCHPO	14.29%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
206	224	3	2169.16	3.6	1	37.8	18.5	95.00%	R.LKPFVIDAVAFMYEALQSK.K		R.LKPFVIDAVAFMYEALQSK.K
282	304	3	2420.22	4.2	1	27.4	22.7	95.00%	R.VGAGPFPTEQLNEIGDHLQSVGR.E		R.VGAGPFPTEQLNEIGDHLQSVGR.E
268	276	2	899.55	4.9	0	44.5	20.5	95.00%	R.IANSIGVVK.A		R.IANSIGVVK.A
126	136	2	1129.57	4.6	1	38.6	23.2	95.00%	R.ADALNEAELGK.Q		R.ADALNEAELGK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
156	SYTC_SCHPO	4.27%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
248	258	2	1187.55	4.2	1	47.1	26.3	95.00%	K.NSSSYFLGDAK.N		K.NSSSYFLGDAK.N
8	26	3	2136.14	4.2	1	27.4	18.9	95.00%	K.GVQASLDNLSLEIPFIQHR.L		K.GVQASLDNLSLEIPFIQHR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
157	PDI1_SCHPO	5.28%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	136	3	1350.87	5.1	1	30.4	6.02	95.00%	R.KQLLPTVKPISK.D		R.KQLLPTVKPISK.D
188	201	2	1436.77	4.3	0	45.1	19.9	95.00%	K.SLGSNFPGIVAFTK.D		K.SLGSNFPGIVAFTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
158	SPI1_SCHPO	12.50%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
110	122	2	1514.77	4.6	0	58.5	24	95.00%	R.VCENIPIVLCGNK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VCENIPIVLCGNK.V
152	165	3	1783.91	4.6	0	29.2	23.2	95.00%	K.SNYNFEKPFLWLAR.K		K.SNYNFEKPFLWLAR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
159	RL14_SCHPO	14.93%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
53	64	3	1345.74	-1.4	0	24.8	21	95.00%	R.YGSVVLTHIVMK.L		R.YGSVVLTHIVMK.L
87	94	2	905.44	5.7	0	30.4	23.9	95.00%	K.WASSAWAK.K		K.WASSAWAK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
160	SPEE_SCHPO	8.39%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	12	2	1291.72	4.1	0	43.5	18.5	95.00%	M.SVQELSHPLIK.D	Acetyl (+42)	-.MSVQELSHPLIK.D
18	31	2	1631.79	4.6	0	31.2	25.2	95.00%	R.EINNMWPGQAMTLK.V		R.EINNMWPGQAMTLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
161	PLR1_SCHPO	7.51%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	66	2	1195.66	-0.52	1	53.2	20.5	95.00%	D.PPTSNLDLLAR.Y		K.QTPDEEAFEVMNYALSQGSNYW DAGEFYGVDPPTSNLDLLAR.Y
194	207	3	1663.91	-0.28	1	46.6	17.9	95.00%	R.KLSIPIIAYSPFCR.G	Carbamidomethyl (+57)	R.KLSIPIIAYSPFCR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
162	RL30A_SCHPO	28.44%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
71	89	2	1997.95	6	1	62.5	25.7	95.00%	K.ANVHHYAGTNIDLGTACGK.L	Carbamidomethyl (+57)	K.ANVHHYAGTNIDLGTACGK.L
47	58	2	1335.77	-1.6	0	25.1	15.8	90.60%	K.LILIAGNCPPLR.K	Carbamidomethyl (+57)	K.LILIAGNCPPLR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
163	RS13_SCHPO	15.23%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
44	55	2	1244.66	3.8	0	40.8	22.5	95.00%	K.GMSPSQIGVTLR.D		K.GMSPSQIGVTLR.D
10	20	2	1132.63	4.4	0	38.6	20.1	95.00%	K.GIASSALPYVR.S		K.GIASSALPYVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
164	RL31_SCHPO	21.24%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
91	105	2	1650.87	4.2	1	39.3	21	95.00%	K.ALYTYVQAVDVANPK.M		K.ALYTYVQAVDVANPK.M
7	15	2	986.56	5	0	39.5	21.7	95.00%	K.SAINQVVTR.D		K.SAINQVVTR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
165	RL11_SCHPO	14.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
36	49	2	1531.83	4.2	0	63.5	20	95.00%	K.VLEQLSGQTPVFSK.A		K.VLEQLSGQTPVFSK.A
154	164	2	1349.67	4.1	1	39.8	24.4	95.00%	K.INAEDTINWFK.Q		K.INAEDTINWFK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
166	RS14_SCHPO	16.55%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
95	105	2	1037.57	5.3	0	47.1	19.9	95.00%	K.TPGPGAQAALR.A		K.TPGPGAQAALR.A
73	84	3	1367.77	4	1	24.2	19.1	95.00%	K.CKEVGITALHIK.I	Carbamidomethyl (+57)	K.CKEVGITALHIK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
167	RL2_SCHPO	15.02%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
92	118	3	2780.44	3.2	0	52	20	95.00%	K.NAALTVGNVLPVGEMPEGTIISNV EEK.A		K.NAALTVGNVLPVGEMPEGTIISNV EEK.A
163	173	2	940.55	4.3	0	54.6	16.4	95.00%	R.GVVGIVAGGGR.I		R.GVVGIVAGGGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
168	Q1L854_SCHPO	7.32%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
14	27	2	1459.74	-1.7	0	28.1	23.2	94.90%	D.LLGEETPAATTTEK.K		K.NLFDLLGEETPAATTTEK.K
10	27	2	1948.96	0.085	1	79.9	24.9	95.00%	K.NLFDLLGEETPAATTTEK.K		K.NLFDLLGEETPAATTTEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
169	RS12A_SCHPO	31.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

99	111	2	1486.76	2.4	1	27.9	23.3	94.60%	K.VLGEWAGLCVLDR.D	Carbamidomethyl (+57)	K.VLGEWAGLCVLDR.D
79	93	2	1671.88	4.1	0	73.8	21.7	95.00%	K.LVEALCAESETPLIK.V	Carbamidomethyl (+57)	K.LVEALCAESETPLIK.V
61	78	3	2208.97	4.2	1	36.3	27	95.00%	R.QAHLCVLCESCDQEAYVK.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.QAHLCVLCESCDQEAYVK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
170	ATPB_SCHPO	7.43%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
167	185	2	2076.03	-0.54	0	69.8	24.4	95.00%	D.APSFEEQSTTPEILETGIK.V		K.YSPIHADAPSFEEQSTTPEILETGIK.V
160	185	3	2859.39	2.5	1	29.4	24.2	95.00%	K.YSPIHADAPSFEEQSTTPEILETGIK.V		K.YSPIHADAPSFEEQSTTPEILETGIK.V
210	222	2	1501.85	0.99	0	36.3	15.8	95.00%	K.TVFIQELINNIAK.A		K.TVFIQELINNIAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
171	RL18B_SCHPO	11.23%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	65	3	1111.64	5.1	0	26.6	18.9	95.00%	K.TNRPPISISK.I		K.TNRPPISISK.I
132	142	2	1127.63	4.1	0	42.3	21	95.00%	R.APTGSNTVLLR.G		R.APTGSNTVLLR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
172	TBB_SCHPO	9.82%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
123	154	3	3205.55	2.6	1	82.9	24	95.00%	R.EAEACDALQGFQLTHSLGGGTGSGMGTLLLSK.I	Carbamidomethyl (+57)	R.EAEACDALQGFQLTHSLGGGTGSGMGTLLLSK.I
163	174	2	1249.62	3.9	0	41.3	24.3	95.00%	R.MMATFSVAPAPK.S		R.MMATFSVAPAPK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
173	Q9P7B4_SCHPO	19.69%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
234	256	3	2522.27	2.7	1	34.8	22.5	95.00%	R.ENVVIADTLVFPSHQGGANHVYR.K		R.ENVVIADTLVFPSHQGGANHVYR.K
163	173	2	1163.64	5.6	0	26.5	19	92.90%	K.SALAQFTSALR.K		K.SALAQFTSALR.K
183	199	2	1918.98	6.8	1	60.8	22.6	95.00%	R.IMEVDPGLVETEFSVVR.F		R.IMEVDPGLVETEFSVVR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
174	PGM_SCHPO	10.65%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
423	435	2	1529.66	4.3	1	62.5	26.4	95.00%	R.YDYEELENEAAGK.V		R.YDYEELENEAAGK.V
350	358	2	1160.54	5.2	1	29	25.3	95.00%	K.FFCNLFDAK.R	Carbamidomethyl (+57)	K.FFCNLFDAK.R
127	142	2	1631.79	4.4	0	81.8	25.3	95.00%	K.YNLGNGGPAPESVTEK.I		K.YNLGNGGPAPESVTEK.I
1	21	3	2330.21	3.2	0	23.9	20.7	94.90%	-.MIETIPTKPYEGQRPGTSGLR.K		-.MIETIPTKPYEGQRPGTSGLR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
175	VATB_SCHPO	8.35%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
415	427	2	1417.68	4.9	1	78	25.4	95.00%	K.SVVGEEALSQEDR.L		K.SVVGEEALSQEDR.L
439	449	2	1284.62	4.2	0	36.9	25.1	95.00%	K.TFISQGAYENR.T		K.TFISQGAYENR.T
42	59	3	2083.09	4.5	1	23.6	21.7	94.60%	R.RPQYNEIVNLNLPDGSVR.S		R.RPQYNEIVNLNLPDGSVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
176	CYSK1_SCHPO	9.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
10	23	2	1341.78	-1.2	0	60.4	17.1	95.00%	K.VPGIVSGFIGAIGR.T		K.VPGIVSGFIGAIGR.T
180	200	2	2019.93	5.1	1	71.4	26.6	95.00%	K.GTVDGFTCSTGTGGTFAGVTK.Y	Carbamidomethyl (+57)	K.GTVDGFTCSTGTGGTFAGVTK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
177	THI22_SCHPO	4.90%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
138	151	2	1403.73	-1.2	1	50.6	23.2	95.00%	D.PVMVATSGDSLVTK.D		K.LVVDPVMVATSGDSLVTK.D	
423	435	2	1516.6	5.3	0	56.7	26	95.00%	K.SCEESPACTAYSR.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.SCEESPACTAYSR.Y	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
178	CH10_SCHPO	22.12%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
73	84	2	1230.7	4	0	31.7	16.6	95.00%	R.VLLPAYGGSNIK.V		R.VLLPAYGGSNIK.V	
62	72	2	1111.6	4.5	1	30.9	20.3	95.00%	K.LAQPSVAVGDR.V		K.LAQPSVAVGDR.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
179	RANG_SCHPO	10.23%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
188	198	2	1253.61	5.8	0	35.7	24.3	95.00%	R.FANSENANLFK.E		R.FANSENANLFK.E	
88	98	2	1353.6	4	0	43.5	25.9	95.00%	K.TNEEEETVEFK.M		K.TNEEEETVEFK.M	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
180	RAD25_SCHPO	14.44%	100%	3								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
63	74	2	1417.75	4.9	1	43.2	22.3	95.00%	R.IISSIEQKEESR.G		R.IISSIEQKEESR.G	
218	226	2	1073.63	0.55	0	44	16.5	95.00%	D.STLIMQLLR.D		K.DSTLIMQLLR.D	
244	261	3	1846.84	4.4	0	24	26	93.80%	K.EEAPAAAAASENEHPEPK.E		K.EEAPAAAAASENEHPEPK.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
181	TBA1_SCHPO	8.79%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
285	308	3	2899.3	3.7	0	55.7	27.3	95.00%	K.AFHESNSVQEITNQCFEPYNQMV K.C	Carbamidomethyl (+57)	K.AFHESNSVQEITNQCFEPYNQMV K.C	
269	284	3	1741.98	0.18	0	21	16.9	90.30%	R.IHFPLVTYSPIVSAAK.A		R.IHFPLVTYSPIVSAAK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
182	RL12_SCHPO	28.48%	100%	3								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
68	83	2	1538.91	3.4	0	50.5	14.3	95.00%	R.QAAVSVVPSASALVIK.A		R.QAAVSVVPSASALVIK.A	
17	31	2	1312.7	3.6	0	46	21.2	95.00%	R.AVGGEVAGGSTLAPK.I		R.AVGGEVAGGSTLAPK.I	
131	146	2	1652.81	4	1	45.9	24.3	95.00%	K.EILGTAFSVGCTVDGK.N	Carbamidomethyl (+57)	K.EILGTAFSVGCTVDGK.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
183	YCO6_SCHPO	10.94%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
15	36	3	2140.01	5.3	0	26.3	26.1	95.00%	K.MSAAPTPHNTPSGTSAPNFGAK. A		K.MSAAPTPHNTPSGTSAPNFGAK. A	
57	77	3	2234.19	0.59	0	28.3	18.3	95.00%	K.LGSLLHLTSEGVSELPEAVQR.R		K.LGSLLHLTSEGVSELPEAVQR.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
184	RL24A_SCHPO	20.81%	100%	3								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
1	12	2	1357.64	4.1	1	34.6	25.3	95.00%	-.MKVEVCSFSGSK.V	Carbamidomethyl (+57)	-.MKVEVCSFSGSK.V	
81	91	2	1097.65	4.7	1	29.4	18.1	95.00%	R.GIVGANLDVIK.E		R.GIVGANLDVIK.E	
36	43	2	978.52	4.9	0	29.5	22.9	95.00%	K.SESLFLQR.K		K.SESLFLQR.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
185	APE1_SCHPO	3.40%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
253	269	2	1912.97	5	1	42.1	23.6	95.00%	K.TLDFFSGVFGEPYPLPK.C		K.TLDFFSGVFGEPYPLPK.C	
137	149	2	1467.71	4.6	0	42.2	24.5	95.00%	K.YLATTQMEPTSAR.R		K.YLATTQMEPTSAR.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
186	YDMC_SCHPO	4.59%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
370	385	2	1877	4	0	39.4	20	95.00%	K.LTSLMESIFPEQTIIR.S		K.LTSLMESIFPEQTIIR.S
82	91	2	1136.53	5	1	33.4	25.5	95.00%	R.NADNSVTNFR.D		R.NADNSVTNFR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
187	CPGL_SCHPO	4.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
40	53	2	1599.79	4.2	1	88.3	24.6	95.00%	K.VVEMADFVVSEFTK.L		K.VVEMADFVVSEFTK.L
113	121	2	1033.54	-0.51	1	30.5	21.4	95.00%	D.PFTLTVDNK.G		K.TVLIYNHFDVQPASLEDGWSTDP FTLTVDNK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
188	YOI1_SCHPO	7.01%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
392	408	2	1726.88	3.3	1	56.2	23.3	95.00%	K.LGEGELGQLAADINAEK.A		K.LGEGELGQLAADINAEK.A
35	48	3	1475.82	-0.076	0	24.6	17.7	95.00%	R.AVEPVGPLFLAHAR.R		R.AVEPVGPLFLAHAR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
189	ARPC1_SCHPO	10.08%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	23	4	2564.32	3.3	0	37.1	20.7	95.00%	M.ATSQVLHILPKPSYEHAFNSQR.T	Acetyl (+42)	- .MATSQVLHILPKPSYEHAFNSQR.T
227	242	2	1698.86	-1.1	0	41.8	24.1	95.00%	D.SSVTIAYPSAPEQPPR.A		R.LPFNTVCAEYPSGGWVHAVGFS PSGNALAYAGHDSSVTIAYPSAPEQ PPR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
190	PROF_SCHPO	26.77%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
54	68	2	1515.81	-0.54	0	47.9	21.4	95.00%	D.PPSMFGTGIILAGQK.Y		R.AGDSVWAASAGFNLSPQEIQGL AAGFQDPPSMFGTGIILAGQK.Y
95	113	3	2098.08	3.5	0	24.5	21.1	95.00%	K.LCILVSHYPETTLPGEAAK.I	Carbamidomethyl (+57)	K.LCILVSHYPETTLPGEAAK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
191	RL20_SCHPO	14.77%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	112	2	1453.67	0.33	1	54.9	25.8	95.00%	R.VGAVEAMYADMAAR.H		R.VGAVEAMYADMAAR.H
165	176	3	1448.76	-0.006	1	29.3	22.6	95.00%	K.KVFAPHRPSTFY.-		K.KVFAPHRPSTFY.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
192	MPG1_SCHPO	11.02%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
270	287	2	1776	4.2	1	35.2	16.3	95.00%	K.IGPNVVIGPNVTIGDGVR.L		K.IGPNVVIGPNVTIGDGVR.L
138	159	4	2530.28	3.4	1	22.1	22.9	95.00%	K.VEEPSKYGVVVHYPNSESLIER.F		K.VEEPSKYGVVVHYPNSESLIER.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
193	SODM_SCHPO	20.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	173	2	1303.7	4.2	1	48.8	21.3	95.00%	R.ITTTANQDTIVK.S		R.ITTTANQDTIVK.S
26	48	2	2502.32	2.9	0	32.8	19.3	95.00%	K.ATLPPLPYAYNALEPALSETIMK.L		K.ATLPPLPYAYNALEPALSETIMK.L
127	135	2	1108.52	5	1	34	25.8	95.00%	K.WGSLEDFQK.E		K.WGSLEDFQK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

194	YBS7_SCHPO	7.97%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
442	471	4	3134.5	-0.033	1	26.4	24.5	95.00%	K.EQPPNKAEPAVPTEASSTKPSEAAEESTPR.F		K.EQPPNKAEPAVPTEASSTKPSEAAEESTPR.F		
128	146	2	1760.86	5.1	0	31.6	25.1	95.00%	R.TSGSSTGLSNAPPSANVSK.A		R.TSGSSTGLSNAPPSANVSK.A		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
195	ODPA_SCHPO	7.33%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
200	229	3	3269.55	4.6	1	77.4	24.9	95.00%	K.YLEKPTTTFALYGDGASNQGQAFEAFNMAK.L		K.YLEKPTTTFALYGDGASNQGQAFEAFNMAK.L		
214	229	2	1669.75	-0.61	0	31.1	27	95.00%	D.GASNQGQAFEAFNMAK.L		K.YLEKPTTTFALYGDGASNQGQAFEAFNMAK.L		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
196	RS3_SCHPO	10.04%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
97	108	2	1362.64	3.8	0	61	25.7	95.00%	R.GLCAVAQCESLR.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GLCAVAQCESLR.Y		
30	42	2	1513.64	4.2	0	70.9	26.3	95.00%	R.ELSEEGYSGCEVR.V	Carbamidomethyl (+57)	R.ELSEEGYSGCEVR.V		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
197	PPID_SCHPO	7.87%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
155	169	2	1686.83	-0.39	0	40.4	24.3	95.00%	D.PVVPVVIEECGTCTK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.NDDPVVPVVIEECGTCTK.D		
214	226	2	1432.74	4.4	1	72	23.8	95.00%	K.QFAQQNLDTAVAK.W		K.QFAQQNLDTAVAK.W		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
198	UBC4_SCHPO	14.97%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
118	128	3	1264.72	-1.3	0	36	17.4	95.00%	D.PLVPEIAHVYK.T		K.VLLSICSLLTDPNPDDPLVPEIAHVYK.T		
91	101	2	1244.65	4.6	1	28.4	23.2	95.00%	R.DQWSPALTISK.V		R.DQWSPALTISK.V		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
199	ODPB_SCHPO	8.20%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
199	213	2	1682.92	-0.0099	0	48.3	18	95.00%	D.PNPVVVLENEILYGK.T		R.DPNPVVVLENEILYGK.T		
220	234	2	1634.86	4.6	1	26.5	21.8	93.00%	K.EALSEDFVLPFGLAK.V		K.EALSEDFVLPFGLAK.V		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
200	RL35_SCHPO	19.67%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
11	24	2	1684.85	4.2	0	72	23.8	95.00%	K.QSQENLAEQLQELR.Q		K.QSQENLAEQLQELR.Q		
56	65	2	1157.65	4.3	0	33.6	20.5	95.00%	R.ILTVINESNR.L		R.ILTVINESNR.L		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
201	RLA0_SCHPO	15.06%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
133	144	2	1308.71	5.2	0	29.1	19.5	95.00%	K.TSFFQALGIPTK.I		K.TSFFQALGIPTK.I		
98	132	3	3513.88	2.7	1	45.6	17.3	95.00%	R.ETIIANVIAAPARPNAIAPLDVFVPAGNTGMEPGK.T		R.ETIIANVIAAPARPNAIAPLDVFVPAGNTGMEPGK.T		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
202	YET4_SCHPO	13.60%	100%	3									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
190	216	3	2686.32	5.5	1	58	24	95.00%	R.NDEQLGNSPASITSKPATTSAAQPSSK.V		R.NDEQLGNSPASITSKPATTSAAQPSSK.V		

419	462	4	4557.19	2.7	1	18.1	22.3	94.50%	K.NEVNVPSTIPTESENPVAVGGTTAEHPVQEAVTAPTETAHDFSK.E		K.NEVNVPSTIPTESENPVAVGGTTAEHPVQEAVTAPTETAHDFSK.E
487	503	3	1712.87	4.4	0	27.8	23.7	95.00%	R.KPSSTGQEPTTPSTPAK.S		R.KPSSTGQEPTTPSTPAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
203	GPD2_SCHPO	10.46%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	88	4	2626.25	3.3	1	19.3	25.2	95.00%	K.IQHEGKECNLTEVFNTTHENVK.Y	Carbamidomethyl (+57)	K.IQHEGKECNLTEVFNTTHENVK.Y
311	327	3	1907.98	3	1	33.8	22.2	95.00%	K.TGKPMHVVEQELLDGQK.L		K.TGKPMHVVEQELLDGQK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
204	DLDH_SCHPO	5.87%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
113	128	2	1663.83	1.7	1	25	24.3	90.40%	R.GIDVSGVSVNLSQMMK.A		R.GIDVSGVSVNLSQMMK.A
155	168	2	1448.76	3.8	1	31.8	22.6	95.00%	K.GTGSFIDPQTLSVK.G		K.GTGSFIDPQTLSVK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
205	YEI3_SCHPO	8.67%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
43	62	2	2148.05	4.6	1	58.6	24.9	95.00%	K.SVLGNPANYPYATIDPEEAK.V		K.SVLGNPANYPYATIDPEEAK.V
329	342	2	1482.75	2.8	1	41.2	24.6	95.00%	K.APQAAGVIHTDFEK.A		K.APQAAGVIHTDFEK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
206	G6PD_SCHPO	5.60%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
468	478	3	1340.68	-0.049	1	28.6	23	95.00%	D.GPECLYSFLKK.F	Carbamidomethyl (+57)	K.YMEEEKPVPEPYEYGSDGPECLYSFLKK.F
451	467	2	2060.86	-0.4	1	30.7	26.8	95.00%	K.YMEEEKPVPEPYEYGSD.G		K.YMEEEKPVPEPYEYGSDGPECLYSFLK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
207	RL7B_SCHPO	14.00%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	21	2	2002.11	4.4	0	37	16	95.00%	M.VASSTVPSVASIFAPESLLK.K		-.MVASSTVPSVASIFAPESLLK.K
168	182	2	1523.86	4.4	1	56.2	15.9	95.00%	R.IPLSDNAIIEAALGK.Y		R.IPLSDNAIIEAALGK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
208	PSB1_SCHPO	18.67%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
186	197	2	1267.61	4.3	1	55.9	24.9	95.00%	K.ITTDAFTSAGER.H		K.ITTDAFTSAGER.H
141	170	4	3152.54	-0.27	1	20.9	23.7	95.00%	R.AGGSAANFITPFLDNQVNLHNQYVPGSHGK.E		R.AGGSAANFITPFLDNQVNLHNQYVPGSHGK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
209	PUR2_SCHPO	4.31%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
678	693	3	1606.82	-1.6	0	23.1	23	94.00%	K.GMAHITGGGLVENVPR.M		K.GMAHITGGGLVENVPR.M
31	48	2	1678.78	1.8	0	54.6	26.3	95.00%	K.VYVAPGNGGTASNGAESK.M	Deamidation (+1)	K.VYVAPGNGGTASNGAESK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
210	LYS4_SCHPO	4.30%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
149	159	2	1179.57	4.4	1	26	24.9	92.20%	K.GQGIDFYPAGR.G		K.GQGIDFYPAGR.G
470	489	2	1872.04	4.8	0	47.2	15.2	95.00%	R.EALAYLASPAVVAASAIAGK.I		R.EALAYLASPAVVAASAIAGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
211	MUG64_SCHPO	11.19%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

224	238	3	1767.86	4.9	1	44.3	25.1	95.00%	K.LDVESAKPENLEHCK.S	Carbamidomethyl (+57)	K.LDVESAKPENLEHCK.S	
108	125	2	1851.02	3.8	0	41.3	17.2	95.00%	R.NLGNLTPLEQTPLASVGK.N		R.NLGNLTPLEQTPLASVGK.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
212	P5CR_SCHPO	15.25%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
116	129	2	1566.76	5	1	85.9	25.3	95.00%	K.TISSLQSMLDESTR.V		K.TISSLQSMLDESTR.V
70	98	3	3111.57	2.6	1	41.3	22.4	95.00%	K.ENAEMAAISNVLLLSCKPQAAEDVLNSPK.M	Carbamidomethyl (+57)	K.ENAEMAAISNVLLLSCKPQAAEDVLNSPK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
213	ACAC_SCHPO	1.49%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1972	1994	3	2667.36	3.2	1	27.8	21.1	95.00%	K.TAQAINDFNHGEQLPLFILANWR.G		K.TAQAINDFNHGEQLPLFILANWR.G
197	207	2	1131.63	6.1	0	34.7	18.8	95.00%	K.ISSTIVAQSAR.V		K.ISSTIVAQSAR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
214	EIF3E_SCHPO	6.59%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
267	284	3	2029.08	4.4	0	22.1	19.4	92.50%	R.YLTVAVVTNQNNANQKPR.N		R.YLTVAVVTNQNNANQKPR.N
477	491	2	1679.84	3.6	0	46.3	24.2	95.00%	K.SLSFESQNLEQSLAK.S		K.SLSFESQNLEQSLAK.S

Supplementary Table S2: All "Scaffold" validated proteins and peptides identified from solprotSP (*S.pombe*) and from SCVMprot (*S.cerevisiae*) samples

***S.cervisiae* - Trypsin - Whole tryptic digest**

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
1	A6ZPV7_YEAS7	41.19%	100%	32							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
150	166	2	2070.07	-1	1	37.1	26	95.00%	R.LDSKPFFKENYDELVVK.I		
310	320	2	1254.66	-0.57	1	61	25	95.00%	K.GKYTVDQVFAK.M		
429	442	2	1679.86	-0.66	0	82.3	26.6	95.00%	K.LQTQLGQEPPEWVR.E		
201	212	2	1513.76	-0.8	0	50.2	28.2	95.00%	K.YWVHPDNITELK.L		
74	86	2	1578.85	-1.3	1	72.5	23.4	95.00%	R.VKEVQEQVQHTVR.L		
324	348	3	2876.46	-0.62	1	75.4	27	95.00%	K.EGKKPMNEIENLEALASEIQYVMLK.K		
362	371	2	1074.55	0.99	0	43.2	26.9	95.00%	R.TAFQLPGDAR.V		
443	455	2	1402.78	-0.086	0	69.7	23	95.00%	R.ELVGSHLVEPVPK.F		
327	348	2	2562.31	-0.043	0	87.8	27.1	95.00%	K.KPMNEIENLEALASEIQYVMLK.K		
576	594	2	2355.09	0.25	0	73	30.9	95.00%	K.YYEIVAFFDHYFNGDQISK.I		
401	410	2	1176.58	-0.79	0	37.5	27.5	95.00%	R.TDIGVDWPFK.Q		
598	606	2	1037.52	0.65	0	36.2	26.8	95.00%	K.GTTFDTQIR.A		
312	320	2	1069.54	-0.76	0	34.7	25.7	95.00%	K.YTVDQVFAK.M		
119	129	3	1359.69	-0.14	1	24.3	27.4	90.30%	K.FSRLNYTGFQK.I		
301	309	3	1156.6	0.86	1	29.1	25.2	95.00%	K.ERHVNDFLK.G		
267	280	2	1676.75	-0.67	0	68.2	29.8	95.00%	R.WYGGMSTDTIFVER.K	Oxidation (+16)	
567	574	2	871.44	2.4	0	28.3	22.3	95.00%	R.NAENPISK.K		
327	349	3	2690.4	-0.48	1	69.9	24.1	95.00%	K.KPMNEIENLEALASEIQYVMLKK.K		
76	86	2	1351.69	1	0	51.3	27.6	95.00%	K.EVQEQVQHTVR.L		
282	291	2	1257.58	1	1	41.3	27.7	95.00%	K.THREDWTGEK.S		
575	594	3	2483.18	0.25	1	39.2	31.2	95.00%	K.KYYEIVAFFDHYFNGDQISK.I		
420	428	2	1064.59	2	0	47.2	23.2	95.00%	R.FPYAVLEVK.L		
138	149	3	1403.83	0.43	0	40.7	15.6	95.00%	K.TGFILKPVFQVR.L		
122	129	2	969.49	-0.013	0	43.3	24.7	95.00%	R.LNYTGFQK.I		
374	384	2	1292.66	-0.1	0	58.1	25.9	95.00%	R.ISLDTELTMVR.E	Oxidation (+16)	
14	26	2	1719.77	-0.1	0	46.5	29.6	95.00%	R.QYSYYYISYDDLK.T		
167	175	2	1077.58	0.45	0	41.3	25.9	95.00%	K.ISQLYDIAR.T		
612	622	2	1296.72	0.7	1	28.9	22.8	95.00%	K.TICVPVRVEPK.V	Carbamidomethyl (+57)	
374	393	2	2324.1	-0.14	1	40.7	30	95.00%	R.ISLDTELTMVREDNFDGVDR.T		
3	9	2	816.41	0.46	0	28.5	25.9	94.30%	K.FGEHLSK.S		
385	393	2	1065.44	0.53	0	30.6	24.7	95.00%	R.EDNFDGVDR.T		
14	35	2	2749.26	-1.2	1	53.4	30.9	95.00%	R.QYSYYYISYDDLKTELEDNLSK.N		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
2	VTC3_YEAST	57.84%	100%	48							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
7	24	2	2243.06	0.8	1	63	30.2	95.00%	K.LANDVYPPWKDSYIDYER.L		
151	166	2	1969.94	0.24	0	56	29	95.00%	K.ELPFNNSEEYSPLLYR.I		
821	835	2	1732.94	-0.24	0	25	23.2	90.50%	R.TLKPIQDFIFNLVGE.-		

227	252	3	2927.39	-0.65	0	73.2	30.2	95.00%	R.HLPALVYASVPNENDDFVDNLESDVR.V	
459	477	3	2301.09	-0.14	1	48.3	29.9	95.00%	R.NPENWHRDDIDSNIPNPLR.F	
398	413	2	1965.98	0.24	1	75.1	27.5	95.00%	K.LSRDFDNIQNFIVEEK.L	
365	372	2	1041.56	0.061	0	30.6	23.7	95.00%	K.FINNFIFK.N	
806	820	2	1637.88	-0.19	1	75.7	23.1	95.00%	R.ERGLVNVSSQPSLPR.T	
330	340	2	1329.75	-0.25	0	39.5	21.5	95.00%	K.LLDKPDIFLEK.R	
316	323	2	813.47	-0.4	0	31.9	22.4	95.00%	K.ISGAPTLR.L	
437	453	2	2010.99	-0.0046	1	61.4	27.8	95.00%	R.VTIDSNIMYIREDSLDK.N	
101	112	2	1476.65	0.68	0	71.2	29.3	95.00%	K.NTLEECLDEAQR.L	Carbamidomethyl (+57)
63	70	2	984.53	-0.21	0	27.3	22.8	94.00%	K.VYTFQISK.Y	
167	175	2	1202.63	0.24	0	55.8	25.8	95.00%	R.ISYLYEFLR.S	
487	495	2	1112.56	0.34	0	34.3	25.4	95.00%	K.FPYSVMEIK.V	
641	649	2	1038.59	0.16	1	34.2	18.9	95.00%	K.FKTNAAFLK.I	
149	166	2	2211.12	-0.82	1	105	26.8	95.00%	R.LKELPFNNSEEYSPLLYR.I	
401	413	2	1609.77	2.3	0	75.6	29	95.00%	R.DFDNIQNFIVEEK.L	
143	148	2	715.42	1.1	0	25.5	25.7	90.30%	K.SLLQVR.L	Deamidation (+1)
560	569	2	1235.53	1.6	0	37.8	26.7	95.00%	K.NPQEAYEEEK.K	
119	126	2	938.52	0.61	0	38.3	22	95.00%	R.LNFTGFIK.I	
437	447	2	1323.69	0.67	0	43.8	26.6	95.00%	R.VTIDSNIMYIR.E	
48	58	2	1265.58	1.4	0	55.2	27.6	95.00%	R.NESDFVEALDK.E	
341	358	2	2116.97	-0.35	1	84.4	29.9	95.00%	K.RTFTENTETGNSSFEEIR.L	
7	16	2	1201.61	-0.85	0	43.6	25.8	95.00%	K.LANDVYPPWK.D	
77	86	2	1203.6	0.89	1	38.6	26.9	95.00%	R.KLDDLEENTK.S	
194	206	2	1493.71	-0.55	0	51.2	28	95.00%	K.LSHFSNLEDASFK.S	
512	524	2	1464.76	-0.9	0	57.6	26.1	95.00%	K.DLTNSHLVNEVPK.F	
808	820	2	1352.74	0.73	0	52.5	22.2	95.00%	R.GLVNVSSQPSLPR.T	
265	282	2	1849.83	-0.0019	0	91.9	29.5	95.00%	K.SNSLSSDGNSNQDVEIGK.S	
591	601	2	1201.63	-1.4	1	29.4	26.1	95.00%	K.ISVPDGKTTER.Q	
699	705	2	886.47	-0.031	0	25.2	23.3	90.90%	K.VWLANER.T	
525	541	2	1887.93	0.73	0	63.2	28.7	95.00%	K.FSLYLQGVASLFGEDDK.Y	
39	58	3	2299.02	-0.44	1	54.4	30.7	95.00%	R.SSVDSWSERNESDFVEALDK.E	
210	221	2	1531.71	-1.1	0	45.1	29.3	95.00%	K.FWVHDDNIMEVK.A	
101	118	3	2237	0.72	1	37.4	30.9	95.00%	K.NTLEECLDEAQRLDNFDR.L	Carbamidomethyl (+57)
643	649	2	763.42	1	0	26.4	24.4	92.90%	K.TNAAFLK.I	
28	38	2	1265.71	-0.57	1	64.2	22.4	95.00%	K.LLKESVIHDGR.S	
17	24	2	1059.45	0.65	0	29	26.3	94.40%	K.DSYIDYER.L	
326	340	3	1814.04	0.99	1	23	18.6	92.10%	R.WIGKLLDKPDIFLEK.R	
379	386	2	1032.57	0.38	0	33.9	22.7	95.00%	K.NYLINQLR.E	
542	559	2	2231.2	0.033	1	71.2	22.7	95.00%	K.YVNILPFWLPDLETDIRK.N	
39	47	2	1051.46	0.65	0	32.4	25.6	95.00%	R.SSVDSWSER.N	
655	681	2	2853.25	-1.6	0	56.8	31.2	95.00%	K.NISENGNDPYSDDTDSASSFQLPPGVK.K	
425	436	2	1331.68	-0.39	0	43	26.9	95.00%	R.TAFQIPGDQSIR.V	
591	597	2	714.39	2.1	0	25.8	20	91.90%	K.ISVPDGK.T	
496	511	2	1977.92	-0.35	0	78.6	29.6	95.00%	K.VINQDNSQMPNYEWIK.D	
342	358	2	1960.86	-0.53	0	83.2	30.3	95.00%	R.TFTENTETGNSSFEEIR.L	

Index AC Coverage Scaffold probability Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
3	PMA1_YEAST	41.72%	100%	30							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
253	271	2	2012.97	-0.26	1	77.7	28.6	95.00%	K.RGEGFMVVTATGDNTFVGR.A		
388	414	3	2960.42	-0.43	0	46.9	30.4	95.00%	K.LSLHEPYTVEGVSPDDLMLTACLAASR.K	Oxidation (+16)/ Carbamidomethyl (+57)	
458	469	2	1271.64	-0.1	0	48.2	27.3	95.00%	K.VTAVVESPEGER.I		
175	184	2	1056.63	0.26	0	70	21.2	95.00%	K.TLANTAVVIR.D		
644	659	2	1544.78	-0.28	1	105	27	95.00%	K.KADTGIAVEGATDAAR.S		
502	508	2	744.41	1.4	0	34.7	28.3	95.00%	K.VAELASR.G		
483	501	2	2293.01	-0.099	0	74.9	31	95.00%	K.TVEEDHPIPEDVHENYENK.V		
417	424	2	858.48	0.55	1	27.3	25.2	93.80%	K.KGLDAIDK.A		
584	615	3	3260.51	-0.56	0	92.7	30.6	95.00%	R.LGLGGGGDMPGSELADFVENADGFAEVFPQHK.Y		
616	625	2	1288.72	-0.55	1	29.5	22.6	95.00%	K.YRVVEILQNR.G		
240	252	2	1455.66	-0.55	0	74.8	28.6	95.00%	K.HYGDQTFSSSTVK.R		
899	909	2	1283.56	0.61	0	65.3	27.3	95.00%	R.SVEDFMAAMQR.V		
475	482	2	843.52	1.5	0	25.8	23.3	92.00%	K.GAPLFVLK.T		
457	469	2	1399.73	0.19	1	78.8	25.7	95.00%	K.KVTAVVESPEGER.I		
185	215	3	3258.66	-0.15	0	42	25.9	95.00%	R.DGQLVEIPANEVVPGDILQLEDGTVIPTDGR.I		
216	239	2	2651.3	-0.37	0	100	29.6	95.00%	R.IVTEDCFLQIDQSAITGESLAVDK.H	Carbamidomethyl (+57)	
483	508	3	3019.41	-1.3	1	55.4	30.6	95.00%	K.TVEEDHPIPEDVHENYENKVAELASR.G		
660	679	2	1984.12	-0.37	0	49	19.6	95.00%	R.SAADIVFLAPGLSAIIDALK.T		
556	566	2	1074.57	-0.48	0	68.1	25.3	95.00%	K.MLTGDAVGIAK.E		
618	625	2	969.56	1.7	0	36.1	21	95.00%	R.VVEILQNR.G		
571	583	2	1447.74	0.68	0	84.7	27.4	95.00%	R.QLGLGTNIYNAER.L		
443	456	2	1704.89	0.1	1	41.2	25.6	95.00%	K.YKVLEFHPFDPVSK.K		
363	379	2	1803.93	-0.1	0	62.3	26.4	95.00%	K.LSAIESLAGVEILCSDK.T	Carbamidomethyl (+57)	
100	109	2	1167.52	0.25	0	33.7	28.1	95.00%	K.YGLNQMADEK.E		
645	659	2	1416.68	-0.87	0	88.8	27.8	95.00%	K.ADTGIAVEGATDAAR.S		
626	643	2	1806.88	-0.45	0	94.4	28.6	95.00%	R.GYLVAMTGDGVNDAPSLK.K		
175	215	3	4297.28	0.44	1	45.7	25.2	95.00%	K.TLANTAVVIRDGQLVEIPANEVVPGDILQLEDGTVIPTDGR.I		
418	428	2	1189.67	-0.45	1	46.2	23	95.00%	K.GLDAIDKAFLK.S		
388	415	3	3072.52	-0.7	1	46.3	27.8	95.00%	K.LSLHEPYTVEGVSPDDLMLTACLAASRK.K	Carbamidomethyl (+57)	
2	28	3	2720.24	0.54	0	62.8	30.8	95.00%	M.TDTSSSSSSSSASSVSAHQPTQEKPAK.T	Acetyl (+42)	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
4	YBT1_YEAST	31.73%	100%	49							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
118	130	2	1403.71	-0.87	0	56.8	26.4	95.00%	K.VNGEPHGTPEIVR.R		
1616	1627	2	1490.74	0.26	0	44.7	27.6	95.00%	K.EYDHPYSLLLNK.Q		
1457	1473	2	1830.01	-0.44	0	57.2	20.3	95.00%	R.SITIIPQDPTLFSGTIK.T		
670	680	2	1321.62	0.51	0	45.7	27.4	95.00%	R.VQDFLNENDTK.K		
228	240	3	1519.83	0.73	0	25.5	24.1	94.80%	R.SIFIHHINSPISR.K		
1584	1596	2	1471.78	-0.15	0	57.2	25.5	95.00%	K.EFQGSTILTIAHR.L		

901	912	2	1326.71	-0.47	0	74.2	24.2	95.00%	R.NAELVVLLEDGR.V	
588	597	2	1216.65	0.15	0	34.8	26	95.00%	R.ENELSLLLMR.S	
115	130	3	1718.89	-0.3	1	31.2	25.5	95.00%	K.SVKVNGEPHGTPEIVR.R	Deamidation (+1)
936	951	2	1748.78	-0.79	1	41	29.1	95.00%	K.SSILSRANSSANLAAK.S	Phospho (+80)/ Phospho (+80)
1422	1430	2	1020.6	0.17	0	49.3	18.8	95.00%	K.STIITALFR.F	
1431	1440	3	1169.61	-0.26	0	33.2	25.6	95.00%	R.FLEPETGHIK.I	
1525	1544	2	2123.01	0.091	0	128	29.5	95.00%	K.FLDLSSEISEGGSNLSQGQR.Q	
1599	1615	3	1893.97	-1.2	1	27	26.6	94.70%	R.SVIDYDKILVMDAGEVK.E	
1583	1596	3	1599.87	-0.061	1	46.9	23.3	95.00%	R.KEFQGSTILTIAHR.L	
1494	1508	2	1684.87	-0.3	0	74.9	26	95.00%	R.VNLISEEQLQQGATR.E	
14	25	2	1595.7	-0.95	0	62	29.3	95.00%	R.FWFYDDVTQYGR.T	
926	935	2	1105.57	0.97	0	31.2	26.3	95.00%	K.GLFGEDELVK.S	
1559	1576	2	1923.97	0.36	0	103	27.5	95.00%	K.IILLDEATASIDYSSDAK.I	
1353	1368	3	2064.95	0.1	1	41.6	30.3	95.00%	R.VKEYMEIEQEPYNEHK.E	
1381	1389	2	1057.58	1.3	0	48.7	25.4	95.00%	K.IEVNDLSLR.Y	
665	680	2	1891.93	0.042	1	60.1	28.2	95.00%	K.VSLDRVQDFLNENDTK.K	
913	925	2	1485.75	-0.75	1	46.5	26.6	95.00%	R.VKDQGDPIDMLQK.G	
952	963	2	1202.65	-0.011	0	49.2	25.5	95.00%	K.SSTSLSNLPAVK.E	
582	597	2	1929.04	-0.17	1	43.6	23	95.00%	K.DINTIRENELSLLLMR.S	
1493	1508	2	1840.98	-0.22	1	70.3	24.9	95.00%	K.RVNLISEEQLQQGATR.E	
887	900	3	1609.9	0.4	0	39.1	20.5	95.00%	R.TCILVSHNIALTLR.N	Carbamidomethyl (+57)
915	925	2	1258.59	0.55	0	42.1	27.6	95.00%	K.DQGDPIDMLQK.G	
427	436	2	1165.66	-0.61	0	36.2	19.2	95.00%	K.SIIISEIYTK.A	
791	803	2	1535.73	-1.4	0	64.7	28.4	95.00%	K.NNILFNSPFNEAR.Y	Deamidation (+1)
964	979	2	1816.83	-0.89	0	67.9	29.8	95.00%	K.EQQVSVNNNSSHFEAK.K	
1417	1430	3	1434.82	-0.42	1	27.4	21	95.00%	R.TGAGKSTIITALFR.F	
694	705	2	1443.67	0.12	0	88.1	28.7	95.00%	R.FAFENSTISWDK.D	
1238	1255	2	2047.08	0.73	0	77	25.7	95.00%	R.SPIYQHFSETLVGVTTIR.A	
560	568	2	1060.57	-0.69	0	56.9	26.2	95.00%	K.LNEAFQAIR.I	
1152	1160	2	1010.48	0.36	0	38.1	28.5	95.00%	R.FFDATPTGR.I	
1606	1627	3	2546.31	-0.78	1	36.6	26.2	95.00%	K.ILVMDAGEVKEYDHPYSLLLNK.Q	
572	581	2	1377.59	-0.023	0	48.9	29	95.00%	K.YFSWEENFEK.D	
1486	1492	2	847.48	1.2	0	31.5	23.6	95.00%	R.QIFEALK.R	
1441	1453	2	1456.75	-1.5	0	97.7	25.8	95.00%	K.IDNIDISGVDLQR.L	
1456	1473	2	1986.11	-1.3	1	79.9	19.3	95.00%	R.RSITIIPQDPTLFSGTIK.T	
822	831	2	1031.51	0.85	0	47.9	27	95.00%	K.AGDLTEIGEK.G	
1474	1485	2	1470.63	-0.56	0	61.9	28.4	95.00%	K.TNLDPYDEFSDR.Q	
1431	1453	3	2608.35	-0.27	1	43.2	25	95.00%	R.FLEPETGHIKIDNIDISGVDLQR.L	
1400	1410	2	1180.57	0.41	0	30.9	26.4	95.00%	K.NVSFSVDAQSK.I	
447	461	3	1741.81	-0.23	0	31.8	29.4	95.00%	K.TKPSNEDPQEINDQK.S	
681	693	2	1532.76	-1.5	1	65.4	27.1	95.00%	K.KYDQLTIDPNGNR.F	
557	568	2	1429.8	0.12	1	57.1	22.6	95.00%	R.IQKLNEAFQAIR.I	
855	886	3	3702.68	0.4	0	65.1	31.9	95.00%	R.HVLLDDCLSAVDSHTASWIYDNCITGPLMEDR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
5	A6ZPA7_YEAS7	37.02%	100%	27

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
334	352	3	2164.2	0.23	1	48	19.8	95.00%	K.ILIAEGWIPRDELATLQAR.L	

305	317	2	1651.78	-0.92	1	54.9	28.9	95.00%	K.ELDSWFQDVTREK.A	
2	10	2	1133.57	0.78	1	58.8	26.7	95.00%	M.AEKEEAIFR.S	Acetyl (+42)
194	205	2	1470.82	-0.69	1	74.5	23.6	95.00%	R.DKVATLEQILWR.V	
196	205	2	1227.7	-0.014	0	46.3	23.1	95.00%	K.VATLEQILWR.V	
11	27	2	1981	0.15	0	69.3	26.8	95.00%	R.SAEMALVQFYIPQEISR.D	
121	135	2	1759.87	-0.17	0	73.7	27.5	95.00%	R.LIQMEDATDQIEVQK.N	
121	142	2	2678.29	-0.26	1	93	28.7	95.00%	R.LIQMEDATDQIEVQKNDLEQYR.F	
54	60	2	877.47	0.31	0	39.4	26.5	95.00%	R.TFVNEIR.R	
360	382	4	2569.37	0.48	0	18.3	24.6	94.20%	R.LGIDVPSIIQVLDTNHTPPTFHR.T	
386	403	2	2155.95	-0.11	0	90.3	30.2	95.00%	K.FTAGFQSICDCYGIAQYR.E	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
28	42	3	1666.87	0.79	0	59.7	26	95.00%	R.DSAYTLGQLGLVQFR.D	
809	825	2	2038.97	-0.17	0	52	29.5	95.00%	K.FFVGEGLPYEPFAFEYK.D	
383	403	3	2499.13	-0.41	1	62.1	31.2	95.00%	R.TNKFTAGFQSICDCYGIAQYR.E	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
251	270	2	2195.04	0.49	1	125	30	95.00%	R.KIAESLDANLYDVDSSNEGR.S	
209	214	2	724.39	0.78	0	31.3	24	95.00%	R.GNLFFK.T	
280	289	2	1164.64	0.25	0	44.7	22.1	95.00%	K.NLSDLYTVLK.T	
234	248	3	1728.97	0.63	1	41.1	20.4	95.00%	K.NAFIVFSHGDLIIKR.I	
113	120	2	980.46	-0.024	0	52.5	26.3	95.00%	R.NASYLEER.L	
305	315	2	1394.65	-0.087	0	65	28.1	95.00%	K.ELDSWFQDVTR.E	
143	154	2	1442.75	0.74	0	41.7	26.6	95.00%	R.FILQSGDEFFLK.G	
215	226	2	1418.73	0.13	0	71.3	26.5	95.00%	K.TVEIEQPVYDVK.T	
91	112	2	2400.15	0.29	0	45.5	29.5	95.00%	K.YLDGSGELYVPPSGSVIDDYVR.N	
252	270	2	2066.94	-0.93	0	130	29.8	95.00%	K.IAESLDANLYDVDSSNEGR.S	
290	304	2	1626.84	0.053	0	54.1	26.5	95.00%	K.TTSTTLESELYAIAK.E	
83	112	3	3321.56	0.069	1	54.7	30	95.00%	K.LYEGDTDKYLDGSGELYVPPSGSVIDDYVR.N	
318	325	2	946.55	-0.031	0	49.3	21.9	95.00%	K.AIFEILNK.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
6	A7A234_YEAS7	43.84%	100%	38

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
500	515	4	1888.99	-0.031	1	33.3	25.1	95.00%	K.KHGQWLNDLTNSHLVK.E	
394	401	2	1001.53	2	0	29.4	26.9	94.20%	K.NELQPVFR.T	
94	102	2	1005.49	-0.03	0	50.7	27	95.00%	K.ALDADAFQR.V	
501	515	3	1760.9	0.52	0	40.8	26.8	95.00%	K.HGQWLNDLTNSHLVK.E	
407	418	2	1359.71	-0.24	1	35.9	25.9	95.00%	R.TAFQIPGDDKIR.V	
380	401	3	2707.39	0.59	1	49.6	25.5	95.00%	R.LEEDFSEIQNFIIKNELQPVFR.T	
7	16	2	1215.63	0.47	0	45.5	25.8	95.00%	K.LANEVYPPWK.G	
750	757	2	1026.59	1.1	1	33.6	21.8	95.00%	K.RVDIIQQR.S	
144	149	2	715.42	1.1	0	25.5	25.7	90.30%	K.SLLEVR.L	
150	166	2	2060.06	-0.25	1	76.6	26.4	95.00%	R.LKELPSHSEEYSPLLYR.I	
347	358	2	1413.73	-0.73	1	49	26.3	95.00%	K.FINGFIFEGDKK.F	
17	26	2	1142.56	-0.36	0	45.8	25.4	95.00%	K.GSYINYEGLK.K	
469	477	2	1112.56	0.34	0	34.3	25.4	95.00%	K.FPYSVMEIK.V	
103	119	2	2021.03	-0.21	1	81.7	26.7	95.00%	R.VLEELLSESTELDNFKR.L	

152	166	3	1818.88	0.94	0	26.8	28.2	92.80%	K.ELPSHSEEYSPLLYR.I	
347	357	2	1285.64	0.9	0	59.3	27.3	95.00%	K.FINGFIFEGDK.K	
53	63	2	1377.7	-0.24	1	51.3	26.4	95.00%	K.FVEELDKELEK.V	
480	496	2	1745.78	-0.92	0	76.4	30.5	95.00%	K.SSLDSSMSASSMISNVK.L	Oxidation (+16)
103	118	2	1864.93	-0.71	0	76.9	27.7	95.00%	R.VLEELLSESTELDNFK.R	
306	322	3	2045.1	0.44	1	34	23.4	95.00%	R.LRWTGQLSDKPDIFLEK.K	
72	78	2	938.43	0.94	0	35.9	27.2	95.00%	K.YNNLMER.L	
191	204	2	1659.76	-0.14	0	69.9	28.6	95.00%	K.FSSIVSNDIDMNFR.S	Oxidation (+16)
308	322	2	1775.91	-0.29	0	52.3	26.4	95.00%	R.WTGQLSDKPDIFLEK.K	
208	219	2	1530.73	-0.73	0	47.6	28.4	95.00%	K.FWVHNDNLMEVK.T	
480	499	2	2068.02	-1.3	1	55.8	28.3	95.00%	K.SSLDSSMSASSMISNVKLPK.K	
407	416	2	1090.53	0.98	0	42.7	27.1	95.00%	R.TAFQIPGDDK.I	
436	447	2	1575.8	-1.1	1	28.2	27	92.50%	R.ERPIRDPNTWHR.T	
273	294	3	2733.26	-0.4	0	65.5	31.4	95.00%	R.SFDPLINTLYFDNEHFELYNDK.L	
176	190	2	1522.73	-0.41	0	102	28.5	95.00%	R.SNFNTASEPLASASK.F	
17	27	2	1270.66	-0.64	1	39.1	26.1	95.00%	K.GSYINYEGLKK.F	
448	459	2	1269.66	0.3	0	64.7	25.9	95.00%	R.TDIDANVANPLK.F	
687	693	2	886.47	-0.031	0	25.2	23.3	90.90%	K.VWLANER.T	
45	59	2	1840.8	-0.4	1	115	29.3	95.00%	R.WDDSDESKFVEELDK.E	
795	807	2	1594.83	-0.89	0	61.3	25.5	95.00%	R.QELQIQNLEVPER.I	
795	821	3	3305.81	-0.24	1	31.9	21.4	95.00%	R.QELQIQNLEVPERIPEVLRPLQNYLFK.L	
587	603	2	1946.91	0.2	0	81.9	29.4	95.00%	K.EPQHQAAVPVSQEENER.I	
298	305	2	870.49	1.7	0	25.7	20.3	91.80%	K.LNSAPTLR.L	
582	603	2	2502.24	-1.2	1	73.1	27.8	95.00%	R.LSNLKEPQHQAAVPVSQEENER.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
7	B3LLD7_YEAS1	31.86%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
481	492	2	1085.55	3	0	53.4	25.7	95.00%	R.STAHGISAASGK.V	
48	64	2	1933.95	1.5	0	94.3	28.9	95.00%	R.LALESIDNEGFGWQQVK.T	Deamidation (+1)
481	512	4	3160.64	-0.17	1	58.6	23.4	95.00%	R.STAHGISAASGKVGAIIAQTALGTLIDHNCAR.D	Carbamidomethyl (+57)
109	131	2	2280.21	0.78	0	108	24.1	95.00%	K.VSTSVGTVIGQFGFGTLADIVGR.K	
548	569	2	2659.31	0.063	1	76.8	28.2	95.00%	R.KTLEEINELYHDEIDPATLNFR.N	
47	64	2	2090.04	-0.017	1	101	27.9	95.00%	R.RLALESIDNEGFGWQQVK.T	Deamidation (+1)
298	314	2	1942.9	-0.68	1	117	29.7	95.00%	K.KIHDTSDEDMAINGLER.A	
315	328	2	1464.72	-1	0	66.2	27.1	95.00%	R.ASTAVESLDNHPPK.A	
19	45	3	3142.43	-0.51	0	49.2	31	95.00%	K.EHLTEGGNMAFHNHLNDFAHIEDPLER.R	
299	314	2	1814.81	0.15	0	81.5	29.7	95.00%	K.IHDTSDEDMAINGLER.A	
549	569	2	2531.22	-1.1	0	85.7	29.6	95.00%	K.TLEEINELYHDEIDPATLNFR.N	
493	512	2	2093.1	-0.95	0	100	23.8	95.00%	K.VGAIIAQTALGTLIDHNCAR.D	Carbamidomethyl (+57)
572	587	2	1754.77	0.85	0	99.7	29.5	95.00%	K.NNDIESSSPSQLQHEA.-	
284	297	2	1471.72	0.94	0	87.3	28	95.00%	K.LELAAAAQEQDGEK.K	
315	332	3	1977.92	-0.12	1	28.5	29.7	93.00%	R.ASTAVESLDNHPPKASFK.D	Phospho (+80)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
8	A7A1M1_YEAS7	28.84%	100%	40							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
966	988	3	2633.33	-0.076	1	42.8	27.1	95.00%	K.LLYRVENPEIVQMFGGNAEGLER.E		
1024	1046	2	2644.25	-0.54	0	74	29.9	95.00%	R.AYPDLQIAYLDEEPPLTEGEEPR.I		
1047	1063	2	1944.94	-0.093	0	58.2	28.6	95.00%	R.IYSALIDGHCEILDNGR.R	Carbamidomethyl (+57)	
1779	1788	2	1213.72	-0.84	0	34.5	19.9	95.00%	R.QIRPPIYSLK.Q		
859	869	2	1406.68	-0.52	1	41.8	27.6	95.00%	R.EIIREDDQFSR.V		
819	852	3	3814.93	1.5	0	60.3	26.1	95.00%	R.ISFFAQSLSTPIPEPLPVDNMPTFTVLTPHYAER.I		
1139	1154	2	1783.88	-0.74	0	68.1	27.2	95.00%	R.YEEQTTNHPVAIVGAR.E		
1010	1023	3	1741.92	0.16	0	45.5	25	95.00%	K.FKPHELENAEFLLR.A		
260	288	3	3237.43	-0.22	1	80.4	32.1	95.00%	K.AMEEANPEDTEETLNKIEGDNSLEAADFR.W		
1117	1138	2	2473.25	-0.62	0	79	26.9	95.00%	R.SVLAEFEELNVEQVNPYAPGLR.Y		
792	811	2	2407.08	-0.15	0	87	30.7	95.00%	R.APTFFVSQDDNNFETEFFPR.D		
970	992	3	2587.26	-0.54	1	47.4	29	95.00%	R.VENPEIVQMFGGNAEGLERELEK.M		
387	405	2	2240.12	-0.093	0	71.6	28.2	95.00%	K.IVGYDDLNQLFWYPEGIAK.I		
775	787	2	1511.8	-0.6	0	50.6	25	95.00%	K.LLYHQVPSEIEGK.R		
426	437	2	1438.71	-0.99	0	49.1	27.7	95.00%	R.LGDVVWDDVFFK.T		
1262	1273	2	1248.6	-0.33	0	89.3	27.9	95.00%	K.IGAGMGEQMLSR.E		
893	915	2	2536.18	-1.7	1	94.3	30.9	95.00%	K.ILAEETAAYEGNENEAEKEDALK.S		
970	988	2	2088	0.32	0	88.9	29	95.00%	R.VENPEIVQMFGGNAEGLER.E		
1083	1094	2	1476.71	-0.48	0	28	28.2	90.10%	K.SDNQNHALIFYR.G		
1173	1182	2	1168.59	-0.63	0	40.8	25.9	95.00%	K.EQTFGTLFAR.T		
658	670	2	1628.71	-0.52	0	64.8	29	95.00%	R.CTGEYWWGAVLCK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	
789	811	3	2777.31	-0.16	1	50.7	30.5	95.00%	R.TLRAPTFFVSQDDNNFETEFFPR.D		
1191	1207	2	2019.96	-0.61	0	60.7	28.9	95.00%	K.LHYGHPDFINATFMTTR.G		
1155	1182	3	3005.48	-0.034	1	58.1	28.5	95.00%	R.EYIFSENSGVLGDVAAGKEQTFGTLFAR.T		
1436	1444	2	1094.61	-0.2	0	48.5	20.8	95.00%	R.IPFSILYSR.F		
1117	1154	4	4239.12	-1.1	1	27.7	26.3	95.00%	R.SVLAEFEELNVEQVNPYAPGLRYEEQTTNHPVAIVGAR.E		
1095	1114	2	2427.13	-0.52	0	84.1	30	95.00%	R.GEYIQLIDANQDNYLEECLK.I	Carbamidomethyl (+57)	
1070	1082	2	1296.7	-0.0085	0	62.1	22.4	95.00%	R.VQLSGNPILGDGK.S		
775	788	3	1667.9	0.13	1	42.1	24.1	95.00%	K.LLYHQVPSEIEGKR.T		
331	344	2	1737.78	-0.023	0	107	28.8	95.00%	K.CALDYLDSPLCQQR.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	
184	196	2	1623.75	-0.63	0	69.7	28.8	95.00%	R.NMFDHFMVLLDSR.S		
916	929	2	1701.81	-0.64	0	65	28.2	95.00%	K.SQIDDLPFYCIGFK.S	Carbamidomethyl (+57)	
1717	1728	2	1383.61	-0.15	0	66	28	95.00%	K.GMGYMAWTQPSR.E		
383	405	3	2734.34	-0.18	1	46.5	28.3	95.00%	R.DHNKIVGYDDLNQLFWYPEGIAK.I		

1155	1172	2	1854.9	-0.98	0	76.5	29.2	95.00%	R.EYIFSENSGVLGDVAAGK.E	
200	222	3	2479.17	-0.88	0	37.7	30.6	95.00%	R.MSPDQALLSLHADYIGGDTANYK.K	
1520	1527	2	993.5	-0.11	0	40.9	25.7	95.00%	R.NSWIGYVR.M	
953	962	2	1174.54	-0.35	0	46.5	27	95.00%	R.TISGFMNYSR.A	
406	422	3	1966.1	-0.36	1	32.1	20.8	95.00%	K.IVLEDGTKLIELPLEER.Y	
870	877	2	977.58	-0.012	0	44.9	15.1	95.00%	R.VTLLEYLK.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
9	B3LFI5_YEAS1	52.83%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
427	438	2	1511.83	-1	1	43.3	23.1	95.00%	K.IENFIKHEILEK.D	
302	309	2	799.48	-0.03	0	33.6	23.1	95.00%	K.VALGALEK.A	
172	187	2	1765.83	-0.18	0	69.4	28.8	95.00%	R.ITDATPASFSSHVDYR.W	
467	474	2	980.48	1.5	0	30.4	28	94.10%	K.LNDMVSFR.A	
239	256	2	2092.98	-0.099	1	54.7	29.8	95.00%	R.DLIDEAQSNGWQYVGDRK.N	
475	498	3	2643.32	-0.18	1	50.8	27.6	95.00%	R.AQIGWTTHGHSAVDVNIYAYANKK.A	
136	158	2	2448.2	0.17	0	45.1	28.5	95.00%	K.SYNGAIGVDPHHRPCGTVLEAAK.L	Carbamidomethyl (+57)
159	171	2	1362.79	-0.15	0	81.9	18.7	95.00%	K.LAGYLTGLVVTTR.I	
206	215	2	1015.55	1.6	0	58.9	26.2	95.00%	R.VVDLLMGGGR.S	
67	86	3	2140.08	-0.047	1	47.5	27	95.00%	K.KNVIFFVTDGMGPASLSMAR.S	
329	343	2	1643.78	0.54	0	47.3	28.9	95.00%	R.IDHAGHQNDPASQVR.E	
188	205	2	2125.06	-0.99	0	73.5	28.3	95.00%	R.WQEDLIATHQLGEYPLGR.V	
1	12	3	1430.66	-0.061	0	39.2	29.1	95.00%	-.MMTHTLPSEQTR.L	
68	86	2	2027.98	-1.7	0	104	29.5	95.00%	K.NVIFFVTDGMGPASLSMAR.S	Oxidation (+16)
413	426	3	1552.8	0.32	1	40.5	25.9	95.00%	K.LVDFVHEHKGASSK.I	
316	328	2	1457.66	-0.64	0	38.8	28.2	95.00%	K.DSNGFFLMVEGSR.I	
113	135	3	2299.11	-0.12	1	26.2	29.1	90.60%	R.TRSSDSLVTDSAAGATAFACALK.S	Carbamidomethyl (+57)
541	566	3	3113.31	-1.3	0	28.8	31.8	90.40%	K.HTSDFDATEIASEVQHYDEYYHELTN.-	
115	135	2	2041.96	-0.63	0	128	29.2	95.00%	R.SSDSLVTDSAAGATAFACALK.S	Carbamidomethyl (+57)
413	421	2	1122.58	-0.2	0	39.5	27.1	95.00%	K.LVDFVHEHK.G	
87	112	3	2981.46	1.4	0	66.2	28.7	95.00%	R.SFNQHVNDLPIDDILTLDEHFIGSSR.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
10	A6ZL63_YEAS7	61.14%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
225	253	3	3318.82	-0.36	1	29.9	21.1	95.00%	K.TLLEAIDAIEQPSRPTDKPLRLPLQDVYK.I	
85	100	2	1857.97	-1.1	1	45.7	25.5	95.00%	K.YQVTVIDAPGHRDFIK.N	
402	421	2	2310.12	-0.17	0	74.3	29	95.00%	K.FVPSKPMCVEAFSEYPPLGR.F	Carbamidomethyl (+57)
370	376	2	892.45	-0.82	0	41	23.9	95.00%	R.FDELLEK.N	
289	311	2	2549.19	-1.4	0	72.4	30.8	95.00%	K.SVEMHHEQLEQGVPGDNVGFNVK.N	

185	210	2	2923.38	-0.63	0	77.9	30.7	95.00%	K.TVPFVPISGWNGDNMIEATTNAPWYK.G	Oxidation (+16)
185	214	3	3407.63	0.41	1	39.9	29.5	95.00%	K.TVPFVPISGWNGDNMIEATTNAPWYKGWEK.E	
85	96	2	1354.7	-0.6	0	61.9	25.3	95.00%	K.YQVTVIDAPGHR.D	
165	177	2	1581.84	-1.1	1	65.4	24.5	95.00%	R.FQEIVKETSNFIK.K	
394	401	2	759.41	1.7	0	40.5	26.8	95.00%	K.SGDAALVK.F	
329	369	4	4444.12	-0.85	1	52.6	28	95.00%	K.NDPPKGCASFNATVIVLNHPGQISAGYSPVLDCHTAHIACR.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)
254	264	2	1024.61	1.8	0	68.3	17.8	95.00%	K.IGGIGTVPVGR.V	
101	129	3	2922.45	0.29	0	72.8	28.3	95.00%	K.NMITGTSQADCAILIIAGGVGEFEAGISK.D	Carbamidomethyl (+57)
429	437	2	913.56	-0.34	0	45.5	20.4	95.00%	R.QTVAVGVIK.S	
6	20	2	1559.84	-0.0025	0	81.3	24.1	95.00%	K.SHINVVVIGHVDSGK.S	
254	288	4	3451.91	-0.6	1	32.1	22.2	95.00%	K.IGGIGTVPVGRVETGVIKPGMVVTFAPAGVTTEVK.S	Oxidation (+16)
265	288	2	2429.32	-1.2	0	52.5	21.2	95.00%	R.VETGVIKPGMVVTFAPAGVTTEVK.S	
334	369	5	3892.85	-0.78	0	21.2	29.9	91.60%	K.GCASFNATVIVLNHPGQISAGYSPVLDCHTAHIACR.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)
246	253	2	974.54	-0.0093	0	40.2	23.9	95.00%	R.LPLQDVYK.I	
101	134	3	3479.7	-0.25	1	67.9	28.8	95.00%	K.NMITGTSQADCAILIIAGGVGEFEAGISKDGQTR.E	Carbamidomethyl (+57)
225	245	3	2362.29	-0.089	0	31.5	21.8	95.00%	K.TLLEAIDAIEQPSRPTDKPLR.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
11	A6ZY95_YEAS7	25.94%	100%	33

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
1251	1273	3	2569.33	-0.9	1	28	26.2	95.00%	K.SEAPLIVEGHRPPKEWPSQGDIK.F	
237	248	2	1478.81	-0.28	1	50.3	24	95.00%	K.YLVEADLYKLPR.N	
1036	1048	2	1466.72	-0.78	0	61.7	28	95.00%	R.APMTFFETTPIGR.I	
717	724	2	1063.45	1.9	0	32.1	25.1	95.00%	R.YDAEFYEK.T	
1349	1364	2	1787.94	-0.62	0	36.3	24.2	95.00%	K.LSIIPQDSQVFEGTVR.E	
237	245	2	1112.58	0.71	0	25.2	24.3	90.90%	K.YLVEADLYK.L	
790	805	3	1777	-0.45	0	52.9	18.9	95.00%	R.HLIEHVLGPNGLLHTK.T	
1365	1380	2	1975.93	-0.87	0	81.5	29.4	95.00%	R.ENIDPINQYTDEAIWR.A	
486	495	2	1141.67	0.25	0	47.6	22.6	95.00%	R.VISEILNNIK.S	
863	875	2	1399.59	1.4	0	69.6	28	95.00%	K.SNEFGDSSESSVR.E	
249	261	2	1537.76	-1.3	1	48.7	28.1	95.00%	R.NFSSEELSQKLEK.N	
1281	1290	3	1244.71	-0.078	0	59.3	21.9	95.00%	R.YRPELDLVLK.H	
1251	1264	3	1528.84	0.78	0	29.3	24.1	95.00%	K.SEAPLIVEGHRPPK.E	
1430	1446	2	1800.94	0.6	0	74.8	26.1	95.00%	K.ILVLDEATAAVDVETDK.V	
1485	1499	2	1618.78	-0.51	0	87.8	28.5	95.00%	K.VAEFDSPGQLLSDNK.S	
192	206	3	1835.99	-0.32	0	32.5	21.6	95.00%	K.KPLMPHQHIHQTLTR.R	
271	281	2	1289.62	0.94	0	53.4	27	95.00%	K.SNPSLSWAICR.T	Carbamidomethyl (+57)
771	789	2	2083.02	-0.49	0	108	28.6	95.00%	R.ADTYLLDDPLAAVDEHVAR.H	
1458	1467	3	1194.68	-0.25	1	39.9	20	95.00%	K.DRTILTIAHR.L	

1126	1143	2	1975.01	-0.82	0	78.2	26.8	95.00%	R.SPIYSHFQETLGGLATVR.G	
1347	1364	2	2053.09	-1.2	1	74	24.2	95.00%	R.HKLSIIPQDSQVFEGTVR.E	
1313	1321	2	1006.58	1.5	0	51.4	21.4	95.00%	K.SSLTLALFR.M	
249	258	2	1167.54	-0.1	0	46.1	27.9	95.00%	R.NFSSEELSQK.L	
1460	1467	2	923.56	0.52	0	30.7	17.2	95.00%	R.TILTIAHR.L	
2	11	2	1146.55	-0.31	0	39.1	26.6	95.00%	M.AGNLVSWACK.L	Acetyl (+42)/ Carbamidomethyl (+57)
1291	1301	3	1341.75	0.22	0	27	22.9	95.00%	K.HINIHIKPNEK.V	
1468	1484	2	1916	-1.8	1	71.9	26.3	95.00%	R.LNTIMDSDRIIVLDNGK.V	
1274	1280	2	900.41	2.6	0	33.3	25.2	95.00%	K.FNNYSTR.Y	
728	743	2	1718.86	-0.17	0	83	26.8	95.00%	K.ACALTIDLAILMDGDK.T	Carbamidomethyl (+57)
207	220	3	1663.84	-0.25	1	57.4	28.2	95.00%	R.RKPNPYDSANIFSR.I	
1389	1415	3	2783.31	-0.39	0	72	30.4	95.00%	K.EHVLSMSNDGLDAQLTEGGGNLSVGQR.Q	
1381	1388	2	909.53	-0.46	0	33.8	14.5	95.00%	R.ALELSHLK.E	
598	614	2	2070.01	0.71	0	76.7	28.9	95.00%	R.LFTFFTNEELQPDSVQR.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
12	B3LSE9_YEAS1	38.26%	100%	22

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
351	365	2	1634.91	0.3	0	106	20.3	95.00%	R.SSDILTVFLIDTIAK.T	
699	710	2	1380.65	-0.15	0	47.4	28.6	95.00%	K.YGMSVAPVTDWR.F	
433	448	2	1862.86	-0.07	0	98.2	29.6	95.00%	K.WEVVNGPLAFDSMENR.L	
427	448	3	2492.2	1.5	1	46.2	29.4	95.00%	K.TLTEGKWEVVNGPLAFDSMENR.L	
793	803	2	1318.67	-0.54	0	44	27.9	95.00%	R.YHNANVIVFDK.L	
117	131	2	1687.79	0.18	0	76.2	29.6	95.00%	K.SVYDDSYNSVLLEGK.T	
544	553	2	1202.67	-0.19	1	46.6	24.3	95.00%	K.ILEDYAVPRK.S	
166	177	2	1449.66	-0.83	0	49.1	28.9	95.00%	R.HSTFGSYFVYDK.S	
748	766	3	2172.04	-0.18	0	56.5	29.7	95.00%	R.FLLMHGTGDDNVHFQNSLK.F	
347	365	3	2108.14	0.19	1	39.1	22.9	95.00%	K.TTDRSSDILTVFLIDTIAK.T	
327	346	2	2113.14	0.61	0	87.6	22.7	95.00%	K.DGSLLITEVTWVGNGNVLVK.T	
557	567	2	1248.63	-0.51	1	45.6	26.6	95.00%	R.ELNLGKDEFGK.D	
265	283	2	2272.08	-0.67	0	95.1	29.9	95.00%	K.IDESEVGEFIIPYYVQDEK.D	
297	312	3	1815.86	0.45	0	30.1	29	95.00%	K.SGTPNPHAELWVYSMK.D	
470	495	3	2858.32	1.3	1	92.9	30.3	95.00%	R.SPNEIIEVTDTSEDGVYDVSFSSGRR.F	
711	719	2	1178.52	-0.098	0	49.4	27.2	95.00%	R.FYDSVYTER.Y	
72	78	2	792.45	0.98	0	26	23.8	92.20%	K.VSFSVVR.N	
222	249	3	3236.44	-0.71	0	72.6	32.3	95.00%	R.AVTNDGSSFLFNGKPDWVYEEEVFEDDK.A	
265	290	3	3176.49	-1.3	1	53.3	30.8	95.00%	K.IDESEVGEFIIPYYVQDEKDIYPEMR.S	
250	264	2	1724.86	-0.3	0	40	28.2	95.00%	K.AAWWSPTGDYLAFLK.I	
810	818	2	1066.56	-0.22	1	30.5	25.1	95.00%	K.RAFDGQFVK.-	
767	792	3	3028.45	-0.92	0	79.5	29.1	95.00%	K.FLDLLDLNGVENYDVHVFPDSDHSIR.Y	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
13	B3LS03_YEAS1	40.31%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
39	50	2	1338.64	-1.1	0	45.8	27.7	95.00%	K.DQLDFYSGGPLK.A	
300	317	2	1954.09	-0.55	0	51.5	21.4	95.00%	K.LIQSDSIPLVLASVACIR.N	Carbamidomethyl (+57)
277	290	2	1607.82	-0.19	0	108	27.5	95.00%	R.NLASDTSYQLEIVR.A	
161	174	3	1448.87	-0.066	1	39.8	13.2	95.00%	K.HKIATSGALIPLTK.L	
203	243	3	4392.22	-0.21	1	101	26.7	95.00%	K.ELVNAGAVPVLVSLLSSTDPDVQYYCTTALSNIAVDEANRK.K	Carbamidomethyl (+57)
186	202	2	1884.91	-0.54	1	74.8	29.4	95.00%	R.NATGALLNMTHSEENRK.E	
267	276	2	1158.65	-0.51	1	29.5	23.9	95.00%	R.VKCQATLALR.N	Carbamidomethyl (+57)
505	515	2	1257.63	-0.42	1	54.3	26.4	95.00%	K.NDDDIINGVRK.M	
163	174	2	1183.72	-0.35	0	66.9	18.3	95.00%	K.IATSGALIPLTK.L	
269	276	2	931.49	1.1	0	44.2	27	95.00%	K.CQATLALR.N	Carbamidomethyl (+57)
26	38	2	1462.79	-0.22	0	68.1	24	95.00%	R.EAVTLLLGYLEDK.D	
66	77	2	1249.66	2.1	0	69.5	26.3	95.00%	R.SAALAFAEITEK.Y	
371	380	2	1141.53	-0.65	0	32.6	27.4	95.00%	K.EFFESGAVEK.C	
341	359	2	2276.11	-1.5	1	65.2	28.8	95.00%	R.LLDYKDSEEIQCHAVSTLR.N	Carbamidomethyl (+57)
256	266	2	1206.59	-0.023	0	52	27.7	95.00%	K.LVSLMDSPSSR.V	Oxidation (+16)
318	340	3	2514.43	-0.32	0	35.7	16.2	95.00%	R.NISIHPLNEGLIVDAGFLKPLVR.L	
516	523	2	967.44	0.49	0	35	28	95.00%	K.MADVTFER.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
14	A6ZVC8_YEAS7	42.97%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
12	27	2	1762.88	-0.46	0	84.6	27.1	95.00%	K.TITLEVESSDTIDNVK.S	
55	72	3	2129.15	-0.51	1	52.1	22.6	95.00%	R.TLSDYNIQKESTLHLVLR.L	
64	72	2	1066.61	0.45	0	62.5	20.5	95.00%	K.ESTLHLVLR.L	
1	6	2	764.43	-0.41	0	35.4	25.9	95.00%	-.MQIFVK.T	
34	42	2	1038.51	0.94	0	39.5	28.1	95.00%	K.EGIPPDQQR.L	
55	63	2	1080.55	-0.0048	0	50.4	25.4	95.00%	R.TLSDYNIQK.E	
49	63	2	1778.88	0.17	1	45.1	28	95.00%	K.QLEDGRTLSDYNIQK.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
15	CBPS_YEAST	29.69%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
108	119	2	1391.6	1.6	0	51.9	29.6	95.00%	K.NPNPADDPDFYK.H	
279	290	2	1302.68	1.7	0	59.6	26.7	95.00%	K.DVFVATPINAEK.G	
419	431	2	1499.77	0.18	0	38.5	25.8	95.00%	R.INLHSSVAEVFER.N	
533	544	2	1331.77	0.061	0	62.1	19.4	95.00%	R.FVGSIIDIDLLK.T	
63	74	2	1433.72	-0.42	1	42.6	27.2	95.00%	K.CEKIEPLSPSFK.H	Carbamidomethyl (+57)
450	470	3	2396.22	0.46	0	57.2	25.4	95.00%	K.NGDDYIIPETELGHIDITLLR.E	
120	130	2	1526.68	-0.015	0	39.3	28.9	95.00%	K.HFYELHDYFEK.T	
522	528	2	972.47	0.61	0	33.8	27	95.00%	K.YYWNLSK.N	
258	278	2	2317.03	-0.78	0	138	30.8	95.00%	R.YGDDGIYSIIDEGEGIMEVDK.D	
361	370	2	1130.59	-0.36	0	32	26.4	95.00%	K.TILGAPFCPR.R	Carbamidomethyl (+57)
391	403	2	1314.72	1.4	0	74.9	24.6	95.00%	R.TTQAVDIINGGVK.A	
373	386	3	1700.89	0.48	1	42.5	25.6	95.00%	K.DKLVEYISNQSHLR.S	
375	386	2	1457.76	0.27	0	60.3	25.8	95.00%	K.LVEYISNQSHLR.S	
75	87	2	1506.76	-0.68	0	81.4	27.6	95.00%	K.HSVDTILHDPAFR.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
16	ATN2_YEAST	35.01%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
784	807	3	2619.28	0.034	1	38.4	28.9	95.00%	K.EASDIVLSDDNFASILNAVEEGRR.M	
582	595	2	1659.85	-0.3	1	73.1	25.3	95.00%	K.ITPLTDCDVETIRK.N	Carbamidomethyl (+57)
614	626	2	1536.74	-0.92	1	68.2	28.5	95.00%	K.SFTKDQVNDDQLK.N	
477	492	2	1696.88	-0.49	0	74.5	25.2	95.00%	K.AHGDPTEIAIQVFATK.M	
414	434	3	2458.11	-0.44	0	28.5	31.3	90.70%	R.FSPYEYSHNEDGDVGILQNFK.D	
389	413	2	2703.31	-0.31	0	88.6	29.2	95.00%	R.FGTITISNSDDPFNPNEGNVSLIPR.F	
633	660	3	2916.52	0.27	1	51.7	24.1	95.00%	R.ATAESDLVFLGLIGIYDPPRNETAGAVK.K	
924	941	3	2173.89	-0.56	1	31	30.3	95.00%	R.LGHDCDGTYNSSCRDVYR.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
661	681	4	2270.16	-0.34	1	30.8	26.1	95.00%	K.KFHQAGINVHMLTGDFVGTAK.A	
156	165	2	1055.56	0.26	0	36.5	24.3	95.00%	K.VGDTIPADLR.L	
596	606	2	1250.63	-0.17	0	44	28.3	95.00%	K.NVYSLSNEGLR.V	
353	370	3	1946.96	0.17	1	33.7	27.2	95.00%	R.KLDSLEALGAVNDICSDK.T	Carbamidomethyl (+57)
751	766	2	1697.74	-0.52	0	83.4	29	95.00%	K.FCAMTGDGVNDSPSLK.M	Carbamidomethyl (+57)
171	188	2	1950.94	-1.2	0	98.6	28.8	95.00%	K.NFDTDESLLTGESLPVSK.D	
239	253	2	1558.79	-1.4	1	77	26.7	95.00%	K.SLQGDSGLISRDPSK.S	
493	504	2	1324.64	-1.6	0	31.2	27.5	95.00%	K.MDLPHNALTGEK.S	
454	476	3	2668.28	-0.66	1	41.5	29.4	95.00%	K.WLETATLANIATVFKDDATDCWK.A	Carbamidomethyl (+57)
8	45	4	4328.99	-0.9	1	60.1	30.7	95.00%	K.ENNNEEFNAYHTLTTEEAAEFIGTSLTEGLTQDESLRR.L	
543	561	3	2352.06	-0.62	1	48.5	31.2	95.00%	K.RMSSVYYNNHNETYNIYGK.G	
254	264	2	1362.69	-0.0057	0	52.6	27.2	95.00%	K.SWLQNTWISTK.K	
124	134	2	1206.65	-0.51	0	30.2	25.7	95.00%	K.NLSSPNAHVIR.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
17	A6ZTJ2_YEAS7	20.78%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
430	439	2	1117.64	0.43	0	41.3	21.2	95.00%	K.TTLLDILAMK.R	
68	78	2	1347.55	-0.21	0	62.4	27.7	95.00%	K.QFSECNSYTGR.C	Carbamidomethyl (+57)
30	39	2	1099.52	0.88	0	36.6	25.7	95.00%	K.TPFFEGTSSK.N	
702	716	2	1689.78	-0.61	1	55.9	29.1	95.00%	R.SLLRDEEDVEGTDGR.R	
860	873	2	1681.8	-0.71	0	38.6	28.4	95.00%	R.SNNYYSPLAYYISK.I	
259	270	2	1352.57	-0.37	0	64.8	27.8	95.00%	K.GPGDFSCDLETR.Q	Carbamidomethyl (+57)
657	688	3	3467.55	-1.3	0	70.7	32.2	95.00%	R.NISDLEAGTDTNDIDNTIHQTTFTSSDGTTQR.E	
245	258	2	1537.79	-0.14	0	71.5	26.8	95.00%	K.GSIDISDFLTETIK.G	
274	295	2	2499.26	-0.65	0	75.4	27	95.00%	K.FSEPSMNDLILTVFGDPYITLK.C	
245	270	3	2872.34	0.15	1	54.1	30.4	95.00%	K.GSIDISDFLTETIKGPGDFSCDLETR.Q	Carbamidomethyl (+57)

49	67	2	2358.96	-0.55	0	44.9	30.4	95.00%	K.GNDTCPPCFNCMLPIFECK.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)
171	178	2	897.56	-0.12	0	27	17.2	93.60%	K.ILQILNGK.I	
79	111	4	3680.59	-1	1	64.3	32.2	95.00%	R.CECIEGFAGDDCSLPLCGGLSPDESGNKDRPIR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)
296	311	2	1913.79	0.19	0	69.1	30.1	95.00%	K.CESGECVHYSEIPGYK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
655	688	3	3736.74	0.11	1	75.8	30.9	95.00%	R.IRNISDLEAGTDTNDIDNTIHQTTFTSSDGTTQR.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
18	ATC2_YEAST	26.77%	100%	24

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
235	251	2	1867.81	-0.69	0	118	30.1	95.00%	K.CEADESSITGESNTIQK.F	Carbamidomethyl (+57)
432	446	2	1602.63	-0.78	0	102	27.7	95.00%	R.SCETMGSATAVCSDK.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
71	83	2	1432.73	1.2	0	27.9	26.9	92.20%	K.NAGISLPEISNYR.K	
71	84	2	1560.82	-1.2	1	29.2	25.4	95.00%	K.NAGISLPEISNYRK.T	
760	770	2	1161.61	0.59	0	34.2	26.6	95.00%	R.MVTGDNILTAK.A	
2	33	3	3644.63	1.4	1	61.3	32	95.00%	M.SRQDENSALLANNENNKPSYTGNENGVYDNFK.L	Acetyl (+42)/ Deamidation (+1)
447	459	2	1419.74	1.7	0	64.5	26.6	95.00%	K.TGTLTENVMTVVR.G	
868	887	2	2165.09	-0.66	0	80.8	26.7	95.00%	R.EASDIILMTDDFSAIVNAIK.W	
4	33	3	3358.5	0.51	0	54.8	31.7	95.00%	R.QDENSALLANNENNKPSYTGNENGVYDNFK.L	
574	583	2	1073.61	2.3	0	62.8	23.7	95.00%	K.TETALLSLAR.L	
727	741	2	1591.93	-0.13	0	49.6	15.7	95.00%	K.GLILDGLLGIQDPLR.A	
37	46	2	1137.58	2	0	31.9	27.5	95.00%	K.SQLSDLHNPK.S	
263	287	3	2779.32	0.65	1	54	29.8	95.00%	K.KFNSIDSHNHSKPLDIGDVNEDGNK.I	
584	597	2	1585.88	-0.13	0	48.8	22.7	95.00%	R.LSLGLQPGELQYLR.D	
54	64	2	1303.64	-0.32	0	47.4	27	95.00%	R.LFGYESNSLFK.Y	
711	726	2	1744.9	0.39	0	75.9	25.8	95.00%	K.DSPNIAALDLLFNSQK.G	
432	459	3	3004.36	-0.0048	1	62.2	31.4	95.00%	R.SCETMGSATAVCSDKTGTLTENVMTVVR.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
497	513	2	1902.98	0.56	0	80.2	26.7	95.00%	R.NDLLANIVLNSTAFENR.D	
831	850	2	1886.9	-0.49	0	95	29.1	95.00%	K.GMGDVVAVTGDGTNDAPALK.L	
264	287	3	2651.22	-0.64	0	62.8	30.6	95.00%	K.FNSIDSHNHSKPLDIGDVNEDGNK.I	
90	99	2	1163.52	-0.79	0	36.9	26.8	95.00%	K.NYGDNSLPER.I	
288	298	2	1221.58	-0.068	0	81.2	27.5	95.00%	K.IADCMLISGSR.I	Carbamidomethyl (+57)
1149	1173	3	2820.2	-0.29	1	83.7	31.6	95.00%	K.NHTGKHDDEEALLEESDSPESTAFY.-	
252	259	2	946.49	0.6	0	26.9	26.7	90.80%	K.FPVDNSLR.D	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
19	ATC9_YEAST	17.93%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
947	958	2	1488.65	-0.35	0	76.3	28.7	95.00%	K.TNNDDVYWSFTK.G	
1049	1065	2	1820.91	0.51	0	60.3	28.7	95.00%	R.TIMCTGDNILTAISVGR.E	Carbamidomethyl (+57)
959	970	2	1315.64	-0.53	0	45.3	27.6	95.00%	K.GAPEVISEICNK.S	Carbamidomethyl (+57)
199	221	3	2438.11	-0.16	0	60.9	30.9	95.00%	R.LGENSDTGFVYHSATHSSSSLSR.Y	
931	940	3	1282.67	-0.09	1	25	25.7	93.60%	R.SFEFLSELRR.M	
264	287	3	2825.24	-0.21	0	47.3	31.2	95.00%	R.GSFSGHDDVHNQHSEYLKPDYHEK.F	
288	300	2	1695.81	-0.53	0	63.2	28.4	95.00%	K.FYPQYAPNLHYQR.F	
890	930	5	4685.17	-1.4	1	33.1	30.8	95.00%	R.HEDDVFPENSEIIPAVVHPDSNNRENTFTDNDPHNFLGVVR.S	
823	835	2	1528.69	-0.19	0	64.3	29.1	95.00%	K.FSLNDCSSPLDFK.S	Carbamidomethyl (+57)
809	817	2	1048.56	0.54	0	76.1	26.2	95.00%	K.FGELLSDIR.Q	
94	109	2	1744.88	0.048	0	73.5	26.9	95.00%	R.LTESEPLVLSSAEQSR.S	
639	649	2	1296.68	-0.48	0	35.5	24.9	95.00%	K.SFLYNGTNIIR.A	
93	109	3	1900.99	0.0014	1	27.7	25.8	95.00%	R.RLTESEPLVLSSAEQSR.S	
1163	1177	2	1825.91	0.38	1	33.9	27.8	95.00%	R.MSPDEKHELMIQLQK.L	
1	14	2	1651.77	-0.58	0	92.7	29.2	95.00%	-.MDIPSSNQIQHGQR.S	Acetyl (+42)
851	864	2	1488.75	0.59	0	60.9	27.8	95.00%	R.SVDGNLLGDPLDFK.M	
760	768	2	1049.53	0.86	0	36.2	26.9	95.00%	K.GIFCISPTR.L	Carbamidomethyl (+57)
1113	1122	2	1087.56	0.26	0	90.7	25.5	95.00%	K.LGNNSVESLR.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
20	KTR1_YEAST	44.78%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
46	57	2	1247.6	-0.076	0	69.9	27.5	95.00%	K.YSTVLSSGSGYK.Y	
327	352	5	3083.43	-0.94	0	45.1	31.3	95.00%	R.SEIHHFGDIGYYHVPFHSCPIDTSIR.L	Carbamidomethyl (+57)
83	92	2	1137.59	-0.012	0	42.2	25.9	95.00%	R.DLYSLAESIK.S	
203	213	3	1423.64	0.17	0	52.6	28.9	95.00%	K.LHCDIDYDVFK.F	Carbamidomethyl (+57)
185	196	2	1695.71	-1.4	0	43	29.6	95.00%	R.HPLMDDYDWYWR.V	
163	172	2	1185.6	-0.0046	0	45	26.2	95.00%	R.IIYGDSISYR.H	
230	243	2	1708.83	-0.89	0	37.8	28.9	95.00%	K.EYEATIPTLWETTR.K	
364	375	2	1531.64	-0.9	0	35	27.7	95.00%	K.DFTWHSYSCTTK.F	Carbamidomethyl (+57)
310	326	2	1823.92	-4.6	0	50.8	26.8	95.00%	R.WGDAPVHSIGAALFLDR.S	
73	80	2	905.53	1.5	0	43.1	20.6	95.00%	K.ATFVTLVR.N	
289	309	3	2552.13	-0.43	1	38.9	31.6	95.00%	R.SPAYSAYFDYLDREGGFFYER.W	
138	150	2	1730.76	-0.54	0	54.5	29.8	95.00%	K.EHWSFPEWIDEEK.A	
177	184	2	1051.48	0.16	0	30.8	26.7	95.00%	R.FESGFFYR.H	
81	92	2	1407.74	-0.3	1	68.2	25.8	95.00%	R.NRDLYSLAESIK.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
21	A6ZYU5_YEAS7	29.63%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
13	35	2	2494.06	-0.52	0	88.9	30.9	95.00%	K.SSENSNADLPSNSSQVMNMPEEK.G	

279	301	2	2605.31	1.1	0	81.4	27.5	95.00%	K.VAPDHPFIQQELEVIEASVEEAR.A	
534	543	2	1117.55	-0.1	0	39.7	27.5	95.00%	K.SASWVPTSQR.G	
1	12	2	1387.66	-0.5	0	48.4	28.2	95.00%	-.MNSTPDLISPQK.S	Acetyl (+42)/ Oxidation (+16)
544	562	3	2197.97	-0.18	1	28.2	30.5	91.60%	R.GANYDADALMHDDQPFYKK.M	
259	270	2	1362.68	0.28	0	95.3	27.7	95.00%	R.YLVEAGQIDEAR.A	
515	533	2	2163.06	0.64	0	72.1	28.6	95.00%	K.GLTLEEVNDMYAEGVLPWK.S	
225	233	2	1153.52	0.85	0	47.9	28.1	95.00%	K.NYSNSVQWR.V	Deamidation (+1)
544	561	2	2069.88	0.14	0	67.7	30.5	95.00%	R.GANYDADALMHDDQPFYK.K	
36	56	2	2246.05	-0.005	0	72.5	30.1	95.00%	K.GVQDDFQAEADQVLTNPNTGK.G	
302	321	4	2111.06	0.43	1	26.6	27.8	95.00%	R.AAGSASWGELFTGKPAMFKR.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
22	A7A0C8_YEAS7	54.20%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
70	86	2	1872	-2.1	0	45.1	24.6	95.00%	K.SEELYPGRPLAIALDTK.G	
217	225	2	1001.55	-0.022	0	39	24.6	95.00%	R.TANDVLTIR.E	
50	61	2	1498.63	-0.14	0	38.7	28.2	95.00%	R.MNFSHGSYEYHK.S	
487	500	2	1340.67	-1	0	30.5	26.8	95.00%	K.AGAGHSNTLQVSTV.-	
178	194	2	1723.9	0.28	0	48.9	25.2	95.00%	K.GVNLPGTDVDLPALSEK.D	
397	409	2	1314.75	0.29	0	41.9	21.6	95.00%	K.AIIVLSTSGTTPR.L	
313	337	2	2521.17	-0.19	0	98.9	30.4	95.00%	R.AEVSDVGNAILDGADCVMLSGETAK.G	Carbamidomethyl (+57)
438	459	3	2568.22	0.03	1	41.1	29.8	95.00%	R.GVFPFVFEKEPVSDWTDDVEAR.I	
31	41	2	1226.66	-0.27	0	53.6	24.2	95.00%	K.TNNPETLVALR.K	
265	281	2	1747.97	-0.53	0	32.1	22.3	95.00%	R.GDLGIEIPAPEVLAVQK.K	
31	42	2	1354.76	-0.68	1	60.5	21.7	95.00%	K.TNNPETLVALRK.A	
241	255	2	1759.87	-0.24	0	51	27.8	95.00%	K.IENQQGVNNFDEILK.V	
69	86	3	2000.09	-0.1	1	29.9	22.1	95.00%	R.KSEELYPGRPLAIALDTK.G	
414	425	2	1500.82	-0.66	0	49.1	23.6	95.00%	K.YRPNCPIILVTR.C	Carbamidomethyl (+57)
370	394	3	2607.28	-0.83	0	40.6	28	95.00%	R.NCTPKPTSTTETVAASAVAAVFEQK.A	Carbamidomethyl (+57)
241	264	3	2688.35	-0.33	1	25	27.5	91.20%	K.IENQQGVNNFDEILKVTDGVMVAR.G	
287	312	3	2934.45	-0.019	0	32.1	27.5	95.00%	K.SNLAGKPVICATQMLESMTYNPRPTR.A	Carbamidomethyl (+57)
92	116	3	2821.27	-0.99	0	45.7	31.3	95.00%	R.TGTTTNDVDYPIPPNHEMIFTTDDK.Y	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
23	KTR4_YEAST	38.58%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
406	426	3	2476.02	0.19	0	56.7	31.3	95.00%	R.DIGYHHTPYTNCPTCPADSDR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
399	405	2	931.47	-0.13	0	31.6	26.4	95.00%	K.SSIHWFR.D	
271	281	2	1417.67	-0.57	0	65.6	28.3	95.00%	K.INYDVFQFMNK.N	
91	103	2	1490.69	-0.83	0	35	28.5	95.00%	K.DTFDPNEVLAENK.Q	

375	381	2	890.39	0.43	0	33.5	26.5	95.00%	K.GGFYYER.W	
406	435	4	3463.41	-0.044	1	26.9	32.3	95.00%	R.DIGYHHTPYTNCPTCPADSDRCNGNCVPGK.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Deamidation (+1)/ Carbamidomethyl (+57)
143	162	2	2366.11	0.29	0	78.4	29.9	95.00%	R.NSDLEDIISSIQQLEEEYNK.N	
83	103	3	2500.21	-1.4	1	45.8	28.9	95.00%	R.LHEPLYEKDTFDPNEVLAENK.Q	
436	453	2	2251.01	-0.17	0	82.2	31.2	95.00%	K.FTPWSDLDNQNCQATWIR.H	Carbamidomethyl (+57)
135	142	2	857.53	-0.6	0	30.8	23.2	95.00%	K.GTILSLVR.N	
62	82	3	2357.03	-0.93	0	41.7	30.6	95.00%	K.TESADELPDHDAEVLDSIMDR.L	
389	398	2	1047.6	-0.12	0	49.9	21.1	95.00%	R.SLALALFADK.S	
245	254	3	1269.65	0.081	0	29.2	26.1	95.00%	K.EFYHHPLLSK.Y	
225	240	2	2041.86	0.65	0	75.6	30.5	95.00%	K.ENIQYAEVESYHNMCR.F	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
24	A6ZQR8_YEAS7	22.39%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
909	929	3	2238.17	-1.4	0	42.6	24.1	95.00%	K.AVEEANSKPVEVIKPNGLSEK.K	Deamidation (+1)
955	967	2	1323.61	-0.15	0	58.7	28.3	95.00%	K.LGDASCAAPFTSK.L	Carbamidomethyl (+57)
806	825	2	2144.92	-0.31	0	45.2	30.8	95.00%	K.DMGYQTLMCGDGTNDVGALK.Q	Carbamidomethyl (+57)
118	132	2	1729.87	-0.12	0	63.3	26.9	95.00%	R.VTEAGSLQTFFQFQK.K	
588	604	3	1756.92	-0.06	1	33.9	25.4	95.00%	K.RSASIASHNDALFAAVK.G	
514	537	3	2460.34	-0.69	0	47.1	20.7	95.00%	R.HLYSAAEAPESTILVIGAAHALVK.L	
589	604	2	1600.82	-0.27	0	70.8	26.6	95.00%	R.SASIASHNDALFAAVK.G	
481	488	2	1055.44	-0.15	0	39.8	25.4	95.00%	R.IDVCCFDK.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
372	383	2	1280.64	-0.56	0	71.7	27.6	95.00%	K.TGFETSQGSLVR.V	
489	513	3	2564.26	0.54	0	35.2	28.7	95.00%	K.TGTLTGEDLVFEGLAGISADSENIR.H	
135	148	3	1746.84	0.8	0	37.8	29.6	95.00%	R.FLWHENEQVFSSPK.F	
930	954	3	2464.28	-0.12	0	29.9	24.9	95.00%	K.KPADLASLLLNSAGDAQGDEAPALK.L	
149	156	2	933.48	-0.03	0	31	25.4	95.00%	K.FLVDESPK.I	
321	335	2	1697.86	-0.66	0	67.1	25.8	95.00%	K.LRPSEDNLQLDGVDK.I	
968	979	2	1269.74	0.14	0	69.8	20.5	95.00%	K.LANVSAVTNIIR.Q	
92	117	3	2867.44	-0.97	0	44.2	27.4	95.00%	K.NVNEATHILIYTTPNNGSDGIVEIQR.V	
355	371	2	1646.89	-0.56	0	29	25.1	95.00%	K.SDIPPPPDGGALAIVTK.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
25	PPN1_YEAST	38.13%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
184	198	2	1707.81	-0.42	0	83.2	29	95.00%	R.TEAQIFDMNNIVADK.M	
335	343	2	1175.46	1.7	0	26.3	25.8	91.40%	K.NFDQSCYDK.F	Carbamidomethyl (+57)
651	660	2	1276.65	-0.18	0	31.1	26.8	95.00%	R.LYENKPAWEK.Y	

51	71	2	2509.21	-1.4	1	45.3	29.5	95.00%	K.FLDDRGDNESLQLLNDIEFTR.L	
571	595	3	2909.44	0.13	1	40.2	28	95.00%	K.TMPIEMPDKYELGPAYVPQLFTPTR.F	Oxidation (+16)
390	407	2	2119.88	0.7	0	100	30.3	95.00%	R.VQQGEDSNEEDEETELNR.I	
661	674	2	1652.7	0.72	1	76.7	29.7	95.00%	K.YVEWSFASSGYKDD.-	
97	126	5	3382.63	-0.3	0	31.1	29.3	95.00%	R.FLHITDIHPDPYYVEGSSIDAVCHTGKPSK.K	Carbamidomethyl (+57)
596	605	2	1258.62	1.1	0	30.5	27.5	94.70%	R.FVQFYADLEK.I	
137	153	2	1907.88	0.06	0	93	29.7	95.00%	K.AMSGCDSPVILMEETLR.W	Carbamidomethyl (+57)
482	500	2	2067.08	0.23	0	83.6	25.5	95.00%	R.YSIVNIGGSVIPTFNPSFR.I	
199	242	4	4877.32	3.3	1	33.7	29.4	95.00%	K.MTELFSAGNEEDPRDFDVSVIPSLGNNDVFPHNMFALGPTLQTR.E	
606	618	2	1543.76	-0.92	0	81.4	27.5	95.00%	K.INQELHNSFVESK.D	
263	274	2	1247.68	0.62	0	34.2	25.4	95.00%	R.SASFLTEVIPGK.L	
580	595	2	1850.96	-0.87	0	36.8	27.1	95.00%	K.YELGPAYVPQLFTPTR.F	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
26	A6ZMV7_YEAS7	24.89%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
203	228	3	3013.42	0.33	1	42.5	30.5	95.00%	R.LSNESQPLLNHDDHDHSHESKKPGHR.S	
358	383	3	2931.43	0.34	0	65.6	29.1	95.00%	K.IFHQHGIHSATVQPEFVSGDVNEDIR.R	
293	309	2	1854.02	-1	0	106	21.5	95.00%	R.ILLQATPSTISADQIQR.E	
385	411	3	2830.3	-0.92	1	73.6	31.1	95.00%	R.RFSIIAGGSPSSSQEAFDSHGNTEHGR.K	
357	383	3	3059.52	-0.78	1	83.7	27.8	95.00%	R.KIFHQHGIHSATVQPEFVSGDVNEDIR.R	
102	112	2	1335.71	-0.61	0	45.7	24.9	95.00%	R.LIEPQEIQNPR.L	
358	384	4	3087.53	-0.64	1	55.5	26.9	95.00%	K.IFHQHGIHSATVQPEFVSGDVNEDIRR.R	
386	411	4	2674.2	-0.14	0	47.5	31	95.00%	R.FSIIAGGSPSSSQEAFDSHGNTEHGR.K	
386	412	3	2802.29	-0.53	1	37.5	31	95.00%	R.FSIIAGGSPSSSQEAFDSHGNTEHGRK.K	
203	223	3	2438.08	-0.28	0	42.1	30.8	95.00%	R.LSNESQPLLNHDDHDHSHESK.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
27	A6ZR77_YEAS7	29.39%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
402	411	2	1107.55	-1.3	0	39.2	26.7	95.00%	R.ISSNPQSFTK.Q	
20	46	4	2920.41	-1.1	1	23.4	29.7	94.70%	K.IGEGSFGVIFEGENILHSCQAQTGSKR.D	Carbamidomethyl (+57)
321	339	3	2204.98	-0.76	1	27.9	30.1	91.60%	R.LNDLKDDGHYDWMDLNGGK.G	
273	295	3	2691.43	-0.22	1	27	22.4	95.00%	K.QKLNPDDLLLNNAIPYQFATYLK.Y	
140	163	4	2969.51	-0.49	1	21	25.4	95.00%	R.AIHDHDLIYRDIKPDNFLISQYQR.I	

468	484	3	1978.92	-0.85	0	43.5	30.1	95.00%	R.SNNEHNLPNHYTNLANK.N	
47	64	2	2016.04	0.13	1	56.3	26.8	95.00%	R.DSSIIMANEPVAIKFEPR.H	
467	484	4	2135.02	-0.32	1	32.2	29.5	95.00%	K.RSNNEHNLPNHYTNLANK.N	
150	163	2	1735.89	-1.2	0	46.3	26.3	95.00%	R.DIKPDNFLISQYQR.I	
20	45	3	2764.31	-0.02	0	64.2	30.9	95.00%	K.IGEGSFGVIFEGENILHSCQAQTGSK.R	Carbamidomethyl (+57)
5	19	3	1591.85	0.39	0	41.1	24.4	95.00%	R.SSQHIVGIHYAVGPK.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
28	YA11B_YEAST	14.02%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
987	1001	2	1640.82	-1.2	0	49.1	27.2	95.00%	R.EVDPNISESNILPSK.K	
400	419	2	2073.92	-0.2	0	113	29.9	95.00%	R.AHNVSTSNNSPSTDNDSISK.S	
331	354	3	2813.38	-0.1	0	72.6	28.8	95.00%	R.HLNMTVAELFLDIHAIYEEQQGSR.N	
1003	1022	3	2072.99	-0.71	1	38.5	29.6	95.00%	K.RSSTPQISNIESTGSGGMHK.L	
471	491	3	2226.08	-0.67	0	88.7	29.5	95.00%	R.SAHHIHSASSNPDINVVDAQK.R	
560	568	2	1163.53	-1.8	0	29.8	27.1	94.50%	K.YGDFYWVSK.K	
25	39	2	1638.78	-0.86	0	78.9	28.4	95.00%	K.EVHTNQDPLDVSASK.T	
25	45	3	2415.09	-0.27	1	54.1	30.8	95.00%	K.EVHTNQDPLDVSASKTEECEK.A	Carbamidomethyl (+57)
1093	1113	3	2202.09	0.046	0	33.6	28.2	95.00%	R.SPSIDASPPENNSSHNIVPIK.T	
1621	1632	2	1318.72	-0.46	0	43.7	24.9	95.00%	K.SQIGNIYLLNGK.V	
308	315	2	989.52	0.32	0	31.3	26.4	95.00%	K.VACQLIMR.G	Carbamidomethyl (+57)
1	24	3	2598.18	-0.31	0	74.4	31	95.00%	-.MESQQLSQHSPISHGSACASVTSK.E	Acetyl (+42)/ Carbamidomethyl (+57)
1234	1242	2	1115.51	0.078	0	55.2	26.5	95.00%	R.YDEAITYNK.D	
658	681	4	2906.4	-0.29	0	21.1	29.8	90.20%	K.YQNSYEPFQYLHTDIFGPVHNLPK.S	
958	975	2	1855.84	-0.6	0	47.1	30.3	95.00%	K.AVSPTDSTPPSTHTEDSK.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
29	COS1_YEAST	37.53%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
157	167	2	1275.75	0.92	1	50	19.9	95.00%	R.TTLLEPFSLKK.D	
102	108	2	935.49	1.7	0	31	24.9	95.00%	K.QLIQFCK.E	Carbamidomethyl (+57)
206	219	2	1525.81	-0.017	1	66.9	24.3	95.00%	K.SWSPVGLEDAKLPK.E	
357	369	2	1544.86	0.83	0	48.5	22.6	95.00%	R.ALSLNVELWPYIK.E	
109	137	3	3320.51	-1.1	0	56.9	31.3	95.00%	K.EVTENTPSSDPHDWEVVAANLNSYLYENK.A	
143	156	2	1828.81	0.87	0	75.3	30	95.00%	K.YFFFNAMVCQEAFR.T	Carbamidomethyl (+57)
291	313	3	2580.22	-0.42	0	41.8	30.2	95.00%	K.MQFLSTIINEQESGANGWDEIAK.K	
25	33	2	1099.64	-0.29	0	27.9	22.6	94.60%	K.IVLPQDLFR.S	
178	192	2	1756.87	1.1	0	61.5	28.6	95.00%	K.DSVPYIEEALGVYFR.E	
206	216	2	1187.58	-0.27	0	57.3	27.1	95.00%	K.SWSPVGLEDAK.L	
157	166	2	1147.65	0.15	0	29.8	23.2	95.00%	R.TTLLEPFSLK.K	
11	18	2	893.49	-0.02	0	26.5	24.8	92.90%	K.SVDVLSFK.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
30	B3LFI3_YEAS1	32.35%	100%	9						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
359	375	2	1791.97	0.15	0	28.6	23	95.00%	R.WGDAPVHSIAAALFLPK.D	
252	262	2	1448.66	-0.61	0	64.3	29.2	95.00%	K.LYCDINYDVFK.W	Carbamidomethyl (+57)
376	398	5	2830.28	-0.96	1	41.7	31.8	95.00%	K.DKIHYFSDIGYHHPPYDNCPLDK.E	Carbamidomethyl (+57)
424	435	2	1409.72	-0.15	0	58.7	25.9	95.00%	K.EYYDAQGLVKPK.N	
105	117	2	1487.7	0.86	0	75.5	28.3	95.00%	K.TTMDYITPSFANK.A	
226	233	2	1089.5	1.4	0	38.4	27	95.00%	R.YQSGFFWR.H	
66	88	2	2526.09	-0.88	1	102	31.8	95.00%	K.KLEQSALNSEASEDSEAMDEESK.A	
343	358	2	2022.87	-0.75	0	49.6	30.2	95.00%	R.EYFDTLDHQGGFFYER.W	
298	317	2	2313.02	-0.27	0	94.8	30.8	95.00%	K.NPEYLDENNLMSFLSNDNGK.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
31	A6ZR26_YEAS7	13.95%	100%	2						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
2	9	2	912.51	3	0	38.6	23.1	95.00%	M.SSAPLLQR.T	Acetyl (+42)
15	24	2	1122.68	-0.56	1	32.8	13	95.00%	K.IALPTRVEPK.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
32	B3LNF5_YEAS1	12.11%	100%	14						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
315	328	2	1622.68	-0.74	0	81.7	28.3	95.00%	R.HSMQGEIYEDAMGR.I	
1032	1049	2	1913.05	-0.0021	0	98.5	22.9	95.00%	K.IQGLEGIILTNIVSNSDK.V	
907	919	2	1487.68	-0.62	0	78	28.3	95.00%	R.SLVSSTDFFQDDK.N	
1022	1031	2	1218.56	-0.43	0	28.2	27.4	91.90%	R.NTFGYVDFEK.I	
1217	1232	2	1685.84	-0.38	0	84.3	27.5	95.00%	R.FLLFGEAADIGGSSFR.T	
648	661	2	1795.72	-0.76	0	70	28.4	95.00%	K.CTEADYECAFEFVR.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
596	611	2	1955.78	-0.87	0	95.8	29.3	95.00%	K.TCEENDFEDWNLAEGK.C	Carbamidomethyl (+57)
1367	1379	3	1335.62	0.25	0	41.1	28	95.00%	K.LDAPSSPHACPGK.E	Carbamidomethyl (+57)
759	772	2	1502.71	-1	0	54.2	28.6	95.00%	R.GEAYISHDGGQTIR.R	
126	136	2	1330.63	-0.81	0	45.6	27.1	95.00%	R.GCYIETHPLNK.N	Carbamidomethyl (+57)
709	719	2	1189.57	0.013	0	33.2	27.4	95.00%	K.SVDISCEGVPK.K	Carbamidomethyl (+57)
196	210	2	1611.72	-0.43	0	74.5	28.1	95.00%	R.NENSAISISDCGFAK.T	Carbamidomethyl (+57)
887	899	2	1599.67	-0.61	0	79.7	29.6	95.00%	K.YPSNEDMVMCQVK.E	Carbamidomethyl (+57)
1267	1279	2	1607.75	-1.1	0	62.2	28.5	95.00%	K.SNCLFGHQTEFLR.K	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
33	A7A1A2_YEAS7	20.70%	100%	9						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
663	674	2	1229.66	-0.49	0	43.2	25.8	95.00%	R.NAVVQGIDSSLK.I	
498	509	2	1339.65	-0.96	0	48	27.6	95.00%	K.VLSAPNHTVDCK.I	Carbamidomethyl (+57)
471	485	2	1826.87	-0.61	1	80.7	28.8	95.00%	R.HRDPNNPDQLTMYVK.A	
185	198	2	1745.86	-1	1	50.7	28.3	95.00%	K.SLIYPSVYKDYNER.T	
453	470	2	2188.04	-0.1	0	100	30.3	95.00%	K.SAWFYSFQSHPFTVLSER.H	

639	662	2	2823.24	-3.3	0	86.6	31.6	95.00%	K.LSELENNNITFYSCGPATFNDDFR.N	Carbamidomethyl (+57)
510	525	3	1739.96	-0.29	0	58.5	22.2	95.00%	K.IFLEGPYGVTVPHIAK.L	
51	67	2	1925.89	-0.35	0	122	29.5	95.00%	K.NINWLGSVTACAYENSK.S	Carbamidomethyl (+57)
414	427	2	1464.73	1.3	0	48.1	27.4	95.00%	K.TATLSTTDDSNVIK.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
34	A6ZV88_YEAS7	29.81%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
169	206	4	4235.83	-0.25	0	78.8	32.4	95.00%	K.SGDNLTVVINSLGWAFEDEDGDDEYATEETLSHHDNNK.G	
138	143	2	705.44	0.11	0	27.5	15.9	94.30%	K.SIVLFK.F	
144	152	2	1058.49	1.6	0	39.9	26.1	95.00%	K.FTSDAYDLK.K	
153	168	2	1957.93	-0.2	1	133	29.1	95.00%	K.KLDEFIDSCLSFLEDK.S	Carbamidomethyl (+57)
29	38	2	1145.53	2.9	0	29.9	27.7	93.80%	K.ESSSFISFDK.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
35	A6ZSR0_YEAS7	26.79%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
219	234	2	1876.91	-0.27	1	118	28.7	95.00%	R.AKLDTDFAYLYSDLDK.G	
235	252	2	2160.12	-0.16	0	50.6	25.7	95.00%	K.GFTPINFVFPNLPLEHYR.K	
354	371	2	2161.13	-0.46	0	64.7	25.6	95.00%	K.ELTYDLLQEMPLLNQTIK.E	
275	289	2	1788.87	-1.3	1	40.8	29.2	95.00%	K.NNDIQDRDLIDSLMK.N	
117	136	2	2060.06	-0.25	0	69.1	26.4	95.00%	K.LADVSAEAAYAHLTTPVFGK.G	
190	210	2	2298.13	0.69	0	63.9	28.7	95.00%	R.TTGTIDVMVTQPEMTIFTASR.S	
455	467	2	1292.65	0.76	0	57.2	26.9	95.00%	K.GVSSPYLPFGGGR.H	
137	146	2	1179.53	0.098	0	29.4	27.8	93.10%	K.GVIYDCPNSR.L	Carbamidomethyl (+57)
221	234	2	1677.78	0.23	0	113	29.4	95.00%	K.LDTDFAYLYSDLDK.G	
260	270	2	1182.63	-0.43	0	43.6	23.7	95.00%	K.AISGTYMSLIK.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
36	A6ZX34_YEAS7	18.75%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
130	143	2	1387.73	-0.011	0	60.9	25.2	95.00%	R.AIASSPSLNSNLSK.N	
340	360	3	2476.05	0.21	0	58.3	31.3	95.00%	R.TFYDGDDPYWTAPDVHYDATK.D	
594	607	2	1634.81	-0.38	0	67.4	27.4	95.00%	R.WFVGDTPTYTIHAK.A	
494	508	2	1572.75	-0.4	0	81.3	28.4	95.00%	R.GAPEIDVLEGETDTK.I	
114	129	2	1752.85	-0.64	0	40	28.4	95.00%	R.AVSTANDNSFLQPPHR.A	
579	593	2	1832.82	-0.55	0	80.2	30.1	95.00%	K.YAIEYLNDDDNGYIR.W	
476	493	2	2013.86	-1.1	0	65	30.2	95.00%	K.LSICTCDGEDHPNQGVGR.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
304	316	2	1358.66	0.13	0	41.9	27.4	95.00%	R.TSLVDPDTPDTAK.T	
393	401	2	1049.5	-0.0072	0	40.2	26.5	95.00%	R.SGMLQSWNK.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
37	A6ZY55_YEAS7	25.32%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
529	548	2	2334.15	-1.4	0	32	28.9	94.90%	K.SVVTNEFQCSLIPPDLTTWK.I	Carbamidomethyl (+57)

218	240	3	2406.99	-0.97	0	42.4	31.1	95.00%	R.SDESAHTSSSPEANNSSLPASPR.S	Phospho (+80)
509	524	2	1737.85	-0.24	1	82.2	28.3	95.00%	R.SSGLSQTAINEDNKFK.Q	
306	320	2	1603.77	-0.45	0	80.9	28.1	95.00%	K.EILDTTDNINSAGNK.S	
673	685	2	1511.74	-0.48	0	55.1	28.4	95.00%	R.NSPPDYGFILFSR.N	
78	90	2	1436.78	-0.22	0	68.3	23.7	95.00%	R.ILSVESSIIDFSK.G	
32	47	2	1817.74	-0.72	0	53.7	29.1	95.00%	K.VTAYDYDNPNDSGMEK.L	
295	305	2	1190.64	-0.68	0	48.6	24.9	95.00%	R.IIDDSIISTSK.E	
718	746	3	3131.33	-0.073	0	111	32.3	95.00%	K.HPHCSSTNYGSVASFGSQSTSASYDDVQR.Y	Carbamidomethyl (+57)
404	414	2	1292.72	0.064	0	48.2	21.1	95.00%	R.NHVVTNDLLLR.D	
661	672	2	1376.68	1.6	0	44.6	28.3	95.00%	R.STTDNEESLLLR.N	
274	285	2	1349.71	-0.61	0	47.5	27.1	95.00%	R.FLLSSEDIEGLK.F	
295	320	3	2776.4	-0.17	1	49.8	27	95.00%	R.IIDDSIISTSKEILDTTDNINSAGNK.S	
342	353	2	1298.68	-0.63	0	30.8	25.5	95.00%	K.NILPSAVQSNEK.Y	
574	590	2	1910.89	0.092	0	68.5	29.3	95.00%	K.LNSDDSLSPDEFFQLGK.D	
509	522	2	1462.69	-0.83	0	73.8	27.4	95.00%	R.SSGLSQTAINEDNK.F	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
38	B3LGF8_YEAS1	17.32%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
79	95	3	1817.92	0.5	0	41.1	27.1	95.00%	K.AVDIDTIDAQPLHEGPK.I	
27	37	2	1300.71	-0.7	1	35.2	24.7	95.00%	K.SVQTLKNEVQR.E	
145	174	3	3306.51	-0.32	0	51.1	31.3	95.00%	R.SVSPLQSITSCNTPMSEHELPVSSSNSFER.A	Carbamidomethyl (+57)
705	719	3	1679.75	0.6	0	29.8	29.5	94.60%	K.HATESSDWVHESAPK.F	
79	108	3	3258.59	0.095	1	49.2	28.2	95.00%	K.AVDIDTIDAQPLHEGPKIDDSPQDEVNSIK.G	
115	144	3	3288.46	-1.2	0	57.7	31.5	95.00%	K.ANEDDLKPPSQHEACGNSALQSSITDFSDR.S	Carbamidomethyl (+57)
175	191	2	1791.79	-0.45	0	73	29.7	95.00%	R.ADDMPVVQADNQTSSSK.S	
96	108	2	1458.68	-0.56	0	62.7	28.7	95.00%	K.IDDSPQDEVNSIK.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
39	B3LS12_YEAS1	25.46%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
485	513	3	3453.61	0.39	0	63.5	31.2	95.00%	K.NFQNSLLIDPDHALNECDNTLTTEEYIFK.A	Carbamidomethyl (+57)
712	725	2	1640.8	-0.13	0	73.8	28.1	95.00%	R.TTHGELITLDEEQR.L	
176	185	2	1333.61	-0.25	1	28.3	28.3	90.50%	R.KYDMFQAFER.I	
473	479	2	890.49	0.65	0	36.2	23.5	95.00%	R.YETLLPR.N	
521	533	3	1454.75	0.21	0	43.9	26.8	95.00%	R.QHQLEAGLFAVDK.S	
685	700	2	1708.74	-0.73	0	88.8	29.8	95.00%	R.ASAGACGGYIWCATHK.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
726	740	2	1703.87	-1.1	0	58.5	26.9	95.00%	R.LHIDAVNTVWSHANK.D	
597	616	3	2230.05	-0.61	1	75.8	30	95.00%	K.RQEAAVEICSGQIAHMSTDK.K	Carbamidomethyl (+57)
113	122	2	1230.6	0.22	0	57.4	27.7	95.00%	K.HFNELSLTDR.C	
129	142	2	1683.8	-0.42	0	76.2	28.9	95.00%	R.TLYTLDDEWTNSVK.K	
274	282	2	1029.59	-0.022	0	30.5	23.9	95.00%	K.VLEQGFLPK.F	

520	533	2	1610.85	-0.26	1	54.1	24.6	95.00%	R.RQHQLEAGLFAVDK.S	
64	99	3	3985.06	-0.15	1	78	23.6	95.00%	K.VLIEAFGSPEVDPVDTIPVSPLELV PFYDQSIDTKR.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
40	A6ZWJ5_YEAS7	35.65%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
171	187	2	1857.91	-0.92	0	83.2	28.7	95.00%	R.QAITDSMNGDPELINIK.F	
423	436	2	1585.7	-0.68	1	35.8	29.2	95.00%	R.SGSCGGHYFDIMKK.D	Carbamidomethyl (+57)
34	46	2	1582.77	-0.5	0	68.5	28	95.00%	K.QMSEQYVTPYLPK.S	
119	128	2	1194.61	0.088	0	59.7	27.6	95.00%	K.ACFVSLITER.D	Carbamidomethyl (+57)
239	250	3	1661.76	0.72	0	34.3	30	95.00%	R.HPVLDEFDWYWR.V	
207	223	2	1713.85	-0.71	0	51.3	27	95.00%	K.AAESLISLANVPDGDSR.A	
257	267	3	1465.67	0.024	0	52.2	28.4	95.00%	K.LYCDIDHDLFR.W	Carbamidomethyl (+57)
188	206	2	2350.08	-0.058	0	67.2	30.5	95.00%	K.FAEIPADEWVYPEWIDENK.A	
62	72	2	1302.63	-1.4	0	67	28.1	95.00%	R.IQSEQEEAELK.Q	
148	165	2	2101	-0.29	0	97.8	29.2	95.00%	K.NFAYPWVFISQGELDGMK.Q	
119	144	3	3009.51	-1.1	1	40.5	26.8	95.00%	K.ACFVSLITERDSMTQILQSIDEVQ VK.F	Carbamidomethyl (+57)
129	144	2	1832.92	0.0052	0	44.3	27.5	95.00%	R.DSMTQILQSIDEVQVK.F	
61	72	2	1458.73	-0.91	1	64.4	26.9	95.00%	R.RIQSEQEEAELK.Q	
423	435	2	1457.61	0.084	0	35.1	27.9	95.00%	R.SGSCGGHYFDIMK.K	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
41	A6ZSG0_YEAS7	21.70%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
53	62	2	1157.61	-0.7	0	34.2	24.8	95.00%	R.YLEGLHEGLK.F	
340	378	4	4263	-0.28	1	70.7	31	95.00%	K.FQQREDHPAPATESSSLMPPANT TATPLNSNHPSYNSIR.H	
453	472	3	2375.1	-0.026	0	58.1	30.7	95.00%	K.YVENSSQSHENEITQQQLNK.N	
713	742	3	3446.59	-1.2	0	45.3	30.4	95.00%	K.MIWQLPIADPTSTAPEQQEQNSH DAPNWSR.S	
72	107	4	4035.01	1.2	1	34.1	27.7	95.00%	K.RSVSSQSPIVHSSNNTLHHHEHQ QHLPPTLESLSSK.S	
131	147	3	1970.74	0.35	0	38.5	27.6	95.00%	R.ELPHDDNDDEDANDDSR.F	
20	36	2	1865.99	0.52	1	79.9	25.6	95.00%	R.LKEEVLTPTTSASTPHR.I	
37	52	2	1902.93	-0.85	1	46.6	28.3	95.00%	R.IFSVDDDPKEIQNDIR.Y	
220	231	2	1353.69	-1	0	51.8	27	95.00%	R.TAAQDIHETQLK.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
42	GNP1_YEAST	17.95%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
42	57	2	1909.89	-0.012	0	62.5	29.3	95.00%	K.QIGSIEPENEVEYFEK.T	
62	79	3	2234.02	-0.36	1	69.5	30.3	95.00%	K.TIENMEYEGEHHASYLRR.F	
11	34	3	2813.14	-1.1	1	62.5	31.3	95.00%	R.NNEGSSNMNMNRNDLDDVSHY EMK.E	
110	122	2	1504.71	-0.14	1	59.3	27.3	95.00%	K.DSSSQLDNELNRK.S	
86	109	3	2414.11	1.5	1	80.9	30.4	95.00%	R.RAEGSHANSPDSSNSNGTTPIST K.D	

87	109	2	2258	-1.5	0	56.5	30.3	95.00%	R.AEGSHANSPDSSNSNGTTPISTK.D	
62	78	3	2077.92	0.49	0	44	30.1	95.00%	K.TIENMEYEGEHHASYLR.R	
418	431	2	1441.77	-0.0067	0	66.7	24.5	95.00%	K.ASPYVIAVSSHGVR.V	
123	132	2	1081.57	1.7	0	34.2	24.2	95.00%	K.SSYITVDGIK.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
43	YNL5_YEAST	26.40%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
610	619	2	1143.59	-1.1	0	48	25.8	95.00%	K.IVEGGHEIYK.Y	
13	36	3	2773.28	-0.87	1	48.2	30.4	95.00%	R.TGMERTDIDSEHPEAQPLLNNNHR.T	
379	407	3	3197.55	-0.2	0	79.5	28.9	95.00%	R.YCLYDRPGYGLSDSPPAPISIAMVAESLR.Y	Carbamidomethyl (+57)
18	36	3	2199.03	0.14	0	51.9	30	95.00%	R.TDIDSEHPEAQPLLNNNHR.T	
297	320	4	2714.41	0.13	1	38.1	24.8	95.00%	R.LTHKLPITVQSPSYEAFHYVDAAK.T	
37	52	2	1469.72	-0.9	0	82.9	27.1	95.00%	R.TLGAGSANGPAVNEGR.D	
563	575	2	1430.7	-0.5	0	77.2	28.4	95.00%	R.DVTNNAESLQNVK.T	
215	235	3	2447.11	-0.41	1	73.5	31.1	95.00%	R.RIDDANISTFNENHTNSTENR.D	
588	596	2	1117.53	1.9	0	34.2	27.5	95.00%	K.SALWGDWQR.D	
550	575	3	2913.47	0.42	1	53.3	27.2	95.00%	K.FLESVTSSILSYRDVTNNAESLQNVK.T	
634	644	2	1186.64	-0.36	1	47.5	25.8	95.00%	R.LIGELGKLTED.-	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
44	A6ZVP9_YEAS7	37.40%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
201	221	3	2158.03	0.47	0	44.3	29.3	95.00%	R.GVAMNPVDHPHGGGNHQHIGK.A	
129	147	3	2097.06	-0.76	1	61.9	27.4	95.00%	R.ASGNYVIIIGHNPDENKTR.V	
94	123	3	3046.59	-0.52	0	30	22.9	95.00%	K.ASLNVGNVLPLGSVPEGTIVSNVEEKPGDR.G	
71	92	3	2491.28	-1.2	1	51.2	25.5	95.00%	R.LREEIFIANEGVHTGQFIYAGK.K	
129	145	2	1839.91	-0.55	0	59.4	28.6	95.00%	R.ASGNYVIIIGHNPDENK.T	
199	221	4	2431.17	1.6	1	24.1	29.6	95.00%	K.TRGVAMNPVDHPHGGGNHQHIGK.A	Oxidation (+16)
93	123	3	3174.69	-0.82	1	67.6	22.5	95.00%	K.KASLNVGNVLPLGSVPEGTIVSNVEEKPGDR.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
45	B3LPA7_YEAS1	22.42%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
83	107	4	2992.37	-0.12	1	26.8	31	95.00%	R.LQVVSHETDINEDEEEAHYEDKHVK.R	
287	300	2	1397.69	-0.8	0	35.5	27.5	95.00%	R.NPGAWGPGIISSDK.S	
504	513	3	1146.6	-0.18	1	23.8	26.3	91.20%	R.GISRDDLPFK.A	
4	16	2	1580.78	-0.84	1	39.4	27.8	95.00%	R.FSNIITSNKWDEK.Q	

17	45	3	3368.47	-1	0	51.6	32.5	95.00%	K.QNNIGEQSMQELPEDQIEHEMEAIDPSNK.T	Oxidation (+16)
588	600	2	1585.75	-0.53	0	37.6	28.4	95.00%	R.EIEAIIWEDDEPK.N	
588	605	2	2256.1	0.027	1	61.4	29.6	95.00%	R.EIEAIIWEDDEPKNLWEK.F	
83	104	3	2628.15	-0.38	0	72.9	31.8	95.00%	R.LQVVSHETDINEDEEEAHYEDK.H	
4	12	2	1022.54	0.18	0	29.1	24.6	95.00%	R.FSNIITSNK.W	
435	441	2	869.44	1.7	0	27.7	24	94.40%	K.QFGYVTR.Q	
62	82	2	2110.08	-0.67	0	120	26.4	95.00%	K.HGSLQGGAIADVNSITNSLTR.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
46	YG35_YEAST	21.91%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
805	817	2	1313.73	0.3	0	28	23.7	94.80%	K.QNNVVSAVIAATK.N	
651	661	2	1358.68	-0.59	1	42.2	26.9	95.00%	R.STVYRDYVQTK.F	
162	189	4	3057.49	0.34	0	44.6	28.3	95.00%	R.GLQNSSLPELEDGYAGGYQSLRPSHNLR.F	
874	890	3	2002.1	-1.9	1	22	21.9	90.30%	K.EYKDDEPVLPILLFALK.Q	
821	830	2	1071.57	1.3	0	35.6	24.1	95.00%	K.IDTIGNGLNR.G	
716	732	2	1882.84	-0.39	0	107	29.6	95.00%	K.NINADNIDYSAAEGFNR.I	
48	75	3	3005.43	-0.094	1	59.5	30.5	95.00%	R.SYMSGFFTGGNSPMINNLSDSKLPISNK.Q	
637	650	2	1547.77	-0.91	0	27.8	27.7	90.70%	K.LQTINGEYNGNVAR.S	
146	161	2	1770.89	-0.63	1	44.7	28.2	95.00%	R.LLLSPASSNVDDDRNR.G	
923	945	3	2583.35	0.28	0	61.6	24.1	95.00%	R.LASQSHLLHADNIFFLVETGMLK.A	
891	902	3	1474.78	-0.6	0	23	26	90.30%	K.QYRPDIISEVQK.V	
709	715	2	910.52	-0.13	0	25.1	19.3	90.70%	K.YLILDFK.N	
839	849	2	1242.64	-0.099	0	35.1	24.7	95.00%	R.NLMSLPTNTPR.N	
850	869	2	2278.16	0.046	0	71.7	26.8	95.00%	R.NYQILSVAQNVFVNDEQAVK.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
47	A6ZM54_YEAS7	52.22%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
181	190	2	1274.51	-0.81	0	53.8	26.8	95.00%	K.MDFEENTFDK.V	
62	93	4	3938.73	1.2	1	71	32.5	95.00%	R.RLEDYNEATHSYYNVVTDFYEYGWGSSFHFSR.F	
356	366	2	1324.7	0.43	0	28.6	24.2	95.00%	K.LFTPMMLFVAR.K	
26	34	2	906.48	-0.12	0	49.7	25.9	95.00%	K.TGLSALMSK.N	
367	383	2	1844.84	-0.39	0	62.2	29.9	95.00%	R.KPENAETPSQTSQEATQ.-	
296	308	2	1555.82	0.5	0	61.4	25	95.00%	K.YVQNLANLATFFR.T	
164	175	2	1486.71	-0.88	1	65.8	28.2	95.00%	K.KYNLSDQMDFVK.G	
140	157	2	2039.97	-0.087	0	71.7	29.5	95.00%	R.FTGCNVIGLNNNDYQIAK.A	Carbamidomethyl (+57)
191	202	2	1358.66	-6.4	0	48.2	27.5	95.00%	K.VYAIEATCHAPK.L	Carbamidomethyl (+57)
94	106	2	1445.73	-0.023	1	69.9	27.2	95.00%	R.FYKGESFAASIAR.H	
213	239	4	3194.51	-0.27	1	64.7	30.3	95.00%	K.VLKPGGTFAVYEWVMTDKYDENNPEHR.K	
120	135	2	1540.77	-1.1	0	69.9	27.1	95.00%	R.GDLVLDVGCGVGGPAR.E	Carbamidomethyl (+57)
191	212	3	2540.26	-0.53	1	34.9	28.2	95.00%	K.VYAIEATCHAPKLEGVYSEIYK.V	Carbamidomethyl (+57)

165	175	2	1358.62	-0.96	0	48.9	28.4	95.00%	K.YNLSDQMDFVK.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
48	XPP_YEAST	25.77%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
200	213	2	1859.82	-0.96	0	97.9	30	95.00%	R.QNEDPITWQEWCVR.E	Carbamidomethyl (+57)
380	397	3	2224.16	-0.36	0	40.2	25.2	95.00%	K.INGIEVRPYEQIWEHLTK.I	
118	140	3	2894.28	-0.79	1	48.3	32	95.00%	K.KHDLCCYIVPSCDEHQSEYVSLR.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)
398	421	3	2689.28	-0.74	0	36.8	29.3	95.00%	K.ITSQASSAEHEFLIPDSASWQMVR.C	
189	199	2	1449.72	-0.49	0	31.8	27.7	95.00%	R.QELDYNWTLLR.Q	
673	680	2	947.5	-0.55	0	35.2	25.3	95.00%	R.IESDMLIK.K	
162	174	2	1498.67	-0.22	0	34.3	29	95.00%	R.DLLNFNDDHPDGK.S	
566	585	3	2373.26	-1.4	1	30.1	24	95.00%	R.TIHLTKPTKEEMDNYTLVLK.G	
422	435	2	1434.68	-0.49	0	74.3	28.6	95.00%	R.CLNTSTNANGAIAK.K	Carbamidomethyl (+57)/ Deamidation (+1)
436	453	3	2025.11	-0.14	1	55.1	20.8	95.00%	K.KMTAQNFAIIHSPIDVLK.S	
593	609	2	1886.99	0.29	0	60.2	25.2	95.00%	R.LIFPENTPGFNIDAIAR.Q	
12	24	4	1428.71	1.1	0	31.2	27.2	95.00%	R.AHSISHVPGTHMR.G	
437	453	3	1897.01	-0.1	0	45.2	24.1	95.00%	K.MTAQNFAIIHSPIDVLK.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
49	MAM3_YEAST	26.20%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
427	457	3	3326.5	-0.78	0	66.6	31.5	95.00%	K.AADQADESSPLLSPSNSNHPSEHPQQDLNNK.S	
637	651	2	1766.75	-0.12	0	80.9	28.7	95.00%	K.SEYGNENINQENSNR.S	
609	619	2	1158.65	0.32	0	41.5	24.3	95.00%	K.NGIVESVITVK.G	Deamidation (+1)
683	691	2	1025.48	0.46	0	29.9	28.4	93.00%	R.SNFTDSLSR.T	
514	535	3	2380.18	0.71	1	46.7	28.2	95.00%	K.IITTHTPHSSKEPSPAPHSNDK.S	
236	251	2	1757.02	-0.065	1	89.9	19.6	95.00%	R.LTKDEVTIISAVLDLK.A	
254	277	3	2766.35	-0.11	1	63.9	29	95.00%	K.RVEEIMTPIENVFTMSADTILDDK.T	
282	289	2	926.46	0.074	0	27.1	23.3	93.70%	K.IFNSGFSR.I	
536	553	3	2011.98	0.21	0	47.4	28.6	95.00%	K.SLSAEEQQLLSDHAELSR.Q	
470	500	3	3211.68	-0.52	0	40	23.3	95.00%	R.SNAVLSPTPQVTEHGTIIPSNLASNPLNVNK.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
50	A6ZPW7_YEAS7	33.22%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
80	89	2	1186.56	0.14	0	57.8	27.3	95.00%	R.NIELNADNER.S	
48	60	3	1482.79	0.21	1	45.6	24.5	95.00%	R.RQSILDHPVGSFK.G	
14	26	3	1582.86	0.57	1	33.6	23	95.00%	K.RSEVHYISIPLNR.G	
113	125	3	1452.83	0.063	1	26.7	20.5	95.00%	R.RLSVTLNNAGRPR.I	
135	178	4	4456.06	0.081	0	66.6	30.6	95.00%	R.VSTASMAIHDDDYGSIQNSTIGDSGSILRPTASLTEMMSGGAGR.R	

180	191	2	1381.66	0.28	0	65	28.6	95.00%	R.FTNNDMDSIVVK.R	
90	112	3	2587.17	-0.78	1	39.1	31.4	95.00%	R.SFFKESNDETYDPDTLAPALDGR.R	
94	113	3	2234.01	0.31	1	48.5	30.2	95.00%	K.ESNDETYDPDTLAPALDGRR.L	
114	125	2	1296.73	-0.021	0	34.5	22.6	95.00%	R.LSVTLNNAGRPR.I	
484	512	3	3113.69	-0.25	0	86.5	20.1	95.00%	K.TPLNARPIVSVLDVLMNVQHIDEAASAIK.R	
27	47	2	2264.96	-0.49	0	91.3	30.9	95.00%	R.GSAFSPDDSVSQFQSDGFMTR.R	
262	283	2	2391.13	-0.58	0	100	30.1	95.00%	R.CLDTDPTLISYADLGYAAFGTK.G	Carbamidomethyl (+57)
15	26	3	1426.76	0.22	0	27.2	23.8	95.00%	R.SEVHYISIPLNR.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
51	PDR5_YEAST	13.37%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
205	220	2	1648.77	-0.62	0	73	28.8	95.00%	K.SISSNTHGFDLGADTK.I	
95	109	2	1663.78	-0.8	0	45.4	29.5	95.00%	K.LDPNSENFSSAAWVK.N	
412	427	2	1738.84	-1.2	0	95.7	28.3	95.00%	R.QTTADFLTSVTSPSER.T	
221	233	2	1431.69	-0.91	1	55.3	28.9	95.00%	K.ISYSGYSGDDIKK.H	
338	349	2	1291.68	-0.26	0	35.4	25.2	95.00%	R.GLDSATALEFIR.A	
945	957	2	1588.76	-1.9	0	41	28.4	95.00%	R.SIGYCQQQDLHLK.T	Carbamidomethyl (+57)
873	881	2	1165.58	0.022	0	27.9	27.3	91.60%	R.NLCYEVQIK.A	Carbamidomethyl (+57)
436	445	3	1117.66	-0.44	1	26.3	19	95.00%	K.KGIHIPQTPK.E	
400	411	2	1522.62	-0.97	0	55.2	28.5	95.00%	K.YFEDMGYVCPSR.Q	Carbamidomethyl (+57)
329	337	2	1196.5	-0.24	0	41.3	26.9	95.00%	K.FQCWDNATR.G	Carbamidomethyl (+57)
1090	1101	2	1344.6	-0.29	0	37.5	28.1	95.00%	K.TVYFGDLGEGCK.T	Carbamidomethyl (+57)
273	297	4	2747.31	0.56	1	47.2	30.2	95.00%	K.GVDRESYANHLAEVAMATYGLSHTR.N	
110	132	3	2641.21	-0.52	0	32.8	31	95.00%	K.NMAHLSAADPDFYKPYSLGCAWK.N	Carbamidomethyl (+57)
49	65	2	1805.86	-0.99	0	112	28.6	95.00%	R.TLTAQSMQNSTQSAPNK.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
52	A6ZKX6_YEAS7	52.76%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
203	217	2	1628.89	-0.81	1	79.4	24.3	95.00%	R.RGPLVVYAEDNGIVK.A	
247	271	3	2799.41	-0.68	1	57	27.5	95.00%	R.FVIWTEAAFTKLDQVWGSETVASSK.V	
145	161	2	1880.05	-0.48	0	58.8	20.2	95.00%	K.IPEIPLVVSTDLESIQK.T	
221	246	4	2610.43	0.51	0	45	20.4	95.00%	R.NVPGVETANVASLNLLQLAPGAHLGR.F	
272	288	2	1844.96	-0.49	0	58	25.5	95.00%	K.VGYTLPSHIISTSDVTR.I	
347	360	2	1462.8	-0.5	0	27.4	22.9	94.10%	K.TGTKPAAVFTETLK.H	
289	309	3	2267.23	-1.2	1	30	21.6	95.00%	R.IINSSEIQSAIRPAGQATQKR.T	
289	308	2	2111.13	-0.098	0	66.7	22.3	95.00%	R.IINSSEIQSAIRPAGQATQK.R	
85	95	2	1183.49	-0.074	0	27.7	25.1	94.40%	R.SGQGAFGNMCR.G	Carbamidomethyl (+57)
258	271	2	1505.74	-0.27	0	76.6	28.1	95.00%	K.LDQVWGSETVASSK.V	
2	44	4	4579.45	-0.97	0	44	26.8	95.00%	M.SRPQVTVHSLTGEATANALPLPAVFSAPIRPDIVHTVFTSVNK.N	Acetyl (+42)

347	362	3	1714.89	-0.24	1	34.9	26.1	95.00%	K.TGTKPAAVFTETLKHD.-	
204	217	2	1472.79	-0.28	0	63.8	24.8	95.00%	R.GPLVVYAEDNGIVK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
53	NCPR_YEAST	28.65%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
318	343	3	3017.6	-1.2	0	42.6	22.7	95.00%	K.VEQFLSIFNLDPETIFDLKPLDPTVK.V	
254	275	2	2355.24	-1.9	0	46	23.3	95.00%	R.NADGIQLGPFDLSQPYIAPIVK.S	
653	664	2	1171.69	0.074	0	31.5	21.6	95.00%	K.GVSTALVGILSR.G	
220	253	4	3909.86	-0.42	0	41.4	29.4	95.00%	K.FTSQFQYTVLNEITDSMSLGEPSAHYLPSHQLNR.N	
452	483	3	3452.83	-0.72	0	64.7	21.9	95.00%	K.QTVHVTSIVENFPNPELPDAPPVVGVTTNLLR.N	
440	451	2	1349.63	-0.22	0	70.5	28.1	95.00%	R.YYSISSSSLSEK.Q	
49	59	2	1229.63	-0.012	0	78.6	26.2	95.00%	R.DIAQVVTENNK.N	
147	165	2	2129.95	-0.1	0	86.4	30.9	95.00%	R.YNMFGLGNSTYEFFNGAAK.K	
598	611	3	1574.79	-0.13	1	45.5	28.4	95.00%	K.KLDGSFEMVVAHSR.L	
582	597	2	2032.87	-0.89	0	55.2	30.7	95.00%	R.NTDDFLYQDEWPEYAK.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
54	SNA3_YEAST	40.60%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
93	125	3	3566.53	0.25	0	68.2	32.5	95.00%	R.DLEAHPAEESQAQPPAYDEDDEAGADVPLMDNK.Q	
1	12	2	1601.68	-0.18	1	46.1	28.8	95.00%	-.MDRDHINDHDHR.M	Acetyl (+42)
84	125	3	4485.01	2.4	1	81	32.2	95.00%	R.HATAPAVDRDLEAHPAEESQAQPPAYDEDDEAGADVPLMDNK.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
55	A6ZL71_YEAS7	35.59%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
258	272	2	1741.89	0.51	0	66.2	26.6	95.00%	R.LALTTAEYLAYQTER.H	
145	166	2	2397.15	-0.96	0	95.9	29.6	95.00%	R.IYPEEMISTGVSAIDTMNSIAR.G	
126	144	2	2153.04	0.17	0	54.1	28.6	95.00%	K.VFAEDYLDINGSPINPYAR.I	
273	289	2	1904.97	0.68	0	92.2	26.4	95.00%	R.HVLTILTDMSSYADALR.E	
15	25	2	1243.67	-0.42	0	49.2	26.5	95.00%	K.AVEQGFNVKPR.L	
273	295	3	2518.29	0.32	1	31.9	25.3	95.00%	R.HVLTILTDMSSYADALREVSAAR.E	
102	111	2	1115.56	-0.74	0	38.8	27.1	95.00%	R.IPVSEDMLGR.I	
49	63	2	1702.89	-1	0	64	26	95.00%	R.YNEIVNLTLPDGTVR.Q	
91	111	3	2336.17	-0.64	1	35.2	27.7	95.00%	K.TTVEFTGESLRIPVSEDMLGR.I	
453	466	2	1663.86	0.83	0	56.9	27.2	95.00%	R.TVFESLDQAWSLLR.I	
303	318	2	1927.87	-0.46	0	82.2	30	95.00%	R.GYPGYMYTDLSTIYER.A	
170	189	2	2193.13	-1.5	0	71.4	25.7	95.00%	K.IPIFSASGLPHNEIAAQICR.Q	Carbamidomethyl (+57)
480	487	2	1069.51	0.069	0	26.9	26.7	90.90%	K.ILDEFYDR.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
56	BPT1_YEAST	14.75%	100%	17							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
1065	1077	2	1468.7	-4	0	48.9	28.6	95.00%	R.SPMTFFETTPVGR.I		
1343	1351	2	1006.58	0.67	0	29	21.2	95.00%	K.STLSLALFR.I		
726	744	3	2358.15	-0.59	1	32.6	28.7	95.00%	R.ENILFGHKFDQDYYDLTIK.A		
1311	1325	3	1799.95	0.61	1	54.1	24.9	95.00%	K.YRENLDPVLNNINVK.I		
487	497	2	1395.63	0.63	0	30.3	28.4	93.40%	K.LYAWEEPMMAR.L		
1431	1448	2	1946.83	-0.73	0	84.3	30	95.00%	R.GDDSNEEDGNVNDILDVK.I		
1523	1532	2	1098.64	1.1	0	25.1	22.1	90.80%	K.IIVLDQGSVR.E		
807	816	2	1160.68	-0.53	0	46.3	19.2	95.00%	K.NIIEYVLIGK.T		
1273	1290	2	2115.02	-0.09	0	58.6	29.5	95.00%	R.IVEYCELPPEAQSINPEK.R	Carbamidomethyl (+57)	
1410	1423	4	1654.93	0.5	1	35.8	21.7	95.00%	K.RAVEQAHLKPHLEK.M		
1504	1513	3	1194.68	-0.25	1	39.9	20	95.00%	K.DRTILTIAHR.I		
1449	1461	2	1386.69	0.64	0	63.5	27.8	95.00%	K.INENGSNLSVGQR.Q		
1377	1394	2	1924.01	-0.0085	0	58	25.9	95.00%	R.SHLAIIPQDAQAFEGTVK.T		
1506	1513	2	923.56	0.52	0	30.7	17.2	95.00%	R.TILTIAHR.I		
611	625	2	1759.93	-0.36	0	55.4	24.8	95.00%	R.ALPAIEMNNITFLWK.S		
745	753	2	1056.56	0.77	0	27	24.7	93.70%	K.ACQLLPDLK.I	Carbamidomethyl (+57)	
628	655	3	2976.49	-0.19	1	67.4	26.4	95.00%	K.EVLTSSQSGDNLRTDEESIIGSSQIALK.N		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
57	HIP1_YEAST	16.92%	100%	8							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
9	30	2	2499.16	-0.86	0	77.7	30.7	95.00%	K.EYWADVVDGFKPATSPAFENEK.E		
53	69	2	1819.82	0.54	0	68.7	30.2	95.00%	K.DSPGINQTTNDITSSDR.F		
31	42	2	1341.67	-0.31	0	56	26.8	95.00%	K.ESTTFVTELTSK.T		
73	88	2	1862.82	1.5	0	90.7	30.3	95.00%	R.NEDTEQEDINNTNLSK.D		
43	69	3	2853.33	0.95	1	74.7	30.8	95.00%	K.TDSAFPLSSKDSPGINQTTNDITSSDR.F		
72	88	2	2018.91	-0.41	1	80.8	29.8	95.00%	R.RNEDTEQEDINNTNLSK.D		
400	412	3	1440.7	-0.18	0	40.7	28.1	95.00%	R.CMVAMAHIGNLPK.F	Carbamidomethyl (+57)	
561	571	3	1291.61	-0.078	1	44.3	28.4	95.00%	K.LEDMDLDTGRK.Q		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
58	A6ZQQ8_YEAS7	30.89%	100%	8							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
494	507	2	1555.84	-0.31	0	58	24.1	95.00%	K.EIGWCLGASLPLLK.A	Carbamidomethyl (+57)	
47	80	3	3787.83	-1.6	1	60.7	29.7	95.00%	K.TPEDISILPVNDEPGYLQDSKTEQNYPELADAVK.S		
375	395	3	2383.08	-0.55	0	35.9	30.8	95.00%	K.DAQCQSPPCSFNGVHQPSLVR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	
111	151	3	4441.12	-1.3	1	55.4	28.8	95.00%	K.FDVCTSPPTLLDEKFDMLEPGLSSFDTDSVGAANSLDPLLK.V	Carbamidomethyl (+57)	
300	310	2	1184.68	-0.013	0	65	23.2	95.00%	K.VNSVLVENALK.D		
37	46	2	1026.57	0.76	0	26.8	21.9	93.40%	R.TVTPNASIPK.T		
413	432	3	2257.19	0.04	0	55.6	24.4	95.00%	R.TRPLGMPLSFTLNELNDLAR.I		
366	374	2	1091.59	-0.025	0	45.6	24.8	95.00%	R.FLTDEILNK.D		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
59	A7A201_YEAS7	58.74%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
28	46	2	2199.99	0.18	0	84.5	30.9	95.00%	R.FSDDTYTNDYISTIGVDFK.I	
11	21	2	1070.63	0.63	0	40	23.1	95.00%	K.LLLIGNSGVGK.S	Deamidation (+1)
72	79	2	989.48	0.9	0	25.5	25.4	90.60%	R.TITSSYYR.G	
101	116	2	1953	-0.36	1	56.3	26.4	95.00%	K.MWLQEIDRYATSTVLK.L	
171	184	2	1636.74	-0.79	0	67.2	29.3	95.00%	K.ESMSQQNLNETTQK.K	
101	108	2	1089.53	-0.2	0	53.5	28.3	95.00%	K.MWLQEIDR.Y	
59	69	2	1315.65	0.75	0	47	27.7	95.00%	K.LQIWDTAGQER.F	
168	184	3	2005.97	-0.13	1	35	28.9	95.00%	R.QIKESMSQQNLNETTQK.K	
145	167	2	2558.2	-0.012	0	102	30.2	95.00%	K.MPFLETSALDSTNVEDAFLTMAR.Q	
22	27	2	760.43	1.9	0	25.1	22.8	90.80%	K.SCLLLR.F	Carbamidomethyl (+57)
1	10	2	1366.58	0.078	0	39.8	28.1	95.00%	-.MNSEYDYLFK.L	Acetyl (+42)/ Oxidation (+16)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
60	B3LPM9_YEAS1	12.53%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
43	72	3	3385.58	-0.68	0	96.2	30.4	95.00%	K.HHVVEPHDANDENLPLLADASPDDQFYISK.F	
115	132	2	2124.08	-0.51	0	75.4	26.8	95.00%	K.ATQLFNQQQQHQLQSVAR.N	
353	359	2	907.39	0.2	0	30.1	25.4	95.00%	K.DMMNLER.K	
73	82	2	1131.63	2.1	0	50.5	24.3	95.00%	K.FVAALNQELK.K	
334	347	3	1761.89	0.68	1	34	27	95.00%	R.ELSSHLRDHVVWER.N	
87	114	3	3290.56	-0.42	1	76.6	29.3	95.00%	K.FYISQETGLIANYNELKDDVMELENTNK.A	
348	359	2	1535.72	-0.73	1	50.3	28.4	95.00%	R.NTVWKDMMNLER.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
61	A6ZM61_YEAS7	39.42%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
161	174	2	1561.77	-0.024	0	85.8	28	95.00%	K.NAINVDTAFEEIAR.S	
57	70	2	1590.75	0.94	0	70.2	28.8	95.00%	K.VATMQVWDTAGQER.F	
39	48	2	1035.56	-0.22	0	43.9	24.3	95.00%	K.ATIGADFLTK.E	
81	101	2	2361.06	-0.15	0	98.4	30.5	95.00%	R.GADCCVLVYDVTNASSFENIK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
148	160	2	1360.76	0.42	0	49.8	21.3	95.00%	K.SLGDIPLFLTSAK.N	
71	80	2	1186.62	1.7	0	41	25.6	95.00%	R.FQSLGVAFYR.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
62	A6ZL18_YEAS7	10.04%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
221	233	2	1277.66	1.2	0	64	26.3	95.00%	K.YVINLEGTGAGGK.A	
816	830	2	1698.94	-0.42	0	61.7	21.3	95.00%	R.SPYEPIVAELLLEVK.E	
605	616	2	1266.55	0.62	0	71.5	27.1	95.00%	K.GSNSMEEGLSTR.E	
726	745	3	2112.07	-0.46	0	78.8	26.9	95.00%	R.FSQNIDLSQGNAASVHVLGR.E	
287	296	2	1237.62	-0.83	0	47.4	26.8	95.00%	R.GWDVAFYKPR.N	
129	140	2	1398.74	-0.0082	0	36.6	25	95.00%	R.VTYFESSNILVK.L	
254	269	2	1905.86	-0.058	0	79.3	29.5	95.00%	K.ENPFGNSIYQQGFYSR.Y	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
63	A6ZSU5_YEAS7	28.57%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
380	394	2	1652.76	-1.3	0	43.1	28.9	95.00%	R.GTFQSSGQNCIGIER.V	Carbamidomethyl (+57)
572	585	2	1463.71	-0.2	0	79.2	27.9	95.00%	K.FGGEEGLLGLCNAK.S	Carbamidomethyl (+57)
144	155	2	1354.59	-0.24	0	44.4	28.8	95.00%	K.AQSTWGNSDFSR.R	
507	532	3	2674.28	0.052	0	63.5	28.7	95.00%	K.NTDHCVQLANSAPFGLGGSVFGADIK.E	Carbamidomethyl (+57)
395	407	2	1520.81	-0.33	1	53.9	25.6	95.00%	R.VIVSKENYDDLVK.I	
327	342	3	1823.01	-0.046	0	22.2	22.1	90.80%	K.HITFIGSQPVAHYILK.C	
470	489	3	2362.17	-0.12	0	32.7	28.5	95.00%	K.YPQGHYFQPTLLVDVTPEMK.I	
81	94	2	1571.77	-0.4	0	49.4	28	95.00%	K.FSLPAPEAAQNNWK.G	
369	379	2	1247.66	0.78	0	62.4	25.8	95.00%	K.NLDALSSIIMR.G	Oxidation (+16)
347	358	2	1197.7	-0.51	0	31.2	21.2	95.00%	K.SLTPVVVELGGK.D	
185	200	2	1749.89	0.39	0	89	27.6	95.00%	K.TMLDASMGEILVTLEK.I	
490	504	2	1688.9	0.17	0	49.6	24.7	95.00%	K.IAQNEVFGPILVMMK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
64	A6ZQK0_YEAS7	9.08%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
1190	1228	4	4131.03	-0.62	0	21.1	27.9	94.10%	R.NGELVMHVVSEHVENAGVHSGDATLIVPPQDLAPETVDR.I	
325	337	3	1398.67	0.24	0	33.2	28.7	95.00%	R.GHNIPCTSTISGR.C	Carbamidomethyl (+57)
599	615	2	1638.8	-0.26	0	58.3	28.5	95.00%	R.AAYALGGLGSGFANNEK.E	
1551	1564	2	1385.78	-0.08	0	32.1	22.6	95.00%	R.SISGPVITDVASLK.A	
752	762	2	1208.71	-0.35	0	32.9	16.6	95.00%	K.LGLNIPLNEVK.N	
855	864	2	1050.59	0.82	0	45.4	23.6	95.00%	R.VFAIANAFAK.K	
467	489	3	2529.41	-0.27	1	28.1	20	95.00%	K.ALKEEGIYTILINPNIATIQTSK.G	
2000	2011	2	1398.66	-0.7	0	34.5	28	95.00%	R.TLACYSDAIVMR.H	Carbamidomethyl (+57)
1242	1253	2	1363.75	-0.38	0	27.9	22.8	94.70%	K.ITGPYNIQFIAK.D	
1635	1650	2	1713.96	0.58	0	29.6	20.8	95.00%	K.TADLASVLLLTSLQNR.S	
575	589	2	1472.75	-0.96	0	59.3	26.4	95.00%	K.SQAANSVDEALAAVK.E	
180	198	2	2143.06	0.36	0	56.6	28.7	95.00%	R.SAFDVPEWVDPNVQNLVSK.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
65	A7A052_YEAS7	11.81%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
318	333	4	1827.93	0.44	1	21.3	27.1	95.00%	K.NKFDFNAAKPSVHPEK.N	
2	16	2	1682.71	5.7	0	47.4	29.3	95.00%	M.LNHPSQGSDDAQDEK.Q	Acetyl (+42)/ Deamidation (+1)
35	48	2	1556.66	1.5	0	60.9	28.9	95.00%	K.DSYVSDDVANSTER.Y	
1	27	4	3042.35	-0.68	1	42.4	32	95.00%	-.MLNHPSQGSDDAQDEKQGDFPVIEEEK.T	
1	16	2	1829.75	5.6	0	55.2	29.3	95.00%	-.MLNHPSQGSDDAQDEK.Q	Acetyl (+42)/ Oxidation (+16)/ Deamidation (+1)
583	596	2	1628.8	-2	0	68.5	26.8	95.00%	K.ANDIEILEPMESLR.S	
17	27	2	1289.61	-0.72	0	27.2	26.7	91.50%	K.QGDFPVIEEEK.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
66	A6ZT96_YEAS7	25.23%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
2	15	3	1575.92	0.83	1	54.7	16.9	95.00%	M.GKLLQLALHPVEMK.A	
340	350	2	1433.66	-0.82	0	44.3	28.9	95.00%	R.GCVEIFDYYLR.D	Carbamidomethyl (+57)
226	235	2	1194.52	-0.35	0	49.5	27.7	95.00%	R.DYNEDLVDGR.S	
121	135	2	1760.93	-0.13	0	70.1	25.1	95.00%	R.AVLTDFESILIEFHK.L	
136	145	3	1245.7	-0.79	0	26.6	24	95.00%	K.LKPEYQEVIK.E	
4	15	2	1390.8	-0.0092	0	46.5	19.1	95.00%	K.LLQLALHPVEMK.A	
356	365	2	1143.63	1.1	0	31.8	23.9	95.00%	K.LAVQDPNFLK.L	
366	372	2	814.49	1.1	0	34.4	24.5	95.00%	K.LNIQISK.I	
136	150	3	1846.01	-0.21	1	32.1	23.1	95.00%	K.LKPEYQEVIKEITEK.M	
373	384	2	1589.67	-0.32	0	65.9	28.7	95.00%	K.IEQFMEEMYQDK.L	
119	135	3	2032.06	0.63	1	54.3	25.2	95.00%	K.DRAVLTDFESILIEFHK.L	
108	118	2	1234.56	-0.1	0	35.4	27.7	95.00%	K.WSFDGNAPDVK.D	
221	235	3	1791.88	0.057	1	46.7	28.2	95.00%	K.TNIIRDYNEDLVDGR.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
67	A6ZNT9_YEAS7	59.52%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
27	36	2	1169.54	0.31	0	52.3	27.3	95.00%	R.FVSNDFAENK.E	
37	48	2	1302.69	-0.41	0	32.8	25.9	95.00%	K.EPTIGAAFLTQR.V	
156	170	2	1590.79	0.047	0	69.8	27.5	95.00%	K.TGENVNDVFLGIGEK.I	
10	20	2	1068.65	-0.019	0	27.6	14.1	94.40%	K.LVLLGEAAVGK.S	
58	68	2	1350.62	-0.24	0	70.8	29.1	95.00%	K.FEIWDTAGQER.F	
27	48	3	2454.22	-0.58	1	35.6	28.8	95.00%	R.FVSNDFAENKEPTIGAAFLTQR.V	
79	97	2	2091.14	-0.53	0	79.3	21.6	95.00%	R.NAQAALVVYDVTKPQSFIK.A	
69	78	2	1217.59	0.15	0	44.1	26.6	95.00%	R.FASLAPMYYR.N	
104	121	3	1977.09	-0.6	1	49.6	20.1	95.00%	K.ELHEQASKDIIIALVGNK.I	
1	9	2	1037.51	0.87	0	34.2	28.1	95.00%	-.MNTSVTSIK.L	Acetyl (+42)/ Oxidation (+16)
146	155	2	1111.59	-0.21	0	48.5	23.6	95.00%	K.GLLFFETSAK.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
68	A6ZNV4_YEAS7	40.64%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
137	152	2	1821.91	-0.28	1	57.2	27.8	95.00%	R.TEAVRQDPESSYISIK.V	
29	42	2	1635.81	-0.38	0	74.8	27.9	95.00%	K.ELSNLIETFAEQSR.V	
142	152	2	1265.61	-0.32	0	41.9	27.9	95.00%	R.QDPESSYISIK.V	
13	26	2	1591.72	0.94	0	72.6	29.5	95.00%	K.GNSQQEPQFSTNQK.T	
102	112	2	1413.66	-0.41	0	69.7	28.6	95.00%	K.YQSLQQSYNQR.K	
223	247	3	2864.3	0.25	0	48.5	30.8	95.00%	K.EQGEQVTTIDENISHLHDNMQNANK.Q	
62	76	3	1821.93	0.41	1	24	26.9	90.50%	R.YKIETELIPNCTSVR.D	Carbamidomethyl (+57)
203	222	3	2203.21	0.28	0	67.6	20.8	95.00%	R.IHTAVQEVNAIFHQLGSLVK.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
69	A6ZKY2_YEAS7	17.34%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
349	369	2	2284.11	2.1	0	78.4	29.2	95.00%	K.VNQGSLDYLAALGVYQEDMAK.A	

121	147	3	2965.39	-1.5	0	47.2	30.7	95.00%	R.DNADLPVDPYHLSPQQQPSNNLFGSGR.L	
103	120	3	1968.02	0.15	1	36.6	25.9	95.00%	K.RAGEAVIHLSEGSNLYPR.D	
246	253	2	883.51	0.085	0	27.4	20.8	94.10%	K.GLLDTLPR.R	
223	232	2	1069.55	0.074	0	38.8	25.8	95.00%	R.MVSDLPPPSK.K	
564	572	2	1130.62	0.63	0	28.2	25	95.00%	R.ILCWELVAK.R	Carbamidomethyl (+57)
93	102	2	1119.56	0.34	0	46.1	26.7	95.00%	R.YAANLQESPK.R	
828	840	2	1585.76	-0.76	0	92	28.4	95.00%	K.QIVETDWPQEVDK.K	
235	245	3	1220.75	-0.0033	1	25.4	12.6	94.80%	K.ALLKLDNPIPK.G	
457	472	2	1621.78	-0.69	0	98.9	28.3	95.00%	K.VFDMDSNVAGAAGQIK.T	
538	548	2	1285.59	-0.092	0	55.9	27.9	95.00%	R.SYFLGETQEGR.D	
264	276	2	1585.71	-0.5	0	38.2	29.5	95.00%	R.YTACTVEPDDFLR.E	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
70	B3LH18_YEAS1	8.52%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
181	195	2	1663.83	-0.079	1	49.9	27.8	95.00%	R.ATLPHGKEDHFIDGK.I	
1	20	2	2175.11	-1.6	1	41.3	26.3	95.00%	-.MDATTPLLTVANSHPARNPK.H	Acetyl (+42)
1	17	2	1835.92	-0.7	0	84.2	27.6	95.00%	-.MDATTPLLTVANSHPAR.N	Acetyl (+42)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
71	A6ZQN6_YEAS7	16.88%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
616	624	2	1100.53	-0.028	0	41.2	27.1	95.00%	K.FFTHFTSSK.D	
1	25	3	2868.36	-0.22	0	41.6	30.6	95.00%	-.MDPGIANHTLPEEFEEVVVPEMLEK.E	Oxidation (+16)
584	599	2	1740.85	0.1	0	53.8	28.8	95.00%	K.LTDSIALEGNDHLESK.N	
600	613	2	1741.84	-0.77	1	71	29.2	95.00%	K.NTFEIEEKEESFLK.N	
520	547	3	3090.49	-3.1	0	47.1	29.3	95.00%	R.ISDPTLAAQAYGSPFTFITTYTWGTPER.I	
259	268	3	1187.66	-0.095	0	44	24.5	95.00%	R.LKPEFEALNK.L	
519	547	3	3246.6	1	1	72.6	27.6	95.00%	K.RISDPTLAAQAYGSPFTFITTYTWGTPER.I	
581	599	3	2120.05	-0.045	1	54.7	28.4	95.00%	R.NHKLTDSIALEGNDHLESK.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
72	A6ZWP0_YEAS7	12.31%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
958	971	2	1612.78	-0.75	1	66.6	28.1	95.00%	R.SQKDFIQAYSDGVR.I	
91	103	2	1443.72	-0.66	0	51.6	27.2	95.00%	K.AQPLISSCPACLK.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
961	971	2	1269.6	0.46	0	46.9	27.6	95.00%	K.DFIQAYSDGVR.I	
33	45	2	1470.73	-0.68	0	34.2	27.6	95.00%	K.SVFGNELPCPVPR.S	Carbamidomethyl (+57)
831	841	2	1272.63	1.1	0	47.3	27.1	95.00%	R.DSLANVLEQER.H	
185	203	3	2082.06	-0.24	0	28	27.2	95.00%	K.FLGDAKPMLGGSPFQINYK.Y	
476	489	2	1687.87	-0.94	0	33.6	26.1	95.00%	K.FPVNCLPTFQQPLK.T	Carbamidomethyl (+57)
161	177	2	1671.79	-0.85	0	88.4	29	95.00%	K.FSATNGYAMDLIGGGAK.N	
104	120	2	2070.88	-0.71	0	61	29.7	95.00%	K.NFNNLFCHFTCAADQGR.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)

521	533	3	1734.88	-0.23	1	29.1	26.9	95.00%	R.WEERLEEYLLDLK.V	
46	58	2	1434.69	0.75	0	29.8	28.5	92.60%	R.SFEPPVLSDETSK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
73	A7A0Z7_YEAS7	35.97%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
14	27	2	1642.73	-1.2	0	73.2	29.1	95.00%	K.NGETISSCFQPFQK.N	Deamidation (+1)/ Carbamidomethyl (+57)
3	13	2	1352.75	0.36	1	31.9	21.8	95.00%	K.RFNVSYVEVIK.N	
108	143	4	4119.01	-0.13	0	37.3	28.3	95.00%	R.ILSGLQEYESNATNELLSSHVGQILDSFHEELVEYR.N	
28	57	3	3401.7	-0.32	0	56.4	28	95.00%	K.NENYGTITSANEQITPVIFHNLIMDMVLPK.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
74	A6ZT03_YEAS7	23.86%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
518	536	2	2149.04	0.5	0	92.5	29	95.00%	K.GLSLEEVNDMYAEGVLPWK.S	
1	12	2	1387.66	-0.5	0	48.4	28.2	95.00%	-.MNSTPDLISPQK.S	Acetyl (+42)/ Oxidation (+16)
546	564	2	2269.97	-1.2	1	65.4	31.4	95.00%	K.RGADYNADDLMHDDQPFYK.S	
305	324	2	2125.04	-2	0	82.3	28.9	95.00%	R.AAGTASWGELFTGKPAMFQR.T	
262	273	3	1390.72	-0.22	1	24.6	26.2	92.60%	R.YLVEAGRIDEAR.A	
282	304	3	2805.26	0.23	0	37.4	31.8	95.00%	K.CPPDHPYIQYELETIEASVEEMR.A	Carbamidomethyl (+57)
228	236	2	1153.52	0.85	0	47.9	28.1	95.00%	K.NYSNSVQWR.V	Deamidation (+1)
537	545	2	959.51	0.5	0	44.9	25.4	95.00%	K.SASWVPVSK.R	
13	25	2	1508.58	0.1	0	48.4	27.4	95.00%	K.SNSSNSYELESGR.S	Phospho (+80)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
75	PMT1_YEAST	14.69%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
408	425	3	2113	-0.28	0	30.5	29.2	95.00%	R.LHSHDHKPPVSESSDWQK.E	
9	22	2	1651.84	-0.14	1	56.1	26.4	95.00%	K.RVEQDDPVPELDIK.Q	
504	525	3	2653.31	-3	1	61.1	28.6	95.00%	R.HDLTLWYVENNSNPLLPEDTKR.I	
799	812	2	1601.83	-0.017	1	76.9	25.9	95.00%	K.MLEEEGANILKVEK.R	
486	503	2	2021.93	0.4	0	98.8	29.9	95.00%	K.LPAWGFEQQEVTCASSGR.H	Carbamidomethyl (+57)
23	42	3	2152.16	-0.24	0	60.1	22.5	95.00%	K.QGPVRPFIVTDPSAELASLR.T	
472	485	3	1678.76	-0.033	0	31.3	29.4	95.00%	R.HAMTGCYLFSHEVK.L	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
76	A6ZQY0_YEAS7	58.74%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
181	215	3	3476.58	-2.1	0	46.5	31.2	95.00%	K.HQMDLGDSSANGNANGASAPNGPTISLTPTPNENK.K	
62	74	2	1514.78	-1.1	1	64.2	26.6	95.00%	R.IKAQIWDTAGQER.Y	
33	43	2	1359.61	-0.39	1	50.4	28.2	95.00%	R.FTKNEFNMDSK.S	
16	26	2	1056.62	0.27	0	32.4	22.8	95.00%	K.IVLIGDSGVGK.S	

143	165	2	2598.24	-0.62	0	125	28.9	95.00%	K.TFAQENQLLFTETSALNSENVDK.A	
64	74	2	1273.61	-0.17	0	64.6	27.7	95.00%	K.AQIWDTAGQER.Y	
181	216	3	3605.67	0.99	1	66.5	31.4	95.00%	K.HQMDLGDSSANGNANGASAPNGPTISLTPTPNENKK.A	Deamidation (+1)
113	127	2	1527.75	-1.3	0	74.8	27.8	95.00%	R.ENADDNVAVGLIGNK.S	
44	53	2	1079.56	0.067	0	61.1	25.3	95.00%	K.STIGVEFATR.T	
166	177	2	1467.76	-0.28	0	44.5	25.7	95.00%	K.AFEELINTIYQK.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
77	ZRT3_YEAST	10.34%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
176	185	2	1188.69	-0.35	1	42.7	20.4	95.00%	K.KMSLIDLLTR.R	
177	185	2	1060.6	0.17	0	48.3	23.1	95.00%	K.MSLIDLLTR.R	
246	266	3	2468.24	-0.71	1	27.4	28.3	93.40%	R.GLVCVENNIGYDLENLSLYRK.N	Carbamidomethyl (+57)
246	265	2	2340.14	-1.1	0	97.3	29	95.00%	R.GLVCVENNIGYDLENLSLYR.K	Carbamidomethyl (+57)
198	218	2	2441.23	-0.14	0	64.4	27	95.00%	K.CTPLLQSEQPEYIACVPPVIK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
78	YIL7_YEAST	26.10%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
273	289	3	1852.9	0.27	1	39	28.1	95.00%	K.LLNSPESDGSVNRNHSK.G	
192	205	2	1566.83	0.18	0	43.7	24.2	95.00%	R.NSLFISPTGDILYK.T	
273	285	2	1386.67	-0.52	0	61.9	27.3	95.00%	K.LLNSPESDGSVNR.N	
272	285	2	1514.77	-1.8	1	85.9	26.3	95.00%	R.KLLNSPESDGSVNR.N	
117	137	3	2513.07	-0.66	0	48.2	31.2	95.00%	K.MFSTQHTQFYGDSPYMDYPAK.E	
162	191	4	3418.69	-0.5	0	26.9	28.2	95.00%	K.DALVSHTNNEKPFLSNFERPLFSLASESNR.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
79	A6ZNR5_YEAS7	11.89%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
285	300	2	1637.73	-1.1	1	89.8	29.7	95.00%	R.VGKGDDEANGATSFDR.T	
176	191	3	1665.87	-0.29	0	25.2	25.6	94.00%	K.AHLAEIQLNGGSISEK.V	
175	191	3	1793.96	0.17	1	34.3	23	95.00%	K.KAHLAEIQLNGGSISEK.V	
38	50	2	1409.79	-0.65	0	37.9	19.9	95.00%	R.SKPVALTSFLGYK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
80	YO092_YEAST	11.36%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
138	162	3	2661.16	-0.42	1	67	31.2	95.00%	R.IDEEMAAPSSDGNAGDDNLREVNSR.N	
1	10	2	1211.67	0.23	0	30.4	22.3	95.00%	-.MQLVPLELNR.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
81	GAS1_YEAST	10.91%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
194	209	2	1793.84	-0.4	1	95.9	28.9	95.00%	K.IPVGYSSNDDEDTRVK.M	

223	236	2	1752.73	-0.39	0	57.8	29.1	95.00%	K.ADFYGINMYEWCGK.S	Carbamidomethyl (+57)
194	207	2	1566.68	-0.84	0	93.4	28.9	95.00%	K.IPVGYSSNDDEDTR.V	
415	424	2	1192.52	0.27	0	36	27.5	95.00%	K.YGAYSFCTPK.E	Carbamidomethyl (+57)
210	222	2	1535.59	-1.4	0	85.3	26.7	95.00%	K.MTDYFACGDDDVK.A	Carbamidomethyl (+57)
83	90	2	956.58	2.2	1	40.2	21.1	95.00%	K.KLNTNVIR.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
82	A7A0E5_YEAS7	14.76%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
353	383	3	3463.62	-0.75	0	111	30.2	95.00%	K.NQALGGSLLHSHIQTYPDGSNQQQVTCYGYK.D	Carbamidomethyl (+57)
426	438	3	1369.75	0.44	0	27	23.1	95.00%	R.NLHTHPVAAPVSK.T	
744	759	2	1985.92	-0.51	1	44	29.2	95.00%	R.YLNWFSTWDIADKQEA.-	
384	393	2	1311.56	-0.11	0	42.3	27.9	95.00%	K.DANNEWFFNR.E	
341	352	2	1187.68	-0.34	0	45.5	22.7	95.00%	R.DIALGSSVVSIK.N	
439	455	2	1866.84	-0.055	0	89.9	29.8	95.00%	K.TQWEVSGYGDNVVGDNK.D	
106	118	4	1574.76	0.079	0	32.8	28.6	95.00%	R.HEFYHDVHPPLGK.M	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
83	A6ZVM2_YEAS7	13.86%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
314	325	2	1292.68	-0.86	0	78.3	25.4	95.00%	K.HADANVQLVAQK.M	
824	852	3	3224.5	-0.16	0	53.9	31.2	95.00%	K.AFSSLNDIPITPSHDNNPHSFAEPMPAYR.G	
36	47	2	1412.6	-1.1	0	83.4	28	95.00%	K.LDAEEEQSSSYR.S	
34	47	2	1669.74	-0.91	1	75.5	29.3	95.00%	K.EKLDAEEEQSSSYR.S	
196	204	2	1094.58	-0.25	0	39.6	25.2	95.00%	R.LSLLAYCQK.V	Carbamidomethyl (+57)
326	345	2	2176.04	0.14	0	114	28.9	95.00%	K.MQQITSSQPTPTSELSSAQR.D	
3	16	2	1670.81	-0.2	0	52.7	28.8	95.00%	K.FADHLTESAIPEWR.D	
797	823	2	2734.26	-2.7	0	64.5	30.9	95.00%	R.VTGDAPLPYPIAQVGDDSMDSSDLGSK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
84	A6ZNT8_YEAS7	13.93%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
465	480	2	1841.82	-1	0	46.2	30.1	95.00%	K.VIDNADDEYMALMSQK.T	
653	667	2	1684.96	0.28	1	79.6	18.1	95.00%	K.KVENLTAVITDLLEK.L	
2	33	3	3450.6	1.6	0	51.4	30.6	95.00%	M.VSANGDLHLPISNEQCMPENNGSLGFEAPTPR.Q	Carbamidomethyl (+57)
125	133	2	1060.53	0.4	0	31.9	26.7	95.00%	R.NLASQQLCK.L	Carbamidomethyl (+57)
49	70	2	2508.26	0.05	0	43.7	27.7	95.00%	K.VVPIVYDPNDIVCDHSEILSPK.V	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
85	A6ZKW1_YEAS7	23.62%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
83	98	2	1920.91	-0.38	0	63.5	29.1	95.00%	K.SFYNNVFNFLMVDSPK.G	
55	80	3	2701.12	0.3	1	52.2	31.5	95.00%	K.YSSSSDAASADDSTPLRDNDEAGNEK.L	
560	569	2	1178.58	-0.85	0	40.1	26.1	95.00%	K.YLDDLLGQDK.T	

536	545	2	1283.6	-0.18	0	31.3	28.2	94.90%	K.NYDIELENFK.V	
320	333	2	1575.79	-0.14	1	58.5	27.5	95.00%	R.NSRDDITPPAVYTK.D	
418	447	4	3435.53	-0.63	1	35.4	31.9	95.00%	R.TRTGVEGYHDEDGFHGVAMLQHDFVQDYGR.Y	
448	458	2	1238.6	-0.25	0	51	28.3	95.00%	R.YLNAMESIGNK.Y	
479	492	2	1733.74	-1.1	0	49.8	29.4	95.00%	K.YTEEFFDNEDLNAK.N	
546	555	2	1236.62	-1.4	0	46	27.6	95.00%	K.VLNEYVCVNK.N	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
86	A6ZXZ5_YEAS7	20.31%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
95	110	3	1943.93	2	1	36.4	29.6	95.00%	K.YNHVQTSTQKEHPGYR.Q	
268	284	2	1788.85	0.43	0	34.8	29.5	95.00%	K.LGYHFGPSDAEAVMAPK.A	
285	300	2	1575.87	-0.34	0	48.8	22.4	95.00%	K.APVASPRPAATPNLSK.D	
18	31	2	1524.77	-0.55	0	71.2	27.1	95.00%	K.INPPTGADFHITSR.G	
285	302	3	1818.99	-0.28	1	22.7	23.1	91.50%	K.APVASPRPAATPNLSKDK.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
87	A6ZMQ9_YEAS7	37.79%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
167	178	2	1413.68	-0.074	0	54.6	28.5	95.00%	R.QTLFQADSYVDK.S	
103	117	2	1691.77	-0.43	0	68.3	29.4	95.00%	R.LFGDLNASNIDDDQR.Q	
118	129	2	1391.79	-0.72	0	46.3	21.5	95.00%	R.QQLLSNHAILQK.S	
21	34	2	1453.75	-0.49	0	51.8	25.5	95.00%	K.ASLAEAPSQPLSQR.N	
2	13	2	1429.7	0.36	0	61	28.5	95.00%	M.SSLLISYESDFK.T	Acetyl (+42)
103	129	3	3065.55	-1.4	1	56	27	95.00%	R.LFGDLNASNIDDDQRQQLLSNHAILQK.S	
140	156	2	1892.9	0.51	0	57.5	29.3	95.00%	R.IANETEGIGSQIMMDLR.S	Oxidation (+16)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
88	A7A077_YEAS7	12.68%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
271	287	3	1889.03	0.11	1	29.9	23	95.00%	K.YKPNLVLGENSLDATKK.H	
104	113	2	1195.56	0.23	0	34.8	28.1	95.00%	R.IDSEEAEYIK.L	
257	270	2	1602.84	0.24	0	59.1	25.7	95.00%	R.GSVPIYWAEINNLK.Y	
294	308	2	1780.9	-0.34	0	61.6	27.8	95.00%	K.ELYGDNYLVNLVNQK.G	
175	188	2	1612.85	-0.38	0	55.1	25.7	95.00%	R.IDSFIQPVIYGYAK.T	
390	398	2	1183.44	0.21	0	45.4	24.8	95.00%	R.TNCMDCLDR.T	Carbamidomethyl (+57)/Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
89	A6ZX41_YEAS7	44.98%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
128	137	2	1212.61	-0.18	0	77.4	27.4	95.00%	R.NDPQTIEQLR.Q	
2	10	2	1029.52	2.1	0	26	25.6	91.10%	M.SQQVGNSIR.R	Acetyl (+42)
104	123	3	2338.23	-0.74	0	25.6	23.4	95.00%	K.WIAEVLHFCQGVPIILVGCK.V	Carbamidomethyl (+57)/Carbamidomethyl (+57)
174	181	2	921.46	1.4	0	32.1	26.7	95.00%	R.EVFEAATR.A	
128	167	3	4410.03	-1.1	1	71.3	30.2	95.00%	R.NDPQTIEQLRQEGQQPVTSQEGQSVADQIGATGYYECSAK.T	Carbamidomethyl (+57)

57	73	2	2035.96	-0.35	1	85.2	29.8	95.00%	R.RVELALWDTAGQEDYDR.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
90	NCB5R_YEAST	39.44%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
37	48	2	1478.75	-0.83	1	48.3	27.8	95.00%	K.RNDFQSFPLVEK.T	
91	102	2	1283.59	-0.71	0	32.9	28.2	95.00%	R.SYTPTSLDGDTK.G	
195	208	2	1589.85	-0.27	0	40	25	95.00%	K.ELEALVAMKPSQFK.I	
209	230	3	2546.23	-0.58	1	27.7	29.5	92.30%	K.IVYYLDSPDREDWTGGVGYITK.D	
60	80	4	2238.25	0.33	0	28.3	18.6	95.00%	K.FGLPHADDVLGLPIGQHIVIK.A	
49	59	2	1307.65	-0.0036	0	57	27.3	95.00%	K.TILTHNTSMYK.F	
147	166	2	2075.04	-0.72	0	51.6	27.2	95.00%	R.SHLGMIAGGTGIAPMYQIMK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
91	A6ZS21_YEAS7	26.11%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
298	314	2	1916.97	-0.85	1	29	27.8	92.50%	R.QAPSMFLDDVLNGREII.-	
271	292	3	2214.16	-0.49	1	46.5	25.5	95.00%	K.RNQSSLGLIPVASATSNTSSPK.K	
142	157	2	1816.83	2	0	58.2	30.1	95.00%	K.HSSSLQSNPFDINDEK.S	
298	311	2	1561.75	-0.78	0	63	28.3	95.00%	R.QAPSMFLDDVLNGR.E	
195	209	2	1738.91	-0.35	0	63	24.9	95.00%	R.SLFISPTLQVSQYEK.S	
122	133	2	1377.59	-0.59	0	49.4	29.1	95.00%	R.FTMTNSYANDSK.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
92	YL001_YEAST	13.11%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
485	496	2	1391.74	-0.3	0	26.8	24.2	93.30%	K.ELNLLDLPSNHK.G	
551	563	2	1377.73	-0.14	0	82.3	26.2	95.00%	K.NLYGNSVSIGVQK.I	
801	844	4	4728.39	-1.5	0	27.5	26.8	95.00%	R.ATTPLIQHSPIIHNPSYSATAHLSPLSQPTFEGSYSVNAIQTPR.D	
302	318	3	1963.02	0.047	0	49.5	26.1	95.00%	R.IFEIGVVHGFSDLDFLR.T	
247	265	2	2086.16	0.38	0	87.2	17.2	95.00%	R.TSLLQELIIDDVYGGILPK.E	
523	530	2	930.53	-0.13	0	41.6	25.3	95.00%	K.TALNLLMR.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
93	A6ZM72_YEAS7	17.38%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
27	37	2	1339.59	-0.49	0	53.2	28.1	95.00%	K.LETDESPIQTK.S	Phospho (+80)
296	309	2	1492.73	-0.69	0	87.2	27.8	95.00%	R.LAGNASWGELFSNK.G	
9	26	3	1924.98	-0.66	0	34.1	26.8	95.00%	R.VESGSQQTSIHSTPIVQK.L	
219	227	2	1153.52	0.77	0	47.9	28.1	95.00%	K.DYSNSVQWR.V	
273	295	2	2562.22	-0.83	0	97.3	29.9	95.00%	K.VTIEDPSIVAEMDTIMANVETER.L	
509	527	3	2220.11	-0.042	0	28.7	28	95.00%	K.GLTLEEVNEMYVEGVKPWK.S	
9	37	3	3166.6	-0.49	1	61.4	26.4	95.00%	R.VESGSQQTSIHSTPIVQKLETDESPIQTK.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
94	A6ZXE6_YEAS7	9.43%	100%	7						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
208	219	3	1520.74	-0.063	0	27.7	27.9	94.10%	K.SDFTLYHTWPVR.V	
2	9	2	842.43	0.47	0	41.8	24.4	95.00%	M.AGAIENAR.K	Acetyl (+42)
356	367	3	1445.71	0.37	0	26.1	27.1	93.40%	K.FTCNATHELVVR.T	Carbamidomethyl (+57)
925	937	2	1645.78	-1.2	0	44.7	29.5	95.00%	K.FYDSNYPEFPVLR.D	
446	455	2	1095.6	-0.29	0	48.3	22.9	95.00%	R.DLSLLGSHVR.K	
89	114	3	2811.52	0.04	0	51	20.7	95.00%	R.TGKPLSVELGPGLMETIYDGIQRPLK.A	
940	959	3	2256.2	-0.12	1	27.7	23.8	95.00%	R.MKEILSNAEELEQVVQLVGK.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
95	G3P3_YEAST	30.72%	100%	7						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
322	331	3	1107.63	-0.8	0	30.6	22.1	95.00%	R.VVDLVEHVAK.-	
161	184	3	2574.3	-0.19	0	43.3	27.2	95.00%	K.VINDAFGIEEGLMTTVHSLTATQK.T	
144	160	2	1818.9	-0.47	0	66.5	27.7	95.00%	K.IVSNASCTTNCLAPLAK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
322	332	2	1178.67	-0.1	1	68.2	22.9	95.00%	R.VVDLVEHVAKA.-	
117	137	2	2206.1	-2.7	0	45.9	27.9	95.00%	K.VVITAPSSTAPMFVMGVNEEK.Y	
308	321	2	1751.78	-0.68	0	69.6	29.8	95.00%	K.LVSWYDNEYGYSTR.V	
199	213	2	1373.71	-0.23	0	53.4	26.3	95.00%	R.TASGNIIPSSTGAAK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
96	B3LKQ2_YEAS1	12.64%	100%	4						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
137	153	3	1878.89	-0.099	0	38.1	29.4	95.00%	R.GSNGSFSDHDLLLQYAR.K	
66	78	3	1576.81	0.15	1	26.9	26.4	94.80%	R.MCFENNVVIPVKK.N	Carbamidomethyl (+57)
317	347	3	3286.6	-0.52	1	66.2	29.3	95.00%	K.SVALPQYGTGDALTPEWEGSIRDPIDATEAK.C	
218	255	4	4337.03	1.9	1	46.6	30.9	95.00%	R.VYSKDDTEGFDIPLNEENFNPMSHNGQLNNIPVIYANK.A	Deamidation (+1)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
97	A6ZQR6_YEAS7	52.23%	100%	5						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
69	86	2	2022.05	0.83	1	81.7	25.1	95.00%	K.KLEDLSPSTHNMEVPVVK.R	
2	28	3	3110.26	-0.79	1	32.5	31.5	95.00%	M.SDEEHTFETADAGSSATYPMQCSALRK.N	Acetyl (+42)/ Phospho (+80)/ Carbamidomethyl (+57)
29	35	2	776.44	-0.31	0	30.2	22.9	95.00%	K.NGFVVIK.S	Deamidation (+1)
57	68	2	1311.75	-0.32	0	66.2	21.2	95.00%	K.VHLVAIDIFTGK.K	
115	132	2	1862.85	-0.5	0	90.2	29.1	95.00%	K.APEGELGDSLQTAFDEGK.D	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
98	A6ZZH5_YEAS7	17.05%	100%	5						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
230	242	2	1526.76	-0.026	0	43.8	27.3	95.00%	K.HNVDAPIPNFFTR.N	

136	169	3	3761.73	-0.66	0	61	31.2	95.00%	K.WTNDHPSSPSQYQYPSQPALSTSIPSQAPSFSNR.K	
68	112	5	4768.36	-0.78	0	32.2	27.6	95.00%	K.KPPLLVNNEAVHASVPDASHTSCNNGTLEVSINNPEPHVVDAVAR.H	Carbamidomethyl (+57)
117	131	2	1598.8	-1	0	99.5	27.5	95.00%	R.NPSNSLQLQGGDITR.D	
355	365	2	1140.49	-0.46	0	51	26.7	95.00%	K.VGVDGYGDMGR.I	Oxidation (+16)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
99	A6ZYN3_YEAS7	27.34%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
276	289	2	1580.7	-1.1	0	38.8	28.9	95.00%	R.IPDEELHPLSDEGM.-	
245	275	4	3590.81	-0.25	1	53.2	26.3	95.00%	R.RIFPPIDDPLPFKPLMDDSDVTLEEAVTHQR.I	
44	61	3	2168.06	0.51	0	29.9	28.9	95.00%	R.QFYINDLTISHPYATTER.V	
132	147	2	1787.91	-0.61	0	47.3	26.1	95.00%	R.CQPVEGLPLDTLFTAK.D	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
100	A6ZZQ2_YEAS7	13.31%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
582	606	2	2589.07	-1.9	0	108	31.3	95.00%	K.SQAYGATMSNESNANNNNSTSNASR.S	
169	179	2	1265.55	-0.024	0	39.3	27.5	95.00%	K.SFVDENSPTDR.R	
517	534	3	2014.05	0.044	0	23.1	24.4	92.10%	K.AFGIHPLTTEDIFLGEVR.E	
567	579	2	1471.69	-0.62	0	52.4	27.8	95.00%	K.QESATLDHESISR.R	
381	393	2	1411.78	-0.78	0	59.6	23	95.00%	R.IQSGLQDNLLVGR.N	
565	579	3	1728.83	-0.11	1	54.1	28.6	95.00%	K.EKQESATLDHESISR.R	
110	126	2	1811.91	0.28	0	41.8	27.9	95.00%	R.EGPQSVSSTVQPQPIMK.F	
394	410	3	2075.03	0.0005	0	28.5	27.3	95.00%	R.NIQYPPHIISNNPEHFR.F	
468	480	2	1344.73	0.89	0	55.6	25.4	95.00%	K.AETVSQLQGLTAK.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
101	A7A1Z8_YEAS7	16.56%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
390	401	2	1360.73	-1.3	0	49.9	25.5	95.00%	R.IYGDNINAQLLK.H	
311	321	2	1332.6	-1.2	0	43.6	28.5	95.00%	R.ALNIEDCDLDR.A	Carbamidomethyl (+57)
311	334	3	2894.37	-0.61	1	47.5	30.2	95.00%	R.ALNIEDCDLDRATNDFYLEPLIER.D	Carbamidomethyl (+57)
322	334	2	1579.79	-0.34	0	54.5	27.9	95.00%	R.ATNDFYLEPLIER.D	
141	158	3	2199.98	-0.92	0	31.3	30.8	94.90%	R.GAFIIHDPEEPFEYDHER.V	
471	484	2	1519.84	-0.34	0	41.6	23.3	95.00%	R.DTVVLEPSGHVVLR.F	
372	383	2	1229.72	-0.58	0	25.8	19.3	91.90%	K.VPTLTTLLTSGK.L	
524	533	2	1280.61	-0.3	0	52.9	27.7	95.00%	K.LNENYLDICK.A	Carbamidomethyl (+57)
159	171	3	1617.78	0.26	0	30.8	28.1	95.00%	R.VITLSDHYHENYK.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
102	A6ZRM3_YEAS7	14.42%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
149	168	2	2298.15	-0.1	0	72.9	27.7	95.00%	K.LMTPLTFSTETNFIPQDISK.I	Oxidation (+16)
109	121	3	1541.86	-0.76	1	27.9	22.8	95.00%	K.VVSYILNHKDQVK.C	

273	286	2	1578.76	0.18	0	58.9	28.5	95.00%	K.VFYGHDASMGLNLR.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
103	B3LJX9_YEAS1	14.35%	100%	4						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
393	411	2	2047.01	-0.59	0	62.3	28.5	95.00%	R.AGDSQGDHLQNDPLSLRPK.T	
213	234	3	2338.05	-0.12	0	40	31	95.00%	K.TPSYSTSSHTIASGGNYTEHNK.R	
302	322	2	2197.19	0.36	0	97	22.8	95.00%	K.ILLQATPSTLSGDQVEGDLLK.I	
213	235	3	2494.15	-0.23	1	69.9	31.1	95.00%	K.TPSYSTSSHTIASGGNYTEHNKR.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
104	B3LQG1_YEAS1	17.68%	100%	4						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
130	146	2	2078.95	0.32	0	99.2	29.9	95.00%	K.FPAFIWQTWSNDEGPER.V	
51	81	3	3458.65	-1.1	0	84.1	30.4	95.00%	K.EISQSINSANNIQSSDSDLVQHFESLAQEIR.H	
349	358	2	1129.68	0.16	0	52	18.2	95.00%	K.LLSDVLVFPK.F	
118	129	3	1407.69	0.72	0	30.8	27.8	95.00%	R.IAMTFPYDSHVK.F	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
105	A6ZWC1_YEAS7	25.25%	100%	5						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
144	152	2	1059.61	0.17	0	70.8	22.7	95.00%	K.VFLDIGLQR.T	
197	224	4	3340.49	-0.35	1	40.4	31.6	95.00%	R.SYIFGGHVSQYMEELADDDEERFSELFK.G	
180	196	2	2091.98	0.072	0	85.4	29.9	95.00%	R.FPGWDFETEEIDPELLR.S	
159	179	3	2173.09	-0.27	1	34.9	27	95.00%	R.VFGALKGASDGGLYVPHSENR.F	
165	179	3	1557.72	0.068	0	32.8	29.4	95.00%	K.GASDGGLYVPHSENR.F	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
106	A7A0U0_YEAS7	9.51%	100%	5						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
401	430	3	3175.58	-0.63	1	62.4	27.5	95.00%	K.LMVVHDENGVVRAPADVNAIADETTPLNSK.H	Deamidation (+1)
66	79	2	1581.75	-0.43	0	60.3	29.1	95.00%	K.LGTITGYDLAENCR.H	Carbamidomethyl (+57)
400	412	3	1494.8	0.81	1	47.8	24.9	95.00%	R.KLMVVHDENGVVR.A	
413	430	2	1825.91	-0.18	0	85.6	27.7	95.00%	R.APADVNAIADETTPLNSK.H	
401	412	2	1366.7	-0.083	0	49.6	26.7	95.00%	K.LMVVHDENGVVR.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
107	A6ZQU5_YEAS7	23.49%	100%	7						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
75	85	2	1305.73	0.74	0	40.3	22.7	95.00%	R.LFDNIIVFPTK.G	
137	161	4	2826.43	-0.55	1	35.2	26.7	95.00%	K.GHVIRDYFSPSSEELVVSSNHLLNK.Y	
26	45	2	2389.19	-0.33	0	76.3	28.3	95.00%	R.TLVLYDQSTEPLEEYSVYLK.D	

266	287	3	2469.16	0.21	1	54.2	30.7	95.00%	K.SVHAVHSHADGTSYDEEPYKIK.D	
350	361	3	1482.76	0.81	1	43.7	25.6	95.00%	R.HGVFTFLTDYRK.I	
266	285	3	2227.98	-0.13	0	44.5	30.6	95.00%	K.SVHAVHSHADGTSYDEEPYK.I	
186	196	2	1248.72	-0.58	0	48.6	21.6	95.00%	R.EQIVPILNAPR.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
108	A7A1W6_YEAS7	24.93%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
164	181	2	2196.97	-0.73	0	106	31	95.00%	K.NCFDTAEELDDMNIEIIR.N	Carbamidomethyl (+57)
322	335	2	1715.84	-0.46	0	69.2	27.9	95.00%	R.NITWIAECIAQNQR.E	Carbamidomethyl (+57)
19	43	3	2942.41	0.15	1	58.8	29.1	95.00%	R.GYRNGLLSNNQYINLTQCDTLEDLK.L	Deamidation (+1)/ Carbamidomethyl (+57)
220	238	2	2043.03	-2.9	0	32.3	26.7	95.00%	R.SINIALNSLQSSDIDPDLK.S	Deamidation (+1)
267	276	2	1168.59	-0.44	0	57.4	25.9	95.00%	R.AALANVYEYR.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
109	A6ZP92_YEAS7	17.04%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
433	454	2	2362.21	-0.17	0	44	27.3	95.00%	K.ADFLVPGENQVTPSSTPYISLK.V	
573	589	2	1889.97	-1.1	0	62.5	26.6	95.00%	K.IPLGQPAPETVGDFFFR.V	
179	189	2	1294.64	-0.092	0	61	27.8	95.00%	K.AYESLTDELVR.Q	
61	72	2	1453.66	-0.22	0	47.3	28.8	95.00%	K.NLNEEYTSDEIK.Q	
511	521	2	1310.57	-0.56	0	35.3	28.1	95.00%	R.GSWCCLVSSQK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
403	414	2	1269.73	-1.2	1	28.5	21.3	95.00%	K.IGEVLGIKDQAK.L	
195	212	4	1888.92	0.76	0	23.8	29.2	95.00%	K.YGHPDGPQSTSHGIALPR.F	
525	534	2	1166.73	2.5	0	25.6	12.8	91.60%	K.ILQTPIIIEK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
110	A6ZNY0_YEAS7	13.66%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
770	785	2	1798.89	-0.68	0	61.3	28.6	95.00%	K.AYLPVNESFGFTGELR.Q	
2	10	2	1065.53	1	0	38.7	26.6	95.00%	M.VAFTVDQMR.S	
244	253	2	1209.58	0.055	0	34.4	28.3	95.00%	R.LWGDSFFNPK.T	
712	723	2	1265.66	-3.6	0	53.3	26.4	95.00%	R.ATYAGFLLADPK.I	
151	162	3	1378.87	0.58	1	24.8	11.5	94.20%	R.IKPVVVINKVDR.A	
618	631	2	1626.7	-0.62	0	81.6	29	95.00%	R.IMADDYGWDVTDAR.K	
33	42	2	1118.59	0.17	0	40.3	25.1	95.00%	K.STLTDSLVQR.A	
353	370	2	1976.92	0.0056	0	81.2	29.8	95.00%	R.AEQLYEGPADDANCIAIK.N	Carbamidomethyl (+57)
565	578	2	1494.7	-0.21	0	70.9	28.3	95.00%	R.ETVESESSQTALSK.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
111	YOL19_YEAST	32.12%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
376	402	3	3114.35	-1.5	0	40.8	31.9	95.00%	R.LLNDIMETSFNEPNDSHINSMSSYNDK.D	
472	501	3	3257.62	-0.24	0	75	27.1	95.00%	R.TTPAGPDPSNVILQSNPYFNVAPNQVPQHR.N	

502	529	3	2950.53	-1.5	0	45.8	25.7	95.00%	R.NPVPGVGFAPNPLPNQSPITQGYKPAYK.R	
540	551	2	1339.65	-0.018	0	37.3	27.5	95.00%	R.ATTSLNNPYGFR.-	
203	214	2	1336.67	-0.31	0	36.9	27.6	95.00%	K.GMLLNDPYLSSK.S	
425	451	3	2898.49	-1.1	0	43.4	24.6	95.00%	R.ETAAGPANIRPYAGQPHPAPLVYPQQR.L	
306	320	2	1586.77	-0.32	0	64	28.2	95.00%	R.STSTYSVIESESGLK.N	
187	202	3	1824.75	0.05	1	61.1	29.4	95.00%	R.SSGSRDDDETEELEEK.G	
403	412	2	1106.56	-0.91	0	40.2	26.8	95.00%	K.DSTLTSISQR.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
112	MNN5_YEAST	23.38%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
310	323	2	1645.73	-0.25	0	53.6	29.8	95.00%	R.YDPFVSNSNDYTPK.E	
504	513	2	1115.57	-0.38	0	40.2	28.1	95.00%	R.FIGPNGEQVR.G	
493	503	2	1400.65	0.34	0	50.1	28.7	95.00%	K.ADPWTLYHENR.F	
78	108	3	3274.42	-1.2	0	71.8	31.8	95.00%	K.LHGAEGCSFANNVAAHDSGHDSDLSYESLSK.C	Carbamidomethyl (+57)
299	309	2	1220.6	-0.26	0	40.4	27.7	95.00%	R.FVSDDISPVSR.Y	
426	439	3	1675.82	0.31	0	27.1	28.4	93.00%	K.GLALLQHDFEQDYK.Q	
450	470	3	2428.18	-0.21	1	29.5	28.7	95.00%	K.ANIEEFSKLDPDYTLDNGFLK.T	
53	77	3	2750.38	-0.032	0	33.2	27.4	95.00%	K.NNFYTTLVQAIVENKPADSSPDLSK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
113	EF3A_YEAST	15.13%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
320	357	4	3987.01	0.59	1	18.1	25.6	92.90%	R.VGNVGEDDAIPELSHAGDVSTTLQVVNELLKDETVAPR.F	
829	842	2	1700.82	0.16	0	32.1	28.3	95.00%	R.WVPMMSVDNAWIPR.G	
650	660	2	1234.62	0.22	0	28.5	26.3	93.80%	K.FPEPGYLEGVK.T	
708	732	3	2802.38	-1.6	0	31.5	28.5	95.00%	K.STLINVLTGELLPTSGEVYTHENCR.I	Carbamidomethyl (+57)
971	987	3	1737.8	-0.45	0	64.7	28.5	95.00%	R.MTPSGHNWVSGQGAGPR.I	
958	967	2	1187.62	0.15	0	26.5	26	91.50%	K.NLTEEVWAVK.D	
775	786	2	1375.6	-0.16	0	37.3	29.1	95.00%	R.QINENDAEAMNK.I	
873	893	4	2465.17	-1.2	1	28.5	29.7	95.00%	R.KEIEEHCSMLGLDPEIVSHSR.I	Carbamidomethyl (+57)
266	275	2	1149.56	2.9	0	47	27.7	95.00%	K.SAVIIDNMCK.L	Carbamidomethyl (+57)
874	893	3	2337.07	-0.45	0	29.3	30.3	93.20%	K.EIEEHCSMLGLDPEIVSHSR.I	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
114	A6ZMK1_YEAS7	37.69%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
158	168	2	1192.55	-0.023	0	49.9	27.2	95.00%	R.AVQDNGESAFR.T	
46	59	3	1614.01	0.8	0	23.1	10.4	92.10%	K.IAPRPLDLLRPVVR.A	
82	91	2	963.52	1.5	0	28.5	24.6	95.00%	K.AAGLTAAYAR.T	
105	115	2	1332.64	-0.47	0	60.8	27.9	95.00%	R.NQEIFDANVQR.L	
129	157	3	2952.48	-0.55	1	51	27.9	95.00%	R.DGKAPEAEQVLSAAATFPIAQPATDVEAR.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
115	B3LKG8_YEAS1	5.92%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
403	412	2	1076.59	1.6	0	34.5	24.9	95.00%	R.NLYALAIDGK.A	
595	602	2	1145.49	1.5	0	33.8	26.5	95.00%	K.NMEWFYEK.F	
16	30	2	1687.69	-0.89	0	56.6	29	95.00%	R.NSSSLDSDHDAYYSK.Q	
403	415	2	1372.77	-0.017	1	70.1	22.5	95.00%	R.NLYALAIDGKAPK.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
116	A6ZSL7_YEAS7	10.94%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
33	43	2	1157.62	2.7	0	41	26.1	95.00%	K.NFGIGQAVQPK.R	
194	204	2	1116.61	-0.56	0	64.5	25.2	95.00%	K.TSAVAALTEVR.A	
52	57	2	848.42	-0.5	0	29.6	25.1	95.00%	K.WPEYVR.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
117	GLRX7_YEAST	33.99%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
166	185	2	2278.11	-0.27	1	90.1	28.9	95.00%	R.GGYTEIAELHKNDELLDSFK.K	
154	165	2	1212.68	-0.76	0	73.1	22.6	95.00%	R.TVPNVIIGGTSR.G	
166	176	3	1216.61	0.0047	0	25.2	27.1	92.10%	R.GGYTEIAELHK.N	
116	140	3	2969.46	-0.027	1	34.7	28.8	95.00%	K.ALLTNSYTFSPSYYVVELDRHEHTK.E	
94	105	2	1424.7	-0.58	0	69.7	27.8	95.00%	K.IMEQSPMIVFSK.T	Oxidation (+16)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
118	A6ZQE5_YEAS7	24.64%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
116	128	2	1414.69	-0.51	0	47.4	26.4	95.00%	R.IEDVTPVPSDSTR.K	
10	19	2	1091.54	0.44	0	47.3	26.9	95.00%	R.DNSQVFGVAR.I	
94	104	2	1023.55	1.4	0	39	23.7	95.00%	K.TPGPGGQAALR.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
119	A6ZZX2_YEAS7	45.05%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
136	149	2	1494.76	1.7	0	62.8	26.8	95.00%	R.TNTFTLLTSPDSAK.I	
108	135	3	2735.25	0.7	0	83.3	30.9	95.00%	R.SAGDDNLSGHSVPSSGSAQATTHQTAPR.T	
22	43	2	2459.99	-0.45	0	102	30.4	95.00%	R.EQQAGYGSQGNANDEYDAEQMR.L	
104	135	4	3264.46	0.22	1	48.5	32.2	95.00%	R.EDERSAGDDNLSGHSVPSSGSAQATTHQTAPR.T	
55	68	2	1643.81	-0.62	1	60	27.5	95.00%	R.EQELRDIVANTNDK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
120	AQR1_YEAST	18.94%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
282	292	2	1140.69	-0.72	0	31	20.5	95.00%	R.TIAGNLSIKPK.R	
493	504	2	1361.6	-0.43	0	49.4	28.5	95.00%	K.SSTASSCFNFVR.C	Carbamidomethyl (+57)
39	54	2	1749.87	0.22	0	75.5	28.5	95.00%	K.LNFEGAYINSHGTLSK.T	

310	326	2	2054.98	-0.3	1	72.8	29.5	95.00%	R.FKYDNPDYETLDPTIPK.L		
505	517	2	1520.68	-0.69	0	60.3	28.8	95.00%	R.CSLSTIFMGCFAK.M	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	
563	572	2	1158.64	-0.27	0	29.8	24.2	95.00%	R.QSWLNTLAVK.A		
4	25	3	2677.21	-0.14	0	42	31.2	95.00%	R.SNSIYTEDIEMYPTHNEQHLTR.E		
298	307	2	1081.67	0.25	0	30.5	15.6	95.00%	R.APIFLLGPVR.R		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
121	A6ZUC1_YEAS7	13.73%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
48	59	2	1209.61	-0.69	0	28.1	27.7	91.10%	R.IVNGFGSLMGSK.E	Deamidation (+1)
376	391	2	1874.94	0.16	0	97.5	28.2	95.00%	K.FSQNAIEEALIQQEQK.K	
426	452	3	2789.5	-0.46	0	40.5	21.4	95.00%	K.GLVIISGIVHDVSGYISEHPGGETLIK.T	
400	414	2	1783.9	-0.46	0	49.1	28	95.00%	K.INWGPVLTDLPMWDK.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
122	VAC7_YEAST	10.73%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
999	1012	2	1699.62	-0.21	0	80.7	26.7	95.00%	K.CDSNGDCTVMEQER.K	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
1141	1150	2	1271.62	-0.18	0	29.4	27.4	93.60%	K.YEVPFFNTQK.S	
606	643	4	4039.94	-0.13	1	49.7	29.4	95.00%	K.VSPHLLSSTSSNGNTISCPNVATNSQELEPNNDISTKK.S	Carbamidomethyl (+57)
277	311	4	3696.65	-0.81	1	24.5	31.8	93.00%	K.NAPANSTTHDNGPVANDGLRIPNHSNADDNENNNK.M	
688	715	4	3273.51	0.57	0	29.9	31.7	95.00%	R.YSGVPDHVNLEDYIEQPHNYPTMQNSVK.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
123	CHS3_YEAST	8.93%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
935	945	2	1290.62	-0.94	0	46.8	27.8	95.00%	R.YSDNVTNTLHK.K	
104	118	2	1772.78	-0.73	0	84.8	29.4	95.00%	R.ETDSYLLQDMNTTDK.K	
1109	1118	2	1244.51	0.21	0	38.4	27.2	95.00%	K.FDDFSWGDTR.T	
598	612	2	1721.84	-0.42	0	50.7	27.9	95.00%	R.NPSTLLPTSSMFWNK.A	
575	586	2	1368.62	0.067	0	62.5	28.3	95.00%	R.GMTTMTTQNAWK.L	
124	153	3	3328.44	0.24	1	61.9	32.6	95.00%	K.ISDEGVAEDEFDKDGDVDNFEESSTQPINK.S	
686	696	2	1259.7	0.018	0	26.7	23.9	93.20%	K.LLMVVCDGLIK.G	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
124	A6ZX57_YEAS7	33.71%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
146	166	3	2297.14	0.088	0	41	28.1	95.00%	R.MMARPLTIASDPMSGFFGLQK.K	
16	24	3	1054.65	-0.29	0	33.5	16.2	95.00%	K.LNIKPLTTR.L	
25	35	2	1180.56	0.23	0	39.4	27.3	95.00%	R.LFAGMSPEMAK.K	
88	107	3	2297.08	-0.54	0	31	29.8	95.00%	K.GQYLVCMDADLQHPPETVPK.L	Carbamidomethyl (+57)

2	15	2	1675.84	-0.88	0	36.1	27.7	95.00%	M.SIEYSVIVPAYHEK.L	Acetyl (+42)
108	122	3	1742.87	0.45	0	36.2	27.5	95.00%	K.LFESLHDHAFTLGTR.Y	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
125	A6ZU19_YEAS7	12.53%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
553	568	2	1731.91	-0.18	0	69.4	26.1	95.00%	K.LTLSDSSTPLTEDLIK.D	
627	655	4	3213.6	-0.081	1	44.6	27.6	95.00%	K.LSVLSGDKLDEMSDDQLANVIDHVNIFAR.A	
690	699	2	1033.52	0.28	0	54.7	26.7	95.00%	K.LSDIGVSMGR.I	
235	245	2	1241.61	-0.38	0	36.4	27.3	95.00%	R.SCIAYMGTLVK.E	Carbamidomethyl (+57)
158	178	3	2321.16	-0.24	0	34.4	27.3	95.00%	R.CGQESHVLASTLVPGDLVHFR.I	Carbamidomethyl (+57)
219	234	2	1788.86	-1.1	0	46.8	29	95.00%	K.SSFNDQPNSIVPISER.S	
531	546	2	1722.77	-0.52	0	106	29.5	95.00%	K.ATINECANSMASEGLR.V	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
126	A6ZT57_YEAS7	8.58%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
369	377	2	1155.59	-0.17	0	51.3	25.4	95.00%	K.SIYQVYLDR.A	
320	333	3	1726.78	0.23	1	31.9	29.2	95.00%	R.FGKDDDNYELQDIR.E	
414	429	2	1811.83	-0.57	0	45.2	28.6	95.00%	K.INNNDNIDNNEVPEAK.H	
638	661	3	2580.3	-1.4	0	29.9	27.7	95.00%	R.QSVVMTNPSDLTAKPSYKPAGSFR.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
127	RL20_YEAST	37.79%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
100	113	2	1552.76	-0.34	0	67.6	28.2	95.00%	R.VAAVETLYQDMAAR.H	Oxidation (+16)
2	12	3	1346.71	0.078	1	29.9	25.3	95.00%	M.AHFKEYQVIGR.R	
13	23	2	1251.68	-0.51	1	38.7	23.6	95.00%	R.RLPTESVPEPK.L	
29	38	2	1090.6	-0.39	0	57.7	23.9	95.00%	R.IFASNEVIAK.S	
54	71	2	1906.97	-0.69	0	56.9	27.3	95.00%	K.ASGEIVSINQINEAHPTK.V	
53	71	3	2035.07	-0.19	1	43.5	24.8	95.00%	K.KASGEIVSINQINEAHPTK.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
128	B3LI54_YEAS1	16.94%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
44	56	3	1598.82	0.5	1	24.6	26.7	91.80%	K.VLIVERDWAMPDR.I	
298	311	2	1519.76	-0.74	0	56.4	28	95.00%	K.SLRPSFDEAVSQGK.F	
218	240	4	2468.22	0.38	0	21.6	29.2	92.60%	K.ELHPDHVPTVGSSFVGMSLFNAK.N	
314	323	2	1118.55	0.16	0	34.8	26.7	95.00%	R.AMPNSYLPAR.Q	
170	182	2	1544.79	-0.57	1	47.6	26.7	95.00%	R.VQGNCIEILKDEK.N	Carbamidomethyl (+57)
159	169	2	1241.64	-0.34	0	47.5	26.4	95.00%	R.NITAQEPNVTR.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
129	A6ZLZ0_YEAS7	9.58%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
598	614	2	1869.02	-0.069	0	82.7	23.3	95.00%	K.IRPLEELEALLSSGNTK.Q	
372	385	2	1500.74	-0.75	0	63.5	27.1	95.00%	K.QTLEEDGVVPSTAR.I	

727	740	2	1272.7	-0.72	0	73.1	24.5	95.00%	K.AINAGGGATTVLTK.D	
786	801	3	1914.98	0.13	0	30	26.8	95.00%	R.LQHIQTCLAGDLLFMR.F	Carbamidomethyl (+57)
524	535	2	1374.71	-0.58	0	40.9	26.6	95.00%	R.IHTSYTADQLVK.T	
804	817	2	1456.64	0.27	0	36	29	95.00%	R.TTTGDAMGMNMISK.G	
67	80	2	1818.76	-0.92	0	71.8	30	95.00%	K.DSNTLFQECSHYYR.D	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
130	YAJ8_YEAST	29.91%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
201	211	2	1248.68	0.39	0	59.9	24	95.00%	R.SDPILMAYVLK.A	
1	11	2	1248.57	1.5	0	27.6	27.6	90.40%	-.MQTPSENTDVK.M	
153	162	3	1294.64	0.41	0	40.3	27	95.00%	K.CHEFFTTLIK.E	Carbamidomethyl (+57)
163	188	2	2563.09	-0.43	0	80.3	31	95.00%	K.EVNSGSHSDSSSNSAEDTQSPVSAGK.T	
189	200	2	1385.66	-0.31	0	48.3	29	95.00%	K.TSNGLNNFYSIR.S	Deamidation (+1)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
131	A7A0B5_YEAS7	8.05%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
133	149	2	1902.98	-1.1	0	71.7	26.8	95.00%	K.QFPGIAYTIPDLDAQVR.V	
99	117	2	2080.01	-0.46	0	80.3	29.3	95.00%	K.TFDLCSLGQVSLCPLSAGR.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
736	762	3	2867.4	-0.55	0	28.8	28.5	94.60%	R.TNLAPNNTSTSSLMKPESSLYLGNSNK.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
132	A6ZLE7_YEAS7	15.59%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
117	134	3	2349.04	0.087	0	28.5	31	91.20%	R.YHYDWVFLNDQPFSDEFK.R	
96	104	2	1087.57	0.35	0	35.3	27.1	95.00%	R.NSDLWNLVK.S	
342	365	4	2844.29	-0.86	0	47.4	31.6	95.00%	K.SEIHFFDGLGFHHPDFTSCPIEQK.I	Carbamidomethyl (+57)
379	390	2	1559.67	0.13	0	28.4	28.6	90.30%	K.DVTWTPDYFCTR.K	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
133	FET4_YEAST	13.41%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
306	316	2	1370.64	-0.021	0	40.9	26.8	95.00%	R.FLVDIFDMDEK.I	
445	454	2	1132.59	-0.46	0	46.1	26.3	95.00%	K.APEINTIGYR.T	
324	340	3	1995.97	-0.96	0	44.5	29.4	95.00%	K.HFNDFETPHPVVTIESK.K	
4	20	4	1884.97	0.64	0	34.6	26.1	95.00%	K.IAEFLGNPGARPDVHHR.A	
248	265	2	1833.81	-1.2	0	98.2	30	95.00%	K.DAGNTPPYTGETTGSNPR.L	
323	340	3	2124.06	-0.66	1	38.1	28.1	95.00%	R.KHFNDFETPHPVVTIESK.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
134	B3LJS4_YEAS1	8.41%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
3	33	3	3432.6	-0.34	0	67.1	30.7	95.00%	R.SSYQPVSTTNFEHENAIPTASSSHNLLMSQR.F	
248	258	2	1205.57	-1	0	43.2	26.7	95.00%	K.ENFNPLSSNGK.L	

299	309	2	1226.72	0.078	0	48	22.3	95.00%	K.LVSQQVLIAEK.F	
384	398	2	1477.66	-0.55	0	91.5	28.6	95.00%	R.LSSGGVTVDDGNSDR.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
135	A6ZLU9_YEAS7	18.88%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
313	325	2	1424.67	0.13	0	30.7	28.3	94.10%	K.DFGQVIGQGFSDR.H	
135	159	3	2866.37	0.21	1	53.7	29.8	95.00%	K.FDDGVQHYLISQFGSEVLTPKDDEK.Y	
279	287	2	1159.5	-0.53	0	44	27.9	95.00%	K.YMDEGYINR.V	
15	26	2	1272.65	-0.57	0	38	27.2	95.00%	K.AMDNGLSLPISR.N	
201	211	2	1217.65	0.22	0	35.4	25.5	95.00%	R.NAADVLPLMFK.H	
501	521	3	2454.18	-2.3	0	28.6	29.4	93.50%	R.VGGLPHYTIWHIYEPSDDDLK.E	
191	200	2	1248.7	0.41	0	24.9	22.8	90.40%	R.DHILLCIPLR.N	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
136	A6ZT02_YEAS7	15.10%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
524	542	2	2212.14	-0.19	0	78.7	26	95.00%	K.GLTLEEVNTLWEEGVLPWK.S	
268	279	2	1376.75	-0.59	1	66.2	24.5	95.00%	R.YLVEVGKIEEAK.R	
288	310	2	2386.16	0.83	0	114	28.6	95.00%	K.VSADDPAVMAEVEVVQATVEAEK.L	
311	324	2	1479.73	-0.83	0	78.9	28.6	95.00%	K.LAGNASWGEIFSTK.T	
552	570	3	2299.98	-0.56	1	37	30.9	95.00%	K.RGTDYNADDLMHDDQPFYK.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
137	VDAC1_YEAST	24.73%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
96	108	2	1341.75	-0.69	0	61.7	23.3	95.00%	K.NELITSLTPGVAK.S	
109	124	2	1799.92	0.093	0	57.9	27.3	95.00%	K.SAVLNTTFTQPFFTAR.G	
165	174	2	1163.57	0.5	0	49.9	26.8	95.00%	R.YAMALSYFAK.D	
66	84	2	2060.03	-0.72	0	87	27.2	95.00%	K.QTGLGLTQGWSNTNNLQTK.L	
237	248	2	1251.67	-0.084	0	78.6	24.5	95.00%	K.VSDSGIVTLAYK.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
138	B3LPM2_YEAS1	8.17%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
16	32	2	1938.93	-0.57	0	71.5	28.9	95.00%	R.VNSLNAPYQALSYDEQK.A	
208	223	2	1867.86	-0.12	0	63.3	29.1	95.00%	R.TENYFLSIAHTSENDK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
139	GLRX6_YEAST	45.02%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
70	84	2	1703.82	-1.1	1	94.2	28.4	95.00%	K.GSSEVDEEINEIKQK.V	
208	219	2	1373.72	-0.3	0	44.4	26.1	95.00%	K.LLESLQVWSDGK.F	
85	105	3	2197.16	-0.17	1	34.2	25.4	95.00%	K.VGLQQPIASVDDSLSAIKNDK.G	
43	57	2	1560.63	-0.54	0	86.9	27.2	95.00%	K.AFSTNMDNMAGGSSR.E	Oxidation (+16)
85	102	2	1839.99	-1.2	0	63.1	23.3	95.00%	K.VGLQQPIASVDDSLSAIK.N	
164	175	2	1438.68	0.41	0	44.7	28.7	95.00%	K.HGHGEELQEYIK.L	
118	133	2	1850.04	-1.1	0	64.7	18.7	95.00%	K.EYSLILDLSPIIIFSK.S	

181	193	2	1324.75	-0.69	0	47.4	22.6	95.00%	R.GTVPNLLVNGVSR.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
140	RTN1_YEAST	24.41%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
236	247	2	1267.67	-0.42	0	55.2	24.7	95.00%	K.LAADVPLEPESK.A	
248	281	4	3832.81	0.45	1	23.6	30.2	94.40%	K.AYTSSAQVMPEVPQHEPSTTQEFNVDELSNELKK.S	
208	216	2	939.58	-0.019	0	45.3	14.6	95.00%	K.LGPISNLVK.S	
219	235	2	1589.79	-0.2	0	77.4	28	95.00%	K.TAPVSSTAGPQTASTSK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
141	A6ZLM5_YEAS7	16.16%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
225	238	2	1458.66	-0.97	0	107	28.7	95.00%	R.MNSSFLSSSSIGDK.I	
327	335	2	940.61	0.51	0	44.5	18.6	95.00%	K.LLIGSIIGR.M	
199	224	3	3155.4	-0.8	0	62	31.6	95.00%	R.TPNIDNEELVNEEQEEQELLEEENNR.M	
179	198	3	2323.1	-0.51	0	51.3	29.7	95.00%	K.WSGENTQHMPPSQVQSLLER.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
142	A6ZXE9_YEAS7	24.07%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
275	305	4	3513.78	1.1	1	31.4	25.5	95.00%	K.IRDIENLVADAVEVNIPFNNPITGFCAFTHK.A	Carbamidomethyl (+57)
32	45	2	1631.71	-0.15	0	66.3	29	95.00%	R.EGEQFANAFFDTEK.K	
377	388	2	1330.7	-0.76	0	49.8	25.9	95.00%	R.SLNIDDVDSIIK.N	
180	192	2	1328.65	-0.6	0	78	27.7	95.00%	R.VGIADTVGCANPR.Q	Carbamidomethyl (+57)
312	332	4	2387.2	0.43	1	31.5	28.2	95.00%	K.AILANPSTYEILDPHDFGMKR.Y	
234	245	2	1269.73	-0.013	0	44	21.3	95.00%	R.LIDVSVLGIGER.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
143	A6ZY13_YEAS7	12.91%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
67	78	2	1376.59	-0.75	0	35	29.1	95.00%	R.LEEDNDLEDGTK.S	
62	78	2	1947.86	-1	1	89.5	29.6	95.00%	R.AESQRLEEDNDLEDGTK.S	
400	412	2	1465.71	-0.047	0	74.9	28.6	95.00%	R.LMCSLAQQGYAPK.F	Carbamidomethyl (+57)
14	48	4	3903.79	0.47	1	44.3	31	95.00%	K.SAEFEVTDSALYNNFNTSTTASLTPEIKEHSEESR.N	
269	281	2	1250.55	-0.67	0	65.6	26.9	95.00%	R.DPGSFAEGSGATR.F	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
144	FUI1_YEAST	11.58%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
75	82	2	995.53	1.1	0	42.4	23.5	95.00%	R.VVEFFEVK.N	
621	635	2	1664.72	-0.012	0	63.7	29.4	95.00%	R.EAFEEYGGVSTGYEK.I	
75	98	3	2798.39	-0.86	1	45.5	28.2	95.00%	R.VVEFFEVKNDSTDLADHKPENPIR.T	
236	245	2	1105.59	-0.93	0	47.8	26.6	95.00%	K.AIFGTNLNTR.I	

109	123	2	1768.9	-0.69	0	59	27.1	95.00%	R.STYLYNTDLRPVEAK.R	
99	108	3	1235.65	-0.000077	1	34.3	26.3	95.00%	R.TFKDLQESLR.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
145	ARN2_YEAST	7.38%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
254	265	2	1531.72	-0.28	1	55	29.5	95.00%	R.NDVEWKELQDEK.S	
1	14	2	1675.78	6.3	1	34.9	29.1	95.00%	-.MIEVPEDNRSSQTK.R	Acetyl (+42)/ Deamidation (+1)
2	9	2	970.47	1.2	0	25.7	25.8	90.30%	M.IEVPEDNR.S	
601	611	2	1314.61	2.6	0	34.6	28.4	95.00%	K.EDDPINDWIAK.R	
591	600	2	1247.65	-0.73	1	31.5	26.2	95.00%	K.LPDREYVQTK.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
146	B3LRN6_YEAS1	40.16%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
199	212	2	1512.75	0.33	0	37.2	27.5	95.00%	K.QTSNSTPAPQNQIK.E	
125	156	4	3644.8	-0.12	1	27.4	27.5	95.00%	K.YLISPDVHPAQNQNIQENKETVEPVVQDSEPK.E	
100	113	2	1578.76	0.49	0	58.8	28.4	95.00%	K.AVADVWSDLEAEFK.Q	
181	190	3	1151.66	-0.085	1	31.8	20.1	95.00%	K.KEEVPPVVQK.T	
166	180	2	1646.85	-0.8	0	41.3	27	95.00%	K.EVPAEPETQPPVQVK.K	
2	14	2	1460.78	0.36	0	36.8	25.3	95.00%	M.SAVEISPDVLVYK.S	Acetyl (+42)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
147	ATG27_YEAS7	28.41%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
73	88	3	1772.92	0.19	1	38.3	26.3	95.00%	K.KNDMLCGLTDVILPGK.D	Carbamidomethyl (+57)
119	130	2	1223.56	0.55	0	42	27.2	95.00%	K.GATWGANSFDAK.L	
89	100	2	1378.7	-0.087	0	34.4	26.9	95.00%	K.DAITTQIIDFDK.N	
101	118	2	1978.03	0.49	0	77.8	25	95.00%	K.NIGFNVEETESALTLTLK.G	
74	88	2	1644.82	-0.29	0	32.5	27.5	95.00%	K.NDMLCGLTDVILPGK.D	Carbamidomethyl (+57)
36	54	2	2096.03	-0.061	1	58.2	28.7	95.00%	K.FSSLTSTERDTPPSTTIEK.W	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
148	AXL2_YEAST	7.29%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
651	664	2	1512.68	-0.6	0	55.9	28.3	95.00%	R.SSSVYMDSEPAVNK.S	
730	740	2	1191.61	-0.093	0	33.6	26.4	95.00%	K.SVTPSPYNVTK.H	
169	183	2	1781.79	0.39	0	48.1	29.5	95.00%	R.SMFTNEESIVSYYGR.S	
184	203	2	2338.16	-0.052	0	56.3	27.6	95.00%	R.SQLYNAPLPNWLFFDSGELK.F	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
149	A6ZZW6_YEAS7	11.79%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
249	265	2	1829.92	0.05	0	59.2	27.2	95.00%	K.VDLMDQGTDVIDILAGR.V	
389	400	2	1232.6	-0.095	0	80.3	27.2	95.00%	K.ELSSQELSGGAR.I	
185	196	2	1320.67	-0.47	0	53.8	27.2	95.00%	K.VPVGDQPPDIER.Q	
205	230	3	2701.43	0.042	0	52.8	23.9	95.00%	K.YISKPNAIILSVNAANTDLANSDGLK.L	
150	165	2	1583.86	-0.32	0	57.7	23.1	95.00%	K.VTGANSGISSVPINLR.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
150	B3LFU9_YEAS1	18.93%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
287	307	2	2463.17	-2.1	1	56.2	30.1	95.00%	R.ELERELYSPEEDSAAQLVTER.T	
291	307	2	1935.91	-0.53	0	80.9	29.9	95.00%	R.ELYSPEEDSAAQLVTER.T	
100	138	4	4306.08	-0.12	1	41.7	29	95.00%	K.LATVGHEPKPLLPELVENGELLREEEDMIQGGSSAESPR.S	Phospho (+80)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
151	A7A0Y7_YEAS7	6.30%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
141	156	2	1817.92	-0.018	0	84.4	27.1	95.00%	K.NGFFQNWLIDGLPAAR.E	
104	117	2	1723.86	-0.58	0	67.9	27.8	95.00%	R.IYNSPFQLNMLQEK.E	
238	249	2	1237.77	1.6	0	36.3	17.2	95.00%	R.VVGVIVEPVSIK.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
152	B5VDM9_YEAST	27.66%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
219	226	2	1128.49	0.59	0	29	25.8	94.90%	K.EAEFEYWR.K	
1	11	2	1248.57	1.5	0	27.6	27.6	90.40%	-.MQTPSENTDVK.L	
189	212	3	2770.41	-1	0	36.5	26.1	95.00%	K.EVSNEMVKPYIFSSDPVLEAYLIK.A	
167	188	2	2226.01	-0.64	0	89.7	30.3	95.00%	R.SNAHLSSPTNGAENTQSNTPAK.E	Deamidation (+1)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
153	A6ZWW2_YEAS7	24.93%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
267	277	2	1215.61	1	0	50	25.6	95.00%	K.DADDNLITAIR.A	
282	314	4	3769.78	0.62	1	29.9	31	95.00%	K.LVQIAEEESDKEIQDLDVIEEQTEADDLSHMAK.S	
201	221	2	2116.14	-0.19	0	73.9	22.3	95.00%	R.ASNILPIAYIPGVTSGLSTDK.L	
241	266	3	2863.35	0.007	0	76.5	30.7	95.00%	R.SHITLGSSILDGLDDEDDEHNQVLNK.D	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
154	RSP5_YEAST	11.25%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
23	38	2	1750.88	-0.47	0	69.7	27.2	95.00%	R.SPDPFAVLTIDGYQTK.S	
138	164	4	2669.23	1.8	0	32.2	30.5	95.00%	K.LPSSSPHSQAPSGHTASSSTNTSSTTR.T	
80	90	2	1202.64	-0.51	0	31.2	26.1	95.00%	K.DQGFLGVVNVR.V	
220	230	2	1378.58	-0.66	0	42.3	28.4	95.00%	R.QYSSFEDQYGR.L	
184	209	3	2561.23	-0.032	0	55.9	29.9	95.00%	R.GTAQAVESTLQSGTTAATNTATTSHR.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
155	A7A1C4_YEAS7	6.65%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
352	364	2	1576.8	0.5	0	49.9	27.4	95.00%	K.EVDAIEYLEQQLK.F	
10	31	3	2484.2	-2	1	47.6	29.8	95.00%	K.SAASYLDTVPDEHHDFRKPTAK.V	
413	429	5	2014.02	-0.16	1	23.4	27.3	95.00%	R.LAPAPHDIKWDHVCLSR.K	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
156	A6ZWJ1_YEAS7	10.47%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
328	340	2	1292.66	-0.015	0	89.4	26.3	95.00%	K.STSDTASATLLAR.Q	
65	73	2	1153.54	0.062	0	44.8	28	95.00%	K.TEDIPEHWK.E	
347	357	2	1323.68	0.27	1	42.5	27.3	95.00%	R.KDSNTNIVLLK.S	Phospho (+80)
348	357	2	1115.62	-0.46	0	31.1	24.5	95.00%	K.DSNTNIVLLK.S	
58	73	4	2037.03	0.7	1	29.3	26.8	95.00%	K.IIHQTYKTEDIPEHWK.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
157	A6ZNH7_YEAS7	18.80%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
207	222	2	1828.77	-0.27	0	104	29.9	95.00%	R.QLAAEYFNCGDEADAR.I	Carbamidomethyl (+57)
192	206	2	1572.83	-0.64	0	82.2	26.2	95.00%	R.QIPVGYSAADIVANR.Q	
34	45	2	1313.56	0.2	0	42	27.4	95.00%	K.GNAFFNSESGER.F	
317	329	2	1679.74	-1.6	1	37.8	29	95.00%	K.LTDFENLKNEYSK.V	Phospho (+80)
250	269	2	2392.13	-3.2	0	48.1	30.1	95.00%	K.LYQDYSVPVFLSEFGCNQVK.S	Carbamidomethyl (+57)
88	102	2	1819.76	-0.97	0	36.2	29.8	95.00%	R.VYTVDNSQDHSHCMK.L	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
158	A6ZRN1_YEAS7	14.36%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
174	191	2	1728.94	-0.94	0	84.5	23.4	95.00%	R.IINEPTAAAIAYGLGAGK.S	
305	314	2	1166.6	-0.37	0	43.3	26.8	95.00%	R.FEDLNAALFK.S	
252	261	2	1061.5	-0.49	0	53.5	27.1	95.00%	K.TGLDISDDAR.A	
456	466	2	1277.65	-0.41	0	56.3	26.5	95.00%	K.ENTLLGEFDLK.N	
502	513	2	1217.64	-0.59	0	69.6	26.4	95.00%	K.SSNITISNAVGR.L	
315	325	2	1241.69	-0.33	0	29.6	24.7	95.00%	K.STLEPVEQVLK.D	
144	157	2	1563.8	-1.2	0	27.2	27	91.00%	K.AVITVPAYFNDAQR.Q	
303	314	2	1393.74	0.26	1	40.8	24.3	95.00%	R.ARFEDLNAALFK.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
159	A7A0C4_YEAS7	26.99%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
185	197	2	1610.74	0.82	1	40.8	28.9	95.00%	K.NIEQCEREGYVSK.I	Carbamidomethyl (+57)
217	244	4	3217.53	-1.1	0	27.6	29.7	95.00%	R.IQGNLHFAPGKPYQNAYGHFHDTSLYDK.T	
351	366	2	1755.87	0.21	0	56.3	27.4	95.00%	R.GGIPGMFVFFEMSPLK.V	
275	289	3	1491.79	0.47	1	33.8	26	95.00%	K.RHGGAVVATSPLDGR.Q	
108	147	4	4128.83	-0.63	0	35	32.6	95.00%	R.LNSEGRPVGDATELHVGGNGDGTAPVNNDPNYCGPCYGAK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
160	A6ZZ86_YEAS7	13.87%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
569	584	2	1954.98	-2.5	1	45.2	27.4	95.00%	R.VHELKYEPTQEIIEDI.-	
288	300	2	1597.76	-0.77	1	56.9	28.6	95.00%	K.RSYTDTSEEIIER.K	
289	300	2	1441.66	1.7	0	51.8	28.6	95.00%	R.SYTDTSEEIIER.K	
42	51	2	1224.65	-0.59	0	62.5	25.5	95.00%	K.ITLESHEIQR.A	
12	38	3	2777.2	0.077	0	61.6	31.6	95.00%	K.TSQSNVGDAVGNADSVEFNSEHDSPSK.R	
301	315	2	1653.93	0.052	1	73.9	20.2	95.00%	R.KVEELVTLNQSIPGK.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
161	YD237_YEAST	25.13%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
230	243	2	1667.77	-0.47	0	30.5	29.2	92.70%	K.SLIDSGYLTYYDMK.K	
171	193	3	2663.27	-1	1	37.1	29.4	95.00%	K.LYTGPLLEILDEVNCQDSDADRK.N	Carbamidomethyl (+57)
151	170	3	2209.16	-0.087	0	46.8	24.1	95.00%	K.ILAVGHNEAYLDPVELTLDK.L	
351	367	2	1910	-0.17	0	50.2	25.2	95.00%	R.IWGAPTWPANLVETISR.Q	
282	295	2	1559.86	0.17	0	39.9	22.1	95.00%	R.FAFLDAPLLSLEPK.Y	
337	346	2	1023.57	-0.6	0	41.4	21.8	95.00%	K.SIIDGAHALK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
162	A6ZWS9_YEAS7	17.99%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
6	17	3	1474.73	0.95	0	25.1	27.6	91.20%	K.ILMDSTHFNEIR.S	
448	460	2	1499.7	-1.3	0	57.8	28.6	95.00%	K.ADIMELLNHSDSR.V	
95	108	2	1515.82	0.59	0	57.2	24.5	95.00%	K.SVQNLIAELLSSDK.Y	
468	478	2	1211.65	-0.59	0	46.8	24.2	95.00%	K.ATQAIIGYTFK.-	
76	94	4	2196.15	-0.52	1	35.7	24.8	95.00%	K.TLIPLIHLLSTSDNEDCKK.S	Carbamidomethyl (+57)
55	71	2	1703.78	-1.1	0	78.9	29.9	95.00%	K.NIGDGLSSSNNAHSGFK.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
163	A6ZSQ1_YEAS7	38.41%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
56	74	2	2050.19	-0.35	0	115	14.8	95.00%	R.QAINLGQVVLTPLTFALPR.G	
32	42	2	1211.71	1.2	0	60.2	19.7	95.00%	K.LAAIVEIIDQK.K	
110	117	2	921.46	-0.26	0	39.1	26.7	95.00%	R.AALTDFER.F	
118	124	2	891.5	0.21	0	27.3	25.8	92.90%	R.FQVMVLR.K	
94	101	2	905.44	0.42	0	28.9	26.7	93.90%	K.WAASSWAK.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
164	FCY2_YEAST	14.07%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
18	29	2	1258.64	-0.41	0	53.7	27.5	95.00%	R.SPVIGSSLENEK.K	
17	29	3	1414.74	-0.071	1	59.5	26.3	95.00%	K.RSPVIGSSLENEK.K	
2	16	2	1791.85	-0.45	0	81.1	29.4	95.00%	M.LEEGNNVYEIQDLEK.R	
63	72	2	1126.57	1.9	0	41.1	25.8	95.00%	K.FFASLNAETK.G	
30	56	3	2934.36	-0.13	1	66.7	30.8	95.00%	K.KVAASETFTATSEDDQQYIVESSEATK.L	
156	164	2	991.55	0.19	0	49.3	24.1	95.00%	R.YLVGNVTAR.I	
1	16	2	1922.89	-0.27	0	109	29.4	95.00%	-.MLEEGNNVYEIQDLEK.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
165	A6ZSA1_YEAS7	15.26%	100%	3						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
193	219	4	3023.53	-0.48	1	38.8	27.2	95.00%	K.LANVKTDENGKPEQPITIGYISSQEHR.V	
250	258	2	1127.54	0.27	0	27.8	27.1	91.60%	K.NYLYQGSQR.K	
234	244	2	1322.6	-1.1	0	57	27.3	95.00%	R.LQDYQNGDLEK.G	Deamidation (+1)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
166	A7A1B6_YEAS7	14.66%	100%	2						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
154	163	2	1225.58	-0.23	0	57.5	28.1	95.00%	K.YVECSALTQR.G	Carbamidomethyl (+57)
167	184	2	1952.1	-0.33	1	70.5	19.6	95.00%	K.NVFDEAIVAALEPPVIKK.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
167	A6ZQA2_YEAS7	29.50%	100%	4						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
201	221	3	2385.17	-0.5	1	57.7	28.3	95.00%	R.HDGGFDLVHIKDSLDNTFVTR.L	
76	100	3	2846.36	0.63	1	47.6	30	95.00%	K.VRTDTTYPAGFMDVITLDATNENFR.L	
222	240	3	2115.17	-0.8	0	27.9	19.4	95.00%	R.LNNVFVIGEQGKPYISLPK.G	
134	145	2	1326.7	-0.54	1	57.3	25.3	95.00%	K.KGVPYVVTHDGR.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
168	ERG2_YEAST	19.37%	100%	4						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
35	46	2	1376.7	1.3	0	44.2	26.9	95.00%	K.TLNEICNSVISK.H	Carbamidomethyl (+57)
47	77	4	3471.63	0.56	1	37.5	30.6	95.00%	K.HNAAEGLSTEDLLQDVRDALASHYGDEYINR.Y	
47	63	2	1866.91	-0.064	0	108	28.5	95.00%	K.HNAAEGLSTEDLLQDVR.D	
64	77	2	1622.73	-1.2	0	68.5	28.6	95.00%	R.DALASHYGDEYINR.Y	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
169	A6ZL12_YEAS7	8.37%	100%	4						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
14	23	2	1103.55	-0.29	0	35.4	27.5	95.00%	K.ETSPDSISIR.S	
24	38	2	1575.68	-0.074	0	96.5	28.8	95.00%	R.SFSAGNNFQSSSSEK.T	
405	417	2	1447.75	-0.74	0	66	27.1	95.00%	R.LICSLAQQGYAPK.F	Carbamidomethyl (+57)
1	13	3	1371.63	-0.14	1	26.9	27.3	93.90%	-.MLSSEDFGSSGKK.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
170	A6ZPF8_YEAS7	6.61%	100%	6						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
205	219	2	1588.83	-0.27	0	41.7	26.8	95.00%	K.ILATNPIMEAFGNAK.T	
581	594	3	1581.81	-0.76	1	26	26.8	93.50%	K.NRDTVSDGHLEVLK.A	
874	890	3	1986.02	-0.14	1	47.1	26.7	95.00%	R.QLKQEHEYNAAVTIQSK.V	
1163	1180	2	2070.11	0.67	0	46	21.5	95.00%	R.LLEDTEILNQEITEGLLK.G	
595	610	2	1743.93	0.68	0	53.7	23.4	95.00%	K.ASTNETLINILEGLEK.A	

514	537	3	2643.34	-1.3	1	36.5	27.3	95.00%	K.LGILSLLDEESRLPAGSDESWTQK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
171	B5VE42_YEAST	12.84%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
146	160	2	1574.82	0.25	0	80.9	26.2	95.00%	K.VGQSLSIVSNDELSK.A	
60	70	2	1330.71	-0.021	1	59.7	25.2	95.00%	K.KVNVFNINNNR.Y	
235	249	2	1622.77	-0.48	0	75	28.4	95.00%	K.LQSNGAIQGDSFVCK.N	Carbamidomethyl (+57)
61	70	2	1202.62	-0.19	0	43.8	27	95.00%	K.VNVFNINNNR.Y	
234	249	3	1750.87	-0.086	1	27.6	27.5	94.50%	K.KLQSNGAIQGDSFVCK.N	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
172	A6ZV40_YEAS7	10.80%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
60	73	2	1615.85	-0.52	0	69.3	26	95.00%	K.QLGILSCIGLICNR.M	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
6	16	2	1309.7	-0.32	0	74.3	23.9	95.00%	R.TFLSQLNVFNK.E	

Carbamidomethyl (+57)/ Deamidation

254	266	2	1516.77	-0.076	0	41.4	26.5	95.00%	K.TLIDNLIDTSEQR.D	
371	385	2	1727.81	-0.81	0	92.9	29.5	95.00%	K.LYAVEGNDQYVQSSR.S	
191	207	2	1942.98	0.46	0	85.8	26.6	95.00%	R.ITAYNVADGFNLNQLYK.F	
141	163	3	2647.36	-0.15	0	28.7	25.6	95.00%	K.LVLIPEDDNLNHFQTLPTNALDR.Q	
488	496	2	1089.62	0.99	0	46	20.8	95.00%	R.IFNDIVTLR.S	
447	458	2	1368.69	-0.087	0	56.8	26.4	95.00%	K.NILGDITFADYK.N	
208	218	2	1341.67	-0.54	0	73.1	26.8	95.00%	K.FLQETHEVSPR.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
177	A7A233_YEAS7	25.58%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
117	134	2	1964	-0.41	0	50.5	27.4	95.00%	K.TVNEHANDEAQLLLVGNK.S	
71	81	2	1315.65	0.75	0	47	27.7	95.00%	K.LQLWDTAGQER.F	
165	178	2	1638.79	-1.6	0	74.2	28.4	95.00%	K.NDDNVNEIFFTLAK.L	
141	152	2	1200.63	-0.6	0	69	25.9	95.00%	R.VVTADQGEALAK.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
178	A6ZQF7_YEAS7	28.26%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
31	43	2	1460.71	-0.44	0	52.3	27.5	95.00%	R.ETAQAINGWELTK.A	Deamidation (+1)
47	56	2	1285.64	-0.78	0	51.2	27.8	95.00%	K.YLDQVLDHQR.A	
112	124	2	1495.81	-0.2	0	61.1	22.8	95.00%	K.LYVSHIQVNQAPK.Q	
90	105	2	1643.86	-0.2	0	80.3	24.4	95.00%	K.FVQGLLQNAAANAEAK.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
179	A7A0U9_YEAS7	7.10%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
259	273	2	1595.86	-0.25	0	40.5	24.1	95.00%	R.YGGVYVGTLSKPEVK.E	
155	179	3	2741.51	-0.39	0	35.6	20.5	95.00%	R.TTYVTQRPVYLGLPANLVDLNVPAK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
180	A6ZL51_YEAS7	35.64%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
65	78	2	1466.63	-0.7	0	61.3	28.8	95.00%	K.YVEPGNAMSGEGEK.L	
155	168	2	1346.66	-1.6	0	57.1	27.3	95.00%	K.APSLFGGMGQTGPK.T	
138	150	3	1395.79	0.28	0	24.5	20.3	93.90%	K.IHLFGKPATGDLK.R	
115	128	2	1623.83	-0.68	0	63.7	27.1	95.00%	K.YTNPLFMQSISPVK.S	
79	90	2	1449.78	-0.62	1	44	24.1	95.00%	K.LQVTTVRDYDLK.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
181	A7A244_YEAS7	9.16%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
492	500	2	1044.57	-0.5	0	27.4	25.4	93.60%	R.IEDDILVTK.D	
213	229	2	2001.92	0.53	0	56.8	29.9	95.00%	R.SLIPSDPNFFYAMDETR.A	
123	145	3	2617.25	-0.29	0	41.7	29.6	95.00%	R.YFYHLSGVDIPASAILFNCSTDK.L	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
182	A6ZXW5_YEAS7	10.23%	100%	4							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
12	33	4	2499.33	0.86	1	36.5	22.5	95.00%	R.HALLHNDIQTSNNSRPSLVQKK.Y		
97	106	2	1235.59	0.89	0	35.7	27	95.00%	K.NQEVYSQVNR.I		
277	288	2	1252.71	-0.56	0	41	20	95.00%	K.LSISHAIAQSVK.I		
12	32	3	2371.23	-0.5	0	35.1	24.8	95.00%	R.HALLHNDIQTSNNSRPSLVQK.K		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
183	CSG2_YEAST	10.49%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
78	90	2	1540.67	-1.2	0	67.6	29.1	95.00%	K.MRPMFVSDSDSNR.N		
91	120	3	3347.46	-0.087	0	95.6	31.8	95.00%	R.NSQFDNNNSGSVTNEDVDTFSHVLDDPQPR.I		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
184	A6ZUF3_YEAS7	13.49%	100%	4							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
79	101	4	2698.37	-0.43	1	23.8	26.7	95.00%	K.QRGNVPQYVIDNSPLLHLYSEEK.Y		
273	287	4	1728.03	-0.16	1	17.4	14.3	92.70%	K.LTNEVIKKPLIFSAR.G		
151	166	2	1793.76	-1.1	0	98.2	29.7	95.00%	R.VSSEGTYMTSLDDFDK.G		
347	355	2	1109.56	-0.02	0	36.5	26.6	95.00%	K.MGLEWLSFK.G		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
185	B3LMA9_YEAS1	14.88%	100%	7							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
283	293	3	1070.59	-0.46	0	32	23	95.00%	K.SGGIFGVLHGK.S		
220	247	3	2982.44	-0.74	1	54	28.6	95.00%	K.IAVEGLDENGRLIEGDTGSGIIPDEQER.Q	Deamidation (+1)	
231	247	2	1827.88	-1.4	0	81.6	29.2	95.00%	R.LIEGDTGSGIIPDEQER.Q		
496	504	2	981.48	0.1	0	36.4	25.9	95.00%	R.GLSSNYQTI.-		
220	230	2	1171.58	-0.71	0	54.9	26.6	95.00%	K.IAVEGLDENGR.L		
84	91	2	963.49	0.71	0	32.4	26.9	95.00%	K.ILDMYGPR.V		
248	266	3	2223.16	-0.32	1	24	24.8	93.30%	R.QSLIAIEREEDSIPSRPQR.R		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
186	A6ZLC2_YEAS7	35.59%	100%	6							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
31	46	2	1747.84	-0.19	1	65.5	29.5	95.00%	K.RIGQEVDGEAVGDEFK.G		
99	115	2	1647.03	-0.31	0	55.7	6.02	95.00%	R.GAIVGPDLAVLALVIVK.K		
15	25	3	1429.7	0.55	1	29.6	28.3	95.00%	K.TFEIDDEHRIR.V		
116	131	2	1743.89	-0.7	1	54.5	26.6	95.00%	K.KGEQELEGLTDTTVPK.R		
3	14	2	1319.67	-0.39	0	56.7	26.8	95.00%	K.LNISYPVNGSQK.T	Deamidation (+1)	
203	214	2	1276.67	1.9	0	58.7	26.4	95.00%	R.EAAAEYAQLLAK.R		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
187	A6ZPF1_YEAS7	8.00%	100%	4							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	

176	198	3	2467.37	-0.48	0	34.2	19.3	95.00%	K.AIFTDNSLLPSLIKPVQAAQDVK.Y	
237	245	2	1084.54	-0.026	0	27.8	26.3	92.90%	K.TFSFDDILK.L	
2	11	2	1060.59	1.2	0	35.5	23.2	95.00%	M.VAQYTVPVGK.A	
620	633	2	1609.75	-1	0	73.9	29.3	95.00%	K.DSSINIENYLEDAK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
188	A6ZKL6_YEAS7	26.28%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
121	128	2	1045.47	1.9	0	47.8	26.6	95.00%	K.ECADLWPR.V	Carbamidomethyl (+57)
33	40	2	932.57	-0.12	0	26.9	16.3	93.50%	R.NLYIIAVK.G	
13	32	2	2014.99	0.21	0	81.3	29.2	95.00%	R.ISLGLPVGAIMNCADNSGAR.N	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
189	A6ZLH4_YEAS7	9.02%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
904	928	3	2880.27	-1.5	1	65.9	31.6	95.00%	R.MPTNRIDTPCESEDSDLDTDLTSIR.D	Carbamidomethyl (+57)
127	136	2	1073.5	0.37	0	54.1	26.5	95.00%	R.GGGAYYMISR.S	
735	746	2	1437.7	-0.33	0	34.9	28.3	95.00%	K.TIDLYPIQMCGK.V	Carbamidomethyl (+57)
5	31	3	2878.42	-0.2	0	48	28.2	95.00%	R.FYQIPGTHRPSSAISSSNESSSLLSAR.R	
33	48	2	1976.89	-1.5	0	73.4	30.2	95.00%	R.ISQTYFNYQATPECQK.V	Carbamidomethyl (+57)
869	879	2	1233.66	-0.018	0	29.6	24.9	95.00%	R.FSTIEPQTIAK.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
190	AVT7_YEAST	5.51%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
441	451	2	1098.67	0.26	0	49.5	21.5	95.00%	K.LIGLDSLAIGK.M	
1	16	2	1650.81	-1.1	0	82.5	28.2	95.00%	-.MEATSSALSSTANLVK.T	Acetyl (+42)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
191	A6ZMW0_YEAS7	10.09%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
485	496	2	1367.7	-0.74	0	60.2	27.5	95.00%	K.LVDVEDLGYFAK.N	
573	588	2	1912.86	-0.35	0	73.9	30.2	95.00%	R.SNPYVQNICVYADENK.V	Carbamidomethyl (+57)
677	688	2	1324.74	-0.17	0	47.4	22.4	95.00%	R.DILAAVKPDVER.V	
2	21	3	2157.99	-0.092	0	62.5	30.5	95.00%	M.TEQYSVAVGEAANEHETAPR.R	
532	541	2	1116.55	-0.29	0	41.4	26.3	95.00%	R.TGDIAEWTPK.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
192	A6ZU02_YEAS7	8.12%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
478	491	2	1607.89	-0.63	1	43.7	20.5	95.00%	K.EVEKDAVTNIHLLK.R	
482	491	2	1122.64	0.52	0	48.8	22.7	95.00%	K.DAVTNIHLLK.R	
62	75	2	1489.75	-0.95	1	94.6	27.2	95.00%	K.KVDAMGVESTGIQR.I	
459	477	2	1959.98	-1.1	0	60.5	28	95.00%	K.EFPTVTGEINGPELVGSSK.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
193	A7A007_YEAS7	19.43%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
232	242	2	1314.64	-0.7	0	44.1	26.9	95.00%	R.FTTVYENNLSK.S	
149	176	3	2900.4	-0.83	1	51.2	29.5	95.00%	K.EIGSSGEENKVTDASSLPHVAELSSTTR.G	
249	264	2	1600.87	-0.51	0	103	24.8	95.00%	K.AIVSTGLDLGNATIEK.L	
159	176	2	1869.95	1.8	0	62.9	26.7	95.00%	K.VTDASSLPHVAELSSTTR.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
194	ZRT1_YEAST	6.91%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
155	172	2	2121.02	-0.33	1	64.9	29.3	95.00%	K.YGLSHDHTHDEIKDTVVR.N	
155	167	3	1550.71	1.1	0	28	29.1	93.20%	K.YGLSHDHTHDEIK.D	
269	276	2	931.52	2.9	0	44.1	23.8	95.00%	R.LSAIEFPR.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
195	A6ZZE8_YEAS7	8.51%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
388	399	2	1417.68	-0.86	0	28.2	28.3	90.20%	K.ETDDILDEIDLK.E	
382	399	3	2155.06	0.6	1	35.7	28.8	95.00%	K.YLFADKETDDILDEIDLK.E	
403	424	3	2424.16	-0.28	0	54.6	29.7	95.00%	R.HIPYVTQGQSFDDEISLGGFSK.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
196	A6ZPF3_YEAS7	11.20%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
172	182	2	1290.61	-0.25	0	38.6	27.8	95.00%	K.DTTPWNESLTK.L	
399	411	2	1583.8	-0.5	0	43.5	27.6	95.00%	R.HYSIIYNDVLGYK.T	
219	235	2	2000.99	-0.51	0	68.6	28.6	95.00%	K.FAAPLTYWFLSNSDLEK.S	
205	218	2	1684.87	0.4	0	57.7	26.1	95.00%	R.SSLDELFFLPNYIK.F	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
197	HSP72_YEAST	14.87%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
297	308	2	1525.74	0.12	1	41.3	28.5	95.00%	R.ARFEELCADLFR.S	Carbamidomethyl (+57)
158	169	2	1198.67	-0.44	0	52.4	24.3	95.00%	K.DAGTIAGLNVLR.I	
548	562	2	1617.78	-1.2	1	29.7	27.8	93.40%	K.NTISEAGDKLEQADK.D	
537	547	2	1264.67	-1	0	39.1	25.6	95.00%	K.NQLESIAYSLK.N	
55	69	2	1590.74	-1	0	63.7	29.1	95.00%	K.NQAAMNPANTVFDAK.R	
170	185	2	1658.89	-0.44	0	68.9	25.9	95.00%	R.IINEPTAAAIAYGLDK.K	
111	124	2	1549.78	-1.2	0	62.2	27.3	95.00%	K.NFTPEQISSMVLGK.M	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
198	B3LP09_YEAS1	11.54%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
375	390	4	1797.89	-0.43	0	21.2	28.4	93.50%	K.KPNLHGYGHPNPPNEK.S	
326	339	2	1718.74	-0.015	0	57.2	29.8	95.00%	R.NLSFEETPDYEGYR.M	
509	524	2	1822.81	-0.77	0	52.7	30	95.00%	K.YPYNAQPTANDEQNAK.N	
431	447	2	1994	0.067	0	93.7	27.3	95.00%	K.VQQQQLQQAQAQQQANR.Y	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
199	A6ZR28_YEAS7	39.26%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
21	32	3	1450.81	0.42	1	47.4	20.1	95.00%	R.KQFVVDVLHPNR.A	
11	20	2	1109.69	0.25	1	49.1	11.5	95.00%	R.KVISNPLLAR.K	
84	90	2	939.48	1.5	1	28.8	26	94.60%	K.KFEPTYR.L	
12	20	2	981.6	0.28	0	25.8	15.3	91.80%	K.VISNPLLAR.K	
69	83	2	1539.79	0.12	0	37.8	25.6	95.00%	K.SVGFGLVYNSVAEAK.K	
53	61	2	996.5	0.17	0	47.5	26.1	95.00%	K.DAVSVFGFR.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
200	B3LHY2_YEAS1	14.42%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
12	49	4	4276.97	-0.95	0	56.9	30.7	95.00%	K.HLVDDVLFISPTNDGSEEKPTEVTFQEDEGHDASLHNR.S	
108	120	2	1258.65	0.7	0	69.9	26.5	95.00%	K.SNIGNAEVAGLSK.D	
274	286	2	1684.77	-0.56	1	36.6	29.1	95.00%	K.NLEDSWFFNKEEK.E	
510	522	2	1590.7	-0.88	0	57	29.8	95.00%	R.CNELGEPIPYDER.L	Carbamidomethyl (+57)
274	283	2	1298.59	-0.1	0	48.3	27.9	95.00%	K.NLEDSWFFNK.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
201	A6ZU59_YEAS7	28.35%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
187	203	2	1833.95	-0.54	0	87.1	26.7	95.00%	K.LLQLAGVEDVYTQSNGK.T	
142	157	2	1728.86	-1.3	0	73.2	27.7	95.00%	R.GYWGTNLGQPHSLATK.T	
50	64	2	1738.99	-0.42	0	46.3	19.3	95.00%	K.ITTIEEIFLHSLPVK.E	
65	88	3	2767.48	0.11	0	25.2	22.2	94.60%	K.EFQIIDTLLPGLQDEVMNIKPVQK.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
202	A6ZM19_YEAS7	8.44%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
253	270	3	2304.03	0.32	1	34.4	30.7	95.00%	K.RATYDDYQTNYYNYVIDK.M	
321	336	2	1986	0.087	0	36.8	27.4	95.00%	K.FILSEEYFVELENNLK.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
203	A7A1T6_YEAS7	8.89%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
659	671	2	1508.74	0.11	0	39.5	28.5	95.00%	R.IIEEHESPIDAEK.N	
487	521	4	3993.91	0.01	1	25.1	29.8	95.00%	R.SIVYNNIEGSDFKPYMDALNIGKDDLHLDGELQDR.Q	
203	214	2	1323.71	-0.47	0	37.9	24	95.00%	K.LSPVFELFASSK.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
204	A6ZYY5_YEAS7	10.91%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
2	13	2	1291.59	8	0	34.5	28.3	95.00%	M.TSSASSPQDLEK.G	Acetyl (+42)/ Deamidation (+1)
61	78	2	1945.88	-0.67	1	77.5	29.8	95.00%	R.DLLNALDRGDGEEGNCAK.Y	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
205	YIP8_YEAST	25.49%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
101	112	3	1314.71	-0.15	0	42	25.6	95.00%	R.QLNASMGTLRPK.K	
137	150	2	1675.79	-0.007	0	71.1	28.8	95.00%	R.DPSYSFMYPLTLSR.K	
113	129	2	1867.97	0.64	1	88.8	25.6	95.00%	K.KQSTAYTNVPVIFSGEK.V	
196	204	2	1112.56	-0.12	0	39.8	24.3	95.00%	R.EFIDSLRPH.-	
114	129	2	1739.87	-0.35	0	72.9	28	95.00%	K.QSTAYTNVPVIFSGEK.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
206	B3LK87_YEAS1	17.00%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
386	402	2	1913.92	-0.26	0	79.7	29.3	95.00%	K.LQEQSGNMDQNLLPAEK.F	
315	340	3	2734.3	-0.18	1	69.5	30.1	95.00%	R.HPEPSPDPIAVADTTSGSDQSTRLEK.N	
372	385	2	1642.83	-0.44	1	52.8	26.9	95.00%	K.NQANIERDILENSK.L	
303	314	2	1398.52	0.98	0	44.9	27.4	95.00%	K.SCPGFGNCQCGR.H	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
207	B5VQ30_YEAST	5.25%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
514	524	2	1171.63	-0.018	0	32.5	24.9	95.00%	K.AMDLLASNLPK.A	
696	715	3	2145.1	-0.65	0	30.5	26.3	95.00%	K.VIPVDTMKPLDGVSDTPSFK.N	
196	204	2	1031.6	1.9	0	34	20.3	95.00%	R.TVLFQTVPK.Q	
56	65	2	1179.58	-0.28	0	53.3	27.1	95.00%	K.SSFNLINEEK.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
208	A6ZSL9_YEAS7	29.15%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
14	27	2	1518.81	0.12	0	77	24.4	95.00%	K.AISLETQTESLLSK.Y	
155	163	2	1102.58	-0.29	0	45.3	26.6	95.00%	R.LISQAWETR.S	
28	44	2	1891.84	-0.42	0	89.7	30.6	95.00%	K.YSTFAQTTSSEQTGQEK.K	
164	179	3	1787.86	0.12	0	32.5	29.6	95.00%	R.SQFHSQSNVLNTANNK.V	
49	57	2	1012.57	-0.31	0	40.6	22.2	95.00%	K.QLEGILGQR.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
209	A6ZVR3_YEAS7	15.41%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
611	621	2	1203.65	0.061	0	45.3	25.7	95.00%	R.EAFVSLNIPSK.A	
156	173	2	2045	-2	0	62	28.5	95.00%	K.SESQYLEGFDFLELIAGK.A	
578	586	2	984.59	-0.42	0	25.1	19	90.70%	K.IGDVIIIDK.S	
216	246	3	3443.59	-1.1	0	69.4	31.5	95.00%	R.QLAVDDINTGHVNCESNPTICEELGFGDLVK.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
433	442	2	1203.59	-0.93	0	33.9	26.3	95.00%	R.NIDAIMDWVK.K	
493	505	3	1642.85	0.98	0	30	26	95.00%	K.NLLLASWEYEHIR.M	
140	155	2	1763.75	-1.8	0	76.8	29.9	95.00%	R.ESMDPNNLDTDLDSAK.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
210	A6ZQ99_YEAS7	7.80%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
196	216	3	2452.26	-0.45	1	32.5	26	95.00%	K.VIDPSNNWVVDEIVNLDEVRK.V	
31	44	4	1646.79	0.87	0	29.5	28.4	95.00%	K.HQDTDAFLHSHLAR.Y	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
211	RAX1_YEAST	18.62%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
222	232	2	1397.71	0.2	1	32.4	26.2	95.00%	R.KYDIEIFDDLK.N	
118	131	2	1498.77	-0.49	0	61.8	25.5	95.00%	K.LLENSGPDVPFSPK.L	
132	140	2	1086.57	0.62	0	42.5	26.4	95.00%	K.LNELLGDWK.H	
213	221	2	1085.61	-0.11	0	28.5	24.3	95.00%	R.IIESVQIER.K	
8	19	2	1468.68	-0.55	0	44.5	28.1	95.00%	K.VSSMQNFEMIQR.E	
20	32	3	1628.93	0.86	1	28.2	19.7	95.00%	R.ERLPTLYEVLIQR.T	
152	164	2	1487.76	0.46	0	80.9	27.1	95.00%	R.NEDVALIVDEIMK.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
212	A6ZYM2_YEAS7	6.57%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
688	702	2	1603.88	0.3	0	68	23.3	95.00%	K.ALNAVVLESEYVLGK.G	
779	795	2	1847.8	-0.87	0	77.6	30.1	95.00%	R.NGYETYMITGDNNSAAK.R	
800	817	2	1926.92	0.87	0	83.6	28.9	95.00%	R.EVGISFENVYSDVSPTGK.C	
169	184	2	1777.87	-2.3	0	44.5	28.4	95.00%	K.AFEDESPLILSSVSER.F	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
213	A6ZYA1_YEAS7	3.24%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
300	308	2	1055.63	0.75	0	31.9	20.1	95.00%	R.SVLDLLLQR.L	
550	564	3	1784.86	-0.49	1	36.6	28.1	95.00%	K.LKHDDEVSCEELLAK.I	Carbamidomethyl (+57)
2	15	2	1580.88	-1.1	0	46.8	19.7	95.00%	M.SLPLKPLTIDSNNK.Q	Acetyl (+42)
78	94	3	1760.99	-0.17	1	31.5	17.9	95.00%	R.RLTSSLSPALPAGVHQK.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
214	A6ZLU0_YEAS7	11.22%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
275	292	2	1990	-1.4	0	65.9	27.6	95.00%	R.LLICGPDGMNNLALQYAK.E	Carbamidomethyl (+57)
96	112	4	1870.02	-0.31	1	19.5	24.1	95.00%	K.TRLESLDIPAGHHVAVR.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
215	A6ZUM5_YEAS7	19.84%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
102	113	2	1402.69	-0.09	0	54.8	28	95.00%	R.FTPGSFTNYITR.S	
89	101	2	1268.66	-1.3	0	40.1	24.8	95.00%	K.FAAHTGATPIAGR.F	
28	52	4	2815.45	-0.2	0	18.5	25.6	93.50%	R.NVQVHQEPYVFNARPDGVHVINVGK.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
216	A6ZRX9_YEAS7	5.19%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
596	606	3	1359.72	0.96	1	30.3	26	95.00%	K.IYVKHDDLTTR.V	

65	90	3	3044.47	-0.39	1	49.3	29.6	95.00%	R.VFVDMSSPNFQTLEDPHRDEIINSVR.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
217	AGP1_YEAST	10.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
92	112	3	2269.06	-0.26	1	51.2	30.2	95.00%	R.QAQELEKNESSDNIGANTGHK.S	
15	57	4	4802.15	0.052	0	37.1	31.6	95.00%	K.NSSTEIHATGQDNEIEYFETGSNDRPSSQPHLGYEQHNTSAVR.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
218	A6ZT41_YEAS7	24.40%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
70	88	2	1955.01	-0.52	0	67.6	25.8	95.00%	K.ALLSNASQLEMVPPSATAR.H	
8	24	2	1776.91	-6.6	1	63.3	26.7	95.00%	K.NQLNTGGVPNGVHNTKK.E	
35	69	4	3854.89	-0.56	1	45.9	27.8	95.00%	K.LGSASFTAINTLTKPALFSFYDDDITKNEGNVYDK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
219	ATG22_YEAS7	16.29%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
512	525	2	1614.77	-0.45	0	53	28.5	95.00%	R.EAEELSQVLPESER.R	
62	79	3	1982.86	-0.48	0	30.1	30.4	94.00%	K.VHDHSIPCLSETGSDSDK.C	Carbamidomethyl (+57)
281	296	2	1801.86	-0.5	0	58.2	28.7	95.00%	R.SPYPGEQDALGQLNWK.N	
2	17	2	1862.81	-0.65	0	75.2	30.1	95.00%	M.SYGTINDMNESVTNYR.I	
189	210	3	2410.14	-0.89	1	47.4	29.8	95.00%	K.CQSQGAYEPDKVDSLTTVISGR.G	Carbamidomethyl (+57)
200	210	2	1146.62	-0.62	0	57.3	25.3	95.00%	K.VDSLTTVISGR.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
220	A6ZN13_YEAS7	5.45%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
41	52	3	1397.76	0.49	0	40.4	22.5	95.00%	K.FGLNLDLDHLLK.E	Deamidation (+1)
449	458	2	1265.59	-0.15	0	29.8	27.1	94.40%	K.DFICNWLGNK.A	Carbamidomethyl (+57)
93	99	2	907.44	-0.027	0	32.5	26.9	95.00%	K.DWDFVVK.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
221	A7A0E6_YEAS7	8.32%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
12	32	3	2272.2	-0.89	0	31.2	23.7	95.00%	K.KPILAVPEPALADTHSEEISR.S	
271	292	3	2507.28	0.48	1	50.6	26.2	95.00%	R.KVNENWNVEDGHITDVLLGSLR.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
222	A6ZQG2_YEAS7	10.61%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
272	299	3	3217.55	0.011	0	97.2	29.4	95.00%	K.NHLYSTFHTFQGIEDLGTGIQSYGYITR.N	
191	204	2	1433.68	0.14	0	38.4	28	95.00%	R.SGIPAYYGYGGTTK.M	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
223	B3LL17_YEAS1	11.65%	100%	3							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
79	103	3	2918.4	-0.79	0	43.8	29.9	95.00%	K.SGWLFNDHVEDIIPEGHIAHYDLNK.L		
142	152	2	1286.73	2	0	48.2	23	95.00%	R.ELIELGFITPR.T		
256	265	2	1131.64	-0.37	0	34.9	24	95.00%	K.AILAANIYQR.F		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
224	B3LK49_YEAS1	6.56%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
332	346	2	1598.74	-0.34	1	38.3	28.6	95.00%	R.LRSSPSASSSSLANR.E	Phospho (+80)	
190	199	2	1179.6	0.26	0	58.5	28	95.00%	K.ATLLNFVCDK.E	Carbamidomethyl (+57)	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
225	A6ZTV6_YEAS7	6.73%	100%	4							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
412	422	2	1194.61	0.16	0	32.9	26	95.00%	R.TAVDTVYEAVK.C		
289	302	2	1672.88	-0.48	0	35	25.8	95.00%	K.TNQLVPEVLEYNVR.F		
400	411	2	1288.7	-0.084	0	66.5	25	95.00%	R.VLSVTSTAQDLR.T		
29	45	2	1705.81	-0.89	0	50.9	28.7	95.00%	K.IYVAPGNGGTATMDPSR.V		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
226	A6ZU67_YEAS7	7.72%	100%	3							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
428	440	2	1502.76	-0.75	1	33.6	27.4	95.00%	R.LVSRDNEIEVDSK.H		
521	551	3	3156.55	-1.1	0	115	28	95.00%	R.DRPGSVLMNVVSGGIAEASAQQAGDLMQDLK.T		
598	609	2	1399.73	0.22	0	43.2	26	95.00%	R.IPTAVVWIDCAR.L	Carbamidomethyl (+57)	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
227	A6ZU78_YEAS7	17.45%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
116	126	2	1190.75	0.15	1	34.6	9.54	95.00%	K.GRIPNVPVIVK.A		
97	111	2	1504.78	-0.21	0	38.5	26.9	95.00%	K.ETAPVIDTLAAGYGK.I		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
228	A6ZV05_YEAS7	3.94%	100%	4							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
1305	1320	2	1769.91	-0.23	0	62	27.1	95.00%	K.ISRPIASQNSLGWNEV.-		
1261	1272	2	1395.65	-0.29	0	57.4	28.2	95.00%	R.MSVQESITQSMR.I		
1260	1272	2	1551.75	-0.84	1	56	28.1	95.00%	K.RMSVQESITQSMR.I		
1273	1295	3	2684.15	-0.62	0	30	31.4	92.70%	R.IQNWMDDSYYGHGLTNNDSTPTR.H		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
229	A6ZU36_YEAS7	29.32%	100%	4							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
92	106	3	1804.95	0.73	0	24.8	25.7	93.50%	R.YVYAHFPINVNIVEK.D		

3	21	2	2160.13	-0.089	0	61.3	25	95.00%	K.YIQTEQQIEVPEGVTVSIK.S	
175	184	3	1177.61	-0.33	0	29.8	26	95.00%	K.FLDGIYVSHK.G	
73	84	2	1276.67	-2.2	0	43.1	26.2	95.00%	K.SLVDNMITGVTK.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
230	A6ZNJ9_YEAS7	12.32%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
290	315	3	2982.31	-0.6	1	80.9	31.2	95.00%	K.FTDSTNPFNYTSYNLSPDSEDRSTPK.S	
326	341	3	1865.97	1.2	1	23.4	26.3	90.60%	K.YRPPSVHLDQLLDGKE.-	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
231	SSO1_YEAST	15.17%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
63	77	3	1793.94	0.22	1	25.9	25.4	94.80%	K.RLLTEVNEEQASHLR.H	
50	62	3	1568.76	-0.88	0	28.8	28	95.00%	K.YDHTINQVDSLHK.R	
78	93	2	1832.91	0.97	0	60.8	28	95.00%	R.HSLDNFVAQATDLQFK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
232	B3LJK2_YEAS1	7.85%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
581	592	2	1265.61	-0.33	0	42.6	27.9	95.00%	K.VESGLFSVDGEK.F	
9	19	2	1170.69	-0.36	0	28.3	21.1	95.00%	R.AILTDEGVLIK.S	
593	608	2	1943.99	0.31	0	49.7	26	95.00%	K.FPLEPLQVEIMPMLCK.T	Carbamidomethyl (+57)
549	558	2	1129.64	0.25	0	31.7	24.3	95.00%	R.MTPILLSLDK.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
233	TCB3_YEAST	3.24%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
1340	1352	2	1358.68	-0.087	0	85	26.7	95.00%	R.SPSNLNSTSVTPR.A	
1339	1352	3	1514.78	2.8	1	28.1	26.4	95.00%	R.RSPSNLNSTSVTPR.A	
40	63	4	2678.19	-0.88	0	24.4	31	94.30%	R.GSDHAPSGHHQYHQLINHDANDTK.T	
1196	1207	2	1517.76	-0.21	0	58.5	28.2	95.00%	K.NQVIFNVLDWDR.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
234	A6ZQP7_YEAS7	33.33%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
32	40	2	880.54	-0.026	0	41.9	15.8	95.00%	K.IGPLGLSPK.K	
147	165	2	2073	-0.16	0	50.5	29.4	95.00%	K.NPHDIIEGINAGEIEIPEN.-	
131	142	2	1289.64	-0.064	0	69.4	27.4	95.00%	K.EILGTAQSVGCR.V	Carbamidomethyl (+57)
17	31	2	1296.7	0.13	0	30	22.4	95.00%	R.AVGGEVGASAALAPK.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
235	A6ZQ10_YEAS7	9.58%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
478	491	2	1464.77	0.42	0	43	24.5	95.00%	R.LGGSSLLECVVFGK.T	Carbamidomethyl (+57)
327	336	2	1150.55	-0.44	0	34.4	26.7	95.00%	R.DTVTMEIQSK.C	
380	395	2	1837.93	0.49	0	79.1	27.1	95.00%	R.QYDLQTTASELVTELK.S	
319	326	2	966.48	0.8	0	29	26	94.70%	R.FTNELSTR.D	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
236	A6ZSL1_YEAS7	6.70%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
16	46	4	3541.55	-0.78	0	54.2	31.9	95.00%	K.HVFMGMEHELNPETHNDSNSDSYGLPQLSEK.Y		
607	617	2	1390.64	-0.24	0	50.1	28.2	95.00%	K.DNDPILDWFEK.L		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
237	A6ZLM1_YEAS7	7.14%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
56	69	2	1619.83	-1.1	0	66.5	27.2	95.00%	K.ATTPNVNDPIYFLR.G		
6	26	3	2414.44	-0.29	0	31.8	11.1	95.00%	R.LIDIVKPILPILPEVELPFEK.L		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
238	EMP47_YEAST	13.26%	100%	5							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
221	227	2	812.38	0.95	0	26	26	90.50%	R.FPSGSYR.I		
333	346	2	1637.87	0.36	0	84.1	24.1	95.00%	K.VQQELLSFMTTITK.Q		
315	326	2	1313.72	-0.018	0	93	24.5	95.00%	K.ILANDINALETK.L		
40	53	2	1562.79	-0.46	0	94.9	27.5	95.00%	K.LSSDYSLPDLINAR.K		
194	205	2	1436.7	-1.2	0	48.5	28.2	95.00%	R.VTYDLEDDNLLK.V		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
239	A6ZRQ7_YEAS7	38.33%	100%	5							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
152	173	3	2420.18	0.45	0	55.1	29.2	95.00%	K.FADGFLIHSGQPVNDFIDTATR.H		
201	223	2	2458.36	-0.016	1	52.7	18.8	95.00%	K.ALPDAVTIIEPKEEEPILAPSVK.D		
28	40	2	1436.68	-0.5	0	73.2	28.6	95.00%	R.ELAEEGYSGVEVR.V		
11	27	3	1989.98	0.35	0	51.6	28.4	95.00%	K.LVADGVFYAELNEFFTR.E		
224	240	2	1903.84	0.3	0	53.2	29.8	95.00%	K.DYRPAEETEAQAEPVEA.-		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
240	A6ZZX8_YEAS7	28.21%	100%	5							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
162	172	2	1351.69	-0.52	0	52.6	27.3	95.00%	K.QYAQEQGLLFR.E		
62	72	2	1350.62	-0.24	0	70.8	29.1	95.00%	K.FEIWDTAGQER.Y		
6	16	2	1086.63	-0.19	0	29.6	22.6	95.00%	K.LVLLGDSSVGK.S		
83	101	2	2091.05	-0.53	0	102	27.9	95.00%	R.NANAALVVYDITQEDSLQK.A		
113	126	2	1532.81	-0.07	0	80.1	26.4	95.00%	K.VGDDDLVIYLLGNK.V		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
241	A6ZNG9_YEAS7	34.51%	100%	4							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
19	35	2	1951.98	-0.78	1	61.1	27.2	95.00%	R.GVDLEKLLEMSTEDFVK.L		
25	35	2	1310.64	-0.093	0	49.2	27.2	95.00%	K.LLEMSTEDFVK.L		
65	77	2	1390.76	-1.3	0	61.5	23.2	95.00%	K.LAAPENEKPAPVR.T		
82	100	2	2033.07	-0.84	0	82.2	25.2	95.00%	R.NMIIVPEMIGSVVGIYNGK.A		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
242	A6ZKM8_YEAS7	14.50%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
165	178	2	1550.76	-1	0	34.9	28.2	95.00%	R.LYACISSRPGQSGR.C	Carbamidomethyl (+57)
78	92	2	1666.88	-0.49	0	26.1	25.4	91.80%	R.IAGVVYHPSNNELVR.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
243	A6ZPG3_YEAS7	20.60%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
167	181	2	1716.89	-0.068	0	44	26.6	95.00%	R.APLEEIVISNDYLNK.D	
93	106	2	1651.79	-0.077	1	28.6	28.3	91.10%	R.EQSLDGIFEETKEK.L	
53	63	2	1264.57	0.29	0	60.2	27.8	95.00%	R.NETNNIDGNFK.S	
220	227	2	905.49	0.091	0	28	24.2	94.80%	R.LELYGPSK.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
244	A6ZQE6_YEAS7	23.08%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
4	19	2	1628.84	-0.075	0	76.2	27	95.00%	R.SSVLADALNAINNAEK.T	
44	57	3	1749.77	0.06	0	38.8	29.1	95.00%	K.HGYIGEFEYIDDHR.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
245	A6ZSR4_YEAS7	32.35%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
85	93	2	1084.54	0.62	0	26.5	26.5	90.50%	R.YTLDVEAFK.S	
35	48	3	1489.78	0.4	0	38.2	25.7	95.00%	K.SHPFGHALVAGIER.Y	
94	107	2	1593.76	-0.76	0	66.9	28.1	95.00%	K.SVVSTETFEQPSQR.E	
127	133	2	955.46	1.8	0	26.9	26.7	90.80%	K.NQWFFSK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
246	A6ZQF2_YEAS7	19.91%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
83	95	4	1542.89	0.088	0	28.1	19	95.00%	R.LIYPHVEHVPVLK.Q	
114	129	3	1897.02	-0.061	1	51.8	24	95.00%	K.RLILKPEENALTDEEK.K	
61	82	3	2263.09	0.71	0	44	29	95.00%	R.SAGASYSPSHGLYINEIPASSR.L	
261	268	2	915.55	0.31	0	31	23.3	95.00%	K.IMDLALLK.N	
291	315	3	2691.32	-0.22	0	40.6	28.3	95.00%	K.IIIPHDADGNIDASSFVIANDFYGK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
247	OST1_YEAST	13.03%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
57	77	2	2308.09	-0.23	0	97.1	29.8	95.00%	K.NIASEPATEYFTAFESGIFSK.V	
198	213	2	1834.82	-1.6	0	47.2	29.5	95.00%	K.ANGNSFEFGPWEDIPR.F	
173	197	3	2724.29	-0.26	0	39.4	30.4	95.00%	K.ASFTLIGSSSFEEYHPPNDESLLGK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
248	A6ZRX1_YEAS7	53.33%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
27	67	4	4491.04	-1.5	1	68.2	31.6	95.00%	K.VYDVSQFKDEHPGGDEIIMDLGGQDATESFVDIGHSDEALR.L	
4	26	3	2765.3	0.005	0	32.2	30.9	95.00%	K.VYSYQEVAEHNGPENFWIIIDDK.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
249	A6ZMP4_YEAS7	13.90%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
54	66	2	1584.79	-0.19	0	45.2	27.8	95.00%	R.YENIINQIDAQHK.D	
44	53	2	1100.59	-1.2	0	72.2	26.4	95.00%	K.INSINANLSR.Y	
238	255	3	1966.9	-0.8	0	41.7	29.8	95.00%	K.NVEDAQQDVEQGVGHTNK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
250	B3LQX5_YEAS1	6.74%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
268	277	2	1117.53	-0.096	0	35.7	27.2	95.00%	K.YSIAYESTGK.L	
470	486	3	1936.01	0.83	0	32.4	26.8	95.00%	R.ITAQTSKPLWSVGTYER.I	
450	461	2	1394.58	-0.52	0	47.3	28.1	95.00%	R.YADTDNFFGSMK.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
251	A6ZN91_YEAS7	12.90%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
57	66	3	1123.65	0.26	0	41.9	17	95.00%	K.INRPPVSVSR.I	
117	130	2	1501.76	-0.057	0	77	27.4	95.00%	K.AGGECITLDQLAVR.A	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
252	B3LJM9_YEAS1	6.79%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
411	425	2	1841.88	-0.55	0	65.7	29	95.00%	R.MADQLTDFLIMQNFR.A	
181	192	2	1237.55	1.9	0	33.2	26.7	95.00%	R.DLMACAQTGSGK.T	Carbamidomethyl (+57)
193	206	2	1527.8	0.11	0	36.2	24.7	95.00%	K.TGGFLFPVLSESFK.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
253	A6ZNU6_YEAS7	27.37%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
125	138	2	1571.88	0.56	0	26.2	22.4	92.60%	K.ILEDLVFPTEIVGK.R	
166	175	2	1197.6	-0.43	0	26.7	26.3	91.20%	K.LESFQAVYNK.L	
8	35	3	3082.61	-0.16	0	56.2	23.5	95.00%	K.ILSQAPTELELQVAQAFVELENSSPELK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
254	A6ZUX1_YEAS7	5.99%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
606	615	2	1249.53	-0.1	0	31.2	26.8	95.00%	R.DFYTAEGEYR.V	
490	504	3	1942.99	0.26	1	26.9	25.6	95.00%	K.LALIDDFREAYYWLR.M	
472	489	2	1832.91	-0.6	0	62.2	27.6	95.00%	R.TAYSSPSVVLPSQTPDGK.L	
490	497	2	961.52	0.18	0	41.7	23.7	95.00%	K.LALIDDFR.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
255	A7A0Y0_YEAS7	32.13%	100%	5							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
83	88	2	757.39	1.1	0	40.1	21.2	95.00%	R.DAFHLR.V		
186	198	2	1363.66	-0.54	1	51.5	28.1	95.00%	R.EAGEVKDDGAFVK.F		
117	128	3	1219.66	-0.0072	0	31.5	25.2	95.00%	R.GAWGKPHGLAAR.V		
41	69	3	3226.58	-0.49	0	54.7	29.2	95.00%	K.ATVDEFPLCVHLVSNELEQLSSEALEAAR.I	Carbamidomethyl (+57)	
129	139	2	1245.71	0.15	0	55.6	22.8	95.00%	R.VDIGQIIFSVR.T		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
256	A6ZRC2_YEAS7	1.72%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
732	749	2	2001.97	0.54	0	54	28.6	95.00%	R.ALSGNSQFYPEEVTFVSK.E		
872	880	2	980.49	0.49	0	32.2	26.3	95.00%	K.GADSIIYSR.L		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
257	A6ZMY7_YEAS7	13.54%	100%	3							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
181	195	2	1589.85	0.79	0	67	24.9	95.00%	K.GSAPLFGNFLEPLTK.T		
16	34	3	2363.07	-0.78	1	43	30.5	95.00%	K.TVQEHNTANDCWVTYQNRK.I	Carbamidomethyl (+57)	
41	58	3	1933.91	0.41	0	30.4	29.8	94.90%	R.FLSEHPGGDESILDYAGK.D		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
258	B3LU76_YEAS1	30.36%	100%	4							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
50	65	3	1766.89	-0.0026	0	31.3	27.6	95.00%	K.MNAPQKPEDIPVATEK.T		
81	94	2	1665.79	-0.74	0	56.2	29.4	95.00%	R.FGNLPAQWSAFWDK.T		
147	176	3	2968.39	-0.81	0	56.4	30	95.00%	K.NSFAELASIEEVHGGSPWGAGTLAGPDGSR.T		
66	80	2	1740.91	-0.017	0	50.5	26	95.00%	K.TLLEYDAFLFGVPTR.F		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
259	B3LMS1_YEAS1	5.94%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
257	264	2	1101.52	0.35	0	45.6	27.7	95.00%	K.QEIQDWQR.S		
57	77	3	2420.09	-0.29	0	36.7	31.2	95.00%	R.FEAPDENISYDDTWVGQHGLK.Q		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
260	A6ZSD5_YEAS7	10.05%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
101	111	2	1246.53	-0.066	0	45.5	27	95.00%	R.GINFDYSGSCK.I	Carbamidomethyl (+57)	
90	100	2	1261.49	-0.079	0	75.5	26.3	95.00%	K.FGSMSCSSMPR.G	Oxidation (+16)/ Carbamidomethyl (+57)	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
261	A6ZVM1_YEAS7	8.34%	100%	6							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
109	126	2	1896.92	-1.3	0	73.7	29	95.00%	K.FTNIASSPPSSSNNIFSK.A		
248	261	3	1744.85	-0.17	1	33.8	28.5	95.00%	R.DRESNNELYHVITR.N		

803	817	3	1763.92	0.23	0	32.5	25.5	95.00%	K.VTRPEGAFNQLEYLK.I	
615	628	4	1614.82	0.081	1	34.8	26.5	95.00%	R.DRHSISLLHEHSGK.T	
629	645	2	2014.01	0.29	0	30	28	93.60%	K.TLNYEILQVFPFNSDSK.R	
487	504	2	2049.06	0.04	1	30.8	25.5	95.00%	R.TSTIPEDLGRIEYLLSDK.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
262	A6ZW48_YEAS7	3.58%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
122	135	2	1532.69	-0.73	0	58.9	29.8	95.00%	K.NIGDNENTATEVEK.A	
500	514	2	1846.9	-0.12	0	43.9	27.6	95.00%	R.WEVDEPEYILENALK.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
263	A6ZT81_YEAS7	6.64%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
244	255	2	1372.63	0.29	0	60.6	27.7	95.00%	K.IGLDCASSEFFK.D	Carbamidomethyl (+57)
376	392	2	1820.92	-0.23	0	46	28.7	95.00%	R.SGETEDTFIADLVVGLR.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
264	A6ZXF1_YEAS7	11.70%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
307	324	2	2056.95	-1.8	0	50.8	30.2	95.00%	K.SFGYTWAVPNENTQNTTK.S	
285	306	3	2472.3	-0.2	1	22	24.6	90.40%	K.LTTLDTGDLSFPIDEEQPILKK.S	
261	284	3	2737.31	-0.17	0	31.5	30	95.00%	K.QLHVPDNSQDDTIIMMNPIDNSLK .L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
265	A6ZL24_YEAS7	7.52%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
581	587	2	822.44	-0.29	0	28.6	24.1	95.00%	K.SGFPFIR.L	
362	378	2	1655.85	0.3	0	61.5	26.4	95.00%	R.GDGTGVGDNVVNQLLAK.M	
425	433	2	1104.62	0.26	0	31.2	23.9	95.00%	R.LQIFDIQTK.K	
588	602	2	1561.76	-0.78	0	53.8	28.1	95.00%	R.LISPNELSGMSESAK.I	
603	611	2	1111.57	0.34	0	31.2	25.5	95.00%	K.IAYIDNTFR.D	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
266	A6ZRQ9_YEAS7	6.76%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
527	544	2	2030.9	-0.71	0	114	29.9	95.00%	R.NTETASANNPFSNEFNFK.A	
622	633	2	1376.68	-0.3	0	90.1	27.8	95.00%	R.NTVQNNSQGFLR.E	
557	569	2	1468.65	-0.42	0	35.3	28	95.00%	R.NVTAMNGSFQNMR.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
267	A6ZR85_YEAS7	17.65%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
43	51	2	941.53	0.29	0	42.1	22.8	95.00%	R.NIVEAAAVR.D	
71	82	3	1485.7	0.86	0	42.8	28.8	95.00%	K.LHYCVSCAIHAR.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
268	COS7_YEAST	24.80%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
157	167	3	1261.73	-0.0015	1	29	21.9	95.00%	R.TTVLEPFSLKK.D	
102	108	2	935.49	1.7	0	31	24.9	95.00%	K.QLIQFCK.E	Carbamidomethyl (+57)
354	369	2	2001.08	-0.26	0	39.5	23	95.00%	K.SMWLLPLNVELWPYIK.E	
25	33	2	1099.64	-0.29	0	27.9	22.6	94.60%	K.IVLPQDLFR.S	
178	196	2	2144.03	-0.98	0	84.1	29.3	95.00%	K.DSVPYIEEALQVYATGFDK.Q	
206	219	2	1553.81	-0.2	0	52.8	25.6	95.00%	K.SWSPVGLEDVQLPK.D	
143	153	2	1391.58	0.28	0	49.9	28.3	95.00%	K.NFFFNATDCEK.M	Carbamidomethyl (+57)
11	18	2	893.49	-0.02	0	26.5	24.8	92.90%	K.SVDVLSFK.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
269	A6ZPF9_YEAS7	31.30%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
28	43	3	1787.92	0.34	1	32.5	26	95.00%	K.TAALRQEIDDTVGIMR.D	
63	75	2	1389.74	-0.38	1	59.6	24.7	95.00%	K.ADNLAISAQGFKR.G	
56	74	3	2020.05	-0.3	1	24.8	25.7	93.40%	R.LTSIEDKADNLAISAQGFK.R	
63	74	2	1233.63	-0.67	0	49.2	26.2	95.00%	K.ADNLAISAQGFK.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
270	A6ZKZ2_YEAS7	23.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
117	133	2	1855	-0.52	0	47.2	23.8	95.00%	R.VQVGDIVTVGQCRPISK.T	Carbamidomethyl (+57)
47	56	2	1095.54	-0.83	0	34.6	26.1	95.00%	K.TAIEGSYIDK.K	
58	67	2	1148.6	0.44	0	68.1	26.5	95.00%	K.CPFTGLVSIR.G	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
271	A6ZM36_YEAS7	37.67%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
2	16	2	1781.94	-0.15	0	67.6	24.6	95.00%	M.SLVVQEQGSFQHILR.L	Acetyl (+42)
89	108	3	2261.06	-0.26	1	52.7	30	95.00%	R.QNDITDGKDYHTLANNVESK.L	
81	88	2	1015.56	1	0	47.3	26.3	95.00%	K.IPAWFLNR.Q	
57	68	2	1429.71	-1	1	48.4	27	95.00%	K.RAGELTQEELER.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
272	A6ZYL7_YEAS7	6.41%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
737	748	2	1380.73	-0.3	0	40.4	24.1	95.00%	K.ALLNGIEVDYFK.L	
242	257	3	1770.89	-0.34	0	25.7	27.6	92.10%	K.IADTEGFTPLHWGTVK.G	
265	276	2	1443.7	-0.7	0	40.9	27.8	95.00%	K.YLIQDGADFFQK.T	
2	10	2	1068.56	0.25	0	51.9	24.6	95.00%	M.VNELENVPR.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
273	A7A0G8_YEAS7	11.42%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
51	62	2	1525.72	-0.39	0	62.5	29	95.00%	K.AQIYDDQLQNYR.D	
108	120	2	1483.79	-0.53	0	45.6	24.4	95.00%	K.ICIQPEAGGWLIK.A	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
274	A6ZSV7_YEAS7	9.84%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification

502	511	2	1089.57	0.17	0	25.9	25.2	91.80%	R.SLVSPAPEYK.D	
39	55	2	1833.92	-0.87	0	72.6	27.3	95.00%	R.TTLQPNSTSQSMIGTLR.K	
475	501	3	3020.39	-0.43	1	82.3	30.8	95.00%	K.KPVADRTEDDETIELEEMGIGSSSQER.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
275	A6ZWP8_YEAS7	4.24%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
552	569	2	2050.88	-0.25	0	43.8	30.2	95.00%	R.VAGTSNFTNLDDYMMNMK.R	
589	602	2	1602.81	0.29	0	62.3	26.5	95.00%	R.IPEPLTFTNSEDLK.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
276	A6ZZV9_YEAS7	32.99%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
38	60	2	2445.14	-1.3	0	95.8	31.4	95.00%	R.AVSDSSVINQMTDSLGSMFTDIK.N	
29	37	2	1057.52	-0.3	0	34.9	26.5	95.00%	R.NINQEIGDR.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
277	A6ZN90_YEAS7	21.53%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
8	24	2	1927.94	0.72	0	65.4	28	95.00%	R.DVAAQDFINAYASFLQR.Q	
25	38	3	1543.86	0.59	1	26.3	22.4	95.00%	R.QGKLEVPGYVDIVK.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
278	A6ZR09_YEAS7	20.66%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
44	60	3	1846.88	-0.18	0	49.9	28.7	95.00%	K.CGDCGSALQGISTLRPR.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
92	99	2	976.52	-0.44	0	29	24.5	95.00%	R.AFLIEEQK.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
279	A6ZKS1_YEAS7	20.63%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
21	38	3	2057.02	0.73	1	30.6	27.8	95.00%	R.KVWLDPNETSEIAQANSR.N	
10	19	2	899.54	-0.46	0	66.1	21.7	95.00%	R.LAASVVGVGK.R	
22	38	2	1928.92	-0.63	0	89.3	29.3	95.00%	K.VWLDPNETSEIAQANSR.N	
118	128	4	1415.76	0.24	1	18.2	25.3	93.40%	K.HLYHVLYKESK.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
280	A6ZM77_YEAS7	5.02%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
362	370	2	1112.63	-0.56	1	41.1	22	95.00%	K.IREEQLAVR.N	
284	301	3	2013.92	-0.76	0	42	30.3	95.00%	K.DHIAAGGKPVCVMDAWCK.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
281	A6ZYE1_YEAS7	9.16%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification

176	199	3	2558.24	-0.23	0	34.2	29	95.00%	R.TVMSLPGNHDIGFGDTVVESSLQR.F	
255	275	3	2559.34	-0.57	1	28.7	23.7	95.00%	R.ILLTHVPLWRDPEQQTCGQLR.E	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
282	A6ZZN6_YEAS7	10.20%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
30	42	2	1494.71	-0.82	0	48.9	28.5	95.00%	K.TDSWFNETLIGGR.A	
174	200	4	2999.63	0.21	0	30.7	19.8	95.00%	R.SLHDIVKPEDFVLNSEHLTTVLVAVPK.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
283	A6ZUT7_YEAS7	2.37%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
148	159	2	1489.66	-1.1	0	73.1	28.7	95.00%	R.MSIETLYDDFEK.N	
666	676	2	1250.63	-0.66	0	53.5	27.9	95.00%	R.DNIIFGSPFNK.E	
763	774	3	1392.81	-0.14	0	30	18.3	95.00%	R.ILATHQLSLIER.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
284	B3LGK8_YEAS1	11.05%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
10	41	4	3711.76	-0.95	1	36.8	30.3	95.00%	R.VPLCEPEELPDDIQKENEYGTLDSPGHLYQVK.S	Carbamidomethyl (+57)
186	194	2	963.48	1.4	0	59.2	26.3	95.00%	K.YSIQSGGPR.A	
173	185	2	1392.62	-0.92	0	72	27.8	95.00%	K.GQCTDAALESVDK.Y	Carbamidomethyl (+57)
540	547	2	1058.54	0.069	0	34.6	26.3	95.00%	R.WDIEEVIR.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
285	A6ZLA4_YEAS7	12.97%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
114	128	3	1677.8	-0.15	1	29.9	29.3	94.90%	K.QSIESCKEGEAVVSR.H	Carbamidomethyl (+57)
386	411	3	2899.37	-0.58	0	36.1	30.6	95.00%	K.LISHIHDGQDGGTQDYFERPTDGTLK.A	
368	385	2	1942.86	-0.41	0	104	29.9	95.00%	K.TGCGEMDLFEILTAGSDK.L	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
286	A6ZNP1_YEAS7	21.88%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
174	201	3	3312.67	0.0038	1	57.5	26.3	95.00%	R.IPGSQIVIERDPINNEEFAYQQNLIEQR.D	
56	66	2	1193.6	-1.6	1	27.6	27.2	91.30%	K.SFIDRGDVSAK.V	
211	220	2	1148.61	2.1	0	32.9	26.3	95.00%	R.GITELNEVFK.D	
118	131	2	1702.79	-0.18	0	57.7	29.2	95.00%	R.DVSYSFQEFQGIQR.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
287	A6ZRQ3_YEAS7	6.84%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
759	782	4	2691.31	-0.097	1	38.9	28.7	95.00%	K.VVRGEDHHHTQVDQSEAHIAGLEK.K	

255	269	2	1638.77	-0.076	0	73.6	28.5	95.00%	R.SGSFSSQLGNFFFSK.N	
670	684	2	1688.71	-1.8	0	66.8	29.6	95.00%	R.TPDPPSYDESHSTEK.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
288	A6ZM38_YEAS7	34.56%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
82	95	2	1590.79	-0.0064	0	69.1	27.5	95.00%	K.DQYVPEVSALDLSR.S	
117	128	2	1295.76	-0.39	0	61.9	19.2	95.00%	K.LPLSVINVSAQR.D	
96	111	2	1702.84	-0.71	0	58.6	27.9	95.00%	R.SNGVLNVDNQTSDLVK.S	Deamidation (+1)
112	128	3	1794.07	0.4	1	22.5	12.3	91.10%	K.SLGLKLPLSVINVSAQR.D	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
289	A6ZLN3_YEAS7	4.53%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
293	306	2	1533.72	1.6	0	66.7	28.5	95.00%	R.NLGTTVSVEDEENK.A	
317	328	2	1456.75	-1	1	37.6	25.7	95.00%	K.NKEDIQEVDLVR.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
290	B3LMC0_YEAS1	2.14%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
933	943	2	1290.76	0.056	0	49.3	17.7	95.00%	R.LTLDIPVVFFK.C	
607	617	2	1253.55	0.22	0	38.6	27.5	95.00%	R.DTTGDFSENIR.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
291	A6ZPF4_YEAS7	4.65%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
420	432	3	1441.77	0.49	0	32.8	24.7	95.00%	K.NLHTHEVPAPISK.S	
13	21	2	1119.52	0.16	0	31.1	26.3	95.00%	K.STDDDLIWR.R	
99	111	4	1574.76	0.079	0	32.8	28.6	95.00%	R.HEFYHDVHPPLGK.M	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
292	A6ZW97_YEAS7	16.90%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
190	204	2	1718.86	-0.49	0	63.2	26.7	95.00%	R.EFEISPELATVDLEK.H	
158	165	2	991.53	-0.028	0	46	25	95.00%	R.TDFLDIIR.T	
166	174	2	974.58	-0.13	0	29.1	16.4	95.00%	R.TSPAVLFIK.S	
75	90	2	1855.86	-0.77	0	86.9	30	95.00%	K.TADSFLSNENELNFQK.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
293	A6ZW73_YEAS7	8.89%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
7	30	4	2618.33	-0.63	1	54	26.7	95.00%	R.TLKSDTDVTSLNASTVSHQSKPFR.Q	
314	326	3	1378.79	0.22	1	53.1	18.9	95.00%	K.KILDVGNTLAAHK.S	
82	93	2	1276.68	-0.013	0	43	25.6	95.00%	R.TISGLNMTALTR.V	
327	348	4	2579.13	-0.41	0	30.1	31.7	95.00%	K.SNQKPSHSDEQFDQEDHIDAPR.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
294	A6ZWB1_YEAS7	32.71%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
100	107	2	965.52	0.19	0	36.2	24.1	95.00%	R.IFLYPSNI.-	
32	48	3	1891.98	0.0037	1	28.9	27.1	95.00%	K.IEGVATPQDAQFYLGKR.I	
22	31	2	1096.62	-0.015	0	27.1	20.8	93.80%	R.VNNPNVSLIK.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
295	A6ZWH0_YEAS7	27.92%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
139	149	2	1302.71	-0.32	0	42	24	95.00%	K.QIVNIPSFMVR.L	
70	78	2	1031.58	-0.42	0	59.2	23.9	95.00%	R.LFEGNALIR.R	
180	197	2	1835.72	-1.1	1	111	29	95.00%	R.KAEASGEAADEADEADEE.-	
155	171	3	1781.9	-0.07	0	28.7	27.4	95.00%	K.HIDFAPTSPFGGARPGR.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
296	A6ZQF9_YEAS7	13.77%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
32	58	2	2783.31	-2.1	0	33.1	30.6	94.20%	K.ATFSPSGGTVSVPVEWMDNGAYPSLSK.I	
84	94	2	1245.61	-0.74	0	37.5	28.1	95.00%	K.ITPSELTQDDK.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
297	A6ZUW4_YEAS7	59.05%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
87	105	2	1872.01	-0.0043	0	77.3	23	95.00%	R.VGVVSILEAGDSDILTTLA.-	
41	52	2	1292.82	0.83	0	49.5	7.78	95.00%	K.LIIIAANTPVLR.K	
65	83	3	2045.02	-0.38	1	47.3	27.2	95.00%	K.TKVYYFQGGNNELGTAVGK.L	
67	83	2	1815.88	-0.33	0	86.2	28.3	95.00%	K.VYYFQGGNNELGTAVGK.L	
53	64	2	1460.72	0.063	1	52	27.6	95.00%	R.KSELEYYAMLSK.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
298	YP13B_YEAST	14.69%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
988	1002	2	1640.82	-1.2	0	49.1	27.2	95.00%	R.EVDPNISESNILPSK.K	
400	419	2	2073.92	-0.2	0	113	29.9	95.00%	R.AHNVSTSNNSPSTDNDSISK.S	
331	354	3	2813.38	-0.1	0	72.6	28.8	95.00%	R.HLNMTVAELFLDIHAIYEEQQGSR.N	
1004	1023	3	2072.99	-0.71	1	38.5	29.6	95.00%	K.RSSTPQISNIESTGSGGMHK.L	
471	491	3	2226.08	-0.67	0	88.7	29.5	95.00%	R.SAHHIHSASSNPDINVVDAQK.R	
560	568	2	1163.53	-1.8	0	29.8	27.1	94.50%	K.YGDFYWVSK.K	
1714	1731	4	2169.06	0.31	1	28.4	28.7	95.00%	R.LRDEVSGNHLHVCYIETK.K	Carbamidomethyl (+57)
25	39	2	1638.78	-0.86	0	78.9	28.4	95.00%	K.EVHTNQDPLDVSASK.I	
1094	1114	3	2202.09	0.046	0	33.6	28.2	95.00%	R.SPSIDASPPENNSSHNIVPIK.T	
1622	1633	2	1318.72	-0.46	0	43.7	24.9	95.00%	K.SQIGNIYLLNGK.V	
308	315	2	989.52	0.32	0	31.3	26.4	95.00%	K.VACQLIMR.G	Carbamidomethyl (+57)
1235	1243	2	1115.51	0.078	0	55.2	26.5	95.00%	R.YDEAITYNK.D	
658	681	4	2906.4	-0.29	0	21.1	29.8	90.20%	K.YQNSYEPFQYLHTDIFGPVHNLPK.S	
959	976	2	1855.84	-0.6	0	47.1	30.3	95.00%	K.AVSPTDSTPPSTHTEDSK.R	

1	24	3	2660.2	0.19	0	63.5	31.4	95.00%	- .MESQQLSNYPHISHGSACASVTSK .E	Acetyl (+42)/ Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
299	VTH1_YEAST	1.48%	100%	2						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
1000	1009	2	1218.56	-0.43	0	28.2	27.4	91.90%	R.NTFGYVDFEK.V	
394	406	2	1445.75	0.2	0	37.6	26.3	95.00%	K.VSVDNGLTWTNLK.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
300	ATG15_YEAS7	7.31%	100%	3						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
194	201	2	971.48	0.39	0	30.2	24.9	95.00%	R.IPQTGDWR.N	
241	260	2	1919.83	-1.3	0	68.2	30.2	95.00%	K.GTSAQGLPGSGEDETTGNDK.I	
417	426	2	1209.57	-0.14	0	44.3	28.2	95.00%	R.VCVYDVVNDK.G	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
301	A6ZLA3_YEAS7	5.85%	100%	2						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
109	119	2	1500.7	-0.15	0	40.1	28.2	95.00%	K.QEYPWFLDTFR.S	
226	236	2	1203.56	1.2	0	76.6	27.7	95.00%	R.WSNTAENGAVR.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
302	A7A001_YEAS7	8.47%	100%	4						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
61	76	3	1822.98	-0.12	1	36.4	24.1	95.00%	K.RVKPIEVDPNLSEAEK.V	
400	408	2	1017.53	0.47	0	39.7	25.5	95.00%	R.TMVALAEQR.F	
77	87	2	1153.71	-0.36	0	53.7	17.4	95.00%	K.VAIITAQTPLK.H	
571	585	2	1770.92	-0.8	1	66.4	25.6	95.00%	R.EVDLDLLKQEIAEEK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
303	A6ZMS7_YEAS7	7.44%	100%	3						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
293	306	2	1513.73	0.12	0	68.2	28.7	95.00%	R.TFDEVSEGLYGGLK.D	
223	233	2	1310.59	-0.44	0	29.4	27.9	92.90%	K.YLQCNSLDGNK.V	Carbamidomethyl (+57)
81	94	2	1580.79	-2	0	77.5	27.7	95.00%	R.DAYAFQQLGVNTVR.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
304	B3LLW4_YEAS1	14.97%	100%	3						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
140	150	2	1370.69	-0.67	0	48.3	26.5	95.00%	K.HQEFQNTNIIK.N	
140	164	4	2963.41	-0.67	1	39.6	29.3	95.00%	K.HQEFQNTNIIKNPTDDDFPHEAV VR.E	
151	164	2	1610.73	-1.4	0	48.5	29.2	95.00%	K.NPTDDDFPHEAVVR.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides						
305	A6ZQC8_YEAS7	5.88%	100%	4						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
151	159	2	1067.64	-0.12	0	30.8	18.3	95.00%	R.ILALLPDWK.C	

77	91	2	1703.82	-0.25	0	34.9	28.5	95.00%	K.GDPTYLPNSPYPEVR.S	
404	415	2	1449.73	-1.7	0	52.5	27.5	95.00%	K.ILNEDYSINLEK.Y	
66	91	3	3010.48	-0.53	1	54	28.4	95.00%	R.HSIQEEGLVWKGDPTYLPNSPYPEVR.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
306	A6ZYT9_YEAS7	22.69%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
61	98	4	4379.89	1.2	0	32.5	32.4	95.00%	R.SLTDDFGSNVHEPNPYLGNIDEEPDLYYHDEEDGELSR.T	
127	147	3	2415	-0.27	1	33.4	31.5	95.00%	R.RYSSVCNSDNEEASQSNTPDR.I	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
307	YJT8_YEAST	2.95%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
311	320	2	1196.66	0.073	0	54	23	95.00%	K.ISQLVTFYAR.I	
321	336	3	1902.01	2.6	1	28.4	24.2	95.00%	R.ITDRPHNISHSKQELK.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
308	A6ZU95_YEAS7	5.54%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
396	408	2	1630.72	0.32	0	30.9	29	93.50%	R.CVDNNYSSLAFWR.A	Carbamidomethyl (+57)
2	19	2	1942.06	0.47	0	53.3	22.1	95.00%	M.SLISILSPLITSEGLDSR.I	Acetyl (+42)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
309	ERV25_YEAST	12.32%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
137	145	3	1095.67	-0.19	0	33.5	15.2	95.00%	K.LKPIEVELR.R	
146	162	2	2064.06	0.23	1	128	26.5	95.00%	R.RVEEITDEIVDELTYLK.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
310	A6ZT39_YEAS7	9.07%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
330	343	2	1592.83	0.31	0	63.8	25.7	95.00%	R.DLENLLELSYGLSK.A	
158	173	4	1747.92	0.35	1	20.7	26.1	95.00%	K.ALHISGNKPESNPEKK.T	
352	360	2	1068.49	1.1	0	29.7	28.7	92.20%	R.NYDVISACK.D	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
311	A6ZNL3_YEAS7	14.81%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
352	365	2	1317.67	-0.25	0	94.2	27.6	95.00%	R.ISNGTFINGGPGGK.N	
316	338	3	2484.08	-0.48	0	54.6	30.8	95.00%	K.LYASSFSSNHGPSSGSFEEEHTK.G	
38	56	2	2216.85	-0.51	0	72.7	29.4	95.00%	K.ADSYNWQSSSHCNSECSAK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
312	A6ZSQ7_YEAS7	9.32%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification

22	35	2	1641.87	0.052	1	96.2	24.6	95.00%	K.RANDVIEQSLQLEK.Q	
300	314	2	1583.77	-0.64	0	53	28.7	95.00%	K.TTGITETEFNIGSSK.F	
281	295	2	1770.81	0.23	0	49.7	29.2	95.00%	K.FASPNYVCTDEDILK.G	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
313	A6ZZM1_YEAS7	13.81%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
125	139	2	1544.78	-1.2	0	63.9	26.6	95.00%	K.QSDDATGVAIRPTSK.S	
32	49	2	1945.93	0.31	0	90	29.2	95.00%	R.SGSDLQYLSVYSDNGTLK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
314	A6ZXD4_YEAS7	8.37%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
21	43	4	2564.26	-0.69	1	40.2	28.7	95.00%	R.AHQLAQDFNSKQDDTALTSLPHK.N	
600	616	2	1973.98	-0.86	0	82.3	28.6	95.00%	K.QNNQAYSSIQNEQILPK.N	
4	20	3	1866.92	-0.85	0	64.2	27.9	95.00%	R.SNKPLTQEANSSAHIDR.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
315	A6ZQQ0_YEAS7	17.58%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
181	202	3	2719.26	0.59	1	46.7	30.2	95.00%	R.TENTIAYINSELDELDREEFYR.L	
170	180	2	1259.73	-0.5	0	26	20.3	92.20%	R.VNAIEHVIIPR.T	
2	12	2	1331.66	-0.15	1	35.7	27.9	95.00%	M.SGNREQVFPTR.M	Acetyl (+42)
169	180	3	1415.84	0.067	1	26.6	16.9	95.00%	R.RVNAIEHVIIPR.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
316	HMX1_YEAST	14.20%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
72	89	2	2042.08	0.38	0	107	23.9	95.00%	R.LLNDPVTEEELQTSTILK.Q	
194	211	2	2045.97	-0.12	1	73.2	29.4	95.00%	K.KGTNFFTFSDLGPTEETR.L	
177	185	2	1063.57	-0.32	0	26.8	25.3	92.90%	R.LGLFPNFEK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
317	A7A200_YEAS7	12.27%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
255	284	4	3291.66	0.49	1	19.1	26.1	93.80%	R.FRAPEALFHPSVLGLESAGIDQTTYNSIMK.C	
239	254	2	1789.88	-0.79	0	76.7	28	95.00%	K.SYELPDGQVITIGNER.F	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
318	A6ZQL2_YEAS7	9.32%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
172	188	3	2034.06	0.054	1	60	25.9	95.00%	R.HETKDPVVNNTHIIVYR.E	
160	171	2	1329.74	-0.24	0	64.3	23.3	95.00%	K.VFGINLNDLVAR.H	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
319	A6ZPM4_YEAS7	5.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
2	17	3	1945.87	0.13	0	57.7	29.9	95.00%	M.SNEAYQHDHTVNPHQK.I	Acetyl (+42)

167	181	2	1621.77	-1.1	0	87.5	28.1	95.00%	R.IQTGSSGSYFVYGTR.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
320	B3LI68_YEAS1	5.78%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
35	48	2	1622.7	-0.61	0	49.8	29.5	95.00%	R.GYTNYNNGSNYTQK.K	
2	21	3	2099.01	-0.091	1	62.7	28.7	95.00%	M.TDETAHPTQSASKQESAALK.Q	
172	192	2	2139.93	0.04	0	51	30.3	95.00%	K.ETSDSTSTSTPTPTPSTNDSK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
321	A6ZT92_YEAS7	1.61%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
1480	1492	2	1480.76	-0.21	0	64	26.1	95.00%	K.IWTTSGDLLNSFK.N	
131	142	2	1434.75	0.21	0	56.2	26.3	95.00%	K.NLQAQYETLSLR.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
322	A6ZV67_YEAS7	18.39%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
36	49	2	1512.81	-0.46	0	72.5	24	95.00%	K.VLEQLSGQTPVQSK.A	
167	174	2	937.44	0.41	0	27.2	25.6	93.20%	K.YDADVLDK.-	
73	82	2	1140.61	-0.21	1	30	24.1	95.00%	R.GPKAEEILER.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
323	A6ZTH2_YEAS7	30.60%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
66	78	2	1521.7	-0.74	0	34.9	28.8	95.00%	R.NFDIISENSNDVR.G	
50	65	3	1801.82	0.28	0	47.4	29.9	95.00%	R.LNDSFADDLENGLHSR.N	
91	102	2	1466.63	-0.63	0	52	28.8	95.00%	K.QIMENDNVDFDK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
324	A6ZT43_YEAS7	15.43%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
368	383	4	1797.89	-0.43	0	21.2	28.4	93.50%	K.KPNLHGYGHPNPPNEK.S	
428	443	2	1935.9	-0.51	0	53.1	29.7	95.00%	K.LDPTSYEAYQHQTQQK.Y	
457	478	3	2805.41	-0.82	0	45.6	27.3	95.00%	K.LQEQQLQEQQLQQQQQQQQQLR.A	
479	499	2	2212.06	-1.3	0	79.8	29.6	95.00%	R.ATGQPPSQPQAQTQSQQFGAR.Y	
360	367	2	958.49	-0.13	0	37.6	25.6	95.00%	R.GWDLNINK.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
325	A6ZQ50_YEAS7	51.09%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
28	36	3	1121.63	-0.17	1	28.7	23.7	95.00%	K.KLEIQQHAR.Y	
50	61	2	1369.56	-0.31	0	49.8	27.1	95.00%	R.GAAGIWTCSCCK.K	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)
63	80	2	1665.87	-1	0	64.9	25.6	95.00%	K.TVAGGAYTVSTAAAATVR.S	
37	44	2	1035.38	1.3	0	30.5	24.7	95.00%	R.YDCSFCGK.K	Carbamidomethyl (+57)/ Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
326	A6ZKL0_YEAS7	23.85%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
73	90	3	2060.1	0.34	1	33.9	22.9	95.00%	K.TFLVANVKDLETLTMHTK.T	
81	90	2	1187.59	-0.18	0	28.9	27.4	93.00%	K.DLETLTMHTK.T	
91	103	2	1387.71	-0.66	0	73.9	27.1	95.00%	K.TYAAEIAHNISAK.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
327	A6ZX25_YEAS7	20.23%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
161	173	2	1340.74	-0.077	1	38.8	23.3	95.00%	R.RTGQVGVPTISQV.-	
95	116	3	2382.06	-0.48	1	76.3	31.4	95.00%	R.AHSCNNSSYVDSNKITQGSGTR.C	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
328	A6ZL34_YEAS7	4.97%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
188	200	2	1563.75	-0.2	0	70.9	28.2	95.00%	K.YSSFSTIEFLQDK.Q	
802	822	3	2146.02	0.7	1	42.1	30	95.00%	K.IAVTGGENNENTQAKDDAATK.T	
782	794	2	1340.69	-0.47	0	52.1	25.1	95.00%	K.LLPDGDAVDALSR.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
329	A6ZMB4_YEAS7	6.52%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
132	141	2	1174.58	0.58	0	48.2	27.3	95.00%	R.QLDESLDSLR.S	
67	77	2	1263.65	0.69	0	47.7	25.9	95.00%	R.MVGFLNEVVEK.H	
160	170	2	1171.63	-0.2	0	49	25.5	95.00%	K.FIEVNPGIAGR.A	
708	733	4	2817.33	-0.73	0	36.7	30.2	95.00%	K.NGGGGRPHGYQSVGNIEHEEQIAQQR.H	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
330	A6ZPU2_YEAS7	6.30%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
206	217	2	1198.67	-0.44	0	52.4	24.3	95.00%	K.DAGTIAGLNVLR.I	
218	233	2	1644.87	-0.5	0	60.3	24.3	95.00%	R.IVNEPTAAAIAYGLDK.S	
103	117	2	1671.86	-1.1	0	72.9	26.3	95.00%	K.NQVAANPQNTIFDIK.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
331	A6ZUA3_YEAS7	19.26%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
176	196	4	2379.29	0.44	0	31.6	22	95.00%	K.YGILSIDDLIHEIITVGPHFK.Q	
159	175	3	1837.01	0.49	1	26.7	21.2	95.00%	K.QRVPLSDNAIIEANLGK.Y	
22	30	2	973.48	2	0	35.2	25.7	95.00%	K.TAEQVAAER.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
332	A6ZVY2_YEAS7	8.35%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
16	29	2	1576.72	-0.78	0	59.2	29	95.00%	K.IETESTTIPNDSDR.S	

252	265	4	1661.84	0.55	0	35	26.9	95.00%	K.YWHDPGAFAKPVFK.N	
43	63	3	2466.15	-0.84	0	54.5	30	95.00%	K.QSNLHVIPEDLENSEQTEQEK.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
333	A6ZZI1_YEAS7	13.87%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
489	514	4	3071.33	0.041	1	46.5	32	95.00%	R.RVFSTSAIDEDNENEHQDDTEDQIHK.E	
460	485	3	2820.26	-1.6	1	67.2	31.2	95.00%	R.THSADRSPLSVQADEADEVHNADNSR.F	
416	428	2	1496.77	-0.89	0	65.2	26.4	95.00%	R.FIEFFNPGNVSVK.T	
84	94	3	1373.69	0.0054	0	34.6	27.5	95.00%	R.TEDNYILTLHR.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
334	A6ZMQ5_YEAS7	14.00%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
87	98	2	1345.67	-0.54	0	60	27.5	95.00%	K.VEEMNNIIAASR.R	
85	98	2	1544.8	0.37	1	78.1	26.9	95.00%	K.AKVEEMNNIIAASR.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
335	A6ZN11_YEAS7	30.96%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
39	69	3	3400.56	-1.2	0	81.9	30.9	95.00%	R.TASVADPILDAVQEAQPFEQAADTFHDNMNR.Q	
70	99	3	3408.57	-0.63	0	36.6	31.9	95.00%	R.QSYFSNEEGHVLCDVFGQPITQADISNPTR.A	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
336	A6ZTG2_YEAS7	9.39%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
6	25	3	2124.02	-0.046	0	62.1	29.6	95.00%	K.LISEAESHFSQGNHAEAVAK.L	
68	84	2	1643.73	-0.011	0	85.3	29.4	95.00%	R.AAGGGSSFMNTLMADSK.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
337	A6ZQ25_YEAS7	1.46%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
1188	1211	3	2535.21	-0.79	0	34.8	29.9	95.00%	K.ILEANTTDYKPAEQMEAADAGVAK.L	
2438	2449	2	1431.69	-1.3	0	36.5	28.6	95.00%	R.FNELDVPEQVDK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
338	A7A1R6_YEAS7	17.99%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
38	61	3	2803.18	-1.3	1	47.8	31.2	95.00%	K.SSSTCDSLNQVTCYCEHENSAVKK.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)
62	80	2	2130.9	-0.64	0	70.4	30.2	95.00%	K.CLDSICPNNDADAAYSAFK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)

38	60	3	2675.09	-0.85	0	42.5	31.1	95.00%	K.SSSTCDSLNQVTCYCEHENSAVK.K	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
339	A6ZMK8_YEAS7	7.69%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
118	128	2	1185.64	-0.019	0	55.5	25.5	95.00%	K.LDAALLQEASR.S	
91	101	2	1319.64	-0.18	0	38.5	27.5	95.00%	K.NLEMAFEPEIK.D	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
340	MHP1_YEAST	5.58%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
242	270	3	3140.38	-0.38	1	32.4	31.3	95.00%	R.TYHSPEEGKVDGTSPADDHNYGGSRPDPR.L	
332	343	3	1280.7	-0.093	0	34.6	23.7	95.00%	K.GRPIPPHPDAPK.L	
113	133	4	2361.1	0.65	0	32	29.2	95.00%	K.SVVETNLSNVEADSGHHHHHR.H	
471	486	4	1746.98	1.3	1	30.7	19	95.00%	R.KGEVEVKPNGSVVIHR.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
341	B3LKB6_YEAS1	8.84%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
80	104	3	2739.45	0.18	0	28.2	24.6	95.00%	K.IFPEEYTLETPTGLVPVATLHSIGR.T	
65	77	2	1308.67	-0.63	0	42.4	26.8	95.00%	K.APVPDVNAPQSSK.N	
380	396	2	1926.83	-0.36	0	86.5	30.3	95.00%	K.IMTEQEAQGVSMGEMMR.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
342	A6ZTY9_YEAS7	12.81%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
80	93	2	1517.73	-1	0	83	28.3	95.00%	R.DTSHGEITLSAPYK.G	
145	156	3	1477.78	0.076	1	36.3	26	95.00%	R.EVKDEQSYIVIR.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
343	A6ZUK7_YEAS7	6.22%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
198	206	2	1134.59	-0.37	0	39	25.5	95.00%	K.IVDLIYDER.Y	
514	529	2	1572.77	0.048	0	56.2	28.1	95.00%	K.NAMQAAEAAVAAATQR.A	
89	97	2	1017.56	-0.22	0	29	25.5	95.00%	R.IQTGLFSPR.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
344	B3LJ36_YEAS1	4.05%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
67	79	2	1379.66	-1.3	0	55.7	28.7	95.00%	K.SPLDGSFDTSNLK.R	
67	80	2	1535.76	-0.73	1	74.6	28.2	95.00%	K.SPLDGSFDTSNLKR.T	
1	10	2	1155.55	0.5	0	26.3	26.2	90.70%	-.MTEDFISSVK.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
345	A6ZU48_YEAS7	6.45%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
79	92	2	1523.69	-1.4	1	49.3	28	95.00%	K.SCGVDAMSVDDLKK.L	Carbamidomethyl (+57)
79	91	2	1395.6	-0.56	0	57.3	27.8	95.00%	K.SCGVDAMSVDDLK.K	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
346	A7A1L9_YEAS7	7.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
65	75	2	1266.61	-1.3	0	45.5	28.5	95.00%	R.GFLSDLPDFEK.L	
111	122	2	1282.67	-0.34	0	35.2	25.7	95.00%	R.AGAVAPEDIWVR.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
347	B3LH47_YEAS1	4.94%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
302	316	3	1832.85	-0.68	1	49.4	30.1	95.00%	K.KITDLGYSCYYSHAR.M	Carbamidomethyl (+57)
336	345	2	1176.62	0.52	0	34.8	26	95.00%	R.TLVCSDLLTR.G	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
348	A6ZW55_YEAS7	10.00%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
41	56	2	1833.81	-1.1	0	90.2	30	95.00%	R.DQLSHESQTAYQQGDK.K	
106	113	2	960.56	0.08	0	27.5	20.4	94.30%	K.EALFILQK.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
349	A7A0W2_YEAS7	5.83%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
525	534	2	1195.66	1.1	0	28.4	23.2	95.00%	K.FNFLNSILTK.S	
175	184	2	1257.67	0.15	0	32.9	25	95.00%	K.SWNQEQLLLK.S	
431	447	2	1900.91	-0.32	0	96.4	29.3	95.00%	K.INDLFQSSYDILDGSSK.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
350	A6ZSI2_YEAS7	1.96%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
667	678	2	1265.63	-0.4	0	70.7	27.5	95.00%	K.SDVTSIESSLTK.F	
1143	1154	2	1388.8	-0.43	0	40	21.2	95.00%	K.NAVILNYQTLLK.E	
1443	1450	2	1018.54	-0.23	0	27.8	24.5	94.50%	R.IIDLFNER.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
351	A6ZUT8_YEAS7	7.35%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
145	156	2	1191.56	-0.51	0	55.9	27.4	95.00%	R.SVVADISDSDGK.S	
129	139	2	1190.58	0.16	0	49.6	27.5	95.00%	R.NDLTASQLSDK.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
352	A6ZN47_YEAS7	5.45%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
610	622	2	1601.8	-1.2	0	70.2	26.8	95.00%	K.LQCININDLMVNR.N	Carbamidomethyl (+57)
389	398	2	1204.56	-0.34	0	27.7	27	91.60%	K.QLDMVDDLEK.A	
188	198	2	1154.6	0.15	0	29.6	25.9	95.00%	K.FLYLDGASAAK.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
353	A6ZVF2_YEAS7	7.41%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
32	41	2	1185.56	0.35	0	69.8	26.8	95.00%	R.NGYLVYACAR.R	Carbamidomethyl (+57)
170	181	3	1439.77	0.62	0	26.9	22.7	95.00%	R.GLHLEMKPFNVR.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
354	A6ZMV1_YEAS7	5.90%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
188	201	2	1563.78	-1.6	0	69.1	27.6	95.00%	K.NTVSNACLFQIAAR.L	Carbamidomethyl (+57)
324	336	2	1422.74	1.2	0	40.3	26.7	95.00%	R.MLGLTSVMAPFTR.D	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
355	A6ZQZ3_YEAS7	15.54%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
1	12	2	1382.71	0.5	0	55.5	25.4	95.00%	-.MFSLQDVITTTK.T	
56	66	3	1239.66	3.5	0	31.8	23.3	95.00%	R.KPTETTHLSAR.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
356	FRE7_YEAST	5.97%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
577	588	2	1414.6	-0.82	0	57.3	28.2	95.00%	R.NCFICSGSDSLR.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
407	418	2	1301.7	-0.32	0	53.5	25.7	95.00%	K.ILIDGPYGGIER.D	
589	601	2	1306.69	-0.54	0	69.8	26.3	95.00%	R.YTVGNSVAGLQAK.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
357	A6ZZA0_YEAS7	33.57%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
134	143	2	1156.69	-0.28	0	39.1	22.2	95.00%	K.LAEILKPVFQ.-	
35	45	3	1227.63	-0.39	0	27.7	26.2	95.00%	K.MVSQETVAHVK.D	
118	130	3	1410.75	0.075	1	42.8	24.7	95.00%	K.HIGGNSDLETLKK.N	
66	79	2	1559.86	0.12	0	37.6	23	95.00%	K.ATLSTLFQELNVPK.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
358	A6ZYD0_YEAS7	3.36%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
408	417	2	1191.52	0.069	0	50.1	28	95.00%	K.MDDPTVNWSK.E	
485	497	2	1421.79	-0.16	0	24.8	22.3	90.00%	R.HINAPFMLPIAAK.M	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
359	A6ZQ79_YEAS7	11.56%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
55	65	2	1263.65	0.55	0	27	26.9	90.60%	K.DASLVDYVQVR.Q	
189	203	2	1585.86	-0.27	0	80.5	25	95.00%	K.TIAETLAEELINAAK.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
360	IRC8_YEAST	3.04%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
218	231	2	1507.71	-0.34	0	66.3	28.7	95.00%	K.TISSDENSNSSVIR.H	
305	315	2	1294.69	1.1	0	41.2	24.9	95.00%	K.SFLNFLALNEK.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
361	A6ZVV4_YEAS7	20.11%	100%	3							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
313	327	3	1658.97	-0.54	0	35.7	17.2	95.00%	K.LSVISIDHLPSLLPR.E		
328	348	3	2455.27	-0.7	1	31	25.8	95.00%	R.EASEFFSHDLLPSLELLPQRK.T		
274	312	4	4074.17	0.67	0	36.2	24.7	95.00%	R.TVVDVSADTTNPHNPIPIYTVATV FNKPTVLVPTTAGPK.L		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
362	A6ZSF8_YEAS7	5.31%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
135	143	2	1135.54	-0.015	0	29	25.7	95.00%	K.TYNTAPQWR.F		
2	14	2	1478.75	-0.69	0	66.3	27.8	95.00%	M.VNFDLGQVGEVFR.R		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
363	A6ZM44_YEAS7	9.16%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
98	118	2	2226.09	-0.81	0	63.8	29.1	95.00%	R.SVDMTSPLLTNLEAGTHANQK.K		
83	97	2	1665.71	-1.2	0	107	28.7	95.00%	R.ELIMEEEGTGSDSNR.S		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
364	A6ZVN8_YEAS7	2.05%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
881	894	3	1617.8	-0.37	0	35.7	28	95.00%	R.DVHAYFVPDGVLMR.V		
868	880	2	1518.77	-1	0	49.6	27.9	95.00%	K.TLEQAEELFGQVR.D		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
365	VPS41_YEAST	3.23%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
654	674	3	2239.06	-0.76	1	41	29.9	95.00%	R.IEAASEPTASSKEEGSNITYR.T		
156	166	2	1206.59	0.35	0	43.3	27.5	95.00%	R.SSILCINTDGK.Y	Carbamidomethyl (+57)	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
366	A6ZW34_YEAS7	4.04%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
701	718	3	1929.94	-0.72	1	26.4	28.7	91.60%	K.ITQQEVSPDRASSSPNSK.S		
610	623	2	1415.74	-0.3	0	73.2	25.5	95.00%	K.SVANELMALGNVAK.D		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
367	A6ZLM4_YEAS7	4.43%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
206	217	2	1399.7	-0.64	0	28.9	26.3	94.40%	K.LVEIPNLGCEEK.D	Carbamidomethyl (+57)	
544	556	2	1528.79	-0.73	0	36.5	25.9	95.00%	K.EVDILNAQQPQFK.Y		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
368	A7A187_YEAS7	4.96%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	
47	57	2	1262.73	0.84	0	48.5	21.4	95.00%	K.LIELVSFAPFK.G		

33	46	2	1624.77	-0.75	0	61	28.6	95.00%	K.EVQEQINDFGAFTK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
369	A6ZM02_YEAS7	11.76%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
65	83	3	2188.06	-0.12	1	55.5	29.6	95.00%	R.VVEVCLADLQGSEDHSFRK.V	Carbamidomethyl (+57)
203	213	2	1350.74	0.21	0	39.1	23.9	95.00%	K.DIFPLQNIHVR.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
370	A6ZTK4_YEAS7	7.36%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
319	353	5	3960.85	0.98	1	25	30.3	95.00%	R.TYSLHEPTDAVHANIDTAPDGCK ESSIFHHVFHTK.V	Carbamidomethyl (+57)
134	143	2	1101.6	0.066	0	36.5	26.6	95.00%	R.TIIGEIATER.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
371	A6ZP37_YEAS7	4.17%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
13	21	2	1115.63	-0.49	1	31	22.6	95.00%	R.FLEIPVKNR.A	Deamidation (+1)
510	525	3	1930.8	-0.21	1	53.5	29.4	95.00%	K.HDDKDYYGAFTDEEAR.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
372	A6ZY29_YEAS7	13.91%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
131	140	2	1123.64	0.16	0	34.1	20.7	95.00%	R.TVAVLPPNWK.Y	
10	20	2	1136.58	0.96	0	41.2	26.3	95.00%	K.GISSSAIPYSR.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
373	CASP_YEAST	3.53%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
1	15	2	1777.83	0.015	0	45.7	28.7	95.00%	-.MDTSVYSHALDIWAK.A	Acetyl (+42)
559	567	2	1095.52	-0.19	0	57.2	26.5	95.00%	R.IDVESQYSR.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
374	A6ZZ10_YEAS7	12.90%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
85	98	2	1671.8	1.2	0	57.4	28.6	95.00%	R.AMPALMELYSIYDR.S	
291	308	2	1718.84	-0.65	0	86.5	27.5	95.00%	R.LGTAPATLSQTSGTDSGR.A	
316	327	2	1303.63	-0.86	0	54.7	27.3	95.00%	R.SGPSNLNQFQGR.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
375	A6ZRM1_YEAS7	7.57%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
424	442	2	1968.95	-0.22	0	37.4	28.6	95.00%	K.SGFDGLLPGDFPESGSIFK.K	
393	402	2	1071.55	0.29	0	43.8	24.6	95.00%	K.APVVNVCTGR.E	Carbamidomethyl (+57)
497	509	2	1394.65	-0.93	0	74.5	27.6	95.00%	K.LACAAFIDGENSK.I	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
376	A6ZV22_YEAS7	14.73%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification

20	29	2	1127.53	0.33	0	28.1	27	92.30%	K.AYFTAPSSER.R	
31	39	2	926.58	1.2	0	27.3	17.4	94.00%	R.VLLSAPLSK.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
377	A7A281_YEAS7	7.12%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
161	169	2	1137.55	-0.076	0	32.7	28.1	95.00%	R.IENFISQCK.Q	Carbamidomethyl (+57)
232	243	2	1349.68	-0.31	0	37	26.6	95.00%	R.IPASVWNMTFGK.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
378	A6ZKK2_YEAS7	11.16%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
200	210	2	1091.54	-0.38	0	38.1	27.1	95.00%	R.MLSSAGVNSAR.G	
37	49	2	1496.73	-0.48	0	104	28.5	95.00%	K.TLFSSWADSLNTR.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
379	A6ZSF6_YEAS7	5.06%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
5	13	2	1032.6	-0.025	0	68.4	19	95.00%	R.LSLTSLFPR.C	
308	315	2	1045.52	0.013	0	28.8	26.7	93.80%	R.CLEDQLLR.R	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
380	A6ZNC5_YEAS7	5.46%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
304	311	2	967.48	-0.56	0	27.5	27	91.50%	R.EALDFFAR.G	
277	287	2	1354.6	-0.7	0	65.5	29.2	95.00%	K.CCSDVFNQVVK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
381	A6ZNT7_YEAS7	2.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
575	586	2	1437.65	0.4	0	59.7	28.6	95.00%	K.WNSDYEAVIADR.R	
721	733	2	1549.75	-0.63	0	79.6	28.9	95.00%	R.ITLQCMDVETVNK.D	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
382	A6ZTW2_YEAS7	4.51%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
290	299	2	1219.65	0.15	0	49.8	26.4	95.00%	K.TQDVIQLFEK.D	
71	86	3	1761.95	0.23	1	39.5	24.3	95.00%	R.KYDTAVKPVIDDATVK.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
383	A6ZZC9_YEAS7	13.50%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
34	50	2	1863.88	-0.44	0	84.7	29.4	95.00%	R.SSVGQFMTFFAETVASR.T	
24	33	2	1244.58	-0.51	0	33.1	27.6	95.00%	K.DLSQFGFFER.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
384	KHA1_YEAST	2.98%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
861	873	3	1586.78	0.5	1	27.2	28.7	92.70%	R.RFDTLIVHHFSSE.-	

620	632	2	1512.77	0.91	0	49.1	26.4	95.00%	K.IPFSSEVIFSTMR.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
385	B3LI87_YEAS1	6.10%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
528	545	3	2056.87	-0.98	0	30.9	30.5	94.80%	K.LSVCTCDNEDHPNQGVGR.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)
34	47	2	1486.7	-0.81	0	35.7	28.3	95.00%	R.QSSSLEPADGQNVR.V	
631	645	2	1832.82	-0.55	0	80.2	30.1	95.00%	K.YAIEYLNDDDNGYIR.W	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
386	A9EDP4_YEAST	6.95%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
324	337	2	1659.82	-0.79	0	94.4	28.4	95.00%	R.NIDIWTVETAQNTR.E	
586	600	3	1613.74	-0.067	1	54.6	29.1	95.00%	R.FKQEFSNAASGSGER.V	
508	521	2	1370.74	-0.81	0	35.6	24.2	95.00%	K.DISASSPNLGGILK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
387	B3LNV3_YEAS1	4.98%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
270	284	2	1694.75	-0.58	0	76.6	29.5	95.00%	R.NTIACTQSEESQATR.G	Carbamidomethyl (+57)
187	203	2	1791.83	0.83	0	74.7	29.5	95.00%	K.TQPAVSANTTNTDTSER.F	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
388	A6ZV49_YEAS7	4.38%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
85	92	2	1167.49	-0.2	0	27	24.9	93.70%	K.YFDEFEYR.V	
50	67	3	1986.97	-0.96	0	33.3	28.3	95.00%	K.TDVTAETTAVEPHPHNLR.H	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
389	A6ZZQ1_YEAS7	9.22%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
170	178	2	1014.57	0.29	0	39.7	25.5	95.00%	K.QISLEGLQK.Q	
131	140	2	1220.6	0.16	0	31.9	27.3	95.00%	K.YQGLINEQEK.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
390	A6ZLE8_YEAS7	8.17%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
431	448	4	2066.94	2.7	1	30	29.6	95.00%	K.HHTSELNSSTSEPDSQRR.S	
325	344	2	2141.87	-0.45	0	98.4	30.1	95.00%	K.CNGQDMSEVGNGPGSYDISR.S	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
391	COS8_YEAST	20.73%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
157	167	2	1275.75	0.92	1	50	19.9	95.00%	K.TTLLEPFSLKK.D	
102	108	2	935.49	1.7	0	31	24.9	95.00%	K.QLIQFCK.E	Carbamidomethyl (+57)
143	153	2	1441.62	-0.55	0	40.4	28	95.00%	K.YFFFNAMSCQK.A	Carbamidomethyl (+57)
178	196	2	2114.02	0.23	0	70.3	29.3	95.00%	K.DSVPYIEEALQVYAAGFDK.E	

291	313	3	2580.22	-0.42	0	41.8	30.2	95.00%	K.MQFLSTIINEQESGANGWDEIAK.K	
157	166	2	1147.65	0.15	0	29.8	23.2	95.00%	K.TTLLEPFSLK.K	
11	18	2	893.49	-0.02	0	26.5	24.8	92.90%	K.SVDVLSFK.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
392	A6ZN84_YEAS7	24.65%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
62	74	2	1445.74	-0.77	0	48.3	26.7	95.00%	K.VIEQPITSETAMK.K	
101	109	2	1106.59	-0.19	0	31.3	24.1	95.00%	K.ELYEVDVLK.V	
126	138	2	1449.71	-0.77	0	87.1	28.2	95.00%	R.LTADYDALDIANR.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
393	A6ZXS1_YEAS7	6.17%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
2	15	4	1728.9	0.31	1	19.9	25.6	95.00%	M.PLSKVEHYLSYHTR.L	
6	15	3	1303.63	0.24	0	27.4	28.1	93.70%	K.VEHYLSYHTR.L	
245	260	2	1912.95	-1.2	1	64.1	28.3	95.00%	K.RLDDQTDVEQSPLLER.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
394	YNS1_YEAST	6.39%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
2	16	2	1582.86	7.2	0	89.8	23.4	95.00%	M.PLNIIGTALLDGTDK.I	Acetyl (+42)/ Deamidation (+1)
113	123	3	1432.71	-0.67	1	28.7	27.1	95.00%	K.CDLSNLWEIRK.F	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
395	A7A1T7_YEAS7	11.41%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
38	49	2	1469.69	-0.39	0	52.5	28.8	95.00%	K.IYCAELDLSQMK.V	Carbamidomethyl (+57)
246	263	2	2010.11	-0.86	0	74.1	19.7	95.00%	R.SRPTVIYANAPIEEKPLI.-	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
396	A6ZRT4_YEAS7	20.93%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
2	15	2	1693.77	1.5	0	32.3	28.9	95.00%	M.SEVAETWVDTWMAK.L	Acetyl (+42)
97	109	2	1547.75	-0.4	0	54.4	27.1	95.00%	R.QQELFENALEEAK.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
397	A6ZLW3_YEAS7	39.32%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
100	117	2	1975.93	-1.4	1	47.8	29.4	95.00%	R.NTGSIEHTMENIFAGKLD.-	
32	59	3	2885.4	-0.63	0	63.6	29.3	95.00%	R.TVQDAKPAPSVATNDPSPEPVPSAPEER.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
398	A6ZXK9_YEAS7	14.77%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
65	86	3	2309.04	-0.35	1	64.8	30.7	95.00%	K.FDLKDTEESLGHDSASASSASR.K	
69	86	2	1805.77	-0.4	0	68.2	29.3	95.00%	K.DTEESLGHDSASASSASR.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
399	A6ZM11_YEAS7	15.17%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
149	163	2	1793.82	-0.68	0	58.2	29.2	95.00%	K.VFNESGYLQNDAYFK.W	
119	130	2	1443.8	-0.98	0	46.6	23.9	95.00%	K.NEPLYLVELVQK.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
400	COS5_YEAST	28.46%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
157	167	2	1275.75	0.92	1	50	19.9	95.00%	R.TTLLEPFSLKK.D	
102	108	2	935.49	1.7	0	31	24.9	95.00%	K.QLIQFCK.E	Carbamidomethyl (+57)
109	137	3	3320.51	-1.1	0	56.9	31.3	95.00%	K.EVTENTPSSDPHDWEVVAANLN SYLYENK.A	
354	369	2	2001.08	-0.26	0	39.5	23	95.00%	K.SMWLLPLNVELWPYIK.E	
25	33	2	1099.64	-0.29	0	27.9	22.6	94.60%	K.IVLPQDLFR.S	
178	192	2	1756.87	1.1	0	61.5	28.6	95.00%	K.DSVPYIEEALGVYFR.E	
206	219	2	1553.81	-0.2	0	52.8	25.6	95.00%	K.SWSPVGLEDVQLPK.D	
157	166	2	1147.65	0.15	0	29.8	23.2	95.00%	R.TTLLEPFSLK.K	
11	18	2	893.49	-0.02	0	26.5	24.8	92.90%	K.SVDVLSFK.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
401	A6ZRB2_YEAS7	1.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
28	47	2	1942.91	-0.51	0	85.3	29.6	95.00%	K.TTTASTASSSSPSSSSQTIR.N	
286	305	2	1968.82	-0.72	0	68.4	29.8	95.00%	K.NDDSSSTTATNSGNDVASAR.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
402	A6ZZL6_YEAS7	3.24%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
149	156	2	1061.42	-0.69	0	28.7	26	94.50%	R.FFDMMDEK.H	
247	257	2	1224.65	-0.75	0	53.8	25.1	95.00%	K.IGGFVTNLNYK.D	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
403	A6ZNT6_YEAS7	6.29%	99%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
99	110	2	1332.62	-0.39	0	29.1	28	92.40%	K.SSNSDTSIFFTK.V	
335	344	2	1159.64	0.32	0	26.1	25.3	91.90%	K.SPAYPFPLLR.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
404	A6ZTZ0_YEAS7	5.53%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
42	53	2	1316.72	-0.16	0	33.5	23.7	95.00%	R.GTLDETVLQTLK.R	
42	54	3	1472.82	0.14	1	42	23.5	95.00%	R.GTLDETVLQTLKR.D	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
405	A6ZND5_YEAS7	3.27%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
2	15	2	1627.88	-0.66	1	61.5	24.5	95.00%	M.SDKIQEEILGLVSR.S	Acetyl (+42)
118	129	2	1398.61	-0.79	0	41.2	28.2	95.00%	K.ALEDSNYNQMSK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
406	AKR2_YEAST	5.34%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
212	222	2	1252.58	-0.82	0	30.3	28	94.00%	K.FGSTVAWTDNR.G	
610	638	3	3037.45	-0.46	0	28.3	30	92.40%	K.GVEDSDMIPEGPSATTITHTISIDGLEPR.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
407	A6ZKK0_YEAS7	3.08%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
923	938	3	1706.79	-0.47	0	37.7	29.2	95.00%	K.FNTGSSEAQAADEKPR.H	
893	908	2	1542.72	-0.0029	0	28.4	27.7	91.60%	R.TSSPSSAVSTSAGNYK.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
408	COS2_YEAST	34.83%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
157	167	2	1275.75	0.92	1	50	19.9	95.00%	R.TTLLEPFSLKK.D	
102	108	2	935.49	1.7	0	31	24.9	95.00%	K.QLIQFCK.E	Carbamidomethyl (+57)
352	367	2	1985.05	0.29	0	47.2	25.4	95.00%	K.SMWPLPLNVELWPYIK.E	
109	142	3	3948.82	1.9	0	47.2	30.9	95.00%	K.EITENTPSSDPHDWEVVAANLNSYLYENNVWNTK.Y	
206	219	2	1525.81	-0.017	1	66.9	24.3	95.00%	K.SWSPVGLEDAKLPK.E	
143	156	2	1828.81	0.87	0	75.3	30	95.00%	K.YFFFNAMVCQEAFR.T	Carbamidomethyl (+57)
25	33	2	1099.64	-0.29	0	27.9	22.6	94.60%	K.IVLPQDLFR.S	
178	196	2	2187.06	-0.46	0	72.1	29.3	95.00%	K.DSVPYIEEALGVYFTEVEK.Q	
206	216	2	1187.58	-0.27	0	57.3	27.1	95.00%	K.SWSPVGLEDAK.L	
157	166	2	1147.65	0.15	0	29.8	23.2	95.00%	R.TTLLEPFSLK.K	
11	18	2	893.49	-0.02	0	26.5	24.8	92.90%	K.SVDVLSFK.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
409	A6ZTX9_YEAS7	33.78%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
62	74	2	1514.78	-1.1	1	64.2	26.6	95.00%	K.IKAQIWDTAGQER.Y	
16	26	2	1056.62	0.27	0	32.4	22.8	95.00%	K.IVLIGDSGVGK.S	
64	74	2	1273.61	-0.17	0	64.6	27.7	95.00%	K.AQIWDTAGQER.Y	
33	43	2	1329.61	-0.1	0	54.8	29.3	95.00%	R.FTTDEFNIESK.S	
113	127	2	1527.75	-1.3	0	74.8	27.8	95.00%	R.ENADDNVAVGLIGNK.S	
44	53	2	1079.56	0.067	0	61.1	25.3	95.00%	K.STIGVEFATR.T	
98	127	3	3404.56	-1.5	1	46.6	31.9	95.00%	K.SSSYENCNHWLTELRENADDNVAVGLIGNK.S	Carbamidomethyl (+57)

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
410	A6ZYY3_YEAS7	21.82%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
50	62	2	1400.75	-1.1	1	58.9	25.7	95.00%	K.GSLEEIIAEGQKK.F	
39	49	2	1201.65	-0.6	0	54.5	24.6	95.00%	R.INELLSSLEGK.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
411	A6ZUX3_YEAS7	11.49%	100%	2

Start	End	charge	Mr(expt)	ppm		MC	Ion score	Identity score	Scaffold probability	Sequence	Modification
211	223	2	1447.65	-0.64		0	77.5	29.2	95.00%	K.MEAPASVETQEEK.A	
81	94	3	1672.83	-0.12		1	25.9	27.4	92.60%	K.EINNLKDEIQSENK.A	

Supplementary Table S2: All "Scaffold" validated proteins and peptides identified from solprotSP (*S.pombe*) and from SCVMprot (*S.cerevisiae*) samples

S.cervisiae **- Glu-C digest of large tryptic peptides (Replicate A)**

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
1	A6ZPV7_YEAS7	48.27%	100%	40

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
310	320	2	1254.66	-0.57	1	61	26.4	95.00%	K.GKYTVDQVFAK.M		K.GKYTVDQVFAK.M
234	245	2	1373.6	1.1	0	44.3	30.3	95.00%	E.DSAITSIYFDNE.N		R.EDSAITSIYFDNENLDLYYGR.L
429	442	2	1679.86	-0.66	1	82.3	27.2	95.00%	K.LQTQLGQEPPEWVR.E		K.LQTQLGQEPPEWVR.E
201	212	2	1513.76	-0.8	1	50.2	28.9	95.00%	K.YWVHPDNITELK.L		K.YWVHPDNITELK.L
362	371	2	1074.55	0.99	0	43.2	27.8	95.00%	R.TAFQLPGDAR.V		R.TAFQLPGDAR.V
579	594	2	1899.92	0.62	0	85.7	29.7	95.00%	E.IVAFFDHYFNGDQISK.I		K.YYEIVAFFDHYFNGDQISK.I
401	415	2	1775.87	0.33	1	48.9	28.6	95.00%	R.TDIGVDWPFKQLDDK.D		R.TDIGVDWPFKQLDDK.D
443	455	2	1402.78	0.48	1	72.3	23.2	95.00%	R.ELVGSHLVEPVPK.F		R.ELVGSHLVEPVPK.F
576	594	2	2355.09	1.1	1	75.9	30.5	95.00%	K.YYEIVAFFDHYFNGDQISK.I		K.YYEIVAFFDHYFNGDQISK.I
150	158	2	1109.58	0.15	1	27.5	27.1	94.70%	R.LDSKPFFKE.N		R.LDSKPFFKENYDELVVK.I
137	149	3	1531.93	1.1	1	27	12.8	95.00%	K.KTGFILKPVFQVR.L		K.KTGFILKPVFQVR.L
401	410	2	1176.58	-0.79	0	37.5	28.1	95.00%	R.TDIGVDWPFK.Q		R.TDIGVDWPFK.Q
598	606	2	1037.52	0.65	0	36.2	28	95.00%	K.GTTFDTQIR.A		K.GTTFDTQIR.A
312	320	2	1069.54	-0.76	0	34.7	27	95.00%	K.YTVDQVFAK.M		K.YTVDQVFAK.M
342	348	2	893.51	0.78	0	32.2	25.1	95.00%	E.IQYVMLK.K		K.KPMNEIENLEALASEIQYVMLK.K
536	554	2	1890.86	1.2	0	73.1	30.4	95.00%	E.SVGYGATSAPTSNTNHVVE.S	Deamidation (+1)	R.SDNEDNDFDEDDEDDAALVAAM TNAPGNSLDIEESVGYGATSAPTSN TNHVVESANAAYYQR.K
400	410	2	1332.68	0.73	1	32	27.5	95.00%	R.RTDIGVDWPFK.Q		R.RTDIGVDWPFK.Q
119	129	3	1359.69	-0.14	1	24.3	28	95.00%	K.FSRLNYTGFQK.I		K.FSRLNYTGFQK.I
386	393	2	936.39	0.82	0	39.5	28.9	95.00%	E.DNFDGVDR.T		R.EDNFDGVDR.T
342	349	2	1021.6	0.49	1	23.8	21.4	92.30%	E.IQYVMLKK.K		K.KPMNEIENLEALASEIQYVMLKK. K
267	280	2	1660.76	1.1	1	71	31.1	95.00%	R.WYGGMSTDTIFVER.K		R.WYGGMSTDTIFVER.K
567	574	2	871.44	2.4	1	28.3	24.1	95.00%	R.NAENPISK.K		R.NAENPISK.K
623	629	2	884.44	0.083	1	24.6	25.4	93.10%	K.VYFATER.T		K.VYFATER.T
487	495	2	1007.57	0.86	0	28.2	23	95.00%	R.KPPLPTNIE.I		R.KPPLPTNIEITRPGR.S
420	428	2	1064.59	2	1	47.2	25.8	95.00%	R.FPYAVLEVK.L		R.FPYAVLEVK.L
138	149	3	1403.83	1.5	0	45	17.2	95.00%	K.TGFILKPVFQVR.L		K.TGFILKPVFQVR.L
122	129	2	969.49	-0.013	0	43.3	26.2	95.00%	R.LNYTGFQK.I		R.LNYTGFQK.I
555	563	2	1042.48	1.7	0	51.2	29	95.00%	E.SANAAYYQR.K		R.SDNEDNDFDEDDEDDAALVAAM TNAPGNSLDIEESVGYGATSAPTSN TNHVVESANAAYYQR.K
87	100	2	1601.76	0.55	0	45.3	29.5	95.00%	R.LLDSNNPPTQLDFE.I		R.LLDSNNPPTQLDFEILEEELSDIIA DVHDLAK.F
106	118	2	1408.76	0.41	0	74.6	24.6	95.00%	E.LSDIIADVHDLAK.F		R.LLDSNNPPTQLDFEILEEELSDIIA DVHDLAK.F
56	64	3	1172.59	0.37	1	23.8	28.2	94.80%	E.LDKVYTFCK.V	Carbamidomethyl (+57)	K.NNGQWTQELETDFLESLEIELDK VYTFCK.V
14	26	2	1719.77	-0.1	0	46.5	30.8	95.00%	R.QYSYYYISYDDLK.T		R.QYSYYYISYDDLK.T
374	384	2	1292.66	-0.1	1	58.1	27.3	95.00%	R.ISLDTELTMVR.E	Oxidation (+16)	R.ISLDTELTMVR.E
167	175	2	1077.58	0.45	0	41.3	26.2	95.00%	K.ISQLYDIAR.T		K.ISQLYDIAR.T
612	622	2	1296.72	0.7	1	28.9	23.4	95.00%	K.TICVPVRVEPK.V	Carbamidomethyl (+57)	K.TICVPVRVEPK.V
14	28	2	1949.86	0.37	1	55.6	30.4	95.00%	R.QYSYYYISYDDLKTE.L		R.QYSYYYISYDDLKTELEDNLSK.N
3	9	2	816.41	0.46	1	28.5	26.6	95.00%	K.FGEHLSK.S		K.FGEHLSK.S
218	229	2	1409.77	1.2	1	57.6	25	95.00%	K.HLPVLVFNTNKE.F		K.HLPVLVFNTNKEFER.E
385	393	2	1065.44	0.53	1	30.6	28.8	95.00%	R.EDNFDGVDR.T		R.EDNFDGVDR.T
487	501	2	1687.97	0.69	1	23.7	18.9	92.10%	R.KPPLPTNIEITRPGR.S		R.KPPLPTNIEITRPGR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
2	VTC3_YEAST	46.59%	100%	42

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
496	508	2	1566.66	-0.0096	0	46.6	29.9	95.00%	K.VINQDNSQMPNYE.W	Oxidation (+16)	K.VINQDNSQMPNYEWIK.D

821	835	2	1732.94	0.1	0	33.2	23.2	95.00%	R.TLKPIQDFIFNLVGE.-		R.TLKPIQDFIFNLVGE.-
542	554	2	1617.85	0.6	0	71.4	26.8	95.00%	K.YVNILPFWLPDLE.T		K.YVNILPFWLPDLETDIR.K
50	58	2	1022.49	1.4	1	29.2	29	94.30%	E.SDFVEALDK.E		R.NESDFVEALDK.E
365	372	2	1041.56	0.061	0	30.6	25.5	95.00%	K.FINNFIFK.N		K.FINNFIFK.N
330	340	2	1329.76	0.35	1	45.4	22.5	95.00%	K.LLDKPDIFLEK.R		K.LLDKPDIFLEK.R
316	323	2	813.47	-0.4	0	31.9	24.5	95.00%	K.ISGAPTLR.L		K.ISGAPTLR.L
63	70	2	984.53	-0.21	0	27.3	24.2	95.00%	K.VYTFQISK.Y		K.VYTFQISK.Y
167	175	2	1202.63	0.24	1	55.8	26.2	95.00%	R.ISYLYEFLR.S		R.ISYLYEFLR.S
487	495	2	1112.56	0.34	1	34.3	27	95.00%	K.FPYSVMEIK.V		K.FPYSVMEIK.V
641	649	2	1038.59	0.16	1	34.2	21.6	95.00%	K.FKTNAAFLK.I		K.FKTNAAFLK.I
227	248	2	2470.16	-1.6	1	56.5	29.9	95.00%	R.HLPALVYASVPNENDDFVDNLE.S		R.HLPALVYASVPNENDDFVDNLESDVR.V
659	681	2	2410.06	0.45	0	68.1	30.4	95.00%	E.NGNDPYSDDTDSASSFQLPPGVK.K		K.NISENGNDPYSDDTDSASSFQLPPGVK.K
143	148	2	715.42	1.1	0	25.5	27.7	90.60%	K.SLLQVR.L	Deamidation (+1)	K.SLLQVR.L
119	126	2	938.52	0.61	0	38.3	23.2	95.00%	R.LNFTGFIK.I		R.LNFTGFIK.I
437	447	2	1323.69	0.67	0	72.5	27.3	95.00%	R.VTIDSNIMYIR.E		R.VTIDSNIMYIR.E
398	411	2	1708.84	0.86	1	29.8	28.8	95.00%	K.LSRDFDNIQNFIVE.E		K.LSRDFDNIQNFIVEEK.L
210	219	2	1304.55	0.9	0	34.3	30.2	95.00%	K.FWVHDDNIME.V		K.FWVHDDNIMEVK.A
365	378	2	1745.88	0.61	1	72	27.7	95.00%	K.FINNFIFKNDPSYK.N		K.FINNFIFKNDPSYK.N
7	16	2	1201.61	-0.85	0	43.6	28.4	95.00%	K.LANDVYPPWK.D		K.LANDVYPPWK.D
194	206	2	1493.71	-0.55	1	51.2	29.3	95.00%	K.LSHFSNLEDASFK.S		K.LSHFSNLEDASFK.S
512	524	2	1464.76	-0.9	1	57.6	26.4	95.00%	K.DLTNSHLVNEVPK.F		K.DLTNSHLVNEVPK.F
401	411	2	1352.63	2.1	0	42.8	30.2	95.00%	R.DFDNIQNFIVE.E		R.DFDNIQNFIVEEK.L
330	339	2	1201.66	0.56	0	33.7	24.9	95.00%	K.LLDKPDIFLE.K		K.LLDKPDIFLEK.R
808	820	2	1352.74	0.73	0	52.5	23.8	95.00%	R.GLVNVSSQPSLPR.T		R.GLVNVSSQPSLPR.T
265	282	2	1849.83	-0.0019	1	91.9	30.2	95.00%	K.SNSLSSDGNSNQDVEIGK.S		K.SNSLSSDGNSNQDVEIGK.S
699	705	2	886.47	-0.031	1	25.2	25.3	94.00%	K.VWLANER.T		K.VWLANER.T
525	541	2	1887.93	2.3	1	72	28.8	95.00%	K.FSLYLQGVASLFGEDDK.Y		K.FSLYLQGVASLFGEDDK.Y
437	448	2	1468.72	0.53	1	59.4	28.4	95.00%	R.VTIDSNIMYIRE.D	Oxidation (+16)	R.VTIDSNIMYIREDSLDK.N
210	221	2	1531.71	-1.1	1	45.1	30.4	95.00%	K.FWVHDDNIMEVK.A		K.FWVHDDNIMEVK.A
643	649	2	763.42	1	0	26.4	26.9	93.40%	K.TNAAFLK.I		K.TNAAFLK.I
17	24	2	1059.45	0.65	1	29	29	94.00%	K.DSYIDYER.L		K.DSYIDYER.L
113	126	2	1698.87	0.39	1	47.3	26.5	95.00%	R.LDNFDRLNFTGFIK.I		R.LDNFDRLNFTGFIK.I
379	386	2	1032.57	0.38	0	33.9	23.9	95.00%	K.NYLINQLR.E		K.NYLINQLR.E
39	47	2	1051.46	0.65	1	32.4	28.6	95.00%	R.SSVDSWSER.N		R.SSVDSWSER.N
655	681	2	2853.25	-1.6	1	56.8	30.6	95.00%	K.NISENGNDPYSDDTDSASSFQLPPGVK.K		K.NISENGNDPYSDDTDSASSFQLPPGVK.K
425	436	2	1331.68	-0.39	0	43	27.8	95.00%	R.TAFQIPGDQSIR.V		R.TAFQIPGDQSIR.V
591	597	2	714.39	2.1	0	25.8	24.4	95.00%	K.ISVPDGK.T		K.ISVPDGK.T
496	511	2	1977.92	-0.35	1	78.6	29.5	95.00%	K.VINQDNSQMPNYEWIK.D		K.VINQDNSQMPNYEWIK.D
462	477	2	1960.95	-0.37	1	67.2	28.8	95.00%	E.NWHRDDIDSNIPNPLR.F		R.NPENWHRDDIDSNIPNPLR.F
160	166	2	910.49	1.7	0	36.5	25.1	95.00%	E.YSPLLYR.I		K.ELPFNNSEEYSPLLYR.I
588	597	3	1122.57	-0.73	1	22.4	27.7	93.50%	R.LSKISVPDGK.T	Phospho (+80)	R.LSKISVPDGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
3	PMA1_YEAST	41.50%	100%	37

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
584	596	2	1145.5	1	0	42.8	29.8	95.00%	R.LGLGGGGDMPGSE.L		R.LGLGGGGDMPGSELADFVENADGFAEVFPQHK.Y
388	397	2	1186.59	0.49	0	38.5	27.3	95.00%	K.LSLHEPYTVE.G		K.LSLHEPYTVEGVSPDDLMLTACLAASR.K
388	414	3	2944.43	-0.39	1	65	28.5	95.00%	K.LSLHEPYTVEGVSPDDLMLTACLAASR.K	Carbamidomethyl (+57)	K.LSLHEPYTVEGVSPDDLMLTACLAASR.K
196	205	2	1081.6	0.63	0	42	22.5	95.00%	E.VVPGDILQLE.D		R.DGQLVEIPANEVVPGDILQLEDGTVIPTDGR.I
526	546	2	2331.06	0.22	1	38.5	30	95.00%	E.ILGVMPCMDPPRDDTAQTVSE.A	Carbamidomethyl (+57)	R.GEGHWEILGVMPCMDPPRDDTAQTVSEAR.H
79	92	2	1587.69	0.38	0	64	30.3	95.00%	E.YLQTDPSYGLTSDE.V		K.TYDDAASESSDDDDIDALIEELQSNHGVDDEDSDNDGPVAAGEARPVPEEYLQTDPSYGLTSDEVLK.R
175	184	2	1056.63	0.26	0	70	21.8	95.00%	K.TLANTAVVIR.D		K.TLANTAVVIR.D

78	92	2	1716.74	-0.35	1	94.7	30.5	95.00%	E.EYLQTDPSYGLTSDE.V		K.TYDDAASESSDDDDIDALIEELQSNHGVDDEDSDNDGPVAAGEARPVPEEYLQTDPSYGLTSDEVLK.R
502	508	2	744.41	1.4	1	34.7	29.2	95.00%	K.VAELASR.G		K.VAELASR.G
417	424	2	858.48	0.55	1	27.3	27	94.50%	K.KGLDAIDK.A		K.KGLDAIDK.A
568	582	2	1708.82	0.25	1	37.2	29.6	95.00%	E.TCRQLGLGTNIYNAE.R	Carbamidomethyl (+57)	K.ETCRQLGLGTNIYNAER.L
220	233	2	1595.71	0.39	0	82.6	30.1	95.00%	E.DCFLQIDQSAITGE.S	Carbamidomethyl (+57)	R.IVTEDCFLQIDQSAITGESLAVDK.H
597	609	2	1396.62	0.62	1	86.8	30	95.00%	E.LADFVENADGFAE.V		R.LGLGGGGDMPGSELADFVENADGFAEVFPQHK.Y
256	271	2	1670.81	0.88	0	87.2	29	95.00%	E.GFMVVTATGDNTFVGR.A		R.GEGFMVVTATGDNTFVGR.A
240	252	2	1455.66	-0.55	0	74.8	29.9	95.00%	K.HYGDQTFSSSTVK.R		K.HYGDQTFSSSTVK.R
448	456	3	1072.54	0.83	0	31.9	27.8	95.00%	E.FHPFDPVSK.K		K.VLEFHPFDPVSK.K
899	909	2	1283.56	0.61	1	65.3	29.2	95.00%	R.SVEDFMAAMQR.V		R.SVEDFMAAMQR.V
475	482	2	843.52	1.5	0	25.8	24.6	95.00%	K.GAPLFVLK.T		K.GAPLFVLK.T
196	215	2	2093.1	-0.72	1	39.3	24.8	95.00%	E.VVPGDILQLEDGTVIPTDGR.I		R.DGQLVEIPANEVVPGDILQLEDGTVIPTDGR.I
50	71	2	2239.91	0.44	1	66	30.6	95.00%	E.LQSNHGVDDEDSDNDGPVAAGE.A		K.TYDDAASESSDDDDIDALIEELQSNHGVDDEDSDNDGPVAAGEARPVPEEYLQTDPSYGLTSDEVLK.R
583	596	2	1301.6	0.059	1	42	29.4	95.00%	E.RLGLGGGGDMPGSE.L		R.QLGLGTNIYNAERLGLGGGGDMPGSELADFVENADGFAEVFPQHK.Y
448	457	3	1200.63	1.2	1	20.9	27.2	91.50%	E.FHPFDPVSKK.V		K.VLEFHPFDPVSKK.V
398	414	2	1775.86	0.91	0	76.4	28.9	95.00%	E.GVSPDDLMLTACLAASR.K	Carbamidomethyl (+57)	K.LSLHEPYTVEGVSPDDLMLTACLAASR.K
660	679	2	1984.13	0.64	0	50.7	19.9	95.00%	R.SAADIVFLAPGLSAIIDALK.T		R.SAADIVFLAPGLSAIIDALK.T
556	566	2	1074.57	-0.48	0	68.1	26.7	95.00%	K.MLTGDAVGIAK.E		K.MLTGDAVGIAK.E
618	625	2	969.56	1.7	1	36.1	22.2	95.00%	R.VVEILQNR.G		R.VVEILQNR.G
571	583	2	1447.74	0.68	1	84.7	27.9	95.00%	R.QLGLGTNIYNAER.L		R.QLGLGTNIYNAER.L
100	109	2	1167.52	0.25	1	33.7	29.7	95.00%	K.YGLNQMADEK.E		K.YGLNQMADEK.E
398	415	2	1903.95	0.32	1	111	28.2	95.00%	E.GVSPDDLMLTACLAASRK.K	Carbamidomethyl (+57)	K.LSLHEPYTVEGVSPDDLMLTACLAASRK.K
175	190	2	1697.93	-0.18	1	29.3	22.7	95.00%	K.TLANTAVVIRDGQLVE.I		K.TLANTAVVIRDGQLVEIPANEVVPGDILQLEDGTVIPTDGR.I
645	659	2	1416.68	-0.87	1	88.8	28.9	95.00%	K.ADTGIAVEGATDAAR.S		K.ADTGIAVEGATDAAR.S
79	95	2	1927.94	0.26	1	83.6	28.4	95.00%	E.YLQTDPSYGLTSDEVLK.R		K.TYDDAASESSDDDDIDALIEELQSNHGVDDEDSDNDGPVAAGEARPVPEEYLQTDPSYGLTSDEVLK.R
626	643	2	1822.88	0.15	0	96.3	28.5	95.00%	R.GYLVAMTGDGVNDAPSLK.K	Oxidation (+16)	R.GYLVAMTGDGVNDAPSLK.K
487	496	2	1186.53	0.48	1	42.4	29	95.00%	E.DHPIPEDVHE.N		K.TVEEDHPIPEDVHENYENK.V
206	219	2	1471.75	0.19	1	35.2	26.8	95.00%	E.DGTVIPTDGRIVTE.D		R.DGQLVEIPANEVVPGDILQLEDGTVIPTDGRIVTEDCFLQIDQSAITGESLAVDK.H
418	428	2	1189.67	-0.45	1	46.2	24.7	95.00%	K.GLDAIDKAFLK.S		K.GLDAIDKAFLK.S
2	28	3	2678.23	0.46	1	63.1	29.7	95.00%	M.TDTSSSSSSSSASSVSAHQPTQEKPAK.T		-.MTDTSSSSSSSSASSVSAHQPTQEKPAK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
4	YBT1_YEAST	26.61%	100%	47

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
118	130	2	1403.71	-0.87	1	56.8	27.2	95.00%	K.VNGEPHGTPEIVR.R		K.VNGEPHGTPEIVR.R
1616	1627	2	1490.74	0.26	1	44.7	28.5	95.00%	K.EYDHPYSLLLNK.Q		K.EYDHPYSLLLNK.Q
1599	1613	2	1666.81	-0.0047	1	39.5	30.2	95.00%	R.SVIDYDKILVMDAGE.V		R.SVIDYDKILVMDAGEVK.E
1457	1473	2	1830.02	0.65	0	76.9	21.8	95.00%	R.SITIIPQDPTLFSGTIK.T		R.SITIIPQDPTLFSGTIK.T
670	680	2	1321.62	0.51	1	45.7	28.9	95.00%	R.VQDFLNENDTK.K		R.VQDFLNENDTK.K
1617	1627	2	1361.7	-0.0049	0	49.8	28.5	95.00%	E.YDHPYSLLLNK.Q		K.EYDHPYSLLLNK.Q
228	240	3	1519.83	0.73	0	33.2	24.7	95.00%	R.SIFIHHINSPISR.K		R.SIFIHHINSPISR.K
1584	1596	2	1471.78	-0.15	1	57.2	26	95.00%	K.EFQGSTILTIAHR.L		K.EFQGSTILTIAHR.L
855	884	3	3431.54	-1.3	0	46.3	29.5	95.00%	R.HVLLDDCLSAVDSHTASWIYDNCITGPLME.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.HVLLDDCLSAVDSHTASWIYDNCITGPLMEDR.T

1238	1246	2	1106.5	0.53	0	34.1	29	95.00%	R.SPIYQHFSE.T		R.SPIYQHFSETLVGVTTIR.A
1482	1489	2	1040.49	1	1	28.4	29	93.20%	E.FSDRQIFE.A		K.TNLDPYDEFSDRQIFEALK.R
936	951	2	1748.78	-0.79	1	41	29.9	95.00%	K.SSILSRANSSANLAAK.S	Phospho (+80)/ Phospho (+80)	K.SSILSRANSSANLAAK.S
1535	1544	2	1002.49	3.7	0	29.2	28.2	95.00%	E.GGSNLSQGQR.Q		K.FLDLSSEISEGGSNLSQGQR.Q
1422	1430	2	1020.6	0.17	0	49.3	20.3	95.00%	K.STIITALFR.F		K.STIITALFR.F
1431	1440	3	1169.61	-0.26	1	33.2	27.3	95.00%	R.FLEPETGHIK.I		R.FLEPETGHIK.I
14	25	2	1595.7	-0.95	0	62	30.4	95.00%	R.FWFYDDVTQYGR.T		R.FWFYDDVTQYGR.T
933	941	2	1081.59	0.88	1	43.9	24.2	95.00%	E.LVKSSILSR.A	Phospho (+80)	K.GLFGEDELVKSSILSR.A
1559	1576	2	1923.97	0.36	1	103	26.8	95.00%	K.IILLDEATASIDYSSDAK.I		K.IILLDEATASIDYSSDAK.I
1381	1389	2	1057.58	1.3	1	48.7	26.1	95.00%	K.IEVNDLSLR.Y		K.IEVNDLSLR.Y
1383	1389	2	816.43	0.32	0	47	28.2	95.00%	E.VNDLSLR.Y	Deamidation (+1)	K.IEVNDLSLR.Y
1565	1576	2	1227.56	0.4	0	60.2	29.1	95.00%	E.ATASIDYSSDAK.I		K.IILLDEATASIDYSSDAK.I
913	925	2	1485.75	-0.48	1	52.8	27.4	95.00%	R.VKDQGDPIDMLQK.G		R.VKDQGDPIDMLQK.G
952	963	2	1202.65	-0.011	0	49.2	25.7	95.00%	K.SSTSLSNLPAVK.E		K.SSTSLSNLPAVK.E
887	900	3	1609.9	0.4	0	39.1	21	95.00%	R.TCILVSHNIALTLR.N	Carbamidomethyl (+57)	R.TCILVSHNIALTLR.N
915	925	2	1258.59	0.55	0	42.1	29	95.00%	K.DQGDPIDMLQK.G		K.DQGDPIDMLQK.G
1247	1255	2	958.58	0.61	0	33	21	95.00%	E.TLVGVTTIR.A		R.SPIYQHFSETLVGVTTIR.A
1370	1382	2	1503.77	-0.21	1	44.8	27.5	95.00%	E.IPPPQWPQDGKIE.V		K.EIPPPQWPQDGKIEVNDLSLR.Y
80	100	2	2423.14	0.26	0	99.4	29.5	95.00%	E.QSPLINNNTITTNYVDNNCTK.D	Carbamidomethyl (+57)	K.NPIDELLYSSTDEDEQSPLINNNTITTNYVDNNCTK.D
427	436	2	1165.66	-0.61	1	36.2	21.4	95.00%	K.SIIISEIYTK.A		K.SIIISEIYTK.A
791	803	2	1535.73	-1.4	1	64.7	29.5	95.00%	K.NNILFNSPFNEAR.Y	Deamidation (+1)	K.NNILFNSPFNEAR.Y
665	676	2	1433.72	0.33	1	34.9	28.8	95.00%	K.VSLDRVQDFLNE.N		K.VSLDRVQDFLNENDTK.K
1417	1430	3	1434.82	0.83	1	44.9	21.8	95.00%	R.TGAGKSTIITALFR.F		R.TGAGKSTIITALFR.F
591	597	2	844.52	1.5	0	33.2	18.5	95.00%	E.LSLLLMR.S		R.ENELSLLLMR.S
694	705	2	1443.67	0.12	1	88.1	29.5	95.00%	R.FAFENSTISWDK.D		R.FAFENSTISWDK.D
1238	1255	2	2047.08	0.73	1	77	25.5	95.00%	R.SPIYQHFSETLVGVTTIR.A		R.SPIYQHFSETLVGVTTIR.A
560	568	2	1060.57	-0.69	1	56.9	27.5	95.00%	K.LNEAFQAIR.I		K.LNEAFQAIR.I
1152	1160	2	1010.48	0.36	0	38.1	29.6	95.00%	R.FFDATPTGR.I		R.FFDATPTGR.I
965	977	2	1488.66	0.6	0	46.5	29.9	95.00%	E.QQVSVNNNSSHFE.A		K.EQQVSVNNNSSHFEAK.K
1486	1492	2	847.48	1.2	1	31.5	24.4	95.00%	R.QIFEALK.R		R.QIFEALK.R
1441	1453	2	1456.75	-1.5	0	97.7	26.6	95.00%	K.IDNIDISGVDLQR.L		K.IDNIDISGVDLQR.L
1436	1453	2	1993.06	0.3	1	73.7	24	95.00%	E.TGHIKIDNIDISGVDLQR.L		R.FLEPETGHIKIDNIDISGVDLQR.L
1456	1473	2	1986.11	-1.3	1	79.9	19.1	95.00%	R.RSITIIPQDPTLFSGTIK.T		R.RSITIIPQDPTLFSGTIK.T
1474	1485	2	1470.63	-0.56	1	61.9	30	95.00%	K.TNLDPYDEFSDR.Q		K.TNLDPYDEFSDR.Q
1400	1410	2	1180.57	0.41	0	30.9	28.5	95.00%	K.NVSFSVDAQSK.I		K.NVSFSVDAQSK.I
681	693	2	1532.76	-1.5	1	65.4	28.2	95.00%	K.KYDQLTIDPNGNR.F		K.KYDQLTIDPNGNR.F
855	886	3	3702.68	0.4	1	65.1	29.9	95.00%	R.HVLLDDCLSAVDSHTASWIYDNCITGPLMEDR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.HVLLDDCLSAVDSHTASWIYDNCITGPLMEDR.T
1585	1596	2	1342.74	0.88	0	54.4	25.5	95.00%	E.FQGSTILTIAHR.L		K.EFQGSTILTIAHR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
5	A6ZPA7_YEAS7	34.29%	100%	26

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
14	24	2	1337.67	1.5	0	33.4	28.4	95.00%	E.MALVQFYIPQE.I		R.SAEMALVQFYIPQEISR.D
196	205	2	1227.7	-0.014	1	46.3	24	95.00%	K.VATLEQILWR.V		K.VATLEQILWR.V
121	132	2	1404.64	0.064	1	60.9	29.4	95.00%	R.LIQMEDATDQIE.V		R.LIQMEDATDQIEVQK.N
255	268	2	1540.65	1.2	0	62.9	30.4	95.00%	E.SLDANLYDVDSSNE.G		K.IAESLDANLYDVDSSNEGR.S
54	60	2	877.47	0.31	1	39.4	27.9	95.00%	R.TFVNEIR.R		R.TFVNEIR.R
71	77	2	932.5	0.74	0	24.4	26.8	90.00%	R.YFYSLLK.K		R.YFYSLLK.K
360	382	3	2569.37	0.35	0	26.2	22.7	95.00%	R.LGIDVPSIIQVLDTNHTPPTFHR.T		R.LGIDVPSIIQVLDTNHTPPTFHR.T
386	403	2	2155.95	-0.11	0	90.3	30	95.00%	K.FTAGFQSICDCYGIAQYR.E	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.FTAGFQSICDCYGIAQYR.E
829	840	2	1022.49	3	0	30.9	28.3	95.00%	E.VAVASASSSASS.-		K.DMEVAVASASSSASS.-
28	42	3	1666.87	0.79	0	59.7	26.7	95.00%	R.DSAYTLGQLGLVQFR.D		R.DSAYTLGQLGLVQFR.D
383	403	2	2499.13	0.063	1	67	30	95.00%	R.TNKFTAGFQSICDCYGIAQYR.E	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.TNKFTAGFQSICDCYGIAQYR.E
98	112	2	1678.86	0.77	0	54.2	27.2	95.00%	E.LYVPPSGSVIDDYVR.N		K.YLDGSGELYVPPSGSVIDDYVR.N
814	823	2	1168.55	1.6	0	41.5	29.5	95.00%	E.GLPYEPFAFE.Y		K.FFVGEGLPYEPFAFEYK.D

209	214	2	724.39	0.78	0	31.3	26.3	95.00%	R.GNLFFK.T	R.GNLFFK.T
699	721	3	2477.17	0.61	1	24.8	29.3	94.80%	E.VGSGSHGEDFGDIMIHQVIHTIE.F	K.SHEPLPSTEADASSEDLEAQQLISAMDADDAEEEEVGSGSHGEDFGDIMIHQVIHTIEFCLNCVSHTASYLR.L
280	289	2	1164.64	0.25	0	44.7	23.8	95.00%	K.NLSDLYTVLK.T	K.NLSDLYTVLK.T
234	248	3	1728.97	0.63	1	41.1	20	95.00%	K.NAFIVFSHGDLIIKR.I	K.NAFIVFSHGDLIIKR.I
305	315	2	1394.65	-0.087	1	65	29.7	95.00%	K.ELDSWFQDVTR.E	K.ELDSWFQDVTR.E
86	97	2	1255.52	0.39	1	71.5	29.5	95.00%	E.GDTDKYLDGSGE.L	K.LYEGDTDKYLDGSGELYVPPSGSVIDDYVR.N
175	193	2	1859.03	1.6	0	102	18.3	95.00%	E.NIAAAIGASVNYVTGVIAR.D	K.GDNTDSTSYMDEDMIDANGENIAAAIGASVNYVTGVIAR.D
527	536	2	1155.59	0.76	0	34	26.7	95.00%	E.NALLFSNSYK.M	K.GESITATSVGTYPIGLDWAWHGTENALLFSNSYK.M
14	27	2	1693.89	-0.0051	1	32.6	25.6	95.00%	E.MALVQFYIPQEISR.D	R.SAEMALVQFYIPQEISR.D
143	154	2	1442.75	0.74	1	41.7	27.6	95.00%	R.FILQSGDEFFLK.G	R.FILQSGDEFFLK.G
91	112	2	2400.15	0.29	1	45.5	28.8	95.00%	K.YLDGSGELYVPPSGSVIDDYVR.N	K.YLDGSGELYVPPSGSVIDDYVR.N
318	325	2	946.55	-0.031	1	49.3	23	95.00%	K.AIFEILNK.S	K.AIFEILNK.S
255	270	2	1753.78	0.39	1	92.1	30.5	95.00%	E.SLDANLYDVDSSNEGR.S	K.IAESLDANLYDVDSSNEGR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
6	A7A234_YEAS7	40.34%	100%	37

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
500	515	3	1888.99	1.2	1	43	25.5	95.00%	K.KHGQWLNDLTNSHLVK.E		K.KHGQWLNDLTNSHLVK.E
394	401	2	1001.53	2	1	29.4	27.8	95.00%	K.NELQPVFR.T		K.NELQPVFR.T
536	548	2	1597.88	0.42	1	34.3	22.5	95.00%	E.KLDILPFWLPDLE.T		K.FSIFVQGVASLYGDDEKLDILPFWLPDLETDIR.Q
94	102	2	1005.49	-0.03	0	50.7	28.4	95.00%	K.ALDADAFQR.V		K.ALDADAFQR.V
208	217	2	1303.57	1.1	0	40.6	30.4	95.00%	K.FWVHNDNLME.V		K.FWVHNDNLMEVK.T
501	515	3	1760.9	1.2	0	49.8	27	95.00%	K.HGQWLNDLTNSHLVK.E		K.HGQWLNDLTNSHLVK.E
407	418	2	1359.71	-0.24	1	35.9	26.9	95.00%	R.TAFQIPGDDKIR.V		R.TAFQIPGDDKIR.V
7	16	2	1215.63	0.47	1	45.5	27	95.00%	K.LANEVYPPWK.G		K.LANEVYPPWK.G
750	757	2	1026.59	1.1	1	33.6	23.1	95.00%	K.RVDIIQQR.S		K.RVDIIQQR.S
144	149	2	715.42	1.1	1	25.5	27.7	90.60%	K.SLLEVR.L		K.SLLEVR.L
273	286	2	1686.78	0.22	0	60.4	29.6	95.00%	R.SFDPLINTLYFDNE.H		R.SFDPLINTLYFDNEHFELYNDK.L
587	600	2	1547.72	0.51	1	66.5	29.6	95.00%	K.EPQHQAAVPVSQEE.N		K.EPQHQAAVPVSQEENER.I
17	26	2	1142.56	-0.36	1	45.8	27.5	95.00%	K.GSYINYEGLK.K		K.GSYINYEGLK.K
469	477	2	1112.56	0.34	1	34.3	27	95.00%	K.FPYSVMEIK.V		K.FPYSVMEIK.V
387	393	2	874.53	0.32	0	36.8	22.7	95.00%	E.IQNFIIK.N		R.LEEDFSEIQNFIIK.N
347	357	2	1285.64	0.9	1	59.3	28.8	95.00%	K.FINGFIFEGDK.K		K.FINGFIFEGDK.K
480	496	2	1745.78	-0.92	0	76.4	31.6	95.00%	K.SSLDSSMSASSMISNVK.L	Oxidation (+16)	K.SSLDSSMSASSMISNVK.L
72	78	2	938.43	0.94	1	35.9	30.2	95.00%	K.YNNLMER.L		K.YNNLMER.L
191	204	2	1659.76	-0.14	0	69.9	30	95.00%	K.FSSIVSNDIDMNFR.S	Oxidation (+16)	K.FSSIVSNDIDMNFR.S
308	322	2	1775.91	0.49	1	61.6	26.8	95.00%	R.WTGQLSDKPDIFLEK.K		R.WTGQLSDKPDIFLEK.K
208	219	2	1530.73	-0.73	1	47.6	29.8	95.00%	K.FWVHNDNLMEVK.T		K.FWVHNDNLMEVK.T
811	821	2	1389.81	0.63	0	44.9	18	95.00%	E.VLRPLQNYLFK.L		R.IPEVLRPLQNYLFK.L
419	430	2	1376.76	0.42	1	29.8	24	95.00%	R.VTIDSNIVFIKE.D		R.VTIDSNIVFIKEDSFDR.E
480	499	2	2068.02	-0.29	1	69.2	28.1	95.00%	K.SSLDSSMSASSMISNVKLPK.K		K.SSLDSSMSASSMISNVKLPK.K
407	416	2	1090.53	0.98	0	42.7	28.8	95.00%	R.TAFQIPGDDK.I		R.TAFQIPGDDK.I
582	599	2	1974.02	0.35	1	64.3	26	95.00%	R.LSNLKEPQHQAAVPVSQE.E		R.LSNLKEPQHQAAVPVSQEENER.I
176	190	2	1522.73	-0.41	0	102	29.5	95.00%	R.SNFNTASEPLASASK.F		R.SNFNTASEPLASASK.F
448	459	2	1269.66	0.3	0	64.7	27.2	95.00%	R.TDIDANVANPLK.F		R.TDIDANVANPLK.F
687	693	2	886.47	-0.031	1	25.2	25.3	94.00%	K.VWLANER.T		K.VWLANER.T
225	237	2	1436.77	0.2	0	29.6	26	95.00%	R.HLPVLVYANVPSE.N		R.HLPVLVYANVPSENDDLVNR.F
662	669	2	851.51	0.67	1	27.6	18.6	95.00%	E.IELPPGVK.K		K.LMGVDSEEEEIELPPGVK.K
308	321	2	1647.82	0.9	0	36	28	95.00%	R.WTGQLSDKPDIFLEK.K		R.WTGQLSDKPDIFLEK.K
387	395	2	1117.61	1.1	1	59	24.8	95.00%	E.IQNFIIKNE.L		R.LEEDFSEIQNFIIKNELQPVFR.T
255	272	2	1809.83	0.26	1	60.2	30.1	95.00%	E.IVGSSSSTSSVEHGLGAR.S	Phospho (+80)	R.FESDISNNDEIVGSSSSTSSVEHGLGAR.S

273	289	2	2100.93	-0.17	1	74.4	30.3	95.00%	R.SFDPLINTLYFDNEHFE.L	Deamidation (+1)	R.SFDPLINTLYFDNEHFELYNDK.L
298	305	2	870.49	1.7	0	25.7	23.7	94.90%	K.LNSAPTLR.L		K.LNSAPTLR.L
160	166	2	910.49	1.7	0	36.5	25.1	95.00%	E.YSPLLYR.I		K.ELPSHSEEYSPLLYR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
7	B3LLD7_YEAS1	20.61%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
481	492	2	1085.55	3	0	53.4	27.4	95.00%	R.STAHGISAASGK.V		R.STAHGISAASGK.V
24	44	3	2377.06	0.29	1	28.5	31	95.00%	E.GGNMAFHNHLNDFAHIEDPLE.R		K.EHLTEGGNMAFHNHLNDFAHIEDPLER.R
481	512	4	3160.64	0.34	1	65.7	21.1	95.00%	R.STAHGISAASGKVGAIIAQTALGTLIDHNCAR.D	Carbamidomethyl (+57)	R.STAHGISAASGKVGAIIAQTALGTLIDHNCAR.D
109	131	2	2280.21	-0.092	0	127	23.1	95.00%	K.VSTSVGTVIGQFGFGTLADIVGR.K		K.VSTSVGTVIGQFGFGTLADIVGR.K
52	64	2	1507.7	0.51	1	87.7	30.1	95.00%	E.SIDNEGFGWQQVK.T	Deamidation (+1)	R.LALESIDNEGFGWQQVK.T
315	328	2	1464.72	-1	1	66.2	28.1	95.00%	R.ASTAVESLDNHPPK.A		R.ASTAVESLDNHPPK.A
561	569	2	1045.56	0.83	0	49.1	28	95.00%	E.IDPATLNFR.N		K.TLEEINELYHDEIDPATLNFR.N
306	314	2	1017.49	0.96	1	27.5	28.2	93.20%	E.DMAINGLER.A		K.IHDTSDEDMAINGLER.A
493	512	2	2093.11	0.0086	0	119	23.5	95.00%	K.VGAIIAQTALGTLIDHNCAR.D	Carbamidomethyl (+57)	K.VGAIIAQTALGTLIDHNCAR.D
57	64	2	948.48	0.83	0	42.7	27.9	95.00%	E.GFGWQQVK.T		R.LALESIDNEGFGWQQVK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
8	A7A1M1_YEAS7	22.01%	100%	40

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	74	2	1191.42	1.8	0	42.4	27.6	95.00%	E.SYDQDYTNGE.Y	Deamidation (+1)	-.MNTDQQPYQGQTDYTQGPDNGQSQEQDYDQYGQPLYPSQADGYYDPNVAAGTEADMYGQQPPNESYDQDYTNGEYYGQPPNMAAQDGENFSDFSSHGPPGTPGYDSYGGQYTPSQMSYGEPNSSGTSTPIYGNYDPNAIAMALPNEPYPAWTADSQSPVSIEQIEDIFIDLTNR.L
1161	1172	2	1086.57	0.72	0	35.3	26.9	95.00%	E.NSGVLGDVAAGK.E		R.EYIFSENSGVLGDVAAGK.E
1047	1063	2	1944.94	-0.093	1	58.2	28.6	95.00%	R.IYSALIDGHCEILDNGR.R	Carbamidomethyl (+57)	R.IYSALIDGHCEILDNGR.R
1779	1788	2	1213.72	0.15	0	39.9	21.3	95.00%	R.QIRPPIYSLK.Q		R.QIRPPIYSLK.Q
819	852	3	3814.93	1.5	1	60.3	23.1	95.00%	R.ISFFAQSLSTPIPEPLPVDNMPTFTVLTPHYAER.I		R.ISFFAQSLSTPIPEPLPVDNMPTFTVLTPHYAER.I
1129	1140	2	1405.7	0.99	1	37.8	28.4	95.00%	E.QVNPYAPGLRYE.E		R.SVLAEFEELNVEQVNPYAPGLRYEEQTTNHPVAIVGAR.E
387	405	2	2240.12	-0.093	1	71.6	27.6	95.00%	K.IVGYDDLNQLFWYPEGIAK.I		K.IVGYDDLNQLFWYPEGIAK.I
1161	1173	2	1215.61	0.81	1	58.7	27.1	95.00%	E.NSGVLGDVAAGKE.Q		R.EYIFSENSGVLGDVAAGKEQTFGTLFAR.T
1047	1057	2	1276.58	0.56	0	66.6	30.2	95.00%	R.IYSALIDGHCE.I	Carbamidomethyl (+57)	R.IYSALIDGHCEILDNGR.R
426	437	2	1438.71	0.82	0	62.9	28.3	95.00%	R.LGDVVWDDVFFK.T		R.LGDVVWDDVFFK.T
1262	1273	2	1248.6	-0.33	1	89.3	28.9	95.00%	K.IGAGMGEQMLSR.E		K.IGAGMGEQMLSR.E
1097	1110	2	1710.81	-0.23	0	42.9	29.4	95.00%	E.YIQLIDANQDNYLE.E		R.GEYIQLIDANQDNYLEECLK.I
1083	1094	2	1476.71	-0.48	0	28	28.9	92.90%	K.SDNQNHALIFYR.G		K.SDNQNHALIFYR.G
75	88	2	1555.63	1.1	0	52.8	30.6	95.00%	E.YYGQPPNMAAQDGE.N	Oxidation (+16)	-.MNTDQQPYQGQTDYTQGPDNGQSQEQDYDQYGQPLYPSQADGYYDPNVAAGTEADMYGQQPPNESYDQDYTNGEYYGQPPNMAAQDGENFSDFSSHGPPGTPGYDSYGGQYTPSQMSYGEPNSSGTSTPIYGNYDPNAIAMALPNEPYPAWTADSQSPVSIEQIEDIFIDLTNR.L
789	805	2	1999.93	-0.12	1	57.1	30.1	95.00%	R.TLRAPTFFVSQDDNNFE.T		R.TLRAPTFFVSQDDNNFETEFFPR.D
1222	1232	2	1253.59	1.3	0	60.5	30.1	95.00%	E.DIYAGMNAMLR.G		K.GLHLNEDIYAGMNAMLR.G
1142	1154	2	1362.74	0.87	0	31.3	25.3	95.00%	E.QTTNHPVAIVGAR.E		R.YEEQTTNHPVAIVGAR.E

1173	1182	2	1168.59	-0.63	1	40.8	27.3	95.00%	K.EQTFGTLFAR.T		K.EQTFGTLFAR.T
1068	1082	2	1599.87	0.55	1	40.9	23.4	95.00%	K.FRVQLSGNPILGDGK.S		K.FRVQLSGNPILGDGK.S
387	401	2	1870.88	0.8	0	34.5	30.1	95.00%	K.IVGYDDLNQLFWYPE.G		K.IVGYDDLNQLFWYPEGIAK.I
658	670	2	1628.71	-0.52	1	64.8	30.3	95.00%	R.CTGEYWWGAVLCK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.CTGEYWWGAVLCK.V
1083	1096	2	1662.78	0.83	1	39.7	29.7	95.00%	K.SDNQNHALIFYRGE.Y		K.SDNQNHALIFYRGEYIQLIDANQDNYLEECLK.I
166	174	2	1105.58	2.8	0	35.1	27.7	95.00%	E.DIFIDLTNR.L		-.MNTDQQPYQGQTDYTQGPDNGQSQEQDYDQYGQPLYPSQADGYYDPNVAAGTEADMYGQQPPNESYDQDYTNGEYYGQPPNMAAQDGENFSDFSSHGPPGTPGYDSYGGQYTPSQMSYGEPNSSGTSTPIYGNYDPNAIAMALPNEPYPAWTADSQSPVSIEQIEDIFIDLTNR.L
1191	1207	3	2019.96	0.79	0	78.3	28.9	95.00%	K.LHYGHPDFINATFMTTR.G		K.LHYGHPDFINATFMTTR.G
200	223	3	2607.27	0.51	1	62	27.7	95.00%	R.MSPDQALLSLHADYIGGDTANYKK.W		R.MSPDQALLSLHADYIGGDTANYKK.W
1436	1444	2	1094.61	-0.2	0	48.5	23.3	95.00%	R.IPFSILYSR.F		R.IPFSILYSR.F
1097	1111	2	1839.85	0.87	1	60.7	29.6	95.00%	E.YIQLIDANQDNYLEE.C		R.GEYIQLIDANQDNYLEECLK.I
1249	1261	2	1425.75	0.54	0	74	26.4	95.00%	R.DLGFGTILNFTTK.I		R.DLGFGTILNFTTK.I
1070	1082	2	1296.7	-0.0085	0	62.1	23.9	95.00%	R.VQLSGNPILGDGK.S		R.VQLSGNPILGDGK.S
331	344	2	1737.78	-0.023	0	107	29.9	95.00%	K.CALDYLDSPLCQQR.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CALDYLDSPLCQQR.Q
184	196	2	1623.75	0.48	0	75	30.1	95.00%	R.NMFDHFMVLLDSR.S		R.NMFDHFMVLLDSR.S
792	805	2	1629.7	0.29	0	43.4	30.2	95.00%	R.APTFFVSQDDNNFE.T		R.APTFFVSQDDNNFETEFFPR.D
1717	1728	2	1383.61	-0.15	0	66	30.1	95.00%	K.GMGYMAWTQPSR.E		K.GMGYMAWTQPSR.E
916	929	2	1701.81	0.19	0	70.8	29.4	95.00%	K.SQIDDLPFYCIGFK.S	Carbamidomethyl (+57)	K.SQIDDLPFYCIGFK.S
200	222	3	2479.17	-0.15	0	76.9	29.5	95.00%	R.MSPDQALLSLHADYIGGDTANYK.K		R.MSPDQALLSLHADYIGGDTANYK.K
792	807	2	1859.79	0.3	1	54.2	30.7	95.00%	R.APTFFVSQDDNNFETE.F		R.APTFFVSQDDNNFETEFFPR.D
1520	1527	2	993.5	-0.11	0	40.9	27.6	95.00%	R.NSWIGYVR.M		R.NSWIGYVR.M
953	962	2	1174.54	-0.35	0	46.5	29.3	95.00%	R.TISGFMNYSR.A		R.TISGFMNYSR.A
870	877	2	977.58	-0.012	1	44.9	16	95.00%	R.VTLLEYLK.Q		R.VTLLEYLK.Q
1174	1182	2	1039.55	1.4	0	33.4	25.3	95.00%	E.QTFGTLFAR.T		K.EQTFGTLFAR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
9	B3LFI5_YEAS1	50.71%	100%	25

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
302	309	2	799.48	-0.03	1	33.6	25.8	95.00%	K.VALGALEK.A		K.VALGALEK.A
172	187	2	1765.83	-0.18	0	69.4	29	95.00%	R.ITDATPASFSSHVDYR.W		R.ITDATPASFSSHVDYR.W
452	466	2	1679.85	0.29	0	80.7	27.7	95.00%	E.TLIHLDDNANAIQDK.L		K.DLGIYDYTDSDLETLIHLDDNANAIQDK.L
467	474	2	980.48	1.5	0	30.4	29.5	95.00%	K.LNDMVSFR.A		K.LNDMVSFR.A
244	255	2	1380.61	0.42	0	52.3	30.3	95.00%	E.AQSNGWQYVGDR.K	Deamidation (+1)	R.DLIDEAQSNGWQYVGDR.K
191	205	2	1681.88	0.7	1	55.5	25.7	95.00%	E.DLIATHQLGEYPLGR.V		R.WQEDLIATHQLGEYPLGR.V
475	498	3	2643.32	-0.18	1	50.8	26.5	95.00%	R.AQIGWTTHGHSAVDVNIYAYANKK.A		R.AQIGWTTHGHSAVDVNIYAYANKK.A
136	158	2	2448.2	0.17	1	45.1	27.9	95.00%	K.SYNGAIGVDPHHRPCGTVLEAAK.L	Carbamidomethyl (+57)	K.SYNGAIGVDPHHRPCGTVLEAAK.L
159	171	2	1362.79	-0.15	0	81.9	20.3	95.00%	K.LAGYLTGLVVTTR.I		K.LAGYLTGLVVTTR.I
136	155	2	2178.03	1.7	0	57.7	30.4	95.00%	K.SYNGAIGVDPHHRPCGTVLE.A	Carbamidomethyl (+57)	K.SYNGAIGVDPHHRPCGTVLEAAK.L
329	344	3	1772.82	1.2	1	53.5	30.2	95.00%	R.IDHAGHQNDPASQVRE.V		R.IDHAGHQNDPASQVREVLAFDEAFQYVLEFAENSDTETVLVSTSDHETGGLVTSR.Q
87	105	2	2197.06	0.54	0	71.8	28.8	95.00%	R.SFNQHVNDLPIDDILTLDE.H		R.SFNQHVNDLPIDDILTLDEHFIGSSR.T
206	215	2	1015.55	1.6	0	58.9	27	95.00%	R.VVDLLMGGGR.S		R.VVDLLMGGGR.S
67	86	3	2140.08	-0.047	1	47.5	26.7	95.00%	K.KNVIFFVTDGMGPASLSMAR.S		K.KNVIFFVTDGMGPASLSMAR.S
329	343	2	1643.78	0.54	0	47.3	29.7	95.00%	R.IDHAGHQNDPASQVR.E		R.IDHAGHQNDPASQVR.E

439	451	2	1517.64	1.2	0	80.2	30.4	95.00%	K.DLGIYDYTDSDLE.T		K.DLGIYDYTDSDLETLIHLDDNANAIQDK.L
244	256	2	1508.7	0.52	1	62.4	30.3	95.00%	E.AQSNGWQYVGDRK.N	Deamidation (+1)	R.DLIDEAQSNGWQYVGDRK.N
1	12	3	1430.66	-0.061	1	39.2	30.4	95.00%	-.MMTHTLPSEQTR.L		-.MMTHTLPSEQTR.L
68	86	2	2027.98	0.23	0	105	29.1	95.00%	K.NVIFFVTDGMGPASLSMAR.S	Oxidation (+16)	K.NVIFFVTDGMGPASLSMAR.S
366	375	2	1086.52	1.4	0	32.5	29	95.00%	E.TVLVSTSDHE.T		R.EVLAFDEAFQYVLEFAENSDTETVLVSTSDHETGGLVTSR.Q
316	328	2	1457.66	-0.64	1	38.8	29.8	95.00%	K.DSNGFFLMVEGSR.I		K.DSNGFFLMVEGSR.I
113	135	2	2299.11	-0.041	1	73.8	28.1	95.00%	R.TRSSDSLVTDSAAGATAFACALK.S	Carbamidomethyl (+57)	R.TRSSDSLVTDSAAGATAFACALK.S
115	135	2	2041.96	-0.63	0	128	29.1	95.00%	R.SSDSLVTDSAAGATAFACALK.S	Carbamidomethyl (+57)	R.SSDSLVTDSAAGATAFACALK.S
413	421	2	1122.58	-0.2	1	39.5	27	95.00%	K.LVDFVHEHK.G		K.LVDFVHEHK.G
87	112	3	2981.46	1.4	1	66.2	27.4	95.00%	R.SFNQHVNDLPIDDILTLDEHFIGSSR.T		R.SFNQHVNDLPIDDILTLDEHFIGSSR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
10	A6ZL63_YEAS7	45.41%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
85	100	2	1857.97	-0.17	1	56.4	25.2	95.00%	K.YQVTVIDAPGHRDFIK.N		K.YQVTVIDAPGHRDFIK.N
267	286	2	1974.05	-0.011	0	69.1	23.7	95.00%	E.TGVIKPGMVVTFAPAGVTTE.V		R.VETGVIKPGMVVTFAPAGVTTEVK.S
299	311	2	1329.67	0.59	0	54.6	29.1	95.00%	E.QGVPGDNVGFNVK.N		K.SVEMHHEQLEQGVPGDNVGFNVK.N
185	210	2	2907.39	-0.32	1	85	29.5	95.00%	K.TVPFVPISGWNGDNMIEATTNAPWYK.G		K.TVPFVPISGWNGDNMIEATTNAPWYK.G
265	286	2	2202.16	0.26	1	54.4	24.1	95.00%	R.VETGVIKPGMVVTFAPAGVTTE.V		R.VETGVIKPGMVVTFAPAGVTTEVK.S
412	421	2	1135.57	0.32	1	43.9	28.8	95.00%	E.AFSEYPPLGR.F		K.FVPSKPMCVEAFSEYPPLGR.F
185	201	2	1874.89	0.41	0	53.1	29.8	95.00%	K.TVPFVPISGWNGDNMIE.A		K.TVPFVPISGWNGDNMIEATTNAPWYK.G
254	266	2	1252.71	0.54	1	43.2	21.7	95.00%	K.IGGIGTVPVGRVE.T		K.IGGIGTVPVGRVETGVIKPGMVVTFAPAGVTTEVK.S
85	96	2	1354.7	-0.6	0	61.9	26.5	95.00%	K.YQVTVIDAPGHR.D		K.YQVTVIDAPGHR.D
394	401	2	759.41	1.7	0	40.5	27.2	95.00%	K.SGDAALVK.F		K.SGDAALVK.F
329	369	4	4444.12	-0.85	1	52.6	24.4	95.00%	K.NDPPKGCASFNATVIVLNHPGQISAGYSPVLDCHTAHIACR.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.NDPPKGCASFNATVIVLNHPGQISAGYSPVLDCHTAHIACR.F
254	264	2	1024.61	1.8	0	68.3	19.3	95.00%	K.IGGIGTVPVGR.V		K.IGGIGTVPVGR.V
267	288	3	2201.22	1	1	20.1	20.8	94.10%	E.TGVIKPGMVVTFAPAGVTTEVK.S		R.VETGVIKPGMVVTFAPAGVTTEVK.S
429	437	2	913.56	-0.34	0	45.5	21.3	95.00%	R.QTVAVGVIK.S		R.QTVAVGVIK.S
6	20	2	1559.84	-0.0025	0	81.3	24.9	95.00%	K.SHINVVVIGHVDSGK.S		K.SHINVVVIGHVDSGK.S
402	411	2	1192.56	1.8	0	32.1	28.9	95.00%	K.FVPSKPMCVE.A	Carbamidomethyl (+57)	K.FVPSKPMCVEAFSEYPPLGR.F
334	369	5	3892.85	-0.78	0	21.2	27.7	95.00%	K.GCASFNATVIVLNHPGQISAGYSPVLDCHTAHIACR.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GCASFNATVIVLNHPGQISAGYSPVLDCHTAHIACR.F
246	253	2	974.54	-0.0093	0	40.2	25.6	95.00%	R.LPLQDVYK.I		R.LPLQDVYK.I
229	245	3	1906.03	0.47	1	24.4	24.1	95.00%	E.AIDAIEQPSRPTDKPLR.L		K.TLLEAIDAIEQPSRPTDKPLR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
11	A6ZY95_YEAS7	22.57%	100%	32

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1488	1499	2	1319.64	1.1	0	64	29.5	95.00%	E.FDSPGQLLSDNK.S		K.VAEFDSPGQLLSDNK.S
1036	1048	2	1466.72	-0.78	1	61.7	28.2	95.00%	R.APMTFFETTPIGR.I		R.APMTFFETTPIGR.I
1349	1364	2	1787.94	-0.62	1	36.3	25	95.00%	K.LSIIPQDSQVFEGTVR.E		K.LSIIPQDSQVFEGTVR.E
237	245	2	1112.58	0.71	1	25.2	26.2	92.70%	K.YLVEADLYK.L		K.YLVEADLYK.L
1340	1346	2	848.48	0.8	0	34.2	25.9	95.00%	E.IGLYDLR.H		R.MIEASEGNIVIDNIAINEIGLYDLR.H
1436	1446	2	1118.55	0.69	1	50	28.3	95.00%	E.ATAAVDVETDK.V		K.ILVLDEATAAVDVETDK.V

790	805	3	1777	-0.45	1	52.9	19.5	95.00%	R.HLIEHVLGPNGLLHTK.T		R.HLIEHVLGPNGLLHTK.T
486	495	2	1141.67	0.25	1	47.6	23.1	95.00%	R.VISEILNNIK.S		R.VISEILNNIK.S
670	682	2	1495.75	1.1	0	47.9	28	95.00%	K.TALLSCMLGDLFR.V	Carbamidomethyl (+57)	K.TALLSCMLGDLFR.V
1347	1360	2	1639.86	0.18	1	48	25.7	95.00%	R.HKLSIIPQDSQVFE.G		R.HKLSIIPQDSQVFEGTVR.E
1389	1405	2	1857.84	1.1	1	60.4	30.7	95.00%	K.EHVLSMSNDGLDAQLTE.G		K.EHVLSMSNDGLDAQLTEGGGNL SVGQR.Q
1281	1290	3	1244.71	-0.078	1	59.3	22.6	95.00%	R.YRPELDLVLK.H		R.YRPELDLVLK.H
840	850	2	1272.67	0.29	1	41.9	27.6	95.00%	E.ITKDADSPLWK.L		K.VSALSIADSIALLDNGEITQQGTY DEITKDADSPLWK.L
1485	1499	2	1618.78	-0.51	1	87.8	29	95.00%	K.VAEFDSPGQLLSDNK.S		K.VAEFDSPGQLLSDNK.S
794	805	3	1284.73	0.084	0	59.7	22.5	95.00%	E.HVLGPNGLLHTK.T		R.HLIEHVLGPNGLLHTK.T
192	206	3	1835.99	-0.32	0	32.5	22.5	95.00%	K.KPLMPHQHIHQTLTR.R		K.KPLMPHQHIHQTLTR.R
271	281	2	1289.62	0.94	0	53.4	28.8	95.00%	K.SNPSLSWAICR.T	Carbamidomethyl (+57)	K.SNPSLSWAICR.T
771	785	2	1619.76	0.79	0	46.2	29.6	95.00%	R.ADTYLLDDPLAAVDE.H		R.ADTYLLDDPLAAVDEHVAR.H
771	789	2	2083.02	-0.49	1	108	28.2	95.00%	R.ADTYLLDDPLAAVDEHVAR.H		R.ADTYLLDDPLAAVDEHVAR.H
1458	1467	3	1194.68	-0.25	1	39.9	20.8	95.00%	K.DRTILTIAHR.L		K.DRTILTIAHR.L
1126	1143	2	1975.02	0.7	1	113	26.7	95.00%	R.SPIYSHFQETLGGLATVR.G		R.SPIYSHFQETLGGLATVR.G
1313	1321	2	1006.58	1.5	0	51.4	22	95.00%	K.SSLTLALFR.M		K.SSLTLALFR.M
1460	1467	2	923.56	0.52	0	30.7	18.5	95.00%	R.TILTIAHR.L		R.TILTIAHR.L
2	11	2	1146.55	-0.31	0	39.1	28.5	95.00%	M.AGNLVSWACK.L	Acetyl (+42)/ Carbamidomethyl (+57)	-.MAGNLVSWACK.L
1291	1301	3	1341.75	0.22	1	27	22.8	95.00%	K.HINIHIKPNEK.V		K.HINIHIKPNEK.V
1468	1484	2	1916	-1.8	1	71.9	25.8	95.00%	R.LNTIMDSDRIIVLDNGK.V		R.LNTIMDSDRIIVLDNGK.V
1274	1280	2	900.41	2.6	0	33.3	28.5	95.00%	K.FNNYSTR.Y		K.FNNYSTR.Y
728	743	2	1718.86	-0.17	0	83	26.9	95.00%	K.ACALTIDLAILMDGDK.T	Carbamidomethyl (+57)	K.ACALTIDLAILMDGDK.T
207	220	3	1663.84	-0.25	1	57.4	28.4	95.00%	R.RKPNPYDSANIFSR.I		R.RKPNPYDSANIFSR.I
1381	1388	2	909.53	-0.46	1	33.8	17	95.00%	R.ALELSHLK.E		R.ALELSHLK.E
814	830	2	1686.87	0.76	0	30.4	26.7	95.00%	K.VSALSIADSIALLDNGE.I		K.VSALSIADSIALLDNGEITQQGTY DEITK.D
379	388	2	1106.63	0.35	0	24.6	22.4	93.60%	K.SALTALIYQK.S		K.SALTALIYQK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
12	B3LSE9_YEAS1	44.38%	100%	31

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
222	241	2	2245.03	0.26	0	57.8	29.9	95.00%	R.AVTNDGSSFLFNGKPDWVYE.E		R.AVTNDGSSFLFNGKPDWVYEEE VFEDDK.A
351	365	2	1634.91	0.3	0	106	21.7	95.00%	R.SSDILTVFLIDTIAK.T		R.SSDILTVFLIDTIAK.T
576	606	3	3543.7	1.5	1	41.8	27.8	95.00%	E.ILPNDFDETLSDHYPVFFFAYGGP NSQQVVK.T		K.DILVNSYEILPNDFDETLSDHYPV FFFAYGGPNSQQVVK.T
699	710	2	1380.65	-0.15	0	47.4	30.1	95.00%	K.YGMSVAPVTDWR.F		K.YGMSVAPVTDWR.F
335	346	2	1285.7	1.4	0	60.7	25.7	95.00%	E.VTWVGNGNVLVK.T	Deamidation (+1)	K.DGSLLITEVTWVGNGNVLVK.T
435	448	2	1548.72	-2.1	1	85.1	29.7	95.00%	E.VVNGPLAFDSMENR.L	Deamidation (+1)	K.WEVVNGPLAFDSMENR.L
565	575	2	1283.64	-0.17	1	41.6	28.6	95.00%	E.FGKDILVNSYE.I		K.DEFGKDILVNSYEILPNDFDETLS DHYPVFFFAYGGPNSQQVVK.T
793	803	2	1318.67	-0.54	0	44	29.2	95.00%	R.YHNANVIVFDK.L		R.YHNANVIVFDK.L
483	494	2	1287.57	1.2	0	50	30.4	95.00%	E.DGVYDVSFSSGR.R		R.SPNEIIEVTDTSEDGVYDVSFSSG R.R
654	672	2	2039.02	0.048	0	42.7	28.3	95.00%	R.DQISAASLYGSLTFVDPQK.I		R.DQISAASLYGSLTFVDPQK.I
117	131	2	1687.79	0.18	1	76.2	30.2	95.00%	K.SVYDDSYNSVLLEGK.T		K.SVYDDSYNSVLLEGK.T
166	177	2	1449.66	0.13	0	60.7	30.3	95.00%	R.HSTFGSYFVYDK.S		R.HSTFGSYFVYDK.S
720	733	2	1744.7	0.044	1	58.6	30.2	95.00%	R.YMHTPQENFDGYVE.S	Oxidation (+16)	R.YMHTPQENFDGYVESSVHNVTA LAQANR.F
89	98	2	1244.64	0.79	1	25.4	27.7	90.30%	E.LQWISDNKIE.S		K.YHELQWISDNKIESNDLGLYVTF MNDSYVVK.S
767	777	2	1246.65	1.2	0	57.6	27.5	95.00%	K.FLDLLDLNGVE.N		K.FLDLLDLNGVENYDVHVFPDSDH SIR.Y
748	766	2	2172.04	0.45	0	109	29.3	95.00%	R.FLLMHGTGDDNVHFQNSLK.F		R.FLLMHGTGDDNVHFQNSLK.F
477	494	2	1919.84	0.67	1	45.2	30.8	95.00%	E.VTDTSEDGVYDVSFSSGR.R		R.SPNEIIEVTDTSEDGVYDVSFSSG R.R
273	283	2	1413.72	0.91	1	29.3	27.5	95.00%	E.FIIPYYVQDEK.D		K.IDESEVGEFIIPYYVQDEK.D
347	365	3	2108.14	0.9	1	43.3	23.4	95.00%	K.TTDRSSDILTVFLIDTIAK.T		K.TTDRSSDILTVFLIDTIAK.T
327	346	2	2113.14	0.61	1	87.6	22.2	95.00%	K.DGSLLITEVTWVGNGNVLVK.T		K.DGSLLITEVTWVGNGNVLVK.T

273	282	2	1285.63	1.9	0	32.9	29.4	95.00%	E.FIIPYYVQDE.K		K.IDESEVGEFIIPYYVQDEK.D
297	312	3	1815.86	0.45	1	30.1	29.8	95.00%	K.SGTPNPHAELWVYSMK.D		K.SGTPNPHAELWVYSMK.D
394	418	3	2908.38	0.68	0	63.1	29.4	95.00%	E.TFDRPHNGYVDILPIGGYNHLAYFE.N	Deamidation (+1)	R.NESSNGGWWEITHNTLFIPANETFDRPHNGYVDILPIGGYNHLAYFENSNSSHYK.T
584	606	3	2601.27	5.2	0	56.3	27.6	95.00%	E.TLSDHYPVFFFAYGGPNSQQVVK.T	Deamidation (+1)	K.DILVNSYEILPNDFDETLSDHYPVFFFAYGGPNSQQVVK.T
435	446	2	1278.58	2.6	0	36.4	29.7	95.00%	E.VVNGPLAFDSME.N	Deamidation (+1)	K.WEVVNGPLAFDSMENR.L
711	719	2	1178.52	-0.098	1	49.4	29.5	95.00%	R.FYDSVYTER.Y		R.FYDSVYTER.Y
72	78	2	792.45	0.98	0	26	24.6	95.00%	K.VSFSVVR.N		K.VSFSVVR.N
778	792	2	1799.82	0.49	0	82.9	29.7	95.00%	E.NYDVHVFPDSDHSIR.Y		K.FLDLLDLNGVENYDVHVFPDSDHSIR.Y
250	264	2	1724.86	0.74	0	57.7	28.4	95.00%	K.AAWWSPTGDYLAFLK.I		K.AAWWSPTGDYLAFLK.I
810	818	2	1066.56	-0.22	1	30.5	26.1	95.00%	K.RAFDGQFVK.-		K.RAFDGQFVK.-
767	792	3	3028.45	-0.92	1	79.5	28.1	95.00%	K.FLDLLDLNGVENYDVHVFPDSDHSIR.Y		K.FLDLLDLNGVENYDVHVFPDSDHSIR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
13	B3LS03_YEAS1	37.72%	100%	23

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
39	50	2	1338.64	-1.1	0	45.8	28.8	95.00%	K.DQLDFYSGGPLK.A		K.DQLDFYSGGPLK.A
300	317	2	1954.09	-0.55	0	51.5	21.4	95.00%	K.LIQSDSIPLVLASVACIR.N	Carbamidomethyl (+57)	K.LIQSDSIPLVLASVACIR.N
26	36	2	1219.67	1.2	1	40.9	25.3	95.00%	R.EAVTLLLGYLE.D		R.EAVTLLLGYLEDK.D
27	36	2	1090.63	0.63	0	29.1	23.7	95.00%	E.AVTLLLGYLE.D		R.EAVTLLLGYLEDK.D
277	290	2	1607.82	-0.19	1	108	27.7	95.00%	R.NLASDTSYQLEIVR.A		R.NLASDTSYQLEIVR.A
142	156	2	1675.81	0.21	0	87.1	28.9	95.00%	E.VQCNAVGCITNLATR.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.LLIVEMGGLEPLINQMMGDNVEVQCNAVGCITNLATR.D
318	326	2	1035.54	1	0	37.4	26.6	95.00%	R.NISIHPLNE.G		R.NISIHPLNEGLIVDAGFLKPLVR.L
161	174	3	1448.87	-0.066	1	39.8	14.8	95.00%	K.HKIATSGALIPLTK.L		K.HKIATSGALIPLTK.L
267	276	2	1158.65	-0.51	1	29.5	25.1	95.00%	R.VKCQATLALR.N	Carbamidomethyl (+57)	R.VKCQATLALR.N
51	65	2	1719.92	0.35	0	62	24.9	95.00%	K.ALTTLVYSDNLNLQR.S		K.ALTTLVYSDNLNLQR.S
27	38	2	1333.75	0.81	1	39.5	22.4	95.00%	E.AVTLLLGYLEDK.D		R.EAVTLLLGYLEDK.D
125	141	2	1846.83	1.1	0	63.3	30.4	95.00%	E.MGGLEPLINQMMGDNVE.V		K.LLIVEMGGLEPLINQMMGDNVEVQCNAVGCITNLATR.D
163	174	2	1183.72	-0.35	0	66.9	19	95.00%	K.IATSGALIPLTK.L		K.IATSGALIPLTK.L
269	276	2	931.49	1.1	0	44.2	29.1	95.00%	K.CQATLALR.N	Carbamidomethyl (+57)	K.CQATLALR.N
505	515	2	1257.63	-0.42	1	54.3	27.9	95.00%	K.NDDDIINGVRK.M		K.NDDDIINGVRK.M
37	50	2	1581.77	-0.39	1	70.7	28.6	95.00%	E.DKDQLDFYSGGPLK.A		R.EAVTLLLGYLEDKDQLDFYSGGPLK.A
350	359	3	1183.61	0.71	0	22.5	25.8	95.00%	E.IQCHAVSTLR.N	Carbamidomethyl (+57)	K.DSEEIQCHAVSTLR.N
186	199	2	1486.67	0.12	1	75.2	30.2	95.00%	R.NATGALLNMTHSEE.N		R.NATGALLNMTHSEENR.K
256	266	2	1206.59	-0.023	0	52	29.1	95.00%	K.LVSLMDSPSSR.V	Oxidation (+16)	K.LVSLMDSPSSR.V
318	340	3	2514.43	-0.32	1	35.7	16.6	95.00%	R.NISIHPLNEGLIVDAGFLKPLVR.L		R.NISIHPLNEGLIVDAGFLKPLVR.L
186	198	2	1357.63	0.72	0	72.9	29.9	95.00%	R.NATGALLNMTHSE.E		R.NATGALLNMTHSEENR.K
516	523	2	967.44	0.49	1	35	30	95.00%	K.MADVTFER.L		K.MADVTFER.L
566	578	2	1629.89	0.25	0	88.6	24.5	95.00%	E.LYNITQQILQFLH.-		K.NPGSNNNPSSNDNNSNNNDTGSEHQPVEDASLELYNITQQILQFLH.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
14	A6ZVC8_YEAS7	36.72%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
64	72	2	1066.61	0.45	1	62.5	21.4	95.00%	K.ESTLHLVLR.L		K.ESTLHLVLR.L
17	27	2	1205.58	0.32	1	47.5	28.5	95.00%	E.VESSDTIDNVK.S		K.TITLEVESSDTIDNVK.S
52	63	2	1408.69	-0.0071	1	45.1	28.3	95.00%	E.DGRTLSDYNIQK.E		K.QLEDGRTLSDYNIQK.E
1	6	2	764.43	-0.41	0	35.4	27.2	95.00%	-.MQIFVK.T		-.MQIFVK.T
55	64	2	1209.59	1.5	1	47.5	29.4	95.00%	R.TLSDYNIQKE.S		R.TLSDYNIQKESTLHLVLR.L
19	27	2	977.47	2	0	33.6	28.8	95.00%	E.SSDTIDNVK.S		K.TITLEVESSDTIDNVK.S
34	42	2	1038.51	0.94	1	39.5	28.9	95.00%	K.EGIPPDQQR.L		K.EGIPPDQQR.L
65	72	2	937.57	0.52	0	53.7	16.1	95.00%	E.STLHLVLR.L		K.ESTLHLVLR.L

55	63	2	1080.55	-0.0048	0	50.4	27.6	95.00%	R.TLSDYNIQK.E		R.TLSDYNIQK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
15	CBPS_YEAST	28.47%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
461	470	3	1149.69	0.091	0	33	16.3	95.00%	E.LGHIDITLLR.E		K.NGDDYIIPETELGHIDITLLR.E
108	119	2	1391.6	1.6	0	51.9	30.7	95.00%	K.NPNPADDPDFYK.H		K.NPNPADDPDFYK.H
279	290	2	1302.68	1.7	1	59.6	27.3	95.00%	K.DVFVATPINAEK.G		K.DVFVATPINAEK.G
195	201	2	879.42	0.99	0	25	26.6	91.70%	E.TDFVWGR.G		K.FPPFSGHYDPETDFVWGR.G
533	544	2	1331.77	0.061	0	62.1	21.1	95.00%	R.FVGSIIDIDLLK.T		R.FVGSIIDIDLLK.T
258	269	2	1358.59	1.2	0	45	30.1	95.00%	R.YGDDGIYSIIDE.G		R.YGDDGIYSIIDEGEGIMEVDK.D
522	528	2	972.47	0.61	0	33.8	28.9	95.00%	K.YYWNLSK.N		K.YYWNLSK.N
241	257	2	1686.87	0.4	1	92.2	26.8	95.00%	E.ASGTLGAASLASFLHER.Y		R.TIVMSLGFDEEASGTLGAASLAS FLHER.Y
361	370	2	1130.59	-0.36	0	32	27.5	95.00%	K.TILGAPFCPR.R	Carbamidomethyl (+57)	K.TILGAPFCPR.R
391	403	2	1314.72	1.4	0	74.9	24.9	95.00%	R.TTQAVDIINGGVK.A		R.TTQAVDIINGGVK.A
375	386	2	1457.76	0.27	1	60.3	27	95.00%	K.LVEYISNQSHLR.S		K.LVEYISNQSHLR.S
75	87	2	1506.76	-0.68	0	81.4	28.4	95.00%	K.HSVDTILHDPAFR.N		K.HSVDTILHDPAFR.N
184	201	3	2152.96	0.13	1	24	30.3	91.50%	K.FPPFSGHYDPETDFVWGR.G		K.FPPFSGHYDPETDFVWGR.G
552	567	2	1752.89	0.85	0	50.6	28.4	95.00%	E.HVDVPGHLSAIAFVYE.Y		K.TLHSVNEHVDVPGHLSAIAFVYE YIVNVNEYA.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
16	ATN2_YEAST	29.61%	100%	25

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
531	542	2	1389.69	0.34	1	42.6	28.2	95.00%	E.HIAEFPFDSTVK.R		K.STNQSNENDQSSLSQHNEKPGS AQFEHIAEFPFDSTVK.R
52	63	2	1381.67	0.13	1	50.9	28.8	95.00%	E.NTLGDDTKIDYK.A		K.AVGENTLGDDTKIDYK.A
14	24	2	1324.59	0.66	1	48.6	29.9	95.00%	E.FNAYHTLTTEE.A		K.ENNNEEFNAYHTLTTEEAAEFIGT SLTEGLTQDESLR.R
424	436	2	1475.74	-0.49	1	39.5	28.2	95.00%	E.DGDVGILQNFKDR.L		R.FSPYEYSHNEDGDVGILQNFKDR .L
614	626	2	1536.74	-0.92	1	68.2	29	95.00%	K.SFTKDQVNDDQLK.N		K.SFTKDQVNDDQLK.N
477	492	2	1696.88	-0.49	1	74.5	25.9	95.00%	K.AHGDPTEIAIQVFATK.M		K.AHGDPTEIAIQVFATK.M
512	530	2	2101.93	0.61	1	51.4	30.1	95.00%	E.NDQSSLSQHNEKPGSAQFE.H		K.STNQSNENDQSSLSQHNEKPGS AQFEHIAEFPFDSTVK.R
389	413	2	2703.31	-0.31	1	88.6	28	95.00%	R.FGTITISNSDDPFNPNEGNVSLIP R.F		R.FGTITISNSDDPFNPNEGNVSLIP R.F
637	654	2	2017.05	-0.46	1	61.1	24.9	95.00%	E.SDLVFLGLIGIYDPPRNE.T		R.ATAESDLVFLGLIGIYDPPRNETA GAVK.K
687	700	2	1632.82	0.61	0	36.7	27.8	95.00%	E.VGILPTNLYHYSQE.I		K.AIAQEVGILPTNLYHYSQEIVDSM VMTGSQFDGLSEEEVDDLPVLPLVI AR.C
359	370	2	1261.6	0.64	0	47.5	29.1	95.00%	E.ALGAVNDICSDK.T	Carbamidomethyl (+57)	K.LDSLEALGAVNDICSDK.T
924	941	3	2173.89	-0.56	1	31	30.7	95.00%	R.LGHDCDGTYNSSCRDVYR.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.LGHDCDGTYNSSCRDVYR.S
661	681	4	2270.16	-0.34	1	30.8	26.2	95.00%	K.KFHQAGINVHMLTGDFVGTAK.A		K.KFHQAGINVHMLTGDFVGTAK.A
662	681	3	2142.07	0.38	0	29.3	28.1	95.00%	K.FHQAGINVHMLTGDFVGTAK.A		K.FHQAGINVHMLTGDFVGTAK.A
156	165	2	1055.56	0.26	0	36.5	25.3	95.00%	K.VGDTIPADLR.L		K.VGDTIPADLR.L
457	476	2	2240.08	0.36	1	130	29.3	95.00%	E.TATLANIATVFKDDATDCWK.A	Carbamidomethyl (+57)	K.WLETATLANIATVFKDDATDCWK. A
596	606	2	1250.63	-0.17	1	44	29.3	95.00%	K.NVYSLSNEGLR.V		K.NVYSLSNEGLR.V
720	732	2	1418.85	1	0	56	13	95.00%	E.VDDLPVLPLVIAR.C		K.AIAQEVGILPTNLYHYSQEIVDSM VMTGSQFDGLSEEEVDDLPVLPLVI AR.C
484	492	2	989.59	1.6	0	23.8	20.1	92.30%	E.IAIQVFATK.M		K.AHGDPTEIAIQVFATK.M
751	766	2	1697.74	-0.52	0	83.4	30.2	95.00%	K.FCAMTGDGVNDSPSLK.M	Carbamidomethyl (+57)	K.FCAMTGDGVNDSPSLK.M
239	253	2	1558.79	-1.4	1	77	27.5	95.00%	K.SLQGDSGLISRDPSK.S		K.SLQGDSGLISRDPSK.S
493	504	2	1324.64	-1.6	1	31.2	28.8	95.00%	K.MDLPHNALTGEK.S		K.MDLPHNALTGEK.S
424	434	2	1204.61	0.81	0	45.5	28.1	95.00%	E.DGDVGILQNFK.D		R.FSPYEYSHNEDGDVGILQNFK.D

254	264	2	1362.69	-0.0057	0	52.6	28.3	95.00%	K.SWLQNTWISTK.K			K.SWLQNTWISTK.K
124	134	2	1206.65	-0.51	0	30.2	26.7	95.00%	K.NLSSPNAHVIR.N			K.NLSSPNAHVIR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
17	A6ZTJ2_YEAS7	26.22%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
193	203	2	1498.66	0.94	0	29.7	30.1	93.50%	E.CNFQFWIDQLE.S	Carbamidomethyl (+57)	K.IPQITFACDKPNQECNFQFWIDQLESFYCGLSDCAFEYDLEQNTSHYK.C
430	439	2	1117.64	0.43	0	41.3	22.5	95.00%	K.TTLLDILAMK.R		K.TTLLDILAMK.R
68	78	2	1347.55	-0.21	1	62.4	30.5	95.00%	K.QFSECNSYTGR.C	Carbamidomethyl (+57)	K.QFSECNSYTGR.C
30	39	2	1099.52	0.88	1	36.6	27.1	95.00%	K.TPFFEGTSSK.N		K.TPFFEGTSSK.N
860	873	2	1681.8	-0.71	0	38.6	29.2	95.00%	R.SNNYYSPLAYYISK.I		R.SNNYYSPLAYYISK.I
259	270	2	1352.57	-0.37	1	64.8	30	95.00%	K.GPGDFSCDLETR.Q	Carbamidomethyl (+57)	K.GPGDFSCDLETR.Q
657	688	3	3467.55	-1.3	1	70.7	30	95.00%	R.NISDLEAGTDTNDIDNTIHQTTFTSSDGTTQR.E		R.NISDLEAGTDTNDIDNTIHQTTFTSSDGTTQR.E
245	258	2	1537.79	-0.14	1	71.5	27.2	95.00%	K.GSIDISDFLTETIK.G		K.GSIDISDFLTETIK.G
274	295	2	2499.26	-0.65	0	75.4	25.8	95.00%	K.FSEPSMNDLILTVFGDPYITLK.C		K.FSEPSMNDLILTVFGDPYITLK.C
301	311	2	1351.62	0.68	1	37.6	29.5	95.00%	E.CVHYSEIPGYK.S	Carbamidomethyl (+57)	K.CESGECVHYSEIPGYK.S
49	67	2	2358.96	-0.55	1	44.9	30.4	95.00%	K.GNDTCPPCFNCMLPIFECK.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GNDTCPPCFNCMLPIFECK.Q
663	688	3	2796.25	0.79	0	82.1	30.4	95.00%	E.AGTDTNDIDNTIHQTTFTSSDGTTQR.E		R.NISDLEAGTDTNDIDNTIHQTTFTSSDGTTQR.E
49	65	2	2070.83	0.18	0	40.7	30.7	95.00%	K.GNDTCPPCFNCMLPIFE.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GNDTCPPCFNCMLPIFECK.Q
171	178	2	897.56	-0.12	0	27	19.1	95.00%	K.ILQILNGK.I		K.ILQILNGK.I
733	741	2	1136.5	0.79	1	39.1	28.4	95.00%	K.YKDSVYYAE.L		K.YKDSVYYAELSQEIEEVLSEGDEESNVLNGDLPTGQQSAGFLQQLSILNSR.S
179	192	2	1659.79	0.43	0	86.8	29.2	95.00%	K.IPQITFACDKPNQE.C	Carbamidomethyl (+57)	K.IPQITFACDKPNQECNFQFWIDQLESFYCGLSDCAFEYDLEQNTSHYK.C
544	570	2	2827.45	0.029	0	72.8	25.1	95.00%	E.LVTSPLVLFLDEPTSGLDASNANNVIE.C		R.VSIACELVTSPLVLFLDEPTSGLDASNANNVIECLVR.L
84	106	2	2352	-0.37	1	101	31	95.00%	E.GFAGDDCSLPLCGGLSPDESGNK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.CECIEGFAGDDCSLPLCGGLSPDESGNK.D
663	689	3	2925.29	-0.063	1	89.1	30.4	95.00%	E.AGTDTNDIDNTIHQTTFTSSDGTTQRE.W		R.NISDLEAGTDTNDIDNTIHQTTFTSSDGTTQREWAHLAAHR.D
757	783	2	2857.46	2.2	0	70.8	25.6	95.00%	E.SNVLNGDLPTGQQSAGFLQQLSILNSR.S	Deamidation (+1)	K.DSVYYAELSQEIEEVLSEGDEESNVLNGDLPTGQQSAGFLQQLSILNSR.S
256	268	2	1437.65	0.073	1	40.6	29.9	95.00%	E.TIKGPGDFSCDLE.T	Carbamidomethyl (+57)	K.GSIDISDFLTETIKGPGDFSCDLETR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
18	ATC2_YEAST	23.53%	100%	22

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
490	511	2	2437.19	0.29	1	37.4	27.8	95.00%	E.NCSSSLRNDLLANIVLNSTAFE.N	Carbamidomethyl (+57)	K.VFEENCSSSLRNDLLANIVLNSTAFENR.D
432	446	2	1602.63	-0.78	1	102	29.4	95.00%	R.SCETMGSATAVCSDK.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.SCETMGSATAVCSDK.T
71	83	2	1432.73	1.2	1	27.9	27.3	94.70%	K.NAGISLPEISNYR.K		K.NAGISLPEISNYR.K
760	770	2	1161.61	0.59	0	34.2	27.6	95.00%	R.MVTGDNILTAK.A		R.MVTGDNILTAK.A
447	459	2	1419.74	1.7	1	64.5	27	95.00%	K.TGTLTENVMTVVR.G		K.TGTLTENVMTVVR.G
868	887	2	2165.09	0.27	1	98.3	25.9	95.00%	R.EASDIILMTDDFSAIVNAIK.W		R.EASDIILMTDDFSAIVNAIK.W
574	583	2	1073.61	2.3	1	62.8	24.1	95.00%	K.TETALLSLAR.L		K.TETALLSLAR.L
727	741	2	1591.93	-0.13	0	49.6	15.6	95.00%	K.GLILDGLLGIQDPLR.A		K.GLILDGLLGIQDPLR.A
709	726	3	1988.02	0.6	1	39.6	26.1	95.00%	R.DKDSPNIAALDLLFNSQK.G		R.DKDSPNIAALDLLFNSQK.G
37	46	2	1137.58	2	0	31.9	28.4	95.00%	K.SQLSDLHNPK.S		K.SQLSDLHNPK.S

584	597	2	1585.88	0.5	1	61.3	22.8	95.00%	R.LSLGLQPGELQYLR.D		R.LSLGLQPGELQYLR.D
54	64	2	1303.64	-0.32	1	47.4	28.1	95.00%	R.LFGYESNSLFK.Y		R.LFGYESNSLFK.Y
711	726	2	1744.9	0.39	0	75.9	26.4	95.00%	K.DSPNIAALDLLFNSQK.G		K.DSPNIAALDLLFNSQK.G
497	513	2	1902.98	0.56	1	80.2	26.3	95.00%	R.NDLLANIVLNSTAFENR.D		R.NDLLANIVLNSTAFENR.D
831	850	2	1886.91	1.3	0	103	29	95.00%	K.GMGDVVAVTGDGTNDAPALK.L		K.GMGDVVAVTGDGTNDAPALK.L
264	287	3	2651.22	-0.64	1	62.8	29.7	95.00%	K.FNSIDSHNHSKPLDIGDVNEDGNK.I		K.FNSIDSHNHSKPLDIGDVNEDGNK.I
688	698	2	1275.59	0.79	1	53.8	29.9	95.00%	R.AISVAHKDFCE.C	Carbamidomethyl (+57)	R.AISVAHKDFCECDSWPPEQLR.D
90	99	2	1163.52	-0.79	1	36.9	29.2	95.00%	K.NYGDNSLPER.I		K.NYGDNSLPER.I
288	298	2	1221.58	-0.068	0	81.2	29.1	95.00%	K.IADCMLISGSR.I	Carbamidomethyl (+57)	K.IADCMLISGSR.I
252	259	2	946.49	0.6	0	26.9	27.9	92.70%	K.FPVDNSLR.D		K.FPVDNSLR.D
435	452	2	1828.82	0.39	1	86.8	30.9	95.00%	E.TMGSATAVCSDKTGTLTE.N	Carbamidomethyl (+57)	R.SCETMGSATAVCSDKTGTLTENVMTVVR.G
16	33	2	2060.91	0.91	1	53.9	30.9	95.00%	E.NNKPSYTGNENGVYDNFK.L	Deamidation (+1)	R.QDENSALLANNENNKPSYTGNENGVYDNFK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
19	ATC9_YEAST	23.37%	100%	27

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1178	1196	2	2031.87	1.2	0	69.1	31.1	95.00%	K.LDYTVGFCGDGANDCGALK.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.LDYTVGFCGDGANDCGALK.A
947	958	2	1488.65	-0.35	0	76.3	30.4	95.00%	K.TNNDDVYWSFTK.G		K.TNNDDVYWSFTK.G
1049	1065	2	1820.91	0.51	0	60.3	28.3	95.00%	R.TIMCTGDNILTAISVGR.E	Carbamidomethyl (+57)	R.TIMCTGDNILTAISVGR.E
443	464	2	2489.17	-0.73	0	65.4	29.2	95.00%	K.TNNNWIDPDWVDLSTVSNGLTK.G	Deamidation (+1)	K.TNNNWIDPDWVDLSTVSNGLTK.G
914	930	3	1973.93	1.4	1	26.1	29	95.00%	R.ENTFTDNDPHNFLGVVR.S		R.ENTFTDNDPHNFLGVVR.S
380	393	2	1748.89	0.1	0	36.8	27.2	95.00%	R.QWYNRPLSTVLPFE.N		R.QWYNRPLSTVLPFENYPNPSYEPNDINLSHHHANEINPNVPILITFEYR.Y
1153	1162	2	1148.66	1.3	0	54.9	22.8	95.00%	E.ILLNSSIYAR.M		R.DENEIPEEYLNEILLNSSIYAR.M
652	665	2	1396.79	0.63	0	79	20.9	95.00%	R.IAPGQTAALAMVVR.T		R.IAPGQTAALAMVVR.T
199	221	3	2438.11	0.71	1	65.3	30.3	95.00%	R.LGENSDTGFVYHSATHSSSSLSR.Y		R.LGENSDTGFVYHSATHSSSSLSR.Y
1021	1030	2	1225.69	0.79	0	57.2	22.6	95.00%	E.FLGFIIFQNK.L		R.EEVESNLEFLGFIIFQNK.L
915	930	2	1844.88	0.42	0	54.2	29.4	95.00%	E.NTFTDNDPHNFLGVVR.S		R.ENTFTDNDPHNFLGVVR.S
901	914	2	1560.79	-1.7	1	46.5	27.4	95.00%	E.IIPAVVHPDSNNRE.N	Deamidation (+1)	R.HEDDVFPENSEIIPAVVHPDSNNRENTFTDNDPHNFLGVVR.S
432	442	2	1356.7	0.5	0	30	27.2	95.00%	K.FIYSPLDDLFK.T		K.FIYSPLDDLFK.T
288	300	2	1695.81	-0.53	0	63.2	29	95.00%	K.FYPQYAPNLHYQR.F		K.FYPQYAPNLHYQR.F
264	278	3	1651.67	3.5	0	32.2	29.9	95.00%	R.GSFSGHDDVHNQHSE.Y		R.GSFSGHDDVHNQHSEYLKPDYHEK.F
823	835	2	1528.69	-0.19	0	64.3	29.9	95.00%	K.FSLNDCSSPLDFK.S	Carbamidomethyl (+57)	K.FSLNDCSSPLDFK.S
202	221	3	2138.96	0.48	0	61.3	30.2	95.00%	E.NSDTGFVYHSATHSSSSLSR.Y		R.LGENSDTGFVYHSATHSSSSLSR.Y
809	817	2	1048.56	0.54	1	76.1	27.2	95.00%	K.FGELLSDIR.Q		K.FGELLSDIR.Q
639	649	2	1296.68	-0.48	0	35.5	25.5	95.00%	K.SFLYNGTNIIR.A		K.SFLYNGTNIIR.A
97	109	2	1401.71	0.34	1	44.5	27.8	95.00%	E.SEPLVLSSAEQSR.S		R.LTESEPLVLSSAEQSR.S
1	14	2	1651.77	-0.58	0	92.7	29.4	95.00%	-.MDIPSSNQIQHGQR.S	Acetyl (+42)	-.MDIPSSNQIQHGQR.S
619	638	2	2384.06	-1.3	0	150	30.8	95.00%	E.TMYQLCDDFQSTQISSFVSK.S	Carbamidomethyl (+57)	K.FPATEETMYQLCDDFQSTQISSFVSK.S
152	163	2	1351.68	-0.23	1	39.1	27.9	95.00%	E.QDRIYGTGLSSR.R		R.FFTQEQISNAEGASTLENTDYDMAWDATPAYEQDRIYGTGLSSR.R
851	864	2	1488.75	0.59	0	60.9	28.4	95.00%	R.SVDGNLLGDPLDFK.M		R.SVDGNLLGDPLDFK.M
760	768	2	1049.53	0.86	0	36.2	28.6	95.00%	K.GIFCISPTR.L	Carbamidomethyl (+57)	K.GIFCISPTR.L
279	287	3	1191.59	1	1	21.6	28.3	90.70%	E.YLKPDYHEK.F		R.GSFSGHDDVHNQHSEYLKPDYHEK.F
1113	1122	2	1087.56	0.26	1	90.7	26.5	95.00%	K.LGNNSVESLR.E		K.LGNNSVESLR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
20	KTR1_YEAST	39.19%	100%	15								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
46	57	2	1247.6	-0.076	0	69.9	29.2	95.00%	K.YSTVLSSGSGYK.Y		K.YSTVLSSGSGYK.Y	
327	352	5	3083.43	-0.94	1	45.1	28.3	95.00%	R.SEIHHFGDIGYYHVPFHSCPIDTSIR.L	Carbamidomethyl (+57)	R.SEIHHFGDIGYYHVPFHSCPIDTSIR.L	
281	288	2	956.55	1	0	34.8	25.7	95.00%	E.IAALDLWR.S		K.FMEAHPELIHENNMLDFVSDDQGLSYNLCHFWSNFEIAALDLWR.S	
83	92	2	1137.59	-0.012	1	42.2	26.7	95.00%	R.DLYSLAESIK.S		R.DLYSLAESIK.S	
203	213	2	1423.65	0.71	0	61.6	30.5	95.00%	K.LHCDIDYDVFK.F	Carbamidomethyl (+57)	K.LHCDIDYDVFK.F	
185	196	2	1695.71	-1.4	0	43	31.2	95.00%	R.HPLMDDYDWYWR.V		R.HPLMDDYDWYWR.V	
310	328	3	2040.01	0.73	1	44.5	28.3	95.00%	R.WGDAPVHSIGAALFLDRSE.I		R.WGDAPVHSIGAALFLDRSEIHHFGDIGYYHVPFHSCPIDTSIR.L	
163	172	2	1185.6	-0.0046	0	45	27.1	95.00%	R.IIYGDSISYR.H		R.IIYGDSISYR.H	
329	352	5	2867.36	0.94	0	30.8	28.7	95.00%	E.IHHFGDIGYYHVPFHSCPIDTSIR.L	Carbamidomethyl (+57)	R.SEIHHFGDIGYYHVPFHSCPIDTSIR.L	
364	375	2	1531.64	-0.9	0	35	30.3	95.00%	K.DFTWHSYSCTTK.F	Carbamidomethyl (+57)	K.DFTWHSYSCTTK.F	
310	326	2	1823.93	-0.017	0	79.6	26.7	95.00%	R.WGDAPVHSIGAALFLDR.S		R.WGDAPVHSIGAALFLDR.S	
73	80	2	905.53	1.5	0	43.1	21.6	95.00%	K.ATFVTLVR.N		K.ATFVTLVR.N	
197	213	4	2105.02	0.65	1	21.1	29.4	94.10%	R.VEPDIKLHCDIDYDVFK.F	Carbamidomethyl (+57)	R.VEPDIKLHCDIDYDVFK.F	
289	302	2	1695.74	1.3	1	108	30.8	95.00%	R.SPAYSAYFDYLDRE.G		R.SPAYSAYFDYLDREGGFFYER.W	
177	184	2	1051.48	0.16	1	30.8	29.1	95.00%	R.FESGFFYR.H		R.FESGFFYR.H	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
21	A6ZYU5_YEAS7	17.99%	100%	10								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
534	543	2	1117.55	-0.1	0	39.7	29	95.00%	K.SASWVPTSQR.G		K.SASWVPTSQR.G	
1	12	2	1387.66	-0.5	0	48.4	29.6	95.00%	-.MNSTPDLISPQK.S	Acetyl (+42)/ Oxidation (+16)	-.MNSTPDLISPQK.S	
544	562	3	2213.97	-0.093	1	35.3	30.8	95.00%	R.GANYDADALMHDDQPFYKK.M	Oxidation (+16)	R.GANYDADALMHDDQPFYKK.M	
311	321	3	1294.72	0.14	1	21.6	22.4	95.00%	E.LFTGKPAMFKR.T		R.AAGSASWGELFTGKPAMFKR.T	
225	233	2	1153.52	0.85	0	47.9	30.1	95.00%	K.NYSNSVQWR.V	Deamidation (+1)	K.NYSNSVQWR.V	
302	320	3	1954.96	0.86	1	34.8	28.1	95.00%	R.AAGSASWGELFTGKPAMFK.R		R.AAGSASWGELFTGKPAMFK.R	
544	561	2	2069.88	0.14	0	95.8	30.6	95.00%	R.GANYDADALMHDDQPFYK.K		R.GANYDADALMHDDQPFYK.K	
36	56	2	2246.05	-0.005	1	72.5	30	95.00%	K.GVQDDFQAEADQVLTNPNTGK.G		K.GVQDDFQAEADQVLTNPNTGK.G	
279	289	2	1279.62	0.14	0	26.9	29.1	90.30%	K.VAPDHPFIQQE.L		K.VAPDHPFIQQELEVIEASVEEAR.A	
311	320	3	1138.62	0.43	0	21.7	22.5	95.00%	E.LFTGKPAMFK.R		R.AAGSASWGELFTGKPAMFK.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
22	A7A0C8_YEAS7	36.00%	100%	14								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
217	225	2	1001.55	-0.022	0	39	25.5	95.00%	R.TANDVLTIR.E		R.TANDVLTIR.E	
50	61	2	1498.63	-0.14	1	38.7	30.1	95.00%	R.MNFSHGSYEYHK.S		R.MNFSHGSYEYHK.S	
92	108	2	1869.84	0.58	0	64	30.5	95.00%	R.TGTTTNDVDYPIPPNHE.M		R.TGTTTNDVDYPIPPNHEMIFTTDDK.Y	
487	500	2	1340.67	-1	0	30.5	28.4	95.00%	K.AGAGHSNTLQVSTV.-		K.AGAGHSNTLQVSTV.-	
178	194	2	1723.9	0.28	1	70.8	25.7	95.00%	K.GVNLPGTDVDLPALSEK.D		K.GVNLPGTDVDLPALSEK.D	
397	409	2	1314.75	0.29	0	41.9	21.5	95.00%	K.AIIVLSTSGTTPR.L		K.AIIVLSTSGTTPR.L	
7	20	2	1499.84	0.92	1	28.5	22.5	95.00%	R.LTSLNVVAGSDLRR.T		R.LTSLNVVAGSDLRR.T	
31	41	2	1226.66	-0.27	1	53.6	25.4	95.00%	K.TNNPETLVALR.K		K.TNNPETLVALR.K	
357	369	2	1568.73	0.5	0	44.3	29.8	95.00%	E.QAIAYLPNYDDMR.N		K.GNYPINAVTTMAETAVIAEQAIAYLPNYDDMR.N	
414	425	2	1500.82	-0.66	0	49.1	23.6	95.00%	K.YRPNCPIILVTR.C	Carbamidomethyl (+57)	K.YRPNCPIILVTR.C	
73	86	2	1526.88	0.049	0	43.4	17.9	95.00%	E.LYPGRPLAIALDTK.G		K.SEELYPGRPLAIALDTK.G	
287	312	4	2934.45	1.1	1	37.3	27.1	95.00%	K.SNLAGKPVICATQMLESMTYNPRPTR.A	Carbamidomethyl (+57)	K.SNLAGKPVICATQMLESMTYNPRPTR.A	
92	116	3	2821.27	-0.99	1	45.7	30.3	95.00%	R.TGTTTNDVDYPIPPNHEMIFTTDDK.Y		R.TGTTTNDVDYPIPPNHEMIFTTDDK.Y	

287	302	2	1730.87	0.53	0	69.4	27.6	95.00%	K.SNLAGKPVICATQMLE.S	Carbamidomethyl (+57)	K.SNLAGKPVICATQMLESMTYNPR PTR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
23	KTR4_YEAST	35.34%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
353	360	2	989.56	1.7	0	47.4	25.8	95.00%	E.IVDLDFLR.S		K.NYDYTQGYSTCHFWTNFEIVDLD FLR.S
406	426	2	2476.01	-1.6	0	67	31.1	95.00%	R.DIGYHHTPYTNCPTCPADSDR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.DIGYHHTPYTNCPTCPADSDR.C
399	405	2	931.47	-0.13	0	31.6	27.4	95.00%	K.SSIHWFR.D		K.SSIHWFR.D
271	281	2	1417.67	-0.57	0	65.6	29.6	95.00%	K.INYDVFQFMNK.N		K.INYDVFQFMNK.N
75	82	2	947.48	0.93	0	51.4	27.8	95.00%	E.VLDSIMDR.L		K.TESADELPDHDAEVLDSIMDR.L
375	381	2	890.39	0.43	1	33.5	28.6	95.00%	K.GGFYYER.W		K.GGFYYER.W
196	213	2	2062.91	0.81	1	68	30.3	95.00%	E.FGTIGPDNWNMPDSIDRE.R		R.VVEFGTIGPDNWNMPDSIDRER. Y
335	352	2	2331.92	0.31	0	49.8	30.6	95.00%	K.NYDYTQGYSTCHFWTNFE.I	Carbamidomethyl (+57)	K.NYDYTQGYSTCHFWTNFEIVDLD FLR.S
406	435	4	3463.41	-0.044	1	26.9	30.5	95.00%	R.DIGYHHTPYTNCPTCPADSDRCN GNCVPGK.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Deamidation (+1)/ Carbamidomethyl (+57)	R.DIGYHHTPYTNCPTCPADSDRCN GNCVPGK.F
114	124	2	1268.71	0.22	1	46.8	23.6	95.00%	E.ISEPKVDNLVR.S		K.QLYEEFLLQEISEPKVDNLVR.S
196	212	2	1933.86	0.86	0	74.4	30.6	95.00%	E.FGTIGPDNWNMPDSIDR.E		R.VVEFGTIGPDNWNMPDSIDR.E
436	453	2	2251.01	-0.17	0	82.2	30.9	95.00%	K.FTPWSDLDNQNCQATWIR.H	Carbamidomethyl (+57)	K.FTPWSDLDNQNCQATWIR.H
135	142	2	857.53	-0.6	0	30.8	24.2	95.00%	K.GTILSLVR.N		K.GTILSLVR.N
389	398	2	1047.6	1.8	0	50	23.6	95.00%	R.SLALALFADK.S		R.SLALALFADK.S
245	254	3	1269.65	0.081	1	29.2	27.3	95.00%	K.EFYHHPLLSK.Y		K.EFYHHPLLSK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
24	A6ZQR8_YEAS7	18.52%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
955	967	2	1323.61	-0.15	0	58.7	30.1	95.00%	K.LGDASCAAPFTSK.L	Carbamidomethyl (+57)	K.LGDASCAAPFTSK.L
806	825	2	2144.92	-0.31	0	45.2	30.8	95.00%	K.DMGYQTLMCGDGTNDVGALK.Q	Carbamidomethyl (+57)	K.DMGYQTLMCGDGTNDVGALK.Q
118	132	2	1729.87	-0.12	1	63.3	27.3	95.00%	R.VTEAGSLQTFFQFQK.K		R.VTEAGSLQTFFQFQK.K
501	513	2	1301.66	1.2	1	52	27.9	95.00%	E.GLAGISADSENIR.H		K.TGTLTGEDLVFEGLAGISADSENI R.H
524	537	2	1391.85	0.35	0	60.2	15.4	95.00%	E.STILVIGAAHALVK.L		R.HLYSAAEAPESTILVIGAAHALVK. L
588	604	3	1756.92	-0.06	1	33.9	25.2	95.00%	K.RSASIASHNDALFAAVK.G		K.RSASIASHNDALFAAVK.G
121	132	2	1400.71	1.1	0	27.7	27.1	94.80%	E.AGSLQTFFQFQK.K		R.VTEAGSLQTFFQFQK.K
96	114	2	2014	0.24	0	33.4	28	95.00%	E.ATHILIYTTPNNGSDGIVE.I		K.NVNEATHILIYTTPNNGSDGIVEIQ R.V
589	604	2	1600.82	0.73	0	77	27	95.00%	R.SASIASHNDALFAAVK.G		R.SASIASHNDALFAAVK.G
481	488	2	1055.44	-0.15	0	39.8	28.6	95.00%	R.IDVCCFDK.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.IDVCCFDK.T
372	383	2	1280.64	-0.56	1	71.7	28.9	95.00%	K.TGFETSQGSLVR.V		K.TGFETSQGSLVR.V
930	954	2	2464.28	-1.6	1	96.7	24.9	95.00%	K.KPADLASLLLNSAGDAQGDEAPA LK.L		K.KPADLASLLLNSAGDAQGDEAPA LK.L
149	156	2	933.48	-0.03	1	31	27.1	95.00%	K.FLVDESPK.I		K.FLVDESPK.I
693	709	2	1765.94	0.9	0	69.6	23.6	95.00%	R.SIMITGDNPLTAVHVAK.E		R.SIMITGDNPLTAVHVAK.E
321	335	2	1697.86	-0.66	1	67.1	26.6	95.00%	K.LRPSEDNLQLDGVDK.I		K.LRPSEDNLQLDGVDK.I
968	979	2	1269.74	0.14	0	69.8	21.9	95.00%	K.LANVSAVTNIIR.Q		K.LANVSAVTNIIR.Q
355	371	2	1646.89	0.77	0	55.3	25.1	95.00%	K.SDIPPPPDGGALAIVTK.T		K.SDIPPPPDGGALAIVTK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
25	PPN1_YEAST	21.66%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
184	198	2	1707.81	-0.42	1	83.2	29.4	95.00%	R.TEAQIFDMNNIVADK.M		R.TEAQIFDMNNIVADK.M
335	343	2	1175.46	1.7	0	26.3	28.4	90.80%	K.NFDQSCYDK.F	Carbamidomethyl (+57)	K.NFDQSCYDK.F

137	150	2	1537.65	0.14	1	30.6	30.2	94.50%	K.AMSGCDSPVILMEE.T	Carbamidomethyl (+57)	K.AMSGCDSPVILMEETLR.W
72	83	2	1334.83	0.13	1	35.5	12.6	95.00%	R.LGLTPREPVIIK.D		R.LGLTPREPVIIK.D
582	595	2	1558.85	0.69	0	51.7	23.7	95.00%	E.LGPAYVPQLFTPTR.F		K.YELGPAYVPQLFTPTR.F
186	198	2	1477.72	0.12	0	56.2	28.2	95.00%	E.AQIFDMNNIVADK.M		R.TEAQIFDMNNIVADK.M
97	126	5	3382.63	-0.3	1	31.1	28.2	95.00%	R.FLHITDIHPDPYYVEGSSIDAVCHTGKPSK.K	Carbamidomethyl (+57)	R.FLHITDIHPDPYYVEGSSIDAVCHTGKPSK.K
596	605	2	1258.62	1.1	1	30.5	28.4	95.00%	R.FVQFYADLEK.I		R.FVQFYADLEK.I
97	111	2	1857.89	0.046	0	74.7	29	95.00%	R.FLHITDIHPDPYYVE.G		R.FLHITDIHPDPYYVEGSSIDAVCHTGKPSK.K
482	500	2	2067.08	0.23	0	83.6	25.1	95.00%	R.YSIVNIGGSVIPTFNPSFR.I		R.YSIVNIGGSVIPTFNPSFR.I
112	126	2	1542.75	1.7	0	56.9	28.8	95.00%	E.GSSIDAVCHTGKPSK.K	Carbamidomethyl (+57)	R.FLHITDIHPDPYYVEGSSIDAVCHTGKPSK.K
263	274	2	1247.68	0.62	1	34.2	26.2	95.00%	R.SASFLTEVIPGK.L		R.SASFLTEVIPGK.L
580	595	2	1850.96	-0.87	1	36.8	26.6	95.00%	K.YELGPAYVPQLFTPTR.F		K.YELGPAYVPQLFTPTR.F
60	68	2	1043.55	1.1	0	34	27.8	95.00%	E.SLQLLNDIE.F		R.GDNESLQLLNDIEFTR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
26	A6ZMV7_YEAS7	26.47%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
194	202	2	1010.59	1.2	0	31.1	20.1	95.00%	E.VLPQSVVNR.L		R.LVLYVGVAGLISNVVGLFLFHDHGSDSLHSHSHGSVESGNNDLDIESNATHSHSHASLPNDNLAIDEDAISSPGPSGQIGEVLPQSVVNR.L
385	399	2	1521.74	0.45	1	72.7	29.1	95.00%	R.RFSIIAGGSPSSSQE.A		R.RFSIIAGGSPSSSQEAFDSHGNTEHGR.K
358	372	2	1699.84	0.52	0	59.4	27.9	95.00%	K.IFHQHGIHSATVQPE.F		K.IFHQHGIHSATVQPEFVSGDVNEDIR.R
386	399	2	1365.64	1.2	0	91.7	29.6	95.00%	R.FSIIAGGSPSSSQE.A		R.FSIIAGGSPSSSQEAFDSHGNTEHGR.K
293	309	2	1854.02	-1	0	106	21.5	95.00%	R.ILLQATPSTISADQIQR.E		R.ILLQATPSTISADQIQR.E
415	442	3	2962.24	0.38	0	95.4	30.5	95.00%	R.SPTAYGATTASSNCIVDDAVNCNTSNCL.-	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.SPTAYGATTASSNCIVDDAVNCNTSNCL.-
414	442	3	3118.34	-0.6	1	78.3	31.2	95.00%	K.RSPTAYGATTASSNCIVDDAVNCNTSNCL.-	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.RSPTAYGATTASSNCIVDDAVNCNTSNCL.-
102	112	2	1335.71	-0.61	1	45.7	25.6	95.00%	R.LIEPQEIQNPR.L		R.LIEPQEIQNPR.L
357	372	2	1827.94	0.27	1	46.3	27	95.00%	R.KIFHQHGIHSATVQPE.F		R.KIFHQHGIHSATVQPEFVSGDVNEDIR.R
400	408	2	976.39	3.5	0	27.7	29	92.20%	E.AFDSHGNTE.H		R.FSIIAGGSPSSSQEAFDSHGNTEHGR.K
373	383	2	1249.59	0.7	1	55.2	28.9	95.00%	E.FVSGDVNEDIR.R		K.IFHQHGIHSATVQPEFVSGDVNEDIR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
27	A6ZR77_YEAS7	28.63%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
439	462	3	2674.22	0.17	0	44.1	30.3	95.00%	K.SQSQTYDSISHTQNSPFVPYSSSK.A		K.SQSQTYDSISHTQNSPFVPYSSSK.A
402	411	2	1107.55	-1.3	0	39.2	28.6	95.00%	R.ISSNPQSFTK.Q		R.ISSNPQSFTK.Q
321	339	3	2204.98	0.32	1	43.6	30.3	95.00%	R.LNDLKDDGHYDWMDLNGGK.G		R.LNDLKDDGHYDWMDLNGGK.G
273	295	2	2691.42	-1.5	1	56.7	22.9	95.00%	K.QKLNPDDLLLNNAIPYQFATYLK.Y		K.QKLNPDDLLLNNAIPYQFATYLK.Y
140	163	4	2969.51	-0.49	1	21	24.6	95.00%	R.AIHDHDLIYRDIKPDNFLISQYQR.I		R.AIHDHDLIYRDIKPDNFLISQYQR.I
468	484	3	1978.92	-0.85	1	43.5	30.2	95.00%	R.SNNEHNLPNHYTNLANK.N		R.SNNEHNLPNHYTNLANK.N
47	64	2	2016.04	1.1	1	60.2	26.4	95.00%	R.DSSIIMANEPVAIKFEPR.H		R.DSSIIMANEPVAIKFEPR.H
150	163	2	1735.89	-1.2	0	46.3	27.1	95.00%	R.DIKPDNFLISQYQR.I		R.DIKPDNFLISQYQR.I
275	295	2	2435.27	-1	0	63	24.3	95.00%	K.LNPDDLLLNNAIPYQFATYLK.Y		K.LNPDDLLLNNAIPYQFATYLK.Y
472	484	2	1534.76	0.12	0	71.4	28.3	95.00%	E.HNLPNHYTNLANK.N		R.SNNEHNLPNHYTNLANK.N
5	19	2	1591.85	0.44	0	69.6	25.3	95.00%	R.SSQHIVGIHYAVGPK.I		R.SSQHIVGIHYAVGPK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
28	YA11B_YEAST	16.01%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	65	2	1587.74	1.1	0	52.3	29.9	95.00%	K.ANSQQTTTPASSAVPE.N		K.ANSQQTTTPASSAVPENPHHASPQTAQSHSPQNGPYPQQCMMTQNQANPSGWSFYGHPSMIPYTPYQMSPMYFPPGPQSQFPQYPSSVGTPLSTPSPESGNTFTDSSSADSDMTSTK.K
400	419	2	2073.92	-0.2	0	113	30.1	95.00%	R.AHNVSTSNNSPSTDNDSISK.S		R.AHNVSTSNNSPSTDNDSISK.S
625	644	2	2328.01	0.54	0	73.7	31.3	95.00%	E.SDVDWSSAIDYQCPDCLIGK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.NNTITYFNESDVDWSSAIDYQCPDCLIGK.S
471	491	3	2226.08	-0.67	0	88.7	29	95.00%	R.SAHHIHSASSNPDINVVDAQK.R		R.SAHHIHSASSNPDINVVDAQK.R
1151	1178	3	2885.41	-0.54	0	59.2	28.1	95.00%	E.LPPINSHQTNSSLGGIGDSNAYTTINSK.K		K.ELPPINSHQTNSSLGGIGDSNAYTTINSK.K
148	167	2	2065.88	0.33	1	86.6	30.8	95.00%	E.SGNTFTDSSSADSDMTSTKK.Y		K.ANSQQTTTPASSAVPENPHHASPQTAQSHSPQNGPYPQQCMMTQNQANPSGWSFYGHPSMIPYTPYQMSPMYFPPGPQSQFPQYPSSVGTPLSTPSPESGNTFTDSSSADSDMTSTKK.Y
560	568	2	1163.53	-1.8	0	29.8	29.4	94.60%	K.YGDFYWVSK.K		K.YGDFYWVSK.K
25	39	2	1638.78	-0.86	1	78.9	29.3	95.00%	K.EVHTNQDPLDVSASK.T		K.EVHTNQDPLDVSASK.T
1093	1113	3	2202.09	-0.77	1	34.9	28.2	95.00%	R.SPSIDASPPENNSSHNIVPIK.T		R.SPSIDASPPENNSSHNIVPIK.T
958	972	2	1525.69	0.052	0	39.9	30	95.00%	K.AVSPTDSTPPSTHTE.D		K.AVSPTDSTPPSTHTEDSK.R
1621	1632	2	1318.72	-0.46	0	43.7	25.8	95.00%	K.SQIGNIYLLNGK.V		K.SQIGNIYLLNGK.V
308	315	2	989.52	0.32	0	31.3	28.1	95.00%	K.VACQLIMR.G	Carbamidomethyl (+57)	K.VACQLIMR.G
1605	1620	2	1787.87	0.79	0	71.7	28.7	95.00%	K.LVAISDASYGNQPYYK.S		K.LVAISDASYGNQPYYK.S
148	166	2	1953.78	0.7	0	94.2	30.7	95.00%	E.SGNTFTDSSSADSDMTSTK.K	Oxidation (+16)	K.ANSQQTTTPASSAVPENPHHASPQTAQSHSPQNGPYPQQCMMTQNQANPSGWSFYGHPSMIPYTPYQMSPMYFPPGPQSQFPQYPSSVGTPLSTPSPESGNTFTDSSSADSDMTSTK.K
3	24	3	2296.09	0.81	0	71.7	29.8	95.00%	E.SQQLSQHSPISHGSACASVTSK.E	Carbamidomethyl (+57)	-.MESQQLSQHSPISHGSACASVTSK.E
1	24	3	2598.18	-0.31	1	74.4	30.3	95.00%	-.MESQQLSQHSPISHGSACASVTSK.E	Acetyl (+42)/ Carbamidomethyl (+57)	-.MESQQLSQHSPISHGSACASVTSK.E
1234	1242	2	1115.51	0.078	1	55.2	28.4	95.00%	R.YDEAITYNK.D		R.YDEAITYNK.D
658	681	4	2906.4	-0.29	0	21.1	29.4	94.20%	K.YQNSYEPFQYLHTDIFGPVHNLPK.S		K.YQNSYEPFQYLHTDIFGPVHNLPK.S
958	975	2	1855.84	-0.6	1	47.1	30.4	95.00%	K.AVSPTDSTPPSTHTEDSK.R		K.AVSPTDSTPPSTHTEDSK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
29	COS1_YEAST	30.97%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
157	167	2	1275.75	0.92	1	50	21.3	95.00%	R.TTLLEPFSLKK.D		R.TTLLEPFSLKK.D
102	108	2	935.49	1.7	0	31	27.4	95.00%	K.QLIQFCK.E	Carbamidomethyl (+57)	K.QLIQFCK.E
186	193	2	953.5	0.6	1	54.1	26.6	95.00%	E.ALGVYFRE.V		K.DSVPYIEEALGVYFREVEK.Q
113	123	2	1283.51	0.84	0	38.3	28.9	95.00%	E.NTPSSDPHDWE.V		K.EVTENTPSSDPHDWEVVAANLNSYLYENK.A
291	300	2	1194.6	1.9	0	35.2	28.7	95.00%	K.MQFLSTIINE.Q		K.MQFLSTIINEQESGANGWDEIAK.K
357	369	2	1544.86	0.83	1	48.5	22.9	95.00%	R.ALSLNVELWPYIK.E		R.ALSLNVELWPYIK.E
22	33	3	1442.83	0.91	1	35.7	20.9	95.00%	E.SQKIVLPQDLFR.S		K.QLESQKIVLPQDLFR.S
143	156	2	1828.81	0.87	1	75.3	30.6	95.00%	K.YFFFNAMVCQEAFR.T	Carbamidomethyl (+57)	K.YFFFNAMVCQEAFR.T
102	109	2	1064.53	0.77	1	37.9	28.6	95.00%	K.QLIQFCKE.V	Carbamidomethyl (+57)	K.QLIQFCKEVTENTPSSDPHDWEVVAANLNSYLYENK.A
25	33	2	1099.64	-0.29	0	27.9	23.4	95.00%	K.IVLPQDLFR.S		K.IVLPQDLFR.S

206	216	2	1187.58	-0.27	1	57.3	28.3	95.00%	K.SWSPVGLEDAK.L		K.SWSPVGLEDAK.L
157	166	2	1147.65	0.67	0	30	23.3	95.00%	R.TTLLEPFSLK.K		R.TTLLEPFSLK.K
11	18	2	893.49	-0.02	0	26.5	25.4	95.00%	K.SVDVLSFK.Q		K.SVDVLSFK.Q
124	135	2	1355.66	0.94	0	41.7	28.9	95.00%	E.VVAANLNSYLYE.N	Deamidation (+1)	K.EVTENTPSSDPHDWEVVAANLN SYLYENK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
30	B3LFI3_YEAS1	33.71%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
240	245	2	987.43	1.6	0	27.1	28.9	91.40%	E.YDWYWR.V		R.HELLEEYDWYWR.V
344	358	3	1893.83	0.74	1	25.5	30.8	93.30%	E.YFDTLDHQGGFFYER.W		R.EYFDTLDHQGGFFYER.W
359	375	3	1791.97	1.1	0	32.8	24	95.00%	R.WGDAPVHSIAAALFLPK.D		R.WGDAPVHSIAAALFLPK.D
252	262	2	1448.66	-0.61	0	64.3	30.6	95.00%	K.LYCDINYDVFK.W	Carbamidomethyl (+57)	K.LYCDINYDVFK.W
376	398	5	2830.28	-0.96	1	41.7	30	95.00%	K.DKIHYFSDIGYHHPPYDNCPLDK. E	Carbamidomethyl (+57)	K.DKIHYFSDIGYHHPPYDNCPLDK. E
424	435	2	1409.72	-0.15	1	58.7	27.1	95.00%	K.EYYDAQGLVKPK.N		K.EYYDAQGLVKPK.N
105	117	2	1487.7	0.86	0	75.5	29.4	95.00%	K.TTMDYITPSFANK.A		K.TTMDYITPSFANK.A
408	423	2	1882.73	0.51	0	66.5	30.6	95.00%	E.CDQGNDFTFQGYSCGK.E	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.EVYNSNNCECDQGNDFTFQGYS CGK.E
226	233	2	1089.5	1.4	0	38.4	29.3	95.00%	R.YQSGFFWR.H		R.YQSGFFWR.H
282	296	2	1794.92	0.097	0	43.3	27.1	95.00%	E.VTIPTLWQTSMDFIK.K	Oxidation (+16)	K.VYGFTVSIHEYEVTIPTLWQTSM DFIK.K
425	435	3	1280.68	1.2	0	34	24.8	95.00%	E.YYDAQGLVKPK.N		K.EYYDAQGLVKPK.N
305	317	2	1452.67	0.19	0	66.3	29.9	95.00%	E.NNLMSFLSNDNGK.T		K.NPEYLDENNLMSFLSNDNGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
31	A6ZR26_YEAS7	13.95%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	9	2	912.51	3	0	38.6	24.3	95.00%	M.SSAPLLQR.T	Acetyl (+42)	-.MSSAPLLQR.T
15	24	2	1122.68	-0.56	1	32.8	16.9	95.00%	K.IALPTRVEPK.V		K.IALPTRVEPK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
32	B3LNF5_YEAS1	21.43%	100%	29

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1032	1049	2	1913.05	-0.0021	1	98.5	23.6	95.00%	K.IQGLEGIILTNIVSNSDK.V		K.IQGLEGIILTNIVSNSDK.V
1096	1106	2	1371.64	0.014	1	56.7	29.3	95.00%	E.CSLHLHGYTER.K	Carbamidomethyl (+57)	K.SLDECSLHLHGYTER.K
907	919	2	1487.68	-0.62	0	78	29.8	95.00%	R.SLVSSTDFFQDDK.N		R.SLVSSTDFFQDDK.N
1540	1558	2	2086.93	-0.0056	0	67.1	30.7	95.00%	E.HTSYTDQPTTTDVPDALPE.G		R.TGPSYSSLIHDQFLDEADDLLAG HDEDANDLSSFMDQGSNFEIEEDD VPTLEEEHTSYTDQPTTTDVPDALP EGNEENIDRPDSTAPSNENQ.-
1022	1031	2	1218.56	-0.43	1	28.2	29	92.90%	R.NTFGYVDFEK.I		R.NTFGYVDFEK.I
687	697	2	1220.79	1.6	0	23.2	10.8	91.30%	K.TVPVKPLQLVK.G		K.TVPVKPLQLVK.G
1217	1232	2	1685.84	-0.38	1	84.3	27.8	95.00%	R.FLLFGEAADIGGSSFR.T		R.FLLFGEAADIGGSSFR.T
1178	1189	2	1319.59	0.6	0	53	29.9	95.00%	E.TDSISYSTDFGK.T		K.TPHQWEYGDHGGILVLVPENSET DSISYSTDFGK.T
854	866	2	1405.59	1.1	0	47	29.7	95.00%	E.CHAVAYLTNDGGE.T	Carbamidomethyl (+57)	K.NCESILSPECHAVAYLTNDGGET FTEMLDNAIHCEFAGSLFK.Y
1367	1379	3	1335.62	0.25	0	41.1	29.7	95.00%	K.LDAPSSPHACPGK.E	Carbamidomethyl (+57)	K.LDAPSSPHACPGK.E
759	772	2	1502.71	-1	1	54.2	29.5	95.00%	R.GEAYISHDGGQTIR.R		R.GEAYISHDGGQTIR.R
854	870	2	1883.8	-0.046	1	69.2	30.4	95.00%	E.CHAVAYLTNDGGETFTE.M	Carbamidomethyl (+57)	K.NCESILSPECHAVAYLTNDGGET FTEMLDNAIHCEFAGSLFK.Y
1563	1577	2	1656.74	0.95	1	55.1	30.2	95.00%	E.NIDRPDSTAPSNENQ.-		R.TGPSYSSLIHDQFLDEADDLLAG HDEDANDLSSFMDQGSNFEIEEDD VPTLEEEHTSYTDQPTTTDVPDALP EGNEENIDRPDSTAPSNENQ.-
39	50	2	1392.73	0.56	0	65.2	26.7	95.00%	E.ILSFDDSNTLIR.K		K.TIAQDSFEILSFDDSNTLIR.K
445	455	2	1432.62	0.5	0	45.4	31.2	95.00%	E.NCSLQNMFYTR.E	Carbamidomethyl (+57)	K.VVDPDNADSFDCDITDFENCSLQ NMFYTR.E
126	136	2	1330.63	-0.81	1	45.6	29.4	95.00%	R.GCYIETHPLNK.N	Carbamidomethyl (+57)	R.GCYIETHPLNK.N
709	719	2	1189.57	0.013	1	33.2	28.6	95.00%	K.SVDISCEGVPK.K	Carbamidomethyl (+57)	K.SVDISCEGVPK.K

530	538	2	1119.52	0.98	0	39.2	27.6	95.00%	E.FYYSLDQGK.T		K.LAFDFPCLYAVGDYGNVIVAIPYNADEDDDPQSEFYYSLDQGK.T
871	879	2	1101.46	1.1	0	49.1	28.9	95.00%	E.MLDNAIHCE.F	Carbamidomethyl (+57)	K.NCESILSPECHAVAYLTNDGGETFTEMLDNAIHCEFAGSLFK.Y
76	89	3	1844.93	0.76	1	21.7	27.5	92.60%	E.ITWIYIDPFNRHDR.A		K.VEGIEDEITWIYIDPFNRHDR.A
1037	1049	2	1372.76	0.65	0	77.7	23.9	95.00%	E.GIILTNIVSNSDK.V		K.IQGLEGIILTNIVSNSDK.V
427	444	2	2072.82	0.68	0	35.7	30.5	95.00%	K.VVDPDNADSFDCDITDFE.N	Carbamidomethyl (+57)	K.VVDPDNADSFDCDITDFENCSLQNMFYTR.E
667	682	2	1908.9	0.55	0	68.5	29.5	95.00%	K.CVPDYNLIVLSDVCDK.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CVPDYNLIVLSDVCDK.T
414	426	2	1445.78	1.7	0	74.3	26	95.00%	K.ISVDNGLTWTVLK.V	Deamidation (+1)	K.ISVDNGLTWTVLK.V
1363	1379	3	1690.85	0.25	1	33.9	27.4	95.00%	E.GGLKLDAPSSPHACPGK.E	Carbamidomethyl (+57)	K.IPLSTCEGGLKLDAPSSPHACPGK.E
1563	1575	2	1414.64	2.6	0	64.4	30.1	95.00%	E.NIDRPDSTAPSNE.N		R.TGPSYSSLIHDQFLDEADDLLAGHDEDANDLSSFMDQGSNFEIEEDDVPTLEEEHTSYTDQPTTTDVPDALPEGNEENIDRPDSTAPSNENQ.-
196	210	2	1611.72	-0.43	1	74.5	29.9	95.00%	R.NENSAISISDCGFAK.T	Carbamidomethyl (+57)	R.NENSAISISDCGFAK.T
887	899	2	1599.67	-0.61	1	79.7	30.6	95.00%	K.YPSNEDMVMCQVK.E	Carbamidomethyl (+57)	K.YPSNEDMVMCQVK.E
1267	1279	2	1607.75	-1.1	1	62.2	29.8	95.00%	K.SNCLFGHQTEFLR.K	Carbamidomethyl (+57)	K.SNCLFGHQTEFLR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
33	A7A1A2_YEAS7	21.14%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
663	674	2	1229.66	-0.49	0	43.2	26.2	95.00%	R.NAVVQGIDSSLK.I		R.NAVVQGIDSSLK.I
135	144	2	1229.64	1.2	0	40.5	27.7	95.00%	E.NYGIHLNLMR.S		K.TVVSQPLMANETAYHYYYEENYGIHLNLMR.S
498	509	2	1339.65	-0.96	0	48	29	95.00%	K.VLSAPNHTVDCK.I	Carbamidomethyl (+57)	K.VLSAPNHTVDCK.I
514	525	2	1237.68	-0.013	0	54	23.2	95.00%	E.GPYGVTVPHIAK.L		K.IFLEGPYGVTVPHIAK.L
471	485	2	1826.87	-0.61	1	80.7	28.6	95.00%	R.HRDPNNPDQLTMYVK.A		R.HRDPNNPDQLTMYVK.A
453	470	2	2188.04	-0.1	1	100	29.8	95.00%	K.SAWFYSFQSHPFTVLSER.H		K.SAWFYSFQSHPFTVLSER.H
644	662	2	2252.94	0.036	0	124	30.9	95.00%	E.NNNITFYSCGPATFNDDFR.N	Deamidation (+1)/ Carbamidomethyl (+57)	K.LSELENNNITFYSCGPATFNDDFR.N
510	525	3	1739.96	-0.29	1	58.5	22.2	95.00%	K.IFLEGPYGVTVPHIAK.L		K.IFLEGPYGVTVPHIAK.L
51	67	2	1925.89	-0.35	1	122	30.1	95.00%	K.NINWLGSVTACAYENSK.S	Carbamidomethyl (+57)	K.NINWLGSVTACAYENSK.S
414	427	2	1464.73	1.3	0	48.1	27.6	95.00%	K.TATLSTTDDSNVIK.I		K.TATLSTTDDSNVIK.I
562	573	3	1533.8	0.98	0	19.5	26.3	90.40%	K.FYWIVNDLSHLK.W		K.FYWIVNDLSHLK.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
34	A6ZV88_YEAS7	17.36%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
138	143	2	705.44	0.11	0	27.5	17.8	95.00%	K.SIVLFK.F		K.SIVLFK.F
115	123	2	1076.5	0.63	1	30.5	29.3	95.00%	E.QFTVDELPE.S		R.FFANDVSLTVHDDSPLNISQSLSPIMEQFTVDELPESASDLLYEYSLDDK.S
157	168	2	1472.69	0.61	1	80.1	29.4	95.00%	E.FIDSCLSFLEDK.S	Carbamidomethyl (+57)	K.LDEFIDSCLSFLEDK.S
144	152	2	1058.49	1.6	0	39.9	28.1	95.00%	K.FTSDAYDLK.K		K.FTSDAYDLK.K
29	38	2	1145.53	2.9	1	29.9	29.7	94.30%	K.ESSSFISFDK.E		K.ESSSFISFDK.E
157	166	2	1229.57	1.7	0	37.4	29.6	95.00%	E.FIDSCLSFLE.D	Carbamidomethyl (+57)	K.LDEFIDSCLSFLEDK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
35	A6ZSR0_YEAS7	36.04%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
500	518	2	1955.01	0.34	0	50.3	25.7	95.00%	K.TVPPPDFTSMVTLPTGPAK.I		K.TVPPPDFTSMVTLPTGPAK.I
390	418	4	3266.58	0.75	1	28.7	27.9	95.00%	K.DMHVPNTSYVIPAGYHVLVSPGYTHLRDE.Y		K.DMHVPNTSYVIPAGYHVLVSPGYTHLRDEYFPNAHQFNIHR.W
219	234	2	1876.91	-0.27	1	118	28.9	95.00%	R.AKLDTDFAYLYSDLDK.G		R.AKLDTDFAYLYSDLDK.G
235	252	2	2160.12	0.77	1	57.6	25.4	95.00%	K.GFTPINFVFPNLPLEHYR.K		K.GFTPINFVFPNLPLEHYR.K
275	289	2	1789.85	-0.74	1	44.9	29.8	95.00%	K.NNDIQDRDLIDSLMK.N	Deamidation (+1)	K.NNDIQDRDLIDSLMK.N
203	210	2	925.47	1.6	0	39.4	27.7	95.00%	E.MTIFTASR.S		R.TTGTIDVMVTQPEMTIFTASR.S
117	136	2	2060.06	-0.25	1	69.1	25.2	95.00%	K.LADVSAEAAYAHLTTPVFGK.G		K.LADVSAEAAYAHLTTPVFGK.G
190	210	2	2298.13	0.69	1	63.9	28.1	95.00%	R.TTGTIDVMVTQPEMTIFTASR.S		R.TTGTIDVMVTQPEMTIFTASR.S

124	136	2	1374.73	0.86	0	62.7	26.6	95.00%	E.AAYAHLTTPVFGK.G		K.LADVSAEAAYAHLTTPVFGK.G
455	467	2	1292.65	0.76	0	57.2	28.7	95.00%	K.GVSSPYLPFGGGR.H		K.GVSSPYLPFGGGR.H
137	146	2	1179.53	0.098	0	29.4	29.7	93.80%	K.GVIYDCPNSR.L	Carbamidomethyl (+57)	K.GVIYDCPNSR.L
445	454	2	1055.53	1.1	0	54.8	26.9	95.00%	E.VDYGFGAISK.G		R.WNNDSASSYSVGEEVDYGFGAISK.G
221	234	2	1677.78	0.23	0	113	30.1	95.00%	K.LDTDFAYLYSDLDK.G		K.LDTDFAYLYSDLDK.G
260	270	2	1182.63	-0.43	0	43.6	25.1	95.00%	K.AISGTYMSLIK.E		K.AISGTYMSLIK.E
363	371	2	1056.6	0.84	0	24	25.3	92.20%	E.MPLLNQTIK.E		K.ELTYDLLQEMPLLNQTIK.E
235	249	2	1703.89	0.56	0	28.5	25.7	95.00%	K.GFTPINFVFPNLPLE.H		K.GFTPINFVFPNLPLEHYR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
36	A6ZX34_YEAS7	28.89%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
196	215	2	2203.98	1.8	0	73.4	30.2	95.00%	E.QDFSPFGGYPASSFPLMIDE.K		R.SPTSSPGNESSASFSSNPFLGEQDFSPFGGYPASSFPLMIDEK.E
130	143	2	1387.73	-0.011	0	60.9	26.2	95.00%	R.AIASSPSLNSNLSK.N		R.AIASSPSLNSNLSK.N
69	91	3	2500.16	0.34	0	85.4	29.7	95.00%	E.SLSSSVHYQPQGSDSSLLHDNSR.L		R.DGESLSSSVHYQPQGSDSSLLHDNSR.L
340	360	2	2476.05	-0.97	0	75.5	31.2	95.00%	R.TFYDGDDPYWTAPDVHYDATK.D		R.TFYDGDDPYWTAPDVHYDATK.D
594	607	2	1634.81	-0.38	0	67.4	28.9	95.00%	R.WFVGDTPTYTIHAK.A		R.WFVGDTPTYTIHAK.A
583	593	2	1357.58	0.2	0	56.3	29.8	95.00%	E.YLNDDDNGYIR.W	Deamidation (+1)	K.YAIEYLNDDDNGYIR.W
411	420	2	1103.57	0.8	0	32	27.2	95.00%	E.ISANLPNYGR.V		K.VCFTQGALEISANLPNYGR.V
697	704	2	897.42	1.2	0	36.6	29.6	95.00%	E.DAGYTFPK.N		R.IYQPSNAISVTCDPSDYPTYDYIQSHLNAFQNANLTTWEDAGYTFPK.N
114	129	2	1752.85	-0.64	0	40	28.8	95.00%	R.AVSTANDNSFLQPPHR.A		R.AVSTANDNSFLQPPHR.A
340	363	2	2833.2	-0.041	1	60.9	30.6	95.00%	R.TFYDGDDPYWTAPDVHYDATKDLE.W		R.TFYDGDDPYWTAPDVHYDATKDLEWYSPDASTTVNGTLQLR.M
579	593	2	1832.82	-0.55	1	80.2	30.8	95.00%	K.YAIEYLNDDDNGYIR.W		K.YAIEYLNDDDNGYIR.W
476	493	2	2013.86	-0.074	1	78	30.8	95.00%	K.LSICTCDGEDHPNQGVGR.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.LSICTCDGEDHPNQGVGR.G
183	195	2	1328.59	0.51	0	59.7	30.3	95.00%	E.SSASFSSNPFLGE.Q		R.SPTSSPGNESSASFSSNPFLGEQDFSPFGGYPASSFPLMIDEK.E
304	316	2	1358.66	0.13	0	41.9	28.8	95.00%	R.TSLVDPDTPDTAK.T		R.TSLVDPDTPDTAK.T
393	401	2	1049.5	-0.0072	0	40.2	28.7	95.00%	R.SGMLQSWNK.V		R.SGMLQSWNK.V
608	618	2	1234.62	-0.67	0	26.1	28.3	90.40%	K.ALHPDGNIGWR.R		K.ALHPDGNIGWR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
37	A6ZY55_YEAS7	32.57%	100%	23

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
529	548	2	2334.15	-1.4	1	32	28.6	95.00%	K.SVVTNEFQCSLIPPDLTTWK.I	Carbamidomethyl (+57)	K.SVVTNEFQCSLIPPDLTTWK.I
307	320	2	1474.73	-0.22	0	93	28.7	95.00%	E.ILDTTDNINSAGNK.S		K.EILDTTDNINSAGNK.S
585	590	2	738.41	0.91	0	27.2	26.4	95.00%	E.FFQLGK.D		K.LNSDDSLSPDEFFQLGK.D
306	320	2	1603.77	-0.45	1	80.9	29.4	95.00%	K.EILDTTDNINSAGNK.S		K.EILDTTDNINSAGNK.S
673	685	2	1511.74	-0.48	0	55.1	29.2	95.00%	R.NSPPDYGFILFSR.N		R.NSPPDYGFILFSR.N
78	90	2	1436.78	-0.22	1	68.3	25.2	95.00%	R.ILSVESSIIDFSK.G		R.ILSVESSIIDFSK.G
32	47	2	1817.74	-0.72	1	53.7	30.4	95.00%	K.VTAYDYDNPNDSGMEK.L		K.VTAYDYDNPNDSGMEK.L
295	305	2	1190.64	-0.68	0	48.6	26.5	95.00%	R.IIDDSIISTSK.E		R.IIDDSIISTSK.E
718	746	3	3131.33	-0.073	0	111	30.6	95.00%	K.HPHCSSTNYGSVASFGSQSTSASYDDVQR.Y	Carbamidomethyl (+57)	K.HPHCSSTNYGSVASFGSQSTSASYDDVQR.Y
570	584	2	1724.74	-0.18	1	52.1	31.2	95.00%	R.DQYKLNSDDSLSPDE.F		R.DQYKLNSDDSLSPDEFFQLGK.D
404	414	2	1292.72	0.064	0	48.2	22.4	95.00%	R.NHVVTNDLLLR.D		R.NHVVTNDLLLR.D
367	390	2	2565.24	0.43	0	52.5	28.1	95.00%	E.GSPLLLTDDNINQHPNMIVSSTAE.D		K.YVSISILDTVGNEGSPLLLTDDNINQHPNMIVSSTAEDTCIVMCHVGGLR.N
597	615	3	2019.96	0.19	1	34.6	29	95.00%	E.FDLTGPINNSQGSVDSGRR.V	Deamidation (+1)	R.LEEEFDLTGPINNSQGSVDSGRR.V
535	548	2	1704.86	0.12	0	30.1	27.5	95.00%	E.FQCSLIPPDLTTWK.I	Carbamidomethyl (+57)	K.SVVTNEFQCSLIPPDLTTWK.I

295	306	2	1319.68	0.6	1	32.8	26.8	95.00%	R.IIDDSIISTSKE.I		R.IIDDSIISTSKEILDTTDNINSAGNK.S
260	267	2	921.48	0.95	0	56.3	27.2	95.00%	E.FDTALIDK.A		K.MIDSSLEFDTALIDK.A
553	569	3	2051.12	1.3	1	37	21.9	95.00%	E.LVHSNELQNDLFQLLLR.D		K.ICLELVHSNELQNDLFQLLLR.D
342	353	2	1298.68	-0.63	1	30.8	26.1	95.00%	K.NILPSAVQSNEK.Y		K.NILPSAVQSNEK.Y
487	502	2	1699.94	0.93	0	58.7	22.5	95.00%	E.SITIGNVSTLPFPILE.I		R.FISADNGDIYLIALDESITIGNVSTLPFPILEIK.K
391	403	2	1516.7	0.63	0	61.2	30.5	95.00%	E.DTCIVMCHVGGLR.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.YVSISILDTVGNEGSPLLLTDDNINQHPNMIVSSTAEDTCIVMCHVGGLR.N
574	590	2	1910.89	0.092	1	68.5	29.5	95.00%	K.LNSDDSLSPDEFFQLGK.D		K.LNSDDSLSPDEFFQLGK.D
509	522	2	1462.69	-0.83	1	73.8	28.9	95.00%	R.SSGLSQTAINEDNK.F		R.SSGLSQTAINEDNK.F
60	70	2	1307.73	1.1	0	31.8	23.2	95.00%	E.FQNVNLFVSLK.I		K.LLNQCSVAFDQEFQNVNLFVSLK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
38	B3LGF8_YEAS1	18.36%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	208	2	1731.87	0.22	1	55.5	27.2	95.00%	K.SLHIVAPSPEVPVSGDE.I		K.SLHIVAPSPEVPVSGDEITSYGYGSIPQSIGDVENGLNPPYVENTSSDELVHDLTR.R
79	95	2	1817.92	0.92	1	80.2	27.3	95.00%	K.AVDIDTIDAQPLHEGPK.I		K.AVDIDTIDAQPLHEGPK.I
192	201	2	1048.56	0.84	0	39.2	27.4	95.00%	K.SLHIVAPSPE.V		K.SLHIVAPSPEVPVSGDEITSYGYGSIPQSIGDVENGLNPPYVENTSSDELVHDLTR.R
79	92	2	1535.75	0.12	0	72.2	29	95.00%	K.AVDIDTIDAQPLHE.G		K.AVDIDTIDAQPLHEGPK.I
209	225	2	1784.85	0.34	0	46.9	29.4	95.00%	E.ITSYGYGSIPQSIGDVE.N		K.SLHIVAPSPEVPVSGDEITSYGYGSIPQSIGDVENGLNPPYVENTSSDELVHDLTR.R
115	127	2	1478.66	0.32	1	60.3	29.4	95.00%	K.ANEDDLKPPSQHE.A		K.ANEDDLKPPSQHEACGNSALQSSITDFSDR.S
93	103	2	1199.53	1.1	1	29.9	29.8	94.30%	E.GPKIDDSPQDE.V		K.AVDIDTIDAQPLHEGPKIDDSPQDEVNSIK.G
145	161	2	1836.82	0.34	0	40.8	30.6	95.00%	R.SVSPLQSITSCNTPMSE.H	Carbamidomethyl (+57)	R.SVSPLQSITSCNTPMSEHELPVSSSNSFER.A
174	191	2	1947.9	0.77	1	87.7	30.2	95.00%	E.RADDMPVVQADNQTSSSK.S		R.SVSPLQSITSCNTPMSEHELPVSSSNSFERADDMPVVQADNQTSSSK.S
164	174	2	1221.6	0.8	1	47.6	29.2	95.00%	E.LPVSSSNSFER.A		R.SVSPLQSITSCNTPMSEHELPVSSSNSFER.A
175	191	2	1791.79	-0.45	0	73	30.9	95.00%	R.ADDMPVVQADNQTSSSK.S		R.ADDMPVVQADNQTSSSK.S
162	173	2	1331.6	1	1	68.8	30.4	95.00%	E.HELPVSSSNSFE.R		R.SVSPLQSITSCNTPMSEHELPVSSSNSFER.A
128	144	2	1827.81	0.45	0	114	30.3	95.00%	E.ACGNSALQSSITDFSDR.S	Carbamidomethyl (+57)	K.ANEDDLKPPSQHEACGNSALQSSITDFSDR.S
96	108	2	1458.68	-0.56	1	62.7	29.8	95.00%	K.IDDSPQDEVNSIK.G		K.IDDSPQDEVNSIK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
39	B3LS12_YEAS1	19.16%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
473	479	2	890.49	0.65	1	36.2	25.1	95.00%	R.YETLLPR.N		R.YETLLPR.N
521	533	3	1454.75	0.21	1	43.9	27.6	95.00%	R.QHQLEAGLFAVDK.S		R.QHQLEAGLFAVDK.S
391	403	2	1568.84	0.88	0	61.4	24.4	95.00%	E.IWFLDVSNTIHPK.W		R.SPDFKPVENNYDNSTNVPQEIWFLDVSNTIHPK.W
685	700	2	1708.74	-0.73	0	88.8	30.5	95.00%	R.ASAGACGGYIWCATHK.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.ASAGACGGYIWCATHK.T
726	740	2	1703.87	0.05	0	81.8	26.9	95.00%	R.LHIDAVNTVWSHANK.D		R.LHIDAVNTVWSHANK.D
113	122	2	1230.6	0.22	1	57.4	28.9	95.00%	K.HFNELSLTDR.C		K.HFNELSLTDR.C
87	99	2	1580.82	0.12	1	53.1	27.1	95.00%	E.LVPFYDQSIDTKR.S		K.VLIEAFGSPEVDPVDTIPVSPLELVPFYDQSIDTKR.S
87	98	2	1424.72	0.62	0	48.5	27.6	95.00%	E.LVPFYDQSIDTK.R		K.VLIEAFGSPEVDPVDTIPVSPLELVPFYDQSIDTK.R

604	616	2	1446.66	0.088	0	58.5	29.8	95.00%	E.ICSGQIAHMSTDK.K	Carbamidomethyl (+57)	R.QEAAVEICSGQIAHMSTDK.K
129	142	2	1683.8	-0.42	1	76.2	29.8	95.00%	R.TLYTLDDEWTNSVK.K		R.TLYTLDDEWTNSVK.K
274	282	2	1029.59	-0.022	1	30.5	24.8	95.00%	K.VLEQGFLPK.F		K.VLEQGFLPK.F
485	500	2	1838.88	0.53	0	71.1	29.7	95.00%	K.NFQNSLLIDPDHALNE.C		K.NFQNSLLIDPDHALNECDNTLTTEEYIFK.A
451	457	2	842.43	-0.024	0	23.8	24.4	92.40%	K.TGTVFYR.E		K.TGTVFYR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
40	A6ZWJ5_YEAS7	41.48%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
171	187	2	1857.91	-0.92	1	83.2	28.2	95.00%	R.QAITDSMNGDPELINIK.F		R.QAITDSMNGDPELINIK.F
129	140	2	1378.63	1	0	58.5	30	95.00%	R.DSMTQILQSIDE.V		R.DSMTQILQSIDEVQVK.F
306	313	2	997.49	0.37	1	26.5	29	90.00%	K.FISENNFK.S		K.FISENNFK.S
423	436	2	1585.7	-0.68	1	35.8	30.5	95.00%	R.SGSCGGHYFDIMKK.D	Carbamidomethyl (+57)	R.SGSCGGHYFDIMKK.D
34	46	2	1582.77	-0.5	1	68.5	28.7	95.00%	K.QMSEQYVTPYLPK.S		K.QMSEQYVTPYLPK.S
148	160	2	1556.73	0.56	0	65.3	29.6	95.00%	K.NFAYPWVFISQGE.L		K.NFAYPWVFISQGELDGMK.Q
210	223	2	1442.74	0.68	0	53.1	28	95.00%	E.SLISLANVPDGDSR.A		K.AAESLISLANVPDGDSR.A
119	128	2	1194.61	0.088	1	59.7	28.4	95.00%	K.ACFVSLITER.D	Carbamidomethyl (+57)	K.ACFVSLITER.D
239	250	3	1661.76	0.72	1	34.3	30.4	95.00%	R.HPVLDEFDWYWR.V		R.HPVLDEFDWYWR.V
207	223	2	1713.85	-0.71	1	51.3	28.1	95.00%	K.AAESLISLANVPDGDSR.A		K.AAESLISLANVPDGDSR.A
257	267	2	1465.67	0.14	0	63.5	29.8	95.00%	K.LYCDIDHDLFR.W	Carbamidomethyl (+57)	K.LYCDIDHDLFR.W
148	165	2	2101	-0.29	1	97.8	29.4	95.00%	K.NFAYPWVFISQGELDGMK.Q		K.NFAYPWVFISQGELDGMK.Q
396	422	3	3456.37	0.9	0	83.1	29.5	95.00%	K.YNNCPLNDDIWNQYNCNCDQGNDFTFR.S	Carbamidomethyl (+57)/Carbamidomethyl (+57)/Carbamidomethyl (+57)	K.YNNCPLNDDIWNQYNCNCDQGNDFTFR.S
129	144	2	1832.92	0.0052	1	44.3	27.1	95.00%	R.DSMTQILQSIDEVQVK.F		R.DSMTQILQSIDEVQVK.F
335	342	2	995.52	1.2	0	54.9	25.9	95.00%	E.IGNLNFYR.S		K.DSEDFNNCEFTSNFEIGNLNFYR.S
128	140	2	1534.73	1.1	1	51.1	29.9	95.00%	E.RDSMTQILQSIDE.V		K.ACFVSLITERDSMTQILQSIDEVQVK.F
423	435	2	1457.61	0.084	0	35.1	29.7	95.00%	R.SGSCGGHYFDIMK.K	Carbamidomethyl (+57)	R.SGSCGGHYFDIMK.K
100	113	3	1634.83	1.3	0	24.8	28.2	95.00%	E.TTLGFMVPSYINHR.G		K.SYGGNETTLGFMVPSYINHR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
41	A6ZSG0_YEAS7	11.34%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
713	731	2	2154.03	-0.56	1	55.2	28.6	95.00%	K.MIWQLPIADPTSTAPEQQE.Q		K.MIWQLPIADPTSTAPEQQEQNSHDAPNWSR.S
72	92	4	2353.11	-0.71	1	44.5	30.3	95.00%	K.RSVSSQSPIVHSSNNTLHHHE.H	Deamidation (+1)	K.RSVSSQSPIVHSSNNTLHHHEHQQHLPPTLESLSSK.S
163	172	2	1183.53	1.5	0	27.9	29.6	91.50%	E.INCQSPSHLE.N	Carbamidomethyl (+57)	R.FIIHDSHGHDLLIDEINCQSPSHLENNDQASNASSTESFTLR.E
24	36	2	1366.72	0.2	0	53.7	26.4	95.00%	E.VLTPTTSASTPHR.I		K.EEVLTPTTSASTPHR.I
353	380	3	3022.42	0.3	1	23.6	29.7	92.10%	E.SSSLMPPANTTATPLNSNHPSYNSIRHE.I		R.EDHPAPATESSSLMPPANTTATPLNSNHPSYNSIRHEIPHAAAQR.R
220	231	2	1353.69	-1	1	51.8	28.2	95.00%	R.TAAQDIHETQLK.T		R.TAAQDIHETQLK.T
73	92	3	2197.01	-0.4	0	33.9	30.3	95.00%	R.SVSSQSPIVHSSNNTLHHHE.H	Deamidation (+1)	R.SVSSQSPIVHSSNNTLHHHEHQQHLPPTLESLSSK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
42	GNP1_YEAST	11.16%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
14	32	2	2196.88	0.63	1	47.6	30.8	95.00%	E.GSSNMNMNRNDLDDVSHYE.M		R.NNEGSSNMNMNRNDLDDVSHYEMK.E
89	109	3	2058.91	0.58	0	29.9	30.7	95.00%	E.GSHANSPDSSNSNGTTPISTK.D	Deamidation (+1)	R.AEGSHANSPDSSNSNGTTPISTK.D
87	109	2	2258	-1.5	1	56.5	31.3	95.00%	R.AEGSHANSPDSSNSNGTTPISTK.D		R.AEGSHANSPDSSNSNGTTPISTK.D
539	546	2	844.43	-9.8	1	33.3	29	95.00%	K.VQGRSLGE.V		K.VQGRSLGEVGYK.S
418	431	2	1441.77	-0.0067	0	66.7	25.8	95.00%	K.ASPYVIAVSSHGVR.V		K.ASPYVIAVSSHGVR.V
123	132	2	1081.57	1.7	0	34.2	26.5	95.00%	K.SSYITVDGIK.Q		K.SSYITVDGIK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
43	YNL5_YEAST	26.55%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
215	226	2	1393.65	0.12	1	36.7	29.2	95.00%	R.RIDDANISTFNE.N		R.RIDDANISTFNENHTNSTENR.D
416	433	3	1941.04	1.2	1	37.5	23	95.00%	K.IKGPFTTVGYDLGGLFTR.V		K.IKGPFTTVGYDLGGLFTR.V
379	407	3	3197.55	-0.2	1	79.5	27.7	95.00%	R.YCLYDRPGYGLSDSPPAPISIAMVAESLR.Y	Carbamidomethyl (+57)	R.YCLYDRPGYGLSDSPPAPISIAMVAESLR.Y
354	369	2	1797.78	-0.95	1	52.9	30.3	95.00%	E.HGGYDTGYLSATWIEE.L		K.QPIILFEHGGYDTGYLSATWIEELYHLDK.I
37	52	2	1469.72	-0.9	1	82.9	28.2	95.00%	R.TLGAGSANGPAVNEGR.D		R.TLGAGSANGPAVNEGR.D
563	575	2	1430.7	-0.5	1	77.2	29	95.00%	R.DVTNNAESLQNVK.T		R.DVTNNAESLQNVK.T
465	487	3	2240.91	-2.2	1	27.6	31.1	95.00%	R.LLPPGRGDGDDGDDGNGNDGDGR.N	Deamidation (+1)	R.LLPPGRGDGDDGDDGNGNDGDGR.N
588	596	2	1117.53	1.9	0	34.2	28.8	95.00%	K.SALWGDWQR.D		K.SALWGDWQR.D
321	336	2	1987.86	-0.18	0	52.3	30.8	95.00%	K.TYQLHITCYGDVFDQE.N	Carbamidomethyl (+57)	K.TYQLHITCYGDVFDQENNTDLSENK.K
18	26	2	1041.43	0.93	1	28.1	28.7	93.30%	R.TDIDSEHPE.A		R.TDIDSEHPEAQPLLNNNHR.T
553	569	2	1854.9	0.21	1	38.1	29.3	95.00%	E.SVTSSILSYRDVTNNAE.S		K.FLESVTSSILSYRDVTNNAESLQNVK.T
379	404	2	2841.33	-2.9	0	48.3	29.7	95.00%	R.YCLYDRPGYGLSDSPPAPISIAMVAE.S	Carbamidomethyl (+57)	R.YCLYDRPGYGLSDSPPAPISIAMVAESLR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
44	A6ZVP9_YEAS7	34.25%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
94	109	2	1564.85	0.31	0	25	24.4	94.10%	K.ASLNVGNVLPLGSVPE.G		K.ASLNVGNVLPLGSVPEGTIVSNVEEKPGDR.G
81	92	2	1276.66	0.85	0	66.2	28.6	95.00%	E.GVHTGQFIYAGK.K		R.EEIFIANEGVHTGQFIYAGK.K
201	221	3	2158.03	0.47	0	44.3	29.2	95.00%	R.GVAMNPVDHPHGGGNHQHIGK.A		R.GVAMNPVDHPHGGGNHQHIGK.A
164	181	3	1748.07	0.86	1	21.9	10.8	95.00%	R.GVIGVIAGGGRVDKPLLK.A		R.GVIGVIAGGGRVDKPLLK.A
81	93	3	1404.75	0.65	1	50	26.5	95.00%	E.GVHTGQFIYAGKK.A		R.EEIFIANEGVHTGQFIYAGKK.A
93	109	2	1692.94	0.64	1	38.6	20	95.00%	K.KASLNVGNVLPLGSVPE.G		K.KASLNVGNVLPLGSVPEGTIVSNVEEKPGDR.G
129	145	2	1839.91	0.32	1	92	27.9	95.00%	R.ASGNYVIIIGHNPDENK.T		R.ASGNYVIIIGHNPDENK.T
199	221	4	2415.17	0.3	1	39.8	28.6	95.00%	K.TRGVAMNPVDHPHGGGNHQHIGK.A		K.TRGVAMNPVDHPHGGGNHQHIGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
45	B3LPA7_YEAS1	15.71%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
287	300	2	1397.69	-0.8	0	35.5	28.6	95.00%	R.NPGAWGPGIISSDK.S		R.NPGAWGPGIISSDK.S
504	513	3	1146.6	-0.18	1	23.8	27.2	95.00%	R.GISRDDLPFK.A		R.GISRDDLPFK.A
573	578	2	834.46	0.68	1	37	26.9	95.00%	R.FIWKLE.D		R.FIWKLEDIDIDSDR.R
591	600	2	1214.58	0.71	1	30.2	29.5	95.00%	E.AIIWEDDEPK.N		R.EIEAIIWEDDEPK.N
4	12	2	1022.54	0.18	0	29.1	25.1	95.00%	R.FSNIITSNK.W		R.FSNIITSNK.W
435	441	2	869.44	1.7	0	27.7	25.9	95.00%	K.QFGYVTR.Q		K.QFGYVTR.Q
83	89	2	810.42	1.1	0	25.5	26	93.50%	R.LQVVSHE.T		R.LQVVSHETDINEDEEEAHYEDK.H
4	15	2	1452.69	0.053	1	51.1	29.3	95.00%	R.FSNIITSNKWDE.K		R.FSNIITSNKWDEK.Q
37	45	2	1003.46	-0.32	1	48.3	29.1	95.00%	E.MEAIDPSNK.T		K.QNNIGEQSMQELPEDQIEHEMEAIDPSNK.T
62	82	2	2110.08	-0.67	0	120	26.6	95.00%	K.HGSLQGGAIADVNSITNSLTR.L		K.HGSLQGGAIADVNSITNSLTR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
46	YG35_YEAST	21.14%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
805	817	2	1313.73	0.3	0	28	24	95.00%	K.QNNVVSAVIAATK.N		K.QNNVVSAVIAATK.N
875	890	3	1873.06	0.37	1	54.2	16.9	95.00%	E.YKDDEPVLPILLFALK.Q		K.EYKDDEPVLPILLFALK.Q
651	661	2	1358.68	-0.59	1	42.2	28	95.00%	R.STVYRDYVQTK.F		R.STVYRDYVQTK.F

923	940	2	2053.07	1	0	38.1	25.3	95.00%	R.LASQSHLLHADNIFFLVE.T		R.LASQSHLLHADNIFFLVETGMLK.A
48	69	2	2353.04	0.8	0	96.7	30.4	95.00%	R.SYMSGFFTGGNSPMINNLSDSK.L		R.SYMSGFFTGGNSPMINNLSDSK.L
821	830	2	1071.57	1.3	0	35.6	25.1	95.00%	K.IDTIGNGLNR.G		K.IDTIGNGLNR.G
716	732	2	1882.84	-0.39	1	107	30.1	95.00%	K.NINADNIDYSAAEGFNR.I		K.NINADNIDYSAAEGFNR.I
48	75	3	3005.43	-0.094	1	64	28.4	95.00%	R.SYMSGFFTGGNSPMINNLSDSKLPISNK.Q		R.SYMSGFFTGGNSPMINNLSDSKLPISNK.Q
637	650	2	1547.77	-0.91	1	27.8	28.5	93.20%	K.LQTINGEYNGNVAR.S		K.LQTINGEYNGNVAR.S
173	189	3	1889.92	1.1	0	39.5	28.8	95.00%	E.DGYAGGYQSLRPSHNLR.F		R.GLQNSSLPELEDGYAGGYQSLRPSHNLR.F
850	865	2	1851.9	0.43	0	77.1	28.3	95.00%	R.NYQILSVAQNVFVNDE.Q		R.NYQILSVAQNVFVNDEQAVK.N
146	161	2	1770.89	0.38	1	51.2	27.7	95.00%	R.LLLSPASSNVDDDRNR.G		R.LLLSPASSNVDDDRNR.G
923	945	3	2583.35	0.043	1	80.2	22.3	95.00%	R.LASQSHLLHADNIFFLVETGMLK.A		R.LASQSHLLHADNIFFLVETGMLK.A
171	189	3	2132.04	0.85	1	31.3	29.2	95.00%	E.LEDGYAGGYQSLRPSHNLR.F		R.GLQNSSLPELEDGYAGGYQSLRPSHNLR.F
803	817	2	1498.85	0.73	1	88.9	21.1	95.00%	E.GKQNNVVSAVIAATK.N		R.LEEGKQNNVVSAVIAATK.N
891	902	3	1474.78	-0.6	1	23	25.9	95.00%	K.QYRPDIISEVQK.V		K.QYRPDIISEVQK.V
709	715	2	910.52	-0.13	0	25.1	21.2	94.20%	K.YLILDFK.N		K.YLILDFK.N
839	849	2	1242.64	-0.099	0	35.1	27.1	95.00%	R.NLMSLPTNTPR.N		R.NLMSLPTNTPR.N
850	869	2	2278.16	0.046	1	71.7	26	95.00%	R.NYQILSVAQNVFVNDEQAVK.N		R.NYQILSVAQNVFVNDEQAVK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
47	A6ZM54_YEAS7	33.16%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
356	366	2	1324.7	0.88	0	49.6	25.2	95.00%	K.LFTPMMLFVAR.K		K.LFTPMMLFVAR.K
83	93	2	1329.59	0.21	0	54	30.2	95.00%	E.YGWGSSFHFSR.F		R.LEDYNEATHSYYNVVTDFYEYGWGSSFHFSR.F
26	34	2	906.48	-0.12	0	49.7	27.2	95.00%	K.TGLSALMSK.N		K.TGLSALMSK.N
296	308	2	1555.82	0.5	0	61.4	25.5	95.00%	K.YVQNLANLATFFR.T		K.YVQNLANLATFFR.T
164	175	2	1486.71	-0.88	1	65.8	29	95.00%	K.KYNLSDQMDFVK.G		K.KYNLSDQMDFVK.G
140	157	2	2039.97	-0.087	0	71.7	28.9	95.00%	R.FTGCNVIGLNNNDYQIAK.A	Carbamidomethyl (+57)	R.FTGCNVIGLNNNDYQIAK.A
191	202	2	1358.66	-6.4	1	48.2	28.9	95.00%	K.VYAIEATCHAPK.L	Carbamidomethyl (+57)	K.VYAIEATCHAPK.L
354	366	3	1539.83	1	1	27.9	24.7	95.00%	K.SKLFTPMMLFVAR.K		K.SKLFTPMMLFVAR.K
225	233	2	1185.5	0.58	1	33.1	29	95.00%	E.WVMTDKYDE.N		K.VLKPGGTFAVYEWVMTDKYDENNPEHR.K
69	82	2	1707.74	0.88	0	40.1	30.6	95.00%	E.ATHSYYNVVTDFYE.Y		R.LEDYNEATHSYYNVVTDFYEYGWGSSFHFSR.F
120	135	2	1540.77	-1.1	0	69.9	28.3	95.00%	R.GDLVLDVGCGVGGPAR.E	Carbamidomethyl (+57)	R.GDLVLDVGCGVGGPAR.E
165	175	2	1358.62	-0.96	0	48.9	29.9	95.00%	K.YNLSDQMDFVK.G		K.YNLSDQMDFVK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
48	XPP_YEAST	25.10%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
519	537	2	1942.97	1.1	0	49.2	27.3	95.00%	E.TISSTGSNAAIIHYSPPVE.N		R.NFMGNSFETISSTGSNAAIIHYSPPVENSSMIDPTK.I
598	609	2	1287.66	0.75	0	26.5	28.3	91.30%	E.NTPGFNIDAIAR.Q		R.LIFPENTPGFNIDAIAR.Q
693	701	2	1138.53	0.98	0	29	29.7	93.00%	E.NMTVVPYCR.K	Carbamidomethyl (+57)	K.FENMTVVPYCR.K
362	376	2	1738.81	0.5	0	35	30.4	95.00%	E.TILFTNNPFNDDISE.Y		R.GSDIDYNPVFFSYVAINEDETILFTNNPFNDDISEYFK.I
189	199	2	1449.72	-0.49	1	31.8	28.2	95.00%	R.QELDYNWTLLR.Q		R.QELDYNWTLLR.Q
673	680	2	947.5	-0.55	1	35.2	27.4	95.00%	R.IESDMLIK.K		R.IESDMLIK.K
162	174	2	1498.67	-0.22	0	34.3	29.8	95.00%	R.DLLNFNDDHPDGK.S		R.DLLNFNDDHPDGK.S
145	161	2	1699.84	0.36	0	79.9	27.9	95.00%	R.AFISGFSGSAGVACITR.D	Carbamidomethyl (+57)	R.AFISGFSGSAGVACITR.D
422	435	2	1434.68	-0.49	0	74.3	30	95.00%	R.CLNTSTNANGAIAK.K	Carbamidomethyl (+57)/ Deamidation (+1)	R.CLNTSTNANGAIAK.K
436	453	3	2025.11	-0.14	1	55.1	20.6	95.00%	K.KMTAQNFAIIHSPIDVLK.S		K.KMTAQNFAIIHSPIDVLK.S
538	558	2	2404.09	-0.61	1	53.9	31.1	95.00%	E.NSSMIDPTKIYLCDSGSQFLE.G	Carbamidomethyl (+57)	R.NFMGNSFETISSTGSNAAIIHYSPPVENSSMIDPTKIYLCDSGSQFLEGTTDITR.T
653	665	2	1424.69	-0.0086	0	27.1	28.7	91.60%	R.AGNIISNEPGYYK.D		R.AGNIISNEPGYYK.D

593	609	2	1886.99	0.29	1	60.2	25.1	95.00%	R.LIFPENTPGFNIDAIAR.Q		R.LIFPENTPGFNIDAIAR.Q
12	24	4	1428.71	1.1	0	31.2	27.8	95.00%	R.AHSISHVPGTHMR.G		R.AHSISHVPGTHMR.G
437	453	3	1897.01	-0.1	0	45.2	23.6	95.00%	K.MTAQNFAIIHSPIDVLK.S		K.MTAQNFAIIHSPIDVLK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
49	MAM3_YEAST	26.06%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
241	251	2	1170.72	1.6	0	66.1	15.7	95.00%	E.VTIISAVLDLK.A		K.DEVTIISAVLDLK.A
264	277	2	1584.74	1.1	0	87.2	29.2	95.00%	E.NVFTMSADTILDDK.T	Oxidation (+16)	R.VEEIMTPIENVFTMSADTILDDK.T
609	619	2	1158.65	0.32	1	41.5	25.3	95.00%	K.NGIVESVITVK.G	Deamidation (+1)	K.NGIVESVITVK.G
258	277	2	2269.09	0.56	1	91.6	28.6	95.00%	E.IMTPIENVFTMSADTILDDK.T	Oxidation (+16)	R.VEEIMTPIENVFTMSADTILDDK.T
483	500	2	1888.02	0.89	0	70.7	24.2	95.00%	E.HGTIIPSNLASNPLNVNK.S		R.SNAVLSPTPQVTEHGTIIPSNLASNPLNVNK.S
683	691	2	1025.48	0.46	0	29.9	30.2	93.70%	R.SNFTDSLSR.T		R.SNFTDSLSR.T
595	608	2	1596.77	0.32	0	88.4	29.5	95.00%	E.NQNVTISTSYQNTK.N		R.NSPDSISIPNSGANHGNENQNVTISTSYQNTK.N
514	535	3	2380.18	0.71	1	46.7	27.9	95.00%	K.IITTHTPHSSKEPSPAPHSNDK.S		K.IITTHTPHSSKEPSPAPHSNDK.S
332	347	2	1899.87	1.2	0	47.5	29.9	95.00%	E.TSPNTSCLNILNYFQE.G	Carbamidomethyl (+57)	R.VLISYDPDDCLPISHFPLATLPETSPNTSCLNILNYFQEGK.A
434	457	3	2626.24	0.58	1	32.5	29.3	95.00%	E.SSPLLSPSNSNHPSEHPQQDLNNK.S		K.AADQADESSPLLSPSNSNHPSEHPQQDLNNK.S
282	289	2	926.46	0.074	0	27.1	25	95.00%	K.IFNSGFSR.I		K.IFNSGFSR.I
470	500	3	3211.68	-0.52	1	40	22.4	95.00%	R.SNAVLSPTPQVTEHGTIIPSNLASNPLNVNK.S		R.SNAVLSPTPQVTEHGTIIPSNLASNPLNVNK.S
577	594	2	1808.79	0.38	0	36.5	30.7	95.00%	R.NSPDSISIPNSGANHGNE.N		R.NSPDSISIPNSGANHGNENQNVTISTSYQNTK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
50	A6ZPW7_YEAS7	30.07%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
48	60	3	1482.8	0.81	1	58.7	25.3	95.00%	R.RQSILDHPVGSFK.G		R.RQSILDHPVGSFK.G
113	125	3	1452.83	0.063	1	26.7	22.3	95.00%	R.RLSVTLNNAGRPR.I		R.RLSVTLNNAGRPR.I
99	112	2	1503.72	0.25	0	33.7	28.8	95.00%	E.TYDPDTLAPALDGR.R		K.ESNDETYDPDTLAPALDGR.R
135	178	4	4456.06	0.081	1	66.6	28	95.00%	R.VSTASMAIHDDDYGSIQNSTIGDSGSILRPTASLTEMMSGGAGR.R		R.VSTASMAIHDDDYGSIQNSTIGDSGSILRPTASLTEMMSGGAGR.R
180	191	2	1381.66	0.28	0	65	29.3	95.00%	R.FTNNDMDSIVVK.R		R.FTNNDMDSIVVK.R
135	170	3	3708.74	0.09	0	42.6	27.9	95.00%	R.VSTASMAIHDDDYGSIQNSTIGDSGSILRPTASLTE.M		R.VSTASMAIHDDDYGSIQNSTIGDSGSILRPTASLTEMMSGGAGR.R
179	191	2	1537.76	0.051	1	55.7	28.1	95.00%	R.RFTNNDMDSIVVK.R		R.RFTNNDMDSIVVK.R
17	26	2	1210.68	1.1	0	36.8	22.1	95.00%	E.VHYISIPLNR.G		R.SEVHYISIPLNR.G
114	125	2	1296.73	-0.021	0	34.5	23.2	95.00%	R.LSVTLNNAGRPR.I		R.LSVTLNNAGRPR.I
484	506	3	2572.37	0.28	0	26.5	21.9	95.00%	K.TPLNARPIVSVLDVLMNVQHIDE.A		K.TPLNARPIVSVLDVLMNVQHIDEAASAIK.R
484	512	3	3113.69	-0.25	1	86.5	19.5	95.00%	K.TPLNARPIVSVLDVLMNVQHIDEAASAIK.R		K.TPLNARPIVSVLDVLMNVQHIDEAASAIK.R
27	47	2	2264.96	-0.49	0	91.3	31.2	95.00%	R.GSAFSPDDSVSQFQSDGFMTR.R		R.GSAFSPDDSVSQFQSDGFMTR.R
262	283	2	2391.13	-0.58	0	100	29.1	95.00%	R.CLDTDPTLISYADLGYAAFGTK.G	Carbamidomethyl (+57)	R.CLDTDPTLISYADLGYAAFGTK.G
15	26	3	1426.76	0.22	1	27.2	25	95.00%	R.SEVHYISIPLNR.G		R.SEVHYISIPLNR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
51	PDR5_YEAST	19.85%	100%	20

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
205	220	2	1648.77	-0.62	0	73	29.3	95.00%	K.SISSNTHGFDLGADTK.I		K.SISSNTHGFDLGADTK.I
95	109	2	1663.78	-0.8	1	45.4	30.2	95.00%	K.LDPNSENFSSAAWVK.N		K.LDPNSENFSSAAWVK.N
188	204	3	1783.04	0.64	0	23.4	17.2	95.00%	E.LLVVLGRPGSGCTTLLK.S	Carbamidomethyl (+57)	K.ETNTFQILKPMDGCLNPGELLVVLGRPGSGCTTLLK.S
412	427	2	1738.84	-1.2	1	95.7	29.2	95.00%	R.QTTADFLTSVTSPSER.T		R.QTTADFLTSVTSPSER.T

221	233	2	1431.69	-0.91	1	55.3	29.4	95.00%	K.ISYSGYSGDDIKK.H		K.ISYSGYSGDDIKK.H
338	349	2	1291.68	-0.26	1	35.4	26.5	95.00%	R.GLDSATALEFIR.A		R.GLDSATALEFIR.A
945	957	2	1588.76	-1.9	0	41	29.4	95.00%	R.SIGYCQQQDLHLK.T	Carbamidomethyl (+57)	R.SIGYCQQQDLHLK.T
286	297	2	1305.65	0.068	0	68.2	28.2	95.00%	E.VAMATYGLSHTR.N		R.ESYANHLAEVAMATYGLSHTR.N
873	881	2	1165.58	0.022	1	27.9	28.8	92.90%	R.NLCYEVQIK.A	Carbamidomethyl (+57)	R.NLCYEVQIK.A
436	445	3	1117.66	-0.44	1	26.3	20.5	95.00%	K.KGIHIPQTPK.E		K.KGIHIPQTPK.E
1128	1143	2	1676.74	0.59	0	32.5	31.1	95.00%	E.VVGAAPGSHANQDYYE.V		K.CPADANPAEWMLEVVGAAPGSHANQDYYEVWR.N
400	411	2	1522.62	-0.97	1	55.2	30.4	95.00%	K.YFEDMGYVCPSR.Q	Carbamidomethyl (+57)	K.YFEDMGYVCPSR.Q
1419	1439	2	2418.11	-0.28	0	76.3	30.3	95.00%	E.FTPPSGMTCGQYMEPYLQLAK.T	Carbamidomethyl (+57)	K.CADYELLEFTPPSGMTCGQYMEPYLQLAK.T
329	337	2	1196.5	-0.24	0	41.3	28.9	95.00%	K.FQCWDNATR.G	Carbamidomethyl (+57)	K.FQCWDNATR.G
1090	1101	2	1344.6	-0.29	1	37.5	29.9	95.00%	K.TVYFGDLGEGCK.T	Carbamidomethyl (+57)	K.TVYFGDLGEGCK.T
170	187	2	2033.96	0.0058	0	32.2	29.3	95.00%	E.TNTFQILKPMDGCLNPGE.L	Carbamidomethyl (+57)	K.ETNTFQILKPMDGCLNPGELLVVLGRPGSGCTTLLK.S
110	132	4	2641.21	0.82	0	38.6	30.1	95.00%	K.NMAHLSAADPDFYKPYSLGCAWK.N	Carbamidomethyl (+57)	K.NMAHLSAADPDFYKPYSLGCAWK.N
78	94	2	1801.85	-0.073	1	52.2	28.8	95.00%	E.GVNPIFSDPEAPGYDPK.L		K.SDAQSIFSSGVEGVNPIFSDPEAPGYDPK.L
49	65	2	1805.86	-0.99	0	112	29.5	95.00%	R.TLTAQSMQNSTQSAPNK.S		R.TLTAQSMQNSTQSAPNK.S
740	761	2	2366.16	0.65	0	68.5	27.7	95.00%	E.SVCTVVGAVPGQDYVLGDDFIR.G	Carbamidomethyl (+57)	R.GPAYANISSTESVCTVVGAVPGQDYVLGDDFIR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
52	A6ZKX6_YEAS7	50.55%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
221	246	4	2610.43	0.51	1	45	20.2	95.00%	R.NVPGVETANVASLNLLQLAPGAHLGR.F		R.NVPGVETANVASLNLLQLAPGAHLGR.F
272	288	2	1844.97	1.2	0	67.2	25.6	95.00%	K.VGYTLPSHIISTSDVTR.I		K.VGYTLPSHIISTSDVTR.I
15	44	3	3145.73	1.3	0	23.3	19.6	95.00%	E.ATANALPLPAVFSAPIRPDIVHTVFTSVNK.N		-.MSRPQVTVHSLTGEATANALPLPAVFSAPIRPDIVHTVFTSVNK.N
347	360	2	1462.8	-0.5	1	27.4	23.5	95.00%	K.TGTKPAAVFTETLK.H		K.TGTKPAAVFTETLK.H
289	308	2	2111.13	-0.098	1	66.7	22.7	95.00%	R.IINSSEIQSAIRPAGQATQK.R		R.IINSSEIQSAIRPAGQATQK.R
85	95	2	1183.49	-0.074	0	27.7	29.3	91.70%	R.SGQGAFGNMCR.G	Carbamidomethyl (+57)	R.SGQGAFGNMCR.G
258	271	2	1505.74	-0.27	1	76.6	29.2	95.00%	K.LDQVWGSETVASSK.V		K.LDQVWGSETVASSK.V
120	138	3	1819.02	0.55	0	28.8	21.6	95.00%	R.YATASAIAATAVASLVLAR.G		R.YATASAIAATAVASLVLAR.G
227	246	3	2015.13	1.1	0	56.2	18	95.00%	E.TANVASLNLLQLAPGAHLGR.F		R.NVPGVETANVASLNLLQLAPGAHLGR.F
253	265	2	1450.71	0.61	1	54.3	28.9	95.00%	E.AAFTKLDQVWGSE.T		R.FVIWTEAAFTKLDQVWGSETVASSK.V
2	44	4	4579.46	1.6	1	49.3	23.6	95.00%	M.SRPQVTVHSLTGEATANALPLPAVFSAPIRPDIVHTVFTSVNK.N	Acetyl (+42)	-.MSRPQVTVHSLTGEATANALPLPAVFSAPIRPDIVHTVFTSVNK.N
2	14	2	1451.74	0.63	0	41.7	28.2	95.00%	M.SRPQVTVHSLTGE.A	Acetyl (+42)	-.MSRPQVTVHSLTGEATANALPLPAVFSAPIRPDIVHTVFTSVNK.N
204	217	2	1472.79	-0.28	1	63.8	25.6	95.00%	R.GPLVVYAEDNGIVK.A		R.GPLVVYAEDNGIVK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
53	NCPR_YEAST	25.18%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
279	291	2	1577.69	-0.88	1	37.4	30.2	95.00%	E.LFSSNDRNCIHSE.F	Carbamidomethyl (+57)	R.ELFSSNDRNCIHSEFDLSGSNIK.Y
462	483	2	2359.26	1.5	1	50.5	21.9	95.00%	E.NFPNPELPDAPPVVGVTTNLLR.N		K.QTVHVTSIVENFPNPELPDAPPVVGVTTNLLR.N
254	275	2	2355.25	-0.17	0	70.6	22	95.00%	R.NADGIQLGPFDLSQPYIAPIVK.S		R.NADGIQLGPFDLSQPYIAPIVK.S
653	664	2	1171.69	0.074	0	31.5	21.9	95.00%	K.GVSTALVGILSR.G		K.GVSTALVGILSR.G
405	413	2	1053.55	0.26	0	23.9	25.2	92.10%	K.YFNIADALK.Y		K.YFNIADALK.Y

220	253	4	3909.87	1	1	42.3	26.9	95.00%	K.FTSQFQYTVLNEITDSMSLGEPS AHYLPSHQLNR.N		K.FTSQFQYTVLNEITDSMSLGEPS AHYLPSHQLNR.N
195	205	2	1369.62	0.35	1	47.3	29.8	95.00%	E.DYMAWKDSILE.V		K.LGEADDGAGTTDEDYMAWKDSI LEVLK.D
468	483	2	1660.95	0.71	0	90.9	18.4	95.00%	E.LPDAPPVVGVTTNLLR.N		K.QTVHVTSIVENFPNPELPDAPPV VGVTTNLLR.N
440	451	2	1349.63	-0.22	1	70.5	29.4	95.00%	R.YYSISSSSLSEK.Q		R.YYSISSSSLSEK.Q
49	59	2	1229.63	-0.012	1	78.6	27.4	95.00%	R.DIAQVVTENNK.N		R.DIAQVVTENNK.N
147	165	2	2129.95	-1	1	89.3	30.7	95.00%	R.YNMFGLGNSTYEFFNGAAK.K		R.YNMFGLGNSTYEFFNGAAK.K
292	300	2	979.5	0.9	0	42.1	26.9	95.00%	E.FDLSGSNIK.Y		R.NCIHSEFDLSGSNIK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
54	SNA3_YEAST	28.57%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
84	95	2	1293.63	0.59	1	51.8	28.8	95.00%	R.HATAPAVDRDLE.A		R.HATAPAVDRDLEAHPAEESQAQ PPAYDEDDEAGADVPLMDNK.Q
1	12	2	1601.68	-0.18	1	46.1	30.2	95.00%	-.MDRDHINDHDHR.M	Acetyl (+42)	-.MDRDHINDHDHR.M
115	125	2	1129.54	0.42	0	54.4	28.6	95.00%	E.AGADVPLMDNK.Q		R.DLEAHPAEESQAQPPAYDEDDE AGADVPLMDNK.Q
112	125	2	1488.64	0.45	1	34.8	30.1	95.00%	E.DDEAGADVPLMDNK.Q		R.DLEAHPAEESQAQPPAYDEDDE AGADVPLMDNK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
55	A6ZL71_YEAS7	34.82%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
126	144	2	2153.04	0.17	1	54.1	28.5	95.00%	K.VFAEDYLDINGSPINPYAR.I		K.VFAEDYLDINGSPINPYAR.I
273	289	2	1904.97	0.47	0	114	26.6	95.00%	R.HVLTILTDMSSYADALR.E		R.HVLTILTDMSSYADALR.E
15	25	2	1243.67	-0.42	1	49.2	27.3	95.00%	K.AVEQGFNVKPR.L		K.AVEQGFNVKPR.L
457	466	2	1187.63	1.4	0	62.6	26.2	95.00%	E.SLDQAWSLLR.I		R.TVFESLDQAWSLLR.I
170	182	2	1380.7	-0.31	0	57.1	27.7	95.00%	K.IPIFSASGLPHNE.I		K.IPIFSASGLPHNEIAAQICR.Q
102	111	2	1115.56	-0.74	1	38.8	28.2	95.00%	R.IPVSEDMLGR.I		R.IPVSEDMLGR.I
49	63	2	1702.89	-1	1	64	26.1	95.00%	R.YNEIVNLTLPDGTVR.Q		R.YNEIVNLTLPDGTVR.Q
238	252	2	1702.89	0.86	1	69.8	26.4	95.00%	R.TSLFLNLANDPTIER.I		R.TSLFLNLANDPTIER.I
453	466	2	1663.86	1.1	1	66.8	27.6	95.00%	R.TVFESLDQAWSLLR.I		R.TVFESLDQAWSLLR.I
150	166	2	1765.87	0.28	0	91.2	28.9	95.00%	E.MISTGVSAIDTMNSIAR.G		R.IYPEEMISTGVSAIDTMNSIAR.G
26	43	2	1930.04	-1.8	1	74.6	22.6	95.00%	R.LNYNTVSGVNGPLVILEK.V	Deamidation (+1)	R.LNYNTVSGVNGPLVILEK.V
303	318	2	1927.87	-0.46	1	82.2	30.9	95.00%	R.GYPGYMYTDLSTIYER.A		R.GYPGYMYTDLSTIYER.A
130	144	2	1706.83	0.87	0	30	29.3	95.00%	E.DYLDINGSPINPYAR.I		K.VFAEDYLDINGSPINPYAR.I
170	189	2	2193.13	-1.5	1	71.4	25.7	95.00%	K.IPIFSASGLPHNEIAAQICR.Q	Carbamidomethyl (+57)	K.IPIFSASGLPHNEIAAQICR.Q
480	487	2	1069.51	0.069	1	26.9	27.7	93.00%	K.ILDEFYDR.A		K.ILDEFYDR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
56	BPT1_YEAST	13.15%	100%	22

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
645	655	2	1115.66	1.2	0	30.7	20.7	95.00%	E.SIIGSSQIALK.N		R.TDEESIIGSSQIALK.N
1377	1390	2	1538.77	0.9	0	49.3	27.5	95.00%	R.SHLAIIPQDAQAFE.G		R.SHLAIIPQDAQAFEGTVK.T
1065	1077	2	1468.7	-4	1	48.9	29.6	95.00%	R.SPMTFFETTPVGR.I		R.SPMTFFETTPVGR.I
1343	1351	2	1006.58	0.67	0	29	21.2	95.00%	K.STLSLALFR.I		K.STLSLALFR.I
389	403	2	1631.86	0.12	0	75	26.2	95.00%	K.STGDILNLMSVDVLR.I		K.STGDILNLMSVDVLR.I
487	497	2	1395.63	0.63	1	30.3	29.7	94.70%	K.LYAWEEPMMAR.L		K.LYAWEEPMMAR.L
897	907	2	1269.68	0.3	1	35.9	25.9	95.00%	E.VDEPLQLKVTE.S		R.SESEVDEPLQLKVTESETEDEVV TESELELIK.A
897	904	2	940.52	1.4	0	27.3	21.3	95.00%	E.VDEPLQLK.V		R.SESEVDEPLQLK.V
617	625	2	1165.6	0.84	0	42.9	27.3	95.00%	E.MNNITFLWK.S		R.ALPAIEMNNITFLWK.S
1523	1532	2	1098.64	1.1	0	25.1	22.4	94.30%	K.IIVLDQGSVR.E		K.IIVLDQGSVR.E
807	816	2	1160.68	-0.53	1	46.3	20.1	95.00%	K.NIIEYVLIGK.T		K.NIIEYVLIGK.T
1504	1513	3	1194.68	-0.25	1	39.9	20.8	95.00%	K.DRTILTIAHR.I		K.DRTILTIAHR.I
875	884	2	1106.45	0.79	0	26.7	28.5	91.30%	E.FDSPIDNGNE.S		K.LLEEFDSPIDNGNESDVQTEHR.S
243	259	2	1913.1	0.93	1	44.3	16.6	95.00%	K.IKDPNQLPLPPVDLNIK.S		K.IKDPNQLPLPPVDLNIK.S
1449	1461	2	1386.69	0.64	1	63.5	28.5	95.00%	K.INENGSNLSVGQR.Q		K.INENGSNLSVGQR.Q

1377	1394	2	1924.01	-0.0085	1	58	25.8	95.00%	R.SHLAIIPQDAQAFEGTVK.T		R.SHLAIIPQDAQAFEGTVK.T
1506	1513	2	923.56	0.52	0	30.7	18.5	95.00%	R.TILTIAHR.I		R.TILTIAHR.I
895	904	2	1156.6	0.76	1	39	27.3	95.00%	E.SEVDEPLQLK.V		R.SESEVDEPLQLK.V
611	625	2	1759.93	0.67	1	63.1	24.4	95.00%	R.ALPAIEMNNITFLWK.S		R.ALPAIEMNNITFLWK.S
745	753	2	1056.56	0.77	0	27	26.3	95.00%	K.ACQLLPDLK.I	Carbamidomethyl (+57)	K.ACQLLPDLK.I
1314	1325	2	1352.73	-2.1	0	35.1	24.9	95.00%	E.NLDPVLNNINVK.I	Deamidation (+1)	R.ENLDPVLNNINVK.I
717	725	2	1062.53	0.83	0	47.6	28.9	95.00%	E.SWIMNASVR.E		R.SSSVAYCSQESWIMNASVR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
57	HIP1_YEAST	12.77%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
9	27	2	2127.98	0.17	1	70	30.4	95.00%	K.EYWADVVDGFKPATSPAFE.N		K.EYWADVVDGFKPATSPAFENEK.E
53	69	2	1819.82	0.54	0	68.7	30.3	95.00%	K.DSPGINQTTNDITSSDR.F		K.DSPGINQTTNDITSSDR.F
10	27	2	1998.94	0.48	0	57.9	29.5	95.00%	E.YWADVVDGFKPATSPAFE.N		K.EYWADVVDGFKPATSPAFENEK.E
43	69	3	2853.33	0.84	1	81.2	29.8	95.00%	K.TDSAFPLSSKDSPGINQTTNDITSSDR.F		K.TDSAFPLSSKDSPGINQTTNDITSSDR.F
400	412	3	1440.7	-0.18	0	40.7	29.6	95.00%	R.CMVAMAHIGNLPK.F	Carbamidomethyl (+57)	R.CMVAMAHIGNLPK.F
265	282	3	2019.92	0.15	0	41.5	29.3	95.00%	K.YWHDPGAFVGHSSGTQFK.G		K.YWHDPGAFVGHSSGTQFK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
58	A6ZQQ8_YEAS7	33.78%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
494	507	2	1555.84	-0.31	1	58	24.5	95.00%	K.EIGWCLGASLPLLK.A	Carbamidomethyl (+57)	K.EIGWCLGASLPLLK.A
375	395	3	2383.08	-0.55	0	35.9	30.5	95.00%	K.DAQCQSPPCSFNGVHQPSLVR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.DAQCQSPPCSFNGVHQPSLVR.T
47	67	2	2329.14	1.1	1	66.6	28.2	95.00%	K.TPEDISILPVNDEPGYLQDSK.T		K.TPEDISILPVNDEPGYLQDSK.T
124	151	2	2966.46	-0.45	1	61.3	26.9	95.00%	E.KFDMLEPGLSSFDTDSVGAANSLDPLLK.V		K.FDVCTSPPTLLDEKFDMLEPGLSSFDTDSVGAANSLDPLLK.V
347	365	2	2154.95	0.14	1	65.1	29.8	95.00%	K.ETYTIDFIGPDEPSGAQCR.F	Carbamidomethyl (+57)	K.ETYTIDFIGPDEPSGAQCR.F
111	123	2	1492.68	1.5	0	59.1	30.2	95.00%	K.FDVCTSPPTLLDE.K	Carbamidomethyl (+57)	K.FDVCTSPPTLLDEK.F
348	365	2	2025.91	0.45	0	88.9	30.7	95.00%	E.TYTIDFIGPDEPSGAQCR.F	Carbamidomethyl (+57)	K.ETYTIDFIGPDEPSGAQCR.F
300	310	2	1184.68	-0.013	1	65	24.8	95.00%	K.VNSVLVENALK.D		K.VNSVLVENALK.D
37	46	2	1026.57	0.76	0	26.8	23.2	95.00%	R.TVTPNASIPK.T		R.TVTPNASIPK.T
413	432	3	2257.19	1.2	1	62.2	24	95.00%	R.TRPLGMPLSFTLNELNDLAR.I		R.TRPLGMPLSFTLNELNDLAR.I
366	374	2	1091.59	-0.025	1	45.6	26.1	95.00%	R.FLTDEILNK.D		R.FLTDEILNK.D
413	426	2	1574.81	0.49	0	63.3	26.4	95.00%	R.TRPLGMPLSFTLNE.L		R.TRPLGMPLSFTLNELNDLAR.I
196	204	2	1092.55	0.16	1	32.8	28.8	95.00%	E.KDYPFPVVE.G		R.DHLEKDYPFPVVEGDGVSIMGGDEEGVFAWITTNYLLGNIGANGPK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
59	A7A201_YEAS7	44.66%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
28	46	2	2199.99	0.18	0	84.5	30.5	95.00%	R.FSDDTYTNDYISTIGVDFK.I		R.FSDDTYTNDYISTIGVDFK.I
139	149	2	1281.61	1.1	1	31.1	29.3	95.00%	E.FADANKMPFLE.T		K.EFADANKMPFLETSALDSTNVEDAFLTMAR.Q
11	21	2	1070.63	0.63	0	40	24.1	95.00%	K.LLLIGNSGVGK.S	Deamidation (+1)	K.LLLIGNSGVGK.S
160	167	2	923.45	0.94	0	38.7	29.2	95.00%	E.DAFLTMAR.Q		K.MPFLETSALDSTNVEDAFLTMAR.Q
101	108	2	1089.53	-0.2	1	53.5	30	95.00%	K.MWLQEIDR.Y		K.MWLQEIDR.Y
59	69	2	1315.65	0.75	1	47	28.5	95.00%	K.LQIWDTAGQER.F		K.LQIWDTAGQER.F
106	116	3	1265.7	0.88	1	34.5	24.1	95.00%	E.IDRYATSTVLK.L		K.MWLQEIDRYATSTVLK.L
22	27	2	760.43	1.9	0	25.1	26.7	91.70%	K.SCLLLR.F	Carbamidomethyl (+57)	K.SCLLLR.F
1	10	2	1366.58	0.078	1	39.8	30.2	95.00%	-.MNSEYDYLFK.L	Acetyl (+42)/ Oxidation (+16)	-.MNSEYDYLFK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
60	B3LPM9_YEAS1	12.53%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	72	2	2006	0.74	0	63.4	26.5	95.00%	E.NLPLLADASPDDQFYISK.F		K.HHVVEPHDANDENLPLLADASPDDQFYISK.F

43	72	3	3385.58	-0.68	1	96.2	29.5	95.00%	K.HHVVEPHDANDENLPLLADASPDDQFYISK.F	K.HHVVEPHDANDENLPLLADASPDDQFYISK.F
115	132	2	2124.08	-0.51	0	75.4	26.1	95.00%	K.ATQLFNQQQQHQLQSVAR.N	K.ATQLFNQQQQHQLQSVAR.N
353	359	2	907.39	0.2	1	30.1	28.5	95.00%	K.DMMNLER.K	K.DMMNLER.K
73	82	2	1131.63	2.1	1	50.5	24.9	95.00%	K.FVAALNQELK.K	K.FVAALNQELK.K
325	333	2	1091.53	1.1	1	57.4	28.2	95.00%	E.VLDFQDAER.E	R.QEVLDFQDAER.E
388	409	2	2156.02	-0.42	0	54.3	29	95.00%	E.SMAMSSGGAGIIAPSTDSLTFR.E	K.LSSSQLRPNANITESMAMSSGGAGIIAPSTDSLTFR.E
755	770	2	1604.88	0.62	0	62.8	23.6	95.00%	K.AVSSSGLLSTMAQLIK.A	K.AVSSSGLLSTMAQLIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
61	A6ZM61_YEAS7	50.96%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
186	198	2	1554.7	0.43	1	68.4	30.7	95.00%	E.AFEDDYNDAINIR.L		R.SALQQNQADTEAFEDDYNDAINIR.L
57	70	2	1590.75	0.94	1	70.2	29.9	95.00%	K.VATMQVWDTAGQER.F		K.VATMQVWDTAGQER.F
118	131	2	1562.83	-0.15	1	32.2	25.6	95.00%	E.TFPFVILGNKIDAE.E		R.DEFLVHANVNSPETFPFVILGNKIDAEESK.K
39	48	2	1035.56	-0.22	0	43.9	25.1	95.00%	K.ATIGADFLTK.E		K.ATIGADFLTK.E
107	117	2	1225.61	0.63	0	42.3	28.4	95.00%	E.FLVHANVNSPE.T		R.DEFLVHANVNSPETFPFVILGNK.I
81	101	2	2361.06	-0.15	1	98.4	29.6	95.00%	R.GADCCVLVYDVTNASSFENIK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GADCCVLVYDVTNASSFENIK.S
148	160	2	1360.76	0.57	0	66.9	22.1	95.00%	K.SLGDIPLFLTSAK.N		K.SLGDIPLFLTSAK.N
71	80	2	1186.62	1.7	0	41	26.9	95.00%	R.FQSLGVAFYR.G		R.FQSLGVAFYR.G
118	127	2	1134.65	1.6	0	32	22.2	95.00%	E.TFPFVILGNK.I		R.DEFLVHANVNSPETFPFVILGNK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
62	A6ZL18_YEAS7	12.60%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
221	233	2	1277.66	1.2	1	64	27.2	95.00%	K.YVINLEGTGAGGK.A		K.YVINLEGTGAGGK.A
880	890	2	1384.7	0.49	1	67.1	28.9	95.00%	E.LQLHKLDFDQE.T		K.SASGINELQLHKLDFDQETYHIGVQWFPK.L
747	761	2	1699.93	-0.011	0	32.2	22.1	95.00%	E.GNFLKPMLQDLPSIK.Y		R.EGNFLKPMLQDLPSIK.Y
891	901	3	1374.71	1.2	0	49.5	27.4	95.00%	E.TYHIGVQWFPK.L		K.LDFDQETYHIGVQWFPK.L
726	745	3	2112.07	-0.46	0	78.8	26.7	95.00%	R.FSQNIDLSQGNAASVHVLGR.E		R.FSQNIDLSQGNAASVHVLGR.E
287	296	2	1237.62	-0.83	0	47.4	28.2	95.00%	R.GWDVAFYKPR.N		R.GWDVAFYKPR.N
129	140	2	1398.74	-0.0082	1	36.6	26.1	95.00%	R.VTYFESSNILVK.L		R.VTYFESSNILVK.L
254	269	2	1905.86	-0.058	1	79.3	30	95.00%	K.ENPFGNSIYQQGFYSR.Y		K.ENPFGNSIYQQGFYSR.Y
529	543	2	1785.7	-0.89	0	46.2	30.5	95.00%	R.DHHSNYSSHSQIDME.R		R.DHHSNYSSHSQIDMER.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
63	A6ZSU5_YEAS7	29.50%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
380	394	2	1652.76	-1.3	1	43.1	29.3	95.00%	R.GTFQSSGQNCIGIER.V	Carbamidomethyl (+57)	R.GTFQSSGQNCIGIER.V
495	504	2	1149.63	0.75	0	36.5	24.8	95.00%	E.VFGPILVMMK.A	Oxidation (+16)	K.IAQNEVFGPILVMMK.A
159	176	3	2067.11	1.1	0	29.1	20.8	95.00%	R.VLASLHDYILNNQDLIAR.V		R.VLASLHDYILNNQDLIAR.V
144	155	2	1354.59	-0.24	0	44.4	30.3	95.00%	K.AQSTWGNSDFSR.R		K.AQSTWGNSDFSR.R
507	532	3	2674.28	0.052	0	63.5	28.2	95.00%	K.NTDHCVQLANSAPFGLGGSVFGADIK.E	Carbamidomethyl (+57)	K.NTDHCVQLANSAPFGLGGSVFGADIK.E
327	342	3	1823.01	0.61	0	42.8	20.5	95.00%	K.HITFIGSQPVAHYILK.C		K.HITFIGSQPVAHYILK.C
413	428	3	1795.85	1	1	26.1	29.4	95.00%	R.MTANPLRQGSDIDHLE.N		R.MTANPLRQGSDIDHLENVDMGAMISDNR.F
470	487	2	2103.03	0.9	0	40.8	28.5	95.00%	K.YPQGHYFQPTLLVDVTPE.M		K.YPQGHYFQPTLLVDVTPEMK.I
470	489	3	2362.17	-0.12	1	32.7	27.2	95.00%	K.YPQGHYFQPTLLVDVTPEMK.I		K.YPQGHYFQPTLLVDVTPEMK.I
81	94	2	1571.77	-0.4	1	49.4	28.8	95.00%	K.FSLPAPEAAQNNWK.G		K.FSLPAPEAAQNNWK.G
369	379	2	1247.66	0.78	0	62.4	27.3	95.00%	K.NLDALSSIIMR.G	Oxidation (+16)	K.NLDALSSIIMR.G
429	443	2	1712.71	-0.31	1	87.6	30.2	95.00%	E.NVDMGAMISDNRFDE.L		R.QGSDIDHLENVDMGAMISDNRFDELEALVK.D
347	358	2	1197.7	-0.51	1	31.2	22.3	95.00%	K.SLTPVVVELGGK.D		K.SLTPVVVELGGK.D
490	504	2	1688.9	0.17	1	49.6	25	95.00%	K.IAQNEVFGPILVMMK.A		K.IAQNEVFGPILVMMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
64	A6ZQK0_YEAS7	13.69%	100%	22

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
998	1007	2	1223.58	0.57	0	72.5	29.7	95.00%	E.FDWCAVTAVR.T	Carbamidomethyl (+57)	R.IGSSVEFDWCAVTAVR.T
325	337	3	1398.67	0.24	0	33.2	29.9	95.00%	R.GHNIPCTSTISGR.C	Carbamidomethyl (+57)	R.GHNIPCTSTISGR.C
472	489	2	1959.11	0.66	0	50.6	18.3	95.00%	E.GIYTILINPNIATIQTSK.G		K.EEGIYTILINPNIATIQTSK.G
1204	1224	2	2100.05	-0.77	0	51.5	27.1	95.00%	E.NAGVHSGDATLIVPPQDLAPE.T		R.NGELVMHVVSEHVENAGVHSGDATLIVPPQDLAPETVDR.I
599	615	2	1638.8	-0.26	1	58.3	29.6	95.00%	R.AAYALGGLGSGFANNEK.E		R.AAYALGGLGSGFANNEK.E
1463	1476	2	1516.85	0.33	0	46.5	23.5	95.00%	R.LAVDYSVPLVTNVK.C		R.LAVDYSVPLVTNVK.C
663	692	3	3303.58	0.91	1	46.4	28.1	95.00%	E.NFDPLGIHTGDSIVVAPSQTLSDEDYNMLR.T		R.DAFDNCITVCNMENFDPLGIHTGDSIVVAPSQTLSDEDYNMLR.T
1551	1564	2	1385.78	-0.08	0	32.1	22.7	95.00%	R.SISGPVITDVASLK.A		R.SISGPVITDVASLK.A
752	762	2	1208.71	-0.35	1	32.9	18.1	95.00%	K.LGLNIPLNEVK.N		K.LGLNIPLNEVK.N
855	864	2	1050.59	0.82	0	45.4	24.8	95.00%	R.VFAIANAFAK.K		R.VFAIANAFAK.K
708	719	2	1405.7	1	0	44	27.7	95.00%	E.CNIQYALNPVSK.D	Carbamidomethyl (+57)	R.HLGVVGECNIQYALNPVSK.D
187	198	2	1397.73	0.065	0	37.4	25.7	95.00%	E.WVDPNVQNLVSK.V		R.SAFDVPEWVDPNVQNLVSK.V
2000	2011	2	1398.66	-0.7	0	34.5	29.2	95.00%	R.TLACYSDAIVMR.H	Carbamidomethyl (+57)	R.TLACYSDAIVMR.H
1311	1318	2	976.51	-0.033	0	23.7	25.4	91.40%	K.VPQFSFPR.L		K.VPQFSFPR.L
1242	1253	2	1363.75	-0.38	0	27.9	23.7	95.00%	K.ITGPYNIQFIAK.D		K.ITGPYNIQFIAK.D
1193	1203	2	1277.64	-0.24	1	26.5	28.4	91.00%	E.LVMHVVSEHVE.N		R.NGELVMHVVSEHVENAGVHSGDATLIVPPQDLAPETVDR.I
1101	1113	2	1499.74	-0.74	0	26.5	28.7	90.50%	R.MLDQIGVDQPAWK.E		R.MLDQIGVDQPAWK.E
647	662	2	1941.84	0.13	1	50.8	30.2	95.00%	E.VVRDAFDNCITVCNME.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.EVEYEVVRDAFDNCITVCNMENFDPLGIHTGDSIVVAPSQTLSDEDYNMLR.T
135	145	2	1146.6	0.16	0	39.9	26.5	95.00%	E.GIPAVYGVDTR.S		K.WLQNEGIPAVYGVDTR.S
575	589	2	1472.75	-0.96	1	59.3	26.8	95.00%	K.SQAANSVDEALAAVK.E		K.SQAANSVDEALAAVK.E
1635	1650	2	1713.96	1	0	46.3	20.8	95.00%	K.TADLASVLLLTSLQNR.S		K.TADLASVLLLTSLQNR.S
180	198	2	2143.06	0.36	1	56.6	28.9	95.00%	R.SAFDVPEWVDPNVQNLVSK.V		R.SAFDVPEWVDPNVQNLVSK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
65	A7A052_YEAS7	8.15%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	16	2	1682.71	5.7	1	47.4	30.4	95.00%	M.LNHPSQGSDDAQDEK.Q	Acetyl (+42)/ Deamidation (+1)	-.MLNHPSQGSDDAQDEK.Q
1	15	2	1642.65	0.54	0	72.9	30.8	95.00%	-.MLNHPSQGSDDAQDE.K		-.MLNHPSQGSDDAQDEK.Q
35	48	2	1556.66	1.5	1	60.9	30.8	95.00%	K.DSYVSDDVANSTER.Y		K.DSYVSDDVANSTER.Y
588	596	2	1102.57	0.42	1	39.6	27.5	95.00%	E.ILEPMESLR.S	Oxidation (+16)	K.ANDIEILEPMESLR.S
1	16	2	1813.75	6.6	1	58.8	31	95.00%	-.MLNHPSQGSDDAQDEK.Q	Acetyl (+42)/ Deamidation (+1)	-.MLNHPSQGSDDAQDEK.Q
573	582	2	1100.59	0.61	0	54.7	26.6	95.00%	E.FDLNPISAPK.A		K.YNDTEEEMNAMDYEEEDEFDLNPISAPK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
66	A6ZT96_YEAS7	20.27%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
340	350	2	1433.66	-0.82	1	44.3	30.4	95.00%	R.GCVEIFDYYLR.D	Carbamidomethyl (+57)	R.GCVEIFDYYLR.D
151	162	2	1328.53	0.88	0	39.4	29.2	95.00%	K.MGNGMADYILDE.N	Deamidation (+1)	K.MGNGMADYILDENYNLNGLQTVHDYDVYCHYVAGLVGDGLTR.L
213	220	2	922.5	1.2	0	36.2	28.1	95.00%	E.SMGLFLQK.T		K.FANESLYSNEQLYESMGLFLQK.T
226	235	2	1194.52	-0.35	1	49.5	29.9	95.00%	R.DYNEDLVDGR.S		R.DYNEDLVDGR.S
89	97	3	1121.66	0.0009	1	23.9	20.9	95.00%	E.HDLKIDLLR.H		R.ALDTIEDDMSIEHDLKIDLLR.H
4	13	2	1131.67	1.5	0	47	22	95.00%	K.LLQLALHPVE.M		K.LLQLALHPVEMK.A
356	365	2	1143.63	1.1	0	31.8	25.6	95.00%	K.LAVQDPNFLK.L		K.LAVQDPNFLK.L
4	15	2	1390.8	0.42	1	48.6	19.9	95.00%	K.LLQLALHPVEMK.A		K.LLQLALHPVEMK.A
366	372	2	814.49	1.1	0	34.4	25.3	95.00%	K.LNIQISK.I		K.LNIQISK.I
108	118	2	1234.56	-0.1	0	35.4	29.7	95.00%	K.WSFDGNAPDVK.D		K.WSFDGNAPDVK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
67	A6ZNT9_YEAS7	42.86%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

27	36	2	1169.54	0.31	1	52.3	29.1	95.00%	R.FVSNDFAENK.E		R.FVSNDFAENK.E
37	48	2	1302.69	-0.41	0	32.8	26.5	95.00%	K.EPTIGAAFLTQR.V		K.EPTIGAAFLTQR.V
60	68	2	1074.51	0.44	1	35.1	29.9	95.00%	E.IWDTAGQER.F		K.FEIWDTAGQER.F
35	48	2	1544.83	0.63	1	55.3	24.9	95.00%	E.NKEPTIGAAFLTQR.V		R.FVSNDFAENKEPTIGAAFLTQR.V
10	20	2	1068.65	-0.019	1	27.6	18.1	95.00%	K.LVLLGEAAVGK.S		K.LVLLGEAAVGK.S
79	97	2	2091.14	-0.53	0	79.3	21.6	95.00%	R.NAQAALVVYDVTKPQSFIK.A		R.NAQAALVVYDVTKPQSFIK.A
69	78	2	1217.59	0.15	0	44.1	27.9	95.00%	R.FASLAPMYYR.N		R.FASLAPMYYR.N
1	9	2	1037.51	0.87	0	34.2	29.3	95.00%	-.MNTSVTSIK.L	Acetyl (+42)/ Oxidation (+16)	-.MNTSVTSIK.L
146	155	2	1111.59	-0.21	1	48.5	25	95.00%	K.GLLFFETSAK.T		K.GLLFFETSAK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
68	A6ZNV4_YEAS7	23.67%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
186	195	2	1242.63	0.63	0	28	28	94.10%	E.LDFQTIIHQE.R		K.VNEQSPLLHNEGQHQLQLQEEQEQQQQGLSQEELDFQTIIHQER.S
186	196	2	1398.73	-0.083	1	60.5	27	95.00%	E.LDFQTIIHQER.S		K.VNEQSPLLHNEGQHQLQLQEEQEQQQQGLSQEELDFQTIIHQER.S
210	222	2	1424.81	0.41	0	70	20.7	95.00%	E.VNAIFHQLGSLVK.E		R.IHTAVQEVNAIFHQLGSLVK.E
142	152	2	1265.61	-0.32	1	41.9	29.6	95.00%	R.QDPESSYISIK.V		R.QDPESSYISIK.V
13	26	2	1591.72	0.94	0	72.6	30.6	95.00%	K.GNSQQEPQFSTNQK.T		K.GNSQQEPQFSTNQK.T
102	112	2	1413.66	-0.41	0	69.7	29.4	95.00%	K.YQSLQQSYNQR.K		K.YQSLQQSYNQR.K
203	222	3	2203.21	0.28	1	67.6	21	95.00%	R.IHTAVQEVNAIFHQLGSLVK.E		R.IHTAVQEVNAIFHQLGSLVK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
69	A6ZKY2_YEAS7	15.26%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
349	369	2	2284.11	2.1	1	78.4	28.9	95.00%	K.VNQGSLDYLAALGVYQEDMAK.A		K.VNQGSLDYLAALGVYQEDMAK.A
121	147	3	2965.4	0.68	0	60.7	29.5	95.00%	R.DNADLPVDPYHLSPQQQPSNNLFGSGR.L		R.DNADLPVDPYHLSPQQQPSNNLFGSGR.L
246	253	2	883.51	0.085	0	27.4	21.8	95.00%	K.GLLDTLPR.R		K.GLLDTLPR.R
264	277	2	1714.75	0.47	1	65.3	31.1	95.00%	R.YTACTVEPDDFLRE.G	Carbamidomethyl (+57)	R.YTACTVEPDDFLREGYTLR.F
46	63	2	1966.9	-0.055	0	65.1	30.3	95.00%	E.DSYDQSNVFQGLPASPSR.A		R.WANPSEESLEDSYDQSNVFQGLPASPSR.A
223	232	2	1069.55	0.074	0	38.8	27.3	95.00%	R.MVSDLPPPSK.K		R.MVSDLPPPSK.K
564	572	2	1130.62	0.63	1	28.2	26	95.00%	R.ILCWELVAK.R	Carbamidomethyl (+57)	R.ILCWELVAK.R
93	102	2	1119.56	0.34	1	46.1	28.1	95.00%	R.YAANLQESPK.R		R.YAANLQESPK.R
235	245	3	1220.75	-0.0033	1	25.4	15.9	95.00%	K.ALLKLDNPIPK.G		K.ALLKLDNPIPK.G
457	472	2	1621.78	-0.69	0	98.9	29.7	95.00%	K.VFDMDSNVAGAAGQIK.T		K.VFDMDSNVAGAAGQIK.T
43	63	2	2296.06	0.26	1	94.1	30.2	95.00%	E.SLEDSYDQSNVFQGLPASPSR.A		R.WANPSEESLEDSYDQSNVFQGLPASPSR.A
264	276	2	1585.71	-0.5	0	38.2	30.7	95.00%	R.YTACTVEPDDFLR.E	Carbamidomethyl (+57)	R.YTACTVEPDDFLR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
70	B3LH18_YEAS1	4.87%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	20	2	2175.11	0.28	1	44.7	26.1	95.00%	-.MDATTPLLTVANSHPARNPK.H	Acetyl (+42)	-.MDATTPLLTVANSHPARNPK.H
1	17	2	1835.92	0.49	0	101	28.1	95.00%	-.MDATTPLLTVANSHPAR.N	Acetyl (+42)	-.MDATTPLLTVANSHPAR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
71	A6ZQN6_YEAS7	7.64%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
616	624	2	1100.53	-0.028	0	41.2	29.1	95.00%	K.FFTHFTSSK.D		K.FFTHFTSSK.D
520	547	2	3090.5	-0.75	1	77.3	27.7	95.00%	R.ISDPTLAAQAYGSPFTFITTYTWGTPER.I		R.ISDPTLAAQAYGSPFTFITTYTWGTPER.I
581	591	2	1239.65	0.47	1	34.7	26.5	95.00%	R.NHKLTDSIALE.G		R.NHKLTDSIALEGNDHLESK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
72	A6ZWP0_YEAS7	15.47%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
958	971	2	1612.78	-0.75	1	66.6	29.1	95.00%	R.SQKDFIQAYSDGVR.I		R.SQKDFIQAYSDGVR.I
91	103	2	1443.72	-0.66	0	51.6	27.9	95.00%	K.AQPLISSCPACLK.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.AQPLISSCPACLK.N
238	251	3	1637.84	0.83	1	24.6	27.1	95.00%	E.SCPHLKPLKDGVCK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CACSDCQESCPHLKPLKDGVCK.V
942	950	2	952.5	1	0	37.9	26.1	95.00%	E.TSVSASVFR.T		R.APYSTALVYNETSVSASVFR.T
961	971	2	1269.6	0.46	0	46.9	29.5	95.00%	K.DFIQAYSDGVR.I		K.DFIQAYSDGVR.I
383	393	2	1439.62	0.67	0	30.6	29.9	94.90%	E.YFDDNFGPFYR.T		K.EYFDDNFGPFYR.T
33	45	2	1470.73	-0.68	1	34.2	28.7	95.00%	K.SVFGNELPCPVPR.S	Carbamidomethyl (+57)	K.SVFGNELPCPVPR.S
185	203	2	2082.06	0.13	0	49.7	27.4	95.00%	K.FLGDAKPMLGGSPFQINYK.Y		K.FLGDAKPMLGGSPFQINYK.Y
220	229	2	1231.52	1.2	0	35.8	29.2	95.00%	E.VYACDDAQYK.C	Carbamidomethyl (+57)	K.EWQEFNDEVYACDDAQYK.C
476	489	2	1687.88	-0.23	0	49.3	26.5	95.00%	K.FPVNCLPTFQQPLK.T	Carbamidomethyl (+57)	K.FPVNCLPTFQQPLK.T
792	808	2	1926	1.7	0	29.4	26.4	95.00%	K.DVYSFLNVGPPVYMVVK.N		K.DVYSFLNVGPPVYMVVK.N
161	177	2	1671.79	-0.85	0	88.4	29.5	95.00%	K.FSATNGYAMDLIGGGAK.N		K.FSATNGYAMDLIGGGAK.N
104	120	2	2070.88	1.2	0	77.1	30.4	95.00%	K.NFNNLFCHFTCAADQGR.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.NFNNLFCHFTCAADQGR.F
46	58	2	1434.69	0.75	1	29.8	30.1	93.60%	R.SFEPPVLSDETSK.L		R.SFEPPVLSDETSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
73	A7A0Z7_YEAS7	31.23%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
14	27	2	1642.73	-1.2	1	73.2	30.4	95.00%	K.NGETISSCFQPFQK.N	Deamidation (+1)/ Carbamidomethyl (+57)	K.NGETISSCFQPFQK.N
40	57	2	2124.15	1.7	0	24	23.3	92.60%	E.QITPVIFHNLIMDMVLPK.V	Oxidation (+16)	K.NENYGTITSANEQITPVIFHNLIMDMVLPK.V
123	138	2	1809.89	2.6	1	51.4	28.4	95.00%	E.LLSSHVGQILDSFHEE.L		R.ILSGLQEYESNATNELLSSHVGQILDSFHEELVEYR.N
69	89	2	2507.01	-1.1	0	43.1	30.7	95.00%	K.MSMNLIDGFDCFYSTDDHDPK.T	Carbamidomethyl (+57)	K.MSMNLIDGFDCFYSTDDHDPK.T
30	57	3	3158.62	0.13	1	53.2	24.6	95.00%	E.NYGTITSANEQITPVIFHNLIMDMVLPK.V		K.NENYGTITSANEQITPVIFHNLIMDMVLPK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
74	A6ZT03_YEAS7	14.56%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
314	324	2	1294.69	0.21	0	39.1	26	95.00%	E.LFTGKPAMFQR.T		R.AAGTASWGELFTGKPAMFQR.T
1	12	2	1387.66	-0.5	0	48.4	29.6	95.00%	-.MNSTPDLISPQK.S	Acetyl (+42)/ Oxidation (+16)	-.MNSTPDLISPQK.S
46	59	2	1392.74	0.71	0	79.1	25.9	95.00%	E.SQVQPAVAPPNTGK.G		K.NESFHDNLSESQVQPAVAPPNTGK.G
546	564	2	2269.97	-1.2	1	65.4	31.3	95.00%	K.RGADYNADDLMHDDQPFYK.S		K.RGADYNADDLMHDDQPFYK.S
305	324	2	2125.04	0.83	1	91.3	28.5	95.00%	R.AAGTASWGELFTGKPAMFQR.T		R.AAGTASWGELFTGKPAMFQR.T
228	236	2	1153.52	0.85	0	47.9	30.1	95.00%	K.NYSNSVQWR.V	Deamidation (+1)	K.NYSNSVQWR.V
537	545	2	959.51	0.5	0	44.9	27.5	95.00%	K.SASWVPVSK.R		K.SASWVPVSK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
75	PMT1_YEAST	9.79%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
408	425	3	2113	-0.28	1	30.5	28.9	95.00%	R.LHSHDHKPPVSESSDWQK.E		R.LHSHDHKPPVSESSDWQK.E
486	495	2	1203.56	0.89	1	36.6	29	95.00%	K.LPAWGFEQQE.V		K.LPAWGFEQQEVTCASSGR.H
319	336	2	1850.06	0.16	0	106	16.2	95.00%	K.IPQNVVADVGIGSIISLR.H		K.IPQNVVADVGIGSIISLR.H
472	483	2	1451.6	0.84	0	45.5	29.8	95.00%	R.HAMTGCYLFSHE.V	Carbamidomethyl (+57)	R.HAMTGCYLFSHEVK.L
23	42	3	2152.16	-0.24	1	60.1	22.6	95.00%	K.QGPVRPFIVTDPSAELASLR.T		K.QGPVRPFIVTDPSAELASLR.T
23	37	2	1611.83	0.35	0	42.6	27.2	95.00%	K.QGPVRPFIVTDPSAE.L		K.QGPVRPFIVTDPSAELASLR.T
472	485	3	1678.76	-0.033	1	31.3	29.9	95.00%	R.HAMTGCYLFSHEVK.L	Carbamidomethyl (+57)	R.HAMTGCYLFSHEVK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
76	A6ZQY0_YEAS7	40.36%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
114	127	2	1398.71	0.41	0	59.8	27.5	95.00%	E.NADDNVAVGLIGNK.S		R.ENADDNVAVGLIGNK.S

181	215	3	3476.58	-2.1	1	46.5	29.7	95.00%	K.HQMDLGDSSANGNANGASAPNGPTISLTPTPNENK.K		K.HQMDLGDSSANGNANGASAPNGPTISLTPTPNENK.K
170	177	2	991.57	0.9	0	36	22.3	95.00%	E.LINTIYQK.V		K.AFEELINTIYQK.V
16	26	2	1056.62	0.27	0	32.4	23.5	95.00%	K.IVLIGDSGVGK.S		K.IVLIGDSGVGK.S
64	74	2	1273.61	-0.17	1	64.6	28.9	95.00%	K.AQIWDTAGQER.Y		K.AQIWDTAGQER.Y
113	127	2	1527.75	-1.3	1	74.8	29	95.00%	R.ENADDNVAVGLIGNK.S		R.ENADDNVAVGLIGNK.S
44	53	2	1079.56	0.067	1	61.1	26.9	95.00%	K.STIGVEFATR.T		K.STIGVEFATR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
77	ZRT3_YEAST	17.69%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
176	185	2	1188.69	0.66	1	59	20.8	95.00%	K.KMSLIDLLTR.R		K.KMSLIDLLTR.R
316	327	3	1440.66	1.7	0	31.6	30.2	95.00%	E.NGSLYPHHHHLE.T	Deamidation (+1)	R.HHHSSESPENYGSNQLSHSFSSPLGNDVTENPAALADTQYHPENGSLYPHHHHLETPFSK.L
177	185	2	1060.6	1.7	0	48.5	24.2	95.00%	K.MSLIDLLTR.R		K.MSLIDLLTR.R
267	272	2	722.37	-0.59	0	23.7	25.9	90.50%	K.NFLSSR.H		K.NFLSSR.H
282	315	3	3660.63	1.4	1	81.7	29.4	95.00%	E.NYGSNQLSHSFSSPLGNDVTENPAALADTQYHPE.N	Deamidation (+1)	R.HHHSSESPENYGSNQLSHSFSSPLGNDVTENPAALADTQYHPENGSLYPHHHHLETPFSK.L
143	159	2	1708.72	1.4	1	57.4	30.2	95.00%	E.NAPSEHGYATSSSSVSE.N		K.SHSHSHSHSHADSHSNFSNDHDLENAPSEHGYATSSSSVSENDPLITK.D
209	218	2	1158.65	0.88	0	43.4	24.4	95.00%	E.YIACVPPVIK.S	Carbamidomethyl (+57)	K.CTPLLQSEQPEYIACVPPVIK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
78	YIL7_YEAST	21.38%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
138	148	2	1344.6	0.44	1	47.5	30.5	95.00%	K.ENFQDQVHISE.S		K.ENFQDQVHISESDISPGNK.D
290	298	2	956.57	1.8	0	24	25	92.60%	K.GNLLVVQSK.R		K.GNLLVVQSK.R
139	148	2	1215.55	1.3	0	47.3	30.4	95.00%	E.NFQDQVHISE.S		K.ENFQDQVHISESDISPGNK.D
192	205	2	1566.83	0.18	0	43.7	24.9	95.00%	R.NSLFISPTGDILYK.T		R.NSLFISPTGDILYK.T
273	285	2	1386.67	-0.52	1	61.9	28.6	95.00%	K.LLNSPESDGSVNR.N		K.LLNSPESDGSVNR.N
117	138	2	2642.11	-0.037	1	61.8	31	95.00%	K.MFSTQHTQFYGDSPYMDYPAKE.N		K.MFSTQHTQFYGDSPYMDYPAKENFQDQVHISESDISPGNK.D
117	137	3	2513.07	-0.66	0	48.2	30.9	95.00%	K.MFSTQHTQFYGDSPYMDYPAK.E		K.MFSTQHTQFYGDSPYMDYPAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
79	A6ZNR5_YEAS7	18.86%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
181	191	2	1144.61	1.1	1	39	26.5	95.00%	E.IQLNGGSISEK.V		K.AHLAEIQLNGGSISEK.V
317	325	2	1106.62	0.79	1	32.1	23.7	95.00%	E.IKNDFIMVK.G		K.TITPMGGFVHYGEIKNDFIMVK.G
304	316	2	1407.65	0.84	0	50.5	30	95.00%	K.TITPMGGFVHYGE.I		K.TITPMGGFVHYGEIK.N
214	222	2	960.53	0.92	0	41.7	26.8	95.00%	E.MIDAIAVTK.G		K.TVAVDSVFEQNEMIDAIAVTK.G
249	266	3	2047	0.31	0	41.2	28.4	95.00%	K.VACIGAWHPAHVMWSVAR.A	Carbamidomethyl (+57)	K.VACIGAWHPAHVMWSVAR.A
38	50	2	1409.79	0.63	0	43.2	21.5	95.00%	R.SKPVALTSFLGYK.A		R.SKPVALTSFLGYK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
80	YO092_YEAST	8.77%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
142	157	2	1589.67	0.046	0	93.4	31	95.00%	E.MAAPSSDGNAGDDNLR.E		R.IDEEMAAPSSDGNAGDDNLR.E
1	10	2	1211.67	0.23	1	30.4	23.4	95.00%	-.MQLVPLELNR.S		-.MQLVPLELNR.S
142	158	2	1718.72	0.041	1	104	31.2	95.00%	E.MAAPSSDGNAGDDNLRE.V		R.IDEEMAAPSSDGNAGDDNLREVNSR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
81	GAS1_YEAST	14.67%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
210	232	2	2739.08	0.59	1	55.3	30.3	95.00%	K.MTDYFACGDDDVKADFYGINMYE.W	Carbamidomethyl (+57)	K.MTDYFACGDDDVKADFYGINMYEWCGK.S

223	236	2	1752.73	-0.39	1	57.8	30	95.00%	K.ADFYGINMYEWCGK.S	Carbamidomethyl (+57)	K.ADFYGINMYEWCGK.S
194	207	2	1566.68	-0.84	1	93.4	30.1	95.00%	K.IPVGYSSNDDEDTR.V		K.IPVGYSSNDDEDTR.V
415	424	2	1192.52	0.27	0	36	29.4	95.00%	K.YGAYSFCTPK.E	Carbamidomethyl (+57)	K.YGAYSFCTPK.E
210	222	2	1535.59	-1.4	0	85.3	28.8	95.00%	K.MTDYFACGDDDVK.A	Carbamidomethyl (+57)	K.MTDYFACGDDDVK.A
83	90	2	956.58	2.2	1	40.2	21.9	95.00%	K.KLNTNVIR.V		K.KLNTNVIR.V
392	400	2	1195.54	1.7	0	39.3	29.9	95.00%	E.TLFNWICNE.V	Carbamidomethyl (+57)	K.YWSAATELPPTPNGGLCSCMNA ANSCVVSDDVDSDDYETLFNWICN EVDCSGISANGTAGK.Y
401	414	2	1336.59	0.15	0	79.5	30.2	95.00%	E.VDCSGISANGTAGK.Y	Carbamidomethyl (+57)/ Deamidation (+1)	K.YWSAATELPPTPNGGLCSCMNA ANSCVVSDDVDSDDYETLFNWICN EVDCSGISANGTAGK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
82	A7A0E5_YEAS7	15.94%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
443	455	2	1322.62	4	0	38.9	29.4	95.00%	E.VSGYGDNVVGDNK.D		K.TQWEVSGYGDNVVGDNK.D
443	461	2	2078.95	-0.58	1	48.8	30.4	95.00%	E.VSGYGDNVVGDNKDNWVIE.I		K.TQWEVSGYGDNVVGDNKDNWVI EIMDQR.G
353	383	3	3463.62	-0.75	0	111	28.8	95.00%	K.NQALGGSLLHSHIQTYPDGSNQQ QVTCYGYK.D	Carbamidomethyl (+57)	K.NQALGGSLLHSHIQTYPDGSNQQ QVTCYGYK.D
426	438	3	1369.75	0.44	0	27	24.7	95.00%	R.NLHTHPVAAPVSK.T		R.NLHTHPVAAPVSK.T
409	417	3	1083.57	1	0	23.1	25.3	95.00%	E.YLKPGTSYR.L		R.GLPSWSENETDIEYLKPGTSYR.L
384	393	2	1311.56	-0.11	1	42.3	30.2	95.00%	K.DANNEWFFNR.E		K.DANNEWFFNR.E
341	352	2	1187.68	-0.34	0	45.5	23.4	95.00%	R.DIALGSSVVSIK.N		R.DIALGSSVVSIK.N
439	455	2	1866.84	-0.055	1	89.9	30.4	95.00%	K.TQWEVSGYGDNVVGDNK.D		K.TQWEVSGYGDNVVGDNK.D
106	118	4	1574.76	0.079	1	32.8	29.1	95.00%	R.HEFYHDVHPPLGK.M		R.HEFYHDVHPPLGK.M
473	482	3	1202.68	1	1	30	23.1	95.00%	E.KLHTLTTSFR.I		R.GDEDPEKLHTLTTSFR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
83	A6ZVM2_YEAS7	14.30%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
314	325	2	1292.68	-0.86	0	78.3	26.3	95.00%	K.HADANVQLVAQK.M		K.HADANVQLVAQK.M
326	339	2	1533.7	0.91	0	39.6	30.5	95.00%	K.MQQITSSQPTPTSE.L		K.MQQITSSQPTPTSELSSAQR.D
360	370	2	1264.65	1.1	0	26.1	27.7	91.70%	E.WFTTALTNSPK.D		K.EPITWLETQITEWFTTALTNSPK. D
824	852	3	3224.5	-0.16	0	53.9	28.6	95.00%	K.AFSSLNDIPITPSHDNNPHSFAEP MPAYR.G		K.AFSSLNDIPITPSHDNNPHSFAEP MPAYR.G
196	204	2	1094.58	-0.25	0	39.6	26	95.00%	R.LSLLAYCQK.V	Carbamidomethyl (+57)	R.LSLLAYCQK.V
326	345	2	2176.04	0.14	1	114	28.9	95.00%	K.MQQITSSQPTPTSELSSAQR.D		K.MQQITSSQPTPTSELSSAQR.D
797	823	2	2734.26	-0.51	0	68.3	29.5	95.00%	R.VTGDAPLPYPIAQVGDDSMDSSD LGSK.A		R.VTGDAPLPYPIAQVGDDSMDSSD LGSK.A
125	137	2	1605.85	0.32	0	56.9	25.5	95.00%	E.VLQSQLHYYSLQK.N		K.FEVLQSQLHYYSLQK.N
111	118	2	1110.61	1.4	1	24.9	23.6	94.00%	E.FYLWLLKE.C		K.CNEFYLWLLKECDK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
84	A6ZNT8_YEAS7	18.07%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
465	480	2	1841.82	-1	1	46.2	30.8	95.00%	K.VIDNADDEYMALMSQK.T		K.VIDNADDEYMALMSQK.T
49	65	2	1969.91	0.063	0	54.5	29.6	95.00%	K.VVPIVYDPNDIVCDHSE.I	Carbamidomethyl (+57)	K.VVPIVYDPNDIVCDHSEILSPK.V
561	588	3	3252.36	0.25	1	100	31.1	95.00%	E.YDTPWDLTDGYLDDDDGLFSDN RNSGMR.A		R.LNDDANEYDTPWDLTDGYLDDD DGLFSDNRNSGMR.A
656	667	2	1328.76	0.51	1	60.7	22.7	95.00%	E.NLTAVITDLLEK.L		K.VENLTAVITDLLEK.L
2	15	2	1465.71	1	0	62.3	29.2	95.00%	M.VSANGDLHLPISNE.Q	Deamidation (+1)	- .MVSANGDLHLPISNEQCMPENNG SLGFEAPTPR.Q
21	33	2	1359.64	0.48	1	70.2	29.6	95.00%	E.NNGSLGFEAPTPR.Q	Deamidation (+1)	- .MVSANGDLHLPISNEQCMPENNG SLGFEAPTPR.Q
125	133	2	1060.53	0.4	0	31.9	28.1	95.00%	R.NLASQQLCK.L	Carbamidomethyl (+57)	R.NLASQQLCK.L

561	583	2	2707.12	0.4	0	78	31	95.00%	E.YDTPWDLTDGYLDDDDGLFSDNR.N		R.LNDDANEYDTPWDLTDGYLDDDDGLFSDNR.N
502	509	2	1009.54	1.5	0	30.5	23.9	95.00%	E.VFMTPIFR.I		R.APDEDVYVSPLNLIEVFMTPIFR.I
49	70	2	2508.26	0.05	1	43.7	27.3	95.00%	K.VVPIVYDPNDIVCDHSEILSPK.V	Carbamidomethyl (+57)	K.VVPIVYDPNDIVCDHSEILSPK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
85	A6ZKW1_YEAS7	13.40%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
83	98	2	1920.91	1.3	0	78.6	29.1	95.00%	K.SFYNNVFNFLMVDSPK.G		K.SFYNNVFNFLMVDSPK.G
560	569	2	1178.58	-0.85	0	40.1	28.5	95.00%	K.YLDDLLGQDK.T		K.YLDDLLGQDK.T
320	333	2	1575.79	-0.14	1	58.5	28.1	95.00%	R.NSRDDITPPAVYTK.D		R.NSRDDITPPAVYTK.D
448	458	2	1238.6	-0.25	1	51	28.8	95.00%	R.YLNAMESIGNK.Y		R.YLNAMESIGNK.Y
429	447	3	2190.99	0.78	0	37.3	30.4	95.00%	E.DGFHGVAMLQHDFVQDYGR.Y		R.TGVEGYHDEDGFHGVAMLQHDFVQDYGR.Y
546	555	2	1236.62	-1.4	1	46	28.7	95.00%	K.VLNEYVCVNK.N	Carbamidomethyl (+57)	K.VLNEYVCVNK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
86	A6ZXZ5_YEAS7	16.25%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
268	278	2	1191.52	0.23	0	27.4	29.5	90.70%	K.LGYHFGPSDAE.A		K.LGYHFGPSDAEAVMAPK.A
268	284	2	1788.85	0.43	1	34.8	29.7	95.00%	K.LGYHFGPSDAEAVMAPK.A		K.LGYHFGPSDAEAVMAPK.A
15	31	3	1836.99	0.54	1	34	24.8	95.00%	E.AIKINPPTGADFHITSR.G		R.GGNEAIKINPPTGADFHITSR.G
285	300	2	1575.87	-0.59	0	93	22.2	95.00%	K.APVASPRPAATPNLSK.D		K.APVASPRPAATPNLSK.D
18	31	2	1524.77	-0.55	0	71.2	27.9	95.00%	K.INPPTGADFHITSR.G		K.INPPTGADFHITSR.G
285	302	3	1818.99	-0.28	1	22.7	22.7	95.00%	K.APVASPRPAATPNLSKDK.K		K.APVASPRPAATPNLSKDK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
87	A6ZMQ9_YEAS7	52.53%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
48	58	2	1336.62	0.36	0	57.7	29.1	95.00%	E.LFDLLDQMDVE.V		K.HVEQQDELFDLLDQMDVEVNNSIGDASER.A
146	156	2	1235.6	0.14	0	32.4	28.4	95.00%	E.GIGSQIMMDLR.S	Oxidation (+16)	R.IANETEGIGSQIMMDLR.S
167	178	2	1413.68	-0.074	0	54.6	29.2	95.00%	R.QTLFQADSYVDK.S		R.QTLFQADSYVDK.S
103	117	2	1691.77	-0.43	0	68.3	30	95.00%	R.LFGDLNASNIDDDQR.Q		R.LFGDLNASNIDDDQR.Q
118	129	2	1391.79	-0.72	0	46.3	22.4	95.00%	R.QQLLSNHAILQK.S		R.QQLLSNHAILQK.S
21	34	2	1453.75	-0.49	1	51.8	26.5	95.00%	K.ASLAEAPSQPLSQR.N		K.ASLAEAPSQPLSQR.N
144	156	2	1449.7	0.82	1	55.3	29.4	95.00%	E.TEGIGSQIMMDLR.S		R.IANETEGIGSQIMMDLR.S
89	102	3	1612.83	0.68	1	37.8	26.5	95.00%	K.RPLQSLVDSGDRDR.L		K.RPLQSLVDSGDRDR.L
2	13	2	1429.7	0.36	1	61	29.3	95.00%	M.SSLLISYESDFK.T	Acetyl (+42)	-.MSSLLISYESDFK.T
103	129	3	3065.55	-1.4	1	56	26	95.00%	R.LFGDLNASNIDDDQRQQLLSNHAILQK.S		R.LFGDLNASNIDDDQRQQLLSNHAILQK.S
59	69	2	1160.54	2.3	1	43.1	29.6	95.00%	E.VNNSIGDASER.A		K.HVEQQDELFDLLDQMDVEVNNSIGDASER.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
88	A7A077_YEAS7	19.74%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
359	369	3	1305.64	-0.0049	1	22.8	28.4	92.90%	K.LGLSNEDFFHK.V		K.LGLSNEDFFHK.V
390	413	3	2877.4	1	1	23.4	28.5	93.80%	R.TNCMDCLDRTNVVQSVLAQWVLQK.E	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.TNCMDCLDRTNVVQSVLAQWVLQK.E
257	270	2	1602.84	0.24	1	59.1	26.1	95.00%	R.GSVPIYWAEINNLK.Y		R.GSVPIYWAEINNLK.Y
2	17	2	1767.92	0.5	0	61.5	25.1	95.00%	M.TGPIVYVQNADGIFFK.L		-.MTGPIVYVQNADGIFFK.L
399	413	2	1711.96	0.53	0	77.3	21	95.00%	R.TNVVQSVLAQWVLQK.E		R.TNVVQSVLAQWVLQK.E
295	308	2	1651.86	0.61	0	88.3	26.4	95.00%	E.LYGDNYLVNLVNQK.G		K.ELYGDNYLVNLVNQK.G
1	17	2	1898.96	0.52	0	32.7	27.6	95.00%	-.MTGPIVYVQNADGIFFK.L		-.MTGPIVYVQNADGIFFK.L
294	308	2	1780.9	0.56	1	66.1	27.6	95.00%	K.ELYGDNYLVNLVNQK.G		K.ELYGDNYLVNLVNQK.G
175	188	2	1612.85	-0.0034	0	58.9	26.5	95.00%	R.IDSFIQPVIYGYAK.T		R.IDSFIQPVIYGYAK.T
189	207	3	2021.2	-0.3	1	19.6	11.5	93.40%	K.TVDAVLNATPIVLGLITRR.S		K.TVDAVLNATPIVLGLITRR.S
189	206	2	1865.1	0.85	0	73	12.6	95.00%	K.TVDAVLNATPIVLGLITR.R		K.TVDAVLNATPIVLGLITR.R

390	398	2	1183.44	0.21	0	45.4	27.6	95.00%	R.TNCMDCLDR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.TNCMDCLDR.T
271	279	2	1031.57	-0.21	0	27.5	24.9	95.00%	K.YKPNLVLGE.N		K.YKPNLVLGENSLDATK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
89	A6ZX41_YEAS7	32.54%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
128	137	2	1212.61	-0.18	1	77.4	28.6	95.00%	R.NDPQTIEQLR.Q		R.NDPQTIEQLR.Q
2	10	2	1029.52	2.1	0	26	27.6	91.50%	M.SQQVGNSIR.R	Acetyl (+42)	-.MSQQVGNSIR.R
60	73	2	1651.75	0.47	1	74.8	29.7	95.00%	E.LALWDTAGQEDYDR.L		R.VELALWDTAGQEDYDR.L
104	123	3	2338.23	-0.74	1	25.6	24.2	95.00%	K.WIAEVLHFCQGVPIILVGCK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.WIAEVLHFCQGVPIILVGCK.V
108	123	2	1838.99	0.47	0	67.4	24	95.00%	E.VLHFCQGVPIILVGCK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.WIAEVLHFCQGVPIILVGCK.V
149	163	2	1557.7	0.9	0	50.7	29.9	95.00%	E.GQSVADQIGATGYYE.C		R.QEGQQPVTSQEGQSVADQIGAT GYYECSAK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
90	NCB5R_YEAST	37.68%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
91	102	2	1283.59	-0.71	0	32.9	29.7	95.00%	R.SYTPTSLDGDTK.G		R.SYTPTSLDGDTK.G
220	230	2	1195.59	1.1	0	35	28.8	95.00%	E.DWTGGVGYITK.D		R.EDWTGGVGYITK.D
178	187	2	1099.57	1.2	0	26.6	27.4	93.00%	K.VSLVFGNVHE.E		K.VSLVFGNVHEEDILLK.K
198	208	2	1218.68	0.23	0	32.8	24.5	95.00%	E.ALVAMKPSQFK.I		K.ELEALVAMKPSQFK.I
209	219	2	1368.66	1.3	1	45.1	29.3	95.00%	K.IVYYLDSPDRE.D		K.IVYYLDSPDREDWTGGVGYITK.D
60	80	3	2238.25	0.54	0	39	17.9	95.00%	K.FGLPHADDVLGLPIGQHIVIK.A		K.FGLPHADDVLGLPIGQHIVIK.A
49	59	2	1307.65	-0.0036	0	57	28.3	95.00%	K.TILTHNTSMYK.F		K.TILTHNTSMYK.F
147	166	2	2075.04	-0.72	0	51.6	27.8	95.00%	R.SHLGMIAGGTGIAPMYQIMK.A		R.SHLGMIAGGTGIAPMYQIMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
91	A6ZS21_YEAS7	31.53%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
297	311	3	1717.86	0.81	1	44.9	27.8	95.00%	K.RQAPSMFLDDVLNGR.E		K.RQAPSMFLDDVLNGR.E
142	156	2	1688.73	0.46	0	68.7	30.2	95.00%	K.HSSSLQSNPFDINDE.K		K.HSSSLQSNPFDINDEK.S
271	292	3	2214.16	-0.49	1	46.5	25.1	95.00%	K.RNQSSLGLIPVASATSNTSSPK.K		K.RNQSSLGLIPVASATSNTSSPK.K
272	292	2	2058.06	1	0	81.4	25.2	95.00%	R.NQSSLGLIPVASATSNTSSPK.K		R.NQSSLGLIPVASATSNTSSPK.K
177	194	3	2059.97	1.2	1	24.8	29	95.00%	E.DAASPFNPIQDPFTDNRR.S		K.SYMQDDWDSMSQLESSQYEDA ASPFNPIQDPFTDNRR.S
142	157	2	1816.83	2	1	58.2	30.8	95.00%	K.HSSSLQSNPFDINDEK.S		K.HSSSLQSNPFDINDEK.S
298	311	2	1561.75	-0.78	0	63	28.5	95.00%	R.QAPSMFLDDVLNGR.E		R.QAPSMFLDDVLNGR.E
195	209	2	1738.91	0.23	1	65	25.2	95.00%	R.SLFISPTLQVSQYEK.S		R.SLFISPTLQVSQYEK.S
122	133	2	1377.59	-0.59	0	49.4	30.6	95.00%	R.FTMTNSYANDSK.N		R.FTMTNSYANDSK.N
298	312	2	1691.78	0.92	1	72.6	29.9	95.00%	R.QAPSMFLDDVLNGRE.I	Deamidation (+1)	R.QAPSMFLDDVLNGREII.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
92	YL001_YEAST	15.78%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
485	496	2	1391.74	-0.3	1	26.8	25.6	95.00%	K.ELNLLDLPSNHK.G		K.ELNLLDLPSNHK.G
833	844	2	1291.65	0.77	0	48.9	28.9	95.00%	E.GSYSVNAIQTPR.D		R.ATTPLIQHSPIIHNPSYSATAHLSP LSQPTFEGSYSVNAIQTPR.D
551	563	2	1377.73	-0.14	0	82.3	26.1	95.00%	K.NLYGNSVSIGVQK.I		K.NLYGNSVSIGVQK.I
474	484	2	1314.68	0.4	0	25.4	26.8	92.10%	E.NHCSISLMLLK.E	Carbamidomethyl (+57)	K.ILNTKPYEIGNTSIYSIDDDLQLPG DLVLSLAPENHCSISLMLLK.E
801	844	4	4728.39	-1.5	1	27.5	25.4	95.00%	R.ATTPLIQHSPIIHNPSYSATAHLSP LSQPTFEGSYSVNAIQTPR.D		R.ATTPLIQHSPIIHNPSYSATAHLSP LSQPTFEGSYSVNAIQTPR.D
302	318	3	1963.02	0.047	1	49.5	26	95.00%	R.IFEIGVVHGFSDLDFLR.T		R.IFEIGVVHGFSDLDFLR.T
801	832	3	3454.75	0.53	0	38.8	23.5	95.00%	R.ATTPLIQHSPIIHNPSYSATAHLSP LSQPTFE.G		R.ATTPLIQHSPIIHNPSYSATAHLSP LSQPTFEGSYSVNAIQTPR.D
253	265	2	1414.81	0.063	0	82.1	22.1	95.00%	E.LIIDDVYGGILPK.E		R.TSLLQELIIDDVYGGILPK.E
247	265	2	2086.16	0.38	1	87.2	18.5	95.00%	R.TSLLQELIIDDVYGGILPK.E		R.TSLLQELIIDDVYGGILPK.E

242	252	2	1288.64	0.76	1	28.9	28.8	94.20%	K.WAADRTSLLQE.L		K.WAADRTSLLQELIIDDVYGGILPK.E
523	530	2	930.53	-0.13	0	41.6	25.3	95.00%	K.TALNLLMR.N		K.TALNLLMR.N
305	318	3	1573.83	1.6	0	42.8	25.5	95.00%	E.IGVVHGFSDLDFLR.T		R.IFEIGVVHGFSDLDFLR.T
97	103	2	914.46	0.077	0	25.1	26.1	92.60%	E.DFLIHDR.V		K.GDQTTDQFEEHFHIEDFLIHDR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
93	A6ZM72_YEAS7	9.61%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
11	28	2	1939	1.4	1	53.5	25.1	95.00%	E.SGSQQTSIHSTPIVQKLE.T		R.VESGSQQTSIHSTPIVQKLETDESPIQTK.S
296	309	2	1492.73	-0.69	1	87.2	28.9	95.00%	R.LAGNASWGELFSNK.G		R.LAGNASWGELFSNK.G
9	26	2	1924.99	1.2	1	86.2	26.6	95.00%	R.VESGSQQTSIHSTPIVQK.L		R.VESGSQQTSIHSTPIVQK.L
219	227	2	1153.52	0.77	0	47.9	30.1	95.00%	K.DYSNSVQWR.V		K.DYSNSVQWR.V
284	292	2	1022.44	2	0	27.1	27.6	93.50%	E.MDTIMANVE.T		K.VTIEDPSIVAEMDTIMANVETER.L
11	26	2	1696.87	-0.17	0	67.7	25.8	95.00%	E.SGSQQTSIHSTPIVQK.L		R.VESGSQQTSIHSTPIVQK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
94	A6ZXE6_YEAS7	8.78%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
208	219	3	1520.74	-0.063	0	27.7	28.9	95.00%	K.SDFTLYHTWPVR.V		K.SDFTLYHTWPVR.V
826	842	2	1763.86	0.16	1	37.5	28.6	95.00%	R.LGEMPADQGFPAYLGAK.L		R.LGEMPADQGFPAYLGAK.L
2	9	2	842.43	0.47	1	41.8	26.4	95.00%	M.AGAIENAR.K	Acetyl (+42)	-.MAGAIENAR.K
356	367	3	1445.71	0.37	1	26.1	28.4	95.00%	K.FTCNATHELVVR.T	Carbamidomethyl (+57)	K.FTCNATHELVVR.T
77	88	2	1197.67	0.065	0	25	23.7	94.20%	E.TAGLTVGDPVLR.T		K.ATIQVYEETAGLTVGDPVLR.T
925	937	2	1645.78	0.71	1	56.3	30	95.00%	K.FYDSNYPEFPVLR.D		K.FYDSNYPEFPVLR.D
950	959	2	1111.66	1.1	1	34.6	21.8	95.00%	E.LEQVVQLVGK.S		K.EILSNAEELEQVVQLVGK.S
446	455	2	1095.6	-0.29	0	48.3	24.4	95.00%	R.DLSLLGSHVR.K		R.DLSLLGSHVR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
95	G3P3_YEAST	21.08%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
322	331	3	1107.63	-0.8	1	30.6	22.7	95.00%	R.VVDLVEHVAK.-		R.VVDLVEHVAK.A
144	160	2	1818.9	-0.47	0	66.5	27.5	95.00%	K.IVSNASCTTNCLAPLAK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.IVSNASCTTNCLAPLAK.V
308	321	2	1751.78	-0.68	1	69.6	30.8	95.00%	K.LVSWYDNEYGYSTR.V		K.LVSWYDNEYGYSTR.V
199	213	2	1373.71	-0.23	0	53.4	27.3	95.00%	R.TASGNIIPSSTGAAK.A		R.TASGNIIPSSTGAAK.A
171	184	2	1486.78	-0.2	0	57	26.5	95.00%	E.GLMTTVHSLTATQK.T		K.VINDAFGIEEGLMTTVHSLTATQK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
96	B3LKQ2_YEAS1	15.84%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	153	3	1879.87	1	0	40.2	29.6	95.00%	R.GSNGSFSDHDLLLQYAR.K	Deamidation (+1)	R.GSNGSFSDHDLLLQYAR.K
335	345	2	1172.57	0.74	1	29.8	28	95.00%	E.GSIRDPIDATE.A		K.SVALPQYGTGDALTPEWEGSIRDPIDATEAK.C
167	184	2	1879.86	-0.27	0	81	30.4	95.00%	E.YISSMPHMSGTSGDAAIR.H		R.DLEYISSMPHMSGTSGDAAIR.H
235	255	3	2401.15	-0.0075	0	47.6	28.6	95.00%	E.NFNPMSHNGQLNNIPVIYANK.A	Oxidation (+16)/ Deamidation (+1)	K.DDTEGFDIPLNEENFNPMSHNGQLNNIPVIYANK.A
539	569	3	3380.7	0.39	0	47	25.2	95.00%	K.VDNVHQFGDWTPYLAQGIPVAIISSPGVMNR.E		K.VDNVHQFGDWTPYLAQGIPVAIISSPGVMNR.E
420	427	2	809.51	0.58	0	23	16.9	90.90%	R.AIVIAAPR.N		R.AIVIAAPR.N
6	23	2	1976.86	-1.1	1	62	30.5	95.00%	R.GYTTLPNVEEPANNSQDE.L		R.GYTTLPNVEEPANNSQDELNSQDFEQAIGMPSEPPVYVEEMGMEEPQAPEAFSEK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
97	A6ZQR6_YEAS7	49.68%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

10	27	2	1885.83	1.1	0	93.1	30.2	95.00%	E.TADAGSSATYPMQCSALR.K	Carbamidomethyl (+57)	- .MSDEEHTFETADAGSSATYPMQC SALR.K
29	35	2	776.44	-0.31	0	30.2	24.8	95.00%	K.NGFVVIK.S	Deamidation (+1)	K.NGFVVIK.S
90	114	3	2876.32	1.9	1	42.7	29.5	95.00%	E.YQLLDIDDGFLSLMNMDGDTKDD VK.A	Oxidation (+16)	R.NEYQLLDIDDGFLSLMNMDGDTK DDVK.A
57	68	2	1311.75	-0.32	0	66.2	21.3	95.00%	K.VHLVAIDIFTGK.K		K.VHLVAIDIFTGK.K
72	86	2	1651.83	0.84	1	50.3	28	95.00%	E.DLSPSTHNMEVPVVK.R		K.LEDLSPSTHNMEVPVVK.R
10	28	2	2013.93	0.26	1	76.4	30	95.00%	E.TADAGSSATYPMQCSALRK.N	Carbamidomethyl (+57)	- .MSDEEHTFETADAGSSATYPMQC SALRK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
98	A6ZZH5_YEAS7	22.98%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
68	76	2	1022.58	0.66	0	35.3	21.5	95.00%	K.KPPLLVNNE.A		K.KPPLLVNNEAVHASVPDASHTSC NNGTLEVSINNPEPHVVDAVAR.H
230	242	2	1526.77	3.1	0	64.4	28.3	95.00%	K.HNVDAPIPNFFTR.N		K.HNVDAPIPNFFTR.N
77	96	2	2066.9	-0.43	0	61.9	30.6	95.00%	E.AVHASVPDASHTSCNNGTLE.V	Carbamidomethyl (+57)/ Deamidation (+1)	K.KPPLLVNNEAVHASVPDASHTSC NNGTLEVSINNPEPHVVDAVAR.H
172	191	2	2039.89	1.1	0	36.7	30.6	95.00%	R.SMSFSAASIASSSHLNNNSE.A		R.SMSFSAASIASSSHLNNNSEANG NPLAAIGLAPAPMTHEEIR.A
97	112	2	1715.9	0.33	0	53.9	26.4	95.00%	E.VSINNPEPHVVDAVAR.H		K.KPPLLVNNEAVHASVPDASHTSC NNGTLEVSINNPEPHVVDAVAR.H
229	242	3	1654.86	0.84	1	35.5	26.5	95.00%	R.KHNVDAPIPNFFTR.N		R.KHNVDAPIPNFFTR.N
136	169	3	3761.73	-0.66	0	61	28.9	95.00%	K.WTNDHPSSPSQYQYPSQPALST SIPSQAPSFSNR.K		K.WTNDHPSSPSQYQYPSQPALST SIPSQAPSFSNR.K
192	211	2	1972.97	1.4	1	52.8	27.5	95.00%	E.ANGNPLAAIGLAPAPMTHEE.I		R.SMSFSAASIASSSHLNNNSEANG NPLAAIGLAPAPMTHEEIR.A
117	131	2	1598.8	-1	0	99.5	28	95.00%	R.NPSNSLQLQGGDITR.D		R.NPSNSLQLQGGDITR.D
355	365	2	1140.49	-0.46	0	51	28.8	95.00%	K.VGVDGYGDMGR.I	Oxidation (+16)	K.VGVDGYGDMGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
99	A6ZYN3_YEAS7	19.72%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	147	2	1174.66	1.3	0	60	23.8	95.00%	E.GLPLDTLFTAK.D		R.CQPVEGLPLDTLFTAK.D
246	268	2	2629.29	-0.21	0	26.2	27.6	92.00%	R.IFPPIDDPLPFKPLMDDSDVTLE.E	Oxidation (+16)	R.IFPPIDDPLPFKPLMDDSDVTLEE AVTHQR.I
44	61	3	2168.06	0.51	1	29.9	28.7	95.00%	R.QFYINDLTISHPYATTER.V		R.QFYINDLTISHPYATTER.V
132	147	2	1787.91	-0.61	1	47.3	26.8	95.00%	R.CQPVEGLPLDTLFTAK.D	Carbamidomethyl (+57)	R.CQPVEGLPLDTLFTAK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
100	A6ZZQ2_YEAS7	11.66%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
582	606	2	2589.07	-1.9	1	108	31	95.00%	K.SQAYGATMSNESNANNNNSTSN ASR.S		K.SQAYGATMSNESNANNNNSTSN ASR.S
169	179	2	1265.55	-0.024	1	39.3	29.8	95.00%	K.SFVDENSPTDR.R		K.SFVDENSPTDR.R
319	335	2	1855.99	0.63	0	45	24.1	95.00%	E.DGILFSKPIVTNIDVPE.L		R.SQAIQDAEAFHFQYDEDEEDGTS NEDGILFSKPIVTNIDVPELGNR.R
381	393	2	1411.78	-0.78	0	59.6	23.7	95.00%	R.IQSGLQDNLLVGR.N		R.IQSGLQDNLLVGR.N
110	126	2	1811.91	0.5	1	44.3	27.9	95.00%	R.EGPQSVSSTVQPQPIMK.F		R.EGPQSVSSTVQPQPIMK.F
394	410	3	2075.03	0.0005	1	28.5	27.8	95.00%	R.NIQYPPHIISNNPEHFR.F		R.NIQYPPHIISNNPEHFR.F
468	480	2	1344.73	0.89	1	55.6	25.8	95.00%	K.AETVSQLQGLTAK.N		K.AETVSQLQGLTAK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
101	A7A1Z8_YEAS7	16.08%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
390	401	2	1360.73	-1.3	0	49.9	26.3	95.00%	R.IYGDNINAQLLK.H		R.IYGDNINAQLLK.H

311	321	2	1332.6	-1.2	1	43.6	30.2	95.00%	R.ALNIEDCDLDR.A	Carbamidomethyl (+57)	R.ALNIEDCDLDR.A
322	334	2	1579.79	-0.34	1	54.5	28.2	95.00%	R.ATNDFYLEPLIER.D		R.ATNDFYLEPLIER.D
471	484	2	1519.84	-0.34	0	41.6	23.8	95.00%	R.DTVVLEPSGHVVLR.F		R.DTVVLEPSGHVVLR.F
159	168	2	1212.58	0.41	0	42.8	28.7	95.00%	R.VITLSDHYHE.N		R.VITLSDHYHENYK.T
372	383	2	1229.72	-0.58	0	25.8	20.1	95.00%	K.VPTLTTLLTSGK.L		K.VPTLTTLLTSGK.L
524	533	2	1280.61	-0.3	1	52.9	29.2	95.00%	K.LNENYLDICK.A	Carbamidomethyl (+57)	K.LNENYLDICK.A
418	432	4	1837.95	0.18	0	17.2	26.2	92.70%	R.HPFHLHGHNFQIVQK.S		R.HPFHLHGHNFQIVQK.S
159	171	3	1617.78	0.26	1	30.8	28.7	95.00%	R.VITLSDHYHENYK.T		R.VITLSDHYHENYK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
102	A6ZRM3_YEAS7	16.87%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
159	168	2	1161.6	0.58	0	35.4	27.8	95.00%	E.TNFIPQDISK.I		K.LMTPLTFSTETNFIPQDISK.I
149	158	2	1138.56	0.95	0	29.4	29.5	94.00%	K.LMTPLTFSTE.T		K.LMTPLTFSTETNFIPQDISK.I
149	168	2	2298.15	-0.1	1	72.9	27.6	95.00%	K.LMTPLTFSTETNFIPQDISK.I	Oxidation (+16)	K.LMTPLTFSTETNFIPQDISK.I
109	121	3	1541.86	-0.76	1	27.9	23	95.00%	K.VVSYILNHKDQVK.C		K.VVSYILNHKDQVK.C
76	83	2	991.52	1.4	1	38.3	28.2	95.00%	E.FIELIDDK.I		K.EYVFVGDVHGNYDEFIELIDDK.I
273	286	2	1578.76	0.31	0	73.1	28.7	95.00%	K.VFYGHDASMGLNLR.R		K.VFYGHDASMGLNLR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
103	B3LJX9_YEAS1	23.01%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
302	317	2	1670.87	0.42	0	38.1	25.5	95.00%	K.ILLQATPSTLSGDQVE.G		K.ILLQATPSTLSGDQVEGDLLK.I
393	411	3	2047.01	-0.14	0	70.9	28.5	95.00%	R.AGDSQGDHLQNDPLSLRPK.T		R.AGDSQGDHLQNDPLSLRPK.T
412	439	3	3030.23	0.66	1	68.6	30.9	95.00%	K.TYGTGISGSTCLIDDAANCNTADCLEDH.-	Carbamidomethyl (+57)/Carbamidomethyl (+57)/Carbamidomethyl (+57)	K.TYGTGISGSTCLIDDAANCNTADCLEDH.-
213	234	3	2338.05	-0.25	1	54	30.7	95.00%	K.TPSYSTSSHTIASGGNYTEHNK.R		K.TPSYSTSSHTIASGGNYTEHNK.R
213	231	2	1958.85	0.87	0	56.3	30	95.00%	K.TPSYSTSSHTIASGGNYTE.H		K.TPSYSTSSHTIASGGNYTEHNK.R
371	381	2	1214.59	0.65	0	27.5	29	91.80%	R.YGIHSATLQPE.F		R.YGIHSATLQPEFITR.E
302	322	2	2197.19	0.36	1	97	23	95.00%	K.ILLQATPSTLSGDQVEGDLLK.I		K.ILLQATPSTLSGDQVEGDLLK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
104	B3LQG1_YEAS1	16.16%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
340	348	3	1109.6	-0.18	0	20.7	23.3	95.00%	K.LFHNLNQPK.L		K.LFHNLNQPK.L
51	74	2	2661.22	0.75	1	88.4	29.8	95.00%	K.EISQSINSANNIQSSDSDLVQHFE.S		K.EISQSINSANNIQSSDSDLVQHFESLAQEIR.H
52	74	2	2532.17	0.24	0	80.9	29.7	95.00%	E.ISQSINSANNIQSSDSDLVQHFE.S		K.EISQSINSANNIQSSDSDLVQHFESLAQEIR.H
107	115	2	1011.54	1.2	1	22.6	24.7	90.10%	K.QTPPEATLR.E		K.QTPPEATLR.E
349	358	2	1129.68	0.16	0	52	19.7	95.00%	K.LLSDVLVFPK.F		K.LLSDVLVFPK.F
118	129	3	1407.69	0.72	0	30.8	29	95.00%	R.IAMTFPYDSHVK.F		R.IAMTFPYDSHVK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
105	A6ZWC1_YEAS7	24.24%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
144	152	2	1059.61	0.17	0	70.8	23.7	95.00%	K.VFLDIGLQR.T		K.VFLDIGLQR.T
159	177	3	1902.95	0.48	1	29.6	28.1	95.00%	R.VFGALKGASDGGLYVPHSE.N		R.VFGALKGASDGGLYVPHSENR.F
178	186	2	1166.52	1.2	1	37.2	28.8	95.00%	E.NRFPGWDFE.T		K.GASDGGLYVPHSENRFPGWDFETEEIDPELLR.S
225	245	2	2312	0.13	1	112	30.7	95.00%	K.GYLADDIDADSLEDIYTSAHE.A		K.GYLADDIDADSLEDIYTSAHEAIR.A
197	210	2	1645.71	0.73	1	58.7	30.6	95.00%	R.SYIFGGHVSQYMEE.L		R.SYIFGGHVSQYMEELADDDEER.F
165	177	2	1287.57	0.77	0	70	30.4	95.00%	K.GASDGGLYVPHSE.N		K.GASDGGLYVPHSENR.F
165	179	3	1557.72	0.068	1	32.8	30.3	95.00%	K.GASDGGLYVPHSENR.F		K.GASDGGLYVPHSENR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
106	A7A0U0_YEAS7	9.30%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
408	423	2	1609.81	0.48	1	65.4	28.2	95.00%	E.NGVVRAPADVNAIADE.T		K.LMVVHDENGVVRAPADVNAIADETTPLNSK.H
66	79	2	1581.75	-0.43	1	60.3	29.5	95.00%	K.LGTITGYDLAENCR.H	Carbamidomethyl (+57)	K.LGTITGYDLAENCR.H
413	430	2	1825.91	-0.18	1	85.6	28.5	95.00%	R.APADVNAIADETTPLNSK.H		R.APADVNAIADETTPLNSK.H
401	412	2	1367.69	0.93	1	50	27.7	95.00%	K.LMVVHDENGVVR.A	Deamidation (+1)	K.LMVVHDENGVVR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
107	A6ZQU5_YEAS7	13.26%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
75	85	2	1305.73	0.9	0	49.8	23.7	95.00%	R.LFDNIIVFPTK.G		R.LFDNIIVFPTK.G
75	88	3	1547.87	0.71	1	45.4	21.4	95.00%	R.LFDNIIVFPTKGGK.N		R.LFDNIIVFPTKGGK.N
350	361	3	1482.76	0.81	1	43.7	26.5	95.00%	R.HGVFTFLTDYRK.I		R.HGVFTFLTDYRK.I
266	285	3	2227.98	0.14	1	53.1	31	95.00%	K.SVHAVHSHADGTSYDEEPYK.I		K.SVHAVHSHADGTSYDEEPYK.I
186	196	2	1248.72	-0.58	1	48.6	20.9	95.00%	R.EQIVPILNAPR.T		R.EQIVPILNAPR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
108	A7A1W6_YEAS7	33.33%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
80	92	3	1529.72	0.79	1	26.5	29.8	95.00%	E.FNYIRDQSSGSTR.K		K.LYHEFNYIRDQSSGSTR.K
248	266	3	2175.11	0.78	1	27	26.1	95.00%	K.LYPLATFHLAQAQDFEGVR.A		K.LYPLATFHLAQAQDFEGVR.A
322	335	2	1715.84	-0.46	1	69.2	28.2	95.00%	R.NITWIAECIAQNQR.E	Carbamidomethyl (+57)	R.NITWIAECIAQNQR.E
220	238	2	2042.05	-0.98	0	96.7	26.6	95.00%	R.SINIALNSLQSSDIDPDLK.S		R.SINIALNSLQSSDIDPDLK.S
248	263	2	1862.92	0.85	0	45.8	27.7	95.00%	K.LYPLATFHLAQAQDFE.G		K.LYPLATFHLAQAQDFEGVR.A
267	276	2	1168.59	-0.44	1	57.4	27.3	95.00%	R.AALANVYEYR.G		R.AALANVYEYR.G
220	247	3	2979.58	-0.2	1	66.6	20.3	95.00%	R.SINIALNSLQSSDIDPDLKSDLLPNIGK.L		R.SINIALNSLQSSDIDPDLKSDLLPNIGK.L
62	70	2	990.52	1.4	0	36.6	26.8	95.00%	E.SLTTSLIQE.Y		K.LQLSSTDYGNFLSSVSSESLTTSLIQEYASSK.L
22	43	2	2566.22	0.4	1	96.5	28.3	95.00%	R.NGLLSNNQYINLTQCDTLEDLK.L	Deamidation (+1)/ Carbamidomethyl (+57)	R.NGLLSNNQYINLTQCDTLEDLK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
109	A6ZP92_YEAS7	15.54%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
441	454	2	1533.81	0.85	0	24.3	25.8	91.70%	E.NQVTPSSTPYISLK.V		K.ADFLVPGENQVTPSSTPYISLK.V
433	454	2	2362.21	-0.17	1	44	25.5	95.00%	K.ADFLVPGENQVTPSSTPYISLK.V		K.ADFLVPGENQVTPSSTPYISLK.V
573	589	2	1889.97	-1.1	1	62.5	26.7	95.00%	K.IPLGQPAPETVGDFFFR.V		K.IPLGQPAPETVGDFFFR.V
483	493	2	1296.6	0.68	1	47.3	30.3	95.00%	E.SQRDPFAMMSK.Q		K.QPLIPTSLIPEENLTEPQDFESQRDPFAMMSK.Q
511	521	2	1310.57	-0.56	0	35.3	29.8	95.00%	R.GSWCCLVSSQK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GSWCCLVSSQK.D
195	212	4	1888.92	0.76	0	23.8	29.3	95.00%	K.YGHPDGPQSTSHGIALPR.F		K.YGHPDGPQSTSHGIALPR.F
525	534	2	1166.73	0.41	1	27.9	14	95.00%	K.ILQTPIIIEK.L		K.ILQTPIIIEK.L
129	142	2	1474.8	0.73	1	34.8	24	95.00%	E.ILGISTSASDRDIK.S		K.LFDPYEILGISTSASDRDIK.S
582	589	2	987.48	1.8	0	38.1	28.8	95.00%	E.TVGDFFFR.V		K.IPLGQPAPETVGDFFFR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
110	A6ZNY0_YEAS7	15.20%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
93	114	2	2363.09	0.63	0	41.3	29.9	95.00%	K.TDGNSFLINLIDSPGHVDFSSE.V		K.TDGNSFLINLIDSPGHVDFSSEVTAALR.V
2	10	2	1065.53	1	0	38.7	28.7	95.00%	M.VAFTVDQMR.S		-.MVAFTVDQMR.S
244	253	2	1209.58	0.055	0	34.4	29.8	95.00%	R.LWGDSFFNPK.T		R.LWGDSFFNPK.T
758	769	2	1371.75	-0.17	1	38	24.2	95.00%	E.EQRPGTPLFTVK.A		R.GQVVSEEQRPGTPLFTVK.A
712	723	2	1265.66	-3.6	0	53.3	27	95.00%	R.ATYAGFLLADPK.I		R.ATYAGFLLADPK.I
151	162	3	1378.87	1	1	29.8	15.3	95.00%	R.IKPVVVINKVDR.A		R.IKPVVVINKVDR.A
618	631	2	1626.7	-0.62	0	81.6	30.4	95.00%	R.IMADDYGWDVTDAR.K		R.IMADDYGWDVTDAR.K

33	42	2	1118.59	0.17	0	40.3	26.9	95.00%	K.STLTDSLVQR.A		K.STLTDSLVQR.A
196	206	2	1215.66	0.48	0	47.3	26.4	95.00%	E.VLGDVQVYPAR.G		R.TVESVNVIVSTYADEVLGDVQVYPAR.G
540	555	4	1843.93	0.14	1	23.6	27.9	95.00%	E.ICLQDLEHDHAGVPLK.I	Carbamidomethyl (+57)	K.SDPCVLTYMSESGEHIVAGTGELHLEICLQDLEHDHAGVPLK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
111	YOL19_YEAST	36.12%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
376	402	3	3114.35	-1.5	1	40.8	30.3	95.00%	R.LLNDIMETSFNEPNDSHINSMSSYNDK.D		R.LLNDIMETSFNEPNDSHINSMSSYNDK.D
383	402	2	2285.95	1.7	0	60.1	31	95.00%	E.TSFNEPNDSHINSMSSYNDK.D		R.LLNDIMETSFNEPNDSHINSMSSYNDK.D
472	501	3	3257.62	-0.24	0	75	25.6	95.00%	R.TTPAGPDPSNVILQSNPYFNVAPNQVPQHR.N		R.TTPAGPDPSNVILQSNPYFNVAPNQVPQHR.N
502	529	3	2950.53	-1.5	0	45.8	24.2	95.00%	R.NPVPGVGFAPNPLPNQSPITQGYKPAYK.R		R.NPVPGVGFAPNPLPNQSPITQGYKPAYK.R
540	551	2	1339.65	-0.018	0	37.3	29	95.00%	R.ATTSLNNPYGFR.-		R.ATTSLNNPYGFR.-
351	365	2	1557.73	0.71	0	95.3	30.2	95.00%	E.ISSSASLASSDYSQR.E		K.TEISSSASLASSDYSQR.E
203	214	2	1336.67	-0.31	0	36.9	28.5	95.00%	K.GMLLNDPYLSSK.S		K.GMLLNDPYLSSK.S
452	471	3	2615.26	0.53	0	21.1	28.1	90.00%	R.LQPQQQQPQQQYHQYNLYQR.T		R.LQPQQQQPQQQYHQYNLYQR.T
425	451	3	2898.49	-1.1	1	43.4	24	95.00%	R.ETAAGPANIRPYAGQPHPAPLVYPQQR.L		R.ETAAGPANIRPYAGQPHPAPLVYPQQR.L
60	77	2	2126.88	-0.14	1	84.3	30.9	95.00%	K.ASYNYHPDELSDSDSNWK.L		K.ASYNYHPDELSDSDSNWK.L
403	412	2	1106.56	-0.91	0	40.2	28.8	95.00%	K.DSTLTSISQR.G		K.DSTLTSISQR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
112	MNN5_YEAST	19.62%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
310	323	2	1645.73	-0.25	0	53.6	30.8	95.00%	R.YDPFVSNSNDYTPK.E		R.YDPFVSNSNDYTPK.E
504	513	2	1115.57	-0.38	1	40.2	28.7	95.00%	R.FIGPNGEQVR.G		R.FIGPNGEQVR.G
493	503	2	1400.65	0.34	1	50.1	29.9	95.00%	K.ADPWTLYHENR.F		K.ADPWTLYHENR.F
299	309	2	1220.6	-0.26	0	40.4	29.1	95.00%	R.FVSDDISPVSR.Y		R.FVSDDISPVSR.Y
426	439	3	1675.82	0.31	1	27.1	28.7	95.00%	K.GLALLQHDFEQDYK.Q		K.GLALLQHDFEQDYK.Q
426	435	2	1141.58	0.77	0	42.1	26.4	95.00%	K.GLALLQHDFE.Q		K.GLALLQHDFEQDYK.Q
278	295	2	1890.03	-0.11	0	44.7	23.9	95.00%	R.VTPPAFYNIIGSSINIGK.R		R.VTPPAFYNIIGSSINIGK.R
53	77	3	2750.38	-0.032	1	33.2	26	95.00%	K.NNFYTTLVQAIVENKPADSSPDLSK.L		K.NNFYTTLVQAIVENKPADSSPDLSK.L
53	65	2	1510.77	-0.2	0	59.8	27.9	95.00%	K.NNFYTTLVQAIVE.N		K.NNFYTTLVQAIVENKPADSSPDLSK.L
414	425	2	1571.69	0.37	1	37.6	30.1	95.00%	E.FDGFFYQKDDYK.G		R.TNFEFDGFFYQKDDYK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
113	EF3A_YEAST	7.57%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
944	954	2	1095.59	0.62	0	41.4	25.5	95.00%	E.GGVIIITHSAE.F		K.EFEGGVIIITHSAEFTK.N
829	842	2	1700.82	0.16	0	32.1	29.5	95.00%	R.WVPMMSVDNAWIPR.G		R.WVPMMSVDNAWIPR.G
650	660	2	1234.62	0.22	1	28.5	27.8	94.90%	K.FPEPGYLEGVK.T		K.FPEPGYLEGVK.T
971	987	3	1737.8	-0.45	0	64.7	29.6	95.00%	R.MTPSGHNWVSGQGAGPR.I		R.MTPSGHNWVSGQGAGPR.I
266	275	2	1149.56	2.9	0	47	29.2	95.00%	K.SAVIIDNMCK.L	Carbamidomethyl (+57)	K.SAVIIDNMCK.L
332	347	2	1668.83	-0.061	0	70.7	27.9	95.00%	E.LSHAGDVSTTLQVVNE.L		R.VGNVGEDDAIPELSHAGDVSTTLQVVNELLK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
114	A6ZMK1_YEAS7	33.67%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
158	168	2	1192.55	-0.023	1	49.9	29	95.00%	R.AVQDNGESAFR.T		R.AVQDNGESAFR.T
46	59	3	1614.01	0.8	0	23.1	10.4	95.00%	K.IAPRPLDLLRPVVR.A		K.IAPRPLDLLRPVVR.A
82	91	2	963.52	1.5	0	28.5	25.6	95.00%	K.AAGLTAAYAR.T		K.AAGLTAAYAR.T
137	157	2	2155.13	-0.013	1	88.8	25.5	95.00%	E.QVLSAAATFPIAQPATDVEAR.A		K.APEAEQVLSAAATFPIAQPATDVEAR.A

105	115	2	1332.64	-0.47	1	60.8	28.8	95.00%	R.NQEIFDANVQR.L		R.NQEIFDANVQR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
115	B3LKG8_YEAS1	8.06%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
403	412	2	1076.59	1.6	0	34.5	26.1	95.00%	R.NLYALAIDGK.A		R.NLYALAIDGK.A
16	30	2	1687.69	-0.89	0	56.6	31	95.00%	R.NSSSLDSDHDAYYSK.Q		R.NSSSLDSDHDAYYSK.Q
31	40	2	1186.56	0.73	1	33.1	29.2	95.00%	K.QNPDNFPVKE.Q		K.QNPDNFPVKEQEIYNIDLEENNVSSR.S
559	569	2	1316.61	0.82	1	60	29.5	95.00%	K.STDVDLYTFKE.I		K.STDVDLYTFKEIYDR.E
403	415	2	1372.77	-0.017	1	70.1	23.6	95.00%	R.NLYALAIDGKAPK.I		R.NLYALAIDGKAPK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
116	A6ZSL7_YEAS7	25.00%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
33	43	2	1157.62	2.7	0	41	26.7	95.00%	K.NFGIGQAVQPK.R		K.NFGIGQAVQPK.R
134	144	2	1226.67	1.5	0	24.4	24.2	93.30%	K.YGLNHVVALIE.N		K.YGLNHVVALIENK.K
214	228	2	1699.79	-0.012	1	35.4	29.7	95.00%	K.LVSTIDANFADKYDE.V		K.LVSTIDANFADKYDEVK.K
194	204	2	1116.61	-0.56	1	64.5	26	95.00%	K.TSAVAALTEVR.A		K.TSAVAALTEVR.A
162	171	2	1158.68	0.87	0	38.7	20.3	95.00%	E.LVVFLPALCK.K	Carbamidomethyl (+57)	K.LVLIANDVDPIELVVFLPALCK.K
52	57	2	848.42	-0.5	1	29.6	26.4	95.00%	K.WPEYVR.V		K.WPEYVR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
117	GLRX7_YEAST	11.82%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
154	165	2	1212.68	-0.76	0	73.1	24.8	95.00%	R.TVPNVIIGGTSR.G		R.TVPNVIIGGTSR.G
94	105	2	1424.7	-0.58	1	69.7	28.4	95.00%	K.IMEQSPMIVFSK.T	Oxidation (+16)	K.IMEQSPMIVFSK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
118	A6ZQE5_YEAS7	56.52%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	71	2	1592.79	0.37	0	76.7	28.1	95.00%	E.SSPYAAMLAAQDVAAK.C		R.DESSPYAAMLAAQDVAAK.C
116	128	2	1414.69	-0.51	1	47.4	27.6	95.00%	R.IEDVTPVPSDSTR.K		R.IEDVTPVPSDSTR.K
20	37	2	2012.99	1.5	0	102	28.8	95.00%	R.IYASFNDTFVHVTDLSGK.E		R.IYASFNDTFVHVTDLSGK.E
10	19	2	1091.54	0.44	0	47.3	28.7	95.00%	R.DNSQVFGVAR.I		R.DNSQVFGVAR.I
94	104	2	1023.55	1.4	0	39	25.3	95.00%	K.TPGPGGQAALR.A		K.TPGPGGQAALR.A
74	83	2	1051.6	-0.21	1	23.1	20.9	91.00%	K.EVGITAVHVK.I		K.EVGITAVHVK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
119	A6ZZX2_YEAS7	32.97%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
136	149	2	1494.76	1.7	0	62.8	27.5	95.00%	R.TNTFTLLTSPDSAK.I		R.TNTFTLLTSPDSAK.I
108	135	3	2735.25	-0.18	0	92.3	29.6	95.00%	R.SAGDDNLSGHSVPSSGSAQATTHQTAPR.T		R.SAGDDNLSGHSVPSSGSAQATTHQTAPR.T
107	135	3	2891.35	-0.17	1	84.6	29.7	95.00%	E.RSAGDDNLSGHSVPSSGSAQATTHQTAPR.T		R.EDERSAGDDNLSGHSVPSSGSAQATTHQTAPR.T
166	182	2	1858	-0.12	0	43.4	23.7	95.00%	E.IFSQSQVNKPGPLTVPF.-		K.LHSNILNEIFSQSQVNKPGPLTVPF.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
120	AQR1_YEAST	12.29%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
282	292	2	1140.69	-0.72	0	31	21	95.00%	R.TIAGNLSIKPK.R		R.TIAGNLSIKPK.R
493	504	2	1361.6	-0.43	0	49.4	30.4	95.00%	K.SSTASSCFNFVR.C	Carbamidomethyl (+57)	K.SSTASSCFNFVR.C
39	54	2	1749.87	0.22	1	75.5	28.9	95.00%	K.LNFEGAYINSHGTLSK.T		K.LNFEGAYINSHGTLSK.T
505	517	2	1520.68	-0.69	0	60.3	29.9	95.00%	R.CSLSTIFMGCFAK.M	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.CSLSTIFMGCFAK.M
43	54	2	1247.61	-0.18	0	43	28.5	95.00%	E.GAYINSHGTLSK.T	Deamidation (+1)	K.LNFEGAYINSHGTLSK.T
563	572	2	1158.64	-0.27	0	29.8	25.3	95.00%	R.QSWLNTLAVK.A		R.QSWLNTLAVK.A
298	307	2	1081.67	0.25	0	30.5	17.3	95.00%	R.APIFLLGPVR.R		R.APIFLLGPVR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
121	A6ZUC1_YEAS7	16.08%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
48	59	2	1209.61	-0.69	0	28.1	28.7	93.20%	R.IVNGFGSLMGSK.E	Deamidation (+1)	R.IVNGFGSLMGSK.E
34	43	2	1013.59	0.77	0	23.8	23.4	92.30%	E.ANILATGLNK.K		K.DDSASSGIVDEVDLTEANILATGLNK.K
426	448	3	2334.19	1	1	46.2	26.1	95.00%	K.GLVIISGIVHDVSGYISEHPGGE.T		K.GLVIISGIVHDVSGYISEHPGGETLIK.T
10	28	2	2049.94	0.58	1	80.2	29.9	95.00%	E.LIDDQFPKDDSASSGIVDE.V		-.MPTSGTTIELIDDQFPKDDSASSGIVDEVDLTEANILATGLNK.K
34	44	2	1141.68	0.85	1	46.5	20.6	95.00%	E.ANILATGLNKK.A		K.DDSASSGIVDEVDLTEANILATGLNKK.A
398	414	3	1983.03	0.91	1	26.6	25.4	95.00%	K.AKINWGPVLTDLPMWDK.Q		K.AKINWGPVLTDLPMWDK.Q
400	414	2	1783.9	0.44	0	61.3	28	95.00%	K.INWGPVLTDLPMWDK.Q		K.INWGPVLTDLPMWDK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
122	VAC7_YEAST	11.67%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1141	1150	2	1271.62	-0.18	1	29.4	29	94.50%	K.YEVPFFNTQK.S		K.YEVPFFNTQK.S
513	553	4	4427.1	0.13	0	33.1	27	95.00%	R.HISTGAILNNTIATISTNPNLNSNVMQNNNNLMSGHNHLDE.L		R.HISTGAILNNTIATISTNPNLNSNVMQNNNNLMSGHNHLDELSSIK.Q
773	784	3	1567.69	1.4	0	24	29.7	92.60%	E.NDIHSMFYYNHK.N		K.FPHGLNFYGDNNVIEEENNGDSSNVNRPQHTNLQHEFIPEDNESDENDIHSMFYYNHK.N
699	715	2	2062.94	-0.24	1	83.2	30.2	95.00%	E.DYIEQPHNYPTMQNSVK.K		R.YSGVPDHVNLEDYIEQPHNYPTMQNSVK.K
14	50	3	3767.95	0.27	1	64.9	24.1	95.00%	E.TVEAPVANNLLLSNNSNVVAPNPSIPSASTSTSPLHR.E		K.LTVETETVEAPVANNLLLSNNSNVVAPNPSIPSASTSTSPLHR.E
744	762	3	2160.96	1.3	0	34.7	30.8	95.00%	E.NNGDSSNVNRPQHTNLQHE.F	Deamidation (+1)	K.FPHGLNFYGDNNVIEEENNGDSSNVNRPQHTNLQHEFIPEDNESDENDIHSMFYYNHK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
123	CHS3_YEAST	15.97%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
722	735	2	1454.78	0.27	0	56.5	26.3	95.00%	E.VKPYSYVAVASGSK.R		K.TTPEIALGMMDDFVTPPDEVKPYSYVAVASGSK.R
707	735	3	3086.5	-1	1	76	27.4	95.00%	E.IALGMMDDFVTPPDEVKPYSYVAVASGSK.R		K.TTPEIALGMMDDFVTPPDEVKPYSYVAVASGSK.R
47	62	3	1962.93	0.46	1	28.8	29	95.00%	R.SRLNNPDNPHFYYAQK.T		R.SRLNNPDNPHFYYAQK.T
935	945	2	1290.62	-0.94	0	46.8	29.1	95.00%	R.YSDNVTNTLHK.K		R.YSDNVTNTLHK.K
104	118	2	1772.78	-0.73	1	84.8	30.1	95.00%	R.ETDSYLLQDMNTTDK.K		R.ETDSYLLQDMNTTDK.K
1109	1118	2	1244.51	0.21	0	38.4	29.6	95.00%	K.FDDFSWGDTR.T		K.FDDFSWGDTR.T
598	612	2	1721.84	-0.42	0	50.7	28.7	95.00%	R.NPSTLLPTSSMFWNK.A		R.NPSTLLPTSSMFWNK.A
892	911	2	2314.03	1.4	1	112	29.7	95.00%	K.AFESVFGSVTCLPGCFSMYR.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.AFESVFGSVTCLPGCFSMYR.I
575	586	2	1368.62	0.067	0	62.5	30.2	95.00%	R.GMTTMTTQNAWK.L		R.GMTTMTTQNAWK.L
917	934	2	1985.99	0.8	1	64.1	28.4	95.00%	K.GSDGYWVPVLANPDIVER.Y		K.GSDGYWVPVLANPDIVER.Y
686	696	2	1259.7	0.018	0	26.7	24.7	95.00%	K.LLMVVCDGLIK.G	Carbamidomethyl (+57)	K.LLMVVCDGLIK.G
349	357	2	1083.54	1.3	1	40.3	27.4	95.00%	E.DRDAFYGLK.S		K.EDRDAFYGLK.S
282	301	3	2289.09	0.27	0	29.1	28.9	95.00%	K.DASFLFQNVNGNCHNLITPK.S	Deamidation (+1)/ Carbamidomethyl (+57)	K.DASFLFQNVNGNCHNLITPK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
124	A6ZX57_YEAS7	47.57%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
200	212	2	1390.76	1.6	1	48	23.8	95.00%	R.VAIGEVPFTFGVR.T		R.VAIGEVPFTFGVR.T
146	166	3	2297.14	0.088	0	41	27.3	95.00%	R.MMARPLTIASDPMSGFFGLQK.K		R.MMARPLTIASDPMSGFFGLQK.K
111	122	3	1353.68	1.3	0	52.3	28.7	95.00%	E.SLHDHAFTLGTR.Y		K.LFESLHDHAFTLGTR.Y
16	24	3	1054.65	-0.29	0	33.5	18	95.00%	K.LNIKPLTTR.L		K.LNIKPLTTR.L
25	35	2	1180.56	0.23	1	39.4	29	95.00%	R.LFAGMSPEMAK.K		R.LFAGMSPEMAK.K

88	107	3	2297.08	-0.54	1	31	29.3	95.00%	K.GQYLVCMDADLQHPPETVPK.L	Carbamidomethyl (+57)	K.GQYLVCMDADLQHPPETVPK.L
5	15	2	1304.68	0.15	1	29.5	26.7	95.00%	E.YSVIVPAYHEK.L		-.MSIEYSVIVPAYHEK.L
123	137	2	1766.85	0.44	1	54.1	29.7	95.00%	R.YAPGVGIDKDWPMYR.R		R.YAPGVGIDKDWPMYR.R
108	122	3	1742.87	0.45	1	36.2	27.6	95.00%	K.LFESLHDHAFTLGTR.Y		K.LFESLHDHAFTLGTR.Y
54	65	2	1341.68	0.067	0	54.7	27.3	95.00%	E.VDALAHQGYNVR.I		K.TELIFVDDNSQDGSVEEVDALAH QGYNVR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
125	A6ZU19_YEAS7	13.16%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
553	568	2	1731.91	-0.18	1	69.4	26.1	95.00%	K.LTLSDSSTPLTEDLIK.D		K.LTLSDSSTPLTEDLIK.D
638	655	2	2057	-1.3	0	72.7	29	95.00%	E.MSDDQLANVIDHVNIFAR.A		K.LDEMSDDQLANVIDHVNIFAR.A
361	372	2	1291.65	0.87	0	69.2	29.2	95.00%	E.TLGSVNVICSDK.T	Carbamidomethyl (+57)	R.LPSVETLGSVNVICSDK.T
627	637	2	1174.61	0.75	1	32	27.5	95.00%	K.LSVLSGDKLDE.M		K.LSVLSGDKLDEMSDDQLANVIDH VNIFAR.A
690	699	2	1033.52	0.28	0	54.7	27.4	95.00%	K.LSDIGVSMGR.I		K.LSDIGVSMGR.I
235	245	2	1241.61	-0.38	0	36.4	28.7	95.00%	R.SCIAYMGTLVK.E	Carbamidomethyl (+57)	R.SCIAYMGTLVK.E
158	178	3	2321.16	-0.24	1	34.4	27.3	95.00%	R.CGQESHVLASTLVPGDLVHFR.I	Carbamidomethyl (+57)	R.CGQESHVLASTLVPGDLVHFR.I
219	234	2	1788.86	-1.1	1	46.8	29.2	95.00%	K.SSFNDQPNSIVPISER.S		K.SSFNDQPNSIVPISER.S
28	37	2	1027.56	0.75	0	38	24.3	95.00%	E.ALSKPSPSLE.Y		R.EILDATAEALSKPSPSLEYCTLSV DETLEK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
126	A6ZT57_YEAS7	13.62%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
369	377	2	1155.59	-0.17	0	51.3	27.2	95.00%	K.SIYQVYLDR.A		K.SIYQVYLDR.A
590	602	2	1376.66	0.33	0	60.1	28.5	95.00%	R.LNGTALNPVDHPE.M	Deamidation (+1)	R.LNGTALNPVDHPEMFYSPTNDAY YAPQQQGQYMK.F
484	498	2	1864.86	0.39	0	53	30.4	95.00%	E.AIQPLNYQDQYQQQE.Q		R.IASSIYSEAIQPLNYQDQYQQQEQ SPVYNGHTQYPGNGYSGNPQQQG YTAQFVQNPQWYGVPTPQQQQHN HPQTLETIGELPTPAYLAQSASSHS LTSFK.R
700	723	3	2581.26	0.42	1	34.8	27.9	95.00%	E.TDVVQPPSVGGILPHSGSQDDLR K.Q	Phospho (+80)	R.VSGILEETDVVQPPSVGGILPHS GSQDDLRK.Q
399	413	3	1705.95	1.4	1	27.7	21.8	95.00%	E.NRVDNIVQNPLPSIK.I		K.ADNANDISQEENRVDNIVQNPLP SIK.I
638	661	3	2580.3	1.6	0	37	26.3	95.00%	R.QSVVMTNPSDLTAKPSYKPAGSF R.S		R.QSVVMTNPSDLTAKPSYKPAGSF R.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
127	RL20_YEAST	13.95%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
100	113	2	1552.76	-0.34	1	67.6	29.2	95.00%	R.VAAVETLYQDMAAR.H	Oxidation (+16)	R.VAAVETLYQDMAAR.H
29	38	2	1090.6	-0.39	1	57.7	25.7	95.00%	R.IFASNEVIAK.S		R.IFASNEVIAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
128	B3LI54_YEAS1	16.13%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
129	138	2	1219.57	0.48	1	31.8	29.3	95.00%	E.DSTIHIKDYE.D		K.VLEDSTIHIKDYEDDER.E
298	311	2	1519.76	-0.74	1	56.4	28.5	95.00%	K.SLRPSFDEAVSQGK.F		K.SLRPSFDEAVSQGK.F
218	240	3	2468.22	1.3	1	51.4	27.5	95.00%	K.ELHPDHVPTVGSSFVGMSLFNAK .N		K.ELHPDHVPTVGSSFVGMSLFNAK .N
314	323	2	1118.55	0.16	0	34.8	28.2	95.00%	R.AMPNSYLPAR.Q		R.AMPNSYLPAR.Q
72	83	2	1317.66	0.68	0	35.7	28.6	95.00%	R.SLGMIQSINNIE.A		R.SLGMIQSINNIEAYPVTGYTVFFN GEQVDIPYPYK.A
159	169	2	1241.64	-0.34	0	47.5	27.6	95.00%	R.NITAQEPNVTR.V		R.NITAQEPNVTR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
129	A6ZLZ0_YEAS7	12.33%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

715	723	2	963.46	1.1	0	34.3	29	95.00%	E.GCLVASAMR.G	Carbamidomethyl (+57)	R.VFGACCENVIGYMPLPVGVIGPLVIDGTSYHIPMATTEGCLVASAMR.G
727	740	2	1272.7	-0.72	0	73.1	25.5	95.00%	K.AINAGGGATTVLTK.D		K.AINAGGGATTVLTK.D
786	801	3	1914.98	0.76	0	35.2	26.7	95.00%	R.LQHIQTCLAGDLLFMR.F	Carbamidomethyl (+57)	R.LQHIQTCLAGDLLFMR.F
837	848	2	1327.61	0.023	0	29.1	30.3	92.40%	E.VVSVSGNYCTDK.K	Carbamidomethyl (+57)	K.QMVEEYGWEDMEVVSVSGNYCTDK.K
123	130	2	920.5	1.4	1	38.7	26.5	95.00%	E.LANTVFEK.D		R.DSSLDGWVSITAHEASELPAPHHYYLLNLNFNSPNETDSIPELANTVFEK.D
524	535	2	1374.71	-0.58	0	40.9	27.2	95.00%	R.IHTSYTADQLVK.T		R.IHTSYTADQLVK.T
804	817	2	1456.64	0.27	0	36	30.1	95.00%	R.TTTGDAMGMNMISK.G		R.TTTGDAMGMNMISK.G
671	683	2	1667.64	0.45	1	33.8	29.7	95.00%	K.NYDYDRVFGACCE.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.NYDYDRVFGACCENVIGYMPLPVGVIGPLVIDGTSYHIPMATTEGCLVASAMR.G
67	80	2	1818.76	-0.92	1	71.8	31.2	95.00%	K.DSNTLFQECSHYYR.D	Carbamidomethyl (+57)	K.DSNTLFQECSHYYR.D
1026	1043	3	1993.02	-0.059	0	20.9	26.4	93.30%	R.KPAEPTKPNNLDATDINR.L		R.KPAEPTKPNNLDATDINR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
130	YAJ8_YEAST	29.49%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
201	211	2	1248.68	1	0	68.9	25.4	95.00%	R.SDPILMAYVLK.A		R.SDPILMAYVLK.A
1	11	2	1248.57	1.5	1	27.6	29	92.00%	-.MQTPSENTDVK.M		-.MQTPSENTDVK.M
153	162	3	1294.64	0.41	1	40.3	28.7	95.00%	K.CHEFFTTLIK.E	Carbamidomethyl (+57)	K.CHEFFTTLIK.E
164	188	3	2434.05	0.87	1	29.9	31.3	95.00%	E.VNSGSHSDSSSNSAEDTQSPVSAGK.T		K.EVNSGSHSDSSSNSAEDTQSPVSAGK.T
189	200	2	1385.66	-0.31	0	48.3	30.3	95.00%	K.TSNGLNNFYSIR.S	Deamidation (+1)	K.TSNGLNNFYSIR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
131	A7A0B5_YEAS7	13.41%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
160	175	2	1747.88	0.34	1	64.2	27.8	95.00%	E.FETPLACVQAILSNGK.T	Carbamidomethyl (+57)/ Deamidation (+1)	R.VVAYAQNDTEFETPLACVQAILSNGK.T
133	149	2	1902.98	-1.1	0	71.7	26.4	95.00%	K.QFPGIAYTIPDLDAQVR.V		K.QFPGIAYTIPDLDAQVR.V
704	729	2	2764.35	0.8	1	71.6	27.6	95.00%	E.VTEQPVQPTSAVMGTGGSFLSPQYQR.A		K.QNSSPFDASEVTEQPVQPTSAVMGTGGSFLSPQYQR.A
736	752	2	1803.87	0.045	0	58	29	95.00%	R.TNLAPNNTSTSSLMKPE.S		R.TNLAPNNTSTSSLMKPESSLYLGNSNK.S
99	117	2	2080.01	0.51	0	96.5	29.3	95.00%	K.TFDLCSLGQVSLCPLSAGR.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.TFDLCSLGQVSLCPLSAGR.I
736	762	3	2867.4	-0.55	1	28.8	27.5	95.00%	R.TNLAPNNTSTSSLMKPESSLYLGNSNK.S		R.TNLAPNNTSTSSLMKPESSLYLGNSNK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
132	A6ZLE7_YEAS7	33.17%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
344	365	3	2628.22	0.46	1	34.1	29.6	95.00%	E.IHFFDGLGFHHPDFTSCPIEQK.I	Carbamidomethyl (+57)	K.SEIHFFDGLGFHHPDFTSCPIEQK.I
117	134	3	2349.04	0.087	1	28.5	30.8	95.00%	R.YHYDWVFLNDQPFSDEFK.R		R.YHYDWVFLNDQPFSDEFK.R
96	104	2	1087.57	0.35	0	35.3	27.8	95.00%	R.NSDLWNLVK.S		R.NSDLWNLVK.S
296	303	2	953.5	1.5	0	56	26.6	95.00%	E.IGSLDFFR.S		K.FISNDDGDTYNMCHFWTNFEIGSLDFFR.S
325	341	3	1825.93	-3.1	0	21.5	27.5	92.30%	R.WGDAPVHSIAASLFLDK.S		R.WGDAPVHSIAASLFLDK.S
276	295	2	2511.97	-0.91	0	43.7	30.4	95.00%	K.FISNDDGDTYNMCHFWTNFE.I	Carbamidomethyl (+57)	K.FISNDDGDTYNMCHFWTNFEIGSLDFFR.S
310	324	2	1864.8	2.1	1	41.8	30.7	95.00%	E.YFDYLDSSGGFFYER.W		R.EYFDYLDSSGGFFYER.W
60	72	2	1513.75	1.3	1	46.6	28.9	95.00%	R.VASKDYLMPFTDK.S		R.VASKDYLMPFTDK.S
117	132	2	2073.88	0.43	0	46.2	31	95.00%	R.YHYDWVFLNDQPFSDE.F		R.YHYDWVFLNDQPFSDEFK.R
379	390	2	1559.67	0.13	0	28.4	30	91.70%	K.DVTWTPDYFCTR.K	Carbamidomethyl (+57)	K.DVTWTPDYFCTR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
133	FET4_YEAST	15.40%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
306	316	2	1370.64	1	1	62	28.9	95.00%	R.FLVDIFDMDEK.I		R.FLVDIFDMDEK.I
445	454	2	1132.59	-0.46	1	46.1	27.3	95.00%	K.APEINTIGYR.T		K.APEINTIGYR.T
32	45	2	1642.72	0.35	1	61.3	29.9	95.00%	E.FGDSNDYKNDDVVR.V		K.QYEEFGDSNDYKNDDVVR.V
4	20	4	1884.97	0.64	1	34.6	25.7	95.00%	K.IAEFLGNPGARPDVHHR.A		K.IAEFLGNPGARPDVHHR.A
324	338	2	1780.84	0.26	1	29.1	29	94.30%	K.HFNDFETPHPVVTIE.S		K.HFNDFETPHPVVTIESK.K
248	265	2	1833.81	-1.2	1	98.2	31.1	95.00%	K.DAGNTPPYTGETTGSNPR.L		K.DAGNTPPYTGETTGSNPR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
134	B3LJS4_YEAS1	18.79%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
61	72	2	1479.66	0.45	1	37.3	30.1	95.00%	E.FDIEDPHDDLHK.R		R.FDDSPPSSNDNSIETNITPPPEPPSYEFDIEDPHDDLHK.R
248	258	2	1205.57	-1	1	43.2	28.5	95.00%	K.ENFNPLSSNGK.L		K.ENFNPLSSNGK.L
742	752	2	1229.67	1.5	0	24	24.9	92.70%	K.NVLFGPTLIQE.D		K.NVLFGPTLIQEDK.S
48	60	2	1440.68	0.4	0	33.5	29.9	95.00%	E.TNITPPPEPPSYE.F		R.FDDSPPSSNDNSIETNITPPPEPPSYEFDIEDPHDDLHK.R
34	47	2	1522.61	0.24	0	41.3	29.6	95.00%	R.FDDSPPSSNDNSIE.T		R.FDDSPPSSNDNSIETNITPPPEPPSYEFDIEDPHDDLHK.R
742	754	2	1472.79	0.6	1	33.8	25.2	95.00%	K.NVLFGPTLIQEDK.S		K.NVLFGPTLIQEDK.S
325	356	3	3357.59	-2.2	1	62.7	28.7	95.00%	E.NIDVVQSKPVGLPQYSTGDASGLNWDGSPVEE.K		K.AVIFISEPYGENIDVVQSKPVGLPQYSTGDASGLNWDGSPVEEK.D
299	309	2	1226.72	0.078	1	48	22.8	95.00%	K.LVSQQVLIAEK.F		K.LVSQQVLIAEK.F
3	16	2	1624.7	0.61	1	61	30	95.00%	R.SSYQPVSTTNFEHE.N		R.SSYQPVSTTNFEHENAIPTASSSHNLLMSQR.F
384	398	2	1477.66	-0.55	0	91.5	30.1	95.00%	R.LSSGGVTVDDGNSDR.S		R.LSSGGVTVDDGNSDR.S
17	33	2	1825.91	-0.55	0	77.8	28.3	95.00%	E.NAIPTASSSHNLLMSQR.F		R.SSYQPVSTTNFEHENAIPTASSSHNLLMSQR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
135	A6ZLU9_YEAS7	20.00%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
313	325	2	1424.67	0.13	0	30.7	29.6	95.00%	K.DFGQVIGQGFSDR.H		K.DFGQVIGQGFSDR.H
279	287	2	1159.5	-0.53	1	44	29.4	95.00%	K.YMDEGYINR.V		K.YMDEGYINR.V
131	150	2	2268.11	1.3	1	35.8	27.7	95.00%	E.VISKFDDGVQHYLISQFGSE.V		K.TIDLEDEEYYDYDFEDIDPEVISKFDDGVQHYLISQFGSEVLTPK.D
15	26	2	1272.65	-0.57	0	38	28.1	95.00%	K.AMDNGLSLPISR.N		K.AMDNGLSLPISR.N
201	211	2	1217.65	0.22	0	35.4	26.9	95.00%	R.NAADVLPLMFK.H		R.NAADVLPLMFK.H
501	521	3	2454.18	-2.3	0	28.6	28.5	95.00%	R.VGGLPHYTIWHIYEPSDDDLK.E		R.VGGLPHYTIWHIYEPSDDDLK.E
191	200	2	1248.7	-0.072	0	33.8	23.3	95.00%	R.DHILLCIPLR.N	Carbamidomethyl (+57)	R.DHILLCIPLR.N
472	482	2	1256.57	2.7	0	28	29.3	92.30%	R.NGVQFPAFTFE.N	Deamidation (+1)	R.NGVQFPAFTFENHAETEAFGK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
136	A6ZT02_YEAS7	10.76%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
10	38	2	2915.36	-1.3	1	75.7	29.3	95.00%	E.DTAVQNTPADALSPVESDSNSALSTPSNK.A		-.MSEEAAYQEDTAVQNTPADALSPVESDSNSALSTPSNK.A
311	324	2	1479.73	-0.83	1	78.9	29	95.00%	K.LAGNASWGEIFSTK.T		K.LAGNASWGEIFSTK.T
552	570	3	2299.98	0.35	1	45.3	31.1	95.00%	K.RGTDYNADDLMHDDQPFYK.K		K.RGTDYNADDLMHDDQPFYK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
137	VDAC1_YEAST	44.88%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
20	40	2	2268.07	-0.28	0	65.7	29.8	95.00%	K.DFYHATPAAFDVQTTTANGIK.F	Deamidation (+1)	K.DFYHATPAAFDVQTTTANGIK.F
96	108	2	1341.75	-0.69	1	61.7	23.1	95.00%	K.NELITSLTPGVAK.S		K.NELITSLTPGVAK.S
133	145	2	1403.64	0.98	0	56.3	30.2	95.00%	K.SPTFVGDLTMAHE.G		K.SPTFVGDLTMAHEGIVGGAEFGYDISAGSISR.Y
51	61	2	1129.56	0.33	1	26.2	27.9	91.50%	K.DGPLSTNVEAK.L		K.DGPLSTNVEAK.L

153	164	2	1271.62	0.46	0	88.8	29.6	95.00%	E.FGYDISAGSISR.Y		K.SPTFVGDLTMAHEGIVGGAEFGY DISAGSISR.Y
109	124	2	1799.92	0.093	0	57.9	26.9	95.00%	K.SAVLNTTFTQPFFTAR.G		K.SAVLNTTFTQPFFTAR.G
165	174	2	1163.57	0.5	0	49.9	28.7	95.00%	R.YAMALSYFAK.D		R.YAMALSYFAK.D
66	84	2	2060.03	-0.72	0	87	27	95.00%	K.QTGLGLTQGWSNTNNLQTK.L		K.QTGLGLTQGWSNTNNLQTK.L
237	248	2	1251.67	-0.084	0	78.6	25.9	95.00%	K.VSDSGIVTLAYK.Q		K.VSDSGIVTLAYK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
138	B3LPM2_YEAS1	22.52%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
210	223	2	1637.77	1.1	1	46.3	30.4	95.00%	E.NYFLSIAHTSENDK.L		R.TENYFLSIAHTSENDK.L
210	220	2	1280.6	0.77	0	51	29.1	95.00%	E.NYFLSIAHTSE.N		R.TENYFLSIAHTSENDK.L
73	89	3	1930.99	1.4	0	25	26.5	95.00%	R.GNQIFQSLHSFLANDLK.F		R.GNQIFQSLHSFLANDLK.F
16	32	2	1938.93	-0.57	1	71.5	29.2	95.00%	R.VNSLNAPYQALSYDEQK.A		R.VNSLNAPYQALSYDEQK.A
260	275	3	1875.94	0.32	1	22.5	28	93.00%	K.YISFTDLPVNPPRDDK.E		K.YISFTDLPVNPPRDDK.E
164	176	2	1410.81	1.6	0	33.6	20.7	95.00%	E.IVIRPNGILVTSE.S	Deamidation (+1)	K.QLEEFMEIVIRPNGILVTSESAHP NK.N
2	15	2	1551.8	1	1	77.1	28.1	95.00%	M.SSSIFGPLTGFLER.V	Acetyl (+42)	-.MSSSIFGPLTGFLER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
139	GLRX6_YEAST	33.33%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
208	219	2	1373.72	-0.3	1	44.4	26.9	95.00%	K.LLESLQVWSDGK.F		K.LLESLQVWSDGK.F
85	105	3	2197.16	0.65	1	40.7	24.5	95.00%	K.VGLQQPIASVDDSLSAIKNDK.G		K.VGLQQPIASVDDSLSAIKNDK.G
43	57	2	1560.63	-0.54	0	86.9	29	95.00%	K.AFSTNMDNMAGGSSR.E	Oxidation (+16)	K.AFSTNMDNMAGGSSR.E
85	102	2	1840	0.33	0	63.9	23.6	95.00%	K.VGLQQPIASVDDSLSAIK.N		K.VGLQQPIASVDDSLSAIK.N
118	133	2	1850.04	-1.1	1	64.7	19.6	95.00%	K.EYSLILDLSPIIIFSK.S		K.EYSLILDLSPIIIFSK.S
181	193	2	1324.75	-0.69	0	47.4	23.2	95.00%	R.GTVPNLLVNGVSR.G		R.GTVPNLLVNGVSR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
140	RTN1_YEAST	20.34%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
236	247	2	1267.67	-0.42	1	55.2	25.8	95.00%	K.LAADVPLEPESK.A		K.LAADVPLEPESK.A
208	216	2	939.58	-0.019	0	45.3	16.7	95.00%	K.LGPISNLVK.S		K.LGPISNLVK.S
248	269	2	2416.09	0.87	1	53.4	30.2	95.00%	K.AYTSSAQVMPEVPQHEPSTTQE. F		K.AYTSSAQVMPEVPQHEPSTTQE FNVDELSNELK.K
219	235	2	1589.79	-0.2	0	77.4	28.8	95.00%	K.TAPVSSTAGPQTASTSK.L		K.TAPVSSTAGPQTASTSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
141	A6ZLM5_YEAS7	9.13%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
225	238	2	1458.66	-0.97	0	107	29.9	95.00%	R.MNSSFLSSSSIGDK.I		R.MNSSFLSSSSIGDK.I
327	335	2	940.61	0.51	0	44.5	19.5	95.00%	K.LLIGSIIGR.M		K.LLIGSIIGR.M
183	198	2	1863.93	0.54	1	69.2	27.5	95.00%	E.NTQHMPPSQVQSLLER.T		K.WSGENTQHMPPSQVQSLLER.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
142	A6ZXE9_YEAS7	19.39%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
156	170	3	1796.93	0.84	1	23	25.9	95.00%	E.DSFRSDLVDLLNIYK.T		R.FSSEDSFRSDLVDLLNIYK.T
2	32	4	3406.72	0.037	1	19.8	25.2	95.00%	M.TAAKPNPYAAKPGDYLSNVNNF QLIDSTLRE.G		- .MTAAKPNPYAAKPGDYLSNVNNF QLIDSTLREGEQFANAFFDTEK.K
160	170	2	1291.7	1.2	0	35.6	25.4	95.00%	R.SDLVDLLNIYK.T		R.SDLVDLLNIYK.T
377	388	2	1330.7	-0.76	0	49.8	26.7	95.00%	R.SLNIDDVDSIIK.N		R.SLNIDDVDSIIK.N
180	192	2	1328.65	-0.6	0	78	29.3	95.00%	R.VGIADTVGCANPR.Q	Carbamidomethyl (+57)	R.VGIADTVGCANPR.Q
234	245	2	1269.73	0.62	1	70.9	23.1	95.00%	R.LIDVSVLGIGER.N		R.LIDVSVLGIGER.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
143	A6ZY13_YEAS7	7.78%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

400	412	2	1465.71	-0.047	0	74.9	29.2	95.00%	R.LMCSLAQQGYAPK.F	Carbamidomethyl (+57)	R.LMCSLAQQGYAPK.F
19	39	2	2245.04	0.35	0	54.1	29.8	95.00%	E.VTDSALYNNFNTSTTASLTPE.I		K.SAEFEVTDSALYNNFNTSTTASLTPEIK.E
269	281	2	1250.55	-0.67	1	65.6	29.1	95.00%	R.DPGSFAEGSGATR.F		R.DPGSFAEGSGATR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
144	FUI1_YEAST	7.98%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
83	98	3	1820.87	0.71	1	30	28.7	95.00%	K.NDSTDLADHKPENPIR.T		K.NDSTDLADHKPENPIR.T
626	635	2	1059.49	1.2	1	39.6	29.5	95.00%	E.YGGVSTGYEK.I		R.EAFEEYGGVSTGYEK.I
236	245	2	1105.59	-0.93	0	47.8	27.9	95.00%	K.AIFGTNLNTR.I		K.AIFGTNLNTR.I
109	123	2	1768.9	0.9	1	62.9	27.2	95.00%	R.STYLYNTDLRPVEAK.R		R.STYLYNTDLRPVEAK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
145	ARN2_YEAST	6.75%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
515	546	3	3446.73	-1.3	0	62.5	25	95.00%	K.LLHYMGDADLATAAYGSPLTFILSNPWGTPVR.S		K.LLHYMGDADLATAAYGSPLTFILSNPWGTPVR.S
601	611	2	1314.61	2.6	1	34.6	30.1	95.00%	K.EDDPINDWIAK.R		K.EDDPINDWIAK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
146	B3LRN6_YEAS1	36.07%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	141	2	1964.96	0.46	0	63.5	28.6	95.00%	K.YLISPDVHPAQNQNIQE.N		K.YLISPDVHPAQNQNIQENK.E
199	212	2	1512.75	0.33	0	37.2	28.5	95.00%	K.QTSNSTPAPQNQIK.E		K.QTSNSTPAPQNQIK.E
125	143	3	2207.1	-0.89	1	22.6	27.8	93.70%	K.YLISPDVHPAQNQNIQENK.E		K.YLISPDVHPAQNQNIQENK.E
24	38	2	1657.8	1.1	0	78.9	29.5	95.00%	E.YASISNNSDQTIAFK.V		K.SPLTEQSTEYASISNNSDQTIAFK.V
145	156	2	1326.67	0.44	0	60.5	27.6	95.00%	E.TVEPVVQDSEPK.E		K.ETVEPVVQDSEPK.E
85	99	2	1676.9	-2.3	0	48.7	25.1	95.00%	K.FLVITLPSPYDLNGK.A	Deamidation (+1)	K.FLVITLPSPYDLNGK.A
2	14	2	1460.78	0.36	1	36.8	25.7	95.00%	M.SAVEISPDVLVYK.S	Acetyl (+42)	-.MSAVEISPDVLVYK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
147	ATG27_YEAS7	22.51%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	88	2	1772.92	0.4	1	42.8	26.4	95.00%	K.KNDMLCGLTDVILPGK.D	Carbamidomethyl (+57)	K.KNDMLCGLTDVILPGK.D
119	130	2	1223.56	0.55	0	42	29.8	95.00%	K.GATWGANSFDAK.L		K.GATWGANSFDAK.L
89	100	2	1378.7	-0.087	0	34.4	27.5	95.00%	K.DAITTQIIDFDK.N		K.DAITTQIIDFDK.N
119	132	2	1465.68	0.66	1	75.2	29.4	95.00%	K.GATWGANSFDAKLE.F		K.GATWGANSFDAKLEFQCNDNMK.Q
74	88	2	1644.82	1.3	0	57.1	27.8	95.00%	K.NDMLCGLTDVILPGK.D	Carbamidomethyl (+57)	K.NDMLCGLTDVILPGK.D
133	143	2	1427.55	0.92	1	27.9	29.9	90.90%	E.FQCNDNMKQDE.L	Carbamidomethyl (+57)	K.LEFQCNDNMKQDELTSHTWADK.S
111	118	2	845.52	1.5	0	44.1	18.5	95.00%	E.SALTLTLK.G		K.NIGFNVEETESALTLTLK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
148	AXL2_YEAST	17.25%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
651	664	2	1512.68	-0.6	0	55.9	30.3	95.00%	R.SSSVYMDSEPAVNK.S		R.SSSVYMDSEPAVNK.S
709	729	3	2329.14	0.39	1	43.2	28	95.00%	R.DVTMSSLDPWNSNISPSPVRK.S		R.DVTMSSLDPWNSNISPSPVRK.S
730	740	2	1191.61	-0.093	0	33.6	28.2	95.00%	K.SVTPSPYNVTK.H		K.SVTPSPYNVTK.H
631	650	2	2276.2	-0.11	1	47.7	24.4	95.00%	E.LLAKPPVQPPESPFFDPQNR.S		K.EELLAKPPVQPPESPFFDPQNR.S
184	203	2	2338.16	-0.052	1	56.3	27.1	95.00%	R.SQLYNAPLPNWLFFDSGELK.F		R.SQLYNAPLPNWLFFDSGELK.F
60	81	2	2594.18	0.24	0	95.7	29.6	95.00%	K.TAQITYNCFDLPSWLSFDSSSR.T	Carbamidomethyl (+57)	K.TAQITYNCFDLPSWLSFDSSSR.T
757	779	2	2385.05	0.071	1	47.1	31	95.00%	K.NGITPTTMSTSSSDDFVPVKDGE.N	Deamidation (+1)	K.NGITPTTMSTSSSDDFVPVKDGENFCWVHSMEPDR.R
432	442	2	1299.65	0.76	0	50.9	28.4	95.00%	E.LYFNIIGMDSK.I		K.ANQGSQSQELYFNIIGMDSK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

149	A6ZZW6_YEAS7	20.88%		100%		8							
Start	End	charge	Mr(expt)		ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
249	265	2	1829.92		0.05	0	59.2	26.9	95.00%	K.VDLMDQGTDVIDILAGR.V		K.VDLMDQGTDVIDILAGR.V	
91	101	2	1286.64		0.37	0	54.9	28.4	95.00%	E.LIDLNINDDDK.K		K.VNQTANELIDLNINDDDK.K	
12	42	3	3019.59		2	0	36.3	22.1	95.00%	K.LQDALAPLGGGSQSPIDLPQITVVGSQSSGK.S		K.LQDALAPLGGGSQSPIDLPQITVVGSQSSGK.S	
166	184	3	2079.2		0.73	0	26.2	13.8	95.00%	R.IYSPHVLTLTLVDLPGLTK.V		R.IYSPHVLTLTLVDLPGLTK.V	
185	196	2	1320.67		-0.47	1	53.8	28.1	95.00%	K.VPVGDQPPDIER.Q		K.VPVGDQPPDIER.Q	
522	536	3	1712.87		-0.052	1	23.6	28	94.80%	K.AEQTYINTAHPDLLK.G		K.AEQTYINTAHPDLLK.G	
205	230	3	2701.43		0.042	0	52.8	22.7	95.00%	K.YISKPNAIILSVNAANTDLANSDGLK.L		K.YISKPNAIILSVNAANTDLANSDGLK.L	
150	165	2	1583.86		-0.32	0	57.7	23.5	95.00%	K.VTGANSGISSVPINLR.I		K.VTGANSGISSVPINLR.I	
Index	AC	Coverage	Scaffold probability		Nb distinct peptides								
150	B3LFU9_YEAS1	9.46%		100%		3							
Start	End	charge	Mr(expt)		ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
100	116	2	1841.03		0.15	1	28.5	18.6	95.00%	K.LATVGHEPKPLLPELVE.N		K.LATVGHEPKPLLPELVENGELLR.E	
126	138	2	1333.59		0.21	1	69.9	30	95.00%	E.DMIQGGSSAESPR.S		R.EEEDMIQGGSSAESPR.S	
100	113	2	1499.84		0.38	0	44.1	23.1	95.00%	K.LATVGHEPKPLLPE.L		K.LATVGHEPKPLLPELVENGELLR.E	
Index	AC	Coverage	Scaffold probability		Nb distinct peptides								
151	A7A0Y7_YEAS7	8.55%		100%		4							
Start	End	charge	Mr(expt)		ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
141	156	2	1817.92		-0.018	0	84.4	26.9	95.00%	K.NGFFQNWLIDGLPAAR.E		K.NGFFQNWLIDGLPAAR.E	
104	117	2	1723.86		-0.58	1	67.9	27.5	95.00%	R.IYNSPFQLNMLQEK.E		R.IYNSPFQLNMLQEK.E	
258	272	2	1591.67		1.1	1	39.1	30.3	95.00%	E.TTGSPLMLDEGNDNE.V		R.SSPGTCETTGSPLMLDEGNDNEVYFTYSVK.F	
238	249	2	1237.77		1.1	0	42.5	17.5	95.00%	R.VVGVIVEPVSIK.R		R.VVGVIVEPVSIK.R	
Index	AC	Coverage	Scaffold probability		Nb distinct peptides								
152	B5VDM9_YEAST	20.00%		100%		3							
Start	End	charge	Mr(expt)		ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
1	11	2	1248.57		1.5	1	27.6	29	92.00%	-.MQTPSENTDVK.L		-.MQTPSENTDVK.L	
194	207	2	1623.82		0.67	0	58.6	28	95.00%	E.MVKPYIFSSDPVLE.A		K.EVSNEMVKPYIFSSDPVLEAYLIK.A	
167	188	2	2226.01		-0.64	1	89.7	30.7	95.00%	R.SNAHLSSPTNGAENTQSNTPAK.E	Deamidation (+1)	R.SNAHLSSPTNGAENTQSNTPAK.E	
Index	AC	Coverage	Scaffold probability		Nb distinct peptides								
153	A6ZWW2_YEAS7	23.56%		100%		6							
Start	End	charge	Mr(expt)		ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
172	191	2	2163.15		0.77	0	66.8	23.1	95.00%	E.SHTLFNTSLVPPTLNVPGNR.S		K.DESHTLFNTSLVPPTLNVPGNR.S	
241	259	2	2029.9		0.29	1	75.4	30.7	95.00%	R.SHITLGSSILDGLDDEDDE.H		R.SHITLGSSILDGLDDEDDEHNQVLNK.D	
201	225	3	2572.41		0.94	1	25.8	17.5	95.00%	R.ASNILPIAYIPGVTSGLSTDKLQSK.L		R.ASNILPIAYIPGVTSGLSTDKLQSK.L	
267	277	2	1215.61		1	0	50	27.1	95.00%	K.DADDNLITAIR.A		K.DADDNLITAIR.A	
47	57	2	1376.58		0.045	0	53.4	31.1	95.00%	E.YCVMTSLTCDK.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GSDGCVVCDSTASCPVCASGEYCVMTSLTCDK.C	
201	221	2	2116.14		-0.19	0	73.9	21.4	95.00%	R.ASNILPIAYIPGVTSGLSTDK.L		R.ASNILPIAYIPGVTSGLSTDK.L	
Index	AC	Coverage	Scaffold probability		Nb distinct peptides								
154	RSP5_YEAST	12.48%		100%		7							
Start	End	charge	Mr(expt)		ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
91	100	2	1052.52		1.3	0	31.2	28	95.00%	R.VGDVLGHLDE.D		R.VGDVLGHLDEDTATSSGRPR.E	
23	38	2	1750.88		0.11	0	95	27.3	95.00%	R.SPDPFAVLTIDGYQTK.S		R.SPDPFAVLTIDGYQTK.S	
191	209	2	1904.92		0.31	0	115	29.3	95.00%	E.STLQSGTTAATNTATTSHR.S		R.GTAQAVESTLQSGTTAATNTATTSHR.S	

138	164	3	2669.23	2	0	91.3	29.5	95.00%	K.LPSSSPHSQAPSGHTASSSTNTSSTTR.T		K.LPSSSPHSQAPSGHTASSSTNTSSTTR.T
80	90	2	1202.64	-0.51	0	31.2	26.5	95.00%	K.DQGFLGVVNVR.V		K.DQGFLGVVNVR.V
220	230	2	1378.58	-0.66	1	42.3	30.7	95.00%	R.QYSSFEDQYGR.L		R.QYSSFEDQYGR.L
184	209	3	2561.23	-0.032	1	55.9	28.6	95.00%	R.GTAQAVESTLQSGTTAATNTATTSHR.S		R.GTAQAVESTLQSGTTAATNTATTSHR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
155	A7A1C4_YEAS7	8.57%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
326	340	2	1718.92	0.17	1	50.1	25.4	95.00%	E.DTILYSQISLGERPK.M		R.QPYSENYHLLGNEQSGAVTHGENVPSSNNNDEDTILYSQISLGERPK.M
742	749	2	921.53	0.094	0	24.3	21.2	93.10%	K.YIALSSIR.E		K.YIALSSIR.E
299	315	2	1824.84	1.4	1	70.3	29.7	95.00%	E.NYHLLGNEQSGAVTHGE.N		R.QPYSENYHLLGNEQSGAVTHGENVPSSNNNDEDTILYSQISLGERPK.M
307	325	2	1954.83	0.71	1	58.2	30.7	95.00%	E.QSGAVTHGENVPSSNNNDE.D		R.QPYSENYHLLGNEQSGAVTHGENVPSSNNNDEDTILYSQISLGERPK.M
299	306	2	958.45	1.7	0	30.2	28.7	95.00%	E.NYHLLGNE.Q		R.QPYSENYHLLGNEQSGAVTHGENVPSSNNNDEDTILYSQISLGERPK.M
413	429	5	2014.02	-0.16	1	23.4	27.2	95.00%	R.LAPAPHDIKWDHVCLSR.K	Carbamidomethyl (+57)	R.LAPAPHDIKWDHVCLSR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
156	A6ZWJ1_YEAS7	9.69%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
328	340	2	1292.66	-0.015	0	89.4	28.1	95.00%	K.STSDTASATLLAR.Q		K.STSDTASATLLAR.Q
347	357	2	1323.68	0.27	1	42.5	27.9	95.00%	R.KDSNTNIVLLK.S	Phospho (+80)	R.KDSNTNIVLLK.S
348	357	2	1115.62	-0.46	0	31.1	25.2	95.00%	K.DSNTNIVLLK.S		K.DSNTNIVLLK.S
146	158	3	1499.89	1.6	1	19.6	15.4	93.30%	R.KLDPLLAFPAFLR.K		R.KLDPLLAFPAFLR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
157	A6ZNH7_YEAS7	15.29%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	206	2	1572.83	0.88	0	93.2	26.3	95.00%	R.QIPVGYSAADIVANR.Q		R.QIPVGYSAADIVANR.Q
237	247	2	1160.57	0.86	0	68.3	28.3	95.00%	E.SSFVVSGYSTK.M		R.IDMFGVNDYSWCGESSFVVSGYSTK.M
250	269	2	2392.13	-3.2	1	48.1	29.3	95.00%	K.LYQDYSVPVFLSEFGCNQVK.S	Carbamidomethyl (+57)	K.LYQDYSVPVFLSEFGCNQVK.S
88	102	2	1819.76	-0.97	0	36.2	31.4	95.00%	R.VYTVDNSQDHSHCMK.L	Carbamidomethyl (+57)	R.VYTVDNSQDHSHCMK.L
301	313	2	1435.7	0.62	0	76.7	29.4	95.00%	E.TNNYGLVQIDGDK.V		K.SSRPFTEIEAIYSTQMSSVFSGGLVYEYSNETNNYGLVQIDGDK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
158	A6ZRN1_YEAS7	14.03%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
174	191	2	1728.94	-0.94	0	84.5	24.1	95.00%	R.IINEPTAAAIAYGLGAGK.S		R.IINEPTAAAIAYGLGAGK.S
305	314	2	1166.6	-0.37	1	43.3	27.8	95.00%	R.FEDLNAALFK.S		R.FEDLNAALFK.S
252	261	2	1061.5	-0.49	0	53.5	29.1	95.00%	K.TGLDISDDAR.A		K.TGLDISDDAR.A
502	513	2	1217.64	-0.59	0	69.6	27.4	95.00%	K.SSNITISNAVGR.L		K.SSNITISNAVGR.L
315	325	2	1241.69	-0.33	1	29.6	25.1	95.00%	K.STLEPVEQVLK.D		K.STLEPVEQVLK.D
144	157	2	1563.8	-1.2	0	27.2	27.3	94.10%	K.AVITVPAYFNDAQR.Q		K.AVITVPAYFNDAQR.Q
555	565	2	1173.63	0.67	0	40.3	26.8	95.00%	E.QTVTDPVLSSK.L		R.LESYVASIEQTVTDPVLSSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
159	A7A0C4_YEAS7	23.61%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
121	147	3	2804.19	-0.12	0	46.5	30.6	95.00%	E.LHVGGNGDGTAPVNNDPNYCGPCYGAK.D	Deamidation (+1)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.LNSEGRPVGDATELHVGGNGDGTAPVNNDPNYCGPCYGAK.D

217	244	4	3217.54	-0.11	0	32.2	27.9	95.00%	R.IQGNLHFAPGKPYQNAYGHFHDTSLYDK.T		R.IQGNLHFAPGKPYQNAYGHFHDTSLYDK.T
351	366	2	1755.87	0.21	1	56.3	27.7	95.00%	R.GGIPGMFVFFEMSPLK.V		R.GGIPGMFVFFEMSPLK.V
275	289	3	1491.79	0.47	1	33.8	26.1	95.00%	K.RHGGAVVATSPLDGR.Q		K.RHGGAVVATSPLDGR.Q
3	14	2	1320.74	-0.32	1	23.9	22.7	92.50%	K.RSTLLSLDAFAK.T		K.RSTLLSLDAFAK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
160	A6ZZ86_YEAS7	4.79%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
305	315	2	1168.68	0.76	0	42.3	21.8	95.00%	E.LVTLNQSIPGK.N		K.VEELVTLNQSIPGK.N
12	28	2	1648.72	-0.13	0	84.7	30.9	95.00%	K.TSQSNVGDAVGNADSVE.F		K.TSQSNVGDAVGNADSVEFNSEHDSPSK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
161	YD237_YEAST	19.49%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
142	150	2	1088.51	0.44	1	28.2	28.4	93.80%	E.ADVWNIDEK.I		K.LPLFEGLAYGASSTEADVWNIDEK.I
230	243	2	1667.77	-1.2	0	66.9	30	95.00%	K.SLIDSGYLTYYDMK.K		K.SLIDSGYLTYYDMK.K
159	170	2	1375.72	0.5	1	40.4	26.7	95.00%	E.AYLDPVELTLDK.L		K.ILAVGHNEAYLDPVELTLDK.L
351	367	2	1910.01	0.25	1	65	25.1	95.00%	R.IWGAPTWPANLVETISR.Q		R.IWGAPTWPANLVETISR.Q
282	295	2	1559.86	0.55	0	54.8	22.4	95.00%	R.FAFLDAPLLSLEPK.Y		R.FAFLDAPLLSLEPK.Y
337	346	2	1023.57	-0.6	0	41.4	22.7	95.00%	K.SIIDGAHALK.L		K.SIIDGAHALK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
162	A6ZWS9_YEAS7	20.92%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
76	90	2	1664.9	0.41	0	59.6	23.7	95.00%	K.TLIPLIHLLSTSDNE.D		K.TLIPLIHLLSTSDNEDCK.K
6	17	3	1474.73	0.95	1	25.1	28.9	95.00%	K.ILMDSTHFNEIR.S		K.ILMDSTHFNEIR.S
448	460	2	1499.7	-1.3	1	57.8	29.4	95.00%	K.ADIMELLNHSDSR.V		K.ADIMELLNHSDSR.V
95	108	2	1515.82	0.59	1	57.2	25	95.00%	K.SVQNLIAELLSSDK.Y		K.SVQNLIAELLSSDK.Y
468	478	2	1211.65	-0.59	0	46.8	25.2	95.00%	K.ATQAIIGYTFK.-		K.ATQAIIGYTFK.-
55	71	2	1703.78	-1.1	0	78.9	30.2	95.00%	K.NIGDGLSSSNNAHSGFK.V		K.NIGDGLSSSNNAHSGFK.V
311	328	2	1951.11	0.2	1	77.9	17.7	95.00%	K.QLLLLGNALPTVQSLSER.K		K.QLLLLGNALPTVQSLSER.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
163	A6ZSQ1_YEAS7	38.41%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	74	2	2050.2	0.63	0	116	14.1	95.00%	R.QAINLGQVVLTPLTFALPR.G		R.QAINLGQVVLTPLTFALPR.G
32	42	2	1211.71	1.2	1	60.2	20.3	95.00%	K.LAAIVEIIDQK.K		K.LAAIVEIIDQK.K
110	117	2	921.46	-0.26	1	39.1	28.5	95.00%	R.AALTDFER.F		R.AALTDFER.F
118	124	2	891.5	0.21	0	27.3	26.2	95.00%	R.FQVMVLR.K		R.FQVMVLR.K
94	101	2	905.44	0.42	0	28.9	28.6	94.50%	K.WAASSWAK.K		K.WAASSWAK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
164	FCY2_YEAST	3.56%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
63	72	2	1126.57	1.9	1	41.1	27.2	95.00%	K.FFASLNAETK.G		K.FFASLNAETK.G
156	164	2	991.55	0.19	0	49.3	25.5	95.00%	R.YLVGNVTAR.I		R.YLVGNVTAR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
165	A6ZSA1_YEAS7	14.61%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
68	80	2	1462.81	-0.41	0	34.4	22.6	95.00%	R.LITIDLYGTMVPK.T		R.LITIDLYGTMVPK.T
250	258	2	1127.54	0.27	0	27.8	28.8	92.50%	K.NYLYQGSQR.K		K.NYLYQGSQR.K
234	244	2	1322.6	-1.1	1	57	29.1	95.00%	R.LQDYQNGDLEK.G	Deamidation (+1)	R.LQDYQNGDLEK.G
176	187	2	1204.68	0.82	0	35.8	23.3	95.00%	E.SVVFGQVTAGLK.D		K.FIIETSETPLEGESVVFGQVTAGLK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
166	A7A1B6_YEAS7	17.80%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

172	184	2	1347.85	0.94	1	31.3	6.02	95.00%	E.AIVAALEPPVIKK.S		K.NVFDEAIVAALEPPVIKK.S
172	183	2	1219.76	0.88	0	43.9	13	95.00%	E.AIVAALEPPVIK.K		K.NVFDEAIVAALEPPVIK.K
154	163	2	1225.58	-0.23	1	57.5	30	95.00%	K.YVECSALTQR.G	Carbamidomethyl (+57)	K.YVECSALTQR.G
134	144	3	1242.67	2.2	1	21.5	26.6	93.70%	R.LRPITSEQGSR.L		R.LRPITSEQGSR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
167	A6ZQA2_YEAS7	32.18%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
76	97	2	2429.14	-2	1	69.8	29.7	95.00%	K.VRTDTTYPAGFMDVITLDATNE.N		K.VRTDTTYPAGFMDVITLDATNENFR.L
201	221	3	2385.17	-0.5	1	57.7	27.4	95.00%	R.HDGGFDLVHIKDSLDNTFVTR.L		R.HDGGFDLVHIKDSLDNTFVTR.L
231	240	3	1129.65	0.81	0	21.7	23.3	95.00%	E.QGKPYISLPK.G		R.LNNVFVIGEQGKPYISLPK.G
222	240	3	2115.17	-0.8	1	27.9	20.3	95.00%	R.LNNVFVIGEQGKPYISLPK.G		R.LNNVFVIGEQGKPYISLPK.G
146	155	3	1215.66	-0.33	1	21.7	26.4	94.40%	R.TIRYPDPNIK.V		R.TIRYPDPNIK.V
134	145	2	1326.7	-0.54	1	57.3	26.2	95.00%	K.KGVPYVVTHDGR.T		K.KGVPYVVTHDGR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
168	ERG2_YEAST	14.86%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	46	2	1376.7	1.3	1	44.2	27.5	95.00%	K.TLNEICNSVISK.H	Carbamidomethyl (+57)	K.TLNEICNSVISK.H
57	73	3	1915.89	1.5	1	44.7	30	95.00%	E.DLLQDVRDALASHYGDE.Y		K.HNAAEGLSTEDLLQDVRDALASHYGDEYINR.Y
64	77	2	1622.73	-1.2	1	68.5	29.8	95.00%	R.DALASHYGDEYINR.Y		R.DALASHYGDEYINR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
169	A6ZW21_YEAS7	10.98%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
41	58	2	1831.03	1	1	56.2	21.9	95.00%	K.SGIGIAGIGTFKPELIMK.S		K.SGIGIAGIGTFKPELIMK.S
41	54	2	1345.73	0.72	0	64.7	25.3	95.00%	K.SGIGIAGIGTFKPE.L		K.SGIGIAGIGTFKPELIMK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
170	A6ZL12_YEAS7	6.24%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
14	23	2	1103.55	-0.29	1	35.4	28.9	95.00%	K.ETSPDSISIR.S		K.ETSPDSISIR.S
24	38	2	1575.68	-0.074	1	96.5	30.7	95.00%	R.SFSAGNNFQSSSSEK.T		R.SFSAGNNFQSSSSEK.T
405	417	2	1447.75	-0.74	0	66	27.2	95.00%	R.LICSLAQQGYAPK.F	Carbamidomethyl (+57)	R.LICSLAQQGYAPK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
171	A6ZPF8_YEAS7	4.76%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
205	219	2	1588.83	-0.27	1	41.7	26.1	95.00%	K.ILATNPIMEAFGNAK.T		K.ILATNPIMEAFGNAK.T
367	381	2	1696.85	-0.58	1	25.5	28	90.00%	K.LACELLGIDAYNFAK.W	Carbamidomethyl (+57)	K.LACELLGIDAYNFAK.W
514	523	2	1100.6	1.2	1	33	25.9	95.00%	K.LGILSLLDEE.S		K.LGILSLLDEESR.L
476	484	2	1160.6	0.49	1	26	26.7	93.20%	E.FNQHVFKLE.Q		K.LQQEFNQHVFKLEQEEYVK.E
1527	1538	2	1321.69	1.8	0	51.7	26.8	95.00%	E.TGPFTDPFSLIK.T		K.GHEHSSSIFITPETGPFTDPFSLIK.T
500	513	2	1718.79	0.7	1	39.1	30	95.00%	E.FNDNQPCIDLIENK.L	Carbamidomethyl (+57)	K.EEIEWSFIEFNDNQPCIDLIENK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
172	B5VE42_YEAST	12.84%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
146	160	2	1574.82	0.25	1	80.9	26.7	95.00%	K.VGQSLSIVSNDELSK.A		K.VGQSLSIVSNDELSK.A
60	70	2	1330.71	-0.021	1	59.7	25.3	95.00%	K.KVNVFNINNNR.Y		K.KVNVFNINNNR.Y
235	249	2	1622.77	-0.48	0	75	29.8	95.00%	K.LQSNGAIQGDSFVCK.N	Carbamidomethyl (+57)	K.LQSNGAIQGDSFVCK.N
61	70	2	1202.62	-0.19	0	43.8	28	95.00%	K.VNVFNINNNR.Y		K.VNVFNINNNR.Y
234	249	2	1751.85	0.0049	1	77.1	28.6	95.00%	K.KLQSNGAIQGDSFVCK.N	Deamidation (+1)/ Carbamidomethyl (+57)	K.KLQSNGAIQGDSFVCK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
173	A6ZV40_YEAS7	6.27%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

60	73	2	1615.85	-0.52	0	69.3	25.9	95.00%	K.QLGILSCIGLICNR.M	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.QLGILSCIGLICNR.M
6	16	2	1309.7	-0.32	0	74.3	25.3	95.00%	R.TFLSQLNVFNK.E		R.TFLSQLNVFNK.E
17	27	2	1290.57	-0.86	1	44.3	29.4	95.00%	K.ENYQFSSSTTK.K		K.ENYQFSSSTTK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
174	A7A1A7_YEAS7	12.73%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
172	181	2	1254.6	0.3	0	49.2	29	95.00%	K.FYDNSNLINR.E		K.FYDNSNLINR.E
60	74	2	1575.72	-1.6	1	88.5	29.9	95.00%	R.NSAQDLENSPMSVGK.D		R.NSAQDLENSPMSVGK.D
45	59	2	1649.76	-1.2	0	70.2	30.1	95.00%	R.HDNLSSSSSDIIYGR.N		R.HDNLSSSSSDIIYGR.N
172	182	2	1383.64	1.1	1	34.6	29.8	95.00%	K.FYDNSNLINRE.I		K.FYDNSNLINREIEDILLEINPNFSD ETIVSFIK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
175	A6ZMI1_YEAS7	25.49%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
129	140	2	1486.78	-0.21	1	55.4	25.9	95.00%	K.YFEVILVDPQHK.A		K.YFEVILVDPQHK.A
148	157	2	1330.61	0.15	0	34.5	30	95.00%	R.YNWICNPVHK.H	Carbamidomethyl (+57)/ Deamidation (+1)	R.YNWICNPVHK.H
115	128	2	1715.81	-0.81	0	68.8	29.3	95.00%	R.VLNSYWVNQDSTYK.Y		R.VLNSYWVNQDSTYK.Y
78	93	2	1675.85	-0.9	1	63.7	27.7	95.00%	K.GATYGKPTNQGVNELK.Y		K.GATYGKPTNQGVNELK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
176	A6ZZN9_YEAS7	13.01%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
143	154	2	1390.71	1.4	0	47.9	28.2	95.00%	E.DDTYVSLNPIVR.C		K.AHNMGPNEVFVEEEYIDEDDTYV SLNPIVR.C
256	264	2	1262.62	0.38	1	36.7	28.7	95.00%	E.WLQDQFDRR.I		R.DEWLQDQFDRR.I
155	163	2	1155.54	-0.25	0	31.1	28.9	95.00%	R.CTPNLYFNK.G	Carbamidomethyl (+57)	R.CTPNLYFNK.G
171	182	2	1485.62	0.14	1	30.4	30.3	94.20%	R.SEPFCTPYENSR.W	Carbamidomethyl (+57)	R.SEPFCTPYENSR.W
188	196	2	1235.6	0.15	0	27.5	28.7	92.40%	K.TYFVTWYTR.F		K.TYFVTWYTR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
177	A7A288_YEAS7	18.13%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
16	26	2	1213.68	0.061	1	35.8	25.3	95.00%	K.RSPSILVTDAR.T		K.RSPSILVTDAR.T
254	266	2	1516.77	-0.076	1	41.4	27.1	95.00%	K.TLIDNLIDTSEQR.D		K.TLIDNLIDTSEQR.D
371	385	2	1727.81	-0.81	1	92.9	30.1	95.00%	K.LYAVEGNDQYVQSSR.S		K.LYAVEGNDQYVQSSR.S
147	163	2	1982.95	0.69	0	72.7	29.5	95.00%	E.DDNLNHFQTLPTNALDR.Q		K.LVLIPEDDNLNHFQTLPTNALDR. Q
191	207	2	1942.98	0.67	0	116	26.9	95.00%	R.ITAYNVADGFNLNQLYK.F		R.ITAYNVADGFNLNQLYK.F
141	163	3	2647.36	-0.15	1	28.7	24.1	95.00%	K.LVLIPEDDNLNHFQTLPTNALDR. Q		K.LVLIPEDDNLNHFQTLPTNALDR. Q
488	496	2	1089.62	0.99	0	46	22	95.00%	R.IFNDIVTLR.S		R.IFNDIVTLR.S
447	458	2	1368.69	-0.087	0	56.8	28	95.00%	K.NILGDITFADYK.N		K.NILGDITFADYK.N
82	101	2	2178.05	0.54	0	83.2	29.6	95.00%	R.FSDISIDNILSDNSDIPSAR.R		R.FSDISIDNILSDNSDIPSAR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
178	A7A233_YEAS7	23.26%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
71	81	2	1315.65	0.75	1	47	28.5	95.00%	K.LQLWDTAGQER.F		K.LQLWDTAGQER.F
165	178	2	1638.79	-1.6	1	74.2	29.5	95.00%	K.NDDNVNEIFFTLAK.L		K.NDDNVNEIFFTLAK.L
126	138	2	1416.73	0.98	1	54.8	27.2	95.00%	E.AQLLLVGNKSDME.T		K.TVNEHANDEAQLLLVGNKSDMET R.V
141	152	2	1200.63	-0.6	1	69	27.5	95.00%	R.VVTADQGEALAK.E		R.VVTADQGEALAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
179	A6ZQF7_YEAS7	21.20%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
47	56	2	1285.64	-0.78	0	51.2	28.9	95.00%	K.YLDQVLDHQR.A		K.YLDQVLDHQR.A
112	124	2	1495.82	0.2	0	66.1	24.4	95.00%	K.LYVSHIQVNQAPK.Q		K.LYVSHIQVNQAPK.Q

90	103	2	1444.73	0.54	0	29.5	27.7	95.00%	K.FVQGLLQNAAANAE.A		K.FVQGLLQNAAANAEAK.G
90	105	2	1643.86	-0.2	1	80.3	24.8	95.00%	K.FVQGLLQNAAANAEAK.G		K.FVQGLLQNAAANAEAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
180	A7A0U9_YEAS7	19.72%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
490	505	2	1781.95	-0.4	0	68.8	24.6	95.00%	E.IQGWDHLSLLPTFGAK.D		K.AQYNEIQGWDHLSLLPTFGAK.D
234	249	2	1776.95	0.61	0	55.4	24.1	95.00%	K.LIDLTQFPAFVTPMGK.G		K.LIDLTQFPAFVTPMGK.G
259	273	2	1595.86	-0.25	1	40.5	24.1	95.00%	R.YGGVYVGTLSKPEVK.E		R.YGGVYVGTLSKPEVK.E
259	271	2	1368.69	0.58	0	60.7	28.2	95.00%	R.YGGVYVGTLSKPE.V		R.YGGVYVGTLSKPEVK.E
200	209	2	1083.69	1.2	0	48.1	15.2	95.00%	E.VIDTILALVK.D		K.EVIDTILALVK.D
155	179	3	2741.51	-0.39	0	35.6	19.1	95.00%	R.TTYVTQRPVYLGLPANLVDLNVPAK.L		R.TTYVTQRPVYLGLPANLVDLNVPAK.L
538	554	2	1912.01	0.93	1	43	23.9	95.00%	E.IMLPVFDAPQNLVEQAK.L		R.MIEIMLPVFDAPQNLVEQAK.L
52	63	2	1254.6	1.3	0	53	29	95.00%	E.LNAAYAADGYAR.I		R.WAGNANELNAAYAADGYAR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
181	A6ZL51_YEAS7	28.19%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
155	168	2	1346.66	-1.6	0	57.1	28.4	95.00%	K.APSLFGGMGQTGPK.T		K.APSLFGGMGQTGPK.T
138	150	3	1395.79	0.28	0	24.5	21.1	95.00%	K.IHLFGKPATGDLK.R		K.IHLFGKPATGDLK.R
115	128	2	1623.83	-0.68	0	63.7	27.7	95.00%	K.YTNPLFMQSISPVK.S		K.YTNPLFMQSISPVK.S
79	90	2	1449.78	-0.62	1	44	24.9	95.00%	K.LQVTTVRDYDLK.E		K.LQVTTVRDYDLK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
182	A7A244_YEAS7	22.99%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	208	2	1991.91	0.54	0	28.2	29.9	91.60%	E.LQDFAIFTTDLDNVHDE.N		K.ELQDFAIFTTDLDNVHDENIAR.S
401	435	4	3870.7	-0.24	0	30.8	30.4	95.00%	R.ASCAFYPHGLGHMLGLDVHDVGGNPNYDDPDPMFR.Y	Carbamidomethyl (+57)	R.ASCAFYPHGLGHMLGLDVHDVGGNPNYDDPDPMFR.Y
492	500	2	1044.57	-0.5	1	27.4	27.8	93.60%	R.IEDDILVTK.D		R.IEDDILVTK.D
191	208	2	2120.96	0.6	1	47.4	31.1	95.00%	K.ELQDFAIFTTDLDNVHDE.N		K.ELQDFAIFTTDLDNVHDENIAR.S
213	229	2	2001.92	0.53	1	56.8	29.9	95.00%	R.SLIPSDPNFFYAMDETR.A		R.SLIPSDPNFFYAMDETR.A
123	145	3	2617.25	-0.29	0	43.4	28.9	95.00%	R.YFYHLSGVDIPASAILFNCSTDK.L	Carbamidomethyl (+57)	R.YFYHLSGVDIPASAILFNCSTDK.L
282	302	2	2354.05	-0.086	0	74.6	30.4	95.00%	R.SLGYDPICCSGPACGTLHYVK.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.SLGYDPICCSGPACGTLHYVK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
183	A6ZXW5_YEAS7	15.58%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
349	364	2	1960.97	0.61	0	48.8	27.9	95.00%	E.IMWSEPQLEPIYQATR.G		R.ININLHGSVLDSPEIMWSEPQLEPIYQATR.G
12	33	4	2499.33	0.86	1	36.5	21.9	95.00%	R.HALLHNDIQTSNNSRPSLVQKK.Y		R.HALLHNDIQTSNNSRPSLVQKK.Y
97	106	2	1235.59	0.89	1	35.7	28.4	95.00%	K.NQEVYSQVNR.I		K.NQEVYSQVNR.I
248	254	2	933.46	1.4	0	40.3	28.5	95.00%	E.FNYYVTK.S		K.LAEEDIQVEEFNYYVTK.S
277	288	2	1252.71	-0.56	0	41	21.7	95.00%	K.LSISHAIAQSVK.I		K.LSISHAIAQSVK.I
12	32	3	2371.23	-0.5	0	35.1	24.3	95.00%	R.HALLHNDIQTSNNSRPSLVQK.K		R.HALLHNDIQTSNNSRPSLVQK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
184	CSG2_YEAST	10.49%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
106	120	2	1739.81	-0.071	0	56.9	29.8	95.00%	E.DVDTFSHVLDDPQPR.I		R.NSQFDNNNSGSVTNEDVDTFSHVLDDPQPR.I
78	90	2	1540.67	-1.2	0	67.6	30.4	95.00%	K.MRPMFVSDSDSNR.N		K.MRPMFVSDSDSNR.N
91	120	3	3347.46	-0.087	1	95.6	29.3	95.00%	R.NSQFDNNNSGSVTNEDVDTFSHVLDDPQPR.I		R.NSQFDNNNSGSVTNEDVDTFSHVLDDPQPR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
185	A6ZUF3_YEAS7	12.85%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
49	56	2	948.4	1.2	0	29	31.3	90.30%	E.MGDEPWSK.D		R.AVLVPWLDDDPFEATLLEMGDEPWSK.D
151	166	2	1793.76	-1.1	1	98.2	31	95.00%	R.VSSEGTYMTSLDDFDK.G		R.VSSEGTYMTSLDDFDK.G
277	287	3	1270.81	0.7	1	34.5	11.8	95.00%	E.VIKKPLIFSAR.G		K.LTNEVIKKPLIFSAR.G
57	72	2	1720.85	0.16	1	32.6	28.5	95.00%	K.DILSSTPPLHPSEVTE.D		K.DILSSTPPLHPSEVTEDNK.S
155	166	2	1391.59	0.78	0	49.6	30.6	95.00%	E.GTYMTSLDDFDK.G		R.VSSEGTYMTSLDDFDK.G
347	355	2	1109.56	-0.02	1	36.5	28	95.00%	K.MGLEWLSFK.G		K.MGLEWLSFK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
186	B3LMA9_YEAS1	7.14%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
283	293	3	1070.59	-0.46	0	32	24.4	95.00%	K.SGGIFGVLHGK.S		K.SGGIFGVLHGK.S
247	254	2	928.54	1.5	1	27.5	25.6	95.00%	E.RQSLIAIE.R		R.LIEGDTGSGIIPDEQERQSLIAIER.E
496	504	2	981.48	0.1	0	36.4	28.5	95.00%	R.GLSSNYQTI.-		R.GLSSNYQTI.-
84	91	2	963.49	0.71	0	32.4	28.9	95.00%	K.ILDMYGPR.V		K.ILDMYGPR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
187	A6ZLC2_YEAS7	12.29%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	115	2	1647.03	-0.31	0	55.7	6.02	95.00%	R.GAIVGPDLAVLALVIVK.K		R.GAIVGPDLAVLALVIVK.K
3	14	2	1319.67	-0.39	0	56.7	27.4	95.00%	K.LNISYPVNGSQK.T	Deamidation (+1)	K.LNISYPVNGSQK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
188	A6ZPF1_YEAS7	13.71%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
524	535	2	1339.64	0.063	0	33.7	29.2	95.00%	E.TSQALTSDGWFK.T		K.NEEETSQALTSDGWFK.T
176	198	3	2467.37	-0.48	0	34.2	17.4	95.00%	K.AIFTDNSLLPSLIKPVQAAQDVK.Y		K.AIFTDNSLLPSLIKPVQAAQDVK.Y
237	245	2	1084.54	-0.026	0	27.8	27.6	94.40%	K.TFSFDDILK.L		K.TFSFDDILK.L
2	11	2	1060.59	1.2	0	35.5	24.5	95.00%	M.VAQYTVPVGK.A		-.MVAQYTVPVGK.A
254	278	3	2776.25	0.71	1	30.8	30.4	95.00%	E.IDVHPPGKDDLCCIMYTSGSTGEPK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.ESCNEIDVHPPGKDDLCCIMYTSGSTGEPK.G
284	300	2	1620.9	0.8	0	61.3	21.8	95.00%	K.HSNVVAGVGGASLNVLK.F		K.HSNVVAGVGGASLNVLK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
189	A6ZUA2_YEAS7	7.99%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
531	542	2	1459.62	0.19	1	75	30.8	95.00%	E.YSNNFDTIEDSR.E		K.EFHALEESENEQAEYSNNFDTIEDSR.E
544	554	2	1165.55	-0.022	1	40.1	29.5	95.00%	E.FSVAASDVELE.N		R.EFSVAASDVELENEHVPWGK.K
5	26	3	2394.01	-0.32	1	49.2	30.5	95.00%	R.NDNASGGYMQPDQSSNASMHKR.D		R.NDNASGGYMQPDQSSNASMHKR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
190	A6ZKL6_YEAS7	39.42%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
46	63	3	1886.01	1.5	1	25.7	22.9	95.00%	R.LNRLPAASLGDMVMATVK.K		R.LNRLPAASLGDMVMATVK.K
121	128	2	1045.47	1.9	1	47.8	29.2	95.00%	K.ECADLWPR.V	Carbamidomethyl (+57)	K.ECADLWPR.V
33	40	2	932.57	-0.12	0	26.9	17.9	95.00%	R.NLYIIAVK.G		R.NLYIIAVK.G
13	32	2	2015	1.2	0	96.5	28	95.00%	R.ISLGLPVGAIMNCADNSGAR.N	Carbamidomethyl (+57)	R.ISLGLPVGAIMNCADNSGAR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
191	A6ZLH4_YEAS7	8.48%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
127	136	2	1073.5	0.37	0	54.1	28.7	95.00%	R.GGGAYYMISR.S		R.GGGAYYMISR.S
1067	1084	2	1882.97	-0.011	0	31.8	26.4	95.00%	K.SSDLIFSTLPVPALGTHE.D		K.SSDLIFSTLPVPALGTHEDHDASLQYVEDLDIWLEGLPPCMLINSQTMTVTTAL.-

735	746	2	1437.7	-0.33	0	34.9	28.9	95.00%	K.TIDLYPIQMCGK.V	Carbamidomethyl (+57)	K.TIDLYPIQMCGK.V
5	31	3	2878.42	-0.2	1	48	26.9	95.00%	R.FYQIPGTHRPSSAISSSNESSSLLSAR.R		R.FYQIPGTHRPSSAISSSNESSSLLSAR.R
5	23	2	2076.99	0.47	0	49.1	29.5	95.00%	R.FYQIPGTHRPSSAISSSNE.S		R.FYQIPGTHRPSSAISSSNESSSLLSAR.R
32	45	2	1716.81	0.52	1	73.7	29.4	95.00%	R.RISQTYFNYQATPE.C		R.RISQTYFNYQATPECQK.V
33	48	2	1976.89	-1.5	1	73.4	30.4	95.00%	R.ISQTYFNYQATPECQK.V	Carbamidomethyl (+57)	R.ISQTYFNYQATPECQK.V
869	879	2	1233.66	-0.018	0	29.6	26.5	95.00%	R.FSTIEPQTIAK.Q		R.FSTIEPQTIAK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
192	AVT7_YEAST	14.29%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
17	31	2	1536.86	0.96	0	37.2	20.5	95.00%	K.TIVGAGTLAIPYSFK.S		K.TIVGAGTLAIPYSFK.S
3	16	2	1348.72	0.21	0	72.4	25.6	95.00%	E.ATSSALSSTANLVK.T		-.MEATSSALSSTANLVK.T
321	348	2	2991.38	0.83	1	69.7	30.4	95.00%	R.ASNLRPISMTVEDPAQPSDALDATSYNE.Q		R.ASNLRPISMTVEDPAQPSDALDATSYNEQECLLPNGNFDNGSIESQENNNDER.G
441	451	2	1098.67	0.26	0	49.5	21.4	95.00%	K.LIGLDSLAIGK.M		K.LIGLDSLAIGK.M
1	16	2	1650.81	-1.1	1	82.5	29.2	95.00%	-.MEATSSALSSTANLVK.T	Acetyl (+42)	-.MEATSSALSSTANLVK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
193	A6ZMW0_YEAS7	12.25%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
485	496	2	1367.7	-0.74	1	60.2	27.8	95.00%	K.LVDVEDLGYFAK.N		K.LVDVEDLGYFAK.N
520	531	2	1356.61	0.63	0	28.5	29.7	92.20%	E.TAAAFTDDGWFR.T		K.NPEETAAAFTDDGWFR.T
573	588	2	1912.86	-0.35	1	73.9	30.4	95.00%	R.SNPYVQNICVYADENK.V	Carbamidomethyl (+57)	R.SNPYVQNICVYADENK.V
677	688	2	1324.74	-0.17	1	47.4	23.4	95.00%	R.DILAAVKPDVER.V		R.DILAAVKPDVER.V
532	541	2	1116.55	-0.29	1	41.4	27	95.00%	R.TGDIAEWTPK.G		R.TGDIAEWTPK.G
256	278	3	2533.2	0.6	1	33.4	29.5	95.00%	E.LHFPKPEDPACIMYTSGSTGTPK.G	Carbamidomethyl (+57)	K.DEVELHFPKPEDPACIMYTSGSTGTPK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
194	A6ZU02_YEAS7	4.15%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
29	41	2	1261.65	1.1	1	86.7	27	95.00%	E.GTAASSLNIATEK.A		K.HTTDVIEFYEEGTAASSLNIATEK.A
482	491	2	1122.64	0.52	0	48.8	23.7	95.00%	K.DAVTNIHLLK.R		K.DAVTNIHLLK.R
481	491	3	1250.74	0.48	1	52.4	18.1	95.00%	E.KDAVTNIHLLK.R		K.EVEKDAVTNIHLLK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
195	A7A007_YEAS7	19.79%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
232	242	2	1314.64	-0.7	1	44.1	28.4	95.00%	R.FTTVYENNLSK.S		R.FTTVYENNLSK.S
202	212	3	1249.65	-0.63	0	22.6	27.8	93.70%	K.YDAIVKPTTDK.L		K.YDAIVKPTTDK.L
249	264	2	1600.87	-0.51	1	103	25	95.00%	K.AIVSTGLDLGNATIEK.L		K.AIVSTGLDLGNATIEK.L
159	170	2	1224.6	0.64	0	48.6	30.1	95.00%	K.VTDASSLPHVAE.L		K.VTDASSLPHVAELSSTTR.G
159	176	2	1869.95	1.8	1	62.9	26.9	95.00%	K.VTDASSLPHVAELSSTTR.G		K.VTDASSLPHVAELSSTTR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
196	ZRT1_YEAST	5.59%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
155	167	3	1550.71	1.1	1	28	29.7	95.00%	K.YGLSHDHTHDEIK.D		K.YGLSHDHTHDEIK.D
269	276	2	931.52	2.9	1	44.1	25	95.00%	R.LSAIEFPR.S		R.LSAIEFPR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
197	A6ZZE8_YEAS7	10.43%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
403	416	2	1634.72	0.85	0	82.9	30.6	95.00%	R.HIPYVTQGQSFDDE.I		R.HIPYVTQGQSFDDEISLGGFSK.V
382	388	2	884.43	1.3	1	28.2	25.7	95.00%	K.YLFADKE.T		K.YLFADKETDDILDEIDLK.E
417	424	2	807.45	0.59	0	27.6	24.9	95.00%	E.ISLGGFSK.V		R.HIPYVTQGQSFDDEISLGGFSK.V

403	424	3	2424.16	-0.28	1	54.6	28.4	95.00%	R.HIPYVTQGQSFDDEISLGGFSK.V		R.HIPYVTQGQSFDDEISLGGFSK.V
348	367	3	2373.09	0.32	0	25.2	29.7	94.80%	E.NYSPCVGTPISQAHFYVDYR.I	Carbamidomethyl (+57)	R.NPFSTDSENYISTCTENYSPCVG TPISQAHFYVDYR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
198	A6ZPF3_YEAS7	17.72%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
172	182	2	1290.61	-0.25	1	38.6	28.8	95.00%	K.DTTPWNESLTK.L		K.DTTPWNESLTK.L
191	204	3	1721.91	1.3	1	18.6	24	91.30%	E.FDRVIYLDNDAILR.S		K.LLVFNQTEFDRVIYLDNDAILR.S
469	486	3	2197	0.35	0	27.5	30.7	95.00%	E.HQACDLWNSVYASYIQSR.E	Carbamidomethyl (+57)	K.LEHQACDLWNSVYASYIQSR.E
399	411	2	1583.8	-0.5	0	43.5	28.1	95.00%	R.HYSIIYNDVLGYK.T		R.HYSIIYNDVLGYK.T
210	218	2	1153.65	1	0	27	22	95.00%	E.LFFLPNYIK.F		R.SSLDELFFLPNYIK.F
219	235	2	2000.99	-0.51	1	68.6	28.7	95.00%	K.FAAPLTYWFLSNSDLEK.S		K.FAAPLTYWFLSNSDLEK.S
205	218	2	1684.87	0.4	1	57.7	25.7	95.00%	R.SSLDELFFLPNYIK.F		R.SSLDELFFLPNYIK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
199	HSP72_YEAST	16.12%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
158	169	2	1198.67	-0.44	0	52.4	25	95.00%	K.DAGTIAGLNVLR.I		K.DAGTIAGLNVLR.I
537	547	2	1264.67	-1	1	39.1	27	95.00%	K.NQLESIAYSLK.N		K.NQLESIAYSLK.N
424	441	2	2026.01	1.3	0	60	28.8	95.00%	E.VFSTYADNQPGVLIQVFE.G		K.SEVFSTYADNQPGVLIQVFEGER. A
55	69	2	1590.74	-1	0	63.7	30.1	95.00%	K.NQAAMNPANTVFDAK.R		K.NQAAMNPANTVFDAK.R
170	185	2	1658.89	1.1	0	93.6	25.3	95.00%	R.IINEPTAAAIAYGLDK.K		R.IINEPTAAAIAYGLDK.K
111	124	2	1549.78	-1.2	1	62.2	27.9	95.00%	K.NFTPEQISSMVLGK.M		K.NFTPEQISSMVLGK.M
137	153	2	1893.92	1.2	0	26.7	28.3	91.70%	K.VNDAVVTVPAYFNDSQR.Q		K.VNDAVVTVPAYFNDSQR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
200	B3LP09_YEAS1	16.85%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
375	390	4	1797.89	-0.43	1	21.2	28.6	95.00%	K.KPNLHGYGHPNPPNEK.S		K.KPNLHGYGHPNPPNEK.S
398	430	4	3862.74	0.91	0	21.2	29.1	94.80%	K.NHQYSSPDHHHHYNQQQQQQQ AQAQAQAQAQAK.V		K.NHQYSSPDHHHHYNQQQQQQQ AQAQAQAQAQAK.V
463	472	2	1109.53	0.97	1	34.3	28.7	95.00%	E.ASKLDPTSYE.A		R.EASKLDPTSYEAYQQQTQQK.Y
509	524	2	1822.81	-0.77	1	52.7	30.9	95.00%	K.YPYNAQPTANDEQNAK.N		K.YPYNAQPTANDEQNAK.N
431	447	2	1994	0.067	0	93.7	27.2	95.00%	K.VQQQQLQQAQAQQQANR.Y		K.VQQQQLQQAQAQQQANR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
201	A6ZR28_YEAS7	39.26%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
21	32	3	1450.81	0.42	1	47.4	21.4	95.00%	R.KQFVVDVLHPNR.A		R.KQFVVDVLHPNR.A
11	20	2	1109.69	0.25	1	49.1	12.8	95.00%	R.KVISNPLLAR.K		R.KVISNPLLAR.K
84	90	2	939.48	1.5	1	28.8	27	95.00%	K.KFEPTYR.L		K.KFEPTYR.L
12	20	2	981.6	0.28	0	25.8	16.9	95.00%	K.VISNPLLAR.K		K.VISNPLLAR.K
69	83	2	1539.79	0.12	1	37.8	26.4	95.00%	K.SVGFGLVYNSVAEAK.K		K.SVGFGLVYNSVAEAK.K
53	61	2	996.5	0.17	0	47.5	27.7	95.00%	K.DAVSVFGFR.T		K.DAVSVFGFR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
202	A6ZTN7_YEAS7	7.77%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
199	211	2	1543.79	0.37	0	46.9	27.6	95.00%	E.YRPVDTIPLNDLE.S		K.EYRPVDTIPLNDLESTPVMVNSA R.G
63	80	3	1965.08	0.0021	1	24.9	21.7	95.00%	K.HLHGLPILQSPSLTPAER.L		K.HLHGLPILQSPSLTPAER.L
281	298	2	1975.11	-0.27	1	64.3	18.4	95.00%	E.IASIEAPPLLPQDIPVFR.I		R.DEDYDNDDDEIASIEAPPLLPQDI PVFR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
203	B3LHY2_YEAS1	7.87%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
307	315	2	1190.63	1.2	0	26.6	27.8	92.20%	E.WFQVWQAVK.D		K.FEWFQVWQAVK.D

108	120	2	1258.65	0.7	1	69.9	27.2	95.00%	K.SNIGNAEVAGLSK.D		K.SNIGNAEVAGLSK.D
513	522	2	1187.58	0.82	1	61.3	28.4	95.00%	E.LGEPIPYDER.L		R.CNELGEPIPYDER.L
274	283	2	1298.59	-0.1	1	48.3	29.6	95.00%	K.NLEDSWFFNK.E		K.NLEDSWFFNK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
204	A6ZU59_YEAS7	12.99%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
187	203	2	1833.95	-0.54	1	87.1	26.9	95.00%	K.LLQLAGVEDVYTQSNGK.T		K.LLQLAGVEDVYTQSNGK.T
142	157	2	1728.86	-1.3	0	73.2	28.3	95.00%	R.GYWGTNLGQPHSLATK.T		R.GYWGTNLGQPHSLATK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
205	A6ZM19_YEAS7	11.41%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
253	270	2	2304.03	-0.038	1	60.8	30.8	95.00%	K.RATYDDYQTNYYNYVIDK.M		K.RATYDDYQTNYYNYVIDK.M
305	316	2	1356.7	0.12	1	27.7	27.4	94.40%	E.DRFTASTFTAIK.T		K.AAAPGIQLVAGEGFQSPLEDRFT ASTFTAIK.T
298	306	2	1047.5	0.74	1	32.7	28.4	95.00%	E.GFQSPLEDR.F		K.AAAPGIQLVAGEGFQSPLEDR.F
61	69	2	1001.48	0.98	0	35.3	27.8	95.00%	K.SIHPGYLSE.G		K.SIHPGYLSEGGCLMFHYEADNEE NLEELNDSKPLIDQLWPGQLVVPE WK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
206	A7A1T6_YEAS7	7.11%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
518	530	3	1583.82	0.14	1	40.7	26	95.00%	E.LQDRQHMYVPAVK.A		K.DDLHLDGELQDRQHMYVPAVK.A
495	517	3	2549.18	1.1	1	30.8	29.7	95.00%	E.GSDFKPYMDALNIGKDDLHLDGE .L		R.SIVYNNIEGSDFKPYMDALNIGKD DLHLDGELQDR.Q
203	214	2	1323.71	-0.47	1	37.9	25.7	95.00%	K.LSPVFELFASSK.N		K.LSPVFELFASSK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
207	A6ZYY5_YEAS7	17.45%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
23	42	2	2070.04	0.48	0	71.8	27.2	95.00%	E.TLPQQGSIAGVSQGFPNIQE.I		K.GVNTLENIETLPQQGSIAGVSQG FPNIQEIYSDR.D
2	13	2	1291.59	8	1	34.5	29.6	95.00%	M.TSSASSPQDLEK.G	Acetyl (+42)/ Deamidation (+1)	-.MTSSASSPQDLEK.G
43	58	2	1892.93	0.36	1	53	27.9	95.00%	E.IYSDRDFITLGSSTYR.R		K.GVNTLENIETLPQQGSIAGVSQG FPNIQEIYSDRDFITLGSSTYR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
208	YIP8_YEAST	28.43%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
130	150	3	2495.2	0.53	1	42.9	28.6	95.00%	K.VNYGMVRDPSYSFMYPLTLSR.K		K.VNYGMVRDPSYSFMYPLTLSR.K
101	112	3	1314.71	-0.15	0	42	25.9	95.00%	R.QLNASMGTLRPK.K		R.QLNASMGTLRPK.K
137	150	2	1675.79	-0.007	0	71.1	29.5	95.00%	R.DPSYSFMYPLTLSR.K		R.DPSYSFMYPLTLSR.K
196	204	2	1112.56	-0.12	1	39.8	26.3	95.00%	R.EFIDSLRPH.-		R.EFIDSLRPH.-
114	129	2	1739.87	-0.35	1	72.9	27.6	95.00%	K.QSTAYTNVPVIFSGEK.V		K.QSTAYTNVPVIFSGEK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
209	B3LK87_YEAS1	6.40%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
389	402	2	1543.73	0.38	1	64.6	29.6	95.00%	E.QSGNMDQNLLPAEK.F		K.LQEQSGNMDQNLLPAEK.F
303	314	2	1398.52	0.98	0	44.9	29.3	95.00%	K.SCPGFGNCQCGR.H	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.SCPGFGNCQCGR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
210	B5VQ30_YEAST	7.03%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

798	809	2	1273.62	0.53	0	49	28.4	95.00%	E.DVPLLADGDTMK.I		R.SESVTEQQVENSIFSENTFEYQFNPANEANADGHAINAENLIEDVPLLADGDTMK.I
514	524	2	1171.63	-0.018	0	32.5	26	95.00%	K.AMDLLASNLPK.A		K.AMDLLASNLPK.A
783	797	2	1550.73	0.56	1	36.1	29.1	95.00%	E.ANADGHAINAENLIE.D		R.SESVTEQQVENSIFSENTFEYQFNPANEANADGHAINAENLIEDVPLLADGDTMK.I
794	809	2	1742.88	-0.47	1	56.5	27.6	95.00%	E.NLIEDVPLLADGDTMK.I		R.SESVTEQQVENSIFSENTFEYQFNPANEANADGHAINAENLIEDVPLLADGDTMK.I
696	715	3	2145.1	-0.65	0	30.5	25.8	95.00%	K.VIPVDTMKPLDGVSDTPSFK.N		K.VIPVDTMKPLDGVSDTPSFK.N
196	204	2	1031.6	1.9	0	34	22.6	95.00%	R.TVLFQTVPK.Q		R.TVLFQTVPK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
211	A6ZSL9_YEAS7	24.66%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
155	163	2	1102.58	-0.29	1	45.3	27.6	95.00%	R.LISQAWETR.S		R.LISQAWETR.S
52	78	3	2885.46	0.68	1	55.6	26.1	95.00%	E.GILGQRQDVIDSLTQICDSNPAISASK.L	Carbamidomethyl (+57)	K.QLEGILGQRQDVIDSLTQICDSNPAISASK.L
164	179	3	1787.86	0.12	0	32.5	29.5	95.00%	R.SQFHSQSNVLNTANNK.V		R.SQFHSQSNVLNTANNK.V
49	57	2	1012.57	-0.31	1	40.6	23.4	95.00%	K.QLEGILGQR.Q		K.QLEGILGQR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
212	A6ZVR3_YEAS7	8.70%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
611	621	2	1203.65	0.061	1	45.3	26.6	95.00%	R.EAFVSLNIPSK.A		R.EAFVSLNIPSK.A
216	230	2	1683.75	0.61	0	83.7	30.7	95.00%	R.QLAVDDINTGHVNCE.S	Carbamidomethyl (+57)	R.QLAVDDINTGHVNCESNPTICEELGFGDLVK.I
578	586	2	984.59	-0.42	0	25.1	21.3	94.30%	K.IGDVIIIDK.S		K.IGDVIIIDK.S
433	442	2	1203.59	-0.93	0	33.9	28.1	95.00%	R.NIDAIMDWVK.K		R.NIDAIMDWVK.K
140	155	2	1763.75	-1.8	1	76.8	31.2	95.00%	R.ESMDPNNLDTDLDSAK.S		R.ESMDPNNLDTDLDSAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
213	A6ZRP5_YEAS7	7.69%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
509	527	2	2072.97	0.35	1	88.2	29.6	95.00%	R.SLALLSSLGCYQDGFAKDE.I	Carbamidomethyl (+57)	R.SLALLSSLGCYQDGFAKDEINEK.K
663	682	2	2177.08	0.031	1	85.2	27.8	95.00%	K.TTESNFGFITVLPGAFSAYR.F		K.TTESNFGFITVLPGAFSAYR.F
148	167	3	2318.1	0.54	1	28.9	29.4	95.00%	E.LIHNGSQTMATPIERPFFNE.N	Deamidation (+1)/ Oxidation (+16)	R.QRPPPATAEYNDVFNTNSQQLPSEHQYNNVPSYPLPSINVIQTTPELIHNGSQTMATPIERPFFNENDYYYNNR.N
179	194	2	1613.67	-0.44	0	42.4	30.8	95.00%	R.TSPSIASSSDGYADQE.A		R.TSPSIASSSDGYADQEARPILEQPNNNMNSGNIPQYHDQPFGYNNGYHGLQAK.D
90	101	3	1469.73	0.61	1	35.4	28.5	95.00%	E.RDIYGGFVNHHR.Q		R.YTNQNASMGSFTPVQSLQFPEQSQQTNMLYNGDDGNNNTINDNERDIYGGFVNHHR.Q
666	682	2	1845.94	0.47	0	60.9	26.7	95.00%	E.SNFGFITVLPGAFSAYR.F		K.TTESNFGFITVLPGAFSAYR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
214	A6ZQR0_YEAS7	11.37%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
100	115	2	1917.78	0.46	1	57.5	30.7	95.00%	E.ADWLYTGDVLDYDDEE.S		K.LGNANTFLGNVSEADWLYTGDVLDYDDEESLILAMPK.N
116	123	2	871.52	0.44	0	33.7	27	95.00%	E.SLILAMPK.N		K.LGNANTFLGNVSEADWLYTGDVLDYDDEESLILAMPK.N
60	74	2	1826.78	0.19	0	72.3	30.9	95.00%	R.YSFSHDSCMPVPICK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.YSFSHDSCMPVPICK.S
46	59	2	1715.68	0.64	0	94	30.2	95.00%	E.CGTGQYCLNNCDVR.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VEAATFCNATQACPEDKPCCSQYGECGTGQYCLNNCDVR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
215	A6ZQ99_YEAS7	17.59%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
138	146	2	1063.61	1.9	0	31.7	23.5	95.00%	E.TLFAFQPLK.K		R.HVATDTYLLAHDVASPFYPTNEEITTVTLEEGDGELYPETLFAFQPLK.K
54	74	2	2378.06	0.42	0	65.2	30.2	95.00%	R.ISSAGQQVTGYTHPDFNNQWE.V		R.ISSAGQQVTGYTHPDFNNQWEVLPPHGSDVGK.G
138	147	2	1191.7	0.39	1	31.5	18.9	95.00%	E.TLFAFQPLKK.S		R.HVATDTYLLAHDVASPFYPTNEEITTVTLEEGDGELYPETLFAFQPLKK.S
99	121	3	2589.2	0.74	1	26	30	95.00%	R.HVATDTYLLAHDVASPFYPTNEE.I		R.HVATDTYLLAHDVASPFYPTNEEITTVTLEEGDGELYPETLFAFQPLK.K
31	44	4	1646.79	0.62	0	42.2	28.9	95.00%	K.HQDTDAFLHSHLAR.Y		K.HQDTDAFLHSHLAR.Y
20	30	2	1325.72	-0.011	0	23.4	24.9	91.70%	K.TVNYFDIITIK.H		K.TVNYFDIITIK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
216	RAX1_YEAST	14.02%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
118	131	2	1498.77	-0.49	1	61.8	27.2	95.00%	K.LLENSGPDVPFSPK.L		K.LLENSGPDVPFSPK.L
132	140	2	1086.57	0.62	1	42.5	27.1	95.00%	K.LNELLGDWK.H		K.LNELLGDWK.H
8	19	2	1468.68	-0.55	1	44.5	29.3	95.00%	K.VSSMQNFEMIQR.E		K.VSSMQNFEMIQR.E
365	390	3	2644.19	1	1	45.4	29.7	95.00%	K.NAGNDEGDASSDTDHVPMILAVFGGR.R		K.NAGNDEGDASSDTDHVPMILAVFGGR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
217	A6ZYM2_YEAS7	6.77%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
445	455	2	1140.61	0.062	1	62.1	25	95.00%	K.IPADGIITRGE.S		K.IPADGIITRGESEIDESLMTGESILVPK.K
404	420	2	1929.03	0.58	1	60	23.5	95.00%	K.LIQLTPSVCSIISDVER.N	Carbamidomethyl (+57)	K.LIQLTPSVCSIISDVER.N
779	795	2	1847.8	-0.87	1	77.6	31.1	95.00%	R.NGYETYMITGDNNSAAK.R		R.NGYETYMITGDNNSAAK.R
174	184	2	1186.66	1.2	1	61.8	25.1	95.00%	E.SPLILSSVSER.F		K.AFEDESPLILSSVSER.F
629	640	2	1253.67	0.71	0	23.5	25.6	90.70%	K.TGTLTTGFMVVK.K		K.TGTLTTGFMVVK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
218	A6ZYA1_YEAS7	2.89%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
300	308	2	1055.63	0.75	0	31.9	22	95.00%	R.SVLDLLLQR.L		R.SVLDLLLQR.L
2	15	2	1580.88	-1.1	0	46.8	21.4	95.00%	M.SLPLKPLTIDSNNK.Q	Acetyl (+42)	-.MSLPLKPLTIDSNNK.Q
78	94	3	1760.99	0.86	1	38.3	18.6	95.00%	R.RLTSSLSPALPAGVHQK.T		R.RLTSSLSPALPAGVHQK.T
839	847	2	1111.61	1.8	0	43.7	22.8	95.00%	E.FQMLAYVLK.T		R.DDLDMLTYEFQMLAYVLK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
219	A6ZLU0_YEAS7	23.40%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
100	112	3	1370.74	0.95	0	41.7	25.2	95.00%	E.SLDIPAGHHVAVR.V		R.LESLDIPAGHHVAVR.V
66	76	2	1365.66	0.5	1	34.2	28.9	95.00%	R.SLYPDRWTSLE.L		R.SLYPDRWTSLELEDQTIISK.N
275	292	2	1990	0.16	0	68.7	27.5	95.00%	R.LLICGPDGMNNLALQYAK.E	Carbamidomethyl (+57)	R.LLICGPDGMNNLALQYAK.E
151	178	3	2990.43	0.3	1	51	29.1	95.00%	K.YFAGLNSGDTVDFKGPIGTLNYEPNSSK.H		K.YFAGLNSGDTVDFKGPIGTLNYEPNSSK.H
272	292	3	2375.17	0.27	1	50.8	28	95.00%	E.DNRLLICGPDGMNNLALQYAK.E	Carbamidomethyl (+57)	R.YLPEYSEDNRLLICGPDGMNNLALQYAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
220	A6ZUM5_YEAS7	32.54%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
63	79	2	1763.98	0.44	1	43.7	20	95.00%	R.IIAAIPNPEDVVAISSR.T		R.IIAAIPNPEDVVAISSR.T
102	113	2	1402.69	-0.09	0	54.8	29.1	95.00%	R.FTPGSFTNYITR.S		R.FTPGSFTNYITR.S
89	101	2	1268.66	-1.3	0	40.1	26.3	95.00%	K.FAAHTGATPIAGR.F		K.FAAHTGATPIAGR.F

28	52	3	2815.45	-1.1	0	22.6	24.8	95.00%	R.NVQVHQEPYVFNARPDGVHVINVGK.T		R.NVQVHQEPYVFNARPDGVHVINVGK.T
13	27	2	1562.85	0.37	0	71.3	24.3	95.00%	E.DAQLLLAANTHLGAR.N		-.MSLPATFDLTPEDAQLLLAANTHLGAR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
221	A6ZRX9_YEAS7	6.03%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
219	235	2	1820.8	0.28	0	97.9	30.2	95.00%	E.SDSINQSSPSSNQDIDK.V		R.QEHQLNDSASSDFTSHESDSINQSSPSSNQDIDK.V
596	606	3	1359.72	0.96	1	30.3	27.2	95.00%	K.IYVKHDDLTTR.V		K.IYVKHDDLTTR.V
204	218	2	1673.69	0.41	0	102	30.7	95.00%	E.HQLNDSASSDFTSHE.S		R.QEHQLNDSASSDFTSHESDSINQSSPSSNQDIDK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
222	A6ZT41_YEAS7	22.34%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	63	3	3178.57	0.88	1	46.4	26.6	95.00%	K.LGSASFTAINTLTKPALFSFYDDDITKNE.G		K.LGSASFTAINTLTKPALFSFYDDDITKNEGNVYDK.A
70	88	2	1955.01	-0.52	1	67.6	25.2	95.00%	K.ALLSNASQLEMVPPSATAR.H		K.ALLSNASQLEMVPPSATAR.H
8	24	2	1776.91	-6.6	1	63.3	26.5	95.00%	K.NQLNTGGVPNGVHNTKK.E		K.NQLNTGGVPNGVHNTKK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
223	ATG22_YEAS7	13.64%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
62	79	3	1982.86	-0.48	1	30.1	31.1	95.00%	K.VHDHSIPCLSETGSDSDK.C	Carbamidomethyl (+57)	K.VHDHSIPCLSETGSDSDK.C
281	296	2	1801.86	-0.5	1	58.2	28.6	95.00%	R.SPYPGEQDALGQLNWK.N		R.SPYPGEQDALGQLNWK.N
2	17	2	1862.81	-0.65	1	75.2	30.9	95.00%	M.SYGTINDMNESVTNYR.I		-.MSYGTINDMNESVTNYR.I
189	210	3	2410.14	-0.89	1	47.4	29.6	95.00%	K.CQSQGAYEPDKVDSLTTVISGR.G	Carbamidomethyl (+57)	K.CQSQGAYEPDKVDSLTTVISGR.G
62	72	2	1292.58	0.17	0	44.3	29.8	95.00%	K.VHDHSIPCLSE.T	Carbamidomethyl (+57)	K.VHDHSIPCLSETGSDSDK.C
200	210	2	1146.62	-0.62	0	57.3	25.7	95.00%	K.VDSLTTVISGR.G		K.VDSLTTVISGR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
224	A6ZN13_YEAS7	11.65%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	77	2	1329.64	0.67	0	28.5	29	93.50%	E.HLYPNQVMSLE.T		K.ELDSNVLDAWAQIEHLYPNQVMSLETSTKPK.F
41	52	3	1397.76	0.49	0	40.4	23.5	95.00%	K.FGLNLDLDHLLK.E	Deamidation (+1)	K.FGLNLDLDHLLK.E
449	458	2	1265.59	-0.15	0	29.8	28.4	95.00%	K.DFICNWLGNK.A	Carbamidomethyl (+57)	K.DFICNWLGNK.A
93	99	2	907.44	-0.027	0	32.5	28.7	95.00%	K.DWDFVVK.N		K.DWDFVVK.N
375	396	2	2603.19	1.6	0	84.4	29.5	95.00%	E.GGNLCYPTLQDIDDYLNQDYVK.E	Carbamidomethyl (+57)	K.DCEGGNLCYPTLQDIDDYLNQDYVK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
225	A7A0E6_YEAS7	8.70%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
57	70	2	1554.83	1.3	0	77	25.2	95.00%	E.QSVSTEPLDTLPLR.K		R.EQSVSTEPLDTLPLR.K
280	292	2	1394.75	0.71	0	39.3	25.1	95.00%	E.DGHITDVLLGSLR.S		K.VNENWNVEDGHITDVLLGSLR.S
12	29	2	1915.99	-0.49	1	74.5	25.9	95.00%	K.KPILAVPEPALADTHSEE.I		K.KPILAVPEPALADTHSEEISR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
226	A6ZQG2_YEAS7	21.21%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
28	44	2	1874.91	0.69	0	80.3	28.9	95.00%	K.LDFTNVGFTGSYVDVNK.F		K.LDFTNVGFTGSYVDVNK.F
272	299	3	3217.55	0.011	1	97.2	27.7	95.00%	K.NHLYSTFHTFQGIEDLGTGIQSYGYITR.N		K.NHLYSTFHTFQGIEDLGTGIQSYGYITR.N
154	168	2	1518.74	0.19	0	51.6	28.7	95.00%	E.ATVLADGTLISSDQE.Y		K.TADNVTFLNHGGEASPCLGNALSYASSNGTGSASEATVLADGTLISSDQEYIIYSNVSCPK.S

58	67	2	1149.59	0.93	1	40.2	27.5	95.00%	E.VGDRVWFSGK.N		K.DITNNESCTCEVGDRVWFSGK.N
191	204	2	1433.68	0.14	0	38.4	29.3	95.00%	R.SGIPAYYGYGGTTK.M		R.SGIPAYYGYGGTTK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
227	B3LL17_YEAS1	16.71%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
331	344	2	1376.68	0.23	0	50.4	28.9	95.00%	E.MALDGVGGGCTLVK.A	Carbamidomethyl (+57)	K.QPSIRPYDFNNWQESDTGLEIASQMGDDEIIVEGYAEIATYRPLMAHFYDANGVPGEEMALDGVGGGCTLVK.A
115	141	4	3410.73	0.93	1	20	24.9	95.00%	K.EHILILTPMQTFHQQYWDNLLQLNYPR.E		K.EHILILTPMQTFHQQYWDNLLQLNYPR.E
256	265	2	1131.64	-0.37	0	34.9	24.8	95.00%	K.AILAANIYQR.F		K.AILAANIYQR.F
350	364	2	1796.82	0.26	0	28.3	29.8	91.80%	R.DGAMFPNFPFYHLIE.T		R.DGAMFPNFPFYHLIETEGFAK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
228	B3LK49_YEAS1	18.64%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
358	370	2	1456.71	0.47	0	68.4	28.7	95.00%	E.IIDSLDINSHTTE.S		R.DMEAQNEIIDSLDINSHTTESDHPTLADNSV.-
149	170	3	2203.16	0.82	0	36.4	25.9	95.00%	E.NNLVSIGDFSTRPALVGGSTAK.K		R.GWGYDTNFTLGICSSPVGEAESQQLSNLTGAFYVDQLNENNLVSIGDFSTRPALVGGSTAK.K
371	381	2	1154.52	1	0	31.9	29.4	95.00%	E.SDHPTLADNSV.-		R.DMEAQNEIIDSLDINSHTTESDHPTLADNSV.-
332	346	2	1598.74	-0.34	1	38.3	29.7	95.00%	R.LRSSPSASSSSLANR.E	Phospho (+80)	R.LRSSPSASSSSLANR.E
190	199	2	1179.6	0.26	0	58.5	29.1	95.00%	K.ATLLNFVCDK.E	Carbamidomethyl (+57)	K.ATLLNFVCDK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
229	A6ZTV6_YEAS7	9.73%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
412	422	2	1194.61	0.16	1	32.9	26.8	95.00%	R.TAVDTVYEAVK.C		R.TAVDTVYEAVK.C
623	646	3	2358.2	0.21	0	65.6	26.3	95.00%	E.MAAGDVLLGLASSGVHSNGFSLVR.K	Deamidation (+1)	K.INEMAAGDVLLGLASSGVHSNGFSLVR.K
504	517	2	1345.71	0.29	0	48.9	26.2	95.00%	E.DTLLVGATDGVGTK.L		R.QNEDTLLVGATDGVGTK.L
400	411	2	1288.7	-0.084	0	66.5	25.6	95.00%	R.VLSVTSTAQDLR.T		R.VLSVTSTAQDLR.T
29	45	2	1705.81	-0.89	0	50.9	29.3	95.00%	K.IYVAPGNGGTATMDPSR.V		K.IYVAPGNGGTATMDPSR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
230	A6ZU67_YEAS7	5.93%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
521	551	3	3156.55	-1.1	1	115	27	95.00%	R.DRPGSVLMNVVSGGIAEASAQQAGDLMQDLK.T		R.DRPGSVLMNVVSGGIAEASAQQAGDLMQDLK.T
521	537	2	1699.86	-0.13	0	57.4	27.3	95.00%	R.DRPGSVLMNVVSGGIAE.A		R.DRPGSVLMNVVSGGIAEASAQQAGDLMQDLK.T
598	609	2	1399.73	0.51	0	51.6	26.4	95.00%	R.IPTAVVWIDCAR.L	Carbamidomethyl (+57)	R.IPTAVVWIDCAR.L
538	551	2	1474.71	0.95	0	68.9	29	95.00%	E.ASAQQAGDLMQDLK.T		R.DRPGSVLMNVVSGGIAEASAQQAGDLMQDLK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
231	A6ZU78_YEAS7	26.17%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
116	126	2	1190.75	0.15	1	34.6	12.6	95.00%	K.GRIPNVPVIVK.A		K.GRIPNVPVIVK.A
98	111	2	1375.74	0.93	0	63.9	25.4	95.00%	E.TAPVIDTLAAGYGK.I		K.ETAPVIDTLAAGYGK.I
97	111	2	1504.78	0.32	1	59.5	26.8	95.00%	K.ETAPVIDTLAAGYGK.I		K.ETAPVIDTLAAGYGK.I
43	55	3	1568.75	0.39	1	25.2	29.4	95.00%	R.INMDKYHPGYFGK.V		R.INMDKYHPGYFGK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
232	A6ZV05_YEAS7	3.86%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

1305	1320	2	1769.91	0.56	1	70.6	27.1	95.00%	K.ISRPIASQNSLGWNEV.-		K.ISRPIASQNSLGWNEV.-
1261	1272	2	1395.65	-0.29	1	57.4	29.2	95.00%	R.MSVQESITQSMR.I		R.MSVQESITQSMR.I
1273	1295	3	2684.16	0.38	0	41.7	30.5	95.00%	R.IQNWMDDSYYGHGLTNNDSTPTR.H		R.IQNWMDDSYYGHGLTNNDSTPTR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
233	A6ZU36_YEAS7	41.36%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
92	106	3	1804.95	1.6	1	26.4	25.4	95.00%	R.YVYAHFPINVNIVEK.D		R.YVYAHFPINVNIVEK.D
136	143	2	938.44	1.1	1	34.4	28.4	95.00%	E.FSTNVKDE.I		R.DGVTIEFSTNVKDEIVLSGNSVEDVSQNAADLQQICR.V
144	166	2	2515.23	-0.14	1	108	27.9	95.00%	E.IVLSGNSVEDVSQNAADLQQICR.V	Carbamidomethyl (+57)	K.DEIVLSGNSVEDVSQNAADLQQICR.V
175	184	3	1177.61	-0.33	0	29.8	27.3	95.00%	K.FLDGIYVSHK.G		K.FLDGIYVSHK.G
73	84	2	1276.67	-2.2	0	43.1	27.8	95.00%	K.SLVDNMITGVTK.G		K.SLVDNMITGVTK.G
125	135	2	1197.64	1.6	1	24.8	25.9	92.40%	R.NVPVRDGVTIE.F		R.NVPVRDGVTIEFSTNVK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
234	A6ZNJ9_YEAS7	22.58%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
251	267	2	1906.82	-2.6	0	78.3	30.2	95.00%	E.ILQSDANNSNTWSQSNE.S		R.SSMFISPTEILQSDANNSNTWSQSNESAIYDSLSSTPR.E
326	341	3	1865.97	1.2	1	23.4	26.1	95.00%	K.YRPPSVHLDQLLDGKE.-		K.YRPPSVHLDQLLDGKE.-
268	289	3	2370.15	-0.64	1	26.2	29	95.00%	E.SAIYDSLSSTPREPGATQILGK.F	Phospho (+80)	R.SSMFISPTEILQSDANNSNTWSQSNESAIYDSLSSTPREPGATQILGK.F
290	311	2	2569.09	0.5	1	77.8	31.2	95.00%	K.FTDSTNPFNYTSYNLSPDSEDR.S		K.FTDSTNPFNYTSYNLSPDSEDR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
235	SSO1_YEAST	14.83%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	62	3	1568.76	-0.88	0	28.8	28.6	95.00%	K.YDHTINQVDSLHK.R		K.YDHTINQVDSLHK.R
78	93	3	1832.91	1.1	0	61.4	27.7	95.00%	R.HSLDNFVAQATDLQFK.L		R.HSLDNFVAQATDLQFK.L
30	39	2	1150.52	0.85	0	48.5	28.5	95.00%	E.GHDFVGFMNK.I		-.MSYNNPYQLETPFEESYELDEGSSAIGAEGHDFVGFMNK.I
46	62	3	2039.99	-0.53	1	46	28.9	95.00%	R.DLDKYDHTINQVDSLHK.R		R.DLDKYDHTINQVDSLHK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
236	B3LJK2_YEAS1	13.14%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	78	2	1397.8	0.69	0	61.1	21	95.00%	E.LLPLNTTIPFNR.I		R.SGDYLSLLNCLSCLDDGTLSSDGGSFDEDDSLELLPLNTTIPFNR.I
9	19	2	1170.69	-0.36	1	28.3	21.9	95.00%	R.AILTDEGVLIK.S		R.AILTDEGVLIK.S
316	348	3	3619.71	0.45	0	34.1	27.5	95.00%	K.LAVTQLPCGSGNAMSISCHWTNNPSYAALCLVK.S	Carbamidomethyl (+57)/Carbamidomethyl (+57)/Carbamidomethyl (+57)	K.LAVTQLPCGSGNAMSISCHWTNNPSYAALCLVK.S
593	608	2	1943.99	0.31	1	49.7	26.6	95.00%	K.FPLEPLQVEIMPMLCK.T	Carbamidomethyl (+57)	K.FPLEPLQVEIMPMLCK.T
549	558	2	1129.64	0.25	0	31.7	24.9	95.00%	R.MTPILLSLDK.G		R.MTPILLSLDK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
237	TCB3_YEAST	5.57%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	178	3	2045.95	0.24	1	28.4	29.4	95.00%	K.FHLDSDDKLFPWQNVGE.F		K.FHLDSDDKLFPWQNVGEFHASGK.G
1340	1352	2	1358.68	-0.087	0	85	27.9	95.00%	R.SPSNLNSTSVTPR.A		R.SPSNLNSTSVTPR.A
783	801	2	1922.92	-0.15	0	87.4	29.1	95.00%	E.MTGAFAAANSVSEPIGCIK.L	Carbamidomethyl (+57)	K.SIEMTGAFAAANSVSEPIGCIK.L
1339	1352	3	1514.78	2.8	1	28.1	26.9	95.00%	R.RSPSNLNSTSVTPR.A		R.RSPSNLNSTSVTPR.A
40	63	3	2678.2	0.46	0	33.9	29.4	95.00%	R.GSDHAPSGHHQYHQLINHDANDTK.T		R.GSDHAPSGHHQYHQLINHDANDTK.T

1196	1207	2	1517.76	-0.21	0	58.5	28.5	95.00%	K.NQVIFNVLDWDR.A		K.NQVIFNVLDWDR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
238	A6ZQP7_YEAS7	21.82%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	40	2	880.54	-0.026	0	41.9	13	95.00%	K.IGPLGLSPK.K		K.IGPLGLSPK.K
131	142	2	1289.64	-0.064	1	69.4	28.2	95.00%	K.EILGTAQSVGCR.V	Carbamidomethyl (+57)	K.EILGTAQSVGCR.V
17	31	2	1296.7	0.13	1	30	23.9	95.00%	R.AVGGEVGASAALAPK.I		R.AVGGEVGASAALAPK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
239	A6ZQ10_YEAS7	13.37%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
404	417	3	1663.86	0.77	0	27.8	27.6	95.00%	K.DTFDRPLIINAFDK.D		K.DTFDRPLIINAFDK.D
272	292	3	2438.16	0.86	1	36.4	29	95.00%	E.LIDMDQVQVHPTGFIDPNDRE.N		K.LGAELIDMDQVQVHPTGFIDPNDRENNWK.F
478	491	2	1464.77	0.42	1	43	25.3	95.00%	R.LGGSSLLECVVFGK.T	Carbamidomethyl (+57)	R.LGGSSLLECVVFGK.T
327	336	2	1150.55	-0.44	1	34.4	28.5	95.00%	R.DTVTMEIQSK.C		R.DTVTMEIQSK.C
319	326	2	966.48	0.8	1	29	28.5	94.60%	R.FTNELSTR.D		R.FTNELSTR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
240	A6ZSL1_YEAS7	7.50%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
29	46	2	1990.89	0.35	1	75.4	30.6	95.00%	E.THNDSNSDSYGLPQLSEK.Y		K.HVFMGMEHELNPETHNDSNSDSYGLPQLSEK.Y
607	617	2	1390.64	-0.24	1	50.1	29.9	95.00%	K.DNDPILDWFEK.L		K.DNDPILDWFEK.L
16	24	2	1115.45	0.16	1	36.6	28.5	95.00%	K.HVFMGMEHE.L		K.HVFMGMEHELNPETHNDSNSDSYGLPQLSEK.Y
543	551	2	1108.53	0.35	0	28	29.7	91.50%	E.TYTWGTPQR.N		R.MGDVALATTAYESPYTFIETYTWGTPQR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
241	A6ZLM1_YEAS7	7.76%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	69	2	1619.83	-1.1	0	66.5	27.5	95.00%	K.ATTPNVNDPIYFLR.G		K.ATTPNVNDPIYFLR.G
400	410	2	1264.66	-0.016	1	46.1	27.1	95.00%	E.FKDQGITLMGR.R		R.DVALEFKDQGITLMGR.R
213	225	2	1365.81	1.3	0	50.9	17.2	95.00%	E.AQGALINLIQGLR.S		K.VGEDDQTEAQGALINLIQGLR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
242	EMP47_YEAST	16.63%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
221	227	2	812.38	0.95	0	26	27.6	91.70%	R.FPSGSYR.I		R.FPSGSYR.I
333	346	2	1637.87	0.49	1	93.2	24.4	95.00%	K.VQQELLSFMTTITK.Q		K.VQQELLSFMTTITK.Q
315	326	2	1313.72	-0.018	1	93	24.8	95.00%	K.ILANDINALETK.L		K.ILANDINALETK.L
40	53	2	1562.79	-0.46	0	94.9	27.2	95.00%	K.LSSDYSLPDLINAR.K		K.LSSDYSLPDLINAR.K
228	242	2	1471.69	-0.29	0	41.4	29.3	95.00%	R.IGVTAQNGAVNNNAE.S	Deamidation (+1)	R.IGVTAQNGAVNNNAESFEIFK.M
194	205	2	1436.7	-1.2	1	48.5	29	95.00%	R.VTYDLEDDNLLK.V		R.VTYDLEDDNLLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
243	A7A0K9_YEAS7	10.53%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
444	461	3	2057.99	0.44	1	23.7	29.1	93.30%	K.ATLINLNTSNNPHDEMFK.V		K.ATLINLNTSNNPHDEMFK.V
643	661	2	2086.06	-0.064	0	42.2	26.4	95.00%	E.LTSFAHIGNARPNFSNVIE.N		R.DQLIHFDDIMTELTSFAHIGNARPNFSNVIENAIK.S
444	458	2	1651.78	-0.013	0	73.2	29.2	95.00%	K.ATLINLNTSNNPHDE.M		K.ATLINLNTSNNPHDEMFK.V
666	688	2	2409.17	-0.73	0	74.8	29.3	95.00%	K.STPPGDSLAVVCCGPPVLVDDVR.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.STPPGDSLAVVCCGPPVLVDDVR.N
33	47	2	1623.83	1.4	0	92.9	27.7	95.00%	E.SNAVLACASYINTLK.W	Carbamidomethyl (+57)	K.DHLESNAVLACASYINTLK.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
244	A6ZZX8_YEAS7	37.18%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

162	172	2	1351.69	-0.52	1	52.6	28.1	95.00%	K.QYAQEQGLLFR.E		K.QYAQEQGLLFR.E
64	72	2	1074.51	0.44	1	35.1	29.9	95.00%	E.IWDTAGQER.Y		K.FEIWDTAGQER.Y
6	16	2	1086.63	-0.19	0	29.6	23.4	95.00%	K.LVLLGDSSVGK.S		K.LVLLGDSSVGK.S
83	101	2	2091.05	-0.53	1	102	27.5	95.00%	R.NANAALVVYDITQEDSLQK.A		R.NANAALVVYDITQEDSLQK.A
34	56	3	2400.2	1.8	1	50.6	27.1	95.00%	E.STIGAAFLSQSITIHPNDGNETK.D		R.ESTIGAAFLSQSITIHPNDGNETK.D
113	126	2	1532.81	-0.07	0	80.1	27.1	95.00%	K.VGDDDLVIYLLGNK.V		K.VGDDDLVIYLLGNK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
245	A6ZNG9_YEAS7	13.38%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
89	100	2	1237.64	1.8	0	43.9	27.5	95.00%	E.MIGSVVGIYNGK.A	Deamidation (+1)	R.NMIIVPEMIGSVVGIYNGK.A
82	100	2	2033.07	-0.84	1	82.2	25	95.00%	R.NMIIVPEMIGSVVGIYNGK.A		R.NMIIVPEMIGSVVGIYNGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
246	A6ZKM8_YEAS7	14.50%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
165	178	2	1550.76	-1	0	34.9	28.9	95.00%	R.LYACISSRPGQSGR.C	Carbamidomethyl (+57)	R.LYACISSRPGQSGR.C
78	92	2	1666.88	-0.49	1	26.1	26.2	94.00%	R.IAGVVYHPSNNELVR.T		R.IAGVVYHPSNNELVR.T
78	89	2	1298.63	0.14	0	44.7	29.3	95.00%	R.IAGVVYHPSNNE.L		R.IAGVVYHPSNNELVR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
247	A6ZPG3_YEAS7	15.45%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
53	63	2	1264.57	0.29	1	60.2	29.8	95.00%	R.NETNNIDGNFK.S		R.NETNNIDGNFK.S
182	198	2	1687.86	0.76	1	36.3	27.1	95.00%	K.DLVSGGVVVSNASDKIE.I		K.DLVSGGVVVSNASDKIEINNTLEER.L
220	227	2	905.49	0.091	1	28	26.4	95.00%	R.LELYGPSK.T		R.LELYGPSK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
248	A6ZSR4_YEAS7	22.06%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
85	93	2	1084.54	0.62	1	26.5	28	91.70%	R.YTLDVEAFK.S		R.YTLDVEAFK.S
35	48	3	1489.78	0.4	1	38.2	26.3	95.00%	K.SHPFGHALVAGIER.Y		K.SHPFGHALVAGIER.Y
127	133	2	955.46	1.8	0	26.9	28.6	91.60%	K.NQWFFSK.L		K.NQWFFSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
249	A6ZQF2_YEAS7	18.72%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
83	95	4	1542.89	0.088	1	28.1	19.1	95.00%	R.LIYPHVEHVPVLK.Q		R.LIYPHVEHVPVLK.Q
61	82	3	2263.09	0.71	1	44	29.4	95.00%	R.SAGASYSPSHGLYINEIPASSR.L		R.SAGASYSPSHGLYINEIPASSR.L
261	268	2	915.55	0.31	0	31	23.9	95.00%	K.IMDLALLK.N		K.IMDLALLK.N
269	279	2	1153.64	-0.53	0	24.4	23.5	93.30%	K.NVPVVANSNIK.T		K.NVPVVANSNIK.T
291	315	3	2691.32	-0.22	0	40.6	27.7	95.00%	K.IIIPHDADGNIDASSFVIANDFYGK.A		K.IIIPHDADGNIDASSFVIANDFYGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
250	B5VDK9_YEAST	14.12%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
170	183	2	1467.74	0.2	0	71.1	27.7	95.00%	E.QDSHLGALSQSIGR.T		K.DEPLQSQLQSQSQPQPPQPMVSNQELFINQQQQLLEQDSHLGALSQSIGR.T
184	194	2	1269.59	1.1	0	38.6	29.7	95.00%	R.THDISLDLNNE.I		R.THDISLDLNNEIVSQNDSLLVDLENLIDNNGR.N
159	169	2	1372.73	-0.58	0	68.1	25.5	95.00%	E.LFINQQQQLLE.Q		K.DEPLQSQLQSQSQPQPPQPMVSNQELFINQQQQLLEQDSHLGALSQSIGR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
251	OST1_YEAST	6.93%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

205	213	2	1115.54	1.3	1	40.8	28.8	95.00%	E.FGPWEDIPR.F		K.ANGNSFEFGPWEDIPR.F
160	171	2	1377.73	0.35	1	60.2	26.1	95.00%	E.TNRLPLSAYDTK.K		K.SFYNTVGIPYPEHVGMSEEQHLLWETNRLPLSAYDTK.K
135	146	2	1385.65	0.49	0	31.8	30.4	95.00%	K.SFYNTVGIPYPE.H		K.SFYNTVGIPYPEHVGMSEEQHLLWETNR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
252	A6ZRX1_YEAS7	20.83%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	67	2	1444.7	0.74	1	62.5	29.1	95.00%	E.SFVDIGHSDEALR.L		K.DEHPGGDEIIMDLGGQDATESFVDIGHSDEALR.L
43	54	2	1261.59	-0.089	0	44.7	29.1	95.00%	E.IIMDLGGQDATE.S		K.DEHPGGDEIIMDLGGQDATESFVDIGHSDEALR.L
55	64	2	1104.47	0.34	0	37.7	29.7	95.00%	E.SFVDIGHSDE.A		K.DEHPGGDEIIMDLGGQDATESFVDIGHSDEALR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
253	A6ZMP4_YEAS7	29.15%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
83	99	2	1999.98	0.66	0	80.5	28.6	95.00%	R.SLDDYISQATDLQYQLK.A		R.SLDDYISQATDLQYQLK.A
54	66	2	1584.79	-0.19	1	45.2	28.1	95.00%	R.YENIINQIDAQHK.D		R.YENIINQIDAQHK.D
44	53	2	1100.59	-1.2	0	72.2	26.9	95.00%	K.INSINANLSR.Y		K.INSINANLSR.Y
166	186	2	2257.15	1	0	62.5	26.6	95.00%	E.AAINDVNGQQIFSQALLNANR.R	Deamidation (+1)	R.QYTIIQPEATDEEVEAAINDVNGQQIFSQALLNANR.R
19	43	3	2739.15	-0.25	1	40	30.8	95.00%	E.MQEDLNNAPTGHSDGSDDFVAFMNK.I		-.MSNANPYENNNPYAENYEMQEDLNNAPTGHSDGSDDFVAFMNK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
254	B3LQX5_YEAS1	12.44%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
157	171	2	1790.8	0.44	0	58.1	30.5	95.00%	K.DFGTYLDSDDQQFIK.D		K.DFGTYLDSDDQQFIK.D
244	261	2	2061.06	1.1	0	61.2	26.6	95.00%	K.SNSIFSIGLTTVPYPYFR.V		K.SNSIFSIGLTTVPYPYFR.V
268	277	2	1117.53	-0.096	1	35.7	28	95.00%	K.YSIAYESTGK.L		K.YSIAYESTGK.L
470	486	2	1936.01	0.67	1	71.2	25.8	95.00%	R.ITAQTSKPLWSVGTYER.I		R.ITAQTSKPLWSVGTYER.I
450	461	2	1394.58	-0.52	0	47.3	30.5	95.00%	R.YADTDNFFGSMK.V		R.YADTDNFFGSMK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
255	A6ZY37_YEAS7	5.88%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
378	392	2	1557.69	-0.52	1	72	29.8	95.00%	R.SSSPSSSFTVSSNER.S		R.SSSPSSSFTVSSNER.S
362	377	2	1800.86	-0.41	1	87.9	29.3	95.00%	E.MEPLGTVEPVDISNER.S	Oxidation (+16)	K.LSEEDSEDEGDNSIPPTIGPNDLEMEPLGTVEPVDISNER.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
256	A6ZN91_YEAS7	12.90%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
57	66	3	1123.65	0.26	0	41.9	19.2	95.00%	K.INRPPVSVSR.I		K.INRPPVSVSR.I
117	130	2	1501.76	-0.057	1	77	28.1	95.00%	K.AGGECITLDQLAVR.A	Carbamidomethyl (+57)	K.AGGECITLDQLAVR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
257	B3LJM9_YEAS1	8.77%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
411	425	2	1841.88	-0.55	0	65.7	29.1	95.00%	R.MADQLTDFLIMQNFR.A		R.MADQLTDFLIMQNFR.A
144	155	2	1300.69	0.82	0	45.6	26.3	95.00%	E.FTSPPLDGLLLE.N		K.DVPEPITEFTSPPLDGLLLENIK.L
181	192	2	1237.55	1.9	0	33.2	29.1	95.00%	R.DLMACAQTGSGK.T	Carbamidomethyl (+57)	R.DLMACAQTGSGK.T
193	206	2	1527.8	0.11	1	36.2	26.1	95.00%	K.TGGFLFPVLSESFK.T		K.TGGFLFPVLSESFK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
258	A6ZWJ0_YEAS7	3.97%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

962	978	2	1833.01	0.11	1	86.7	22.3	95.00%	K.IITLLGMQNYAEALVGK.T		K.IITLLGMQNYAEALVGK.T
918	931	2	1551.61	0.53	0	55.2	29.5	95.00%	R.SCGYVAQADNHMAE.L	Carbamidomethyl (+57)	R.SCGYVAQADNHMAELSVR.E
1418	1433	2	1971.88	1.1	0	36.4	30.4	95.00%	E.NCQYCPYTVQDQVVAK.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.TCGEFLSTYMDNNTGYLVNPTATENCQYCPYTVQDQVVAK.Y
105	117	2	1317.66	0.97	0	27.8	28.6	93.10%	E.QGIEPGDSGIAFK.N		R.QLEQGIEPGDSGIAFK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
259	A6ZNU6_YEAS7	20.00%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	127	2	1238.69	0.15	1	27.2	24.3	95.00%	R.TLTAVHDKILE.D		R.TLTAVHDKILEDLVFPTEIVGK.R
166	175	2	1197.6	-0.43	1	26.7	28	92.20%	K.LESFQAVYNK.L		K.LESFQAVYNK.L
36	44	2	1100.63	-0.85	1	23.9	24.4	92.60%	K.AELRPLQFK.S		K.AELRPLQFK.S
158	167	2	1249.62	-0.16	1	31.7	28.7	95.00%	K.DVQQIDYKLE.S		K.DVQQIDYKLESFQAVYNK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
260	A6ZSS5_YEAS7	35.37%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	17	2	1718.93	0.34	1	64.6	24.6	95.00%	M.VLVQDLLHPTAASEAR.K		-.MVLVQDLLHPTAASEAR.K
2	15	2	1491.79	0.66	0	85	25.7	95.00%	M.VLVQDLLHPTAASE.A		-.MVLVQDLLHPTAASEAR.K
58	70	2	1366.62	0.11	0	43.5	29.3	95.00%	E.SCSTVLCTPTGGK.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CPGCLNITTVFSHAQTAVTCESCSTVLCTPTGGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
261	A6ZUX1_YEAS7	8.50%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
513	529	2	1957.88	0.92	0	70.7	30.3	95.00%	K.VAAWWDYGYQIGGMADR.T		K.VAAWWDYGYQIGGMADR.T
472	489	2	1832.91	-0.6	0	62.2	27	95.00%	R.TAYSSPSVVLPSQTPDGK.L		R.TAYSSPSVVLPSQTPDGK.L
490	497	2	961.52	0.18	0	41.7	26	95.00%	K.LALIDDFR.E		K.LALIDDFR.E
632	649	3	2074.94	0.67	1	40.4	29.9	95.00%	K.MSYKDFPQLFNGGQATDR.V	Deamidation (+1)	K.MSYKDFPQLFNGGQATDR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
262	A7A0Y0_YEAS7	18.10%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
83	88	2	757.39	1.1	0	40.1	24.4	95.00%	R.DAFHLR.V		R.DAFHLR.V
170	180	3	1361.67	1.4	1	28.5	29.1	95.00%	K.KWGFTNLDRPE.Y		K.KWGFTNLDRPEYLK.K
117	128	3	1219.66	-0.0072	0	31.5	26.4	95.00%	R.GAWGKPHGLAAR.V		R.GAWGKPHGLAAR.V
129	139	2	1245.71	0.15	0	55.6	23.4	95.00%	R.VDIGQIIFSVR.T		R.VDIGQIIFSVR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
263	A6ZRC2_YEAS7	3.31%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
357	372	2	1812.82	0.38	0	36.2	30.1	95.00%	R.VSADYGRPSLDYDNLE.Q		R.VSADYGRPSLDYDNLEQGAGEANIVDR.S
1025	1039	2	1590.81	0.24	1	74.1	27.1	95.00%	E.FGSEPSEIVDALLSK.Y		K.EFGSEPSEIVDALLSK.Y
872	880	2	980.49	0.49	0	32.2	27.6	95.00%	K.GADSIIYSR.L		K.GADSIIYSR.L
955	966	2	1269.73	0.85	1	31.7	23.1	95.00%	E.LILLGGTAIEDR.L		R.ELILLGGTAIEDR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
264	A6ZMY7_YEAS7	10.94%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
51	62	2	1323.66	0.59	1	26.9	28.1	92.50%	E.SILDYAGKDITE.I		R.FLSEHPGGDESILDYAGKDITEIMK.D
181	195	2	1589.85	0.54	0	80.5	25.3	95.00%	K.GSAPLFGNFLEPLTK.T		K.GSAPLFGNFLEPLTK.T
20	34	3	1906.83	-2	1	77.2	30	95.00%	E.HNTANDCWVTYQNRK.I	Deamidation (+1)/ Carbamidomethyl (+57)	K.TVQEHNTANDCWVTYQNRK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
265	B3LU76_YEAS1	19.43%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
81	94	2	1665.79	-0.74	0	56.2	29.8	95.00%	R.FGNLPAQWSAFWDK.T		R.FGNLPAQWSAFWDK.T
158	176	2	1777.85	-0.014	0	77.7	29.3	95.00%	E.VHGGSPWGAGTLAGPDGSR.T		K.NSFAELASIEEVHGGSPWGAGTLAGPDGSR.T

66	80	2	1740.91	-0.017	1	50.5	25.6	95.00%	K.TLLEYDAFLFGVPTR.F		K.TLLEYDAFLFGVPTR.F
70	80	2	1284.65	0.83	0	60.7	28.1	95.00%	E.YDAFLFGVPTR.F		K.TLLEYDAFLFGVPTR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
266	B3LMS1_YEAS1	5.74%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
257	264	2	1101.52	0.35	1	45.6	29	95.00%	K.QEIQDWQR.S		K.QEIQDWQR.S
278	297	4	2360.19	0.91	1	29.6	26.5	95.00%	E.THSGPTLWQYVTDPSYKKPR.T		R.DPESSEETHSGPTLWQYVTDPSYKKPR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
267	A6ZSD5_YEAS7	13.70%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
101	111	2	1246.53	-0.066	0	45.5	29.2	95.00%	R.GINFDYSGSCK.I	Carbamidomethyl (+57)	R.GINFDYSGSCK.I
90	100	2	1261.49	-0.079	0	75.5	29.1	95.00%	K.FGSMSCSSMPR.G	Oxidation (+16)/ Carbamidomethyl (+57)	K.FGSMSCSSMPR.G
174	181	2	914.46	0.63	0	36.2	27.9	95.00%	E.SEPLLDLE.V		R.LETSLEESEPLLDLEVQEDAR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
268	A6ZVM1_YEAS7	3.04%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
109	126	2	1896.92	-1.3	0	73.7	28.9	95.00%	K.FTNIASSPPSSSNNIFSK.A		K.FTNIASSPPSSSNNIFSK.A
629	645	2	2014.01	0.29	1	30	27.7	95.00%	K.TLNYEILQVFPFNSDSK.R		K.TLNYEILQVFPFNSDSK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
269	A6ZW48_YEAS7	6.91%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
362	372	2	1334.66	0.58	1	34.2	28.5	95.00%	E.TLKDDEPIIYE.Y		K.IDEWTSLLAETLKDDEPIIYEYDENADSEEDEEEGNGSDELGDVEDIGGK.G
768	782	2	1564.74	0.79	0	63.9	29.3	95.00%	E.WALFGNGGFAPGNTR.V	Deamidation (+1)	K.TPEWALFGNGGFAPGNTR.V
392	401	2	1001.5	0.78	1	52.4	27.8	95.00%	E.LGDVEDIGGK.G		K.DDEPIIYEYDENADSEEDEEEGNGSDELGDVEDIGGK.G
199	218	3	2128.14	0.26	0	52.3	23.1	95.00%	E.TLLSSQIYVLYSSLQGAASK.A		K.SALTISNETLLSSQIYVLYSSLQGAASK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
270	A6ZT81_YEAS7	20.14%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
244	255	2	1372.63	0.29	1	60.6	29.7	95.00%	K.IGLDCASSEFFK.D	Carbamidomethyl (+57)	K.IGLDCASSEFFK.D
313	330	2	1853.99	0.8	0	76.6	24.1	95.00%	K.TAGIQIVADDLTVTNPAR.I		K.TAGIQIVADDLTVTNPAR.I
61	79	2	1944.02	-0.37	0	45.7	24.8	95.00%	K.GVMNAVNNVNNVIAAAFVK.A		K.GVMNAVNNVNNVIAAAFVK.A
33	45	2	1239.61	0.55	0	35.9	29	95.00%	R.SIVPSGASTGVHE.A		R.SIVPSGASTGVHEALEMR.D
273	288	3	1892.92	0.96	1	25	28.1	95.00%	K.WLTGVELADMYHSLMK.R		K.WLTGVELADMYHSLMK.R
225	234	2	1069.64	1.4	0	37.5	22	95.00%	E.ALDLIVDAIK.A		R.YGASAGNVGDEGGVAPNIQTAEEALDLIVDAIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
271	A7A0V2_YEAS7	15.31%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
360	375	3	1792.02	1.4	0	21.8	17.6	95.00%	E.LSFISKPTVPFNITTK.S		K.YYITGAFEPELSFISKPTVPFNITTK.S
583	598	2	1747.88	-0.46	1	40.7	27.9	95.00%	K.IIEPPAQDPCLEAAPK.K	Carbamidomethyl (+57)	K.IIEPPAQDPCLEAAPK.K
650	662	2	1458.8	0.88	0	47	23.3	95.00%	E.YLSQVWVLAAGPR.G		R.DHAEYLSQVWVLAAGPR.G
670	682	3	1481.68	0.67	1	37	30	95.00%	K.RWATDGGLHFHGE.S		K.RWATDGGLHFHGESFAL.-
469	484	2	1940.77	-0.76	0	59.4	30.1	95.00%	E.IDYIDYHDCAADINDE.V	Carbamidomethyl (+57)	K.NNFEGMEIYISGTEGNEQDIEIDYIDYHDCAADINDEVR.S
546	554	2	1118.54	1	0	41.6	27.5	95.00%	E.IDFTYAFSR.S		K.TNDIPDINADDEIDFTYAFSR.S
268	289	2	2368.35	-0.6	1	85.9	15.6	95.00%	R.VTIVPISSSLSLLEFPLTDLPK.K		R.VTIVPISSSLSLLEFPLTDLPK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
272	A6ZXF1_YEAS7	14.44%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
307	324	2	2056.95	-1.8	1	50.8	30.1	95.00%	K.SFGYTWAVPNENTQNTTK.S		K.SFGYTWAVPNENTQNTTK.S
261	284	3	2737.31	-0.17	0	31.5	28.8	95.00%	K.QLHVPDNSQDDTIIMMNPIDNSLK.L		K.QLHVPDNSQDDTIIMMNPIDNSLK.L
221	242	3	2506.21	-0.47	1	25.5	29.3	95.00%	R.NDSSSISNNVYSSEYHPIKPLR.S		R.NDSSSISNNVYSSEYHPIKPLR.S
285	299	2	1635.79	-0.44	0	30.3	29.3	95.00%	K.LTTLDTGDLSFPIDE.E		K.LTTLDTGDLSFPIDEEQPILK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
273	A6ZL24_YEAS7	8.05%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
581	587	2	822.44	-0.29	0	28.6	24.9	95.00%	K.SGFPFIR.L		K.SGFPFIR.L
362	378	2	1655.85	0.3	0	61.5	26.2	95.00%	R.GDGTGVGDNVVNQLLAK.M		R.GDGTGVGDNVVNQLLAK.M
379	397	3	2130.09	0.38	1	25.5	26.6	95.00%	K.MDGVDQLNNILVIGMTNRK.D		K.MDGVDQLNNILVIGMTNRK.D
425	433	2	1104.62	0.26	0	31.2	24.8	95.00%	R.LQIFDIQTK.K		R.LQIFDIQTK.K
603	611	2	1111.57	0.34	0	31.2	26.7	95.00%	K.IAYIDNTFR.D		K.IAYIDNTFR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
274	A6ZRQ9_YEAS7	4.09%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
621	633	2	1532.78	-0.6	1	75.8	27	95.00%	E.RNTVQNNSQGFLR.E		R.GLDNDISHDERNTVQNNSQGFLR.E
622	633	2	1376.68	-0.3	0	90.1	28.5	95.00%	R.NTVQNNSQGFLR.E		R.NTVQNNSQGFLR.E
557	569	2	1468.65	-0.42	0	35.3	29.4	95.00%	R.NVTAMNGSFQNMR.S		R.NVTAMNGSFQNMR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
275	A6ZR85_YEAS7	17.65%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
43	51	2	941.53	0.29	1	42.1	25.3	95.00%	R.NIVEAAAVR.D		R.NIVEAAAVR.D
71	82	3	1485.7	0.86	0	42.8	29.6	95.00%	K.LHYCVSCAIHAR.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.LHYCVSCAIHAR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
276	A6ZQX5_YEAS7	11.96%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	201	2	1115.63	-0.11	0	45.3	23.7	95.00%	R.FNVTVAQLPK.D		R.FNVTVAQLPK.D
45	66	2	2285.19	0.38	0	76.3	24.8	95.00%	R.ASSIFSINTTPLAPPNATDIQK.F		R.ASSIFSINTTPLAPPNATDIQK.F
44	66	3	2441.29	1	1	26.5	23.5	95.00%	R.RASSIFSINTTPLAPPNATDIQK.F		R.RASSIFSINTTPLAPPNATDIQK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
277	COS7_YEAST	26.63%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
157	167	3	1261.73	-0.0015	1	29	22.1	95.00%	R.TTVLEPFSLKK.D		R.TTVLEPFSLKK.D
102	108	2	935.49	1.7	0	31	27.4	95.00%	K.QLIQFCK.E	Carbamidomethyl (+57)	K.QLIQFCK.E
113	123	2	1283.51	0.84	0	38.3	28.9	95.00%	E.NTPSSDPHDWE.V		K.EITENTPSSDPHDWEVVVANLNSYLYENK.A
22	33	3	1442.83	0.91	1	35.7	20.9	95.00%	E.SQKIVLPQDLFR.S		K.QLESQKIVLPQDLFR.S
354	369	2	2001.08	-0.26	1	39.5	23.1	95.00%	K.SMWLLPLNVELWPYIK.E		K.SMWLLPLNVELWPYIK.E
102	109	2	1064.53	0.77	1	37.9	28.6	95.00%	K.QLIQFCKE.I	Carbamidomethyl (+57)	K.QLIQFCKEITENTPSSDPHDWEVVVANLNSYLYENK.A
25	33	2	1099.64	-0.29	0	27.9	23.4	95.00%	K.IVLPQDLFR.S		K.IVLPQDLFR.S
206	219	2	1553.81	-0.2	1	52.8	26.7	95.00%	K.SWSPVGLEDVQLPK.D		K.SWSPVGLEDVQLPK.D
143	153	2	1391.58	0.28	1	49.9	29.7	95.00%	K.NFFFNATDCEK.M	Carbamidomethyl (+57)	K.NFFFNATDCEK.M
186	196	2	1211.62	1.1	0	50.2	27.3	95.00%	E.ALQVYATGFDK.Q		K.DSVPYIEEALQVYATGFDK.Q
11	18	2	893.49	-0.02	0	26.5	25.4	95.00%	K.SVDVLSFK.Q		K.SVDVLSFK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
278	A6ZPF9_YEAS7	19.13%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
63	75	2	1389.74	-0.38	1	59.6	25.7	95.00%	K.ADNLAISAQGFKR.G		K.ADNLAISAQGFKR.G
63	74	2	1233.63	-0.67	0	49.2	27.6	95.00%	K.ADNLAISAQGFK.R		K.ADNLAISAQGFK.R

35	43	2	1018.51	0.67	0	53.3	27.5	95.00%	E.IDDTVGIMR.D		R.QEIDDTVGIMR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
279	A6ZKZ2_YEAS7	23.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	133	2	1855	-0.52	0	47.2	23.2	95.00%	R.VQVGDIVTVGQCRPISK.T	Carbamidomethyl (+57)	R.VQVGDIVTVGQCRPISK.T
47	56	2	1095.54	-0.83	1	34.6	27.6	95.00%	K.TAIEGSYIDK.K		K.TAIEGSYIDK.K
58	67	2	1148.6	0.44	0	68.1	27.6	95.00%	K.CPFTGLVSIR.G	Carbamidomethyl (+57)	K.CPFTGLVSIR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
280	A6ZM36_YEAS7	15.75%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	16	2	1781.94	-0.15	1	67.6	24.6	95.00%	M.SLVVQEQGSFQHILR.L	Acetyl (+42)	-.MSLVVQEQGSFQHILR.L
81	88	2	1015.56	1	0	47.3	27	95.00%	K.IPAWFLNR.Q		K.IPAWFLNR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
281	A6ZYL7_YEAS7	11.13%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
737	748	2	1380.73	-0.3	1	40.4	25.8	95.00%	K.ALLNGIEVDYFK.L		K.ALLNGIEVDYFK.L
242	257	3	1770.89	-0.34	1	25.7	27.5	95.00%	K.IADTEGFTPLHWGTVK.G		K.IADTEGFTPLHWGTVK.G
644	658	2	1525.81	-0.079	0	43.8	25	95.00%	E.SNDTVLAPVPGSTIR.K		K.SIGPDGLSFNENFNTTPEGFAPSI DPGEESNDTVLAPVPGSTIR.K
265	276	2	1443.7	-0.7	0	40.9	28.4	95.00%	K.YLIQDGADFFQK.T		K.YLIQDGADFFQK.T
122	138	2	1788.94	3.5	0	47.2	24.8	95.00%	R.LSVVDFLVSQGADVNAR.A		R.LSVVDFLVSQGADVNAR.A
109	121	3	1517.79	1.1	0	30.6	27.2	95.00%	E.HITGLHWASINNR.L		K.EHITGLHWASINNR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
282	A6ZTE7_YEAS7	10.39%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
655	677	3	2735.38	0.58	1	26.8	26.1	95.00%	K.EFMATPYTPVIPINDNFIITHFR.N		K.EFMATPYTPVIPINDNFIITHFR.N
696	711	2	1855.88	0.4	0	39.3	29.1	95.00%	E.STSIICDLGLDVFCTR.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.NLLPGSDSQLISIPTNLESTSIICD LGLDVFCTR.I
572	596	4	2837.36	0.93	0	21.8	29	95.00%	R.LSNSSDNFSYDPLTGHINKPQFQ TK.Q		R.LSNSSDNFSYDPLTGHINKPQFQ TK.Q
467	481	2	1588.83	-1.3	1	40.9	25.7	95.00%	R.ETTNLNTLGITLGDK.S		R.ETTNLNTLGITLGDK.S
468	481	2	1459.79	0.33	0	77.6	24.4	95.00%	E.TTNLNTLGITLGDK.S		R.ETTNLNTLGITLGDK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
283	A7A0G8_YEAS7	16.89%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
114	120	2	743.43	0.91	0	28.8	26.4	95.00%	E.AGGWLIK.A		K.ICIQPEAGGWLIK.A
51	62	2	1525.72	-0.39	0	62.5	29.9	95.00%	K.AQIYDDQLQNYR.D		K.AQIYDDQLQNYR.D
108	120	2	1483.79	-0.53	1	45.6	25.1	95.00%	K.ICIQPEAGGWLIK.A	Carbamidomethyl (+57)	K.ICIQPEAGGWLIK.A
78	89	2	1451.72	-0.28	0	34.2	29.3	95.00%	E.TFDDNHLVVHQK.G		R.DAGAQDFGVLIDIEETFDDNHLVV HQK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
284	A6ZSV7_YEAS7	10.38%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
492	501	2	1050.48	1.5	1	40	28.3	95.00%	E.MGIGSSSQER.S		R.TEDDETIELEEMGIGSSSQER.S
502	511	2	1089.57	0.17	1	25.9	26.5	93.40%	R.SLVSPAPEYK.D		R.SLVSPAPEYK.D
39	55	2	1833.92	-0.87	0	72.6	27.2	95.00%	R.TTLQPNSTSQSMIGTLR.K		R.TTLQPNSTSQSMIGTLR.K
15	34	2	2193.91	0.36	0	134	30.5	95.00%	E.SQTNNDSVNDAYADVNTTHE.S		- .MTSQEYEPIQWSDESQTNNDSVN DAYADVNTTHESR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
285	A6ZWP8_YEAS7	5.97%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
552	569	2	2050.88	-0.25	0	43.8	30.9	95.00%	R.VAGTSNFTNLDDYMMNMK.R		R.VAGTSNFTNLDDYMMNMK.R
742	754	2	1445.69	-0.079	0	68.2	29.3	95.00%	E.SFMSNTLFNSSLV.-		K.GNNVPNNDSESFMSNTLFNSSLV .-

589	602	2	1602.81	0.29	1	62.3	27.5	95.00%	R.IPEPLTFTNSEDLK.Q		R.IPEPLTFTNSEDLK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
286	A6ZZV9_YEAS7	32.99%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
38	60	2	2445.14	0.37	0	101	29.5	95.00%	R.AVSDSSVINQMTDSLGSMFTDIK.N		R.AVSDSSVINQMTDSLGSMFTDIK.N
29	37	2	1057.52	-0.3	1	34.9	28.3	95.00%	R.NINQEIGDR.A		R.NINQEIGDR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
287	A6ZN90_YEAS7	18.06%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
111	119	2	954.58	0.084	1	24.2	18.7	92.90%	K.IGIVEISPK.G		K.IGIVEISPK.G
8	24	2	1927.94	1	0	68.3	28.4	95.00%	R.DVAAQDFINAYASFLQR.Q		R.DVAAQDFINAYASFLQR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
288	A6ZKS1_YEAS7	10.58%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	146	2	1120.66	1.5	1	22.7	19.7	90.20%	R.ALVEHIIQAK.A		R.ALVEHIIQAK.A
10	19	2	899.54	-0.46	0	66.1	22.4	95.00%	R.LAASVVGVGK.R		R.LAASVVGVGK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
289	A6ZM77_YEAS7	7.81%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
284	301	3	2013.92	-0.76	0	42	30.2	95.00%	K.DHIAAGGKPVCVMDAWCK.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.DHIAAGGKPVCVMDAWCK.L
425	440	2	1736.88	0.68	0	69.5	27.2	95.00%	K.GAMLIPTLYPALHDPE.V		K.GAMLIPTLYPALHDPEVYENPDEFIPER.W
378	385	2	956.56	1	1	26.9	23.6	95.00%	E.LNLDLIEK.M		R.NNDMSTELNLDLIEK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
290	A6ZYE1_YEAS7	12.02%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
176	194	2	1986.94	0.75	0	45.7	29.2	95.00%	R.TVMSLPGNHDIGFGDTVVE.S		R.TVMSLPGNHDIGFGDTVVESSLQR.F
255	267	3	1587.88	0.75	1	40	21.6	95.00%	R.ILLTHVPLWRDPE.Q		R.ILLTHVPLWRDPEQQTCGQLR.E
176	199	3	2558.24	-0.23	1	34.2	27.6	95.00%	R.TVMSLPGNHDIGFGDTVVESSLQR.F		R.TVMSLPGNHDIGFGDTVVESSLQR.F
309	330	3	2587.16	0.25	0	27.3	31.1	95.00%	E.ILFSGDDHDHCQISHSYPFQGK.T	Carbamidomethyl (+57)	K.TQPEILFSGDDHDHCQISHSYPFQGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
291	A6ZZN6_YEAS7	9.95%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
344	358	2	1599.81	0.17	0	89.2	27.6	95.00%	E.LIDAFGFLGGNAFMK.D		K.SELIDAFGFLGGNAFMK.D
190	200	2	1176.72	0.75	0	36.3	14.5	95.00%	E.HLTTVLVAVPK.S		R.SLHDIVKPEDFVLNSEHLTTVLVAVPK.S
30	42	2	1494.71	-0.82	1	48.9	29.3	95.00%	K.TDSWFNETLIGGR.A		K.TDSWFNETLIGGR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
292	A6ZUT7_YEAS7	3.39%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
666	676	2	1250.63	-0.66	0	53.5	28.9	95.00%	R.DNIIFGSPFNK.E		R.DNIIFGSPFNK.E
1413	1424	3	1461.69	1.2	0	48.1	29.3	95.00%	E.FGDCTILCIAHR.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.IVEEFGDCTILCIAHR.L
729	743	2	1726.84	-1.2	0	42.8	29.4	95.00%	K.DIYLFDDVLSAVDSR.V		K.DIYLFDDVLSAVDSR.V
763	774	3	1392.81	-0.14	1	30	19	95.00%	R.ILATHQLSLIER.A		R.ILATHQLSLIER.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
293	B3LGK8_YEAS1	10.70%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

349	366	3	1995.04	-0.05	1	23.2	25.8	95.00%	E.IFGVDPKDVDILMGTFTK.S		R.GVCEIFGVDPKDVDILMGTFTK.S
397	416	2	2029.04	0.54	0	87	26.5	95.00%	E.SMPAPVLAQTISSLQTISGE.I		R.LDLTTVSYSESMPAPVLAQTISSLQTISGEICPGQGTER.L
186	194	2	963.48	1.4	0	59.2	27.7	95.00%	K.YSIQSGGPR.A		K.YSIQSGGPR.A
173	185	2	1392.62	-0.92	1	72	29.8	95.00%	K.GQCTDAALESVDK.Y	Carbamidomethyl (+57)	K.GQCTDAALESVDK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
294	A6ZLA4_YEAS7	12.31%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
309	321	2	1288.62	0.6	0	40.8	28.6	95.00%	E.GIPAYHGFGGADK.I		R.EGIPAYHGFGGADK.I
431	447	2	1924.9	-0.52	0	59.8	29.5	95.00%	E.SFDATLSDDVVDQWLSK.S		K.TIHIIEVDESFDATLSDDVVDQWLSK.S
386	411	3	2899.37	-0.58	1	36.1	29	95.00%	K.LISHIHDGQDGGTQDYFERPTDGTLK.A		K.LISHIHDGQDGGTQDYFERPTDGTLK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
295	A6ZNP1_YEAS7	18.06%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
191	201	2	1408.71	-0.077	1	52.4	28.3	95.00%	E.FAYQQNLIEQR.D		R.DPINNEEFAYQQNLIEQR.D
40	55	2	1762.95	-0.41	0	57.4	23.9	95.00%	E.INGQISTLQQFTATLK.S	Deamidation (+1)	K.EEVAAELFEINGQISTLQQFTATLK.S
56	66	2	1193.6	-1.6	1	27.6	28.6	92.70%	K.SFIDRGDVSAK.V		K.SFIDRGDVSAK.V
118	131	2	1702.79	-0.18	1	57.7	29.6	95.00%	R.DVSYSFQEFQGIQR.Q		R.DVSYSFQEFQGIQR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
296	B3LTD1_YEAS1	16.29%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
37	80	4	4761.74	1.2	0	71.4	28	95.00%	R.SSSQPSHHHSGGTNNNNNNNNNNNNSNNNNGNDGGNDDDYDYE.M	Deamidation (+1)/ Deamidation (+1)	R.SSSQPSHHHSGGTNNNNNNNNNNNNSNNNNGNDGGNDDDYDYEMQDYRPSPQSARPTPTYVPQYSVESGTAFPIQEVIPSAYINTQDINHK.D
162	176	3	1661.77	-0.66	1	32.8	29.8	95.00%	K.NADDAHTIPESHLSR.R		K.NADDAHTIPESHLSR.R
81	104	3	2812.31	0.15	0	24.1	28.8	94.50%	E.MQDYRPSPQSARPTPTYVPQYSVE.S	Oxidation (+16)	R.SSSQPSHHHSGGTNNNNNNNNNNNNSNNNNGNDGGNDDDYDYEMQDYRPSPQSARPTPTYVPQYSVESGTAFPIQEVIPSAYINTQDINHK.D
183	208	3	2520.09	0.79	1	36.3	31	95.00%	R.ATSNAGHSANTGATNGRTTGAQTNME.S	Deamidation (+1)	R.ATSNAGHSANTGATNGRTTGAQTNMESNESPR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
297	A7A0W1_YEAS7	5.21%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	19	2	2263.11	0.41	1	89.6	28.6	95.00%	-.MDLVLEVADHYVLDDLYAK.V	Acetyl (+42)	-.MDLVLEVADHYVLDDLYAK.V
7	19	2	1520.75	0.26	0	53.7	28.5	95.00%	E.VADHYVLDDLYAK.V		-.MDLVLEVADHYVLDDLYAK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
298	B3LM88_YEAS1	23.44%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
77	86	2	1091.54	1.2	0	41.6	28.7	95.00%	E.ATYQVSGNPR.N		K.SNQVFTGPGFYDPVDELLIEPSLPGLSYSFTEDGWYEEATYQVSGNPR.N
39	54	2	1770.77	-0.12	0	58	30.8	95.00%	K.SNQVFTGPGFYDPVDE.L		K.SNQVFTGPGFYDPVDELLIEPSLPGLSYSFTEDGWYEEATYQVSGNPR.N
76	86	2	1220.58	0.72	1	45.3	28.9	95.00%	E.EATYQVSGNPR.N		K.SNQVFTGPGFYDPVDELLIEPSLPGLSYSFTEDGWYEEATYQVSGNPR.N
121	137	2	1959.83	1	0	90.6	30.3	95.00%	R.QLFSDPCNDDGVSTYSR.Y	Carbamidomethyl (+57)	R.QLFSDPCNDDGVSTYSR.Y

55	70	2	1764.92	1.5	0	44.6	25.1	95.00%	E.LLIEPSLPGLSYSFTE.D		K.SNQVFTGPGFYDPVDELLIEPSLPGLSYSFTEDGWYEEATYQVSGNPR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
299	A6ZS93_YEAS7	8.88%	100%	3							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
130	144	2	1694.88	0.87	0	61.5	26.8	95.00%	E.HRPSILDGSVNEPFK.T		R.QGSSNFISYFDDMSFEHRPSILDGSVNEPFK.T
52	79	3	2839.36	-0.071	0	71.1	29.7	95.00%	E.HTATTITQNHSVVASNGDVAFIPGTATE.G	Deamidation (+1)	R.QSITVDDEGELYGLDTSGNSPANEHTATTITQNHSVVASNGDVAFIPGTATEGNTEIVTEEVIETDDNMFK.T
38	51	2	1436.64	0.55	0	74.4	29.8	95.00%	E.LYGLDTSGNSPANE.H		R.QSITVDDEGELYGLDTSGNSPANEHTATTITQNHSVVASNGDVAFIPGTATEGNTEIVTEEVIETDDNMFK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
300	A6ZM38_YEAS7	34.56%	100%	5							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
88	95	2	859.48	0.79	0	39.9	27.8	95.00%	E.VSALDLSR.S		K.DQYVPEVSALDLSR.S
82	95	2	1590.79	-0.0064	1	69.1	27.8	95.00%	K.DQYVPEVSALDLSR.S		K.DQYVPEVSALDLSR.S
117	128	2	1295.76	-0.39	0	61.9	21.4	95.00%	K.LPLSVINVSAQR.D		K.LPLSVINVSAQR.D
96	111	2	1702.84	-0.71	0	58.6	29	95.00%	R.SNGVLNVDNQTSDLVK.S	Deamidation (+1)	R.SNGVLNVDNQTSDLVK.S
112	128	3	1794.07	0.4	1	22.5	12.8	95.00%	K.SLGLKLPLSVINVSAQR.D		K.SLGLKLPLSVINVSAQR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
301	YM12B_YEAST	14.87%	100%	18							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	65	2	1587.74	1.1	0	52.3	29.9	95.00%	K.ANSQQTTTPASSAVPE.N		K.ANSQQTTTPASSAVPENPHHASPQPASVPPPQNGPYPQQCMMTQNQANPSGWSFYGHPSMIPYTPYQMSPMYFPPGPQSQFPQYPSSVGTPLSTPSPESGNTFTDSSSADSDMTSTK.K
400	419	2	2073.92	-0.2	0	113	30.1	95.00%	R.AHNVSTSNNSPSTDNDSISK.S		R.AHNVSTSNNSPSTDNDSISK.S
471	491	3	2226.08	-0.67	0	88.7	29	95.00%	R.SAHHIHSASSNPDINVVDAQK.R		R.SAHHIHSASSNPDINVVDAQK.R
1151	1178	3	2885.41	-0.54	0	59.2	28.1	95.00%	E.LPPINSHQTNSSLGGIGDSNAYTTINSK.K		K.ELPPINSHQTNSSLGGIGDSNAYTTINSK.K
148	167	2	2065.88	0.33	1	86.6	30.8	95.00%	E.SGNTFTDSSSADSDMTSTKK.Y		K.ANSQQTTTPASSAVPENPHHASPQPASVPPPQNGPYPQQCMMTQNQANPSGWSFYGHPSMIPYTPYQMSPMYFPPGPQSQFPQYPSSVGTPLSTPSPESGNTFTDSSSADSDMTSTKK.Y
560	568	2	1163.53	-1.8	0	29.8	29.4	94.60%	K.YGDFYWVSK.K		K.YGDFYWVSK.K
3	24	3	2336.1	1.1	0	50.5	29.5	95.00%	E.SQQLSQHSHISHGSACASVTSK.E	Carbamidomethyl (+57)	-.MESQQLSQHSHISHGSACASVTSK.E
25	39	2	1638.78	-0.86	1	78.9	29.3	95.00%	K.EVHTNQDPLDVSASK.T		K.EVHTNQDPLDVSASK.T
1093	1113	3	2202.09	-0.77	1	34.9	28.2	95.00%	R.SPSIDASPPENNSSHNIVPIK.T		R.SPSIDASPPENNSSHNIVPIK.T
958	972	2	1525.69	0.052	0	39.9	30	95.00%	K.AVSPTDSTPPSTHTE.D		K.AVSPTDSTPPSTHTEDSK.R
1621	1632	2	1318.72	-0.46	0	43.7	25.8	95.00%	K.SQIGNIYLLNGK.V		K.SQIGNIYLLNGK.V
308	315	2	989.52	0.32	0	31.3	28.1	95.00%	K.VACQLIMR.G	Carbamidomethyl (+57)	K.VACQLIMR.G
1605	1620	2	1787.87	0.79	0	71.7	28.7	95.00%	K.LVAISDASYGNQPYYK.S		K.LVAISDASYGNQPYYK.S

148	166	2	1953.78	0.7	0	94.2	30.7	95.00%	E.SGNTFTDSSSADSDMTSTK.K	Oxidation (+16)	K.ANSQQTTTPASSAVPENPHHAS PQPASVPPPQNGPYPQQCMMTQN QANPSGWSFYGHPSMIPYTPYQM SPMYFPPGPQSQFPQYPSSVGTPL STPSPESGNTFTDSSSADSDMTST K.K
1	24	4	2638.19	-0.25	1	34.7	29.6	95.00%	-.MESQQLSQHSHISHGSACASVTSK.E	Acetyl (+42)/ Carbamidomethyl (+57)	-.MESQQLSQHSHISHGSACASVTSK.E
1234	1242	2	1115.51	0.078	1	55.2	28.4	95.00%	R.YDEAITYNK.D		R.YDEAITYNK.D
658	681	4	2906.4	-0.29	0	21.1	29.4	94.20%	K.YQNSYEPFQYLHTDIFGPVHNLP K.S		K.YQNSYEPFQYLHTDIFGPVHNLP K.S
958	975	2	1855.84	-0.6	1	47.1	30.4	95.00%	K.AVSPTDSTPPSTHTEDSK.R		K.AVSPTDSTPPSTHTEDSK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
302	B3LMC0_YEAS1	3.79%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
199	207	2	1033.59	0.65	0	24.5	22.3	93.40%	R.ILLFNTTGR.N		R.ILLFNTTGR.N
933	943	2	1290.76	0.056	0	49.3	18.9	95.00%	R.LTLDIPVVFFK.C		R.LTLDIPVVFFK.C
607	617	2	1253.55	0.22	1	38.6	30	95.00%	R.DTTGDFSENIR.T		R.DTTGDFSENIR.T
783	790	2	981.5	1.8	0	31.9	28	95.00%	E.MDLLSTFR.A		K.IDIASFANDNPEMDLLSTFR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
303	A6ZPF4_YEAS7	7.04%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
420	432	3	1441.77	0.49	1	32.8	25.9	95.00%	K.NLHTHEVPAPISK.S		K.NLHTHEVPAPISK.S
13	21	2	1119.52	0.16	0	31.1	28.5	95.00%	K.STDDDLIWR.R		K.STDDDLIWR.R
346	363	2	1913.97	-0.37	0	45.9	27	95.00%	K.NQALGGALLHSHVQPFPE.G		K.NQALGGALLHSHVQPFPEGSEQ QQVTVYGYSDANNEWFFQR.I
99	111	4	1574.76	0.079	1	32.8	29.1	95.00%	R.HEFYHDVHPPLGK.M		R.HEFYHDVHPPLGK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
304	A6ZW97_YEAS7	11.97%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
158	165	2	991.53	-0.028	0	46	26.9	95.00%	R.TDFLDIIR.T		R.TDFLDIIR.T
166	174	2	974.58	-0.13	0	29.1	18.1	95.00%	R.TSPAVLFIK.S		R.TSPAVLFIK.S
230	246	2	1921.03	0.98	0	99.2	24	95.00%	E.SIQSPYLFLNGISVINR.G	Deamidation (+1)	K.LNIDTSAALESIQSPYLFLNGISVI NR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
305	A6ZW73_YEAS7	8.14%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
401	416	2	1778.86	0.28	1	79.8	28.6	95.00%	E.NYAPNMILSQSTGVER.R		K.DIEGHSLLENYAPNMILSQSTGVE R.R
7	30	4	2618.33	-0.63	1	54	26.3	95.00%	R.TLKSDTDVTSLNASTVSHQSKPF R.Q		R.TLKSDTDVTSLNASTVSHQSKPF R.Q
314	326	3	1378.79	0.22	1	53.1	19.3	95.00%	K.KILDVGNTLAAHK.S		K.KILDVGNTLAAHK.S
82	93	2	1276.68	-0.013	0	43	26.3	95.00%	R.TISGLNMTALTR.V		R.TISGLNMTALTR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
306	A6ZWB1_YEAS7	31.78%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
100	107	2	965.52	0.19	0	36.2	26.8	95.00%	R.IFLYPSNI.-		R.IFLYPSNI.-
32	47	2	1735.88	0.28	1	51	28.1	95.00%	K.IEGVATPQDAQFYLGK.R		K.IEGVATPQDAQFYLGK.R
22	31	2	1096.62	-0.015	0	27.1	21.9	95.00%	R.VNNPNVSLIK.I		R.VNNPNVSLIK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
307	A6ZWH0_YEAS7	18.78%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
139	149	2	1302.71	-0.32	0	42	25	95.00%	K.QIVNIPSFMVR.L		K.QIVNIPSFMVR.L
70	78	2	1031.58	-0.42	1	59.2	24.7	95.00%	R.LFEGNALIR.R		R.LFEGNALIR.R
155	171	3	1781.9	-0.07	0	28.7	27.7	95.00%	K.HIDFAPTSPFGGARPGR.V		K.HIDFAPTSPFGGARPGR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
308	A6ZQF9_YEAS7	13.77%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	58	2	2784.3	0.74	1	59.3	29.2	95.00%	K.ATFSPSGGTVSVPVEWMDNGAYPSLSK.I	Deamidation (+1)	K.ATFSPSGGTVSVPVEWMDNGAYPSLSK.I
84	94	2	1245.61	-0.74	1	37.5	29.4	95.00%	K.ITPSELTQDDK.V		K.ITPSELTQDDK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
309	A6ZUW4_YEAS7	45.71%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
87	105	2	1872.01	-0.0043	1	77.3	23.3	95.00%	R.VGVVSILEAGDSDILTTLA.-		R.VGVVSILEAGDSDILTTLA.-
41	52	2	1292.82	0.83	0	49.5	10	95.00%	K.LIIIAANTPVLR.K		K.LIIIAANTPVLR.K
67	83	2	1815.88	-0.33	1	86.2	29.2	95.00%	K.VYYFQGGNNELGTAVGK.L		K.VYYFQGGNNELGTAVGK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
310	YP13B_YEAST	16.00%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	65	2	1587.74	1.1	0	52.3	29.9	95.00%	K.ANSQQTTTPASSAVPE.N		K.ANSQQTTTPASSAVPENPHHASPQPASVPPPQNGPYPQQCMMTQNQANPSGWSFYGHPSMIPYTPYQMSPMYFPPGPQSQFPQYPSSVGTPLSTPSPESGNTFTDSSSADSDMTSTK.K
400	419	2	2073.92	-0.2	0	113	30.1	95.00%	R.AHNVSTSNNSPSTDNDSISK.S		R.AHNVSTSNNSPSTDNDSISK.S
625	644	2	2328.01	0.54	0	73.7	31.3	95.00%	E.SDVDWSSAIDYQCPDCLIGK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.NNTITYFNESDVDWSSAIDYQCPDCLIGK.S
471	491	3	2226.08	-0.67	0	88.7	29	95.00%	R.SAHHIHSASSNPDINVVDAQK.R		R.SAHHIHSASSNPDINVVDAQK.R
1152	1179	3	2885.41	-0.54	0	59.2	28.1	95.00%	E.LPPINSHQTNSSLGGIGDSNAYTTINSK.K		K.ELPPINSHQTNSSLGGIGDSNAYTTINSK.K
148	167	2	2065.88	0.33	1	86.6	30.8	95.00%	E.SGNTFTDSSSADSDMTSTKK.Y		K.ANSQQTTTPASSAVPENPHHASPQPASVPPPQNGPYPQQCMMTQNQANPSGWSFYGHPSMIPYTPYQMSPMYFPPGPQSQFPQYPSSVGTPLSTPSPESGNTFTDSSSADSDMTSTKK.Y
560	568	2	1163.53	-1.8	0	29.8	29.4	94.60%	K.YGDFYWVSK.K		K.YGDFYWVSK.K
25	39	2	1638.78	-0.86	1	78.9	29.3	95.00%	K.EVHTNQDPLDVSASK.I		K.EVHTNQDPLDVSASK.I
1094	1114	3	2202.09	-0.77	1	34.9	28.2	95.00%	R.SPSIDASPPENNSSHNIVPIK.T		R.SPSIDASPPENNSSHNIVPIK.T
959	973	2	1525.69	0.052	0	39.9	30	95.00%	K.AVSPTDSTPPSTHTE.D		K.AVSPTDSTPPSTHTEDSK.R
1622	1633	2	1318.72	-0.46	0	43.7	25.8	95.00%	K.SQIGNIYLLNGK.V		K.SQIGNIYLLNGK.V
308	315	2	989.52	0.32	0	31.3	28.1	95.00%	K.VACQLIMR.G	Carbamidomethyl (+57)	K.VACQLIMR.G
1606	1621	2	1787.87	0.79	0	71.7	28.7	95.00%	K.LVAISDASYGNQPYYK.S		K.LVAISDASYGNQPYYK.S
3	24	3	2358.1	0.33	0	44.6	30	95.00%	E.SQQLSNYPHISHGSACASVTSK.E	Carbamidomethyl (+57)	-.MESQQLSNYPHISHGSACASVTSK.E
148	166	2	1953.78	0.7	0	94.2	30.7	95.00%	E.SGNTFTDSSSADSDMTSTK.K	Oxidation (+16)	K.ANSQQTTTPASSAVPENPHHASPQPASVPPPQNGPYPQQCMMTQNQANPSGWSFYGHPSMIPYTPYQMSPMYFPPGPQSQFPQYPSSVGTPLSTPSPESGNTFTDSSSADSDMTSTK.K
1235	1243	2	1115.51	0.078	1	55.2	28.4	95.00%	R.YDEAITYNK.D		R.YDEAITYNK.D
658	681	4	2906.4	-0.29	0	21.1	29.4	94.20%	K.YQNSYEPFQYLHTDIFGPVHNLPK.S		K.YQNSYEPFQYLHTDIFGPVHNLPK.S
959	976	2	1855.84	-0.6	1	47.1	30.4	95.00%	K.AVSPTDSTPPSTHTEDSK.R		K.AVSPTDSTPPSTHTEDSK.R
1	24	3	2660.2	0.19	1	63.5	30.2	95.00%	-.MESQQLSNYPHISHGSACASVTSK.E	Acetyl (+42)/ Carbamidomethyl (+57)	-.MESQQLSNYPHISHGSACASVTSK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
311	VTH1_YEAST	8.07%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1074	1084	2	1371.64	0.014	1	56.7	29.3	95.00%	K.CSLHLHGYTER.K	Carbamidomethyl (+57)	K.CSLHLHGYTER.K
1000	1009	2	1218.56	-0.43	1	28.2	29	92.90%	R.NTFGYVDFEK.V		R.NTFGYVDFEK.V
1156	1167	2	1319.59	0.6	0	53	29.9	95.00%	E.TDSISYSTDFGK.T		K.GPHQWEYGDHGGVLVLVPENAETDSISYSTDFGK.T
1263	1275	2	1538.75	-0.78	1	28.2	28.1	94.20%	K.CFIGNIPLSEFSR.N	Carbamidomethyl (+57)	K.CFIGNIPLSEFSR.N
1015	1027	2	1386.77	0.93	1	68.3	23.3	95.00%	E.GIIITNIVSNSEK.V		K.VQGLEGIIITNIVSNSEK.V
510	518	2	1119.52	0.98	0	39.2	27.6	95.00%	K.FYYSLDQGK.T		K.FYYSLDQGK.T
849	857	2	1101.46	1.1	0	49.1	28.9	95.00%	E.MLDNAIHCE.F	Carbamidomethyl (+57)	K.DGGETFTEMLDNAIHCEFAGTLFK.Y
1518	1533	2	1622.86	0.6	0	84.9	26	95.00%	R.TDLLGASNIPDALPAR.S		R.TDLLGASNIPDALPAR.S
192	210	2	2054.92	0.83	1	80.9	30.4	95.00%	K.SSEDSDLGGNDASILCLFR.N	Carbamidomethyl (+57)	K.SSEDSDLGGNDASILCLFR.N
394	406	2	1445.75	0.2	0	37.6	26.9	95.00%	K.VSVDNGLTWTNLK.V		K.VSVDNGLTWTNLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
312	ATG15_YEAS7	5.58%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
84	94	2	1180.58	1.2	0	35.6	28.7	95.00%	E.VISAAGMLYQE.T		R.LEVTPEVISAAGMLYQETTTQGQDFEDQEPLWTTNAEYATTNPFDFEFELR.R
194	201	2	971.48	0.39	0	30.2	27.5	95.00%	R.IPQTGDWR.N		R.IPQTGDWR.N
417	426	2	1209.57	-0.14	0	44.3	29.5	95.00%	R.VCVYDVVNDK.G	Carbamidomethyl (+57)	R.VCVYDVVNDK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
313	A6ZQP1_YEAS7	2.19%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
621	634	2	1689.9	0.99	1	43.9	25.4	95.00%	K.TDLIFDQVRDILDK.L		K.TDLIFDQVRDILDK.L
621	629	2	1105.58	0.072	0	35.8	27.6	95.00%	K.TDLIFDQVR.D		K.TDLIFDQVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
314	A6ZLA3_YEAS7	5.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
109	119	2	1500.7	-0.15	1	40.1	29.3	95.00%	K.QEYPWFLDTFR.S		K.QEYPWFLDTFR.S
226	236	2	1203.56	1.2	1	76.6	29.2	95.00%	R.WSNTAENGAVR.I		R.WSNTAENGAVR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
315	A7A001_YEAS7	3.32%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
400	408	2	1017.53	0.47	1	39.7	27.3	95.00%	R.TMVALAEQR.F		R.TMVALAEQR.F
77	87	2	1153.71	-0.36	0	53.7	18.4	95.00%	K.VAIITAQTPLK.H		K.VAIITAQTPLK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
316	A6ZMS7_YEAS7	9.54%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	46	2	1624.72	0.48	1	68.5	29.8	95.00%	R.FIKPSSATNSESDNE.V		R.FIKPSSATNSESDNEVFFVK.G
274	283	2	1102.59	1.7	0	46.8	26.1	95.00%	E.DAVIPLIFSE.Y		K.LNSTFEDAVIPLIFSEYGCNK.N
223	233	2	1310.59	-0.44	0	29.4	30	93.20%	K.YLQCNSLDGNK.V	Carbamidomethyl (+57)	K.YLQCNSLDGNK.V
81	94	2	1580.79	-2	0	77.5	28.3	95.00%	R.DAYAFQQLGVNTVR.I		R.DAYAFQQLGVNTVR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
317	B3LLW4_YEAS1	23.95%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
140	150	2	1370.69	-0.67	1	48.3	27.9	95.00%	K.HQEFQNTNIIK.N		K.HQEFQNTNIIK.N
143	160	3	2143.98	0.79	1	44.5	30	95.00%	E.FQNTNIIKNPTDDDFPHE.A		K.HQEFQNTNIIKNPTDDDFPHEAVVR.E
151	164	2	1610.73	-1.4	1	48.5	30.2	95.00%	K.NPTDDDFPHEAVVR.E		K.NPTDDDFPHEAVVR.E
2	16	2	1532.84	0.52	0	56.5	21.8	95.00%	M.ALSLGQFINVGGMVK.D		-.MALSLGQFINVGGMVK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
318	A6ZZW2_YEAS7	9.98%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

337	353	2	1851.84	1.4	1	47.2	30.3	95.00%	K.YDISKSDPLAADSNDIE.S		K.YDISKSDPLAADSNDIESVPLSNLELDFDLNMTDEPSVSPSLFDGSTSVSR.S
24	34	3	1251.68	0.49	0	32	24.7	95.00%	E.TSLDPHQTLLK.V		R.WFLSERPPNCHVADLETSLDPHQTLLK.V
388	399	2	1149.62	-0.62	0	59.6	25	95.00%	R.SSATSITSLGVK.R		R.SSATSITSLGVK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
319	A6ZQC8_YEAS7	3.63%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
72	89	2	2032	0.48	1	69	28.5	95.00%	E.GLVWKGDPTYLPNSPYPE.V		R.HSIQEEGLVWKGDPTYLPNSPYPEVR.S
151	159	2	1067.64	-0.12	0	30.8	19.6	95.00%	R.ILALLPDWK.C		R.ILALLPDWK.C
77	91	2	1703.82	-0.25	1	34.9	29.8	95.00%	K.GDPTYLPNSPYPEVR.S		K.GDPTYLPNSPYPEVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
320	A6ZMB7_YEAS7	11.64%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
329	349	3	2356.16	0.47	1	25.5	27.3	95.00%	K.EAIYGEPDHVITVDVVMDNLK.N		K.EAIYGEPDHVITVDVVMDNLK.N
385	396	2	1393.69	0.28	0	33.2	28.2	95.00%	E.IYGSNTHTFILE.K		K.VPTLMTVLSSGDQANNSEIYGSNTHTFILEK.D
302	328	3	3179.5	-0.84	1	49.9	28.5	95.00%	K.TAALPTQNYVDSIDNFLDDFYLQPYEK.E		K.TAALPTQNYVDSIDNFLDDFYLQPYEK.E
458	471	2	1706.91	0.11	0	45	24.4	95.00%	R.DTLYVRPQSNFVIR.F		R.DTLYVRPQSNFVIR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
321	YJT8_YEAST	5.56%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
311	320	2	1196.66	0.073	0	54	24.3	95.00%	K.ISQLVTFYAR.I		K.ISQLVTFYAR.I
353	363	2	1190.55	1.9	0	31.1	28.7	95.00%	K.DMLGLLSQADE.L		K.DMLGLLSQADELTPK.E
15	24	2	1371.52	0.66	0	49.5	29.2	95.00%	E.WQNHYMDYSE.L		K.YNAVPEWQNHYMDYSELK.N
130	147	2	2041.99	2.3	1	99.5	28.8	95.00%	E.NLQLDTYDTFVGDLTAEK.Q		R.SSSASSVSSTANENLQLDTYDTFVGDLTAEK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
322	A6ZU95_YEAS7	5.54%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
396	408	2	1630.72	0.32	0	30.9	30.4	94.70%	R.CVDNNYSSLAFWR.A	Carbamidomethyl (+57)	R.CVDNNYSSLAFWR.A
2	14	2	1413.8	0.3	0	60.5	22.3	95.00%	M.SLISILSPLITSE.G	Acetyl (+42)	-.MSLISILSPLITSEGLDSR.I
2	19	2	1942.06	0.47	1	53.3	22	95.00%	M.SLISILSPLITSEGLDSR.I	Acetyl (+42)	-.MSLISILSPLITSEGLDSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
323	A6ZYP2_YEAS7	7.81%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
261	273	2	1338.73	-0.097	0	41.3	24.8	95.00%	E.IIAPVTAHAGFDK.A		R.GITEPEIIAPVTAHAGFDK.A
569	579	2	1250.73	0.79	0	46.4	17.7	95.00%	K.LIVGFLDALYK.L		K.LIVGFLDALYK.L
169	190	3	2385.2	0.054	1	39.8	26.3	95.00%	K.VSGAVYHGGDDLIHLQTIAYEK.Y		K.VSGAVYHGGDDLIHLQTIAYEK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
324	ERV25_YEAST	13.74%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
33	42	2	1265.61	0.56	1	27.8	29.3	91.90%	E.QVCIRDFVTE.G	Carbamidomethyl (+57)	-.MQVLQLWLTTLISLVVAVQGLHFDIAASTDPEQVCIRDFVTEGQLVVADIHSDGSVGDGQK.L
43	61	2	1880.92	0.37	0	78.4	28.7	95.00%	E.GQLVVADIHSDGSVGDGQK.L		R.DFVTEGQLVVADIHSDGSVGDGQK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
325	A6ZT39_YEAS7	8.84%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

48	62	2	1777.86	1.4	0	53.2	29.3	95.00%	R.DVIAPLTDDYDVWTR.S		R.DVIAPLTDDYDVWTR.S
92	105	2	1602.82	0.18	0	33.8	26.5	95.00%	E.LIQNTLPTSQMMAR.E		K.EIGEQINDGQVIIDNMNELIQNTLPTSQMMAR.E
352	360	2	1068.49	1.1	0	29.7	29.6	94.30%	R.NYDVISACK.D	Carbamidomethyl (+57)	R.NYDVISACK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
326	A6ZNL3_YEAS7	12.43%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
24	37	2	1649.74	1.3	0	63.8	30.4	95.00%	E.YVNCFSSLPSDFSK.A	Carbamidomethyl (+57)	K.TSLLLALLSILSQANAYEYVNCFSSLPSDFSK.A
352	365	2	1317.67	-0.25	0	94.2	28.8	95.00%	R.ISNGTFINGGPGGK.N		R.ISNGTFINGGPGGK.N
38	56	2	2216.85	-0.51	1	72.7	30.2	95.00%	K.ADSYNWQSSSHCNSECSAK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.ADSYNWQSSSHCNSECSAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
327	A6ZSH5_YEAS7	12.46%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	47	2	1535.8	-0.51	0	55.6	26	95.00%	K.YSTVVISCEPIIR.Q	Carbamidomethyl (+57)	K.YSTVVISCEPIIR.Q
11	31	2	2232.01	0.45	0	35	30.3	95.00%	E.QSSHLYGQPASSQDGNAFIPE.D		-.MSGPPPPYEEQSSHLYGQPASSQDGNAFIPEDFK.Y
11	34	3	2622.2	0.62	1	41.3	29.4	95.00%	E.QSSHLYGQPASSQDGNAFIPEDFK.Y		-.MSGPPPPYEEQSSHLYGQPASSQDGNAFIPEDFK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
328	A6ZN12_YEAS7	10.93%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
402	415	2	1575.76	-0.26	0	74.5	29.1	95.00%	K.LMDSNNDAVQTLQK.L		K.LMDSNNDAVQTLQK.L
228	250	3	2492.33	-0.83	1	31.7	21.9	95.00%	K.RGDVIVADDQVSLPVQNALQLSR.S		K.RGDVIVADDQVSLPVQNALQLSR.S
80	92	2	1438.74	0.48	0	46.8	27.7	95.00%	K.SLQAQKPNLSPQE.I		K.SLQAQKPNLSPQEIDALIEDWEPEPLVDPSATDEQSWR.V
127	137	2	1322.71	0.44	0	48.8	25.3	95.00%	E.MPIQNHITITR.N		K.TPVTMEMPIQNHITITR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
329	A6ZSQ7_YEAS7	8.90%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
269	280	2	1376.63	0.57	1	48.5	29.7	95.00%	E.GSAAYYFDNIEK.F		R.SNEFQLEGSAAYYFDNIEK.F
281	295	2	1770.81	0.23	1	49.7	29.5	95.00%	K.FASPNYVCTDEDILK.G	Carbamidomethyl (+57)	K.FASPNYVCTDEDILK.G
98	112	3	1741.87	0.31	1	44.9	28.1	95.00%	R.KLGIQLDCDDPINNK.D	Carbamidomethyl (+57)	R.KLGIQLDCDDPINNK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
330	A6ZXE1_YEAS7	15.83%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
16	26	3	1241.73	0.26	1	41.3	20.8	95.00%	E.QLASQLVDLKK.E		K.EQLASQLVDLKK.E
36	43	2	896.54	0.19	0	23.6	17.2	92.00%	K.LSRPSLPK.I		K.LSRPSLPK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
331	A6ZZM1_YEAS7	13.81%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	139	2	1544.78	-1.2	0	63.9	27.4	95.00%	K.QSDDATGVAIRPTSK.S		K.QSDDATGVAIRPTSK.S
32	49	2	1945.93	0.31	0	90	29.4	95.00%	R.SGSDLQYLSVYSDNGTLK.L		R.SGSDLQYLSVYSDNGTLK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
332	A6ZXD4_YEAS7	8.37%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
21	43	4	2564.26	-0.69	1	40.2	27.4	95.00%	R.AHQLAQDFNSKQDDTALTSLPHK.N		R.AHQLAQDFNSKQDDTALTSLPHK.N
600	616	2	1973.98	-0.86	1	82.3	27.5	95.00%	K.QNNQAYSSIQNEQILPK.N		K.QNNQAYSSIQNEQILPK.N
4	20	3	1866.92	-0.85	1	64.2	28.4	95.00%	R.SNKPLTQEANSSAHIDR.A		R.SNKPLTQEANSSAHIDR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
333	A7A200_YEAS7	9.87%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
271	284	2	1527.73	0.78	0	69.2	29.3	95.00%	E.SAGIDQTTYNSIMK.C		R.APEALFHPSVLGLESAGIDQTTYNSIMK.C
73	84	2	1443.65	0.4	1	44	30	95.00%	E.HGIVTNWDDMEK.I		R.YPIEHGIVTNWDDMEK.I
260	270	2	1181.64	-0.27	0	27.2	24.5	95.00%	E.ALFHPSVLGLE.S		R.APEALFHPSVLGLESAGIDQTTYNSIMK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
334	A6ZQL2_YEAS7	14.15%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
160	171	2	1329.74	-0.24	0	64.3	24.1	95.00%	K.VFGINLNDLVAR.H		K.VFGINLNDLVAR.H
17	48	3	3402.76	0.53	0	33.4	23.3	95.00%	K.NAPSVPQVDASLDKPLDIDAPPTIYSVNLKPE.Y		K.NAPSVPQVDASLDKPLDIDAPPTIYSVNLKPEYGTAALNLSADFIR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
335	A6ZPM4_YEAS7	8.57%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	17	3	1945.87	0.13	1	57.7	30.4	95.00%	M.SNEAYQHDHTVNPHQK.I	Acetyl (+42)	-.MSNEAYQHDHTVNPHQK.I
167	181	2	1621.77	-1.1	0	87.5	29.5	95.00%	R.IQTGSSGSYFVYGTR.A		R.IQTGSSGSYFVYGTR.A
39	59	2	2077.97	0.43	0	91.2	30.3	95.00%	K.NPITHASPGVGSNAQNSDIAE.A		K.NPITHASPGVGSNAQNSDIAEAPQVFHPSYQSLVNVPSESPRPDQTSGSNPAVGLLHNTEDK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
336	A7A105_YEAS7	8.36%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
313	327	2	1683.82	0.94	0	68.1	28.2	95.00%	E.IDPTGMSDVFAYIQK.K		K.TQEIDPTGMSDVFAYIQK.K
310	327	2	2041.97	-0.74	1	60.3	29	95.00%	K.TQEIDPTGMSDVFAYIQK.K		K.TQEIDPTGMSDVFAYIQK.K
187	197	2	1319.73	-2.6	1	23.5	23.9	91.90%	K.YLSLNDIELLK.T		K.YLSLNDIELLK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
337	B3LI68_YEAS1	3.68%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	48	2	1622.7	-0.61	0	49.8	30.3	95.00%	R.GYTNYNNGSNYTQK.K		R.GYTNYNNGSNYTQK.K
172	192	2	2139.93	0.04	1	51	30.5	95.00%	K.ETSDSTSTSTPTPTPSTNDSK.A		K.ETSDSTSTSTPTPTPSTNDSK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
338	A6ZT92_YEAS7	1.61%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1480	1492	2	1480.76	-0.21	0	64	27.3	95.00%	K.IWTTSGDLLNSFK.N		K.IWTTSGDLLNSFK.N
131	142	2	1434.75	0.21	1	56.2	26.8	95.00%	K.NLQAQYETLSLR.T		K.NLQAQYETLSLR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
339	A6ZV67_YEAS7	12.64%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
36	49	2	1512.81	-0.46	1	72.5	24.3	95.00%	K.VLEQLSGQTPVQSK.A		K.VLEQLSGQTPVQSK.A
167	174	2	937.44	0.41	0	27.2	27.9	93.20%	K.YDADVLDK.-		K.YDADVLDK.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
340	A6ZTH2_YEAS7	30.60%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
66	78	2	1521.7	-0.74	1	34.9	29.8	95.00%	R.NFDIISENSNDVR.G		R.NFDIISENSNDVR.G
50	65	3	1802.81	0.93	1	53.3	30.2	95.00%	R.LNDSFADDLENGLHSR.N	Deamidation (+1)	R.LNDSFADDLENGLHSR.N
91	102	2	1466.63	-0.63	1	52	30.2	95.00%	K.QIMENDNVDFDK.A		K.QIMENDNVDFDK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
341	A6ZT43_YEAS7	13.94%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
368	383	4	1797.89	-0.43	1	21.2	28.6	95.00%	K.KPNLHGYGHPNPPNEK.S		K.KPNLHGYGHPNPPNEK.S

465	478	2	1808.93	0.8	0	46.4	27	95.00%	E.QQLQQQQQQQQQLR.A			K.LQEQQLQEQQLQQQQQQQQQLR.A
428	443	2	1935.9	-0.51	1	53.1	29.6	95.00%	K.LDPTSYEAYQHQTQQK.Y			K.LDPTSYEAYQHQTQQK.Y
479	499	2	2212.06	-1.3	0	79.8	29.9	95.00%	R.ATGQPPSQPQAQTQSQQFGAR.Y			R.ATGQPPSQPQAQTQSQQFGAR.Y
360	367	2	958.49	-0.13	0	37.6	27.2	95.00%	R.GWDLNINK.K			R.GWDLNINK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
342	A6ZQ50_YEAS7	41.30%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	61	2	1369.56	-0.31	0	49.8	29.1	95.00%	R.GAAGIWTCSCCK.K	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GAAGIWTCSCCK.K
63	80	2	1665.87	1	0	98.8	26.9	95.00%	K.TVAGGAYTVSTAAAATVR.S		K.TVAGGAYTVSTAAAATVR.S
37	44	2	1035.38	1.3	0	30.5	26.9	95.00%	R.YDCSFCGK.K	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.YDCSFCGK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
343	A6ZKL0_YEAS7	23.85%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	83	2	1247.68	1.1	1	44.1	26	95.00%	K.TFLVANVKDLE.T		K.TFLVANVKDLETLTMHTK.T
81	90	2	1187.59	-0.18	1	28.9	28.6	94.40%	K.DLETLTMHTK.T		K.DLETLTMHTK.T
91	103	2	1387.71	-0.66	1	73.9	28.2	95.00%	K.TYAAEIAHNISAK.N		K.TYAAEIAHNISAK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
344	A6ZX25_YEAS7	20.23%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
161	173	2	1340.74	-0.077	1	38.8	23.5	95.00%	R.RTGQVGVPTISQV.-		R.RTGQVGVPTISQV.-
95	116	3	2382.06	-0.48	1	76.3	31	95.00%	R.AHSCNNSSYVDSNKITQGSGTR.C	Carbamidomethyl (+57)	R.AHSCNNSSYVDSNKITQGSGTR.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
345	A6ZM25_YEAS7	4.75%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
428	437	2	1145.59	1.5	0	52.9	27.8	95.00%	E.LDMIAQNVSR.S		K.IAPYSISVDLTNQEYELDMIAQNVSR.S
400	410	2	1254.59	-0.016	1	73.8	29.2	95.00%	K.GFQDFEQLGSK.K		K.GFQDFEQLGSK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
346	A6ZL34_YEAS7	2.75%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
188	200	2	1563.75	-0.2	1	70.9	29.3	95.00%	K.YSSFSTIEFLQDK.Q		K.YSSFSTIEFLQDK.Q
782	794	2	1340.69	-0.47	0	52.1	26.7	95.00%	K.LLPDGDAVDALSR.K		K.LLPDGDAVDALSR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
347	A6ZMB4_YEAS7	2.36%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
132	141	2	1174.58	0.58	1	48.2	28.8	95.00%	R.QLDESLDSLR.S		R.QLDESLDSLR.S
160	170	2	1171.63	-0.2	1	49	26.5	95.00%	K.FIEVNPGIAGR.A		K.FIEVNPGIAGR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
348	A6ZPU2_YEAS7	8.80%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
206	217	2	1198.67	-0.44	0	52.4	25	95.00%	K.DAGTIAGLNVLR.I		K.DAGTIAGLNVLR.I
218	233	2	1644.87	-0.5	0	60.3	24.8	95.00%	R.IVNEPTAAAIAYGLDK.S		R.IVNEPTAAAIAYGLDK.S
103	117	2	1671.86	-1.1	0	72.9	26.9	95.00%	K.NQVAANPQNTIFDIK.R		K.NQVAANPQNTIFDIK.R
468	484	2	1877.96	0.32	0	68.8	26.4	95.00%	K.SQIFSTAVDNQPTVMIK.V		K.SQIFSTAVDNQPTVMIK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
349	A6ZMX9_YEAS7	12.81%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
144	154	2	1319.62	-0.066	1	37.9	29	95.00%	K.NMICAENLLDK.F	Carbamidomethyl (+57)	K.NMICAENLLDK.F

72	86	2	1728.93	0.22	1	29.2	25.8	95.00%	E.TVQNLAPNLHPEQIR.Y		R.VNGGHPVTTQMVETVQNLAPNLHPEQIR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
350	A6ZUA3_YEAS7	8.61%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
176	196	4	2379.29	0.44	1	31.6	21.5	95.00%	K.YGILSIDDLIHEIITVGPHFK.Q		K.YGILSIDDLIHEIITVGPHFK.Q
176	187	2	1386.7	0.35	0	44.8	27.7	95.00%	K.YGILSIDDLIHE.I		K.YGILSIDDLIHEIITVGPHFK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
351	A6ZZI1_YEAS7	4.38%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
416	428	2	1496.77	-0.89	1	65.2	27	95.00%	R.FIEFFNPGNVSVK.T		R.FIEFFNPGNVSVK.T
84	94	3	1373.69	0.0054	1	34.6	28.6	95.00%	R.TEDNYILTLHR.I		R.TEDNYILTLHR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
352	A6ZN11_YEAS7	15.23%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
53	69	2	1990.86	-0.016	1	71.3	30.8	95.00%	E.AQPFEQAADTFHDNMNR.Q		R.TASVADPILDAVQEAQPFEQAADTFHDNMNR.Q
168	180	2	1554.74	0.074	0	52.1	29.4	95.00%	E.QAVYQPQQHVQTE.E		R.VRPDFPVFGAAVTYDANGMPQQVGGASSQMYGEQAVYQPQQHVQTEEK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
353	A6ZTG2_YEAS7	8.63%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
358	374	3	1905.8	1.4	0	37.3	30.5	95.00%	E.YGRPQYGGNQNSNGQHE.S	Deamidation (+1)	K.SGNNSQGQGQGQGQGQGQGQGQGQGSFTALASLASSFMNSNNNNQQGQNQSSGGSSFGALASMASSFMHSNNNQNSNNSQQGYNQSYQNGNQNSQGYNNQQYQGGNGGYQQQQGQSGGAFSSLASMAQSYLGGGQTQSNQQQYNQQGQNYQHQQQGQQQQQGHSSSFSALASMASSYLGNNSNSNSSYGGQQQANEYGRPQQNGQQQSNEYGRPQYGGNQNSNGQHESFNFSGNFSQQNNNGNQNR.Y
68	84	2	1643.73	-0.011	0	89.7	30.3	95.00%	R.AAGGGSSFMNTLMADSK.G		R.AAGGGSSFMNTLMADSK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
354	A7A1R6_YEAS7	15.48%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
62	80	2	2130.9	0.3	0	87.9	30.2	95.00%	K.CLDSICPNNDADAAYSAFK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CLDSICPNNDADAAYSAFK.S
38	55	2	2175.82	0.51	1	106	30.1	95.00%	K.SSSTCDSLNQVTCYCEHE.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.SSSTCDSLNQVTCYCEHENSAVK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
355	A6ZMK8_YEAS7	9.79%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
118	128	2	1185.64	-0.019	1	55.5	26.6	95.00%	K.LDAALLQEASR.S		K.LDAALLQEASR.S
74	90	2	1884.05	0.25	0	52.7	20.8	95.00%	E.STNKPFQNTLLIGLPNK.N		R.IGIDETVPTTITVEDPNEVIQVNFAIESTNKPFQNTLLIGLPNK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
356	A6ZTY6_YEAS7	7.99%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
217	241	2	2777.41	-1.7	1	51.1	26.4	95.00%	K.ALLIGNGWIDPNTQSLSYLPFAMEK.K		K.ALLIGNGWIDPNTQSLSYLPFAMEK.K

283	293	2	1318.76	0.98	0	60.6	21.2	95.00%	E.NILNLLLSYTR.E		K.HLTNAHENCQNLINSASTDEAAHFSYQECENILNLLLSYTR.E
313	324	2	1440.58	0.64	0	42	30	95.00%	K.DSYPSCGMNWPK.D	Carbamidomethyl (+57)	K.DSYPSCGMNWPK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
357	B3LRN4_YEAS1	15.80%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
284	304	2	2338.07	-0.21	0	72.5	30.4	95.00%	E.TTMGDTLGLYSDIGDDNFIYK.A		K.ETNDNSNNQTNTNIGNTFDTDFSNGNTETTMGDTLGLYSDIGDDNFIYK.A
328	337	2	1128.62	1	1	47.1	26.1	95.00%	E.ILQVSDIEGR.W		K.ALYPYDADDDDAYEISFEQNEILQVSDIEGR.W
182	196	2	1781.83	0.11	0	50.4	29.8	95.00%	R.NTTPYQNNVYNDAIR.D		R.NTTPYQNNVYNDAIR.D
236	247	2	1405.78	0.56	0	58.9	23	95.00%	E.AVNLHLNTLQQR.I		R.DSGYATQFDGYPQQQPSHTNYVSSTALAGFENTQPNTSEAVNLHLNTLQQR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
358	MHP1_YEAST	1.93%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
332	343	3	1280.7	-0.093	0	34.6	24.9	95.00%	K.GRPIPPHPDAPK.L		K.GRPIPPHPDAPK.L
62	76	2	1525.71	0.33	0	91.6	29.7	95.00%	E.TSVDSSSSILSSNDK.G		K.ANSVAPDIQMDTARPPVFETSVDSSSSILSSNDK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
359	B3LKB6_YEAS1	4.66%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	77	2	1308.67	-0.63	0	42.4	28.2	95.00%	K.APVPDVNAPQSSK.N		K.APVPDVNAPQSSK.N
89	104	2	1617.92	0.36	0	63.5	19.8	95.00%	E.TPTGLVPVATLHSIGR.T		K.IFPEEYTLETPTGLVPVATLHSIGR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
360	A6ZRV2_YEAS7	21.05%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
7	21	2	1787.9	-0.68	1	66.5	27.1	95.00%	E.IKDDVVQLDEPQFSR.N		-.MVELTEIKDDVVQLDEPQFSR.N
129	145	2	1862.9	-1.4	1	84.9	28.5	95.00%	K.TFDLQSDANNILAQGEK.D		K.TFDLQSDANNILAQGEK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
361	A6ZLB9_YEAS7	8.87%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
163	184	3	2304.33	1	0	62.2	16.5	95.00%	E.VDLPLVVILHGLAGGSHEPIIR.S		R.EVDLPLVVILHGLAGGSHEPIIR.S
97	114	3	2083.97	0.5	1	27	30	95.00%	K.FSDGGVCTADWLIDSWKK.D	Carbamidomethyl (+57)	K.FSDGGVCTADWLIDSWKK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
362	A6ZUG8_YEAS7	5.29%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
30	45	3	1813.92	0.72	0	33.7	27.2	95.00%	R.SSNVTFKPPVTHDMVR.S		R.SSNVTFKPPVTHDMVR.S
680	695	2	1926.91	2.5	1	38.8	29.5	95.00%	K.MPIELYNGDDWIGLYK.V	Deamidation (+1)	K.MPIELYNGDDWIGLYK.V
666	679	2	1628.89	1.3	0	34.2	23.2	95.00%	E.TNFVLPTPVTLNWK.M		K.IENEQIETNFVLPTPVTLNWK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
363	RAS1_YEAST	10.03%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
57	70	2	1501.75	1.1	1	35.7	27.9	95.00%	K.VSILDILDTAGQEE.Y		K.VSILDILDTAGQEEYSAMR.E
163	169	2	868.48	0.89	0	30.7	23.2	95.00%	E.AFYSLIR.L		K.QAINVDEAFYSLIR.L
100	109	2	1310.7	1	0	50.6	25.6	95.00%	E.LLSYYQQIQR.V		R.NSFDELLSYYQQIQR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
364	A6ZP65_YEAS7	18.49%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

91	112	2	2308.06	0.3	0	60.8	30.1	95.00%	E.LTHYFDTANNSNVATGTSVAPE.Q		K.IAEELTHYFDTANNSNVATGTSVAPEQNNYYIHCIIGTEELTQAELANEDLK.D
2	19	2	1890.91	0.79	1	67.7	29.5	95.00%	M.SAEPLLPTHNGSQGGEVR.S	Acetyl (+42)/ Deamidation (+1)	-.MSAEPLLPTHNGSQGGEVR.S
113	126	2	1752.78	0.13	1	34.3	30.7	95.00%	E.QNNYYIHCIIGTEE.L	Carbamidomethyl (+57)	K.IAEELTHYFDTANNSNVATGTSVAPEQNNYYIHCIIGTEELTQAELANEDLK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
365	A6ZSX8_YEAS7	3.83%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
237	249	2	1436.83	0.21	0	27.5	19.7	95.00%	R.GVYIPVSYLSLVK.F		R.GVYIPVSYLSLVK.F
449	463	2	1626.75	-0.91	1	53.3	30.1	95.00%	K.TQGYTVADCTAEAIK.A	Carbamidomethyl (+57)	K.TQGYTVADCTAEAIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
366	A6ZUK7_YEAS7	6.22%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
198	206	2	1134.59	-0.37	1	39	27.4	95.00%	K.IVDLIYDER.Y		K.IVDLIYDER.Y
514	529	2	1572.77	0.048	1	56.2	28.7	95.00%	K.NAMQAAEAAVAAATQR.A		K.NAMQAAEAAVAAATQR.A
89	97	2	1017.56	-0.22	0	29	26.2	95.00%	R.IQTGLFSPR.L		R.IQTGLFSPR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
367	B3LJ36_YEAS1	4.05%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	79	2	1379.66	-1.3	0	55.7	29.7	95.00%	K.SPLDGSFDTSNLK.R		K.SPLDGSFDTSNLK.R
67	80	2	1535.76	-0.73	1	74.6	28.7	95.00%	K.SPLDGSFDTSNLKR.T		K.SPLDGSFDTSNLKR.T
1	10	2	1155.55	0.5	1	26.3	28.6	90.20%	-.MTEDFISSVK.R		-.MTEDFISSVK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
368	A6ZU48_YEAS7	14.29%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
131	147	3	1844.91	0.11	1	21.8	28.1	91.50%	K.AGKFPTPVSHNDDLYGK.V		K.AGKFPTPVSHNDDLYGK.V
79	92	2	1523.69	-1.4	1	49.3	29.4	95.00%	K.SCGVDAMSVDDLKK.L	Carbamidomethyl (+57)	K.SCGVDAMSVDDLKK.L
79	91	2	1395.6	-0.56	0	57.3	29.7	95.00%	K.SCGVDAMSVDDLK.K	Carbamidomethyl (+57)	K.SCGVDAMSVDDLK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
369	A7A1L9_YEAS7	7.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	75	2	1266.61	-1.3	1	45.5	29.6	95.00%	R.GFLSDLPDFEK.L		R.GFLSDLPDFEK.L
111	122	2	1282.67	-0.34	1	35.2	27	95.00%	R.AGAVAPEDIWVR.A		R.AGAVAPEDIWVR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
370	B3LT91_YEAS1	16.11%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
139	154	2	1661.86	0.89	0	77.3	26.6	95.00%	E.VTSIDVDAPSSGFVIR.N		K.TLGHDHGDHGEVTSIDVDAPSSGFVIR.N
239	250	2	1382.65	0.21	0	46.5	28.9	95.00%	E.NDHQDVSQLATR.I		K.DHYSHENDHQDVSQLATR.I
194	210	2	1848.84	-0.5	1	50.1	30.3	95.00%	K.EPGSNVTNYDLEPGKTE.S		K.EPGSNVTNYDLEPGKTESLANELVPTSSHATNLASVPGK.D
216	238	3	2446.19	-0.61	1	31.2	29	95.00%	E.LVPTSSHATNLASVPGKDHYSHE.N		K.TESLANELVPTSSHATNLASVPGKDHYSHENDHQDVSQLATR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
371	B3LH47_YEAS1	7.71%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
493	506	2	1649.7	1.1	0	44.1	30.8	95.00%	E.HFMAMPPGQSQPQY.-	Oxidation (+16)/ Oxidation (+16)	K.SLYVAENDETVPVPFPIEQQSYHQQAIPQQQLPSQQQFAIPPQQHHPQFMVPPSHQQQQAYPPPQMPSQQGYPPQQEHFMAMPPGQSQPQY.-
302	316	3	1832.85	-0.68	1	49.4	30.7	95.00%	K.KITDLGYSCYYSHAR.M	Carbamidomethyl (+57)	K.KITDLGYSCYYSHAR.M
336	345	2	1176.62	0.52	0	34.8	26.3	95.00%	R.TLVCSDLLTR.G	Carbamidomethyl (+57)	R.TLVCSDLLTR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
372	A6ZUK0_YEAS7	5.30%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
238	251	2	1705.77	-0.0098	1	52.9	30.6	95.00%	E.TNYNDAPFTMYIEK.V		R.VLSNTSSEGYPQSPMYLMMGIWAGGDPDNAAGTIEWAGGETNYNDAPFTMYIEK.V
80	91	2	1241.6	-0.73	0	67.2	28.8	95.00%	K.YGSDGLSMTLAK.R		K.YGSDGLSMTLAK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
373	A6ZW55_YEAS7	13.75%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
97	105	3	1056.6	0.11	0	24.4	24.6	95.00%	E.IDLHGLYVK.E		K.TAEDFNMQAAEYVFVENNADSSSNEIDLHGLYVK.E
41	56	2	1833.81	-1.1	1	90.2	31.1	95.00%	R.DQLSHESQTAYQQGDK.K		R.DQLSHESQTAYQQGDK.K
106	113	2	960.56	0.08	1	27.5	21.7	95.00%	K.EALFILQK.R		K.EALFILQK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
374	A7A0W2_YEAS7	8.19%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
525	534	2	1195.66	1.1	0	28.4	23.3	95.00%	K.FNFLNSILTK.S		K.FNFLNSILTK.S
152	166	2	1694.87	-0.42	0	38.8	26.8	95.00%	K.IQPAMQLPPDVDMIK.Q		K.IQPAMQLPPDVDMIK.Q
175	184	2	1257.67	0.15	1	32.9	26.3	95.00%	K.SWNQEQLLLK.S		K.SWNQEQLLLK.S
431	447	2	1900.91	-0.32	0	96.4	29.9	95.00%	K.INDLFQSSYDILDGSSK.N		K.INDLFQSSYDILDGSSK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
375	A6ZSI2_YEAS7	2.63%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
667	678	2	1265.63	-0.4	1	70.7	28.7	95.00%	K.SDVTSIESSLTK.F		K.SDVTSIESSLTK.F
1143	1154	2	1388.8	-0.43	0	40	22.4	95.00%	K.NAVILNYQTLLK.E		K.NAVILNYQTLLK.E
1443	1450	2	1018.54	-0.23	1	27.8	26.3	95.00%	R.IIDLFNER.Q		R.IIDLFNER.Q
1600	1610	2	1266.77	1.2	0	42	17.5	95.00%	E.NLQTLSPLILR.T		K.QIGVENLQTLSPLILR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
376	A6ZUT8_YEAS7	11.82%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
145	156	2	1191.56	-0.51	0	55.9	29.3	95.00%	R.SVVADISDSDGK.S		R.SVVADISDSDGK.S
280	293	2	1562.72	-0.53	1	48.5	30	95.00%	E.DWKPNTSGTSDVEK.H		R.AWGVNVIVFEAFDEDWKPNTSGTSDVEK.H
129	139	2	1190.58	0.16	0	49.6	29.2	95.00%	R.NDLTASQLSDK.I		R.NDLTASQLSDK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
377	A6ZN47_YEAS7	8.65%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
82	101	3	2137.12	1.2	0	35.2	24.2	95.00%	R.QSPSDIHPVGVSYFPAVIPK.G		R.QSPSDIHPVGVSYFPAVIPK.G
610	622	2	1601.8	-1.2	0	70.2	28.3	95.00%	K.LQCININDLMVNR.N	Carbamidomethyl (+57)	K.LQCININDLMVNR.N
389	398	2	1204.56	-0.34	1	27.7	29.1	92.00%	K.QLDMVDDLEK.A		K.QLDMVDDLEK.A
188	198	2	1154.6	0.15	0	29.6	27.5	95.00%	K.FLYLDGASAAK.T		K.FLYLDGASAAK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
378	A6ZVF2_YEAS7	12.79%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	41	2	1185.56	0.35	0	69.8	29.2	95.00%	R.NGYLVYACAR.R	Carbamidomethyl (+57)	R.NGYLVYACAR.R
170	181	3	1439.77	0.62	1	26.9	24.3	95.00%	R.GLHLEMKPFNVR.V		R.GLHLEMKPFNVR.V
182	197	2	1556.84	0.5	0	103	24.5	95.00%	R.VINAITGGVATDIADK.R		R.VINAITGGVATDIADK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
379	A6ZLK4_YEAS7	15.08%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
63	71	2	1074.51	0.44	1	35.1	29.9	95.00%	E.IWDTAGQER.Y		R.IHMEIWDTAGQER.Y
153	162	2	1171.55	-0.19	0	36	28.4	95.00%	K.TGYNFDTLNK.I		K.TGYNFDTLNK.I
92	102	2	1176.58	0.87	0	33.4	27.8	95.00%	E.LGDVSSLQCAK.T	Carbamidomethyl (+57)	R.DANIALIVFELGDVSSLQCAK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
380	A6ZMV1_YEAS7	5.90%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
188	201	2	1563.78	-1.6	0	69.1	28.1	95.00%	K.NTVSNACLFQIAAR.L	Carbamidomethyl (+57)	K.NTVSNACLFQIAAR.L
324	336	2	1422.74	1.2	0	40.3	27.1	95.00%	R.MLGLTSVMAPFTR.D		R.MLGLTSVMAPFTR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
381	A6ZQZ3_YEAS7	15.54%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	12	2	1382.71	0.5	0	55.5	26.4	95.00%	-.MFSLQDVITTTK.T		-.MFSLQDVITTTK.T
56	66	3	1239.66	3.5	1	31.8	25	95.00%	R.KPTETTHLSAR.T		R.KPTETTHLSAR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
382	FRE7_YEAST	7.90%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
577	588	2	1414.6	-0.82	0	57.3	29.9	95.00%	R.NCFICSGSDSLR.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.NCFICSGSDSLR.Y
407	418	2	1301.7	-0.32	1	53.5	26.5	95.00%	K.ILIDGPYGGIER.D		K.ILIDGPYGGIER.D
348	359	3	1404.7	0.86	0	23.6	27.6	95.00%	E.MAYSPGQHIFVR.T		K.DVEMAYSPGQHIFVR.T
589	601	2	1306.69	-0.54	0	69.8	27.1	95.00%	R.YTVGNSVAGLQAK.V		R.YTVGNSVAGLQAK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
383	A6ZZA0_YEAS7	24.48%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
134	143	2	1156.69	-0.28	1	39.1	23.2	95.00%	K.LAEILKPVFQ.-		K.LAEILKPVFQ.-
35	45	3	1227.63	-0.39	1	27.7	27.7	95.00%	K.MVSQETVAHVK.D		K.MVSQETVAHVK.D
66	79	2	1559.86	0.12	1	37.6	23.8	95.00%	K.ATLSTLFQELNVPK.S		K.ATLSTLFQELNVPK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
384	A6ZY59_YEAS7	2.62%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
855	865	2	1171.59	-0.26	0	30.7	27.9	95.00%	R.QLGYSFVGSSK.S		R.QLGYSFVGSSK.S
1068	1082	2	1629.87	0.054	0	74.4	25.4	95.00%	E.FGSDPIQVVNNLVTK.Y		K.ASGEDVEEFGSDPIQVVNNLVTK.Y
998	1009	2	1269.73	0.85	1	31.7	23.1	95.00%	E.LILLGGTAIEDR.L		R.ELILLGGTAIEDR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
385	A6ZYD0_YEAS7	5.69%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
408	417	2	1191.52	0.069	0	50.1	29.9	95.00%	K.MDDPTVNWSK.E		K.MDDPTVNWSK.E
485	497	2	1421.79	0.12	0	30.2	22.7	95.00%	R.HINAPFMLPIAAK.M		R.HINAPFMLPIAAK.M
274	289	2	1654.83	1.4	0	88.6	28.6	95.00%	K.STMGGNLLYLTGSVDK.R		K.STMGGNLLYLTGSVDK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
386	A6ZQ79_YEAS7	10.67%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	65	2	1263.65	0.55	0	27	28.1	92.40%	K.DASLVDYVQVR.Q		K.DASLVDYVQVR.Q
20	31	2	1282.72	1.7	0	23.2	23.2	91.40%	E.FTPVVLATPIPE.E		-.MSDTEAPVEVQEDFEVVEEFTPVVLATPIPEEVQQAQTEIK.L
20	32	2	1411.76	1.1	1	30.8	24.7	95.00%	E.FTPVVLATPIPEE.V		-.MSDTEAPVEVQEDFEVVEEFTPVVLATPIPEEVQQAQTEIK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
387	IRC8_YEAST	4.14%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
218	231	2	1507.71	-0.34	1	66.3	30.1	95.00%	K.TISSDENSNSSVIR.H		K.TISSDENSNSSVIR.H
305	315	2	1294.69	1.1	1	41.2	25.7	95.00%	K.SFLNFLALNEK.N		K.SFLNFLALNEK.N

422	430	2	1064.6	1.1	0	25.9	23.1	95.00%	E.LQDIPQVPR.I		K.MISPQQSTQNEDSYQATPLIPQV EVDDDFYVGDILMTNELQDIPQVPR .I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
388	A6ZSP5_YEAS7	5.38%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
13	23	2	1074.61	1.9	0	51.7	24.2	95.00%	E.TALAVVATAMK.K		- .MVDDSNYLTPHETALAVVATAMK. K
549	559	2	1135.6	0.33	0	36	26.2	95.00%	K.ANSTTLGGLFR.A		K.ANSTTLGGLFR.A
367	378	2	1325.7	0.65	0	28.9	26.3	95.00%	E.SDLGEPVPFIPR.S		R.SLNSLLSIPSSVVTSDNATMESDL GEPVPFIPR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
389	A6ZVV4_YEAS7	14.48%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
313	327	3	1658.97	-0.54	0	35.7	17.1	95.00%	K.LSVISIDHLPSLLPR.E		K.LSVISIDHLPSLLPR.E
274	312	4	4074.17	0.67	0	36.2	24.2	95.00%	R.TVVDVSADTTNPHNPIPIYTVATV FNKPTVLVPTTAGPK.L		R.TVVDVSADTTNPHNPIPIYTVATV FNKPTVLVPTTAGPK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
390	A6ZSF8_YEAS7	8.94%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
135	143	2	1135.54	-0.015	0	29	28.1	95.00%	K.TYNTAPQWR.F		K.TYNTAPQWR.F
207	221	4	1639.84	0.4	0	31.7	26.8	95.00%	E.TVHDATGINCKPLSK.N	Carbamidomethyl (+57)	R.GEDASYETVHDATGINCKPLSK.N
2	14	2	1478.75	-0.69	1	66.3	28.3	95.00%	M.VNFDLGQVGEVFR.R		-.MVNFDLGQVGEVFR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
391	A6ZM44_YEAS7	5.34%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
98	118	2	2226.09	-0.81	1	63.8	28.8	95.00%	R.SVDMTSPLLTNLEAGTHANQK.K		R.SVDMTSPLLTNLEAGTHANQK.K
98	110	2	1418.7	1.1	0	52.4	29.1	95.00%	R.SVDMTSPLLTNLE.A		R.SVDMTSPLLTNLEAGTHANQK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
392	A6ZMK2_YEAS7	32.87%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
31	45	2	1635.92	-0.56	1	70.5	20	95.00%	K.VNGSPITLVEPEILR.F		K.VNGSPITLVEPEILR.F
48	66	3	2203.23	0.82	1	33.6	20.6	95.00%	K.VYEPLLLVGLDKFSNIDIR.V		K.VYEPLLLVGLDKFSNIDIR.V
115	127	3	1494.85	0.59	1	27.4	21.3	95.00%	R.TLLIADSRRPEPK.K		R.TLLIADSRRPEPK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
393	A6ZYP1_YEAS7	3.36%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
480	495	2	1651.75	-0.55	0	55.8	29.6	95.00%	R.SSTINNDSDSLSSPTK.S		R.SSTINNDSDSLSSPTK.S
124	149	4	2968.21	-0.16	1	50.6	30.2	95.00%	R.NNSGYYHNSYDNNNNSNNPGSN SHRK.T	Deamidation (+1)	R.NNSGYYHNSYDNNNNSNNPGSN SHRK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
394	A6ZVN8_YEAS7	4.47%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
24	40	2	1798.74	-0.33	0	42	30.7	95.00%	E.TDTATFNDDAPSGATCR.I	Carbamidomethyl (+57)	K.VANEETDTATFNDDAPSGATCR.I
881	894	3	1617.8	-0.37	0	35.7	28.2	95.00%	R.DVHAYFVPDGVLMR.V		R.DVHAYFVPDGVLMR.V
402	429	3	3086.61	0.29	0	46.2	23.4	95.00%	E.FDDLIAAQQNAINRPNAPVFIPPP AQNR.A		R.AQNEFDDLIAAQQNAINRPNAPV FIPPPAQNR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
395	VPS41_YEAST	3.73%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
435	444	2	1026.54	8.7	1	25.1	26.2	92.40%	E.NLLAKGNAPE.L	Deamidation (+1)	K.RPENLLAKGNAPELK.I
156	166	2	1206.59	0.35	0	43.3	28.8	95.00%	R.SSILCINTDGK.Y	Carbamidomethyl (+57)	R.SSILCINTDGK.Y
919	934	2	1816.89	0.49	0	104	29.1	95.00%	R.GMSDDLQIDNLQDIIK.H		R.GMSDDLQIDNLQDIIK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
396	A6ZW34_YEAS7	3.53%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
755	768	2	1472.65	-1.1	0	60.5	30.2	95.00%	E.DAASSTQMHAMPAR.D		R.QESEANNGLINAYEDEQFSLMEPSILEDAASSTQMHAMPAR.D
610	623	2	1415.74	-0.3	1	73.2	26.5	95.00%	K.SVANELMALGNVAK.D		K.SVANELMALGNVAK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
397	A6ZLM4_YEAS7	8.69%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
464	485	2	2151.05	-1.5	1	91.3	28.6	95.00%	R.SDYVGFINNGIPAGGIATGAEK.N	Deamidation (+1)	R.SDYVGFINNGIPAGGIATGAEK.N
519	532	2	1522.73	0.58	0	46.5	29.4	95.00%	K.LIAHSVATYADSFE.G		K.LIAHSVATYADSFEGFPK.R
544	556	2	1528.79	-0.73	1	36.5	26.1	95.00%	K.EVDILNAQQPQFK.Y		K.EVDILNAQQPQFK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
398	A7A187_YEAS7	5.56%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
389	405	2	1896.91	0.47	1	63.2	29.1	95.00%	R.IDNYSEEPSNVFGSVLK.K		R.IDNYSEEPSNVFGSVLK.K
47	57	2	1262.73	0.84	1	48.5	21.4	95.00%	K.LIELVSFAPFK.G		K.LIELVSFAPFK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
399	A6ZM69_YEAS7	5.87%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
237	247	2	1195.6	0.33	0	46.7	28	95.00%	R.GGVGYTWSTLR.E		R.GGVGYTWSTLR.E
288	302	2	1680.78	0.64	0	67.7	29.5	95.00%	E.MGSWDPTLNAFTDVK.Y		R.YPGTTVINLNATLFEFNPFEMGSWDPTLNAFTDVK.Y
495	507	2	1543.88	1.1	0	31.5	20.8	95.00%	E.YIPPLIVYIPNSR.H		R.NLTDLEYIPPLIVYIPNSR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
400	A6ZM02_YEAS7	9.02%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
223	234	2	1258.6	1.3	0	81.5	29	95.00%	K.FDVGALMALHGE.G		K.FDVGALMALHGEGSGEEK.G
203	213	2	1350.74	0.21	0	39.1	24.5	95.00%	K.DIFPLQNIHVR.K		K.DIFPLQNIHVR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
401	A6ZQV0_YEAS7	20.35%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
64	77	2	1561.83	-0.72	0	61.1	25.7	95.00%	E.MNPQVLFTALATTR.A		K.WSQLITNEMNPQVLFTALATTR.A
161	175	2	1448.74	-1.6	0	54.2	26.9	95.00%	K.QSGFGGNLTAALGTR.V		K.QSGFGGNLTAALGTR.V
1	18	2	1833.93	1.2	0	40.2	27.1	95.00%	-.MNGLVLGATGLCGGGFLR.H	Acetyl (+42)/ Carbamidomethyl (+57)	-.MNGLVLGATGLCGGGFLR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
402	A6ZXN6_YEAS7	7.91%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
172	181	2	1161.57	0.27	1	34	28.5	95.00%	E.LLDACSEQVK.F	Carbamidomethyl (+57)	K.SIMQNSYTELLDACSEQVK.F
436	452	2	1835.91	0.76	1	27.8	28.2	93.60%	K.ISDVSGIYPSGNIVMER.L		K.ISDVSGIYPSGNIVMER.L
338	346	2	1256.67	-0.015	1	31.7	25.9	95.00%	R.IENQWLLWR.K		R.IENQWLLWR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
403	A6ZLT5_YEAS7	4.62%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	75	2	1256.71	1.4	1	31.2	23.3	95.00%	E.NIRDDLSALLK.S		R.NDHVSPSCNVTFNELNAINENIRDDLSALLK.S

89	103	2	1854.78	-0.25	0	66.1	30.5	95.00%	K.QCSFWDANDGLCLNR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.QCSFWDANDGLCLNR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
404	B3LUC7_YEAS1	14.47%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
49	61	2	1480.78	-0.75	1	59.6	25.6	95.00%	R.GIITIEYFDPVSK.S		R.GIITIEYFDPVSK.S
121	140	2	2063.08	1.2	0	27.8	26.7	95.00%	K.YIQGGVVAPDVGPFTVYGPK.F		K.YIQGGVVAPDVGPFTVYGPK.F
97	109	3	1564.73	0.2	1	29.6	29.4	95.00%	E.GKDPNDIHTYSYR.K		K.AVIEGKDPNDIHTYSYR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
405	A6ZT94_YEAS7	4.59%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
275	289	3	1661.92	0.41	1	31.8	22.1	95.00%	R.GERPIPKPLDGNTLR.C		R.GERPIPKPLDGNTLR.C
387	399	3	1412.85	1.2	0	21	15.6	95.00%	K.VTPIVPVPIHVSR.S		K.VTPIVPVPIHVSR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
406	A6ZNW6_YEAS7	7.05%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
502	510	2	1112.59	1.7	0	28.9	25.2	95.00%	E.LHFLIQDVE.V		K.EENSPYELHFLIQDVEVWGCGGE K.E
554	567	2	1328.6	0.53	0	41.5	30	95.00%	E.MAGLVGQHQGGGSM.-		R.ALLEMAGLVGQHQGGGSM.-
477	493	2	1765.83	0.73	1	114	28.6	95.00%	R.NTGYGGSLDPGLLSMER.K		R.NTGYGGSLDPGLLSMER.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
407	A6ZXS0_YEAS7	9.14%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
225	239	2	1639.88	0.72	0	98.6	24.5	95.00%	K.DFLSGTVLYLNSLAK.R		K.DFLSGTVLYLNSLAK.R
269	286	2	1776.97	-0.18	0	38.9	22.6	95.00%	K.IGPDVVIGPNVTIGDGVR.I		K.IGPDVVIGPNVTIGDGVR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
408	A7A1Q4_YEAS7	2.92%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
6	14	2	1106.6	1.5	0	45.3	26	95.00%	R.VLDLFKPFE.S		R.VLDLFKPFESFLPEVIAPER.K
6	19	2	1679.88	0.57	1	33.6	25.1	95.00%	R.VLDLFKPFESFLPE.V		R.VLDLFKPFESFLPEVIAPER.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
409	A6ZRZ3_YEAS7	2.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1134	1155	2	2107.12	1.5	0	104	24.1	95.00%	K.AGSTVFALGTNVVSTGLGTIDK.V		K.AGSTVFALGTNVVSTGLGTIDK.V
1080	1092	2	1387.74	0.49	0	37.4	25.6	95.00%	E.SDTTFNIPLVGPK.G		K.AVVPLSTIDPESDTTFNIPLVGPK. G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
410	B3LRK1_YEAS1	17.54%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
71	82	2	1311.7	0.75	0	24.9	24.9	94.00%	E.DSNVAPQLDLLK.Q		K.EDSNVAPQLDLLK.Q
33	54	3	2164.08	0.83	1	33.5	27.9	95.00%	K.ITGQASSHLNAESPLDAPSAAK.T		K.ITGQASSHLNAESPLDAPSAAK.T
55	70	2	1649.83	-0.14	1	65.1	28.9	95.00%	K.TTPPASVHSATPDIKE.D		K.TTPPASVHSATPDIKEDSNVAPQ LDLLK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
411	A6ZY29_YEAS7	13.91%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
131	140	2	1123.64	0.16	0	34.1	21.9	95.00%	R.TVAVLPPNWK.Y		R.TVAVLPPNWK.Y
10	20	2	1136.58	0.96	0	41.2	27.3	95.00%	K.GISSSAIPYSR.N		K.GISSSAIPYSR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
412	A6ZQ18_YEAS7	7.09%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

225	242	2	2054.02	0.66	1	49.7	27.3	95.00%	R.MLPLPIANPNDFLPEDMK.Q		R.MLPLPIANPNDFLPEDMK.Q
567	581	2	1756.79	-0.11	1	34.6	30.6	95.00%	E.TCVEPNDDDLVRVPE.L	Carbamidomethyl (+57)	R.YTMDDLFNDPFFQQIETCVEPNDDDLVRVPELR.K
53	77	3	2288.11	1.4	1	125	28	95.00%	R.KRPTSPSISGSGSGGGNSPSSSAGAR.Q		R.KRPTSPSISGSGSGGGNSPSSSAGAR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
413	A7A1K8_YEAS7	30.77%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
47	61	2	1523.78	-0.0027	0	52.6	26.8	95.00%	R.GSSSLYTLVINDAGK.A		R.GSSSLYTLVINDAGK.A
5	13	2	1105.6	-0.11	1	27.9	24.8	95.00%	E.ITDIKQFLE.L		R.EITDIKQFLELTR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
414	CASP_YEAST	3.53%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	15	2	1777.83	0.015	0	45.7	29.7	95.00%	-.MDTSVYSHALDIWAK.A	Acetyl (+42)	-.MDTSVYSHALDIWAK.A
559	567	2	1095.52	-0.19	1	57.2	28.5	95.00%	R.IDVESQYSR.V		R.IDVESQYSR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
415	A6ZZ10_YEAS7	12.90%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
85	98	2	1671.8	1.2	1	57.4	29.3	95.00%	R.AMPALMELYSIYDR.S		R.AMPALMELYSIYDR.S
291	308	2	1718.84	-0.65	0	86.5	28.4	95.00%	R.LGTAPATLSQTSGTDSGR.A		R.LGTAPATLSQTSGTDSGR.A
316	327	2	1303.63	-0.86	0	54.7	29	95.00%	R.SGPSNLNQFQGR.G		R.SGPSNLNQFQGR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
416	A6ZRM1_YEAS7	7.57%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
424	442	2	1968.95	-0.22	1	37.4	29.3	95.00%	K.SGFDGLLPGDFPESGSIFK.K		K.SGFDGLLPGDFPESGSIFK.K
393	402	2	1071.55	0.29	0	43.8	27	95.00%	K.APVVNVCTGR.E	Carbamidomethyl (+57)	K.APVVNVCTGR.E
497	509	2	1394.65	-0.93	1	74.5	29.3	95.00%	K.LACAAFIDGENSK.I	Carbamidomethyl (+57)	K.LACAAFIDGENSK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
417	A6ZV22_YEAS7	15.50%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
20	29	2	1127.53	0.33	1	28.1	28.7	93.20%	K.AYFTAPSSER.R		K.AYFTAPSSER.R
30	39	2	1082.68	-0.2	1	24	16.3	92.70%	R.RVLLSAPLSK.E		R.RVLLSAPLSK.E
31	39	2	926.58	1.2	0	27.3	17.6	95.00%	R.VLLSAPLSK.E		R.VLLSAPLSK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
418	A7A281_YEAS7	7.12%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
161	169	2	1137.55	-0.076	1	32.7	29.8	95.00%	R.IENFISQCK.Q	Carbamidomethyl (+57)	R.IENFISQCK.Q
232	243	2	1349.68	-0.31	0	37	27.8	95.00%	R.IPASVWNMTFGK.S		R.IPASVWNMTFGK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
419	A6ZKK2_YEAS7	11.16%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
200	210	2	1091.54	-0.38	0	38.1	28.8	95.00%	R.MLSSAGVNSAR.G		R.MLSSAGVNSAR.G
37	49	2	1496.73	-0.48	0	104	29.7	95.00%	K.TLFSSWADSLNTR.A		K.TLFSSWADSLNTR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
420	A6ZSF6_YEAS7	5.06%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
5	13	2	1032.6	-0.025	0	68.4	20.9	95.00%	R.LSLTSLFPR.C		R.LSLTSLFPR.C
308	315	2	1045.52	0.013	1	28.8	28.2	94.80%	R.CLEDQLLR.R	Carbamidomethyl (+57)	R.CLEDQLLR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
421	A6ZNC5_YEAS7	5.46%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
304	311	2	967.48	-0.56	1	27.5	28.6	92.60%	R.EALDFFAR.G		R.EALDFFAR.G

277	287	2	1354.6	-0.7	0	65.5	30.7	95.00%	K.CCSDVFNQVVK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CCSDVFNQVVK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
422	A6ZTV9_YEAS7	12.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
63	72	2	1169.68	-0.42	0	23.5	24.4	91.90%	K.NQITVLQVQK.A		K.NQITVLQVQK.A
178	190	2	1564.69	-2.4	0	34.7	30.2	95.00%	R.IAHYNNGLQWFSD.-	Deamidation (+1)	R.IAHYNNGLQWFSD.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
423	B3LKX9_YEAS1	12.77%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	27	3	2341.19	1.7	0	36.6	26.2	95.00%	M.SAVGPGSNAGASVNGGSATAIA TLLR.N	Acetyl (+42)/ Deamidation (+1)	- .MSAVGPGSNAGASVNGGSATAIA TLLR.N
137	145	2	1257.59	0.86	0	46.3	29.3	95.00%	E.YFVWNYNPR.T		K.AQLEADEYFVWNYNPR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
424	A6ZNT7_YEAS7	3.29%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
603	616	2	1557.84	0.31	0	88.1	25.3	95.00%	E.IGSTIQTLNDLIDR.S		K.GEEIGSTIQTLNDLIDR.S
575	586	2	1437.65	0.4	1	59.7	30.3	95.00%	K.WNSDYEAVIADR.R		K.WNSDYEAVIADR.R
721	733	2	1549.75	-0.63	1	79.6	29.4	95.00%	R.ITLQCMDVETVNK.D	Carbamidomethyl (+57)	R.ITLQCMDVETVNK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
425	A6ZTW2_YEAS7	4.51%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
290	299	2	1219.65	0.15	1	49.8	27.7	95.00%	K.TQDVIQLFEK.D		K.TQDVIQLFEK.D
71	86	3	1761.95	0.57	1	50.1	24.5	95.00%	R.KYDTAVKPVIDDATVK.V		R.KYDTAVKPVIDDATVK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
426	A6ZZC9_YEAS7	13.50%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
34	50	2	1863.88	0.74	1	92.2	29.4	95.00%	R.SSVGQFMTFFAETVASR.T		R.SSVGQFMTFFAETVASR.T
24	33	2	1244.58	-0.51	1	33.1	29	95.00%	K.DLSQFGFFER.S		K.DLSQFGFFER.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
427	KHA1_YEAST	2.98%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
861	873	3	1586.79	1.3	1	34.7	28.8	95.00%	R.RFDTLIVHHFSSE.-		R.RFDTLIVHHFSSE.-
620	632	2	1512.77	0.91	1	49.1	27.5	95.00%	K.IPFSSEVIFSTMR.E		K.IPFSSEVIFSTMR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
428	A7A257_YEAS7	1.41%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2173	2184	2	1363.71	-0.018	0	44.3	26.2	95.00%	R.ASVWNDTLFLAK.M		R.ASVWNDTLFLAK.M
368	387	2	2228.02	0.77	1	103	30.3	95.00%	E.VYLLNDDDVQSIMTSGEDSK.L		R.SSNTNPYSHSHSHLHLISQDNHN GTDLHDPVAATDNPQQQNEVYLLN DDDVQSIMTSGEDSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
429	A7A1E2_YEAS7	14.88%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
61	71	2	1315.65	0.75	1	47	28.5	95.00%	R.LQLWDTAGQER.F		R.LQLWDTAGQER.F
116	125	2	1128.63	0.73	0	41.4	24.9	95.00%	E.NVILCIVGNK.S	Carbamidomethyl (+57)	R.GDENVILCIVGNK.S
13	23	2	1145.64	-0.54	1	37.9	23.2	95.00%	K.IVFLGEQGVGK.T		K.IVFLGEQGVGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
430	A6ZSX0_YEAS7	4.46%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
72	80	2	1050.54	0.16	0	31.1	27.5	95.00%	R.DFIGLPFDK.C		R.DFIGLPFDK.C
308	322	2	1643.86	0.96	0	83	25.3	95.00%	K.VFAQFSSFVDSVIAK.A		K.VFAQFSSFVDSVIAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
431	A6ZKX1_YEAS7	5.33%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
105	115	2	1183.65	1.2	0	52.3	24.6	95.00%	E.GLGNAFLSHIR.S		K.GASAGEGLGNAFLSHIR.S
116	125	2	1164.61	-0.34	0	44.5	27	95.00%	R.SVDSIYQVVR.C		R.SVDSIYQVVR.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
432	B5VMB7_YEAST	4.59%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	45	2	1319.56	-0.12	0	35.9	29.6	95.00%	K.NYQVCAGMYSK.E	Carbamidomethyl (+57)	K.NYQVCAGMYSK.E
134	146	2	1450.68	1.1	0	28.4	29	93.20%	R.SLANPIMTFSQNE.V		R.SLANPIMTFSQNEVGLHDTR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
433	A6ZM71_YEAS7	7.16%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
378	397	2	2146.96	-0.19	1	76.2	30.8	95.00%	K.ALKQDSNDTSDSPQDDQVGK.S		K.ALKQDSNDTSDSPQDDQVGK.S
365	373	2	1090.6	0.72	0	48.5	25.9	95.00%	E.LDLFNTLQK.D		R.HQHHPNDSNSPSDEDESEMYELDLFNTLQK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
434	A7A048_YEAS7	2.31%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
641	654	2	1534.84	0.05	0	50.6	23.2	95.00%	K.TPFQFADSVIGLIK.A		K.TPFQFADSVIGLIK.A
68	74	2	787.46	4.7	1	31.7	26.5	95.00%	R.LQTGKNK.T		R.LQTGKNK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
435	B3LI87_YEAS1	6.10%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
635	645	2	1357.58	0.2	0	56.3	29.8	95.00%	E.YLNDDDNGYIR.W	Deamidation (+1)	K.YAIEYLNDDDNGYIR.W
528	545	3	2056.87	-0.98	1	30.9	31.3	95.00%	K.LSVCTCDNEDHPNQGVGR.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.LSVCTCDNEDHPNQGVGR.G
34	47	2	1486.7	-0.81	0	35.7	29.1	95.00%	R.QSSSLEPADGQNVR.V		R.QSSSLEPADGQNVR.V
631	645	2	1832.82	-0.55	1	80.2	30.8	95.00%	K.YAIEYLNDDDNGYIR.W		K.YAIEYLNDDDNGYIR.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
436	A9EDP4_YEAST	4.52%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
324	337	2	1659.82	-0.79	1	94.4	29	95.00%	R.NIDIWTVETAQNTR.E		R.NIDIWTVETAQNTR.E
508	521	2	1370.74	-0.81	0	35.6	25.8	95.00%	K.DISASSPNLGGILK.A		K.DISASSPNLGGILK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
437	A6ZP32_YEAS7	7.55%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
111	126	4	1953.89	1	1	36.1	30.2	95.00%	K.RHYSHVDCPGHADYIK.N	Carbamidomethyl (+57)	K.RHYSHVDCPGHADYIK.N
45	61	4	1794.95	0.74	0	27.1	24.8	95.00%	R.SKPHVNIGTIGHVDHGK.T		R.SKPHVNIGTIGHVDHGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
438	A6ZV49_YEAS7	3.04%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	67	3	1370.71	1.2	0	24.2	26.5	95.00%	E.TTAVEPHPHNLR.H		K.TDVTAETTAVEPHPHNLR.H
50	67	3	1986.97	-0.96	1	33.3	28.4	95.00%	K.TDVTAETTAVEPHPHNLR.H		K.TDVTAETTAVEPHPHNLR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
439	A6ZZQ1_YEAS7	16.99%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
170	178	2	1014.57	0.29	1	39.7	25.7	95.00%	K.QISLEGLQK.Q		K.QISLEGLQK.Q
73	98	3	2643.33	0.01	0	41.4	26.1	95.00%	R.VSLYHNDNSGSIGSSAVTPIQALASR.A		R.VSLYHNDNSGSIGSSAVTPIQALASR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
440	A6ZLE8_YEAS7	7.10%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
325	344	2	2141.87	-0.45	1	98.4	30.7	95.00%	K.CNGQDMSEVGNGPGSYDISR.S	Carbamidomethyl (+57)	K.CNGQDMSEVGNGPGSYDISR.S
401	413	2	1626.85	0.55	0	31.2	26.3	95.00%	K.YGYIPYLPISWQK.K		K.YGYIPYLPISWQK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
441	COS8_YEAST	18.64%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
157	167	2	1275.75	0.92	1	50	21.3	95.00%	K.TTLLEPFSLKK.D		K.TTLLEPFSLKK.D
102	108	2	935.49	1.7	0	31	27.4	95.00%	K.QLIQFCK.E	Carbamidomethyl (+57)	K.QLIQFCK.E
143	153	2	1441.62	-0.55	0	40.4	30	95.00%	K.YFFFNAMSCQK.A	Carbamidomethyl (+57)	K.YFFFNAMSCQK.A
124	135	2	1388.66	0.71	0	63.3	29.8	95.00%	E.VVAANLNSYFYE.N		K.EITEDTPSSDPHDWEVVAANLNS YFYENK.T
291	300	2	1194.6	1.9	0	35.2	28.7	95.00%	K.MQFLSTIINE.Q		K.MQFLSTIINEQESGANGWDEIAK. K
102	109	2	1064.53	0.77	1	37.9	28.6	95.00%	K.QLIQFCKE.I	Carbamidomethyl (+57)	K.QLIQFCKEITEDTPSSDPHDWEV VAANLNSYFYENK.T
186	196	2	1181.61	0.58	0	47.5	26.5	95.00%	E.ALQVYAAGFDK.E		K.DSVPYIEEALQVYAAGFDK.E
157	166	2	1147.65	0.67	0	30	23.3	95.00%	K.TTLLEPFSLK.K		K.TTLLEPFSLK.K
11	18	2	893.49	-0.02	0	26.5	25.4	95.00%	K.SVDVLSFK.Q		K.SVDVLSFK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
442	A6ZZ58_YEAS7	10.71%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
148	164	2	1957.89	0.61	1	57.1	30.1	95.00%	K.TMQNLHIQAQTMGDELE.N		K.TMQNLHIQAQTMGDELENQGQL LDNMDEGMDGVVNK.L
22	28	2	892.48	0.43	0	35.5	25.9	95.00%	R.INNYITR.H		R.INNYITR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
443	A7A0T2_YEAS7	17.94%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
141	151	2	1272.69	-0.16	0	32.8	27	95.00%	K.NVVNLLNTQMK.N		K.NVVNLLNTQMK.N
178	215	3	4105.81	0.59	0	45.5	28.9	95.00%	K.LTTDTGHAPADDQTQSNHAADLT TYNNSNPFMTSLLDE.S		K.LTTDTGHAPADDQTQSNHAADLT TYNNSNPFMTSLLDESSEK.N
244	255	2	1419.71	0.42	1	43.7	28.4	95.00%	E.GQLSNNVYLQER.N		K.NNNSSNQGELSFPQNDSQLMLM EEGQLSNNVYLQER.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
444	A6ZLT3_YEAS7	30.61%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
157	167	2	1275.75	0.92	1	50	21.3	95.00%	R.TTLLEPFSLKK.D		R.TTLLEPFSLKK.D
102	108	2	935.49	1.7	0	31	27.4	95.00%	K.QLIQFCK.E	Carbamidomethyl (+57)	K.QLIQFCK.E
352	367	2	2001.05	0.93	1	49.3	25.7	95.00%	K.SMWPLPLNVELWPYIK.E	Oxidation (+16)	K.SMWPLPLNVELWPYIK.E
186	193	2	953.5	0.6	1	54.1	26.6	95.00%	E.ALGVYFRE.V		K.DSVPYIEEALGVYFREVEK.Q
113	123	2	1283.51	0.84	0	38.3	28.9	95.00%	E.NTPSSDPHDWE.V		K.EVTENTPSSDPHDWEVVAANLN SYLYENK.A
289	298	2	1194.6	1.9	0	35.2	28.7	95.00%	K.MQFLSTIINE.Q		K.MQFLSTIINEQESGANGWDEIAR. K
22	33	3	1442.83	0.91	1	35.7	20.9	95.00%	E.SQKIVLPQDLFR.S		K.QLESQKIVLPQDLFR.S
102	109	2	1064.53	0.77	1	37.9	28.6	95.00%	K.QLIQFCKE.V	Carbamidomethyl (+57)	K.QLIQFCKEVTENTPSSDPHDWEV VAANLNSYLYENK.A
25	33	2	1099.64	-0.29	0	27.9	23.4	95.00%	K.IVLPQDLFR.S		K.IVLPQDLFR.S
337	345	3	1362.63	0.94	0	25.4	29.6	95.00%	E.WFFNHFFYR.V		K.NEEFFFDGIDCEWFFNHFFYR.V
206	216	2	1187.58	-0.27	1	57.3	28.3	95.00%	K.SWSPVGLEDAK.L		K.SWSPVGLEDAK.L
157	166	2	1147.65	0.67	0	30	23.3	95.00%	R.TTLLEPFSLK.K		R.TTLLEPFSLK.K
11	18	2	893.49	-0.02	0	26.5	25.4	95.00%	K.SVDVLSFK.Q		K.SVDVLSFK.Q
124	135	2	1355.66	0.94	0	41.7	28.9	95.00%	E.VVAANLNSYLYE.N	Deamidation (+1)	K.EVTENTPSSDPHDWEVVAANLN SYLYENK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

445	A6ZR56_YEAS7	10.40%		100%		2							
Start	End	charge	Mr(expt)		ppm	MC	Ion score	Identity score	Scaffold probability	Sequence		Modification	Extended sequence
37	50	3	1660.83		0.97	0	30.3	28.2	95.00%	E.WHYIITGPADTPYK.G			K.LMVENPPPYILARPNEDNILEWHYIITGPADTPYK.G
138	149	2	1441.7		0.13	0	51.1	28.9	95.00%	R.NSISYNTFQNVR.F			R.NSISYNTFQNVR.F
Index	AC	Coverage	Scaffold probability		Nb distinct peptides								
446	A6ZW91_YEAS7	13.19%		100%		3							
Start	End	charge	Mr(expt)		ppm	MC	Ion score	Identity score	Scaffold probability	Sequence		Modification	Extended sequence
263	273	2	1181.56		-1.2	0	35.7	29	95.00%	K.DNNISSYGSII.-			K.DNNISSYGSII.-
230	240	2	1237.58		0.62	1	58.4	29.8	95.00%	E.SLTITNAENFE.T			R.LHSESLTITNAENFETNTFLNDEIPDLSEISNEVPNK.D
241	254	2	1606.74		-0.39	1	40.7	30.5	95.00%	E.TNTFLNDEIPDLSE.I			R.LHSESLTITNAENFETNTFLNDEIPDLSEISNEVPNK.D
Index	AC	Coverage	Scaffold probability		Nb distinct peptides								
447	A6ZMI9_YEAS7	3.14%		100%		3							
Start	End	charge	Mr(expt)		ppm	MC	Ion score	Identity score	Scaffold probability	Sequence		Modification	Extended sequence
782	799	2	1910.04		-0.58	0	71.5	21.8	95.00%	K.TPVFTTGGDYILSLVSIK.D			K.TPVFTTGGDYILSLVSIK.D
5	13	2	1124.52		-0.38	0	32.6	29.8	95.00%	R.YNVFNDTPR.G			R.YNVFNDTPR.G
820	834	2	1723.85		0.55	1	31.4	28	95.00%	R.DIPSAAFNFFEPIKE.A			R.DIPSAAFNFFEPIKEAK.I
Index	AC	Coverage	Scaffold probability		Nb distinct peptides								
448	A6ZS70_YEAS7	13.20%		100%		3							
Start	End	charge	Mr(expt)		ppm	MC	Ion score	Identity score	Scaffold probability	Sequence		Modification	Extended sequence
76	88	2	1450.68		0.68	0	71.2	29.2	95.00%	R.GNVTSVSFQQDNR.W			R.GNVTSVSFQQDNR.W
27	39	3	1525.75		0.34	1	37.5	28.9	95.00%	R.TIQHSDSQVNRLE.I			R.TIQHSDSQVNRLEITNDK.K
2	15	2	1571.83		-0.62	0	23.8	25.6	91.20%	M.SVILVSAGYDHTIR.F		Acetyl (+42)	-.MSVILVSAGYDHTIR.F
Index	AC	Coverage	Scaffold probability		Nb distinct peptides								
449	B3LFN6_YEAS1	4.66%		100%		2							
Start	End	charge	Mr(expt)		ppm	MC	Ion score	Identity score	Scaffold probability	Sequence		Modification	Extended sequence
842	859	2	2031.02		-0.4	1	28	27.5	94.60%	E.SSLPKPNQTLFSNLEDLE.I			R.YTESSLPKPNQTLFSNLEDLEIEDIDDNGSVSDVHIEELDALDEELYK.R
810	833	3	2611.26		0.52	0	37.5	28.8	95.00%	E.FSTGSQTCLPSTAYTTPLHTNSIK.L		Carbamidomethyl (+57)	K.LHGLGTESCTTDDPDTGNQITNEFSTGSQTCLPSTAYTTPLHTNSIK.L
Index	AC	Coverage	Scaffold probability		Nb distinct peptides								
450	A6ZMR5_YEAS7	8.79%		100%		2							
Start	End	charge	Mr(expt)		ppm	MC	Ion score	Identity score	Scaffold probability	Sequence		Modification	Extended sequence
29	46	2	2007.96		0.84	0	127	29.4	95.00%	K.GNFFSSNPISSFVVDTYK.Q			K.GNFFSSNPISSFVVDTYK.Q
10	25	2	1606.93		0.61	0	39.9	15.4	95.00%	E.ASQIPTIPALSPLTAK.Q			-.MSAPTPLAEASQIPTIPALSPLTAK.Q
Index	AC	Coverage	Scaffold probability		Nb distinct peptides								
451	A6ZTM4_YEAS7	18.11%		100%		2							
Start	End	charge	Mr(expt)		ppm	MC	Ion score	Identity score	Scaffold probability	Sequence		Modification	Extended sequence
1	12	2	1295.73		0.83	0	39.2	21.8	95.00%	-.MIPAPLDASLLR.E			-.MIPAPLDASLLR.E
58	68	2	1401.66		1.4	0	61.2	28.8	95.00%	E.VYDYSVCDIIR.G		Carbamidomethyl (+57)	K.YGLGYFNYGLVIDDEVYDYSVCDIIR.G
Index	AC	Coverage	Scaffold probability		Nb distinct peptides								
452	A6ZQR4_YEAS7	4.80%		100%		2							
Start	End	charge	Mr(expt)		ppm	MC	Ion score	Identity score	Scaffold probability	Sequence		Modification	Extended sequence
315	326	3	1353.64		0.51	1	42.7	30.1	95.00%	R.TGSHFPAFSFEK.H			R.TGSHFPAFSFEK.H
298	309	2	1141.67		0.42	0	46.9	23.1	95.00%	E.LDGIGGVSILAK.A			R.DPNGNPEDEMELDGIGGVSILAK.A
Index	AC	Coverage	Scaffold probability		Nb distinct peptides								

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
453	A6ZP61_YEAS7	5.59%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
191	205	2	1653.83	1.3	0	41.9	28.5	95.00%	R.LLGQDSDPGLYFTTK.E		R.LLGQDSDPGLYFTTK.E
355	370	2	1800.87	0.32	0	85.3	28.9	95.00%	E.VLASDQAIWWAPDDSK.A		K.DIFNAKPDWIYEEEVLASDQAIWWAPDDSK.A
54	74	2	2369.21	-0.18	1	45.2	25.9	95.00%	E.IRPTEATIDVTDVPQTPFLQE.Q		K.SSNSSMDKPFFPNNDSVANTDPQSDENGHTINEIRPTEATIDVTDVPQTPFLQEQYSMRPR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
454	A6ZVG8_YEAS7	4.86%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
751	765	2	1780.76	0.053	0	29	30.6	91.80%	K.NIYPDVYSLHDMADE.A		K.NIYPDVYSLHDMADEAGLPVQTEDGEATGTIVLPQPINATSSLFER.Y
174	183	2	1134.57	0.42	0	45.8	28	95.00%	E.LSNASPDYIR.S		R.MLVPSELSNASPDYIR.S
777	796	2	2114.14	0.98	1	74	22.5	95.00%	E.ATGTIVLPQPINATSSLFER.Y		K.NIYPDVYSLHDMADEAGLPVQTEDGEATGTIVLPQPINATSSLFER.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
455	A6ZRY2_YEAS7	15.84%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
144	151	2	950.41	9.1	0	28.1	28.2	93.90%	K.QMNAPFLE.T	Deamidation (+1)/ Deamidation (+1)	K.QMNAPFLETSAK.Q
252	280	3	3046.41	0.4	1	72	29.3	95.00%	K.TQTDRTNIDNSTGQAGQANAQSANTVNNR.V		K.TQTDRTNIDNSTGQAGQANAQSANTVNNR.V
57	70	2	1501.75	1.1	1	35.7	27.9	95.00%	E.VSILDILDTAGQEE.Y		K.QVVIDDEVSILDILDTAGQEEYSAMR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
456	B3LMI6_YEAS1	27.33%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	136	2	1963.83	0.35	1	65.3	30.7	95.00%	E.DKGEPGYVAYVGYDTDSE.L		R.DYEPNDEHLSFCIIENDNVPPVHYPIHEDKGEPGYVAYVGYDTDSELVQELCADSTIYHM.-
141	150	2	1209.52	0.93	0	52.5	29.5	95.00%	E.LCADSTIYHM.-	Carbamidomethyl (+57)	K.GEPGYVAYVGYDTDSELVQELCADSTIYHM.-
106	118	2	1529.73	0.31	0	45.7	29.8	95.00%	E.NDNVPPVHYPIHE.D		R.DYEPNDEHLSFCIIENDNVPPVHYPIHEDK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
457	A6ZZF1_YEAS7	6.47%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
44	53	2	1277.6	0.38	0	30.6	29.6	95.00%	E.HFNYDQVLDK.S		R.ENIVHFDPNGLFDNLHTIVHEDDSQENEEAEHFNYDQVLDK.S
4	13	2	1206.63	0.73	1	52	27.3	95.00%	E.YTLLADNIRE.N		-.MPEYTLLADNIRENIVHFDPNGLFDNLHTIVHEDDSQENEEAEHFNYDQVLDK.S
13	33	3	2459.19	1.3	1	47.4	28.6	95.00%	R.ENIVHFDPNGLFDNLHTIVHE.D		R.ENIVHFDPNGLFDNLHTIVHEDDSQENEEAEHFNYDQVLDK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
458	A6ZUD1_YEAS7	17.93%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
102	110	2	959.59	2.2	1	27.1	14.5	95.00%	E.VLLAGFGRK.G		K.VTAFVPNDGCLNFVDENDEVLLAGFGRK.G
82	98	2	1923.9	0.31	1	49	30.5	95.00%	K.KVTAFVPNDGCLNFVDE.N	Carbamidomethyl (+57)	K.KVTAFVPNDGCLNFVDENDEVLLAGFGR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
459	A6ZZT0_YEAS7	3.56%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
668	683	2	1866.88	-0.81	0	34.6	29.7	95.00%	K.HTIPDGYSYFKPLSNE.Y		K.HTIPDGYSYFKPLSNEYISEHGGGTAEHTVDCAICMSDVPIYIEEIPETHK.V
172	182	2	1403.57	-0.36	1	33.2	29.5	95.00%	E.TYWSEWPSYGE.L		R.FYEPATDFSEDIPPEGETYWSEWPSYGELHNVSFQHGEIAIQISHMSNLQDNNNYLR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
460	A6ZX09_YEAS7	13.33%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
74	86	3	1487.8	0.94	0	26.1	24.5	95.00%	E.WHTHITAVTVAPR.F		K.TTEWHTHITAVTVAPR.F
2	14	2	1575.82	0.45	0	33.4	26.8	95.00%	M.TTIQPFEPVDLFK.T	Acetyl (+42)	-.MTTIQPFEPVDLFK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
461	A6ZM11_YEAS7	15.17%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
149	163	2	1793.82	-0.68	1	58.2	30.4	95.00%	K.VFNESGYLQNDAYFK.W		K.VFNESGYLQNDAYFK.W
119	130	2	1443.8	-0.98	1	46.6	23.9	95.00%	K.NEPLYLVELVQK.K		K.NEPLYLVELVQK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
462	COS5_YEAST	26.11%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
157	167	2	1275.75	0.92	1	50	21.3	95.00%	R.TTLLEPFSLKK.D		R.TTLLEPFSLKK.D
102	108	2	935.49	1.7	0	31	27.4	95.00%	K.QLIQFCK.E	Carbamidomethyl (+57)	K.QLIQFCK.E
186	193	2	953.5	0.6	1	54.1	26.6	95.00%	E.ALGVYFRE.V		K.DSVPYIEEALGVYFREVEK.Q
113	123	2	1283.51	0.84	0	38.3	28.9	95.00%	E.NTPSSDPHDWE.V		K.EVTENTPSSDPHDWEVVAANLNSYLYENK.A
22	33	3	1442.83	0.91	1	35.7	20.9	95.00%	E.SQKIVLPQDLFR.S		K.QLESQKIVLPQDLFR.S
354	369	2	2001.08	-0.26	1	39.5	23.1	95.00%	K.SMWLLPLNVELWPYIK.E		K.SMWLLPLNVELWPYIK.E
102	109	2	1064.53	0.77	1	37.9	28.6	95.00%	K.QLIQFCKE.V	Carbamidomethyl (+57)	K.QLIQFCKEVTENTPSSDPHDWEVVAANLNSYLYENK.A
25	33	2	1099.64	-0.29	0	27.9	23.4	95.00%	K.IVLPQDLFR.S		K.IVLPQDLFR.S
206	219	2	1553.81	-0.2	1	52.8	26.7	95.00%	K.SWSPVGLEDVQLPK.D		K.SWSPVGLEDVQLPK.D
157	166	2	1147.65	0.67	0	30	23.3	95.00%	R.TTLLEPFSLK.K		R.TTLLEPFSLK.K
11	18	2	893.49	-0.02	0	26.5	25.4	95.00%	K.SVDVLSFK.Q		K.SVDVLSFK.Q
124	135	2	1355.66	0.94	0	41.7	28.9	95.00%	E.VVAANLNSYLYE.N	Deamidation (+1)	K.EVTENTPSSDPHDWEVVAANLNSYLYENK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
463	A6ZRB2_YEAS7	1.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
28	47	2	1942.91	-0.51	0	85.3	29.2	95.00%	K.TTTASTASSSSPSSSSQTIR.N		K.TTTASTASSSSPSSSSQTIR.N
286	305	2	1968.82	-0.72	0	68.4	30.7	95.00%	K.NDDSSSTTATNSGNDVASAR.S		K.NDDSSSTTATNSGNDVASAR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
464	A6ZZL6_YEAS7	3.24%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
149	156	2	1061.42	-0.69	1	28.7	28.5	94.30%	R.FFDMMDEK.H		R.FFDMMDEK.H
247	257	2	1224.65	-0.75	0	53.8	26.4	95.00%	K.IGGFVTNLNYK.D		K.IGGFVTNLNYK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
465	A7A0Y2_YEAS7	7.79%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	10	2	1201.59	0.1	0	31.1	27.7	95.00%	-.MNALYNHAVK.Q	Acetyl (+42)	-.MNALYNHAVK.Q
13	21	2	1098.58	-0.19	1	24.5	25.5	92.60%	K.NQLQQELAR.F		K.NQLQQELAR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
466	A6ZNT6_YEAS7	6.29%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	110	2	1332.62	-0.39	0	29.1	29.2	94.00%	K.SSNSDTSIFFTK.V		K.SSNSDTSIFFTK.V

335	344	2	1159.64	0.32	0	26.1	25.1	95.00%	K.SPAYPFPLLR.L		K.SPAYPFPLLR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
467	A6ZVN0_YEAS7	4.86%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
322	332	2	1217.53	-0.57	1	53.8	29.6	95.00%	R.EGLCVDGPDTR.Y	Carbamidomethyl (+57)	R.EGLCVDGPDTR.Y
357	368	2	1379.68	0.72	0	50.3	28.2	95.00%	E.SVSNQVLNMIFE.N		R.SQNHLSESVSNQVLNMIFENGKP GIILTGHDHEGCETVYNK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
468	B3LNE5_YEAS1	2.25%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
95	112	3	2153.03	1.1	1	32.9	28.5	95.00%	E.NDVFDVFDDKDADWLLVK.S		R.AIYDYEQVQNADEELTFHENDVF DVFDDKDADWLLVK.S
36	45	2	1263.58	-0.73	0	42.5	28.6	95.00%	K.SDIDDWWTVK.K		K.SDIDDWWTVK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
469	A6ZQ13_YEAS7	3.82%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
291	299	2	1115.48	0.69	1	41.2	29	95.00%	E.SQTFDDFKE.V		K.TGLLESQTFDDFKEVENK.I
121	130	2	1150.6	0.43	0	34.4	26.9	95.00%	R.NLNSVLNYSK.F		R.NLNSVLNYSK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
470	A6ZZ91_YEAS7	5.73%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
341	351	2	1256.72	0.3	0	34.3	23.6	95.00%	K.NFDLRPGVLVK.E		K.NFDLRPGVLVK.E
138	148	2	1174.74	0.32	0	63.9	14	95.00%	E.GLPLTILLAHK.L		K.SLEDLGAGDQGIMFGYATDETPE GLPLTILLAHK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
471	A6ZT09_YEAS7	7.16%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
246	254	2	1111.53	-0.38	0	38.5	28.7	95.00%	R.LSFNDYTPR.F		R.LSFNDYTPR.F
214	228	2	1758	1.9	0	43.7	21.1	95.00%	E.SIIPIQIFPDIFDIK.S		R.TILAQIPSPEQNVIYTSLNPGTTLA HESIIPIQIFPDIFDIK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
472	SNQ2_YEAST	2.00%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1082	1092	2	1326.66	-0.7	1	47.8	28	95.00%	K.NSATILNYFER.N		K.NSATILNYFER.N
417	435	3	2133.08	0.88	0	24.1	26.7	95.00%	E.FLTALTDPNGFHLIKPGYE.N	Deamidation (+1)	R.QATAEFLTALTDPNGFHLIKPGYE NK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
473	A6ZTG3_YEAS7	4.69%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
225	237	2	1452.66	0.75	0	32.3	29.8	95.00%	E.SSMPSYNDLPSQK.T		K.VVDAFLYTKPPNIVHIESSMPSYN DLPSQK.T
429	439	2	1164.58	0.42	1	38.2	27.9	95.00%	K.YNGEASVQLGK.T		K.YNGEASVQLGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
474	A7A0I6_YEAS7	2.02%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
814	829	2	1813.99	0.48	0	60	22.1	95.00%	K.LTLPVSFNEPTSLLQR.V		K.LTLPVSFNEPTSLLQR.V
1167	1174	2	1056.47	0.92	1	32.3	28.6	95.00%	K.FNGEYWNK.R		K.FNGEYWNK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
475	A6ZND7_YEAS7	12.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
265	286	2	2027.99	0.028	0	41.5	29	95.00%	E.AATAATGNGNTGNSGPTSLPLR. G	Deamidation (+1)	R.ATVEAATAATGNGNTGNSGPTSL PLR.G
244	260	2	1569.82	-0.47	0	102	25.9	95.00%	R.ANVAIAANAATNTAAAR.A		R.ANVAIAANAATNTAAAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
476	A6ZUL4_YEAS7	2.75%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
316	328	2	1424.79	0.34	0	32.5	22.1	95.00%	K.LLTPVPSDIDISR.A		K.LLTPVPSDIDISR.A
171	183	2	1326.74	-0.013	1	31.2	24.1	95.00%	R.SDIVGSPVAELLK.S		R.SDIVGSPVAELLK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
477	A6ZL20_YEAS7	16.67%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
58	70	2	1457.75	-0.35	1	78.4	27.2	95.00%	K.NSINEINSVNNLK.M		K.NSINEINSVNNLK.M
15	28	3	1675.86	0.84	0	20.9	27.2	91.60%	E.NTLKPYDLHSVDFK.T		K.GFLENTLKPYDLHSVDFK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
478	A6ZYA4_YEAS7	4.87%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
305	321	3	1987.06	1.3	0	23	23.4	95.00%	K.YAGDLYTIPIINTLQHR.G		K.YAGDLYTIPIINTLQHR.G
260	271	2	1475.71	0.13	0	28	29.1	92.60%	K.SYTYNNFPMVLK.N		K.SYTYNNFPMVLK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
479	A6ZYE8_YEAS7	4.95%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
555	574	2	2155.12	0.79	0	109	25.8	95.00%	K.TIPITNVVDAIMDPLNSSQK.N		K.TIPITNVVDAIMDPLNSSQK.N
318	330	2	1732.75	1.7	1	36.4	30.3	95.00%	K.KYDIEPNDFFWME.N		K.KYDIEPNDFFWMENSHLPFPEAA ENVEAALNTYK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
480	INP54_YEAST	8.07%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	68	2	1568.85	0.43	0	41.2	24.1	95.00%	E.VVPIWQGSFPAVNR.D		K.QLLFPYDDGISQLELQDLYVLGFQ EVVPIWQGSFPAVNR.D
305	321	3	1910	0.95	0	37.4	25.5	95.00%	R.SNALLFSDHQPVNLTVR.L		R.SNALLFSDHQPVNLTVR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
481	A6ZS90_YEAS7	1.12%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
282	291	2	1101.63	0.7	0	36.6	23.7	95.00%	E.IPGSPIFIMK.L		R.EEDFIALYHQAANEIPGSPIFIMK. L
1133	1147	2	1639.86	1.4	0	42.5	25.5	95.00%	K.FQLPSAAFSTFPTVK.S		K.FQLPSAAFSTFPTVK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
482	A6ZT54_YEAS7	3.44%	99%	1

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
300	315	2	1715.9	0.33	0	44.2	26.9	95.00%	E.AVTPLINEPEPLPTPE.A		K.EVAHNVQELTPQVEAVTPLINEP EPLPTPEAQISIPESSK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
483	A6ZLZ8_YEAS7	6.53%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
102	112	2	1386.66	1.8	1	40.6	29.8	95.00%	E.EMPFFIPYDTK.V		K.LVLEELQLEEMPFFIPYDTK.V
252	263	2	1472.65	0.47	0	28.4	30.4	90.90%	E.VDTNQYSVNDYR.Y		K.LGAEVDTNQYSVNDYR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
484	A6ZMS6_YEAS7	9.28%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
94	118	3	2329.02	0.84	1	50.3	31.2	95.00%	K.NGGGGGGPGGPGAGGFHDPFDI FER.M	Deamidation (+1)	K.NGGGGGGPGGPGAGGFHDPFDI FER.M
71	80	2	1135.54	-0.017	1	51.5	28.2	95.00%	E.AYDVLSDPEK.K		K.FIEVGEAYDVLSDPEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
485	YD206_YEAST	3.41%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

263	276	2	1525.81	0.24	1	62.5	25	95.00%	E.DNAISLDPTRLPSK.S		R.YVRPLGDTQIDEDNAISLDPTRLPSK.S
251	262	2	1404.69	0.63	0	48.9	28.5	95.00%	R.YVRPLGDTQIDE.D		R.YVRPLGDTQIDEDNAISLDPTR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
486	A6ZXW8_YEAS7	16.19%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
165	186	3	2627.22	0.52	1	49.8	30.2	95.00%	E.FDFNLLRPTMNNFVNGQSNRNE.Q	Deamidation (+1)	R.IPSESEFDFNLLRPTMNNFVNGQSNRNEQHSPTVESSSFDVNNAPAR.A
194	205	2	1263.59	1.6	0	34.8	29.3	95.00%	E.SSSFDVNNAPAR.A		R.NEQHSPTVESSSFDVNNAPAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
487	A6ZQQ7_YEAS7	3.14%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
667	678	2	1415.62	1.3	0	42.5	30.2	95.00%	E.TDYPDNISNYSK.G		R.SNLWTTAQFAQPSHQQVSTELDQAFEYDNANHLISGLQNMIYDETDYPDNISNYSK.G
649	666	2	2108.95	0.0017	0	46.2	30.3	95.00%	E.YDNANHLISGLQNMIYDE.T		R.SNLWTTAQFAQPSHQQVSTELDQAFEYDNANHLISGLQNMIYDETDYPDNISNYSK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
488	A6ZT21_YEAS7	5.92%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
301	309	2	1150.44	0.35	1	35.7	28	95.00%	R.LMACFDHEE.I	Carbamidomethyl (+57)	R.LMACFDHEEIGSSSAQGADSNFLPNILER.L
310	329	2	2075.03	0.47	1	56	28	95.00%	E.IGSSSAQGADSNFLPNILER.L		R.LMACFDHEEIGSSSAQGADSNFLPNILER.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
489	A6ZKV2_YEAS7	10.80%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
131	142	2	1253.67	1.7	0	25.7	25.7	94.10%	K.AAYVAPPPLVQE.C		K.AAYVAPPPLVQECSSESVNSLERPPAAVVHQANSLDTDYGLTRPSNGR.V
114	124	2	1351.58	1.8	1	34.5	30.2	95.00%	E.HDLGYYDQRGE.F		R.TDDYVPEYTETANEHDLGYYDQRGEFHPNDK.A

Supplementary Table S2: All "Scaffold" validated proteins and peptides identified from solprotSP (*S.pombe*) and from SCVMprot (*S.cerevisiae*) samples

***S.cervisiae* - Glu-C digest of large tryptic peptides (Replicate B)**

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
1	A6ZPV7_YEAS7	57.98%	100%	52								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
310	320	2	1254.66	2.6	1	56.4	26.5	95.00%	K.GKYTVDQVFAK.M		K.GKYTVDQVFAK.M	
429	442	2	1679.87	2.4	1	72.1	26.8	95.00%	K.LQTQLGQEPPEWVR.E		K.LQTQLGQEPPEWVR.E	
201	212	2	1513.76	2.6	1	56.7	28	95.00%	K.YWVHPDNITELK.L		K.YWVHPDNITELK.L	
362	371	2	1074.55	3.4	0	46	28	95.00%	R.TAFQLPGDAR.V		R.TAFQLPGDAR.V	
579	594	2	1900.9	-0.65	0	100	30.3	95.00%	E.IVAFFDHYFNGDQISK.I	Deamidation (+1)	K.YYEIVAFFDHYFNGDQISK.I	
401	415	2	1775.88	2.8	1	54.2	28.6	95.00%	R.TDIGVDWPFKQLDDK.D		R.TDIGVDWPFKQLDDK.D	
443	455	2	1402.78	1.5	1	83.6	23.5	95.00%	R.ELVGSHLVEPVPK.F		R.ELVGSHLVEPVPK.F	
444	455	2	1273.74	1.8	0	44.5	20.5	95.00%	E.LVGSHLVEPVPK.F		R.ELVGSHLVEPVPK.F	
416	426	2	1381.67	2.1	1	29.7	28.8	95.00%	K.DICRFPYAVLE.V	Carbamidomethyl (+57)	K.DICRFPYAVLEVK.L	
380	385	2	747.4	2.2	1	29.6	26.8	95.00%	E.LTMVRE.D		R.ISLDTELTMVREDNFDGVDR.T	
576	594	2	2355.08	-0.6	1	78.5	30.7	95.00%	K.YYEIVAFFDHYFNGDQISK.I		K.YYEIVAFFDHYFNGDQISK.I	
137	149	2	1531.93	2.1	1	30.8	12.8	95.00%	K.KTGFILKPVFQVR.L		K.KTGFILKPVFQVR.L	
459	470	2	1326.73	1.3	0	62.2	24.4	95.00%	K.FIHGVATLLNDK.V		K.FIHGVATLLNDK.V	
401	410	2	1176.59	2.8	0	54.4	28	95.00%	R.TDIGVDWPFK.Q		R.TDIGVDWPFK.Q	
598	606	2	1037.52	2.2	0	37.2	28.5	95.00%	K.GTTFDTQIR.A		K.GTTFDTQIR.A	
312	320	2	1069.54	-1.3	0	24.5	26.9	91.20%	K.YTVDQVFAK.M		K.YTVDQVFAK.M	
342	348	2	893.51	1.9	0	51.5	23.1	95.00%	E.IQYVMLK.K		K.KPMNEIENLEALASEIQYVMLK.K	
471	486	2	1929.96	-0.99	0	32.7	27.3	95.00%	K.VDSIPFWLPQMDVDIR.K		K.VDSIPFWLPQMDVDIR.K	
536	554	2	1889.88	0.1	0	71	30.3	95.00%	E.SVGYGATSAPTSNTNHVVE.S		R.SDNEDNDFDEDDEDDAALVAAM TNAPGNSLDIEESVGYGATSAPTSN TNHVVESANAAYYQR.K	
515	535	2	2131.96	0.59	1	65.3	30	95.00%	E.DDAALVAAMTNAPGNSLDIEE.S	Oxidation (+16)	R.SDNEDNDFDEDDEDDAALVAAM TNAPGNSLDIEESVGYGATSAPTSN TNHVVESANAAYYQR.K	
119	129	2	1359.7	2.6	1	40	27.7	95.00%	K.FSRLNYTGFQK.I		K.FSRLNYTGFQK.I	
400	410	2	1332.68	-1.1	1	34.8	27.6	95.00%	R.RTDIGVDWPFK.Q		R.RTDIGVDWPFK.Q	
267	280	2	1660.76	2	1	82.6	30.7	95.00%	R.WYGGMSTDTIFVER.K		R.WYGGMSTDTIFVER.K	
163	175	3	1516.9	2.4	1	54.5	16.7	95.00%	E.LVVKISQLYDIAR.T		K.ENYDELVVKISQLYDIAR.T	
567	574	2	871.44	-0.15	1	28.2	25	95.00%	R.NAENPISK.K		R.NAENPISK.K	
246	253	2	1013.48	1.7	0	26	27.8	92.50%	E.NLDLYYGR.L	Deamidation (+1)	R.EDSAITSIYFDNENLDLYYGR.L	
176	190	3	1416.73	-0.42	1	35.1	26.6	95.00%	R.TSGRPIKGDSSAGGK.Q		R.TSGRPIKGDSSAGGK.Q	
67	72	2	773.38	0.35	1	31.4	26.5	95.00%	K.HSEVFR.R		K.HSEVFR.R	
487	495	2	1007.57	3	0	23	24.8	92.00%	R.KPPLPTNIE.I		R.KPPLPTNIEITRPGR.S	
598	611	2	1487.78	2.1	1	32	27	95.00%	K.GTTFDTQIRAPPGK.T		K.GTTFDTQIRAPPGK.T	
201	210	2	1272.58	1.2	0	26.7	29.5	90.60%	K.YWVHPDNITE.L		K.YWVHPDNITELK.L	
420	428	2	1064.59	0.35	1	47.5	25.5	95.00%	R.FPYAVLEVK.L		R.FPYAVLEVK.L	
138	149	3	1403.83	3.6	0	58.5	16.5	95.00%	K.TGFILKPVFQVR.L		K.TGFILKPVFQVR.L	
122	129	2	969.49	1	0	47.2	26.5	95.00%	R.LNYTGFQK.I		R.LNYTGFQK.I	
555	563	2	1042.49	2.5	0	38.4	29.2	95.00%	E.SANAAYYQR.K		R.SDNEDNDFDEDDEDDAALVAAM TNAPGNSLDIEESVGYGATSAPTSN TNHVVESANAAYYQR.K	
87	100	2	1601.76	2.7	0	42.9	29.6	95.00%	R.LLDSNNPPTQLDFE.I		R.LLDSNNPPTQLDFEILEEELSDIIA DVHDLAK.F	
579	597	3	2239.13	1.5	1	24.3	27.1	95.00%	E.IVAFFDHYFNGDQISKIPK.G	Deamidation (+1)	K.YYEIVAFFDHYFNGDQISKIPK.G	
106	118	2	1408.76	1.8	0	74.6	25	95.00%	E.LSDIIADVHDLAK.F		R.LLDSNNPPTQLDFEILEEELSDIIA DVHDLAK.F	
14	26	2	1719.77	1.8	0	50.8	30.4	95.00%	R.QYSYYYISYDDLK.T		R.QYSYYYISYDDLK.T	
374	384	2	1276.67	3.6	1	57.4	27	95.00%	R.ISLDTELTMVR.E		R.ISLDTELTMVR.E	
167	175	2	1077.58	-0.47	0	46.9	25.5	95.00%	K.ISQLYDIAR.T		K.ISQLYDIAR.T	
197	210	2	1730.83	1.8	1	27.5	29.8	91.50%	R.QTTKYWVHPDNITE.L		R.QTTKYWVHPDNITELK.L	

612	622	2	1296.72	1.6	1	31	23.2	95.00%	K.TICVPVRVEPK.V	Carbamidomethyl (+57)	K.TICVPVRVEPK.V
233	245	2	1502.65	2.7	1	33	30.6	95.00%	R.EDSAITSIYFDNE.N		R.EDSAITSIYFDNENLDLYYGR.L
14	28	2	1949.86	2.1	1	51.6	30.7	95.00%	R.QYSYYYISYDDLKTE.L		R.QYSYYYISYDDLKTELEDNLSK.N
515	534	2	1986.92	1.9	0	51.7	29.5	95.00%	E.DDAALVAAMTNAPGNSLDIE.E		R.SDNEDNDFDEDDEDDAALVAAMTNAPGNSLDIEESVGYGATSAPTSNTNHVVESANAAYYQR.K
80	100	3	2450.22	2	1	31	26.8	95.00%	E.QVQHTVRLLDSNNPPTQLDFE.I		K.EVQEQVQHTVRLLDSNNPPTQLDFEILEEELSDIIADVHDLAK.F
218	229	2	1410.75	-0.38	1	57.4	26.1	95.00%	K.HLPVLVFNTNKE.F	Deamidation (+1)	K.HLPVLVFNTNKEFER.E
357	371	3	1741.86	1.8	1	34.2	28.7	95.00%	R.SFYNRTAFQLPGDAR.V		R.SFYNRTAFQLPGDAR.V
487	501	2	1687.97	-1.2	1	24.8	18.8	94.70%	R.KPPLPTNIEITRPGR.S		R.KPPLPTNIEITRPGR.S
218	228	2	1280.73	1.6	0	27.4	21.8	95.00%	K.HLPVLVFNTNK.E		K.HLPVLVFNTNK.E
459	486	3	3238.69	2.7	1	53	22.4	95.00%	K.FIHGVATLLNDKVDSIPFWLPQMDVDIR.K		K.FIHGVATLLNDKVDSIPFWLPQMDVDIR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
2	VTC3_YEAST	52.34%	100%	47

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
285	312	3	3404.59	0.061	0	54.8	29.6	95.00%	K.SVIFPQSYDPTITTLYFDNDFFDLYNNR.L		K.SVIFPQSYDPTITTLYFDNDFFDLYNNR.L
496	508	2	1566.67	3.3	0	53.2	29.9	95.00%	K.VINQDNSQMPNYE.W	Oxidation (+16)	K.VINQDNSQMPNYEWIK.D
821	835	2	1732.94	-1.3	0	37.9	23.4	95.00%	R.TLKPIQDFIFNLVGE.-		R.TLKPIQDFIFNLVGE.-
542	554	2	1617.85	3.7	0	56.3	27	95.00%	K.YVNILPFWLPDLE.T		K.YVNILPFWLPDLETDIR.K
365	372	2	1041.57	3.5	0	37.6	24.9	95.00%	K.FINNFIFK.N		K.FINNFIFK.N
330	340	2	1329.76	1.7	1	53.4	22.5	95.00%	K.LLDKPDIFLEK.R		K.LLDKPDIFLEK.R
316	323	2	813.47	-0.4	0	28.3	24.5	95.00%	K.ISGAPTLR.L		K.ISGAPTLR.L
63	70	2	984.53	4.3	0	26.3	25.6	95.00%	K.VYTFQISK.Y		K.VYTFQISK.Y
167	175	2	1202.63	-0.096	1	70.6	26.6	95.00%	R.ISYLYEFLR.S		R.ISYLYEFLR.S
173	186	4	1676.83	1.8	1	26.5	28.7	95.00%	E.FLRSNYDHPNTVSK.S		R.ISYLYEFLRSNYDHPNTVSK.S
487	495	2	1112.56	3.4	1	49	26.3	95.00%	K.FPYSVMEIK.V		K.FPYSVMEIK.V
641	649	2	1038.58	-6	1	28.3	23.1	95.00%	K.FKTNAAFLK.I		K.FKTNAAFLK.I
227	248	2	2470.17	2.5	1	65.7	29.3	95.00%	R.HLPALVYASVPNENDDFVDNLE.S		R.HLPALVYASVPNENDDFVDNLESDVR.V
659	681	2	2411.04	1.3	0	72.5	30.7	95.00%	E.NGNDPYSDDTDSASSFQLPPGVK.K	Deamidation (+1)	K.NISENGNDPYSDDTDSASSFQLPPGVK.K
143	148	2	715.42	-0.041	0	26.7	27.6	93.70%	K.SLLQVR.L	Deamidation (+1)	K.SLLQVR.L
807	820	2	1508.84	0.85	1	37.2	21.6	95.00%	E.RGLVNVSSQPSLPR.T		R.ERGLVNVSSQPSLPR.T
119	126	2	938.52	1.5	0	36	23.2	95.00%	R.LNFTGFIK.I		R.LNFTGFIK.I
176	186	2	1260.57	-0.33	0	33.5	29.7	95.00%	R.SNYDHPNTVSK.S		R.SNYDHPNTVSK.S
437	447	2	1323.68	-0.69	0	55.4	27.4	95.00%	R.VTIDSNIMYIR.E		R.VTIDSNIMYIR.E
363	372	2	1240.7	-0.35	1	27.7	22.8	95.00%	K.AKFINNFIFK.N		K.AKFINNFIFK.N
398	411	2	1708.85	2.4	1	42.5	28.6	95.00%	K.LSRDFDNIQNFIVE.E		K.LSRDFDNIQNFIVEEK.L
210	219	2	1304.55	2.7	0	38.4	30.5	95.00%	K.FWVHDDNIME.V		K.FWVHDDNIMEVK.A
365	378	2	1745.88	1.9	1	58.8	28	95.00%	K.FINNFIFKNDPSYK.N		K.FINNFIFKNDPSYK.N
7	16	2	1201.62	3.3	0	48.5	27.8	95.00%	K.LANDVYPPWK.D		K.LANDVYPPWK.D
512	524	2	1464.76	2.2	1	57	26.4	95.00%	K.DLTNSHLVNEVPK.F		K.DLTNSHLVNEVPK.F
194	206	2	1493.72	2	1	57.2	29	95.00%	K.LSHFSNLEDASFK.S		K.LSHFSNLEDASFK.S
401	411	2	1352.63	3.3	0	37.7	30.3	95.00%	R.DFDNIQNFIVE.E		R.DFDNIQNFIVEEK.L
330	339	2	1201.66	2.6	0	26.2	24.9	95.00%	K.LLDKPDIFLE.K		K.LLDKPDIFLEK.R
542	558	2	2103.1	-0.44	1	68.2	25	95.00%	K.YVNILPFWLPDLETDIR.K		K.YVNILPFWLPDLETDIR.K
265	282	2	1849.83	-1.3	1	98.2	30.4	95.00%	K.SNSLSSDGNSNQDVEIGK.S		K.SNSLSSDGNSNQDVEIGK.S
808	820	2	1352.74	0.88	0	41.5	23.8	95.00%	R.GLVNVSSQPSLPR.T		R.GLVNVSSQPSLPR.T
699	705	2	886.47	2.2	1	32.7	28.6	95.00%	K.VWLANER.T		K.VWLANER.T
577	586	3	1227.6	-0.57	1	20.7	27.7	90.10%	K.SIHDKLDNMR.R		K.SIHDKLDNMR.R
525	541	2	1887.92	-0.96	1	56.8	28.8	95.00%	K.FSLYLQGVASLFGEDDK.Y		K.FSLYLQGVASLFGEDDK.Y
437	448	2	1468.73	2.6	1	36.5	27.8	95.00%	R.VTIDSNIMYIRE.D	Oxidation (+16)	R.VTIDSNIMYIREDSLDK.N
210	221	2	1531.72	1.7	1	52.9	30.2	95.00%	K.FWVHDDNIMEVK.A		K.FWVHDDNIMEVK.A
17	24	2	1059.45	2	1	53.9	29	95.00%	K.DSYIDYER.L		K.DSYIDYER.L

113	126	2	1698.88	2.5	1	43.6	26.2	95.00%	R.LDNFDRLNFTGFIK.I		R.LDNFDRLNFTGFIK.I
379	386	2	1032.57	3.1	0	38.1	22.1	95.00%	K.NYLINQLR.E		K.NYLINQLR.E
39	47	2	1051.46	-0.11	1	32.8	28.3	95.00%	R.SSVDSWSER.N		R.SSVDSWSER.N
94	100	2	864.43	-0.37	1	30	28.5	95.00%	K.INSEQFK.N		K.INSEQFK.N
655	681	2	2854.24	-0.19	1	59.3	30.4	95.00%	K.NISENGNDPYSDDTDSASSFQLPPGVK.K	Deamidation (+1)	K.NISENGNDPYSDDTDSASSFQLPPGVK.K
401	412	2	1481.67	3	1	42.7	30	95.00%	R.DFDNIQNFIVEE.K		R.DFDNIQNFIVEEK.L
425	436	2	1331.69	3.2	0	47.9	27.4	95.00%	R.TAFQIPGDQSIR.V		R.TAFQIPGDQSIR.V
496	511	2	1993.93	2.8	1	78	30.3	95.00%	K.VINQDNSQMPNYEWIK.D	Oxidation (+16)	K.VINQDNSQMPNYEWIK.D
462	477	2	1960.95	1.6	1	62	28.3	95.00%	E.NWHRDDIDSNIPNPLR.F		R.NPENWHRDDIDSNIPNPLR.F
588	597	2	1122.57	-0.31	1	27.6	27.6	94.90%	R.LSKISVPDGK.T	Phospho (+80)	R.LSKISVPDGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
3	A6ZPA7_YEAS7	42.14%	100%	35

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
136	142	2	937.41	0.71	1	26.1	28.3	91.80%	K.NDLEQYR.F	Deamidation (+1)	K.NDLEQYR.F
353	359	2	788.42	0.095	1	56	29.7	95.00%	R.LGEMIAR.L		R.LGEMIAR.L
14	24	2	1337.67	4.3	0	41.4	28.3	95.00%	E.MALVQFYIPQE.I		R.SAEMALVQFYIPQEISR.D
196	205	2	1227.7	-0.5	1	59.4	24.1	95.00%	K.VATLEQILWR.V		K.VATLEQILWR.V
121	132	2	1404.65	2.1	1	47.4	29.4	95.00%	R.LIQMEDATDQIE.V		R.LIQMEDATDQIEVQK.N
255	268	2	1540.66	2.8	0	97.8	30.4	95.00%	E.SLDANLYDVDSSNE.G		K.IAESLDANLYDVDSSNEGR.S
28	47	3	2224.16	2.8	1	41.4	25.7	95.00%	R.DSAYTLGQLGLVQFRDLNSK.V		R.DSAYTLGQLGLVQFRDLNSK.V
151	166	2	1868.78	2.3	1	82.1	31.2	95.00%	E.FFLKGDNTDSTSYMDE.D		R.FILQSGDEFFLKGDNTDSTSYMDEDMIDANGENIAAAIGASVNYVTGVIAR.D
167	193	2	2705.34	3.8	1	122	26.4	95.00%	E.DMIDANGENIAAAIGASVNYVTGVIAR.D	Deamidation (+1)	K.GDNTDSTSYMDEDMIDANGENIAAAIGASVNYVTGVIAR.D
54	60	2	877.47	1.4	1	44.8	27	95.00%	R.TFVNEIR.R		R.TFVNEIR.R
140	150	2	1354.65	1.9	1	40	29.1	95.00%	E.QYRFILQSGDE.F		K.NDLEQYRFILQSGDEFFLK.G
360	382	2	2569.37	3	0	61.8	22.5	95.00%	R.LGIDVPSIIQVLDTNHTPPTFHR.T		R.LGIDVPSIIQVLDTNHTPPTFHR.T
386	403	2	2155.95	2.7	0	93.4	30.1	95.00%	K.FTAGFQSICDCYGIAQYR.E	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.FTAGFQSICDCYGIAQYR.E
829	840	2	1022.49	4.8	0	49	28.1	95.00%	E.VAVASASSSASS.-		K.DMEVAVASASSSASS.-
28	42	3	1666.87	-0.11	0	59.2	26.7	95.00%	R.DSAYTLGQLGLVQFR.D		R.DSAYTLGQLGLVQFR.D
383	403	2	2499.14	1.7	1	70	30.1	95.00%	R.TNKFTAGFQSICDCYGIAQYR.E	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.TNKFTAGFQSICDCYGIAQYR.E
234	247	2	1572.87	-0.97	0	46.4	23.2	95.00%	K.NAFIVFSHGDLIIK.R		K.NAFIVFSHGDLIIK.R
98	112	2	1678.86	2.6	0	61.2	27.2	95.00%	E.LYVPPSGSVIDDYVR.N		K.YLDGSGELYVPPSGSVIDDYVR.N
209	214	2	724.39	-0.6	0	33	25.8	95.00%	R.GNLFFK.T		R.GNLFFK.T
699	721	3	2477.17	2.9	1	23	29.3	91.60%	E.VGSGSHGEDFGDIMIHQVIHTIE.F		K.SHEPLPSTEADASSEDLEAQQLISAMDADDAEEEEVGSGSHGEDFGDIMIHQVIHTIEFCLNCVSHTASYLR.L
280	289	2	1164.64	0.25	0	44.1	23.8	95.00%	K.NLSDLYTVLK.T		K.NLSDLYTVLK.T
234	248	3	1728.97	-0.58	1	34.2	19.7	95.00%	K.NAFIVFSHGDLIIKR.I		K.NAFIVFSHGDLIIKR.I
305	315	2	1394.65	2.2	1	68.5	29.4	95.00%	K.ELDSWFQDVTR.E		K.ELDSWFQDVTR.E
206	214	3	1092.65	1.1	1	19.6	18.8	93.50%	R.VLRGNLFFK.T		R.VLRGNLFFK.T
86	97	2	1255.52	2	1	53.3	29.6	95.00%	E.GDTDKYLDGSGE.L		K.LYEGDTDKYLDGSGELYVPPSGSVIDDYVR.N
175	193	2	1859.04	4.6	0	113	17.6	95.00%	E.NIAAAIGASVNYVTGVIAR.D		K.GDNTDSTSYMDEDMIDANGENIAAAIGASVNYVTGVIAR.D
527	536	2	1155.59	2.1	0	28.7	26.8	95.00%	E.NALLFSNSYK.M		K.GESITATSVGTYPIGLDWAWHGTENALLFSNSYK.M
14	27	2	1693.89	2.9	1	43.1	25.9	95.00%	E.MALVQFYIPQEISR.D		R.SAEMALVQFYIPQEISR.D
143	154	2	1442.74	-0.23	1	39.9	27.7	95.00%	R.FILQSGDEFFLK.G		R.FILQSGDEFFLK.G
91	112	2	2400.14	-2.2	1	27.7	29.1	93.00%	K.YLDGSGELYVPPSGSVIDDYVR.N		K.YLDGSGELYVPPSGSVIDDYVR.N

334	343	2	1166.69	3.5	1	42.4	19.1	95.00%	K.ILIAEGWIPR.D		K.ILIAEGWIPR.D
505	526	2	2361.13	1.5	0	50.1	29.3	95.00%	E.SITATSVGTYPIGLDWAWHGTE.N		K.GESITATSVGTYPIGLDWAWHGTENALLFSNSYK.M
318	325	2	946.55	-0.031	1	39.5	23	95.00%	K.AIFEILNK.S		K.AIFEILNK.S
344	352	2	1015.53	1.3	1	58.2	26.1	95.00%	R.DELATLQAR.L		R.DELATLQAR.L
255	270	2	1753.78	1.4	1	86.5	30.4	95.00%	E.SLDANLYDVDSSNEGR.S		K.IAESLDANLYDVDSSNEGR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
4	PMA1_YEAST	36.93%	100%	33

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
660	682	3	2328.31	3.9	1	23.9	17.1	95.00%	R.SAADIVFLAPGLSAIIDALKTSR.Q		R.SAADIVFLAPGLSAIIDALKTSR.Q
388	414	2	2944.44	4.1	1	78.6	27.8	95.00%	K.LSLHEPYTVEGVSPDDLMLTACLAASR.K	Carbamidomethyl (+57)	K.LSLHEPYTVEGVSPDDLMLTACLAASR.K
196	205	2	1081.6	2.3	0	36	21.5	95.00%	E.VVPGDILQLE.D		R.DGQLVEIPANEVVPGDILQLEDGTVIPTDGR.I
526	546	2	2347.05	0.68	1	37	30.7	95.00%	E.ILGVMPCMDPPRDDTAQTVSE.A	Carbamidomethyl (+57)/ Oxidation (+16)	R.GEGHWEILGVMPCMDPPRDDTAQTVSEAR.H
79	92	2	1587.7	1.4	0	75.8	30.3	95.00%	E.YLQTDPSYGLTSDE.V		K.TYDDAASESSDDDDIDALIEELQSNHGVDDEDSDNDGPVAAGEARPVPEEYLQTDPSYGLTSDEVLK.R
175	184	2	1056.63	-0.3	0	53.9	21.8	95.00%	K.TLANTAVVIR.D		K.TLANTAVVIR.D
78	92	2	1716.74	1.9	1	80.4	30.4	95.00%	E.EYLQTDPSYGLTSDE.V		K.TYDDAASESSDDDDIDALIEELQSNHGVDDEDSDNDGPVAAGEARPVPEEYLQTDPSYGLTSDEVLK.R
568	582	2	1708.82	2.2	1	39.1	29.7	95.00%	E.TCRQLGLGTNIYNAE.R	Carbamidomethyl (+57)	K.ETCRQLGLGTNIYNAER.L
220	233	2	1595.72	1.6	0	67.7	30.1	95.00%	E.DCFLQIDQSAITGE.S	Carbamidomethyl (+57)	R.IVTEDCFLQIDQSAITGESLAVDK.H
256	271	2	1670.81	2	0	83.5	29.1	95.00%	E.GFMVVTATGDNTFVGR.A		R.GEGFMVVTATGDNTFVGR.A
445	456	2	1413.73	-0.66	1	30.9	27.2	95.00%	K.VLEFHPFDPVSK.K		K.VLEFHPFDPVSK.K
386	397	2	1428.73	1.3	1	56	27.1	95.00%	K.NKLSLHEPYTVE.G		K.NKLSLHEPYTVEGVSPDDLMLTACLAASR.K
240	252	2	1455.66	-0.69	0	70.9	29.9	95.00%	K.HYGDQTFSSSTVK.R		K.HYGDQTFSSSTVK.R
448	456	3	1072.54	1.7	0	28.2	27.8	95.00%	E.FHPFDPVSK.K		K.VLEFHPFDPVSK.K
899	909	2	1315.55	-0.039	1	80.1	29.2	95.00%	R.SVEDFMAAMQR.V	Oxidation (+16)/ Oxidation (+16)	R.SVEDFMAAMQR.V
475	482	2	843.52	0.085	0	23.4	24.6	92.70%	K.GAPLFVLK.T		K.GAPLFVLK.T
1	28	3	2868.27	6.4	1	36.9	30.9	95.00%	-.MTDTSSSSSSSSASSVSAHQPTQEKPAK.T	Acetyl (+42)/ Oxidation (+16)/ Deamidation (+1)	-.MTDTSSSSSSSSASSVSAHQPTQEKPAK.T
196	215	2	2093.11	2.1	1	36.9	23.5	95.00%	E.VVPGDILQLEDGTVIPTDGR.I		R.DGQLVEIPANEVVPGDILQLEDGTVIPTDGR.I
50	71	2	2239.91	0.44	1	73.4	30.6	95.00%	E.LQSNHGVDDEDSDNDGPVAAGE.A		K.TYDDAASESSDDDDIDALIEELQSNHGVDDEDSDNDGPVAAGEARPVPEEYLQTDPSYGLTSDEVLK.R
583	596	2	1301.61	1.3	1	47.2	29.5	95.00%	E.RLGLGGGGDMPGSE.L		R.QLGLGTNIYNAERLGLGGGGDMPGSELADFVENADGFAEVFPQHK.Y
398	414	2	1791.85	1.5	0	86.8	30.2	95.00%	E.GVSPDDLMLTACLAASR.K	Oxidation (+16)/ Carbamidomethyl (+57)	K.LSLHEPYTVEGVSPDDLMLTACLAASR.K
660	679	2	1984.13	3.9	0	71.4	18.1	95.00%	R.SAADIVFLAPGLSAIIDALK.T		R.SAADIVFLAPGLSAIIDALK.T
556	566	2	1074.58	3.2	0	57.6	26.6	95.00%	K.MLTGDAVGIAK.E		K.MLTGDAVGIAK.E
618	625	2	969.56	-0.33	1	33.8	21.2	95.00%	R.VVEILQNR.G		R.VVEILQNR.G
571	583	2	1447.75	2.8	1	85.2	27.5	95.00%	R.QLGLGTNIYNAER.L		R.QLGLGTNIYNAER.L
556	567	2	1203.62	0.73	1	26.6	27.8	93.50%	K.MLTGDAVGIAKE.T		K.MLTGDAVGIAKETCR.Q
2	24	2	2253.95	1.2	0	85	31.1	95.00%	M.TDTSSSSSSSSASSVSAHQPTQE.K		-.MTDTSSSSSSSSASSVSAHQPTQEKPAK.T
398	415	2	1903.95	1.5	1	82.6	28.1	95.00%	E.GVSPDDLMLTACLAASRK.K	Carbamidomethyl (+57)	K.LSLHEPYTVEGVSPDDLMLTACLAASRK.K

645	659	2	1416.69	1.4	1	87.4	28.6	95.00%	K.ADTGIAVEGATDAAR.S		K.ADTGIAVEGATDAAR.S
626	643	2	1806.89	2.6	0	103	29	95.00%	R.GYLVAMTGDGVNDAPSLK.K		R.GYLVAMTGDGVNDAPSLK.K
487	496	2	1186.53	0.82	1	36	29.6	95.00%	E.DHPIPEDVHE.N		K.TVEEDHPIPEDVHENYENK.V
206	219	2	1471.76	2	1	28.8	26.7	95.00%	E.DGTVIPTDGRIVTE.D		R.DGQLVEIPANEVVPGDILQLEDGTVIPTDGRIVTEDCFLQIDQSAITGESLAVDK.H
2	28	3	2758.19	-1	1	52	30.8	95.00%	M.TDTSSSSSSSSASSVSAHQPTQEKPAK.T	Phospho (+80)	-.MTDTSSSSSSSSASSVSAHQPTQEKPAK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
5	B3LLD7_YEAS1	20.78%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
481	492	2	1085.55	-0.29	0	40.9	27	95.00%	R.STAHGISAASGK.V		R.STAHGISAASGK.V
481	512	3	3160.65	2.5	1	76.7	21.1	95.00%	R.STAHGISAASGKVGAIIAQTALGTLIDHNCAR.D	Carbamidomethyl (+57)	R.STAHGISAASGKVGAIIAQTALGTLIDHNCAR.D
109	131	2	2280.22	5.2	0	122	22.3	95.00%	K.VSTSVGTVIGQFGFGTLADIVGR.K		K.VSTSVGTVIGQFGFGTLADIVGR.K
286	296	2	1101.5	3	1	29.1	27.2	95.00%	E.LAAAAQEQDGE.K		K.LELAAAAQEQDGEK.K
276	283	2	949.49	0.31	0	40.6	27.7	95.00%	R.YQLDVNAK.L		R.YQLDVNAK.L
315	328	2	1544.69	-0.81	1	55.2	29.6	95.00%	R.ASTAVESLDNHPPK.A	Phospho (+80)	R.ASTAVESLDNHPPK.A
561	569	2	1045.56	3.5	0	48.3	27.3	95.00%	E.IDPATLNFR.N		K.TLEEINELYHDEIDPATLNFR.N
298	305	2	943.43	1.9	1	46.4	27.3	95.00%	K.KIHDTSDE.D		K.KIHDTSDEDMAINGLER.A
306	314	2	1017.49	2.3	1	30.4	28.2	95.00%	E.DMAINGLER.A		K.IHDTSDEDMAINGLER.A
493	512	2	2093.11	0.0086	0	119	23.5	95.00%	K.VGAIIAQTALGTLIDHNCAR.D	Carbamidomethyl (+57)	K.VGAIIAQTALGTLIDHNCAR.D
57	64	2	948.48	1.5	0	39.4	27.9	95.00%	E.GFGWQQVK.T		R.LALESIDNEGFGWQQVK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
6	YBT1_YEAST	28.90%	100%	46

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
118	130	3	1403.72	0.92	1	25.3	27.4	95.00%	K.VNGEPHGTPEIVR.R		K.VNGEPHGTPEIVR.R
1616	1627	2	1490.75	2.9	1	41.6	27.8	95.00%	K.EYDHPYSLLLNK.Q		K.EYDHPYSLLLNK.Q
1457	1473	2	1830.01	-1.1	0	49	21.8	95.00%	R.SITIIPQDPTLFSGTIK.T		R.SITIIPQDPTLFSGTIK.T
670	680	2	1321.62	3.1	1	56.9	28.8	95.00%	R.VQDFLNENDTK.K		R.VQDFLNENDTK.K
1617	1627	3	1361.7	1.5	0	51.9	28.3	95.00%	E.YDHPYSLLLNK.Q		K.EYDHPYSLLLNK.Q
228	240	3	1519.83	1.3	0	23	24.4	95.00%	R.SIFIHHINSPISR.K		R.SIFIHHINSPISR.K
1584	1596	2	1471.78	2.6	1	60.5	25.7	95.00%	K.EFQGSTILTIAHR.L		K.EFQGSTILTIAHR.L
855	884	3	3431.56	2.2	0	48.3	29.5	95.00%	R.HVLLDDCLSAVDSHTASWIYDNCITGPLME.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.HVLLDDCLSAVDSHTASWIYDNCITGPLMEDR.T
764	790	2	2938.45	2.4	0	74.3	27.6	95.00%	E.LIVDANGTTNSIAYCSQAAWLLNDTVK.N	Deamidation (+1)/ Carbamidomethyl (+57)	R.QELIVDANGTTNSIAYCSQAAWLLNDTVK.N
936	951	2	1748.79	2.1	1	32	30.2	95.00%	K.SSILSRANSSANLAAK.S	Phospho (+80)/ Phospho (+80)	K.SSILSRANSSANLAAK.S
1422	1430	2	1020.6	-0.025	0	44.2	20.3	95.00%	K.STIITALFR.F		K.STIITALFR.F
14	25	2	1595.7	-0.82	0	70.4	30.4	95.00%	R.FWFYDDVTQYGR.T		R.FWFYDDVTQYGR.T
933	941	2	1081.59	2.2	1	30.8	24	95.00%	E.LVKSSILSR.A	Phospho (+80)	K.GLFGEDELVKSSILSR.A
1559	1576	2	1923.96	-2.7	1	80	26.9	95.00%	K.IILLDEATASIDYSSDAK.I		K.IILLDEATASIDYSSDAK.I
1381	1389	2	1057.58	2.8	1	45.4	26.1	95.00%	K.IEVNDLSLR.Y		K.IEVNDLSLR.Y
469	488	2	2036.07	3	0	40.3	25.6	95.00%	E.STSSANLGAIINLMAIDAFK.V		K.SINGDEESTSSANLGAIINLMAIDAFK.V
1565	1576	2	1227.57	3.3	0	65.8	28.9	95.00%	E.ATASIDYSSDAK.I		K.IILLDEATASIDYSSDAK.I
913	925	2	1485.75	2.3	1	63	27.1	95.00%	R.VKDQGDPIDMLQK.G		R.VKDQGDPIDMLQK.G
952	963	2	1282.62	3.2	0	42.4	29	95.00%	K.SSTSLSNLPAVK.E	Phospho (+80)	K.SSTSLSNLPAVK.E
887	900	3	1609.9	2.8	0	31.3	20.4	95.00%	R.TCILVSHNIALTLR.N	Carbamidomethyl (+57)	R.TCILVSHNIALTLR.N
714	720	2	877.46	3.4	1	29.9	29	95.00%	K.DLNIEFK.T		K.DLNIEFK.T
915	925	2	1258.59	2.6	0	33.5	29.2	95.00%	K.DQGDPIDMLQK.G		K.DQGDPIDMLQK.G
1247	1255	2	958.58	1.4	0	26.3	21	95.00%	E.TLVGVTTIR.A		R.SPIYQHFSETLVGVTTIR.A
549	556	2	901.46	0.53	0	29.2	27.5	95.00%	K.NLAVTDNR.I		K.NLAVTDNR.I
1370	1382	2	1503.77	0.98	1	48.9	27.4	95.00%	E.IPPPQWPQDGKIE.V		K.EIPPPQWPQDGKIEVNDLSLR.Y

80	100	2	2423.14	1.1	0	101	29.4	95.00%	E.QSPLINNNTITTNYVDNNCTK.D	Carbamidomethyl (+57)	K.NPIDELLYSSTDEDEQSPLINNNTITTNYVDNNCTK.D
427	436	2	1165.66	-0.44	1	29.7	21.6	95.00%	K.SIIISEIYTK.A		K.SIIISEIYTK.A
791	803	2	1535.74	1.9	1	53.3	29.5	95.00%	K.NNILFNSPFNEAR.Y	Deamidation (+1)	K.NNILFNSPFNEAR.Y
665	676	2	1433.72	2.7	1	28.1	28.2	94.80%	K.VSLDRVQDFLNE.N		K.VSLDRVQDFLNENDTK.K
1417	1430	3	1434.82	3.1	1	43.7	20.2	95.00%	R.TGAGKSTIITALFR.F		R.TGAGKSTIITALFR.F
694	705	2	1443.67	1.1	1	62.9	29.3	95.00%	R.FAFENSTISWDK.D		R.FAFENSTISWDK.D
1238	1255	2	2047.07	-1.2	1	68.1	25.9	95.00%	R.SPIYQHFSETLVGVTTIR.A		R.SPIYQHFSETLVGVTTIR.A
560	568	2	1060.57	2.9	1	58.5	25.7	95.00%	K.LNEAFQAIR.I		K.LNEAFQAIR.I
1152	1160	2	1010.48	0.95	0	73.2	29.7	95.00%	R.FFDATPTGR.I		R.FFDATPTGR.I
965	977	2	1488.66	2.5	0	49.2	30	95.00%	E.QQVSVNNNSSHFE.A		K.EQQVSVNNNSSHFEAK.K
1486	1492	2	847.48	-0.028	1	26.8	24.4	95.00%	R.QIFEALK.R		R.QIFEALK.R
1441	1453	2	1456.76	2.9	0	76.1	26.8	95.00%	K.IDNIDISGVDLQR.L		K.IDNIDISGVDLQR.L
1436	1453	2	1993.06	0.9	1	78.9	23.9	95.00%	E.TGHIKIDNIDISGVDLQR.L		R.FLEPETGHIKIDNIDISGVDLQR.L
1456	1473	2	1986.11	-1.2	1	64.8	18.9	95.00%	R.RSITIIPQDPTLFSGTIK.T		R.RSITIIPQDPTLFSGTIK.T
1474	1485	2	1470.63	3.2	1	49	30.1	95.00%	K.TNLDPYDEFSDR.Q		K.TNLDPYDEFSDR.Q
1400	1410	2	1180.56	-6.4	0	33.6	29	95.00%	K.NVSFSVDAQSK.I		K.NVSFSVDAQSK.I
964	977	2	1617.71	3	1	49.2	30.5	95.00%	K.EQQVSVNNNSSHFE.A		K.EQQVSVNNNSSHFEAK.K
681	693	2	1532.76	2	1	49.3	28.6	95.00%	K.KYDQLTIDPNGNR.F		K.KYDQLTIDPNGNR.F
855	886	3	3702.67	-1.2	1	61.3	30	95.00%	R.HVLLDDCLSAVDSHTASWIYDNCITGPLMEDR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.HVLLDDCLSAVDSHTASWIYDNCITGPLMEDR.T
1585	1596	2	1342.74	2.8	0	61.4	24.2	95.00%	E.FQGSTILTIAHR.L		K.EFQGSTILTIAHR.L
724	735	2	1140.65	-0.36	0	24.7	22.9	94.60%	K.LNVVIGPTGSGK.T		K.LNVVIGPTGSGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
7	A7A234_YEAS7	39.61%	100%	35

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
500	515	2	1889	2.5	1	64.6	25.4	95.00%	K.KHGQWLNDLTNSHLVK.E		K.KHGQWLNDLTNSHLVK.E
536	548	2	1597.88	3.7	1	35.3	22.7	95.00%	E.KLDILPFWLPDLE.T		K.FSIFVQGVASLYGDDEKLDILPFWLPDLETDIR.Q
94	102	2	1005.49	1.4	0	49.3	28.6	95.00%	K.ALDADAFQR.V		K.ALDADAFQR.V
208	217	2	1304.55	2.8	0	38.4	30.5	95.00%	K.FWVHNDNLME.V	Deamidation (+1)	K.FWVHNDNLMEVK.T
501	515	3	1760.9	2.9	0	60.9	26.6	95.00%	K.HGQWLNDLTNSHLVK.E		K.HGQWLNDLTNSHLVK.E
7	16	2	1215.63	-0.35	1	33.4	27.4	95.00%	K.LANEVYPPWK.G		K.LANEVYPPWK.G
419	429	2	1247.71	0.79	0	37.2	22	95.00%	R.VTIDSNIVFIK.E		R.VTIDSNIVFIK.E
144	149	2	715.42	-0.031	1	26.7	27.6	93.70%	K.SLLEVR.L		K.SLLEVR.L
273	286	2	1686.78	2.2	0	76.8	29.6	95.00%	R.SFDPLINTLYFDNE.H		R.SFDPLINTLYFDNEHFELYNDK.L
587	600	2	1547.72	1.7	1	36.9	29.6	95.00%	K.EPQHQAAVPVSQEE.N		K.EPQHQAAVPVSQEENER.I
17	26	2	1142.57	3.8	1	42.1	28.3	95.00%	K.GSYINYEGLK.K		K.GSYINYEGLK.K
469	477	2	1112.56	3.4	1	49	26.3	95.00%	K.FPYSVMEIK.V		K.FPYSVMEIK.V
347	357	2	1286.62	3.5	1	60.7	29.8	95.00%	K.FINGFIFEGDK.K	Deamidation (+1)	K.FINGFIFEGDK.K
797	806	2	1181.63	2.6	1	31.1	24.1	95.00%	E.LQIQNLEVPE.R		R.QELQIQNLEVPER.I
480	496	2	1745.79	2.3	0	87	31.4	95.00%	K.SSLDSSMSASSMISNVK.L	Oxidation (+16)	K.SSLDSSMSASSMISNVK.L
238	246	2	1120.52	1.7	1	47.2	29.6	95.00%	E.NDDLVNRFE.S		R.HLPVLVYANVPSENDDLVNRFESDISNNDEIVGSSSSTSSVEHGLGAR.S
72	78	2	938.43	-0.13	1	31	29.9	95.00%	K.YNNLMER.L		K.YNNLMER.L
191	204	2	1643.76	2	0	85.8	30	95.00%	K.FSSIVSNDIDMNFR.S		K.FSSIVSNDIDMNFR.S
167	175	2	1137.65	0.16	0	52	21.6	95.00%	R.ISFLYNILR.S		R.ISFLYNILR.S
308	322	2	1775.91	2.5	1	68.6	26.6	95.00%	R.WTGQLSDKPDIFLEK.K		R.WTGQLSDKPDIFLEK.K
208	219	2	1531.72	1.7	1	52.9	30.2	95.00%	K.FWVHNDNLMEVK.T	Deamidation (+1)	K.FWVHNDNLMEVK.T
811	821	2	1389.82	2.2	0	48.1	18	95.00%	E.VLRPLQNYLFK.L		R.IPEVLRPLQNYLFK.L
480	499	2	2068.02	0.68	1	45.4	28.2	95.00%	K.SSLDSSMSASSMISNVKLPK.K		K.SSLDSSMSASSMISNVKLPK.K
407	416	2	1090.53	3.4	0	47.6	28.4	95.00%	R.TAFQIPGDDK.I		R.TAFQIPGDDK.I
582	599	2	1974.02	0.96	1	68.2	25.9	95.00%	R.LSNLKEPQHQAAVPVSQE.E		R.LSNLKEPQHQAAVPVSQEENER.I
176	190	2	1522.73	0.77	0	87.7	29.6	95.00%	R.SNFNTASEPLASASK.F		R.SNFNTASEPLASASK.F
448	459	2	1269.66	3	0	58.3	27	95.00%	R.TDIDANVANPLK.F		R.TDIDANVANPLK.F

687	693	2	886.47	2.2	1	32.7	28.6	95.00%	K.VWLANER.T		K.VWLANER.T
662	669	2	851.51	2.1	1	25.2	18.6	95.00%	E.IELPPGVK.K		K.LMGVDSEEEEIELPPGVK.K
387	395	2	1117.62	2.3	1	54.3	24.9	95.00%	E.IQNFIIKNE.L		R.LEEDFSEIQNFIIKNELQPVFR.T
677	686	2	997.52	0.57	1	34.7	26	95.00%	K.NAGPVNVEAK.V		K.NAGPVNVEAK.V
273	289	2	2100.94	2.7	1	77.3	30.1	95.00%	R.SFDPLINTLYFDNEHFE.L	Deamidation (+1)	R.SFDPLINTLYFDNEHFELYNDK.L
306	321	2	1917	1.3	1	23.8	25.8	91.90%	R.LRWTGQLSDKPDIFLE.K		R.LRWTGQLSDKPDIFLEK.K
603	611	2	1017.51	3.9	1	27.3	27.6	94.50%	E.RITSQGDLE.A		K.EPQHQAAVPVSQEENERITSQGDLEADGSSDEETEQEPHSK.R
298	305	2	870.49	-0.83	0	38.2	23.8	95.00%	K.LNSAPTLR.L		K.LNSAPTLR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
8	A7A1M1_YEAS7	26.97%	100%	43

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
163	174	2	1475.77	2.6	1	54.2	27.3	95.00%	E.QIEDIFIDLTNR.L		-.MNTDQQPYQGQTDYTQGPDNGQSQEQDYDQYGQPLYPSQADGYYDPNVAAGTEADMYGQQPPNESYDQDYTNGEYYGQPPNMAAQDGENFSDFSSHGPPGTPGYDSYGGQYTPSQMSYGEPNSSGTSTPIYGNYDPNAIAMALPNEPYPAWTADSQSPVSIEQIEDIFIDLTNR.L
1047	1063	2	1944.94	1	1	69.2	28.6	95.00%	R.IYSALIDGHCEILDNGR.R	Carbamidomethyl (+57)	R.IYSALIDGHCEILDNGR.R
1779	1788	2	1213.72	2.1	0	23.2	21.2	92.30%	R.QIRPPIYSLK.Q		R.QIRPPIYSLK.Q
819	852	3	3814.94	3.1	1	53.8	23.3	95.00%	R.ISFFAQSLSTPIPEPLPVDNMPTFTVLTPHYAER.I		R.ISFFAQSLSTPIPEPLPVDNMPTFTVLTPHYAER.I
320	330	2	1450.67	2.8	1	42	29.9	95.00%	R.FTAECLCFIYK.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.FTAECLCFIYK.C
975	984	2	1064.5	2	0	28.4	29.6	93.30%	E.IVQMFGGNAE.G		R.VENPEIVQMFGGNAEGLER.E
387	405	2	2240.11	-1.9	1	47	28	95.00%	K.IVGYDDLNQLFWYPEGIAK.I		K.IVGYDDLNQLFWYPEGIAK.I
367	376	2	1205.61	2.2	1	28.3	28.5	94.70%	R.NQVYEIIDGR.F		R.NQVYEIIDGR.F
1161	1173	2	1215.61	1.8	1	68.6	27.2	95.00%	E.NSGVLGDVAAGKE.Q		R.EYIFSENSGVLGDVAAGKEQTFGTLFAR.T
1047	1057	2	1276.58	1.7	0	64.6	30.2	95.00%	R.IYSALIDGHCE.I	Carbamidomethyl (+57)	R.IYSALIDGHCEILDNGR.R
426	437	2	1438.72	3	0	70.7	28.4	95.00%	R.LGDVVWDDVFFK.T		R.LGDVVWDDVFFK.T
1262	1273	2	1248.6	2.9	1	86.4	28.9	95.00%	K.IGAGMGEQMLSR.E		K.IGAGMGEQMLSR.E
75	88	2	1539.63	0.19	0	40.8	29.9	95.00%	E.YYGQPPNMAAQDGE.N		-.MNTDQQPYQGQTDYTQGPDNGQSQEQDYDQYGQPLYPSQADGYYDPNVAAGTEADMYGQQPPNESYDQDYTNGEYYGQPPNMAAQDGENFSDFSSHGPPGTPGYDSYGGQYTPSQMSYGEPNSSGTSTPIYGNYDPNAIAMALPNEPYPAWTADSQSPVSIEQIEDIFIDLTNR.L
789	805	2	1999.93	1.9	1	89.2	30.2	95.00%	R.TLRAPTFFVSQDDNNFE.T		R.TLRAPTFFVSQDDNNFETEFFPR.D
1222	1232	2	1253.59	3.1	0	51.8	29.9	95.00%	E.DIYAGMNAMLR.G		K.GLHLNEDIYAGMNAMLR.G
1183	1207	4	2804.41	0.048	1	18.4	27.1	93.10%	R.TLSQIGGKLHYGHPDFINATFMTTR.G		R.TLSQIGGKLHYGHPDFINATFMTTR.G
1142	1154	2	1362.74	0.87	0	46.5	25.3	95.00%	E.QTTNHPVAIVGAR.E		R.YEEQTTNHPVAIVGAR.E
1173	1182	2	1168.59	-0.28	1	52.2	27.4	95.00%	K.EQTFGTLFAR.T		K.EQTFGTLFAR.T
383	401	2	2365.11	2.4	1	49.7	30.1	95.00%	R.DHNKIVGYDDLNQLFWYPE.G		R.DHNKIVGYDDLNQLFWYPEGIAK.I
1083	1096	2	1662.78	1.8	1	37.3	29.7	95.00%	K.SDNQNHALIFYRGE.Y		K.SDNQNHALIFYRGEYIQLIDANQDNYLEECLK.I

166	174	2	1105.58	3.3	0	40.1	27.9	95.00%	E.DIFIDLTNR.L		- .MNTDQQPYQGQTDYTQGPDNGQ SQEQDYDQYGQPLYPSQADGYYD PNVAAGTEADMYGQQPPNESYDQ DYTNGEYYGQPPNMAAQDGENFS DFSSHGPPGTPGYDSYGGQYTPS QMSYGEPNSSGTSTPIYGNYDPNAI AMALPNEPYPAWTADSQSPVSIEQI EDIFIDLTNR.L
1191	1207	2	2019.97	2.4	0	79.1	28.7	95.00%	K.LHYGHPDFINATFMTTR.G		K.LHYGHPDFINATFMTTR.G
200	223	3	2607.27	1.9	1	61.4	27.6	95.00%	R.MSPDQALLSLHADYIGGDTANYK K.W		R.MSPDQALLSLHADYIGGDTANYK K.W
1436	1444	2	1094.62	3.4	0	52.9	24	95.00%	R.IPFSILYSR.F		R.IPFSILYSR.F
1	25	3	2888.13	-1.5	0	40.2	30.3	95.00%	- .MNTDQQPYQGQTDYTQGPDNGQ SQE.Q	Acetyl (+42)/ Oxidation (+16)/ Deamidation (+1)	- .MNTDQQPYQGQTDYTQGPDNGQ SQEQDYDQYGQPLYPSQADGYYD PNVAAGTEADMYGQQPPNESYDQ DYTNGEYYGQPPNMAAQDGENFS DFSSHGPPGTPGYDSYGGQYTPS QMSYGEPNSSGTSTPIYGNYDPNAI AMALPNEPYPAWTADSQSPVSIEQI EDIFIDLTNR.L
1097	1111	2	1839.86	2.1	1	69	29.7	95.00%	E.YIQLIDANQDNYLEE.C		R.GEYIQLIDANQDNYLEECLK.I
1249	1261	2	1425.75	-0.019	0	69.1	26.3	95.00%	R.DLGFGTILNFTTK.I		R.DLGFGTILNFTTK.I
1070	1082	2	1296.71	0.92	0	44.2	23.9	95.00%	R.VQLSGNPILGDGK.S		R.VQLSGNPILGDGK.S
1141	1154	2	1491.78	0.39	1	47.8	27	95.00%	E.EQTTNHPVAIVGAR.E		R.YEEQTTNHPVAIVGAR.E
26	53	2	3124.33	2	0	35.5	30.7	95.00%	E.QDYDQYGQPLYPSQADGYYDPN VAAGTE.A		- .MNTDQQPYQGQTDYTQGPDNGQ SQEQDYDQYGQPLYPSQADGYYD PNVAAGTEADMYGQQPPNESYDQ DYTNGEYYGQPPNMAAQDGENFS DFSSHGPPGTPGYDSYGGQYTPS QMSYGEPNSSGTSTPIYGNYDPNAI AMALPNEPYPAWTADSQSPVSIEQI EDIFIDLTNR.L
331	344	2	1737.78	0.32	0	100	30	95.00%	K.CALDYLDSPLCQQR.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CALDYLDSPLCQQR.Q
184	196	2	1623.75	-0.75	0	75.1	30.1	95.00%	R.NMFDHFMVLLDSR.S		R.NMFDHFMVLLDSR.S
916	929	2	1701.81	-0.99	0	58.6	29.5	95.00%	K.SQIDDLPFYCIGFK.S	Carbamidomethyl (+57)	K.SQIDDLPFYCIGFK.S
792	805	2	1629.7	2.4	0	50.8	30.3	95.00%	R.APTFFVSQDDNNFE.T		R.APTFFVSQDDNNFETEFFPR.D
1717	1728	2	1383.61	3.3	0	66.4	30.1	95.00%	K.GMGYMAWTQPSR.E		K.GMGYMAWTQPSR.E
293	301	2	1086.55	3.5	1	25.1	27.5	91.40%	K.MNQLSPLER.V		K.MNQLSPLER.V
200	222	3	2479.17	2	0	52.4	29.4	95.00%	R.MSPDQALLSLHADYIGGDTANYK. K		R.MSPDQALLSLHADYIGGDTANYK. K
792	807	2	1859.79	2	1	47.9	30.7	95.00%	R.APTFFVSQDDNNFETE.F		R.APTFFVSQDDNNFETEFFPR.D
1520	1527	2	993.5	0.087	0	45.7	28.7	95.00%	R.NSWIGYVR.M		R.NSWIGYVR.M
953	962	2	1174.55	2	0	46.4	29.4	95.00%	R.TISGFMNYSR.A		R.TISGFMNYSR.A
870	877	2	977.58	3.3	1	51.5	19.9	95.00%	R.VTLLEYLK.Q		R.VTLLEYLK.Q
54	74	2	2437.92	0.98	1	46.7	29.5	95.00%	E.ADMYGQQPPNESYDQDYTNGE. Y	Oxidation (+16)/ Deamidation (+1)	- .MNTDQQPYQGQTDYTQGPDNGQ SQEQDYDQYGQPLYPSQADGYYD PNVAAGTEADMYGQQPPNESYDQ DYTNGEYYGQPPNMAAQDGENFS DFSSHGPPGTPGYDSYGGQYTPS QMSYGEPNSSGTSTPIYGNYDPNAI AMALPNEPYPAWTADSQSPVSIEQI EDIFIDLTNR.L
1174	1182	2	1039.55	2.4	0	27.7	24.8	95.00%	E.QTFGTLFAR.T		K.EQTFGTLFAR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
9	A6ZY95_YEAS7	27.19%	100%	37

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
620	638	2	2117.05	-1.4	0	36.1	27.7	95.00%	K.NIGDVAINIGDDATFLWQR.K		K.NIGDVAINIGDDATFLWQR.K
1053	1066	3	1609.85	3.7	1	29.7	25	95.00%	R.FSNDIYKVDALLGR.T		R.FSNDIYKVDALLGR.T
221	231	2	1299.64	-0.32	0	72.8	29.6	95.00%	R.ITFSWMSGLMK.T		R.ITFSWMSGLMK.T
1036	1048	2	1466.73	2.8	1	60.5	28	95.00%	R.APMTFFETTPIGR.I		R.APMTFFETTPIGR.I
1349	1364	2	1787.95	2.3	1	34.5	24.6	95.00%	K.LSIIPQDSQVFEGTVR.E		K.LSIIPQDSQVFEGTVR.E
1365	1376	2	1449.63	3.1	1	39.4	30.5	95.00%	R.ENIDPINQYTDE.A		R.ENIDPINQYTDEAIWR.A
1340	1346	2	848.48	1.5	0	51	25.9	95.00%	E.IGLYDLR.H		R.MIEASEGNIVIDNIAINEIGLYDLR.H
1436	1446	2	1118.55	3.9	1	41.4	28	95.00%	E.ATAAVDVETDK.V		K.ILVLDEATAAVDVETDK.V
790	805	2	1777	0.61	1	83.5	19.4	95.00%	R.HLIEHVLGPNGLLHTK.T		R.HLIEHVLGPNGLLHTK.T
1159	1174	2	1825.85	3.1	0	50.7	30	95.00%	R.IDNNMSAFYPSINANR.W		R.IDNNMSAFYPSINANR.W
486	495	2	1141.67	3.6	1	67.1	22.8	95.00%	R.VISEILNNIK.S		R.VISEILNNIK.S
670	682	2	1495.75	-0.73	0	73.1	27.9	95.00%	K.TALLSCMLGDLFR.V	Carbamidomethyl (+57)	K.TALLSCMLGDLFR.V
1347	1360	2	1639.86	2.1	1	39.4	25.7	95.00%	R.HKLSIIPQDSQVFE.G		R.HKLSIIPQDSQVFEGTVR.E
1389	1405	2	1857.84	1.6	1	59.9	30.5	95.00%	K.EHVLSMSNDGLDAQLTE.G		K.EHVLSMSNDGLDAQLTEGGGNLSVGQR.Q
1281	1290	3	1244.72	2.8	1	43.5	22.1	95.00%	R.YRPELDLVLK.H		R.YRPELDLVLK.H
840	850	3	1272.67	1.5	1	27.1	27.8	95.00%	E.ITKDADSPLWK.L		K.VSALSIADSIALLDNGEITQQGTYDEITKDADSPLWK.L
655	664	2	1088.6	-0.72	1	27.5	25.1	95.00%	K.KGNLTCIVGK.V	Carbamidomethyl (+57)	K.KGNLTCIVGK.V
1485	1499	2	1618.79	2.6	1	74.9	29.1	95.00%	K.VAEFDSPGQLLSDNK.S		K.VAEFDSPGQLLSDNK.S
794	805	3	1285.72	2.2	0	55.2	25.3	95.00%	E.HVLGPNGLLHTK.T	Deamidation (+1)	R.HLIEHVLGPNGLLHTK.T
192	206	4	1836	2.5	0	28.3	22.1	95.00%	K.KPLMPHQHIHQTLTR.R		K.KPLMPHQHIHQTLTR.R
271	281	2	1289.62	1.9	0	49	28.6	95.00%	K.SNPSLSWAICR.T	Carbamidomethyl (+57)	K.SNPSLSWAICR.T
771	785	2	1619.76	2.6	0	53.4	29.6	95.00%	R.ADTYLLDDPLAAVDE.H		R.ADTYLLDDPLAAVDEHVAR.H
771	789	2	2083.02	-2.4	1	97.8	28	95.00%	R.ADTYLLDDPLAAVDEHVAR.H		R.ADTYLLDDPLAAVDEHVAR.H
1458	1467	3	1194.68	-0.5	1	38.8	20.8	95.00%	K.DRTILTIAHR.L		K.DRTILTIAHR.L
1126	1143	2	1975.02	2.9	1	90.5	26.3	95.00%	R.SPIYSHFQETLGGLATVR.G		R.SPIYSHFQETLGGLATVR.G
1313	1321	2	1006.58	3.4	0	41.4	22.3	95.00%	K.SSLTLALFR.M		K.SSLTLALFR.M
1406	1415	2	943.49	2.7	0	38.9	27.1	95.00%	E.GGGNLSVGQR.Q		K.EHVLSMSNDGLDAQLTEGGGNLSVGQR.Q
1366	1376	2	1320.59	1.7	0	48.1	29.9	95.00%	E.NIDPINQYTDE.A		R.ENIDPINQYTDEAIWR.A
1460	1467	2	923.55	-1.9	0	32.8	18.5	95.00%	R.TILTIAHR.L		R.TILTIAHR.L
891	905	2	1728.78	2.8	0	45.4	30.3	95.00%	K.LNDLDFGNSDAISLR.R	Phospho (+80)	K.LNDLDFGNSDAISLR.R
2	11	2	1104.54	3.3	0	55.8	28.4	95.00%	M.AGNLVSWACK.L	Carbamidomethyl (+57)	-.MAGNLVSWACK.L
1468	1484	2	1916.01	2.5	1	73.1	25.2	95.00%	R.LNTIMDSDRIIVLDNGK.V		R.LNTIMDSDRIIVLDNGK.V
728	743	2	1718.86	-1.6	0	79.2	27.5	95.00%	K.ACALTIDLAILMDGDK.T	Carbamidomethyl (+57)	K.ACALTIDLAILMDGDK.T
207	220	2	1663.85	2.4	1	61.1	28.7	95.00%	R.RKPNPYDSANIFSR.I		R.RKPNPYDSANIFSR.I
1416	1422	2	872.49	-0.56	0	28.1	27.7	95.00%	R.QLLCLAR.A	Carbamidomethyl (+57)	R.QLLCLAR.A
1381	1388	2	909.52	-7.3	1	35.3	19.5	95.00%	R.ALELSHLK.E		R.ALELSHLK.E
379	388	2	1106.63	-0.37	0	29.1	21.6	95.00%	K.SALTALIYQK.S		K.SALTALIYQK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
10	A6ZL63_YEAS7	51.75%	100%	22

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
85	100	2	1857.98	1	1	65.9	25.2	95.00%	K.YQVTVIDAPGHRDFIK.N		K.YQVTVIDAPGHRDFIK.N
267	286	2	1974.05	1.2	0	49.4	23.6	95.00%	E.TGVIKPGMVVTFAPAGVTTE.V		R.VETGVIKPGMVVTFAPAGVTTEVK.S
299	311	2	1329.67	1.6	0	35.9	28.7	95.00%	E.QGVPGDNVGFNVK.N		K.SVEMHHEQLEQGVPGDNVGFNVK.N
185	210	2	2907.4	2.4	1	73.5	29.1	95.00%	K.TVPFVPISGWNGDNMIEATTNAPWYK.G		K.TVPFVPISGWNGDNMIEATTNAPWYK.G
265	286	2	2202.17	3	1	66.3	24	95.00%	R.VETGVIKPGMVVTFAPAGVTTE.V		R.VETGVIKPGMVVTFAPAGVTTEVK.S
412	421	2	1135.57	2.1	1	33.1	29	95.00%	E.AFSEYPPLGR.F		K.FVPSKPMCVEAFSEYPPLGR.F

185	201	2	1874.89	3.5	0	64.5	29.5	95.00%	K.TVPFVPISGWNGDNMIE.A		K.TVPFVPISGWNGDNMIEATTNAPWYK.G
254	266	2	1252.71	-0.096	1	49.8	21.7	95.00%	K.IGGIGTVPVGRVE.T		K.IGGIGTVPVGRVETGVIKPGMVVTFAPAGVTTEVK.S
85	96	2	1354.7	2.5	0	66.3	26.7	95.00%	K.YQVTVIDAPGHR.D		K.YQVTVIDAPGHR.D
394	401	2	759.41	-0.42	0	45.9	27.5	95.00%	K.SGDAALVK.F		K.SGDAALVK.F
56	64	2	1134.65	2.6	1	33.6	22.2	95.00%	K.YAWVLDKLK.A		K.YAWVLDKLK.A
147	154	2	883.55	-0.35	0	43.7	20.4	95.00%	R.QLIVAVNK.M		R.QLIVAVNK.M
329	369	4	4444.12	-0.85	1	53.5	24.4	95.00%	K.NDPPKGCASFNATVIVLNHPGQISAGYSPVLDCHTAHIACR.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.NDPPKGCASFNATVIVLNHPGQISAGYSPVLDCHTAHIACR.F
254	264	2	1024.61	3.2	0	65.4	18.3	95.00%	K.IGGIGTVPVGR.V		K.IGGIGTVPVGR.V
267	288	2	2201.22	0.99	1	72.2	20.8	95.00%	E.TGVIKPGMVVTFAPAGVTTEVK.S		R.VETGVIKPGMVVTFAPAGVTTEVK.S
429	437	2	913.56	0.54	0	47.8	21.3	95.00%	R.QTVAVGVIK.S		R.QTVAVGVIK.S
6	20	2	1559.84	1.5	0	87.7	24.6	95.00%	K.SHINVVVIGHVDSGK.S		K.SHINVVVIGHVDSGK.S
402	411	2	1192.56	1.8	0	28.1	28.9	93.80%	K.FVPSKPMCVE.A	Carbamidomethyl (+57)	K.FVPSKPMCVEAFSEYPPLGR.F
135	146	2	1325.75	-0.022	1	62.4	23	95.00%	R.EHALLAFTLGVR.Q		R.EHALLAFTLGVR.Q
334	369	5	3892.86	0.25	0	25.3	27.8	95.00%	K.GCASFNATVIVLNHPGQISAGYSPVLDCHTAHIACR.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GCASFNATVIVLNHPGQISAGYSPVLDCHTAHIACR.F
246	253	2	974.55	3.5	0	30	26.6	95.00%	R.LPLQDVYK.I		R.LPLQDVYK.I
229	245	3	1906.03	0.15	1	32.2	24.1	95.00%	E.AIDAIEQPSRPTDKPLR.L		K.TLLEAIDAIEQPSRPTDKPLR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
11	B3LFI5_YEAS1	52.30%	100%	30

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
172	187	2	1765.83	1.4	0	73.2	28.7	95.00%	R.ITDATPASFSSHVDYR.W		R.ITDATPASFSSHVDYR.W
452	466	2	1679.85	1.4	0	79.8	27.8	95.00%	E.TLIHLDDNANAIQDK.L		K.DLGIYDYTDSDLETLIHLDDNANAIQDK.L
467	474	2	996.47	1.4	0	33.9	29.4	95.00%	K.LNDMVSFR.A	Oxidation (+16)	K.LNDMVSFR.A
439	466	3	3179.49	3.2	1	48.8	28.8	95.00%	K.DLGIYDYTDSDLETLIHLDDNANAIQDK.L		K.DLGIYDYTDSDLETLIHLDDNANAIQDK.L
244	255	2	1380.61	1.9	0	68.8	30.7	95.00%	E.AQSNGWQYVGDR.K	Deamidation (+1)	R.DLIDEAQSNGWQYVGDR.K
376	383	2	789.44	2.1	0	40.6	26	95.00%	E.TGGLVTSR.Q		R.EVLAFDEAFQYVLEFAENSDTETVLVSTSDHETGGLVTSR.Q
191	205	2	1681.88	1.8	1	60.5	24.9	95.00%	E.DLIATHQLGEYPLGR.V		R.WQEDLIATHQLGEYPLGR.V
499	513	2	1745.8	2.2	0	32.9	30.8	95.00%	K.ATWSYVLNNLQGNHE.N	Deamidation (+1)	K.ATWSYVLNNLQGNHENTEVGQFLENFLELNLSEVTDLIR.D
475	498	3	2643.33	3.2	1	55.4	26	95.00%	R.AQIGWTTHGHSAVDVNIYAYANKK.A		R.AQIGWTTHGHSAVDVNIYAYANKK.A
136	158	3	2448.2	2.4	1	45.5	27.6	95.00%	K.SYNGAIGVDPHHRPCGTVLEAAK.L	Carbamidomethyl (+57)	K.SYNGAIGVDPHHRPCGTVLEAAK.L
159	171	2	1362.79	2.6	0	69.1	19.4	95.00%	K.LAGYLTGLVVTTR.I		K.LAGYLTGLVVTTR.I
136	155	2	2179.02	1.7	0	54	30.5	95.00%	K.SYNGAIGVDPHHRPCGTVLE.A	Deamidation (+1)/ Carbamidomethyl (+57)	K.SYNGAIGVDPHHRPCGTVLEAAK.L
329	344	3	1772.82	3	1	31.8	29.9	95.00%	R.IDHAGHQNDPASQVRE.V		R.IDHAGHQNDPASQVREVLAFDEAFQYVLEFAENSDTETVLVSTSDHETGGLVTSR.Q
452	474	4	2658.31	2.5	1	20.9	27.7	95.00%	E.TLIHLDDNANAIQDKLNDMVSFR.A	Oxidation (+16)	K.DLGIYDYTDSDLETLIHLDDNANAIQDKLNDMVSFR.A
87	105	2	2197.06	2.4	0	67.5	28.6	95.00%	R.SFNQHVNDLPIDDILTLDE.H		R.SFNQHVNDLPIDDILTLDEHFIGSSR.T
206	215	2	1031.54	-0.9	0	57.7	28.2	95.00%	R.VVDLLMGGGR.S	Oxidation (+16)	R.VVDLLMGGGR.S
67	86	3	2140.08	-1.6	1	41	27.4	95.00%	K.KNVIFFVTDGMGPASLSMAR.S		K.KNVIFFVTDGMGPASLSMAR.S
329	343	3	1643.78	-0.36	0	26.3	29.9	95.00%	R.IDHAGHQNDPASQVR.E		R.IDHAGHQNDPASQVR.E
439	451	2	1517.64	2	0	40.9	30.4	95.00%	K.DLGIYDYTDSDLE.T		K.DLGIYDYTDSDLETLIHLDDNANAIQDK.L

244	256	2	1508.7	1	1	86.4	30.2	95.00%	E.AQSNGWQYVGDRK.N	Deamidation (+1)	R.DLIDEAQSNGWQYVGDRK.N
1	12	3	1430.67	0.57	1	37.6	30.5	95.00%	-.MMTHTLPSEQTR.L		-.MMTHTLPSEQTR.L
68	86	2	2027.98	-0.76	0	95.4	28.9	95.00%	K.NVIFFVTDGMGPASLSMAR.S	Oxidation (+16)	K.NVIFFVTDGMGPASLSMAR.S
498	513	2	1872.91	1.1	1	34.3	28.8	95.00%	K.KATWSYVLNNLQGNHE.N		K.KATWSYVLNNLQGNHENTEVGQFLENFLELNLSEVTDLIR.D
366	375	2	1086.52	1.7	0	32.8	29	95.00%	E.TVLVSTSDHE.T		R.EVLAFDEAFQYVLEFAENSDTETVLVSTSDHETGGLVTSR.Q
172	190	3	2209.01	1.4	1	29.5	31.5	95.00%	R.ITDATPASFSSHVDYRWQE.D		R.ITDATPASFSSHVDYRWQEDLIATHQLGEYPLGR.V
316	328	2	1457.66	-1.5	1	45.5	29.7	95.00%	K.DSNGFFLMVEGSR.I		K.DSNGFFLMVEGSR.I
113	135	2	2299.12	1.7	1	117	28	95.00%	R.TRSSDSLVTDSAAGATAFACALK.S	Carbamidomethyl (+57)	R.TRSSDSLVTDSAAGATAFACALK.S
115	135	2	2041.96	-1.6	0	110	29.1	95.00%	R.SSDSLVTDSAAGATAFACALK.S	Carbamidomethyl (+57)	R.SSDSLVTDSAAGATAFACALK.S
475	497	2	2515.23	2.8	0	35.9	28	95.00%	R.AQIGWTTHGHSAVDVNIYAYANK.K		R.AQIGWTTHGHSAVDVNIYAYANK.K
87	112	3	2981.45	-0.3	1	86.3	27.7	95.00%	R.SFNQHVNDLPIDDILTLDEHFIGSSR.T		R.SFNQHVNDLPIDDILTLDEHFIGSSR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
12	B3LSE9_YEAS1	49.14%	100%	38

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
222	241	2	2245.04	2	0	56.8	29.9	95.00%	R.AVTNDGSSFLFNGKPDWVYE.E		R.AVTNDGSSFLFNGKPDWVYEEEVFEDDK.A
351	365	2	1634.92	5.1	0	105	21.2	95.00%	R.SSDILTVFLIDTIAK.T		R.SSDILTVFLIDTIAK.T
699	710	2	1380.65	3	0	28.9	30.3	93.00%	K.YGMSVAPVTDWR.F		K.YGMSVAPVTDWR.F
335	346	2	1284.72	2.3	0	61.5	23.6	95.00%	E.VTWVGNGNVLVK.T		K.DGSLLITEVTWVGNGNVLVK.T
615	630	2	1637.95	3.2	0	93.1	14.8	95.00%	E.VVASQLNAIVVVVDGR.G		K.TFSVGFNEVVASQLNAIVVVVDGR.G
435	448	2	1563.74	1.4	1	46.4	29.5	95.00%	E.VVNGPLAFDSMENR.L	Oxidation (+16)	K.WEVVNGPLAFDSMENR.L
565	575	2	1283.64	2.2	1	46.4	28.4	95.00%	E.FGKDILVNSYE.I		K.DEFGKDILVNSYEILPNDFDETLSDHYPVFFFAYGGPNSQQVVK.T
793	803	2	1318.67	1.7	0	37.3	29.1	95.00%	R.YHNANVIVFDK.L		R.YHNANVIVFDK.L
449	455	2	898.49	-0.022	0	23.9	24.1	93.50%	R.LYFISTR.K		R.LYFISTR.K
654	672	2	2039.02	0.048	0	72.2	28.3	95.00%	R.DQISAASLYGSLTFVDPQK.I		R.DQISAASLYGSLTFVDPQK.I
117	131	2	1687.8	0.53	1	76.2	30	95.00%	K.SVYDDSYNSVLLEGK.T		K.SVYDDSYNSVLLEGK.T
166	177	2	1449.66	4	0	35.4	30	95.00%	R.HSTFGSYFVYDK.S		R.HSTFGSYFVYDK.S
720	733	2	1744.7	0.5	1	30	30.3	94.60%	R.YMHTPQENFDGYVE.S	Oxidation (+16)	R.YMHTPQENFDGYVESSVHNVTALAQANR.F
89	98	2	1244.64	2.1	1	33.5	27.5	95.00%	E.LQWISDNKIE.S		K.YHELQWISDNKIESNDLGLYVTFMNDSYVVK.S
767	777	2	1246.65	3.3	0	43.9	27.3	95.00%	K.FLDLLDLNGVE.N		K.FLDLLDLNGVENYDVHVFPDSDHSIR.Y
748	766	2	2172.05	2.3	0	103	29.1	95.00%	R.FLLMHGTGDDNVHFQNSLK.F		R.FLLMHGTGDDNVHFQNSLK.F
273	283	2	1413.72	1.8	1	27.8	27.4	95.00%	E.FIIPYYVQDEK.D		K.IDESEVGEFIIPYYVQDEK.D
158	165	2	1003.48	0.58	0	34.1	28.8	95.00%	R.TNSVQNWR.H		R.TNSVQNWR.H
347	365	3	2108.15	5.3	1	29.1	21.6	95.00%	K.TTDRSSDILTVFLIDTIAK.T		K.TTDRSSDILTVFLIDTIAK.T
327	346	2	2113.14	-2.2	1	85.6	22	95.00%	K.DGSLLITEVTWVGNGNVLVK.T		K.DGSLLITEVTWVGNGNVLVK.T
496	502	2	840.47	-0.26	0	36.9	23.6	95.00%	R.FGLLTYK.G		R.FGLLTYK.G
483	495	2	1443.68	2.3	1	29	29.3	94.50%	E.DGVYDVSFSSGRR.F		R.SPNEIIEVTDTSEDGVYDVSFSSGRR.F
222	242	2	2375.06	1.7	1	52.9	30.9	95.00%	R.AVTNDGSSFLFNGKPDWVYEE.E	Deamidation (+1)	R.AVTNDGSSFLFNGKPDWVYEEEVFEDDK.A
273	282	2	1285.63	2.2	0	41	29.3	95.00%	E.FIIPYYVQDE.K		K.IDESEVGEFIIPYYVQDEK.D
297	312	2	1815.86	0.21	1	69.8	29.9	95.00%	K.SGTPNPHAELWVYSMK.D		K.SGTPNPHAELWVYSMK.D
394	418	3	2907.4	2.2	0	31.8	28.8	95.00%	E.TFDRPHNGYVDILPIGGYNHLAYFE.N		R.NESSNGGWWEITHNTLFIPANETFDRPHNGYVDILPIGGYNHLAYFENSNSSHYK.T
433	446	2	1592.72	1.9	1	36.1	30.4	95.00%	K.WEVVNGPLAFDSME.N		K.WEVVNGPLAFDSMENR.L

584	606	3	2601.26	1.9	0	34.7	27.6	95.00%	E.TLSDHYPVFFFAYGGPNSQQVVK.T	Deamidation (+1)	K.DILVNSYEILPNDFDETLSDHYPVFFFAYGGPNSQQVVK.T
435	446	2	1278.58	2.2	0	48.7	29.7	95.00%	E.VVNGPLAFDSME.N	Deamidation (+1)	K.WEVVNGPLAFDSMENR.L
711	719	2	1178.53	3.3	1	52.9	29.2	95.00%	R.FYDSVYTER.Y		R.FYDSVYTER.Y
72	78	2	792.45	3	0	43.9	24.4	95.00%	K.VSFSVVR.N		K.VSFSVVR.N
117	129	2	1502.68	2.5	0	29.1	30.3	93.40%	K.SVYDDSYNSVLLE.G		K.SVYDDSYNSVLLEGK.T
366	373	2	917.46	1.8	1	37.4	28.4	95.00%	K.TSNVVRNE.S		K.TSNVVRNESSNGGWWEITHNTLFIPANETFDRPHNGYVDILPIGGYNHLAYFENSNSSHYK.T
778	792	2	1799.83	2	0	90.7	29.8	95.00%	E.NYDVHVFPDSDHSIR.Y		K.FLDLLDLNGVENYDVHVFPDSDHSIR.Y
250	264	2	1724.86	-0.072	0	46.6	28.7	95.00%	K.AAWWSPTGDYLAFLK.I		K.AAWWSPTGDYLAFLK.I
810	818	2	1066.56	-0.59	1	25	26.1	93.50%	K.RAFDGQFVK.-		K.RAFDGQFVK.-
767	792	3	3028.47	3	1	78.7	27.7	95.00%	K.FLDLLDLNGVENYDVHVFPDSDHSIR.Y		K.FLDLLDLNGVENYDVHVFPDSDHSIR.Y
250	267	2	2082.02	3.5	1	44.6	28.2	95.00%	K.AAWWSPTGDYLAFLKIDE.S		K.AAWWSPTGDYLAFLKIDESEVGEFIIPYYVQDEK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
13	A7A160_YEAS7	48.03%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
64	72	2	1066.62	3.4	1	51.7	20.1	95.00%	K.ESTLHLVLR.L		K.ESTLHLVLR.L
17	27	2	1205.58	2.6	1	38.5	28.9	95.00%	E.VESSDTIDNVK.S		K.TITLEVESSDTIDNVK.S
52	63	2	1408.7	0.84	1	51.5	28.6	95.00%	E.DGRTLSDYNIQK.E		K.QLEDGRTLSDYNIQK.E
1	6	2	764.43	3.8	0	35.4	23.4	95.00%	-.MQIFVK.T		-.MQIFVK.T
120	136	2	1860.83	2.3	1	85.7	30	95.00%	R.ECSNPTCGAGVFLANHK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.ECSNPTCGAGVFLANHK.D
55	64	2	1209.59	2.1	1	52.3	29.2	95.00%	R.TLSDYNIQKE.S		R.TLSDYNIQKESTLHLVLR.L
19	27	2	977.47	3.7	0	56.5	28.4	95.00%	E.SSDTIDNVK.S		K.TITLEVESSDTIDNVK.S
49	54	2	716.35	-0.31	1	24.1	27.1	90.10%	K.QLEDGR.T		K.QLEDGR.T
34	42	2	1038.51	-0.21	1	38.7	29.7	95.00%	K.EGIPPDQQR.L		K.EGIPPDQQR.L
65	72	2	937.57	1.6	0	34	16.1	95.00%	E.STLHLVLR.L		K.ESTLHLVLR.L
55	63	2	1080.55	0.55	0	50	28.2	95.00%	R.TLSDYNIQK.E		R.TLSDYNIQK.E
43	51	2	1017.59	1.4	1	23	24.4	92.10%	R.LIFAGKQLE.D		R.LIFAGKQLEDGR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
14	CBPS_YEAST	41.84%	100%	25

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
108	119	2	1391.6	2.3	0	53.2	30.7	95.00%	K.NPNPADDPDFYK.H		K.NPNPADDPDFYK.H
195	201	2	879.43	1.9	0	28.2	28.8	94.10%	E.TDFVWGR.G		K.FPPFSGHYDPETDFVWGR.G
533	544	2	1331.77	-0.39	0	55.2	21.1	95.00%	R.FVGSIIDIDLLK.T		R.FVGSIIDIDLLK.T
178	194	2	1993.93	2.1	1	43.8	30.3	95.00%	E.TLSSWKFPPFSGHYDPE.T		K.VNELGLLYTWEGSDPDLKPLLLMAHQDVVPVNNETLSSWKFPPFSGHYDPETDFVWGR.G
258	269	2	1358.59	2.1	0	48.8	30.1	95.00%	R.YGDDGIYSIIDE.G		R.YGDDGIYSIIDEGEGIMEVDK.D
147	154	2	993.52	2.4	0	26.4	27.6	93.40%	E.LGLLYTWE.G		K.VNELGLLYTWEGSDPDLKPLLLMAHQDVVPVNNETLSSWK.F
360	370	3	1258.69	3	1	46.3	24.4	95.00%	K.KTILGAPFCPR.R	Carbamidomethyl (+57)	K.KTILGAPFCPR.R
413	418	2	798.45	-0.79	0	24.3	22	94.00%	R.FLINHR.I		R.FLINHR.I
522	528	2	972.47	-0.0068	0	34.1	28.9	95.00%	K.YYWNLSK.N		K.YYWNLSK.N
257	269	2	1514.69	1.4	1	58	30.1	95.00%	E.RYGDDGIYSIIDE.G		R.TIVMSLGFDEEASGTLGAASLASFLHERYGDDGIYSIIDEGEGIMEVDK.D
241	257	2	1686.87	1.9	1	98.6	26.7	95.00%	E.ASGTLGAASLASFLHER.Y		R.TIVMSLGFDEEASGTLGAASLASFLHER.Y
361	370	2	1130.59	2.8	0	29.6	26.7	95.00%	K.TILGAPFCPR.R	Carbamidomethyl (+57)	K.TILGAPFCPR.R
391	403	2	1314.71	-0.23	0	87.6	25.2	95.00%	R.TTQAVDIINGGVK.A		R.TTQAVDIINGGVK.A
65	74	2	1144.65	1.1	1	25.1	23.6	95.00%	E.KIEPLSPSFK.H		K.CEKIEPLSPSFK.H

506	521	2	1778.84	1.5	1	59.6	29.3	95.00%	E.EFYVTTGLFSGNTDTK.Y		R.ELEPAPLSPSSGPVWDILAGTIQDVFENGVLQNNEEFYVTTGLFSGNTDTK.Y
375	386	2	1457.77	2.9	1	59.4	26.8	95.00%	K.LVEYISNQSHLR.S		K.LVEYISNQSHLR.S
378	386	2	1116.57	3.8	0	28	26.9	95.00%	E.YISNQSHLR.S		K.LVEYISNQSHLR.S
75	87	2	1506.76	2.2	0	69.8	27.9	95.00%	K.HSVDTILHDPAFR.N		K.HSVDTILHDPAFR.N
241	256	2	1530.77	2.2	0	57.8	27.3	95.00%	E.ASGTLGAASLASFLHE.R		R.TIVMSLGFDEEASGTLGAASLASFLHER.Y
184	201	2	2152.96	-0.48	1	36.6	30.4	95.00%	K.FPPFSGHYDPETDFVWGR.G		K.FPPFSGHYDPETDFVWGR.G
219	229	3	1299.73	2.2	0	25.3	23.5	95.00%	E.QLLIDGFKPNR.T		K.NLLIAEFEAIEQLLIDGFKPNR.T
94	107	3	1538.88	2	1	21.7	20	95.00%	K.LSNAVRIPTVVQDK.N		K.LSNAVRIPTVVQDK.N
507	521	2	1649.8	2	0	90.9	29	95.00%	E.FYVTTGLFSGNTDTK.Y		R.ELEPAPLSPSSGPVWDILAGTIQDVFENGVLQNNEEFYVTTGLFSGNTDTK.Y
471	497	2	2866.44	2.6	1	70.6	27	95.00%	R.ELEPAPLSPSSGPVWDILAGTIQDVFE.N		R.ELEPAPLSPSSGPVWDILAGTIQDVFENGVLQNNEEFYVTTGLFSGNTDTK.Y
552	567	2	1752.89	3	0	57	28.3	95.00%	E.HVDVPGHLSAIAFVYE.Y		K.TLHSVNEHVDVPGHLSAIAFVYEYIVNVNEYA.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
15	ATC9_YEAST	25.88%	100%	27							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1075	1101	3	3087.58	3.7	1	20.9	24.7	95.00%	R.VYVPSINDTPLHGEPVIVWRDVNEPDK.I		R.VYVPSINDTPLHGEPVIVWRDVNEPDK.I
1178	1196	2	2031.87	1.2	0	43.7	31.1	95.00%	K.LDYTVGFCGDGANDCGALK.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.LDYTVGFCGDGANDCGALK.A
947	958	2	1488.66	3.4	0	70.7	30	95.00%	K.TNNDDVYWSFTK.G		K.TNNDDVYWSFTK.G
1049	1065	2	1820.91	-0.7	0	49	28.4	95.00%	R.TIMCTGDNILTAISVGR.E	Carbamidomethyl (+57)	R.TIMCTGDNILTAISVGR.E
1124	1136	2	1500.71	3.1	0	62.7	29.5	95.00%	E.CNYTLAVSGDVFR.L	Carbamidomethyl (+57)	R.ECNYTLAVSGDVFR.L
443	464	2	2488.18	-1.5	0	74.8	28.7	95.00%	K.TNNNWIDPDWVDLSTVSNGLTK.G		K.TNNNWIDPDWVDLSTVSNGLTK.G
1153	1162	2	1148.66	2.3	0	34.2	22.8	95.00%	E.ILLNSSIYAR.M		R.DENEIPEEYLNEILLNSSIYAR.M
652	665	2	1396.79	1.2	0	70.3	20.9	95.00%	R.IAPGQTAALAMVVR.T		R.IAPGQTAALAMVVR.T
199	221	3	2438.12	2.2	1	69.8	30.3	95.00%	R.LGENSDTGFVYHSATHSSSSLSR.Y		R.LGENSDTGFVYHSATHSSSSLSR.Y
287	300	3	1823.91	2.1	1	32.4	27.4	95.00%	E.KFYPQYAPNLHYQR.F		R.GSFSGHDDVHNQHSEYLKPDYHEKFYPQYAPNLHYQR.F
915	930	2	1844.88	0.85	0	67	28.9	95.00%	E.NTFTDNDPHNFLGVVR.S		R.ENTFTDNDPHNFLGVVR.S
901	914	2	1560.79	-0.28	1	55.4	27.8	95.00%	E.IIPAVVHPDSNNRE.N	Deamidation (+1)	R.HEDDVFPENSEIIPAVVHPDSNNRENTFTDNDPHNFLGVVR.S
59	88	3	3182.52	1.7	0	36.9	27.2	95.00%	E.AVPSSIVSFHHPHSFQSSNLPSPHSSGNLE.Q		R.ASFSSTATTSTAATLTSAMVLDQNNSEPYAGATFEAVPSSIVSFHHPHSFQSSNLPSPHSSGNLEQR.G
432	442	2	1356.7	2.7	0	30.4	27.6	95.00%	K.FIYSPLDDLFK.T		K.FIYSPLDDLFK.T
288	300	2	1695.82	2.1	0	67.8	28.9	95.00%	K.FYPQYAPNLHYQR.F		K.FYPQYAPNLHYQR.F
823	835	2	1528.69	1.5	0	64.4	29.8	95.00%	K.FSLNDCSSPLDFK.S	Carbamidomethyl (+57)	K.FSLNDCSSPLDFK.S
202	221	3	2138.96	1.2	0	67.1	30.1	95.00%	E.NSDTGFVYHSATHSSSSLSR.Y		R.LGENSDTGFVYHSATHSSSSLSR.Y
809	817	2	1048.56	3.8	1	61.2	27.4	95.00%	K.FGELLSDIR.Q		K.FGELLSDIR.Q
97	109	2	1401.71	1.6	1	34.6	27.9	95.00%	E.SEPLVLSSAEQSR.S		R.LTESEPLVLSSAEQSR.S
1	14	2	1651.78	2.1	0	99.4	29.3	95.00%	-.MDIPSSNQIQHGQR.S	Acetyl (+42)	-.MDIPSSNQIQHGQR.S
577	600	2	2673.3	3.5	0	29.9	27.6	95.00%	E.VSDPNITILPCDSILLSSDCIVNE.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.FWTTISSSELVPGDIYEVSDPNITILPCDSILLSSDCIVNESMLTGESVPVSK.F
152	163	2	1351.68	-0.23	1	45.5	27.9	95.00%	E.QDRIYGTGLSSR.R		R.FFTQEQISNAEGASTLENTDYDMAWDATPAYEQDRIYGTGLSSR.R

783	805	2	2370.2	2.4	1	79.6	26.5	95.00%	K.TGTLTEDGLDVLGVQISEPNGVR.G	Deamidation (+1)	K.TGTLTEDGLDVLGVQISEPNGVR.G
851	864	2	1488.75	2.5	0	62.7	28.2	95.00%	R.SVDGNLLGDPLDFK.M		R.SVDGNLLGDPLDFK.M
372	379	2	986.56	2	0	25.6	27.3	92.50%	E.FVIQPIDR.Q		K.AEWVVIENEFGEFVIQPIDR.Q
760	768	2	1049.54	3.3	0	39.3	28.1	95.00%	K.GIFCISPTR.L	Carbamidomethyl (+57)	K.GIFCISPTR.L
789	805	2	1767.91	3.4	0	71.7	26.7	95.00%	E.DGLDVLGVQISEPNGVR.G	Deamidation (+1)	K.TGTLTEDGLDVLGVQISEPNGVR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
16	B3LFI3_YEAS1	43.21%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
240	245	2	987.43	2.4	0	27.8	28.8	93.60%	E.YDWYWR.V		R.HELLEEYDWYWR.V
344	357	2	1737.74	2.3	0	33.4	31	95.00%	E.YFDTLDHQGGFFYE.R		R.EYFDTLDHQGGFFYER.W
344	358	2	1893.84	2.2	1	83.8	30.8	95.00%	E.YFDTLDHQGGFFYER.W		R.EYFDTLDHQGGFFYER.W
359	375	3	1791.97	0.27	0	29.7	24	95.00%	R.WGDAPVHSIAAALFLPK.D		R.WGDAPVHSIAAALFLPK.D
252	262	2	1448.67	0.64	0	49.6	30.5	95.00%	K.LYCDINYDVFK.W	Carbamidomethyl (+57)	K.LYCDINYDVFK.W
376	398	4	2830.28	0.7	1	48.7	29.8	95.00%	K.DKIHYFSDIGYHHPPYDNCPLDK.E	Carbamidomethyl (+57)	K.DKIHYFSDIGYHHPPYDNCPLDK.E
32	54	2	2432.15	2.9	0	85.6	29.9	95.00%	R.TQQYIPSSISAAFDFTSGSISPE.Q		R.TQQYIPSSISAAFDFTSGSISPEQQVISEENDAK.K
359	377	3	2035.1	3.2	1	26.2	23	95.00%	R.WGDAPVHSIAAALFLPKDK.I		R.WGDAPVHSIAAALFLPKDK.I
424	435	2	1409.72	2.8	1	64.2	26.3	95.00%	K.EYYDAQGLVKPK.N		K.EYYDAQGLVKPK.N
105	117	2	1487.69	-5.5	0	76.3	29.7	95.00%	K.TTMDYITPSFANK.A		K.TTMDYITPSFANK.A
212	221	2	1193.54	-0.17	1	52.2	29.5	95.00%	K.YIYGGSESYR.H		K.YIYGGSESYR.H
408	423	2	1882.73	1.7	0	84.4	30.6	95.00%	E.CDQGNDFTFQGYSCGK.E	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.EVYNSNNCECDQGNDFTFQGYSCGK.E
123	130	2	980.51	3.2	0	30.8	27.3	95.00%	K.ACYVTLVR.N	Carbamidomethyl (+57)	K.ACYVTLVR.N
152	167	2	2028.92	3.3	1	48.7	30.6	95.00%	K.FPYPWVFLNDEPFTEE.F		K.FPYPWVFLNDEPFTEEFK.E
226	233	2	1089.5	-0.11	0	44.2	29.5	95.00%	R.YQSGFFWR.H		R.YQSGFFWR.H
378	398	2	2587.16	-0.72	0	56.9	31	95.00%	K.IHYFSDIGYHHPPYDNCPLDK.E	Carbamidomethyl (+57)	K.IHYFSDIGYHHPPYDNCPLDK.E
425	435	2	1280.68	1.2	0	41.9	24.9	95.00%	E.YYDAQGLVKPK.N		K.EYYDAQGLVKPK.N
305	317	2	1469.65	2.1	0	62.1	29.7	95.00%	E.NNLMSFLSNDNGK.T	Oxidation (+16)/ Deamidation (+1)	K.NPEYLDENNLMSFLSNDNGK.T
408	424	2	2011.77	1.8	1	92.1	30.3	95.00%	E.CDQGNDFTFQGYSCGKE.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.EVYNSNNCECDQGNDFTFQGYSCGKEYYDAQGLVKPK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
17	ATN2_YEAST	30.89%	100%	26

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
531	542	2	1389.69	1.2	1	44.1	28.2	95.00%	E.HIAEFPFDSTVK.R		K.STNQSNENDQSSLSQHNEKPGSAQFEHIAEFPFDSTVK.R
52	63	2	1381.67	1.4	1	62.6	28.8	95.00%	E.NTLGDDTKIDYK.A		K.AVGENTLGDDTKIDYK.A
14	24	2	1324.6	1.9	1	43.9	30.1	95.00%	E.FNAYHTLTTEE.A		K.ENNNEEFNAYHTLTTEEAAEFIGTSLTEGLTQDESLR.R
424	436	2	1475.74	1.7	1	54.9	28.3	95.00%	E.DGDVGILQNFKDR.L		R.FSPYEYSHNEDGDVGILQNFKDR.L
14	23	2	1195.55	0.57	0	26.7	29.2	91.20%	E.FNAYHTLTTE.E		K.ENNNEEFNAYHTLTTEEAAEFIGTSLTEGLTQDESLR.R
562	577	2	1850.8	2.9	1	60	30.2	95.00%	K.GAFESIISCCSSWYGK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GAFESIISCCSSWYGK.D
477	492	2	1696.88	2.2	1	64	25.3	95.00%	K.AHGDPTEIAIQVFATK.M		K.AHGDPTEIAIQVFATK.M
512	530	2	2101.93	1.6	1	51.5	30.1	95.00%	E.NDQSSLSQHNEKPGSAQFE.H		K.STNQSNENDQSSLSQHNEKPGSAQFEHIAEFPFDSTVK.R
389	413	2	2703.32	1.9	1	94.2	27.6	95.00%	R.FGTITISNSDDPFNPNEGNVSLIPR.F		R.FGTITISNSDDPFNPNEGNVSLIPR.F
637	654	2	2017.06	5.5	1	22.5	24	91.10%	E.SDLVFLGLIGIYDPPRNE.T		R.ATAESDLVFLGLIGIYDPPRNETAGAVK.K
359	370	2	1261.6	2.1	0	36.6	28.7	95.00%	E.ALGAVNDICSDK.T	Carbamidomethyl (+57)	K.LDSLEALGAVNDICSDK.T
924	941	3	2173.9	3.2	1	29.2	30.9	95.00%	R.LGHDCDGTYNSSCRDVYR.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.LGHDCDGTYNSSCRDVYR.S

661	681	4	2270.17	2.7	1	48.5	25.9	95.00%	K.KFHQAGINVHMLTGDFVGTAK.A		K.KFHQAGINVHMLTGDFVGTAK.A
662	681	3	2142.07	-0.88	0	21.5	28.2	90.90%	K.FHQAGINVHMLTGDFVGTAK.A		K.FHQAGINVHMLTGDFVGTAK.A
156	165	2	1055.56	-0.5	0	46.8	25.4	95.00%	K.VGDTIPADLR.L		K.VGDTIPADLR.L
140	155	2	1756.94	1.4	1	43.4	23.9	95.00%	E.TINSKDVVPGDICLVK.V	Carbamidomethyl (+57)	K.SETINSKDVVPGDICLVK.V
457	476	2	2240.09	3	1	111	29.3	95.00%	E.TATLANIATVFKDDATDCWK.A	Carbamidomethyl (+57)	K.WLETATLANIATVFKDDATDCWK.A
596	606	2	1250.63	2.5	1	48.6	28.9	95.00%	K.NVYSLSNEGLR.V		K.NVYSLSNEGLR.V
720	732	2	1418.85	2.6	0	43.2	12.8	95.00%	E.VDDLPVLPLVIAR.C		K.AIAQEVGILPTNLYHYSQEIVDSMVMTGSQFDGLSEEEVDDLPVLPLVIAR.C
484	492	2	989.59	2.4	0	56.4	20.1	95.00%	E.IAIQVFATK.M		K.AHGDPTEIAIQVFATK.M
785	804	2	2121.02	3.8	1	56.5	29.4	95.00%	E.ASDIVLSDDNFASILNAVEE.G		K.EASDIVLSDDNFASILNAVEEGR.R
751	766	2	1697.74	2.2	0	72	30.1	95.00%	K.FCAMTGDGVNDSPSLK.M	Carbamidomethyl (+57)	K.FCAMTGDGVNDSPSLK.M
493	504	2	1324.65	2.3	1	32.7	28.2	95.00%	K.MDLPHNALTGEK.S		K.MDLPHNALTGEK.S
239	253	3	1558.8	0.91	1	22.9	27.5	94.60%	K.SLQGDSGLISRDPSK.S		K.SLQGDSGLISRDPSK.S
424	434	2	1204.61	3.3	0	38.9	27.6	95.00%	E.DGDVGILQNFK.D		R.FSPYEYSHNEDGDVGILQNFK.D
254	264	2	1362.69	-0.74	0	43.3	28.4	95.00%	K.SWLQNTWISTK.K		K.SWLQNTWISTK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
18	ADP1_YEAST	27.45%	100%	23

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
193	203	2	1498.66	2.4	0	37	30.5	95.00%	E.CNFQFWIDQLE.S	Carbamidomethyl (+57)	K.IPQITFACDKPNQECNFQFWIDQLESFYCGLSDCAFEYDLEQNTSHYK.C
430	439	2	1117.64	-0.46	0	45.1	22.1	95.00%	K.TTLLDILAMK.R		K.TTLLDILAMK.R
68	78	2	1347.55	-0.36	1	44	30.5	95.00%	K.QFSECNSYTGR.C	Carbamidomethyl (+57)	K.QFSECNSYTGR.C
30	39	2	1099.52	4	1	34.3	28.2	95.00%	K.TPFFEGTSSK.N		K.TPFFEGTSSK.N
860	873	2	1681.8	1.5	0	38.8	29.2	95.00%	R.SNNYYSPLAYYISK.I		R.SNNYYSPLAYYISK.I
259	270	2	1352.57	2.6	1	54.3	30	95.00%	K.GPGDFSCDLETR.Q	Carbamidomethyl (+57)	K.GPGDFSCDLETR.Q
84	102	2	1965.81	1.3	0	44.7	30.3	95.00%	E.GFAGDDCSLPLCGGLSPDE.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.CECIEGFAGDDCSLPLCGGLSPDESGNK.D
245	258	2	1537.79	-1.4	1	45.6	27.2	95.00%	K.GSIDISDFLTETIK.G		K.GSIDISDFLTETIK.G
274	295	2	2499.27	3.4	0	43.7	25.9	95.00%	K.FSEPSMNDLILTVFGDPYITLK.C		K.FSEPSMNDLILTVFGDPYITLK.C
301	311	2	1351.63	1.6	1	35.6	29.8	95.00%	E.CVHYSEIPGYK.S	Carbamidomethyl (+57)	K.CESGECVHYSEIPGYK.S
49	67	2	2358.95	-1.4	1	27.7	30.4	90.70%	K.GNDTCPPCFNCMLPIFECK.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GNDTCPPCFNCMLPIFECK.Q
663	688	3	2797.23	0.89	0	84.1	30.6	95.00%	E.AGTDTNDIDNTIHQTTFTSSDGTTQR.E	Deamidation (+1)	R.NISDLEAGTDTNDIDNTIHQTTFTSSDGTTQR.E
171	178	2	897.56	-0.35	0	35.4	19.1	95.00%	K.ILQILNGK.I		K.ILQILNGK.I
733	741	2	1136.51	2.5	1	43.8	28.7	95.00%	K.YKDSVYYAE.L		K.YKDSVYYAELSQEIEEVLSEGDEESNVLNGDLPTGQQSAGFLQQLSILNSR.S
592	600	2	1145.58	-0.28	0	39.1	27.8	95.00%	R.SNIFYLFDK.L		R.SNIFYLFDK.L
179	192	2	1659.8	1.8	0	82.6	29.7	95.00%	K.IPQITFACDKPNQE.C	Carbamidomethyl (+57)	K.IPQITFACDKPNQECNFQFWIDQLESFYCGLSDCAFEYDLEQNTSHYK.C
582	591	2	1162.69	3.3	0	57.6	19	95.00%	R.TLVLSIHQPR.S		R.TLVLSIHQPR.S
544	570	2	2827.46	4.3	0	86.7	22.7	95.00%	E.LVTSPLVLFLDEPTSGLDASNANNVIE.C		R.VSIACELVTSPLVLFLDEPTSGLDASNANNVIECLVR.L
84	106	2	2352	1.3	1	90.6	30.8	95.00%	E.GFAGDDCSLPLCGGLSPDESGNK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.CECIEGFAGDDCSLPLCGGLSPDESGNK.D
663	689	3	2925.29	1.5	1	78.6	30.4	95.00%	E.AGTDTNDIDNTIHQTTFTSSDGTTQRE.W		R.NISDLEAGTDTNDIDNTIHQTTFTSSDGTTQREWAHLAAHR.D

234	244	2	1218.58	1.4	0	26.2	28.2	92.10%	K.CVPDTVLCGAK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CVPDTVLCGAK.G
388	403	2	1722.8	2.1	1	48.4	30.1	95.00%	E.NITYSVPSINSDGVEE.T		R.LPDEDAVNNFLQNEDDTLATLSFENITYSVPSINSDGVEETVLNEISGIVKPGQILAIMGGSGAGK.T
256	268	2	1437.64	-0.2	1	28	30.2	91.90%	E.TIKGPGDFSCDLE.T	Carbamidomethyl (+57)	K.GSIDISDFLTETIKGPGDFSCDLETR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
19	ATC2_YEAST	22.68%	100%	23

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
490	511	2	2437.2	2.8	1	69.5	27.5	95.00%	E.NCSSSLRNDLLANIVLNSTAFE.N	Carbamidomethyl (+57)	K.VFEENCSSSLRNDLLANIVLNSTAFENR.D
497	511	2	1632.84	4.6	0	39.3	26.3	95.00%	R.NDLLANIVLNSTAFE.N		R.NDLLANIVLNSTAFENR.D
432	446	2	1602.63	-0.15	1	102	29.4	95.00%	R.SCETMGSATAVCSDK.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.SCETMGSATAVCSDK.T
71	83	2	1432.73	-0.15	1	45.8	27.8	95.00%	K.NAGISLPEISNYR.K		K.NAGISLPEISNYR.K
760	770	2	1161.61	-0.79	0	41.5	27.5	95.00%	R.MVTGDNILTAK.A		R.MVTGDNILTAK.A
447	459	2	1419.74	-0.85	1	52.8	27	95.00%	K.TGTLTENVMTVVR.G		K.TGTLTENVMTVVR.G
868	887	2	2165.09	-0.66	1	94.7	26	95.00%	R.EASDIILMTDDFSAIVNAIK.W		R.EASDIILMTDDFSAIVNAIK.W
574	583	2	1073.61	0.07	1	45.8	24.3	95.00%	K.TETALLSLAR.L		K.TETALLSLAR.L
709	726	2	1988.02	-1.3	1	67.1	26.5	95.00%	R.DKDSPNIAALDLLFNSQK.G		R.DKDSPNIAALDLLFNSQK.G
727	741	2	1591.93	-1.3	0	34.9	15.6	95.00%	K.GLILDGLLGIQDPLR.A		K.GLILDGLLGIQDPLR.A
37	46	2	1137.58	-0.63	0	43.1	29.5	95.00%	K.SQLSDLHNPK.S		K.SQLSDLHNPK.S
584	597	2	1585.88	-0.38	1	49.8	23.1	95.00%	R.LSLGLQPGELQYLR.D		R.LSLGLQPGELQYLR.D
54	64	2	1303.65	3.2	1	46.6	28.1	95.00%	R.LFGYESNSLFK.Y		R.LFGYESNSLFK.Y
711	726	2	1744.9	-0.76	0	65.5	26.7	95.00%	K.DSPNIAALDLLFNSQK.G		K.DSPNIAALDLLFNSQK.G
26	33	2	956.43	1.9	0	25.4	27.6	91.60%	E.NGVYDNFK.L	Deamidation (+1)	R.QDENSALLANNENNKPSYTGNENGVYDNFK.L
497	513	2	1902.98	-0.49	1	68.7	26.4	95.00%	R.NDLLANIVLNSTAFENR.D		R.NDLLANIVLNSTAFENR.D
264	287	4	2651.22	-0.97	1	31	29.7	95.00%	K.FNSIDSHNHSKPLDIGDVNEDGNK.I		K.FNSIDSHNHSKPLDIGDVNEDGNK.I
688	698	2	1275.59	1.7	1	53.6	29.6	95.00%	R.AISVAHKDFCE.C	Carbamidomethyl (+57)	R.AISVAHKDFCECDSWPPEQLR.D
831	850	2	1886.91	1.2	0	106	29	95.00%	K.GMGDVVAVTGDGTNDAPALK.L		K.GMGDVVAVTGDGTNDAPALK.L
288	298	2	1221.59	3	0	62.1	29.3	95.00%	K.IADCMLISGSR.I	Carbamidomethyl (+57)	K.IADCMLISGSR.I
252	259	2	946.49	1.2	0	28.5	27.9	95.00%	K.FPVDNSLR.D		K.FPVDNSLR.D
435	452	2	1828.82	0.94	1	82.2	31	95.00%	E.TMGSATAVCSDKTGTLTE.N	Carbamidomethyl (+57)	R.SCETMGSATAVCSDKTGTLTENVMTVVR.G
16	33	2	2060.91	1.9	1	56.5	31	95.00%	E.NNKPSYTGNENGVYDNFK.L	Deamidation (+1)	R.QDENSALLANNENNKPSYTGNENGVYDNFK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
20	KTR1_YEAST	49.11%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
102	113	2	1589.67	2	1	37.9	30.5	95.00%	K.FNYDWVFLNDEE.F		K.FNYDWVFLNDEEFTDEFK.N
46	57	2	1247.6	0.56	0	77.6	29.1	95.00%	K.YSTVLSSGSGYK.Y		K.YSTVLSSGSGYK.Y
327	352	5	3083.43	-0.78	1	47.3	28.3	95.00%	R.SEIHHFGDIGYYHVPFHSCPIDTSIR.L	Carbamidomethyl (+57)	R.SEIHHFGDIGYYHVPFHSCPIDTSIR.L
281	288	2	956.55	1.9	0	44.8	25.6	95.00%	E.IAALDLWR.S		K.FMEAHPELIHENNMLDFVSDDQGLSYNLCHFWSNFEIAALDLWR.S
83	92	2	1137.6	3.9	1	44.3	27	95.00%	R.DLYSLAESIK.S		R.DLYSLAESIK.S
203	213	2	1423.65	1.6	0	55.7	30.4	95.00%	K.LHCDIDYDVFK.F	Carbamidomethyl (+57)	K.LHCDIDYDVFK.F
185	196	2	1695.72	1.6	0	47.4	31.1	95.00%	R.HPLMDDYDWYWR.V		R.HPLMDDYDWYWR.V
310	328	2	2040.01	2.3	1	72.6	28.3	95.00%	R.WGDAPVHSIGAALFLDRSE.I		R.WGDAPVHSIGAALFLDRSEIHHFGDIGYYHVPFHSCPIDTSIR.L
163	172	2	1185.61	2.5	0	40.8	27.2	95.00%	R.IIYGDSISYR.H		R.IIYGDSISYR.H

256	280	2	3051.29	2.3	0	50.8	31	95.00%	E.NNMLDFVSDDQGLSYNLCHFWSNFE.I	Carbamidomethyl (+57)	K.FMEAHPELIHENNMLDFVSDDQGLSYNLCHFWSNFEIAALDLWR.S
289	301	2	1566.7	3.2	0	74.7	29.9	95.00%	R.SPAYSAYFDYLDR.E		R.SPAYSAYFDYLDR.E
162	172	2	1341.71	2.2	1	49.6	27	95.00%	K.RIIYGDSISYR.H		K.RIIYGDSISYR.H
364	375	2	1531.64	2.1	0	28.2	30.3	91.90%	K.DFTWHSYSCTTK.F	Carbamidomethyl (+57)	K.DFTWHSYSCTTK.F
310	326	2	1823.94	2.6	0	79	26.6	95.00%	R.WGDAPVHSIGAALFLDR.S		R.WGDAPVHSIGAALFLDR.S
73	80	2	905.54	3.9	0	59.6	21.9	95.00%	K.ATFVTLVR.N		K.ATFVTLVR.N
357	375	3	2393.94	0.34	1	55	30.3	95.00%	K.CDCDPSKDFTWHSYSCTTK.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CDCDPSKDFTWHSYSCTTK.F
289	302	2	1695.75	2.3	1	89.9	30.8	95.00%	R.SPAYSAYFDYLDRE.G		R.SPAYSAYFDYLDREGGFFYER.W
177	184	2	1051.48	-0.034	1	38.6	29	95.00%	R.FESGFFYR.H		R.FESGFFYR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
21	A6ZMV7_YEAS7	29.41%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
194	202	2	1010.59	1.2	0	28.2	20.1	95.00%	E.VLPQSVVNR.L		R.LVLYVGVAGLISNVVGLFLFHDHGSDSLHSHSHGSVESGNNDLDIESNATHSHSHASLPNDNLAIDEDAISSPGPSGQIGEVLPQSVVNR.L
203	221	3	2302.93	2	1	25.4	30.9	93.40%	R.LSNESQPLLNHDDHDHSHE.S	Phospho (+80)	R.LSNESQPLLNHDDHDHSHESK.K
385	399	2	1521.74	1.2	1	106	29.1	95.00%	R.RFSIIAGGSPSSSQE.A		R.RFSIIAGGSPSSSQEAFDSHGNTEHGR.K
358	372	2	1699.85	1.2	0	53.5	27.9	95.00%	K.IFHQHGIHSATVQPE.F		K.IFHQHGIHSATVQPEFVSGDVNEDIR.R
386	399	2	1365.64	2.6	0	88.2	29.4	95.00%	R.FSIIAGGSPSSSQE.A		R.FSIIAGGSPSSSQEAFDSHGNTEHGR.K
180	193	2	1313.61	0.82	0	36	29.1	95.00%	E.DAISSPGPSGQIGE.V		R.LVLYVGVAGLISNVVGLFLFHDHGSDSLHSHSHGSVESGNNDLDIESNATHSHSHASLPNDNLAIDEDAISSPGPSGQIGEVLPQSVVNR.L
293	309	2	1854.03	3.8	0	104	20.9	95.00%	R.ILLQATPSTISADQIQR.E		R.ILLQATPSTISADQIQR.E
415	442	2	2962.24	1.9	0	97.5	30.7	95.00%	R.SPTAYGATTASSNCIVDDAVNCNTSNCL.-	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.SPTAYGATTASSNCIVDDAVNCNTSNCL.-
414	442	3	3118.35	2.3	1	96.3	31.2	95.00%	K.RSPTAYGATTASSNCIVDDAVNCNTSNCL.-	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.RSPTAYGATTASSNCIVDDAVNCNTSNCL.-
357	372	2	1827.94	1.8	1	45.3	26.8	95.00%	R.KIFHQHGIHSATVQPE.F		R.KIFHQHGIHSATVQPEFVSGDVNEDIR.R
373	383	2	1249.6	1.7	1	62.8	28.7	95.00%	E.FVSGDVNEDIR.R		K.IFHQHGIHSATVQPEFVSGDVNEDIR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
22	PPN1_YEAST	21.07%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
184	198	2	1707.82	2.9	1	82.5	29.5	95.00%	R.TEAQIFDMNNIVADK.M		R.TEAQIFDMNNIVADK.M
137	150	2	1537.65	3.1	1	38.3	29.8	95.00%	K.AMSGCDSPVILMEE.T	Carbamidomethyl (+57)	K.AMSGCDSPVILMEETLR.W
72	83	2	1334.83	1.8	1	22.3	13.2	90.80%	R.LGLTPREPVIIK.D		R.LGLTPREPVIIK.D
582	595	2	1558.86	2.7	0	54	22.8	95.00%	E.LGPAYVPQLFTPTR.F		K.YELGPAYVPQLFTPTR.F
186	198	2	1478.71	2.1	0	36.5	29.1	95.00%	E.AQIFDMNNIVADK.M	Deamidation (+1)	R.TEAQIFDMNNIVADK.M
97	126	3	3382.63	0.46	1	56.3	28.2	95.00%	R.FLHITDIHPDPYYVEGSSIDAVCHTGKPSK.K	Carbamidomethyl (+57)	R.FLHITDIHPDPYYVEGSSIDAVCHTGKPSK.K
596	605	2	1258.63	3	1	35.3	28.5	95.00%	R.FVQFYADLEK.I		R.FVQFYADLEK.I
97	111	2	1857.9	1.7	0	75.4	29.1	95.00%	R.FLHITDIHPDPYYVE.G		R.FLHITDIHPDPYYVEGSSIDAVCHTGKPSK.K

482	500	2	2067.09	3.1	0	87.4	24.2	95.00%	R.YSIVNIGGSVIPTFNPSFR.I		R.YSIVNIGGSVIPTFNPSFR.I
161	174	2	1690.87	3.4	1	43.9	26.1	95.00%	R.DKIDFVIWTGDNIR.H		R.DKIDFVIWTGDNIR.H
263	274	2	1247.68	0.46	1	31.7	26.2	95.00%	R.SASFLTEVIPGK.L		R.SASFLTEVIPGK.L
580	595	2	1850.95	-1.7	1	46.2	26.7	95.00%	K.YELGPAYVPQLFTPTR.F		K.YELGPAYVPQLFTPTR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
23	A6ZQR8_YEAS7	27.08%	100%	22

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
248	260	3	1538.83	3	0	41.6	24	95.00%	R.TMGIKPYTINVFR.N		R.TMGIKPYTINVFR.N
620	626	2	943.43	1.2	1	23.6	26.1	91.20%	K.NYDEIYK.S		K.NYDEIYK.S
955	967	2	1323.62	3	0	81.8	30.1	95.00%	K.LGDASCAAPFTSK.L	Carbamidomethyl (+57)	K.LGDASCAAPFTSK.L
806	825	2	2144.92	2.5	0	83.2	30.8	95.00%	K.DMGYQTLMCGDGTNDVGALK.Q	Carbamidomethyl (+57)	K.DMGYQTLMCGDGTNDVGALK.Q
118	132	2	1729.87	-0.82	1	58	27.2	95.00%	R.VTEAGSLQTFFQFQK.K		R.VTEAGSLQTFFQFQK.K
501	513	2	1301.66	1.7	1	59.7	27.6	95.00%	E.GLAGISADSENIR.H		K.TGTLTGEDLVFEGLAGISADSENIR.H
524	537	2	1391.85	2.1	0	29.5	13.8	95.00%	E.STILVIGAAHALVK.L		R.HLYSAAEAPESTILVIGAAHALVK.L
663	681	2	2250.11	0.88	1	35	27.4	95.00%	E.LTFNGFLIFHCPLKDDAIE.T	Deamidation (+1)/ Carbamidomethyl (+57)	R.DDVESELTFNGFLIFHCPLKDDAIETIK.M
798	805	2	976.56	3.7	1	22.5	24.9	91.10%	K.EFLLNTLK.D		K.EFLLNTLK.D
96	114	2	2014	1.2	0	49.5	27.9	95.00%	E.ATHILIYTTPNNGSDGIVE.I		K.NVNEATHILIYTTPNNGSDGIVEIQR.V
264	282	2	2198.18	2.9	1	56.2	22.3	95.00%	K.WVALQTNELLPMDLVSITR.T		K.WVALQTNELLPMDLVSITR.T
757	774	2	2043.04	1.9	1	41.8	27	95.00%	K.LFDRYDIAVTGYALNALE.G		K.LFDRYDIAVTGYALNALEGHSQLR.D
589	604	2	1600.83	2.7	0	80.6	27.1	95.00%	R.SASIASHNDALFAAVK.G		R.SASIASHNDALFAAVK.G
481	488	2	1055.44	2.9	0	38	28.9	95.00%	R.IDVCCFDK.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.IDVCCFDK.T
372	383	2	1280.64	1.6	1	75.5	28.6	95.00%	K.TGFETSQGSLVR.V		K.TGFETSQGSLVR.V
930	954	2	2464.28	0.84	1	94.1	24.5	95.00%	K.KPADLASLLLNSAGDAQGDEAPALK.L		K.KPADLASLLLNSAGDAQGDEAPALK.L
580	587	2	926.49	4.4	0	22.7	25.4	90.80%	R.FQFSSALK.R		R.FQFSSALK.R
693	709	2	1765.94	1.9	0	66.7	22.7	95.00%	R.SIMITGDNPLTAVHVAK.E		R.SIMITGDNPLTAVHVAK.E
321	335	2	1697.86	0.87	1	93.3	26.8	95.00%	K.LRPSEDNLQLDGVDK.I		K.LRPSEDNLQLDGVDK.I
968	979	2	1269.74	3.3	0	75.9	20.1	95.00%	K.LANVSAVTNIIR.Q		K.LANVSAVTNIIR.Q
867	887	2	2345.24	2.1	0	36.7	23.2	95.00%	R.WNQPQPPVPEPIAHLFPPGPK.N		R.WNQPQPPVPEPIAHLFPPGPK.N
355	371	2	1646.89	2.7	0	28.3	24.5	95.00%	K.SDIPPPPDGGALAIVTK.T		K.SDIPPPPDGGALAIVTK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
24	XPP_YEAST	28.97%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
519	537	2	1942.97	2.3	0	28.4	27.1	95.00%	E.TISSTGSNAAIIHYSPPVE.N		R.NFMGNSFETISSTGSNAAIIHYSPPVENSSMIDPTK.I
598	609	2	1287.66	2.8	0	37.2	27.8	95.00%	E.NTPGFNIDAIAR.Q		R.LIFPENTPGFNIDAIAR.Q
342	359	2	2048.94	2.3	0	45.6	30.2	95.00%	R.GSDIDYNPVFFSYVAINE.D		R.GSDIDYNPVFFSYVAINEDETILFTNNPFNDDISEYFK.I
727	740	2	1659.9	2.5	0	50.5	23.6	95.00%	R.TIVHFLQPQSISYK.W		R.TIVHFLQPQSISYK.W
362	376	2	1738.81	2.2	0	59.8	30.5	95.00%	E.TILFTNNPFNDDISE.Y		R.GSDIDYNPVFFSYVAINEDETILFTNNPFNDDISEYFK.I
189	199	2	1449.73	2.4	1	55.7	27.6	95.00%	R.QELDYNWTLLR.Q		R.QELDYNWTLLR.Q
342	361	2	2293.01	0.47	1	28.3	30.6	91.60%	R.GSDIDYNPVFFSYVAINEDE.T		R.GSDIDYNPVFFSYVAINEDETILFTNNPFNDDISEYFK.I
162	174	2	1498.67	1.6	0	51.1	29.9	95.00%	R.DLLNFNDDHPDGK.S		R.DLLNFNDDHPDGK.S
2	24	3	2487.21	1.9	1	41.8	27.6	95.00%	M.TSKPSTSDGRAHSISHVPGTHMR.G	Acetyl (+42)	-.MTSKPSTSDGRAHSISHVPGTHMR.G
145	161	2	1699.84	3.2	0	71.1	28.3	95.00%	R.AFISGFSGSAGVACITR.D	Carbamidomethyl (+57)	R.AFISGFSGSAGVACITR.D

436	453	3	2025.11	1.2	1	32.2	20	95.00%	K.KMTAQNFAIIHSPIDVLK.S		K.KMTAQNFAIIHSPIDVLK.S
538	558	2	2420.09	1.5	1	63.9	30.7	95.00%	E.NSSMIDPTKIYLCDSGSQFLE.G	Oxidation (+16)/ Carbamidomethyl (+57)	R.NFMGNSFETISSTGSNAAIIHYSPPVENSSMIDPTKIYLCDSGSQFLEGTTDITR.T
653	668	2	1725.79	0.17	1	31.1	29.7	95.00%	R.AGNIISNEPGYYKDGE.Y		R.AGNIISNEPGYYKDGEYGIR.I
653	665	2	1424.7	3.2	0	53	28.6	95.00%	R.AGNIISNEPGYYK.D		R.AGNIISNEPGYYK.D
593	609	2	1886.99	-1.3	1	65.6	25.1	95.00%	R.LIFPENTPGFNIDAIAR.Q		R.LIFPENTPGFNIDAIAR.Q
12	24	4	1428.7	-0.26	0	29.8	28.7	95.00%	R.AHSISHVPGTHMR.G		R.AHSISHVPGTHMR.G
409	421	2	1548.78	2.5	0	29	28	95.00%	E.FLIPDSASWQMVR.C		K.ITSQASSAEHEFLIPDSASWQMVR.C
437	453	2	1897.02	3.3	0	73.9	23.6	95.00%	K.MTAQNFAIIHSPIDVLK.S		K.MTAQNFAIIHSPIDVLK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
25	B3LNF5_YEAS1	18.96%	100%	26

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
90	99	2	1113.51	-1.2	1	31.8	29.4	95.00%	R.AVATSMYESR.L		R.AVATSMYESR.L
1032	1049	2	1913.05	-0.73	1	90.6	23.8	95.00%	K.IQGLEGIILTNIVSNSDK.V		K.IQGLEGIILTNIVSNSDK.V
427	455	3	3487.44	3.1	1	36.9	30.3	95.00%	K.VVDPDNADSFDCDITDFENCSLQNMFYTR.E	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.VVDPDNADSFDCDITDFENCSLQNMFYTR.E
907	919	2	1487.68	-1	0	72	29.9	95.00%	R.SLVSSTDFFQDDK.N		R.SLVSSTDFFQDDK.N
1540	1558	2	2086.94	1.9	0	58.4	30.6	95.00%	E.HTSYTDQPTTTDVPDALPE.G		R.TGPSYSSLIHDQFLDEADDLLAGHDEDANDLSSFMDQGSNFEIEEDDVPTLEEEHTSYTDQPTTTDVPDALPEGNEENIDRPDSTAPSNENQ.-
1022	1031	2	1218.56	3.5	1	30.1	28.9	95.00%	R.NTFGYVDFEK.I		R.NTFGYVDFEK.I
1217	1232	2	1685.84	-1.3	1	60.2	27.9	95.00%	R.FLLFGEAADIGGSSFR.T		R.FLLFGEAADIGGSSFR.T
1178	1189	2	1319.59	1.7	0	57.2	30.1	95.00%	E.TDSISYSTDFGK.T		K.TPHQWEYGDHGGILVLVPENSETDSISYSTDFGK.T
1328	1339	2	1201.58	0.34	0	35.4	29	95.00%	K.GLSPANAADVCK.K	Carbamidomethyl (+57)	K.GLSPANAADVCK.K
854	866	2	1405.59	1.1	0	74.9	29.7	95.00%	E.CHAVAYLTNDGGE.T	Carbamidomethyl (+57)	K.NCESILSPECHAVAYLTNDGGETFTEMLDNAIHCEFAGSLFK.Y
1295	1300	2	764.43	9.9	1	28.5	27.2	95.00%	E.FSRNIK.N	Deamidation (+1)	K.TDENCFIGNIPLSEFSRNIK.N
1307	1317	2	1527.6	2.4	1	47.6	29.5	95.00%	R.QDFECDYNFYK.A	Carbamidomethyl (+57)	R.QDFECDYNFYK.A
1563	1577	2	1657.72	2.6	1	45.4	30.1	95.00%	E.NIDRPDSTAPSNENQ.-	Deamidation (+1)	R.TGPSYSSLIHDQFLDEADDLLAGHDEDANDLSSFMDQGSNFEIEEDDVPTLEEEHTSYTDQPTTTDVPDALPEGNEENIDRPDSTAPSNENQ.-
384	395	2	1307.69	1.8	0	47.7	26.4	95.00%	K.GTMIASLYPLSR.R		K.GTMIASLYPLSR.R
445	455	2	1432.63	2.5	0	57.7	31.1	95.00%	E.NCSLQNMFYTR.E	Carbamidomethyl (+57)	K.VVDPDNADSFDCDITDFENCSLQNMFYTR.E
709	719	2	1189.57	0.18	1	29.1	28.4	95.00%	K.SVDISCEGVPK.K	Carbamidomethyl (+57)	K.SVDISCEGVPK.K
530	538	2	1119.53	1.3	0	40.6	27.6	95.00%	E.FYYSLDQGK.T		K.LAFDFPCLYAVGDYGNVIVAIPYNADEDDDPQSEFYYSLDQGK.T
1037	1049	2	1373.74	1.9	0	76	25.8	95.00%	E.GIILTNIVSNSDK.V	Deamidation (+1)	K.IQGLEGIILTNIVSNSDK.V
427	444	2	2072.82	1.6	0	49.4	30.5	95.00%	K.VVDPDNADSFDCDITDFE.N	Carbamidomethyl (+57)	K.VVDPDNADSFDCDITDFENCSLQNMFYTR.E
1439	1451	2	1498.79	1.3	1	36.4	25.7	95.00%	E.NNNTDRVVNNIVK.S		R.LGDDGLIENNNTDRVVNNIVK.S
667	682	2	1908.9	3.4	0	46	29.1	95.00%	K.CVPDYNLIVLSDVCDK.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CVPDYNLIVLSDVCDK.T
414	426	2	1444.8	2.6	0	89.7	23.6	95.00%	K.ISVDNGLTWTVLK.V		K.ISVDNGLTWTVLK.V
198	210	2	1368.64	2.8	0	31.4	29.1	95.00%	E.NSAISISDCGFAK.T	Carbamidomethyl (+57)	R.NENSAISISDCGFAK.T
196	210	2	1611.72	-0.18	1	56.4	29.9	95.00%	R.NENSAISISDCGFAK.T	Carbamidomethyl (+57)	R.NENSAISISDCGFAK.T
887	899	2	1599.68	2.5	1	68.7	30.6	95.00%	K.YPSNEDMVMCQVK.E	Carbamidomethyl (+57)	K.YPSNEDMVMCQVK.E
1267	1279	2	1607.76	2.9	1	65.6	29.5	95.00%	K.SNCLFGHQTEFLR.K	Carbamidomethyl (+57)	K.SNCLFGHQTEFLR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
26	KTR4_YEAST	39.01%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

353	360	2	989.56	2.7	0	65.7	25.6	95.00%	E.IVDLDFLR.S		K.NYDYTQGYSTCHFWTNFEIVDLDFLR.S
382	388	2	799.4	-0.16	0	31.8	23.7	95.00%	R.WGDAPVR.S		R.WGDAPVR.S
406	426	3	2476.02	0.8	0	71.5	31.1	95.00%	R.DIGYHHTPYTNCPTCPADSDR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.DIGYHHTPYTNCPTCPADSDR.C
271	281	2	1417.67	-0.43	0	70.4	29.6	95.00%	K.INYDVFQFMNK.N		K.INYDVFQFMNK.N
75	82	2	947.48	2.2	0	43.1	27.7	95.00%	E.VLDSIMDR.L		K.TESADELPDHDAEVLDSIMDR.L
375	381	2	890.39	2	1	32.1	28.9	95.00%	K.GGFYYER.W		K.GGFYYER.W
196	213	2	2062.91	3.7	1	63.8	30.5	95.00%	E.FGTIGPDNWNMPDSIDRE.R		R.VVEFGTIGPDNWNMPDSIDRER.Y
335	352	2	2331.92	1.2	0	64.6	30.6	95.00%	K.NYDYTQGYSTCHFWTNFE.I	Carbamidomethyl (+57)	K.NYDYTQGYSTCHFWTNFEIVDLDFLR.S
75	89	2	1828.91	2.8	1	52.7	28.6	95.00%	E.VLDSIMDRLHEPLYE.K		K.TESADELPDHDAEVLDSIMDRLHEPLYEK.D
406	435	4	3463.41	-0.51	1	26.7	30.5	95.00%	R.DIGYHHTPYTNCPTCPADSDRCNGNCVPGK.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Deamidation (+1)/ Carbamidomethyl (+57)	R.DIGYHHTPYTNCPTCPADSDRCNGNCVPGK.F
114	124	2	1268.71	-1	1	44.4	23.8	95.00%	E.ISEPKVDNLVR.S		K.QLYEEFLLQEISEPKVDNLVR.S
196	212	2	1933.87	1.8	0	70.8	30.6	95.00%	E.FGTIGPDNWNMPDSIDR.E		R.VVEFGTIGPDNWNMPDSIDR.E
436	453	2	2251.02	1.6	0	68	30.9	95.00%	K.FTPWSDLDNQNCQATWIR.H	Carbamidomethyl (+57)	K.FTPWSDLDNQNCQATWIR.H
135	142	2	857.53	-0.6	0	41.8	24.2	95.00%	K.GTILSLVR.N		K.GTILSLVR.N
389	398	2	1047.6	-0.12	0	52.3	21.4	95.00%	R.SLALALFADK.S		R.SLALALFADK.S
245	254	3	1269.65	2.7	1	26.9	26.9	95.00%	K.EFYHHPLLSK.Y		K.EFYHHPLLSK.Y
148	157	2	1144.6	2.2	0	61.4	27.3	95.00%	E.DIISSIQQLE.E		R.NSDLEDIISSIQQLEEEYNK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
27	A6ZYU5_YEAS7	17.99%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
534	543	2	1117.55	0.61	0	34	28.5	95.00%	K.SASWVPTSQR.G		K.SASWVPTSQR.G
1	12	2	1371.67	2.8	0	27.7	28.5	93.90%	-.MNSTPDLISPQK.S	Acetyl (+42)	-.MNSTPDLISPQK.S
544	562	3	2197.98	2.8	1	50	30.9	95.00%	R.GANYDADALMHDDQPFYKK.M		R.GANYDADALMHDDQPFYKK.M
311	321	3	1294.72	0.84	1	43.6	22.7	95.00%	E.LFTGKPAMFKR.T		R.AAGSASWGELFTGKPAMFKR.T
225	233	2	1153.52	2.9	0	49.9	30.3	95.00%	K.NYSNSVQWR.V	Deamidation (+1)	K.NYSNSVQWR.V
302	320	2	1954.96	1.1	1	71.4	28.1	95.00%	R.AAGSASWGELFTGKPAMFK.R		R.AAGSASWGELFTGKPAMFK.R
544	561	2	2069.88	1.1	0	95.4	30.7	95.00%	R.GANYDADALMHDDQPFYK.K		R.GANYDADALMHDDQPFYK.K
36	56	2	2246.05	1.8	1	86.1	29.7	95.00%	K.GVQDDFQAEADQVLTNPNTGK.G		K.GVQDDFQAEADQVLTNPNTGK.G
279	289	2	1279.63	4	0	26.6	28.6	92.20%	K.VAPDHPFIQQE.L		K.VAPDHPFIQQELEVIEASVEEAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
28	B3LGF8_YEAS1	24.74%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
79	95	2	1817.92	0.7	1	80.1	27.2	95.00%	K.AVDIDTIDAQPLHEGPK.I		K.AVDIDTIDAQPLHEGPK.I
192	208	2	1731.87	2.1	1	58	27	95.00%	K.SLHIVAPSPEVPVSGDE.I		K.SLHIVAPSPEVPVSGDEITSYGYGSIPQSIGDVENGLNPPYVENTSSDELVHDLTR.R
79	92	2	1535.75	1.6	0	61.9	29	95.00%	K.AVDIDTIDAQPLHE.G		K.AVDIDTIDAQPLHEGPK.I
431	443	2	1518.82	1.8	0	33.3	24.5	95.00%	K.STLYGRPTPTLWK.R		K.STLYGRPTPTLWK.R
209	225	2	1784.85	1.9	0	34.7	29.2	95.00%	E.ITSYGYGSIPQSIGDVE.N		K.SLHIVAPSPEVPVSGDEITSYGYGSIPQSIGDVENGLNPPYVENTSSDELVHDLTR.R
115	127	3	1478.67	1.7	1	34.8	29.7	95.00%	K.ANEDDLKPPSQHE.A		K.ANEDDLKPPSQHEACGNSALQSSITDFSDR.S
431	444	3	1674.92	0.54	1	30.5	23.2	95.00%	K.STLYGRPTPTLWKR.F		K.STLYGRPTPTLWKR.F
345	358	2	1378.73	0.37	0	47.8	26.1	95.00%	R.CVTGFGGGSLIALK.S	Carbamidomethyl (+57)	R.CVTGFGGGSLIALK.S

145	161	2	1836.83	1.9	0	44.9	30.5	95.00%	R.SVSPLQSITSCNTPMSE.H	Carbamidomethyl (+57)	R.SVSPLQSITSCNTPMSEHELPVSSSNSFER.A
174	191	2	1947.9	0.15	1	86.1	30.1	95.00%	E.RADDMPVVQADNQTSSSK.S		R.SVSPLQSITSCNTPMSEHELPVSSSNSFERADDMPVVQADNQTSSSK.S
164	174	2	1221.6	0.96	1	53.3	28.5	95.00%	E.LPVSSSNSFER.A		R.SVSPLQSITSCNTPMSEHELPVSSSNSFER.A
209	234	2	2769.31	2.6	1	68.8	28.8	95.00%	E.ITSYGYGSIPQSIGDVENGLNPPYVE.N	Deamidation (+1)	K.SLHIVAPSPEVPVSGDEITSYGYGSIPQSIGDVENGLNPPYVENTSSDELVHDLTR.R
44	56	2	1401.71	1.2	1	28.5	28	95.00%	R.TSNQIALGNDKIE.E		R.TSNQIALGNDKIEEINENSPLLSAPSK.Q
175	191	2	1791.79	-0.11	0	77.9	30.9	95.00%	R.ADDMPVVQADNQTSSSK.S		R.ADDMPVVQADNQTSSSK.S
162	173	2	1411.57	1.3	1	72.5	30.6	95.00%	E.HELPVSSSNSFE.R	Phospho (+80)	R.SVSPLQSITSCNTPMSEHELPVSSSNSFER.A
128	144	2	1828.79	0.33	0	128	30.8	95.00%	E.ACGNSALQSSITDFSDR.S	Carbamidomethyl (+57)/ Deamidation (+1)	K.ANEDDLKPPSQHEACGNSALQSSITDFSDR.S
61	72	2	1269.66	1.8	1	43.8	26.9	95.00%	E.NSPLLSAPSKQE.E		K.IEEINENSPLLSAPSKQEEVSIPK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
29	YBS4_YEAST	20.49%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
297	311	3	1809.93	0.79	1	27.5	27.2	95.00%	R.NLYHTIKDSIQYTSK.A		R.NLYHTIKDSIQYTSK.A
549	585	3	3969.72	-0.063	1	93.4	29.9	95.00%	E.NLEQPQDQLTSSQDDQASIQDDNVSTTSAGPSHNVDE.D		R.DGQENLEQPQDQLTSSQDDQASIQDDNVSTTSAGPSHNVDEDHGMDSSSQQHDER.V
221	233	2	1277.67	2.7	1	65.4	27.3	95.00%	K.YVINLEGTGAGGK.A		K.YVINLEGTGAGGK.A
950	965	2	1870.95	1.5	1	28.4	27.5	95.00%	E.LINYAPLSFSFTNEQK.G		K.IPAFDELINYAPLSFSFTNEQK.G
411	418	2	976.54	4.7	0	28.6	25.9	95.00%	K.LFSNDIIR.S		K.LFSNDIIR.S
880	890	2	1384.7	1.1	1	47.1	28.8	95.00%	E.LQLHKLDFDQE.T		K.SASGINELQLHKLDFDQETYHIGVQWFPK.L
747	761	2	1699.94	2.2	0	45.8	22.4	95.00%	E.GNFLKPMLQDLPSIK.Y		R.EGNFLKPMLQDLPSIK.Y
191	201	2	1353.62	2.2	1	47	30.2	95.00%	R.TLIFNFNNNEE.F		R.TLIFNFNNNEEFGLLGASTYFDHSWSNLTK.Y
891	901	2	1374.71	2.4	0	34.3	27.9	95.00%	E.TYHIGVQWFPK.L		K.LDFDQETYHIGVQWFPK.L
255	269	2	1776.83	2.8	0	39.6	29.4	95.00%	E.NPFGNSIYQQGFYSR.Y		K.ENPFGNSIYQQGFYSR.Y
950	963	2	1614.8	2.6	0	40	28.4	95.00%	E.LINYAPLSFSFTNE.Q		K.IPAFDELINYAPLSFSFTNEQK.G
885	901	2	2123.01	6.2	1	37.6	29.8	95.00%	K.LDFDQETYHIGVQWFPK.L	Deamidation (+1)	K.LDFDQETYHIGVQWFPK.L
726	745	2	2112.07	1	0	95.7	26.5	95.00%	R.FSQNIDLSQGNAASVHVLGR.E		R.FSQNIDLSQGNAASVHVLGR.E
129	140	2	1398.74	2.4	1	31.1	25.7	95.00%	R.VTYFESSNILVK.L		R.VTYFESSNILVK.L
254	269	2	1905.87	1.5	1	93.8	30.1	95.00%	K.ENPFGNSIYQQGFYSR.Y		K.ENPFGNSIYQQGFYSR.Y
529	543	2	1785.7	0.67	0	45.8	30.5	95.00%	R.DHHSNYSSHSQIDME.R		R.DHHSNYSSHSQIDMER.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
30	A6ZX34_YEAS7	28.61%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
196	215	2	2219.98	2.3	0	40.3	29.8	95.00%	E.QDFSPFGGYPASSFPLMIDE.K	Oxidation (+16)	R.SPTSSPGNESSASFSSNPFLGEQDFSPFGGYPASSFPLMIDEK.E
130	143	2	1387.73	2.6	0	60.2	25.9	95.00%	R.AIASSPSLNSNLSK.N		R.AIASSPSLNSNLSK.N
69	91	3	2500.16	0.82	0	69.2	29.7	95.00%	E.SLSSSVHYQPQGSDSSLLHDNSR.L		R.DGESLSSSVHYQPQGSDSSLLHDNSR.L
340	360	2	2476.06	2.3	0	65.1	31.4	95.00%	R.TFYDGDDPYWTAPDVHYDATK.D		R.TFYDGDDPYWTAPDVHYDATK.D
594	607	2	1634.81	0.72	0	59.7	28.8	95.00%	R.WFVGDTPTYTIHAK.A		R.WFVGDTPTYTIHAK.A
583	593	2	1357.58	1.1	0	56.1	29.6	95.00%	E.YLNDDDNGYIR.W	Deamidation (+1)	K.YAIEYLNDDDNGYIR.W

411	420	2	1103.57	1.9	0	34	27.1	95.00%	E.ISANLPNYGR.V		K.VCFTQGALEISANLPNYGR.V
402	420	2	2109.03	-1.9	1	56.3	28.8	95.00%	K.VCFTQGALEISANLPNYGR.V	Carbamidomethyl (+57)	K.VCFTQGALEISANLPNYGR.V
697	704	2	897.42	1.6	0	40	29.6	95.00%	E.DAGYTFPK.N		R.IYQPSNAISVTCDPSDYPTYDYIQSHLNAFQNANLTTWEDAGYTFPK.N
114	129	2	1752.86	1.6	0	46	29.1	95.00%	R.AVSTANDNSFLQPPHR.A		R.AVSTANDNSFLQPPHR.A
340	363	3	2833.21	2.5	1	40.1	30.1	95.00%	R.TFYDGDDPYWTAPDVHYDATKDLE.W		R.TFYDGDDPYWTAPDVHYDATKDLEWYSPDASTTVNGTLQLR.M
579	593	2	1832.82	-0.77	1	97.8	30.8	95.00%	K.YAIEYLNDDDNGYIR.W		K.YAIEYLNDDDNGYIR.W
476	493	2	2013.87	0.92	1	90.4	30.9	95.00%	K.LSICTCDGEDHPNQGVGR.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.LSICTCDGEDHPNQGVGR.G
183	195	2	1328.59	2.6	0	35.2	30.1	95.00%	E.SSASFSSNPFLGE.Q		R.SPTSSPGNESSASFSSNPFLGEQDFSPFGGYPASSFPLMIDEK.E
304	316	2	1358.66	-0.9	0	51.5	29.1	95.00%	R.TSLVDPDTPDTAK.T		R.TSLVDPDTPDTAK.T
393	401	2	1049.5	3.4	0	51.8	28.3	95.00%	R.SGMLQSWNK.V		R.SGMLQSWNK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
31	A6ZY55_YEAS7	33.14%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
307	320	2	1474.73	1	0	84.9	28.7	95.00%	E.ILDTTDNINSAGNK.S		K.EILDTTDNINSAGNK.S
306	320	2	1603.77	2.7	1	54.9	29.3	95.00%	K.EILDTTDNINSAGNK.S		K.EILDTTDNINSAGNK.S
673	685	2	1511.74	-0.88	0	38.9	29.3	95.00%	R.NSPPDYGFILFSR.N		R.NSPPDYGFILFSR.N
78	90	2	1436.78	-0.91	1	86.9	25.2	95.00%	R.ILSVESSIIDFSK.G		R.ILSVESSIIDFSK.G
32	47	2	1817.75	2.6	1	74.5	30.3	95.00%	K.VTAYDYDNPNDSGMEK.L		K.VTAYDYDNPNDSGMEK.L
295	305	2	1190.64	2.7	0	44.9	26.6	95.00%	R.IIDDSIISTSK.E		R.IIDDSIISTSK.E
48	59	2	1422.65	1.7	0	31	29.9	95.00%	K.LLNQCSVAFDQE.F	Carbamidomethyl (+57)	K.LLNQCSVAFDQEFQNVNLFVSLK.I
718	746	3	3131.33	1.8	0	103	30.3	95.00%	K.HPHCSSTNYGSVASFGSQSTSASYDDVQR.Y	Carbamidomethyl (+57)	K.HPHCSSTNYGSVASFGSQSTSASYDDVQR.Y
570	584	2	1724.74	0.86	1	62.5	31	95.00%	R.DQYKLNSDDSLSPDE.F		R.DQYKLNSDDSLSPDEFFQLGK.D
404	414	2	1292.72	2.8	0	46.9	21.8	95.00%	R.NHVVTNDLLLR.D		R.NHVVTNDLLLR.D
367	390	2	2565.24	1.2	0	54.6	28.2	95.00%	E.GSPLLLTDDNINQHPNMIVSSTAE.D		K.YVSISILDTVGNEGSPLLLTDDNINQHPNMIVSSTAEDTCIVMCHVGGLR.N
597	615	3	2018.98	1.2	1	22.6	28.5	92.70%	E.FDLTGPINNSQGSVDSGRR.V		R.LEEEFDLTGPINNSQGSVDSGRR.V
646	660	2	1714.75	2	0	69.7	31.1	95.00%	E.DNLDNAFYIDTNGSR.S	Deamidation (+1)	R.YWNEFDEQEEDNLDNAFYIDTNGSR.S
447	456	3	1251.68	3.3	1	40.2	25.2	95.00%	K.IALEWIQSHR.L		K.IALEWIQSHR.L
342	353	2	1298.69	1.7	1	55.2	25.3	95.00%	K.NILPSAVQSNEK.Y		K.NILPSAVQSNEK.Y
487	502	2	1699.95	4.3	0	34.1	21.5	95.00%	E.SITIGNVSTLPFPILE.I		R.FISADNGDIYLIALDESITIGNVSTLPFPILEIK.K
391	403	2	1516.7	1.7	0	53.5	30.3	95.00%	E.DTCIVMCHVGGLR.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.YVSISILDTVGNEGSPLLLTDDNINQHPNMIVSSTAEDTCIVMCHVGGLR.N
574	590	2	1910.89	-0.95	1	63.3	29.7	95.00%	K.LNSDDSLSPDEFFQLGK.D		K.LNSDDSLSPDEFFQLGK.D
327	339	2	1488.76	2.5	0	72.8	27.8	95.00%	K.SFNDLQHTLSLSK.Q		K.SFNDLQHTLSLSK.Q
509	522	2	1462.69	-0.55	1	62.4	28.5	95.00%	R.SSGLSQTAINEDNK.F		R.SSGLSQTAINEDNK.F
60	70	2	1307.73	3.1	0	28.5	23	95.00%	E.FQNVNLFVSLK.I		K.LLNQCSVAFDQEFQNVNLFVSLK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
32	A7A0C8_YEAS7	39.00%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
381	392	2	1134.59	2.4	0	33.2	27.4	95.00%	E.TVAASAVAAVFE.Q		R.NCTPKPTSTTETVAASAVAAVFEQK.A
217	225	2	1001.55	3.8	0	28	25.6	95.00%	R.TANDVLTIR.E		R.TANDVLTIR.E

92	108	2	1869.84	0.68	0	38.2	30.6	95.00%	R.TGTTTNDVDYPIPPNHE.M		R.TGTTTNDVDYPIPPNHEMIFTTDDK.Y
397	409	2	1314.75	2.9	0	41.1	21.6	95.00%	K.AIIVLSTSGTTPR.L		K.AIIVLSTSGTTPR.L
31	41	2	1226.66	1.2	1	48.4	24.6	95.00%	K.TNNPETLVALR.K		K.TNNPETLVALR.K
7	20	2	1499.84	-0.15	1	34.8	22.6	95.00%	R.LTSLNVVAGSDLRR.T		R.LTSLNVVAGSDLRR.T
178	193	2	1595.81	2.3	0	62.4	27.6	95.00%	K.GVNLPGTDVDLPALSE.K		K.GVNLPGTDVDLPALSEK.D
357	369	2	1568.73	1.8	0	28.4	29.5	93.50%	E.QAIAYLPNYDDMR.N		K.GNYPINAVTTMAETAVIAEQAIAYLPNYDDMR.N
315	337	2	2321.09	1.4	1	109	29.5	95.00%	E.VSDVGNAILDGADCVMLSGETAK.G	Carbamidomethyl (+57)	R.AEVSDVGNAILDGADCVMLSGETAK.G
460	466	2	819.45	-0.16	1	35.5	26.2	95.00%	R.INFGIEK.A		R.INFGIEK.A
414	425	2	1500.83	1.3	0	39.4	23.3	95.00%	K.YRPNCPIILVTR.C	Carbamidomethyl (+57)	K.YRPNCPIILVTR.C
73	86	2	1526.89	2.3	0	39.9	17.8	95.00%	E.LYPGRPLAIALDTK.G		K.SEELYPGRPLAIALDTK.G
287	312	4	2934.46	1.8	1	37.3	27.3	95.00%	K.SNLAGKPVICATQMLESMTYNPRPTR.A	Carbamidomethyl (+57)	K.SNLAGKPVICATQMLESMTYNPRPTR.A
92	116	3	2821.28	0.71	1	37.8	30.6	95.00%	R.TGTTTNDVDYPIPPNHEMIFTTDDK.Y		R.TGTTTNDVDYPIPPNHEMIFTTDDK.Y
287	302	2	1730.87	1.7	0	73.8	27.5	95.00%	K.SNLAGKPVICATQMLE.S	Carbamidomethyl (+57)	K.SNLAGKPVICATQMLESMTYNPRPTR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
33	BPT1_YEAST	16.93%	100%	25

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
645	655	2	1115.66	2.8	0	48.7	20.5	95.00%	E.SIIGSSQIALK.N		R.TDEESIIGSSQIALK.N
1065	1077	2	1468.71	2.8	1	78.5	29.3	95.00%	R.SPMTFFETTPVGR.I		R.SPMTFFETTPVGR.I
1313	1325	2	1480.79	2.4	1	58.9	24.8	95.00%	R.ENLDPVLNNINVK.I		R.ENLDPVLNNINVK.I
1343	1351	2	1006.58	-0.72	0	30.7	21.4	95.00%	K.STLSLALFR.I		K.STLSLALFR.I
389	403	2	1631.86	2.9	0	87.6	25.2	95.00%	K.STGDILNLMSVDVLR.I		K.STGDILNLMSVDVLR.I
897	907	2	1269.68	0.93	1	23.6	25.9	91.40%	E.VDEPLQLKVTE.S		R.SESEVDEPLQLKVTESETEDEVVTESELELIK.A
1438	1448	2	1200.6	2	0	33.9	26.8	95.00%	E.DGNVNDILDVK.I		R.GDDSNEEDGNVNDILDVK.I
629	643	2	1620.76	0.86	1	109	29.1	95.00%	E.VLTSSQSGDNLRTDE.E		K.EVLTSSQSGDNLRTDEESIIGSSQIALK.N
930	950	4	2253.3	0.23	1	18.3	13.2	95.00%	R.ASLATLRPRPFVGAQLDSVKK.T		R.ASLATLRPRPFVGAQLDSVKK.T
897	904	2	940.53	2.2	0	27.3	24.1	95.00%	E.VDEPLQLK.V		R.SESEVDEPLQLK.V
617	625	2	1181.59	3.3	0	25.9	28.3	91.40%	E.MNNITFLWK.S	Oxidation (+16)	R.ALPAIEMNNITFLWK.S
62	71	3	1177.65	2.4	1	19.5	24.8	93.40%	R.FKNFPTLPSK.I		R.FKNFPTLPSK.I
807	816	2	1160.68	-0.18	1	23.9	22.4	93.50%	K.NIIEYVLIGK.T		K.NIIEYVLIGK.T
788	806	2	2049.05	-1.3	1	59.5	26.8	95.00%	R.ADIYLLDDILSAVDAEVSK.N		R.ADIYLLDDILSAVDAEVSK.N
1504	1513	3	1194.68	-0.5	1	38.8	20.8	95.00%	K.DRTILTIAHR.I		K.DRTILTIAHR.I
243	259	2	1913.1	2.2	1	41.5	16.2	95.00%	K.IKDPNQLPLPPVDLNIK.S		K.IKDPNQLPLPPVDLNIK.S
1449	1461	2	1387.67	0.051	1	66.3	29.8	95.00%	K.INENGSNLSVGQR.Q	Deamidation (+1)	K.INENGSNLSVGQR.Q
1377	1394	3	1924.01	2.5	1	70.6	25.7	95.00%	R.SHLAIIPQDAQAFEGTVK.T		R.SHLAIIPQDAQAFEGTVK.T
1506	1513	2	923.55	-1.9	0	32.8	18.5	95.00%	R.TILTIAHR.I		R.TILTIAHR.I
1506	1522	3	1910.05	3.1	1	27	20.5	95.00%	R.TILTIAHRIDTVLDSDK.I		R.TILTIAHRIDTVLDSDK.I
611	625	2	1759.93	-0.58	1	57.7	24.7	95.00%	R.ALPAIEMNNITFLWK.S		R.ALPAIEMNNITFLWK.S
745	753	2	1056.57	4	0	25.8	25.4	95.00%	K.ACQLLPDLK.I	Carbamidomethyl (+57)	K.ACQLLPDLK.I
1462	1468	2	872.49	-0.56	0	28.1	27.7	95.00%	R.QLLCLAR.A	Carbamidomethyl (+57)	R.QLLCLAR.A
1314	1325	2	1351.75	2.2	0	35.4	24.3	95.00%	E.NLDPVLNNINVK.I		R.ENLDPVLNNINVK.I
595	602	2	993.48	2.4	1	42.7	28.2	95.00%	E.IDDSFIER.I		K.SFLLSDEIDDSFIER.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
34	A6ZR26_YEAS7	19.38%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	9	2	912.51	3.2	0	42.8	24.3	95.00%	M.SSAPLLQR.T	Acetyl (+42)	-.MSSAPLLQR.T
25	31	2	881.44	1.8	1	27.1	28	93.80%	K.VFFANER.T		K.VFFANER.T
15	24	2	1122.68	2.6	1	41.8	15.1	95.00%	K.IALPTRVEPK.V		K.IALPTRVEPK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
35	A6ZSR0_YEAS7	34.34%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
500	518	2	1955.01	2.6	0	55.8	25.4	95.00%	K.TVPPPDFTSMVTLPTGPAK.I		K.TVPPPDFTSMVTLPTGPAK.I
390	418	4	3266.59	3.4	1	41.9	27.7	95.00%	K.DMHVPNTSYVIPAGYHVLVSPGYTHLRDE.Y		K.DMHVPNTSYVIPAGYHVLVSPGYTHLRDEYFPNAHQFNIHR.W
219	234	2	1876.92	3.1	1	98.8	29	95.00%	R.AKLDTDFAYLYSDLDK.G		R.AKLDTDFAYLYSDLDK.G
235	252	2	2160.11	-2	1	53.7	25.9	95.00%	K.GFTPINFVFPNLPLEHYR.K		K.GFTPINFVFPNLPLEHYR.K
275	289	2	1804.87	1.9	1	44.5	29.1	95.00%	K.NNDIQDRDLIDSLMK.N	Oxidation (+16)	K.NNDIQDRDLIDSLMK.N
203	210	2	925.47	2	0	35.9	27.2	95.00%	E.MTIFTASR.S		R.TTGTIDVMVTQPEMTIFTASR.S
117	136	2	2060.06	2.7	1	59.4	25	95.00%	K.LADVSAEAAYAHLTTPVFGK.G		K.LADVSAEAAYAHLTTPVFGK.G
190	210	2	2298.13	2.4	1	58.2	27.8	95.00%	R.TTGTIDVMVTQPEMTIFTASR.S		R.TTGTIDVMVTQPEMTIFTASR.S
124	136	2	1374.73	1.9	0	70.4	26.1	95.00%	E.AAYAHLTTPVFGK.G		K.LADVSAEAAYAHLTTPVFGK.G
455	467	2	1292.65	1.5	0	41.1	28.5	95.00%	K.GVSSPYLPFGGGR.H		K.GVSSPYLPFGGGR.H
137	146	2	1179.53	0.27	0	28.4	29.7	93.30%	K.GVIYDCPNSR.L	Carbamidomethyl (+57)	K.GVIYDCPNSR.L
445	454	2	1055.53	2.3	0	33.3	27.3	95.00%	E.VDYGFGAISK.G		R.WNNDSASSYSVGEEVDYGFGAISK.G
221	234	2	1677.78	-1.3	0	124	30.2	95.00%	K.LDTDFAYLYSDLDK.G		K.LDTDFAYLYSDLDK.G
260	270	2	1182.64	3	0	53.7	25	95.00%	K.AISGTYMSLIK.E		K.AISGTYMSLIK.E
235	249	2	1703.9	4.4	0	47.1	25.2	95.00%	K.GFTPINFVFPNLPLE.H		K.GFTPINFVFPNLPLEHYR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
36	B3LPA7_YEAS1	12.77%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
39	53	2	1649.78	1.4	1	33.3	29.5	95.00%	E.AIDPSNKTTPYSIDE.K		K.QNNIGEQSMQELPEDQIEHEMEAIDPSNKTTPYSIDEK.Q
287	300	2	1397.7	3.3	0	31.2	28	95.00%	R.NPGAWGPGIISSDK.S		R.NPGAWGPGIISSDK.S
504	513	2	1146.61	2.7	1	29.1	26.8	95.00%	R.GISRDDLPFK.A		R.GISRDDLPFK.A
573	578	2	834.47	1.9	1	29.6	26.9	95.00%	R.FIWKLE.D		R.FIWKLEDIDIDSDR.R
4	12	2	1022.54	2.3	0	55.3	25.5	95.00%	R.FSNIITSNK.W		R.FSNIITSNK.W
4	15	2	1452.69	2.7	1	62.1	29.1	95.00%	R.FSNIITSNKWDE.K		R.FSNIITSNKWDEK.Q
62	82	2	2110.08	2.2	0	116	26.2	95.00%	K.HGSLQGGAIADVNSITNSLTR.L		K.HGSLQGGAIADVNSITNSLTR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
37	YNL5_YEAST	22.52%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
553	562	2	1111.59	3.2	0	55.7	25.1	95.00%	E.SVTSSILSYR.D		K.FLESVTSSILSYR.D
215	226	2	1393.65	1.3	1	64.4	29.3	95.00%	R.RIDDANISTFNE.N		R.RIDDANISTFNENHTNSTENR.D
416	433	2	1941.04	2.9	1	68.4	22.8	95.00%	K.IKGPFTTVGYDLGGLFTR.V		K.IKGPFTTVGYDLGGLFTR.V
379	407	3	3197.56	2.6	1	85.7	27.8	95.00%	R.YCLYDRPGYGLSDSPPAPISIAMVAESLR.Y	Carbamidomethyl (+57)	R.YCLYDRPGYGLSDSPPAPISIAMVAESLR.Y
37	52	2	1469.72	-1	1	69.6	28.3	95.00%	R.TLGAGSANGPAVNEGR.D		R.TLGAGSANGPAVNEGR.D
563	575	2	1430.7	0.061	1	66.7	29.3	95.00%	R.DVTNNAESLQNVK.T		R.DVTNNAESLQNVK.T
465	487	2	2240.92	2.7	1	68.5	30.8	95.00%	R.LLPPGRGDGDDGDDGNGNDGDGR.N	Deamidation (+1)	R.LLPPGRGDGDDGDDGNGNDGDGR.N
588	596	2	1117.53	1.7	0	39.1	28.4	95.00%	K.SALWGDWQR.D		K.SALWGDWQR.D
553	569	2	1854.9	2.5	1	61.2	29.2	95.00%	E.SVTSSILSYRDVTNNAE.S		K.FLESVTSSILSYRDVTNNAESLQNVK.T
297	311	2	1711.92	0.46	1	39.9	25.3	95.00%	R.LTHKLPITVQSPSYE.A		R.LTHKLPITVQSPSYEAFHYVDAAK.T
418	433	2	1699.86	-1.2	0	75.6	27.3	95.00%	K.GPFTTVGYDLGGLFTR.V		K.GPFTTVGYDLGGLFTR.V
379	404	2	2841.34	0.64	0	51	29.1	95.00%	R.YCLYDRPGYGLSDSPPAPISIAMVAE.S	Carbamidomethyl (+57)	R.YCLYDRPGYGLSDSPPAPISIAMVAESLR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
38	A6ZWJ5_YEAS7	41.03%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
171	187	2	1857.92	2.5	1	74.2	28.1	95.00%	R.QAITDSMNGDPELINIK.F		R.QAITDSMNGDPELINIK.F
129	140	2	1378.63	1.7	0	62	29.4	95.00%	R.DSMTQILQSIDE.V		R.DSMTQILQSIDEVQVK.F

423	436	3	1585.71	2.5	1	28.9	30.8	95.00%	R.SGSCGGHYFDIMKK.D	Carbamidomethyl (+57)	R.SGSCGGHYFDIMKK.D
34	46	2	1582.77	2.9	1	63.2	28.5	95.00%	K.QMSEQYVTPYLPK.S		K.QMSEQYVTPYLPK.S
210	223	2	1442.74	1.2	0	44.9	28	95.00%	E.SLISLANVPDGDSR.A		K.AAESLISLANVPDGDSR.A
119	128	2	1194.61	0.92	1	60.3	27.7	95.00%	K.ACFVSLITER.D	Carbamidomethyl (+57)	K.ACFVSLITER.D
207	223	2	1713.86	3	1	54.3	28	95.00%	K.AAESLISLANVPDGDSR.A		K.AAESLISLANVPDGDSR.A
257	267	2	1465.67	2.2	0	54.9	30	95.00%	K.LYCDIDHDLFR.W	Carbamidomethyl (+57)	K.LYCDIDHDLFR.W
231	238	2	1092.52	1.4	0	40.2	29.2	95.00%	R.YFAGFFWR.H		R.YFAGFFWR.H
364	380	3	1910.03	-0.51	0	34.6	22.9	95.00%	K.WSDSIIHTIGLSMLLPK.D		K.WSDSIIHTIGLSMLLPK.D
381	387	2	934.46	0.93	1	25.7	27.1	92.90%	K.DKIHFFE.N		K.DKIHFFENIGFHYDK.Y
148	165	2	2101	-1.2	1	90.8	29.2	95.00%	K.NFAYPWVFISQGELDGMK.Q		K.NFAYPWVFISQGELDGMK.Q
396	422	3	3456.37	0.9	0	65.7	29.5	95.00%	K.YNNCPLNDDIWNQYNCNCDQGNDFTFR.S	Carbamidomethyl (+57)/Carbamidomethyl (+57)/Carbamidomethyl (+57)	K.YNNCPLNDDIWNQYNCNCDQGNDFTFR.S
129	144	2	1832.92	-1.5	1	52.7	27	95.00%	R.DSMTQILQSIDEVQVK.F		R.DSMTQILQSIDEVQVK.F
335	342	2	995.52	2.6	0	67.3	25.7	95.00%	E.IGNLNFYR.S		K.DSEDFNNCEFTSNFEIGNLNFYR.S
128	140	2	1534.74	3.3	1	41.9	29.4	95.00%	E.RDSMTQILQSIDE.V		K.ACFVSLITERDSMTQILQSIDEVQVK.F
423	435	2	1457.61	2.4	0	37	30.1	95.00%	R.SGSCGGHYFDIMK.K	Carbamidomethyl (+57)	R.SGSCGGHYFDIMK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
39	A6ZR77_YEAS7	29.77%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
173	194	2	2420.04	-1.4	0	48.4	30.4	95.00%	K.SCASSSNNDPNLIYMVDFGMAK.Q	Carbamidomethyl (+57)	K.SCASSSNNDPNLIYMVDFGMAK.Q
402	411	2	1107.56	-0.74	0	33.7	28.4	95.00%	R.ISSNPQSFTK.Q		R.ISSNPQSFTK.Q
219	228	2	1224.57	3.2	0	26.5	29.6	90.10%	R.YMSINTHFGR.E		R.YMSINTHFGR.E
321	339	3	2204.99	2.4	1	42.3	30.4	95.00%	R.LNDLKDDGHYDWMDLNGGK.G		R.LNDLKDDGHYDWMDLNGGK.G
140	163	3	2969.52	0.14	1	36.6	24.5	95.00%	R.AIHDHDLIYRDIKPDNFLISQYQR.I		R.AIHDHDLIYRDIKPDNFLISQYQR.I
468	484	3	1978.92	-0.55	1	35	30.3	95.00%	R.SNNEHNLPNHYTNLANK.N		R.SNNEHNLPNHYTNLANK.N
47	64	2	2016.04	2.1	1	56.6	26.4	95.00%	R.DSSIIMANEPVAIKFEPR.H		R.DSSIIMANEPVAIKFEPR.H
150	163	2	1735.89	2.6	0	49.5	27	95.00%	R.DIKPDNFLISQYQR.I		R.DIKPDNFLISQYQR.I
275	295	2	2435.28	3.9	0	103	22.9	95.00%	K.LNPDDLLLNNAIPYQFATYLK.Y		K.LNPDDLLLNNAIPYQFATYLK.Y
472	484	2	1535.75	2.6	0	47.8	29.3	95.00%	E.HNLPNHYTNLANK.N	Deamidation (+1)	R.SNNEHNLPNHYTNLANK.N
5	19	2	1591.85	2.6	0	62.9	24.8	95.00%	R.SSQHIVGIHYAVGPK.I		R.SSQHIVGIHYAVGPK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
40	A6ZPW7_YEAS7	32.56%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
48	60	2	1482.8	1.1	1	54.2	25.3	95.00%	R.RQSILDHPVGSFK.G		R.RQSILDHPVGSFK.G
126	170	4	4720.26	2.2	1	21.4	25.5	95.00%	R.ITNLANNDRVSTASMAIHDDDYGSIQNSTIGDSGSILRPTASLTE.M		R.ITNLANNDRVSTASMAIHDDDYGSIQNSTIGDSGSILRPTASLTEMMSGGAGR.R
368	388	2	2275.08	-1.4	1	42.2	29.5	95.00%	K.SSSPGSLVNPMETSMWPIDLK.H		K.SSSPGSLVNPMETSMWPIDLK.H
135	178	4	4456.05	-0.82	1	29.8	28	95.00%	R.VSTASMAIHDDDYGSIQNSTIGDSGSILRPTASLTEMMSGGAGR.R		R.VSTASMAIHDDDYGSIQNSTIGDSGSILRPTASLTEMMSGGAGR.R
180	191	2	1381.66	2.4	0	81.9	29.2	95.00%	R.FTNNDMDSIVVK.R		R.FTNNDMDSIVVK.R
135	170	3	3708.75	0.9	0	63.6	27.8	95.00%	R.VSTASMAIHDDDYGSIQNSTIGDSGSILRPTASLTE.M		R.VSTASMAIHDDDYGSIQNSTIGDSGSILRPTASLTEMMSGGAGR.R
179	191	2	1537.76	2.5	1	71.4	28	95.00%	R.RFTNNDMDSIVVK.R		R.RFTNNDMDSIVVK.R
17	26	2	1210.69	2.3	0	25.2	22.4	95.00%	E.VHYISIPLNR.G		R.SEVHYISIPLNR.G
114	125	2	1296.73	-0.33	0	32.9	23.2	95.00%	R.LSVTLNNAGRPR.I		R.LSVTLNNAGRPR.I
380	388	2	1089.56	2.7	0	29	28.9	94.90%	E.TSMWPIDLK.H		K.SSSPGSLVNPMETSMWPIDLK.H
484	512	3	3113.7	3.6	1	78.5	18.9	95.00%	K.TPLNARPIVSVLDVLMNVQHIDEAASAIK.R		K.TPLNARPIVSVLDVLMNVQHIDEAASAIK.R

27	47	2	2280.96	1.7	0	126	31.1	95.00%	R.GSAFSPDDSVSQFQSDGFMTR.R	Oxidation (+16)	R.GSAFSPDDSVSQFQSDGFMTR.R
262	283	2	2391.13	-1.4	0	89.3	29.3	95.00%	R.CLDTDPTLISYADLGYAAFGTK.G	Carbamidomethyl (+57)	R.CLDTDPTLISYADLGYAAFGTK.G
15	26	2	1426.76	2.9	1	22.4	24.2	91.00%	R.SEVHYISIPLNR.G		R.SEVHYISIPLNR.G
49	60	2	1326.7	3.1	0	31.9	26.3	95.00%	R.QSILDHPVGSFK.G		R.QSILDHPVGSFK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
41	PTR2_YEAST	14.31%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	15	2	1701.66	8.6	0	35.7	30.1	95.00%	-.MLNHPSQGSDDAQDE.K	Acetyl (+42)/ Oxidation (+16)/ Deamidation (+1)	-.MLNHPSQGSDDAQDEK.Q
2	16	2	1682.71	6.1	1	36.1	30.2	95.00%	M.LNHPSQGSDDAQDEK.Q	Acetyl (+42)/ Deamidation (+1)	-.MLNHPSQGSDDAQDEK.Q
35	48	2	1556.66	0.63	1	54.6	30.6	95.00%	K.DSYVSDDVANSTER.Y		K.DSYVSDDVANSTER.Y
588	596	2	1102.57	2.2	1	41.5	27.6	95.00%	E.ILEPMESLR.S	Oxidation (+16)	K.ANDIEILEPMESLR.S
1	16	2	1813.76	8	1	62.5	30.9	95.00%	-.MLNHPSQGSDDAQDEK.Q	Acetyl (+42)/ Deamidation (+1)	-.MLNHPSQGSDDAQDEK.Q
94	116	2	2674.17	-1.2	1	48.7	30.4	95.00%	R.FSYYGLSAPFQNYMEYGPNDSPK.G		R.FSYYGLSAPFQNYMEYGPNDSPK.G
94	108	2	1815.79	2.9	0	52.7	30.7	95.00%	R.FSYYGLSAPFQNYME.Y		R.FSYYGLSAPFQNYMEYGPNDSPK.G
320	333	4	1585.79	2.5	1	23.1	27.6	95.00%	K.FDFNAAKPSVHPEK.N		K.FDFNAAKPSVHPEK.N
573	582	2	1100.59	2.2	0	38.9	26.4	95.00%	E.FDLNPISAPK.A		K.YNDTEEEMNAMDYEEEDEFDLNPISAPK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
42	YA11B_YEAST	15.44%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
625	644	2	2328.01	2.3	0	83.9	31.3	95.00%	E.SDVDWSSAIDYQCPDCLIGK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.NNTITYFNESDVDWSSAIDYQCPDCLIGK.S
471	491	3	2226.08	-0.4	0	86.8	29.1	95.00%	R.SAHHIHSASSNPDINVVDAQK.R		R.SAHHIHSASSNPDINVVDAQK.R
1151	1178	3	2885.42	0.91	0	59.7	27.9	95.00%	E.LPPINSHQTNSSLGGIGDSNAYTTINSK.K		K.ELPPINSHQTNSSLGGIGDSNAYTTINSK.K
148	167	2	2065.88	0.33	1	107	30.8	95.00%	E.SGNTFTDSSSADSDMTSTKK.Y		K.ANSQQTTTPASSAVPENPHHASPQTAQSHSPQNGPYPQQCMMTQNQANPSGWSFYGHPSMIPYTPYQMSPMYFPPGPQSQFPQYPSSVGTPLSTPSPESGNTFTDSSSADSDMTSTKK.Y
239	250	2	1411.69	2.6	0	32.7	29.3	95.00%	K.DILSVDYTDIMK.I		K.DILSVDYTDIMK.I
560	568	2	1163.53	2.7	0	33.5	29.5	95.00%	K.YGDFYWVSK.K		K.YGDFYWVSK.K
1496	1503	2	893.54	1.6	0	22.9	22.8	91.90%	K.LNVPLNPK.G		K.LNVPLNPK.G
25	39	2	1638.79	0.24	1	32.3	29.6	95.00%	K.EVHTNQDPLDVSASK.T		K.EVHTNQDPLDVSASK.T
1093	1113	3	2202.1	2.2	1	29.1	27.6	95.00%	R.SPSIDASPPENNSSHNIVPIK.T		R.SPSIDASPPENNSSHNIVPIK.T
784	807	3	2803.42	2.6	1	58.3	27.2	95.00%	R.TQLQCSGLPNHLWFSAIEFSTIVR.N	Carbamidomethyl (+57)	R.TQLQCSGLPNHLWFSAIEFSTIVR.N
1621	1632	2	1318.73	3.3	0	51.9	24.7	95.00%	K.SQIGNIYLLNGK.V		K.SQIGNIYLLNGK.V
516	531	2	1810.95	3.6	0	28.7	25.2	95.00%	K.VLHTPNIAYDLLSLNE.L		K.VLHTPNIAYDLLSLNELAAVDITACFTK.N
308	315	2	989.52	1.9	0	40.9	27.7	95.00%	K.VACQLIMR.G	Carbamidomethyl (+57)	K.VACQLIMR.G
148	166	2	1937.78	0.46	0	109	31.1	95.00%	E.SGNTFTDSSSADSDMTSTK.K		K.ANSQQTTTPASSAVPENPHHASPQTAQSHSPQNGPYPQQCMMTQNQANPSGWSFYGHPSMIPYTPYQMSPMYFPPGPQSQFPQYPSSVGTPLSTPSPESGNTFTDSSSADSDMTSTK.K
3	24	2	2296.09	2.1	0	91.7	29.6	95.00%	E.SQQLSQHSPISHGSACASVTSK.E	Carbamidomethyl (+57)	-.MESQQLSQHSPISHGSACASVTSK.E

1	24	3	2598.18	-0.65	1	59.5	30.2	95.00%	-.MESQQLSQHSPISHGSACASVTSK.E	Acetyl (+42)/ Carbamidomethyl (+57)	-.MESQQLSQHSPISHGSACASVTSK.E
570	588	2	2097.08	3.4	0	37.9	26.8	95.00%	K.YLLPSNISVPTINNVHTSE.S		K.YLLPSNISVPTINNVHTSESTR.K
532	543	2	1308.68	2.4	0	27.4	27.4	94.90%	E.LAAVDITACFTK.N	Carbamidomethyl (+57)	K.VLHTPNIAYDLLSLNELAAVDITACFTK.N
26	41	3	1739.84	2.2	1	40.4	28.5	95.00%	E.VHTNQDPLDVSASKTE.E		K.EVHTNQDPLDVSASKTEECEK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
43	B3LPM9_YEAS1	20.13%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	72	2	2006.01	2.7	0	72.2	26.6	95.00%	E.NLPLLADASPDDQFYISK.F		K.HHVVEPHDANDENLPLLADASPDDQFYISK.F
43	72	3	3385.58	-0.68	1	67.6	29.5	95.00%	K.HHVVEPHDANDENLPLLADASPDDQFYISK.F		K.HHVVEPHDANDENLPLLADASPDDQFYISK.F
115	132	2	2124.09	2.3	0	73.7	25.5	95.00%	K.ATQLFNQQQQHQLQSVAR.N		K.ATQLFNQQQQHQLQSVAR.N
374	387	2	1528.79	0.97	0	23.6	26.3	90.70%	K.LSSSQLRPNANITE.S		K.LSSSQLRPNANITESMAMSSGGAGIIAPSTDSLTFR.E
73	82	2	1131.63	2.6	1	55.5	24.9	95.00%	K.FVAALNQELK.K		K.FVAALNQELK.K
325	333	2	1091.53	2.2	1	51.5	28.6	95.00%	E.VLDFQDAER.E		R.QEVLDFQDAER.E
37	54	3	2117.94	1.7	1	29.3	30.4	95.00%	K.LYSNNKHHVVEPHDANDE.N	Deamidation (+1)	K.LYSNNKHHVVEPHDANDENLPLLADASPDDQFYISK.F
388	409	2	2156.03	1.4	0	96.2	28.9	95.00%	E.SMAMSSGGAGIIAPSTDSLTFR.E		K.LSSSQLRPNANITESMAMSSGGAGIIAPSTDSLTFR.E
755	770	2	1604.88	-0.37	0	63.8	23.8	95.00%	K.AVSSSGLLSTMAQLIK.A		K.AVSSSGLLSTMAQLIK.A
260	272	3	1538.78	3.5	0	41.3	27.3	95.00%	K.FHSHVFNPATINR.I		K.FHSHVFNPATINR.I
860	869	2	1169.64	0.071	0	44.2	24.6	95.00%	R.YLTVGTFITR.G		R.YLTVGTFITR.G
93	101	2	993.48	2.1	0	48	28.2	95.00%	E.TGLIANYNE.L		K.FYISQETGLIANYNELK.D
341	347	2	939.46	-0.025	1	25.9	26.7	93.90%	R.DHVVWER.N		R.DHVVWER.N
3	18	2	1892.91	2.6	1	57	28.9	95.00%	K.FSHSLQFNSVPEWSTK.Y		K.FSHSLQFNSVPEWSTK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
44	A6ZV88_YEAS7	30.57%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
138	143	2	705.45	3.8	0	27.6	17.8	95.00%	K.SIVLFK.F		K.SIVLFK.F
169	185	2	1820.9	4.2	0	73.1	28.3	95.00%	K.SGDNLTVVINSLGWAFE.D		K.SGDNLTVVINSLGWAFEDEDGDDEYATEETLSHHDNNK.G
157	168	2	1472.69	2.5	1	71.8	29.4	95.00%	E.FIDSCLSFLEDK.S	Carbamidomethyl (+57)	K.LDEFIDSCLSFLEDK.S
144	152	2	1058.49	-6.2	0	38.5	29.5	95.00%	K.FTSDAYDLK.K		K.FTSDAYDLK.K
88	114	2	2976.41	0.33	0	43.2	28.7	95.00%	R.FFANDVSLTVHDDSPLNISQSLSPIME.Q	Deamidation (+1)	R.FFANDVSLTVHDDSPLNISQSLSPIMEQFTVDELPESASDLLYEYSLDDK.S
29	38	2	1145.53	3.3	1	34.5	29.8	95.00%	K.ESSSFISFDK.E		K.ESSSFISFDK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
45	B3LS12_YEAS1	14.83%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
724	740	4	1988.04	3.4	1	31.3	25.4	95.00%	E.QRLHIDAVNTVWSHANK.D		R.TTHGELITLDEEQRLHIDAVNTVWSHANK.D
100	107	2	933.5	4.2	0	25	26.8	92.40%	R.SSSWLINK.K		R.SSSWLINK.K
391	403	3	1568.84	2.4	0	37.8	24.2	95.00%	E.IWFLDVSNTIHPK.W		R.SPDFKPVENNYDNSTNVPQEIWFLDVSNTIHPK.W
726	740	2	1703.87	0.05	0	50.6	26.9	95.00%	R.LHIDAVNTVWSHANK.D		R.LHIDAVNTVWSHANK.D
113	122	2	1230.6	3.5	1	55.1	28.1	95.00%	K.HFNELSLTDR.C		K.HFNELSLTDR.C
87	99	2	1580.82	2.5	1	50.2	26.2	95.00%	E.LVPFYDQSIDTKR.S		K.VLIEAFGSPEVDPVDTIPVSPLELVPFYDQSIDTKR.S
87	98	2	1424.72	2.4	0	47.2	27.1	95.00%	E.LVPFYDQSIDTK.R		K.VLIEAFGSPEVDPVDTIPVSPLELVPFYDQSIDTK.R

604	616	2	1446.66	1.7	0	61.3	29.6	95.00%	E.ICSGQIAHMSTDK.K	Carbamidomethyl (+57)	R.QEAAVEICSGQIAHMSTDK.K
129	142	2	1683.8	0.77	1	85.9	29.7	95.00%	R.TLYTLDDEWTNSVK.K		R.TLYTLDDEWTNSVK.K
192	207	2	1934.94	-0.098	1	48.7	29	95.00%	R.CFMQANPVNIQEIFPK.S	Carbamidomethyl (+57)	R.CFMQANPVNIQEIFPK.S
274	282	2	1029.59	-0.41	1	39.1	24.8	95.00%	K.VLEQGFLPK.F		K.VLEQGFLPK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
46	NCPR_YEAST	39.07%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
279	291	2	1577.69	1.8	1	33.3	30.3	95.00%	E.LFSSNDRNCIHSE.F	Carbamidomethyl (+57)	R.ELFSSNDRNCIHSEFDLSGSNIK.Y
462	483	3	2359.26	3.1	1	38	21.6	95.00%	E.NFPNPELPDAPPVVGVTTNLLR.N		K.QTVHVTSIVENFPNPELPDAPPVVGVTTNLLR.N
484	509	3	2916.49	0.59	1	45.1	25.1	95.00%	R.NIQLAQNNVNIAETNLPVHYDLNGPR.K		R.NIQLAQNNVNIAETNLPVHYDLNGPR.K
254	275	2	2355.25	2.4	0	63.6	22	95.00%	R.NADGIQLGPFDLSQPYIAPIVK.S		R.NADGIQLGPFDLSQPYIAPIVK.S
653	664	2	1171.7	3.1	0	42.5	20.2	95.00%	K.GVSTALVGILSR.G		K.GVSTALVGILSR.G
405	413	2	1053.55	3.5	0	40.6	25.6	95.00%	K.YFNIADALK.Y		K.YFNIADALK.Y
220	253	4	3909.86	-2.1	1	33.6	27.1	95.00%	K.FTSQFQYTVLNEITDSMSLGEPSAHYLPSHQLNR.N		K.FTSQFQYTVLNEITDSMSLGEPSAHYLPSHQLNR.N
195	205	2	1385.62	2	1	35.2	29.7	95.00%	E.DYMAWKDSILE.V	Oxidation (+16)	K.LGEADDGAGTTDEDYMAWKDSILEVLK.D
468	483	2	1660.95	1.5	0	51.7	18.6	95.00%	E.LPDAPPVVGVTTNLLR.N		K.QTVHVTSIVENFPNPELPDAPPVVGVTTNLLR.N
582	594	2	1670.68	2.5	1	38.2	30.4	95.00%	R.NTDDFLYQDEWPE.Y		R.NTDDFLYQDEWPEYAK.K
421	439	2	2260.1	-1.2	1	59.7	28.3	95.00%	K.WDTVPMQFLVESVPQMTPR.Y		K.WDTVPMQFLVESVPQMTPR.Y
440	451	2	1349.64	2.4	1	61	29.6	95.00%	R.YYSISSSSLSEK.Q		R.YYSISSSSLSEK.Q
421	431	2	1363.65	3.3	0	38.8	29.5	95.00%	K.WDTVPMQFLVE.S		K.WDTVPMQFLVESVPQMTPR.Y
49	59	2	1229.63	1.1	1	54.2	26.7	95.00%	R.DIAQVVTENNK.N		R.DIAQVVTENNK.N
528	549	2	2207.18	1.8	0	36.3	22.3	95.00%	R.LPSNPSTPVIMIGPGTGVAPFR.G		R.LPSNPSTPVIMIGPGTGVAPFR.G
369	384	2	1776.94	-0.18	0	60.3	24.6	95.00%	R.QLFSSLIQFAPNADVK.E		R.QLFSSLIQFAPNADVK.E
220	231	2	1475.7	2.8	0	39.4	29.7	95.00%	K.FTSQFQYTVLNE.I		K.FTSQFQYTVLNEITDSMSLGEPSAHYLPSHQLNR.N
147	165	2	2129.95	-1	1	70.5	30.7	95.00%	R.YNMFGLGNSTYEFFNGAAK.K		R.YNMFGLGNSTYEFFNGAAK.K
292	300	2	979.5	1.9	0	27.6	27.3	95.00%	E.FDLSGSNIK.Y		R.NCIHSEFDLSGSNIK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
47	YG35_YEAST	19.50%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
805	817	2	1313.73	0.45	0	45.7	24	95.00%	K.QNNVVSAVIAATK.N		K.QNNVVSAVIAATK.N
910	920	2	1487.7	-1.1	0	55.5	29.5	95.00%	K.FWAQLCPYFTR.R	Carbamidomethyl (+57)	K.FWAQLCPYFTR.R
875	890	3	1873.07	3.6	1	36.8	16.1	95.00%	E.YKDDEPVLPILLFALK.Q		K.EYKDDEPVLPILLFALK.Q
923	940	2	2053.07	2	0	27.2	25.2	95.00%	R.LASQSHLLHADNIFFLVE.T		R.LASQSHLLHADNIFFLVETGMLK.A
48	69	2	2353.03	-0.9	0	82	30.5	95.00%	R.SYMSGFFTGGNSPMINNLSDSK.L		R.SYMSGFFTGGNSPMINNLSDSK.L
716	732	2	1882.85	2.4	1	108	29.9	95.00%	K.NINADNIDYSAAEGFNR.I		K.NINADNIDYSAAEGFNR.I
48	75	3	3005.43	1.9	1	70.6	27.8	95.00%	R.SYMSGFFTGGNSPMINNLSDSKLPISNK.Q		R.SYMSGFFTGGNSPMINNLSDSKLPISNK.Q
173	189	3	1889.92	2.5	0	26.7	29.1	95.00%	E.DGYAGGYQSLRPSHNLR.F		R.GLQNSSLPELEDGYAGGYQSLRPSHNLR.F
850	865	2	1851.9	2.4	0	78.8	28.2	95.00%	R.NYQILSVAQNVFVNDE.Q		R.NYQILSVAQNVFVNDEQAVK.N
146	161	2	1770.89	1.6	1	36.8	27.6	95.00%	R.LLLSPASSNVDDDRNR.G		R.LLLSPASSNVDDDRNR.G
923	945	3	2583.36	3.2	1	47	21.8	95.00%	R.LASQSHLLHADNIFFLVETGMLK.A		R.LASQSHLLHADNIFFLVETGMLK.A
803	817	2	1498.85	2.6	1	84.2	20.3	95.00%	E.GKQNNVVSAVIAATK.N		R.LEEGKQNNVVSAVIAATK.N
891	902	3	1474.78	2.9	1	30.1	25.3	95.00%	K.QYRPDIISEVQK.V		K.QYRPDIISEVQK.V
709	715	2	910.52	0.089	0	34.7	21.2	95.00%	K.YLILDFK.N		K.YLILDFK.N

662	674	2	1493.81	-0.81	1	38.6	24.5	95.00%	K.FLDGIGEQIYVLK.L		K.FLDGIGEQIYVLK.L
839	849	2	1242.64	2.6	0	36.8	26.7	95.00%	R.NLMSLPTNTPR.N		R.NLMSLPTNTPR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
48	A6ZSG0_YEAS7	12.11%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
37	46	2	1163.54	2	1	28.4	29.4	93.60%	R.IFSVDDDPKE.I		R.IFSVDDDPKEIQNDIR.Y
93	102	2	1198.61	0.66	0	26.6	27.9	93.30%	E.HQQHLPPTLE.S		R.SVSSQSPIVHSSNNTLHHHEHQQHLPPTLESLSSK.S
713	731	2	2154.04	3.2	1	37.9	28.2	95.00%	K.MIWQLPIADPTSTAPEQQE.Q		K.MIWQLPIADPTSTAPEQQEQNSHDAPNWSR.S
72	92	3	2353.12	3.2	1	47.2	29.2	95.00%	K.RSVSSQSPIVHSSNNTLHHHE.H	Deamidation (+1)	K.RSVSSQSPIVHSSNNTLHHHEHQQHLPPTLESLSSK.S
192	204	2	1496.74	2.6	1	27.9	28.7	93.90%	R.QDAINETHPFGIR.I		R.QDAINETHPFGIR.I
163	172	2	1183.53	1.4	0	38.7	29.6	95.00%	E.INCQSPSHLE.N	Carbamidomethyl (+57)	R.FIIHDSHGHDLLIDEINCQSPSHLENNDQASNASSTESFTLR.E
148	162	3	1759.86	2.2	0	21.8	28.1	91.70%	R.FIIHDSHGHDLLIDE.I		R.FIIHDSHGHDLLIDEINCQSPSHLENNDQASNASSTESFTLR.E
220	231	2	1353.69	-1.9	1	28.2	28.1	95.00%	R.TAAQDIHETQLK.T		R.TAAQDIHETQLK.T
73	92	3	2197.02	1.1	0	45.2	30.1	95.00%	R.SVSSQSPIVHSSNNTLHHHE.H	Deamidation (+1)	R.SVSSQSPIVHSSNNTLHHHEHQQHLPPTLESLSSK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
49	A6ZKY2_YEAS7	19.00%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
349	369	2	2284.1	-1.4	1	72.1	29.4	95.00%	K.VNQGSLDYLAALGVYQEDMAK.A		K.VNQGSLDYLAALGVYQEDMAK.A
26	35	2	1142.51	1	0	43.9	29.2	95.00%	K.FYANANSNSR.W		K.FYANANSNSR.W
114	147	3	3752.8	2.1	1	36.4	27.1	95.00%	E.GSNLYPRDNADLPVDPYHLSPQQQPSNNLFGSGR.L		R.AGEAVIHLSEGSNLYPRDNADLPVDPYHLSPQQQPSNNLFGSGR.L
121	147	3	2965.4	1.8	0	63.8	29.3	95.00%	R.DNADLPVDPYHLSPQQQPSNNLFGSGR.L		R.DNADLPVDPYHLSPQQQPSNNLFGSGR.L
400	411	2	1429.8	2.5	0	37.3	23.4	95.00%	K.DIVPVQLVFCLK.E	Carbamidomethyl (+57)	K.DIVPVQLVFCLK.E
482	495	2	1668.85	-0.67	1	57.2	27.2	95.00%	K.LFNPLVASQNFEYK.I		K.LFNPLVASQNFEYK.I
950	961	3	1395.79	1.9	1	36	20	95.00%	E.VSKLDLPNVFHK.K		K.VEGSGSWEVSKLDLPNVFHK.K
246	253	2	883.52	3	0	41.9	22.6	95.00%	K.GLLDTLPR.R		K.GLLDTLPR.R
46	63	2	1966.9	1.1	0	65	30.2	95.00%	E.DSYDQSNVFQGLPASPSR.A		R.WANPSEESLEDSYDQSNVFQGLPASPSR.A
400	412	2	1558.85	3.3	1	24.7	24.5	94.60%	K.DIVPVQLVFCLKE.E	Carbamidomethyl (+57)	K.DIVPVQLVFCLKEENK.K
564	572	2	1130.62	1.9	1	27.5	26	95.00%	R.ILCWELVAK.R	Carbamidomethyl (+57)	R.ILCWELVAK.R
93	102	2	1119.56	-0.55	1	34.7	28.1	95.00%	R.YAANLQESPK.R		R.YAANLQESPK.R
107	113	2	767.42	1.4	0	36.1	23.6	95.00%	E.AVIHLSE.G		R.AGEAVIHLSEGSNLYPR.D
235	245	2	1220.75	2.5	1	35.7	15.1	95.00%	K.ALLKLDNPIPK.G		K.ALLKLDNPIPK.G
349	365	2	1838.91	2.9	0	65.4	28.3	95.00%	K.VNQGSLDYLAALGVYQE.D		K.VNQGSLDYLAALGVYQEDMAK.A
457	472	2	1621.78	2.5	0	99.7	29.5	95.00%	K.VFDMDSNVAGAAGQIK.T		K.VFDMDSNVAGAAGQIK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
50	PDR5_YEAST	17.21%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
922	938	2	1753.98	2.9	0	47.5	21.4	95.00%	R.VTMGVITGDILVNGIPR.D		R.VTMGVITGDILVNGIPR.D
95	109	2	1663.79	3.3	1	37.4	29.9	95.00%	K.LDPNSENFSSAAWVK.N		K.LDPNSENFSSAAWVK.N
412	427	2	1738.84	2.5	1	92	29.6	95.00%	R.QTTADFLTSVTSPSER.T		R.QTTADFLTSVTSPSER.T
221	233	3	1431.69	0.99	1	32.5	29.4	95.00%	K.ISYSGYSGDDIKK.H		K.ISYSGYSGDDIKK.H
338	349	2	1291.68	2.8	1	31.4	25.9	95.00%	R.GLDSATALEFIR.A		R.GLDSATALEFIR.A
286	297	2	1305.65	1.6	0	87.3	27.9	95.00%	E.VAMATYGLSHTR.N		R.ESYANHLAEVAMATYGLSHTR.N

912	921	2	1190.6	-0.25	1	26.3	28.5	91.80%	K.TTLLDCLAER.V	Carbamidomethyl (+57)	K.TTLLDCLAER.V
865	872	2	1044.52	2.6	1	50.3	28.3	95.00%	K.SEAIFHWR.N		K.SEAIFHWR.N
1128	1143	2	1676.75	1.9	0	33.5	31	95.00%	E.VVGAAPGSHANQDYYE.V		K.CPADANPAEWMLEVVGAAPGSHANQDYYEVWR.N
887	911	3	2469.31	2.1	0	30.8	21.6	95.00%	R.ILNNVDGWVKPGTLTALMGASGAGK.T		R.ILNNVDGWVKPGTLTALMGASGAGK.T
400	411	2	1522.63	2.7	1	60.9	30.5	95.00%	K.YFEDMGYVCPSR.Q	Carbamidomethyl (+57)	K.YFEDMGYVCPSR.Q
1419	1439	2	2418.11	2.2	0	69.6	30.2	95.00%	E.FTPPSGMTCGQYMEPYLQLAK.T	Carbamidomethyl (+57)	K.CADYELLEFTPPSGMTCGQYMEPYLQLAK.T
329	337	2	1196.51	3.6	0	30	29	95.00%	K.FQCWDNATR.G	Carbamidomethyl (+57)	K.FQCWDNATR.G
1090	1101	2	1344.61	2.1	1	27.7	29.8	91.80%	K.TVYFGDLGEGCK.T	Carbamidomethyl (+57)	K.TVYFGDLGEGCK.T
110	132	3	2641.21	2	0	42.4	30.1	95.00%	K.NMAHLSAADPDFYKPYSLGCAWK.N	Carbamidomethyl (+57)	K.NMAHLSAADPDFYKPYSLGCAWK.N
49	65	2	1805.86	-0.55	0	104	29.5	95.00%	R.TLTAQSMQNSTQSAPNK.S		R.TLTAQSMQNSTQSAPNK.S
740	761	2	2366.16	2.3	0	76.5	27.7	95.00%	E.SVCTVVGAVPGQDYVLGDDFIR.G	Carbamidomethyl (+57)	R.GPAYANISSTESVCTVVGAVPGQDYVLGDDFIR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
51	A6ZZF0_YEAS7	14.12%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
176	185	2	1188.69	0.66	1	59.8	20.8	95.00%	K.KMSLIDLLTR.R		K.KMSLIDLLTR.R
177	185	2	1060.6	-0.2	0	70.3	24	95.00%	K.MSLIDLLTR.R		K.MSLIDLLTR.R
282	315	3	3659.65	1.4	1	60	29.4	95.00%	E.NYGSNQLSHSFSSPLGNDVTENPAALADTQYHPE.N		R.HHHSSESPENYGSNQLSHSFSSPLGNDVTENPAALADTQYHPENGSLYPHHHHLETPFSK.L
143	159	2	1708.72	2	1	74.8	30.1	95.00%	E.NAPSEHGYATSSSSVSE.N		K.SHSHSHSHSHADSHSNFSNDHDLENAPSEHGYATSSSSVSENDPLITK.D
282	302	2	2252	1.5	0	56.9	31.1	95.00%	E.NYGSNQLSHSFSSPLGNDVTE.N		R.HHHSSESPENYGSNQLSHSFSSPLGNDVTENPAALADTQYHPENGSLYPHHHHLETPFSK.L
148	159	2	1210.51	3.5	0	28.4	29.4	93.70%	E.HGYATSSSSVSE.N		K.SHSHSHSHSHADSHSNFSNDHDLENAPSEHGYATSSSSVSENDPLITK.D
209	218	2	1158.65	2.6	0	30.5	25.3	95.00%	E.YIACVPPVIK.S	Carbamidomethyl (+57)	K.CTPLLQSEQPEYIACVPPVIK.S
303	315	2	1425.65	1.3	0	68.1	30	95.00%	E.NPAALADTQYHPE.N		R.HHHSSESPENYGSNQLSHSFSSPLGNDVTENPAALADTQYHPENGSLYPHHHHLETPFSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
52	A6ZVM2_YEAS7	20.51%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
314	325	2	1292.68	-0.24	0	78.4	26.2	95.00%	K.HADANVQLVAQK.M		K.HADANVQLVAQK.M
326	339	2	1549.7	2.5	0	44.1	30.1	95.00%	K.MQQITSSQPTPTSE.L	Oxidation (+16)	K.MQQITSSQPTPTSELSSAQR.D
360	370	2	1264.65	2.2	0	26.9	27.9	93.60%	E.WFTTALTNSPK.D		K.EPITWLETQITEWFTTALTNSPK.D
48	63	2	1913.91	-1.2	0	71.3	29.8	95.00%	R.SWMPSVSVYQTAFQQR.E		R.SWMPSVSVYQTAFQQR.E
824	852	3	3224.5	1.7	0	44.2	28.5	95.00%	K.AFSSLNDIPITPSHDNNPHSFAEPMPAYR.G		K.AFSSLNDIPITPSHDNNPHSFAEPMPAYR.G
634	649	2	1787.87	3.1	0	42.8	29.2	95.00%	R.FADSGDWFPHLLNAAK.Y		R.FADSGDWFPHLLNAAK.Y
48	67	2	2325.12	-1.6	1	51.8	29	95.00%	R.SWMPSVSVYQTAFQQREPGK.S		R.SWMPSVSVYQTAFQQREPGK.S
196	204	2	1094.58	2.1	0	56.3	26.2	95.00%	R.LSLLAYCQK.V	Carbamidomethyl (+57)	R.LSLLAYCQK.V
326	345	2	2176.05	2	1	113	28.5	95.00%	K.MQQITSSQPTPTSELSSAQR.D		K.MQQITSSQPTPTSELSSAQR.D
797	823	2	2734.27	1.7	0	89.1	29	95.00%	R.VTGDAPLPYPIAQVGDDSMDSSDLGSK.A		R.VTGDAPLPYPIAQVGDDSMDSSDLGSK.A
147	165	2	1885.89	3	0	65.7	29.9	95.00%	R.SSSNVDMSTSLYAAGLAGR.S		R.SSSNVDMSTSLYAAGLAGR.S
346	354	2	1129.57	2	1	35.3	27.5	95.00%	R.DKEPITWLE.T		R.DKEPITWLETQITEWFTTALTNSPK.D

125	137	2	1605.85	1.4	0	56.6	24.9	95.00%	E.VLQSQLHYYSLQK.N		K.FEVLQSQLHYYSLQK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
53	A6ZKX6_YEAS7	52.21%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
221	246	2	2610.44	6.5	1	57.3	18.9	95.00%	R.NVPGVETANVASLNLLQLAPGAHLGR.F		R.NVPGVETANVASLNLLQLAPGAHLGR.F
272	288	2	1844.97	1.4	0	70.6	25.7	95.00%	K.VGYTLPSHIISTSDVTR.I		K.VGYTLPSHIISTSDVTR.I
289	308	2	2111.14	1.8	1	91.9	22.2	95.00%	R.IINSSEIQSAIRPAGQATQK.R		R.IINSSEIQSAIRPAGQATQK.R
247	257	2	1311.69	0.05	1	50.8	26.1	95.00%	R.FVIWTEAAFTK.L		R.FVIWTEAAFTK.L
85	95	2	1183.49	-0.58	0	46.1	29.3	95.00%	R.SGQGAFGNMCR.G	Carbamidomethyl (+57)	R.SGQGAFGNMCR.G
258	271	2	1505.74	2.3	1	65.9	29.3	95.00%	K.LDQVWGSETVASSK.V		K.LDQVWGSETVASSK.V
120	138	3	1819.02	-0.27	0	24.2	21.6	95.00%	R.YATASAIAATAVASLVLAR.G		R.YATASAIAATAVASLVLAR.G
227	246	2	2015.13	2.8	0	71.8	18.5	95.00%	E.TANVASLNLLQLAPGAHLGR.F		R.NVPGVETANVASLNLLQLAPGAHLGR.F
253	265	2	1450.71	1.7	1	38.6	28.7	95.00%	E.AAFTKLDQVWGSE.T		R.FVIWTEAAFTKLDQVWGSETVASSK.V
2	44	4	4579.45	-1.8	1	59.5	23.4	95.00%	M.SRPQVTVHSLTGEATANALPLPAVFSAPIRPDIVHTVFTSVNK.N	Acetyl (+42)	-.MSRPQVTVHSLTGEATANALPLPAVFSAPIRPDIVHTVFTSVNK.N
56	69	3	1443.65	0.074	1	30.2	29.5	95.00%	K.AGHQTSAESWGTGR.A		K.AGHQTSAESWGTGR.A
2	14	2	1451.74	1.9	0	35.9	28.3	95.00%	M.SRPQVTVHSLTGE.A	Acetyl (+42)	-.MSRPQVTVHSLTGEATANALPLPAVFSAPIRPDIVHTVFTSVNK.N
204	217	2	1472.79	2	1	35	25	95.00%	R.GPLVVYAEDNGIVK.A		R.GPLVVYAEDNGIVK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
54	GAS1_YEAST	24.15%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
210	232	2	2739.09	1.3	1	55.5	30.2	95.00%	K.MTDYFACGDDDVKADFYGINMYE.W	Carbamidomethyl (+57)	K.MTDYFACGDDDVKADFYGINMYEWCGK.S
223	236	2	1752.73	-0.62	1	57.6	30	95.00%	K.ADFYGINMYEWCGK.S	Carbamidomethyl (+57)	K.ADFYGINMYEWCGK.S
361	391	3	3359.33	3.5	0	41.6	30.9	95.00%	E.LPPTPNGGLCSCMNAANSCVVSDDVDSDDYE.T	Deamidation (+1)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.YWSAATELPPTPNGGLCSCMNAANSCVVSDDVDSDDYETLFNWICNEVDCSGISANGTAGK.Y
106	141	3	3967.96	2.5	1	65.5	25.3	95.00%	K.ALNDADIYVIADLAAPATSINRDDPTWTVDLFNSYK.T		K.ALNDADIYVIADLAAPATSINRDDPTWTVDLFNSYK.T
194	207	2	1566.68	-0.71	1	74.9	30.1	95.00%	K.IPVGYSSNDDEDTR.V		K.IPVGYSSNDDEDTR.V
415	424	2	1192.52	-0.24	0	35.4	29.5	95.00%	K.YGAYSFCTPK.E	Carbamidomethyl (+57)	K.YGAYSFCTPK.E
210	222	2	1535.59	0.34	0	71.5	28.8	95.00%	K.MTDYFACGDDDVK.A	Carbamidomethyl (+57)	K.MTDYFACGDDDVK.A
83	90	2	956.58	0.5	1	36.9	21.9	95.00%	K.KLNTNVIR.V		K.KLNTNVIR.V
392	400	2	1195.54	3.7	0	43.6	29.9	95.00%	E.TLFNWICNE.V	Carbamidomethyl (+57)	K.YWSAATELPPTPNGGLCSCMNAANSCVVSDDVDSDDYETLFNWICNEVDCSGISANGTAGK.Y
128	141	2	1699.77	-1	0	48.1	30.2	95.00%	R.DDPTWTVDLFNSYK.T		R.DDPTWTVDLFNSYK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
55	MAM3_YEAST	22.52%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
264	277	2	1568.74	2.2	0	87.7	29.4	95.00%	E.NVFTMSADTILDDK.T		R.VEEIMTPIENVFTMSADTILDDK.T
577	608	3	3387.56	0.25	1	42.7	29.5	95.00%	R.NSPDSISIPNSGANHGNENQNVTISTSYQNTK.N		R.NSPDSISIPNSGANHGNENQNVTISTSYQNTK.N
258	277	2	2253.1	3.6	1	94.3	27.9	95.00%	E.IMTPIENVFTMSADTILDDK.T		R.VEEIMTPIENVFTMSADTILDDK.T
483	500	2	1888.02	1.7	0	72.6	24.1	95.00%	E.HGTIIPSNLASNPLNVNK.S		R.SNAVLSPTPQVTEHGTIIPSNLASNPLNVNK.S
657	669	2	1313.65	2.2	0	40.5	28.6	95.00%	E.SSSSNASLFSSIK.N		R.ESSSSNASLFSSIK.N

683	691	2	1025.48	2.6	0	34.1	29.7	95.00%	R.SNFTDSLSR.T		R.SNFTDSLSR.T
595	608	2	1596.78	2.2	0	84.8	29.5	95.00%	E.NQNVTISTSYQNTK.N		R.NSPDSISIPNSGANHGNENQNVTISTSYQNTK.N
408	423	4	1979.01	-0.025	1	34.2	26.4	95.00%	K.RHITSYLHHLYTSSHK.E		K.RHITSYLHHLYTSSHK.E
514	535	3	2380.17	-1.2	1	58.7	28.4	95.00%	K.IITTHTPHSSKEPSPAPHSNDK.S		K.IITTHTPHSSKEPSPAPHSNDK.S
332	347	2	1899.87	1.6	0	41.9	29.9	95.00%	E.TSPNTSCLNILNYFQE.G	Carbamidomethyl (+57)	R.VLISYDPDDCLPISHFPLATLPETSPNTSCLNILNYFQEGK.A
470	500	3	3211.69	0.41	1	37.7	22.3	95.00%	R.SNAVLSPTPQVTEHGTIIPSNLASNPLNVNK.S		R.SNAVLSPTPQVTEHGTIIPSNLASNPLNVNK.S
577	594	2	1808.8	1.6	0	59.7	30.7	95.00%	R.NSPDSISIPNSGANHGNE.N		R.NSPDSISIPNSGANHGNENQNVTISTSYQNTK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
56	A6ZNT9_YEAS7	43.81%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
37	48	2	1302.7	2.8	0	34.1	26.2	95.00%	K.EPTIGAAFLTQR.V		K.EPTIGAAFLTQR.V
159	170	2	1303.68	2.5	1	31.7	26.6	95.00%	E.NVNDVFLGIGEK.I		K.TGENVNDVFLGIGEK.I
35	48	2	1544.83	2	1	67.3	24.9	95.00%	E.NKEPTIGAAFLTQR.V		R.FVSNDFAENKEPTIGAAFLTQR.V
10	20	2	1068.65	-1.1	1	24	18.4	93.70%	K.LVLLGEAAVGK.S		K.LVLLGEAAVGK.S
112	127	2	1799.98	2.5	1	33.2	23.2	95.00%	K.DIIIALVGNKIDMLQE.G	Oxidation (+16)	K.DIIIALVGNKIDMLQEGGER.K
112	121	2	1054.64	1.5	0	46.2	19.2	95.00%	K.DIIIALVGNK.I		K.DIIIALVGNK.I
79	97	2	2091.14	2.3	0	64.5	21.4	95.00%	R.NAQAALVVYDVTKPQSFIK.A		R.NAQAALVVYDVTKPQSFIK.A
69	78	2	1217.59	3.4	0	39.5	27.6	95.00%	R.FASLAPMYYR.N		R.FASLAPMYYR.N
146	155	2	1111.6	3.4	1	49.4	25.7	95.00%	K.GLLFFETSAK.T		K.GLLFFETSAK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
57	A6ZQQ8_YEAS7	36.29%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
152	160	2	1033.57	3.9	0	25.2	24.3	95.00%	K.VAMNYVPIK.A		K.VAMNYVPIK.A
495	507	2	1426.81	3	0	32.6	22.8	95.00%	E.IGWCLGASLPLLK.A	Carbamidomethyl (+57)	K.EIGWCLGASLPLLK.A
50	67	2	2001.99	1.8	0	35.4	27.9	95.00%	E.DISILPVNDEPGYLQDSK.T		K.TPEDISILPVNDEPGYLQDSK.T
494	507	2	1555.84	-0.57	1	53.3	24.5	95.00%	K.EIGWCLGASLPLLK.A	Carbamidomethyl (+57)	K.EIGWCLGASLPLLK.A
375	395	3	2384.07	1.6	0	41.3	30.9	95.00%	K.DAQCQSPPCSFNGVHQPSLVR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Deamidation (+1)	K.DAQCQSPPCSFNGVHQPSLVR.T
238	264	3	2847.48	2.3	1	34.9	24.1	95.00%	K.LPTAAVFDLGGGSTQIVFEPTFPINEK.M		K.LPTAAVFDLGGGSTQIVFEPTFPINEK.M
124	151	3	2982.46	2.2	1	59.3	26.6	95.00%	E.KFDMLEPGLSSFDTDSVGAANSLDPLLK.V	Oxidation (+16)	K.FDVCTSPPTLLDEKFDMLEPGLSSFDTDSVGAANSLDPLLK.V
347	365	2	2154.96	2	1	82.6	30.1	95.00%	K.ETYTIDFIGPDEPSGAQCR.F	Carbamidomethyl (+57)	K.ETYTIDFIGPDEPSGAQCR.F
50	69	2	2232.08	1.5	1	58.7	28.4	95.00%	E.DISILPVNDEPGYLQDSKTE.Q		K.TPEDISILPVNDEPGYLQDSKTEQNYPELADAVK.S
348	365	2	2025.91	1.4	0	101	30.8	95.00%	E.TYTIDFIGPDEPSGAQCR.F	Carbamidomethyl (+57)	K.ETYTIDFIGPDEPSGAQCR.F
300	310	2	1184.68	0.49	1	48.4	24.8	95.00%	K.VNSVLVENALK.D		K.VNSVLVENALK.D
37	46	2	1026.57	-0.22	0	31.2	23.7	95.00%	R.TVTPNASIPK.T		R.TVTPNASIPK.T
413	432	3	2257.19	-0.49	1	58.8	24.5	95.00%	R.TRPLGMPLSFTLNELNDLAR.I		R.TRPLGMPLSFTLNELNDLAR.I
366	374	2	1091.59	-1.1	1	26.9	26.2	95.00%	R.FLTDEILNK.D		R.FLTDEILNK.D
413	426	2	1574.82	1.9	0	49.9	26.7	95.00%	R.TRPLGMPLSFTLNE.L		R.TRPLGMPLSFTLNELNDLAR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
58	A7A201_YEAS7	35.44%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
28	46	2	2200.97	2	0	93.1	31	95.00%	R.FSDDTYTNDYISTIGVDFK.I	Deamidation (+1)	R.FSDDTYTNDYISTIGVDFK.I
11	21	2	1069.65	-0.48	0	24.2	20.6	94.00%	K.LLLIGNSGVGK.S		K.LLLIGNSGVGK.S
101	108	2	1089.53	4	1	41.9	29.1	95.00%	K.MWLQEIDR.Y		K.MWLQEIDR.Y
59	69	2	1315.65	-0.16	1	49.1	28.3	95.00%	K.LQIWDTAGQER.F		K.LQIWDTAGQER.F
106	116	3	1265.7	2.1	1	37.9	24	95.00%	E.IDRYATSTVLK.L		K.MWLQEIDRYATSTVLK.L

22	27	2	760.42	-8.9	0	28.8	26.6	95.00%	K.SCLLLR.F	Carbamidomethyl (+57)	K.SCLLLR.F
1	10	2	1350.58	-0.58	1	36.9	30	95.00%	-.MNSEYDYLFK.L	Acetyl (+42)	-.MNSEYDYLFK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
59	A7A1A2_YEAS7	21.14%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
663	674	2	1229.67	3.1	0	37.8	25.5	95.00%	R.NAVVQGIDSSLK.I		R.NAVVQGIDSSLK.I
135	144	2	1229.63	0.4	0	26.7	27.6	93.80%	E.NYGIHLNLMR.S		K.TVVSQPLMANETAYHYYYEENYGIHLNLMR.S
498	509	2	1339.65	-1.3	0	39.8	29.2	95.00%	K.VLSAPNHTVDCK.I	Carbamidomethyl (+57)	K.VLSAPNHTVDCK.I
514	525	2	1237.68	1.4	0	45.3	22.4	95.00%	E.GPYGVTVPHIAK.L		K.IFLEGPYGVTVPHIAK.L
471	485	2	1826.88	2	1	86.5	28.5	95.00%	R.HRDPNNPDQLTMYVK.A		R.HRDPNNPDQLTMYVK.A
453	470	2	2188.04	-0.1	1	95.7	29.8	95.00%	K.SAWFYSFQSHPFTVLSER.H		K.SAWFYSFQSHPFTVLSER.H
644	662	2	2252.94	0.036	0	131	30.9	95.00%	E.NNNITFYSCGPATFNDDFR.N	Deamidation (+1)/ Carbamidomethyl (+57)	K.LSELENNNITFYSCGPATFNDDFR.N
510	525	2	1739.97	2.9	1	48.2	22	95.00%	K.IFLEGPYGVTVPHIAK.L		K.IFLEGPYGVTVPHIAK.L
51	67	2	1925.9	2.6	1	108	29.9	95.00%	K.NINWLGSVTACAYENSK.S	Carbamidomethyl (+57)	K.NINWLGSVTACAYENSK.S
414	427	2	1464.73	0.61	0	67.9	27.5	95.00%	K.TATLSTTDDSNVIK.I		K.TATLSTTDDSNVIK.I
562	573	2	1533.8	-0.53	0	36.3	26.5	95.00%	K.FYWIVNDLSHLK.W		K.FYWIVNDLSHLK.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
60	A6ZM54_YEAS7	23.76%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
356	366	2	1324.7	-0.78	0	27.5	25.5	95.00%	K.LFTPMMLFVAR.K		K.LFTPMMLFVAR.K
83	93	2	1329.59	2.5	0	41.1	30.1	95.00%	E.YGWGSSFHFSR.F		R.LEDYNEATHSYYNVVTDFYEYGWGSSFHFSR.F
296	308	2	1555.81	-0.14	0	55.9	25.8	95.00%	K.YVQNLANLATFFR.T		K.YVQNLANLATFFR.T
140	157	2	2039.98	2.9	0	65.8	28.7	95.00%	R.FTGCNVIGLNNNDYQIAK.A	Carbamidomethyl (+57)	R.FTGCNVIGLNNNDYQIAK.A
354	366	3	1539.83	-0.13	1	31.4	25	95.00%	K.SKLFTPMMLFVAR.K		K.SKLFTPMMLFVAR.K
225	233	2	1185.5	2.6	1	26.7	28.7	92.00%	E.WVMTDKYDE.N		K.VLKPGGTFAVYEWVMTDKYDENNPEHR.K
120	135	2	1540.77	0.85	0	56.6	28.2	95.00%	R.GDLVLDVGCGVGGPAR.E	Carbamidomethyl (+57)	R.GDLVLDVGCGVGGPAR.E
165	175	2	1358.62	2.9	0	36.8	29.7	95.00%	K.YNLSDQMDFVK.G		K.YNLSDQMDFVK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
61	YO092_YEAST	13.96%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	140	2	1835.92	1.2	1	29.8	28	95.00%	E.QQPLLNSQGQPNRIDE.E		K.SSDGLSLLFVVLWLAGDVFNLMGAVMQHLLSTMIILAAYYTVADIILLGQCLWYDNEEKPAVDPIHLSPANPINENVLHDVFNEQQPLLNSQGQPNRIDEEMAAPSSDGNAGDDNLR.E
142	157	2	1590.65	-2.9	0	72.1	30.5	95.00%	E.MAAPSSDGNAGDDNLR.E	Deamidation (+1)	R.IDEEMAAPSSDGNAGDDNLR.E
1	10	2	1211.67	0.89	1	40.1	23.2	95.00%	-.MQLVPLELNR.S		-.MQLVPLELNR.S
142	158	2	1718.72	1.8	1	101	31.3	95.00%	E.MAAPSSDGNAGDDNLRE.V		R.IDEEMAAPSSDGNAGDDNLREVNSR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
62	A6ZM61_YEAS7	56.25%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
186	198	2	1554.7	2.1	1	58.1	30.7	95.00%	E.AFEDDYNDAINIR.L		R.SALQQNQADTEAFEDDYNDAINIR.L
189	198	2	1207.55	2	0	51	29.3	95.00%	E.DDYNDAINIR.L		R.SALQQNQADTEAFEDDYNDAINIR.L
57	70	2	1606.75	3.2	1	72.5	30	95.00%	K.VATMQVWDTAGQER.F	Oxidation (+16)	K.VATMQVWDTAGQER.F
118	131	2	1562.84	1.8	1	46.7	24.8	95.00%	E.TFPFVILGNKIDAE.E		R.DEFLVHANVNSPETFPFVILGNKIDAEESK.K
39	48	2	1035.56	2.9	0	28.6	26.4	95.00%	K.ATIGADFLTK.E		K.ATIGADFLTK.E

107	117	2	1225.61	1.6	0	59.5	28.3	95.00%	E.FLVHANVNSPE.T		R.DEFLVHANVNSPETFPFVILGNK.I
81	101	2	2361.06	-2.7	1	101	29.8	95.00%	R.GADCCVLVYDVTNASSFENIK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GADCCVLVYDVTNASSFENIK.S
148	160	2	1360.76	3.1	0	63.7	21.6	95.00%	K.SLGDIPLFLTSAK.N		K.SLGDIPLFLTSAK.N
11	21	2	1056.62	2.9	0	27.1	24.5	95.00%	K.VIILGDSGVGK.T		K.VIILGDSGVGK.T
71	80	2	1186.61	-1.7	0	41.4	27.7	95.00%	R.FQSLGVAFYR.G		R.FQSLGVAFYR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
63	A6ZVP9_YEAS7	38.19%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
94	109	2	1564.85	3.2	0	37	23.8	95.00%	K.ASLNVGNVLPLGSVPE.G		K.ASLNVGNVLPLGSVPEGTIVSNVEEKPGDR.G
164	174	2	954.56	3.5	0	55.4	17.7	95.00%	R.GVIGVIAGGGR.V		R.GVIGVIAGGGR.V
81	92	2	1276.66	1.6	0	46.8	28.6	95.00%	E.GVHTGQFIYAGK.K		R.EEIFIANEGVHTGQFIYAGK.K
201	221	2	2158.02	-0.33	0	50.1	29.2	95.00%	R.GVAMNPVDHPHGGGNHQHIGK.A		R.GVAMNPVDHPHGGGNHQHIGK.A
10	21	3	1260.66	0.078	1	55.2	26.8	95.00%	R.KGAGSIFTSHTR.L		R.KGAGSIFTSHTR.L
164	181	3	1748.07	2.2	1	38.1	10.8	95.00%	R.GVIGVIAGGGRVDKPLLK.A		R.GVIGVIAGGGRVDKPLLK.A
81	93	3	1404.75	1.7	1	46.1	26.2	95.00%	E.GVHTGQFIYAGKK.A		R.EEIFIANEGVHTGQFIYAGKK.A
129	145	2	1839.91	1.2	1	97.2	27.8	95.00%	R.ASGNYVIIIGHNPDENK.T		R.ASGNYVIIIGHNPDENK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
64	PMT1_YEAST	15.18%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
408	425	2	2113	-0.19	1	40.8	28.8	95.00%	R.LHSHDHKPPVSESSDWQK.E		R.LHSHDHKPPVSESSDWQK.E
559	569	2	1330.71	3.6	0	33.8	25.5	95.00%	E.SQPTSWPFLLR.G		K.NLVEPHVYESQPTSWPFLLR.G
550	569	3	2411.24	3.2	1	31.5	25.7	95.00%	K.NLVEPHVYESQPTSWPFLLR.G		K.NLVEPHVYESQPTSWPFLLR.G
486	495	2	1203.56	2.7	1	32.7	29	95.00%	K.LPAWGFEQQE.V		K.LPAWGFEQQEVTCASSGR.H
472	483	2	1451.6	2.2	0	42.4	30	95.00%	R.HAMTGCYLFSHE.V	Carbamidomethyl (+57)	R.HAMTGCYLFSHEVK.L
570	579	2	1194.55	3.9	1	30.9	29.5	95.00%	R.GISYWGENNR.N		R.GISYWGENNR.N
358	376	2	2318.03	0.82	0	30.9	30.6	95.00%	E.QQQSTLYPHMDANNDWLLE.L	Oxidation (+16)	R.HLSTMGGYLHSHSHNYPAGSEQQQSTLYPHMDANNDWLLELYNAPGESLTTFQNLTDGTK.V
23	42	3	2152.16	-0.37	1	46.7	22.5	95.00%	K.QGPVRPFIVTDPSAELASLR.T		K.QGPVRPFIVTDPSAELASLR.T
91	103	2	1474.73	1.7	0	35.5	28.6	95.00%	R.GTYFMDVHPPLAK.M		R.GTYFMDVHPPLAK.M
23	37	2	1611.83	0.6	0	30.9	27.1	95.00%	K.QGPVRPFIVTDPSAE.L		K.QGPVRPFIVTDPSAELASLR.T
472	485	2	1678.76	2.5	1	63.8	30.2	95.00%	R.HAMTGCYLFSHEVK.L	Carbamidomethyl (+57)	R.HAMTGCYLFSHEVK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
65	A6ZXE9_YEAS7	28.04%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
246	257	2	1198.65	3.6	0	29.1	24.8	95.00%	R.NGITPLGGLMAR.M		R.NGITPLGGLMAR.M
322	332	3	1327.67	1.7	1	20.7	27.4	90.90%	E.ILDPHDFGMKR.Y		K.AILANPSTYEILDPHDFGMKR.Y
350	363	2	1627.84	1.7	0	81.8	27.1	95.00%	R.VDQLNLNLTDDQIK.E		R.VDQLNLNLTDDQIK.E
350	364	2	1756.89	2.2	1	42.3	27.3	95.00%	R.VDQLNLNLTDDQIKE.V		R.VDQLNLNLTDDQIKEVTAK.I
312	331	3	2231.1	2.8	1	21.3	27.5	92.00%	K.AILANPSTYEILDPHDFGMK.R		K.AILANPSTYEILDPHDFGMK.R
160	170	2	1291.71	3	0	36.2	25.1	95.00%	R.SDLVDLLNIYK.T		R.SDLVDLLNIYK.T
105	118	2	1345.71	2.6	0	43.4	26	95.00%	E.TGVDGVDVVIGTSK.F		K.VAVETGVDGVDVVIGTSK.F
377	388	2	1330.7	2.5	0	53.5	26	95.00%	R.SLNIDDVDSIIK.N		R.SLNIDDVDSIIK.N
258	267	2	1105.59	3.2	0	40	26.2	95.00%	R.MIVAAPDYVK.S		R.MIVAAPDYVK.S
180	192	2	1328.65	0.46	0	87.7	28.7	95.00%	R.VGIADTVGCANPR.Q	Carbamidomethyl (+57)	R.VGIADTVGCANPR.Q
234	245	2	1269.73	1.6	1	67.6	21.9	95.00%	R.LIDVSVLGIGER.N		R.LIDVSVLGIGER.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
66	A6ZT96_YEAS7	30.18%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
25	44	2	2417.13	2.6	0	101	30.1	95.00%	R.TPLFSIYDQSTSPYLLHCFE.L	Carbamidomethyl (+57)	R.TPLFSIYDQSTSPYLLHCFELLNLTSR.S

340	350	2	1433.66	-0.69	1	78.7	30.3	95.00%	R.GCVEIFDYYLR.D	Carbamidomethyl (+57)	R.GCVEIFDYYLR.D
151	162	2	1328.53	2.1	0	40.8	29.3	95.00%	K.MGNGMADYILDE.N	Deamidation (+1)	K.MGNGMADYILDENYNLNGLQTV HDYDVYCHYVAGLVGDGLTR.L
226	235	2	1194.52	0.65	1	49.6	29.9	95.00%	R.DYNEDLVDGR.S		R.DYNEDLVDGR.S
89	97	3	1121.66	1.9	1	28.5	20.2	95.00%	E.HDLKIDLLR.H		R.ALDTIEDDMSIEHDLKIDLLR.H
108	120	3	1505.7	3.6	1	30.8	29.1	95.00%	K.WSFDGNAPDVKDR.A		K.WSFDGNAPDVKDR.A
4	13	2	1131.67	2.7	0	40.4	22	95.00%	K.LLQLALHPVE.M		K.LLQLALHPVEMK.A
151	192	4	4736.13	1.8	1	37.1	28.2	95.00%	K.MGNGMADYILDENYNLNGLQTV HDYDVYCHYVAGLVGDGLTR.L	Deamidation (+1)/ Carbamidomethyl (+57)	K.MGNGMADYILDENYNLNGLQTV HDYDVYCHYVAGLVGDGLTR.L
25	51	3	3214.61	3.7	1	60.8	25.4	95.00%	R.TPLFSIYDQSTSPYLLHCFELLNLT SR.S	Carbamidomethyl (+57)	R.TPLFSIYDQSTSPYLLHCFELLNLT SR.S
356	365	2	1143.63	2.5	0	26.7	25.5	95.00%	K.LAVQDPNFLK.L		K.LAVQDPNFLK.L
4	15	2	1390.8	2.7	1	59.8	20.4	95.00%	K.LLQLALHPVEMK.A		K.LLQLALHPVEMK.A
108	118	2	1234.57	3.1	0	33.7	30.2	95.00%	K.WSFDGNAPDVK.D		K.WSFDGNAPDVK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
67	A6ZNR5_YEAS7	21.71%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
181	191	2	1145.6	2.7	1	47.9	27.6	95.00%	E.IQLNGGSISEK.V	Deamidation (+1)	K.AHLAEIQLNGGSISEK.V
75	97	2	2351.32	2.3	1	59.5	18.7	95.00%	E.AVTVVDTPPVVVVGVVGYVETPR .G		R.EVVEAVTVVDTPPVVVVGVVGYV ETPR.G
317	325	3	1106.62	1.7	1	31.3	23.7	95.00%	E.IKNDFIMVK.G		K.TITPMGGFVHYGEIKNDFIMVK.G
248	266	4	2175.1	2.9	1	66.2	26.5	95.00%	R.KVACIGAWHPAHVMWSVAR.A	Carbamidomethyl (+57)	R.KVACIGAWHPAHVMWSVAR.A
214	222	2	960.53	2	0	34.5	27.4	95.00%	E.MIDAIAVTK.G		K.TVAVDSVFEQNEMIDAIAVTK.G
249	266	2	2047.01	3	0	49.1	28.3	95.00%	K.VACIGAWHPAHVMWSVAR.A	Carbamidomethyl (+57)	K.VACIGAWHPAHVMWSVAR.A
38	50	2	1409.79	0.48	0	41.5	21.5	95.00%	R.SKPVALTSFLGYK.A		R.SKPVALTSFLGYK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
68	A6ZNV4_YEAS7	19.79%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
186	195	2	1242.63	2.6	0	33.5	27.8	95.00%	E.LDFQTIIHQE.R		K.VNEQSPLLHNEGQHQLQLQEEQ EQQQQGLSQEELDFQTIIHQER.S
186	196	2	1398.73	3.1	1	64.6	26.1	95.00%	E.LDFQTIIHQER.S		K.VNEQSPLLHNEGQHQLQLQEEQ EQQQQGLSQEELDFQTIIHQER.S
210	222	2	1424.82	2	0	35.8	20.7	95.00%	E.VNAIFHQLGSLVK.E		R.IHTAVQEVNAIFHQLGSLVK.E
13	26	2	1591.72	0.81	0	52.5	30.7	95.00%	K.GNSQQEPQFSTNQK.T		K.GNSQQEPQFSTNQK.T
102	112	2	1413.66	-0.98	0	73.2	29.4	95.00%	K.YQSLQQSYNQR.K		K.YQSLQQSYNQR.K
203	222	3	2203.21	-0.67	1	43	21.3	95.00%	R.IHTAVQEVNAIFHQLGSLVK.E		R.IHTAVQEVNAIFHQLGSLVK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
69	A6ZQU5_YEAS7	22.56%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
151	161	3	1222.71	2.5	0	21.8	21	95.00%	E.LVVSSNHLLNK.Y		R.DYFSPSSEELVVSSNHLLNK.Y
75	85	2	1305.73	-0.18	0	40.6	23.8	95.00%	R.LFDNIIVFPTK.G		R.LFDNIIVFPTK.G
107	123	2	1785.89	2.6	0	40	28.1	95.00%	E.GNILCMSSPGAVPNTIR.L	Carbamidomethyl (+57)	K.FFENEGNILCMSSPGAVPNTIR.L
75	88	2	1547.88	2.6	1	76.1	20.8	95.00%	R.LFDNIIVFPTKGGK.N		R.LFDNIIVFPTKGGK.N
187	196	2	1119.68	1.7	0	22.8	16.9	91.80%	E.QIVPILNAPR.T		R.EQIVPILNAPR.T
350	361	3	1482.77	2.8	1	51.1	26.2	95.00%	R.HGVFTFLTDYRK.I		R.HGVFTFLTDYRK.I
266	285	2	2227.98	2	1	67.1	30.9	95.00%	K.SVHAVHSHADGTSYDEEPYK.I		K.SVHAVHSHADGTSYDEEPYK.I
186	196	2	1248.72	1.2	1	24.5	18.5	94.20%	R.EQIVPILNAPR.T		R.EQIVPILNAPR.T
304	315	2	1482.72	1.9	0	47.6	29.2	95.00%	E.WLPHIADDIQFE.L		K.VIYSVGFSEWNGEEWLPHIADDI QFELR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
70	GNP1_YEAST	9.95%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
14	32	2	2196.88	0.63	1	51.3	30.8	95.00%	E.GSSNMNMNRNDLDDVSHYE.M		R.NNEGSSNMNMNRNDLDDVSHYEMK.E
89	109	3	2058.92	3.8	0	26.3	30.6	95.00%	E.GSHANSPDSSNSNGTTPISTK.D	Deamidation (+1)	R.AEGSHANSPDSSNSNGTTPISTK.D
657	663	2	994.47	0.11	1	30	29.4	95.00%	K.RVLDFWC.-	Carbamidomethyl (+57)	K.RVLDFWC.-
110	121	2	1376.62	-0.74	1	37.8	29.8	95.00%	K.DSSSQLDNELNR.K		K.DSSSQLDNELNR.K
23	32	2	1205.49	1.9	0	32.2	29.7	95.00%	R.NDLDDVSHYE.M		R.NDLDDVSHYEMK.E
472	478	2	987.42	3.8	0	32.2	28.5	95.00%	K.CFDYIDR.E	Carbamidomethyl (+57)	K.CFDYIDR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
71	B3LH18_YEAS1	7.54%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
26	36	2	1295.72	4.3	0	39.9	23	95.00%	R.AAVYDLQYILK.A		R.AAVYDLQYILK.A
1	20	2	2175.11	1.2	1	65.8	26.1	95.00%	-.MDATTPLLTVANSHPARNPK.H	Acetyl (+42)	-.MDATTPLLTVANSHPARNPK.H
1	17	2	1836.91	2.8	0	111	28.6	95.00%	-.MDATTPLLTVANSHPAR.N	Acetyl (+42)/ Deamidation (+1)	-.MDATTPLLTVANSHPAR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
72	VAC7_YEAST	23.26%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
799	824	3	2982.17	1.6	1	64.5	30.3	95.00%	E.DEDVDDYDRPNATFNSYYGSASNTHE.L	Deamidation (+1)	K.NDLETKPLISDYGEDEDVDDYDRPNATFNSYYGSASNTHELPLHGR.M
789	798	2	1121.56	1.9	0	32.9	29	95.00%	E.TKPLISDYGE.D		K.NDLETKPLISDYGEDEDVDDYDRPNATFNSYYGSASNTHELPLHGR.M
249	261	3	1552.82	1.9	1	30.5	25.2	95.00%	K.IIERPTMHVTNSR.E		K.IIERPTMHVTNSR.E
115	148	4	3568.74	2.3	0	54.3	25.4	95.00%	E.HIGSVSSTNNNSNNALINHNPLSSHLSNPSSSLR.N		R.AGTSMSTSDIPTDLHLEHIGSVSSTNNNSNNALINHNPLSSHLSNPSSSLR.N
743	762	3	2289.02	2.7	1	33	31.3	95.00%	E.ENNGDSSNVNRPQHTNLQHE.F		K.FPHGLNFYGDNNVIEEENNGDSSNVNRPQHTNLQHEFIPEDNESDENDIHSMFYYNHK.N
460	492	3	3830.86	-2	1	26	26.3	95.00%	K.NLIFPDSSSQQQQQQQQPPKQQQQQQNHGITSK.I		K.NLIFPDSSSQQQQQQQQPPKQQQQQQNHGITSK.I
98	114	2	1789.81	1.8	0	55.7	30.2	95.00%	R.AGTSMSTSDIPTDLHLE.H	Oxidation (+16)	R.AGTSMSTSDIPTDLHLEHIGSVSSTNNNSNNALINHNPLSSHLSNPSSSLR.N
396	417	2	2288.94	0.78	0	143	30.7	95.00%	K.NSNADLSASTSNNNAINDDSHE.S		K.NSNADLSASTSNNNAINDDSHESNSEKPTK.A
1062	1071	2	1096.54	0.45	0	54.9	27.9	95.00%	R.NYDVSVSSVK.L		R.NYDVSVSSVK.L
699	715	2	2062.94	0.73	1	74	30.2	95.00%	E.DYIEQPHNYPTMQNSVK.K		R.YSGVPDHVNLEDYIEQPHNYPTMQNSVK.K
727	742	2	1864.82	-4.7	1	35.9	30.7	95.00%	K.FPHGLNFYGDNNVIEE.E	Deamidation (+1)	K.FPHGLNFYGDNNVIEEENNGDSSNVNRPQHTNLQHEFIPEDNESDENDIHSMFYYNHK.N
152	167	2	1605.79	2.5	0	77	28.9	95.00%	K.SSLLVASNPAFASDVE.L		K.SSLLVASNPAFASDVELSK.K
801	824	3	2737.12	1.7	0	72.6	30.6	95.00%	E.DVDDYDRPNATFNSYYGSASNTHE.L		K.NDLETKPLISDYGEDEDVDDYDRPNATFNSYYGSASNTHELPLHGR.M
14	50	3	3767.95	1.1	1	99.4	24	95.00%	E.TVEAPVANNLLLSNNSNVVAPNPSIPSASTSTSPLHR.E		K.LTVETETVEAPVANNLLLSNNSNVVAPNPSIPSASTSTSPLHR.E
744	762	2	2160.96	2.9	0	33.7	30.7	95.00%	E.NNGDSSNVNRPQHTNLQHE.F	Deamidation (+1)	K.FPHGLNFYGDNNVIEEENNGDSSNVNRPQHTNLQHEFIPEDNESDENDIHSMFYYNHK.N
789	800	2	1365.63	1	1	33.5	29.4	95.00%	E.TKPLISDYGEDE.D		K.NDLETKPLISDYGEDEDVDDYDRPNATFNSYYGSASNTHELPLHGR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
73	A6ZNT8_YEAS7	19.70%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
465	480	2	1841.82	2.4	1	60.2	30.5	95.00%	K.VIDNADDEYMALMSQK.T		K.VIDNADDEYMALMSQK.T
49	65	2	1969.91	2.5	0	38.8	29.8	95.00%	K.VVPIVYDPNDIVCDHSE.I	Carbamidomethyl (+57)	K.VVPIVYDPNDIVCDHSEILSPK.V
561	588	3	3252.37	2.1	1	88.4	31	95.00%	E.YDTPWDLTDGYLDDDDGLFSDNRNSGMR.A		R.LNDDANEYDTPWDLTDGYLDDDDGLFSDNRNSGMR.A
219	229	2	1267.71	1.2	0	31.4	23.3	95.00%	E.VSLISHFNPVR.L		K.DDSLAEVSLISHFNPVR.L
2	15	2	1465.71	1	0	31.1	29.2	95.00%	M.VSANGDLHLPISNE.Q	Deamidation (+1)	-.MVSANGDLHLPISNEQCMPENNGSLGFEAPTPR.Q
21	33	2	1358.66	2.3	1	73.5	28.9	95.00%	E.NNGSLGFEAPTPR.Q		-.MVSANGDLHLPISNEQCMPENNGSLGFEAPTPR.Q
198	218	2	2319.13	1.7	1	67.1	28.5	95.00%	R.GWIVQNGLDPTTFIKDDSLAE.V	Deamidation (+1)	R.GWIVQNGLDPTTFIKDDSLAEVSLISHFNPVR.L
561	583	2	2707.13	2.6	0	80.8	31.1	95.00%	E.YDTPWDLTDGYLDDDDGLFSDNR.N		R.LNDDANEYDTPWDLTDGYLDDDDGLFSDNR.N
502	509	2	1025.54	2.9	0	25.2	23.7	95.00%	E.VFMTPIFR.I	Oxidation (+16)	R.APDEDVYVSPLNLIEVFMTPIFR.I
49	70	2	2508.26	2.4	1	46	26.9	95.00%	K.VVPIVYDPNDIVCDHSEILSPK.V	Carbamidomethyl (+57)	K.VVPIVYDPNDIVCDHSEILSPK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
74	A6ZZH5_YEAS7	26.73%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
68	76	2	1023.56	1.6	0	36.6	24	95.00%	K.KPPLLVNNE.A	Deamidation (+1)	K.KPPLLVNNEAVHASVPDASHTSCNNGTLEVSINNPEPHVVDAVAR.H
230	242	2	1526.77	3.1	0	45.7	28.3	95.00%	K.HNVDAPIPNFFTR.N		K.HNVDAPIPNFFTR.N
113	131	3	2118.13	0.29	1	53.5	23.7	95.00%	R.HLIRNPSNSLQLQGGDITR.D		R.HLIRNPSNSLQLQGGDITR.D
77	96	2	2066.9	0.53	0	64.8	30.4	95.00%	E.AVHASVPDASHTSCNNGTLE.V	Carbamidomethyl (+57)/ Deamidation (+1)	K.KPPLLVNNEAVHASVPDASHTSCNNGTLEVSINNPEPHVVDAVAR.H
172	191	2	2040.87	1.1	0	86	31.2	95.00%	R.SMSFSAASIASSSHLNNNSE.A	Deamidation (+1)	R.SMSFSAASIASSSHLNNNSEANGNPLAAIGLAPAPMTHEEIR.A
97	112	2	1715.9	1.6	0	74.8	26.9	95.00%	E.VSINNPEPHVVDAVAR.H		K.KPPLLVNNEAVHASVPDASHTSCNNGTLEVSINNPEPHVVDAVAR.H
229	242	3	1654.86	1.4	1	42.2	26.5	95.00%	R.KHNVDAPIPNFFTR.N		R.KHNVDAPIPNFFTR.N
136	169	3	3761.74	2.5	0	85.9	28.6	95.00%	K.WTNDHPSSPSQYQYPSQPALSTSIPSQAPSFSNR.K		K.WTNDHPSSPSQYQYPSQPALSTSIPSQAPSFSNR.K
192	211	2	1973.95	0.68	1	44.7	28.4	95.00%	E.ANGNPLAAIGLAPAPMTHEE.I	Deamidation (+1)	R.SMSFSAASIASSSHLNNNSEANGNPLAAIGLAPAPMTHEEIR.A
117	131	2	1598.81	2.6	0	88.2	27.9	95.00%	R.NPSNSLQLQGGDITR.D		R.NPSNSLQLQGGDITR.D
583	596	2	1562.77	-0.081	1	47.3	28.8	95.00%	R.ILENWTFPSNASGK.Y		R.ILENWTFPSNASGK.Y
355	365	2	1124.49	0.52	0	51	29.8	95.00%	K.VGVDGYGDMGR.I		K.VGVDGYGDMGR.I
212	219	2	872.5	0.3	1	30.6	25.9	95.00%	E.IRAPGGFR.R		R.SMSFSAASIASSSHLNNNSEANGNPLAAIGLAPAPMTHEEIRAPGGFR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
75	EF3A_YEAST	13.98%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
829	842	2	1700.82	-0.54	0	29.2	29.3	94.70%	R.WVPMMSVDNAWIPR.G		R.WVPMMSVDNAWIPR.G
971	987	2	1737.8	0.11	0	79.9	29.7	95.00%	R.MTPSGHNWVSGQGAGPR.I		R.MTPSGHNWVSGQGAGPR.I
459	469	2	1181.5	-0.8	0	36.2	28.5	95.00%	R.YGICGPNGCGK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.YGICGPNGCGK.S

751	759	2	1178.58	3.2	1	37.4	29.4	95.00%	K.TPSEYIQWR.F		K.TPSEYIQWR.F
296	307	2	1290.62	2.6	1	69.5	28.9	95.00%	K.SNFATIADPEAR.E		K.SNFATIADPEAR.E
276	289	2	1524.86	2.3	1	35.2	22	95.00%	K.LVEDPQVIAPFLGK.L		K.LVEDPQVIAPFLGK.L
113	127	2	1550.94	2.7	0	53.9	7.78	95.00%	E.TLISIVNAVNPVAIK.A		K.EIQSVASETLISIVNAVNPVAIK.A
128	139	2	1289.74	2.3	0	25.9	21.4	95.00%	K.ALLPHLTNAIVE.T		K.ALLPHLTNAIVETNK.W
669	696	3	3247.54	2.2	1	30.7	28.1	95.00%	K.VTNMEFQYPGTSKPQITDINFQCSLSSR.I	Carbamidomethyl (+57)	K.VTNMEFQYPGTSKPQITDINFQCSLSSR.I
536	549	2	1460.76	3.5	0	27.2	27.4	94.70%	E.MIAMPISALSGGWK.M		K.LIEFGFTDEMIAMPISALSGGWK.M
674	696	3	2673.29	1.8	0	30.1	28	95.00%	E.FQYPGTSKPQITDINFQCSLSSR.I	Carbamidomethyl (+57)	K.VTNMEFQYPGTSKPQITDINFQCSLSSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
76	A7A077_YEAS7	23.27%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
359	369	3	1305.64	3	1	33.7	28	95.00%	K.LGLSNEDFFHK.V		K.LGLSNEDFFHK.V
390	413	3	2877.39	-1.8	1	26.7	28.6	95.00%	R.TNCMDCLDRTNVVQSVLAQWVLQK.E	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.TNCMDCLDRTNVVQSVLAQWVLQK.E
21	39	3	1992.02	1.9	1	42.1	26.7	95.00%	E.GKGTNDAVIHLANQDQGVR.V		K.LAEGKGTNDAVIHLANQDQGVR.V
257	270	2	1602.84	-0.88	1	59	26.1	95.00%	R.GSVPIYWAEINNLK.Y		R.GSVPIYWAEINNLK.Y
2	17	2	1767.93	3.4	0	39.3	24.8	95.00%	M.TGPIVYVQNADGIFFK.L		-.MTGPIVYVQNADGIFFK.L
399	413	2	1711.96	-1.2	0	77.1	20.9	95.00%	R.TNVVQSVLAQWVLQK.E		R.TNVVQSVLAQWVLQK.E
295	308	2	1651.86	2.1	0	59.7	25.9	95.00%	E.LYGDNYLVNLVNQK.G		K.ELYGDNYLVNLVNQK.G
294	308	2	1780.9	-1.7	1	64	27.8	95.00%	K.ELYGDNYLVNLVNQK.G		K.ELYGDNYLVNLVNQK.G
175	188	2	1612.85	-1.4	0	43.4	26.8	95.00%	R.IDSFIQPVIYGYAK.T		R.IDSFIQPVIYGYAK.T
189	207	3	2021.2	-0.59	1	24.7	11.5	95.00%	K.TVDAVLNATPIVLGLITRR.S		K.TVDAVLNATPIVLGLITRR.S
189	206	2	1865.1	-0.54	0	61.6	12.6	95.00%	K.TVDAVLNATPIVLGLITR.R		K.TVDAVLNATPIVLGLITR.R
390	398	2	1183.44	-0.13	0	49.6	27.7	95.00%	R.TNCMDCLDR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.TNCMDCLDR.T
471	483	2	1410.69	2.9	0	101	29.1	95.00%	R.LGAFNDFLNSASR.Y		R.LGAFNDFLNSASR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
77	A7A0Z7_YEAS7	30.83%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
17	29	2	1584.73	1.7	1	40.3	29.8	95.00%	E.TISSCFQPFQKNE.N	Carbamidomethyl (+57)	K.NGETISSCFQPFQKNENYGTITSANEQITPVIFHNLIMDMVLPK.V
14	27	2	1641.75	2.9	1	72.9	30.1	95.00%	K.NGETISSCFQPFQK.N	Carbamidomethyl (+57)	K.NGETISSCFQPFQK.N
196	202	2	772.47	-3.5	0	22.9	25.5	90.90%	R.VSLLVDK.T		R.VSLLVDK.T
40	57	3	2124.15	2.4	0	25.8	23.1	95.00%	E.QITPVIFHNLIMDMVLPK.V	Oxidation (+16)	K.NENYGTITSANEQITPVIFHNLIMDMVLPK.V
123	138	2	1809.89	1.8	1	81	28.7	95.00%	E.LLSSHVGQILDSFHEE.L		R.ILSGLQEYESNATNELLSSHVGQILDSFHEELVEYR.N
69	89	2	2507.02	3.6	0	31.8	31.1	95.00%	K.MSMNLIDGFDCFYSTDDHDPK.T	Carbamidomethyl (+57)	K.MSMNLIDGFDCFYSTDDHDPK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
78	A6ZV40_YEAS7	8.36%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
542	554	2	1468.62	2	0	71.5	30.2	95.00%	K.VYDDTIGDVDTQE.D		K.VYDDTIGDVDTQEDGVIETNIIEHYK.S
60	73	2	1615.85	-0.65	0	69	25.9	95.00%	K.QLGILSCIGLICNR.M	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.QLGILSCIGLICNR.M
6	16	2	1309.7	-0.47	0	68.2	25.5	95.00%	R.TFLSQLNVFNK.E		R.TFLSQLNVFNK.E
527	536	2	1192.55	1.3	1	39.6	29.2	95.00%	K.DVLGEDGFWR.V		K.DVLGEDGFWR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
79	A6ZX41_YEAS7	38.76%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
60	69	2	1102.53	2.9	0	45.5	28.5	95.00%	E.LALWDTAGQE.D		R.VELALWDTAGQEDYDR.L
128	137	2	1212.61	0.15	1	68.8	28.6	95.00%	R.NDPQTIEQLR.Q		R.NDPQTIEQLR.Q
2	10	2	1029.52	-0.26	0	37	27.6	95.00%	M.SQQVGNSIR.R	Acetyl (+42)	-.MSQQVGNSIR.R
124	134	2	1298.65	1.7	1	30.5	28.7	95.00%	K.VDLRNDPQTIE.Q		K.VDLRNDPQTIEQLR.Q
60	73	2	1651.75	2.3	1	42.7	29.7	95.00%	E.LALWDTAGQEDYDR.L		R.VELALWDTAGQEDYDR.L
104	123	2	2338.24	2.6	1	49.3	23.7	95.00%	K.WIAEVLHFCQGVPIILVGCK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.WIAEVLHFCQGVPIILVGCK.V
108	123	2	1838.99	2.4	0	61.1	24.1	95.00%	E.VLHFCQGVPIILVGCK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.WIAEVLHFCQGVPIILVGCK.V
24	32	2	1079.61	3.5	0	39	22.6	95.00%	K.TCLLIVFSK.G	Carbamidomethyl (+57)	K.TCLLIVFSK.G
149	163	2	1557.7	2.2	0	52.4	29.8	95.00%	E.GQSVADQIGATGYYE.C		R.QEGQQPVTSQEGQSVADQIGATGYYECSAK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
80	A6ZT03_YEAS7	12.98%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
314	324	3	1294.69	1.8	0	34.2	26.1	95.00%	E.LFTGKPAMFQR.T		R.AAGTASWGELFTGKPAMFQR.T
547	564	2	2113.87	2.1	0	65.4	30.4	95.00%	R.GADYNADDLMHDDQPFYK.S		R.GADYNADDLMHDDQPFYK.S
1	12	2	1371.67	2.8	0	27.7	28.5	93.90%	-.MNSTPDLISPQK.S	Acetyl (+42)	-.MNSTPDLISPQK.S
46	59	2	1392.74	2.7	0	64	25.5	95.00%	E.SQVQPAVAPPNTGK.G		K.NESFHDNLSESQVQPAVAPPNTGK.G
546	564	2	2269.97	1.4	1	75.4	31.3	95.00%	K.RGADYNADDLMHDDQPFYK.S		K.RGADYNADDLMHDDQPFYK.S
305	324	2	2125.05	2.7	1	94.5	28	95.00%	R.AAGTASWGELFTGKPAMFQR.T		R.AAGTASWGELFTGKPAMFQR.T
228	236	2	1153.52	2.9	0	49.9	30.3	95.00%	K.NYSNSVQWR.V	Deamidation (+1)	K.NYSNSVQWR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
81	RL20_YEAST	28.49%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
100	113	2	1536.76	2.5	1	60.2	28	95.00%	R.VAAVETLYQDMAAR.H		R.VAAVETLYQDMAAR.H
147	155	3	1121.64	3.1	1	24	21.9	95.00%	K.DLKFPLPHR.V		K.DLKFPLPHR.V
74	80	2	876.46	0.084	0	30.8	27.2	95.00%	K.NFGVWVR.Y		K.NFGVWVR.Y
29	38	2	1090.6	2.2	1	60.7	25.7	95.00%	R.IFASNEVIAK.S		R.IFASNEVIAK.S
58	66	2	1028.55	1.7	0	27.7	27.2	95.00%	E.IVSINQINE.A		K.ASGEIVSINQINEAHPTK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
82	B3LQG1_YEAS1	18.18%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
51	74	2	2661.22	1.5	1	105	29.6	95.00%	K.EISQSINSANNIQSSDSDLVQHFE.S		K.EISQSINSANNIQSSDSDLVQHFESLAQEIR.H
52	74	2	2532.18	1.8	0	98.8	29.5	95.00%	E.ISQSINSANNIQSSDSDLVQHFE.S		K.EISQSINSANNIQSSDSDLVQHFESLAQEIR.H
107	115	2	1011.53	-0.42	1	25.4	24.5	95.00%	K.QTPPEATLR.E		K.QTPPEATLR.E
349	358	2	1129.68	0.16	0	56.3	19.7	95.00%	K.LLSDVLVFPK.F		K.LLSDVLVFPK.F
359	375	2	2074.92	1.2	1	40.6	30.6	95.00%	K.FSFNCPNQIDNDDPHKK.F	Carbamidomethyl (+57)	K.FSFNCPNQIDNDDPHKK.F
118	129	2	1407.69	0.63	0	33	29	95.00%	R.IAMTFPYDSHVK.F		R.IAMTFPYDSHVK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
83	A6ZSU5_YEAS7	24.84%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
380	394	2	1652.76	2.1	1	69.1	29	95.00%	R.GTFQSSGQNCIGIER.V	Carbamidomethyl (+57)	R.GTFQSSGQNCIGIER.V
495	504	2	1149.63	2.8	0	32.5	25.1	95.00%	E.VFGPILVMMK.A	Oxidation (+16)	K.IAQNEVFGPILVMMK.A
159	176	2	2067.12	1.9	0	85.7	20.8	95.00%	R.VLASLHDYILNNQDLIAR.V		R.VLASLHDYILNNQDLIAR.V
144	155	2	1354.59	0.94	0	48.9	30.3	95.00%	K.AQSTWGNSDFSR.R		K.AQSTWGNSDFSR.R
507	532	3	2674.29	2.9	0	34.8	27.7	95.00%	K.NTDHCVQLANSAPFGLGGSVFGADIK.E	Carbamidomethyl (+57)	K.NTDHCVQLANSAPFGLGGSVFGADIK.E
327	342	3	1823.02	3.1	0	32.6	20.2	95.00%	K.HITFIGSQPVAHYILK.C		K.HITFIGSQPVAHYILK.C

470	487	2	2103.04	1.9	0	32.7	28.4	95.00%	K.YPQGHYFQPTLLVDVTPE.M		K.YPQGHYFQPTLLVDVTPEMK.I
81	94	2	1571.78	3.2	1	50.7	27.7	95.00%	K.FSLPAPEAAQNNWK.G		K.FSLPAPEAAQNNWK.G
369	379	2	1231.66	-0.094	0	52.8	27.1	95.00%	K.NLDALSSIIMR.G		K.NLDALSSIIMR.G
429	443	2	1712.72	1.6	1	74.2	30.2	95.00%	E.NVDMGAMISDNRFDE.L		R.QGSDIDHLENVDMGAMISDNRFDELEALVK.D
490	504	2	1688.9	-0.54	1	41.5	25	95.00%	K.IAQNEVFGPILVMMK.A		K.IAQNEVFGPILVMMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
84	A6ZNY0_YEAS7	16.98%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
633	651	2	2130.02	-0.65	0	63.1	29.4	95.00%	K.IWCFGPDGNGPNLVIDQTK.A	Carbamidomethyl (+57)	K.IWCFGPDGNGPNLVIDQTK.A
786	814	3	3117.46	2.4	0	31.5	29.2	95.00%	R.QATGGQAFPQMVFDHWSTLGSDPLDPTSK.A		R.QATGGQAFPQMVFDHWSTLGSDPLDPTSK.A
244	253	2	1209.58	1.7	0	38.1	29.4	95.00%	R.LWGDSFFNPK.T		R.LWGDSFFNPK.T
632	651	3	2259.11	2.4	1	22.2	28.6	91.40%	R.KIWCFGPDGNGPNLVIDQTK.A	Carbamidomethyl (+57)/ Deamidation (+1)	R.KIWCFGPDGNGPNLVIDQTK.A
712	723	2	1265.67	-0.42	0	36.8	26.2	95.00%	R.ATYAGFLLADPK.I		R.ATYAGFLLADPK.I
151	162	2	1378.87	2.8	1	55.1	13	95.00%	R.IKPVVVINKVDR.A		R.IKPVVVINKVDR.A
618	631	2	1626.7	2	0	60.1	30.2	95.00%	R.IMADDYGWDVTDAR.K		R.IMADDYGWDVTDAR.K
441	465	2	2742.44	3.1	0	85.9	24	95.00%	R.FVEPIDDCPAGNIIGLVGIDQFLLK.T	Carbamidomethyl (+57)	R.FVEPIDDCPAGNIIGLVGIDQFLLK.T
33	42	2	1118.6	3.2	0	46.5	26.2	95.00%	K.STLTDSLVQR.A		K.STLTDSLVQR.A
618	632	2	1754.8	2	1	33.9	30.1	95.00%	R.IMADDYGWDVTDARK.I		R.IMADDYGWDVTDARK.I
196	206	2	1215.66	2.1	0	51.8	25.9	95.00%	E.VLGDVQVYPAR.G		R.TVESVNVIVSTYADEVLGDVQVYPAR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
85	A6ZXZ5_YEAS7	15.31%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
268	278	2	1191.52	1.4	0	29.1	29.9	93.90%	K.LGYHFGPSDAE.A		K.LGYHFGPSDAEAVMAPK.A
268	284	2	1788.85	0.66	1	63.6	29.7	95.00%	K.LGYHFGPSDAEAVMAPK.A		K.LGYHFGPSDAEAVMAPK.A
285	300	2	1575.88	1.9	0	68.3	21.9	95.00%	K.APVASPRPAATPNLSK.D		K.APVASPRPAATPNLSK.D
18	31	2	1524.77	3.1	0	55.6	27.3	95.00%	K.INPPTGADFHITSR.G		K.INPPTGADFHITSR.G
285	302	2	1819	-0.077	1	64.8	22.7	95.00%	K.APVASPRPAATPNLSKDK.K		K.APVASPRPAATPNLSKDK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
86	A6ZU19_YEAS7	16.95%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	178	3	1847.01	2.7	0	27	23.4	95.00%	E.SHVLASTLVPGDLVHFR.I		R.CGQESHVLASTLVPGDLVHFR.I
88	94	2	868.44	2.5	0	32.1	30.2	95.00%	K.FLSNFIE.D		K.FLSNFIEDR.M
553	568	2	1731.91	-0.87	1	63.2	25.9	95.00%	K.LTLSDSSTPLTEDLIK.D		K.LTLSDSSTPLTEDLIK.D
507	516	2	1215.64	2.9	1	24.7	26.8	91.80%	R.ILEYSTSYLK.S		R.ILEYSTSYLK.S
638	655	2	2057.01	2.6	0	76.9	28.5	95.00%	E.MSDDQLANVIDHVNIFAR.A		K.LDEMSDDQLANVIDHVNIFAR.A
361	372	2	1291.65	1.5	0	53	28.5	95.00%	E.TLGSVNVICSDK.T	Carbamidomethyl (+57)	R.LPSVETLGSVNVICSDK.T
627	637	2	1174.61	1.1	1	40.7	27.5	95.00%	K.LSVLSGDKLDE.M		K.LSVLSGDKLDEMSDDQLANVIDHVNIFAR.A
690	699	2	1033.53	2.8	0	76.1	27.6	95.00%	K.LSDIGVSMGR.I		K.LSDIGVSMGR.I
235	245	2	1241.62	3.2	0	43.1	28.6	95.00%	R.SCIAYMGTLVK.E	Carbamidomethyl (+57)	R.SCIAYMGTLVK.E
158	178	4	2321.16	2.4	1	43.6	27.1	95.00%	R.CGQESHVLASTLVPGDLVHFR.I	Carbamidomethyl (+57)	R.CGQESHVLASTLVPGDLVHFR.I
219	234	2	1788.87	3.5	1	54.1	29	95.00%	K.SSFNDQPNSIVPISER.S		K.SSFNDQPNSIVPISER.S
28	37	2	1027.56	1.3	0	38.5	26.2	95.00%	E.ALSKPSPSLE.Y		R.EILDATAEALSKPSPSLEYCTLSVDETLEK.L
569	587	3	2084.08	2.7	0	24.8	25.9	95.00%	K.DLTFTGLIGMNDPPRPNVK.F		K.DLTFTGLIGMNDPPRPNVK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
87	A6ZKW1_YEAS7	22.61%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
83	98	2	1920.91	-0.9	0	68.3	29.4	95.00%	K.SFYNNVFNFLMVDSPK.G		K.SFYNNVFNFLMVDSPK.G

337	356	2	2086.99	3.6	0	44.7	29.1	95.00%	K.DLSDVPLSDLDGTIPDVSTE.S			K.DLSDVPLSDLDGTIPDVSTESGQLMINK.T
448	458	2	1238.6	3.5	1	64	28.6	95.00%	R.YLNAMESIGNK.Y			R.YLNAMESIGNK.Y
227	236	2	1234.64	0.58	0	24.8	27	91.70%	K.CIYVSDILPR.E	Carbamidomethyl (+57)		K.CIYVSDILPR.E
108	123	3	1856.92	0.72	1	24.4	27.5	95.00%	E.ACLLKGDIGDRPDHYK.D	Carbamidomethyl (+57)		K.QYNEACLLKGDIGDRPDHYK.D
429	447	3	2191	2.7	0	27	30.3	95.00%	E.DGFHGVAMLQHDFVQDYGR.Y			R.TGVEGYHDEDGFHGVAMLQHDFVQDYGR.Y
55	75	2	2201.89	0.95	1	84.5	30.1	95.00%	K.YSSSSDAASADDSTPLRDNDE.A			K.YSSSSDAASADDSTPLRDNDEAGNEK.L
493	514	4	2649.28	3.5	1	38.2	27.8	95.00%	K.NHVDVMFIHSNFPKFDPYDLSK.S			K.NHVDVMFIHSNFPKFDPYDLSK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
88	YHF0_YEAST	2.15%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
411	419	2	1018.48	1.4	1	31.6	29.5	95.00%	R.MAWEALAVE.R		R.MAWEALAVER.M
201	206	2	764.43	2.2	0	29.9	24.4	95.00%	R.MFNLIK.E		R.MFNLIK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
89	B3LJX9_YEAS1	20.73%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
302	317	2	1670.88	2.1	0	30.7	25.6	95.00%	K.ILLQATPSTLSGDQVE.G		K.ILLQATPSTLSGDQVEGDLLK.I
393	411	2	2047.01	2.3	0	59.8	28.2	95.00%	R.AGDSQGDHLQNDPLSLRPK.T		R.AGDSQGDHLQNDPLSLRPK.T
412	439	3	3030.24	2.6	1	50.2	30.8	95.00%	K.TYGTGISGSTCLIDDAANCNTADCLEDH.-	Carbamidomethyl (+57)/Carbamidomethyl (+57)/Carbamidomethyl (+57)	K.TYGTGISGSTCLIDDAANCNTADCLEDH.-
213	234	3	2338.05	0.52	1	47.1	30.7	95.00%	K.TPSYSTSSHTIASGGNYTEHNK.R		K.TPSYSTSSHTIASGGNYTEHNK.R
213	231	2	1958.85	0.97	0	55.2	30	95.00%	K.TPSYSTSSHTIASGGNYTE.H		K.TPSYSTSSHTIASGGNYTEHNK.R
302	322	2	2197.19	1.3	1	78.3	22.9	95.00%	K.ILLQATPSTLSGDQVEGDLLK.I		K.ILLQATPSTLSGDQVEGDLLK.I
392	411	4	2203.11	1.2	1	22.4	26.6	95.00%	E.RAGDSQGDHLQNDPLSLRPK.T		R.EVTSTERAGDSQGDHLQNDPLSLRPK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
90	A7A0E5_YEAS7	12.65%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
443	461	2	2078.96	1.3	1	36.6	30.4	95.00%	E.VSGYGDNVVGDNKDNWVIE.I		K.TQWEVSGYGDNVVGDNKDNWVIEIMDQR.G
353	383	3	3463.62	0.12	0	63	28.1	95.00%	K.NQALGGSLLHSHIQTYPDGSNQQQVTCYGYK.D	Carbamidomethyl (+57)	K.NQALGGSLLHSHIQTYPDGSNQQQVTCYGYK.D
330	352	3	2253.24	2	1	36.1	20.4	95.00%	R.LVGSDVGQGPRDIALGSSVVSIK.N		R.LVGSDVGQGPRDIALGSSVVSIK.N
341	352	2	1187.68	2.5	0	40.7	22.6	95.00%	R.DIALGSSVVSIK.N		R.DIALGSSVVSIK.N
106	118	3	1574.77	2.6	1	33.7	28.9	95.00%	R.HEFYHDVHPPLGK.M		R.HEFYHDVHPPLGK.M
473	482	2	1202.68	1.1	1	27.3	23.1	95.00%	E.KLHTLTTSFR.I		R.GDEDPEKLHTLTTSFR.I
108	118	3	1308.66	1.8	0	23.3	28.2	94.30%	E.FYHDVHPPLGK.M		R.HEFYHDVHPPLGK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
91	A7A0U0_YEAS7	9.30%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
408	423	2	1610.79	0.59	1	57.7	28.8	95.00%	E.NGVVRAPADVNAIADE.T	Deamidation (+1)	K.LMVVHDENGVVRAPADVNAIADETTPLNSK.H
66	79	2	1581.75	2.2	1	52.2	29.4	95.00%	K.LGTITGYDLAENCR.H	Carbamidomethyl (+57)	K.LGTITGYDLAENCR.H
413	430	2	1825.91	-0.29	1	82.6	28.5	95.00%	R.APADVNAIADETTPLNSK.H		R.APADVNAIADETTPLNSK.H
401	412	2	1366.71	2.7	1	52.5	26.9	95.00%	K.LMVVHDENGVVR.A		K.LMVVHDENGVVR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
92	A6ZRM3_YEAS7	28.22%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
159	168	2	1161.6	0.93	0	30.3	27.7	95.00%	E.TNFIPQDISK.I		K.LMTPLTFSTETNFIPQDISK.I
149	158	2	1138.56	2.9	0	42.8	29.1	95.00%	K.LMTPLTFSTE.T		K.LMTPLTFSTETNFIPQDISK.I
149	168	2	2282.16	2	1	111	27.1	95.00%	K.LMTPLTFSTETNFIPQDISK.I		K.LMTPLTFSTETNFIPQDISK.I
63	75	2	1512.65	1.5	0	33.5	30.7	95.00%	E.YVFVGDVHGNYDE.F		K.EYVFVGDVHGNYDEFIELIDDK.I
79	89	2	1128.61	2.1	1	49.5	26.9	95.00%	E.LIDDKIGGLGE.N		K.EYVFVGDVHGNYDEFIELIDDKIGGLGENITMILLGDFIHK.G
109	121	2	1541.86	1.2	1	75.1	22.6	95.00%	K.VVSYILNHKDQVK.C		K.VVSYILNHKDQVK.C
129	142	2	1640.84	2.9	0	33.8	27.2	95.00%	E.ILVMMAYLNPDFSK.W		K.CVLGNHEILVMMAYLNPDFSK.W
122	142	3	2450.19	3.6	1	33.6	28.7	95.00%	K.CVLGNHEILVMMAYLNPDFSK.W	Carbamidomethyl (+57)	K.CVLGNHEILVMMAYLNPDFSK.W
273	286	2	1578.77	2.3	0	77.9	29.1	95.00%	K.VFYGHDASMGLNLR.R		K.VFYGHDASMGLNLR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
93	A7A1W6_YEAS7	42.03%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
248	266	3	2175.11	-0.87	1	30.6	26.1	95.00%	K.LYPLATFHLAQAQDFEGVR.A		K.LYPLATFHLAQAQDFEGVR.A
322	335	2	1715.84	1.1	1	69.3	27.9	95.00%	R.NITWIAECIAQNQR.E	Carbamidomethyl (+57)	R.NITWIAECIAQNQR.E
19	40	2	2586.21	2	1	66.4	29.9	95.00%	R.GYRNGLLSNNQYINLTQCDTLE.D	Deamidation (+1)/ Carbamidomethyl (+57)	R.GYRNGLLSNNQYINLTQCDTLEDLK.L
220	238	2	2042.06	2.9	0	102	25.6	95.00%	R.SINIALNSLQSSDIDPDLK.S		R.SINIALNSLQSSDIDPDLK.S
239	247	2	955.54	1.7	0	33.9	24.9	95.00%	K.SDLLPNIGK.L		K.SDLLPNIGK.L
267	276	2	1168.59	-0.44	1	58.1	27.3	95.00%	R.AALANVYEYR.G		R.AALANVYEYR.G
220	247	3	2979.58	2.2	1	67	20.6	95.00%	R.SINIALNSLQSSDIDPDLKSDLLPNIGK.L		R.SINIALNSLQSSDIDPDLKSDLLPNIGK.L
41	61	2	2289.11	1.8	1	134	28.3	95.00%	E.DLKLQLSSTDYGNFLSSVSSE.S		R.NGLLSNNQYINLTQCDTLEDLKLQLSSTDYGNFLSSVSSESLTTSLIQEYASSK.L
62	70	2	990.53	1.8	0	44.2	26.7	95.00%	E.SLTTSLIQE.Y		K.LQLSSTDYGNFLSSVSSESLTTSLIQEYASSK.L
151	163	2	1462.81	1.8	0	53.2	22.6	95.00%	E.TVLVDTPLAPYFK.N		R.CHPLGWFDTLPTLSVATDLESLYETVLVDTPLAPYFK.N
76	84	3	1253.62	3	1	27.8	27.4	95.00%	K.LYHEFNYIR.D		K.LYHEFNYIR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
94	A6ZWP0_YEAS7	9.66%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
958	971	2	1612.79	2.2	1	71.4	29.1	95.00%	R.SQKDFIQAYSDGVR.I		R.SQKDFIQAYSDGVR.I
91	103	2	1443.72	-0.52	0	31.2	27.9	95.00%	K.AQPLISSCPACLK.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.AQPLISSCPACLK.N
79	90	2	1397.77	2.9	1	41.2	23.4	95.00%	K.DQVVALRDNLQK.A		K.DQVVALRDNLQK.A
961	971	2	1269.6	3.5	0	44.2	29.3	95.00%	K.DFIQAYSDGVR.I		K.DFIQAYSDGVR.I
383	393	2	1439.62	2.9	0	35.7	29.9	95.00%	E.YFDDNFGPFYR.T		K.EYFDDNFGPFYR.T
33	45	2	1470.73	3	1	28.6	28.5	95.00%	K.SVFGNELPCPVPR.S	Carbamidomethyl (+57)	K.SVFGNELPCPVPR.S
185	203	3	2098.06	2.6	0	34.9	27.5	95.00%	K.FLGDAKPMLGGSPFQINYK.Y	Oxidation (+16)	K.FLGDAKPMLGGSPFQINYK.Y
476	489	2	1687.88	2.1	0	35.6	26.1	95.00%	K.FPVNCLPTFQQPLK.T	Carbamidomethyl (+57)	K.FPVNCLPTFQQPLK.T
104	120	2	2070.88	2.2	0	84	30.3	95.00%	K.NFNNLFCHFTCAADQGR.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.NFNNLFCHFTCAADQGR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
95	YL001_YEAST	15.89%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
833	844	2	1291.65	1.2	0	38.7	28.9	95.00%	E.GSYSVNAIQTPR.D		R.ATTPLIQHSPIIHNPSYSATAHLSPLSQPTFEGSYSVNAIQTPR.D
801	844	4	4728.39	-1.5	1	29.6	25.4	95.00%	R.ATTPLIQHSPIIHNPSYSATAHLSPLSQPTFEGSYSVNAIQTPR.D		R.ATTPLIQHSPIIHNPSYSATAHLSPLSQPTFEGSYSVNAIQTPR.D
302	318	3	1963.03	4	1	46.6	25.5	95.00%	R.IFEIGVVHGFSDLDFLR.T		R.IFEIGVVHGFSDLDFLR.T

801	832	3	3454.75	0.53	0	43	23.5	95.00%	R.ATTPLIQHSPIIHNPSYSATAHLSPLSQPTFE.G		R.ATTPLIQHSPIIHNPSYSATAHLSPLSQPTFEGSYSVNAIQTPR.D
253	265	2	1414.81	1.5	0	70.3	22.1	95.00%	E.LIIDDVYGGILPK.E		R.TSLLQELIIDDVYGGILPK.E
440	447	2	976.52	1.8	0	41.3	27.7	95.00%	K.ILNTKPYE.I		K.ILNTKPYEIGNTSIYSIDDDLQLPGDLVLSLAPENHCSISLMLLK.E
247	265	2	2086.16	-0.58	1	58.9	18.5	95.00%	R.TSLLQELIIDDVYGGILPK.E		R.TSLLQELIIDDVYGGILPK.E
523	530	2	930.54	3.5	0	31.4	25.4	95.00%	K.TALNLLMR.N		K.TALNLLMR.N
486	496	3	1262.7	3.2	0	20.1	23.3	94.30%	E.LNLLDLPSNHK.G		K.ELNLLDLPSNHK.G
305	318	3	1573.83	3.5	0	48.9	25.9	95.00%	E.IGVVHGFSDLDFLR.T		R.IFEIGVVHGFSDLDFLR.T
385	414	3	3449.65	2.6	1	42.5	27.3	95.00%	K.IDLEQDFSSLRPIQYAPTQIYDSAFCSSAK.R	Carbamidomethyl (+57)	K.IDLEQDFSSLRPIQYAPTQIYDSAFCSSAK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
96	A6ZMQ9_YEAS7	52.53%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
48	58	2	1336.63	2.2	0	46.8	29.2	95.00%	E.LFDLLDQMDVE.V		K.HVEQQQDELFDLLDQMDVEVNNSIGDASER.A
146	156	2	1235.6	2.6	0	49	28.5	95.00%	E.GIGSQIMMDLR.S	Oxidation (+16)	R.IANETEGIGSQIMMDLR.S
167	178	2	1413.68	2.6	0	60.1	28.7	95.00%	R.QTLFQADSYVDK.S		R.QTLFQADSYVDK.S
21	34	2	1453.75	-0.63	1	42.6	26.4	95.00%	K.ASLAEAPSQPLSQR.N		K.ASLAEAPSQPLSQR.N
144	156	2	1449.7	3	1	72.6	29.6	95.00%	E.TEGIGSQIMMDLR.S		R.IANETEGIGSQIMMDLR.S
89	102	3	1612.83	0.68	1	23.6	26.5	95.00%	K.RPLQSLVDSGDRDR.L		K.RPLQSLVDSGDRDR.L
2	13	2	1429.7	-0.75	1	30.8	29.2	95.00%	M.SSLLISYESDFK.T	Acetyl (+42)	-.MSSLLISYESDFK.T
103	129	3	3065.56	1.5	1	42.4	25.4	95.00%	R.LFGDLNASNIDDDQRQQLLSNHAILQK.S		R.LFGDLNASNIDDDQRQQLLSNHAILQK.S
59	69	2	1160.55	3.2	1	36.5	29.7	95.00%	E.VNNSIGDASER.A		K.HVEQQQDELFDLLDQMDVEVNNSIGDASER.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
97	A6ZL71_YEAS7	24.56%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
126	144	2	2154.03	0.17	1	58.7	28.8	95.00%	K.VFAEDYLDINGSPINPYAR.I	Deamidation (+1)	K.VFAEDYLDINGSPINPYAR.I
273	289	3	1904.97	-0.46	0	30	26.8	95.00%	R.HVLTILTDMSSYADALR.E		R.HVLTILTDMSSYADALR.E
99	106	2	899.51	2.4	1	42.4	26.8	95.00%	E.SLRIPVSE.D		K.TTVEFTGESLRIPVSEDMLGR.I
457	466	2	1187.63	2.9	0	75.8	26.6	95.00%	E.SLDQAWSLLR.I		R.TVFESLDQAWSLLR.I
170	182	2	1380.71	2.2	0	62.7	26.9	95.00%	K.IPIFSASGLPHNE.I		K.IPIFSASGLPHNEIAAQICR.Q
49	63	2	1702.89	1.9	1	49.5	26.4	95.00%	R.YNEIVNLTLPDGTVR.Q		R.YNEIVNLTLPDGTVR.Q
453	466	2	1663.86	-0.25	1	66.6	27.8	95.00%	R.TVFESLDQAWSLLR.I		R.TVFESLDQAWSLLR.I
26	43	2	1929.06	2.6	1	52	21.5	95.00%	R.LNYNTVSGVNGPLVILEK.V		R.LNYNTVSGVNGPLVILEK.V
303	318	2	1927.87	-0.67	1	76.7	30.7	95.00%	R.GYPGYMYTDLSTIYER.A		R.GYPGYMYTDLSTIYER.A
130	144	2	1707.81	0.51	0	70.1	29.4	95.00%	E.DYLDINGSPINPYAR.I	Deamidation (+1)	K.VFAEDYLDINGSPINPYAR.I
170	189	3	2193.13	-1.3	1	44.1	25.7	95.00%	K.IPIFSASGLPHNEIAAQICR.Q	Carbamidomethyl (+57)	K.IPIFSASGLPHNEIAAQICR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
98	A6ZP92_YEAS7	21.27%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
494	508	2	1737.91	-0.54	0	25.2	25.8	94.20%	K.QPLVPYSFAPFFPTK.R		K.QPLVPYSFAPFFPTK.R
433	454	2	2362.2	-1	1	68.5	25.5	95.00%	K.ADFLVPGENQVTPSSTPYISLK.V		K.ADFLVPGENQVTPSSTPYISLK.V
573	589	2	1889.97	-1.3	1	35.1	26.5	95.00%	K.IPLGQPAPETVGDFFFR.V		K.IPLGQPAPETVGDFFFR.V
358	379	3	2519.33	3.4	0	23.9	23.4	95.00%	K.CIVQAVPLTPNCQILQLPNVDK.E	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CIVQAVPLTPNCQILQLPNVDK.E
483	493	2	1296.6	1.3	1	47.2	30.4	95.00%	E.SQRDPFAMMSK.Q		K.QPLIPTSLIPEENLTEPQDFESQRDPFAMMSK.Q
539	549	2	1369.62	2.7	1	51	30.4	95.00%	K.NLNDDKDFFDK.R		K.NLNDDKDFFDK.R
511	521	2	1310.58	2	0	40.8	29.4	95.00%	R.GSWCCLVSSQK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GSWCCLVSSQK.D
195	212	3	1888.92	1.8	0	40	29.2	95.00%	K.YGHPDGPQSTSHGIALPR.F		K.YGHPDGPQSTSHGIALPR.F
129	142	2	1474.8	1.3	1	43.5	24.2	95.00%	E.ILGISTSASDRDIK.S		K.LFDPYEILGISTSASDRDIK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
99	A7A1A7_YEAS7	21.74%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
172	181	2	1254.6	3.8	0	49.4	28.6	95.00%	K.FYDNSNLINR.E		K.FYDNSNLINR.E
88	99	2	1349.67	0.57	0	47.6	28.4	95.00%	K.ANLGFFQSVDPR.V		K.ANLGFFQSVDPR.V
8	16	2	984.6	3.2	0	40.2	23.5	95.00%	K.NAVVTLIQK.A		K.NAVVTLIQK.A
37	59	3	2439.11	2.9	1	64.7	30.6	95.00%	R.GSNSNSSRHDNLSSSSSDIIYGR.N		R.GSNSNSSRHDNLSSSSSDIIYGR.N
60	74	2	1575.72	2.6	1	93.5	29.9	95.00%	R.NSAQDLENSPMSVGK.D		R.NSAQDLENSPMSVGK.D
45	59	2	1649.77	1.9	0	68.7	30	95.00%	R.HDNLSSSSSDIIYGR.N		R.HDNLSSSSSDIIYGR.N
172	182	2	1383.64	0.56	1	43.2	29.8	95.00%	K.FYDNSNLINRE.I		K.FYDNSNLINREIEDILLEINPNFSDETIVSFIK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
100	A6ZQY0_YEAS7	36.32%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
114	127	2	1398.71	1.6	0	51	27.7	95.00%	E.NADDNVAVGLIGNK.S		R.ENADDNVAVGLIGNK.S
2	15	2	1755.75	-1.5	1	57.4	30.9	95.00%	M.SSEDYGYDYDLLFK.I	Acetyl (+42)	-.MSSEDYGYDYDLLFK.I
128	134	2	810.43	-1.3	0	48.4	24.7	95.00%	K.SDLAHLR.A		K.SDLAHLR.A
16	26	2	1056.62	2.9	0	27.1	24.5	95.00%	K.IVLIGDSGVGK.S		K.IVLIGDSGVGK.S
64	74	2	1273.6	-1.7	1	41.6	28.8	95.00%	K.AQIWDTAGQER.Y		K.AQIWDTAGQER.Y
113	127	2	1527.75	1.2	1	68.2	29.2	95.00%	R.ENADDNVAVGLIGNK.S		R.ENADDNVAVGLIGNK.S
44	53	2	1079.56	3.4	1	61.2	27.6	95.00%	K.STIGVEFATR.T		K.STIGVEFATR.T
85	97	2	1304.74	2.5	0	42.2	23.2	95.00%	R.GAVGALIVYDISK.S		R.GAVGALIVYDISK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
101	A6ZLM5_YEAS7	14.05%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
44	61	2	2092.17	3.3	0	65.6	19.8	95.00%	K.IISLLNVDLFTPCLIFSK.L	Carbamidomethyl (+57)	K.IISLLNVDLFTPCLIFSK.L
225	238	2	1458.67	3.7	0	99.4	29.6	95.00%	R.MNSSFLSSSSIGDK.I		R.MNSSFLSSSSIGDK.I
183	197	2	1723.82	-0.0071	0	33.3	28.8	95.00%	E.NTQHMPPSQVQSLLE.R	Oxidation (+16)	K.WSGENTQHMPPSQVQSLLER.T
327	335	2	940.61	0.94	0	47.1	19.5	95.00%	K.LLIGSIIGR.M		K.LLIGSIIGR.M
183	198	2	1879.92	1	1	57.5	27.7	95.00%	E.NTQHMPPSQVQSLLER.T	Oxidation (+16)	K.WSGENTQHMPPSQVQSLLER.T
222	238	2	1842.86	1.5	1	44.3	29.6	95.00%	E.NNRMNSSFLSSSSIGDK.I		R.TPNIDNEELVNEEQEEQELLEEENNRMNSSFLSSSSIGDK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
102	SNA3_YEAST	26.32%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
84	95	3	1293.63	1.7	1	44.6	29.5	95.00%	R.HATAPAVDRDLE.A		R.HATAPAVDRDLEAHPAEESQAQPPAYDEDDEAGADVPLMDNK.Q
1	12	3	1601.68	0.14	1	33.7	30.2	95.00%	-.MDRDHINDHDHR.M	Acetyl (+42)	-.MDRDHINDHDHR.M
115	125	2	1129.55	1.7	0	62.7	28.5	95.00%	E.AGADVPLMDNK.Q		R.DLEAHPAEESQAQPPAYDEDDEAGADVPLMDNK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
103	B3LI54_YEAS1	23.39%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
129	138	2	1219.57	1.6	1	29.8	29.1	95.00%	E.DSTIHIKDYE.D		K.VLEDSTIHIKDYEDDER.E
298	311	2	1519.77	2.8	1	32.4	28.3	95.00%	K.SLRPSFDEAVSQGK.F		K.SLRPSFDEAVSQGK.F
218	240	3	2468.22	2.8	1	46.6	27.4	95.00%	K.ELHPDHVPTVGSSFVGMSLFNAK.N		K.ELHPDHVPTVGSSFVGMSLFNAK.N
314	323	2	1118.56	3.6	0	30.7	27.2	95.00%	R.AMPNSYLPAR.Q		R.AMPNSYLPAR.Q
324	340	2	1892.85	-0.46	0	73.3	30.4	95.00%	R.QNDVTGMCVIGDALNMR.H	Carbamidomethyl (+57)	R.QNDVTGMCVIGDALNMR.H

84	106	2	2668.29	5.1	1	58.6	28.3	95.00%	E.AYPVTGYTVFFNGEQVDIPYPYK.A	Deamidation (+1)	R.SLGMIQSINNIEAYPVTGYTVFFNGEQVDIPYPYK.A
377	384	3	1091.54	2	1	28.6	29	95.00%	E.LLDYHFER.K		K.VLDELLDYHFER.K
159	169	2	1241.64	-0.66	0	40.2	27.6	95.00%	R.NITAQEPNVTR.V		R.NITAQEPNVTR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
104	YAJ8_YEAST	27.35%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
201	211	2	1248.68	-0.57	0	58.4	25.5	95.00%	R.SDPILMAYVLK.A		R.SDPILMAYVLK.A
123	138	2	1993.91	2.7	1	37.8	30.4	95.00%	K.EWGTVAYNMNQYLFMK.R		K.EWGTVAYNMNQYLFMK.R
164	188	3	2434.05	2.7	1	27.6	31.3	95.00%	E.VNSGSHSDSSSNSAEDTQSPVSAGK.T		K.EVNSGSHSDSSSNSAEDTQSPVSAGK.T
189	200	2	1385.66	0.99	0	44	30.3	95.00%	K.TSNGLNNFYSIR.S	Deamidation (+1)	K.TSNGLNNFYSIR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
105	CHS3_YEAST	13.48%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
722	735	2	1454.78	1.4	0	62.8	26.2	95.00%	E.VKPYSYVAVASGSK.R		K.TTPEIALGMMDDFVTPPDEVKPYSYVAVASGSK.R
47	62	3	1962.94	3.1	1	36.9	29.1	95.00%	R.SRLNNPDNPHFYYAQK.T		R.SRLNNPDNPHFYYAQK.T
394	407	3	1666.81	2.5	1	31.2	29.9	95.00%	E.KDDVDYPVVFDDLK.T		R.NLIVYNGDVLDLDLLDWLEKDDVDYPVVFDDLK.T
497	511	2	1813.83	1.6	1	92.2	30.8	95.00%	K.HTNDIEDWSNNIQTK.A		K.HTNDIEDWSNNIQTK.A
1109	1118	2	1244.51	3.3	0	43.3	29.1	95.00%	K.FDDFSWGDTR.T		K.FDDFSWGDTR.T
598	612	2	1721.84	-1.1	0	29.3	28.8	95.00%	R.NPSTLLPTSSMFWNK.A		R.NPSTLLPTSSMFWNK.A
892	911	2	2314.02	-0.28	1	80.2	29.8	95.00%	K.AFESVFGSVTCLPGCFSMYR.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.AFESVFGSVTCLPGCFSMYR.I
917	934	2	1985.98	-1.2	1	53.4	28.4	95.00%	K.GSDGYWVPVLANPDIVER.Y		K.GSDGYWVPVLANPDIVER.Y
267	281	2	1609.73	2	0	32.8	30.1	95.00%	E.VDSDTLYGPWSDAGK.D		R.SGIQDVEVDSDTLYGPWSDAGK.D
282	301	2	2289.09	2	0	45.3	28.8	95.00%	K.DASFLFQNVNGNCHNLITPK.S	Deamidation (+1)/ Carbamidomethyl (+57)	K.DASFLFQNVNGNCHNLITPK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
106	A6ZZX2_YEAS7	32.97%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
136	149	2	1494.76	-1	0	69.3	27.7	95.00%	R.TNTFTLLTSPDSAK.I		R.TNTFTLLTSPDSAK.I
108	135	3	2735.26	2.2	0	87.9	29.4	95.00%	R.SAGDDNLSGHSVPSSGSAQATTHQTAPR.T		R.SAGDDNLSGHSVPSSGSAQATTHQTAPR.T
107	135	3	2891.36	2	1	86.2	29.5	95.00%	E.RSAGDDNLSGHSVPSSGSAQATHQTAPR.T		R.EDERSAGDDNLSGHSVPSSGSAQATTHQTAPR.T
166	182	2	1858	2.3	0	35.7	23.3	95.00%	E.IFSQSQVNKPGPLTVPF.-		K.LHSNILNEIFSQSQVNKPGPLTVPF.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
107	A6ZL51_YEAS7	29.26%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
155	168	2	1346.67	1.8	0	64.3	27.8	95.00%	K.APSLFGGMGQTGPK.T		K.APSLFGGMGQTGPK.T
136	150	3	1622.96	2.6	1	19.8	16.9	93.90%	E.VKIHLFGKPATGDLK.R		K.SALEHNEVKIHLFGKPATGDLK.R
138	150	2	1395.79	0.62	0	38.4	21.1	95.00%	K.IHLFGKPATGDLK.R		K.IHLFGKPATGDLK.R
115	128	2	1623.84	2.8	0	63.9	27.6	95.00%	K.YTNPLFMQSISPVK.S		K.YTNPLFMQSISPVK.S
79	90	2	1449.79	2.8	1	31.3	24	95.00%	K.LQVTTVRDYDLK.E		K.LQVTTVRDYDLK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
108	A7A0U9_YEAS7	21.49%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
490	505	2	1781.95	2.7	0	56.4	24.3	95.00%	E.IQGWDHLSLLPTFGAK.D		K.AQYNEIQGWDHLSLLPTFGAK.D

234	249	2	1776.95	3	0	61.4	24.1	95.00%	K.LIDLTQFPAFVTPMGK.G	K.LIDLTQFPAFVTPMGK.G
538	551	2	1584.83	3	0	44.9	26	95.00%	E.IMLPVFDAPQNLVE.Q	R.MIEIMLPVFDAPQNLVEQAK.L
485	505	3	2387.2	3.9	1	37.7	27.5	95.00%	K.AQYNEIQGWDHLSLLPTFGAK.D	K.AQYNEIQGWDHLSLLPTFGAK.D
259	273	2	1595.86	-0.13	1	42	24.1	95.00%	R.YGGVYVGTLSKPEVK.E	R.YGGVYVGTLSKPEVK.E
259	271	2	1368.7	1.9	0	73.6	27.9	95.00%	R.YGGVYVGTLSKPE.V	R.YGGVYVGTLSKPEVK.E
200	209	2	1083.69	2.3	0	55.8	15.2	95.00%	E.VIDTILALVK.D	K.EVIDTILALVK.D
155	179	3	2741.52	2.8	0	34.4	19.3	95.00%	R.TTYVTQRPVYLGLPANLVDLNVPAK.L	R.TTYVTQRPVYLGLPANLVDLNVPAK.L
52	63	2	1254.6	2.5	0	37	28.6	95.00%	E.LNAAYAADGYAR.I	R.WAGNANELNAAYAADGYAR.I
199	209	2	1212.73	-0.097	1	38	18.2	95.00%	K.EVIDTILALVK.D	K.EVIDTILALVK.D
45	63	2	1996.9	0.59	1	113	30.6	95.00%	R.WAGNANELNAAYAADGYAR.I	R.WAGNANELNAAYAADGYAR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
109	A6ZZQ2_YEAS7	11.15%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
582	606	2	2590.06	0.46	1	93.4	31.2	95.00%	K.SQAYGATMSNESNANNNNSTSNASR.S	Deamidation (+1)	K.SQAYGATMSNESNANNNNSTSNASR.S
517	526	2	1084.56	1.4	0	26.2	26.1	95.00%	K.AFGIHPLTTE.D		K.AFGIHPLTTEDIFLGEVR.E
470	480	2	1144.65	0.26	0	36.5	24.1	95.00%	E.TVSQLQGLTAK.N		K.AETVSQLQGLTAK.N
381	393	2	1411.78	3	0	53.2	23.7	95.00%	R.IQSGLQDNLLVGR.N		R.IQSGLQDNLLVGR.N
11	25	2	1599.86	1.6	0	34.7	24	95.00%	E.GVPLLSPYSSSPQLR.K		K.DEGVPLLSPYSSSPQLR.K
394	407	2	1634.81	1	0	40	29.1	95.00%	R.NIQYPPHIISNNPE.H		R.NIQYPPHIISNNPEHFR.F
110	126	2	1811.91	2.3	1	52.5	27.9	95.00%	R.EGPQSVSSTVQPQPIMK.F		R.EGPQSVSSTVQPQPIMK.F
394	410	3	2075.04	2	1	24.2	27.6	95.00%	R.NIQYPPHIISNNPEHFR.F		R.NIQYPPHIISNNPEHFR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
110	A6ZS21_YEAS7	27.71%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
297	311	2	1717.86	2.4	1	46.2	27.5	95.00%	K.RQAPSMFLDDVLNGR.E		K.RQAPSMFLDDVLNGR.E
142	156	2	1688.73	1.1	0	66.8	30.2	95.00%	K.HSSSLQSNPFDINDE.K		K.HSSSLQSNPFDINDEK.S
271	292	2	2214.16	1.4	1	92.4	25.3	95.00%	K.RNQSSLGLIPVASATSNTSSPK.K		K.RNQSSLGLIPVASATSNTSSPK.K
272	292	2	2058.06	2	0	76	24.6	95.00%	R.NQSSLGLIPVASATSNTSSPK.K		R.NQSSLGLIPVASATSNTSSPK.K
177	194	3	2059.98	2.9	1	26.4	28.8	95.00%	E.DAASPFNPIQDPFTDNRR.S		K.SYMQDDWDSMSQLESSQYEDAASPFNPIQDPFTDNRR.S
142	157	2	1816.83	3.2	1	82.5	30.9	95.00%	K.HSSSLQSNPFDINDEK.S		K.HSSSLQSNPFDINDEK.S
298	311	2	1561.75	-1.4	0	46	28.7	95.00%	R.QAPSMFLDDVLNGR.E		R.QAPSMFLDDVLNGR.E
195	209	2	1738.92	2.5	1	62.8	24.8	95.00%	R.SLFISPTLQVSQYEK.S		R.SLFISPTLQVSQYEK.S
298	312	2	1691.79	2.6	1	77.6	29.8	95.00%	R.QAPSMFLDDVLNGREI.I	Deamidation (+1)	R.QAPSMFLDDVLNGREII.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
111	A6ZT57_YEAS7	13.08%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
369	377	2	1155.6	3.8	0	40.7	27	95.00%	K.SIYQVYLDR.A		K.SIYQVYLDR.A
590	602	2	1376.66	1.8	0	47.3	28.6	95.00%	R.LNGTALNPVDHPE.M	Deamidation (+1)	R.LNGTALNPVDHPEMFYSPTNDAYYAPQQQGQYMK.F
484	498	2	1864.86	0.6	0	53.7	30.3	95.00%	E.AIQPLNYQDQYQQQE.Q		R.IASSIYSEAIQPLNYQDQYQQQEQSPVYNGHTQYPGNGYSGNPQQQGYTAQFVQNPQWYGVPTPQQQQHNHPQTLETIGELPTPAYLAQSASSHSLTSFK.R
399	413	2	1705.95	1.2	1	70.6	21.8	95.00%	E.NRVDNIVQNPLPSIK.I		K.ADNANDISQEENRVDNIVQNPLPSIK.I
176	187	2	1507.7	2.4	0	40.2	30.1	95.00%	R.SWYVDPFQLPQE.S		R.SWYVDPFQLPQESNDSNSLR.D
176	195	2	2381.1	2.9	1	73.1	30.6	95.00%	R.SWYVDPFQLPQESNDSNSLR.D		R.SWYVDPFQLPQESNDSNSLR.D

638	661	4	2580.31	3.2	0	44.1	26.1	95.00%	R.QSVVMTNPSDLTAKPSYKPAGSFR.S		R.QSVVMTNPSDLTAKPSYKPAGSFR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
112	YOL19_YEAST	31.58%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
376	402	3	3114.36	0.45	1	58.4	30.3	95.00%	R.LLNDIMETSFNEPNDSHINSMSSYNDK.D		R.LLNDIMETSFNEPNDSHINSMSSYNDK.D
383	402	3	2285.95	1.5	0	31.2	31	95.00%	E.TSFNEPNDSHINSMSSYNDK.D		R.LLNDIMETSFNEPNDSHINSMSSYNDK.D
472	501	3	3257.63	3.4	0	69.7	25	95.00%	R.TTPAGPDPSNVILQSNPYFNVAPNQVPQHR.N		R.TTPAGPDPSNVILQSNPYFNVAPNQVPQHR.N
502	529	3	2950.54	0.95	0	50.5	23.5	95.00%	R.NPVPGVGFAPNPLPNQSPITQGYKPAYK.R		R.NPVPGVGFAPNPLPNQSPITQGYKPAYK.R
540	551	2	1339.66	2.7	0	44.1	29	95.00%	R.ATTSLNNPYGFR.-		R.ATTSLNNPYGFR.-
351	365	2	1557.73	1.7	0	31.4	30.4	95.00%	E.ISSSASLASSDYSQR.E		K.TEISSSASLASSDYSQR.E
452	471	2	2615.27	4	0	44.1	27.9	95.00%	R.LQPQQQQPQQQYHQYNLYQR.T		R.LQPQQQQPQQQYHQYNLYQR.T
425	451	3	2898.49	0.9	1	45.2	23.4	95.00%	R.ETAAGPANIRPYAGQPHPAPLVYPQQR.L		R.ETAAGPANIRPYAGQPHPAPLVYPQQR.L
69	83	3	1705.81	2.4	1	25	29.6	94.80%	E.LSDSDSNWKLNSNAR.S		K.ASYNYHPDELSDSDSNWKLNSNAR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
113	A6ZLU9_YEAS7	25.42%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
313	325	2	1424.67	2.5	0	58.6	29.5	95.00%	K.DFGQVIGQGFSDR.H		K.DFGQVIGQGFSDR.H
279	287	2	1159.5	0.85	1	37.4	29.4	95.00%	K.YMDEGYINR.V		K.YMDEGYINR.V
15	26	2	1272.65	3.5	0	32.8	27.4	95.00%	K.AMDNGLSLPISR.N		K.AMDNGLSLPISR.N
201	211	2	1217.65	0.22	0	60	26.9	95.00%	R.NAADVLPLMFK.H		R.NAADVLPLMFK.H
501	521	3	2454.19	2.7	0	39.6	28.4	95.00%	R.VGGLPHYTIWHIYEPSDDDLK.E		R.VGGLPHYTIWHIYEPSDDDLK.E
452	466	2	1412.79	1.1	0	30.1	24.9	95.00%	E.AVDLDGVGGVSILAK.A		R.DAEGDPNEAVDLDGVGGVSILAK.A
191	200	2	1248.7	1.8	0	43	22.9	95.00%	R.DHILLCIPLR.N	Carbamidomethyl (+57)	R.DHILLCIPLR.N
472	482	2	1256.58	3.4	0	37.5	29.2	95.00%	R.NGVQFPAFTFE.N	Deamidation (+1)	R.NGVQFPAFTFENHAETEAFGK.M
135	150	2	1840.83	2.2	0	35	30.3	95.00%	K.FDDGVQHYLISQFGSE.V		K.FDDGVQHYLISQFGSEVLTPK.D
361	378	2	1975.92	-1	1	53.9	30.2	95.00%	R.DADVELCPGSVIQDLMSK.N	Carbamidomethyl (+57)	R.DADVELCPGSVIQDLMSK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
114	A6ZQK0_YEAS7	7.18%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1204	1224	2	2100.05	1.1	0	48.9	26.9	95.00%	E.NAGVHSGDATLIVPPQDLAPE.T		R.NGELVMHVVSEHVENAGVHSGDATLIVPPQDLAPETVDR.I
599	615	2	1638.81	3	1	43	28.9	95.00%	R.AAYALGGLGSGFANNEK.E		R.AAYALGGLGSGFANNEK.E
1463	1476	2	1516.85	2.2	0	48	22.5	95.00%	R.LAVDYSVPLVTNVK.C		R.LAVDYSVPLVTNVK.C
1551	1564	2	1385.78	3.1	0	23.2	22.2	92.40%	R.SISGPVITDVASLK.A		R.SISGPVITDVASLK.A
1978	1989	2	1267.75	3.1	0	34	18.9	95.00%	R.IVNVNPLVSSVK.K		R.IVNVNPLVSSVK.K
663	686	2	2511.22	1.7	0	51	28.6	95.00%	E.NFDPLGIHTGDSIVVAPSQTLSDE.D		R.DAFDNCITVCNMENFDPLGIHTGDSIVVAPSQTLSDEDYNMLR.T
855	864	2	1050.59	3.9	0	25.3	24.8	95.00%	R.VFAIANAFAK.K		R.VFAIANAFAK.K
2000	2011	2	1398.67	2.4	0	29.2	29.8	94.20%	R.TLACYSDAIVMR.H	Carbamidomethyl (+57)	R.TLACYSDAIVMR.H
1635	1650	2	1713.97	2.8	0	46.2	20.8	95.00%	K.TADLASVLLLTSLQNR.S		K.TADLASVLLLTSLQNR.S
180	198	2	2143.06	-0.57	1	41.7	28.9	95.00%	R.SAFDVPEWVDPNVQNLVSK.V		R.SAFDVPEWVDPNVQNLVSK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
115	YD237_YEAST	14.36%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

142	150	2	1088.52	2.5	1	30.7	28.5	95.00%	E.ADVWNIDEK.I		K.LPLFEGLAYGASSTEADVWNIDEK.I
278	295	3	2018.09	3.1	1	23.9	22.5	95.00%	E.SSQRFAFLDAPLLSLEPK.Y		K.DEIIWRPVTVILTGNYPTSLDILDNGNDNGYFESSQRFAFLDAPLLSLEPK.Y
159	170	2	1375.73	2.2	1	29.4	26.1	95.00%	E.AYLDPVELTLDK.L		K.ILAVGHNEAYLDPVELTLDK.L
351	367	2	1910	-1.2	1	39.7	25.5	95.00%	R.IWGAPTWPANLVETISR.Q		R.IWGAPTWPANLVETISR.Q
282	295	2	1559.86	-1.1	0	46.6	22.9	95.00%	R.FAFLDAPLLSLEPK.Y		R.FAFLDAPLLSLEPK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
116	A7A1T6_YEAS7	8.00%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
518	530	3	1583.83	0.52	1	21.4	26.1	94.50%	E.LQDRQHMYVPAVK.A		K.DDLHLDGELQDRQHMYVPAVK.A
457	464	2	1026.5	3.4	0	35.2	27.1	95.00%	R.LSIFTMCR.A	Carbamidomethyl (+57)	R.LSIFTMCR.A
412	422	2	1223.61	2.5	0	31.4	28.9	95.00%	E.TNAATFMPMLK.I		K.WAETNAATFMPMLK.I
203	214	2	1323.71	0.13	1	38	25.8	95.00%	K.LSPVFELFASSK.N		K.LSPVFELFASSK.N
477	486	2	1203.54	-1.2	0	33.6	29	95.00%	K.SHAVQNMDFR.S		K.SHAVQNMDFR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
117	AQR1_YEAST	11.95%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
310	318	2	1189.5	2	1	31.1	29.4	95.00%	R.FKYDNPDYE.T		R.FKYDNPDYETLDPTIPK.L
493	504	2	1361.61	4.1	0	41.7	29.5	95.00%	K.SSTASSCFNFVR.C	Carbamidomethyl (+57)	K.SSTASSCFNFVR.C
39	54	2	1749.87	1.1	1	75.7	28.7	95.00%	K.LNFEGAYINSHGTLSK.T		K.LNFEGAYINSHGTLSK.T
505	517	2	1520.68	-0.69	0	35.4	29.9	95.00%	R.CSLSTIFMGCFAK.M	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.CSLSTIFMGCFAK.M
43	54	2	1246.63	2.6	0	42.8	28.5	95.00%	E.GAYINSHGTLSK.T		K.LNFEGAYINSHGTLSK.T
563	572	2	1158.64	0.25	0	32.1	25.1	95.00%	R.QSWLNTLAVK.A		R.QSWLNTLAVK.A
298	307	2	1081.67	3.4	0	31.1	17.3	95.00%	R.APIFLLGPVR.R		R.APIFLLGPVR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
118	B3LMA9_YEAS1	3.77%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
331	341	2	1273.7	2.5	0	43.3	25.7	95.00%	E.YLLNDPDLALK.L		R.TQEEYLLNDPDLALK.L
84	91	2	963.49	4.4	0	31.2	27.7	95.00%	K.ILDMYGPR.V		K.ILDMYGPR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
119	B3LP09_YEAS1	12.09%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
375	390	4	1797.89	-0.88	1	24.1	28.5	95.00%	K.KPNLHGYGHPNPPNEK.S		K.KPNLHGYGHPNPPNEK.S
303	319	2	1904.01	-0.63	0	53	24.2	95.00%	R.LTNVYDLAQGLPIQFGR.Y		R.LTNVYDLAQGLPIQFGR.Y
509	524	2	1822.81	-0.77	1	74.3	30.9	95.00%	K.YPYNAQPTANDEQNAK.N		K.YPYNAQPTANDEQNAK.N
431	447	2	1994	-0.94	0	81	27.3	95.00%	K.VQQQQLQQAQAQQQANR.Y		K.VQQQQLQQAQAQQQANR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
120	GLRX6_YEAST	33.33%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
208	219	2	1373.72	0.58	1	51.5	26.8	95.00%	K.LLESLQVWSDGK.F		K.LLESLQVWSDGK.F
85	105	2	2197.17	2.8	1	67.7	24.3	95.00%	K.VGLQQPIASVDDSLSAIKNDK.G		K.VGLQQPIASVDDSLSAIKNDK.G
43	57	2	1544.64	2.4	0	82.2	29.7	95.00%	K.AFSTNMDNMAGGSSR.E		K.AFSTNMDNMAGGSSR.E
85	102	2	1840	2.7	0	53.1	23.6	95.00%	K.VGLQQPIASVDDSLSAIK.N		K.VGLQQPIASVDDSLSAIK.N
118	133	2	1850.04	-1.2	1	73.8	19.6	95.00%	K.EYSLILDLSPIIIFSK.S		K.EYSLILDLSPIIIFSK.S
181	193	2	1324.75	3.7	0	70.1	23.2	95.00%	R.GTVPNLLVNGVSR.G		R.GTVPNLLVNGVSR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
121	A6ZQR6_YEAS7	36.31%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

10	27	2	1885.83	0.7	0	90.4	30.3	95.00%	E.TADAGSSATYPMQCSALR.K	Carbamidomethyl (+57)	-.MSDEEHTFETADAGSSATYPMQCSALR.K
120	130	2	1194.54	2.2	0	45.7	29.8	95.00%	E.LGDSLQTAFDE.G		K.APEGELGDSLQTAFDEGK.D
57	68	2	1311.76	-0.015	0	35.4	21.3	95.00%	K.VHLVAIDIFTGK.K		K.VHLVAIDIFTGK.K
72	86	2	1651.83	1.1	1	52.1	27.9	95.00%	E.DLSPSTHNMEVPVVK.R		K.LEDLSPSTHNMEVPVVK.R
10	28	2	2013.93	1.3	1	86.9	30.1	95.00%	E.TADAGSSATYPMQCSALRK.N	Carbamidomethyl (+57)	-.MSDEEHTFETADAGSSATYPMQCSALRK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
122	ATG27_YEAS7	15.50%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	88	2	1772.92	2.5	1	68.2	26.1	95.00%	K.KNDMLCGLTDVILPGK.D	Carbamidomethyl (+57)	K.KNDMLCGLTDVILPGK.D
119	130	2	1223.56	3.3	0	68.7	29.9	95.00%	K.GATWGANSFDAK.L		K.GATWGANSFDAK.L
89	100	2	1378.7	2.7	0	45.8	27	95.00%	K.DAITTQIIDFDK.N		K.DAITTQIIDFDK.N
119	132	2	1465.69	2	1	50.5	29.7	95.00%	K.GATWGANSFDAKLEF.Q		K.GATWGANSFDAKLEFQCNDNMK.Q
74	88	2	1644.83	3.7	0	55.1	27.4	95.00%	K.NDMLCGLTDVILPGK.D	Carbamidomethyl (+57)	K.NDMLCGLTDVILPGK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
123	A6ZQA2_YEAS7	31.80%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
76	97	2	2429.15	2.1	1	92.9	29.4	95.00%	K.VRTDTTYPAGFMDVITLDATNE.N		K.VRTDTTYPAGFMDVITLDATNENFR.L
201	221	3	2385.18	2.6	1	50.6	27.4	95.00%	R.HDGGFDLVHIKDSLDNTFVTR.L		R.HDGGFDLVHIKDSLDNTFVTR.L
78	100	2	2591.18	-0.7	1	76.1	30.5	95.00%	R.TDTTYPAGFMDVITLDATNENFR.L		R.TDTTYPAGFMDVITLDATNENFR.L
222	240	2	2115.17	-0.76	1	78	20.3	95.00%	R.LNNVFVIGEQGKPYISLPK.G		R.LNNVFVIGEQGKPYISLPK.G
146	155	3	1215.66	2.4	1	21.8	26	95.00%	R.TIRYPDPNIK.V		R.TIRYPDPNIK.V
180	187	2	863.49	0.1	0	31.3	25.1	95.00%	K.LVYVTGGR.N		K.LVYVTGGR.N
212	221	2	1166.56	3.4	0	31.9	29.1	95.00%	K.DSLDNTFVTR.L		K.DSLDNTFVTR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
124	ECM33_YEAS7	15.38%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
248	262	2	1574.82	1.8	1	88.2	26.9	95.00%	K.VGQSLSIVSNDELSK.A		K.VGQSLSIVSNDELSK.A
162	172	2	1330.71	1.9	1	63.7	25.4	95.00%	K.KVNVFNINNNR.Y		K.KVNVFNINNNR.Y
173	182	2	1186.55	2.1	0	33	29.2	95.00%	R.YLNSFQSSLE.S		R.YLNSFQSSLESVSDSLQFSSNGDNTTLAFDNLVWANNITLR.D
337	351	2	1622.78	2.4	0	74.4	29.5	95.00%	K.LQSNGAIQGDSFVCK.N	Carbamidomethyl (+57)	K.LQSNGAIQGDSFVCK.N
106	119	2	1477.81	2.5	0	30.8	22.9	95.00%	E.LIILTSASFGSLQE.V		K.ITGDLNMQELIILTSASFGSLQEVDSINMVTLPAISTFSTDLQNANNIIVSDTTLESVEGFSTLK.K
163	172	2	1202.62	3.8	0	54.4	27.6	95.00%	K.VNVFNINNNR.Y		K.VNVFNINNNR.Y
336	351	2	1750.87	2.5	1	95.5	28.1	95.00%	K.KLQSNGAIQGDSFVCK.N	Carbamidomethyl (+57)	K.KLQSNGAIQGDSFVCK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
125	B3LRN6_YEAS1	18.44%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	141	2	1964.96	0.46	0	28.2	28.6	94.50%	K.YLISPDVHPAQNQNIQE.N		K.YLISPDVHPAQNQNIQENK.E
24	38	2	1657.8	2	0	68.6	29.5	95.00%	E.YASISNNSDQTIAFK.V		K.SPLTEQSTEYASISNNSDQTIAFK.V
2	14	2	1460.78	2.5	1	41.4	25	95.00%	M.SAVEISPDVLVYK.S	Acetyl (+42)	-.MSAVEISPDVLVYK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
126	A6ZU59_YEAS7	16.93%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
187	203	2	1834.93	0.97	1	75.4	27.2	95.00%	K.LLQLAGVEDVYTQSNGK.T	Deamidation (+1)	K.LLQLAGVEDVYTQSNGK.T

142	157	2	1728.86	1.2	0	68.1	27.7	95.00%	R.GYWGTNLGQPHSLATK.T		R.GYWGTNLGQPHSLATK.T
56	65	3	1181.68	1.9	1	36.9	21.2	95.00%	E.IFLHSLPVKE.F		K.ITTIEEIFLHSLPVKEFQIIDTLLPGLQDEVMNIKPVQK.Q
56	64	2	1052.64	1.8	0	40.9	16.8	95.00%	E.IFLHSLPVK.E		K.ITTIEEIFLHSLPVK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
127	A7A0C4_YEAS7	31.57%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
245	268	4	2732.42	2.2	0	21	24	95.00%	K.TSNLNFNHIINHLSFGKPIQSHSK.L		K.TSNLNFNHIINHLSFGKPIQSHSK.L
121	147	3	2803.21	1.3	0	42.5	30.5	95.00%	E.LHVGGNGDGTAPVNNDPNYCGPCYGAK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.LNSEGRPVGDATELHVGGNGDGTAPVNNDPNYCGPCYGAK.D
217	244	3	3217.54	0.29	0	64.1	27.9	95.00%	R.IQGNLHFAPGKPYQNAYGHFHDTSLYDK.T		R.IQGNLHFAPGKPYQNAYGHFHDTSLYDK.T
351	366	2	1755.87	-2	1	38.8	27.8	95.00%	R.GGIPGMFVFFEMSPLK.V		R.GGIPGMFVFFEMSPLK.V
275	289	2	1491.79	-0.35	1	39.7	26.5	95.00%	K.RHGGAVVATSPLDGR.Q		K.RHGGAVVATSPLDGR.Q
176	184	2	997.47	2.6	0	49.5	28.8	95.00%	E.AGWAFFDGK.N		R.SAYLEAGWAFFDGK.N
3	14	2	1320.74	3.5	1	25.2	21.4	95.00%	K.RSTLLSLDAFAK.T		K.RSTLLSLDAFAK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
128	A6ZQN6_YEAS7	6.53%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
520	547	2	3090.51	3.8	1	93.2	27.7	95.00%	R.ISDPTLAAQAYGSPFTFITTYTWGTPER.I		R.ISDPTLAAQAYGSPFTFITTYTWGTPER.I
1	13	2	1422.65	1.9	1	29.8	29.9	94.70%	-.MDPGIANHTLPEE.F		-.MDPGIANHTLPEEFEEVVVPEMLEK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
129	ZRT1_YEAST	5.32%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
11	22	2	1387.67	2.8	1	32	29.5	95.00%	K.QWDPSEVTLADK.T		K.QWDPSEVTLADK.T
269	276	2	931.51	-0.57	1	39.5	24.5	95.00%	R.LSAIEFPR.S		R.LSAIEFPR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
130	A6ZX57_YEAS7	31.84%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
200	212	2	1390.76	2.3	1	25.4	23.5	95.00%	R.VAIGEVPFTFGVR.T		R.VAIGEVPFTFGVR.T
146	166	3	2297.14	2	0	50.8	27.3	95.00%	R.MMARPLTIASDPMSGFFGLQK.K		R.MMARPLTIASDPMSGFFGLQK.K
111	122	3	1353.68	2.8	0	46.7	28.6	95.00%	E.SLHDHAFTLGTR.Y		K.LFESLHDHAFTLGTR.Y
146	167	4	2425.24	3.8	1	26.1	25.7	95.00%	R.MMARPLTIASDPMSGFFGLQKK.Y		R.MMARPLTIASDPMSGFFGLQKK.Y
25	35	2	1180.57	2.8	1	40.1	29	95.00%	R.LFAGMSPEMAK.K		R.LFAGMSPEMAK.K
123	137	2	1766.85	2.7	1	57	29.5	95.00%	R.YAPGVGIDKDWPMYR.R		R.YAPGVGIDKDWPMYR.R
54	65	2	1341.68	1.7	0	56.9	27.9	95.00%	E.VDALAHQGYNVR.I		K.TELIFVDDNSQDGSVEEVDALAHQGYNVR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
131	A7A233_YEAS7	30.70%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
71	81	2	1315.65	-0.16	1	49.1	28.3	95.00%	K.LQLWDTAGQER.F		K.LQLWDTAGQER.F
165	178	2	1638.79	-0.51	1	82.5	29.5	95.00%	K.NDDNVNEIFFTLAK.L		K.NDDNVNEIFFTLAK.L
126	138	2	1416.73	1.5	1	49.9	27.2	95.00%	E.AQLLLVGNKSDME.T		K.TVNEHANDEAQLLLVGNKSDMETR.V
141	152	2	1200.64	0.57	1	50.8	26.8	95.00%	R.VVTADQGEALAK.E		R.VVTADQGEALAK.E
43	58	2	1841.96	2.5	1	39.9	25.6	95.00%	E.DKFNPSFITTIGIDFK.I		R.FVEDKFNPSFITTIGIDFK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

132	A6ZM72_YEAS7	11.65%		100%		6						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
11	28	2	1939	1.1	1	43.2	25.1	95.00%	E.SGSQQTSIHSTPIVQKLE.T		R.VESGSQQTSIHSTPIVQKLETDESPIQTK.S	
296	309	2	1492.74	2.8	1	78.6	28.9	95.00%	R.LAGNASWGELFSNK.G		R.LAGNASWGELFSNK.G	
95	105	2	1274.58	3.1	0	62.8	29	95.00%	K.SDGTYYLSDVR.T		K.SDGTYYLSDVR.T	
9	26	2	1924.98	-0.57	1	68.3	26.7	95.00%	R.VESGSQQTSIHSTPIVQK.L		R.VESGSQQTSIHSTPIVQK.L	
219	227	2	1153.52	2.9	0	49.9	30.3	95.00%	K.DYSNSVQWR.V		K.DYSNSVQWR.V	
284	292	2	1022.44	2.8	0	25.4	26.8	93.10%	E.MDTIMANVE.T		K.VTIEDPSIVAEMDTIMANVETER.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
133	A6ZWW2_YEAS7	26.03%		100%		7						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
172	191	3	2163.15	2.9	0	22.2	23.1	95.00%	E.SHTLFNTSLVPPTLNVPGNR.S		K.DESHTLFNTSLVPPTLNVPGNR.S	
241	259	2	2029.9	1.3	1	87.1	30.7	95.00%	R.SHITLGSSILDGLDDEDDE.H		R.SHITLGSSILDGLDDEDDEHNQVLNK.D	
201	225	2	2572.41	-0.039	1	73.3	18.1	95.00%	R.ASNILPIAYIPGVTSGLSTDKLQSK.L		R.ASNILPIAYIPGVTSGLSTDKLQSK.L	
260	277	3	2049.06	1.8	1	80.8	25.9	95.00%	E.HNQVLNKDADDNLITAIR.A		R.SHITLGSSILDGLDDEDDEHNQVLNKDADDNLITAIR.A	
47	57	2	1376.58	1.8	0	45.9	30.5	95.00%	E.YCVMTSLTCDK.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GSDGCVVCDSTASCPVCASGEYCVMTSLTCDK.C	
201	221	2	2116.14	-0.19	0	69.1	21.4	95.00%	R.ASNILPIAYIPGVTSGLSTDK.L		R.ASNILPIAYIPGVTSGLSTDK.L	
199	221	3	2373.3	3.5	1	28.7	19.2	95.00%	R.TRASNILPIAYIPGVTSGLSTDK.L		R.TRASNILPIAYIPGVTSGLSTDK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
134	A7A1Z8_YEAS7	11.09%		100%		7						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
322	334	2	1579.79	-0.083	1	54.4	28.1	95.00%	R.ATNDFYLEPLIER.D		R.ATNDFYLEPLIER.D	
471	484	2	1519.84	2.6	0	40.2	23.3	95.00%	R.DTVVLEPSGHVVLR.F		R.DTVVLEPSGHVVLR.F	
372	383	2	1229.73	3.2	0	50.7	20.5	95.00%	K.VPTLTTLLTSGK.L		K.VPTLTTLLTSGK.L	
524	533	2	1280.61	3.8	1	38.2	29.6	95.00%	K.LNENYLDICK.A	Carbamidomethyl (+57)	K.LNENYLDICK.A	
158	168	2	1368.68	0.72	1	33.5	29	95.00%	E.RVITLSDHYHE.N		R.GAFIIHDPEEPFEYDHERVITLSDHYHENYK.T	
316	333	2	2197.99	2.4	1	29.8	30.7	93.70%	E.DCDLDRATNDFYLEPLIE.R	Carbamidomethyl (+57)	R.ALNIEDCDLDRATNDFYLEPLIER.D	
159	171	3	1617.78	2.9	1	27.3	28.3	95.00%	R.VITLSDHYHENYK.T		R.VITLSDHYHENYK.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
135	B3LJS4_YEAS1	17.68%		100%		10						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
61	72	2	1479.67	1.5	1	36.2	30.1	95.00%	E.FDIEDPHDDLHK.R		R.FDDSPPSSNDNSIETNITPPPEPPSYEFDIEDPHDDLHK.R	
87	104	3	2100.21	2.8	1	22.1	16.5	95.00%	K.ILEPLMENIIHPLLQISK.F		K.ILEPLMENIIHPLLQISK.F	
248	258	2	1205.57	3.1	1	38.4	28.5	95.00%	K.ENFNPLSSNGK.L		K.ENFNPLSSNGK.L	
742	752	2	1229.67	2	0	32.7	25.5	95.00%	K.NVLFGPTLIQE.D		K.NVLFGPTLIQEDK.S	
34	47	2	1522.61	1.8	0	58	30	95.00%	R.FDDSPPSSNDNSIE.T		R.FDDSPPSSNDNSIETNITPPPEPPSYEFDIEDPHDDLHK.R	
742	754	2	1472.79	1.4	1	40.2	25.2	95.00%	K.NVLFGPTLIQEDK.S		K.NVLFGPTLIQEDK.S	
325	356	3	3357.61	1.4	1	71.2	28.3	95.00%	E.NIDVVQSKPVGLPQYSTGDASGLNWDGSPVEE.K		K.AVIFISEPYGENIDVVQSKPVGLPQYSTGDASGLNWDGSPVEEK.D	
299	309	2	1226.73	3.2	1	31	21.2	95.00%	K.LVSQQVLIAEK.F		K.LVSQQVLIAEK.F	
384	398	2	1477.66	-0.96	0	69.4	30.3	95.00%	R.LSSGGVTVDDGNSDR.S		R.LSSGGVTVDDGNSDR.S	
17	33	2	1825.91	0.87	0	38.3	28.2	95.00%	E.NAIPTASSSHNLLMSQR.F		R.SSYQPVSTTNFEHENAIPTASSSHNLLMSQR.F	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
136	RSP5_YEAST	11.00%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
91	110	3	2081.02	2.1	1	52	28.6	95.00%	R.VGDVLGHLDEDTATSSGRPR.E		R.VGDVLGHLDEDTATSSGRPR.E
23	38	2	1750.88	-0.47	0	68.6	27.5	95.00%	R.SPDPFAVLTIDGYQTK.S		R.SPDPFAVLTIDGYQTK.S
191	209	2	1904.92	2.5	0	110	29.1	95.00%	E.STLQSGTTAATNTATTSHR.S		R.GTAQAVESTLQSGTTAATNTATTSHR.S
138	164	3	2669.23	1.5	0	48	29.4	95.00%	K.LPSSSPHSQAPSGHTASSSTNTSSTTR.T		K.LPSSSPHSQAPSGHTASSSTNTSSTTR.T
184	209	3	2561.23	1	1	54.3	28.8	95.00%	R.GTAQAVESTLQSGTTAATNTATTSHR.S		R.GTAQAVESTLQSGTTAATNTATTSHR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
137	A6ZSR4_YEAS7	30.15%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
85	93	2	1084.54	-0.11	1	27.9	27.6	95.00%	R.YTLDVEAFK.S		R.YTLDVEAFK.S
35	48	2	1489.78	1.7	1	61.8	25.9	95.00%	K.SHPFGHALVAGIER.Y		K.SHPFGHALVAGIER.Y
74	84	2	1324.73	2.6	0	36	23.6	95.00%	K.VVNYNHLLPTR.Y		K.VVNYNHLLPTR.Y
127	133	2	955.46	0.078	0	28.4	28	95.00%	K.NQWFFSK.L		K.NQWFFSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
138	A6ZLA4_YEAS7	22.20%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
308	321	3	1417.67	3.5	1	24.2	29.8	93.20%	R.EGIPAYHGFGGADK.I		R.EGIPAYHGFGGADK.I
327	351	2	2743.27	1.9	0	91.7	29.5	95.00%	E.FSMPSDTSGSAYNQDMPAIWLLNAK.I		K.IFVFEFSMPSDTSGSAYNQDMPAIWLLNAK.I
309	321	2	1288.62	1.4	0	34.9	28.6	95.00%	E.GIPAYHGFGGADK.I		R.EGIPAYHGFGGADK.I
82	87	2	757.42	1.5	0	31.5	23.8	95.00%	E.LSVHFR.G		K.LSITALVGLFSSVVSLVNADCTYSGGNYYCAQTDAIIYSNVGLSATYQDVTNMDESSCACTQADFTASGSLAPFNEELSVHFR.G
431	447	2	1924.91	2.6	0	69	29.1	95.00%	E.SFDATLSDDVVDQWLSK.S		K.TIHIIEVDESFDATLSDDVVDQWLSK.S
386	411	3	2899.37	0.14	1	35.6	29	95.00%	K.LISHIHDGQDGGTQDYFERPTDGTLK.A		K.LISHIHDGQDGGTQDYFERPTDGTLK.A
355	367	2	1574.65	2	0	45.3	30.5	95.00%	R.TLQYGDASCSCWK.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.TLQYGDASCSCWK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
139	GLRX7_YEAST	12.32%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
154	165	2	1212.69	3	0	58.7	23.3	95.00%	R.TVPNVIIGGTSR.G		R.TVPNVIIGGTSR.G
153	165	2	1368.79	2.8	1	33.5	20.9	95.00%	R.RTVPNVIIGGTSR.G		R.RTVPNVIIGGTSR.G
94	105	2	1408.71	2.8	1	37	27.9	95.00%	K.IMEQSPMIVFSK.T		K.IMEQSPMIVFSK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
140	YIL7_YEAST	24.53%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
180	188	2	1018.55	2.4	0	38.8	26.7	95.00%	E.RPLFSLASE.S		K.DALVSHTNNEKPFLSNFERPLFSLASESNR.N
139	148	2	1215.55	2.3	0	51.1	29.8	95.00%	E.NFQDQVHISE.S		K.ENFQDQVHISESDISPGNK.D
192	205	2	1566.83	-0.97	0	44.7	24.7	95.00%	R.NSLFISPTGDILYK.T		R.NSLFISPTGDILYK.T
273	285	2	1466.64	-0.44	1	42.9	29.8	95.00%	K.LLNSPESDGSVNR.N	Phospho (+80)	K.LLNSPESDGSVNR.N
117	138	2	2642.11	1.5	1	56.6	30.9	95.00%	K.MFSTQHTQFYGDSPYMDYPAKE.N		K.MFSTQHTQFYGDSPYMDYPAKENFQDQVHISESDISPGNK.D
149	158	2	1060.47	1.7	1	37.7	29.6	95.00%	E.SDISPGNKDE.S		K.ENFQDQVHISESDISPGNKDESVK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
141	UIP3_YEAST	20.85%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	44	2	1650.72	2.5	0	48.9	30.8	95.00%	E.DTFNSYWSYILNE.I		K.LDTLDEPSAHLIEENVALPEDTFNSYWSYILNEIAR.C
194	207	2	1623.82	1.8	0	54.7	28.1	95.00%	E.MVKPYIFSSDPVLE.A		K.EVSNEMVKPYIFSSDPVLEAYLIK.A
167	188	2	2226.02	0.25	1	90.1	30.6	95.00%	R.SNAHLSSPTNGAENTQSNTPAK.E	Deamidation (+1)	R.SNAHLSSPTNGAENTQSNTPAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
142	RL14A_YEAST	38.41%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	74	2	2050.2	2.6	0	103	14.1	95.00%	R.QAINLGQVVLTPLTFALPR.G		R.QAINLGQVVLTPLTFALPR.G
32	42	2	1211.72	2.9	1	34.8	20.3	95.00%	K.LAAIVEIIDQK.K		K.LAAIVEIIDQK.K
110	117	2	921.46	3.4	1	44.3	28.2	95.00%	R.AALTDFER.F		R.AALTDFER.F
118	124	2	891.5	3.6	0	24.4	24.7	94.10%	R.FQVMVLR.K		R.FQVMVLR.K
94	101	2	905.44	4.2	0	32.2	28.3	95.00%	K.WAASSWAK.K		K.WAASSWAK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
143	AXL2_YEAST	16.04%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
651	664	2	1512.68	0.72	0	59.7	30.2	95.00%	R.SSSVYMDSEPAVNK.S		R.SSSVYMDSEPAVNK.S
709	729	2	2329.14	1.8	1	77.7	28	95.00%	R.DVTMSSLDPWNSNISPSPVRK.S		R.DVTMSSLDPWNSNISPSPVRK.S
730	740	2	1191.61	0.75	0	33.2	27.7	95.00%	K.SVTPSPYNVTK.H		K.SVTPSPYNVTK.H
668	680	2	1419.74	2.2	0	42.4	26.9	95.00%	R.YTGNLSPVSDIVR.D		R.YTGNLSPVSDIVR.D
631	650	3	2356.17	2.3	1	33.8	27.3	95.00%	E.LLAKPPVQPPESPFFDPQNR.S	Phospho (+80)	K.EELLAKPPVQPPESPFFDPQNR.S
184	203	2	2338.16	-1.8	1	63.5	27.5	95.00%	R.SQLYNAPLPNWLFFDSGELK.F		R.SQLYNAPLPNWLFFDSGELK.F
60	81	2	2594.17	-1.3	0	74.9	29.6	95.00%	K.TAQITYNCFDLPSWLSFDSSSR.T	Carbamidomethyl (+57)	K.TAQITYNCFDLPSWLSFDSSSR.T
432	442	2	1299.66	2.1	0	51	28.4	95.00%	E.LYFNIIGMDSK.I		K.ANQGSQSQELYFNIIGMDSK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
144	A7A244_YEAS7	23.93%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	208	2	1991.92	2.4	0	43.3	29.9	95.00%	E.LQDFAIFTTDLDNVHDE.N		K.ELQDFAIFTTDLDNVHDENIAR.S
173	187	2	1696.86	-0.13	1	55.2	27.3	95.00%	R.VFDIDEALYISDLGK.K		R.VFDIDEALYISDLGK.K
401	435	4	3870.71	2.4	0	36.8	30.3	95.00%	R.ASCAFYPHGLGHMLGLDVHDVGGNPNYDDPDPMFR.Y	Carbamidomethyl (+57)	R.ASCAFYPHGLGHMLGLDVHDVGGNPNYDDPDPMFR.Y
213	229	2	2001.91	-0.46	1	43.4	29.9	95.00%	R.SLIPSDPNFFYAMDETR.A		R.SLIPSDPNFFYAMDETR.A
123	145	2	2617.26	2.7	0	83.2	28.6	95.00%	R.YFYHLSGVDIPASAILFNCSTDK.L	Carbamidomethyl (+57)	R.YFYHLSGVDIPASAILFNCSTDK.L
282	302	2	2354.06	2.5	0	78.4	30.4	95.00%	R.SLGYDPICCSGPACGTLHYVK.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.SLGYDPICCSGPACGTLHYVK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
145	B3LKQ2_YEAS1	21.33%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
365	375	2	1128.68	2.6	0	28.5	20.3	95.00%	K.ILAILSDTGVK.F		K.ILAILSDTGVK.F
352	364	2	1338.72	2.3	0	38.8	25.4	95.00%	K.IPSIPISANQGDK.I		K.IPSIPISANQGDK.I
335	345	2	1172.57	2.4	1	28	27.8	95.00%	E.GSIRDPIDATE.A		K.SVALPQYGTGDALTPEWEGSIRDPIDATEAK.C
167	184	2	1879.86	1.1	0	95.4	30.2	95.00%	E.YISSMPHMSGTSGDAAIR.H		R.DLEYISSMPHMSGTSGDAAIR.H
235	255	3	2401.15	1.1	0	46.1	28.5	95.00%	E.NFNPMSHNGQLNNIPVIYANK.A	Oxidation (+16)/ Deamidation (+1)	K.DDTEGFDIPLNEENFNPMSHNGQLNNIPVIYANK.A

539	569	3	3380.71	3.1	0	37.2	25.3	95.00%	K.VDNVHQFGDWTPYLAQGIPVAIISSPGVMNR.E			K.VDNVHQFGDWTPYLAQGIPVAIISSPGVMNR.E
747	767	2	2301.18	3.5	0	111	25.8	95.00%	K.DWSSVQVQANTLGTILQNTAR.Y			K.DWSSVQVQANTLGTILQNTAR.Y
352	375	3	2449.38	1.9	1	36.4	15.2	95.00%	K.IPSIPISANQGDKILAILSDTGVK.F			K.IPSIPISANQGDKILAILSDTGVK.F
516	528	3	1609.87	2.5	0	27.2	24.3	95.00%	E.IQCHPLLVDLFQK.N	Carbamidomethyl (+57)		K.SEIYTIIDVGQIGIWDDSNNLEIQCHPLLVDLFQK.N
31	45	2	1644.77	1.7	1	36	30	95.00%	E.QAIGMPSEPPVYVEE.M			R.GYTTLPNVEEPANNSQDELNSQDFEQAIGMPSEPPVYVEEMGMEEPQAPEAFSEK.V
298	310	2	1536.79	2.5	0	25.9	27.5	92.70%	K.AIIFISEPYQDNK.D			K.AIIFISEPYQDNK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
146	A6ZMW0_YEAS7	19.88%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
163	171	2	971.48	2.9	0	29.4	28.7	95.00%	E.SGLIHSMVE.T		K.TFLGCMSQGIPVVTAYDTLGESGLIHSMVETDSVAIFTDNQLLSK.L
485	496	2	1367.7	-0.45	1	62.5	27.7	95.00%	K.LVDVEDLGYFAK.N		K.LVDVEDLGYFAK.N
573	588	2	1912.87	2.3	1	101	30.2	95.00%	R.SNPYVQNICVYADENK.V	Carbamidomethyl (+57)	R.SNPYVQNICVYADENK.V
677	688	2	1324.74	2.5	1	35	23.2	95.00%	R.DILAAVKPDVER.V		R.DILAAVKPDVER.V
589	604	3	1656.01	3	0	18.7	9.03	91.70%	K.VKPVGIVVPNLGHLSK.L		K.VKPVGIVVPNLGHLSK.L
142	162	2	2258.07	2.3	0	53.8	29.4	95.00%	K.TFLGCMSQGIPVVTAYDTLGE.S	Carbamidomethyl (+57)	K.TFLGCMSQGIPVVTAYDTLGESGLIHSMVETDSVAIFTDNQLLSK.L
532	541	2	1116.55	3.1	1	52.9	27.9	95.00%	R.TGDIAEWTPK.G		R.TGDIAEWTPK.G
26	44	2	2130.14	1.5	1	51	23.3	95.00%	R.VKDQPLIRPINSSASTLYE.F		R.VKDQPLIRPINSSASTLYEFALECFTK.G
256	278	3	2533.2	2.1	1	32.4	29.3	95.00%	E.LHFPKPEDPACIMYTSGSTGTPK.G	Carbamidomethyl (+57)	K.DEVELHFPKPEDPACIMYTSGSTGTPK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
147	B3LQX5_YEAS1	18.83%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
157	171	2	1790.8	2.2	0	61.1	30.4	95.00%	K.DFGTYLDSDDQQFIK.D		K.DFGTYLDSDDQQFIK.D
244	261	2	2061.05	-1.8	0	38.8	26.5	95.00%	K.SNSIFSIGLTTVPYPYFR.V		K.SNSIFSIGLTTVPYPYFR.V
280	292	2	1414.79	2	0	57.2	24.1	95.00%	R.INNPFTASTLLPK.L		R.INNPFTASTLLPK.L
191	203	2	1526.78	2	0	30.4	27.5	95.00%	E.YGNFLPSFIVQDK.L		R.GIQSYFLLPSINDNIDEYGNFLPSFIVQDK.L
268	277	2	1117.53	0.083	1	41.5	28.5	95.00%	K.YSIAYESTGK.L		K.YSIAYESTGK.L
470	486	2	1936.01	2.3	1	59.8	25.6	95.00%	R.ITAQTSKPLWSVGTYER.I		R.ITAQTSKPLWSVGTYER.I
146	156	2	1323.61	3	1	27.9	29.7	92.40%	K.EFQMMSPPMVK.D		K.EFQMMSPPMVK.D
450	461	2	1394.58	2.5	0	64.7	30.5	95.00%	R.YADTDNFFGSMK.V		R.YADTDNFFGSMK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
148	A7A288_YEAS7	17.67%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
254	264	2	1232.62	2.4	0	29	28.8	95.00%	K.TLIDNLIDTSE.Q		K.TLIDNLIDTSEQR.D
459	467	2	1099.57	1.9	0	34.3	27.4	95.00%	K.NLMIRPLDE.Q		K.NLMIRPLDEQDIETEQFHFEYDR.D
254	266	2	1516.78	3.1	1	42.7	27.1	95.00%	K.TLIDNLIDTSEQR.D		K.TLIDNLIDTSEQR.D
371	385	2	1727.82	2.4	1	90	30.1	95.00%	K.LYAVEGNDQYVQSSR.S		K.LYAVEGNDQYVQSSR.S
147	163	2	1982.95	1.3	0	77.5	29.4	95.00%	E.DDNLNHFQTLPTNALDR.Q		K.LVLIPEDDNLNHFQTLPTNALDR.Q
191	207	2	1942.98	-1.3	0	87.6	27.1	95.00%	R.ITAYNVADGFNLNQLYK.F		R.ITAYNVADGFNLNQLYK.F
447	458	2	1368.69	-0.087	0	50.9	28	95.00%	K.NILGDITFADYK.N		K.NILGDITFADYK.N
223	236	2	1606.89	4.2	0	31.3	22.1	95.00%	E.CLYVAYTLPLLPGK.G	Carbamidomethyl (+57)	R.LYDECLYVAYTLPLLPGK.G
82	101	2	2178.04	-0.38	0	82.3	29.6	95.00%	R.FSDISIDNILSDNSDIPSAR.R		R.FSDISIDNILSDNSDIPSAR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
149	A6ZLE7_YEAS7	24.75%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	134	3	2349.04	-0.42	1	39.8	30.8	95.00%	R.YHYDWVFLNDQPFSDEFK.R		R.YHYDWVFLNDQPFSDEFK.R
96	104	2	1087.57	0.35	0	31.4	27.8	95.00%	R.NSDLWNLVK.S		R.NSDLWNLVK.S
296	303	2	953.5	2.4	0	47	26.3	95.00%	E.IGSLDFFR.S		K.FISNDDGDTYNMCHFWTNFEIGSLDFFR.S
325	341	3	1825.94	-0.77	0	33.8	27.1	95.00%	R.WGDAPVHSIAASLFLDK.S		R.WGDAPVHSIAASLFLDK.S
276	295	2	2511.98	1.5	0	38.2	30.4	95.00%	K.FISNDDGDTYNMCHFWTNFE.I	Carbamidomethyl (+57)	K.FISNDDGDTYNMCHFWTNFEIGSLDFFR.S
310	324	2	1864.8	2.6	1	77.2	30.8	95.00%	E.YFDYLDSSGGFFYER.W		R.EYFDYLDSSGGFFYER.W
60	72	2	1513.75	2.9	1	44.2	28.9	95.00%	R.VASKDYLMPFTDK.S		R.VASKDYLMPFTDK.S
117	132	2	2073.88	2.4	0	61.6	31	95.00%	R.YHYDWVFLNDQPFSDE.F		R.YHYDWVFLNDQPFSDEFK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
150	A6ZRX9_YEAS7	9.68%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
31	45	2	1738.88	0.97	1	58.2	27.7	95.00%	R.RAQSTVLNSNPFYSR.K		R.RAQSTVLNSNPFYSR.K
135	150	2	1690.82	1.3	0	80.7	28.9	95.00%	E.TNLSSAGGDITHDIYK.L		K.NSSASTIAAANVDSDDDETNLSSAGGDITHDIYK.L
219	235	2	1820.81	1.5	0	87.3	30.3	95.00%	E.SDSINQSSPSSNQDIDK.V		R.QEHQLNDSASSDFTSHESDSINQSSPSSNQDIDK.V
236	241	2	731.44	3.5	0	31.4	24	95.00%	K.VPFLTR.N		K.VPFLTR.N
204	218	2	1673.69	1.8	0	71.5	30.8	95.00%	E.HQLNDSASSDFTSHE.S		R.QEHQLNDSASSDFTSHESDSINQSSPSSNQDIDK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
151	A7A0Y0_YEAS7	18.10%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
41	56	2	1828.87	2.3	1	26.2	28.8	90.90%	K.ATVDEFPLCVHLVSNE.L	Carbamidomethyl (+57)	K.ATVDEFPLCVHLVSNELEQLSSEALEAAR.I
46	56	2	1313.65	2.1	0	29.2	28.2	95.00%	E.FPLCVHLVSNE.L	Carbamidomethyl (+57)	K.ATVDEFPLCVHLVSNELEQLSSEALEAAR.I
129	139	2	1245.71	-0.33	0	52.1	23.4	95.00%	R.VDIGQIIFSVR.T		R.VDIGQIIFSVR.T
171	183	2	1637.82	1.6	1	41.3	27.6	95.00%	K.WGFTNLDRPEYLK.K		K.WGFTNLDRPEYLK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
152	A7A0B5_YEAS7	14.94%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
707	729	3	2435.2	2.4	0	29.2	27.3	95.00%	E.QPVQPTSAVMGTGGSFLSPQYQR.A		K.QNSSPFDASEVTEQPVQPTSAVMGTGGSFLSPQYQR.A
160	175	2	1746.91	4.4	1	65.9	25.6	95.00%	E.FETPLACVQAILSNGK.T	Carbamidomethyl (+57)	R.VVAYAQNDTEFETPLACVQAILSNGK.T
133	149	2	1902.98	-1.1	0	72.1	26.4	95.00%	K.QFPGIAYTIPDLDAQVR.V		K.QFPGIAYTIPDLDAQVR.V
704	729	2	2764.35	-0.65	1	56.5	27.6	95.00%	E.VTEQPVQPTSAVMGTGGSFLSPQYQR.A		K.QNSSPFDASEVTEQPVQPTSAVMGTGGSFLSPQYQR.A
682	693	2	1361.6	2.8	1	64.1	30.4	95.00%	R.LFDDETSSSSFK.Q		R.LFDDETSSSSFK.Q
736	752	2	1803.87	0.82	0	69.7	29	95.00%	R.TNLAPNNTSTSSLMKPE.S		R.TNLAPNNTSTSSLMKPESSLYLGNSNK.S
99	117	2	2080.01	-1.4	0	54.2	29.4	95.00%	K.TFDLCSLGQVSLCPLSAGR.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.TFDLCSLGQVSLCPLSAGR.I
736	762	3	2867.4	0.91	1	28	27.2	95.00%	R.TNLAPNNTSTSSLMKPESSLYLGNSNK.S		R.TNLAPNNTSTSSLMKPESSLYLGNSNK.S
162	175	2	1471.77	2.3	0	51.4	25.7	95.00%	E.TPLACVQAILSNGK.T	Carbamidomethyl (+57)/ Deamidation (+1)	R.VVAYAQNDTEFETPLACVQAILSNGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
153	FET4_YEAST	12.68%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
306	316	2	1370.65	2.7	1	57.2	29	95.00%	R.FLVDIFDMDEK.I		R.FLVDIFDMDEK.I

445	454	2	1132.59	2.7	1	35.9	26.8	95.00%	K.APEINTIGYR.T		K.APEINTIGYR.T
32	45	2	1642.73	2.1	1	66	30	95.00%	E.FGDSNDYKNDDVVR.V		K.QYEEFGDSNDYKNDDVVR.V
4	20	3	1884.98	3.2	1	36	25.7	95.00%	K.IAEFLGNPGARPDVHHR.A		K.IAEFLGNPGARPDVHHR.A
248	265	2	1833.81	-0.4	1	77.2	31.1	95.00%	K.DAGNTPPYTGETTGSNPR.L		K.DAGNTPPYTGETTGSNPR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
154	A6ZQF7_YEAS7	24.46%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
47	56	2	1285.64	1.7	0	50.9	28.8	95.00%	K.YLDQVLDHQR.A		K.YLDQVLDHQR.A
112	124	2	1495.82	1.9	0	64.3	24.3	95.00%	K.LYVSHIQVNQAPK.Q		K.LYVSHIQVNQAPK.Q
90	103	2	1444.74	2.9	0	44.9	27.5	95.00%	K.FVQGLLQNAAANAE.A		K.FVQGLLQNAAANAEAK.G
106	124	3	2081.13	0.4	1	27.8	24	95.00%	K.GLDATKLYVSHIQVNQAPK.Q		K.GLDATKLYVSHIQVNQAPK.Q
90	105	2	1643.87	1.5	1	78.4	25.2	95.00%	K.FVQGLLQNAAANAEAK.G		K.FVQGLLQNAAANAEAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
155	A6ZWC1_YEAS7	26.26%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
222	237	2	1783.85	1.5	1	65.7	29.7	95.00%	E.LFKGYLADDIDADSLE.D		R.FSELFKGYLADDIDADSLEDIYTSAHEAIR.A
144	152	2	1059.61	0.74	0	62.7	24	95.00%	K.VFLDIGLQR.T		K.VFLDIGLQR.T
159	177	2	1902.95	0.36	1	31.3	28.1	95.00%	R.VFGALKGASDGGLYVPHSE.N		R.VFGALKGASDGGLYVPHSENR.F
178	186	2	1166.52	1.8	1	27.7	29.1	93.10%	E.NRFPGWDFE.T		K.GASDGGLYVPHSENRFPGWDFETEEIDPELLR.S
197	210	2	1661.71	1.4	1	32.2	30.4	95.00%	R.SYIFGGHVSQYMEE.L	Oxidation (+16)	R.SYIFGGHVSQYMEELADDDEER.F
238	248	2	1274.63	1	1	34.4	29	95.00%	E.DIYTSAHEAIR.A		K.GYLADDIDADSLEDIYTSAHEAIR.A
165	177	2	1287.58	1.9	0	38.7	30.3	95.00%	K.GASDGGLYVPHSE.N		K.GASDGGLYVPHSENR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
156	A6ZQS1_YEAS7	31.87%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	34	3	3423.7	2.8	1	51.2	25.6	95.00%	M.TELCPVYAPFFGAIGCASAIIFTSLGAAYGTAK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	-.MTELCPVYAPFFGAIGCASAIIFTSLGAAYGTAK.S
35	52	2	2005.06	3.1	0	55.3	24.2	95.00%	K.SGVGICATCVLRPDLLFK.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.SGVGICATCVLRPDLLFK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
157	B3LPM2_YEAS1	24.01%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
250	259	2	1041.62	3	0	34.5	22.9	95.00%	E.VLSQAGNLLK.Y		K.LPNNFVYMSDVNQLSGFMFHYSKPYEVLSQAGNLLK.Y
224	259	4	4150.04	1.3	1	32	27.4	95.00%	K.LPNNFVYMSDVNQLSGFMFHYSKPYEVLSQAGNLLK.Y		K.LPNNFVYMSDVNQLSGFMFHYSKPYEVLSQAGNLLK.Y
73	89	2	1931	3.7	0	66.4	26.4	95.00%	R.GNQIFQSLHSFLANDLK.F		R.GNQIFQSLHSFLANDLK.F
16	32	2	1938.94	2.8	1	94.5	29.3	95.00%	R.VNSLNAPYQALSYDEQK.A		R.VNSLNAPYQALSYDEQK.A
164	176	2	1410.81	2.3	0	23.7	20.6	93.20%	E.IVIRPNGILVTSE.S	Deamidation (+1)	K.QLEEFMEIVIRPNGILVTSESAHPNK.N
2	15	2	1551.79	-0.9	1	59.9	28	95.00%	M.SSSIFGPLTGFLER.V	Acetyl (+42)	-.MSSSIFGPLTGFLER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
158	A6ZYN3_YEAS7	19.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
246	268	2	2613.3	3.2	0	29	26.9	95.00%	R.IFPPIDDPLPFKPLMDDSDVTLE.E		R.IFPPIDDPLPFKPLMDDSDVTLEEAVTHQR.I
44	61	2	2168.06	2.5	1	82.7	28.2	95.00%	R.QFYINDLTISHPYATTER.V		R.QFYINDLTISHPYATTER.V
132	147	2	1787.91	-2	1	50.4	27	95.00%	R.CQPVEGLPLDTLFTAK.D	Carbamidomethyl (+57)	R.CQPVEGLPLDTLFTAK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
159	B3RHC6_YEAS1	5.37%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
326	340	2	1718.92	1.8	1	45.9	25.3	95.00%	E.DTILYSQISLGERPK.M		R.QPYSENYHLLGNEQSGAVTHGENVPSSNNNDEDTILYSQISLGERPK.M
299	315	2	1824.84	0.82	1	64	29.7	95.00%	E.NYHLLGNEQSGAVTHGE.N		R.QPYSENYHLLGNEQSGAVTHGENVPSSNNNDEDTILYSQISLGERPK.M
307	325	2	1955.81	0.6	1	39.2	30.7	95.00%	E.QSGAVTHGENVPSSNNNDE.D	Deamidation (+1)	R.QPYSENYHLLGNEQSGAVTHGENVPSSNNNDEDTILYSQISLGERPK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
160	HSP76_YEAST	12.40%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
174	191	2	1728.95	2.3	0	84	23.9	95.00%	R.IINEPTAAAIAYGLGAGK.S		R.IINEPTAAAIAYGLGAGK.S
305	314	2	1166.6	0.65	1	50.4	27.7	95.00%	R.FEDLNAALFK.S		R.FEDLNAALFK.S
115	128	2	1550.8	-0.33	1	36.9	27.1	95.00%	K.TFSPQEISAMVLTK.M		K.TFSPQEISAMVLTK.M
431	451	2	2417.15	1.4	1	87.8	29.6	95.00%	R.TFTTVSDNQTTVQFPVYQGER.V		R.TFTTVSDNQTTVQFPVYQGER.V
39	51	2	1478.74	1.7	1	45.7	28.5	95.00%	R.VTPSFVAFTPQER.L	Deamidation (+1)	R.VTPSFVAFTPQER.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
161	HSP72_YEAST	18.15%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
158	169	2	1198.67	-0.1	0	53.6	25	95.00%	K.DAGTIAGLNVLR.I		K.DAGTIAGLNVLR.I
537	547	2	1264.67	2.1	1	31.7	26.6	95.00%	K.NQLESIAYSLK.N		K.NQLESIAYSLK.N
424	441	2	2026.01	3.3	0	47.2	28.7	95.00%	E.VFSTYADNQPGVLIQVFE.G		K.SEVFSTYADNQPGVLIQVFEGER.A
55	69	2	1590.75	0.11	0	56.5	30.1	95.00%	K.NQAAMNPANTVFDAK.R		K.NQAAMNPANTVFDAK.R
170	185	2	1658.89	2.5	0	87.7	25	95.00%	R.IINEPTAAAIAYGLDK.K		R.IINEPTAAAIAYGLDK.K
111	124	2	1549.78	-0.72	1	48.9	27.7	95.00%	K.NFTPEQISSMVLGK.M		K.NFTPEQISSMVLGK.M
137	153	2	1893.93	2.7	0	41.2	28.1	95.00%	K.VNDAVVTVPAYFNDSQR.Q		K.VNDAVVTVPAYFNDSQR.Q
35	47	2	1456.69	2.4	1	34.5	29.5	95.00%	R.TTPSFVGFTDTER.L		R.TTPSFVGFTDTER.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
162	OST1_YEAST	20.17%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
114	128	2	1704.84	0.58	1	48	28	95.00%	R.YGIIQFPNAISPQEE.V		R.YGIIQFPNAISPQEEVSLVIK.S
205	213	2	1115.54	2.9	1	50.3	28.9	95.00%	E.FGPWEDIPR.F		K.ANGNSFEFGPWEDIPR.F
389	404	2	1791.9	1.8	0	39.6	28.2	95.00%	E.IFDIDSPVPFTNVSIE.T		K.FVASIPILNGPPDTVYDNVELSVFLPEGAEIFDIDSPVPFTNVSIETQK.S
38	49	2	1366.68	1.9	1	43	28.8	95.00%	K.RTIDVSNAYISE.T		K.RTIDVSNAYISETIEITIK.N
219	238	3	2277.28	2.3	1	26.1	17.6	95.00%	E.TLAIVYSHNAPLNQVVNLRR.D		R.FSSNETLAIVYSHNAPLNQVVNLRR.D
160	171	2	1377.73	1.1	1	60.1	26.5	95.00%	E.TNRLPLSAYDTK.K		K.SFYNTVGIPYPEHVGMSEEQHLLWETNRLPLSAYDTK.K
135	146	2	1385.65	1.6	0	46.3	30.2	95.00%	K.SFYNTVGIPYPE.H		K.SFYNTVGIPYPEHVGMSEEQHLLWETNR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
163	NCB5R_YEAST	26.41%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
91	102	2	1283.59	-0.87	0	35.3	29.5	95.00%	R.SYTPTSLDGDTK.G		R.SYTPTSLDGDTK.G
198	208	3	1218.68	2.2	0	22.9	24.4	95.00%	E.ALVAMKPSQFK.I		K.ELEALVAMKPSQFK.I

209	219	2	1368.66	2.3	1	40	29.1	95.00%	K.IVYYLDSPDRE.D		K.IVYYLDSPDREDWTGGVGYITK.D
60	80	4	2238.26	2.5	0	19.7	17.4	95.00%	K.FGLPHADDVLGLPIGQHIVIK.A		K.FGLPHADDVLGLPIGQHIVIK.A
147	166	2	2075.04	2.2	0	48.8	27.1	95.00%	R.SHLGMIAGGTGIAPMYQIMK.A		R.SHLGMIAGGTGIAPMYQIMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
164	A6ZKQ4_YEAS7	8.76%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
326	334	2	1043.61	1.6	0	22.5	23.6	91.10%	K.TVLAWSVIR.A		K.TVLAWSVIR.A
83	98	3	1820.87	2.7	1	26.3	28.7	95.00%	K.NDSTDLADHKPENPIR.T		K.NDSTDLADHKPENPIR.T
69	74	2	787.44	3.5	0	26.9	29.5	91.00%	K.VSWLQR.V		K.VSWLQR.V
236	245	2	1105.59	2.7	0	51.9	27.1	95.00%	K.AIFGTNLNTR.I		K.AIFGTNLNTR.I
109	123	2	1768.9	2.1	1	53.8	27.1	95.00%	R.STYLYNTDLRPVEAK.R		R.STYLYNTDLRPVEAK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
165	A6ZW21_YEAS7	10.98%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
41	58	2	1831.03	1.5	1	54.8	21.8	95.00%	K.SGIGIAGIGTFKPELIMK.S		K.SGIGIAGIGTFKPELIMK.S
41	54	2	1345.73	3.1	0	62.9	24.8	95.00%	K.SGIGIAGIGTFKPE.L		K.SGIGIAGIGTFKPELIMK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
166	A6ZTN7_YEAS7	12.36%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
222	250	3	2970.39	2.4	1	60.9	29.1	95.00%	R.GSPSPSSNRDTLFSLSSDTTTATATNNNK.R		R.GSPSPSSNRDTLFSLSSDTTTATATNNNK.R
199	211	2	1543.79	2.1	0	38.6	27.8	95.00%	E.YRPVDTIPLNDLE.S		K.EYRPVDTIPLNDLESTPVMVNSAR.G
63	80	3	1965.08	2.6	1	45.4	20	95.00%	K.HLHGLPILQSPSLTPAER.L		K.HLHGLPILQSPSLTPAER.L
286	298	2	1461.84	2.6	0	48	15.4	95.00%	E.APPLLPQDIPVFR.I		R.DEDYDNDDDEIASIEAPPLLPQDIPVFR.I
281	298	2	1975.12	1.7	1	31.4	18.9	95.00%	E.IASIEAPPLLPQDIPVFR.I		R.DEDYDNDDDEIASIEAPPLLPQDIPVFR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
167	A6ZNH7_YEAS7	12.19%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	206	2	1572.83	2.7	0	84.3	26.3	95.00%	R.QIPVGYSAADIVANR.Q		R.QIPVGYSAADIVANR.Q
237	247	2	1160.57	2.2	0	36.3	28.2	95.00%	E.SSFVVSGYSTK.M		R.IDMFGVNDYSWCGESSFVVSGYSTK.M
250	269	2	2392.14	-2.3	1	42.2	29.5	95.00%	K.LYQDYSVPVFLSEFGCNQVK.S	Carbamidomethyl (+57)	K.LYQDYSVPVFLSEFGCNQVK.S
301	313	2	1436.68	-0.36	0	77.2	29.6	95.00%	E.TNNYGLVQIDGDK.V	Deamidation (+1)	K.SSRPFTEIEAIYSTQMSSVFSGGLVYEYSNETNNYGLVQIDGDK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
168	A6ZVR3_YEAS7	9.42%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
611	621	2	1203.65	3.7	1	38.1	26.4	95.00%	R.EAFVSLNIPSK.A		R.EAFVSLNIPSK.A
415	432	2	2033.9	-0.4	1	30.1	30.2	94.80%	K.DGDPISYVFPGYSTTEMR.N		K.DGDPISYVFPGYSTTEMR.N
578	586	2	984.59	1	0	25.3	20.1	95.00%	K.IGDVIIIDK.S		K.IGDVIIIDK.S
22	31	2	1044.51	-6.5	0	26.3	29.1	90.50%	K.FTIAAAEPPE.G		K.FTIAAAEPPEGFPEPLNPTNFK.E
239	246	2	847.48	2.4	0	29.4	24.3	95.00%	E.LGFGDLVK.I		R.QLAVDDINTGHVNCESNPTICEELGFGDLVK.I
415	430	2	1746.77	3.5	0	30.4	31.4	93.70%	K.DGDPISYVFPGYSTTE.M		K.DGDPISYVFPGYSTTEMR.N
433	442	2	1203.6	0.068	0	29.9	28.1	95.00%	R.NIDAIMDWVK.K		R.NIDAIMDWVK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
169	ERG2_YEAST	14.86%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

57	63	2	857.46	1.6	0	31.9	26.5	95.00%	E.DLLQDVR.D		K.HNAAEGLSTEDLLQDVR.D
35	46	2	1376.7	2.6	1	59.7	27	95.00%	K.TLNEICNSVISK.H	Carbamidomethyl (+57)	K.TLNEICNSVISK.H
57	73	2	1915.9	2.1	1	43.4	30	95.00%	E.DLLQDVRDALASHYGDE.Y		K.HNAAEGLSTEDLLQDVRDALASHYGDEYINR.Y
64	77	2	1622.74	2.9	1	64.2	30	95.00%	R.DALASHYGDEYINR.Y		R.DALASHYGDEYINR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
170	A6ZZ86_YEAS7	4.79%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
305	315	2	1168.68	2	0	46.5	21.3	95.00%	E.LVTLNQSIPGK.N		K.VEELVTLNQSIPGK.N
12	28	2	1648.72	1.8	0	85.7	30.6	95.00%	K.TSQSNVGDAVGNADSVE.F		K.TSQSNVGDAVGNADSVEFNSEHDSPSK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
171	A7A0Y7_YEAS7	9.75%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
94	103	2	1049.55	2.8	0	39	26.8	95.00%	E.SLGSVIFGDR.I		K.QPESLGSVIFGDR.I
141	156	2	1818.91	5	0	64.9	27.7	95.00%	K.NGFFQNWLIDGLPAAR.E	Deamidation (+1)	K.NGFFQNWLIDGLPAAR.E
104	117	2	1723.86	-1.3	1	64.7	27.6	95.00%	R.IYNSPFQLNMLQEK.E		R.IYNSPFQLNMLQEK.E
104	116	2	1595.77	3	0	47.9	28.7	95.00%	R.IYNSPFQLNMLQE.K		R.IYNSPFQLNMLQEK.E
67	79	2	1808.77	3	1	84.3	31.2	95.00%	K.ENFLYSYDYYYNR.F		K.ENFLYSYDYYYNR.F
238	249	2	1237.77	1.3	0	41.5	17.5	95.00%	R.VVGVIVEPVSIK.R		R.VVGVIVEPVSIK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
172	A6ZVM1_YEAS7	9.12%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
300	310	2	1251.6	2.3	1	67.3	29.7	95.00%	E.SFIKTDQLDGE.T		R.IPADLVLLQSSEPSGESFIKTDQLDGETDWK.L
109	126	2	1896.93	2	0	57.1	28.9	95.00%	K.FTNIASSPPSSSNNIFSK.A		K.FTNIASSPPSSSNNIFSK.A
334	343	2	1015.55	-0.61	1	50.2	26.5	95.00%	R.ISITASAPEK.S		R.ISITASAPEK.S
317	333	2	1955.98	3.1	1	96.1	27.1	95.00%	R.VACPLTQNLSENDLINR.I	Carbamidomethyl (+57)	R.VACPLTQNLSENDLINR.I
529	544	2	1752.92	1.5	0	84.8	25.2	95.00%	E.TLDIVSDYVQSLVSSK.N		K.IHLGTVSYTSETLDIVSDYVQSLVSSK.N
629	645	2	2014	-1.7	1	32.2	28	95.00%	K.TLNYEILQVFPFNSDSK.R		K.TLNYEILQVFPFNSDSK.R
821	836	2	1779.89	-0.11	1	36	28.2	95.00%	R.NACLLIDGESLGMFLK.H	Carbamidomethyl (+57)	R.NACLLIDGESLGMFLK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
173	AVT7_YEAST	14.29%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
17	31	2	1536.86	2	0	40.3	21.1	95.00%	K.TIVGAGTLAIPYSFK.S		K.TIVGAGTLAIPYSFK.S
3	16	2	1348.72	2.4	0	89	26.4	95.00%	E.ATSSALSSTANLVK.T		-.MEATSSALSSTANLVK.T
321	348	2	2991.38	2.2	1	83	30.3	95.00%	R.ASNLRPISMTVEDPAQPSDALDATSYNE.Q		R.ASNLRPISMTVEDPAQPSDALDATSYNEQECLLPNGNFDNGSIESQENNNDER.G
441	451	2	1098.67	3.2	0	55.7	20.6	95.00%	K.LIGLDSLAIGK.M		K.LIGLDSLAIGK.M
1	16	2	1650.81	-1.1	1	80.9	29.2	95.00%	-.MEATSSALSSTANLVK.T	Acetyl (+42)	-.MEATSSALSSTANLVK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
174	A6ZWS9_YEAS7	15.06%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
76	90	2	1664.9	3.1	0	47.9	23.6	95.00%	K.TLIPLIHLLSTSDNE.D		K.TLIPLIHLLSTSDNEDCK.K
6	17	3	1474.73	3.6	1	22.3	28.6	91.80%	K.ILMDSTHFNEIR.S		K.ILMDSTHFNEIR.S
448	460	2	1499.7	-0.21	1	44.9	29.6	95.00%	K.ADIMELLNHSDSR.V		K.ADIMELLNHSDSR.V
95	108	2	1515.81	-0.6	1	72.3	24.6	95.00%	K.SVQNLIAELLSSDK.Y		K.SVQNLIAELLSSDK.Y
311	328	2	1951.11	-0.93	1	75.7	17.4	95.00%	K.QLLLLGNALPTVQSLSER.K		K.QLLLLGNALPTVQSLSER.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
175	A6ZLD1_YEAS7	15.62%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

145	160	2	1744.91	3.6	1	42.1	26.1	95.00%	E.GNVPQTLAPVPYETFI.-		R.IVSTEGNVPQTLAPVPYETFI.-
70	78	2	915.54	0.097	0	48.2	23.2	95.00%	K.SSVGVIINK.M		K.SSVGVIINK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
176	SMF1_YEAST	4.35%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	19	2	1748.88	1.4	1	103	27.7	95.00%	M.VNVGPSHAAVAVDASEAR.K		-.MVNVGPSHAAVAVDASEAR.K
291	297	2	864.46	1.8	0	31.1	26.3	95.00%	R.LLDYDVK.H		R.LLDYDVK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
177	EMP47_YEAST	13.93%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
221	227	2	812.38	-0.52	0	26.1	28.5	91.40%	R.FPSGSYR.I		R.FPSGSYR.I
333	346	2	1637.87	-0.25	1	94.7	24.8	95.00%	K.VQQELLSFMTTITK.Q		K.VQQELLSFMTTITK.Q
315	326	2	1313.72	2.4	1	81	24.5	95.00%	K.ILANDINALETK.L		K.ILANDINALETK.L
40	53	2	1562.8	3.4	0	73.7	26.9	95.00%	K.LSSDYSLPDLINAR.K		K.LSSDYSLPDLINAR.K
228	242	2	1471.69	2.7	0	70.2	29.1	95.00%	R.IGVTAQNGAVNNNAE.S	Deamidation (+1)	R.IGVTAQNGAVNNNAESFEIFK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
178	A6ZQE5_YEAS7	36.23%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	71	2	1592.79	3.5	0	72.7	27.6	95.00%	E.SSPYAAMLAAQDVAAK.C		R.DESSPYAAMLAAQDVAAK.C
116	128	2	1414.7	0.62	1	54.4	27.3	95.00%	R.IEDVTPVPSDSTR.K		R.IEDVTPVPSDSTR.K
10	19	2	1091.54	0.62	0	45.2	28.7	95.00%	R.DNSQVFGVAR.I		R.DNSQVFGVAR.I
94	104	2	1023.55	-0.12	0	50.9	26.7	95.00%	K.TPGPGGQAALR.A		K.TPGPGGQAALR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
179	A6ZL12_YEAS7	5.91%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
24	38	2	1575.68	-0.074	1	102	30.7	95.00%	R.SFSAGNNFQSSSSEK.T		R.SFSAGNNFQSSSSEK.T
405	417	2	1447.75	1.1	0	54.5	26.8	95.00%	R.LICSLAQQGYAPK.F	Carbamidomethyl (+57)	R.LICSLAQQGYAPK.F
489	496	2	923.46	1.4	1	33.2	27	95.00%	R.SLDELGYK.A		R.SLDELGYK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
180	A6ZQE6_YEAS7	19.23%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
4	19	2	1628.84	3.5	1	89.9	26.6	95.00%	R.SSVLADALNAINNAEK.T		R.SSVLADALNAINNAEK.T
89	97	2	1040.58	3.5	0	26.7	24.3	95.00%	K.WTANLLPAR.Q		K.WTANLLPAR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
181	A6ZN13_YEAS7	9.59%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
100	109	2	1234.6	3.5	1	50.9	28.7	95.00%	K.NDAIENYQLR.V		K.NDAIENYQLR.V
449	458	2	1265.59	0.48	0	34.1	28.4	95.00%	K.DFICNWLGNK.A	Carbamidomethyl (+57)	K.DFICNWLGNK.A
375	396	2	2603.19	2.3	0	78.8	29.5	95.00%	E.GGNLCYPTLQDIDDYLNQDYVK.E	Carbamidomethyl (+57)	K.DCEGGNLCYPTLQDIDDYLNQDYVK.E
32	40	2	985.54	-3.4	1	40.9	25.8	95.00%	K.DVLLQAAEK.F		K.DVLLQAAEK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
182	A6ZTV6_YEAS7	9.60%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
620	646	3	2713.39	3	1	30.6	24.1	95.00%	K.INEMAAGDVLLGLASSGVHSNGFSLVR.K		K.INEMAAGDVLLGLASSGVHSNGFSLVR.K
623	647	4	2486.3	1.9	1	43.2	24	95.00%	E.MAAGDVLLGLASSGVHSNGFSLVRK.I	Deamidation (+1)	K.INEMAAGDVLLGLASSGVHSNGFSLVRK.I
623	646	3	2374.2	0.67	0	47.1	26.5	95.00%	E.MAAGDVLLGLASSGVHSNGFSLVR.K	Oxidation (+16)/ Deamidation (+1)	K.INEMAAGDVLLGLASSGVHSNGFSLVR.K
504	517	2	1345.71	2.4	0	60	26.5	95.00%	E.DTLLVGATDGVGTK.L		R.QNEDTLLVGATDGVGTK.L

400	411	2	1288.7	4.3	0	41.2	25.1	95.00%	R.VLSVTSTAQDLR.T		R.VLSVTSTAQDLR.T
478	500	3	2323.14	4.1	0	21.7	28	91.70%	R.RPGADSDIGGFGGLFDLAQAGFR.Q		R.RPGADSDIGGFGGLFDLAQAGFR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
183	A6ZLM1_YEAS7	14.29%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	69	2	1619.83	2	0	40.5	26.7	95.00%	K.ATTPNVNDPIYFLR.G		K.ATTPNVNDPIYFLR.G
400	410	2	1264.66	0.62	1	25.6	27.1	92.90%	E.FKDQGITLMGR.R		R.DVALEFKDQGITLMGR.R
213	225	2	1365.81	3.1	0	54.1	14.6	95.00%	E.AQGALINLIQGLR.S		K.VGEDDQTEAQGALINLIQGLR.S
70	77	2	920.42	0.32	0	26.4	29	91.00%	R.GVFGCEPR.T	Carbamidomethyl (+57)	R.GVFGCEPR.T
335	358	2	2571.42	2.8	0	31.9	18.1	95.00%	E.NANNLLAVPTFPLSLLAPPTSFFK.G		K.IMGHYENANNLLAVPTFPLSLLAPPTSFFK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
184	A6ZM36_YEAS7	43.84%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	16	2	1781.94	-1.3	1	65.7	24.7	95.00%	M.SLVVQEQGSFQHILR.L	Acetyl (+42)	-.MSLVVQEQGSFQHILR.L
89	106	2	2045.93	2	1	32.6	29.9	95.00%	R.QNDITDGKDYHTLANNVE.S		R.QNDITDGKDYHTLANNVESK.L
81	88	2	1015.56	1.8	0	49	27	95.00%	K.IPAWFLNR.Q		K.IPAWFLNR.Q
69	80	3	1470.77	3.6	0	33.8	25.8	95.00%	R.IVQIMQNPTHYK.I		R.IVQIMQNPTHYK.I
17	27	2	1199.65	1.2	0	25.2	24.9	95.00%	R.LLNTNVDGNIK.I		R.LLNTNVDGNIK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
185	A6ZLH4_YEAS7	7.14%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
127	136	2	1073.5	3.3	0	45.5	28.6	95.00%	R.GGGAYYMISR.S		R.GGGAYYMISR.S
5	31	3	2878.42	0.21	1	69.4	26.9	95.00%	R.FYQIPGTHRPSSAISSSNESSSLLSAR.R		R.FYQIPGTHRPSSAISSSNESSSLLSAR.R
5	23	2	2076.99	1.4	0	58.4	29.4	95.00%	R.FYQIPGTHRPSSAISSSNE.S		R.FYQIPGTHRPSSAISSSNESSSLLSAR.R
704	719	2	1743.9	1.2	0	83.2	25.7	95.00%	E.DLSLMQSNIAIAHGFK.N		K.VNVQQWVQIVEDLSLMQSNIAIAHGFK.N
693	719	3	3066.61	3.9	1	30	21.8	95.00%	K.VNVQQWVQIVEDLSLMQSNIAIAHGFK.N		K.VNVQQWVQIVEDLSLMQSNIAIAHGFK.N
33	48	2	1976.89	0.17	1	66	30.6	95.00%	R.ISQTYFNYQATPECQK.V	Carbamidomethyl (+57)	R.ISQTYFNYQATPECQK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
186	A6ZQL2_YEAS7	32.48%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
49	62	2	1510.78	2.1	0	62.5	26.9	95.00%	E.YGTAALNLSADFIR.Q		K.NAPSVPQVDASLDKPLDIDAPPTIYSVNLKPEYGTAALNLSADFIR.Q
208	219	2	1335.67	1.1	0	62.9	28.4	95.00%	E.NLVMSVTTVGCR.R	Carbamidomethyl (+57)	R.ETPIALISLAPNMTLSTDENLVMSVTTVGCR.R
160	171	2	1329.74	-0.24	0	37.1	24.1	95.00%	K.VFGINLNDLVAR.H		K.VFGINLNDLVAR.H
174	188	3	1767.97	2.8	1	24.2	23.7	95.00%	E.TKDPVVNNTHIIVYR.E		R.HETKDPVVNNTHIIVYR.E
17	48	3	3402.76	2.3	0	55.8	23	95.00%	K.NAPSVPQVDASLDKPLDIDAPPTIYSVNLKPE.Y		K.NAPSVPQVDASLDKPLDIDAPPTIYSVNLKPEYGTAALNLSADFIR.Q
225	240	3	1826.92	-0.54	1	28.9	28	95.00%	K.SGIIEDLIDWAMLHSK.N		K.SGIIEDLIDWAMLHSK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
187	A6ZUC1_YEAS7	11.37%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
10	28	2	2049.94	1.6	1	62.3	30.1	95.00%	E.LIDDQFPKDDSASSGIVDE.V		-.MPTSGTTIELIDDQFPKDDSASSGIVDEVDLTEANILATGLNK.K
470	482	3	1425.68	3.2	0	23.5	29.4	92.50%	R.HSNAAQNVLADMR.V		R.HSNAAQNVLADMR.V

34	44	2	1141.68	1.4	1	25.7	20.6	95.00%	E.ANILATGLNKK.A		K.DDSASSGIVDEVDLTEANILATGLNKK.A
400	414	2	1783.9	-0.68	0	45.9	28.1	95.00%	K.INWGPVLTDLPMWDK.Q		K.INWGPVLTDLPMWDK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
188	A6ZUW3_YEAS7	15.48%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
3	12	2	1051.52	1.9	1	28.6	28.3	95.00%	K.VEIDSFSGAK.I		K.VEIDSFSGAK.I
78	91	2	1481.86	2.3	0	48.6	18.1	95.00%	K.AQRPITGASLDLIK.E		K.AQRPITGASLDLIK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
189	CSG2_YEAST	7.32%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
106	120	2	1739.81	1.4	0	72.2	29.6	95.00%	E.DVDTFSHVLDDPQPR.I		R.NSQFDNNNSGSVTNEDVDTFSHVLDDPQPR.I
91	105	2	1625.66	2.5	0	61	30.6	95.00%	R.NSQFDNNNSGSVTNE.D		R.NSQFDNNNSGSVTNEDVDTFSHVLDDPQPR.I
91	120	3	3347.46	1.7	1	112	29	95.00%	R.NSQFDNNNSGSVTNEDVDTFSHVLDDPQPR.I		R.NSQFDNNNSGSVTNEDVDTFSHVLDDPQPR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
190	ATG22_YEAS7	13.64%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
62	79	3	1982.87	2.1	1	77.4	30.4	95.00%	K.VHDHSIPCLSETGSDSDK.C	Carbamidomethyl (+57)	K.VHDHSIPCLSETGSDSDK.C
281	296	2	1801.86	-0.73	1	72.2	28.5	95.00%	R.SPYPGEQDALGQLNWK.N		R.SPYPGEQDALGQLNWK.N
2	17	2	1862.81	2.3	1	85.4	30.8	95.00%	M.SYGTINDMNESVTNYR.I		-.MSYGTINDMNESVTNYR.I
189	210	2	2410.14	-0.11	1	76.1	29.6	95.00%	K.CQSQGAYEPDKVDSLTTVISGR.G	Carbamidomethyl (+57)	K.CQSQGAYEPDKVDSLTTVISGR.G
62	72	2	1292.58	2	0	33.3	29.7	95.00%	K.VHDHSIPCLSE.T	Carbamidomethyl (+57)	K.VHDHSIPCLSETGSDSDK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
191	A6ZLU0_YEAS7	20.51%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
250	259	2	1138.57	3	0	36.9	28.7	95.00%	R.WTGDVGYITK.D		R.WTGDVGYITK.D
275	292	2	1990	-1.2	0	60.2	27.7	95.00%	R.LLICGPDGMNNLALQYAK.E	Carbamidomethyl (+57)	R.LLICGPDGMNNLALQYAK.E
151	178	3	2990.44	2.4	1	46.2	28.8	95.00%	K.YFAGLNSGDTVDFKGPIGTLNYEPNSSK.H		K.YFAGLNSGDTVDFKGPIGTLNYEPNSSK.H
219	226	2	958.5	1.7	1	52.2	29.2	95.00%	E.NDILLKDE.L		K.VSLLYANETENDILLKDELDEMAEK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
192	A6ZRY2_YEAS7	19.88%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
252	280	3	3046.41	1.4	1	66	29.2	95.00%	K.TQTDRTNIDNSTGQAGQANAQSANTVNNR.V		K.TQTDRTNIDNSTGQAGQANAQSANTVNNR.V
57	70	2	1501.76	3.1	1	55.2	28.1	95.00%	E.VSILDILDTAGQEE.Y		K.QVVIDDEVSILDILDTAGQEEYSAMR.E
257	280	2	2445.12	-0.57	0	100	29.9	95.00%	R.TNIDNSTGQAGQANAQSANTVNNR.V		R.TNIDNSTGQAGQANAQSANTVNNR.V
95	109	2	1858.91	-0.43	1	72.6	28	95.00%	K.SSLDELMTYYQQILR.V		K.SSLDELMTYYQQILR.V
257	286	3	3102.44	3	1	85.6	29.5	95.00%	R.TNIDNSTGQAGQANAQSANTVNNRVNNNSK.A	Deamidation (+1)	R.TNIDNSTGQAGQANAQSANTVNNRVNNNSK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
193	A6ZXW5_YEAS7	21.63%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
349	364	2	1960.98	2.2	0	53.5	27.5	95.00%	E.IMWSEPQLEPIYQATR.G		R.ININLHGSVLDSPEIMWSEPQLEPIYQATR.G

12	33	5	2499.33	-0.45	1	27.7	21.7	95.00%	R.HALLHNDIQTSNNSRPSLVQKK.Y		R.HALLHNDIQTSNNSRPSLVQKK.Y
260	268	2	1153.62	3.6	0	25.6	26.1	94.30%	R.IYNDFITLR.D		R.IYNDFITLR.D
97	106	2	1235.59	-0.083	1	43.9	28.4	95.00%	K.NQEVYSQVNR.I		K.NQEVYSQVNR.I
326	334	2	1046.61	-0.12	1	57.6	20.3	95.00%	K.SIGELFILR.I		K.SIGELFILR.I
130	142	2	1482.61	-0.52	0	81.8	29.9	95.00%	R.STAYCTASSYNMK.E	Carbamidomethyl (+57)	R.STAYCTASSYNMK.E
46	59	2	1442.67	-1.3	0	53.1	30.1	95.00%	R.ASYTGSAMINPTSK.Q	Oxidation (+16)	R.ASYTGSAMINPTSK.Q
12	32	3	2371.23	-0.5	0	54.1	24.3	95.00%	R.HALLHNDIQTSNNSRPSLVQK.K		R.HALLHNDIQTSNNSRPSLVQK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
194	A6ZUF3_YEAS7	6.85%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
277	287	3	1270.82	1.9	1	32.9	11.5	95.00%	E.VIKKPLIFSAR.G		K.LTNEVIKKPLIFSAR.G
155	166	2	1391.6	2.5	0	68.2	30.1	95.00%	E.GTYMTSLDDFDK.G		R.VSSEGTYMTSLDDFDK.G
347	355	2	1109.56	-0.2	1	40.7	28	95.00%	K.MGLEWLSFK.G		K.MGLEWLSFK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
195	A6ZSL9_YEAS7	17.49%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
58	78	2	2261.09	2	0	125	28.7	95.00%	R.QDVIDSLTQICDSNPAISASK.L	Carbamidomethyl (+57)	R.QDVIDSLTQICDSNPAISASK.L
155	163	2	1102.58	3.3	1	43.7	26.8	95.00%	R.LISQAWETR.S		R.LISQAWETR.S
52	78	3	2885.46	1.8	1	53	25.8	95.00%	E.GILGQRQDVIDSLTQICDSNPAISASK.L	Carbamidomethyl (+57)	K.QLEGILGQRQDVIDSLTQICDSNPAISASK.L
49	57	2	1012.57	4	1	23.4	23.8	92.70%	K.QLEGILGQR.Q		K.QLEGILGQR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
196	SSO1_YEAST	22.07%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	62	3	1568.76	0.27	0	31.9	28.5	95.00%	K.YDHTINQVDSLHK.R		K.YDHTINQVDSLHK.R
162	182	2	2172.13	1.2	0	71.1	25.1	95.00%	E.AAISDVGGQQIFSQALLNANR.R		R.QYMIIQPEATEDEVEAAISDVGGQQIFSQALLNANR.R
78	93	2	1832.9	-1.4	0	73.1	28	95.00%	R.HSLDNFVAQATDLQFK.L		R.HSLDNFVAQATDLQFK.L
30	39	2	1150.52	1.4	0	34.2	28.6	95.00%	E.GHDFVGFMNK.I		-.MSYNNPYQLETPFEESYELDEGSSAIGAEGHDFVGFMNK.I
46	62	3	2039.99	-0.53	1	49.4	28.9	95.00%	R.DLDKYDHTINQVDSLHK.R		R.DLDKYDHTINQVDSLHK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
197	A6ZXE1_YEAS7	20.83%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	63	2	1629.85	2.2	1	58.4	25.8	95.00%	K.SIACVLTVINEQQR.E	Carbamidomethyl (+57)	K.SIACVLTVINEQQR.E
16	26	2	1241.74	1.4	1	42.5	17.6	95.00%	E.QLASQLVDLKK.E		K.EQLASQLVDLKK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
198	A6ZT16_YEAS7	14.53%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
350	360	2	1319.63	2.6	0	33.3	29.5	95.00%	E.INLIDFNDLDE.A		K.NGDSNAASQIHPSHVSAPLQQSSGALTNEINLIDFNDLDEAPSQGNNNTNGTGTPAAAETSVNDLLGDLTDLSISNPSTANQASFGLGGDIVLGSSQPAPPVTTTNNSNNTLDLLGLSTPQLPTNSQAVNSSGFDLLMGFNPTTGTTTAPAR.T

321	349	3	2916.36	1.5	0	59.5	29.1	95.00%	K.NGDSNAASQIHPSHVSAPLQQSSGALTNE.I			K.NGDSNAASQIHPSHVSAPLQQSSGALTNEINLIDFNDLDEAPSQGNNNTNGTGTPAAAETSVNDLLGDLTDLSISNPSTANQASFGLGGDIVLGSSQPAPPVTTTNNSNNTLDLLGLSTPQLPTNSQAVNSSGFDLLMGFNPTTGTTTAPAR.T
295	304	2	1128.61	2.6	0	45.1	26.5	95.00%	E.DDALVQDLLK.F			K.IIEEEQEDDALVQDLLK.F
171	186	3	1740.97	3	1	35.8	21.6	95.00%	K.ISESDLAVLKPSNQLK.T			K.ISESDLAVLKPSNQLK.T
350	379	3	3073.38	2.3	1	37.7	30.1	95.00%	E.INLIDFNDLDEAPSQGNNNTNGTGTPAAAE.T	Deamidation (+1)		K.NGDSNAASQIHPSHVSAPLQQSSGALTNEINLIDFNDLDEAPSQGNNNTNGTGTPAAAETSVNDLLGDLTDLSISNPSTANQASFGLGGDIVLGSSQPAPPVTTTNNSNNTLDLLGLSTPQLPTNSQAVNSSGFDLLMGFNPTTGTTTAPAR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
199	YIP8_YEAST	30.39%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
185	195	2	1370.66	1.1	1	38.6	28.8	95.00%	E.NDFTNYTVNKR.E		K.LDDPYENDFTNYTVNKR.E
101	112	3	1314.71	1.7	0	40.9	25.6	95.00%	R.QLNASMGTLRPK.K		R.QLNASMGTLRPK.K
137	150	2	1675.79	-0.96	0	68.4	29.5	95.00%	R.DPSYSFMYPLTLSR.K		R.DPSYSFMYPLTLSR.K
196	204	2	1112.57	3.1	1	39.7	26.6	95.00%	R.EFIDSLRPH.-		R.EFIDSLRPH.-
114	129	2	1739.87	1	1	39.6	27.6	95.00%	K.QSTAYTNVPVIFSGEK.V		K.QSTAYTNVPVIFSGEK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
200	A6ZKL6_YEAS7	39.42%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
46	63	3	1886.01	0.11	1	41.2	23.2	95.00%	R.LNRLPAASLGDMVMATVK.K		R.LNRLPAASLGDMVMATVK.K
121	128	2	1045.47	-0.19	1	33.1	29.7	95.00%	K.ECADLWPR.V	Carbamidomethyl (+57)	K.ECADLWPR.V
33	40	2	932.57	2.7	0	25.3	20.5	95.00%	R.NLYIIAVK.G		R.NLYIIAVK.G
13	32	2	2015	3.2	0	93.9	28.1	95.00%	R.ISLGLPVGAIMNCADNSGAR.N	Carbamidomethyl (+57)	R.ISLGLPVGAIMNCADNSGAR.N
49	63	2	1502.79	3	0	71.4	26.4	95.00%	R.LPAASLGDMVMATVK.K		R.LPAASLGDMVMATVK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
201	A6ZY13_YEAS7	3.48%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
400	412	2	1465.71	2.5	0	67.5	29.2	95.00%	R.LMCSLAQQGYAPK.F	Carbamidomethyl (+57)	R.LMCSLAQQGYAPK.F
573	580	2	1021.49	3.4	1	28.9	28.8	95.00%	R.VYDPEIMR.Q		R.VYDPEIMR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
202	B3LKG8_YEAS1	8.06%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
403	412	2	1076.59	2.9	0	23.1	25.9	90.50%	R.NLYALAIDGK.A		R.NLYALAIDGK.A
16	30	2	1767.66	-0.81	0	41.6	30.6	95.00%	R.NSSSLDSDHDAYYSK.Q	Phospho (+80)	R.NSSSLDSDHDAYYSK.Q
31	40	2	1186.56	1.6	1	45.2	29.3	95.00%	K.QNPDNFPVKE.Q		K.QNPDNFPVKEQEIYNIDLEENNVSSR.S
559	569	2	1316.62	1.4	1	49.7	29.7	95.00%	K.STDVDLYTFKE.I		K.STDVDLYTFKEIYDR.E
403	415	2	1372.77	2.3	1	79.8	23.3	95.00%	R.NLYALAIDGKAPK.I		R.NLYALAIDGKAPK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
203	A6ZYY5_YEAS7	17.45%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
23	42	2	2070.04	2.4	0	50.2	27.2	95.00%	E.TLPQQGSIAGVSQGFPNIQE.I		K.GVNTLENIETLPQQGSIAGVSQGFPNIQEIYSDR.D
2	13	2	1290.59	-0.91	1	45.7	29.1	95.00%	M.TSSASSPQDLEK.G	Acetyl (+42)	-.MTSSASSPQDLEK.G
43	58	2	1892.93	2.4	1	44.5	27.7	95.00%	E.IYSDRDFITLGSSTYR.R		K.GVNTLENIETLPQQGSIAGVSQGFPNIQEIYSDRDFITLGSSTYR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
204	A6ZUM5_YEAS7	35.71%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	27	2	2776.45	2.7	1	55	24.1	95.00%	M.SLPATFDLTPEDAQLLLAANTHLGAR.N	Acetyl (+42)	-.MSLPATFDLTPEDAQLLLAANTHLGAR.N
102	113	2	1402.69	0.19	0	26.7	29	91.50%	R.FTPGSFTNYITR.S		R.FTPGSFTNYITR.S
120	127	2	911.55	1.6	0	41.2	19.3	95.00%	R.LVIVTDPR.S		R.LVIVTDPR.S
136	154	2	2003.02	2.7	0	106	26.9	95.00%	E.ASYVNIPVIALTDLDSPSE.F		K.EASYVNIPVIALTDLDSPSEFVDVAIPCNNR.G
28	52	3	2815.45	-0.77	0	43.1	24.9	95.00%	R.NVQVHQEPYVFNARPDGVHVINVGK.T		R.NVQVHQEPYVFNARPDGVHVINVGK.T
13	27	2	1562.86	1.4	0	73.9	24.7	95.00%	E.DAQLLLAANTHLGAR.N		-.MSLPATFDLTPEDAQLLLAANTHLGAR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
205	A6ZSS5_YEAS7	60.98%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
37	57	2	2365.05	1.3	0	96.5	30.7	95.00%	K.CPGCLNITTVFSHAQTAVTCE.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CPGCLNITTVFSHAQTAVTCESCSTVLCTPTGGK.A
2	17	3	1718.93	1.7	1	43.9	24.4	95.00%	M.VLVQDLLHPTAASEAR.K		-.MVLVQDLLHPTAASEAR.K
2	15	2	1491.8	2	0	61.9	25.3	95.00%	M.VLVQDLLHPTAASE.A		-.MVLVQDLLHPTAASEAR.K
37	70	3	3713.67	1.9	1	42.9	29.5	95.00%	K.CPGCLNITTVFSHAQTAVTCESCSTVLCTPTGGK.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CPGCLNITTVFSHAQTAVTCESCSTVLCTPTGGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
206	A6ZU78_YEAS7	26.17%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
116	126	2	1190.75	3	1	26	10.4	95.00%	K.GRIPNVPVIVK.A		K.GRIPNVPVIVK.A
98	111	2	1375.74	2.1	0	27.4	24.9	95.00%	E.TAPVIDTLAAGYGK.I		K.ETAPVIDTLAAGYGK.I
97	111	2	1504.78	2.2	1	75.8	26.4	95.00%	K.ETAPVIDTLAAGYGK.I		K.ETAPVIDTLAAGYGK.I
43	55	3	1568.75	1.5	1	25.9	29.5	95.00%	R.INMDKYHPGYFGK.V		R.INMDKYHPGYFGK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
207	A6ZR28_YEAS7	33.33%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
21	32	3	1450.81	0.62	1	42.4	21.4	95.00%	R.KQFVVDVLHPNR.A		R.KQFVVDVLHPNR.A
12	20	2	981.6	3.5	0	33.3	18.7	95.00%	K.VISNPLLAR.K		K.VISNPLLAR.K
69	83	2	1539.8	3.1	1	26.5	25.7	95.00%	K.SVGFGLVYNSVAEAK.K		K.SVGFGLVYNSVAEAK.K
53	61	2	996.5	-0.43	0	42.8	27.3	95.00%	K.DAVSVFGFR.T		K.DAVSVFGFR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
208	B3LK49_YEAS1	25.46%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
60	85	3	2826.38	3.1	0	25.5	27.1	95.00%	E.DLFCAVTNPVTGSYIDLSQLSSTPNK.L	Carbamidomethyl (+57)	K.SENDEDLFCAVTNPVTGSYIDLSQLSSTPNK.L
358	370	2	1456.71	1	0	55.2	28.8	95.00%	E.IIDSLDINSHTTE.S		R.DMEAQNEIIDSLDINSHTTESDHPTLADNSV.-
149	170	2	2203.16	0.72	0	79.3	25.9	95.00%	E.NNLVSIGDFSTRPALVGGSTAK.K		R.GWGYDTNFTLGICSSPVGEAESQQLSNLTGAFYVDQLNENNLVSIGDFSTRPALVGGSTAK.K
371	381	2	1154.52	0.5	0	29.8	29.5	95.00%	E.SDHPTLADNSV.-		R.DMEAQNEIIDSLDINSHTTESDHPTLADNSV.-

332	346	2	1678.71	-0.64	1	32.3	30.7	95.00%	R.LRSSPSASSSSLANR.E	Phospho (+80)/ Phospho (+80)	R.LRSSPSASSSSLANR.E
190	199	2	1179.6	0.77	0	42.5	28.8	95.00%	K.ATLLNFVCDK.E	Carbamidomethyl (+57)	K.ATLLNFVCDK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
209	A6ZSA1_YEAS7	20.13%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
81	93	2	1576.73	2.3	0	31.3	29.6	95.00%	K.TVMTFCQYVDSVK.D	Carbamidomethyl (+57)	K.TVMTFCQYVDSVK.D
40	60	2	2308.15	3.3	0	25.5	27.5	92.10%	K.YAPDPPITHNVNIGIVFTDPE.S		K.YAPDPPITHNVNIGIVFTDPESSEEAGR.L
234	244	2	1322.6	-0.62	1	39.4	29.1	95.00%	R.LQDYQNGDLEK.G	Deamidation (+1)	R.LQDYQNGDLEK.G
201	217	2	1859.93	2	1	59.2	27.2	95.00%	E.NGKPEQPITIGYISSQE.H		K.TDENGKPEQPITIGYISSQEHR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
210	A6ZLC2_YEAS7	12.29%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	115	2	1647.03	-0.43	0	62.6	6.02	95.00%	R.GAIVGPDLAVLALVIVK.K		R.GAIVGPDLAVLALVIVK.K
3	14	2	1319.68	3.8	0	27.1	26.8	95.00%	K.LNISYPVNGSQK.T	Deamidation (+1)	K.LNISYPVNGSQK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
211	A6ZM19_YEAS7	13.90%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
253	270	2	2304.04	1.7	1	56	30.8	95.00%	K.RATYDDYQTNYYNYVIDK.M		K.RATYDDYQTNYYNYVIDK.M
305	316	2	1356.71	1.6	1	44.3	27.5	95.00%	E.DRFTASTFTAIK.T		K.AAAPGIQLVAGEGFQSPLEDRFTASTFTAIK.T
70	78	2	1112.44	2	0	27.8	28.8	93.60%	E.GGCLMFHYE.A	Carbamidomethyl (+57)	K.SIHPGYLSEGGCLMFHYEADNEENLEELNDSKPLIDQLWPGQLVVPEWK.L
254	270	2	2147.94	1.4	0	64.3	30.4	95.00%	R.ATYDDYQTNYYNYVIDK.M		R.ATYDDYQTNYYNYVIDK.M
37	53	3	1926.04	-0.62	1	21.5	22.2	95.00%	K.TGLADLMVLRPSIFHEK.E		K.TGLADLMVLRPSIFHEK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
212	A6ZYE1_YEAS7	10.59%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
176	194	2	1986.94	-0.36	0	34.4	29.1	95.00%	R.TVMSLPGNHDIGFGDTVVE.S		R.TVMSLPGNHDIGFGDTVVESSLQR.F
240	254	3	1728.85	3.9	0	32.5	28.8	95.00%	R.QFLDNFAMGSHPLPR.I		R.QFLDNFAMGSHPLPR.I
255	267	2	1587.88	2.8	1	40	20.3	95.00%	R.ILLTHVPLWRDPE.Q		R.ILLTHVPLWRDPEQQTCGQLR.E
176	199	3	2558.25	2.5	1	38.3	27.5	95.00%	R.TVMSLPGNHDIGFGDTVVESSLQR.F		R.TVMSLPGNHDIGFGDTVVESSLQR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
213	A6ZQ99_YEAS7	9.80%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
138	146	2	1063.61	2.5	0	32.4	23.5	95.00%	E.TLFAFQPLK.K		R.HVATDTYLLAHDVASPFYPTNEEITTVTLEEGDGELYPETLFAFQPLK.K
54	74	2	2378.06	1.3	0	46.1	30.3	95.00%	R.ISSAGQQVTGYTHPDFNNQWE.V		R.ISSAGQQVTGYTHPDFNNQWEVLPPHGSDVGK.G
31	44	4	1646.8	3.1	0	34.9	28.8	95.00%	K.HQDTDAFLHSHLAR.Y		K.HQDTDAFLHSHLAR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
214	A6ZXQ3_YEAS7	26.55%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
51	61	2	1281.71	3.1	1	26	24	95.00%	R.LAPELNQAIWK.R		R.LAPELNQAIWK.R
87	102	2	1732.94	-0.76	0	49.5	23.4	95.00%	K.NPLFSYVEPVLVASAK.G		K.NPLFSYVEPVLVASAK.G
84	102	3	2047.11	3	1	52.8	23.6	95.00%	E.DAKNPLFSYVEPVLVASAK.G		R.NEEEDAKNPLFSYVEPVLVASAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
215	COS6_YEAST	23.88%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
157	167	2	1275.75	3.6	1	33.3	20.9	95.00%	R.TTLLEPFSLKK.D		R.TTLLEPFSLKK.D
124	135	2	1388.66	2	0	45.5	29.5	95.00%	E.VVAANLNSYFYE.N		K.NTPSSDPHDWEVVAANLNSYFYENK.A
113	123	2	1283.51	1.9	0	33.8	29.2	95.00%	K.NTPSSDPHDWE.V		K.NTPSSDPHDWEVVAANLNSYFYENK.A
291	300	2	1194.6	2.6	0	39.6	28.7	95.00%	K.MQFLSTIINE.Q		K.MQFLSTIINEQESGANGWDEIAK.K
357	369	2	1544.86	-0.59	1	57.8	23.2	95.00%	R.ALSLNVELWPYIK.E		R.ALSLNVELWPYIK.E
143	156	2	1789.76	-0.95	1	41.7	31	95.00%	K.YFFFSAMSCQEAFR.T	Carbamidomethyl (+57)	K.YFFFSAMSCQEAFR.T
25	33	2	1087.6	-0.48	0	22.9	24.7	92.00%	K.TVLPQDLFR.S		K.TVLPQDLFR.S
206	216	2	1187.59	3.1	1	36.3	28.5	95.00%	K.SWSPVGLEDAK.L		K.SWSPVGLEDAK.L
157	166	2	1147.65	4.2	0	35.1	23.1	95.00%	R.TTLLEPFSLK.K		R.TTLLEPFSLK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
216	A6ZR09_YEAS7	19.83%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
44	60	3	1846.88	3.1	0	51.2	29.2	95.00%	K.CGDCGSALQGISTLRPR.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CGDCGSALQGISTLRPR.Q
25	31	2	712.42	-0.46	0	24.7	23.4	94.50%	K.TPGGILR.A		K.TPGGILR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
217	ARN2_YEAST	8.32%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
515	546	3	3446.74	3	0	47.9	24	95.00%	K.LLHYMGDADLATAAYGSPLTFILSNPWGTPVR.S		K.LLHYMGDADLATAAYGSPLTFILSNPWGTPVR.S
601	611	2	1314.61	-0.78	1	33	29.6	95.00%	K.EDDPINDWIAK.R		K.EDDPINDWIAK.R
339	348	2	1101.66	0.6	0	27.6	19.2	95.00%	R.LALVPFAPFK.L		R.LALVPFAPFK.L
602	611	2	1185.57	1.7	0	35.2	28.9	95.00%	E.DDPINDWIAK.R		K.EDDPINDWIAK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
218	B3LTD0_YEAS1	11.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
33	43	2	1157.62	3.3	0	47	26.2	95.00%	K.NFGIGQAVQPK.R		K.NFGIGQAVQPK.R
173	181	2	990.56	3.7	0	28.4	23.4	95.00%	K.MGVPYAIIK.G		K.MGVPYAIIK.G
162	171	2	1158.69	2.6	0	26.7	20.4	95.00%	E.LVVFLPALCK.K	Carbamidomethyl (+57)	K.LVLIANDVDPIELVVFLPALCK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
219	B3LFU9_YEAS1	9.46%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
100	116	2	1841.03	1.3	1	27	18.6	95.00%	K.LATVGHEPKPLLPELVE.N		K.LATVGHEPKPLLPELVENGELLR.E
126	138	2	1333.6	1.4	1	85.9	30.1	95.00%	E.DMIQGGSSAESPR.S		R.EEEDMIQGGSSAESPR.S
100	113	2	1499.84	1.2	0	42.5	22.9	95.00%	K.LATVGHEPKPLLPE.L		K.LATVGHEPKPLLPELVENGELLR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
220	A6ZLZ0_YEAS7	5.31%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
727	740	2	1272.7	-0.25	0	23.3	25.5	91.70%	K.AINAGGGATTVLTK.D		K.AINAGGGATTVLTK.D
786	801	3	1914.98	-0.5	0	35.7	27	95.00%	R.LQHIQTCLAGDLLFMR.F	Carbamidomethyl (+57)	R.LQHIQTCLAGDLLFMR.F
123	130	2	920.5	1.2	1	25.4	26.5	93.50%	E.LANTVFEK.D		R.DSSLDGWVSITAHEASELPAPHHYYLLNLNFNSPNETDSIPELANTVFEK.D
1026	1043	3	1993.02	0.54	0	22.5	26	95.00%	R.KPAEPTKPNNLDATDINR.L		R.KPAEPTKPNNLDATDINR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
221	A7A0K9_YEAS7	11.80%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
643	661	2	2086.06	1.9	0	47.2	25.8	95.00%	E.LTSFAHIGNARPNFSNVIE.N		R.DQLIHFDDIMTELTSFAHIGNARPNFSNVIENAIK.S
444	458	2	1651.78	1.6	0	99.1	29.3	95.00%	K.ATLINLNTSNNPHDE.M		K.ATLINLNTSNNPHDEMFK.V
666	688	2	2409.17	2.6	0	65.7	29	95.00%	K.STPPGDSLAVVCCGPPVLVDDVR.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.STPPGDSLAVVCCGPPVLVDDVR.N
631	642	2	1491.66	2	0	50.7	30.9	95.00%	R.DQLIHFDDIMTE.L	Oxidation (+16)	R.DQLIHFDDIMTELTSFAHIGNARPNFSNVIENAIK.S
33	47	2	1623.83	2.1	0	88.8	27.7	95.00%	E.SNAVLACASYINTLK.W	Carbamidomethyl (+57)	K.DHLESNAVLACASYINTLK.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
222	A6ZXE6_YEAS7	3.73%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
826	842	2	1763.86	2.3	1	41.8	28.7	95.00%	R.LGEMPADQGFPAYLGAK.L		R.LGEMPADQGFPAYLGAK.L
925	937	2	1645.78	4	1	44.1	29.4	95.00%	K.FYDSNYPEFPVLR.D		K.FYDSNYPEFPVLR.D
446	455	2	1095.61	3.2	0	28.2	24.4	95.00%	R.DLSLLGSHVR.K		R.DLSLLGSHVR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
223	A6ZQ50_YEAS7	33.70%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	61	2	1369.56	1.2	0	59.3	28.6	95.00%	R.GAAGIWTCSCCK.K	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GAAGIWTCSCCK.K
62	80	2	1793.97	1.3	1	135	23.7	95.00%	K.KTVAGGAYTVSTAAAATVR.S		K.KTVAGGAYTVSTAAAATVR.S
63	80	2	1665.87	1.4	0	81.1	27	95.00%	K.TVAGGAYTVSTAAAATVR.S		K.TVAGGAYTVSTAAAATVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
224	B3LI68_YEAS1	4.52%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	48	2	1623.68	-0.87	0	68.5	30	95.00%	R.GYTNYNNGSNYTQK.K	Deamidation (+1)	R.GYTNYNNGSNYTQK.K
363	375	2	1316.65	-0.4	1	55.1	28.2	95.00%	E.SATTPAIPTKSDE.A		K.EETEVAETEQSNIDESATTPAIPTKSDEAEAEVEAEAGDAGTK.I
404	419	3	1725.9	3.4	0	21.9	25.6	95.00%	E.TDDGTNTVSHILNVLK.D		K.IGLEAEIETTTDETDDGTNTVSHILNVLK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
225	B3LM88_YEAS1	26.17%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
138	145	2	1030.45	-10	1	31.5	28.4	95.00%	R.YNQTETFK.E	Deamidation (+1)	R.YNQTETFK.E
77	86	2	1091.54	3.6	0	50.1	29.2	95.00%	E.ATYQVSGNPR.N		K.SNQVFTGPGFYDPVDELLIEPSLPGLSYSFTEDGWYEEATYQVSGNPR.N
39	54	2	1770.78	0.78	0	66.7	30.8	95.00%	K.SNQVFTGPGFYDPVDE.L		K.SNQVFTGPGFYDPVDELLIEPSLPGLSYSFTEDGWYEEATYQVSGNPR.N
121	137	2	1959.83	2.4	0	97.7	30.2	95.00%	R.QLFSDPCNDDGVSTYSR.Y	Carbamidomethyl (+57)	R.QLFSDPCNDDGVSTYSR.Y
55	70	2	1764.92	2.4	0	55	24.9	95.00%	E.LLIEPSLPGLSYSFTE.D		K.SNQVFTGPGFYDPVDELLIEPSLPGLSYSFTEDGWYEEATYQVSGNPR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
226	A6ZY37_YEAS7	12.33%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
13	22	2	1209.56	1.4	0	38.7	29.2	95.00%	K.NMYNASLNQR.N		K.NMYNASLNQR.N
1	12	2	1354.73	-0.9	0	38.4	24.4	95.00%	-.MNVIFSLASFVK.N		-.MNVIFSLASFVK.N
271	282	3	1320.68	-0.52	0	23	27.5	94.80%	R.VDSHLGTHLNTK.G		R.VDSHLGTHLNTK.G
378	392	2	1557.69	-0.27	1	80.7	29.8	95.00%	R.SSSPSSSFTVSSNER.S		R.SSSPSSSFTVSSNER.S

362	377	2	1800.86	0.92	1	87.7	29.4	95.00%	E.MEPLGTVEPVDISNER.S	Oxidation (+16)	K.LSEEDSEDEGDNSIPPTIGPNDLEMEPLGTVEPVDISNER.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
227	B3LGK8_YEAS1	7.66%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
96	107	2	1418.63	2.4	0	47.2	29.9	95.00%	E.HDGLAPWFSNFE.S		K.HLDLLEHDGLAPWFSNFESFYVR.R
173	185	2	1392.62	-0.49	1	85.4	29.7	95.00%	K.GQCTDAALESVDK.Y	Carbamidomethyl (+57)	K.GQCTDAALESVDK.Y
367	384	2	1909.94	1.6	0	38	28.3	95.00%	K.SFGAAGGYIAADQWIIDR.L		K.SFGAAGGYIAADQWIIDR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
228	A6ZQ79_YEAS7	16.44%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
168	180	2	1338.8	3	0	46.9	17.6	95.00%	R.VNQAIALLTIGAR.E		R.VNQAIALLTIGAR.E
55	65	2	1263.65	3.6	0	56.4	27.3	95.00%	K.DASLVDYVQVR.Q		K.DASLVDYVQVR.Q
20	31	2	1282.72	2.2	0	31.7	22.9	95.00%	E.FTPVVLATPIPE.E		-.MSDTEAPVEVQEDFEVVEEFTPVVLATPIPEEVQQAQTEIK.L
20	32	2	1411.76	2.7	1	56.1	24	95.00%	E.FTPVVLATPIPEE.V		-.MSDTEAPVEVQEDFEVVEEFTPVVLATPIPEEVQQAQTEIK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
229	A6ZQR0_YEAS7	12.45%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
100	115	2	1917.78	2.8	1	63	30.6	95.00%	E.ADWLYTGDVLDYDDEE.S		K.LGNANTFLGNVSEADWLYTGDVLDYDDEESLILAMPK.N
276	295	2	2303.05	3.1	0	44.5	30.6	95.00%	E.INWDASDISNPGYYYAIVNE.V		K.VDISIWPGGNSTNAPGTIAWSGGEINWDASDISNPGYYYAIVNEVNITCYDPPSDTK.K
116	123	2	871.52	1.1	0	54.1	27	95.00%	E.SLILAMPK.N		K.LGNANTFLGNVSEADWLYTGDVLDYDDEESLILAMPK.N
46	59	2	1716.67	0.63	0	85.6	30	95.00%	E.CGTGQYCLNNCDVR.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Deamidation (+1)/ Carbamidomethyl (+57)	R.VEAATFCNATQACPEDKPCCSQYGECGTGQYCLNNCDVR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
230	A6ZMI1_YEAS7	25.49%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
129	140	2	1486.79	2.6	1	55.5	25.4	95.00%	K.YFEVILVDPQHK.A		K.YFEVILVDPQHK.A
148	157	2	1330.61	1.1	0	32.8	29.9	95.00%	R.YNWICNPVHK.H	Carbamidomethyl (+57)/ Deamidation (+1)	R.YNWICNPVHK.H
115	128	2	1715.82	2.2	0	80.2	29	95.00%	R.VLNSYWVNQDSTYK.Y		R.VLNSYWVNQDSTYK.Y
78	93	2	1675.85	-0.66	1	74.7	27.5	95.00%	K.GATYGKPTNQGVNELK.Y		K.GATYGKPTNQGVNELK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
231	A6ZNP1_YEAS7	20.14%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
191	201	2	1408.71	1.3	1	36.8	28	95.00%	E.FAYQQNLIEQR.D		R.DPINNEEFAYQQNLIEQR.D
40	55	2	1762.95	1.9	0	48.3	23.8	95.00%	E.INGQISTLQQFTATLK.S	Deamidation (+1)	K.EEVAAELFEINGQISTLQQFTATLK.S
221	237	2	1811.93	2.5	0	38.8	26.3	95.00%	K.DLGSVVQQQGVLVDNIE.A		K.DLGSVVQQQGVLVDNIEANIYTTSDNTQLASDELR.K
118	131	2	1702.8	0.76	1	71.4	29.7	95.00%	R.DVSYSFQEFQGIQR.Q		R.DVSYSFQEFQGIQR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
232	A6ZPU2_YEAS7	11.44%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
206	217	2	1198.67	-0.1	0	53.6	25	95.00%	K.DAGTIAGLNVLR.I		K.DAGTIAGLNVLR.I
218	233	2	1644.88	2.9	0	64.2	25.6	95.00%	R.IVNEPTAAAIAYGLDK.S		R.IVNEPTAAAIAYGLDK.S
264	281	2	1938.86	0.82	1	81.9	30.7	95.00%	E.VQATSGDTHLGGEDFDYK.I		K.EHQIIVYDLGGGTFDVSLLSIENG VFEVQATSGDTHLGGEDFDYK.I
103	117	2	1671.86	3.2	0	66	26.6	95.00%	K.NQVAANPQNTIFDIK.R		K.NQVAANPQNTIFDIK.R
468	484	2	1877.96	2	0	38.3	26.6	95.00%	K.SQIFSTAVDNQPTVMIK.V		K.SQIFSTAVDNQPTVMIK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
233	A6ZZW6_YEAS7	6.68%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
249	265	2	1829.93	5.5	0	51.3	26.2	95.00%	K.VDLMDQGTDVIDILAGR.V		K.VDLMDQGTDVIDILAGR.V
166	184	3	2079.2	2.2	0	28.1	13.8	95.00%	R.IYSPHVLTLTLVDLPGLTK.V		R.IYSPHVLTLTLVDLPGLTK.V
579	589	2	1180.56	0.053	0	39.4	29	95.00%	K.SGFFGGFFSTK.N		K.SGFFGGFFSTK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
234	B3LHY2_YEAS1	4.31%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
108	120	2	1258.65	1.2	1	64	26.8	95.00%	K.SNIGNAEVAGLSK.D		K.SNIGNAEVAGLSK.D
513	522	2	1187.58	1.7	1	61.5	28.2	95.00%	E.LGEPIPYDER.L		R.CNELGEPIPYDER.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
235	A6ZQG2_YEAS7	18.18%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
28	44	2	1874.91	2.8	0	80.2	28.8	95.00%	K.LDFTNVGFTGSYVDVNK.F		K.LDFTNVGFTGSYVDVNK.F
272	299	3	3217.56	2.8	1	77.9	27.2	95.00%	K.NHLYSTFHTFQGIEDLGTGIQSYG YITR.N		K.NHLYSTFHTFQGIEDLGTGIQSYG YITR.N
191	204	2	1433.69	2.4	0	37.9	28.6	95.00%	R.SGIPAYYGYGGTTK.M		R.SGIPAYYGYGGTTK.M
68	80	2	1501.77	3	0	54.8	26.3	95.00%	K.NAPLADYLSVHFR.G		K.NAPLADYLSVHFR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
236	A6ZKM8_YEAS7	14.50%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
165	178	2	1550.76	-0.5	0	55.3	29	95.00%	R.LYACISSRPGQSGR.C	Carbamidomethyl (+57)	R.LYACISSRPGQSGR.C
78	92	2	1666.88	2.5	1	30.9	25.8	95.00%	R.IAGVVYHPSNNELVR.T		R.IAGVVYHPSNNELVR.T
78	89	2	1298.63	2.1	0	54	29.1	95.00%	R.IAGVVYHPSNNE.L		R.IAGVVYHPSNNELVR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
237	RTN1_YEAST	20.34%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
236	247	2	1267.67	2.4	1	42.5	25.6	95.00%	K.LAADVPLEPESK.A		K.LAADVPLEPESK.A
208	216	2	939.58	3.4	0	36.8	19.8	95.00%	K.LGPISNLVK.S		K.LGPISNLVK.S
248	269	2	2416.09	1.7	1	37.4	30.2	95.00%	K.AYTSSAQVMPEVPQHEPSTTQE. F		K.AYTSSAQVMPEVPQHEPSTTQE FNVDELSNELK.K
219	235	2	1589.79	-0.45	0	43.7	28.8	95.00%	K.TAPVSSTAGPQTASTSK.L		K.TAPVSSTAGPQTASTSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
238	A7A0F5_YEAS7	14.12%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
170	183	3	1467.75	1.4	0	55.6	27.7	95.00%	E.QDSHLGALSQSIGR.T		K.DEPLQSQLQSLSQPQPPQPMVS NQELFINQQQQLLEQDSHLGALSQ SIGR.T
159	169	2	1373.72	2.8	0	65.3	26.5	95.00%	E.LFINQQQQLLE.Q	Deamidation (+1)	K.DEPLQSQLQSLSQPQPPQPMVS NQELFINQQQQLLEQDSHLGALSQ SIGR.T
42	52	2	1240.74	0.077	1	33.9	20.3	95.00%	R.QLGSILELLQK.C		R.QLGSILELLQK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
239	PSS_YEAST	22.83%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
7	24	2	2072.94	2.2	1	41.5	29.8	95.00%	E.DFAPQEFPHTDTDVIVNE.H		-.MVESDEDFAPQEFPHTDTDVIVNEHR.D
192	201	2	1115.64	3.8	0	50.5	23.8	95.00%	R.FNVTVAQLPK.D		R.FNVTVAQLPK.D
45	66	2	2285.2	2.1	0	72.5	24.7	95.00%	R.ASSIFSINTTPLAPPNATDIQK.F		R.ASSIFSINTTPLAPPNATDIQK.F
44	66	3	2441.3	2.3	1	21.3	23.5	95.00%	R.RASSIFSINTTPLAPPNATDIQK.F		R.RASSIFSINTTPLAPPNATDIQK.F
67	78	3	1523.63	3.2	1	36.9	29.8	95.00%	K.FTSDEHHFSMMR.N		K.FTSDEHHFSMMR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
240	B3LTD1_YEAS1	15.84%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
37	80	4	4762.74	5.4	0	48.9	26.7	95.00%	R.SSSQPSHHHSGGTNNNNNNNNNNNNSNNNNNGNDGGNDDDYDYE.M	Deamidation (+1)/ Deamidation (+1)/ Deamidation (+1)	R.SSSQPSHHHSGGTNNNNNNNNNNNNSNNNNNGNDGGNDDDYDYEMQDYRPSPQSARPTPTYVPQYSVESGTAFPIQEVIPSAYINTQDINHK.D
183	208	3	2600.07	4.5	1	41	30.8	95.00%	R.ATSNAGHSANTGATNGRTTGAQTNME.S	Phospho (+80)/ Deamidation (+1)	R.ATSNAGHSANTGATNGRTTGAQTNMESNESPR.N
224	244	3	2411.25	1.7	0	21.4	24.3	95.00%	K.TLYQNPQTPTVLPSTYHPINK.W		K.TLYQNPQTPTVLPSTYHPINK.W
114	128	2	1711.89	1.3	0	33.5	27.2	95.00%	E.VIPSAYINTQDINHK.D		R.SSSQPSHHHSGGTNNNNNNNNNNNNSNNNNNGNDGGNDDDYDYEMQDYRPSPQSARPTPTYVPQYSVESGTAFPIQEVIPSAYINTQDINHK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
241	A6ZU02_YEAS7	4.15%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
29	41	2	1261.65	1.6	1	72.3	27	95.00%	E.GTAASSLNIATEK.A		K.HTTDVIEFYEEGTAASSLNIATEK.A
482	491	2	1122.64	2.5	0	38.2	23.5	95.00%	K.DAVTNIHLLK.R		K.DAVTNIHLLK.R
481	491	3	1250.74	1.9	1	39.2	16.5	95.00%	E.KDAVTNIHLLK.R		K.EVEKDAVTNIHLLK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
242	A7A200_YEAS7	13.60%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
5	18	2	1434.69	0.7	0	59.3	29.9	95.00%	E.VAALVIDNGSGMCK.A	Deamidation (+1)/ Carbamidomethyl (+57)	-.MDSEVAALVIDNGSGMCK.A
271	284	2	1527.73	1.4	0	46.3	29.2	95.00%	E.SAGIDQTTYNSIMK.C		R.APEALFHPSVLGLESAGIDQTTYNSIMK.C
73	84	2	1443.65	1.6	1	37.2	29.6	95.00%	E.HGIVTNWDDMEK.I		R.YPIEHGIVTNWDDMEK.I
260	270	2	1181.65	3.1	0	34.5	23.7	95.00%	E.ALFHPSVLGLE.S		R.APEALFHPSVLGLESAGIDQTTYNSIMK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
243	A6ZUA3_YEAS7	15.57%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
176	196	3	2379.29	3.7	1	35.5	20.9	95.00%	K.YGILSIDDLIHEIITVGPHFK.Q		K.YGILSIDDLIHEIITVGPHFK.Q
171	187	3	1869.99	2.5	1	23.8	24.8	95.00%	E.ANLGKYGILSIDDLIHE.I		R.VPLSDNAIIEANLGKYGILSIDDLIHEIITVGPHFK.Q
207	218	2	1225.62	3.2	0	39	28	95.00%	K.LSNPSGGWGVPR.K		K.LSNPSGGWGVPR.K
176	187	2	1386.71	2.9	0	52.8	27.1	95.00%	K.YGILSIDDLIHE.I		K.YGILSIDDLIHEIITVGPHFK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
244	A6ZW48_YEAS7	6.91%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
136	150	2	1755.88	-0.53	1	37.4	27.5	95.00%	K.AVNYPVTVDFTEVFR.K		K.AVNYPVTVDFTEVFR.K

768	782	2	1564.74	0.92	0	59.5	29.3	95.00%	E.WALFGNGGFAPGNTR.V	Deamidation (+1)	K.TPEWALFGNGGFAPGNTR.V
483	488	2	926.39	-0.28	0	34.5	27.2	95.00%	K.CVFCWR.H	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CVFCWR.H
199	218	3	2128.15	4.1	0	67.2	21.6	95.00%	E.TLLSSQIYVLYSSLQGAASK.A		K.SALTISNETLLSSQIYVLYSSLQGAASK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
245	COS7_YEAST	24.80%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
157	167	2	1261.73	2.6	1	24.9	22.2	94.70%	R.TTVLEPFSLKK.D		R.TTVLEPFSLKK.D
113	123	2	1283.51	1.9	0	33.8	29.2	95.00%	E.NTPSSDPHDWE.V		K.EITENTPSSDPHDWEVVVANLNSYLYENK.A
22	33	2	1442.83	2.4	1	38.4	19.2	95.00%	E.SQKIVLPQDLFR.S		K.QLESQKIVLPQDLFR.S
354	369	2	2001.08	-0.26	1	27.3	23.1	95.00%	K.SMWLLPLNVELWPYIK.E		K.SMWLLPLNVELWPYIK.E
102	109	2	1064.54	2.8	1	38.7	28.6	95.00%	K.QLIQFCKE.I	Carbamidomethyl (+57)	K.QLIQFCKEITENTPSSDPHDWEVVVANLNSYLYENK.A
25	33	2	1099.64	-0.29	0	24.9	23.4	94.80%	K.IVLPQDLFR.S		K.IVLPQDLFR.S
206	219	2	1553.81	3.3	1	69.3	25.8	95.00%	K.SWSPVGLEDVQLPK.D		K.SWSPVGLEDVQLPK.D
186	196	2	1211.62	3	0	48.6	27.3	95.00%	E.ALQVYATGFDK.Q		K.DSVPYIEEALQVYATGFDK.Q
124	135	2	1382.71	2.9	0	41.9	26.5	95.00%	E.VVVANLNSYLYE.N		K.EITENTPSSDPHDWEVVVANLNSYLYENK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
246	A6ZZN9_YEAS7	5.36%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
143	154	2	1390.71	2.2	0	65.6	28	95.00%	E.DDTYVSLNPIVR.C		K.AHNMGPNEVFVEEEYIDEDDTYVSLNPIVR.C
188	196	2	1235.6	-1.3	0	28.8	28.9	94.80%	K.TYFVTWYTR.F		K.TYFVTWYTR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
247	YCE5_YEAST	6.71%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
115	125	2	1478.67	1.7	1	30.9	29.4	95.00%	K.YDLHDWFLLEE.G		K.YDLHDWFLLEEGVDNAPSTTILPQSSYLNDQVSIK.N
572	596	4	2837.37	1.9	0	33.5	28.7	95.00%	R.LSNSSDNFSYDPLTGHINKPQFQTK.Q		R.LSNSSDNFSYDPLTGHINKPQFQTK.Q
467	481	2	1588.83	-0.58	1	41.1	26.1	95.00%	R.ETTNLNTLGITLGDK.S		R.ETTNLNTLGITLGDK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
248	A6ZSD5_YEAS7	10.05%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
101	111	2	1246.53	2.5	0	55.4	29.4	95.00%	R.GINFDYSGSCK.I	Carbamidomethyl (+57)	R.GINFDYSGSCK.I
90	100	2	1245.49	0.33	0	45.2	29.5	95.00%	K.FGSMSCSSMPR.G	Carbamidomethyl (+57)	K.FGSMSCSSMPR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
249	A6ZNJ9_YEAS7	16.13%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
251	267	2	1906.83	0.31	0	83.5	30.2	95.00%	E.ILQSDANNSNTWSQSNE.S		R.SSMFISPTEILQSDANNSNTWSQSNESAIYDSLSSTPR.E
326	341	3	1865.97	2	1	30.1	25.8	95.00%	K.YRPPSVHLDQLLDGKE.-		K.YRPPSVHLDQLLDGKE.-
290	311	2	2569.09	2.1	1	83.7	31.4	95.00%	K.FTDSTNPFNYTSYNLSPDSEDR.S		K.FTDSTNPFNYTSYNLSPDSEDR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
250	ERV25_YEAST	19.43%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
86	101	2	1747.78	2.8	0	40.2	30.7	95.00%	R.VAFTAPSSTAFDVCFE.N	Carbamidomethyl (+57)	R.VAFTAPSSTAFDVCFENQAQYR.G

43	61	2	1880.93	1.3	0	117	28.7	95.00%	E.GQLVVADIHSDGSVGDGQK.L		R.DFVTEGQLVVADIHSDGSVGDGQK.L
62	67	2	760.46	-0.69	0	26.1	21.9	95.00%	K.LNLFVR.D		K.LNLFVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
251	A6ZPF3_YEAS7	13.03%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
131	150	2	2163.11	3.4	0	84.8	25.5	95.00%	K.DLLDPNTSSNVAYISSLLNK.I		K.DLLDPNTSSNVAYISSLLNK.I
399	411	2	1583.8	2.4	0	41.1	27.3	95.00%	R.HYSIIYNDVLGYK.T		R.HYSIIYNDVLGYK.T
210	218	2	1153.66	3.4	0	25	20.7	94.80%	E.LFFLPNYIK.F		R.SSLDELFFLPNYIK.F
219	235	2	2000.99	-1.5	1	62.8	28.8	95.00%	K.FAAPLTYWFLSNSDLEK.S		K.FAAPLTYWFLSNSDLEK.S
205	218	2	1684.87	-0.43	1	63.1	26	95.00%	R.SSLDELFFLPNYIK.F		R.SSLDELFFLPNYIK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
252	A6ZT54_YEAS7	16.99%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
181	192	2	1284.66	2.2	1	37.4	28	95.00%	E.ETPLAEPTNVSK.E		R.EETPLAEPTNVSK.E
300	315	2	1715.9	1.5	0	55.7	26.8	95.00%	E.AVTPLINEPEPLPTPE.A		K.EVAHNVQELTPQVEAVTPLINEPEPLPTPEAQISIPESSK.V
19	37	3	2145.15	2.2	1	21.8	22.3	95.00%	K.DVILTGTFDDWRGTLPLVK.T		K.DVILTGTFDDWRGTLPLVK.T
85	95	2	1304.66	2.5	0	53.3	27.7	95.00%	E.NNFLQITDLVE.T		K.EHVSEGIENNFLQITDLVETQEVAGASR.I
108	118	2	1124.61	0.62	0	47.2	24.6	95.00%	E.AGGLLCGKPPR.S	Carbamidomethyl (+57)	R.IPEAGGLLCGKPPR.S
364	373	2	1144.65	2.3	0	25.2	23.6	95.00%	E.VFTLDPIVNK.A		K.DEEVFTLDPIVNK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
253	A6ZMK2_YEAS7	39.16%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
31	45	2	1636.9	-0.7	1	52.5	21.8	95.00%	K.VNGSPITLVEPEILR.F	Deamidation (+1)	K.VNGSPITLVEPEILR.F
69	82	2	1442.76	-0.0011	0	82	26.6	95.00%	R.VTGGGHVSQVYAIR.Q		R.VTGGGHVSQVYAIR.Q
46	59	2	1632.95	-0.32	1	52.6	17.6	95.00%	R.FKVYEPLLLVGLDK.F		R.FKVYEPLLLVGLDK.F
115	127	3	1494.86	2.4	1	20.5	20.4	94.90%	R.TLLIADSRRPEPK.K		R.TLLIADSRRPEPK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
254	A7A1L9_YEAS7	14.42%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	75	2	1266.61	-0.34	1	44.8	29.5	95.00%	R.GFLSDLPDFEK.L		R.GFLSDLPDFEK.L
123	144	3	2279.17	3	1	18.6	25.6	90.20%	R.AVNTGMEPGKTSFFQALGVPTK.I		R.AVNTGMEPGKTSFFQALGVPTK.I
111	122	2	1282.67	-0.49	1	38.6	27	95.00%	R.AGAVAPEDIWVR.A		R.AGAVAPEDIWVR.A
133	144	2	1294.7	3.4	0	25	25.4	94.40%	K.TSFFQALGVPTK.I		K.TSFFQALGVPTK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
255	A6ZNC5_YEAS7	8.91%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
304	311	2	967.48	-0.15	1	26.8	28.5	92.60%	R.EALDFFAR.G		R.EALDFFAR.G
277	287	2	1354.61	3.1	0	58.8	31	95.00%	K.CCSDVFNQVVK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CCSDVFNQVVK.S
288	299	2	1250.67	2.6	0	76.2	26.2	95.00%	K.SISIVGSYVGNR.A		K.SISIVGSYVGNR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
256	A6ZRP5_YEAS7	7.16%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
418	431	2	1649.78	2.4	1	56.7	29.6	95.00%	R.YQAVTCEPNQLAEK.N	Carbamidomethyl (+57)	R.YQAVTCEPNQLAEK.N
663	682	2	2177.08	-1.8	1	66.4	28	95.00%	K.TTESNFGFITVLPGAFSAYR.F		K.TTESNFGFITVLPGAFSAYR.F
148	167	3	2302.11	1.8	1	31.8	29.5	95.00%	E.LIHNGSQTMATPIERPFFNE.N	Deamidation (+1)	R.QRPPPATAEYNDVFNTNSQQLPSEHQYNNVPSYPLPSINVIQTTPELIHNGSQTMATPIERPFFNENDYYYNNR.N

111	125	2	1754.78	1.8	0	43.1	30.8	95.00%	E.YNDVFNTNSQQLPSE.H		R.QRPPPATAEYNDVFNTNSQQLPSEHQYNNVPSYPLPSINVIQTTPELIHNGSQTMATPIERPFFNENDYYYNNR.N
90	101	4	1469.73	1.4	1	19.6	28.6	92.30%	E.RDIYGGFVNHHR.Q		R.YTNQNASMGSFTPVQSLQFPEQSQQTNMLYNGDDGNNNTINDNERDIYGGFVNHHR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
257	A7A105_YEAS7	12.97%	100%	4							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
313	327	2	1683.82	3	0	44.1	28.1	95.00%	E.IDPTGMSDVFAYIQK.K		K.TQEIDPTGMSDVFAYIQK.K
208	218	2	1284.75	3.5	0	58.5	21.4	95.00%	R.LVDLLHLATYK.D		R.LVDLLHLATYK.D
187	197	2	1319.73	-0.61	1	37.8	23.4	95.00%	K.YLSLNDIELLK.T		K.YLSLNDIELLK.T
284	291	2	931.48	1.1	1	34.2	29	95.00%	R.LANPNFEK.Q		R.LANPNFEK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
258	ATG15_YEAS7	9.23%	100%	4							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
261	273	2	1641.71	1.7	0	39.1	30.6	95.00%	K.INDNLLFSCCCAR.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.INDNLLFSCCCAR.V
84	94	2	1180.58	3	0	37.1	28.8	95.00%	E.VISAAGMLYQE.T		R.LEVTPEVISAAGMLYQETTTQGQDFEDQEPLWTTNAEYATTNPFDFEFELR.R
274	287	2	1792.82	0.095	0	47.6	30.3	95.00%	R.VSYLWTTVCDCYVK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VSYLWTTVCDCYVK.S
417	426	2	1209.57	3.5	0	46.4	29.6	95.00%	R.VCVYDVVNDK.G	Carbamidomethyl (+57)	R.VCVYDVVNDK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
259	A6ZQF9_YEAS7	13.77%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	58	2	2784.3	2.2	1	61	28.9	95.00%	K.ATFSPSGGTVSVPVEWMDNGAYPSLSK.I	Deamidation (+1)	K.ATFSPSGGTVSVPVEWMDNGAYPSLSK.I
84	94	2	1245.61	1.4	1	38.3	29.4	95.00%	K.ITPSELTQDDK.V		K.ITPSELTQDDK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
260	B3LGB1_YEAS1	5.11%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
274	289	2	1654.83	2.5	0	78	28.5	95.00%	K.STMGGNLLYLTGSVDK.R		K.STMGGNLLYLTGSVDK.R
223	241	2	1998.96	0.39	1	120	29.3	95.00%	E.STHNTNNANVTSADALIKE.Q		K.ISESTHNTNNANVTSADALIKEQEEEVDDEVVNDMFGGK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
261	A6ZTK4_YEAS7	9.49%	100%	3							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
319	342	3	2640.18	1.3	1	53.1	30.4	95.00%	R.TYSLHEPTDAVHANIDTAPDGCKE.S	Carbamidomethyl (+57)	R.TYSLHEPTDAVHANIDTAPDGCKESSIFHHVFHTK.V
575	594	3	2177.96	2.4	1	58.8	30.6	95.00%	E.LHGQGSEDAYNSQSQSSDLR.M		K.IAPIDDNENELHGQGSEDAYNSQSQSSDLR.M
120	133	2	1441.81	3	0	31.1	22.1	95.00%	R.SLMGLLNGNVGVIR.T		R.SLMGLLNGNVGVIR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
262	A6ZUT8_YEAS7	11.18%	100%	3							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
145	156	2	1191.56	-0.011	0	89.5	29.3	95.00%	R.SVVADISDSDGK.S		R.SVVADISDSDGK.S
280	293	2	1562.72	2.2	1	49.9	29.4	95.00%	E.DWKPNTSGTSDVEK.H		R.AWGVNVIVFEAFDEDWKPNTSGTSDVEK.H
102	110	2	1003.57	3.9	0	32.6	24.3	95.00%	K.AALQTYLPK.I		K.AALQTYLPK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
263	A6ZWB1_YEAS7	30.84%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
100	107	2	965.53	3.7	0	25.9	26.9	93.60%	R.IFLYPSNI.-		R.IFLYPSNI.-
34	47	2	1493.75	1.9	0	57.4	28.4	95.00%	E.GVATPQDAQFYLGK.R		K.IEGVATPQDAQFYLGK.R
22	31	2	1096.63	1.4	0	22.9	22.5	91.90%	R.VNNPNVSLIK.I		R.VNNPNVSLIK.I
34	48	2	1649.86	2.7	1	41.9	27.2	95.00%	E.GVATPQDAQFYLGKR.I		K.IEGVATPQDAQFYLGKR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
264	A6ZYA1_YEAS7	2.36%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
300	308	2	1055.63	-0.011	0	42	21.2	95.00%	R.SVLDLLLQR.L		R.SVLDLLLQR.L
2	15	2	1580.88	-0.62	0	30.4	21	95.00%	M.SLPLKPLTIDSNNK.Q	Acetyl (+42)	-.MSLPLKPLTIDSNNK.Q
78	94	3	1760.99	2.6	1	44.5	18.8	95.00%	R.RLTSSLSPALPAGVHQK.T		R.RLTSSLSPALPAGVHQK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
265	A6ZQV0_YEAS7	19.48%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
184	196	2	1408.72	-0.0055	1	28.2	27.4	95.00%	R.LLGYPVYGDEVGK.V		R.LLGYPVYGDEVGK.V
64	77	2	1561.83	3.1	0	41	25.8	95.00%	E.MNPQVLFTALATTR.A		K.WSQLITNEMNPQVLFTALATTR.A
1	18	2	1834.91	3	0	92.1	27.5	95.00%	-.MNGLVLGATGLCGGGFLR.H	Acetyl (+42)/ Deamidation (+1)/ Carbamidomethyl (+57)	-.MNGLVLGATGLCGGGFLR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
266	A6ZPF4_YEAS7	10.49%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
420	432	3	1441.77	0.07	1	32.5	25.9	95.00%	K.NLHTHEVPAPISK.S		K.NLHTHEVPAPISK.S
479	491	2	1409.7	3	0	44.4	27.9	95.00%	K.NSILGCYLAQSGK.H	Carbamidomethyl (+57)	K.NSILGCYLAQSGK.H
13	21	2	1119.52	3.7	0	40.9	27.7	95.00%	K.STDDDLIWR.R		K.STDDDLIWR.R
334	345	2	1201.69	0.57	0	34.6	22.3	95.00%	R.DVALGSSIISIK.N		R.DVALGSSIISIK.N
437	455	2	2171.01	3.4	1	34	29.8	95.00%	E.VSAYGDVDLGDYKDNWIIE.I		K.SEYEVSAYGDVDLGDYKDNWIIEI VEQVGEEDPTLLHPLSTSFR.I
99	111	3	1574.77	2.6	1	33.7	28.9	95.00%	R.HEFYHDVHPPLGK.M		R.HEFYHDVHPPLGK.M
101	111	3	1308.66	1.8	0	23.3	28.2	94.30%	E.FYHDVHPPLGK.M		R.HEFYHDVHPPLGK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
267	MKAR_YEAST	18.16%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
266	278	2	1487.79	3.2	0	27.7	25.9	95.00%	R.SSLMIPNPQQFVK.S		R.SSLMIPNPQQFVK.S
64	77	2	1440.66	2.2	1	76.2	29.8	95.00%	K.YCAITGASDGIGKE.F	Carbamidomethyl (+57)	K.YCAITGASDGIGKEFAR.Q
168	187	2	2164.28	-1.9	0	67.3	12.3	95.00%	R.NIITINNTATLLITQIIAPK.I		R.NIITINNTATLLITQIIAPK.I
228	243	2	1722.86	-0.76	1	66.2	27.7	95.00%	K.SFLQGWSNSLAGELSK.D		K.SFLQGWSNSLAGELSK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
268	A6ZWJ1_YEAS7	12.57%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
328	340	2	1292.66	0.91	0	73.2	28	95.00%	K.STSDTASATLLAR.Q		K.STSDTASATLLAR.Q
347	357	2	1323.68	2.8	1	26.2	27.7	92.80%	R.KDSNTNIVLLK.S	Phospho (+80)	R.KDSNTNIVLLK.S
237	247	2	1346.64	3.4	0	29.5	29.7	94.60%	K.MHSYSFFSITK.G		K.MHSYSFFSITK.G
146	158	2	1499.89	-0.43	1	34.9	17.2	95.00%	R.KLDPLLAFPAFLR.K		R.KLDPLLAFPAFLR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
269	A6ZU67_YEAS7	8.83%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
164	184	2	2103.12	2.5	1	31.2	24.4	95.00%	E.KLPFPSGSATATLISVLNGTE.I	Deamidation (+1)	R.EKLPFPSGSATATLISVLNGTEILQ EVSK.S

521	551	3	3156.56	2.7	1	73.2	26.7	95.00%	R.DRPGSVLMNVVSGGIAEASAQQ AGDLMQDLK.T			R.DRPGSVLMNVVSGGIAEASAQQ AGDLMQDLK.T
521	537	2	1699.86	1.6	0	31.8	27	95.00%	R.DRPGSVLMNVVSGGIAE.A			R.DRPGSVLMNVVSGGIAEASAQQ AGDLMQDLK.T
598	609	2	1399.73	2.9	0	47.4	26.4	95.00%	R.IPTAVVWIDCAR.L	Carbamidomethyl (+57)		R.IPTAVVWIDCAR.L
538	551	2	1474.71	3	0	49.9	29	95.00%	E.ASAQQAGDLMQDLK.T			R.DRPGSVLMNVVSGGIAEASAQQ AGDLMQDLK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
270	A6ZMY7_YEAS7	15.10%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
181	195	2	1589.85	2.6	0	52.1	25.2	95.00%	K.GSAPLFGNFLEPLTK.T		K.GSAPLFGNFLEPLTK.T
20	34	3	1905.86	1.8	1	52.5	30	95.00%	E.HNTANDCWVTYQNRK.I	Carbamidomethyl (+57)	K.TVQEHNTANDCWVTYQNRK.I
147	160	3	1741.01	0.46	0	24.2	17	95.00%	K.FLDLNRPLLMQILR.S		K.FLDLNRPLLMQILR.S
367	380	2	1463.77	2	0	25.3	25.2	94.90%	E.VFGTYLGPDAPLSK.M		K.NYQLGFGVTSWFWDEVFGTYLG PDAPLSK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
271	SNQ2_YEAST	3.46%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1082	1092	2	1326.66	1.3	1	49.3	28.3	95.00%	K.NSATILNYFER.N		K.NSATILNYFER.N
417	435	3	2132.1	2	0	28.6	26.5	95.00%	E.FLTALTDPNGFHLIKPGYE.N		R.QATAEFLTALTDPNGFHLIKPGYE NK.V
285	294	2	1167.63	-0.1	0	29.2	25.6	95.00%	R.DLYATIFGLR.H		R.DLYATIFGLR.H
338	349	2	1237.62	3.1	1	64.3	28.5	95.00%	R.GLDASTALEYAK.A		R.GLDASTALEYAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
272	AKR2_YEAST	12.28%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
695	713	2	2276.12	-0.58	0	44.6	28.5	95.00%	K.TNLTDFWLNSDVTAPLWQR.F		K.TNLTDFWLNSDVTAPLWQR.F
72	84	2	1416.65	1.1	1	56.5	30.2	95.00%	E.SGAVDINNDRIDE.L		K.DVVESGAVDINNDRIDELSGLHW ACINNR.F
270	283	3	1699.81	2.9	1	35.5	29.1	95.00%	K.SLFEQALQHHGYDR.L		K.SLFEQALQHHGYDR.L
620	638	3	1965.02	2	0	45.6	25.3	95.00%	E.GPSATTITHTISIDGLEPR.N		K.GVEDSDMIPEGPSATTITHTISIDG LEPR.N
85	96	3	1439.71	2	0	26.1	28.4	95.00%	E.LSGLHWACINNR.F	Carbamidomethyl (+57)	R.IDELSGLHWACINNR.F
223	237	2	1613.78	1	0	38.6	29.2	95.00%	R.GFNALHCALVGGDQR.V	Carbamidomethyl (+57)	R.GFNALHCALVGGDQR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
273	A6ZR85_YEAS7	13.45%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
71	82	3	1485.7	1.3	0	39.6	29.7	95.00%	K.LHYCVSCAIHAR.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.LHYCVSCAIHAR.I
67	82	4	1991.95	3.6	1	22.5	29.7	95.00%	K.TYNKLHYCVSCAIHAR.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.TYNKLHYCVSCAIHAR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
274	A6ZMN0_YEAS7	6.00%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
146	164	2	2229.19	2.6	1	62.6	23.6	95.00%	E.YIKQNPPFLLNQGLLQQSE.D		K.QGEEYIKQNPPFLLNQGLLQQSE DSNPDATR.E
75	88	3	1617.79	2.9	1	29.4	28.2	95.00%	R.LITAYYNEHGPGQR.I		R.LITAYYNEHGPGQR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
275	A6ZQ73_YEAS7	9.27%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
417	440	3	2794.31	2.4	1	26.1	29	95.00%	K.NLSTMNVDPLYSSYHYSHPTLAE R.L		K.NLSTMNVDPLYSSYHYSHPTLAE R.L
409	416	2	912.57	3	0	29.2	23.2	95.00%	R.ALIDLQIK.N		R.ALIDLQIK.N

441	450	2	1137.6	3.2	1	25.6	26.8	93.40%	R.LTALDYVSEK.K		R.LTALDYVSEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
276	A6ZYL7_YEAS7	9.03%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
737	748	2	1380.73	-0.88	1	31.5	25.8	95.00%	K.ALLNGIEVDYFK.L		K.ALLNGIEVDYFK.L
644	658	2	1525.81	1.2	0	46.1	25.2	95.00%	E.SNDTVLAPVPGSTIR.K		K.SIGPDGLSFNENFNTTPEGFAPSIDPGEESNDTVLAPVPGSTIR.K
265	276	2	1443.71	2.3	0	30	28.3	95.00%	K.YLIQDGADFFQK.T		K.YLIQDGADFFQK.T
122	138	2	1788.94	3	0	57.2	25	95.00%	R.LSVVDFLVSQGADVNAR.A		R.LSVVDFLVSQGADVNAR.A
109	121	2	1517.79	1.6	0	59.4	27.3	95.00%	E.HITGLHWASINNR.L		K.EHITGLHWASINNR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
277	A6ZRZ3_YEAS7	5.35%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1080	1094	2	1573.8	2.5	1	29.4	27.3	95.00%	E.SDTTFNIPLVGPKGE.D		K.AVVPLSTIDPESDTTFNIPLVGPKGEDGGVLHLEFEFEPR.Y
642	653	2	1293.68	2	0	36.8	26.2	95.00%	K.SVGYTTPIGMLR.V		K.SVGYTTPIGMLR.V
1134	1155	2	2107.12	2.4	0	96.9	23.7	95.00%	K.AGSTVFALGTNVVSTGLGTIDK.V		K.AGSTVFALGTNVVSTGLGTIDK.V
973	986	2	1499.79	1.5	0	42.9	25.5	95.00%	E.LPQSDLITNSGDLK.I		K.LLVQVSWFPVTATELPQSDLITNSGDLK.I
1080	1092	2	1387.74	1.8	0	23.9	25.3	93.10%	E.SDTTFNIPLVGPK.G		K.AVVPLSTIDPESDTTFNIPLVGPK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
278	A6ZZE8_YEAS7	4.68%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
403	416	2	1634.73	2.3	0	82	30.6	95.00%	R.HIPYVTQGQSFDDE.I		R.HIPYVTQGQSFDDEISLGGFSK.V
403	424	2	2424.16	-1.1	1	78.3	28.6	95.00%	R.HIPYVTQGQSFDDEISLGGFSK.V		R.HIPYVTQGQSFDDEISLGGFSK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
279	A6ZM77_YEAS7	9.11%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
249	260	2	1416.84	2.5	0	32	17.2	95.00%	E.LVNFPIIIPYTK.T		K.IADDYYLVTAALELVNFPIIIPYTK.T
274	283	2	1210.55	-0.24	1	46.4	29.5	95.00%	K.IFENCAQMAK.D	Carbamidomethyl (+57)	K.IFENCAQMAK.D
235	248	2	1583.81	1.5	1	29.5	27.3	95.00%	R.KIADDYYLVTAALE.L		R.KIADDYYLVTAALELVNFPIIIPYTK.T
399	411	2	1559.89	2.2	0	24.5	20	94.20%	R.YRPPVLMVPYVVK.K		R.YRPPVLMVPYVVK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
280	A6ZKZ2_YEAS7	25.64%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
104	116	4	1486.82	0.55	1	25.1	23.6	95.00%	R.HKNVPVHVSPAFR.V		R.HKNVPVHVSPAFR.V
117	133	2	1855	2.3	0	70.7	22.8	95.00%	R.VQVGDIVTVGQCRPISK.T	Carbamidomethyl (+57)	R.VQVGDIVTVGQCRPISK.T
58	67	2	1148.6	2.5	0	39.4	27.4	95.00%	K.CPFTGLVSIR.G	Carbamidomethyl (+57)	K.CPFTGLVSIR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
281	A6ZT02_YEAS7	5.73%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
311	324	2	1479.74	2.7	1	30.4	28.2	95.00%	K.LAGNASWGEIFSTK.T		K.LAGNASWGEIFSTK.T
552	570	3	2299.99	2.3	1	45.7	31.3	95.00%	K.RGTDYNADDLMHDDQPFYK.K		K.RGTDYNADDLMHDDQPFYK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
282	A6ZY29_YEAS7	15.89%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

10	20	2	1136.58	0.6	0	45.4	27.3	95.00%	K.GISSSAIPYSR.N		K.GISSSAIPYSR.N
43	55	2	1380.85	2.1	1	30.3	14.1	95.00%	R.KGLTPSQIGVLLR.D		R.KGLTPSQIGVLLR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
283	RAX1_YEAST	4.83%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
132	140	2	1086.58	3.7	1	37.4	27.2	95.00%	K.LNELLGDWK.H		K.LNELLGDWK.H
8	19	2	1468.69	3.5	1	58.8	29.5	95.00%	K.VSSMQNFEMIQR.E		K.VSSMQNFEMIQR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
284	A6ZVQ4_YEAS7	6.83%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
75	85	2	1312.72	1.7	0	40.4	23.2	95.00%	R.LSAYFLPFLSR.S		R.LSAYFLPFLSR.S
130	147	2	1981.98	4.5	1	83.6	28.5	95.00%	K.FYNVDGVDNTLASLLGER.L		K.FYNVDGVDNTLASLLGER.L
217	230	2	1729.73	2.5	0	55.2	30.8	95.00%	E.SSNFNGNFWSNWNR.L	Deamidation (+1)	K.TVMWPIITDMTTGEAVPASEVDMESSNFNGNFWSNWNR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
285	A6ZZX8_YEAS7	19.66%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	172	2	1351.69	2.3	1	44.3	27.3	95.00%	K.QYAQEQGLLFR.E		K.QYAQEQGLLFR.E
34	54	2	2171.05	1.7	0	27.5	29.1	92.70%	E.STIGAAFLSQSITIHPNDGNE.T		R.ESTIGAAFLSQSITIHPNDGNETK.D
113	126	2	1532.81	2.5	0	88.5	26.4	95.00%	K.VGDDDLVIYLLGNK.V		K.VGDDDLVIYLLGNK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
286	A6ZM02_YEAS7	9.02%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
223	234	2	1258.61	3.2	0	87.5	28.9	95.00%	K.FDVGALMALHGE.G		K.FDVGALMALHGEGSGEEK.G
203	213	2	1350.74	1.4	0	29	24.6	95.00%	K.DIFPLQNIHVR.K		K.DIFPLQNIHVR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
287	A6ZQF2_YEAS7	15.17%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
16	24	2	1079.51	-0.11	0	28.5	29	94.30%	R.SVGSQWFNR.L		R.SVGSQWFNR.L
83	95	4	1542.89	1.1	1	28.3	19.2	95.00%	R.LIYPHVEHVPVLK.Q		R.LIYPHVEHVPVLK.Q
61	82	3	2263.09	0.71	1	48	29.4	95.00%	R.SAGASYSPSHGLYINEIPASSR.L		R.SAGASYSPSHGLYINEIPASSR.L
261	268	2	915.55	1.2	0	29.7	23.9	95.00%	K.IMDLALLK.N		K.IMDLALLK.N
316	327	2	1414.79	3.1	0	60.4	23.7	95.00%	K.ALIDYLNDPLLR.N		K.ALIDYLNDPLLR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
288	A6ZUA2_YEAS7	3.91%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
5	26	3	2473.97	-1.3	1	47	30.3	95.00%	R.NDNASGGYMQPDQSSNASMHKR.D	Phospho (+80)	R.NDNASGGYMQPDQSSNASMHKR.D
5	25	3	2237.91	-0.61	0	32.3	30.8	95.00%	R.NDNASGGYMQPDQSSNASMHK.R		R.NDNASGGYMQPDQSSNASMHK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
289	A6ZSN7_YEAS7	19.01%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
90	101	2	1386.78	2.6	1	52.1	22.2	95.00%	R.YIDLEAPVQIVK.R		R.YIDLEAPVQIVK.R
33	43	2	1229.66	0.89	1	42.7	25.4	95.00%	K.QLENVSSNIVK.N		K.QLENVSSNIVK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
290	B5VLK6_YEAST	8.04%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
413	426	2	1663.86	2.1	0	43.7	27.6	95.00%	K.DTFDRPLIINAFDK.D		K.DTFDRPLIINAFDK.D

439	451	2	1370.74	1.1	0	26.6	25.8	95.00%	E.VTPVVHFTMGGVK.I		K.DISTESTVYVGEVTPVVHFTMGGVK.I
487	500	2	1464.76	-0.67	1	39.2	25.5	95.00%	R.LGGSSLLECVVFGK.T	Carbamidomethyl (+57)	R.LGGSSLLECVVFGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
291	A6ZN11_YEAS7	22.34%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
53	69	2	1990.86	1.1	1	88.1	30.9	95.00%	E.AQPFEQAADTFHDNMNR.Q		R.TASVADPILDAVQEAQPFEQAADTFHDNMNR.Q
168	180	2	1554.74	1.1	0	49.6	29.4	95.00%	E.QAVYQPQQHVQTE.E		R.VRPDFPVFGAAVTYDANGMPQQVGGASSQMYGEQAVYQPQQHVQTEEK.Q
114	127	2	1561.75	3.1	0	35.7	28.8	95.00%	E.YAVSGDPVWAQQLE.T		R.SFEYAVSGDPVWAQQLETPTYGFR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
292	A7A0W1_YEAS7	8.77%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	19	2	2263.12	3.1	1	92.4	28.1	95.00%	-.MDLVLEVADHYVLDDLYAK.V	Acetyl (+42)	-.MDLVLEVADHYVLDDLYAK.V
20	32	2	1291.79	2.3	0	26.6	14.9	95.00%	K.VLPASLAANIPVK.W		K.VLPASLAANIPVK.W
7	19	2	1520.75	1	0	45.6	28.4	95.00%	E.VADHYVLDDLYAK.V		-.MDLVLEVADHYVLDDLYAK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
293	A6ZWP8_YEAS7	6.90%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
742	754	2	1445.69	3.4	0	65.5	29.2	95.00%	E.SFMSNTLFNSSLV.-		K.GNNVPNNDSESFMSNTLFNSSLV.-
13	22	2	1095.5	-0.56	0	30.2	28.9	95.00%	R.MSYSSTAPPR.F		R.MSYSSTAPPR.F
589	602	2	1602.82	2.3	1	50.4	27	95.00%	R.IPEPLTFTNSEDLK.Q		R.IPEPLTFTNSEDLK.Q
710	724	2	1753.78	2.9	0	28.9	30.6	92.60%	E.TYSPYFDSIDAALYE.I		R.AQANNNENNSSNTFSDAGETYSPYFDSIDAALYEIEK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
294	AGP1_YEAST	4.74%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
34	49	2	1743.78	0.74	0	43.3	31.1	95.00%	E.TGSNDRPSSQPHLGYE.Q		K.NSSTEIHATGQDNEIEYFETGSNDRPSSQPHLGYEQHNTSAVR.R
389	402	2	1425.77	1.2	0	63.8	24	95.00%	K.ASPYVIAVASHGVR.V		K.ASPYVIAVASHGVR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
295	A6ZNU6_YEAS7	10.53%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	127	2	1238.69	1.8	1	35.3	23.8	95.00%	R.TLTAVHDKILE.D		R.TLTAVHDKILEDLVFPTEIVGK.R
18	26	2	1003.54	2.6	0	36.7	27.1	95.00%	E.LQVAQAFVE.L		K.ILSQAPTELELQVAQAFVELENSSPELK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
296	KHA1_YEAST	5.61%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
861	873	3	1586.79	1.8	1	39.9	28.5	95.00%	R.RFDTLIVHHFSSE.-		R.RFDTLIVHHFSSE.-
620	632	2	1512.76	-0.81	1	47.3	28.2	95.00%	K.IPFSSEVIFSTMR.E		K.IPFSSEVIFSTMR.E
563	573	2	1158.64	2.9	1	30	25.3	95.00%	K.LTPFEGVGALR.A		K.LTPFEGVGALR.A
643	654	2	1357.75	-0.45	0	45.2	25.1	95.00%	K.MDSTDLILLPLK.G		K.MDSTDLILLPLK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
297	A6ZLE8_YEAS7	10.75%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
325	344	2	2141.88	1.4	1	114	30.7	95.00%	K.CNGQDMSEVGNGPGSYDISR.S	Carbamidomethyl (+57)	K.CNGQDMSEVGNGPGSYDISR.S

333	344	2	1221.56	1.1	0	84.2	28.7	95.00%	E.VGNGPGSYDISR.S	Deamidation (+1)	K.CNGQDMSEVGNGPGSYDISR.S
312	324	2	1590.81	0.57	1	58.1	27	95.00%	K.GVWQLELQDYVNK.C		K.GVWQLELQDYVNK.C
449	465	2	1675.83	2.4	1	91.4	28.6	95.00%	R.SKDSSVPLIIDSSGSAN.-		R.SKDSSVPLIIDSSGSAN.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
298	A6ZUX1_YEAS7	3.62%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
490	498	2	1090.57	2.7	1	38.1	27.2	95.00%	K.LALIDDFRE.A		K.LALIDDFREAYYWLR.M
513	529	2	1957.88	-0.51	0	86.8	30.2	95.00%	K.VAAWWDYGYQIGGMADR.T		K.VAAWWDYGYQIGGMADR.T
490	497	2	961.52	0.38	0	41.1	26	95.00%	K.LALIDDFR.E		K.LALIDDFR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
299	A6ZKL0_YEAS7	23.85%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	83	2	1247.68	2.1	1	42.5	25.6	95.00%	K.TFLVANVKDLE.T		K.TFLVANVKDLETLTMHTK.T
81	90	2	1187.59	3.4	1	45.3	28.2	95.00%	K.DLETLTMHTK.T		K.DLETLTMHTK.T
73	80	2	890.53	3.5	0	25.7	24.2	95.00%	K.TFLVANVK.D		K.TFLVANVK.D
91	103	2	1387.71	3.2	1	82.5	28.1	95.00%	K.TYAAEIAHNISAK.N		K.TYAAEIAHNISAK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
300	A6ZQP1_YEAS7	2.19%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
621	634	2	1689.9	2.9	1	55.3	25.3	95.00%	K.TDLIFDQVRDILDK.L		K.TDLIFDQVRDILDK.L
621	629	2	1105.58	-0.29	0	28.6	27	95.00%	K.TDLIFDQVR.D		K.TDLIFDQVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
301	A6ZLN3_YEAS7	3.83%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
248	256	2	1116.59	4	0	37.2	26.8	95.00%	K.VLDQDWTLK.L		K.VLDQDWTLK.L
257	262	2	775.46	-0.94	0	23.1	23	92.30%	K.LIDIFR.G		K.LIDIFR.G
263	269	2	844.41	2.2	0	29.3	28.6	95.00%	R.GPSFYFK.S		R.GPSFYFK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
302	B3LML0_YEAS1	7.67%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
384	403	2	2165.07	2.9	0	60.9	27.7	95.00%	R.LIQALGASGQLPSVCSYMDR.K	Carbamidomethyl (+57)	R.LIQALGASGQLPSVCSYMDR.K
252	265	4	1661.84	2.5	0	28.3	27.6	95.00%	K.YWHDPGAFAKPVFK.N		K.YWHDPGAFAKPVFK.N
571	581	2	1356.75	1.8	0	59.5	23.3	95.00%	E.QLIASKPFYYK.I		K.EAEEQLIASKPFYYK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
303	A6ZP14_YEAS7	8.17%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
503	514	2	1384.73	2	0	53.1	25.9	95.00%	E.LTDNLTIFYTGK.M		K.MDSELTDNLTIFYTGK.M
67	78	2	1397.81	1.4	0	44.2	21.1	95.00%	E.LLPLNTTIPFNR.I		R.SGDSLFLLSCLSCLDDGTLSSDG GSFDEDDSLELLPLNTTIPFNR.I
9	19	2	1170.69	1.5	1	32.9	21.6	95.00%	R.AILTDEGVLIK.S		R.AILTDEGVLIK.S
593	608	2	1943.99	0.42	1	30.3	26.6	95.00%	K.FPLEPLQVEIMPMLCK.T	Carbamidomethyl (+57)	K.FPLEPLQVEIMPMLCK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
304	A6ZL24_YEAS7	5.80%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
173	193	2	2112.06	1.2	0	42.1	27.5	95.00%	R.NVQAIDLGDIEPTSAVATGIE.T		R.NVQAIDLGDIEPTSAVATGIETK.G
362	378	2	1655.85	1.9	0	58.9	26.1	95.00%	R.GDGTGVGDNVVNQLLAK.M		R.GDGTGVGDNVVNQLLAK.M
101	106	2	739.39	3.3	0	37.9	27.1	95.00%	K.AFDLFK.Y		K.AFDLFK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
305	MHP1_YEAST	2.29%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
62	76	2	1525.71	1.9	0	80.6	29.6	95.00%	E.TSVDSSSSILSSNDK.G		K.ANSVAPDIQMDTARPPVFETSVDSSSSILSSNDK.G
987	1003	2	1887.93	-1.9	1	58.8	28.8	95.00%	R.LNYFSMLGTELDLASSK.A		R.LNYFSMLGTELDLASSK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
306	B3LMS1_YEAS1	5.74%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
257	264	2	1101.52	-0.19	1	35.2	29	95.00%	K.QEIQDWQR.S		K.QEIQDWQR.S
278	297	4	2360.2	2.8	1	27.8	26.4	95.00%	E.THSGPTLWQYVTDPSYKKPR.T		R.DPESSEETHSGPTLWQYVTDPSYKKPR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
307	A6ZMP4_YEAS7	20.68%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
83	99	2	1999.98	2.7	0	71.8	28.7	95.00%	R.SLDDYISQATDLQYQLK.A		R.SLDDYISQATDLQYQLK.A
54	66	2	1584.79	2.2	1	31.2	28.1	95.00%	R.YENIINQIDAQHK.D		R.YENIINQIDAQHK.D
44	53	2	1100.59	-0.11	0	78.1	25.3	95.00%	K.INSINANLSR.Y		K.INSINANLSR.Y
166	186	2	2257.15	1	0	98.4	26.6	95.00%	E.AAINDVNGQQIFSQALLNANR.R	Deamidation (+1)	R.QYTIIQPEATDEEVEAAINDVNGQQIFSQALLNANR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
308	A6ZW73_YEAS7	8.76%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
401	416	2	1778.86	1.4	1	36	28.5	95.00%	E.NYAPNMILSQSTGVER.R		K.DIEGHSLLENYAPNMILSQSTGVER.R
432	447	2	1761.69	1.7	1	27.1	30.1	90.00%	E.IHDSGEHMASGDTFNE.L	Oxidation (+16)	R.FENSSSIQNSLGNEIHDSGEHMASGDTFNELDDGK.L
378	391	2	1458.76	1.8	0	65.7	27.2	95.00%	E.DLIKPDDISSAGTK.D		K.LLNEEEDLIKPDDISSAGTK.D
7	30	4	2618.33	-0.94	1	51.3	26.2	95.00%	R.TLKSDTDVTSLNASTVSHQSKPFR.Q		R.TLKSDTDVTSLNASTVSHQSKPFR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
309	A6ZSV7_YEAS7	10.38%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
492	501	2	1050.48	3	1	32.2	28.3	95.00%	E.MGIGSSSQER.S		R.TEDDETIELEEMGIGSSSQER.S
502	511	2	1089.57	0.35	1	36	26.8	95.00%	R.SLVSPAPEYK.D		R.SLVSPAPEYK.D
39	55	2	1833.93	1.3	0	55.4	27.2	95.00%	R.TTLQPNSTSQSMIGTLR.K		R.TTLQPNSTSQSMIGTLR.K
15	34	2	2193.91	1.3	0	122	30.4	95.00%	E.SQTNNDSVNDAYADVNTTHE.S		-.MTSQEYEPIQWSDESQTNNDSVNDAYADVNTTHESR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
310	A6ZSP5_YEAS7	7.28%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
13	23	2	1074.61	2.1	0	27.5	24.2	95.00%	E.TALAVVATAMK.K		-.MVDDSNYLTPHETALAVVATAMK.K
549	559	2	1135.6	3.7	0	33.6	26.5	95.00%	K.ANSTTLGGLFR.A		K.ANSTTLGGLFR.A
412	420	2	954.53	2.8	0	32.3	24.6	95.00%	R.SPPGVFPVR.G		R.SPPGVFPVR.G
592	606	2	1568.86	2.2	1	77	24	95.00%	R.ITANNVAGIVNLNKE.D		R.ITANNVAGIVNLNKEDLDSIPR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
311	B3LLW4_YEAS1	22.16%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
143	160	3	2143.99	2.2	1	39.2	30	95.00%	E.FQNTNIIKNPTDDDFPHE.A		K.HQEFQNTNIIKNPTDDDFPHEAVVR.E
151	164	2	1610.74	2.6	1	28.8	30.1	93.10%	K.NPTDDDFPHEAVVR.E		K.NPTDDDFPHEAVVR.E
2	16	2	1532.84	3.1	0	65.4	22.6	95.00%	M.ALSLGQFINVGGMVK.D		-.MALSLGQFINVGGMVK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
312	B3LSP7_YEAS1	19.24%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	63	3	3178.58	2.8	1	43.7	26.1	95.00%	K.LGSASFTAINTLTKPALFSFYDDDITKNE.G		K.LGSASFTAINTLTKPALFSFYDDDITKNEGNVYDK.A
70	88	2	1955.02	2.6	1	64.9	24.9	95.00%	K.ALLSNASQLEMVPPSATAR.H		K.ALLSNASQLEMVPPSATAR.H
130	137	2	877.49	3.6	0	32.8	27.5	95.00%	K.GDIVSFLK.H		K.GDIVSFLK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
313	A6ZL34_YEAS7	3.17%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
188	200	2	1563.75	1.1	1	59.4	29.1	95.00%	K.YSSFSTIEFLQDK.Q		K.YSSFSTIEFLQDK.Q
2	18	2	1976.99	0.58	0	42.2	27.6	95.00%	M.SQTITSLDPNCVIVFNK.T	Acetyl (+42)/ Carbamidomethyl (+57)	-.MSQTITSLDPNCVIVFNK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
314	A6ZMX9_YEAS7	18.23%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
34	54	3	2134.11	2.8	0	23.9	25.6	95.00%	R.LSATGVNAHGRPQGSTQNALR.R		R.LSATGVNAHGRPQGSTQNALR.R
34	55	3	2290.21	2.5	1	39.4	23.9	95.00%	R.LSATGVNAHGRPQGSTQNALRR.T		R.LSATGVNAHGRPQGSTQNALRR.T
72	86	3	1728.93	0.58	1	26.3	25.9	95.00%	E.TVQNLAPNLHPEQIR.Y		R.VNGGHPVTTQMVETVQNLAPNLHPEQIR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
315	A6ZKY5_YEAS7	6.58%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
597	609	2	1491.82	2.7	0	28.3	23.1	95.00%	R.LNLPSYAMPLFVK.F		R.LNLPSYAMPLFVK.F
512	523	2	1546.71	-1.2	1	53.8	30	95.00%	K.ADEYGLWYFLDR.M		K.ADEYGLWYFLDR.M
182	200	2	2128.08	1.5	1	57.1	27.1	95.00%	K.ISNITQVFIDPDASNPIRE.S		K.ISNITQVFIDPDASNPIRESEEEIK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
316	A6ZR74_YEAS7	7.81%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
66	73	2	851.45	2.5	0	24.6	26.6	92.10%	R.ASFSALTR.L		R.ASFSALTR.L
295	307	2	1521.76	2.2	1	44.4	27.8	95.00%	R.ASIHQILQHFAEE.N		R.ASIHQILQHFAEENVSISATSADEPTVATESSPLIR.D
325	338	2	1544.77	1.9	1	47.3	27.8	95.00%	E.SSPLIRDSSLDLNE.V		R.ASIHQILQHFAEENVSISATSADEPTVATESSPLIRDSSLDLNEVIEEESIYQPK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
317	A6ZTJ7_YEAS7	4.09%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
852	868	3	2034.77	1.4	1	33.4	30.3	95.00%	E.TSGMHDIDPSDDDRWCE.Y	Carbamidomethyl (+57)	K.LMGNTTRPAILLSYLVVDPGEGNYNTYVSETSGMHDIDPSDDDRWCEYILYK.G
940	950	3	1402.64	2	0	23.3	29.8	91.40%	R.GHFYHVFDEPR.Y		R.GHFYHVFDEPR.Y
893	903	2	1246.7	2.9	1	37.3	23.2	95.00%	E.LQVGKFQVLSE.Q		R.GTITDTELQVGKFQVLSEQVLVEHSDSMYEYGHMSEPEYEDMK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
318	A6ZNL3_YEAS7	15.61%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

24	37	2	1649.74	2.5	0	50.8	30.3	95.00%	E.YVNCFSSLPSDFSK.A	Carbamidomethyl (+57)	K.TSLLLALLSILSQANAYEYVNCFSSLPSDFSK.A
352	365	2	1317.67	-0.25	0	76.4	28.8	95.00%	R.ISNGTFINGGPGGK.N		R.ISNGTFINGGPGGK.N
339	350	2	1363.6	3.1	0	60.9	30.5	95.00%	K.GQTDINPFDDSR.R		K.GQTDINPFDDSR.R
38	56	3	2216.85	-0.55	1	29.6	30.2	95.00%	K.ADSYNWQSSSHCNSECSAK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.ADSYNWQSSSHCNSECSAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
319	A6ZLM4_YEAS7	9.75%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
348	366	2	1826.94	1.3	0	89.3	26.6	95.00%	E.GPGINDDGSGTISLLNVAK.Q		K.HGDPDNIVALGAHSDSVEEGPGINDDGSGTISLLNVAK.Q
464	485	2	2150.07	1.3	1	65.7	27.5	95.00%	R.SDYVGFINNGIPAGGIATGAEK.N		R.SDYVGFINNGIPAGGIATGAEK.N
519	532	2	1522.73	1.8	0	54.7	29.4	95.00%	K.LIAHSVATYADSFE.G		K.LIAHSVATYADSFEGFPK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
320	A6ZM38_YEAS7	24.26%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	128	2	1295.76	1.8	0	76.2	19.3	95.00%	K.LPLSVINVSAQR.D		K.LPLSVINVSAQR.D
96	111	2	1701.86	2	0	42.2	27.1	95.00%	R.SNGVLNVDNQTSDLVK.S		R.SNGVLNVDNQTSDLVK.S
112	128	2	1794.07	-0.9	1	26.3	15.3	95.00%	K.SLGLKLPLSVINVSAQR.D		K.SLGLKLPLSVINVSAQR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
321	A6ZN47_YEAS7	5.29%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
82	101	3	2137.13	2.6	0	35.4	24.3	95.00%	R.QSPSDIHPVGVSYFPAVIPK.G		R.QSPSDIHPVGVSYFPAVIPK.G
610	622	2	1601.81	2.8	0	65.8	28.2	95.00%	K.LQCININDLMVNR.N	Carbamidomethyl (+57)	K.LQCININDLMVNR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
322	B3LH47_YEAS1	6.32%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
302	316	3	1832.85	-0.35	1	30.1	30.6	95.00%	K.KITDLGYSCYYSHAR.M	Carbamidomethyl (+57)	K.KITDLGYSCYYSHAR.M
336	345	2	1176.62	2.7	0	41.3	26	95.00%	R.TLVCSDLLTR.G	Carbamidomethyl (+57)	R.TLVCSDLLTR.G
24	30	2	755.46	3.4	0	24.1	20.2	93.80%	K.TALNIPK.K		K.TALNIPK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
323	A6ZT43_YEAS7	11.52%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
368	383	4	1797.89	-0.88	1	24.1	28.5	95.00%	K.KPNLHGYGHPNPPNEK.S		K.KPNLHGYGHPNPPNEK.S
296	312	2	1863.95	-1.6	0	69.9	27	95.00%	R.STNVYDLAQGLPVQFGR.Y		R.STNVYDLAQGLPVQFGR.Y
479	499	2	2212.06	-0.4	0	66.7	30	95.00%	R.ATGQPPSQPQAQTQSQQFGAR.Y		R.ATGQPPSQPQAQTQSQQFGAR.Y
360	367	2	958.49	-0.13	0	34.2	27.2	95.00%	R.GWDLNINK.K		R.GWDLNINK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
324	B3LHS1_YEAS1	7.11%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
257	271	2	1593.66	-0.01	1	52.2	29.6	95.00%	E.ASTDVEDSTDVNVNE.Q		K.DTHGIHGSVTHEPSSEDMVLTVSTMESDEEELTTTSTQTVVETITLDQEEASAVANHAHDDEASTDVEDSTDVNVNEQALLQEDFDMWSETILQK.T
290	299	2	1219.65	1.3	1	27.7	27.5	95.00%	K.TQDVIQLFEK.D		K.TQDVIQLFEK.D
71	86	3	1761.96	2.6	1	28.8	24.3	95.00%	R.KYDTAVKPVIDDATVK.V		R.KYDTAVKPVIDDATVK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
325	A6ZU95_YEAS7	5.54%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

396	408	2	1630.72	1.7	0	49.3	30.4	95.00%	R.CVDNNYSSLAFWR.A	Carbamidomethyl (+57)	R.CVDNNYSSLAFWR.A
2	14	2	1413.8	5.2	0	30.3	21.5	95.00%	M.SLISILSPLITSE.G	Acetyl (+42)	-.MSLISILSPLITSEGLDSR.I
2	19	2	1942.07	4.9	1	60.1	21.2	95.00%	M.SLISILSPLITSEGLDSR.I	Acetyl (+42)	-.MSLISILSPLITSEGLDSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
326	B3LT28_YEAS1	6.12%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
152	166	2	1694.88	2.5	0	26.5	26.4	94.90%	K.IQPAMQLPPDVDMIK.Q		K.IQPAMQLPPDVDMIK.Q
175	184	2	1257.67	1.4	1	26.5	25.9	95.00%	K.SWNQEQLLLK.S		K.SWNQEQLLLK.S
605	614	2	1192.62	1.8	1	27	27.1	94.70%	E.FDGLLPQKFE.L		K.YILPSSLLEMSEIITQSCFMLMEEFDGLLPQKFELDPCTDETNGNCEFNGEIK.S
431	447	2	1900.9	-0.53	0	83.2	30	95.00%	K.INDLFQSSYDILDGSSK.N		K.INDLFQSSYDILDGSSK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
327	A6ZXS0_YEAS7	16.07%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
225	239	2	1639.88	0.36	0	83.1	24.6	95.00%	K.DFLSGTVLYLNSLAK.R		K.DFLSGTVLYLNSLAK.R
215	224	2	1163.55	2.5	0	39.3	28.6	95.00%	E.GFWMDVGQPK.D		K.QLYSFDLEGFWMDVGQPK.D
306	320	2	1749.83	1.7	0	85.6	29.7	95.00%	K.STIVGWNSTVGQWCR.L	Carbamidomethyl (+57)	K.STIVGWNSTVGQWCR.L
269	286	2	1776.98	2.7	0	36.9	22.4	95.00%	K.IGPDVVIGPNVTIGDGVR.I		K.IGPDVVIGPNVTIGDGVR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
328	VTH1_YEAST	5.62%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1000	1009	2	1218.56	3.5	1	30.1	28.9	95.00%	R.NTFGYVDFEK.V		R.NTFGYVDFEK.V
1156	1167	2	1319.59	1.7	0	57.2	30.1	95.00%	E.TDSISYSTDFGK.T		K.GPHQWEYGDHGGVLVLVPENAETDSISYSTDFGK.T
1285	1295	2	1527.6	2.4	1	47.6	29.5	95.00%	R.QDFECDYNFYK.A	Carbamidomethyl (+57)	R.QDFECDYNFYK.A
1015	1027	2	1386.78	2.2	1	72.4	22.8	95.00%	E.GIIITNIVSNSEK.V		K.VQGLEGIIITNIVSNSEK.V
510	518	2	1119.53	1.3	0	40.6	27.6	95.00%	K.FYYSLDQGK.T		K.FYYSLDQGK.T
192	210	2	2054.93	2.8	1	68.3	30.4	95.00%	K.SSEDSDLGGNDASILCLFR.N	Carbamidomethyl (+57)	K.SSEDSDLGGNDASILCLFR.N
394	406	2	1445.76	3.1	0	39.9	27	95.00%	K.VSVDNGLTWTNLK.V		K.VSVDNGLTWTNLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
329	A6ZSI2_YEAS7	2.20%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1143	1154	2	1388.81	1.9	0	31.1	21.1	95.00%	K.NAVILNYQTLLK.E		K.NAVILNYQTLLK.E
55	70	3	1912.98	3.3	1	20.4	26.6	91.90%	E.RHPDFALPFVLACQSR.N	Carbamidomethyl (+57)	R.VHSFEELERHPDFALPFVLACQSR.N
1443	1450	2	1018.55	0.17	1	39.5	26.2	95.00%	R.IIDLFNER.Q		R.IIDLFNER.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
330	A6ZV05_YEAS7	2.95%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1305	1320	2	1769.91	2.7	1	66.3	27.1	95.00%	K.ISRPIASQNSLGWNEV.-		K.ISRPIASQNSLGWNEV.-
1273	1295	3	2684.16	1.6	0	46.7	30.7	95.00%	R.IQNWMDDSYYGHGLTNNDSTPTR.H		R.IQNWMDDSYYGHGLTNNDSTPTR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
331	A7A0G8_YEAS7	16.89%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
51	62	2	1525.72	2.5	0	58.6	29.5	95.00%	K.AQIYDDQLQNYR.D		K.AQIYDDQLQNYR.D
108	120	2	1483.79	1.8	1	45.6	25	95.00%	K.ICIQPEAGGWLIK.A	Carbamidomethyl (+57)	K.ICIQPEAGGWLIK.A
78	89	2	1451.72	0.82	0	46.4	29.2	95.00%	E.TFDDNHLVVHQK.G		R.DAGAQDFGVLIDIEETFDDNHLVVHQK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
332	A6ZME5_YEAS7	7.65%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
123	131	2	1035.54	3.6	1	32.1	26.4	95.00%	R.NVTEFSIAR.A		R.NVTEFSIAR.A
284	292	2	1100.66	0.43	1	23.1	20.6	92.30%	K.ILPFELLTR.S		K.ILPFELLTR.S
132	156	2	2446.24	2.6	0	130	25.4	95.00%	R.AICGIGAGGLNAISSIAVSDICTAR.E	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.AICGIGAGGLNAISSIAVSDICTAR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
333	A6ZWH0_YEAS7	14.21%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
139	149	2	1302.72	3.4	0	31.6	24.2	95.00%	K.QIVNIPSFMVR.L		K.QIVNIPSFMVR.L
155	171	3	1781.9	3.3	0	31.9	27.1	95.00%	K.HIDFAPTSPFGGARPGR.V		K.HIDFAPTSPFGGARPGR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
334	A6ZXS3_YEAS7	9.24%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
150	159	2	1174.62	3.1	1	25.5	27.5	92.10%	R.ALWVFPEGTR.S		R.ALWVFPEGTR.S
183	200	2	1849.09	0.05	0	26.2	11.8	95.00%	K.IPIVPVVVSNTSTLVSPK.Y		K.IPIVPVVVSNTSTLVSPK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
335	B3LTT3_YEAS1	6.00%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
298	308	3	1386.71	3.5	0	25.6	27.1	95.00%	R.WVNFPWDAKPK.L		R.WVNFPWDAKPK.L
209	214	2	1001.44	-0.016	1	26.5	29.2	90.70%	K.YEWYWR.I		K.YEWYWR.I
371	384	2	1749.82	-0.81	1	68.1	29.5	95.00%	R.VDLFDNEIYNAYFK.F		R.VDLFDNEIYNAYFK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
336	A6ZT81_YEAS7	16.25%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
244	255	2	1372.63	0.44	1	73.7	29.7	95.00%	K.IGLDCASSEFFK.D	Carbamidomethyl (+57)	K.IGLDCASSEFFK.D
313	330	2	1853.99	2.2	0	52.7	23.9	95.00%	K.TAGIQIVADDLTVTNPAR.I		K.TAGIQIVADDLTVTNPAR.I
273	288	2	1892.92	-0.0022	1	52.4	28.5	95.00%	K.WLTGVELADMYHSLMK.R		K.WLTGVELADMYHSLMK.R
89	103	2	1577.8	1.6	0	58.1	28.1	95.00%	K.AVDDFLLSLDGTANK.S		K.AVDDFLLSLDGTANK.S
225	234	2	1069.64	3.1	0	46	22	95.00%	E.ALDLIVDAIK.A		R.YGASAGNVGDEGGVAPNIQTAEEALDLIVDAIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
337	A6ZTG2_YEAS7	8.63%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
358	374	3	1905.8	2.2	0	32.2	30.6	95.00%	E.YGRPQYGGNQNSNGQHE.S	Deamidation (+1)	K.SGNNSQGQGQGQGQGQGQGQGQGQGSFTALASLASSFMNSNNNNQQGQNQSSGGSSFGALASMASSFMHSNNNQNSNNSQQGYNQSYQNGNQNSQGYNNQQYQGGNGGYQQQQGQSGGAFSSLASMAQSYLGGGQTQSNQQQYNQQGQNYQHQQQGQQQQQGHSSSFSALASMASSYLGNNSNSNSSYGGQQQANEYGRPQQNGQQQSNEYGRPQYGGNQNSNGQHESFNFSGNFSQQNNNGNQNR.Y
68	84	2	1643.73	3	0	65	30.3	95.00%	R.AAGGGSSFMNTLMADSK.G		R.AAGGGSSFMNTLMADSK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
338	INP54_YEAST	6.77%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	68	2	1568.85	2.7	0	56.8	24	95.00%	E.VVPIWQGSFPAVNR.D		K.QLLFPYDDGISQLELQDLYVLGFQEVVPIWQGSFPAVNR.D
74	85	2	1362.68	0.89	1	34.3	28.6	95.00%	R.ITTTAVNCLNEK.V	Carbamidomethyl (+57)	R.ITTTAVNCLNEK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
339	A6ZY59_YEAS7	2.55%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1068	1082	2	1629.87	0.79	0	56.7	25.2	95.00%	E.FGSDPIQVVNNLVTK.Y		K.ASGEDVEEFGSDPIQVVNNLVTK.Y
998	1009	2	1269.73	1.8	1	25.7	22.4	95.00%	E.LILLGGTAIEDR.L		R.ELILLGGTAIEDR.L
727	736	2	1126.51	-0.26	0	56.1	29.4	95.00%	K.CTINGVSYGR.A	Carbamidomethyl (+57)/ Deamidation (+1)	K.CTINGVSYGR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
340	A6ZMS6_YEAS7	16.45%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
169	191	3	2505.99	2.6	1	37.7	29.8	95.00%	E.CDACHGSGSADGKLAQCPDCQGR.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.QFYSGSSIEFTLNLNDECDACHGSGSADGKLAQCPDCQGR.G
200	213	2	1680.76	2.1	0	85.6	29.7	95.00%	R.MGIMTQQIQQMCGR.C	Carbamidomethyl (+57)	R.MGIMTQQIQQMCGR.C
94	118	3	2329.02	2.6	1	36.3	31.3	95.00%	K.NGGGGGGPGGPGAGGFHDPFDIFER.M	Deamidation (+1)	K.NGGGGGGPGGPGAGGFHDPFDIFER.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
341	A6ZUT7_YEAS7	3.86%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1068	1085	2	2012.98	-2.2	1	55.5	28.5	95.00%	R.SFVYNNLNEVLGGMDTIK.A		R.SFVYNNLNEVLGGMDTIK.A
1413	1424	3	1461.69	2.4	0	57.8	29.5	95.00%	E.FGDCTILCIAHR.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.IVEEFGDCTILCIAHR.L
729	743	2	1726.85	6.2	0	58.3	28.6	95.00%	K.DIYLFDDVLSAVDSR.V		K.DIYLFDDVLSAVDSR.V
616	627	2	1233.68	2.1	0	35.5	25.1	95.00%	E.FIMITGPIGTGK.S		K.GEFIMITGPIGTGK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
342	A6ZTZ3_YEAS7	0.94%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
988	996	2	1030.51	1.9	1	29.6	29.3	95.00%	E.AFEDPSIPR.I		K.AEFVEEDEEEEHLLLAMEIISVHAEAFEDPSIPR.I
1211	1226	3	1798.96	3.2	1	21.8	24.4	95.00%	K.FLVDDGGLVDREPIVR.Q		K.FLVDDGGLVDREPIVR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
343	A6ZUW4_YEAS7	45.71%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
87	105	2	1872.01	-1.4	1	41.3	23.4	95.00%	R.VGVVSILEAGDSDILTTLA.-		R.VGVVSILEAGDSDILTTLA.-
41	52	2	1292.82	2.5	0	38.8	10	95.00%	K.LIIIAANTPVLR.K		K.LIIIAANTPVLR.K
95	105	2	1075.54	3.6	0	27.7	28.7	93.60%	E.AGDSDILTTLA.-		R.VGVVSILEAGDSDILTTLA.-
67	83	2	1815.88	2.2	1	91	29.1	95.00%	K.VYYFQGGNNELGTAVGK.L		K.VYYFQGGNNELGTAVGK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
344	A6ZYM2_YEAS7	2.49%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
230	243	2	1654.84	2.6	0	76.2	28.1	95.00%	K.FTVFSNLDNTTQLR.L		K.FTVFSNLDNTTQLR.L
174	184	2	1186.66	2.1	1	48.8	24.4	95.00%	E.SPLILSSVSER.F		K.AFEDESPLILSSVSER.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
345	A6ZW97_YEAS7	8.80%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
158	165	2	991.54	3.8	0	49.9	27.8	95.00%	R.TDFLDIIR.T		R.TDFLDIIR.T
230	246	2	1921.04	2.7	0	99.4	23.7	95.00%	E.SIQSPYLFLNGISVINR.G	Deamidation (+1)	K.LNIDTSAALESIQSPYLFLNGISVINR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
346	A6ZRM1_YEAS7	5.59%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
424	442	2	1968.94	-2.9	1	29.9	29.6	95.00%	K.SGFDGLLPGDFPESGSIFK.K		K.SGFDGLLPGDFPESGSIFK.K
160	171	2	1304.62	-0.16	0	28.5	29.1	94.10%	R.YLSTGSTSNFTK.S		R.YLSTGSTSNFTK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
347	A6ZUG8_YEAS7	4.83%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
858	869	2	1359.7	-0.6	1	40	27.5	95.00%	R.AWDIKQTLDSLA.-		R.AWDIKQTLDSLA.-
30	45	3	1813.92	1.9	0	22.6	27.3	94.60%	R.SSNVTFKPPVTHDMVR.S		R.SSNVTFKPPVTHDMVR.S
666	679	2	1628.9	2.6	0	40.2	22.7	95.00%	E.TNFVLPTPVTLNWK.M		K.IENEQIETNFVLPTPVTLNWK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
348	A6ZZW2_YEAS7	16.46%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
337	353	2	1851.84	1.6	1	64.7	30.3	95.00%	K.YDISKSDPLAADSNDIE.S		K.YDISKSDPLAADSNDIESVPLSNLELDFDLNMTDEPSVSPSLFDGSTSVSR.S
362	387	2	2815.28	-0.93	0	76.9	28.9	95.00%	E.LDFDLNMTDEPSVSPSLFDGSTSVSR.S		K.SDPLAADSNDIESVPLSNLELDFDLNMTDEPSVSPSLFDGSTSVSR.S
24	34	3	1251.69	2.9	0	25.8	23.7	95.00%	E.TSLDPHQTLLK.V		R.WFLSERPPNCHVADLETSLDPHQTLLK.V
388	399	2	1149.63	3.6	0	54.4	24.8	95.00%	R.SSATSITSLGVK.R		R.SSATSITSLGVK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
349	A6ZN12_YEAS7	8.24%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
377	398	2	2395.13	2.8	0	97.8	30.5	95.00%	R.IGSNAYCFSACLPAYTVTSVSK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.IGSNAYCFSACLPAYTVTSVSK.V
80	92	2	1438.74	0.76	0	51.5	28	95.00%	K.SLQAQKPNLSPQE.I		K.SLQAQKPNLSPQEIDALIEDWEPEPLVDPSATDEQSWR.V
127	137	2	1322.72	1.5	0	58.4	24.7	95.00%	E.MPIQNHITITR.N		K.TPVTMEMPIQNHITITR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
350	B3LKB6_YEAS1	4.66%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	77	2	1308.67	-0.47	0	45.8	28.2	95.00%	K.APVPDVNAPQSSK.N		K.APVPDVNAPQSSK.N
89	104	2	1617.92	1.8	0	44.5	19.7	95.00%	E.TPTGLVPVATLHSIGR.T		K.IFPEEYTLETPTGLVPVATLHSIGR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
351	A6ZNT7_YEAS7	5.14%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
603	616	2	1557.84	2.1	0	65.5	25.1	95.00%	E.IGSTIQTLNDLIDR.S		K.GEEIGSTIQTLNDLIDR.S
575	586	2	1437.66	3	1	61.4	30.1	95.00%	K.WNSDYEAVIADR.R		K.WNSDYEAVIADR.R
1062	1083	2	2378.1	0.96	1	78.9	30.1	95.00%	K.VMDWDSTSADDTIGTAEIPLNK.V		K.VMDWDSTSADDTIGTAEIPLNK.V
721	733	2	1549.75	1.3	1	67.4	29.5	95.00%	R.ITLQCMDVETVNK.D	Carbamidomethyl (+57)	R.ITLQCMDVETVNK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
352	A6ZP61_YEAS7	3.33%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
191	205	2	1653.83	3.1	0	29.1	28	95.00%	R.LLGQDSDPGLYFTTK.E		R.LLGQDSDPGLYFTTK.E
59	74	2	1772.89	2.1	0	31.4	27.7	95.00%	E.ATIDVTDVPQTPFLQE.Q		K.SSNSSMDKPFFPNNDSVANTDPQSDENGHTINEIRPTEATIDVTDVPQTPFLQEQYSMRPR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
353	A6ZPF8_YEAS7	3.11%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
205	219	2	1588.83	-0.9	1	41.9	26	95.00%	K.ILATNPIMEAFGNAK.T		K.ILATNPIMEAFGNAK.T
476	484	2	1160.6	1.2	1	26.1	26.7	94.20%	E.FNQHVFKLE.Q		K.LQQEFNQHVFKLEQEEYVK.E
1527	1538	2	1321.69	2.1	0	47.6	26.4	95.00%	E.TGPFTDPFSLIK.T		K.GHEHSSSIFITPETGPFTDPFSLIK.T
1547	1559	2	1445.8	2.8	0	37.9	24.1	95.00%	E.AYIPAWLSLPSTK.R		K.FDQVEAYIPAWLSLPSTK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
354	A6ZWX4_YEAS7	9.48%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
343	355	2	1444.78	1.9	1	24.8	24.4	94.60%	K.IKTPGFLDDLVVE.K		K.IKTPGFLDDLVVEK.V
204	219	2	1802.9	2.3	0	32.8	27.4	95.00%	K.NHNVILPHFDPLTSAE.S		K.NHNVILPHFDPLTSAESNNGDISTNDTTHEYQSQFHSSNQFFLYFDNNMDK.E
463	473	2	1220.68	3.3	0	27.5	25	95.00%	K.LSYNVVTNAIK.S		K.LSYNVVTNAIK.S
256	266	2	1399.68	2.7	0	52.8	28.5	95.00%	E.DWYYQLINASK.N		K.EDWYYQLINASK.N
267	288	3	2222.13	2.3	0	34.7	26.9	95.00%	K.NSNSLSTGLLDPNVSANAAHLK.T		K.NSNSLSTGLLDPNVSANAAHLK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
355	A6ZT50_YEAS7	6.65%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
13	22	2	1126.64	-1.2	0	30	23.4	95.00%	K.TPLPLCSVIK.S	Carbamidomethyl (+57)	K.TPLPLCSVIK.S
2	12	2	1215.56	3.6	0	43.7	29.6	95.00%	M.AFSDFAAICSK.T	Carbamidomethyl (+57)	-.MAFSDFAAICSK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
356	A6ZVN8_YEAS7	3.41%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
24	40	2	1798.74	0.78	0	80.1	30.7	95.00%	E.TDTATFNDDAPSGATCR.I	Carbamidomethyl (+57)	K.VANEETDTATFNDDAPSGATCR.I
402	429	3	3086.61	1.3	0	33.3	23.3	95.00%	E.FDDLIAAQQNAINRPNAPVFIPPPAQNR.A		R.AQNEFDDLIAAQQNAINRPNAPVFIPPPAQNR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
357	A6ZUV7_YEAS7	9.17%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
205	220	3	1927.06	0.004	0	24.3	21.5	95.00%	K.SWLNNIIDLNKPIPYK.N		K.SWLNNIIDLNKPIPYK.N
232	243	2	1261.71	2.5	0	33.7	22.9	95.00%	E.ISHQPGLVIGIE.A		K.NSKPSLLSSDEISHQPGLVIGIEADPDR.D
383	398	2	1661.81	0.95	1	62.4	28.5	95.00%	E.SATTPAKDVDNDTLSK.S		K.NDEEGSESATTPAKDVDNDTLSK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
358	A7A0E6_YEAS7	6.00%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
280	292	2	1394.76	2.1	0	47	24.8	95.00%	E.DGHITDVLLGSLR.S		K.VNENWNVEDGHITDVLLGSLR.S
12	29	2	1915.99	1.1	1	47.5	25.5	95.00%	K.KPILAVPEPALADTHSEE.I		K.KPILAVPEPALADTHSEEISR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
359	A6ZV22_YEAS7	24.03%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
20	29	2	1127.52	0.15	1	28.4	28.7	94.50%	K.AYFTAPSSER.R		K.AYFTAPSSER.R
92	105	3	1431.79	3.7	0	24.4	24	95.00%	K.VNGASVPINLHPSK.L		K.VNGASVPINLHPSK.L
80	86	2	805.43	0.97	0	32.2	26.3	95.00%	K.FAVQVDK.V		K.FAVQVDK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
360	A6ZYP1_YEAS7	4.48%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

480	495	2	1731.72	0.092	0	62.8	29.8	95.00%	R.SSTINNDSDSLSSPTK.S	Phospho (+80)	R.SSTINNDSDSLSSPTK.S
124	149	4	2967.22	-0.83	1	26.1	30.1	95.00%	R.NNSGYYHNSYDNNNNSNNPGSNSHRK.T		R.NNSGYYHNSYDNNNNSNNPGSNSHRK.T
276	289	2	1684.83	3.8	0	49.3	28.5	95.00%	R.NQSQQPQQQLSPFR.H		R.NQSQQPQQQLSPFR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
361	B3LRN4_YEAS1	11.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
284	304	2	2338.07	1.5	0	81.2	30.4	95.00%	E.TTMGDTLGLYSDIGDDNFIYK.A		K.ETNDNSNNQTNTNIGNTFDTDFSNGNTETTMGDTLGLYSDIGDDNFIYK.A
328	337	2	1128.62	0.87	1	27.8	26.1	95.00%	E.ILQVSDIEGR.W		K.ALYPYDADDDDAYEISFEQNEILQVSDIEGR.W
236	247	3	1405.78	2.1	0	29.8	23	95.00%	E.AVNLHLNTLQQR.I		R.DSGYATQFDGYPQQQPSHTNYVSSTALAGFENTQPNTSEAVNLHLNTLQQR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
362	A6ZT92_YEAS7	3.34%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1480	1492	2	1480.76	-0.62	0	46.6	27.6	95.00%	K.IWTTSGDLLNSFK.N		K.IWTTSGDLLNSFK.N
1440	1466	3	3130.38	0.83	0	45.2	29.5	95.00%	E.SFVDQNVTSQYGSQQKPTTMTCMQVHE.H	Carbamidomethyl (+57)	R.SEDPVESFVDQNVTSQYGSQQKPTTMTCMQVHEHAPIIATGTK.Q
1310	1321	2	1415.78	-0.15	1	46.3	24.4	95.00%	R.STGLLTEWLQIR.G		R.STGLLTEWLQIR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
363	A6ZMI9_YEAS7	3.52%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
782	799	2	1910.03	-2.9	0	47.2	22.6	95.00%	K.TPVFTTGGDYILSLVSIK.D		K.TPVFTTGGDYILSLVSIK.D
42	52	2	1327.56	-0.24	1	42.1	30.4	95.00%	R.FQYSDDEPAEK.I		R.FQYSDDEPAEK.I
1048	1065	2	2002.03	3	0	35.7	26.9	95.00%	R.ACAANVDQISFLEPINLK.F	Carbamidomethyl (+57)	R.ACAANVDQISFLEPINLK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
364	A6ZMV1_YEAS7	5.90%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
188	201	2	1563.79	2.9	0	67.7	27.2	95.00%	K.NTVSNACLFQIAAR.L	Carbamidomethyl (+57)	K.NTVSNACLFQIAAR.L
324	336	2	1422.74	2.2	0	53.3	26.9	95.00%	R.MLGLTSVMAPFTR.D		R.MLGLTSVMAPFTR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
365	A6ZSL4_YEAS7	6.96%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	63	2	962.47	0.6	1	27	29.5	91.10%	R.FMEVPQGR.H		R.FMEVPQGR.H
527	541	2	1785.97	-0.62	1	26.9	23	95.00%	K.ITYLHDGLIVTEWVK.K		K.ITYLHDGLIVTEWVK.K
323	337	2	1486.88	1.7	0	32.2	17.9	95.00%	E.IVSAGPLVGSVLFTK.L		K.VLTYEEIVSAGPLVGSVLFTK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
366	A6ZSF8_YEAS7	8.21%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
135	143	2	1135.54	1.6	0	30	28.2	95.00%	K.TYNTAPQWR.F		K.TYNTAPQWR.F
311	322	2	1495.71	2	0	27.7	29.9	91.70%	E.FQNWMRPGAFDK.I		K.MYPDGYNETNIPDIQDWEEFQNWMRPGAFDK.I
2	14	2	1478.75	-0.42	1	56	28.4	95.00%	M.VNFDLGQVGEVFR.R		-.MVNFDLGQVGEVFR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
367	B3LJ36_YEAS1	2.36%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	79	2	1379.66	2.6	0	40.6	29.9	95.00%	K.SPLDGSFDTSNLK.R		K.SPLDGSFDTSNLK.R
67	80	2	1535.76	3	1	52.1	28.6	95.00%	K.SPLDGSFDTSNLKR.T		K.SPLDGSFDTSNLKR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
368	A6ZXF1_YEAS7	7.31%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
307	324	2	2056.96	3.1	1	52.4	29.8	95.00%	K.SFGYTWAVPNENTQNTTK.S		K.SFGYTWAVPNENTQNTTK.S
221	242	3	2506.22	3.2	1	40.2	28.9	95.00%	R.NDSSSISNNVYSSEYHPIKPLR.S		R.NDSSSISNNVYSSEYHPIKPLR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
369	A6ZP65_YEAS7	12.33%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
113	126	2	1752.78	3.1	1	34	30.5	95.00%	E.QNNYYIHCIIGTEE.L	Carbamidomethyl (+57)	K.IAEELTHYFDTANNSNVATGTSVAPEQNNYYIHCIIGTEELTQAELANEDLK.D
136	157	3	2413.07	0.86	1	29	30.6	95.00%	E.DLKDDATPSNDSMTTQAIGFDR.L	Oxidation (+16)	K.IAEELTHYFDTANNSNVATGTSVAPEQNNYYIHCIIGTEELTQAELANEDLKDDATPSNDSMTTQAIGFDR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
370	IRC8_YEAST	5.96%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
407	421	2	1744.75	1.9	0	75.6	30.6	95.00%	E.VDDDFYVGDILMTNE.L		K.MISPQQSTQNEDSYQATPLIPQVEVDDDFYVGDILMTNELQDIPQVPR.I
218	231	2	1587.68	-1.5	1	76.7	31	95.00%	K.TISSDENSNSSVIR.H	Phospho (+80)	K.TISSDENSNSSVIR.H
422	430	2	1064.6	1.7	0	41.3	23.1	95.00%	E.LQDIPQVPR.I		K.MISPQQSTQNEDSYQATPLIPQVEVDDDFYVGDILMTNELQDIPQVPR.I
368	378	2	1226.68	2.8	0	28.7	23.3	95.00%	R.INSALLPACLR.V	Carbamidomethyl (+57)	R.INSALLPACLR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
371	ERV41_YEAST	13.07%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
173	182	2	1044.58	0.18	1	60.9	26	95.00%	R.VSGELQITAK.S		R.VSGELQITAK.S
144	153	2	1184.5	2.7	1	26.1	28.7	90.90%	R.SFFDESDPNK.A		R.SFFDESDPNK.A
159	172	2	1603.76	2	0	42.6	29.2	95.00%	E.FNGCHVFGSIPVNR.V	Deamidation (+1)/ Carbamidomethyl (+57)	K.AHLPEFNGCHVFGSIPVNR.V
252	263	2	1472.66	2.4	0	67	30.3	95.00%	E.VDTNQYSVNDYR.Y		K.LGAEVDTNQYSVNDYR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
372	A7A1K8_YEAS7	21.79%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
45	61	3	1778.96	2.3	1	25.4	22.7	95.00%	K.VRGSSSLYTLVINDAGK.A		K.VRGSSSLYTLVINDAGK.A
47	61	2	1523.79	2.6	0	60.8	26.9	95.00%	R.GSSSLYTLVINDAGK.A		R.GSSSLYTLVINDAGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
373	A6ZWJ0_YEAS7	2.65%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
962	978	2	1833.01	-0.77	1	83.5	22.6	95.00%	K.IITLLGMQNYAEALVGK.T		K.IITLLGMQNYAEALVGK.T
895	917	3	2457.29	2.7	0	22.3	22.6	95.00%	R.INMGVITGDMLVNAKPLPASFNR.S		R.INMGVITGDMLVNAKPLPASFNR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
374	A7A0G2_YEAS7	22.33%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
69	85	2	1806.89	1.8	1	41.8	28.7	95.00%	E.IDFDITAPDGSVITSEK.Q		K.ECLYYDMVTEDDSLAVGYQVLTGGNFEIDFDITAPDGSVITSEK.Q
102	115	2	1684.76	0.54	0	31.9	30.6	95.00%	K.YTFCFSNNYGTALK.K	Carbamidomethyl (+57)	K.YTFCFSNNYGTALK.K

52	68	2	1783.83	2.6	0	91.9	29.7	95.00%	E.DDSLAVGYQVLTGGNFE.I		K.ECLYYDMVTEDDSLAVGYQVLTG GNFEIDFDITAPDGSVITSEK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
375	B3LSC3_YEAS1	11.23%	100%	3							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
75	90	2	1863.95	-0.75	0	60.8	26.7	95.00%	R.LQYAQVIWADAIQSMK.I		R.LQYAQVIWADAIQSMK.I
126	147	2	2344.16	2	0	84	28.2	95.00%	K.ALDYINASVAGGSDFLNDYVLK.Y		K.ALDYINASVAGGSDFLNDYVLK.Y
281	295	2	1770.82	2.3	1	39.2	29.3	95.00%	K.FASPNYVCTDEDILK.G	Carbamidomethyl (+57)	K.FASPNYVCTDEDILK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
376	A6ZPW0_YEAS7	7.04%	100%	3							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
441	450	2	1052.66	2.3	0	47.6	17.2	95.00%	R.TPGLLQLAIK.Q		R.TPGLLQLAIK.Q
388	399	2	1344.63	-0.69	1	72.3	29.6	95.00%	R.GATQNNLDDIER.A		R.GATQNNLDDIER.A
474	491	2	1892.02	2.3	0	45.1	22.2	95.00%	E.VLPNLYAAHNVTEPGAVK.T		R.TLAETAGLDVNEVLPNLYAAHNV TEPGAVK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
377	A6ZM69_YEAS7	5.87%	100%	3							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
237	247	2	1195.6	3.2	0	30.2	28.2	95.00%	R.GGVGYTWSTLR.E		R.GGVGYTWSTLR.E
288	302	2	1680.79	1.8	0	74	29.5	95.00%	E.MGSWDPTLNAFTDVK.Y		R.YPGTTVINLNATLFEFNPFEMGS WDPTLNAFTDVK.Y
495	507	2	1543.88	2.1	0	26.2	20.8	95.00%	E.YIPPLIVYIPNSR.H		R.NLTDLEYIPPLIVYIPNSR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
378	A6ZXN6_YEAS7	8.35%	100%	3							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
392	401	2	1198.57	1.9	0	28.6	28.9	94.60%	E.LQLHDMLNSE.N		K.FDASLPTEEIYAFVELQLHDMLNS ENDTLPVYQPANYQHQYSFK.L
338	346	2	1256.67	-0.81	1	41.9	25.9	95.00%	R.IENQWLLWR.K		R.IENQWLLWR.K
402	420	2	2312.09	3.1	0	56.1	29.2	95.00%	E.NDTLPVYQPANYQHQYSFK.L		K.FDASLPTEEIYAFVELQLHDMLNS ENDTLPVYQPANYQHQYSFK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
379	A6ZYP2_YEAS7	4.07%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
261	273	2	1338.73	1.8	0	36.1	24.2	95.00%	E.IIAPVTAHAGFDK.A		R.GITEPEIIAPVTAHAGFDK.A
569	579	2	1250.73	-0.49	0	54	17.9	95.00%	K.LIVGFLDALYK.L		K.LIVGFLDALYK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
380	A6ZPG3_YEAS7	16.31%	100%	3							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
53	63	2	1264.57	-0.18	1	68.2	29.8	95.00%	R.NETNNIDGNFK.S		R.NETNNIDGNFK.S
172	181	2	1177.64	2.1	0	48.4	26.2	95.00%	E.IVISNDYLNK.D		R.APLEEIVISNDYLNK.D
182	198	2	1687.86	0.88	1	25.2	26.9	92.60%	K.DLVSGGVVVSNASDKIE.I		K.DLVSGGVVVSNASDKIEINNTLEE R.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
381	YP162_YEAST	9.16%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
263	273	2	1181.56	-0.34	0	46.2	29	95.00%	K.DNNISSYGSII.-		K.DNNISSYGSII.-
241	254	2	1606.74	2.2	1	45.1	30.6	95.00%	E.TNTFLNDEIPDLSE.V		R.LHSESLTITNAENFETNTFLNDEIP DLSEVSNEVPNK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
382	A6ZPF9_YEAS7	9.57%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
33	43	2	1275.62	2.6	1	29.3	29.2	95.00%	R.QEIDDTVGIMR.D		R.QEIDDTVGIMR.D
35	43	2	1018.51	1.3	0	45.5	28	95.00%	E.IDDTVGIMR.D		R.QEIDDTVGIMR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
383	A7A0V2_YEAS7	7.87%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
583	598	2	1747.89	2.3	1	42.7	27.5	95.00%	K.IIEPPAQDPCLEAAPK.K	Carbamidomethyl (+57)	K.IIEPPAQDPCLEAAPK.K
670	682	3	1481.68	2.3	1	31	29.8	95.00%	K.RWATDGGLHFHGE.S		K.RWATDGGLHFHGESFAL.-
469	484	2	1940.78	1.2	0	37	30.1	95.00%	E.IDYIDYHDCAADINDE.V	Carbamidomethyl (+57)	K.NNFEGMEIYISGTEGNEQDIEIDYIDYHDCAADINDEVR.S
546	554	2	1118.54	2.8	0	46.4	28	95.00%	E.IDFTYAFSR.S		K.TNDIPDINADDEIDFTYAFSR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
384	A6ZVN0_YEAS7	10.57%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
322	332	2	1217.53	-0.24	1	37.3	29.6	95.00%	R.EGLCVDGPDTR.Y	Carbamidomethyl (+57)	R.EGLCVDGPDTR.Y
79	91	2	1465.8	1.8	0	38	24.3	95.00%	E.DIHILAFGDPQIK.G		R.EQWHGSHASAGNDEDIHILAFGDPQIK.G
357	368	2	1379.68	2.6	0	46.9	28.1	95.00%	E.SVSNQVLNMIFE.N		R.SQNHLSESVSNQVLNMIFENGKPGIILTGHDHEGCETVYNK.K
369	382	3	1487.74	0.86	0	23.4	28.5	94.00%	E.NGKPGIILTGHDHE.G	Deamidation (+1)	R.SQNHLSESVSNQVLNMIFENGKPGIILTGHDHEGCETVYNK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
385	A6ZTY9_YEAS7	11.82%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
94	103	2	1313.55	2.7	0	27.6	30	91.30%	K.GHFQYCFLNE.N	Carbamidomethyl (+57)	K.GHFQYCFLNENTGIETK.D
80	93	2	1517.74	2.6	1	59.7	29.1	95.00%	R.DTSHGEITLSAPYK.G		R.DTSHGEITLSAPYK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
386	A6ZZF9_YEAS7	3.26%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
76	84	2	1092.6	3.4	1	24.2	24.9	93.90%	K.TEFLAPFIR.S		K.TEFLAPFIR.S
243	254	2	1444.79	2.8	0	49	24.1	95.00%	K.YIDDQIPILIDK.V		K.YIDDQIPILIDK.V
386	394	2	1145.58	2	0	30.7	27.7	95.00%	E.VIDSQFFYK.E		K.QDEVIDSQFFYK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
387	A6ZV20_YEAS7	13.77%	100%	22

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1798	1807	2	1213.72	2.1	0	23.2	21.2	92.30%	R.QIRPPIYSLK.Q		R.QIRPPIYSLK.Q
838	871	3	3814.94	3.1	1	53.8	23.3	95.00%	R.ISFFAQSLSTPIPEPLPVDNMPTFTVLTPHYAER.I		R.ISFFAQSLSTPIPEPLPVDNMPTFTVLTPHYAER.I
445	456	2	1464.73	2.2	1	26.1	27.5	93.10%	K.LGEIPWDDVFFK.T		K.LGEIPWDDVFFK.T
1180	1192	2	1215.61	1.8	1	68.6	27.2	95.00%	E.NSGVLGDVAAGKE.Q		R.EYIFSENSGVLGDVAAGKEQTFGTLFAR.T
1066	1076	2	1276.58	1.7	0	64.6	30.2	95.00%	R.IYSALIDGHCE.I	Carbamidomethyl (+57)	R.IYSALIDGHCEILENGR.R
1281	1292	2	1248.6	2.9	1	86.4	28.9	95.00%	K.IGAGMGEQMLSR.E		K.IGAGMGEQMLSR.E
808	824	2	1999.93	1.9	1	89.2	30.2	95.00%	R.TLRAPTFFVSQDDNNFE.T		R.TLRAPTFFVSQDDNNFETEFFPR.D
1192	1201	2	1168.59	-0.28	1	52.2	27.4	95.00%	K.EQTFGTLFAR.T		K.EQTFGTLFAR.T
1102	1115	2	1662.78	1.8	1	37.3	29.7	95.00%	K.SDNQNHALIFYRGE.Y		K.SDNQNHALIFYRGEYIQLIDANQDNYLEECLK.I
1210	1226	2	2019.97	2.4	0	79.1	28.7	95.00%	K.LHYGHPDFINATFMTTR.G		K.LHYGHPDFINATFMTTR.G
1455	1463	2	1094.62	3.4	0	52.9	24	95.00%	R.IPFSILYSR.F		R.IPFSILYSR.F
1116	1130	2	1839.86	2.1	1	69	29.7	95.00%	E.YIQLIDANQDNYLEE.C		R.GEYIQLIDANQDNYLEECLK.I
1268	1280	2	1425.75	-0.019	0	69.1	26.3	95.00%	R.DLGFGTILNFTTK.I		R.DLGFGTILNFTTK.I

1089	1101	2	1296.71	0.92	0	44.2	23.9	95.00%	R.VQLSGNPILGDGK.S		R.VQLSGNPILGDGK.S
935	948	2	1701.81	-0.99	0	58.6	29.5	95.00%	K.SQIDDLPFYCIGFK.S	Carbamidomethyl (+57)	K.SQIDDLPFYCIGFK.S
811	824	2	1629.7	2.4	0	50.8	30.3	95.00%	R.APTFFVSQDDNNFE.T		R.APTFFVSQDDNNFETEFFPR.D
223	242	3	2177.12	2.1	1	60.8	26	95.00%	E.QALLSLHADYIGGDTANYKK.W		R.MSPEQALLSLHADYIGGDTANYKK.W
811	826	2	1859.79	2	1	47.9	30.7	95.00%	R.APTFFVSQDDNNFETE.F		R.APTFFVSQDDNNFETEFFPR.D
1539	1546	2	993.5	0.087	0	45.7	28.7	95.00%	R.NSWIGYVR.M		R.NSWIGYVR.M
972	981	2	1174.55	2	0	46.4	29.4	95.00%	R.TISGFMNYSR.A		R.TISGFMNYSR.A
889	896	2	977.58	3.3	1	51.5	19.9	95.00%	R.VTLLEYLK.Q		R.VTLLEYLK.Q
1193	1201	2	1039.55	2.4	0	27.7	24.8	95.00%	E.QTFGTLFAR.T		K.EQTFGTLFAR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
388	B3LMI6_YEAS1	27.33%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	136	2	1963.83	1.2	1	79.9	30.8	95.00%	E.DKGEPGYVAYVGYDTDSE.L		R.DYEPNDEHLSFCIIENDNVPPVHYPIHEDKGEPGYVAYVGYDTDSELVQELCADSTIYHM.-
141	150	2	1209.52	1.4	0	39.4	29.6	95.00%	E.LCADSTIYHM.-	Carbamidomethyl (+57)	K.GEPGYVAYVGYDTDSELVQELCADSTIYHM.-
106	118	2	1529.73	0.44	0	36.9	29.7	95.00%	E.NDNVPPVHYPIHE.D		R.DYEPNDEHLSFCIIENDNVPPVHYPIHEDK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
389	A6ZUP8_YEAS7	3.95%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
74	85	2	1345.67	1.7	1	43	28.6	95.00%	E.VDASGFRIPQQE.A		K.LSEVDASGFRIPQQEATNK.A
517	530	2	1512.81	2.4	1	31.3	24.5	95.00%	E.FTPETPSPLIGILE.N		K.AVLEFTPETPSPLIGILENK.I
574	586	2	1411.65	0.69	1	40.8	30.5	95.00%	E.NFLSTTVKDDGSE.L		R.DTEFIELYENFLSTTVKDDGSELLPVSDR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
390	A6ZS93_YEAS7	7.32%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
130	144	3	1694.88	1.5	0	60.9	26.4	95.00%	E.HRPSILDGSVNEPFK.T		R.QGSSNFISYFDDMSFEHRPSILDGSVNEPFK.T
112	129	2	2191.92	1.7	1	100	30.8	95.00%	R.YRQGSSNFISYFDDMSFE.H		R.YRQGSSNFISYFDDMSFEHRPSILDGSVNEPFK.T
38	51	2	1436.64	-0.15	0	63.9	29.8	95.00%	E.LYGLDTSGNSPANE.H		R.QSITVDDEGELYGLDTSGNSPANEHTATTITQNHSVVASNGDVAFIPGTATEGNTEIVTEEVIETDDNMFK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
391	A6ZRT4_YEAS7	11.63%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
66	80	2	1587.76	0.42	1	54.3	29	95.00%	R.SKDLIDKPDDAATAE.T		R.SKDLIDKPDDAATAETTSFGWGK.K
68	80	2	1372.64	1.8	0	48.2	29.7	95.00%	K.DLIDKPDDAATAE.T		K.DLIDKPDDAATAETTSFGWGK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
392	A6ZQP7_YEAS7	16.36%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
131	142	2	1289.64	-0.22	1	67.4	28.8	95.00%	K.EILGTAQSVGCR.V	Carbamidomethyl (+57)	K.EILGTAQSVGCR.V
17	31	2	1296.71	2.9	1	37.8	23.5	95.00%	R.AVGGEVGASAALAPK.I		R.AVGGEVGASAALAPK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
393	A6ZY70_YEAS7	7.89%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

90	99	2	1049.55	2.8	0	39	26.8	95.00%	E.SLGSVIFGDR.I		K.QPESLGSVIFGDR.I
137	152	2	1776.89	-2	0	32.2	27.7	95.00%	K.SGFFQNWLVDGLPAAR.K		K.SGFFQNWLVDGLPAAR.K
217	230	2	1721.83	1.9	1	26.5	29.3	90.40%	K.TVELPYFVNHFDIE.V		K.TVELPYFVNHFDIEVEFHDR.G
243	255	2	1379.82	3.6	1	36.9	14	95.00%	R.VVGVIVNPVSIER.S		R.VVGVIVNPVSIER.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
394	A6ZZC9_YEAS7	19.50%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
34	50	2	1863.88	-0.98	1	94.9	29.4	95.00%	R.SSVGQFMTFFAETVASR.T		R.SSVGQFMTFFAETVASR.T
132	143	2	1381.62	-0.81	0	71.7	30.4	95.00%	K.YQDPSQADAIMK.V	Oxidation (+16)	K.YQDPSQADAIMK.V
24	33	2	1244.58	-1.2	1	40.8	30.1	95.00%	K.DLSQFGFFER.S		K.DLSQFGFFER.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
395	A6ZKK2_YEAS7	16.74%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
200	210	2	1091.54	-1.5	0	28.5	28.6	94.70%	R.MLSSAGVNSAR.G		R.MLSSAGVNSAR.G
50	61	2	1389.73	0.069	0	63.1	26.8	95.00%	R.AQDIYQTLPVSR.Q		R.AQDIYQTLPVSR.Q
37	49	2	1496.72	-0.88	0	110	29.7	95.00%	K.TLFSSWADSLNTR.A		K.TLFSSWADSLNTR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
396	A6ZM15_YEAS7	6.29%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
284	291	2	966.53	0.9	0	35.3	24	95.00%	K.GINFFTIR.K		K.GINFFTIR.K
60	70	2	1410.64	-0.27	0	48.2	29.4	95.00%	R.WTFWGACLQDK.D	Carbamidomethyl (+57)	R.WTFWGACLQDK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
397	A6ZVG8_YEAS7	5.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
345	358	3	1691.87	-0.092	0	29.8	26.8	95.00%	R.ISILCVDNAIHYFK.I	Carbamidomethyl (+57)	R.ISILCVDNAIHYFK.I
471	484	2	1688.78	2.3	1	31.1	30.2	95.00%	K.ETAQLLSCQDSFYK.N	Carbamidomethyl (+57)	K.ETAQLLSCQDSFYK.N
777	796	2	2114.14	0.98	1	50.6	22.5	95.00%	E.ATGTIVLPQPINATSSLFER.Y		K.NIYPDVYSLHDMADEAGLPVQTE DGEATGTIVLPQPINATSSLFER.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
398	A6ZTR4_YEAS7	1.99%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
489	500	2	1439.71	-0.78	1	48.1	28.9	95.00%	R.QIGWEGFDTFLK.T		R.QIGWEGFDTFLK.T
446	460	2	1642.9	2.7	0	66.7	22.3	95.00%	K.IIINSDDAPIANFLK.S		K.IIINSDDAPIANFLK.S
2085	2099	2	1727.76	-1.4	1	87.5	30.1	95.00%	K.YTTSEQDDQSATINR.R		K.YTTSEQDDQSATINR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
399	A6ZLI8_YEAS7	7.84%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
190	201	2	1221.68	2.6	0	38.6	23.9	95.00%	E.LASGLSFPVGFK.N		R.ELASGLSFPVGFK.N
189	201	2	1350.72	4.3	1	47	26.1	95.00%	R.ELASGLSFPVGFK.N		R.ELASGLSFPVGFK.N
121	136	2	1786.89	1.8	0	71.2	27.7	95.00%	K.GLINDPDVNNTFNINK.G		K.GLINDPDVNNTFNINK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
400	A7A0I6_YEAS7	2.02%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
797	804	2	914.56	2.8	0	30.3	23	95.00%	K.IGLWSVLK.S		K.IGLWSVLK.S
814	829	2	1813.99	-0.51	0	75.8	22	95.00%	K.LTLPVSFNEPTSLLQR.V		K.LTLPVSFNEPTSLLQR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
401	B3LGD6_YEAS1	8.39%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

247	259	2	1341.68	1.3	0	69.3	27.3	95.00%	E.STYSGVSLSSVQK.S		K.SSTFNSNNTEFSIAYGDTTFASGTWGHDQLSLNDLNITGLSFAVANETNSTVGVLGIGLPGLESTYSGVSLSSVQK.S
355	374	2	2176.18	2.3	1	77.6	21.6	95.00%	K.IPVLLDSGTTISYMPTELVK.M		K.IPVLLDSGTTISYMPTELVK.M
305	321	3	1987.05	-0.69	0	21.6	23.5	95.00%	K.YAGDLYTIPIINTLQHR.G		K.YAGDLYTIPIINTLQHR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
402	A7A281_YEAS7	13.22%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
199	225	3	2936.46	2.8	1	37	26.7	95.00%	R.FSDVYVVEPDGSETLISPDTLDKPSVK.N		R.FSDVYVVEPDGSETLISPDTLDKPSVK.N
212	225	2	1512.84	1.4	0	55.7	22	95.00%	E.TLISPDTLDKPSVK.N		R.FSDVYVVEPDGSETLISPDTLDKPSVK.N
232	243	2	1349.68	2.6	0	48.8	28.4	95.00%	R.IPASVWNMTFGK.S		R.IPASVWNMTFGK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
403	A6ZLA3_YEAS7	2.93%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
109	119	2	1500.7	-0.42	1	30.1	29.3	95.00%	K.QEYPWFLDTFR.S		K.QEYPWFLDTFR.S
111	119	2	1243.61	2.7	0	32.5	28.5	95.00%	E.YPWFLDTFR.S		K.QEYPWFLDTFR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
404	A6ZZN6_YEAS7	6.89%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
68	81	3	1428.8	1.9	1	23.6	23.2	95.00%	E.LSKVDNQIGASIGK.I		K.IGSLDTLIVESEELSKVDNQIGASIGK.I
30	42	2	1494.71	1.6	1	50.2	29.6	95.00%	K.TDSWFNETLIGGR.A		K.TDSWFNETLIGGR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
405	B3LRK1_YEAS1	13.33%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
33	54	3	2164.08	1.4	1	47.2	27.7	95.00%	K.ITGQASSHLNAESPLDAPSAAK.T		K.ITGQASSHLNAESPLDAPSAAK.T
55	70	2	1649.83	1.6	1	34.3	28.9	95.00%	K.TTPPASVHSATPDIKE.D		K.TTPPASVHSATPDIKEDSNVAPQLDLLK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
406	SNG1_YEAST	6.40%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
514	529	3	1572.77	-0.19	1	39.6	28.8	95.00%	K.NAMQAAEAAVAAATQR.A		K.NAMQAAEAAVAAATQR.A
10	28	2	1957.92	2	1	81.7	28.9	95.00%	E.SQYIEDPSFAAAAAFTGGR.D		K.SVGDEESQYIEDPSFAAAAAFTGGR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
407	A6ZRQ9_YEAS7	3.93%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
622	633	2	1376.68	0.43	0	63.7	28.9	95.00%	R.NTVQNNSQGFLR.E		R.NTVQNNSQGFLR.E
557	569	2	1468.66	3	0	27.4	29.4	92.00%	R.NVTAMNGSFQNMR.S		R.NVTAMNGSFQNMR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
408	A6ZM44_YEAS7	5.34%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
98	118	2	2226.1	1.9	1	97.1	28.8	95.00%	R.SVDMTSPLLTNLEAGTHANQK.K		R.SVDMTSPLLTNLEAGTHANQK.K
98	110	2	1418.7	2.7	0	30.1	28.6	95.00%	R.SVDMTSPLLTNLE.A		R.SVDMTSPLLTNLEAGTHANQK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

409	A6ZT39_YEAS7	6.28%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
92	105	2	1602.83	2.2	0	54.2	26.1	95.00%	E.LIQNTLPTSQMMAR.E		K.EIGEQINDGQVIIDNMNELIQNTLPTSQMMAR.E	
137	149	2	1410.76	1.9	1	36.3	25.4	95.00%	R.SFPSLVAVEHLGR.T		R.SFPSLVAVEHLGR.T	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
410	A6ZTY6_YEAS7	6.16%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
217	241	3	2778.41	4.9	1	32.6	25.9	95.00%	K.ALLIGNGWIDPNTQSLSYLPFAMEK.K	Deamidation (+1)	K.ALLIGNGWIDPNTQSLSYLPFAMEK.K	
313	324	2	1440.58	2.9	0	43	29.9	95.00%	K.DSYPSCGMNWPK.D	Carbamidomethyl (+57)	K.DSYPSCGMNWPK.D	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
411	A6ZKK0_YEAS7	3.56%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
271	291	2	2217.16	3.7	1	75.3	24.3	95.00%	K.LSDQASLGDLNVASPLLTFEK.L		K.LSDQASLGDLNVASPLLTFEK.L	
893	908	2	1542.72	-0.39	0	89.9	29.5	95.00%	R.TSSPSSAVSTSAGNYK.N		R.TSSPSSAVSTSAGNYK.N	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
412	A6ZW34_YEAS7	5.17%	100%	3								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
290	302	2	1509.8	2.4	0	60.7	26	95.00%	E.NVLYGNSNTLIFR.G		R.AENVLYGNSNTLIFR.G	
755	768	2	1472.65	1.1	0	71.8	30.5	95.00%	E.DAASSTQMHAMPAR.D		R.QESEANNGLINAYEDEQFSLMEPSILEDAASSTQMHAMPAR.D	
610	623	2	1415.75	3	1	54.3	26	95.00%	K.SVANELMALGNVAK.D		K.SVANELMALGNVAK.D	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
413	A6ZSL1_YEAS7	5.42%	100%	3								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
602	616	2	1868.85	2.6	1	36	30.5	95.00%	E.YVDTKDNDPILDWFE.K		K.LTDTVAVEYIEDGEYVDTKDNDPILDWFEK.L	
29	46	2	1990.89	1.8	1	103	30.6	95.00%	E.THNDSNSDSYGLPQLSEK.Y		K.HVFMGMEHELNPETHNDSNSDSYGLPQLSEK.Y	
607	617	2	1390.64	-0.53	1	53.7	29.9	95.00%	K.DNDPILDWFEK.L		K.DNDPILDWFEK.L	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
414	A6ZVF2_YEAS7	8.75%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
32	41	2	1185.56	3.9	0	43.1	28.9	95.00%	R.NGYLVYACAR.R	Carbamidomethyl (+57)	R.NGYLVYACAR.R	
182	197	2	1556.85	2.4	0	61.3	24.5	95.00%	R.VINAITGGVATDIADK.R		R.VINAITGGVATDIADK.R	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
415	A6ZXK3_YEAS7	4.91%	100%	3								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
306	322	2	1825.98	-0.24	1	35	23.6	95.00%	K.NAPAIIFIDEIDSIAPK.R		K.NAPAIIFIDEIDSIAPK.R	
211	221	2	1238.57	0.5	1	45.9	30.1	95.00%	E.VGYDDIGGCRK.Q	Carbamidomethyl (+57)	R.EDEENNMNEVGYDDIGGCRK.Q	
464	476	2	1374.69	-1.6	1	51.2	28.4	95.00%	R.FALGNSNPSALRE.T		R.FALGNSNPSALRETVVESVNVTWDDVGGLEEIK.E	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
416	A6ZMK8_YEAS7	14.34%	100%	3								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
118	128	2	1185.64	2.2	1	53.3	25.9	95.00%	K.LDAALLQEASR.S		K.LDAALLQEASR.S	
74	90	2	1884.05	2.2	0	89.8	20.5	95.00%	E.STNKPFQNTLLIGLPNK.N		R.IGIDETVPTTITVEDPNEVIQVNFAIESTNKPFQNTLLIGLPNK.N	
52	64	2	1414.68	0.9	1	37.7	29	95.00%	E.TVPTTITVEDPNE.V		R.IGIDETVPTTITVEDPNEVIQVNFAIESTNKPFQNTLLIGLPNK.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
417	YJ12B_YEAST	13.85%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
625	644	2	2328.01	2.3	0	83.9	31.3	95.00%	E.SDVDWSSAIDYQCPDCLIGK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.NNTITYFNESDVDWSSAIDYQCPDCLIGK.S
471	491	3	2226.08	-0.4	0	86.8	29.1	95.00%	R.SAHHIHSASSNPDINVVDAQK.R		R.SAHHIHSASSNPDINVVDAQK.R
148	167	2	2065.88	0.33	1	107	30.8	95.00%	E.SGNTFTDSSSADSDMTSTKK.Y		K.ANSQQTTTPASSAVPENPHHASPQTAQSHSPQNGPYPQQCMMTQNQANPSGWSFYGHPSMIPYTPYQMSPMYFPPGPQSQFPQYPSSVGTPLSTPSPESGNTFTDSSSADSDMTSTKK.Y
239	250	2	1411.69	2.6	0	32.7	29.3	95.00%	K.DILSVDYTDIMK.I		K.DILSVDYTDIMK.I
560	568	2	1163.53	2.7	0	33.5	29.5	95.00%	K.YGDFYWVSK.K		K.YGDFYWVSK.K
1496	1503	2	893.54	1.6	0	22.9	22.8	91.90%	K.LNVPLNPK.G		K.LNVPLNPK.G
25	39	2	1638.79	0.24	1	32.3	29.6	95.00%	K.EVHTNQDPLDVSASK.T		K.EVHTNQDPLDVSASK.T
3	24	3	2336.1	3.2	0	39.2	29.5	95.00%	E.SQQLSQHSHISHGSACASVTSK.E	Carbamidomethyl (+57)	-.MESQQLSQHSHISHGSACASVTSK.E
1093	1113	3	2202.1	2.2	1	29.1	27.6	95.00%	R.SPSIDASPPENNSSHNIVPIK.T		R.SPSIDASPPENNSSHNIVPIK.T
784	807	3	2803.42	2.6	1	58.3	27.2	95.00%	R.TQLQCSGLPNHLWFSAIEFSTIVR.N	Carbamidomethyl (+57)	R.TQLQCSGLPNHLWFSAIEFSTIVR.N
1621	1632	2	1318.73	3.3	0	51.9	24.7	95.00%	K.SQIGNIYLLNGK.V		K.SQIGNIYLLNGK.V
516	531	2	1810.95	3.6	0	28.7	25.2	95.00%	K.VLHTPNIAYDLLSLNE.L		K.VLHTPNIAYDLLSLNELAAVDITACFTK.N
308	315	2	989.52	1.9	0	40.9	27.7	95.00%	K.VACQLIMR.G	Carbamidomethyl (+57)	K.VACQLIMR.G
148	166	2	1937.78	0.46	0	109	31.1	95.00%	E.SGNTFTDSSSADSDMTSTK.K		K.ANSQQTTTPASSAVPENPHHASPQTAQSHSPQNGPYPQQCMMTQNQANPSGWSFYGHPSMIPYTPYQMSPMYFPPGPQSQFPQYPSSVGTPLSTPSPESGNTFTDSSSADSDMTSTK.K
1	24	4	2638.19	-0.1	1	28.4	29.6	95.00%	-.MESQQLSQHSHISHGSACASVTSK.E	Acetyl (+42)/ Carbamidomethyl (+57)	-.MESQQLSQHSHISHGSACASVTSK.E
570	588	2	2097.08	3.4	0	37.9	26.8	95.00%	K.YLLPSNISVPTINNVHTSE.S		K.YLLPSNISVPTINNVHTSESTR.K
532	543	2	1308.68	2.4	0	27.4	27.4	94.90%	E.LAAVDITACFTK.N	Carbamidomethyl (+57)	K.VLHTPNIAYDLLSLNELAAVDITACFTK.N
26	41	3	1739.84	2.2	1	40.4	28.5	95.00%	E.VHTNQDPLDVSASKTE.E		K.EVHTNQDPLDVSASKTEECEK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
418	A7A171_YEAS7	7.59%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
182	199	3	2049.03	1.9	1	35.7	27.2	95.00%	R.WVPQRIDTVVVSAQHADE.I		R.WVPQRIDTVVVSAQHADEITTEDLR.A
136	146	2	1174.75	2.2	0	33.9	14	95.00%	E.GLPLTILLAHK.L		K.DLEDIGAGDQGIMFGYATDETPEGLPLTILLAHK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
419	A6ZX09_YEAS7	17.95%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
74	86	3	1487.8	2.4	0	45.1	24.2	95.00%	E.WHTHITAVTVAPR.F		K.TTEWHTHITAVTVAPR.F
111	119	2	1093.62	2.7	0	35.6	22.7	95.00%	E.VNFIDLFVK.C		K.LCNTLETMTDVMPHEVNFIDLFVK.C
2	14	2	1575.82	3.4	0	33.9	26.6	95.00%	M.TTIQPFEPVDLFK.T	Acetyl (+42)	-.MTTIQPFEPVDLFK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
420	A6ZMB7_YEAS7	3.93%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
163	173	3	1389.7	1.7	0	25.2	27.9	95.00%	E.WYHDLVTDLTK.S		K.DDSFPYEYDEELSLSLSEWYHDLVTDLTK.S
458	471	2	1706.91	2.3	0	34.7	24.3	95.00%	R.DTLYVRPQSNFVIR.F		R.DTLYVRPQSNFVIR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
421	PLB2_YEAST	5.24%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
362	385	2	2730.23	0.54	1	58.5	29.1	95.00%	K.YVNNLSQDDDDIAIYAANPFKDTE.F		K.YVNNLSQDDDDIAIYAANPFKDTEFVDR.N
497	509	2	1515.87	2.4	0	22.6	20.5	91.30%	E.YIPPLVVYIPNTK.H		K.NLTDLEYIPPLVVYIPNTK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
422	B3LKX9_YEAS1	15.69%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
113	129	4	1916.07	2	1	16.4	22	93.30%	E.HGLKPSKDFPHLIVSNK.A		K.EHGLKPSKDFPHLIVSNK.A
2	27	3	2341.19	2.1	0	48.2	26.2	95.00%	M.SAVGPGSNAGASVNGGSATAIATLLR.N	Acetyl (+42)/ Deamidation (+1)	-.MSAVGPGSNAGASVNGGSATAIATLLR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
423	YD206_YEAST	3.41%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
263	276	3	1525.81	1.6	1	27.4	25.2	95.00%	E.DNAISLDPTRLPSK.S		R.YVRPLGDTQIDEDNAISLDPTRLPSK.S
251	262	2	1404.69	1.9	0	39.2	28.5	95.00%	R.YVRPLGDTQIDE.D		R.YVRPLGDTQIDEDNAISLDPTR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
424	COS5_YEAST	25.59%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
157	167	2	1275.75	3.6	1	33.3	20.9	95.00%	R.TTLLEPFSLKK.D		R.TTLLEPFSLKK.D
143	156	2	1786.76	-0.73	1	72.9	30.5	95.00%	R.YFFFNAMGCQEAFR.T	Carbamidomethyl (+57)	R.YFFFNAMGCQEAFR.T
143	153	2	1412.56	3	0	35.9	29.7	95.00%	R.YFFFNAMGCQE.A	Carbamidomethyl (+57)	R.YFFFNAMGCQEAFR.T
113	123	2	1283.51	1.9	0	33.8	29.2	95.00%	E.NTPSSDPHDWE.V		K.EVTENTPSSDPHDWEVVAANLNSYLYENK.A
22	33	2	1442.83	2.4	1	38.4	19.2	95.00%	E.SQKIVLPQDLFR.S		K.QLESQKIVLPQDLFR.S
354	369	2	2001.08	-0.26	1	27.3	23.1	95.00%	K.SMWLLPLNVELWPYIK.E		K.SMWLLPLNVELWPYIK.E
102	109	2	1064.54	2.8	1	38.7	28.6	95.00%	K.QLIQFCKE.V	Carbamidomethyl (+57)	K.QLIQFCKEVTENTPSSDPHDWEVVAANLNSYLYENK.A
25	33	2	1099.64	-0.29	0	24.9	23.4	94.80%	K.IVLPQDLFR.S		K.IVLPQDLFR.S
206	219	2	1553.81	3.3	1	69.3	25.8	95.00%	K.SWSPVGLEDVQLPK.D		K.SWSPVGLEDVQLPK.D
157	166	2	1147.65	4.2	0	35.1	23.1	95.00%	R.TTLLEPFSLK.K		R.TTLLEPFSLK.K
124	135	2	1354.68	2.3	0	35.5	27.8	95.00%	E.VVAANLNSYLYE.N		K.EVTENTPSSDPHDWEVVAANLNSYLYENK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
425	A7A1I1_YEAS7	5.58%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
424	437	2	1648.83	1.6	0	27.4	28.1	94.10%	R.LMFNGLFPQPLTDR.K	Deamidation (+1)	R.LMFNGLFPQPLTDR.K
106	116	2	1424.64	0.42	0	31	30.4	95.00%	R.LQSHWSTFYQE.Q		R.LQSHWSTFYQEQDFANIASQGFNLVR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
426	B3LMC0_YEAS1	2.14%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
933	943	2	1290.76	-0.41	0	42.3	18.9	95.00%	R.LTLDIPVVFFK.C		R.LTLDIPVVFFK.C

607	617	2	1253.55	0.38	1	55.2	30	95.00%	R.DTTGDFSENIR.T		R.DTTGDFSENIR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
427	A6ZXD4_YEAS7	5.87%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
21	43	4	2564.26	0.72	1	29.2	27.6	95.00%	R.AHQLAQDFNSKQDDTALTSLPHK.N		R.AHQLAQDFNSKQDDTALTSLPHK.N
4	20	3	1866.92	-0.37	1	74.8	28.4	95.00%	R.SNKPLTQEANSSAHIDR.A		R.SNKPLTQEANSSAHIDR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
428	A6ZT94_YEAS7	5.41%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
194	211	2	2043.03	-1.7	1	42.3	27	95.00%	R.ASLPNEPICTENLTPFIK.L	Carbamidomethyl (+57)	R.ASLPNEPICTENLTPFIK.L
275	289	3	1661.93	2.4	1	27.3	22.1	95.00%	R.GERPIPKPLDGNTLR.C		R.GERPIPKPLDGNTLR.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
429	A6ZZ10_YEAS7	9.38%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
85	98	2	1671.8	-1	1	28.9	29.4	94.30%	R.AMPALMELYSIYDR.S		R.AMPALMELYSIYDR.S
291	308	2	1718.84	-0.3	0	113	28.4	95.00%	R.LGTAPATLSQTSGTDSGR.A		R.LGTAPATLSQTSGTDSGR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
430	B5VMB7_YEAST	3.44%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
159	168	2	1220.57	4.3	0	63.5	29.5	95.00%	E.TGFYCVTAFR.S	Carbamidomethyl (+57)	K.ETGFYCVTAFR.S
175	182	2	965.51	3.2	0	31.2	27.5	95.00%	K.FNAVVNFR.N		K.FNAVVNFR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
431	A6ZQ13_YEAS7	3.82%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
291	299	2	1115.48	0.87	1	42.2	29	95.00%	E.SQTFDDFKE.V		K.TGLLESQTFDDFKEVENK.I
121	130	2	1150.6	4.1	0	38.4	26.9	95.00%	R.NLNSVLNYSK.F		R.NLNSVLNYSK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
432	A7A1T7_YEAS7	9.89%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
246	259	2	1558.81	3.9	1	27.7	27	95.00%	R.SRPTVIYANAPIEE.K		R.SRPTVIYANAPIEEKPLI.-
38	49	2	1469.69	2.1	1	32	29.8	95.00%	K.IYCAELDLSQMK.V	Carbamidomethyl (+57)	K.IYCAELDLSQMK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
433	A6ZQ18_YEAS7	5.26%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
225	242	2	2054.03	1.6	1	34.6	27	95.00%	R.MLPLPIANPNDFLPEDMK.Q		R.MLPLPIANPNDFLPEDMK.Q
53	77	3	2288.11	-1.2	1	122	28.4	95.00%	R.KRPTSPSISGSGSGGNSPSSSAGAR.Q		R.KRPTSPSISGSGSGGNSPSSSAGAR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
434	A6ZZL6_YEAS7	3.75%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
247	257	2	1224.65	3.3	0	45.1	25.1	95.00%	K.IGGFVTNLNYK.D		K.IGGFVTNLNYK.D
4	14	2	1322.62	2.4	0	37	29.1	95.00%	K.YLNSFVDHLSE.W		K.YLNSFVDHLSEWSSR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
435	A6ZM25_YEAS7	4.75%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
428	437	2	1145.59	1.3	0	74.9	27.8	95.00%	E.LDMIAQNVSR.S		K.IAPYSISVDLTNQEYELDMIAQNVSR.S
400	410	2	1254.59	3.5	1	66.6	29.4	95.00%	K.GFQDFEQLGSK.K		K.GFQDFEQLGSK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
436	A6ZND7_YEAS7	12.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
265	286	2	2027.99	2	0	107	28.7	95.00%	E.AATAATGNGNTGNSGPTSLPLR.G	Deamidation (+1)	R.ATVEAATAATGNGNTGNSGPTSLPLR.G
244	260	2	1569.83	2.8	0	26.1	26	95.00%	R.ANVAIAANAATNTAAAR.A		R.ANVAIAANAATNTAAAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
437	A7A0L8_YEAS7	1.21%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
435	452	2	1872.87	1.7	0	62.8	29.6	95.00%	E.DSPTPTASSNIEPQTSNK.S		K.LGMSEDSPTPTASSNIEPQTSNK.S
1292	1311	2	2281.13	0.99	1	27.5	26.9	95.00%	E.NIGLLFNIDRDPLPQDDTPE.L		R.EGQLSSNLNFDGSSQQLYLVENIGLLFNIDRDPLPQDDTPELK.V

Supplementary Table S2: All "Scaffold" validated proteins and peptides identified from solprotSP (*S.pombe*) and from SCVMprot (*S.cerevisiae*) samples

***S.cervisiae* - Chymotrypsin digest of large tryptic peptides (Replicate A)**

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
1	VTC3_YEAST	58.32%	100%	50								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
821	835	2	1732.94	1.3	1	35.4	27.6	95.00%	R.TLKPIQDFIFNLVGE.-		R.TLKPIQDFIFNLVGE.-	
227	252	3	2927.39	-0.65	1	73.2	32.1	95.00%	R.HLPALVYASVPNENDDFVDNLESDVR.V		R.HLPALVYASVPNENDDFVDNLESDVR.V	
611	631	3	2450.99	0.87	0	38.3	34.2	95.00%	R.HVIADLEDHESSDEEGTALPK.K	Phospho (+80)/ Phospho (+80)	R.HVIADLEDHESSDEEGTALPK.K	
459	477	3	2301.09	-0.14	1	48.3	32.9	95.00%	R.NPENWHRDDIDSNIPNPLR.F		R.NPENWHRDDIDSNIPNPLR.F	
389	400	3	1416.76	-0.14	1	38.6	29.4	95.00%	R.GTQKEELEKLSR.D		R.GTQKEELEKLSR.D	
806	820	2	1637.89	1.1	1	76.5	26.9	95.00%	R.ERGLVNVSSQPSLPR.T		R.ERGLVNVSSQPSLPR.T	
330	340	2	1329.76	1.3	1	49.3	27.1	95.00%	K.LLDKPDIFLEK.R		K.LLDKPDIFLEK.R	
316	323	2	813.47	-0.4	0	31.9	25.2	95.00%	K.ISGAPTLR.L		K.ISGAPTLR.L	
437	453	2	2010.99	-0.0046	1	61.4	32.2	95.00%	R.VTIDSNIMYIREDSLDK.N		R.VTIDSNIMYIREDSLDK.N	
101	112	2	1476.65	0.68	0	71.2	33.8	95.00%	K.NTLEECLDEAQR.L	Carbamidomethyl (+57)	K.NTLEECLDEAQR.L	
234	252	2	2133.95	2.9	1	101	33.8	95.00%	Y.ASVPNENDDFVDNLESDVR.V		R.HLPALVYASVPNENDDFVDNLESDVR.V	
63	70	2	984.53	-0.21	1	27.3	26.6	95.00%	K.VYTFQISK.Y		K.VYTFQISK.Y	
234	258	3	2814.31	2.2	1	63.7	32.5	95.00%	Y.ASVPNENDDFVDNLESDVRVQPEAR.L		R.HLPALVYASVPNENDDFVDNLESDVRVQPEAR.L	
487	495	2	1112.56	0.34	1	34.3	30.7	95.00%	K.FPYSVMEIK.V		K.FPYSVMEIK.V	
401	413	2	1609.77	2.3	1	75.6	33.2	95.00%	R.DFDNIQNFIVEEK.L		R.DFDNIQNFIVEEK.L	
143	148	2	715.42	1.1	0	25.5	28.2	90.80%	K.SLLQVR.L	Deamidation (+1)	K.SLLQVR.L	
560	569	2	1235.53	1.6	1	37.8	32.3	95.00%	K.NPQEAYEEEK.K		K.NPQEAYEEEK.K	
611	632	2	2579.09	0.82	1	37.6	34	95.00%	R.HVIADLEDHESSDEEGTALPKK.S	Phospho (+80)/ Phospho (+80)	R.HVIADLEDHESSDEEGTALPKK.S	
119	126	2	938.52	0.61	1	38.3	26.9	95.00%	R.LNFTGFIK.I		R.LNFTGFIK.I	
437	447	2	1323.69	0.67	1	43.8	30.7	95.00%	R.VTIDSNIMYIR.E		R.VTIDSNIMYIR.E	
48	58	2	1265.58	1.4	1	55.2	32.2	95.00%	R.NESDFVEALDK.E		R.NESDFVEALDK.E	
409	419	2	1322.79	1.7	1	45.6	19.9	95.00%	F.IVEEKLQPVLR.A		R.DFDNIQNFIVEEKLQPVLR.A	
7	16	2	1201.61	-0.85	1	43.6	30.5	95.00%	K.LANDVYPPWK.D		K.LANDVYPPWK.D	
512	524	2	1464.76	-0.9	0	57.6	31.2	95.00%	K.DLTNSHLVNEVPK.F		K.DLTNSHLVNEVPK.F	
194	206	2	1493.72	1.6	1	58.5	32.7	95.00%	K.LSHFSNLEDASFK.S		K.LSHFSNLEDASFK.S	
77	86	2	1203.6	0.89	1	38.6	31.3	95.00%	R.KLDDLEENTK.S		R.KLDDLEENTK.S	
529	541	2	1377.68	2	1	74.9	32	95.00%	Y.LQGVASLFGEDDK.Y		K.FSLYLQGVASLFGEDDK.Y	
808	820	2	1352.74	0.73	0	52.5	26.8	95.00%	R.GLVNVSSQPSLPR.T		R.GLVNVSSQPSLPR.T	
27	38	3	1393.8	0.14	1	43.1	23.3	95.00%	K.KLLKESVIHDGR.S		K.KLLKESVIHDGR.S	
265	282	2	1849.83	-0.0019	0	91.9	34.1	95.00%	K.SNSLSSDGNSNQDVEIGK.S		K.SNSLSSDGNSNQDVEIGK.S	
550	559	3	1198.66	1.7	1	22.3	27.2	94.10%	W.LPDLETDIRK.N		K.YVNILPFWLPDLETDIRK.N	
306	312	2	940.44	-0.24	1	37.8	31	95.00%	F.FDLYNNR.L		K.SVIFPQSYDPTITTLYFDNDFFDLYNNR.L	
591	601	2	1201.63	-1.4	1	29.4	29.9	94.10%	K.ISVPDGKTTER.Q		K.ISVPDGKTTER.Q	
699	705	2	886.47	-0.031	1	25.2	27.6	91.30%	K.VWLANER.T		K.VWLANER.T	
210	221	2	1547.71	1.2	1	50.6	33.2	95.00%	K.FWVHDDNIMEVK.A	Oxidation (+16)	K.FWVHDDNIMEVK.A	
101	118	3	2237	0.72	2	37.4	34.4	95.00%	K.NTLEECLDEAQRLDNFDR.L	Carbamidomethyl (+57)	K.NTLEECLDEAQRLDNFDR.L	
344	358	2	1712.75	1.2	1	77.5	33.8	95.00%	F.TENTETGNSSFEEIR.L		R.TFTENTETGNSSFEEIR.L	
481	489	2	1060.49	2	2	39.7	31.6	95.00%	R.AGEYSKFPY.S		R.AGEYSKFPYSVMEIK.V	
28	38	2	1265.71	-0.57	1	64.2	26.5	95.00%	K.LLKESVIHDGR.S		K.LLKESVIHDGR.S	
542	548	2	864.48	2.9	1	38.6	29.4	95.00%	K.YVNILPF.W		K.YVNILPFWLPDLETDIR.K	
17	24	2	1059.45	0.65	1	29	31.7	90.70%	K.DSYIDYER.L		K.DSYIDYER.L	
45	58	2	1637.76	1	2	53.5	33.3	95.00%	W.SERNESDFVEALDK.E		R.SSVDSWSERNESDFVEALDK.E	
379	386	2	1032.57	0.38	1	33.9	27.6	95.00%	K.NYLINQLR.E		K.NYLINQLR.E	
39	47	2	1051.46	0.65	1	32.4	30.1	95.00%	R.SSVDSWSER.N		R.SSVDSWSER.N	
655	681	2	2853.25	-1.6	1	56.8	33	95.00%	K.NISENGNDPYSDDTDSASSFQLPPGVK.K		K.NISENGNDPYSDDTDSASSFQLPPGVK.K	
549	559	2	1384.74	1.8	1	56	28.6	95.00%	F.WLPDLETDIRK.N		K.YVNILPFWLPDLETDIRK.N	
425	436	2	1331.68	-0.39	1	43	31.2	95.00%	R.TAFQIPGDQSIR.V		R.TAFQIPGDQSIR.V	

591	597	2	714.39	2.1	0	25.8	23.6	95.00%	K.ISVPDGK.T		K.ISVPDGK.T
496	511	2	1977.92	-0.35	1	78.6	33.5	95.00%	K.VINQDNSQMPNYEWIK.D		K.VINQDNSQMPNYEWIK.D
342	358	2	1960.87	1.2	1	102	34.2	95.00%	R.TFTENTETGNSSFEEIR.L		R.TFTENTETGNSSFEEIR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
2	A6ZPV7_YEAS7	50.76%	100%	43

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
540	560	2	2061.93	1.8	1	55.1	33.8	95.00%	Y.GATSAPTSNTNHVVESANAAY.Y	Deamidation (+1)	R.SDNEDNDFDEDDEDDAALVAAM TNAPGNSLDIEESVGYGATSAPTSN TNHVVESANAAYYQR.K
429	442	2	1679.86	-0.66	1	82.3	31.1	95.00%	K.LQTQLGQEPPEWVR.E		K.LQTQLGQEPPEWVR.E
201	212	2	1513.76	1.2	1	56.8	31.4	95.00%	K.YWVHPDNITELK.L		K.YWVHPDNITELK.L
74	86	2	1578.85	-1.3	1	72.5	28.5	95.00%	R.VKEVQEQVQHTVR.L		R.VKEVQEQVQHTVR.L
269	280	2	1311.62	2.1	1	45.1	32.3	95.00%	Y.GGMSTDTIFVER.K		R.WYGGMSTDTIFVER.K
324	348	3	2876.46	-0.62	2	75.4	29.2	95.00%	K.EGKKPMNEIENLEALASEIQYVML K.K		K.EGKKPMNEIENLEALASEIQYVML K.K
362	371	2	1074.55	0.99	1	43.2	30.4	95.00%	R.TAFQLPGDAR.V		R.TAFQLPGDAR.V
401	415	2	1775.88	1.7	1	38.7	32.3	95.00%	R.TDIGVDWPFKQLDDK.D		R.TDIGVDWPFKQLDDK.D
443	455	2	1402.78	1.9	0	75.1	27.2	95.00%	R.ELVGSHLVEPVPK.F		R.ELVGSHLVEPVPK.F
327	348	2	2562.31	-0.043	1	87.8	29.9	95.00%	K.KPMNEIENLEALASEIQYVMLK.K		K.KPMNEIENLEALASEIQYVMLK.K
540	561	2	2224.99	2	1	69.7	33.9	95.00%	Y.GATSAPTSNTNHVVESANAAYY. Q	Deamidation (+1)	R.SDNEDNDFDEDDEDDAALVAAM TNAPGNSLDIEESVGYGATSAPTSN TNHVVESANAAYYQR.K
323	344	3	2533.28	2	2	34.7	30.3	95.00%	R.KEGKKPMNEIENLEALASEIQY.V		R.KEGKKPMNEIENLEALASEIQYV MLK.K
401	410	2	1176.58	-0.79	1	37.5	31.9	95.00%	R.TDIGVDWPFK.Q		R.TDIGVDWPFK.Q
598	606	2	1037.52	0.65	1	36.2	31.2	95.00%	K.GTTFDTQIR.A		K.GTTFDTQIR.A
312	320	2	1069.54	-0.76	1	34.7	30.1	95.00%	K.YTVDQVFAK.M		K.YTVDQVFAK.M
324	344	2	2421.18	0.77	2	43.1	31.9	95.00%	K.EGKKPMNEIENLEALASEIQY.V	Oxidation (+16)	K.EGKKPMNEIENLEALASEIQYVML K.K
400	410	2	1332.68	1.5	2	51.4	31.1	95.00%	R.RTDIGVDWPFK.Q		R.RTDIGVDWPFK.Q
301	309	3	1156.6	0.86	2	29.1	29.8	95.00%	K.ERHVNDFLK.G		K.ERHVNDFLK.G
411	422	2	1568.73	1.5	2	57	33.5	95.00%	K.QLDDKDICRFPY.A	Carbamidomethyl (+57)	K.QLDDKDICRFPYAVLEVK.L
327	344	2	2091.02	1.9	1	72.9	32.5	95.00%	K.KPMNEIENLEALASEIQY.V		K.KPMNEIENLEALASEIQYVMLK.K
477	486	2	1271.64	2.2	1	40.3	31.1	95.00%	F.WLPQMDVDIR.K		K.VDSIPFWLPQMDVDIR.K
36	58	2	2750.3	2.5	1	92.7	32.5	95.00%	K.NNGQWTQELETDFLESLEIELDK. V		K.NNGQWTQELETDFLESLEIELDK. V
567	574	2	871.44	2.4	0	28.3	26.8	95.00%	R.NAENPISK.K		R.NAENPISK.K
327	349	3	2690.4	-0.48	1	69.9	27.4	95.00%	K.KPMNEIENLEALASEIQYVMLKK. K		K.KPMNEIENLEALASEIQYVMLKK. K
76	86	2	1351.69	1	0	51.3	32.1	95.00%	K.EVQEQVQHTVR.L		K.EVQEQVQHTVR.L
254	264	3	1280.66	1.9	1	46.1	31	95.00%	R.LRKDEGAEAHR.L		R.LRKDEGAEAHR.L
73	86	3	1734.95	1.6	1	61.8	27.2	95.00%	R.RVKEVQEQVQHTVR.L		R.RVKEVQEQVQHTVR.L
282	291	2	1257.58	1	2	41.3	32.7	95.00%	K.THREDWTGEK.S		K.THREDWTGEK.S
420	428	2	1064.59	2	1	47.2	27.6	95.00%	R.FPYAVLEVK.L		R.FPYAVLEVK.L
540	563	3	2509.16	3.5	1	44.7	33.6	95.00%	Y.GATSAPTSNTNHVVESANAAYYQ R.K	Deamidation (+1)	R.SDNEDNDFDEDDEDDAALVAAM TNAPGNSLDIEESVGYGATSAPTSN TNHVVESANAAYYQR.K
138	149	3	1403.83	1.9	1	44.9	20.2	95.00%	K.TGFILKPVFQVR.L		K.TGFILKPVFQVR.L
141	149	3	1098.69	1.7	1	38.3	21.5	95.00%	F.ILKPVFQVR.L		K.TGFILKPVFQVR.L
122	129	2	969.49	-0.013	1	43.3	29.6	95.00%	R.LNYTGFQK.I		R.LNYTGFQK.I
374	384	2	1276.67	1.7	0	67.5	30.6	95.00%	R.ISLDTELTMVR.E		R.ISLDTELTMVR.E
167	175	2	1077.58	0.45	1	41.3	29.7	95.00%	K.ISQLYDIAR.T		K.ISQLYDIAR.T
612	622	2	1296.72	0.7	1	28.9	26.7	95.00%	K.TICVPVRVEPK.V	Carbamidomethyl (+57)	K.TICVPVRVEPK.V
374	393	2	2324.1	-0.14	2	40.7	32.9	95.00%	R.ISLDTELTMVREDNFDGVDR.T		R.ISLDTELTMVREDNFDGVDR.T
20	35	2	1881.92	2	1	72.2	32.4	95.00%	Y.ISYDDLKTELEDNLSK.N		R.QYSYYYISYDDLKTELEDNLSK.N
3	9	2	816.41	0.46	1	28.5	29.9	93.00%	K.FGEHLSK.S		K.FGEHLSK.S
385	393	2	1065.44	0.53	1	30.6	31.2	94.00%	R.EDNFDGVDR.T		R.EDNFDGVDR.T
584	594	2	1322.59	1.2	1	51	33.3	95.00%	F.DHYFNGDQISK.I		K.YYEIVAFFDHYFNGDQISK.I

487	501	2	1687.97	0.69	0	23.7	22.2	93.00%	R.KPPLPTNIEITRPGR.S		R.KPPLPTNIEITRPGR.S
218	230	3	1556.84	2.2	2	22.6	29	91.60%	K.HLPVLVFNTNKEF.E		K.HLPVLVFNTNKEFER.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
3	PMA1_YEAST	42.48%	100%	40

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
483	498	2	1921.84	1.8	1	56.4	33.8	95.00%	K.TVEEDHPIPEDVHENY.E		K.TVEEDHPIPEDVHENYENK.V
388	414	3	2960.42	-0.43	1	46.9	31.2	95.00%	K.LSLHEPYTVEGVSPDDLMLTACLAASR.K	Oxidation (+16)/ Carbamidomethyl (+57)	K.LSLHEPYTVEGVSPDDLMLTACLAASR.K
457	474	2	1999.08	2.1	1	75.2	27.6	95.00%	K.KVTAVVESPEGERIVCVK.G	Carbamidomethyl (+57)	K.KVTAVVESPEGERIVCVK.G
80	95	2	1764.88	2.4	1	87.5	32.1	95.00%	Y.LQTDPSYGLTSDEVLK.R		K.TYDDAASESSDDDDIDALIEELQSNHGVDDEDSDNDGPVAAGEARPVPEEYLQTDPSYGLTSDEVLK.R
458	469	2	1271.64	-0.1	0	48.2	31.1	95.00%	K.VTAVVESPEGER.I		K.VTAVVESPEGER.I
175	184	2	1056.63	0.26	0	70	25.9	95.00%	K.TLANTAVVIR.D		K.TLANTAVVIR.D
80	96	2	1920.98	1.5	1	92.8	31.1	95.00%	Y.LQTDPSYGLTSDEVLKR.R		K.TYDDAASESSDDDDIDALIEELQSNHGVDDEDSDNDGPVAAGEARPVPEEYLQTDPSYGLTSDEVLKR.R
644	659	2	1544.78	1	1	121	30.9	95.00%	K.KADTGIAVEGATDAAR.S		K.KADTGIAVEGATDAAR.S
502	508	2	744.41	1.4	0	34.7	30.3	95.00%	K.VAELASR.G		K.VAELASR.G
483	501	2	2293.01	-0.099	1	74.9	33.9	95.00%	K.TVEEDHPIPEDVHENYENK.V		K.TVEEDHPIPEDVHENYENK.V
388	394	2	857.43	2	1	27.7	28.2	94.10%	K.LSLHEPY.T		K.LSLHEPYTVEGVSPDDLMLTACLAASR.K
417	424	2	858.48	0.55	1	27.3	28.1	93.70%	K.KGLDAIDK.A		K.KGLDAIDK.A
2	30	3	2942.34	2.1	2	54.1	32.8	95.00%	M.TDTSSSSSSSSASSVSAHQPTQEKPAKTY.D		-.MTDTSSSSSSSSASSVSAHQPTQEKPAKTYDDAASESSDDDDIDALIEELQSNHGVDDEDSDNDGPVAAGEARPVPEEYLQTDPSYGLTSDEVLK.R
584	615	3	3260.51	-0.56	1	92.7	32.1	95.00%	R.LGLGGGGDMPGSELADFVENADGFAEVFPQHK.Y		R.LGLGGGGDMPGSELADFVENADGFAEVFPQHK.Y
616	625	2	1288.72	-0.55	1	29.5	28.5	95.00%	K.YRVVEILQNR.G		K.YRVVEILQNR.G
240	252	2	1455.66	-0.55	1	74.8	33.1	95.00%	K.HYGDQTFSSSTVK.R		K.HYGDQTFSSSTVK.R
223	239	2	1786.94	2.1	0	108	29.5	95.00%	F.LQIDQSAITGESLAVDK.H		R.IVTEDCFLQIDQSAITGESLAVDK.H
253	268	2	1716.78	1.6	2	70.2	34	95.00%	K.RGEGFMVVTATGDNTF.V	Oxidation (+16)	K.RGEGFMVVTATGDNTFVGR.A
899	909	2	1283.56	0.61	1	65.3	32.2	95.00%	R.SVEDFMAAMQR.V		R.SVEDFMAAMQR.V
475	482	2	843.52	1.5	1	25.8	27.3	92.80%	K.GAPLFVLK.T		K.GAPLFVLK.T
395	414	2	2105.01	-0.041	0	54.4	33.1	95.00%	Y.TVEGVSPDDLMLTACLAASR.K	Carbamidomethyl (+57)	K.LSLHEPYTVEGVSPDDLMLTACLAASR.K
667	679	2	1280.77	2	0	39.6	19.5	95.00%	F.LAPGLSAIIDALK.T		R.SAADIVFLAPGLSAIIDALK.T
457	469	2	1399.73	0.19	1	78.8	29.6	95.00%	K.KVTAVVESPEGER.I		K.KVTAVVESPEGER.I
185	215	3	3258.67	1.7	0	58.6	27.2	95.00%	R.DGQLVEIPANEVVPGDILQLEDGTVIPTDGR.I		R.DGQLVEIPANEVVPGDILQLEDGTVIPTDGR.I
584	607	2	2324.03	0.98	1	61.1	34.4	95.00%	R.LGLGGGGDMPGSELADFVENADGF.A		R.LGLGGGGDMPGSELADFVENADGFAEVFPQHK.Y
216	239	2	2651.3	-0.37	1	100	32	95.00%	R.IVTEDCFLQIDQSAITGESLAVDK.H	Carbamidomethyl (+57)	R.IVTEDCFLQIDQSAITGESLAVDK.H
483	508	3	3019.41	-1.3	1	55.4	32	95.00%	K.TVEEDHPIPEDVHENYENKVAELASR.G		K.TVEEDHPIPEDVHENYENKVAELASR.G
87	96	2	1116.62	1.6	1	32.8	29.3	95.00%	Y.GLTSDEVLKR.R		K.TYDDAASESSDDDDIDALIEELQSNHGVDDEDSDNDGPVAAGEARPVPEEYLQTDPSYGLTSDEVLKR.R
660	679	2	1984.13	1	1	67.7	23.3	95.00%	R.SAADIVFLAPGLSAIIDALK.T		R.SAADIVFLAPGLSAIIDALK.T
556	566	2	1074.57	-0.48	0	68.1	29.5	95.00%	K.MLTGDAVGIAK.E		K.MLTGDAVGIAK.E
618	625	2	969.56	1.7	0	36.1	24.8	95.00%	R.VVEILQNR.G		R.VVEILQNR.G
571	583	2	1447.74	0.68	1	84.7	31.7	95.00%	R.QLGLGTNIYNAER.L		R.QLGLGTNIYNAER.L
363	379	2	1803.93	-0.1	0	62.3	31	95.00%	K.LSAIESLAGVEILCSDK.T	Carbamidomethyl (+57)	K.LSAIESLAGVEILCSDK.T
100	109	2	1167.52	0.25	1	33.7	32.7	95.00%	K.YGLNQMADEK.E		K.YGLNQMADEK.E

645	659	2	1416.68	-0.87	0	88.8	31.9	95.00%	K.ADTGIAVEGATDAAR.S		K.ADTGIAVEGATDAAR.S
626	643	2	1806.88	-0.45	1	94.4	32.8	95.00%	R.GYLVAMTGDGVNDAPSLK.K		R.GYLVAMTGDGVNDAPSLK.K
175	215	3	4297.29	1.8	1	52	26.8	95.00%	K.TLANTAVVIRDGQLVEIPANEVVPGDILQLEDGTVIPTDGR.I		K.TLANTAVVIRDGQLVEIPANEVVPGDILQLEDGTVIPTDGR.I
418	428	2	1189.67	-0.45	2	46.2	27.9	95.00%	K.GLDAIDKAFLK.S		K.GLDAIDKAFLK.S
388	415	3	3072.52	-0.7	1	46.3	29.7	95.00%	K.LSLHEPYTVEGVSPDDLMLTACLAASRK.K	Carbamidomethyl (+57)	K.LSLHEPYTVEGVSPDDLMLTACLAASRK.K
2	28	3	2720.24	0.54	0	62.8	33.3	95.00%	M.TDTSSSSSSSSASSVSAHQPTQEKPAK.T	Acetyl (+42)	-.MTDTSSSSSSSSASSVSAHQPTQEKPAK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
4	B3LLD7_YEAS1	31.86%	100%	20

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
19	29	2	1204.52	2.4	1	38.8	32.5	95.00%	K.EHLTEGGNMAF.H		K.EHLTEGGNMAFHNHLNDFAHIEDPLER.R
481	492	2	1085.55	3	0	53.4	30.6	95.00%	R.STAHGISAASGK.V		R.STAHGISAASGK.V
48	64	2	1933.95	1.5	1	94.3	32.7	95.00%	R.LALESIDNEGFGWQQVK.T	Deamidation (+1)	R.LALESIDNEGFGWQQVK.T
47	60	2	1606.77	1.6	2	63.7	32.8	95.00%	R.RLALESIDNEGFGW.Q	Deamidation (+1)	R.RLALESIDNEGFGWQQVK.T
481	512	4	3160.64	-0.17	1	58.6	26	95.00%	R.STAHGISAASGKVGAIIAQTALGTLIDHNCAR.D	Carbamidomethyl (+57)	R.STAHGISAASGKVGAIIAQTALGTLIDHNCAR.D
109	131	2	2280.22	1.7	1	117	27.5	95.00%	K.VSTSVGTVIGQFGFGTLADIVGR.K		K.VSTSVGTVIGQFGFGTLADIVGR.K
37	45	3	1078.54	1.4	0	37.7	30.8	95.00%	F.AHIEDPLER.R		K.EHLTEGGNMAFHNHLNDFAHIEDPLER.R
298	314	2	1942.9	-0.68	1	117	33.8	95.00%	K.KIHDTSDEDMAINGLER.A		K.KIHDTSDEDMAINGLER.A
315	328	2	1464.72	-1	0	66.2	32.4	95.00%	R.ASTAVESLDNHPPK.A		R.ASTAVESLDNHPPK.A
30	45	2	1955.93	2.2	1	60.9	33.2	95.00%	F.HNHLNDFAHIEDPLER.R		K.EHLTEGGNMAFHNHLNDFAHIEDPLER.R
30	46	3	2112.03	1.6	1	44.2	32.5	95.00%	F.HNHLNDFAHIEDPLERR.R		K.EHLTEGGNMAFHNHLNDFAHIEDPLERR.R
121	131	2	1104.6	2.4	1	53.6	30	95.00%	F.GFGTLADIVGR.K		K.VSTSVGTVIGQFGFGTLADIVGR.K
19	45	3	3142.43	-0.51	1	49.2	32.7	95.00%	K.EHLTEGGNMAFHNHLNDFAHIEDPLER.R		K.EHLTEGGNMAFHNHLNDFAHIEDPLER.R
48	60	2	1450.66	1.7	1	53.8	32.9	95.00%	R.LALESIDNEGFGW.Q	Deamidation (+1)	R.LALESIDNEGFGWQQVK.T
299	314	2	1814.81	1.1	0	95.8	33.9	95.00%	K.IHDTSDEDMAINGLER.A		K.IHDTSDEDMAINGLER.A
549	569	2	2531.22	-1.1	1	85.7	32.4	95.00%	K.TLEEINELYHDEIDPATLNFR.N		K.TLEEINELYHDEIDPATLNFR.N
493	512	2	2093.11	0.96	0	127	28.8	95.00%	K.VGAIIAQTALGTLIDHNCAR.D	Carbamidomethyl (+57)	K.VGAIIAQTALGTLIDHNCAR.D
572	587	2	1754.77	0.85	0	99.7	33.4	95.00%	K.NNDIESSSPSQLQHEA.-		K.NNDIESSSPSQLQHEA.-
284	297	2	1471.72	0.94	0	87.3	32.2	95.00%	K.LELAAAAQEQDGEK.K		K.LELAAAAQEQDGEK.K
315	332	3	1977.92	1.5	2	31.1	33.6	95.00%	R.ASTAVESLDNHPPKASFK.D	Phospho (+80)	R.ASTAVESLDNHPPKASFK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
5	A7A234_YEAS7	56.76%	100%	50

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
232	245	2	1588.75	1.8	2	44.1	32.9	95.00%	Y.ANVPSENDDLVNRF.E		R.HLPVLVYANVPSENDDLVNRFESDISNNDEIVGSSSSTSSVEHGLGAR.S
309	322	3	1589.83	1.9	1	31.8	30.8	95.00%	W.TGQLSDKPDIFLEK.K		R.WTGQLSDKPDIFLEK.K
500	515	4	1888.99	1.9	2	35.1	29.4	95.00%	K.KHGQWLNDLTNSHLVK.E		K.KHGQWLNDLTNSHLVK.E
543	556	3	1724.88	1.9	1	25.1	31.2	92.00%	F.WLPDLETDIRQDPK.Q		K.LDILPFWLPDLETDIRQDPK.Q
394	401	2	1001.53	2	1	29.4	30.2	93.80%	K.NELQPVFR.T		K.NELQPVFR.T
94	102	2	1005.49	-0.03	1	50.7	30.5	95.00%	K.ALDADAFQR.V		K.ALDADAFQR.V
793	807	3	1837.97	1.6	1	27.2	29.2	95.00%	K.SRQELQIQNLEVPER.I		K.SRQELQIQNLEVPER.I
501	515	3	1760.9	1.7	1	50.2	31.6	95.00%	K.HGQWLNDLTNSHLVK.E		K.HGQWLNDLTNSHLVK.E
79	93	2	1682.89	0.76	1	53	29.1	95.00%	R.LSHLEKQTDTEAAIK.A		R.LSHLEKQTDTEAAIK.A
407	418	2	1359.71	-0.24	1	35.9	30.1	95.00%	R.TAFQIPGDDKIR.V		R.TAFQIPGDDKIR.V
7	16	2	1215.63	0.47	1	45.5	30	95.00%	K.LANEVYPPWK.G		K.LANEVYPPWK.G
750	757	2	1026.59	1.1	1	33.6	24.9	95.00%	K.RVDIIQQR.S		K.RVDIIQQR.S
144	149	2	715.42	1.1	0	25.5	28.2	90.80%	K.SLLEVR.L		K.SLLEVR.L
505	515	2	1252.68	1.7	0	39.4	27.7	95.00%	W.LNDLTNSHLVK.E		K.HGQWLNDLTNSHLVK.E

17	26	2	1142.56	-0.36	1	45.8	30.9	95.00%	K.GSYINYEGLK.K		K.GSYINYEGLK.K
469	477	2	1112.56	0.34	1	34.3	30.7	95.00%	K.FPYSVMEIK.V		K.FPYSVMEIK.V
652	669	2	1985.95	1.9	0	64.8	33	95.00%	K.LMGVDSEEEEIELPPGVK.K	Oxidation (+16)	K.LMGVDSEEEEIELPPGVK.K
103	119	2	2021.03	-0.21	1	81.7	31	95.00%	R.VLEELLSESTELDNFKR.L		R.VLEELLSESTELDNFKR.L
152	166	3	1818.88	0.94	1	26.8	32.4	93.10%	K.ELPSHSEEYSPLLYR.I		K.ELPSHSEEYSPLLYR.I
273	282	2	1181.6	2.8	1	33.6	31.5	95.00%	R.SFDPLINTLY.F		R.SFDPLINTLYFDNEHFELYNDK.L
604	628	3	2904.14	0.81	1	71.8	33.4	95.00%	R.ITSQGDLEADGSSDEETEQEPHSKR.S	Phospho (+80)/ Phospho (+80)	R.ITSQGDLEADGSSDEETEQEPHSKR.S
53	63	2	1377.7	-0.24	1	51.3	31.4	95.00%	K.FVEELDKELEK.V		K.FVEELDKELEK.V
232	244	2	1441.68	0.88	0	46.4	32.6	95.00%	Y.ANVPSENDDLVNR.F		R.HLPVLVYANVPSENDDLVNR.F
480	496	2	1745.78	-0.92	0	76.4	34.3	95.00%	K.SSLDSSMSASSMISNVK.L	Oxidation (+16)	K.SSLDSSMSASSMISNVK.L
103	118	2	1864.93	1.9	1	80	31.6	95.00%	R.VLEELLSESTELDNFK.R		R.VLEELLSESTELDNFK.R
72	78	2	938.43	0.94	1	35.9	31.8	95.00%	K.YNNLMER.L		K.YNNLMER.L
524	542	2	2078.06	1.9	2	35.1	31	95.00%	F.VQGVASLYGDDEKLDILPF.W		K.FSIFVQGVASLYGDDEKLDILPFWLPDLETDIR.Q
376	390	2	1882.86	0.41	2	52.5	33.5	95.00%	R.DLERLEEDFSEIQNF.I		R.DLERLEEDFSEIQNFIIK.N
191	204	2	1659.76	-0.14	1	69.9	33.2	95.00%	K.FSSIVSNDIDMNFR.S	Oxidation (+16)	K.FSSIVSNDIDMNFR.S
308	322	2	1775.91	2.3	1	64.4	30.8	95.00%	R.WTGQLSDKPDIFLEK.K		R.WTGQLSDKPDIFLEK.K
391	401	3	1355.8	2.1	2	48.9	24.5	95.00%	F.IIKNELQPVFR.T		R.LEEDFSEIQNFIIKNELQPVFR.T
208	219	2	1547.71	1.3	1	50.6	33.2	95.00%	K.FWVHNDNLMEVK.T	Deamidation (+1)/ Oxidation (+16)	K.FWVHNDNLMEVK.T
480	499	2	2068.02	-1.3	1	55.8	32.2	95.00%	K.SSLDSSMSASSMISNVKLPK.K		K.SSLDSSMSASSMISNVKLPK.K
308	319	2	1405.69	1.3	1	52.9	32	95.00%	R.WTGQLSDKPDIF.L		R.WTGQLSDKPDIFLEK.K
407	416	2	1090.53	0.98	1	42.7	30.8	95.00%	R.TAFQIPGDDK.I		R.TAFQIPGDDK.I
176	190	2	1522.73	-0.41	1	102	32.7	95.00%	R.SNFNTASEPLASASK.F		R.SNFNTASEPLASASK.F
448	459	2	1269.66	0.3	0	64.7	29.6	95.00%	R.TDIDANVANPLK.F		R.TDIDANVANPLK.F
687	693	2	886.47	-0.031	1	25.2	27.6	91.30%	K.VWLANER.T		K.VWLANER.T
795	818	3	2917.57	2.2	2	39.9	23.7	95.00%	R.QELQIQNLEVPERIPEVLRPLQNY.L		R.QELQIQNLEVPERIPEVLRPLQNYLFK.L
103	117	2	1736.84	1.9	1	31.3	33	92.60%	R.VLEELLSESTELDNF.K		R.VLEELLSESTELDNFK.R
323	336	2	1566.78	1.3	2	56.5	32.1	95.00%	K.KTLIEDEATGKSEF.D		K.KTLIEDEATGKSEFDLTK.L
324	336	2	1438.68	0.46	2	61.8	33.4	95.00%	K.TLIEDEATGKSEF.D		K.TLIEDEATGKSEFDLTK.L
795	807	2	1594.83	-0.89	0	61.3	29.9	95.00%	R.QELQIQNLEVPER.I		R.QELQIQNLEVPER.I
324	340	3	1895.94	1.9	2	25.9	32.6	90.90%	K.TLIEDEATGKSEFDLTK.L		K.TLIEDEATGKSEFDLTK.L
232	272	3	4303.98	1.4	2	86.2	29.1	95.00%	Y.ANVPSENDDLVNRFESDISNNDEIVGSSSSTSSVEHGLGAR.S		R.HLPVLVYANVPSENDDLVNRFESDISNNDEIVGSSSSTSSVEHGLGAR.S
587	603	2	1946.91	0.2	0	81.9	33.5	95.00%	K.EPQHQAAVPVSQEENER.I		K.EPQHQAAVPVSQEENER.I
298	305	2	870.49	1.7	0	25.7	25	95.00%	K.LNSAPTLR.L		K.LNSAPTLR.L
446	459	2	1562.82	1.5	1	63	30.7	95.00%	W.HRTDIDANVANPLK.F		R.DPNTWHRTDIDANVANPLK.F
581	603	3	2658.35	-0.22	1	60	29.8	95.00%	R.RLSNLKEPQHQAAVPVSQEENER.I		R.RLSNLKEPQHQAAVPVSQEENER.I
582	603	2	2502.24	-1.2	1	73.1	31.1	95.00%	R.LSNLKEPQHQAAVPVSQEENER.I		R.LSNLKEPQHQAAVPVSQEENER.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
6	A6ZPA7_YEAS7	35.00%	100%	34

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
143	152	2	1201.57	2.5	1	40	32.8	95.00%	R.FILQSGDEFF.L		R.FILQSGDEFFLK.G
334	352	3	2164.2	0.23	1	48	23.6	95.00%	K.ILIAEGWIPRDELATLQAR.L		K.ILIAEGWIPRDELATLQAR.L
32	42	2	1230.71	2.3	1	52.3	26.3	95.00%	Y.TLGQLGLVQFR.D		R.DSAYTLGQLGLVQFR.D
2	10	2	1133.57	0.78	2	58.8	30.6	95.00%	M.AEKEEAIFR.S	Acetyl (+42)	-.MAEKEEAIFR.S
152	163	2	1346.6	1.1	2	50.3	33.5	95.00%	F.FLKGDNTDSTSY.M		R.FILQSGDEFFLKGDNTDSTSYMDEDMIDANGENIAAAIGASVNYVTGVIAR.D
194	205	2	1470.82	-0.69	2	74.5	28.6	95.00%	R.DKVATLEQILWR.V		R.DKVATLEQILWR.V
196	205	2	1227.7	-0.014	1	46.3	27.2	95.00%	K.VATLEQILWR.V		K.VATLEQILWR.V
360	380	2	2276.21	1.7	1	74.9	28.1	95.00%	R.LGIDVPSIIQVLDTNHTPPTF.H		R.LGIDVPSIIQVLDTNHTPPTFHR.T
187	193	2	714.44	1.9	0	27.8	28.6	93.70%	Y.VTGVIAR.D		K.GDNTDSTSYMDEDMIDANGENIAAAIGASVNYVTGVIAR.D
11	27	2	1981	0.15	1	69.3	31.6	95.00%	R.SAEMALVQFYIPQEISR.D		R.SAEMALVQFYIPQEISR.D

723	733	2	1310.54	2.6	1	37.4	32	95.00%	F.CLNCVSHTASY.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.SHEPLPSTEADASSEDLEAQQLI SAMDADDAEEEEVGSGSHGEDFG DIMIHQVIHTIEFCLNCVSHTASYLR. L
121	135	2	1759.87	1.4	0	74.2	31.8	95.00%	R.LIQMEDATDQIEVQK.N		R.LIQMEDATDQIEVQK.N
121	142	2	2678.29	1.2	2	99.5	31.6	95.00%	R.LIQMEDATDQIEVQKNDLEQYR.F		R.LIQMEDATDQIEVQKNDLEQYR.F
54	60	2	877.47	0.31	1	39.4	30.4	95.00%	R.TFVNEIR.R		R.TFVNEIR.R
360	382	4	2569.37	3	1	36.5	26.8	95.00%	R.LGIDVPSIIQVLDTNHTPPTFHR.T		R.LGIDVPSIIQVLDTNHTPPTFHR.T
28	42	3	1666.87	0.79	1	59.7	29.9	95.00%	R.DSAYTLGQLGLVQFR.D		R.DSAYTLGQLGLVQFR.D
143	151	2	1054.5	1.5	1	47.8	31.8	95.00%	R.FILQSGDEF.F		R.FILQSGDEFFLK.G
32	41	2	1074.61	0.83	1	45.1	27.9	95.00%	Y.TLGQLGLVQF.R		R.DSAYTLGQLGLVQFR.D
251	270	2	2195.04	1.4	2	133	33.7	95.00%	R.KIAESLDANLYDVDSSNEGR.S		R.KIAESLDANLYDVDSSNEGR.S
386	397	2	1467.58	1.4	1	46.6	32.6	95.00%	K.FTAGFQSICDCY.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.FTAGFQSICDCYGIAQYR.E
21	31	2	1277.63	2	2	39.1	31.8	95.00%	Y.IPQEISRDSAY.T		R.SAEMALVQFYIPQEISRDSAYTLG QLGLVQFR.D
251	261	2	1235.64	1.9	2	51.8	30.8	95.00%	R.KIAESLDANLY.D		R.KIAESLDANLYDVDSSNEGR.S
209	214	2	724.39	0.78	1	31.3	27.2	95.00%	R.GNLFFK.T		R.GNLFFK.T
280	289	2	1164.64	0.25	1	44.7	27.8	95.00%	K.NLSDLYTVLK.T		K.NLSDLYTVLK.T
113	120	2	980.46	-0.024	1	52.5	30.5	95.00%	R.NASYLEER.L		R.NASYLEER.L
100	112	2	1402.71	1.8	1	49.4	31.5	95.00%	Y.VPPSGSVIDDYVR.N		K.YLDGSGELYVPPSGSVIDDYVR.N
305	315	2	1394.65	-0.087	1	65	32.8	95.00%	K.ELDSWFQDVTR.E		K.ELDSWFQDVTR.E
194	204	2	1314.72	2.6	2	51.5	28.9	95.00%	R.DKVATLEQILW.R		R.DKVATLEQILWR.V
825	840	2	1525.7	1.6	1	74.8	32.9	95.00%	Y.KDMEVAVASASSSASS.-		K.FFVGEGLPYEPFAFEYKDMEVAV ASASSSASS.-
215	226	2	1418.73	0.13	1	71.3	30.5	95.00%	K.TVEIEQPVYDVK.T		K.TVEIEQPVYDVK.T
252	270	2	2066.94	1	1	138	33.6	95.00%	K.IAESLDANLYDVDSSNEGR.S		K.IAESLDANLYDVDSSNEGR.S
290	304	2	1626.84	0.053	1	54.1	30.3	95.00%	K.TTSTTLESELYAIAK.E		K.TTSTTLESELYAIAK.E
20	31	2	1440.69	1.6	2	31.6	32.7	93.30%	F.YIPQEISRDSAY.T		R.SAEMALVQFYIPQEISRDSAYTLG QLGLVQFR.D
318	325	2	946.55	-0.031	1	49.3	26.6	95.00%	K.AIFEILNK.S		K.AIFEILNK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
7	YBT1_YEAST	31.49%	100%	55

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1456	1468	2	1499.84	1.7	2	45.3	27.2	95.00%	R.RSITIIPQDPTLFS.S		R.RSITIIPQDPTLFSGTIK.T
118	130	2	1403.71	-0.87	0	56.8	30.7	95.00%	K.VNGEPHGTPEIVR.R		K.VNGEPHGTPEIVR.R
1616	1627	2	1490.74	0.26	1	44.7	31.6	95.00%	K.EYDHPYSLLLNK.Q		K.EYDHPYSLLLNK.Q
1365	1380	2	1898.93	1.1	2	62.1	32.4	95.00%	Y.NEHKEIPPPQWPQDGK.I		K.EYMEIEQEPYNEHKEIPPPQWPQ DGK.I
1457	1473	2	1830.01	-0.44	1	57.2	26	95.00%	R.SITIIPQDPTLFSGTIK.T		R.SITIIPQDPTLFSGTIK.T
670	680	2	1321.62	0.51	1	45.7	31.9	95.00%	R.VQDFLNENDTK.K		R.VQDFLNENDTK.K
228	240	3	1519.83	1.5	1	45	28.1	95.00%	R.SIFIHHINSPISR.K		R.SIFIHHINSPISR.K
1584	1596	2	1471.78	-0.15	1	57.2	29.9	95.00%	K.EFQGSTILTIAHR.L		K.EFQGSTILTIAHR.L
901	912	2	1326.72	1.9	0	79.5	28.5	95.00%	R.NAELVVLLEDGR.V		R.NAELVVLLEDGR.V
588	597	2	1216.65	0.15	0	34.8	30.3	95.00%	R.ENELSLLLMR.S		R.ENELSLLLMR.S
115	130	3	1718.89	-0.3	1	31.2	30.4	95.00%	K.SVKVNGEPHGTPEIVR.R	Deamidation (+1)	K.SVKVNGEPHGTPEIVR.R
936	951	2	1748.78	-0.79	1	41	33.7	95.00%	K.SSILSRANSSANLAAK.S	Phospho (+80)/ Phospho (+80)	K.SSILSRANSSANLAAK.S
1422	1430	2	1020.6	0.17	1	49.3	23.5	95.00%	K.STIITALFR.F		K.STIITALFR.F
1365	1389	3	2938.5	1.1	2	35.6	28.3	95.00%	Y.NEHKEIPPPQWPQDGKIEVNDLS LR.Y		K.EYMEIEQEPYNEHKEIPPPQWPQ DGKIEVNDLSLR.Y
1431	1440	3	1169.61	-0.26	1	33.2	29.4	95.00%	R.FLEPETGHIK.I		R.FLEPETGHIK.I
1525	1544	2	2123.01	0.091	1	128	33.2	95.00%	K.FLDLSSEISEGGSNLSQGQR.Q		K.FLDLSSEISEGGSNLSQGQR.Q
1599	1615	2	1893.98	1.8	1	76.6	29.9	95.00%	R.SVIDYDKILVMDAGEVK.E		R.SVIDYDKILVMDAGEVK.E
1583	1596	3	1599.87	-0.061	2	46.9	28.4	95.00%	R.KEFQGSTILTIAHR.L		R.KEFQGSTILTIAHR.L
1494	1508	2	1684.88	1.8	0	86.1	29.5	95.00%	R.VNLISEEQLQQGATR.E		R.VNLISEEQLQQGATR.E
1353	1364	2	1556.71	0.058	2	41.5	33.3	95.00%	R.VKEYMEIEQEPY.N		R.VKEYMEIEQEPYNEHK.E
926	935	2	1105.57	0.97	1	31.2	31.2	94.70%	K.GLFGEDELVK.S		K.GLFGEDELVK.S
1559	1576	2	1923.97	0.36	1	103	31.4	95.00%	K.IILLDEATASIDYSSDAK.I		K.IILLDEATASIDYSSDAK.I

1381	1389	2	1057.58	1.3	0	48.7	29.5	95.00%	K.IEVNDLSLR.Y		K.IEVNDLSLR.Y
665	680	2	1891.93	1.6	2	79.3	32	95.00%	K.VSLDRVQDFLNENDTK.K		K.VSLDRVQDFLNENDTK.K
913	925	2	1485.75	-0.75	1	46.5	30.6	95.00%	R.VKDQGDPIDMLQK.G		R.VKDQGDPIDMLQK.G
952	963	2	1202.65	-0.011	0	49.2	29.9	95.00%	K.SSTSLSNLPAVK.E		K.SSTSLSNLPAVK.E
582	597	2	1929.04	-0.17	1	43.6	28	95.00%	K.DINTIRENELSLLLMR.S		K.DINTIRENELSLLLMR.S
1493	1508	2	1840.98	1.3	1	70.7	28.4	95.00%	K.RVNLISEEQLQQGATR.E		K.RVNLISEEQLQQGATR.E
887	900	3	1609.9	0.4	0	39.1	25.3	95.00%	R.TCILVSHNIALTLR.N	Carbamidomethyl (+57)	R.TCILVSHNIALTLR.N
915	925	2	1258.59	0.55	0	42.1	32.3	95.00%	K.DQGDPIDMLQK.G		K.DQGDPIDMLQK.G
855	872	2	2024.93	2.5	1	63.8	33.4	95.00%	R.HVLLDDCLSAVDSHTASW.I	Carbamidomethyl (+57)	R.HVLLDDCLSAVDSHTASWIYDNCITGPLMEDR.T
1606	1621	2	1877.89	1.3	2	40.4	32.9	95.00%	K.ILVMDAGEVKEYDHPY.S		K.ILVMDAGEVKEYDHPYSLLLNK.Q
1633	1649	2	1943.94	2.9	0	42.1	32.5	95.00%	Y.SMCEHSGELDILIELAK.K	Carbamidomethyl (+57)	K.QSAFYSMCEHSGELDILIELAK.K
1606	1617	2	1365.69	2.6	2	62.1	32.3	95.00%	K.ILVMDAGEVKEY.D		K.ILVMDAGEVKEYDHPYSLLLNK.Q
1633	1650	3	2072.03	1.4	1	35.3	31.1	95.00%	Y.SMCEHSGELDILIELAKK.A	Carbamidomethyl (+57)	K.QSAFYSMCEHSGELDILIELAKK.A
427	436	2	1165.66	-0.61	1	36.2	24.1	95.00%	K.SIIISEIYTK.A		K.SIIISEIYTK.A
791	803	2	1535.73	-1.4	1	64.7	32.8	95.00%	K.NNILFNSPFNEAR.Y	Deamidation (+1)	K.NNILFNSPFNEAR.Y
964	979	2	1816.83	-0.89	1	67.9	34	95.00%	K.EQQVSVNNNSSHFEAK.K		K.EQQVSVNNNSSHFEAK.K
1417	1430	3	1434.82	-0.42	2	27.4	25.2	95.00%	R.TGAGKSTIITALFR.F		R.TGAGKSTIITALFR.F
1238	1255	2	2047.08	1.7	1	98.1	29	95.00%	R.SPIYQHFSETLVGVTTIR.A		R.SPIYQHFSETLVGVTTIR.A
560	568	2	1060.57	-0.69	1	56.9	30.8	95.00%	K.LNEAFQAIR.I		K.LNEAFQAIR.I
1152	1160	2	1010.48	0.36	1	38.1	32.4	95.00%	R.FFDATPTGR.I		R.FFDATPTGR.I
1486	1492	2	847.48	1.2	1	31.5	27.4	95.00%	R.QIFEALK.R		R.QIFEALK.R
1441	1453	2	1456.75	-1.5	0	97.7	30	95.00%	K.IDNIDISGVDLQR.L		K.IDNIDISGVDLQR.L
1456	1473	2	1986.11	-1.3	2	79.9	25.3	95.00%	R.RSITIIPQDPTLFSGTIK.T		R.RSITIIPQDPTLFSGTIK.T
822	831	2	1031.51	0.85	0	47.9	30.8	95.00%	K.AGDLTEIGEK.G		K.AGDLTEIGEK.G
1474	1485	2	1470.63	-0.56	1	61.9	32.9	95.00%	K.TNLDPYDEFSDR.Q		K.TNLDPYDEFSDR.Q
1431	1453	3	2608.35	1.2	1	62.9	27.2	95.00%	R.FLEPETGHIKIDNIDISGVDLQR.L		R.FLEPETGHIKIDNIDISGVDLQR.L
1400	1410	2	1180.57	0.41	1	30.9	31.6	93.90%	K.NVSFSVDAQSK.I		K.NVSFSVDAQSK.I
447	461	3	1741.81	-0.23	0	31.8	33.5	95.00%	K.TKPSNEDPQEINDQK.S		K.TKPSNEDPQEINDQK.S
681	693	2	1532.76	-1.5	2	65.4	31.5	95.00%	K.KYDQLTIDPNGNR.F		K.KYDQLTIDPNGNR.F
557	568	2	1429.8	0.12	2	57.1	27.1	95.00%	R.IQKLNEAFQAIR.I		R.IQKLNEAFQAIR.I
855	886	3	3702.68	0.4	1	65.1	31.9	95.00%	R.HVLLDDCLSAVDSHTASWIYDNCITGPLMEDR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.HVLLDDCLSAVDSHTASWIYDNCITGPLMEDR.T
901	925	3	2794.45	0.15	1	43.1	27	95.00%	R.NAELVVLLEDGRVKDQGDPIDMLQK.G		R.NAELVVLLEDGRVKDQGDPIDMLQK.G
873	886	2	1695.76	1.4	1	73.4	33.8	95.00%	W.IYDNCITGPLMEDR.T	Carbamidomethyl (+57)	R.HVLLDDCLSAVDSHTASWIYDNCITGPLMEDR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
8	B5VNN6_YEAST	26.71%	100%	45

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1024	1046	2	2644.26	1.7	1	104	32.5	95.00%	R.AYPDLQIAYLDEEPPLTEGEEPR.I		R.AYPDLQIAYLDEEPPLTEGEEPR.I
980	992	2	1400.69	2.2	1	31.8	31.3	95.00%	F.GGNAEGLERELEK.M		R.VENPEIVQMFGGNAEGLERELEK.M
1047	1063	2	1944.94	-0.093	1	58.2	32.2	95.00%	R.IYSALIDGHCEILDNGR.R	Carbamidomethyl (+57)	R.IYSALIDGHCEILDNGR.R
1779	1788	2	1213.72	-0.84	1	34.5	24.9	95.00%	R.QIRPPIYSLK.Q		R.QIRPPIYSLK.Q
859	869	2	1406.68	-0.52	2	41.8	32.1	95.00%	R.EIIREDDQFSR.V		R.EIIREDDQFSR.V
1139	1154	2	1783.89	1.8	1	84.9	32	95.00%	R.YEEQTTNHPVAIVGAR.E		R.YEEQTTNHPVAIVGAR.E
1010	1023	3	1741.92	0.16	1	45.5	29.7	95.00%	K.FKPHELENAEFLLR.A		K.FKPHELENAEFLLR.A
778	788	3	1278.67	2.8	1	41.1	30.1	95.00%	Y.HQVPSEIEGKR.T		K.LLYHQVPSEIEGKR.T
260	288	3	3237.43	-0.22	2	80.4	33.1	95.00%	K.AMEEANPEDTEETLNKIEGDNSLEAADFR.W		K.AMEEANPEDTEETLNKIEGDNSLEAADFR.W
1117	1138	2	2473.25	-0.62	1	79	30.5	95.00%	R.SVLAEFEELNVEQVNPYAPGLR.Y		R.SVLAEFEELNVEQVNPYAPGLR.Y
1033	1046	2	1609.75	1.6	0	64.6	33.8	95.00%	Y.LDEEPPLTEGEEPR.I		R.AYPDLQIAYLDEEPPLTEGEEPR.I

970	992	3	2587.26	-0.54	1	47.4	31.8	95.00%	R.VENPEIVQMFGGNAEGLERELEK.M		R.VENPEIVQMFGGNAEGLERELEK.M
775	787	2	1511.8	-0.6	1	50.6	28.9	95.00%	K.LLYHQVPSEIEGK.R		K.LLYHQVPSEIEGK.R
58	66	2	1018.44	4.1	1	31.8	31.5	95.00%	Y.GQQPPNESY.D		-.MNTDQQPYQGQTDYTQGPDNGQSQEQDYDQYGQPLYPSQADGYYDPNVAAGTEADMYGQQPPNESYDQDYTNGEYYGQPPNMAAQDGENFSDFSSYGPPGTPGYDSYGGQYTPSQMSYGEPNSSGTSTPIYGNYDPNAIAMALPNEPYPAWTADSQSPVSIEQIEDIFIDLTNR.L
969	979	2	1360.68	1.5	2	34.7	31.5	95.00%	Y.RVENPEIVQMF.G		K.LLYRVENPEIVQMFGGNAEGLER.E
1262	1273	2	1248.6	-0.33	0	89.3	31.5	95.00%	K.IGAGMGEQMLSR.E		K.IGAGMGEQMLSR.E
893	915	2	2536.18	-1.7	1	94.3	33.2	95.00%	K.ILAEETAAYEGNENEAEKEDALK.S		K.ILAEETAAYEGNENEAEKEDALK.S
970	988	2	2088	0.32	1	88.9	33.1	95.00%	R.VENPEIVQMFGGNAEGLER.E		R.VENPEIVQMFGGNAEGLER.E
1010	1020	2	1359.65	1.8	1	29.7	31.6	92.20%	K.FKPHELENAEF.L		K.FKPHELENAEFLLR.A
77	93	2	1823.75	1.5	1	39	33.7	95.00%	Y.GQPPNMAAQDGENFSDF.S		-.MNTDQQPYQGQTDYTQGPDNGQSQEQDYDQYGQPLYPSQADGYYDPNVAAGTEADMYGQQPPNESYDQDYTNGEYYGQPPNMAAQDGENFSDFSSYGPPGTPGYDSYGGQYTPSQMSYGEPNSSGTSTPIYGNYDPNAIAMALPNEPYPAWTADSQSPVSIEQIEDIFIDLTNR.L
1173	1182	2	1168.59	-0.63	1	40.8	31.1	95.00%	K.EQTFGTLFAR.T		K.EQTFGTLFAR.T
1068	1082	2	1599.88	1.9	1	45.4	27.9	95.00%	K.FRVQLSGNPILGDGK.S		K.FRVQLSGNPILGDGK.S
44	57	2	1531.62	0.83	1	42.9	32.6	95.00%	Y.YDPNVAAGTEADMY.G	Oxidation (+16)	-.MNTDQQPYQGQTDYTQGPDNGQSQEQDYDQYGQPLYPSQADGYYDPNVAAGTEADMYGQQPPNESYDQDYTNGEYYGQPPNMAAQDGENFSDFSSYGPPGTPGYDSYGGQYTPSQMSYGEPNSSGTSTPIYGNYDPNAIAMALPNEPYPAWTADSQSPVSIEQIEDIFIDLTNR.L
1134	1154	4	2278.19	1.5	2	43.4	29.3	95.00%	Y.APGLRYEEQTTNHPVAIVGAR.E		R.SVLAEFEELNVEQVNPYAPGLRYEEQTTNHPVAIVGAR.E
1436	1444	2	1094.61	-0.2	1	48.5	25.9	95.00%	R.IPFSILYSR.F		R.IPFSILYSR.F
1095	1114	2	2427.13	2.8	1	103	33.1	95.00%	R.GEYIQLIDANQDNYLEECLK.I	Carbamidomethyl (+57)	R.GEYIQLIDANQDNYLEECLK.I
77	90	2	1490.61	2.2	1	71.2	33.5	95.00%	Y.GQPPNMAAQDGENF.S	Oxidation (+16)	-.MNTDQQPYQGQTDYTQGPDNGQSQEQDYDQYGQPLYPSQADGYYDPNVAAGTEADMYGQQPPNESYDQDYTNGEYYGQPPNMAAQDGENFSDFSSYGPPGTPGYDSYGGQYTPSQMSYGEPNSSGTSTPIYGNYDPNAIAMALPNEPYPAWTADSQSPVSIEQIEDIFIDLTNR.L
1070	1082	2	1296.7	-0.0085	0	62.1	27.4	95.00%	R.VQLSGNPILGDGK.S		R.VQLSGNPILGDGK.S
775	788	3	1667.9	0.13	1	42.1	27.9	95.00%	K.LLYHQVPSEIEGKR.T		K.LLYHQVPSEIEGKR.T
797	811	2	1843.81	2.6	1	58.8	33.8	95.00%	F.VSQDDNNFETEFFPR.D		R.APTFFVSQDDNNFETEFFPR.D
331	344	2	1737.78	-0.023	1	107	33.7	95.00%	K.CALDYLDSPLCQQR.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CALDYLDSPLCQQR.Q
184	196	2	1623.75	-0.63	1	69.7	32.8	95.00%	R.NMFDHFMVLLDSR.S		R.NMFDHFMVLLDSR.S
823	852	3	3320.68	1.7	1	26	28.1	95.00%	F.AQSLSTPIPEPLPVDNMPTFTVLTPHYAER.I		R.ISFFAQSLSTPIPEPLPVDNMPTFTVLTPHYAER.I
1717	1728	2	1383.61	-0.15	1	66	32.9	95.00%	K.GMGYMAWTQPSR.E		K.GMGYMAWTQPSR.E

200	222	3	2479.17	-0.88	1	37.7	32.3	95.00%	R.MSPDQALISLHADYIGGDTANYK.K		R.MSPDQALISLHADYIGGDTANYK.K
1098	1114	2	2078	2	1	91.3	32.8	95.00%	Y.IQLIDANQDNYLEECLK.I	Carbamidomethyl (+57)	R.GEYIQLIDANQDNYLEECLK.I
1155	1172	2	1854.9	2.5	1	88.4	32.9	95.00%	R.EYIFSENSGVLGDVAAGK.E		R.EYIFSENSGVLGDVAAGK.E
1049	1063	2	1668.79	0.49	0	56.3	33.2	95.00%	Y.SALIDGHCEILDNGR.R	Carbamidomethyl (+57)	R.IYSALIDGHCEILDNGR.R
97	107	2	1109.47	2.1	1	34.4	31.3	95.00%	Y.GPPGTPGYDSY.G		-.MNTDQQPYQGQTDYTQGPDNGQSQEQDYDQYGQPLYPSQADGYYDPNVAAGTEADMYGQQPPNESYDQDYTNGEYYGQPPNMAAQDGENFSDFSSYGPPGTPGYDSYGGQYTPSQMSYGEPNSSGTSTPIYGNYDPNAIAMALPNEPYPAWTADSQSPVSIEQIEDIFIDLTNR.L
1520	1527	2	993.5	-0.11	1	40.9	29.7	95.00%	R.NSWIGYVR.M		R.NSWIGYVR.M
953	962	2	1174.54	-0.35	1	46.5	31.9	95.00%	R.TISGFMNYSR.A		R.TISGFMNYSR.A
406	422	3	1966.1	1.9	1	44.8	23.4	95.00%	K.IVLEDGTKLIELPLEER.Y		K.IVLEDGTKLIELPLEER.Y
870	877	2	977.58	-0.012	1	44.9	19.8	95.00%	R.VTLLEYLK.Q		R.VTLLEYLK.Q
1191	1203	2	1530.73	1.9	1	66.8	33	95.00%	K.LHYGHPDFINATF.M		K.LHYGHPDFINATFMTTR.G
1117	1133	2	1978.96	1.5	1	54.2	32.9	95.00%	R.SVLAEFEELNVEQVNPY.A		R.SVLAEFEELNVEQVNPYAPGLR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
9	A6ZL63_YEAS7	58.73%	100%	27

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
321	338	2	1892.82	0.97	2	32.9	34.7	92.30%	R.GNVCGDAKNDPPKGCASF.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GNVCGDAKNDPPKGCASFNATVIVLNHPGQISAGYSPVLDCHTAHIACR.F
225	253	3	3318.82	-0.36	2	29.9	22.1	95.00%	K.TLLEAIDAIEQPSRPTDKPLRLPLQDVYK.I		K.TLLEAIDAIEQPSRPTDKPLRLPLQDVYK.I
265	278	2	1491.8	1.6	1	71.4	29.2	95.00%	R.VETGVIKPGMVVTF.A	Oxidation (+16)	R.VETGVIKPGMVVTFAPAGVTTEVK.S
402	421	2	2310.12	-0.17	1	74.3	32.5	95.00%	K.FVPSKPMCVEAFSEYPPLGR.F	Carbamidomethyl (+57)	K.FVPSKPMCVEAFSEYPPLGR.F
370	376	2	892.45	-0.82	1	41	29.1	95.00%	R.FDELLEK.N		R.FDELLEK.N
289	311	2	2549.19	-1.4	1	72.4	33	95.00%	K.SVEMHHEQLEQGVPGDNVGFNVK.N		K.SVEMHHEQLEQGVPGDNVGFNVK.N
195	210	2	1823.82	1.8	1	75.3	33.2	95.00%	W.NGDNMIEATTNAPWYK.G		K.TVPFVPISGWNGDNMIEATTNAPWYK.G
185	208	2	2617.22	2	1	59.1	33	95.00%	K.TVPFVPISGWNGDNMIEATTNAPW.Y	Deamidation (+1)	K.TVPFVPISGWNGDNMIEATTNAPWYK.G
279	288	2	971.53	2.4	0	26	28.8	90.80%	F.APAGVTTEVK.S		R.VETGVIKPGMVVTFAPAGVTTEVK.S
85	96	2	1354.7	-0.6	1	61.9	29.7	95.00%	K.YQVTVIDAPGHR.D		K.YQVTVIDAPGHR.D
195	208	2	1532.66	1.5	1	61.2	33.4	95.00%	W.NGDNMIEATTNAPW.Y		K.TVPFVPISGWNGDNMIEATTNAPWYK.G
225	252	3	3190.73	2.8	2	25.3	22.7	95.00%	K.TLLEAIDAIEQPSRPTDKPLRLPLQDVY.K		K.TLLEAIDAIEQPSRPTDKPLRLPLQDVYK.I
394	401	2	759.41	1.7	0	40.5	29.4	95.00%	K.SGDAALVK.F		K.SGDAALVK.F
254	264	2	1024.61	1.8	0	68.3	21.7	95.00%	K.IGGIGTVPVGR.V		K.IGGIGTVPVGR.V
101	129	3	2922.45	0.29	1	72.8	30.1	95.00%	K.NMITGTSQADCAILIIAGGVGEFEAGISK.D	Carbamidomethyl (+57)	K.NMITGTSQADCAILIIAGGVGEFEAGISK.D
429	437	2	913.56	-0.34	0	45.5	23.6	95.00%	R.QTVAVGVIK.S		R.QTVAVGVIK.S
339	355	2	1752.92	1.4	1	70.7	29.3	95.00%	F.NATVIVLNHPGQISAGY.S		K.GCASFNATVIVLNHPGQISAGYSPVLDCHTAHIACR.F
6	20	2	1559.85	2.3	0	97.2	29.1	95.00%	K.SHINVVVIGHVDSGK.S		K.SHINVVVIGHVDSGK.S
254	288	4	3451.91	-0.6	2	32.1	24.2	95.00%	K.IGGIGTVPVGRVETGVIKPGMVVTFAPAGVTTEVK.S	Oxidation (+16)	K.IGGIGTVPVGRVETGVIKPGMVVTFAPAGVTTEVK.S
265	288	2	2429.33	1.3	1	64.1	24.7	95.00%	R.VETGVIKPGMVVTFAPAGVTTEVK.S		R.VETGVIKPGMVVTFAPAGVTTEVK.S
246	253	2	974.54	-0.0093	1	40.2	28.4	95.00%	R.LPLQDVYK.I		R.LPLQDVYK.I

356	369	2	1635.76	0.7	0	78	33	95.00%	Y.SPVLDCHTAHIACR.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GCASFNATVIVLNHPGQISAGYS PVLDCHTAHIACR.F
101	134	3	3479.7	-0.25	1	67.9	29.5	95.00%	K.NMITGTSQADCAILIIAGGVGEFE AGISKDGQTR.E	Carbamidomethyl (+57)	K.NMITGTSQADCAILIIAGGVGEFE AGISKDGQTR.E
225	245	3	2362.29	0.93	0	49	24	95.00%	K.TLLEAIDAIEQPSRPTDKPLR.L		K.TLLEAIDAIEQPSRPTDKPLR.L
85	98	2	1616.8	2.8	2	36.3	31.3	95.00%	K.YQVTVIDAPGHRDF.I		K.YQVTVIDAPGHRDFIK.N
356	376	3	2510.21	1.6	2	35.5	32.2	95.00%	Y.SPVLDCHTAHIACRFDELLEK.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GCASFNATVIVLNHPGQISAGYS PVLDCHTAHIACRFDELLEK.N
289	308	2	2207.99	1.2	1	53.8	33.6	95.00%	K.SVEMHHEQLEQGVPGDNVGF.N		K.SVEMHHEQLEQGVPGDNVGFNV K.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
10	A6ZY95_YEAS7	29.04%	100%	37

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1251	1273	3	2569.33	1.4	2	30.5	28.2	95.00%	K.SEAPLIVEGHRPPKEWPSQGDIK. F		K.SEAPLIVEGHRPPKEWPSQGDIK. F
1036	1048	2	1466.72	-0.78	1	61.7	32.9	95.00%	R.APMTFFETTPIGR.I		R.APMTFFETTPIGR.I
1349	1364	2	1787.94	-0.62	1	36.3	29.3	95.00%	K.LSIIPQDSQVFEGTVR.E		K.LSIIPQDSQVFEGTVR.E
775	789	2	1632.85	1.5	0	64.7	30.8	95.00%	Y.LLDDPLAAVDEHVAR.H		R.ADTYLLDDPLAAVDEHVAR.H
814	842	3	3064.55	1.5	1	28.6	28.4	95.00%	K.VSALSIADSIALLDNGEITQQGTY DEITK.D		K.VSALSIADSIALLDNGEITQQGTY DEITK.D
790	805	3	1777	-0.45	0	52.9	24.3	95.00%	R.HLIEHVLGPNGLLHTK.T		R.HLIEHVLGPNGLLHTK.T
1133	1143	2	1143.63	1.5	0	64.2	28.5	95.00%	F.QETLGGLATVR.G		R.SPIYSHFQETLGGLATVR.G
1365	1380	2	1975.93	2	1	96.3	33.7	95.00%	R.ENIDPINQYTDEAIWR.A		R.ENIDPINQYTDEAIWR.A
486	495	2	1141.67	0.25	0	47.6	26.4	95.00%	R.VISEILNNIK.S		R.VISEILNNIK.S
863	875	2	1399.59	1.4	1	69.6	32.9	95.00%	K.SNEFGDSSESSVR.E		K.SNEFGDSSESSVR.E
863	890	3	3066.43	1.5	1	48.6	32.2	95.00%	K.SNEFGDSSESSVRESSIPVEGEL EQLQK.L		K.SNEFGDSSESSVRESSIPVEGEL EQLQK.L
249	261	2	1537.76	-1.3	1	48.7	32.4	95.00%	R.NFSSEELSQKLEK.N		R.NFSSEELSQKLEK.N
1281	1290	3	1244.71	-0.078	1	59.3	26.8	95.00%	R.YRPELDLVLK.H		R.YRPELDLVLK.H
1251	1264	4	1528.84	1.4	0	36.1	28.3	95.00%	K.SEAPLIVEGHRPPK.E		K.SEAPLIVEGHRPPK.E
1430	1446	2	1800.94	0.6	0	74.8	30.3	95.00%	K.ILVLDEATAAVDVETDK.V		K.ILVLDEATAAVDVETDK.V
1485	1499	2	1618.78	-0.51	1	87.8	32.3	95.00%	K.VAEFDSPGQLLSDNK.S		K.VAEFDSPGQLLSDNK.S
1347	1359	2	1510.82	1.5	2	50.1	27.4	95.00%	R.HKLSIIPQDSQVF.E		R.HKLSIIPQDSQVFEGTVR.E
192	206	3	1835.99	-0.32	0	32.5	26.8	95.00%	K.KPLMPHQHIHQTLTR.R		K.KPLMPHQHIHQTLTR.R
207	218	2	1420.71	0.75	2	56.2	32	95.00%	R.RKPNPYDSANIF.S		R.RKPNPYDSANIFSR.I
271	281	2	1289.62	0.94	1	53.4	32	95.00%	K.SNPSLSWAICR.T	Carbamidomethyl (+57)	K.SNPSLSWAICR.T
771	789	2	2083.02	-0.49	1	108	32.3	95.00%	R.ADTYLLDDPLAAVDEHVAR.H		R.ADTYLLDDPLAAVDEHVAR.H
1458	1467	3	1194.68	-0.25	1	39.9	23.2	95.00%	K.DRTILTIAHR.L		K.DRTILTIAHR.L
1126	1143	2	1975.02	0.8	1	81.1	30.9	95.00%	R.SPIYSHFQETLGGLATVR.G		R.SPIYSHFQETLGGLATVR.G
1347	1364	2	2053.09	-1.2	2	74	28.1	95.00%	R.HKLSIIPQDSQVFEGTVR.E		R.HKLSIIPQDSQVFEGTVR.E
1313	1321	2	1006.58	1.5	1	51.4	24.7	95.00%	K.SSLTLALFR.M		K.SSLTLALFR.M
249	258	2	1167.54	-0.1	1	46.1	32.5	95.00%	R.NFSSEELSQK.L		R.NFSSEELSQK.L
1460	1467	2	923.56	0.52	0	30.7	19.6	95.00%	R.TILTIAHR.L		R.TILTIAHR.L
603	614	2	1414.67	1.6	0	61.6	32.4	95.00%	F.TNEELQPDSVQR.L		R.LFTFFTNEELQPDSVQR.L
2	11	2	1146.55	-0.31	1	39.1	30.9	95.00%	M.AGNLVSWACK.L	Acetyl (+42)/ Carbamidomethyl (+57)	-.MAGNLVSWACK.L
1291	1301	3	1341.75	0.22	0	27	27.6	95.00%	K.HINIHIKPNEK.V		K.HINIHIKPNEK.V
1468	1484	2	1916	-1.8	1	71.9	29.6	95.00%	R.LNTIMDSDRIIVLDNGK.V		R.LNTIMDSDRIIVLDNGK.V
1274	1280	2	900.41	2.6	1	33.3	30.4	95.00%	K.FNNYSTR.Y		K.FNNYSTR.Y
728	743	2	1718.86	-0.17	0	83	31.5	95.00%	K.ACALTIDLAILMDGDK.T	Carbamidomethyl (+57)	K.ACALTIDLAILMDGDK.T
1389	1415	3	2783.32	2.5	0	76	32.3	95.00%	K.EHVLSMSNDGLDAQLTEGGGNL SVGQR.Q		K.EHVLSMSNDGLDAQLTEGGGNL SVGQR.Q
1381	1388	2	909.53	-0.46	0	33.8	20.2	95.00%	R.ALELSHLK.E		R.ALELSHLK.E
907	926	3	2093.99	1.6	1	55.1	32.7	95.00%	R.ASDATLGSIDFGDDENIAKR.E		R.ASDATLGSIDFGDDENIAKR.E
379	388	2	1106.63	0.35	1	24.6	25.5	93.60%	K.SALTALIYQK.S		K.SALTALIYQK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
11	B3LFI5_YEAS1	59.36%	100%	31

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
355	383	3	3092.48	1.4	1	74.1	31	95.00%	Y.VLEFAENSDTETVLVSTSDHETG GLVTSR.Q		R.EVLAFDEAFQYVLEFAENSDTET VLVSTSDHETGGLVTSR.Q

87	107	2	2481.19	2.4	1	68.4	32.6	95.00%	R.SFNQHVNDLPIDDILTLDEHF.I	R.SFNQHVNDLPIDDILTLDEHFIGSSR.T
427	438	2	1511.84	1.1	1	47.3	27	95.00%	K.IENFIKHEILEK.D	K.IENFIKHEILEK.D
302	309	2	799.48	-0.03	0	33.6	25.6	95.00%	K.VALGALEK.A	K.VALGALEK.A
172	187	2	1765.83	-0.18	1	69.4	33	95.00%	R.ITDATPASFSSHVDYR.W	R.ITDATPASFSSHVDYR.W
236	249	2	1574.7	1.3	2	70.6	33.8	95.00%	K.DGRDLIDEAQSNGW.Q	K.DGRDLIDEAQSNGWQYVGDR.K
467	474	2	980.48	1.5	1	30.4	31.7	93.10%	K.LNDMVSFR.A	K.LNDMVSFR.A
439	466	3	3179.48	1.4	1	48.4	31.9	95.00%	K.DLGIYDYTDSDLETLIHLDDNANAIQDK.L	K.DLGIYDYTDSDLETLIHLDDNANAIQDK.L
113	130	2	1755.83	2	2	59.3	33.1	95.00%	R.TRSSDSLVTDSAAGATAF.A	R.TRSSDSLVTDSAAGATAFACALK.S
546	557	2	1361.61	2	1	51.8	32.9	95.00%	F.DATEIASEVQHY.D	K.HTSDFDATEIASEVQHYDEYYHELTN.-
136	158	2	2448.2	0.17	1	45.1	32.1	95.00%	K.SYNGAIGVDPHHRPCGTVLEAAK.L	Carbamidomethyl (+57)	K.SYNGAIGVDPHHRPCGTVLEAAK.L
159	171	2	1362.79	-0.15	1	81.9	24.1	95.00%	K.LAGYLTGLVVTTR.I	K.LAGYLTGLVVTTR.I
321	328	2	937.47	2	1	38.6	32.2	95.00%	F.FLMVEGSR.I	K.DSNGFFLMVEGSR.I
187	205	4	2281.16	1.7	2	47.5	30.4	95.00%	Y.RWQEDLIATHQLGEYPLGR.V	R.ITDATPASFSSHVDYRWQEDLIATHQLGEYPLGR.V
163	171	2	958.58	2.1	0	36.8	26	95.00%	Y.LTGLVVTTR.I	K.LAGYLTGLVVTTR.I
278	291	2	1675.77	1.2	1	44.3	33.3	95.00%	F.ADNDIPFEIDRDEK.E	K.SHGENVTLPFLGLFADNDIPFEIDRDEK.E
206	215	2	1015.55	1.6	0	58.9	30.1	95.00%	R.VVDLLMGGGR.S	R.VVDLLMGGGR.S
239	249	2	1246.55	1.7	1	57	32.9	95.00%	R.DLIDEAQSNGW.Q	R.DLIDEAQSNGWQYVGDR.K
236	251	2	1866.81	1.6	2	79.1	34.3	95.00%	K.DGRDLIDEAQSNGWQY.V	Deamidation (+1)	K.DGRDLIDEAQSNGWQYVGDR.K
285	297	2	1620.8	1.4	2	54.1	32.5	95.00%	F.EIDRDEKEYPSLK.E	K.SHGENVTLPFLGLFADNDIPFEIDRDEKEYPSLK.E
329	343	2	1643.78	0.54	0	47.3	32.9	95.00%	R.IDHAGHQNDPASQVR.E	R.IDHAGHQNDPASQVR.E
188	205	2	2125.06	1.8	1	88.3	31.3	95.00%	R.WQEDLIATHQLGEYPLGR.V	R.WQEDLIATHQLGEYPLGR.V
1	12	3	1430.66	-0.061	0	39.2	33.2	95.00%	-.MMTHTLPSEQTR.L	-.MMTHTLPSEQTR.L
68	86	2	2027.98	-1.7	1	104	32.9	95.00%	K.NVIFFVTDGMGPASLSMAR.S	Oxidation (+16)	K.NVIFFVTDGMGPASLSMAR.S
235	249	2	1702.79	1.2	2	48.4	33.5	95.00%	R.KDGRDLIDEAQSNGW.Q	R.KDGRDLIDEAQSNGWQYVGDR.K
413	426	3	1552.8	0.32	1	40.5	30.7	95.00%	K.LVDFVHEHKGASSK.I	K.LVDFVHEHKGASSK.I
316	328	2	1457.66	-0.64	1	38.8	33.3	95.00%	K.DSNGFFLMVEGSR.I	K.DSNGFFLMVEGSR.I
113	135	3	2299.11	-0.12	2	26.2	32.2	92.40%	R.TRSSDSLVTDSAAGATAFACALK.S	Carbamidomethyl (+57)	R.TRSSDSLVTDSAAGATAFACALK.S
115	135	2	2041.96	-0.63	1	128	33.7	95.00%	R.SSDSLVTDSAAGATAFACALK.S	Carbamidomethyl (+57)	R.SSDSLVTDSAAGATAFACALK.S
413	421	2	1122.58	-0.2	1	39.5	31.2	95.00%	K.LVDFVHEHK.G	K.LVDFVHEHK.G
87	112	3	2981.46	1.9	1	82.2	30.5	95.00%	R.SFNQHVNDLPIDDILTLDEHFIGSSR.T	R.SFNQHVNDLPIDDILTLDEHFIGSSR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
12	B3LSE9_YEAS1	35.70%	100%	29

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
594	606	2	1393.7	1.4	1	65.5	31.5	95.00%	F.FAYGGPNSQQVVK.T	K.DILVNSYEILPNDFDETLSDHYPVFFFAYGGPNSQQVVK.T
351	365	2	1634.91	0.3	1	106	24.8	95.00%	R.SSDILTVFLIDTIAK.T	R.SSDILTVFLIDTIAK.T
748	761	2	1601.73	1.7	1	70.2	33.9	95.00%	R.FLLMHGTGDDNVHF.Q	R.FLLMHGTGDDNVHFQNSLK.F
92	105	2	1579.78	1.8	2	58.5	32.5	95.00%	W.ISDNKIESNDLGLY.V	K.YHELQWISDNKIESNDLGLYVTFMNDSYVVK.S
575	593	2	2297.06	1.9	1	39.4	33.5	95.00%	Y.EILPNDFDETLSDHYPVFF.F	K.DILVNSYEILPNDFDETLSDHYPVFFFAYGGPNSQQVVK.T
699	710	2	1380.65	-0.15	1	47.4	32.9	95.00%	K.YGMSVAPVTDWR.F	K.YGMSVAPVTDWR.F
433	448	2	1862.86	0.79	1	102	33.9	95.00%	K.WEVVNGPLAFDSMENR.L	K.WEVVNGPLAFDSMENR.L
793	803	2	1318.67	-0.54	1	44	31.6	95.00%	R.YHNANVIVFDK.L	R.YHNANVIVFDK.L
117	131	2	1687.79	0.18	1	76.2	33.5	95.00%	K.SVYDDSYNSVLLEGK.T	K.SVYDDSYNSVLLEGK.T
544	553	2	1202.67	-0.19	1	46.6	28.5	95.00%	K.ILEDYAVPRK.S	K.ILEDYAVPRK.S

575	592	2	2149.99	1.3	1	32.9	33.5	94.00%	Y.EILPNDFDETLSDHYPVF.F		K.DILVNSYEILPNDFDETLSDHYPVFFFAYGGPNSQQVVK.T
396	411	3	1785.87	2.3	1	28.8	32.3	95.00%	F.DRPHNGYVDILPIGGY.N	Deamidation (+1)	R.NESSNGGWWEITHNTLFIPANETFDRPHNGYVDILPIGGYNHLAYFENSNSSHYK.T
748	766	3	2172.04	-0.18	1	56.5	33.3	95.00%	R.FLLMHGTGDDNVHFQNSLK.F		R.FLLMHGTGDDNVHFQNSLK.F
563	574	2	1398.67	2.1	2	33.2	32.7	95.00%	K.DEFGKDILVNSY.E		K.DEFGKDILVNSYEILPNDFDETLSDHYPVFFFAYGGPNSQQVVK.T
434	448	2	1676.78	1.1	1	82.8	33.1	95.00%	W.EVVNGPLAFDSMENR.L		K.WEVVNGPLAFDSMENR.L
347	365	3	2108.14	0.19	2	39.1	25.8	95.00%	K.TTDRSSDILTVFLIDTIAK.T		K.TTDRSSDILTVFLIDTIAK.T
278	290	2	1684.78	1.7	2	55.7	33.4	95.00%	Y.YVQDEKDIYPEMR.S		K.IDESEVGEFIIPYYVQDEKDIYPEMR.S
327	346	2	2113.14	0.61	1	87.6	27.4	95.00%	K.DGSLLITEVTWVGNGNVLVK.T		K.DGSLLITEVTWVGNGNVLVK.T
222	232	2	1156.54	3.3	1	43.8	32.2	95.00%	R.AVTNDGSSFLF.N		R.AVTNDGSSFLFNGKPDWVYEEEVFEDDK.A
557	567	2	1248.63	-0.51	2	45.6	31.3	95.00%	R.ELNLGKDEFGK.D		R.ELNLGKDEFGK.D
297	312	3	1815.86	0.45	1	30.1	33.4	95.00%	K.SGTPNPHAELWVYSMK.D		K.SGTPNPHAELWVYSMK.D
595	606	2	1246.63	1.4	1	31	30.7	95.00%	F.AYGGPNSQQVVK.T		K.DILVNSYEILPNDFDETLSDHYPVFFFAYGGPNSQQVVK.T
72	78	2	792.45	0.98	1	26	28.1	91.90%	K.VSFSVVR.N		K.VSFSVVR.N
372	388	2	1990.88	1.5	1	43.7	34.2	95.00%	R.NESSNGGWWEITHNTLF.I		R.NESSNGGWWEITHNTLFIPANETFDRPHNGYVDILPIGGYNHLAYFENSNSSHYK.T
780	793	3	1685.78	1.8	2	29	33.6	94.50%	Y.DVHVFPDSDHSIRY.H		K.FLDLLDLNGVENYDVHVFPDSDHSIRYHNANVIVFDK.L
780	792	2	1522.72	1.6	1	43.3	33.1	95.00%	Y.DVHVFPDSDHSIR.Y		K.FLDLLDLNGVENYDVHVFPDSDHSIR.Y
749	761	3	1454.67	2.6	1	40.9	33	95.00%	F.LLMHGTGDDNVHF.Q		R.FLLMHGTGDDNVHFQNSLK.F
767	792	3	3028.46	2	1	86.3	30.8	95.00%	K.FLDLLDLNGVENYDVHVFPDSDHSIR.Y		K.FLDLLDLNGVENYDVHVFPDSDHSIR.Y
767	779	2	1523.75	2	1	57	32.6	95.00%	K.FLDLLDLNGVENY.D		K.FLDLLDLNGVENYDVHVFPDSDHSIR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
13	A6ZVC8_YEAS7	47.66%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
12	27	2	1762.89	2.9	0	99.9	31.3	95.00%	K.TITLEVESSDTIDNVK.S		K.TITLEVESSDTIDNVK.S
49	59	2	1295.6	1.3	2	39.3	32.2	95.00%	K.QLEDGRTLSDY.N		K.QLEDGRTLSDYNIQK.E
55	72	3	2129.15	-0.51	1	52.1	27.4	95.00%	R.TLSDYNIQKESTLHLVLR.L		R.TLSDYNIQKESTLHLVLR.L
64	72	2	1066.61	0.45	0	62.5	24.5	95.00%	K.ESTLHLVLR.L		K.ESTLHLVLR.L
1	6	2	764.43	-0.41	1	35.4	30.4	95.00%	-.MQIFVK.T		-.MQIFVK.T
34	42	2	1038.51	0.94	0	39.5	32.1	95.00%	K.EGIPPDQQR.L		K.EGIPPDQQR.L
55	63	2	1080.55	-0.0048	1	50.4	30.4	95.00%	R.TLSDYNIQK.E		R.TLSDYNIQK.E
60	72	3	1549.9	1.8	1	33.6	23.3	95.00%	Y.NIQKESTLHLVLR.L		R.TLSDYNIQKESTLHLVLR.L
49	63	2	1778.88	0.17	2	45.1	32.2	95.00%	K.QLEDGRTLSDYNIQK.E		K.QLEDGRTLSDYNIQK.E
28	42	4	1737.9	0.19	1	29.7	30.5	95.00%	K.SKIQDKEGIPPDQQR.L		K.SKIQDKEGIPPDQQR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
14	PPN1_YEAST	34.72%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
184	198	2	1707.81	-0.42	1	83.2	32.8	95.00%	R.TEAQIFDMNNIVADK.M		R.TEAQIFDMNNIVADK.M
651	660	2	1276.65	-0.18	1	31.1	31.6	94.10%	R.LYENKPAWEK.Y		R.LYENKPAWEK.Y
72	83	2	1334.83	1.2	1	31.2	14.3	95.00%	R.LGLTPREPVIIK.D		R.LGLTPREPVIIK.D
390	407	2	2119.88	0.7	0	106	33.9	95.00%	R.VQQGEDSNEEDEETELNR.I		R.VQQGEDSNEEDEETELNR.I
109	126	3	1933.92	1.6	1	44.6	33.4	95.00%	Y.YVEGSSIDAVCHTGKPSK.K	Carbamidomethyl (+57)	R.FLHITDIHPDPYYVEGSSIDAVCHTGKPSK.K
533	554	2	2508.14	2.1	0	115	33.6	95.00%	K.IMEDSLLEDEMDSSNIEVGINR.E		K.IMEDSLLEDEMDSSNIEVGINR.E
97	108	2	1466.72	1.8	1	41	32.6	95.00%	R.FLHITDIHPDPY.Y		R.FLHITDIHPDPYYVEGSSIDAVCHTGKPSK.K

204	233	3	3334.49	0.98	2	47.1	32.3	95.00%	F.SAGNEEDPRDFDVSVIPSLGNNDVFPHNMF.A	Oxidation (+16)	K.MTELFSAGNEEDPRDFDVSVIPSLGNNDVFPHNMFALGPTLQTR.E
72	86	3	1677.02	0.36	1	24.8	16.6	95.00%	R.LGLTPREPVIIKDVK.T		R.LGLTPREPVIIKDVK.T
204	214	2	1235.51	1.3	2	30.9	32.1	93.20%	F.SAGNEEDPRDF.D		K.MTELFSAGNEEDPRDFDVSVIPSLGNNDVFPHNMFALGPTLQTR.E
137	153	2	1907.88	0.06	0	93	33.6	95.00%	K.AMSGCDSPVILMEETLR.W	Carbamidomethyl (+57)	K.AMSGCDSPVILMEETLR.W
361	375	3	1708.84	1.7	1	32.6	32.8	95.00%	Y.GHMNIDHFIPTDGKK.A		R.DIIIGGLYGHMNIDHFIPTDGKK.A
51	69	2	2252.06	1.5	2	39	33	95.00%	K.FLDDRGDNESLQLLNDIEF.T		K.FLDDRGDNESLQLLNDIEFTR.L
215	233	2	2101	1.7	1	42.2	33.4	95.00%	F.DVSVIPSLGNNDVFPHNMF.A		R.DFDVSVIPSLGNNDVFPHNMFALGPTLQTR.E
390	416	4	3070.38	1.6	1	22.4	32.5	90.40%	R.VQQGEDSNEEDEETELNRILDHAMAAK.E		R.VQQGEDSNEEDEETELNRILDHAMAAK.E
234	242	2	955.55	1.2	0	45.8	24.3	95.00%	F.ALGPTLQTR.E		R.DFDVSVIPSLGNNDVFPHNMFALGPTLQTR.E
606	618	2	1543.76	-0.92	1	81.4	31.7	95.00%	K.INQELHNSFVESK.D		K.INQELHNSFVESK.D
263	274	2	1247.68	0.62	1	34.2	29.8	95.00%	R.SASFLTEVIPGK.L		R.SASFLTEVIPGK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
15	CBPS_YEAST	27.26%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
446	470	3	2782.44	1.2	2	63.6	27.1	95.00%	Y.GLSKNGDDYIIPETELGHIDITLLR.E	Deamidation (+1)	K.YGYGLSKNGDDYIIPETELGHIDITLLR.E
108	119	2	1391.6	1.6	1	51.9	33.6	95.00%	K.NPNPADDPDFYK.H		K.NPNPADDPDFYK.H
279	290	2	1302.68	1.7	1	59.6	30.7	95.00%	K.DVFVATPINAEK.G		K.DVFVATPINAEK.G
419	431	2	1499.77	0.18	1	38.5	30.4	95.00%	R.INLHSSVAEVFER.N		R.INLHSSVAEVFER.N
533	544	2	1331.77	0.061	1	62.1	23.7	95.00%	R.FVGSIIDIDLLK.T		R.FVGSIIDIDLLK.T
63	74	2	1433.72	-0.42	2	42.6	31.5	95.00%	K.CEKIEPLSPSFK.H	Carbamidomethyl (+57)	K.CEKIEPLSPSFK.H
450	470	3	2396.22	0.46	1	57.2	29.6	95.00%	K.NGDDYIIPETELGHIDITLLR.E		K.NGDDYIIPETELGHIDITLLR.E
265	278	2	1549.72	1.1	0	71.4	33	95.00%	Y.SIIDEGEGIMEVDK.D	Oxidation (+16)	R.YGDDGIYSIIDEGEGIMEVDK.D
258	278	2	2317.03	0.95	1	138	34	95.00%	R.YGDDGIYSIIDEGEGIMEVDK.D		R.YGDDGIYSIIDEGEGIMEVDK.D
361	370	2	1130.59	-0.36	1	32	30.8	95.00%	K.TILGAPFCPR.R	Carbamidomethyl (+57)	K.TILGAPFCPR.R
391	403	2	1314.72	1.4	0	74.9	29.3	95.00%	R.TTQAVDIINGGVK.A		R.TTQAVDIINGGVK.A
373	386	3	1700.89	0.48	2	42.5	29.5	95.00%	K.DKLVEYISNQSHLR.S		K.DKLVEYISNQSHLR.S
375	386	2	1457.76	0.27	1	60.3	30.3	95.00%	K.LVEYISNQSHLR.S		K.LVEYISNQSHLR.S
75	87	2	1506.76	-0.68	1	81.4	32.2	95.00%	K.HSVDTILHDPAFR.N		K.HSVDTILHDPAFR.N
265	281	2	1894.89	0.78	2	51.5	33.5	95.00%	Y.SIIDEGEGIMEVDKDVF.V		R.YGDDGIYSIIDEGEGIMEVDKDVFVATPINAEK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
16	B3LS03_YEAS1	42.21%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
39	50	2	1338.64	-1.1	1	45.8	32.3	95.00%	K.DQLDFYSGGPLK.A		K.DQLDFYSGGPLK.A
203	227	2	2648.36	1.1	1	61.2	29	95.00%	K.ELVNAGAVPVLVSLLSSTDPDVQYY.C		K.ELVNAGAVPVLVSLLSSTDPDVQYYCTTALSNIAVDEANR.K
300	317	2	1954.09	-0.55	0	51.5	25.9	95.00%	K.LIQSDSIPLVLASVACIR.N	Carbamidomethyl (+57)	K.LIQSDSIPLVLASVACIR.N
228	242	2	1633.78	1.5	0	116	32.6	95.00%	Y.CTTALSNIAVDEANR.K	Carbamidomethyl (+57)	K.ELVNAGAVPVLVSLLSSTDPDVQYYCTTALSNIAVDEANR.K
277	290	2	1607.82	-0.19	1	108	31.7	95.00%	R.NLASDTSYQLEIVR.A		R.NLASDTSYQLEIVR.A
161	174	3	1448.88	2.6	1	42.1	17.9	95.00%	K.HKIATSGALIPLTK.L		K.HKIATSGALIPLTK.L
186	202	2	1884.91	-0.54	1	74.8	32.8	95.00%	R.NATGALLNMTHSEENRK.E		R.NATGALLNMTHSEENRK.E
267	276	2	1158.65	-0.51	1	29.5	28	95.00%	R.VKCQATLALR.N	Carbamidomethyl (+57)	R.VKCQATLALR.N
505	515	2	1257.63	-0.42	1	54.3	30.8	95.00%	K.NDDDIINGVRK.M		K.NDDDIINGVRK.M
163	174	2	1183.72	-0.35	0	66.9	22.7	95.00%	K.IATSGALIPLTK.L		K.IATSGALIPLTK.L
269	276	2	931.49	1.1	0	44.2	30.4	95.00%	K.CQATLALR.N	Carbamidomethyl (+57)	K.CQATLALR.N
26	38	2	1462.79	-0.22	1	68.1	28.9	95.00%	R.EAVTLLLGYLEDK.D		R.EAVTLLLGYLEDK.D
568	578	2	1353.74	2.4	1	48.2	26.8	95.00%	Y.NITQQILQFLH.-		K.NPGSNNNPSSNDNNSNNNDTGSEHQPVEDASLELYNITQQILQFLH.-
66	77	2	1249.66	1.4	1	71.6	30.6	95.00%	R.SAALAFAEITEK.Y		R.SAALAFAEITEK.Y

228	243	2	1761.87	1.8	1	116	32.7	95.00%	Y.CTTALSNIAVDEANRK.K	Carbamidomethyl (+57)	K.ELVNAGAVPVLVSLLSSTDPDVQ YYCTTALSNIAVDEANRK.K
371	380	2	1141.53	-0.65	1	32.6	31.5	95.00%	K.EFFESGAVEK.C		K.EFFESGAVEK.C
227	243	2	1924.93	1.8	1	73.7	33.1	95.00%	Y.CTTALSNIAVDEANRK.K	Carbamidomethyl (+57)	K.ELVNAGAVPVLVSLLSSTDPDVQ YYCTTALSNIAVDEANRK.K
341	359	2	2276.11	-1.5	1	65.2	32.3	95.00%	R.LLDYKDSEEIQCHAVSTLR.N	Carbamidomethyl (+57)	R.LLDYKDSEEIQCHAVSTLR.N
256	266	2	1206.59	-0.023	0	52	32.1	95.00%	K.LVSLMDSPSSR.V	Oxidation (+16)	K.LVSLMDSPSSR.V
318	340	3	2514.43	-0.32	1	35.7	20.6	95.00%	R.NISIHPLNEGLIVDAGFLKPLVR.L		R.NISIHPLNEGLIVDAGFLKPLVR.L
516	523	2	967.44	0.49	1	35	32	95.00%	K.MADVTFER.L		K.MADVTFER.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
17	A6ZYU5_YEAS7	25.57%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
544	559	2	1794.72	1.8	1	53.3	33.5	95.00%	R.GANYDADALMHDDQPF.Y	Oxidation (+16)	R.GANYDADALMHDDQPFYK.K
13	35	2	2494.06	0.28	0	94.8	33.8	95.00%	K.SSENSNADLPSNSSQVMNMPEE K.G		K.SSENSNADLPSNSSQVMNMPEE K.G
279	301	2	2605.31	1.1	1	81.4	30.7	95.00%	K.VAPDHPFIQQELEVIEASVEEAR. A		K.VAPDHPFIQQELEVIEASVEEAR. A
534	543	2	1117.55	-0.1	1	39.7	31.6	95.00%	K.SASWVPTSQR.G		K.SASWVPTSQR.G
1	12	2	1387.66	-0.5	0	48.4	32.6	95.00%	-.MNSTPDLISPQK.S	Acetyl (+42)/ Oxidation (+16)	-.MNSTPDLISPQK.S
259	270	2	1362.68	0.28	1	95.3	32	95.00%	R.YLVEAGQIDEAR.A		R.YLVEAGQIDEAR.A
515	533	2	2163.06	1.6	1	76.1	32	95.00%	K.GLTLEEVNDMYAEGVLPWK.S		K.GLTLEEVNDMYAEGVLPWK.S
225	233	2	1153.52	0.85	1	47.9	32.1	95.00%	K.NYSNSVQWR.V	Deamidation (+1)	K.NYSNSVQWR.V
36	56	2	2246.05	-0.005	1	72.5	33.6	95.00%	K.GVQDDFQAEADQVLTNPNTGK.G		K.GVQDDFQAEADQVLTNPNTGK.G
286	301	2	1841.94	1.9	0	80.4	30.6	95.00%	F.IQQELEVIEASVEEAR.A		K.VAPDHPFIQQELEVIEASVEEAR. A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
18	A6ZQR8_YEAS7	27.57%	100%	22

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
909	929	3	2238.18	0.88	0	43.9	28	95.00%	K.AVEEANSKPVEVIKPNGLSEK.K	Deamidation (+1)	K.AVEEANSKPVEVIKPNGLSEK.K
118	128	2	1198.59	2.1	1	35.9	31.3	95.00%	R.VTEAGSLQTFF.Q		R.VTEAGSLQTFFQFQK.K
955	967	2	1323.61	-0.15	1	58.7	32.8	95.00%	K.LGDASCAAPFTSK.L	Carbamidomethyl (+57)	K.LGDASCAAPFTSK.L
806	825	2	2144.92	-0.31	1	45.2	33.9	95.00%	K.DMGYQTLMCGDGTNDVGALK.Q	Carbamidomethyl (+57)	K.DMGYQTLMCGDGTNDVGALK.Q
103	117	2	1600.77	0.98	0	59.8	33	95.00%	Y.TTPNNGSDGIVEIQR.V	Deamidation (+1)	K.NVNEATHILIYTTPNNGSDGIVEIQ R.V
669	684	2	1912.01	0.63	1	62.7	27.6	95.00%	F.LIFHCPLKDDAIETIK.M	Carbamidomethyl (+57)	R.DDVESELTFNGFLIFHCPLKDDAI ETIK.M
588	604	3	1756.92	-0.06	2	33.9	29.3	95.00%	K.RSASIASHNDALFAAVK.G		K.RSASIASHNDALFAAVK.G
514	537	3	2460.34	-0.69	1	47.1	25.4	95.00%	R.HLYSAAEAPESTILVIGAAHALVK. L		R.HLYSAAEAPESTILVIGAAHALVK. L
672	684	2	1538.78	2	1	50.5	30.9	95.00%	F.HCPLKDDAIETIK.M	Carbamidomethyl (+57)	R.DDVESELTFNGFLIFHCPLKDDAI ETIK.M
264	282	2	2198.18	1	1	54.3	27.2	95.00%	K.WVALQTNELLPMDLVSITR.T		K.WVALQTNELLPMDLVSITR.T
589	604	2	1600.82	-0.27	1	70.8	31.5	95.00%	R.SASIASHNDALFAAVK.G		R.SASIASHNDALFAAVK.G
481	488	2	1055.44	-0.15	1	39.8	31	95.00%	R.IDVCCFDK.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.IDVCCFDK.T
372	383	2	1280.64	-0.56	1	71.7	31.8	95.00%	K.TGFETSQGSLVR.V		K.TGFETSQGSLVR.V
489	513	2	2564.27	2.5	1	112	31.4	95.00%	K.TGTLTGEDLVFEGLAGISADSENI R.H		K.TGTLTGEDLVFEGLAGISADSENI R.H
930	954	3	2464.29	2.1	0	41.8	28.4	95.00%	K.KPADLASLLLNSAGDAQGDEAPA LK.L		K.KPADLASLLLNSAGDAQGDEAPA LK.L
283	316	3	3556.8	1.8	0	52.2	26.6	95.00%	R.TAEESAIPCDLILLDGSAIVNEAML SGESTPLLK.E	Carbamidomethyl (+57)	R.TAEESAIPCDLILLDGSAIVNEAML SGESTPLLK.E
149	156	2	933.48	-0.03	1	31	29.8	95.00%	K.FLVDESPK.I		K.FLVDESPK.I
321	335	2	1697.86	-0.66	0	67.1	31	95.00%	K.LRPSEDNLQLDGVDK.I		K.LRPSEDNLQLDGVDK.I
769	780	2	1307.7	1.7	0	57.3	30.2	95.00%	Y.ALNALEGHSQLR.D		R.YDIAVTGYALNALEGHSQLR.D
968	979	2	1269.74	0.14	0	69.8	25.4	95.00%	K.LANVSAVTNIIR.Q		K.LANVSAVTNIIR.Q

92	117	3	2867.44	-0.97	1	44.2	30.3	95.00%	K.NVNEATHILIYTTPNNGSDGIVEIQR.V		K.NVNEATHILIYTTPNNGSDGIVEIQR.V
355	371	2	1646.89	-0.56	0	29	29.4	94.20%	K.SDIPPPPDGGALAIVTK.T		K.SDIPPPPDGGALAIVTK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
19	ATC2_YEAST	25.83%	100%	23

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
235	251	2	1867.81	-0.69	0	118	34.2	95.00%	K.CEADESSITGESNTIQK.F	Carbamidomethyl (+57)	K.CEADESSITGESNTIQK.F
432	446	2	1602.63	-0.78	0	102	32.5	95.00%	R.SCETMGSATAVCSDK.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.SCETMGSATAVCSDK.T
71	84	2	1560.82	-1.2	1	29.2	29.9	93.90%	K.NAGISLPEISNYRK.T		K.NAGISLPEISNYRK.T
760	770	2	1161.61	0.59	0	34.2	30.9	95.00%	R.MVTGDNILTAK.A		R.MVTGDNILTAK.A
657	672	3	1918.88	-1.1	1	75.1	33.8	95.00%	K.RNSDDTLEEINEDNKK.E		K.RNSDDTLEEINEDNKK.E
447	459	2	1419.74	1.7	0	64.5	30.9	95.00%	K.TGTLTENVMTVVR.G		K.TGTLTENVMTVVR.G
868	887	2	2165.09	0.27	1	100	30.9	95.00%	R.EASDIILMTDDFSAIVNAIK.W		R.EASDIILMTDDFSAIVNAIK.W
658	679	3	2593.15	-0.2	1	47.1	33.9	95.00%	R.NSDDTLEEINEDNKKETDDEIK.N		R.NSDDTLEEINEDNKKETDDEIK.N
574	583	2	1073.61	2.3	0	62.8	27.6	95.00%	K.TETALLSLAR.L		K.TETALLSLAR.L
727	741	2	1591.93	-0.13	0	49.6	22	95.00%	K.GLILDGLLGIQDPLR.A		K.GLILDGLLGIQDPLR.A
37	46	2	1137.58	2	0	31.9	31.4	95.00%	K.SQLSDLHNPK.S		K.SQLSDLHNPK.S
263	287	3	2779.32	0.65	2	54	31.9	95.00%	K.KFNSIDSHNHSKPLDIGDVNEDGNK.I		K.KFNSIDSHNHSKPLDIGDVNEDGNK.I
584	597	2	1585.88	-0.13	1	48.8	28.1	95.00%	R.LSLGLQPGELQYLR.D		R.LSLGLQPGELQYLR.D
711	726	2	1744.9	1.3	1	77.5	30.3	95.00%	K.DSPNIAALDLLFNSQK.G		K.DSPNIAALDLLFNSQK.G
823	830	2	970.62	-0.44	1	23.8	21.8	93.20%	K.RLLVETLK.G		K.RLLVETLK.G
432	459	3	3004.36	-0.0048	1	62.2	33.2	95.00%	R.SCETMGSATAVCSDKTGTLTENVMTVVR.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.SCETMGSATAVCSDKTGTLTENVMTVVR.G
497	513	2	1902.98	0.56	1	80.2	30.5	95.00%	R.NDLLANIVLNSTAFENR.D		R.NDLLANIVLNSTAFENR.D
831	850	2	1886.91	1.2	0	98.4	33.1	95.00%	K.GMGDVVAVTGDGTNDAPALK.L		K.GMGDVVAVTGDGTNDAPALK.L
264	287	3	2651.22	-0.64	1	62.8	33	95.00%	K.FNSIDSHNHSKPLDIGDVNEDGNK.I		K.FNSIDSHNHSKPLDIGDVNEDGNK.I
90	99	2	1163.52	-0.79	1	36.9	31.9	95.00%	K.NYGDNSLPER.I		K.NYGDNSLPER.I
288	298	2	1221.58	-0.068	0	81.2	31.9	95.00%	K.IADCMLISGSR.I	Carbamidomethyl (+57)	K.IADCMLISGSR.I
1149	1173	3	2820.2	-0.29	2	83.7	33.7	95.00%	K.NHTGKHDDEEALLEESDSPESTAFY.-		K.NHTGKHDDEEALLEESDSPESTAFY.-
789	797	2	1026.45	2.7	1	43.3	32.2	95.00%	Y.SAMEGTEFR.K		R.NCAILSTDISSEAYSAMEGTEFR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
20	ATN2_YEAST	30.16%	100%	23

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
784	807	3	2619.28	0.034	1	38.4	31.6	95.00%	K.EASDIVLSDDNFASILNAVEEGRR.M		K.EASDIVLSDDNFASILNAVEEGRR.M
505	529	3	2813.16	1.4	1	29.3	33.7	94.70%	K.STNQSNENDQSSLSQHNEKPGSAQF.E	Phospho (+80)	K.STNQSNENDQSSLSQHNEKPGSAQFEHIAEFPFDSTVK.R
582	595	2	1659.85	-0.3	1	73.1	30.1	95.00%	K.ITPLTDCDVETIRK.N	Carbamidomethyl (+57)	K.ITPLTDCDVETIRK.N
29	45	3	1874.97	1.1	1	48.6	29.9	95.00%	F.IGTSLTEGLTQDESLRR.L		K.ENNNEEFNAYHTLTTEEAAEFIGTSLTEGLTQDESLRR.L
614	626	2	1536.74	-0.92	1	68.2	32.7	95.00%	K.SFTKDQVNDDQLK.N		K.SFTKDQVNDDQLK.N
477	492	2	1696.88	-0.49	1	74.5	30	95.00%	K.AHGDPTEIAIQVFATK.M		K.AHGDPTEIAIQVFATK.M
389	413	2	2703.31	-0.31	1	88.6	31.1	95.00%	R.FGTITISNSDDPFNPNEGNVSLIPR.F		R.FGTITISNSDDPFNPNEGNVSLIPR.F
418	434	2	1963.89	0.25	1	89.7	33.9	95.00%	Y.EYSHNEDGDVGILQNFK.D		R.FSPYEYSHNEDGDVGILQNFK.D
29	44	2	1718.87	1.6	0	91.5	31.7	95.00%	F.IGTSLTEGLTQDESLR.R		K.ENNNEEFNAYHTLTTEEAAEFIGTSLTEGLTQDESLR.R
124	144	3	2266.17	1.5	1	36.2	29.8	95.00%	K.NLSSPNAHVIRNGKSETINSK.D	Deamidation (+1)	K.NLSSPNAHVIRNGKSETINSK.D
156	165	2	1055.56	0.26	0	36.5	27.9	95.00%	K.VGDTIPADLR.L		K.VGDTIPADLR.L
530	542	2	1518.74	3.1	1	35	32.6	95.00%	F.EHIAEFPFDSTVK.R		K.STNQSNENDQSSLSQHNEKPGSAQFEHIAEFPFDSTVK.R
596	606	2	1250.63	-0.17	1	44	32.2	95.00%	K.NVYSLSNEGLR.V		K.NVYSLSNEGLR.V

353	370	2	1946.97	2.1	1	136	31.3	95.00%	R.KLDSLEALGAVNDICSDK.T	Carbamidomethyl (+57)	R.KLDSLEALGAVNDICSDK.T
751	766	2	1697.74	-0.52	1	83.4	33.8	95.00%	K.FCAMTGDGVNDSPSLK.M	Carbamidomethyl (+57)	K.FCAMTGDGVNDSPSLK.M
752	766	2	1550.67	1.5	0	68.2	33.5	95.00%	F.CAMTGDGVNDSPSLK.M	Carbamidomethyl (+57)	K.FCAMTGDGVNDSPSLK.M
642	660	3	1983.08	2.4	1	18.9	25.9	90.20%	F.LGLIGIYDPPRNETAGAVK.K		R.ATAESDLVFLGLIGIYDPPRNETAGAVK.K
171	188	2	1950.94	-1.2	1	98.6	32.6	95.00%	K.NFDTDESLLTGESLPVSK.D		K.NFDTDESLLTGESLPVSK.D
239	253	2	1558.79	-1.4	1	77	30.7	95.00%	K.SLQGDSGLISRDPSK.S		K.SLQGDSGLISRDPSK.S
493	504	2	1324.64	-1.6	0	31.2	32.8	92.70%	K.MDLPHNALTGEK.S		K.MDLPHNALTGEK.S
682	695	2	1500.82	0.86	1	58.9	28.9	95.00%	K.AIAQEVGILPTNLY.H		K.AIAQEVGILPTNLYHYSQEIVDSMVMTGSQFDGLSEEEVDDLPVLPLVIAR.C
254	264	2	1362.69	-0.0057	1	52.6	31.5	95.00%	K.SWLQNTWISTK.K		K.SWLQNTWISTK.K
124	134	2	1206.65	-0.51	0	30.2	29.2	95.00%	K.NLSSPNAHVIR.N		K.NLSSPNAHVIR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
21	A7A0C8_YEAS7	50.80%	100%	20

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
70	86	2	1872	-2.1	1	45.1	29.7	95.00%	K.SEELYPGRPLAIALDTK.G		K.SEELYPGRPLAIALDTK.G
217	225	2	1001.55	-0.022	0	39	29.3	95.00%	R.TANDVLTIR.E		R.TANDVLTIR.E
487	500	2	1340.67	-1	0	30.5	31.3	93.80%	K.AGAGHSNTLQVSTV.-		K.AGAGHSNTLQVSTV.-
178	194	2	1723.9	0.28	0	48.9	29.8	95.00%	K.GVNLPGTDVDLPALSEK.D		K.GVNLPGTDVDLPALSEK.D
397	409	2	1314.75	0.29	0	41.9	27.9	95.00%	K.AIIVLSTSGTTPR.L		K.AIIVLSTSGTTPR.L
313	337	2	2521.17	-0.19	0	98.9	33.5	95.00%	R.AEVSDVGNAILDGADCVMLSGETAK.G	Carbamidomethyl (+57)	R.AEVSDVGNAILDGADCVMLSGETAK.G
31	41	2	1226.66	-0.27	0	53.6	28.2	95.00%	K.TNNPETLVALR.K		K.TNNPETLVALR.K
265	281	2	1747.97	-0.53	0	32.1	26.5	95.00%	R.GDLGIEIPAPEVLAVQK.K		R.GDLGIEIPAPEVLAVQK.K
370	391	2	2222.09	1.1	1	49	32	95.00%	R.NCTPKPTSTTETVAASAVAAVF.E	Carbamidomethyl (+57)	R.NCTPKPTSTTETVAASAVAAVFEQK.A
31	42	2	1354.76	-0.68	1	60.5	26	95.00%	K.TNNPETLVALRK.A		K.TNNPETLVALRK.A
287	306	2	2213.06	1.9	1	68.4	32.6	95.00%	K.SNLAGKPVICATQMLESMTY.N	Carbamidomethyl (+57)	K.SNLAGKPVICATQMLESMTYNPRPTR.A
241	255	2	1759.87	-0.24	1	51	31.5	95.00%	K.IENQQGVNNFDEILK.V		K.IENQQGVNNFDEILK.V
362	369	2	1022.45	1.5	1	42.2	31.2	95.00%	Y.LPNYDDMR.N		K.GNYPINAVTTMAETAVIAEQAIAYLPNYDDMR.N
69	86	3	2000.09	-0.1	2	29.9	26.6	95.00%	R.KSEELYPGRPLAIALDTK.G		R.KSEELYPGRPLAIALDTK.G
153	161	2	1043.55	1.9	0	36.5	29.8	95.00%	F.QVLEVVDDK.T		R.IIYVDDGVLSFQVLEVVDDK.T
414	425	2	1500.82	-0.66	1	49.1	28.7	95.00%	K.YRPNCPIILVTR.C	Carbamidomethyl (+57)	K.YRPNCPIILVTR.C
370	394	3	2607.28	-0.83	1	40.6	31.4	95.00%	R.NCTPKPTSTTETVAASAVAAVFEQK.A	Carbamidomethyl (+57)	R.NCTPKPTSTTETVAASAVAAVFEQK.A
241	264	3	2688.36	2.6	1	39.1	29.9	95.00%	K.IENQQGVNNFDEILKVTDGVMVAR.G		K.IENQQGVNNFDEILKVTDGVMVAR.G
287	312	3	2934.45	-0.019	1	32.1	29.6	95.00%	K.SNLAGKPVICATQMLESMTYNPRPTR.A	Carbamidomethyl (+57)	K.SNLAGKPVICATQMLESMTYNPRPTR.A
92	116	3	2821.27	-0.99	1	45.7	33.3	95.00%	R.TGTTTNDVDYPIPPNHEMIFTTDDK.Y		R.TGTTTNDVDYPIPPNHEMIFTTDDK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
22	A6ZTJ2_YEAS7	22.02%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
430	439	2	1117.64	0.43	0	41.3	26.5	95.00%	K.TTLLDILAMK.R		K.TTLLDILAMK.R
68	78	2	1347.55	-0.21	1	62.4	33.1	95.00%	K.QFSECNSYTGR.C	Carbamidomethyl (+57)	K.QFSECNSYTGR.C
30	39	2	1099.52	0.88	1	36.6	30.8	95.00%	K.TPFFEGTSSK.N		K.TPFFEGTSSK.N
702	716	2	1689.78	1.2	1	64.6	33.8	95.00%	R.SLLRDEEDVEGTDGR.R		R.SLLRDEEDVEGTDGR.R
657	679	2	2534.14	0.86	1	119	34	95.00%	R.NISDLEAGTDTNDIDNTIHQTTF.T		R.NISDLEAGTDTNDIDNTIHQTTFTSSDGTTQR.E
774	783	2	1171.66	1.1	0	39.5	28.4	95.00%	F.LQQLSILNSR.S	Deamidation (+1)	K.DSVYYAELSQEIEEVLSEGDEESNVLNGDLPTGQQSAGFLQQLSILNSR.S
259	270	2	1352.57	-0.37	1	64.8	32.7	95.00%	K.GPGDFSCDLETR.Q	Carbamidomethyl (+57)	K.GPGDFSCDLETR.Q
657	688	3	3467.55	-1.3	1	70.7	32	95.00%	R.NISDLEAGTDTNDIDNTIHQTTFTSSDGTTQR.E		R.NISDLEAGTDTNDIDNTIHQTTFTSSDGTTQR.E
245	258	2	1537.79	-0.14	1	71.5	31.3	95.00%	K.GSIDISDFLTETIK.G		K.GSIDISDFLTETIK.G

655	679	3	2803.33	1.5	2	79.3	31.9	95.00%	R.IRNISDLEAGTDTNDIDNTIHQTTF.T		R.IRNISDLEAGTDTNDIDNTIHQTTFTSSDGTTQR.E
49	67	2	2358.96	2	1	69.8	34.1	95.00%	K.GNDTCPPCFNCMLPIFECK.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GNDTCPPCFNCMLPIFECK.Q
505	513	3	1147.66	-0.43	1	20	26.5	91.40%	R.VYKVLEELR.I		R.VYKVLEELR.I
171	178	2	897.56	-0.12	0	27	19.5	95.00%	K.ILQILNGK.I		K.ILQILNGK.I
702	717	3	1845.88	1.3	1	58.4	32.8	95.00%	R.SLLRDEEDVEGTDGRR.G		R.SLLRDEEDVEGTDGRR.G
79	111	4	3680.59	-1	1	64.3	32.5	95.00%	R.CECIEGFAGDDCSLPLCGGLSPDESGNKDRPIR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.CECIEGFAGDDCSLPLCGGLSPDESGNKDRPIR.A
296	311	2	1913.79	0.19	1	69.1	34.3	95.00%	K.CESGECVHYSEIPGYK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CESGECVHYSEIPGYK.S
185	195	2	1381.54	2.2	1	30	32.9	90.60%	F.ACDKPNQECNF.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.IPQITFACDKPNQECNFQFWIDQLESFYCGLSDCAFEYDLEQNTSHYK.C
274	291	2	2043.95	1.6	1	44.4	33.2	95.00%	K.FSEPSMNDLILTVFGDPY.I		K.FSEPSMNDLILTVFGDPYITLK.C
655	688	3	3736.74	0.11	2	75.8	30.6	95.00%	R.IRNISDLEAGTDTNDIDNTIHQTTFTSSDGTTQR.E		R.IRNISDLEAGTDTNDIDNTIHQTTFTSSDGTTQR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
23	KTR1_YEAST	39.19%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
46	57	2	1247.6	-0.076	1	69.9	31.6	95.00%	K.YSTVLSSGSGYK.Y		K.YSTVLSSGSGYK.Y
245	270	3	3050.35	2.7	1	36.7	33.3	95.00%	K.FMEAHPELIHENNMLDFVSDDQGLSY.N		K.FMEAHPELIHENNMLDFVSDDQGLSYNLCHFWSNFEIAALDLWR.S
310	323	2	1439.72	1.8	1	37.8	31.3	95.00%	R.WGDAPVHSIGAALF.L		R.WGDAPVHSIGAALFLDR.S
83	92	2	1137.59	-0.012	1	42.2	30.6	95.00%	R.DLYSLAESIK.S		R.DLYSLAESIK.S
203	213	2	1423.65	1.6	1	52.8	33.1	95.00%	K.LHCDIDYDVFK.F	Carbamidomethyl (+57)	K.LHCDIDYDVFK.F
163	172	2	1185.6	-0.0046	1	45	30.2	95.00%	R.IIYGDSISYR.H		R.IIYGDSISYR.H
280	288	2	1085.59	2	1	65.5	28.9	95.00%	F.EIAALDLWR.S		K.FMEAHPELIHENNMLDFVSDDQGLSYNLCHFWSNFEIAALDLWR.S
230	243	2	1708.83	-0.89	1	37.8	33.2	95.00%	K.EYEATIPTLWETTR.K		K.EYEATIPTLWETTR.K
327	338	2	1436.64	2	1	50.2	32.6	95.00%	R.SEIHHFGDIGYY.H		R.SEIHHFGDIGYYHVPFHSCPIDTSIR.L
310	326	2	1823.92	-4.6	1	50.8	31.2	95.00%	R.WGDAPVHSIGAALFLDR.S		R.WGDAPVHSIGAALFLDR.S
73	80	2	905.53	1.5	1	43.1	24.6	95.00%	K.ATFVTLVR.N		K.ATFVTLVR.N
138	150	2	1730.76	1.7	1	68	34	95.00%	K.EHWSFPEWIDEEK.A		K.EHWSFPEWIDEEK.A
81	92	2	1407.74	-0.3	2	68.2	30.5	95.00%	R.NRDLYSLAESIK.S		R.NRDLYSLAESIK.S
343	352	2	1184.56	1.8	0	30.5	32	92.80%	F.HSCPIDTSIR.L	Carbamidomethyl (+57)	R.SEIHHFGDIGYYHVPFHSCPIDTSIR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
24	A6ZMV7_YEAS7	29.41%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
360	383	3	2671.28	1.7	1	79.4	32.4	95.00%	F.HQHGIHSATVQPEFVSGDVNEDIR.R		K.IFHQHGIHSATVQPEFVSGDVNEDIR.R
203	228	3	3013.42	1.3	1	45.3	31.7	95.00%	R.LSNESQPLLNHDDHDHSHESKKPGHR.S		R.LSNESQPLLNHDDHDHSHESKKPGHR.S
358	383	3	2931.43	1.1	1	78	30.9	95.00%	K.IFHQHGIHSATVQPEFVSGDVNEDIR.R		K.IFHQHGIHSATVQPEFVSGDVNEDIR.R
293	309	2	1854.02	-1	0	106	26.3	95.00%	R.ILLQATPSTISADQIQR.E		R.ILLQATPSTISADQIQR.E
102	112	2	1335.71	-0.61	0	45.7	30	95.00%	R.LIEPQEIQNPR.L		R.LIEPQEIQNPR.L
386	401	2	1583.75	2.2	1	63.7	33.8	95.00%	R.FSIIAGGSPSSSQEAF.D		R.FSIIAGGSPSSSQEAFDSHGNTEHGR.K
385	401	2	1739.85	1.9	2	62.6	32.4	95.00%	R.RFSIIAGGSPSSSQEAF.D		R.RFSIIAGGSPSSSQEAFDSHGNTEHGR.K

386	411	2	2674.2	0.96	1	79.7	33.7	95.00%	R.FSIIAGGSPSSSQEAFDSHGNTEHGR.K		R.FSIIAGGSPSSSQEAFDSHGNTEHGR.K
420	442	2	2443.01	0.98	0	116	34.1	95.00%	Y.GATTASSNCIVDDAVNCNTSNCL.-	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.SPTAYGATTASSNCIVDDAVNCNTSNCL.-
203	223	2	2438.09	1.1	0	58.8	33.9	95.00%	R.LSNESQPLLNHDDHDHSHESK.K		R.LSNESQPLLNHDDHDHSHESK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
25	KTR4_YEAST	40.95%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
436	451	2	1981.83	2.3	1	55.8	34.3	95.00%	K.FTPWSDLDNQNCQATW.I	Carbamidomethyl (+57)	K.FTPWSDLDNQNCQATWIR.H
406	426	3	2476.02	0.19	1	56.7	33.8	95.00%	R.DIGYHHTPYTNCPTCPADSDR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.DIGYHHTPYTNCPTCPADSDR.C
399	405	2	931.47	-0.13	1	31.6	29.7	95.00%	K.SSIHWFR.D		K.SSIHWFR.D
415	426	2	1392.54	1.2	0	30.8	32.1	93.20%	Y.TNCPTCPADSDR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.DIGYHHTPYTNCPTCPADSDR.C
91	103	2	1490.69	-0.83	1	35	32.8	95.00%	K.DTFDPNEVLAENK.Q		K.DTFDPNEVLAENK.Q
193	204	2	1332.64	1.6	1	55.5	31.9	95.00%	R.VVEFGTIGPDNW.N		R.VVEFGTIGPDNWNMPDSIDR.E
110	118	2	1055.59	2.1	0	41.5	26.2	95.00%	F.LLQEISEPK.V		K.QLYEEFLLQEISEPK.V
110	124	2	1751.98	1.8	1	38.2	25.3	95.00%	F.LLQEISEPKVDNLVR.S		K.QLYEEFLLQEISEPKVDNLVR.S
143	162	2	2366.12	1.1	1	86.1	32.6	95.00%	R.NSDLEDIISSIQQLEEEYNK.N		R.NSDLEDIISSIQQLEEEYNK.N
440	451	2	1450.58	0.84	1	50.3	33.2	95.00%	W.SDLDNQNCQATW.I	Carbamidomethyl (+57)	K.FTPWSDLDNQNCQATWIR.H
415	435	2	2378.95	-0.38	1	37.6	33.7	95.00%	Y.TNCPTCPADSDRCNGNCVPGK.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.DIGYHHTPYTNCPTCPADSDRCNGNCVPGK.F
349	360	2	1480.76	2.6	1	73.2	30.7	95.00%	W.TNFEIVDLDFLR.S		K.NYDYTQGYSTCHFWTNFEIVDLDFLR.S
406	414	2	1101.49	2	1	30.5	32.1	92.70%	R.DIGYHHTPY.T		R.DIGYHHTPYTNCPTCPADSDR.C
135	142	2	857.53	-0.6	0	30.8	26.3	95.00%	K.GTILSLVR.N		K.GTILSLVR.N
62	82	3	2357.04	1.9	0	53.7	34.1	95.00%	K.TESADELPDHDAEVLDSIMDR.L		K.TESADELPDHDAEVLDSIMDR.L
389	398	2	1047.6	-0.12	1	49.9	26.1	95.00%	R.SLALALFADK.S		R.SLALALFADK.S
245	254	3	1269.65	0.081	1	29.2	29.9	95.00%	K.EFYHHPLLSK.Y		K.EFYHHPLLSK.Y
225	240	2	2041.86	0.65	1	75.6	34.4	95.00%	K.ENIQYAEVESYHNMCR.F	Carbamidomethyl (+57)	K.ENIQYAEVESYHNMCR.F
352	360	2	1118.6	2.4	1	44	29.9	95.00%	F.EIVDLDFLR.S		K.NYDYTQGYSTCHFWTNFEIVDLDFLR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
26	A6ZR26_YEAS7	14.73%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
14	24	2	1250.77	-0.027	1	25.3	17.1	95.00%	K.KIALPTRVEPK.V		K.KIALPTRVEPK.V
2	9	2	912.51	3	0	38.6	26.5	95.00%	M.SSAPLLQR.T	Acetyl (+42)	-.MSSAPLLQR.T
15	24	2	1122.68	-0.56	1	32.8	18.3	95.00%	K.IALPTRVEPK.V		K.IALPTRVEPK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
27	A6ZL71_YEAS7	42.94%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
96	111	3	1758.9	2.3	1	58.9	31	95.00%	F.TGESLRIPVSEDMLGR.I		K.TTVEFTGESLRIPVSEDMLGR.I
258	272	2	1741.89	0.51	1	66.2	30.2	95.00%	R.LALTTAEYLAYQTER.H		R.LALTTAEYLAYQTER.H
145	166	2	2397.15	-0.96	1	95.9	32.7	95.00%	R.IYPEEMISTGVSAIDTMNSIAR.G		R.IYPEEMISTGVSAIDTMNSIAR.G
273	289	2	1904.97	0.68	1	92.2	31.3	95.00%	R.HVLTILTDMSSYADALR.E		R.HVLTILTDMSSYADALR.E
15	25	2	1243.67	-0.42	1	49.2	30.4	95.00%	K.AVEQGFNVKPR.L		K.AVEQGFNVKPR.L
242	252	2	1254.66	2.1	0	41.2	29.2	95.00%	F.LNLANDPTIER.I		R.TSLFLNLANDPTIER.I
285	295	3	1157.62	1.7	1	34.9	29.1	95.00%	Y.ADALREVSAAR.E		R.HVLTILTDMSSYADALREVSAAR.E
273	295	3	2518.29	0.32	1	31.9	29.4	95.00%	R.HVLTILTDMSSYADALREVSAAR.E		R.HVLTILTDMSSYADALREVSAAR.E
322	352	3	3377.69	2.4	2	39.9	28.5	95.00%	R.VEGRNGSITQIPILTMPNDDITHPIPDLTGY.I	Deamidation (+1)	R.VEGRNGSITQIPILTMPNDDITHPIPDLTGYITEGQIFVDR.Q

353	362	2	1176.62	1.8	1	58.6	30.5	95.00%	Y.ITEGQIFVDR.Q		R.NGSITQIPILTMPNDDITHPIPDLTGYITEGQIFVDR.Q
102	111	2	1115.56	-0.74	0	38.8	31.1	95.00%	R.IPVSEDMLGR.I		R.IPVSEDMLGR.I
49	63	2	1702.89	-1	1	64	30.4	95.00%	R.YNEIVNLTLPDGTVR.Q		R.YNEIVNLTLPDGTVR.Q
91	111	3	2336.17	-0.64	1	35.2	31.6	95.00%	K.TTVEFTGESLRIPVSEDMLGR.I		K.TTVEFTGESLRIPVSEDMLGR.I
453	466	2	1663.86	0.83	1	56.9	31.1	95.00%	R.TVFESLDQAWSLLR.I		R.TVFESLDQAWSLLR.I
273	284	2	1378.68	2.1	1	33.4	32.1	95.00%	R.HVLTILTDMSSY.A		R.HVLTILTDMSSYADALR.E
26	43	2	1929.06	1.1	1	83.3	26	95.00%	R.LNYNTVSGVNGPLVILEK.V		R.LNYNTVSGVNGPLVILEK.V
170	189	2	2193.13	-1.5	1	71.4	30.1	95.00%	K.IPIFSASGLPHNEIAAQICR.Q	Carbamidomethyl (+57)	K.IPIFSASGLPHNEIAAQICR.Q
213	223	2	1131.57	2.1	0	77.4	30.8	95.00%	F.AAMGVNLETAR.F		K.DVHDGHEENFSIVFAAMGVNLETAR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
28	A6ZWJ5_YEAS7	33.41%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
171	187	2	1857.91	-0.92	0	83.2	32.4	95.00%	R.QAITDSMNGDPELINIK.F		R.QAITDSMNGDPELINIK.F
34	46	2	1582.77	-0.5	1	68.5	32.4	95.00%	K.QMSEQYVTPYLPK.S		K.QMSEQYVTPYLPK.S
410	422	2	1646.62	1.8	1	69.5	32.9	95.00%	Y.NCNCDQGNDFTFR.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.YNNCPLNDDIWNQYNCNCDQGNDFTFR.S
119	128	2	1194.61	0.088	1	59.7	32.1	95.00%	K.ACFVSLITER.D	Carbamidomethyl (+57)	K.ACFVSLITER.D
122	144	3	2631.39	2.4	1	28.8	27	95.00%	F.VSLITERDSMTQILQSIDEVQVK.F		K.ACFVSLITERDSMTQILQSIDEVQVK.F
207	223	2	1713.85	-0.71	0	51.3	31.6	95.00%	K.AAESLISLANVPDGDSR.A		K.AAESLISLANVPDGDSR.A
257	267	3	1465.67	0.024	1	52.2	33	95.00%	K.LYCDIDHDLFR.W	Carbamidomethyl (+57)	K.LYCDIDHDLFR.W
154	170	2	1979.98	1.7	1	66.3	32	95.00%	W.VFISQGELDGMKQEMIR.Q		K.NFAYPWVFISQGELDGMKQEMIR.Q
154	165	2	1322.66	1.3	1	69.9	32	95.00%	W.VFISQGELDGMK.Q		K.NFAYPWVFISQGELDGMK.Q
197	206	2	1291.61	2.1	1	33.1	32.3	95.00%	W.VYPEWIDENK.A		K.FAEIPADEWVYPEWIDENK.A
62	72	2	1302.63	-1.4	0	67	32.2	95.00%	R.IQSEQEEAELK.Q		R.IQSEQEEAELK.Q
119	144	3	3009.51	-1.1	1	40.5	29.7	95.00%	K.ACFVSLITERDSMTQILQSIDEVQVK.F	Carbamidomethyl (+57)	K.ACFVSLITERDSMTQILQSIDEVQVK.F
129	144	2	1832.92	2	0	67.9	31.6	95.00%	R.DSMTQILQSIDEVQVK.F		R.DSMTQILQSIDEVQVK.F
61	72	2	1458.73	-0.91	1	64.4	31.4	95.00%	R.RIQSEQEEAELK.Q		R.RIQSEQEEAELK.Q
423	435	2	1457.61	0.084	1	35.1	32.1	95.00%	R.SGSCGGHYFDIMK.K	Carbamidomethyl (+57)	R.SGSCGGHYFDIMK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
29	B3LPA7_YEAS1	22.91%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
83	107	4	2992.37	-0.12	1	26.8	32.7	95.00%	R.LQVVSHETDINEDEEEAHYEDKHVK.R		R.LQVVSHETDINEDEEEAHYEDKHVK.R
287	300	2	1397.69	-0.8	1	35.5	31.9	95.00%	R.NPGAWGPGIISSDK.S		R.NPGAWGPGIISSDK.S
504	513	3	1146.6	-0.18	2	23.8	30.4	91.10%	R.GISRDDLPFK.A		R.GISRDDLPFK.A
83	101	3	2255.99	1.6	1	50.2	34.2	95.00%	R.LQVVSHETDINEDEEEAHY.E		R.LQVVSHETDINEDEEEAHYEDK.H
17	45	3	3368.47	-1	0	51.6	33.2	95.00%	K.QNNIGEQSMQELPEDQIEHEMEAIDPSNK.T	Oxidation (+16)	K.QNNIGEQSMQELPEDQIEHEMEAIDPSNK.T
588	600	2	1585.75	-0.53	1	37.6	32.9	95.00%	R.EIEAIIWEDDEPK.N		R.EIEAIIWEDDEPK.N
83	104	3	2628.15	1.8	1	89.9	33.7	95.00%	R.LQVVSHETDINEDEEEAHYEDK.H		R.LQVVSHETDINEDEEEAHYEDK.H
4	12	2	1022.54	0.18	1	29.1	29.1	94.70%	R.FSNIITSNK.W		R.FSNIITSNK.W
576	587	3	1473.75	2.2	1	56.7	31.1	95.00%	W.KLEDIDIDSDRR.E		R.FIWKLEDIDIDSDRR.E
435	441	2	869.44	1.7	1	27.7	26.1	95.00%	K.QFGYVTR.Q		K.QFGYVTR.Q
62	82	2	2110.08	-0.67	0	120	30.2	95.00%	K.HGSLQGGAIADVNSITNSLTR.L		K.HGSLQGGAIADVNSITNSLTR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
30	A6ZQN6_YEAS7	12.26%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
603	613	2	1379.69	2.2	2	37.5	32.2	95.00%	F.EIEEKEESFLK.N		K.NTFEIEEKEESFLK.N
1	25	3	2894.38	1.8	1	44.7	31.9	95.00%	-.MDPGIANHTLPEEFEEVVVPEMLEK.E	Acetyl (+42)	-.MDPGIANHTLPEEFEEVVVPEMLEK.E
584	599	2	1740.86	1	0	79	32.4	95.00%	K.LTDSIALEGNDHLESK.N		K.LTDSIALEGNDHLESK.N

519	530	2	1304.67	1.3	2	47.8	31.2	95.00%	K.RISDPTLAAQAY.G		K.RISDPTLAAQAYGSPFTFITTYTWGTPER.I
259	268	3	1187.66	-0.095	1	44	29.4	95.00%	R.LKPEFEALNK.L		R.LKPEFEALNK.L
581	599	3	2120.05	1.4	1	56.7	31.9	95.00%	R.NHKLTDSIALEGNDHLESK.N		R.NHKLTDSIALEGNDHLESK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
31	A6ZPC6_YEAS7	18.95%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1178	1196	2	2031.87	1.2	1	44.4	34.1	95.00%	K.LDYTVGFCGDGANDCGALK.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.LDYTVGFCGDGANDCGALK.A
1049	1065	2	1820.92	1.8	0	78.4	31.8	95.00%	R.TIMCTGDNILTAISVGR.E	Carbamidomethyl (+57)	R.TIMCTGDNILTAISVGR.E
74	90	2	1836.88	2.9	0	79.5	32.8	95.00%	F.QSSNLPSPHSSGNLEQR.G		R.ASFSSTATTSTAATLTSAMVLDQNNSEPYAGATFEAVPSSIVSFHHPHHSFQSSNLPSPHSSGNLEQR.G
443	464	2	2489.18	4.1	1	72.5	32.7	95.00%	K.TNNNWIDPDWVDLSTVSNGLTK.G	Deamidation (+1)	K.TNNNWIDPDWVDLSTVSNGLTK.G
959	970	2	1315.64	-0.53	0	45.3	31.6	95.00%	K.GAPEVISEICNK.S	Carbamidomethyl (+57)	K.GAPEVISEICNK.S
199	221	3	2438.11	-0.16	1	60.9	34.1	95.00%	R.LGENSDTGFVYHSATHSSSSLSR.Y		R.LGENSDTGFVYHSATHSSSSLSR.Y
542	549	2	947.42	2.5	1	30.7	31.5	93.80%	R.NLAEMSHF.H		R.NLAEMSHFHCDVR.V
1075	1093	2	2134.12	2.5	1	27.4	29.6	91.50%	R.VYVPSINDTPLHGEPVIVW.R		R.VYVPSINDTPLHGEPVIVWR.D
264	279	2	1814.73	1.6	1	47.5	33.1	95.00%	R.GSFSGHDDVHNQHSEY.L		R.GSFSGHDDVHNQHSEYLKPDYHEK.F
823	835	2	1528.69	-0.19	1	64.3	33.5	95.00%	K.FSLNDCSSPLDFK.S	Carbamidomethyl (+57)	K.FSLNDCSSPLDFK.S
809	817	2	1048.56	0.54	1	76.1	30.6	95.00%	K.FGELLSDIR.Q		K.FGELLSDIR.Q
94	109	2	1744.88	0.048	0	73.5	30.9	95.00%	R.LTESEPLVLSSAEQSR.S		R.LTESEPLVLSSAEQSR.S
639	649	2	1296.68	-0.48	1	35.5	29	95.00%	K.SFLYNGTNIIR.A		K.SFLYNGTNIIR.A
93	109	3	1900.99	0.0014	1	27.7	29.8	95.00%	R.RLTESEPLVLSSAEQSR.S		R.RLTESEPLVLSSAEQSR.S
1163	1177	2	1825.91	0.38	1	33.9	31.6	95.00%	R.MSPDEKHELMIQLQK.L		R.MSPDEKHELMIQLQK.L
1	14	2	1651.77	-0.58	0	92.7	33.1	95.00%	-.MDIPSSNQIQHGQR.S	Acetyl (+42)	-.MDIPSSNQIQHGQR.S
1127	1136	2	1063.57	1.9	1	41.2	30.2	95.00%	Y.TLAVSGDVFR.L		R.ECNYTLAVSGDVFR.L
1113	1126	2	1653.74	1.1	2	61.9	33.7	95.00%	K.LGNNSVESLRECNY.T	Carbamidomethyl (+57)	K.LGNNSVESLRECNYTLAVSGDVFR.L
851	864	2	1488.75	1.8	1	64.6	31.6	95.00%	R.SVDGNLLGDPLDFK.M		R.SVDGNLLGDPLDFK.M
760	768	2	1049.53	0.86	1	36.2	31.5	95.00%	K.GIFCISPTR.L	Carbamidomethyl (+57)	K.GIFCISPTR.L
1113	1122	2	1087.56	0.26	0	90.7	29.9	95.00%	K.LGNNSVESLR.E		K.LGNNSVESLR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
32	XPP_YEAST	31.64%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
443	453	2	1204.72	1.4	0	31.4	20.1	95.00%	F.AIIHSPIDVLK.S		K.MTAQNFAIIHSPIDVLK.S
200	213	2	1859.82	-0.96	1	97.9	33.9	95.00%	R.QNEDPITWQEWCVR.E	Carbamidomethyl (+57)	R.QNEDPITWQEWCVR.E
549	565	2	1898.87	0.59	1	81	33.3	95.00%	Y.LCDSGSQFLEGTTDITR.T	Carbamidomethyl (+57)	K.IYLCDSGSQFLEGTTDITR.T
533	548	2	1776.86	0.95	2	35.2	32.7	95.00%	Y.SPPVENSSMIDPTKIY.L		R.NFMGNSFETISSTGSNAAIIHYSPPVENSSMIDPTKIYLCDSGSQFLEGTTDITR.T
533	546	2	1500.71	1.1	0	54.7	32.8	95.00%	Y.SPPVENSSMIDPTK.I		R.NFMGNSFETISSTGSNAAIIHYSPPVENSSMIDPTK.I
389	397	2	1182.61	1.5	1	40.5	30	95.00%	Y.EQIWEHLTK.I		K.INGIEVRPYEQIWEHLTK.I
380	397	3	2224.16	-0.36	1	40.2	28.9	95.00%	K.INGIEVRPYEQIWEHLTK.I		K.INGIEVRPYEQIWEHLTK.I
398	417	2	2175.02	1.6	1	30.5	33.5	90.20%	K.ITSQASSAEHEFLIPDSASW.Q		K.ITSQASSAEHEFLIPDSASWQMVR.C
398	421	3	2689.28	-0.74	1	36.8	32.3	95.00%	K.ITSQASSAEHEFLIPDSASWQMVR.C		K.ITSQASSAEHEFLIPDSASWQMVR.C
547	565	2	2175.02	0.79	1	36.8	33.5	95.00%	K.IYLCDSGSQFLEGTTDITR.T	Carbamidomethyl (+57)	K.IYLCDSGSQFLEGTTDITR.T
189	199	2	1449.72	-0.49	1	31.8	31.8	94.80%	R.QELDYNWTLLR.Q		R.QELDYNWTLLR.Q
673	680	2	947.5	-0.55	0	35.2	30.5	95.00%	R.IESDMLIK.K		R.IESDMLIK.K
162	174	2	1498.67	-0.22	1	34.3	33.5	95.00%	R.DLLNFNDDHPDGK.S		R.DLLNFNDDHPDGK.S
125	136	2	1462.61	1.6	1	37.4	33.2	95.00%	Y.IVPSCDEHQSEY.V	Carbamidomethyl (+57)	K.HDLCCYIVPSCDEHQSEYVSLR.D
566	585	3	2373.26	-1.4	2	30.1	27.5	95.00%	R.TIHLTKPTKEEMDNYTLVLK.G		R.TIHLTKPTKEEMDNYTLVLK.G

422	435	2	1434.68	-0.49	0	74.3	32.8	95.00%	R.CLNTSTNANGAIAK.K	Carbamidomethyl (+57)/ Deamidation (+1)	R.CLNTSTNANGAIAK.K
436	453	3	2025.11	-0.14	2	55.1	26.6	95.00%	K.KMTAQNFAIIHSPIDVLK.S		K.KMTAQNFAIIHSPIDVLK.S
511	532	2	2360.08	0.5	1	90	33.8	95.00%	R.NFMGNSFETISSTGSNAAIIHY.S		R.NFMGNSFETISSTGSNAAIIHYSPPVENSSMIDPTK.I
593	609	2	1886.99	0.29	1	60.2	29.5	95.00%	R.LIFPENTPGFNIDAIAR.Q		R.LIFPENTPGFNIDAIAR.Q
12	24	4	1428.71	1.1	0	31.2	31.3	95.00%	R.AHSISHVPGTHMR.G		R.AHSISHVPGTHMR.G
437	453	3	1897.01	-0.1	1	45.2	28.6	95.00%	K.MTAQNFAIIHSPIDVLK.S		K.MTAQNFAIIHSPIDVLK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
33	B3LFI3_YEAS1	31.67%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
359	375	3	1791.97	2.4	1	37	26.9	95.00%	R.WGDAPVHSIAAALFLPK.D		R.WGDAPVHSIAAALFLPK.D
45	65	2	2280.04	0.83	1	78.1	33.4	95.00%	F.DFTSGSISPEQQVISEENDAK.K		R.TQQYIPSSISAAFDFTSGSISPEQQVISEENDAK.K
424	435	2	1409.72	-0.15	1	58.7	31.2	95.00%	K.EYYDAQGLVKPK.N		K.EYYDAQGLVKPK.N
105	117	2	1487.7	0.86	1	75.5	32.8	95.00%	K.TTMDYITPSFANK.A		K.TTMDYITPSFANK.A
66	88	2	2526.09	-0.88	1	102	33.9	95.00%	K.KLEQSALNSEASEDSEAMDEESK.A		K.KLEQSALNSEASEDSEAMDEESK.A
378	386	2	1113.52	2.1	1	29.9	31.9	92.00%	K.IHYFSDIGY.H		K.IHYFSDIGYHHPPYDNCPLDK.E
298	317	2	2313.02	-0.27	1	94.8	33.9	95.00%	K.NPEYLDENNLMSFLSNDNGK.T		K.NPEYLDENNLMSFLSNDNGK.T
343	354	2	1427.6	1.6	1	54.4	33.3	95.00%	R.EYFDTLDHQGGF.F		R.EYFDTLDHQGGFFYER.W
345	354	2	1135.5	1.9	1	32.2	32	94.90%	Y.FDTLDHQGGF.F		R.EYFDTLDHQGGFFYER.W
32	44	2	1411.7	2.5	1	30.7	32	93.00%	R.TQQYIPSSISAAF.D		R.TQQYIPSSISAAFDFTSGSISPEQQVISEENDAK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
34	B3LS12_YEAS1	24.54%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
147	168	3	2346.99	1.1	1	32.3	34.3	95.00%	Y.SINDNEGVDEGKDANGNPMDEK.S		K.LEYSINDNEGVDEGKDANGNPMDEK.S
712	725	2	1640.8	1.3	0	76.2	33	95.00%	R.TTHGELITLDEEQR.L		R.TTHGELITLDEEQR.L
520	529	2	1197.63	1.9	2	31.2	28.3	95.00%	R.RQHQLEAGLF.A		R.RQHQLEAGLFAVDK.S
132	142	2	1306.61	0.9	1	45	32.3	95.00%	Y.TLDDEWTNSVK.K		R.TLYTLDDEWTNSVK.K
394	403	2	1122.61	2.1	0	34.1	29.5	95.00%	F.LDVSNTIHPK.W		R.SPDFKPVENNYDNSTNVPQEIWFLDVSNTIHPK.W
473	479	2	890.49	0.65	1	36.2	28.3	95.00%	R.YETLLPR.N		R.YETLLPR.N
521	533	3	1454.75	0.21	1	43.9	30.7	95.00%	R.QHQLEAGLFAVDK.S		R.QHQLEAGLFAVDK.S
393	403	3	1269.67	1.6	1	46.1	28.9	95.00%	W.FLDVSNTIHPK.W		R.SPDFKPVENNYDNSTNVPQEIWFLDVSNTIHPK.W
685	700	2	1708.74	-0.73	1	88.8	34	95.00%	R.ASAGACGGYIWCATHK.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.ASAGACGGYIWCATHK.T
726	740	2	1703.87	-1.1	1	58.5	30.7	95.00%	R.LHIDAVNTVWSHANK.D		R.LHIDAVNTVWSHANK.D
597	616	3	2230.05	1.9	1	94.9	33.1	95.00%	K.RQEAAVEICSGQIAHMSTDK.K	Carbamidomethyl (+57)	K.RQEAAVEICSGQIAHMSTDK.K
113	122	2	1230.6	0.22	1	57.4	32	95.00%	K.HFNELSLTDR.C		K.HFNELSLTDR.C
129	142	2	1683.8	-0.42	1	76.2	33.3	95.00%	R.TLYTLDDEWTNSVK.K		R.TLYTLDDEWTNSVK.K
192	207	2	1934.94	2.7	1	55.2	32.6	95.00%	R.CFMQANPVNIQEIFPK.S	Carbamidomethyl (+57)	R.CFMQANPVNIQEIFPK.S
274	282	2	1029.59	-0.022	1	30.5	29.4	95.00%	K.VLEQGFLPK.F		K.VLEQGFLPK.F
520	533	2	1610.85	-0.26	2	54.1	29.1	95.00%	R.RQHQLEAGLFAVDK.S		R.RQHQLEAGLFAVDK.S
451	457	2	842.43	-0.024	1	23.8	26.8	90.20%	K.TGTVFYR.E		K.TGTVFYR.E
353	364	2	1387.7	1.6	1	69.6	31.4	95.00%	Y.RGDELSQELVDK.L		R.FEGNTLPIQVVYRGDELSQELVDK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
35	GNP1_YEAST	17.80%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
42	57	2	1909.9	1.9	1	69.7	33.2	95.00%	K.QIGSIEPENEVEYFEK.T		K.QIGSIEPENEVEYFEK.T
11	34	3	2813.14	-1.1	2	62.5	33.8	95.00%	R.NNEGSSNMNMNRNDLDDVSHYEMK.E		R.NNEGSSNMNMNRNDLDDVSHYEMK.E
110	122	2	1504.71	-0.14	1	59.3	32.4	95.00%	K.DSSSQLDNELNRK.S		K.DSSSQLDNELNRK.S
86	109	3	2414.11	1.5	1	80.9	33.1	95.00%	R.RAEGSHANSPDSSNSNGTTPISTK.D		R.RAEGSHANSPDSSNSNGTTPISTK.D

87	109	2	2258	-1.5	0	56.5	34	95.00%	R.AEGSHANSPDSSNSNGTTPISTK.D		R.AEGSHANSPDSSNSNGTTPISTK.D
62	78	3	2077.92	0.49	1	44	34.2	95.00%	K.TIENMEYEGEHHASYLR.R		K.TIENMEYEGEHHASYLR.R
418	431	2	1441.77	-0.0067	1	66.7	28.5	95.00%	K.ASPYVIAVSSHGVR.V		K.ASPYVIAVSSHGVR.V
62	76	2	1808.73	1.5	1	52.5	33.7	95.00%	K.TIENMEYEGEHHASY.L		K.TIENMEYEGEHHASYLR.R
123	132	2	1081.57	1.7	1	34.2	29.1	95.00%	K.SSYITVDGIK.Q		K.SSYITVDGIK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
36	MAM3_YEAST	27.48%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
427	457	3	3326.51	1.9	0	69.5	32.3	95.00%	K.AADQADESSPLLSPSNSNHPSEHPQQDLNNK.S		K.AADQADESSPLLSPSNSNHPSEHPQQDLNNK.S
391	399	2	1165.55	1.1	0	49.6	32.3	95.00%	F.VDMHQHIMR.Q		K.EPGSSHGAIGVLTLEDVIEELIGEEIVDESDVFVDMHQHIMR.Q
637	651	2	1766.75	-0.12	1	80.9	33.8	95.00%	K.SEYGNENINQENSNR.S		K.SEYGNENINQENSNR.S
609	619	2	1158.65	0.32	0	41.5	28.5	95.00%	K.NGIVESVITVK.G	Deamidation (+1)	K.NGIVESVITVK.G
683	691	2	1025.48	0.46	1	29.9	32.3	91.30%	R.SNFTDSLSR.T		R.SNFTDSLSR.T
514	535	3	2380.18	2.5	1	51.2	31.3	95.00%	K.IITTHTPHSSKEPSPAPHSNDK.S		K.IITTHTPHSSKEPSPAPHSNDK.S
254	266	2	1575.8	1.7	2	40	31.4	95.00%	K.RVEEIMTPIENVF.T		K.RVEEIMTPIENVFTMSADTILDDK.T
267	277	2	1224.56	0.95	0	57.6	32.6	95.00%	F.TMSADTILDDK.T	Oxidation (+16)	R.VEEIMTPIENVFTMSADTILDDK.T
236	251	2	1757.02	-0.065	1	89.9	22.5	95.00%	R.LTKDEVTIISAVLDLK.A		R.LTKDEVTIISAVLDLK.A
254	277	3	2766.35	-0.11	2	63.9	31.3	95.00%	K.RVEEIMTPIENVFTMSADTILDDK.T		K.RVEEIMTPIENVFTMSADTILDDK.T
282	289	2	926.46	0.074	1	27.1	29.1	92.00%	K.IFNSGFSR.I		K.IFNSGFSR.I
536	553	3	2011.98	0.21	0	47.4	32.5	95.00%	K.SLSAEEQQLLSDHAELSR.Q		K.SLSAEEQQLLSDHAELSR.Q
470	500	3	3211.68	-0.52	0	40	25.8	95.00%	R.SNAVLSPTPQVTEHGTIIPSNLASNPLNVNK.S		R.SNAVLSPTPQVTEHGTIIPSNLASNPLNVNK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
37	YD089_YEAST	22.09%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
529	548	2	2334.16	2.8	1	35.3	31.3	95.00%	K.SVVTNEFQCSLIPPDLTTWK.I	Carbamidomethyl (+57)	K.SVVTNEFQCSLIPPDLTTWK.I
218	240	3	2406.99	-0.97	0	42.4	34.2	95.00%	R.SDESAHTSSSPEANNSSLPASPR.S	Phospho (+80)	R.SDESAHTSSSPEANNSSLPASPR.S
509	524	2	1737.85	-0.24	2	82.2	32.9	95.00%	R.SSGLSQTAINEDNKFK.Q		R.SSGLSQTAINEDNKFK.Q
306	320	2	1603.77	-0.45	0	80.9	32.6	95.00%	K.EILDTTDNINSAGNK.S		K.EILDTTDNINSAGNK.S
78	90	2	1436.78	-0.22	1	68.3	28.6	95.00%	R.ILSVESSIIDFSK.G		R.ILSVESSIIDFSK.G
32	47	2	1817.74	1.7	1	66.4	33.8	95.00%	K.VTAYDYDNPNDSGMEK.L		K.VTAYDYDNPNDSGMEK.L
295	305	2	1190.64	-0.68	0	48.6	29.6	95.00%	R.IIDDSIISTSK.E		R.IIDDSIISTSK.E
404	414	2	1292.72	0.064	0	48.2	26.6	95.00%	R.NHVVTNDLLLR.D		R.NHVVTNDLLLR.D
661	672	2	1376.68	1.6	0	44.6	32	95.00%	R.STTDNEESLLLR.N		R.STTDNEESLLLR.N
733	746	2	1499.65	2.7	1	64.3	33.2	95.00%	F.GSQSTSASYDDVQR.Y		K.HPHCSSTNYGSVASFGSQSTSASYDDVQR.Y
274	285	2	1349.71	1.8	1	55	30.9	95.00%	R.FLLSSEDIEGLK.F		R.FLLSSEDIEGLK.F
295	320	3	2776.4	2.3	1	55.8	29.3	95.00%	R.IIDDSIISTSKEILDTTDNINSAGNK.S		R.IIDDSIISTSKEILDTTDNINSAGNK.S
342	353	2	1298.68	-0.63	0	30.8	29.6	95.00%	K.NILPSAVQSNEK.Y		K.NILPSAVQSNEK.Y
574	590	2	1910.89	0.092	1	68.5	33.2	95.00%	K.LNSDDSLSPDEFFQLGK.D		K.LNSDDSLSPDEFFQLGK.D
509	522	2	1462.69	-0.83	0	73.8	32.3	95.00%	R.SSGLSQTAINEDNK.F		R.SSGLSQTAINEDNK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
38	YJ12B_YEAST	16.13%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
987	1001	2	1640.82	-1.2	0	49.1	31.3	95.00%	R.EVDPNISESNILPSK.K		R.EVDPNISESNILPSK.K
400	419	2	2073.92	-0.2	0	113	34.1	95.00%	R.AHNVSTSNNSPSTDNDSISK.S		R.AHNVSTSNNSPSTDNDSISK.S
1050	1075	3	2789.22	1.3	1	70.9	33.7	95.00%	R.HSDSYSENETNHTNVPISSTGGTNNK.T		R.HSDSYSENETNHTNVPISSTGGTNNK.T
278	289	2	1236.56	1.8	1	29.8	32.3	91.20%	Y.NGSTPADAFETK.V		K.MQSDTQEANDIVTLANLQYNGSTPADAFETK.V

331	354	3	2813.38	-0.1	1	72.6	31.5	95.00%	R.HLNMTVAELFLDIHAIYEEQQGSR.N		R.HLNMTVAELFLDIHAIYEEQQGSR.N
1003	1022	3	2072.99	-0.71	1	38.5	33.1	95.00%	K.RSSTPQISNIESTGSGGMHK.L		K.RSSTPQISNIESTGSGGMHK.L
471	491	3	2226.08	1.6	0	89	32.9	95.00%	R.SAHHIHSASSNPDINVVDAQK.R		R.SAHHIHSASSNPDINVVDAQK.R
1713	1730	4	2169.06	0.31	2	28.4	32.2	95.00%	R.LRDEVSGNHLHVCYIETK.K	Carbamidomethyl (+57)	R.LRDEVSGNHLHVCYIETK.K
25	39	2	1638.78	-0.86	0	78.9	32.7	95.00%	K.EVHTNQDPLDVSASK.T		K.EVHTNQDPLDVSASK.T
25	45	2	2415.09	1.3	1	69.7	33.5	95.00%	K.EVHTNQDPLDVSASKTEECEK.A	Carbamidomethyl (+57)	K.EVHTNQDPLDVSASKTEECEK.A
1093	1113	3	2202.09	0.046	0	33.6	31.9	95.00%	R.SPSIDASPPENNSSHNIVPIK.T		R.SPSIDASPPENNSSHNIVPIK.T
1621	1632	2	1318.72	-0.46	1	43.7	29.1	95.00%	K.SQIGNIYLLNGK.V		K.SQIGNIYLLNGK.V
308	315	2	989.52	0.32	0	31.3	30.3	95.00%	K.VACQLIMR.G	Carbamidomethyl (+57)	K.VACQLIMR.G
1	24	4	2638.19	-0.25	0	34.7	33.6	95.00%	-.MESQQLSQHSHISHGSACASVTSK.E	Acetyl (+42)/ Carbamidomethyl (+57)	-.MESQQLSQHSHISHGSACASVTSK.E
837	850	2	1517.76	1.9	0	44.1	32.1	95.00%	F.GQPVIVNDHNPNSK.I		R.QHAGLAGLDISTLLPFGQPVIVNDHNPNSK.I
1234	1242	2	1115.51	0.078	1	55.2	31.3	95.00%	R.YDEAITYNK.D		R.YDEAITYNK.D
958	975	2	1855.84	-0.6	0	47.1	34	95.00%	K.AVSPTDSTPPSTHTEDSK.R		K.AVSPTDSTPPSTHTEDSK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
39	A6ZKX6_YEAS7	48.34%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
203	217	2	1628.89	1.3	2	81.1	28.1	95.00%	R.RGPLVVYAEDNGIVK.A		R.RGPLVVYAEDNGIVK.A
145	161	2	1880.05	2	0	80	24	95.00%	K.IPEIPLVVSTDLESIQK.T		K.IPEIPLVVSTDLESIQK.T
275	288	2	1525.81	1.4	0	45.6	28.9	95.00%	Y.TLPSHIISTSDVTR.I		K.VGYTLPSHIISTSDVTR.I
221	246	4	2610.43	0.51	0	45	23.6	95.00%	R.NVPGVETANVASLNLLQLAPGAHLGR.F		R.NVPGVETANVASLNLLQLAPGAHLGR.F
272	288	2	1844.96	-0.49	1	58	30	95.00%	K.VGYTLPSHIISTSDVTR.I		K.VGYTLPSHIISTSDVTR.I
347	360	2	1462.8	-0.5	1	27.4	27.7	94.40%	K.TGTKPAAVFTETLK.H		K.TGTKPAAVFTETLK.H
139	161	4	2586.44	0.79	1	25.7	21.4	95.00%	R.GHRVEKIPEIPLVVSTDLESIQK.T		R.GHRVEKIPEIPLVVSTDLESIQK.T
289	309	3	2267.23	-1.2	1	30	25.7	95.00%	R.IINSSEIQSAIRPAGQATQKR.T		R.IINSSEIQSAIRPAGQATQKR.T
289	308	2	2111.14	1.8	0	69.7	27.1	95.00%	R.IINSSEIQSAIRPAGQATQK.R		R.IINSSEIQSAIRPAGQATQK.R
258	271	2	1505.74	-0.27	1	76.6	32	95.00%	K.LDQVWGSETVASSK.V		K.LDQVWGSETVASSK.V
2	26	2	2617.39	1.9	1	60.7	26	95.00%	M.SRPQVTVHSLTGEATANALPLPAVF.S	Acetyl (+42)	-.MSRPQVTVHSLTGEATANALPLPAVFSAPIRPDIVHTVFTSVNK.N
2	44	4	4579.45	-0.97	1	44	28.5	95.00%	M.SRPQVTVHSLTGEATANALPLPAVFSAPIRPDIVHTVFTSVNK.N	Acetyl (+42)	-.MSRPQVTVHSLTGEATANALPLPAVFSAPIRPDIVHTVFTSVNK.N
347	362	3	1714.89	-0.24	1	34.9	30.3	95.00%	K.TGTKPAAVFTETLKHD.-		K.TGTKPAAVFTETLKHD.-
204	217	2	1472.79	-0.28	1	63.8	29.1	95.00%	R.GPLVVYAEDNGIVK.A		R.GPLVVYAEDNGIVK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
40	A6ZR77_YEAS7	19.27%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
402	411	2	1107.55	-1.3	1	39.2	32	95.00%	R.ISSNPQSFTK.Q		R.ISSNPQSFTK.Q
468	484	3	1978.92	-0.85	1	43.5	33.8	95.00%	R.SNNEHNLPNHYTNLANK.N		R.SNNEHNLPNHYTNLANK.N
47	64	2	2016.04	1.1	2	67.7	30.6	95.00%	R.DSSIIMANEPVAIKFEPR.H		R.DSSIIMANEPVAIKFEPR.H
467	484	4	2135.02	-0.32	2	32.2	33	95.00%	K.RSNNEHNLPNHYTNLANK.N		K.RSNNEHNLPNHYTNLANK.N
150	163	2	1735.89	-1.2	1	46.3	31.3	95.00%	R.DIKPDNFLISQYQR.I		R.DIKPDNFLISQYQR.I
20	45	3	2764.31	0.74	1	76	32.5	95.00%	K.IGEGSFGVIFEGENILHSCQAQTGSK.R	Carbamidomethyl (+57)	K.IGEGSFGVIFEGENILHSCQAQTGSK.R
5	19	3	1591.85	1.9	1	43.7	28.9	95.00%	R.SSQHIVGIHYAVGPK.I		R.SSQHIVGIHYAVGPK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
41	BPT1_YEAST	16.23%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1065	1077	2	1468.7	-4	1	48.9	33	95.00%	R.SPMTFFETTPVGR.I		R.SPMTFFETTPVGR.I
588	602	2	1784.85	2.3	1	87.8	32.6	95.00%	K.SFLLSDEIDDSFIER.I		K.SFLLSDEIDDSFIER.I
1343	1351	2	1006.58	0.67	1	29	24.2	95.00%	K.STLSLALFR.I		K.STLSLALFR.I

1311	1325	2	1799.96	1.5	1	56.6	28.8	95.00%	K.YRENLDPVLNNINVK.I		K.YRENLDPVLNNINVK.I
487	497	2	1395.63	0.63	1	30.3	32.7	91.30%	K.LYAWEEPMMAR.L		K.LYAWEEPMMAR.L
1431	1448	2	1946.83	-0.73	0	84.3	34.1	95.00%	R.GDDSNEEDGNVNDILDVK.I		R.GDDSNEEDGNVNDILDVK.I
807	816	2	1160.68	-0.53	1	46.3	23.2	95.00%	K.NIIEYVLIGK.T		K.NIIEYVLIGK.T
1273	1290	2	2115.02	-0.09	1	58.6	33	95.00%	R.IVEYCELPPEAQSINPEK.R	Carbamidomethyl (+57)	R.IVEYCELPPEAQSINPEK.R
1410	1423	4	1654.93	0.5	1	35.8	26.1	95.00%	K.RAVEQAHLKPHLEK.M		K.RAVEQAHLKPHLEK.M
1504	1513	3	1194.68	-0.25	1	39.9	23.2	95.00%	K.DRTILTIAHR.I		K.DRTILTIAHR.I
243	259	2	1913.1	2.5	1	42.1	22.4	95.00%	K.IKDPNQLPLPPVDLNIK.S		K.IKDPNQLPLPPVDLNIK.S
1449	1461	2	1386.69	0.64	0	63.5	31.9	95.00%	K.INENGSNLSVGQR.Q		K.INENGSNLSVGQR.Q
1377	1394	2	1924.01	1.4	1	78.5	29.6	95.00%	R.SHLAIIPQDAQAFEGTVK.T		R.SHLAIIPQDAQAFEGTVK.T
1506	1513	2	923.56	0.52	0	30.7	19.6	95.00%	R.TILTIAHR.I		R.TILTIAHR.I
611	625	2	1759.93	-0.36	1	55.4	29.5	95.00%	R.ALPAIEMNNITFLWK.S		R.ALPAIEMNNITFLWK.S
745	753	2	1056.56	0.77	0	27	28.8	92.50%	K.ACQLLPDLK.I	Carbamidomethyl (+57)	K.ACQLLPDLK.I
1377	1389	2	1409.73	1.8	1	53.4	30.6	95.00%	R.SHLAIIPQDAQAF.E		R.SHLAIIPQDAQAFEGTVK.T
843	862	2	2307.08	0.51	1	85.9	33.4	95.00%	Y.ALENGEIVEQGNYEDVMNRK.N		K.HSQMIYALENGEIVEQGNYEDVMNRK.N
628	655	3	2976.49	-0.19	1	67.4	29.4	95.00%	K.EVLTSSQSGDNLRTDEESIIGSSQIALK.N		K.EVLTSSQSGDNLRTDEESIIGSSQIALK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
42	A6ZV88_YEAS7	31.70%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
183	206	2	2780.1	1.2	1	65.6	33.8	95.00%	W.AFEDEDGDDEYATEETLSHHDNNK.G		K.SGDNLTVVINSLGWAFEDEDGDDEYATEETLSHHDNNK.G
138	143	2	705.44	0.11	1	27.5	21.8	95.00%	K.SIVLFK.F		K.SIVLFK.F
117	137	2	2401.11	0.45	1	81.3	33.6	95.00%	F.TVDELPESASDLLYEYSLDDK.S		R.FFANDVSLTVHDDSPLNISQSLSPIMEQFTVDELPESASDLLYEYSLDDK.S
169	182	2	1473.75	2.8	1	55.8	30.6	95.00%	K.SGDNLTVVINSLGW.A		K.SGDNLTVVINSLGWAFEDEDGDDEYATEETLSHHDNNK.G
144	152	2	1058.49	1.6	1	39.9	30.8	95.00%	K.FTSDAYDLK.K		K.FTSDAYDLK.K
29	38	2	1145.53	2.9	1	29.9	32.3	91.30%	K.ESSSFISFDK.E		K.ESSSFISFDK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
43	B3LGF8_YEAS1	29.17%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
79	95	3	1817.92	0.5	0	41.1	31.2	95.00%	K.AVDIDTIDAQPLHEGPK.I		K.AVDIDTIDAQPLHEGPK.I
27	37	2	1300.71	-0.7	1	35.2	29.1	95.00%	K.SVQTLKNEVQR.E		K.SVQTLKNEVQR.E
44	70	3	2881.47	1.9	1	44.2	27.9	95.00%	R.TSNQIALGNDKIEEINENSPLLSAPSK.Q		R.TSNQIALGNDKIEEINENSPLLSAPSK.Q
44	78	3	3791.94	-1.9	1	68.2	26.8	95.00%	R.TSNQIALGNDKIEEINENSPLLSAPSKQEEVSIPK.A		R.TSNQIALGNDKIEEINENSPLLSAPSKQEEVSIPK.A
145	174	3	3306.51	-0.32	1	51.1	32.4	95.00%	R.SVSPLQSITSCNTPMSEHELPVSSSNSFER.A	Carbamidomethyl (+57)	R.SVSPLQSITSCNTPMSEHELPVSSSNSFER.A
705	719	3	1679.76	1.7	1	49.3	33.4	95.00%	K.HATESSDWVHESAPK.F		K.HATESSDWVHESAPK.F
79	108	3	3258.6	1.9	1	62.1	29.4	95.00%	K.AVDIDTIDAQPLHEGPKIDDSPQDEVNSIK.G		K.AVDIDTIDAQPLHEGPKIDDSPQDEVNSIK.G
115	141	3	2930.3	1.5	1	44.4	33.1	95.00%	K.ANEDDLKPPSQHEACGNSALQSSITDF.S	Carbamidomethyl (+57)	K.ANEDDLKPPSQHEACGNSALQSSITDFSDR.S
215	247	3	3552.69	0.9	1	66.1	30.2	95.00%	Y.GSIPQSIGDVENGLNPPYVENTSSDELVHDLTR.R	Deamidation (+1)	K.SLHIVAPSPEVPVSGDEITSYGYGSIPQSIGDVENGLNPPYVENTSSDELVHDLTR.R
115	144	3	3288.46	-1.2	1	57.7	32.8	95.00%	K.ANEDDLKPPSQHEACGNSALQSSITDFSDR.S	Carbamidomethyl (+57)	K.ANEDDLKPPSQHEACGNSALQSSITDFSDR.S
192	212	2	2196.1	1	1	71	31	95.00%	K.SLHIVAPSPEVPVSGDEITSY.G		K.SLHIVAPSPEVPVSGDEITSYGYGSIPQSIGDVENGLNPPYVENTSSDELVHDLTR.R
175	191	2	1791.79	-0.45	0	73	33.9	95.00%	R.ADDMPVVQADNQTSSSK.S		R.ADDMPVVQADNQTSSSK.S
173	191	2	2076.94	2.4	1	95.8	33.9	95.00%	F.ERADDMPVVQADNQTSSSK.S		R.SVSPLQSITSCNTPMSEHELPVSSSNSFERADDMPVVQADNQTSSSK.S
96	108	2	1458.68	-0.56	0	62.7	32.7	95.00%	K.IDDSPQDEVNSIK.G		K.IDDSPQDEVNSIK.G

213	247	3	3772.77	0.37	1	88	30.1	95.00%	Y.GYGSIPQSIGDVENGLNPPYVENTSSDELVHDLTR.R	Deamidation (+1)	K.SLHIVAPSPEVPVSGDEITSYGYGSIPQSIGDVENGLNPPYVENTSSDELVHDLTR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
44	PTR2_YEAST	15.31%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
321	333	3	1438.72	1.5	1	42.2	31.7	95.00%	F.DFNAAKPSVHPEK.N		K.FDFNAAKPSVHPEK.N
2	16	2	1682.71	5.7	0	47.4	33.5	95.00%	M.LNHPSQGSDDAQDEK.Q	Acetyl (+42)/ Deamidation (+1)	-.MLNHPSQGSDDAQDEK.Q
35	48	2	1556.66	1.5	1	60.9	33.5	95.00%	K.DSYVSDDVANSTER.Y		K.DSYVSDDVANSTER.Y
1	27	4	3042.35	-0.68	2	42.4	33.1	95.00%	-.MLNHPSQGSDDAQDEKQGDFPVIEEEK.T		-.MLNHPSQGSDDAQDEKQGDFPVIEEEK.T
1	16	2	1829.75	5.6	0	55.2	33.5	95.00%	-.MLNHPSQGSDDAQDEK.Q	Acetyl (+42)/ Oxidation (+16)/ Deamidation (+1)	-.MLNHPSQGSDDAQDEK.Q
49	72	2	2812.21	1.8	1	59.9	33.7	95.00%	R.YNLSPSPEDEDFEGPTEEEMQTLR.H		R.YNLSPSPEDEDFEGPTEEEMQTLR.H
583	596	2	1628.81	1	0	68.5	31.9	95.00%	K.ANDIEILEPMESLR.S		K.ANDIEILEPMESLR.S
35	49	2	1799.69	1.1	2	72.8	33.2	95.00%	K.DSYVSDDVANSTERY.N	Phospho (+80)	K.DSYVSDDVANSTERYNLSPSPEDEDFEGPTEEEMQTLR.H
50	72	2	2649.15	3.9	1	103	34.1	95.00%	Y.NLSPSPEDEDFEGPTEEEMQTLR.H		R.YNLSPSPEDEDFEGPTEEEMQTLR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
45	A7A1A2_YEAS7	16.03%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
639	650	2	1455.69	2.3	1	33	32.7	95.00%	K.LSELENNNITFY.S		K.LSELENNNITFYSCGPATFNDDFR.N
663	674	2	1229.66	-0.49	0	43.2	30	95.00%	R.NAVVQGIDSSLK.I		R.NAVVQGIDSSLK.I
498	509	2	1339.65	-0.96	0	48	32.4	95.00%	K.VLSAPNHTVDCK.I	Carbamidomethyl (+57)	K.VLSAPNHTVDCK.I
471	485	2	1826.87	-0.61	2	80.7	33.2	95.00%	R.HRDPNNPDQLTMYVK.A		R.HRDPNNPDQLTMYVK.A
651	662	2	1385.57	1.4	1	51.8	33	95.00%	Y.SCGPATFNDDFR.N	Carbamidomethyl (+57)	K.LSELENNNITFYSCGPATFNDDFR.N
510	525	3	1739.96	-0.29	1	58.5	26.2	95.00%	K.IFLEGPYGVTVPHIAK.L		K.IFLEGPYGVTVPHIAK.L
51	67	2	1925.89	-0.35	1	122	33.8	95.00%	K.NINWLGSVTACAYENSK.S	Carbamidomethyl (+57)	K.NINWLGSVTACAYENSK.S
471	483	2	1599.71	1.8	2	63.1	34	95.00%	R.HRDPNNPDQLTMY.V		R.HRDPNNPDQLTMYVK.A
414	427	2	1464.73	1.3	0	48.1	32.6	95.00%	K.TATLSTTDDSNVIK.I		K.TATLSTTDDSNVIK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
46	A6ZT96_YEAS7	29.95%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
182	192	2	1056.6	2.3	0	38.5	28.7	95.00%	Y.VAGLVGDGLTR.L		K.MGNGMADYILDENYNLNGLQTVHDYDVYCHYVAGLVGDGLTR.L
2	15	3	1575.92	0.83	1	54.7	20.6	95.00%	M.GKLLQLALHPVEMK.A		-.MGKLLQLALHPVEMK.A
159	178	2	2397.11	0.34	1	34.7	33.3	95.00%	Y.ILDENYNLNGLQTVHDYDVY.C		K.MGNGMADYILDENYNLNGLQTVHDYDVYCHYVAGLVGDGLTR.L
226	235	2	1194.52	-0.35	1	49.5	32.3	95.00%	R.DYNEDLVDGR.S		R.DYNEDLVDGR.S
121	135	2	1760.93	-0.13	1	70.1	29.4	95.00%	R.AVLTDFESILIEFHK.L		R.AVLTDFESILIEFHK.L
136	145	3	1245.7	-0.79	1	26.6	27.8	95.00%	K.LKPEYQEVIK.E		K.LKPEYQEVIK.E
356	365	2	1143.63	1.1	1	31.8	29	95.00%	K.LAVQDPNFLK.L		K.LAVQDPNFLK.L
4	15	2	1390.8	1.6	0	48.1	22.7	95.00%	K.LLQLALHPVEMK.A		K.LLQLALHPVEMK.A
366	372	2	814.49	1.1	0	34.4	27.1	95.00%	K.LNIQISK.I		K.LNIQISK.I
136	150	3	1846.01	-0.21	1	32.1	27.7	95.00%	K.LKPEYQEVIKEITEK.M		K.LKPEYQEVIKEITEK.M
165	178	2	1649.77	1.8	1	45	33	95.00%	Y.NLNGLQTVHDYDVY.C		K.MGNGMADYILDENYNLNGLQTVHDYDVYCHYVAGLVGDGLTR.L
373	384	2	1589.67	-0.32	1	65.9	33.5	95.00%	K.IEQFMEEMYQDK.L		K.IEQFMEEMYQDK.L
179	192	2	1516.75	1.3	1	50	32.1	95.00%	Y.CHYVAGLVGDGLTR.L	Carbamidomethyl (+57)	K.MGNGMADYILDENYNLNGLQTVHDYDVYCHYVAGLVGDGLTR.L
108	118	2	1234.56	-0.1	1	35.4	32.2	95.00%	K.WSFDGNAPDVK.D		K.WSFDGNAPDVK.D
221	235	3	1791.88	0.057	2	46.7	32.4	95.00%	K.TNIIRDYNEDLVDGR.S		K.TNIIRDYNEDLVDGR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
47	A6ZVP9_YEAS7	35.83%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
201	221	3	2158.03	1.9	0	54.6	33.4	95.00%	R.GVAMNPVDHPHGGGNHQHIGK.A		R.GVAMNPVDHPHGGGNHQHIGK.A
129	147	3	2097.06	-0.76	1	61.9	30.9	95.00%	R.ASGNYVIIIGHNPDENKTR.V		R.ASGNYVIIIGHNPDENKTR.V
134	147	2	1604.87	1.5	1	62.1	29.1	95.00%	Y.VIIIGHNPDENKTR.V		R.ASGNYVIIIGHNPDENKTR.V
94	123	3	3046.59	-0.52	0	30	26.1	95.00%	K.ASLNVGNVLPLGSVPEGTIVSNVEEKPGDR.G		K.ASLNVGNVLPLGSVPEGTIVSNVEEKPGDR.G
164	181	3	1748.07	0.35	1	19.8	12	93.60%	R.GVIGVIAGGGRVDKPLLK.A		R.GVIGVIAGGGRVDKPLLK.A
129	145	2	1839.91	-0.55	1	59.4	31.8	95.00%	R.ASGNYVIIIGHNPDENK.T		R.ASGNYVIIIGHNPDENK.T
199	221	5	2431.18	3.6	1	26.2	32.5	92.60%	K.TRGVAMNPVDHPHGGGNHQHIGK.A	Oxidation (+16)	K.TRGVAMNPVDHPHGGGNHQHIGK.A
134	145	2	1347.72	1.2	0	64	30.5	95.00%	Y.VIIIGHNPDENK.T		R.ASGNYVIIIGHNPDENK.T
93	123	3	3174.69	-0.82	1	67.6	24.8	95.00%	K.KASLNVGNVLPLGSVPEGTIVSNVEEKPGDR.G		K.KASLNVGNVLPLGSVPEGTIVSNVEEKPGDR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
48	COS1_YEAST	30.18%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
157	167	2	1275.75	0.92	1	50	23.9	95.00%	R.TTLLEPFSLKK.D		R.TTLLEPFSLKK.D
102	108	2	935.49	1.7	1	31	30.5	95.00%	K.QLIQFCK.E	Carbamidomethyl (+57)	K.QLIQFCK.E
206	219	2	1525.81	-0.017	1	66.9	28.7	95.00%	K.SWSPVGLEDAKLPK.E		K.SWSPVGLEDAKLPK.E
357	369	2	1544.86	2.1	1	63.7	26.9	95.00%	R.ALSLNVELWPYIK.E		R.ALSLNVELWPYIK.E
19	33	3	1813.01	2.7	2	23.5	25.3	95.00%	K.QLESQKIVLPQDLFR.S		K.QLESQKIVLPQDLFR.S
291	313	2	2580.22	1	1	96.5	33.1	95.00%	K.MQFLSTIINEQESGANGWDEIAK.K		K.MQFLSTIINEQESGANGWDEIAK.K
25	33	2	1099.64	-0.29	1	27.9	27.1	95.00%	K.IVLPQDLFR.S		K.IVLPQDLFR.S
206	216	2	1187.58	-0.27	1	57.3	31.8	95.00%	K.SWSPVGLEDAK.L		K.SWSPVGLEDAK.L
157	166	2	1147.65	0.15	1	29.8	27.7	95.00%	R.TTLLEPFSLK.K		R.TTLLEPFSLK.K
11	18	2	893.49	-0.02	1	26.5	28.9	91.20%	K.SVDVLSFK.Q		K.SVDVLSFK.Q
109	132	2	2673.19	1.6	1	47.2	34	95.00%	K.EVTENTPSSDPHDWEVVAANLNSY.L		K.EVTENTPSSDPHDWEVVAANLNSYLYENK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
49	YNL5_YEAST	24.22%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
610	619	2	1143.59	-1.1	1	48	29.8	95.00%	K.IVEGGHEIYK.Y		K.IVEGGHEIYK.Y
13	36	3	2773.28	-0.87	1	48.2	32.3	95.00%	R.TGMERTDIDSEHPEAQPLLNNNHR.T		R.TGMERTDIDSEHPEAQPLLNNNHR.T
383	407	3	2598.32	3.1	1	61.2	29.1	95.00%	Y.DRPGYGLSDSPPAPISIAMVAESLR.Y		R.YCLYDRPGYGLSDSPPAPISIAMVAESLR.Y
18	36	3	2199.03	0.14	0	51.9	33.4	95.00%	R.TDIDSEHPEAQPLLNNNHR.T		R.TDIDSEHPEAQPLLNNNHR.T
37	52	2	1469.72	-0.9	0	82.9	32.2	95.00%	R.TLGAGSANGPAVNEGR.D		R.TLGAGSANGPAVNEGR.D
563	575	2	1430.7	-0.5	0	77.2	31.8	95.00%	R.DVTNNAESLQNVK.T		R.DVTNNAESLQNVK.T
465	491	3	2734.16	1.1	1	34.1	33.7	95.00%	R.LLPPGRGDGDDGDDGNGNDGDGRNHDK.T		R.LLPPGRGDGDDGDDGNGNDGDGRNHDK.T
215	235	3	2447.11	-0.41	2	73.5	33.8	95.00%	R.RIDDANISTFNENHTNSTENR.D		R.RIDDANISTFNENHTNSTENR.D
588	596	2	1117.53	1.9	1	34.2	31.6	95.00%	K.SALWGDWQR.D		K.SALWGDWQR.D
388	407	2	2010.05	0.83	0	74.4	29.7	95.00%	Y.GLSDSPPAPISIAMVAESLR.Y		R.YCLYDRPGYGLSDSPPAPISIAMVAESLR.Y
634	644	2	1186.64	-0.36	1	47.5	30.2	95.00%	R.LIGELGKLTED.-		R.LIGELGKLTED.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
50	A6ZZQ2_YEAS7	23.74%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
146	161	2	1868.88	1.7	1	53.5	33.3	95.00%	R.SLVSDLSPSELESWLK.R	Phospho (+80)	R.SLVSDLSPSELESWLK.R
582	606	2	2589.07	-1.9	1	108	34.2	95.00%	K.SQAYGATMSNESNANNNNSTSNASR.S		K.SQAYGATMSNESNANNNNSTSNASR.S
169	179	2	1265.55	-0.024	1	39.3	32.2	95.00%	K.SFVDENSPTDR.R		K.SFVDENSPTDR.R
517	534	2	2014.05	0.38	1	65.2	28.6	95.00%	K.AFGIHPLTTEDIFLGEVR.E		K.AFGIHPLTTEDIFLGEVR.E
74	88	3	1645.76	1.6	0	31.3	33.6	95.00%	W.GMLHESDSTSNDIIK.S		R.RPTQLLHDNLQHNHGQITDFDQIDSWGMLHESDSTSNDIIK.S

567	579	2	1471.69	-0.62	0	52.4	32.7	95.00%	K.QESATLDHESISR.R		K.QESATLDHESISR.R
304	323	2	2358.94	0.46	1	66.1	33.8	95.00%	F.HFQYDEDEEDGTSNEDGILF.S		R.SQAIQDAEAFHFQYDEDEEDGTS NEDGILFSKPIVTNIDVPELGNR.R
381	393	2	1411.78	-0.78	0	59.6	26.6	95.00%	R.IQSGLQDNLLVGR.N		R.IQSGLQDNLLVGR.N
565	579	3	1728.83	-0.11	1	54.1	33.1	95.00%	K.EKQESATLDHESISR.R		K.EKQESATLDHESISR.R
416	436	3	2191.15	1.7	0	27.8	29	95.00%	R.VDLDSTVHSPTISGLLQPGQK.F		R.VDLDSTVHSPTISGLLQPGQK.F
324	339	2	1750.96	1.3	0	65.4	25.9	95.00%	F.SKPIVTNIDVPELGNR.R		R.SQAIQDAEAFHFQYDEDEEDGTS NEDGILFSKPIVTNIDVPELGNR.R
110	126	2	1811.91	0.83	0	48.1	31.7	95.00%	R.EGPQSVSSTVQPQPIMK.F		R.EGPQSVSSTVQPQPIMK.F
394	410	3	2075.03	0.0005	1	28.5	31.4	95.00%	R.NIQYPPHIISNNPEHFR.F		R.NIQYPPHIISNNPEHFR.F
292	303	2	1347.68	1.8	2	58.5	31	95.00%	R.LRSQAIQDAEAF.H		R.LRSQAIQDAEAFHFQYDEDEEDG TSNEDGILFSKPIVTNIDVPELGNR. R
324	340	4	1907.06	1.8	1	25.8	24.9	95.00%	F.SKPIVTNIDVPELGNRR.V		R.SQAIQDAEAFHFQYDEDEEDGTS NEDGILFSKPIVTNIDVPELGNRR.V
294	303	2	1078.5	1.9	1	40.4	30.9	95.00%	R.SQAIQDAEAF.H		R.SQAIQDAEAFHFQYDEDEEDGTS NEDGILFSKPIVTNIDVPELGNR.R
468	480	2	1344.73	0.89	0	55.6	30.1	95.00%	K.AETVSQLQGLTAK.N		K.AETVSQLQGLTAK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
51	A6ZX34_YEAS7	20.00%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
130	143	2	1387.73	-0.011	0	60.9	30.2	95.00%	R.AIASSPSLNSNLSK.N		R.AIASSPSLNSNLSK.N
202	232	3	3549.55	0.53	2	60.7	32.3	95.00%	F.GGYPASSFPLMIDEKEEDDYLHN PDPEEEAR.L		R.SPTSSPGNESSASFSSNPFLGEQ DFSPFGGYPASSFPLMIDEKEEDD YLHNPDPEEEAR.L
188	201	2	1570.7	0.87	1	41.4	33.1	95.00%	F.SSNPFLGEQDFSPF.G		R.SPTSSPGNESSASFSSNPFLGEQ DFSPFGGYPASSFPLMIDEK.E
494	508	2	1572.75	-0.4	0	81.3	32.5	95.00%	R.GAPEIDVLEGETDTK.I		R.GAPEIDVLEGETDTK.I
114	129	2	1752.85	-0.64	1	40	32.7	95.00%	R.AVSTANDNSFLQPPHR.A		R.AVSTANDNSFLQPPHR.A
476	493	2	2013.86	-1.1	0	65	34.4	95.00%	K.LSICTCDGEDHPNQGVGR.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.LSICTCDGEDHPNQGVGR.G
304	316	2	1358.66	0.13	0	41.9	31.7	95.00%	R.TSLVDPDTPDTAK.T		R.TSLVDPDTPDTAK.T
393	401	2	1049.5	-0.0072	1	40.2	30.5	95.00%	R.SGMLQSWNK.V		R.SGMLQSWNK.V
174	187	2	1353.57	1.8	1	58.3	32.9	95.00%	R.SPTSSPGNESSASF.S		R.SPTSSPGNESSASFSSNPFLGEQ DFSPFGGYPASSFPLMIDEK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
52	NCPR_YEAST	27.64%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
227	245	2	2062.96	1.7	1	84.5	33.1	95.00%	Y.TVLNEITDSMSLGEPSAHY.L		K.FTSQFQYTVLNEITDSMSLGEPS AHYLPSHQLNR.N
254	275	2	2355.24	-1.9	1	46	27.5	95.00%	R.NADGIQLGPFDLSQPYIAPIVK.S		R.NADGIQLGPFDLSQPYIAPIVK.S
200	219	3	2351.23	1.8	1	55.7	28.6	95.00%	W.KDSILEVLKDELHLDEQEAK.F		K.LGEADDGAGTTDEDYMAWKDSI LEVLKDELHLDEQEAK.F
653	664	2	1171.69	0.074	0	31.5	26.4	95.00%	K.GVSTALVGILSR.G		K.GVSTALVGILSR.G
326	343	2	2054.1	1.6	1	69.1	27.7	95.00%	F.NLDPETIFDLKPLDPTVK.V		K.VEQFLSIFNLDPETIFDLKPLDPTV K.V
429	439	2	1255.66	2	0	42.5	29.1	95.00%	F.LVESVPQMTPR.Y		K.WDTVPMQFLVESVPQMTPR.Y
452	483	3	3452.83	-0.72	1	64.7	25.1	95.00%	K.QTVHVTSIVENFPNPELPDAPPV VGVTTNLLR.N		K.QTVHVTSIVENFPNPELPDAPPV VGVTTNLLR.N
484	503	2	2264.16	1.1	1	97.1	29.9	95.00%	R.NIQLAQNNVNIAETNLPVHY.D		R.NIQLAQNNVNIAETNLPVHYDLNG PR.K
440	451	2	1349.63	-0.22	1	70.5	32.2	95.00%	R.YYSISSSSLSEK.Q		R.YYSISSSSLSEK.Q
201	219	3	2223.13	0.59	1	34.7	30.2	95.00%	K.DSILEVLKDELHLDEQEAK.F		K.DSILEVLKDELHLDEQEAK.F

49	59	2	1229.63	-0.012	0	78.6	30.8	95.00%	R.DIAQVVTENNK.N		R.DIAQVVTENNK.N
598	611	3	1574.79	1.8	2	56.2	31.7	95.00%	K.KLDGSFEMVVAHSR.L		K.KLDGSFEMVVAHSR.L
334	343	2	1124.65	1.4	0	38.1	22.9	95.00%	F.DLKPLDPTVK.V		K.VEQFLSIFNLDPETIFDLKPLDPTVK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
53	A6ZNT9_YEAS7	59.05%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
27	36	2	1169.54	0.31	1	52.3	32.7	95.00%	R.FVSNDFAENK.E		R.FVSNDFAENK.E
37	48	2	1302.69	-0.41	1	32.8	29.9	95.00%	K.EPTIGAAFLTQR.V		K.EPTIGAAFLTQR.V
49	58	2	1186.64	1.8	2	39	30.1	95.00%	R.VTINEHTVKF.E		R.VTINEHTVKFEIWDTAGQER.F
156	170	2	1590.79	1.4	1	71.8	31.6	95.00%	K.TGENVNDVFLGIGEK.I		K.TGENVNDVFLGIGEK.I
10	20	2	1068.66	1.5	0	31.7	22.1	95.00%	K.LVLLGEAAVGK.S		K.LVLLGEAAVGK.S
58	68	2	1350.62	-0.24	1	70.8	33.2	95.00%	K.FEIWDTAGQER.F		K.FEIWDTAGQER.F
79	97	2	2091.14	-0.53	1	79.3	26.5	95.00%	R.NAQAALVVYDVTKPQSFIK.A		R.NAQAALVVYDVTKPQSFIK.A
104	121	3	1977.09	1.8	1	50.7	25.6	95.00%	K.ELHEQASKDIIIALVGNK.I		K.ELHEQASKDIIIALVGNK.I
1	9	2	1037.51	0.87	0	34.2	32	95.00%	-.MNTSVTSIK.L	Acetyl (+42)/ Oxidation (+16)	-.MNTSVTSIK.L
146	155	2	1111.59	-0.21	1	48.5	27.3	95.00%	K.GLLFFETSAK.T		K.GLLFFETSAK.T
59	68	2	1203.55	1.6	1	43.6	32.4	95.00%	F.EIWDTAGQER.F		K.FEIWDTAGQER.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
54	A6ZM54_YEAS7	30.81%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
181	190	2	1274.51	-0.81	1	53.8	32.2	95.00%	K.MDFEENTFDK.V		K.MDFEENTFDK.V
356	366	2	1324.7	0.43	1	28.6	29.2	93.90%	K.LFTPMMLFVAR.K		K.LFTPMMLFVAR.K
26	34	2	906.48	-0.12	0	49.7	30.7	95.00%	K.TGLSALMSK.N		K.TGLSALMSK.N
367	383	2	1844.84	-0.39	0	62.2	34.1	95.00%	R.KPENAETPSQTSQEATQ.-		R.KPENAETPSQTSQEATQ.-
240	253	2	1544.85	1.2	2	84.7	28.5	95.00%	R.KIAYEIELGDGIPK.M		R.KIAYEIELGDGIPK.M
140	157	2	2039.97	-0.087	1	71.7	33.3	95.00%	R.FTGCNVIGLNNNDYQIAK.A	Carbamidomethyl (+57)	R.FTGCNVIGLNNNDYQIAK.A
364	383	3	2171.05	2.7	1	51.3	32.7	95.00%	F.VARKPENAETPSQTSQEATQ.-		K.LFTPMMLFVARKPENAETPSQTSQEATQ.-
191	202	2	1358.66	-6.4	1	48.2	31.7	95.00%	K.VYAIEATCHAPK.L	Carbamidomethyl (+57)	K.VYAIEATCHAPK.L
120	135	2	1540.77	-1.1	0	69.9	32.1	95.00%	R.GDLVLDVGCGVGGPAR.E	Carbamidomethyl (+57)	R.GDLVLDVGCGVGGPAR.E
241	253	2	1416.75	2.3	1	68.4	29.5	95.00%	K.IAYEIELGDGIPK.M		K.IAYEIELGDGIPK.M
165	175	2	1358.62	-0.96	1	48.9	33.2	95.00%	K.YNLSDQMDFVK.G		K.YNLSDQMDFVK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
55	PDR5_YEAST	16.02%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
205	220	2	1648.77	-0.62	1	73	32.9	95.00%	K.SISSNTHGFDLGADTK.I		K.SISSNTHGFDLGADTK.I
146	155	2	1147.63	2.2	1	35.7	29.4	95.00%	Y.QSTVVNIPYK.I		K.NLSASGASADVAYQSTVVNIPYK.I
95	109	2	1663.78	-0.8	1	45.4	33	95.00%	K.LDPNSENFSSAAWVK.N		K.LDPNSENFSSAAWVK.N
826	844	3	2101.96	-0.24	1	32	33.8	95.00%	K.NANDPENVGERSDLSSDRK.M		K.NANDPENVGERSDLSSDRK.M
412	427	2	1738.84	-1.2	1	95.7	32.9	95.00%	R.QTTADFLTSVTSPSER.T		R.QTTADFLTSVTSPSER.T
338	349	2	1291.68	-0.26	1	35.4	30.6	95.00%	R.GLDSATALEFIR.A		R.GLDSATALEFIR.A
945	957	2	1588.76	-1.9	1	41	32.6	95.00%	R.SIGYCQQQDLHLK.T	Carbamidomethyl (+57)	R.SIGYCQQQDLHLK.T
1102	1114	2	1534.69	0.31	1	49.8	33.4	95.00%	K.TMIDYFESHGAHK.C		K.TMIDYFESHGAHK.C
436	445	3	1117.66	-0.44	1	26.3	24.5	95.00%	K.KGIHIPQTPK.E		K.KGIHIPQTPK.E
280	291	2	1289.61	2.5	1	33.4	32.1	95.00%	Y.ANHLAEVAMATY.G		R.ESYANHLAEVAMATYGLSHTR.N
329	337	2	1196.5	-0.24	1	41.3	31.6	95.00%	K.FQCWDNATR.G	Carbamidomethyl (+57)	K.FQCWDNATR.G
1090	1101	2	1344.6	-0.29	1	37.5	33	95.00%	K.TVYFGDLGEGCK.T	Carbamidomethyl (+57)	K.TVYFGDLGEGCK.T
73	94	2	2261.05	1	1	67	33.4	95.00%	F.SSGVEGVNPIFSDPEAPGYDPK.L		K.SDAQSIFSSGVEGVNPIFSDPEAPGYDPK.L
49	65	2	1805.86	-0.99	0	112	32.9	95.00%	R.TLTAQSMQNSTQSAPNK.S		R.TLTAQSMQNSTQSAPNK.S
1125	1142	2	1920.87	2.7	1	33.2	33.7	94.20%	W.MLEVVGAAPGSHANQDYY.E		K.CPADANPAEWMLEVVGAAPGSHANQDYYEVWR.N
110	125	2	1838.83	1.2	1	53.5	33.4	95.00%	K.NMAHLSAADPDFYKPY.S		K.NMAHLSAADPDFYKPYSLGCAWK.N
971	982	2	1397.75	1.3	1	52.8	28	95.00%	Y.LRQPAEVSIEEK.N		R.FSAYLRQPAEVSIEEK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
56	A6ZSG0_YEAS7	17.51%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
53	62	2	1157.61	-0.7	1	34.2	29.3	95.00%	R.YLEGLHEGLK.F		R.YLEGLHEGLK.F
453	472	3	2375.1	-0.026	1	58.1	33.4	95.00%	K.YVENSSQSHENEITQQQLNK.N		K.YVENSSQSHENEITQQQLNK.N
713	742	3	3446.59	-1.2	1	45.3	31.8	95.00%	K.MIWQLPIADPTSTAPEQQEQNSHDAPNWSR.S		K.MIWQLPIADPTSTAPEQQEQNSHDAPNWSR.S
72	107	4	4035.01	1.2	1	34.1	27	95.00%	K.RSVSSQSPIVHSSNNTLHHHEHQQHLPPTLESLSSK.S		K.RSVSSQSPIVHSSNNTLHHHEHQQHLPPTLESLSSK.S
716	742	3	3016.39	0.93	1	49.9	32.5	95.00%	W.QLPIADPTSTAPEQQEQNSHDAPNWSR.S		K.MIWQLPIADPTSTAPEQQEQNSHDAPNWSR.S
131	147	3	1970.74	0.35	0	38.5	32.8	95.00%	R.ELPHDDNDDEDANDDSR.F		R.ELPHDDNDDEDANDDSR.F
20	36	2	1865.99	0.52	1	79.9	28.7	95.00%	R.LKEEVLTPTTSASTPHR.I		R.LKEEVLTPTTSASTPHR.I
37	52	2	1902.94	1.5	1	59.5	32.1	95.00%	R.IFSVDDDPKEIQNDIR.Y		R.IFSVDDDPKEIQNDIR.Y
220	231	2	1353.69	-1	0	51.8	30.9	95.00%	R.TAAQDIHETQLK.T		R.TAAQDIHETQLK.T
131	148	2	2117.81	1.2	2	101	32.4	95.00%	R.ELPHDDNDDEDANDDSRF.I		R.ELPHDDNDDEDANDDSRFIIHDSHGHDLLIDEINCQSPSHLENNDQASNASSTESFTLR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
57	A6ZM61_YEAS7	52.88%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
161	174	2	1561.77	-0.024	1	85.8	32.1	95.00%	K.NAINVDTAFEEIAR.S		K.NAINVDTAFEEIAR.S
57	70	2	1590.75	0.94	1	70.2	32.9	95.00%	K.VATMQVWDTAGQER.F		K.VATMQVWDTAGQER.F
122	134	2	1414.77	1	1	80.8	29	95.00%	F.VILGNKIDAEESK.K		R.DEFLVHANVNSPETFPFVILGNKIDAEESK.K
122	135	2	1542.87	2	1	39.6	27.6	95.00%	F.VILGNKIDAEESKK.I		R.DEFLVHANVNSPETFPFVILGNKIDAEESKK.I
39	48	2	1035.56	-0.22	1	43.9	28.7	95.00%	K.ATIGADFLTK.E		K.ATIGADFLTK.E
81	101	2	2361.06	-0.15	1	98.4	33.8	95.00%	R.GADCCVLVYDVTNASSFENIK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GADCCVLVYDVTNASSFENIK.S
148	160	2	1360.76	1.9	1	65.6	27.5	95.00%	K.SLGDIPLFLTSAK.N		K.SLGDIPLFLTSAK.N
175	198	2	2740.22	0.72	1	123	33.6	95.00%	R.SALQQNQADTEAFEDDYNDAINIR.L		R.SALQQNQADTEAFEDDYNDAINIR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
58	YG35_YEAST	14.67%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
805	817	2	1313.73	0.3	0	28	28.1	94.60%	K.QNNVVSAVIAATK.N		K.QNNVVSAVIAATK.N
162	189	4	3057.49	0.34	1	44.6	30.6	95.00%	R.GLQNSSLPELEDGYAGGYQSLRPSHNLR.F		R.GLQNSSLPELEDGYAGGYQSLRPSHNLR.F
821	830	2	1071.57	1.3	0	35.6	28.8	95.00%	K.IDTIGNGLNR.G		K.IDTIGNGLNR.G
716	732	2	1882.84	-0.39	1	107	33.9	95.00%	K.NINADNIDYSAAEGFNR.I		K.NINADNIDYSAAEGFNR.I
798	817	3	2155.16	1.2	1	53.5	27	95.00%	K.ERLEEGKQNNVVSAVIAATK.N		K.ERLEEGKQNNVVSAVIAATK.N
146	161	2	1770.89	-0.63	1	44.7	31.7	95.00%	R.LLLSPASSNVDDDRNR.G		R.LLLSPASSNVDDDRNR.G
923	945	3	2583.35	0.28	1	61.6	27.1	95.00%	R.LASQSHLLHADNIFFLVETGMLK.A		R.LASQSHLLHADNIFFLVETGMLK.A
709	715	2	910.52	-0.13	1	25.1	25.5	94.30%	K.YLILDFK.N		K.YLILDFK.N
839	849	2	1242.64	-0.099	0	35.1	29.3	95.00%	R.NLMSLPTNTPR.N		R.NLMSLPTNTPR.N
850	869	2	2278.16	0.046	1	71.7	30.6	95.00%	R.NYQILSVAQNVFVNDEQAVK.N		R.NYQILSVAQNVFVNDEQAVK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
59	HIP1_YEAST	13.60%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
71	88	3	2175.02	2.5	1	61.7	33.3	95.00%	F.RRNEDTEQEDINNTNLSK.D		R.FRRNEDTEQEDINNTNLSK.D
53	69	2	1819.82	0.54	0	68.7	33.8	95.00%	K.DSPGINQTTNDITSSDR.F		K.DSPGINQTTNDITSSDR.F
31	42	2	1341.67	-0.31	1	56	31.3	95.00%	K.ESTTFVTELTSK.T		K.ESTTFVTELTSK.T
73	88	2	1862.82	1.5	0	90.7	34.3	95.00%	R.NEDTEQEDINNTNLSK.D		R.NEDTEQEDINNTNLSK.D
43	69	3	2853.33	0.95	1	74.7	32.7	95.00%	K.TDSAFPLSSKDSPGINQTTNDITSSDR.F		K.TDSAFPLSSKDSPGINQTTNDITSSDR.F
53	71	2	2122.99	1.5	2	46	33.2	95.00%	K.DSPGINQTTNDITSSDRFR.R		K.DSPGINQTTNDITSSDRFR.R
72	88	2	2018.91	-0.41	1	80.8	33.6	95.00%	R.RNEDTEQEDINNTNLSK.D		R.RNEDTEQEDINNTNLSK.D

400	412	3	1440.7	-0.18	0	40.7	32.3	95.00%	R.CMVAMAHIGNLPK.F	Carbamidomethyl (+57)	R.CMVAMAHIGNLPK.F
561	571	3	1291.61	-0.078	1	44.3	32.2	95.00%	K.LEDMDLDTGRK.Q		K.LEDMDLDTGRK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
60	A6ZSU5_YEAS7	34.01%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
289	305	2	2126.9	0.56	2	75.3	34.4	95.00%	R.KCLEACDEDPDLVQLCY.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.KCLEACDEDPDLVQLCYCLPPTENDDSANYFTSHPGFK.H
380	394	2	1652.76	-1.3	1	43.1	33.4	95.00%	R.GTFQSSGQNCIGIER.V	Carbamidomethyl (+57)	R.GTFQSSGQNCIGIER.V
476	489	2	1616.85	1.3	1	47.5	30.2	95.00%	Y.FQPTLLVDVTPEMK.I		K.YPQGHYFQPTLLVDVTPEMK.I
521	532	2	1119.6	2.3	1	48.6	30.8	95.00%	F.GLGGSVFGADIK.E		K.NTDHCVQLANSAPFGLGGSVFGADIK.E
572	585	2	1463.71	-0.2	1	79.2	32.3	95.00%	K.FGGEEGLLGLCNAK.S	Carbamidomethyl (+57)	K.FGGEEGLLGLCNAK.S
144	155	2	1354.59	-0.24	1	44.4	33	95.00%	K.AQSTWGNSDFSR.R		K.AQSTWGNSDFSR.R
507	532	3	2674.28	0.052	1	63.5	32.1	95.00%	K.NTDHCVQLANSAPFGLGGSVFGADIK.E	Carbamidomethyl (+57)	K.NTDHCVQLANSAPFGLGGSVFGADIK.E
395	407	2	1520.81	1.4	2	80.8	29.9	95.00%	R.VIVSKENYDDLVK.I		R.VIVSKENYDDLVK.I
327	342	3	1823.01	-0.046	1	22.2	25.3	95.00%	K.HITFIGSQPVAHYILK.C		K.HITFIGSQPVAHYILK.C
123	140	2	1952.94	0.96	1	73.6	33.1	95.00%	Y.LGSFPSKTEADIDEMVSK.A		R.SVSTNIWNPEEPNFIQCHCPATGQYLGSFPSKTEADIDEMVSK.A
470	489	3	2362.17	-0.12	1	32.7	32.1	95.00%	K.YPQGHYFQPTLLVDVTPEMK.I		K.YPQGHYFQPTLLVDVTPEMK.I
81	94	2	1571.77	-0.4	1	49.4	32.2	95.00%	K.FSLPAPEAAQNNWK.G		K.FSLPAPEAAQNNWK.G
369	379	2	1247.66	0.78	0	62.4	30.6	95.00%	K.NLDALSSIIMR.G	Oxidation (+16)	K.NLDALSSIIMR.G
347	358	2	1197.7	-0.51	0	31.2	25.3	95.00%	K.SLTPVVVELGGK.D		K.SLTPVVVELGGK.D
185	200	2	1749.89	1.4	0	103	31.4	95.00%	K.TMLDASMGEILVTLEK.I		K.TMLDASMGEILVTLEK.I
490	504	2	1688.9	2.3	1	53	29	95.00%	K.IAQNEVFGPILVMMK.A		K.IAQNEVFGPILVMMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
61	B3LNF5_YEAS1	17.82%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
315	328	2	1622.68	-0.74	1	81.7	33.7	95.00%	R.HSMQGEIYEDAMGR.I		R.HSMQGEIYEDAMGR.I
1032	1049	2	1913.05	-0.0021	0	98.5	26.9	95.00%	K.IQGLEGIILTNIVSNSDK.V		K.IQGLEGIILTNIVSNSDK.V
907	919	2	1487.68	-0.62	1	78	33.4	95.00%	R.SLVSSTDFFQDDK.N		R.SLVSSTDFFQDDK.N
1356	1381	4	2748.36	-0.7	1	29.9	30.4	95.00%	K.IPLSTCEGGLKLDAPSSPHACPGKEK.E	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.IPLSTCEGGLKLDAPSSPHACPGKEK.E
845	859	2	1748.75	2.7	1	48.7	34	95.00%	K.NCESILSPECHAVAY.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.NCESILSPECHAVAYLTNDGGETFTEMLDNAIHCEFAGSLFK.Y
297	305	2	1022.51	1.9	1	44.1	31.2	95.00%	W.VSNDLSNFK.M		R.YNDMSSMDVWVSNDLSNFK.M
596	611	2	1955.78	-0.87	1	95.8	33.8	95.00%	K.TCEENDFEDWNLAEGK.C	Carbamidomethyl (+57)	K.TCEENDFEDWNLAEGK.C
1367	1379	3	1335.62	0.25	0	41.1	32.3	95.00%	K.LDAPSSPHACPGK.E	Carbamidomethyl (+57)	K.LDAPSSPHACPGK.E
211	228	2	1986.92	3.2	2	42.5	33.7	95.00%	K.TGKDSDLESSDTSIICLF.Q	Carbamidomethyl (+57)	K.TGKDSDLESSDTSIICLFQNMQLIMDEFSSPYTESK.L
759	772	2	1502.71	-1	1	54.2	32.9	95.00%	R.GEAYISHDGGQTIR.R		R.GEAYISHDGGQTIR.R
126	136	2	1330.63	-0.81	1	45.6	31.8	95.00%	R.GCYIETHPLNK.N	Carbamidomethyl (+57)	R.GCYIETHPLNK.N
709	719	2	1189.57	0.013	0	33.2	31.6	95.00%	K.SVDISCEGVPK.K	Carbamidomethyl (+57)	K.SVDISCEGVPK.K
667	682	2	1908.9	0.76	1	73.6	32.9	95.00%	K.CVPDYNLIVLSDVCDK.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CVPDYNLIVLSDVCDK.T
860	880	2	2413.03	2	1	106	34.6	95.00%	Y.LTNDGGETFTEMLDNAIHCEF.A	Carbamidomethyl (+57)	K.NCESILSPECHAVAYLTNDGGETFTEMLDNAIHCEFAGSLFK.Y
1280	1295	2	1882.88	2	2	40.9	33.2	95.00%	R.KTDENCFIGNIPLSEF.S	Carbamidomethyl (+57)	R.KTDENCFIGNIPLSEFSR.N
544	565	2	2365.11	1	1	60.3	32.8	95.00%	Y.QLETTIYPNEVMNTTPDGSGAK.F		K.TWTEYQLETTIYPNEVMNTTPDGSGAK.F
196	210	2	1611.72	-0.43	1	74.5	33.8	95.00%	R.NENSAISISDCGFAK.T	Carbamidomethyl (+57)	R.NENSAISISDCGFAK.T
887	899	2	1599.67	-0.61	1	79.7	33.4	95.00%	K.YPSNEDMVMCQVK.E	Carbamidomethyl (+57)	K.YPSNEDMVMCQVK.E
1267	1279	2	1607.75	-1.1	1	62.2	33.1	95.00%	K.SNCLFGHQTEFLR.K	Carbamidomethyl (+57)	K.SNCLFGHQTEFLR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
62	A6ZSR0_YEAS7	23.21%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
354	371	2	2161.13	-0.46	1	64.7	29	95.00%	K.ELTYDLLQEMPLLNQTIK.E		K.ELTYDLLQEMPLLNQTIK.E

440	454	2	1556.74	1.3	1	71.7	33.6	95.00%	Y.SVGEEVDYGFGAISK.G		R.WNNDSASSYSVGEEVDYGFGAISK.G
275	289	2	1788.87	-1.3	1	40.8	32.6	95.00%	K.NNDIQDRDLIDSLMK.N		K.NNDIQDRDLIDSLMK.N
127	136	3	1069.59	2.2	1	28.9	26.8	95.00%	Y.AHLTTPVFGK.G		K.LADVSAEAAYAHLTTPVFGK.G
117	136	2	2060.06	-0.25	1	69.1	29.6	95.00%	K.LADVSAEAAYAHLTTPVFGK.G		K.LADVSAEAAYAHLTTPVFGK.G
190	210	2	2298.13	0.69	1	63.9	31.7	95.00%	R.TTGTIDVMVTQPEMTIFTASR.S		R.TTGTIDVMVTQPEMTIFTASR.S
455	467	2	1292.65	0.76	1	57.2	31.8	95.00%	K.GVSSPYLPFGGGR.H		K.GVSSPYLPFGGGR.H
137	146	2	1179.53	0.098	1	29.4	31.9	91.20%	K.GVIYDCPNSR.L	Carbamidomethyl (+57)	K.GVIYDCPNSR.L
260	270	2	1182.63	-0.43	1	43.6	27.9	95.00%	K.AISGTYMSLIK.E		K.AISGTYMSLIK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
63	GAS1_YEAST	15.03%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
194	209	2	1793.84	-0.4	1	95.9	32.8	95.00%	K.IPVGYSSNDDEDTRVK.M		K.IPVGYSSNDDEDTRVK.M
114	132	2	2025.02	1.2	2	57.7	31.4	95.00%	Y.VIADLAAPATSINRDDPTW.T		K.ALNDADIYVIADLAAPATSINRDDPTWTVDLFNSYK.T
430	437	2	1058.51	1.9	1	32.1	32.3	94.50%	F.VMNLYYEK.S		K.EQLSFVMNLYYEK.S
114	127	2	1410.79	1.9	0	55.7	26	95.00%	Y.VIADLAAPATSINR.D		K.ALNDADIYVIADLAAPATSINR.D
215	226	2	1374.54	1.9	2	35.7	31.5	95.00%	F.ACGDDDVKADFY.G	Carbamidomethyl (+57)	K.MTDYFACGDDDVKADFYGINMYEWCGK.S
194	207	2	1566.68	-0.84	1	93.4	33.2	95.00%	K.IPVGYSSNDDEDTR.V		K.IPVGYSSNDDEDTR.V
261	271	2	1310.56	1.9	1	63	32.6	95.00%	F.SEYGCNEVTPR.L	Carbamidomethyl (+57)	K.NLSIPVFFSEYGCNEVTPR.L
114	137	2	2600.32	1.9	2	45.8	29.8	95.00%	Y.VIADLAAPATSINRDDPTWTVDLF.N		K.ALNDADIYVIADLAAPATSINRDDPTWTVDLFNSYK.T
210	222	2	1535.59	-1.4	1	85.3	32.1	95.00%	K.MTDYFACGDDDVK.A	Carbamidomethyl (+57)	K.MTDYFACGDDDVK.A
83	90	2	956.58	2.2	1	40.2	25.2	95.00%	K.KLNTNVIR.V		K.KLNTNVIR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
64	A6ZZF0_YEAS7	20.28%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
176	185	2	1188.69	1.7	1	60	24.7	95.00%	K.KMSLIDLLTR.R		K.KMSLIDLLTR.R
273	292	3	2279.96	1.4	1	71.8	34.2	95.00%	R.HHHSSESPENYGSNQLSHSF.S		R.HHHSSESPENYGSNQLSHSFSSPLGNDVTENPAALADTQYHPENGSLYPHHHHLETPFSK.L
151	166	2	1634.8	1.2	0	69	32.1	95.00%	Y.ATSSSSVSENDPLITK.D		K.SHSHSHSHSHADSHSNFSNDHDLENAPSEHGYATSSSSVSENDPLITK.D
177	185	2	1060.6	2.4	0	72.1	28.3	95.00%	K.MSLIDLLTR.R		K.MSLIDLLTR.R
257	265	2	1121.57	2.7	1	30.8	31.1	94.30%	Y.DLENLSLYR.K		R.GLVCVENNIGYDLENLSLYR.K
136	150	2	1683.68	2.2	1	59.9	33.6	95.00%	F.SNDHDLENAPSEHGY.A		K.SHSHSHSHSHADSHSNFSNDHDLENAPSEHGYATSSSSVSENDPLITK.D
246	265	2	2340.14	-1.1	1	97.3	32.4	95.00%	R.GLVCVENNIGYDLENLSLYR.K	Carbamidomethyl (+57)	R.GLVCVENNIGYDLENLSLYR.K
198	218	2	2441.24	0.68	1	89.6	29.8	95.00%	K.CTPLLQSEQPEYIACVPPVIK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CTPLLQSEQPEYIACVPPVIK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
65	A6ZS87_YEAS7	12.30%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
74	82	2	984.56	1.6	0	30.7	26.3	95.00%	F.VAALNQELK.K		K.FVAALNQELK.K
43	72	3	3385.58	-0.68	1	96.2	31.3	95.00%	K.HHVVEPHDANDENLPLLADASPDDQFYISK.F		K.HHVVEPHDANDENLPLLADASPDDQFYISK.F
115	132	2	2124.08	-0.51	1	75.4	30.5	95.00%	K.ATQLFNQQQQHQLQSVAR.N		K.ATQLFNQQQQHQLQSVAR.N
353	359	2	907.39	0.2	0	30.1	29.7	95.00%	K.DMMNLER.K		K.DMMNLER.K
73	82	2	1131.63	2.1	1	50.5	28.3	95.00%	K.FVAALNQELK.K		K.FVAALNQELK.K
100	114	2	1790.84	1.2	1	83.6	33.3	95.00%	Y.NELKDDVMELENTNK.A		K.FYISQETGLIANYNELKDDVMELENTNK.A
43	69	3	3057.38	0.92	1	74.3	33	95.00%	K.HHVVEPHDANDENLPLLADASPDDQFY.I		K.HHVVEPHDANDENLPLLADASPDDQFYISK.F
334	347	3	1761.89	0.68	2	34	31.8	95.00%	R.ELSSHLRDHVVWER.N		R.ELSSHLRDHVVWER.N
89	114	3	2980.44	2.2	1	35.3	31.1	95.00%	Y.ISQETGLIANYNELKDDVMELENTNK.A		K.FYISQETGLIANYNELKDDVMELENTNK.A

348	359	2	1535.72	-0.73	1	50.3	32.9	95.00%	R.NTVWKDMMNLER.K		R.NTVWKDMMNLER.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
66	A6ZPW7_YEAS7	28.90%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
80	89	2	1186.56	0.14	0	57.8	32.4	95.00%	R.NIELNADNER.S		R.NIELNADNER.S
48	60	3	1482.79	0.21	2	45.6	28.1	95.00%	R.RQSILDHPVGSFK.G		R.RQSILDHPVGSFK.G
94	112	2	2077.91	0.71	1	104	34.2	95.00%	K.ESNDETYDPDTLAPALDGR.R		K.ESNDETYDPDTLAPALDGR.R
14	26	3	1582.86	0.57	2	33.6	27.6	95.00%	K.RSEVHYISIPLNR.G		K.RSEVHYISIPLNR.G
368	388	2	2275.09	1.2	1	73.1	32.6	95.00%	K.SSSPGSLVNPMETSMWPIDLK.H		K.SSSPGSLVNPMETSMWPIDLK.H
113	125	3	1452.83	0.063	1	26.7	24.7	95.00%	R.RLSVTLNNAGRPR.I		R.RLSVTLNNAGRPR.I
135	178	4	4456.06	0.081	1	66.6	28.8	95.00%	R.VSTASMAIHDDDYGSIQNSTIGDSGSILRPTASLTEMMSGGAGR.R		R.VSTASMAIHDDDYGSIQNSTIGDSGSILRPTASLTEMMSGGAGR.R
180	191	2	1381.66	0.28	1	65	32.9	95.00%	R.FTNNDMDSIVVK.R		R.FTNNDMDSIVVK.R
94	113	3	2234.01	0.31	1	48.5	33.8	95.00%	K.ESNDETYDPDTLAPALDGRR.L		K.ESNDETYDPDTLAPALDGRR.L
114	125	2	1296.73	-0.021	0	34.5	26.6	95.00%	R.LSVTLNNAGRPR.I		R.LSVTLNNAGRPR.I
484	512	3	3113.69	-0.25	0	86.5	23.4	95.00%	K.TPLNARPIVSVLDVLMNVQHIDEAASAIK.R		K.TPLNARPIVSVLDVLMNVQHIDEAASAIK.R
15	26	3	1426.76	0.22	1	27.2	29.5	95.00%	R.SEVHYISIPLNR.G		R.SEVHYISIPLNR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
67	A6ZQQ8_YEAS7	35.71%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
494	507	2	1555.84	-0.31	1	58	28.4	95.00%	K.EIGWCLGASLPLLK.A	Carbamidomethyl (+57)	K.EIGWCLGASLPLLK.A
47	80	3	3787.83	-1.6	2	60.7	28.8	95.00%	K.TPEDISILPVNDEPGYLQDSKTEQNYPELADAVK.S		K.TPEDISILPVNDEPGYLQDSKTEQNYPELADAVK.S
423	432	2	1157.61	1.8	0	35	29.3	95.00%	F.TLNELNDLAR.I		R.TRPLGMPLSFTLNELNDLAR.I
245	264	2	2148.08	2.4	1	55.7	31.3	95.00%	F.DLGGGSTQIVFEPTFPINEK.M		K.LPTAAVFDLGGGSTQIVFEPTFPINEK.M
375	395	3	2383.08	-0.55	1	35.9	33.7	95.00%	K.DAQCQSPPCSFNGVHQPSLVR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.DAQCQSPPCSFNGVHQPSLVR.T
47	67	2	2329.14	1.1	1	67.4	31.9	95.00%	K.TPEDISILPVNDEPGYLQDSK.T		K.TPEDISILPVNDEPGYLQDSK.T
347	365	2	2154.96	1.1	1	81.6	34.4	95.00%	K.ETYTIDFIGPDEPSGAQCR.F	Carbamidomethyl (+57)	K.ETYTIDFIGPDEPSGAQCR.F
227	237	2	1053.58	2	0	44	26.7	95.00%	Y.LLGNIGANGPK.L	Deamidation (+1)	K.DYPFPVVEGDGVSIMGGDEEGVFAWITTNYLLGNIGANGPK.L
350	365	2	1761.8	1.4	1	59.5	33.5	95.00%	Y.TIDFIGPDEPSGAQCR.F	Carbamidomethyl (+57)	K.ETYTIDFIGPDEPSGAQCR.F
300	310	2	1184.68	-0.013	0	65	27.2	95.00%	K.VNSVLVENALK.D		K.VNSVLVENALK.D
37	46	2	1026.57	0.76	0	26.8	24.1	95.00%	R.TVTPNASIPK.T		R.TVTPNASIPK.T
413	432	3	2257.19	0.04	1	55.6	28.9	95.00%	R.TRPLGMPLSFTLNELNDLAR.I		R.TRPLGMPLSFTLNELNDLAR.I
136	151	2	1614.81	1.4	0	100	31.4	95.00%	F.DTDSVGAANSLDPLLK.V		K.FDMLEPGLSSFDTDSVGAANSLDPLLK.V
366	374	2	1091.59	-0.025	1	45.6	28.5	95.00%	R.FLTDEILNK.D		R.FLTDEILNK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
68	A6ZY13_YEAS7	11.09%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	78	2	1376.59	-0.75	0	35	33.6	95.00%	R.LEEDNDLEDGTK.S		R.LEEDNDLEDGTK.S
62	78	2	1947.87	1	1	91.4	33.9	95.00%	R.AESQRLEEDNDLEDGTK.S		R.AESQRLEEDNDLEDGTK.S
400	412	2	1465.71	-0.047	1	74.9	32.9	95.00%	R.LMCSLAQQGYAPK.F	Carbamidomethyl (+57)	R.LMCSLAQQGYAPK.F
26	41	2	1736.86	1.8	1	88.6	32.6	95.00%	Y.NNFNTSTTASLTPEIK.E		K.SAEFEVTDSALYNNFNTSTTASLTPEIK.E
61	78	2	2103.97	1.1	1	61.4	34	95.00%	R.RAESQRLEEDNDLEDGTK.S		R.RAESQRLEEDNDLEDGTK.S
29	48	3	2216.06	1.3	1	42.3	32.9	95.00%	F.NTSTTASLTPEIKEHSEESR.N		K.SAEFEVTDSALYNNFNTSTTASLTPEIKEHSEESR.N
26	48	3	2591.21	1	1	50.4	33.4	95.00%	Y.NNFNTSTTASLTPEIKEHSEESR.N		K.SAEFEVTDSALYNNFNTSTTASLTPEIKEHSEESR.N
269	281	2	1250.55	-0.67	1	65.6	31.9	95.00%	R.DPGSFAEGSGATR.F		R.DPGSFAEGSGATR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
69	A6ZQY0_YEAS7	60.54%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

153	165	2	1406.66	1.8	0	53.7	32.9	95.00%	F.TETSALNSENVDK.A		K.TFAQENQLLFTETSALNSENVDK.A
181	215	3	3476.58	-2.1	0	46.5	31.9	95.00%	K.HQMDLGDSSANGNANGASAPNGPTISLTPTPNENK.K		K.HQMDLGDSSANGNANGASAPNGPTISLTPTPNENK.K
108	127	3	2126.1	1.7	1	40.1	29.7	95.00%	W.LSELRENADDNVAVGLIGNK.S		K.SSSYENCNHWLSELRENADDNVAVGLIGNK.S
62	74	2	1514.78	-1.1	2	64.2	30.2	95.00%	R.IKAQIWDTAGQER.Y		R.IKAQIWDTAGQER.Y
98	107	2	1282.47	2	1	33	31.4	95.00%	K.SSSYENCNHW.L	Carbamidomethyl (+57)	K.SSSYENCNHWLSELR.E
16	26	2	1056.62	0.27	0	32.4	25.5	95.00%	K.IVLIGDSGVGK.S		K.IVLIGDSGVGK.S
143	165	2	2598.24	-0.62	1	125	32	95.00%	K.TFAQENQLLFTETSALNSENVDK.A		K.TFAQENQLLFTETSALNSENVDK.A
64	74	2	1273.61	-0.17	1	64.6	32.4	95.00%	K.AQIWDTAGQER.Y		K.AQIWDTAGQER.Y
181	216	3	3605.67	0.99	1	66.5	31.3	95.00%	K.HQMDLGDSSANGNANGASAPNGPTISLTPTPNENKK.A	Deamidation (+1)	K.HQMDLGDSSANGNANGASAPNGPTISLTPTPNENKK.A
113	127	2	1527.75	-1.3	0	74.8	32.7	95.00%	R.ENADDNVAVGLIGNK.S		R.ENADDNVAVGLIGNK.S
44	53	2	1079.56	0.067	1	61.1	29.8	95.00%	K.STIGVEFATR.T		K.STIGVEFATR.T
166	177	2	1467.76	-0.28	1	44.5	30	95.00%	K.AFEELINTIYQK.V		K.AFEELINTIYQK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
70	A7A201_YEAS7	37.38%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
11	21	2	1070.63	0.63	0	40	27	95.00%	K.LLLIGNSGVGK.S	Deamidation (+1)	K.LLLIGNSGVGK.S
171	184	2	1636.74	-0.79	0	67.2	33.6	95.00%	K.ESMSQQNLNETTQK.K		K.ESMSQQNLNETTQK.K
101	108	2	1089.53	-0.2	1	53.5	31.6	95.00%	K.MWLQEIDR.Y		K.MWLQEIDR.Y
59	69	2	1315.65	0.75	1	47	31.6	95.00%	K.LQIWDTAGQER.F		K.LQIWDTAGQER.F
168	184	3	2005.97	-0.13	1	35	33	95.00%	R.QIKESMSQQNLNETTQK.K		R.QIKESMSQQNLNETTQK.K
145	167	2	2558.2	-0.012	1	102	32.9	95.00%	K.MPFLETSALDSTNVEDAFLTMAR.Q		K.MPFLETSALDSTNVEDAFLTMAR.Q
22	27	2	760.43	1.9	0	25.1	26.5	93.00%	K.SCLLLR.F	Carbamidomethyl (+57)	K.SCLLLR.F
101	109	2	1252.59	2.8	2	48.8	33.2	95.00%	K.MWLQEIDRY.A		K.MWLQEIDRYATSTVLK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
71	SNA3_YEAST	40.60%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
93	125	3	3566.53	0.25	1	68.2	32.6	95.00%	R.DLEAHPAEESQAQPPAYDEDDEAGADVPLMDNK.Q		R.DLEAHPAEESQAQPPAYDEDDEAGADVPLMDNK.Q
1	12	2	1601.68	-0.18	1	46.1	34.1	95.00%	-.MDRDHINDHDHR.M	Acetyl (+42)	-.MDRDHINDHDHR.M
84	125	3	4485.01	2.4	2	81	29.8	95.00%	R.HATAPAVDRDLEAHPAEESQAQPPAYDEDDEAGADVPLMDNK.Q		R.HATAPAVDRDLEAHPAEESQAQPPAYDEDDEAGADVPLMDNK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
72	A6ZKY2_YEAS7	18.38%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	201	2	1158.52	0.4	2	39.9	31.8	95.00%	F.SADTFNETKF.E		K.YLTSTTSYDDQSTIFSADTFNETKFELNHPTR.Q
349	369	2	2284.11	2.1	1	82.8	32.6	95.00%	K.VNQGSLDYLAALGVYQEDMAK.A		K.VNQGSLDYLAALGVYQEDMAK.A
131	143	2	1508.74	1.6	1	43.9	32.7	95.00%	Y.HLSPQQQPSNNLF.G		R.DNADLPVDPYHLSPQQQPSNNLFGSGR.L
121	147	3	2965.39	-1.5	1	47.2	32.4	95.00%	R.DNADLPVDPYHLSPQQQPSNNLFGSGR.L		R.DNADLPVDPYHLSPQQQPSNNLFGSGR.L
103	120	3	1968.02	1.2	2	73.9	29.6	95.00%	K.RAGEAVIHLSEGSNLYPR.D		K.RAGEAVIHLSEGSNLYPR.D
246	253	2	883.51	0.085	0	27.4	23.1	95.00%	K.GLLDTLPR.R		K.GLLDTLPR.R
223	232	2	1069.55	0.074	0	38.8	30	95.00%	R.MVSDLPPPSK.K		R.MVSDLPPPSK.K
564	572	2	1130.62	0.63	1	28.2	28.8	94.00%	R.ILCWELVAK.R	Carbamidomethyl (+57)	R.ILCWELVAK.R
93	102	2	1119.56	0.34	1	46.1	31.1	95.00%	R.YAANLQESPK.R		R.YAANLQESPK.R
828	840	2	1585.76	-0.76	1	92	32.9	95.00%	K.QIVETDWPQEVDK.K		K.QIVETDWPQEVDK.K
235	245	3	1220.75	-0.0033	1	25.4	17.5	95.00%	K.ALLKLDNPIPK.G		K.ALLKLDNPIPK.G
457	472	2	1621.78	-0.69	1	98.9	32.8	95.00%	K.VFDMDSNVAGAAGQIK.T		K.VFDMDSNVAGAAGQIK.T
538	548	2	1285.59	-0.092	1	55.9	33	95.00%	R.SYFLGETQEGR.D		R.SYFLGETQEGR.D
264	276	2	1585.71	-0.5	1	38.2	33.4	95.00%	R.YTACTVEPDDFLR.E	Carbamidomethyl (+57)	R.YTACTVEPDDFLR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
73	YIL7_YEAST	32.39%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
273	289	3	1852.9	0.27	1	39	32.6	95.00%	K.LLNSPESDGSVNRNHSK.G		K.LLNSPESDGSVNRNHSK.G
196	205	2	1105.6	1.9	1	41.4	29.4	95.00%	F.ISPTGDILYK.T		R.NSLFISPTGDILYK.T
119	131	2	1529.64	1.6	1	43.6	33.2	95.00%	F.STQHTQFYGDSPY.M		K.MFSTQHTQFYGDSPYMDYPAK.E
272	289	3	1981	0.36	1	38.7	31.6	95.00%	R.KLLNSPESDGSVNRNHSK.G		R.KLLNSPESDGSVNRNHSK.G
175	183	2	1121.59	2	1	41.6	30.3	95.00%	F.LSNFERPLF.S		K.DALVSHTNNEKPFLSNFERPLFS LASESNR.N
192	205	2	1566.83	0.18	1	43.7	28.8	95.00%	R.NSLFISPTGDILYK.T		R.NSLFISPTGDILYK.T
138	161	3	2701.25	2	1	53.3	32.7	95.00%	K.ENFQDQVHISESDISPGNKDESV K.D		K.ENFQDQVHISESDISPGNKDESV K.D
273	285	2	1386.67	-0.52	0	61.9	31.8	95.00%	K.LLNSPESDGSVNR.N		K.LLNSPESDGSVNR.N
162	174	2	1470.71	1.8	1	50.8	33	95.00%	K.DALVSHTNNEKPF.L		K.DALVSHTNNEKPFLSNFERPLFS LASESNR.N
272	285	2	1514.77	-1.8	1	85.9	30.6	95.00%	R.KLLNSPESDGSVNR.N		R.KLLNSPESDGSVNR.N
307	318	2	1456.65	1.8	1	65	33.4	95.00%	Y.LEHMLEGKEQDE.-		R.KPTPSTYLEHMLEGKEQDE.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
74	A7A0Z7_YEAS7	28.46%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
116	143	3	3215.54	1.9	1	73.1	30.8	95.00%	Y.ESNATNELLSSHVGQILDSFHEEL VEYR.N		R.ILSGLQEYESNATNELLSSHVGQI LDSFHEELVEYR.N
14	27	2	1642.73	-1.2	1	73.2	33.7	95.00%	K.NGETISSCFQPFQK.N	Deamidation (+1)/ Carbamidomethyl (+57)	K.NGETISSCFQPFQK.N
32	57	3	2881.51	1.8	1	47.8	25.3	95.00%	Y.GTITSANEQITPVIFHNLIMDMVLP K.V		K.NENYGTITSANEQITPVIFHNLIMD MVLPK.V
28	57	3	3401.7	-0.32	1	56.4	28.7	95.00%	K.NENYGTITSANEQITPVIFHNLIMD MVLPK.V		K.NENYGTITSANEQITPVIFHNLIMD MVLPK.V
47	57	2	1309.69	1.1	0	52.6	29.4	95.00%	F.HNLIMDMVLPK.V		K.NENYGTITSANEQITPVIFHNLIMD MVLPK.V
28	46	2	2110.03	1.7	1	58.2	32.4	95.00%	K.NENYGTITSANEQITPVIF.H		K.NENYGTITSANEQITPVIFHNLIMD MVLPK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
75	A7A0U0_YEAS7	9.51%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
400	430	4	3302.69	-0.93	1	19.1	28.2	92.80%	R.KLMVVHDENGVVRAPADVNAIAD ETTPLNSK.H		R.KLMVVHDENGVVRAPADVNAIAD ETTPLNSK.H
401	430	3	3174.61	2.2	1	64.5	28.5	95.00%	K.LMVVHDENGVVRAPADVNAIADE TTPLNSK.H		K.LMVVHDENGVVRAPADVNAIADE TTPLNSK.H
66	79	2	1581.75	-0.43	1	60.3	33.1	95.00%	K.LGTITGYDLAENCR.H	Carbamidomethyl (+57)	K.LGTITGYDLAENCR.H
400	412	2	1494.8	0.99	1	71.1	29.3	95.00%	R.KLMVVHDENGVVR.A		R.KLMVVHDENGVVR.A
413	430	2	1825.91	-0.18	0	85.6	31.7	95.00%	R.APADVNAIADETTPLNSK.H		R.APADVNAIADETTPLNSK.H
401	412	2	1367.69	1.7	0	66.3	31.6	95.00%	K.LMVVHDENGVVR.A	Deamidation (+1)	K.LMVVHDENGVVR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
76	B3LGY9_YEAS1	13.83%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
408	425	3	2113	1.1	1	30.5	33.3	95.00%	R.LHSHDHKPPVSESSDWQK.E		R.LHSHDHKPPVSESSDWQK.E
9	22	2	1651.84	0.95	1	66.9	31.2	95.00%	K.RVEQDDPVPELDIK.Q		K.RVEQDDPVPELDIK.Q
799	812	2	1601.83	-0.017	1	76.9	30.1	95.00%	K.MLEEEGANILKVEK.R		K.MLEEEGANILKVEK.R
486	503	2	2021.93	0.4	1	98.8	33.8	95.00%	K.LPAWGFEQQEVTCASSGR.H	Carbamidomethyl (+57)	K.LPAWGFEQQEVTCASSGR.H
510	524	2	1731.83	1.1	1	34.8	32.5	95.00%	W.YVENNSNPLLPEDTK.R		R.HDLTLWYVENNSNPLLPEDTK.R
30	42	2	1370.74	1.6	0	58	28.6	95.00%	F.IVTDPSAELASLR.T		K.QGPVRPFIVTDPSAELASLR.T
23	42	3	2152.16	-0.24	1	60.1	26.4	95.00%	K.QGPVRPFIVTDPSAELASLR.T		K.QGPVRPFIVTDPSAELASLR.T
472	485	3	1678.76	-0.033	1	31.3	33.5	95.00%	R.HAMTGCYLFSHEVK.L	Carbamidomethyl (+57)	R.HAMTGCYLFSHEVK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
77	A6ZQK0_YEAS7	11.92%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1190	1228	4	4131.03	-0.62	0	21.1	27.8	95.00%	R.NGELVMHVVSEHVENAGVHSGDATLIVPPQDLAPETVDR.I		R.NGELVMHVVSEHVENAGVHSGDATLIVPPQDLAPETVDR.I
325	337	3	1398.67	0.24	0	33.2	33	95.00%	R.GHNIPCTSTISGR.C	Carbamidomethyl (+57)	R.GHNIPCTSTISGR.C
599	615	2	1638.8	-0.26	1	58.3	32.8	95.00%	R.AAYALGGLGSGFANNEK.E		R.AAYALGGLGSGFANNEK.E
1551	1564	2	1385.78	-0.08	0	32.1	27.3	95.00%	R.SISGPVITDVASLK.A		R.SISGPVITDVASLK.A
752	762	2	1208.71	-0.35	0	32.9	22.1	95.00%	K.LGLNIPLNEVK.N		K.LGLNIPLNEVK.N
562	571	2	1131.54	1.9	0	31.1	31	94.80%	F.SNAIDEINEK.C		R.ELFSNAIDEINEK.C
855	864	2	1050.59	0.82	1	45.4	27.4	95.00%	R.VFAIANAFAK.K		R.VFAIANAFAK.K
467	489	3	2529.41	-0.27	2	28.1	21.7	95.00%	K.ALKEEGIYTILINPNIATIQTSK.G		K.ALKEEGIYTILINPNIATIQTSK.G
381	394	2	1584.77	1.1	1	38.4	32.6	95.00%	Y.FSVQFHPESTPGPR.D		R.CYITSQNHGFAVDVDTLTSGWKPLFVNANDDSNEGIYHSELPYFSVQFHPESTPGPR.D
2000	2011	2	1398.66	-0.7	1	34.5	32.5	95.00%	R.TLACYSDAIVMR.H	Carbamidomethyl (+57)	R.TLACYSDAIVMR.H
2176	2188	3	1644.78	1.6	2	28	33.1	93.70%	R.VNEIKEEVDYDHR.A		R.VNEIKEEVDYDHR.A
1242	1253	2	1363.75	-0.38	1	27.9	28.1	94.60%	K.ITGPYNIQFIAK.D		K.ITGPYNIQFIAK.D
1038	1045	2	1020.53	1.7	1	28.1	31.2	90.00%	Y.FETINLER.V		R.LYFETINLER.V
1635	1650	2	1713.96	0.58	0	29.6	25.5	95.00%	K.TADLASVLLLTSLQNR.S		K.TADLASVLLLTSLQNR.S
575	589	2	1472.75	-0.96	0	59.3	31	95.00%	K.SQAANSVDEALAAVK.E		K.SQAANSVDEALAAVK.E
544	561	2	2032.08	2.1	2	36.9	29.1	95.00%	K.VLGTPIDTIITTEDRELF.S		K.VLGTPIDTIITTEDRELFSNAIDEINEK.C
180	198	2	2143.06	2.2	1	66.4	31.8	95.00%	R.SAFDVPEWVDPNVQNLVSK.V		R.SAFDVPEWVDPNVQNLVSK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
78	VAC7_YEAST	18.54%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
999	1012	2	1699.62	-0.21	0	80.7	32	95.00%	K.CDSNGDCTVMEQER.K	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CDSNGDCTVMEQER.K
817	830	2	1474.73	1.3	0	72.7	32	95.00%	Y.GSASNTHELPLHGR.M		K.NDLETKPLISDYGEDEDVDDYDRPNATFNSYYGSASNTHELPLHGR.M
785	812	3	3245.42	1.1	1	58.8	33.1	95.00%	K.NDLETKPLISDYGEDEDVDDYDRPNATF.N		K.NDLETKPLISDYGEDEDVDDYDRPNATFNSYYGSASNTHELPLHGR.M
606	643	4	4039.94	-0.13	1	49.7	28.1	95.00%	K.VSPHLLSSTSSNGNTISCPNVATNSQELEPNNDISTKK.S	Carbamidomethyl (+57)	K.VSPHLLSSTSSNGNTISCPNVATNSQELEPNNDISTKK.S
816	830	3	1637.79	2.1	1	41.8	33.2	95.00%	Y.YGSASNTHELPLHGR.M		K.NDLETKPLISDYGEDEDVDDYDRPNATFNSYYGSASNTHELPLHGR.M
262	274	2	1471.78	1.3	0	44.5	30	95.00%	R.EILLGENLLDDTK.A		R.EILLGENLLDDTK.A
396	425	4	3160.38	0.64	0	35.9	33.5	95.00%	K.NSNADLSASTSNNNAINDDSHESNSEKPTK.A		K.NSNADLSASTSNNNAINDDSHESNSEKPTK.A
581	592	2	1259.6	2.4	0	52.7	31.6	95.00%	Y.TSDNPDSNVIAK.S		K.QEPPHQLQQQQPPMDVQSVDSYTSDNPDSNVIAK.S
277	311	4	3696.65	-0.81	1	24.5	31.4	95.00%	K.NAPANSTTHDNGPVANDGLRIPNHSNADDNENNNK.M		K.NAPANSTTHDNGPVANDGLRIPNHSNADDNENNNK.M
688	715	4	3273.51	0.57	1	29.9	32.4	95.00%	R.YSGVPDHVNLEDYIEQPHNYPTMQNSVK.K		R.YSGVPDHVNLEDYIEQPHNYPTMQNSVK.K
813	830	3	2001.93	2.7	1	27.6	33.9	91.80%	F.NSYYGSASNTHELPLHGR.M		K.NDLETKPLISDYGEDEDVDDYDRPNATFNSYYGSASNTHELPLHGR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
79	G3P3_YEAST	29.82%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
322	331	3	1107.63	-0.8	0	30.6	26	95.00%	R.VVDLVEHVAK.-		R.VVDLVEHVAK.A
161	184	3	2574.31	2.4	1	58.5	29.5	95.00%	K.VINDAFGIEEGLMTTVHSLTATQK.T		K.VINDAFGIEEGLMTTVHSLTATQK.T
294	304	2	1085.57	1.8	0	51.8	28.8	95.00%	F.DASAGIQLSPK.F		K.GVLGYTEDAVVSSDFLGDSHSSIFDASAGIQLSPK.F

144	160	2	1818.9	-0.47	0	66.5	32.1	95.00%	K.IVSNASCTTNCLAPLAK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.IVSNASCTTNCLAPLAK.V
322	332	2	1178.67	-0.1	1	68.2	26.6	95.00%	R.VVDLVEHVAKA.-		R.VVDLVEHVAKA.-
117	137	2	2206.11	1.8	1	71.2	30.8	95.00%	K.VVITAPSSTAPMFVMGVNEEK.Y		K.VVITAPSSTAPMFVMGVNEEK.Y
199	213	2	1373.71	-0.23	0	53.4	30.8	95.00%	R.TASGNIIPSSTGAAK.A		R.TASGNIIPSSTGAAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
80	A6ZNV4_YEAS7	40.64%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	152	2	1821.91	-0.28	2	57.2	31.8	95.00%	R.TEAVRQDPESSYISIK.V		R.TEAVRQDPESSYISIK.V
29	42	2	1635.81	-0.38	1	74.8	32.4	95.00%	K.ELSNLIETFAEQSR.V		K.ELSNLIETFAEQSR.V
142	152	2	1265.61	-0.32	1	41.9	32.5	95.00%	R.QDPESSYISIK.V		R.QDPESSYISIK.V
13	26	2	1591.72	0.94	1	72.6	33.1	95.00%	K.GNSQQEPQFSTNQK.T		K.GNSQQEPQFSTNQK.T
102	112	2	1413.66	-0.41	1	69.7	32.8	95.00%	K.YQSLQQSYNQR.K		K.YQSLQQSYNQR.K
137	148	2	1380.62	1.9	2	67	32.8	95.00%	R.TEAVRQDPESSY.I		R.TEAVRQDPESSYISIK.V
223	247	3	2864.31	2	0	49.6	32.8	95.00%	K.EQGEQVTTIDENISHLHDNMQNANK.Q		K.EQGEQVTTIDENISHLHDNMQNANK.Q
62	76	2	1821.93	0.67	1	57.6	30.9	95.00%	R.YKIETELIPNCTSVR.D	Carbamidomethyl (+57)	R.YKIETELIPNCTSVR.D
203	222	3	2203.21	0.28	1	67.6	24.9	95.00%	R.IHTAVQEVNAIFHQLGSLVK.E		R.IHTAVQEVNAIFHQLGSLVK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
81	A6ZYN3_YEAS7	25.61%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
276	289	2	1580.7	0.93	0	58.7	33.1	95.00%	R.IPDEELHPLSDEGM.-		R.IPDEELHPLSDEGM.-
257	275	3	2183.06	1.6	0	74.1	32.8	95.00%	F.KPLMDDSDVTLEEAVTHQR.I		R.IFPPIDDPLPFKPLMDDSDVTLEEAVTHQR.I
47	56	2	1171.59	2	1	63.5	30.8	95.00%	Y.INDLTISHPY.A		R.QFYINDLTISHPYATTER.V
245	256	2	1425.77	1.7	2	27.9	27.6	95.00%	R.RIFPPIDDPLPF.K		R.RIFPPIDDPLPFKPLMDDSDVTLEEAVTHQR.I
245	275	4	3590.81	-0.25	2	53.2	26.9	95.00%	R.RIFPPIDDPLPFKPLMDDSDVTLEEAVTHQR.I		R.RIFPPIDDPLPFKPLMDDSDVTLEEAVTHQR.I
132	147	2	1787.91	-0.61	1	47.3	30.7	95.00%	R.CQPVEGLPLDTLFTAK.D	Carbamidomethyl (+57)	R.CQPVEGLPLDTLFTAK.D
44	56	2	1609.78	2	1	92.4	33.2	95.00%	R.QFYINDLTISHPY.A		R.QFYINDLTISHPYATTER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
82	A7A1W6_YEAS7	35.65%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
277	289	2	1540.69	2.3	1	67.8	33.2	95.00%	R.GFLETGNLEDHFY.Q		R.GFLETGNLEDHFYQLEMELCR.D
164	181	2	2196.97	-0.73	1	106	34.3	95.00%	K.NCFDTAEELDDMNIEIIR.N	Carbamidomethyl (+57)	K.NCFDTAEELDDMNIEIIR.N
255	266	2	1369.68	1.4	1	68.8	32.1	95.00%	F.HLAQAQDFEGVR.A		K.LYPLATFHLAQAQDFEGVR.A
322	335	2	1715.84	-0.46	1	69.2	32.4	95.00%	R.NITWIAECIAQNQR.E	Carbamidomethyl (+57)	R.NITWIAECIAQNQR.E
31	43	2	1561.77	1.7	0	68.6	32	95.00%	Y.INLTQCDTLEDLK.L	Carbamidomethyl (+57)	R.NGLLSNNQYINLTQCDTLEDLK.L
220	238	2	2043.03	-2.9	0	32.3	30.8	95.00%	R.SINIALNSLQSSDIDPDLK.S	Deamidation (+1)	R.SINIALNSLQSSDIDPDLK.S
267	276	2	1168.59	-0.44	1	57.4	31.1	95.00%	R.AALANVYEYR.G		R.AALANVYEYR.G
194	205	2	1372.69	1.2	1	43.3	30.9	95.00%	Y.NFVTEEIPEPAK.E		K.AYLEDFYNFVTEEIPEPAK.E
7	18	2	1331.69	1.8	1	68.6	31	95.00%	F.NIDNGFIEGVVR.G		-.MEGVYFNIDNGFIEGVVR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
83	B3LQG1_YEAS1	21.21%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
51	81	3	3458.65	-1.1	1	84.1	30.7	95.00%	K.EISQSINSANNIQSSDSDLVQHFESLAQEIR.H		K.EISQSINSANNIQSSDSDLVQHFESLAQEIR.H
340	348	3	1109.6	-0.18	1	20.7	27.7	90.40%	K.LFHNLNQPK.L		K.LFHNLNQPK.L
130	138	2	1194.59	2.3	1	41.6	31.8	95.00%	K.FPAFIWQTW.S		K.FPAFIWQTWSNDEGPER.V
139	151	2	1485.71	0.86	1	32.5	32.5	94.70%	W.SNDEGPERVQDIK.G		K.FPAFIWQTWSNDEGPERVQDIK.G
349	358	2	1129.68	0.16	1	52	25.4	95.00%	K.LLSDVLVFPK.F		K.LLSDVLVFPK.F
118	129	3	1407.69	0.72	1	30.8	32.5	95.00%	R.IAMTFPYDSHVK.F		R.IAMTFPYDSHVK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
84	MNN5_YEAST	24.23%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
332	356	3	2720.28	0.93	0	46.5	32.5	95.00%	K.HVPLHDLDGTMPDLSSESGQMVIDK.I		K.HVPLHDLDGTMPDLSSESGQMVIDK.I
504	513	2	1115.57	-0.38	1	40.2	31.8	95.00%	R.FIGPNGEQVR.G		R.FIGPNGEQVR.G
493	503	2	1400.65	0.34	1	50.1	33.3	95.00%	K.ADPWTLYHENR.F		K.ADPWTLYHENR.F
78	108	3	3274.42	-1.2	1	71.8	33.1	95.00%	K.LHGAEGCSFANNVAAHDSGHDSDLSYESLSK.C	Carbamidomethyl (+57)	K.LHGAEGCSFANNVAAHDSGHDSDLSYESLSK.C
299	309	2	1220.6	-0.26	1	40.4	31.8	95.00%	R.FVSDDISPVSR.Y		R.FVSDDISPVSR.Y
87	108	2	2316.03	0.86	1	88.7	34.1	95.00%	F.ANNVAAHDSGHDSDLSYESLSK.C		K.LHGAEGCSFANNVAAHDSGHDSDLSYESLSK.C
426	439	3	1675.82	0.31	1	27.1	32.5	93.40%	K.GLALLQHDFEQDYK.Q		K.GLALLQHDFEQDYK.Q
380	394	2	1555.69	1.5	2	47.5	33.7	95.00%	K.MISQGTAGEGDKDTF.F		K.MISQGTAGEGDKDTFFAAAHALNMPYYQVR.T
57	77	3	2212.16	1.5	0	43.8	28.7	95.00%	Y.TTLVQAIVENKPADSSPDLSK.L		K.NNFYTTLVQAIVENKPADSSPDLSK.L
53	77	3	2750.38	-0.032	1	33.2	30.1	95.00%	K.NNFYTTLVQAIVENKPADSSPDLSK.L		K.NNFYTTLVQAIVENKPADSSPDLSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
85	YNF8_YEAST	35.13%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
300	316	2	1917.95	-0.12	1	57.5	31.7	95.00%	R.QAPSMFLDDVLNGREII.-	Deamidation (+1)	R.QAPSMFLDDVLNGREII.-
273	294	3	2214.16	-0.49	1	46.5	29.1	95.00%	K.RNQSSLGLIPVASATSNTSSPK.K		K.RNQSSLGLIPVASATSNTSSPK.K
273	295	3	2342.25	-0.63	1	36.5	26.6	95.00%	K.RNQSSLGLIPVASATSNTSSPKK.A		K.RNQSSLGLIPVASATSNTSSPKK.A
142	157	2	1816.83	2	1	58.2	34.1	95.00%	K.HSSSLQSNPFDINDEK.S		K.HSSSLQSNPFDINDEK.S
300	313	2	1561.75	-0.78	1	63	32.5	95.00%	R.QAPSMFLDDVLNGR.E		R.QAPSMFLDDVLNGR.E
218	229	2	1471.69	2.1	1	40.3	32.5	95.00%	K.DTNIFIDDPFLY.V		K.DTNIFIDDPFLYVGTYLEEEEEEEEER.K
195	209	2	1738.91	-0.35	1	63	29.5	95.00%	R.SLFISPTLQVSQYEK.S		R.SLFISPTLQVSQYEK.S
122	133	2	1377.59	-0.59	1	49.4	34	95.00%	R.FTMTNSYANDSK.N		R.FTMTNSYANDSK.N
230	244	2	1868.78	0.51	1	53	34.2	95.00%	Y.VGTYLEEEEEEEEER.K		K.DTNIFIDDPFLYVGTYLEEEEEEEEER.K
198	209	2	1391.73	1.8	1	46.2	30.3	95.00%	F.ISPTLQVSQYEK.S		R.SLFISPTLQVSQYEK.S
230	245	2	1996.88	1.6	1	103	33.9	95.00%	Y.VGTYLEEEEEEEEERK.L		K.DTNIFIDDPFLYVGTYLEEEEEEEEERK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
86	FCY2_YEAST	12.57%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
38	56	2	2100.94	0.86	1	132	34.1	95.00%	F.TATSEDDQQYIVESSEATK.L		K.VAASETFTATSEDDQQYIVESSEATK.L
18	29	2	1258.64	-0.41	0	53.7	30.9	95.00%	R.SPVIGSSLENEK.K		R.SPVIGSSLENEK.K
17	29	3	1414.74	-0.071	1	59.5	29.8	95.00%	K.RSPVIGSSLENEK.K		K.RSPVIGSSLENEK.K
2	16	2	1791.85	-0.45	1	81.1	32.8	95.00%	M.LEEGNNVYEIQDLEK.R		-.MLEEGNNVYEIQDLEK.R
63	72	2	1126.57	1.9	1	41.1	31	95.00%	K.FFASLNAETK.G		K.FFASLNAETK.G
156	164	2	991.55	0.19	1	49.3	29.2	95.00%	R.YLVGNVTAR.I		R.YLVGNVTAR.I
1	16	2	1922.89	-0.27	1	109	33.6	95.00%	-.MLEEGNNVYEIQDLEK.R		-.MLEEGNNVYEIQDLEK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
87	B3LH18_YEAS1	8.52%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
181	195	2	1663.83	-0.079	2	49.9	31.8	95.00%	R.ATLPHGKEDHFIDGK.I		R.ATLPHGKEDHFIDGK.I
1	20	2	2175.11	-1.6	1	41.3	30.5	95.00%	-.MDATTPLLTVANSHPARNPK.H	Acetyl (+42)	-.MDATTPLLTVANSHPARNPK.H
1	17	2	1851.92	1.5	0	92.6	32	95.00%	-.MDATTPLLTVANSHPAR.N	Acetyl (+42)/ Oxidation (+16)	-.MDATTPLLTVANSHPAR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
88	A6ZT03_YEAS7	17.02%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

518	536	2	2149.04	0.5	1	92.5	32.3	95.00%	K.GLSLEEVNDMYAEGVLPWK.S		K.GLSLEEVNDMYAEGVLPWK.S
1	12	2	1387.66	-0.5	0	48.4	32.6	95.00%	-.MNSTPDLISPQK.S	Acetyl (+42)/ Oxidation (+16)	-.MNSTPDLISPQK.S
262	273	3	1390.72	-0.22	1	24.6	30.7	92.20%	R.YLVEAGRIDEAR.A		R.YLVEAGRIDEAR.A
282	304	3	2805.27	1.2	1	48.9	33.3	95.00%	K.CPPDHPYIQYELETIEASVEEMR.A	Carbamidomethyl (+57)	K.CPPDHPYIQYELETIEASVEEMR.A
228	236	2	1153.52	0.85	1	47.9	32.1	95.00%	K.NYSNSVQWR.V	Deamidation (+1)	K.NYSNSVQWR.V
289	304	3	1938.93	1.9	1	41.3	33	95.00%	Y.IQYELETIEASVEEMR.A		K.CPPDHPYIQYELETIEASVEEMR.A
537	545	2	959.51	0.5	1	44.9	29.4	95.00%	K.SASWVPVSK.R		K.SASWVPVSK.R
292	304	2	1550.72	1.4	0	71.2	33	95.00%	Y.ELETIEASVEEMR.A	Oxidation (+16)	K.CPPDHPYIQYELETIEASVEEMR.A
13	25	2	1508.58	0.1	1	48.4	32.8	95.00%	K.SNSSNSYELESGR.S	Phospho (+80)	K.SNSSNSYELESGR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
89	A6ZXZ5_YEAS7	15.31%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
268	284	2	1788.85	0.99	1	41.2	32.9	95.00%	K.LGYHFGPSDAEAVMAPK.A		K.LGYHFGPSDAEAVMAPK.A
285	300	2	1575.87	0.93	0	62.4	26.8	95.00%	K.APVASPRPAATPNLSK.D		K.APVASPRPAATPNLSK.D
18	31	2	1524.77	-0.55	1	71.2	31.6	95.00%	K.INPPTGADFHITSR.G		K.INPPTGADFHITSR.G
285	302	3	1819	2	1	22.8	27.5	94.30%	K.APVASPRPAATPNLSKDK.K		K.APVASPRPAATPNLSKDK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
90	A7A1T6_YEAS7	10.37%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
308	319	2	1251.62	2.9	1	31.6	32.4	93.80%	K.AAMGALTDLLNY.T		K.AAMGALTDLLNYTTNQTELLTSVESLALSTEAASSTNQLVALDEILSASANASTVVSIIPTLESQLANNTVLLK.Y
659	671	2	1508.74	1	0	52.9	32.6	95.00%	R.IIEEHESPIDAEK.N		R.IIEEHESPIDAEK.N
201	210	2	1179.66	2.2	2	47.5	25.4	95.00%	K.TKLSPVFELF.A		K.TKLSPVFELFASSK.N
502	521	2	2267.09	0.74	1	67.1	32.9	95.00%	Y.MDALNIGKDDLHLDGELQDR.Q		R.SIVYNNIEGSDFKPYMDALNIGKDDLHLDGELQDR.Q
203	214	2	1323.71	2.2	1	38.4	28.3	95.00%	K.LSPVFELFASSK.N		K.LSPVFELFASSK.N
491	501	2	1282.59	2	1	46.4	33	95.00%	Y.NNIEGSDFKPY.M		R.SIVYNNIEGSDFKPYMDALNIGK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
91	A6ZL18_YEAS7	10.04%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
221	233	2	1277.66	1.2	1	64	30.5	95.00%	K.YVINLEGTGAGGK.A		K.YVINLEGTGAGGK.A
165	181	2	1659.85	1.8	0	66.5	30.4	95.00%	Y.GATDDGMGVVSLLANLK.Y		K.NPEEEGLLLSAHFDSVPTGYGATDDGMGVVSLLANLK.Y
816	830	2	1698.95	1.9	1	73.9	26	95.00%	R.SPYEPIVAELLLEVK.E		R.SPYEPIVAELLLEVK.E
605	616	2	1266.55	0.62	0	71.5	32.1	95.00%	K.GSNSMEEGLSTR.E		K.GSNSMEEGLSTR.E
893	901	2	1110.6	1.9	1	41.5	28	95.00%	Y.HIGVQWFPK.L		K.LDFDQETYHIGVQWFPK.L
726	745	3	2112.07	-0.46	1	78.8	30.7	95.00%	R.FSQNIDLSQGNAASVHVLGR.E		R.FSQNIDLSQGNAASVHVLGR.E
129	140	2	1398.74	-0.0082	1	36.6	29.2	95.00%	R.VTYFESSNILVK.L		R.VTYFESSNILVK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
92	A6ZM72_YEAS7	17.38%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
27	37	2	1339.59	-0.49	0	53.2	32.6	95.00%	K.LETDESPIQTK.S	Phospho (+80)	K.LETDESPIQTK.S
296	309	2	1492.73	-0.69	1	87.2	32.7	95.00%	R.LAGNASWGELFSNK.G		R.LAGNASWGELFSNK.G
9	26	2	1924.99	0.89	0	70.8	30.4	95.00%	R.VESGSQQTSIHSTPIVQK.L		R.VESGSQQTSIHSTPIVQK.L
219	227	2	1153.52	0.77	1	47.9	32.1	95.00%	K.DYSNSVQWR.V		K.DYSNSVQWR.V
273	295	2	2562.22	1.5	0	107	32.8	95.00%	K.VTIEDPSIVAEMDTIMANVETER.L		K.VTIEDPSIVAEMDTIMANVETER.L
509	527	3	2220.11	-0.042	1	28.7	31.2	95.00%	K.GLTLEEVNEMYVEGVKPWK.S		K.GLTLEEVNEMYVEGVKPWK.S
9	37	3	3166.6	-0.49	1	61.4	28	95.00%	R.VESGSQQTSIHSTPIVQKLETDESPIQTK.S		R.VESGSQQTSIHSTPIVQKLETDESPIQTK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

93	RL20_YEAST	31.40%	100%	5									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
100	113	2	1552.76	-0.34	1	67.6	32.5	95.00%	R.VAAVETLYQDMAAR.H	Oxidation (+16)	R.VAAVETLYQDMAAR.H		
13	23	2	1251.68	-0.51	1	38.7	28.4	95.00%	R.RLPTESVPEPK.L		R.RLPTESVPEPK.L		
29	38	2	1090.6	-0.39	1	57.7	28.6	95.00%	R.IFASNEVIAK.S		R.IFASNEVIAK.S		
54	71	2	1906.98	1.1	0	63.5	30.8	95.00%	K.ASGEIVSINQINEAHPTK.V		K.ASGEIVSINQINEAHPTK.V		
53	71	3	2035.07	1.4	1	80.6	28.7	95.00%	K.KASGEIVSINQINEAHPTK.V		K.KASGEIVSINQINEAHPTK.V		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
94	B3LJX9_YEAS1	20.50%	100%	4									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
393	411	2	2047.01	-0.59	0	62.3	32.5	95.00%	R.AGDSQGDHLQNDPLSLRPK.T		R.AGDSQGDHLQNDPLSLRPK.T		
412	439	2	3030.23	1.1	1	94.3	33.5	95.00%	K.TYGTGISGSTCLIDDAANCNTADCLEDH.-	Carbamidomethyl (+57)/Carbamidomethyl (+57)/Carbamidomethyl (+57)	K.TYGTGISGSTCLIDDAANCNTADCLEDH.-		
213	234	3	2338.05	-0.12	1	40	34.2	95.00%	K.TPSYSTSSHTIASGGNYTEHNK.R		K.TPSYSTSSHTIASGGNYTEHNK.R		
302	322	2	2197.19	0.36	0	97	27.3	95.00%	K.ILLQATPSTLSGDQVEGDLLK.I		K.ILLQATPSTLSGDQVEGDLLK.I		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
95	YO092_YEAST	11.36%	100%	3									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
138	162	3	2661.16	-0.42	1	67	34	95.00%	R.IDEEMAAPSSDGNAGDDNLREVNSR.N		R.IDEEMAAPSSDGNAGDDNLREVNSR.N		
138	157	2	2075.87	1.4	0	76.1	33.9	95.00%	R.IDEEMAAPSSDGNAGDDNLR.E		R.IDEEMAAPSSDGNAGDDNLR.E		
1	10	2	1211.67	0.23	0	30.4	26.5	95.00%	-.MQLVPLELNR.S		-.MQLVPLELNR.S		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
96	A6ZX41_YEAS7	45.93%	100%	6									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
128	137	2	1212.61	-0.18	0	77.4	31.2	95.00%	R.NDPQTIEQLR.Q		R.NDPQTIEQLR.Q		
104	123	3	2338.24	2.5	1	26.7	27.4	95.00%	K.WIAEVLHFCQGVPIILVGCK.V	Carbamidomethyl (+57)/Carbamidomethyl (+57)	K.WIAEVLHFCQGVPIILVGCK.V		
174	181	2	921.46	1.4	1	32.1	30.9	95.00%	R.EVFEAATR.A		R.EVFEAATR.A		
58	73	2	1879.86	2.1	1	35.9	33.6	95.00%	R.VELALWDTAGQEDYDR.L		R.VELALWDTAGQEDYDR.L		
124	161	3	4155.02	1.5	2	83.2	27.4	95.00%	K.VDLRNDPQTIEQLRQEGQQPVTSQEGQSVADQIGATGY.Y		K.VDLRNDPQTIEQLRQEGQQPVTSQEGQSVADQIGATGYYECSAK.T		
90	103	2	1585.79	1.7	0	69.1	31.7	95.00%	F.SIDLPDSLENVQEK.W		R.LRPLSYPDSNVVLICFSIDLPDSLENVQEK.W		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
97	A6ZMQ9_YEAS7	51.61%	100%	8									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
167	178	2	1413.68	-0.074	1	54.6	33.1	95.00%	R.QTLFQADSYVDK.S		R.QTLFQADSYVDK.S		
103	117	2	1691.77	-0.43	1	68.3	33.3	95.00%	R.LFGDLNASNIDDDQR.Q		R.LFGDLNASNIDDDQR.Q		
118	129	2	1391.79	-0.72	0	46.3	25.3	95.00%	R.QQLLSNHAILQK.S		R.QQLLSNHAILQK.S		
21	34	2	1453.75	-0.49	0	51.8	29.9	95.00%	K.ASLAEAPSQPLSQR.N		K.ASLAEAPSQPLSQR.N		
40	69	3	3472.57	1.4	1	87.3	31.9	95.00%	K.HVEQQQDELFDLLDQMDVEVNNSIGDASER.A		K.HVEQQQDELFDLLDQMDVEVNNSIGDASER.A		
2	13	2	1429.7	2	1	71.8	31.4	95.00%	M.SSLLISYESDFK.T	Acetyl (+42)	-.MSSLLISYESDFK.T		
103	129	3	3065.55	-1.4	1	56	28.3	95.00%	R.LFGDLNASNIDDDQRQQLLSNHAILQK.S		R.LFGDLNASNIDDDQRQQLLSNHAILQK.S		
140	156	2	1892.9	0.51	0	57.5	33.4	95.00%	R.IANETEGIGSQIMMDLR.S	Oxidation (+16)	R.IANETEGIGSQIMMDLR.S		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
98	A6ZVM2_YEAS7	12.97%	100%	8									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
314	325	2	1292.68	-0.86	0	78.3	29.8	95.00%	K.HADANVQLVAQK.M		K.HADANVQLVAQK.M		
36	47	2	1412.6	-1.1	1	83.4	32.7	95.00%	K.LDAEEEQSSSYR.S		K.LDAEEEQSSSYR.S		
34	47	2	1669.74	-0.91	2	75.5	33.7	95.00%	K.EKLDAEEEQSSSYR.S		K.EKLDAEEEQSSSYR.S		
196	204	2	1094.58	-0.25	1	39.6	29.9	95.00%	R.LSLLAYCQK.V	Carbamidomethyl (+57)	R.LSLLAYCQK.V		

326	345	2	2176.04	0.14	0	114	32.4	95.00%	K.MQQITSSQPTPTSELSSAQR.D		K.MQQITSSQPTPTSELSSAQR.D
3	16	2	1670.81	1.7	1	52.8	32.8	95.00%	K.FADHLTESAIPEWR.D		K.FADHLTESAIPEWR.D
824	844	3	2309.08	2	1	55.7	33.2	95.00%	K.AFSSLNDIPITPSHDNNPHSF.A		K.AFSSLNDIPITPSHDNNPHSFAEPMPAYR.G
797	823	2	2734.27	0.22	1	66.7	32.9	95.00%	R.VTGDAPLPYPIAQVGDDSMDSSDLGSK.A		R.VTGDAPLPYPIAQVGDDSMDSSDLGSK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
99	A6ZZE8_YEAS7	20.21%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
388	399	2	1417.69	1.5	0	53.2	32.4	95.00%	K.ETDDILDEIDLK.E		K.ETDDILDEIDLK.E
407	424	2	1913.9	1.3	1	90	33.3	95.00%	Y.VTQGQSFDDEISLGGFSK.V		R.HIPYVTQGQSFDDEISLGGFSK.V
342	363	2	2531.11	-0.13	1	40.3	34.7	95.00%	Y.ISTCTENYSPCVGTPISQAHFY.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.NPFSTDSENYISTCTENYSPCVGTPISQAHFYVDYR.I
433	448	2	1813.76	2	1	76.4	33.9	95.00%	K.LHNSASSNFEGESLCY.S	Carbamidomethyl (+57)	K.LHNSASSNFEGESLCYSPASK.E
383	399	3	1992	2.8	1	32.6	31.7	95.00%	Y.LFADKETDDILDEIDLK.E		K.YLFADKETDDILDEIDLK.E
449	470	2	2324.91	2	1	42.2	33.9	95.00%	Y.SPASKEENSSSNEHSSENTAGP.-	Phospho (+80)	K.LHNSASSNFEGESLCYSPASKEENSSSNEHSSENTAGP.-
342	362	2	2368.05	1.2	1	69.5	33.7	95.00%	Y.ISTCTENYSPCVGTPISQAHF.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.NPFSTDSENYISTCTENYSPCVGTPISQAHFYVDYR.I
350	363	2	1562.72	1.3	1	44.4	32.9	95.00%	Y.SPCVGTPISQAHFY.V	Carbamidomethyl (+57)	R.NPFSTDSENYISTCTENYSPCVGTPISQAHFYVDYR.I
385	399	3	1731.85	2.9	1	30.5	32.2	95.00%	F.ADKETDDILDEIDLK.E		K.YLFADKETDDILDEIDLK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
100	A6ZNY0_YEAS7	14.25%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
193	206	2	1530.77	1.6	1	35.2	31.6	95.00%	Y.ADEVLGDVQVYPAR.G		R.TVESVNVIVSTYADEVLGDVQVYPAR.G
2	10	2	1065.53	1	1	38.7	31.4	95.00%	M.VAFTVDQMR.S		-.MVAFTVDQMR.S
712	723	2	1265.66	-3.6	1	53.3	30.8	95.00%	R.ATYAGFLLADPK.I		R.ATYAGFLLADPK.I
151	162	3	1378.87	0.58	1	24.8	14.5	95.00%	R.IKPVVVINKVDR.A		R.IKPVVVINKVDR.A
786	801	2	1818.82	1.7	1	38.6	33.9	95.00%	R.QATGGQAFPQMVFDHW.S		R.QATGGQAFPQMVFDHWSTLGSDPLDPTSK.A
618	631	2	1626.7	-0.62	1	81.6	33.5	95.00%	R.IMADDYGWDVTDAR.K		R.IMADDYGWDVTDAR.K
33	42	2	1118.59	0.17	0	40.3	30.1	95.00%	K.STLTDSLVQR.A		K.STLTDSLVQR.A
564	578	2	1650.81	1.7	1	90.5	32.5	95.00%	Y.RETVESESSQTALSK.S		K.ISPPVVAYRETVESESSQTALSK.S
353	370	2	1976.92	0.0056	1	81.2	33.7	95.00%	R.AEQLYEGPADDANCIAIK.N	Carbamidomethyl (+57)	R.AEQLYEGPADDANCIAIK.N
565	578	2	1494.7	-0.21	0	70.9	32.6	95.00%	R.ETVESESSQTALSK.S		R.ETVESESSQTALSK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
101	AQR1_YEAST	16.04%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
282	292	2	1140.69	-0.72	0	31	22.6	95.00%	R.TIAGNLSIKPK.R		R.TIAGNLSIKPK.R
493	504	2	1361.6	-0.43	1	49.4	33.3	95.00%	K.SSTASSCFNFVR.C	Carbamidomethyl (+57)	K.SSTASSCFNFVR.C
39	54	2	1749.87	0.22	1	75.5	32.4	95.00%	K.LNFEGAYINSHGTLSK.T		K.LNFEGAYINSHGTLSK.T
505	517	2	1520.68	-0.69	1	60.3	33.2	95.00%	R.CSLSTIFMGCFAK.M	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.CSLSTIFMGCFAK.M
563	572	2	1158.64	-0.27	1	29.8	28.9	95.00%	R.QSWLNTLAVK.A		R.QSWLNTLAVK.A
4	25	3	2677.21	1.4	1	44.3	33.7	95.00%	R.SNSIYTEDIEMYPTHNEQHLTR.E		R.SNSIYTEDIEMYPTHNEQHLTR.E
298	307	2	1081.67	0.25	1	30.5	19.7	95.00%	R.APIFLLGPVR.R		R.APIFLLGPVR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
102	B3LFU9_YEAS1	18.93%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
287	307	2	2463.17	-2.1	2	56.2	32.6	95.00%	R.ELERELYSPEEDSAAQLVTER.T		R.ELERELYSPEEDSAAQLVTER.T
294	307	2	1530.72	1.8	0	93.9	33.2	95.00%	Y.SPEEDSAAQLVTER.T		R.ELYSPEEDSAAQLVTER.T

291	307	2	1935.91	1	1	83.3	33.3	95.00%	R.ELYSPEEDSAAQLVTER.T		R.ELYSPEEDSAAQLVTER.T
100	138	4	4306.08	-0.12	1	41.7	27.6	95.00%	K.LATVGHEPKPLLPELVENGELLR EEEDMIQGGSSAESPR.S	Phospho (+80)	K.LATVGHEPKPLLPELVENGELLR EEEDMIQGGSSAESPR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
103	A6ZKQ4_YEAS7	13.30%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
75	82	2	995.53	1.1	1	42.4	28.5	95.00%	R.VVEFFEVK.N		R.VVEFFEVK.N
83	98	3	1820.87	1.2	0	38.1	32.7	95.00%	K.NDSTDLADHKPENPIR.T		K.NDSTDLADHKPENPIR.T
14	30	2	2027.93	1.2	2	37.9	33.5	95.00%	K.TMKDDTIPTEDYEEITK.E		K.TMKDDTIPTEDYEEITK.E
627	635	2	896.43	4.4	1	32.4	32.2	94.90%	Y.GGVSTGYEK.I		R.EAFEEYGGVSTGYEK.I
236	245	2	1105.59	-0.93	1	47.8	31.2	95.00%	K.AIFGTNLNTR.I		K.AIFGTNLNTR.I
109	123	2	1768.9	-0.69	1	59	31.3	95.00%	R.STYLYNTDLRPVEAK.R		R.STYLYNTDLRPVEAK.R
112	123	2	1417.76	1.7	1	61.8	30.1	95.00%	Y.LYNTDLRPVEAK.R		R.STYLYNTDLRPVEAK.R
80	98	4	2177.07	1.5	1	40.3	32.1	95.00%	F.EVKNDSTDLADHKPENPIR.T		R.VVEFFEVKNDSTDLADHKPENPI R.T
99	108	3	1235.65	-0.000077	1	34.3	30.8	95.00%	R.TFKDLQESLR.S		R.TFKDLQESLR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
104	A6ZNR5_YEAS7	17.31%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
285	300	2	1637.73	-1.1	2	89.8	33.7	95.00%	R.VGKGDDEANGATSFDR.T		R.VGKGDDEANGATSFDR.T
176	191	2	1666.85	0.52	0	80.3	30.9	95.00%	K.AHLAEIQLNGGSISEK.V	Deamidation (+1)	K.AHLAEIQLNGGSISEK.V
175	191	3	1794.95	2.2	1	68.3	28.3	95.00%	K.KAHLAEIQLNGGSISEK.V	Deamidation (+1)	K.KAHLAEIQLNGGSISEK.V
202	222	2	2279.14	1.7	1	88.8	31.1	95.00%	K.TVAVDSVFEQNEMIDAIAVTK.G		K.TVAVDSVFEQNEMIDAIAVTK.G
38	50	2	1409.79	-0.65	1	37.9	24.7	95.00%	R.SKPVALTSFLGYK.A		R.SKPVALTSFLGYK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
105	B3LKG8_YEAS1	8.88%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
16	28	2	1472.57	1.6	1	30.1	32.2	91.90%	R.NSSSLDSDHDAYY.S		R.NSSSLDSDHDAYYSK.Q
403	412	2	1076.59	1.6	1	34.5	29.6	95.00%	R.NLYALAIDGK.A		R.NLYALAIDGK.A
16	30	2	1687.69	-0.89	1	56.6	34	95.00%	R.NSSSLDSDHDAYYSK.Q		R.NSSSLDSDHDAYYSK.Q
45	56	2	1388.66	1.8	0	73	32.9	95.00%	Y.NIDLEENNVSSR.S		K.EQEIYNIDLEENNVSSR.S
29	44	2	1934.94	1.5	2	39.2	32.8	95.00%	Y.SKQNPDNFPVKEQEIY.N		R.NSSSLDSDHDAYYSKQNPDNFP VKEQEIYNIDLEENNVSSR.S
403	415	2	1372.77	-0.017	1	70.1	27.2	95.00%	R.NLYALAIDGKAPK.I		R.NLYALAIDGKAPK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
106	B3LTD0_YEAS1	19.92%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
194	213	2	2015.06	0.92	1	57.8	29.6	95.00%	K.TSAVAALTEVRAEDEAALAK.L		K.TSAVAALTEVRAEDEAALAK.L
33	43	2	1157.62	2.7	1	41	29.6	95.00%	K.NFGIGQAVQPK.R		K.NFGIGQAVQPK.R
134	147	3	1612.9	1.6	1	57.7	26.3	95.00%	K.YGLNHVVSLIENKK.A		K.YGLNHVVSLIENKK.A
194	204	2	1116.61	-0.56	0	64.5	29.9	95.00%	K.TSAVAALTEVR.A		K.TSAVAALTEVR.A
52	57	2	848.42	-0.5	1	29.6	27.7	95.00%	K.WPEYVR.L		K.WPEYVR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
107	A6ZKW1_YEAS7	13.57%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	80	3	2701.13	1.2	1	55.1	34.1	95.00%	K.YSSSSDAASADDSTPLRDNDEA GNEK.L		K.YSSSSDAASADDSTPLRDNDEA GNEK.L
560	569	2	1178.58	-0.85	1	40.1	31.1	95.00%	K.YLDDLLGQDK.T		K.YLDDLLGQDK.T
536	545	2	1283.6	-0.18	1	31.3	32.7	93.00%	K.NYDIELENFK.V		K.NYDIELENFK.V
320	333	2	1575.79	-0.14	2	58.5	31.5	95.00%	R.NSRDDITPPAVYTK.D		R.NSRDDITPPAVYTK.D
448	458	2	1238.6	-0.25	1	51	32.5	95.00%	R.YLNAMESIGNK.Y		R.YLNAMESIGNK.Y
546	555	2	1236.62	-1.4	1	46	31.9	95.00%	K.VLNEYVCVNK.N	Carbamidomethyl (+57)	K.VLNEYVCVNK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
108	A6ZWC1_YEAS7	28.28%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
144	152	2	1059.61	0.17	1	70.8	26.3	95.00%	K.VFLDIGLQR.T		K.VFLDIGLQR.T

208	223	2	1973.82	1.3	2	56.2	34	95.00%	Y.MEELADDDEERFSELF.K		R.SYIFGGHVSQYMEELADDDEERFSELFK.G
241	258	3	1968.01	1.5	2	26.8	30.4	95.00%	Y.TSAHEAIRADPAFKPTEK.K		K.GYLADDIDADSLEDIYTSAHEAIRADPAFKPTEK.K
180	196	2	2091.98	0.072	1	85.4	33.1	95.00%	R.FPGWDFETEEIDPELLR.S		R.FPGWDFETEEIDPELLR.S
199	207	2	1006.49	2.2	1	29.3	30.6	93.10%	Y.IFGGHVSQY.M		R.SYIFGGHVSQYMEELADDDEER.F
165	179	3	1557.72	0.068	1	32.8	33.8	95.00%	K.GASDGGLYVPHSENR.F		K.GASDGGLYVPHSENR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
109	NCB5R_YEAST	35.92%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
183	194	3	1393.76	1.4	1	52.6	28.5	95.00%	F.GNVHEEDILLKK.E		K.VSLVFGNVHEEDILLKK.E
37	48	2	1478.75	-0.83	2	48.3	31.8	95.00%	K.RNDFQSFPLVEK.T		K.RNDFQSFPLVEK.T
91	102	2	1283.59	-0.71	1	32.9	32.8	94.80%	R.SYTPTSLDGDTK.G		R.SYTPTSLDGDTK.G
195	208	2	1589.85	-0.27	1	40	29.5	95.00%	K.ELEALVAMKPSQFK.I		K.ELEALVAMKPSQFK.I
60	80	3	2238.26	1.9	1	40.9	22.4	95.00%	K.FGLPHADDVLGLPIGQHIVIK.A		K.FGLPHADDVLGLPIGQHIVIK.A
49	59	2	1307.65	-0.0036	1	57	31.5	95.00%	K.TILTHNTSMYK.F		K.TILTHNTSMYK.F
147	166	2	2075.04	-0.72	1	51.6	31.2	95.00%	R.SHLGMIAGGTGIAPMYQIMK.A		R.SHLGMIAGGTGIAPMYQIMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
110	A6ZQE5_YEAS7	43.48%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
116	128	2	1414.69	-0.51	0	47.4	30.8	95.00%	R.IEDVTPVPSDSTR.K		R.IEDVTPVPSDSTR.K
113	129	4	1869	2.5	1	30.6	28.1	95.00%	R.IGRIEDVTPVPSDSTRK.K		R.IGRIEDVTPVPSDSTRK.K
60	71	2	1158.61	1.4	0	51.4	30.2	95.00%	Y.AAMLAAQDVAAK.C		R.DESSPYAAMLAAQDVAAK.C
113	128	2	1740.9	1.5	1	54.7	30	95.00%	R.IGRIEDVTPVPSDSTR.K		R.IGRIEDVTPVPSDSTR.K
10	19	2	1091.54	0.44	1	47.3	30.8	95.00%	R.DNSQVFGVAR.I		R.DNSQVFGVAR.I
94	104	2	1023.55	1.4	0	39	29.2	95.00%	K.TPGPGGQAALR.A		K.TPGPGGQAALR.A
74	83	2	1051.6	-0.21	0	23.1	24.1	92.10%	K.EVGITAVHVK.I		K.EVGITAVHVK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
111	A6ZT02_YEAS7	11.81%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
524	542	2	2212.15	1.6	1	84.1	29.1	95.00%	K.GLTLEEVNTLWEEGVLPWK.S		K.GLTLEEVNTLWEEGVLPWK.S
268	279	2	1376.76	1.3	1	66.8	28.2	95.00%	R.YLVEVGKIEEAK.R		R.YLVEVGKIEEAK.R
288	310	2	2386.16	2.5	0	126	31.8	95.00%	K.VSADDPAVMAEVEVVQATVEAEK.L		K.VSADDPAVMAEVEVVQATVEAEK.L
311	324	2	1479.73	-0.83	1	78.9	32.6	95.00%	K.LAGNASWGEIFSTK.T		K.LAGNASWGEIFSTK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
112	B3LI54_YEAS1	23.19%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
44	56	3	1598.82	0.5	2	24.6	30.2	92.90%	K.VLIVERDWAMPDR.I		K.VLIVERDWAMPDR.I
298	311	2	1519.76	-0.74	1	56.4	32	95.00%	K.SLRPSFDEAVSQGK.F		K.SLRPSFDEAVSQGK.F
218	240	4	2468.22	0.38	1	21.6	31.4	91.40%	K.ELHPDHVPTVGSSFVGMSLFNAK.N		K.ELHPDHVPTVGSSFVGMSLFNAK.N
314	323	2	1118.55	0.16	1	34.8	30.8	95.00%	R.AMPNSYLPAR.Q		R.AMPNSYLPAR.Q
373	384	3	1547.77	1.9	1	37.4	31.8	95.00%	K.VLDELLDYHFER.K		K.VLDELLDYHFER.K
44	51	2	1028.57	3.2	2	32.9	28.7	95.00%	K.VLIVERDW.A		K.VLIVERDWAMPDR.I
170	182	2	1544.79	-0.57	1	47.6	30.5	95.00%	R.VQGNCIEILKDEK.N	Carbamidomethyl (+57)	R.VQGNCIEILKDEK.N
50	68	3	2126.04	0.8	1	31	31.8	95.00%	R.DWAMPDRIVGELMQPGGVR.A		R.DWAMPDRIVGELMQPGGVR.A
170	189	4	2242.17	1.7	1	21.9	28.7	95.00%	R.VQGNCIEILKDEKNEVVGAK.V	Carbamidomethyl (+57)	R.VQGNCIEILKDEKNEVVGAK.V
159	169	2	1241.64	-0.34	0	47.5	30.5	95.00%	R.NITAQEPNVTR.V		R.NITAQEPNVTR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
113	B3LMA9_YEAS1	17.46%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
283	293	3	1070.59	-0.46	1	32	27.5	95.00%	K.SGGIFGVLHGK.S		K.SGGIFGVLHGK.S
220	247	3	2982.45	1.7	1	68.1	30.9	95.00%	K.IAVEGLDENGRLIEGDTGSGIIPDEQER.Q	Deamidation (+1)	K.IAVEGLDENGRLIEGDTGSGIIPDEQER.Q
231	247	2	1827.89	1.2	0	94	32.9	95.00%	R.LIEGDTGSGIIPDEQER.Q		R.LIEGDTGSGIIPDEQER.Q

269	281	2	1550.82	1.7	1	58	28.8	95.00%	K.SVLETYVEDKLQK.K		K.SVLETYVEDKLQK.K
496	504	2	981.48	0.1	1	36.4	31.1	95.00%	R.GLSSNYQTI.-		R.GLSSNYQTI.-
220	230	2	1171.58	-0.71	0	54.9	31	95.00%	K.IAVEGLDENGR.L		K.IAVEGLDENGR.L
84	91	2	963.49	0.71	1	32.4	30.9	95.00%	K.ILDMYGPR.V		K.ILDMYGPR.V
248	266	3	2223.16	1.2	1	28.9	28.5	95.00%	R.QSLIAIEREEDSIPSRPQR.R		R.QSLIAIEREEDSIPSRPQR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
114	ARN2_YEAST	7.38%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
254	265	2	1531.72	-0.28	1	55	33.4	95.00%	R.NDVEWKELQDEK.S		R.NDVEWKELQDEK.S
1	14	2	1675.78	6.3	1	34.9	33.3	95.00%	-.MIEVPEDNRSSQTK.R	Acetyl (+42)/ Deamidation (+1)	-.MIEVPEDNRSSQTK.R
597	611	3	1770.88	1.6	2	44	31.6	95.00%	Y.VQTKEDDPINDWIAK.R		R.EYVQTKEDDPINDWIAK.R
597	608	2	1458.67	1.4	2	42	33.6	95.00%	Y.VQTKEDDPINDW.I		R.EYVQTKEDDPINDWIAK.R
601	611	2	1314.61	2.6	1	34.6	33	95.00%	K.EDDPINDWIAK.R		K.EDDPINDWIAK.R
591	600	2	1247.65	-0.73	2	31.5	30.6	95.00%	K.LPDREYVQTK.E		K.LPDREYVQTK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
115	A7A1Z8_YEAS7	13.67%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
390	401	2	1360.73	-1.3	1	49.9	29.7	95.00%	R.IYGDNINAQLLK.H		R.IYGDNINAQLLK.H
311	321	2	1332.6	-1.2	0	43.6	33.2	95.00%	R.ALNIEDCDLDR.A	Carbamidomethyl (+57)	R.ALNIEDCDLDR.A
322	334	2	1579.79	1.9	1	58.2	31.9	95.00%	R.ATNDFYLEPLIER.D		R.ATNDFYLEPLIER.D
471	484	2	1519.84	-0.34	0	41.6	27.6	95.00%	R.DTVVLEPSGHVVLR.F		R.DTVVLEPSGHVVLR.F
372	383	2	1229.72	-0.58	0	25.8	24.1	95.00%	K.VPTLTTLLTSGK.L		K.VPTLTTLLTSGK.L
524	533	2	1280.61	-0.3	1	52.9	32.3	95.00%	K.LNENYLDICK.A	Carbamidomethyl (+57)	K.LNENYLDICK.A
159	171	2	1617.78	1	1	60	32.4	95.00%	R.VITLSDHYHENYK.T		R.VITLSDHYHENYK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
116	UIP3_YEAST	18.30%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
199	209	2	1239.6	2	1	40.9	32.4	95.00%	Y.IFSSDPVLEAY.L		K.EVSNEMVKPYIFSSDPVLEAYLIK.A
167	188	2	2226.01	-0.64	0	89.7	33.9	95.00%	R.SNAHLSSPTNGAENTQSNTPAK.E	Deamidation (+1)	R.SNAHLSSPTNGAENTQSNTPAK.E
167	198	4	3402.57	2	2	49.1	31.5	95.00%	R.SNAHLSSPTNGAENTQSNTPAKEVSNEMVKPY.I	Deamidation (+1)	R.SNAHLSSPTNGAENTQSNTPAKEVSNEMVKPYIFSSDPVLEAYLIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
117	B3LJW5_YEAS1	28.51%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
118	131	2	1498.77	-0.49	1	61.8	30.6	95.00%	K.LLENSGPDVPFSPK.L		K.LLENSGPDVPFSPK.L
251	264	2	1703.84	1.4	1	46.7	31.8	95.00%	R.VALHNIHDEISDWR.F		R.VALHNIHDEISDWR.F
132	140	2	1086.57	0.62	1	42.5	30.1	95.00%	K.LNELLGDWK.H		K.LNELLGDWK.H
237	246	2	1313.58	2	1	41.5	32.9	95.00%	Y.QFLEMDCFPK.F	Carbamidomethyl (+57)	K.NLTYQFLEMDCFPK.F
213	221	2	1085.61	-0.11	0	28.5	27.4	95.00%	R.IIESVQIER.K		R.IIESVQIER.K
8	19	2	1468.68	-0.55	1	44.5	33.2	95.00%	K.VSSMQNFEMIQR.E		K.VSSMQNFEMIQR.E
141	164	3	2664.37	4	1	41.9	29.2	95.00%	K.HQSGIGQEALRNEDVALIVDEIMK.R		K.HQSGIGQEALRNEDVALIVDEIMK.R
20	32	3	1628.93	0.86	2	28.2	24.3	95.00%	R.ERLPTLYEVLIQR.T		R.ERLPTLYEVLIQR.T
152	164	2	1487.76	1.9	0	84.1	31	95.00%	R.NEDVALIVDEIMK.R		R.NEDVALIVDEIMK.R
99	117	2	2088.04	2.6	0	70.7	31.3	95.00%	F.DLLNALIEEGHLDPEAPDK.L		K.SLINFPQEQQQNGSTSTATFDLLNALIEEGHLDPEAPDK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
118	A6ZNT8_YEAS7	17.19%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
465	480	2	1841.82	-1	1	46.2	34	95.00%	K.VIDNADDEYMALMSQK.T		K.VIDNADDEYMALMSQK.T
653	667	2	1684.96	1.4	1	95.5	23.9	95.00%	K.KVENLTAVITDLLEK.L		K.KVENLTAVITDLLEK.L
553	565	2	1607.69	1.9	2	37.7	33.8	95.00%	K.RLNDDANEYDTPW.D		K.RLNDDANEYDTPWDLTDGYLDDDDGLFSDNR.N

2	33	3	3450.6	0.76	1	55.4	31.2	95.00%	M.VSANGDLHLPISNEQCMPENNGSLGFEAPTPR.Q	Carbamidomethyl (+57)	-.MVSANGDLHLPISNEQCMPENNGSLGFEAPTPR.Q
603	611	2	1074.47	3	1	33.4	33.2	94.90%	R.TAEQEDVHF.K		R.TAEQEDVHFK.V
125	133	2	1060.53	0.4	0	31.9	30.5	95.00%	R.NLASQQLCK.L	Carbamidomethyl (+57)	R.NLASQQLCK.L
49	70	2	2508.26	0.05	1	43.7	30.6	95.00%	K.VVPIVYDPNDIVCDHSEILSPK.V	Carbamidomethyl (+57)	K.VVPIVYDPNDIVCDHSEILSPK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
119	A6ZLZ0_YEAS7	13.38%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
598	614	2	1869.02	0.57	0	98.4	26.7	95.00%	K.IRPLEELEALLSSGNTK.Q		K.IRPLEELEALLSSGNTK.Q
372	385	2	1500.74	-0.75	0	63.5	31.5	95.00%	K.QTLEEDGVVPSTAR.I		K.QTLEEDGVVPSTAR.I
727	740	2	1272.7	-0.72	0	73.1	29.6	95.00%	K.AINAGGGATTVLTK.D		K.AINAGGGATTVLTK.D
689	706	2	1826.99	3.1	1	44.2	28	95.00%	Y.MPLPVGVIGPLVIDGTSY.H		R.VFGACCENVIGYMPLPVGVIGPLVIDGTSYHIPMATTEGCLVASAMR.G
786	801	3	1914.98	0.13	1	30	30.7	95.00%	R.LQHIQTCLAGDLLFMR.F	Carbamidomethyl (+57)	R.LQHIQTCLAGDLLFMR.F
524	535	2	1374.71	-0.58	1	40.9	31.1	95.00%	R.IHTSYTADQLVK.T		R.IHTSYTADQLVK.T
804	817	2	1456.64	0.27	0	36	33.6	95.00%	R.TTTGDAMGMNMISK.G		R.TTTGDAMGMNMISK.G
652	669	2	1898.06	3	2	57.9	25.2	95.00%	K.ALSILAEAPVLASDRLPY.K		K.ALSILAEAPVLASDRLPYK.N
1026	1043	3	1993.03	1.1	0	31.4	30.3	95.00%	R.KPAEPTKPNNLDATDINR.L		R.KPAEPTKPNNLDATDINR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
120	A6ZNU6_YEAS7	31.58%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	139	4	2593.45	2.5	2	37.1	21.6	95.00%	R.TLTAVHDKILEDLVFPTEIVGKR.V		R.TLTAVHDKILEDLVFPTEIVGKR.V
117	138	3	2437.35	2.5	2	21.2	23	95.00%	R.TLTAVHDKILEDLVFPTEIVGK.R		R.TLTAVHDKILEDLVFPTEIVGK.R
165	173	2	1083.56	2	2	34.4	29.3	95.00%	Y.KLESFQAVY.N		K.DVQQIDYKLESFQAVYNK.L
125	138	2	1571.88	2.1	1	45.6	26	95.00%	K.ILEDLVFPTEIVGK.R		K.ILEDLVFPTEIVGK.R
25	35	2	1243.63	1.3	0	54.1	30.7	95.00%	F.VELENSSPELK.A		K.ILSQAPTELELQVAQAFVELENSSPELK.A
8	35	3	3082.61	-0.16	1	56.2	26.7	95.00%	K.ILSQAPTELELQVAQAFVELENSSPELK.A		K.ILSQAPTELELQVAQAFVELENSSPELK.A
125	139	2	1727.99	1.6	1	39.4	23.6	95.00%	K.ILEDLVFPTEIVGKR.V		K.ILEDLVFPTEIVGKR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
121	YOL19_YEAST	29.76%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
376	402	3	3114.35	-1.5	1	40.8	33.4	95.00%	R.LLNDIMETSFNEPNDSHINSMSSYNDK.D		R.LLNDIMETSFNEPNDSHINSMSSYNDK.D
490	501	2	1405.72	0.98	1	49.8	31.4	95.00%	Y.FNVAPNQVPQHR.N		R.TTPAGPDPSNVILQSNPYFNVAPNQVPQHR.N
452	466	2	1940.91	0.9	1	31.3	33.4	91.90%	R.LQPQQQQPQQQYHQY.N		R.LQPQQQQPQQQYHQYNLYQR.T
425	436	2	1258.63	2	1	54.7	31.3	95.00%	R.ETAAGPANIRPY.A		R.ETAAGPANIRPYAGQPHPAPLVYPQQR.L
472	501	3	3257.62	-0.24	1	75	28.4	95.00%	R.TTPAGPDPSNVILQSNPYFNVAPNQVPQHR.N		R.TTPAGPDPSNVILQSNPYFNVAPNQVPQHR.N
540	551	2	1339.65	-0.018	1	37.3	32.3	95.00%	R.ATTSLNNPYGFR.-		R.ATTSLNNPYGFR.-
203	214	2	1336.67	-0.31	1	36.9	31.8	95.00%	K.GMLLNDPYLSSK.S		K.GMLLNDPYLSSK.S
425	451	3	2898.49	-1.1	1	43.4	27.8	95.00%	R.ETAAGPANIRPYAGQPHPAPLVYPQQR.L		R.ETAAGPANIRPYAGQPHPAPLVYPQQR.L
306	320	2	1586.77	-0.32	1	64	32.4	95.00%	R.STSTYSVIESESGLK.N		R.STSTYSVIESESGLK.N
452	463	2	1512.73	1.5	1	32.5	32.7	94.50%	R.LQPQQQQPQQQY.H		R.LQPQQQQPQQQYHQYNLYQR.T
187	202	3	1824.75	0.05	1	61.1	33.9	95.00%	R.SSGSRDDDETEELEEK.G		R.SSGSRDDDETEELEEK.G
403	412	2	1106.56	-0.91	0	40.2	31.6	95.00%	K.DSTLTSISQR.G		K.DSTLTSISQR.G
472	489	2	1869.91	1.4	1	66.8	32.4	95.00%	R.TTPAGPDPSNVILQSNPY.F		R.TTPAGPDPSNVILQSNPYFNVAPNQVPQHR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
122	A6ZWP0_YEAS7	9.66%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
91	103	2	1443.72	-0.66	0	51.6	31.2	95.00%	K.AQPLISSCPACLK.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.AQPLISSCPACLK.N
961	971	2	1269.6	0.46	1	46.9	32.8	95.00%	K.DFIQAYSDGVR.I		K.DFIQAYSDGVR.I
33	45	2	1470.73	-0.68	1	34.2	32.2	95.00%	K.SVFGNELPCPVPR.S	Carbamidomethyl (+57)	K.SVFGNELPCPVPR.S
831	841	2	1272.63	1.1	0	47.3	31.4	95.00%	R.DSLANVLEQER.H		R.DSLANVLEQER.H
825	841	3	2066.97	2	1	61.2	33.5	95.00%	K.FTTCERDSLANVLEQER.H	Carbamidomethyl (+57)	K.FTTCERDSLANVLEQER.H
476	489	2	1687.87	-0.94	1	33.6	30.1	95.00%	K.FPVNCLPTFQQPLK.T	Carbamidomethyl (+57)	K.FPVNCLPTFQQPLK.T
161	177	2	1671.79	-0.85	1	88.4	33.5	95.00%	K.FSATNGYAMDLIGGGAK.N		K.FSATNGYAMDLIGGGAK.N
873	887	3	1731.84	1.6	2	41.2	32.5	95.00%	K.KGTDEVCPPSFPSRR.C	Carbamidomethyl (+57)	K.KGTDEVCPPSFPSRR.C
46	58	2	1434.69	0.75	1	29.8	32.7	90.20%	R.SFEPPVLSDETSK.L		R.SFEPPVLSDETSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
123	A7A1C4_YEAS7	12.15%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
742	749	2	921.53	0.094	1	24.3	24.1	93.90%	K.YIALSSIR.E		K.YIALSSIR.E
331	340	2	1113.62	2	0	37.3	27.4	95.00%	Y.SQISLGERPK.M		R.QPYSENYHLLGNEQSGAVTHGENVPSSNNNDEDTILYSQISLGERPK.M
352	364	2	1576.8	1.5	1	68	31.5	95.00%	K.EVDAIEYLEQQLK.F		K.EVDAIEYLEQQLK.F
301	330	3	3223.47	2.1	1	52.9	32.7	95.00%	Y.HLLGNEQSGAVTHGENVPSSNNNDEDTILY.S		R.QPYSENYHLLGNEQSGAVTHGENVPSSNNNDEDTILYSQISLGERPK.M
10	26	4	1958.88	2.1	1	31.3	33.8	95.00%	K.SAASYLDTVPDEHHDFR.K		K.SAASYLDTVPDEHHDFR.K
413	429	5	2014.02	-0.16	2	23.4	30.9	90.20%	R.LAPAPHDIKWDHVCLSR.K	Carbamidomethyl (+57)	R.LAPAPHDIKWDHVCLSR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
124	ATC1_YEAST	20.00%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
553	568	2	1731.91	-0.18	0	69.4	29.9	95.00%	K.LTLSDSSTPLTEDLIK.D		K.LTLSDSSTPLTEDLIK.D
445	460	2	1713.9	2.1	1	53.6	29.3	95.00%	F.LGNPTDVALLEQLANF.E		R.ETLTIGNLCNNASFSQEHAIFLGNPTDVALLEQLANFEMPDIR.N
670	689	3	2013.03	1.4	1	69.5	30	95.00%	R.KRGDVVAMTGDGVNDAPALK.L		R.KRGDVVAMTGDGVNDAPALK.L
627	655	4	3213.6	-0.081	2	44.6	28.6	95.00%	K.LSVLSGDKLDEMSDDQLANVIDHVNIFAR.A		K.LSVLSGDKLDEMSDDQLANVIDHVNIFAR.A
690	699	2	1033.52	0.28	0	54.7	30.2	95.00%	K.LSDIGVSMGR.I		K.LSDIGVSMGR.I
39	54	2	1835.88	1.1	1	97	32.2	95.00%	Y.CTLSVDEALEKLDTDK.N	Carbamidomethyl (+57)	R.EILDATAEALSKPSPSLEYCTLSVDEALEKLDTDK.N
235	245	2	1241.61	-0.38	1	36.4	31.8	95.00%	R.SCIAYMGTLVK.E	Carbamidomethyl (+57)	R.SCIAYMGTLVK.E
158	178	3	2321.16	-0.24	1	34.4	31.4	95.00%	R.CGQESHVLASTLVPGDLVHFR.I	Carbamidomethyl (+57)	R.CGQESHVLASTLVPGDLVHFR.I
219	234	2	1788.86	-1.1	1	46.8	32.6	95.00%	K.SSFNDQPNSIVPISER.S		K.SSFNDQPNSIVPISER.S
531	546	2	1722.77	-0.52	0	106	33.6	95.00%	K.ATINECANSMASEGLR.V	Carbamidomethyl (+57)	K.ATINECANSMASEGLR.V
20	38	2	2033.02	1.4	1	41.1	31.5	95.00%	R.EILDATAEALSKPSPSLEY.C		R.EILDATAEALSKPSPSLEYCTLSVDEALEK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
125	A6ZQU5_YEAS7	12.09%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
340	349	2	1147.59	1.6	1	28.4	29.8	92.90%	Y.TTGEFILPDR.H		R.LTLSPSGNDSETQYYTTGEFILPDR.H
75	85	2	1305.74	2.3	1	56.2	26.3	95.00%	R.LFDNIIVFPTK.G		R.LFDNIIVFPTK.G
266	285	3	2227.98	-0.13	1	44.5	33.9	95.00%	K.SVHAVHSHADGTSYDEEPYK.I		K.SVHAVHSHADGTSYDEEPYK.I
186	196	2	1248.72	-0.58	0	48.6	25.4	95.00%	R.EQIVPILNAPR.T		R.EQIVPILNAPR.T
266	284	2	2099.89	1.6	1	84.5	34.3	95.00%	K.SVHAVHSHADGTSYDEEPY.K		K.SVHAVHSHADGTSYDEEPYK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
126	A6ZQR6_YEAS7	68.15%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
69	86	2	2022.05	0.83	1	81.7	29.9	95.00%	K.KLEDLSPSTHNMEVPVVK.R		K.KLEDLSPSTHNMEVPVVK.R

2	28	3	3110.26	-0.79	1	32.5	33.5	95.00%	M.SDEEHTFETADAGSSATYPMQCSALRK.N	Acetyl (+42)/ Phospho (+80)/ Carbamidomethyl (+57)	-.MSDEEHTFETADAGSSATYPMQCSALRK.N
69	87	4	2178.15	-0.35	1	40.8	28.6	95.00%	K.KLEDLSPSTHNMEVPVVKR.N		K.KLEDLSPSTHNMEVPVVKR.N
29	35	2	776.44	-0.31	1	30.2	27.5	95.00%	K.NGFVVIK.S	Deamidation (+1)	K.NGFVVIK.S
57	68	2	1311.75	-0.32	1	66.2	25.6	95.00%	K.VHLVAIDIFTGK.K		K.VHLVAIDIFTGK.K
91	114	3	2697.26	1.6	1	67.2	32.9	95.00%	Y.QLLDIDDGFLSLMNMDGDTKDDVK.A		R.NEYQLLDIDDGFLSLMNMDGDTKDDVK.A
115	132	2	1862.86	2.3	1	122	33.7	95.00%	K.APEGELGDSLQTAFDEGK.D		K.APEGELGDSLQTAFDEGK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
127	A6ZYM2_YEAS7	14.44%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
425	444	3	2277.27	0.27	0	18	21.8	90.20%	K.EIPIELLQVNDIVEIKPGMK.I		K.EIPIELLQVNDIVEIKPGMK.I
688	702	2	1603.88	0.3	1	68	27.8	95.00%	K.ALNAVVLESEYVLGK.G		K.ALNAVVLESEYVLGK.G
779	795	2	1847.8	-0.87	1	77.6	34.3	95.00%	R.NGYETYMITGDNNSAAK.R		R.NGYETYMITGDNNSAAK.R
757	770	2	1664.77	1	2	50.7	33.4	95.00%	F.GLFEINDEVKHDSY.A		K.SGFINSNVDQGNTVSYVSVNGHVFGLFEINDEVKHDSYATVQYLQR.N
760	770	2	1347.6	2	2	38.1	33.2	95.00%	F.EINDEVKHDSY.A		K.SGFINSNVDQGNTVSYVSVNGHVFGLFEINDEVKHDSYATVQYLQR.N
101	128	3	3114.55	1.6	1	90.8	29.8	95.00%	K.QVEGIEGVESVVVSLVTEECHVIYEPSK.T	Carbamidomethyl (+57)	K.QVEGIEGVESVVVSLVTEECHVIYEPSK.T
800	817	2	1926.92	0.87	1	83.6	33.3	95.00%	R.EVGISFENVYSDVSPTGK.C		R.EVGISFENVYSDVSPTGK.C
169	184	2	1777.87	-2.3	1	44.5	32.5	95.00%	K.AFEDESPLILSSVSER.F		K.AFEDESPLILSSVSER.F
716	732	2	1914.02	1.7	1	99.9	28.7	95.00%	Y.DICIGNEALILEDALKK.S	Carbamidomethyl (+57)	K.CQVNGNTYDICIGNEALILEDALKK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
128	B3LRN6_YEAS1	50.82%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
69	80	2	1289.65	1.3	1	38.5	32.2	95.00%	F.LGLTEEPAADFK.C		K.FYCVRPNAAVVAPGETIQVQVIFLGLTEEPAADFK.C
25	38	2	1494.73	1.3	1	56.1	32.7	95.00%	Y.ASISNNSDQTIAFK.V		K.SPLTEQSTEYASISNNSDQTIAFK.V
199	212	2	1512.75	0.33	0	37.2	31.6	95.00%	K.QTSNSTPAPQNQIK.E		K.QTSNSTPAPQNQIK.E
125	156	4	3644.8	-0.12	1	27.4	28	95.00%	K.YLISPDVHPAQNQNIQENKETVEPVVQDSEPK.E		K.YLISPDVHPAQNQNIQENKETVEPVVQDSEPK.E
100	113	2	1578.76	2	1	73.1	32.8	95.00%	K.AVADVWSDLEAEFK.Q		K.AVADVWSDLEAEFK.Q
181	190	3	1151.66	-0.085	1	31.8	24.7	95.00%	K.KEEVPPVVQK.T		K.KEEVPPVVQK.T
166	180	2	1646.85	-0.8	0	41.3	31	95.00%	K.EVPAEPETQPPVQVK.K		K.EVPAEPETQPPVQVK.K
2	14	2	1460.78	0.36	1	36.8	30.4	95.00%	M.SAVEISPDVLVYK.S	Acetyl (+42)	-.MSAVEISPDVLVYK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
129	ERG2_YEAST	19.37%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	46	2	1376.7	1.3	0	44.2	31.5	95.00%	K.TLNEICNSVISK.H	Carbamidomethyl (+57)	K.TLNEICNSVISK.H
47	70	3	2624.25	1.5	2	45.8	32	95.00%	K.HNAAEGLSTEDLLQDVRDALASHY.G		K.HNAAEGLSTEDLLQDVRDALASHYGDEYINR.Y
47	63	2	1866.91	1.3	0	113	32.8	95.00%	K.HNAAEGLSTEDLLQDVR.D		K.HNAAEGLSTEDLLQDVR.D
64	77	2	1622.73	-1.2	1	68.5	33.1	95.00%	R.DALASHYGDEYINR.Y		R.DALASHYGDEYINR.Y
47	74	3	3088.41	1.6	2	32.4	32.9	95.00%	K.HNAAEGLSTEDLLQDVRDALASHYGDEY.I		K.HNAAEGLSTEDLLQDVRDALASHYGDEYINR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
130	A7A077_YEAS7	20.22%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
271	287	3	1889.03	0.11	1	29.9	28	95.00%	K.YKPNLVLGENSLDATKK.H		K.YKPNLVLGENSLDATKK.H
104	113	2	1195.56	0.23	1	34.8	32.4	95.00%	R.IDSEEAEYIK.L		R.IDSEEAEYIK.L
257	270	2	1602.84	0.24	1	59.1	30.1	95.00%	R.GSVPIYWAEINNLK.Y		R.GSVPIYWAEINNLK.Y

453	464	2	1252.64	1.5	2	32.3	31.2	95.00%	Y.SGTGALKTDFTR.T		K.EFESADVVATGSTWEDNAPLLTSYQNLWADNADAVSVAYSGTGALKTDFTR.T
8	17	2	1137.58	1.8	1	43.2	31.4	95.00%	Y.VQNADGIFFK.L		-.MTGPIVYVQNADGIFFK.L
370	389	3	2208.12	1.4	0	24.2	30.5	91.70%	K.VIDSNGNTVEIVNEQHSVVR.T		K.VIDSNGNTVEIVNEQHSVVR.T
294	308	2	1780.9	-0.34	1	61.6	31.6	95.00%	K.ELYGDNYLVNLVNQK.G		K.ELYGDNYLVNLVNQK.G
189	207	3	2021.2	-0.3	1	19.6	16.3	93.40%	K.TVDAVLNATPIVLGLITRR.S		K.TVDAVLNATPIVLGLITRR.S
390	398	2	1183.44	0.21	0	45.4	31.3	95.00%	R.TNCMDCLDR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.TNCMDCLDR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
131	GLRX7_YEAST	17.24%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
154	165	2	1212.68	-0.76	0	73.1	26.7	95.00%	R.TVPNVIIGGTSR.G		R.TVPNVIIGGTSR.G
166	176	3	1216.61	0.0047	1	25.2	31.1	92.50%	R.GGYTEIAELHK.N		R.GGYTEIAELHK.N
94	105	2	1424.7	-0.58	1	69.7	32.5	95.00%	K.IMEQSPMIVFSK.T	Oxidation (+16)	K.IMEQSPMIVFSK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
132	A6ZZ86_YEAS7	13.87%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
569	584	2	1954.98	-2.5	2	45.2	31.5	95.00%	R.VHELKYEPTQEIIEDI.-		R.VHELKYEPTQEIIEDI.-
288	300	2	1597.76	1.2	2	57.9	33.1	95.00%	K.RSYTDTSEEIIER.K		K.RSYTDTSEEIIER.K
289	300	2	1441.66	1.7	1	51.8	33.5	95.00%	R.SYTDTSEEIIER.K		R.SYTDTSEEIIER.K
42	51	2	1224.65	-0.59	0	62.5	30.2	95.00%	K.ITLESHEIQR.A		K.ITLESHEIQR.A
12	38	3	2777.2	0.077	1	61.6	34	95.00%	K.TSQSNVGDAVGNADSVEFNSEHDSPSK.R		K.TSQSNVGDAVGNADSVEFNSEHDSPSK.R
301	315	2	1653.93	0.052	1	73.9	25.6	95.00%	R.KVEELVTLNQSIPGK.N		R.KVEELVTLNQSIPGK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
133	A6ZLU9_YEAS7	15.51%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
313	325	2	1424.67	0.13	1	30.7	33.3	90.90%	K.DFGQVIGQGFSDR.H		K.DFGQVIGQGFSDR.H
279	287	2	1159.5	-0.53	1	44	32.9	95.00%	K.YMDEGYINR.V		K.YMDEGYINR.V
15	26	2	1272.65	-0.57	0	38	31.1	95.00%	K.AMDNGLSLPISR.N		K.AMDNGLSLPISR.N
201	211	2	1217.65	0.22	1	35.4	30.4	95.00%	R.NAADVLPLMFK.H		R.NAADVLPLMFK.H
191	200	2	1248.7	0.41	0	24.9	27	91.80%	R.DHILLCIPLR.N	Carbamidomethyl (+57)	R.DHILLCIPLR.N
511	521	2	1330.61	1.3	1	35.8	33.3	95.00%	W.HIYEPSDDDLK.E		R.VGGLPHYTIWHIYEPSDDDLK.E
143	159	2	1904.97	0.62	1	69.1	31.1	95.00%	Y.LISQFGSEVLTPKDDEK.Y		K.FDDGVQHYLISQFGSEVLTPKDDEK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
134	YL001_YEAST	11.14%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
485	496	2	1391.74	-0.3	0	26.8	29.6	90.50%	K.ELNLLDLPSNHK.G		K.ELNLLDLPSNHK.G
836	844	2	984.54	2.6	0	44.9	26.7	95.00%	Y.SVNAIQTPR.D		R.ATTPLIQHSPIIHNPSYSATAHLSPLSQPTFEGSYSVNAIQTPR.D
385	399	2	1822.91	1.5	1	41	32.2	95.00%	K.IDLEQDFSSLRPIQY.A		K.IDLEQDFSSLRPIQYAPTQIYDSAFCSSAK.R
551	563	2	1377.73	-0.14	1	82.3	30.5	95.00%	K.NLYGNSVSIGVQK.I		K.NLYGNSVSIGVQK.I
509	519	2	1350.64	1.5	1	32.9	32.2	95.00%	W.DNNDLTIDYLR.S		K.GYTILLPCMNSWDNNDLTIDYLR.S
247	265	2	2086.16	1.3	1	98	22.7	95.00%	R.TSLLQELIIDDVYGGILPK.E		R.TSLLQELIIDDVYGGILPK.E
523	530	2	930.53	-0.13	0	41.6	28.6	95.00%	K.TALNLLMR.N		K.TALNLLMR.N
73	81	2	959.55	2.5	1	43	28.3	95.00%	F.APINSAFIK.G		K.TGHVQYLNELQNFTLFAPINSAFIK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
135	A6ZLM5_YEAS7	18.74%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
225	238	2	1458.66	-0.97	1	107	33.6	95.00%	R.MNSSFLSSSSIGDK.I		R.MNSSFLSSSSIGDK.I
327	335	2	940.61	0.51	0	44.5	20.4	95.00%	K.LLIGSIIGR.M		K.LLIGSIIGR.M

199	224	3	3155.4	-0.8	0	62	33.2	95.00%	R.TPNIDNEELVNEEQEEQELLEEENNR.M	R.TPNIDNEELVNEEQEEQELLEEENNR.M
179	198	3	2323.1	-0.51	1	51.3	32.8	95.00%	K.WSGENTQHMPPSQVQSLLER.T	K.WSGENTQHMPPSQVQSLLER.T
98	108	2	1321.64	1	2	37.6	32.5	95.00%	R.ILDLDKDETNF.V	R.ILDLDKDETNFVVANSVFGNSNSLPVSLTLSLAYTLPNLTWDQIPNDNR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
136	B5VQ30_YEAST	12.70%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
514	524	2	1171.63	-0.018	0	32.5	29.3	95.00%	K.AMDLLASNLPK.A		K.AMDLLASNLPK.A
858	876	2	2260.07	2.2	2	66.3	33.2	95.00%	Y.DYPAVSAQCPELWIPRDPF.G	Carbamidomethyl (+57)	R.VNDFDISHAYDYPAVSAQCPELWIPRDPFGFSK.L
858	873	2	1900.92	1.1	1	69.5	32.8	95.00%	Y.DYPAVSAQCPELWIPR.D	Carbamidomethyl (+57)	R.VNDFDISHAYDYPAVSAQCPELWIPR.D
840	857	2	2060.95	1.6	2	34.3	33.8	95.00%	Y.GLVDPDERVNDFDISHAY.D		R.LPEIYGLVDPDERVNDFDISHAYDYPAVSAQCPELWIPR.D
696	715	2	2145.11	1.1	1	43.2	29.7	95.00%	K.VIPVDTMKPLDGVSDTPSFK.N		K.VIPVDTMKPLDGVSDTPSFK.N
776	809	3	3622.69	1.7	1	50	31.3	95.00%	Y.QFNPANEANADGHAINAENLIEDVPLLADGDTMK.I	Oxidation (+16)	R.SESVTEQQVENSIFSENTFEYQFNPANEANADGHAINAENLIEDVPLLADGDTMK.I
196	204	2	1031.6	1.9	1	34	25.7	95.00%	R.TVLFQTVPK.Q		R.TVLFQTVPK.Q
56	65	2	1179.58	-0.28	1	53.3	31.9	95.00%	K.SSFNLINEEK.K		K.SSFNLINEEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
137	ATG27_YEAS7	35.42%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	88	2	1772.92	0.74	1	51.6	30.2	95.00%	K.KNDMLCGLTDVILPGK.D	Carbamidomethyl (+57)	K.KNDMLCGLTDVILPGK.D
119	130	2	1223.56	0.55	1	42	32.4	95.00%	K.GATWGANSFDAK.L		K.GATWGANSFDAK.L
89	100	2	1378.7	-0.087	1	34.4	31.5	95.00%	K.DAITTQIIDFDK.N		K.DAITTQIIDFDK.N
101	118	2	1978.03	0.49	1	77.8	30.1	95.00%	K.NIGFNVEETESALTLTLK.G		K.NIGFNVEETESALTLTLK.G
74	88	2	1644.82	-0.29	0	32.5	31.9	95.00%	K.NDMLCGLTDVILPGK.D	Carbamidomethyl (+57)	K.NDMLCGLTDVILPGK.D
131	149	3	2395.03	2.1	2	49.1	34	95.00%	K.LEFQCNDNMKQDELTSHTW.A	Carbamidomethyl (+57)	K.LEFQCNDNMKQDELTSHTWADK.S
36	54	2	2096.03	1.8	1	63.2	32	95.00%	K.FSSLTSTERDTPPSTTIEK.W		K.FSSLTSTERDTPPSTTIEK.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
138	ZRT1_YEAST	6.91%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
155	172	3	2121.03	0.52	1	71.2	32.9	95.00%	K.YGLSHDHTHDEIKDTVVR.N		K.YGLSHDHTHDEIKDTVVR.N
155	167	3	1550.71	1.1	1	28	33.2	93.70%	K.YGLSHDHTHDEIK.D		K.YGLSHDHTHDEIK.D
269	276	2	931.52	2.9	1	44.1	28.3	95.00%	R.LSAIEFPR.S		R.LSAIEFPR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
139	EF3A_YEAST	14.18%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
320	357	4	3987.01	0.59	1	18.1	26.9	93.40%	R.VGNVGEDDAIPELSHAGDVSTTLQVVNELLKDETVAPR.F		R.VGNVGEDDAIPELSHAGDVSTTLQVVNELLKDETVAPR.F
829	842	2	1700.82	0.16	1	32.1	32.8	93.90%	R.WVPMMSVDNAWIPR.G		R.WVPMMSVDNAWIPR.G
650	660	2	1234.62	0.22	1	28.5	31.3	90.50%	K.FPEPGYLEGVK.T		K.FPEPGYLEGVK.T
708	732	3	2802.38	-1.6	1	31.5	30.8	95.00%	K.STLINVLTGELLPTSGEVYTHENCR.I	Carbamidomethyl (+57)	K.STLINVLTGELLPTSGEVYTHENCR.I
708	726	2	2005.07	2.6	1	26.8	28.7	92.30%	K.STLINVLTGELLPTSGEVY.T		K.STLINVLTGELLPTSGEVYTHENCR.I
971	987	3	1737.8	-0.45	1	64.7	32.9	95.00%	R.MTPSGHNWVSGQGAGPR.I		R.MTPSGHNWVSGQGAGPR.I
775	786	2	1375.6	-0.16	0	37.3	33.5	95.00%	R.QINENDAEAMNK.I		R.QINENDAEAMNK.I
873	893	4	2465.17	-1.2	1	28.5	33	95.00%	R.KEIEEHCSMLGLDPEIVSHSR.I	Carbamidomethyl (+57)	R.KEIEEHCSMLGLDPEIVSHSR.I
266	275	2	1149.56	2.9	0	47	31.9	95.00%	K.SAVIIDNMCK.L	Carbamidomethyl (+57)	K.SAVIIDNMCK.L
874	893	3	2337.07	-0.45	0	29.3	34.2	94.10%	K.EIEEHCSMLGLDPEIVSHSR.I	Carbamidomethyl (+57)	K.EIEEHCSMLGLDPEIVSHSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

140	A7A288_YEAS7	22.21%		100%		11							
Start	End	charge	Mr(expt)		ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
16	26	2	1213.68		0.061	1	35.8	28.1	95.00%	K.RSPSILVTDAR.T		K.RSPSILVTDAR.T	
254	266	2	1516.77		-0.076	0	41.4	30.9	95.00%	K.TLIDNLIDTSEQR.D		K.TLIDNLIDTSEQR.D	
371	385	2	1727.81		-0.81	1	92.9	33.5	95.00%	K.LYAVEGNDQYVQSSR.S		K.LYAVEGNDQYVQSSR.S	
154	163	2	1127.6		1.8	0	50.6	28.7	95.00%	F.QTLPTNALDR.Q		K.LVLIPEDDNLNHFQTLPTNALDR.Q	
141	163	3	2647.36		-0.15	1	28.7	29	95.00%	K.LVLIPEDDNLNHFQTLPTNALDR.Q		K.LVLIPEDDNLNHFQTLPTNALDR.Q	
343	364	3	2509.08		1.4	1	46.8	34.2	95.00%	R.INMLKKEENDSDASCGNDNNNK.N	Carbamidomethyl (+57)	R.INMLKKEENDSDASCGNDNNNK.N	
488	496	2	1089.62		0.99	1	46	26.7	95.00%	R.IFNDIVTLR.S		R.IFNDIVTLR.S	
447	458	2	1368.69		-0.087	1	56.8	31.4	95.00%	K.NILGDITFADYK.N		K.NILGDITFADYK.N	
82	101	2	2178.05		2.4	1	95	32.6	95.00%	R.FSDISIDNILSDNSDIPSAR.R		R.FSDISIDNILSDNSDIPSAR.R	
208	218	2	1341.67		-0.54	1	73.1	31.3	95.00%	K.FLQETHEVSPR.L		K.FLQETHEVSPR.L	
327	337	2	1313.69		1.6	1	40.1	30	95.00%	F.AEETPLEIEKR.E		R.DHHYEYYSGVETVEDANNNYELETSGNNNNANQDTTTVPDHLPNPVGQQDSFNPMEPQFFAEETPLEIEKR.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
141	A7A0E5_YEAS7	13.18%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
353	383	3	3463.62	-0.75	1	111	30.8	95.00%	K.NQALGGSLLHSHIQTYPDGSNQQQVTCYGYK.D	Carbamidomethyl (+57)	K.NQALGGSLLHSHIQTYPDGSNQQQVTCYGYK.D
426	438	3	1369.75	0.44	0	27	27.6	95.00%	R.NLHTHPVAAPVSK.T		R.NLHTHPVAAPVSK.T
341	352	2	1187.68	-0.34	0	45.5	28.1	95.00%	R.DIALGSSVVSIK.N		R.DIALGSSVVSIK.N
439	455	2	1866.84	-0.055	1	89.9	34	95.00%	K.TQWEVSGYGDNVVGDNK.D		K.TQWEVSGYGDNVVGDNK.D
106	118	4	1574.76	0.079	1	32.8	33.1	95.00%	R.HEFYHDVHPPLGK.M		R.HEFYHDVHPPLGK.M
492	505	2	1574.79	1.4	1	55.8	32.1	95.00%	Y.LAQTGNSLPEWGFR.Q		K.NLEMGCYLAQTGNSLPEWGFR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
142	A6ZLC2_YEAS7	36.02%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
31	46	2	1747.84	-0.19	2	65.5	33.1	95.00%	K.RIGQEVDGEAVGDEFK.G		K.RIGQEVDGEAVGDEFK.G
99	115	2	1647.03	-0.31	0	55.7	13.8	95.00%	R.GAIVGPDLAVLALVIVK.K		R.GAIVGPDLAVLALVIVK.K
15	25	3	1429.7	2	1	40.6	32.2	95.00%	K.TFEIDDEHRIR.V		K.TFEIDDEHRIR.V
116	131	2	1743.89	-0.7	1	54.5	31	95.00%	K.KGEQELEGLTDTTVPK.R		K.KGEQELEGLTDTTVPK.R
3	14	2	1319.67	-0.39	1	56.7	31.3	95.00%	K.LNISYPVNGSQK.T	Deamidation (+1)	K.LNISYPVNGSQK.T
203	214	2	1276.67	1.9	1	58.7	30.9	95.00%	R.EAAAEYAQLLAK.R		R.EAAAEYAQLLAK.R
116	132	3	1899.99	0.53	1	46.5	29.8	95.00%	K.KGEQELEGLTDTTVPKR.L		K.KGEQELEGLTDTTVPKR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
143	A6ZMK1_YEAS7	37.69%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
158	168	2	1192.55	-0.023	1	49.9	31.9	95.00%	R.AVQDNGESAFR.T		R.AVQDNGESAFR.T
46	59	3	1614.01	0.8	0	23.1	13.4	95.00%	K.IAPRPLDLLRPVVR.A		K.IAPRPLDLLRPVVR.A
82	91	2	963.52	1.5	1	28.5	29.1	94.00%	K.AAGLTAAYAR.T		K.AAGLTAAYAR.T
105	115	2	1332.64	-0.47	1	60.8	31.9	95.00%	R.NQEIFDANVQR.L		R.NQEIFDANVQR.L
129	157	3	2952.48	-0.55	2	51	29.2	95.00%	R.DGKAPEAEQVLSAAATFPIAQPATDVEAR.A		R.DGKAPEAEQVLSAAATFPIAQPATDVEAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
144	A7A0C4_YEAS7	21.93%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
185	197	2	1610.74	0.82	2	40.8	34	95.00%	K.NIEQCEREGYVSK.I	Carbamidomethyl (+57)	K.NIEQCEREGYVSK.I
234	244	3	1318.6	1.7	1	31.4	33.3	95.00%	Y.GHFHDTSLYDK.T		R.IQGNLHFAPGKPYQNAYGHFHDTSLYDK.T
275	289	3	1491.79	0.47	1	33.8	30.3	95.00%	K.RHGGAVVATSPLDGR.Q		K.RHGGAVVATSPLDGR.Q
3	14	2	1320.74	-0.32	2	23.9	26.7	90.50%	K.RSTLLSLDAFAK.T		K.RSTLLSLDAFAK.T

108	147	4	4128.83	-0.63	1	35	31.6	95.00%	R.LNSEGRPVGDATELHVGGNGDGTAPVNNDPNYCGPCYGAK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.LNSEGRPVGDATELHVGGNGDGTAPVNNDPNYCGPCYGAK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
145	A6ZUA2_YEAS7	14.92%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
516	531	2	1951.85	2.9	2	60.6	34.4	95.00%	K.KEFHALEESENEQAEY.S		K.KEFHALEESENEQAEYSNNFDTIEDSR.E
545	560	2	1780.83	1.5	1	68.1	33.1	95.00%	F.SVAASDVELENEHVPW.G		R.EFSVAASDVELENEHVPWGK.K
517	531	2	1823.75	1.4	1	51.2	33.5	95.00%	K.EFHALEESENEQAEY.S		K.EFHALEESENEQAEYSNNFDTIEDSR.E
543	560	2	2056.94	2.8	1	61.9	33.8	95.00%	R.EFSVAASDVELENEHVPW.G		R.EFSVAASDVELENEHVPWGK.K
5	26	3	2394.01	-0.32	1	49.2	34.2	95.00%	R.NDNASGGYMQPDQSSNASMHKR.D		R.NDNASGGYMQPDQSSNASMHKR.D
532	544	2	1572.67	1.5	2	52	33.1	95.00%	Y.SNNFDTIEDSREF.S		K.EFHALEESENEQAEYSNNFDTIEDSREFSVAASDVELENEHVPWGK.K
27	43	4	2030.99	2.3	1	42.7	32.2	95.00%	R.DLRVEEEIKPLDDMDSK.G		R.DLRVEEEIKPLDDMDSK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
146	A6ZP92_YEAS7	18.55%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
433	454	2	2362.21	-0.17	1	44	30.8	95.00%	K.ADFLVPGENQVTPSSTPYISLK.V		K.ADFLVPGENQVTPSSTPYISLK.V
462	488	3	3139.54	2.8	2	38.6	30.6	95.00%	K.QPLIPTSLIPEENLTEPQDFESQRDPF.A		K.QPLIPTSLIPEENLTEPQDFESQRDPFAMMSK.Q
179	189	2	1294.64	-0.092	1	61	32.3	95.00%	K.AYESLTDELVR.Q		K.AYESLTDELVR.Q
61	72	2	1453.66	-0.22	1	47.3	33.2	95.00%	K.NLNEEYTSDEIK.Q		K.NLNEEYTSDEIK.Q
511	521	2	1310.57	-0.56	1	35.3	32.6	95.00%	R.GSWCCLVSSQK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GSWCCLVSSQK.D
403	414	2	1269.73	-1.2	1	28.5	25.5	95.00%	K.IGEVLGIKDQAK.L		K.IGEVLGIKDQAK.L
195	212	3	1888.92	1.8	1	56.9	32.7	95.00%	K.YGHPDGPQSTSHGIALPR.F		K.YGHPDGPQSTSHGIALPR.F
525	534	2	1166.73	2.5	0	25.6	17	95.00%	K.ILQTPIIIEK.L		K.ILQTPIIIEK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
147	A6ZRN1_YEAS7	19.25%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
174	191	2	1728.94	-0.94	1	84.5	28.1	95.00%	R.IINEPTAAAIAYGLGAGK.S		R.IINEPTAAAIAYGLGAGK.S
305	314	2	1166.6	-0.37	1	43.3	31.1	95.00%	R.FEDLNAALFK.S		R.FEDLNAALFK.S
544	565	3	2449.28	2.5	2	55.1	28.6	95.00%	R.QRLESYVASIEQTVTDPVLSSK.L		R.QRLESYVASIEQTVTDPVLSSK.L
550	565	2	1672.89	1.3	0	57.6	29.6	95.00%	Y.VASIEQTVTDPVLSSK.L		R.LESYVASIEQTVTDPVLSSK.L
252	261	2	1061.5	-0.49	0	53.5	31.1	95.00%	K.TGLDISDDAR.A		K.TGLDISDDAR.A
456	466	2	1277.65	-0.41	1	56.3	31.4	95.00%	K.ENTLLGEFDLK.N		K.ENTLLGEFDLK.N
502	513	2	1217.64	-0.59	0	69.6	31.2	95.00%	K.SSNITISNAVGR.L		K.SSNITISNAVGR.L
315	325	2	1241.69	-0.33	0	29.6	27.7	95.00%	K.STLEPVEQVLK.D		K.STLEPVEQVLK.D
574	597	3	2538.32	1.8	1	61.1	28.1	95.00%	K.IEAALSDALAALQIEDPSADELRK.A		K.IEAALSDALAALQIEDPSADELRK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
148	A6ZT57_YEAS7	18.94%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
369	377	2	1155.59	-0.17	1	51.3	29.9	95.00%	K.SIYQVYLDR.A		K.SIYQVYLDR.A
524	534	2	1380.65	3	1	30.8	33	91.80%	Y.TAQFVQNPQWY.G		R.IASSIYSEAIQPLNYQDQYQQQEQSPVYNGHTQYPGNGYSGNPQQQGYTAQFVQNPQWYGVPTPQQQQHNHPQTLETIGELPTPAYLAQSASSHSLTSFK.R
590	604	2	1654.77	1.9	1	50	33.2	95.00%	R.LNGTALNPVDHPEMF.Y	Deamidation (+1)	R.LNGTALNPVDHPEMFYSPTNDAYYAPQQQGQYMK.F

456	475	2	2218.06	2.3	1	109	33.3	95.00%	K.QYPVQDTLTVNDTEAAPSNR.I		K.QYPVQDTLTVNDTEAAPSNR.I
693	723	4	3228.67	2.3	1	29.9	26	95.00%	R.VSGILEETDVVQPPSVGGILPHSGSQDDLRK.Q		R.VSGILEETDVVQPPSVGGILPHSGSQDDLRK.Q
414	429	2	1811.83	-0.57	0	45.2	33.3	95.00%	K.INNNDNIDNNEVPEAK.H		K.INNNDNIDNNEVPEAK.H
482	494	2	1567.72	3.8	1	51.2	33.1	95.00%	Y.SEAIQPLNYQDQY.Q		R.IASSIYSEAIQPLNYQDQYQQQEQSPVYNGHTQYPGNGYSGNPQQQGYTAQFVQNPQWYGVPTPQQQQHNHPQTLETIGELPTPAYLAQSASSHSLTSFK.R
638	661	3	2580.3	-1.4	1	29.9	30.5	95.00%	R.QSVVMTNPSDLTAKPSYKPAGSFR.S		R.QSVVMTNPSDLTAKPSYKPAGSFR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
149	B3LHY2_YEAS1	11.99%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
12	49	4	4276.97	-0.95	1	56.9	29	95.00%	K.HLVDDVLFISPTNDGSEEKPTEVTFQEDEGHDASLHNR.S		K.HLVDDVLFISPTNDGSEEKPTEVTFQEDEGHDASLHNR.S
20	49	3	3338.5	1.6	1	78.2	32.5	95.00%	F.ISPTNDGSEEKPTEVTFQEDEGHDASLHNR.S		K.HLVDDVLFISPTNDGSEEKPTEVTFQEDEGHDASLHNR.S
108	120	2	1258.65	0.7	0	69.9	30.6	95.00%	K.SNIGNAEVAGLSK.D		K.SNIGNAEVAGLSK.D
20	36	2	1849.86	1.9	1	43.8	33.4	95.00%	F.ISPTNDGSEEKPTEVTF.Q		K.HLVDDVLFISPTNDGSEEKPTEVTFQEDEGHDASLHNR.S
510	522	2	1590.7	-0.88	1	57	34.4	95.00%	R.CNELGEPIPYDER.L	Carbamidomethyl (+57)	R.CNELGEPIPYDER.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
150	GLRX6_YEAST	45.02%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
70	84	2	1703.82	-1.1	1	94.2	32.9	95.00%	K.GSSEVDEEINEIKQK.V		K.GSSEVDEEINEIKQK.V
208	219	2	1373.72	-0.3	1	44.4	30.8	95.00%	K.LLESLQVWSDGK.F		K.LLESLQVWSDGK.F
85	105	3	2197.16	2.3	1	43.5	28.1	95.00%	K.VGLQQPIASVDDSLSAIKNDK.G		K.VGLQQPIASVDDSLSAIKNDK.G
43	57	2	1560.63	-0.54	1	86.9	32.7	95.00%	K.AFSTNMDNMAGGSSR.E	Oxidation (+16)	K.AFSTNMDNMAGGSSR.E
85	102	2	1840	1.3	0	63.6	27.3	95.00%	K.VGLQQPIASVDDSLSAIK.N		K.VGLQQPIASVDDSLSAIK.N
164	175	2	1438.69	0.82	1	44.8	33.1	95.00%	K.HGHGEELQEYIK.L		K.HGHGEELQEYIK.L
118	133	2	1850.04	-1.1	1	64.7	23.8	95.00%	K.EYSLILDLSPIIIFSK.S		K.EYSLILDLSPIIIFSK.S
181	193	2	1324.75	-0.69	0	47.4	26	95.00%	R.GTVPNLLVNGVSR.G		R.GTVPNLLVNGVSR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
151	A6ZZW6_YEAS7	17.47%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
249	265	2	1829.92	1.5	0	68.5	31.1	95.00%	K.VDLMDQGTDVIDILAGR.V		K.VDLMDQGTDVIDILAGR.V
443	453	2	1190.66	2.2	1	57.6	28.6	95.00%	F.VGTEAFEVLVK.Q		R.TIMYNSSGSAPSLFVGTEAFEVLVK.Q
166	184	3	2079.2	2.2	1	31.2	21.4	95.00%	R.IYSPHVLTLTLVDLPGLTK.V		R.IYSPHVLTLTLVDLPGLTK.V
389	400	2	1232.6	-0.095	0	80.3	31.7	95.00%	K.ELSSQELSGGAR.I		K.ELSSQELSGGAR.I
527	536	3	1120.63	2.1	0	30.4	27.3	95.00%	Y.INTAHPDLLK.G		K.AEQTYINTAHPDLLK.G
185	196	2	1320.67	-0.47	0	53.8	32	95.00%	K.VPVGDQPPDIER.Q		K.VPVGDQPPDIER.Q
205	230	3	2701.43	0.042	1	52.8	26.7	95.00%	K.YISKPNAIILSVNAANTDLANSDGLK.L		K.YISKPNAIILSVNAANTDLANSDGLK.L
150	165	2	1583.86	-0.32	0	57.7	28.1	95.00%	K.VTGANSGISSVPINLR.I		K.VTGANSGISSVPINLR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
152	A6ZWJ1_YEAS7	8.90%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
328	340	2	1292.66	-0.015	0	89.4	31	95.00%	K.STSDTASATLLAR.Q		K.STSDTASATLLAR.Q
65	73	2	1153.54	0.062	1	44.8	32.6	95.00%	K.TEDIPEHWK.E		K.TEDIPEHWK.E
347	357	2	1323.68	0.27	1	42.5	31.3	95.00%	R.KDSNTNIVLLK.S	Phospho (+80)	R.KDSNTNIVLLK.S
348	357	2	1115.62	-0.46	0	31.1	28.6	95.00%	K.DSNTNIVLLK.S		K.DSNTNIVLLK.S
64	73	2	1281.64	1.5	2	43.7	31.9	95.00%	Y.KTEDIPEHWK.E		K.IIHQTYKTEDIPEHWK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
153	A6ZXE6_YEAS7	10.55%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

208	219	3	1520.74	-0.063	1	27.7	32.2	94.60%	K.SDFTLYHTWPVR.V		K.SDFTLYHTWPVR.V
2	9	2	842.43	0.47	0	41.8	29.1	95.00%	M.AGAIENAR.K	Acetyl (+42)	-.MAGAIENAR.K
356	367	3	1445.71	0.37	1	26.1	31.8	92.90%	K.FTCNATHELVVR.T	Carbamidomethyl (+57)	K.FTCNATHELVVR.T
925	937	2	1645.78	-1.2	1	44.7	33.3	95.00%	K.FYDSNYPEFPVLR.D		K.FYDSNYPEFPVLR.D
446	455	2	1095.6	-0.29	0	48.3	26.8	95.00%	R.DLSLLGSHVR.K		R.DLSLLGSHVR.K
89	114	3	2811.52	0.04	1	51	23.4	95.00%	R.TGKPLSVELGPGLMETIYDGIQR PLK.A		R.TGKPLSVELGPGLMETIYDGIQR PLK.A
186	197	2	1305.65	1.8	1	35.5	32	95.00%	W.IAPAGEYTLDEK.I		R.GTITWIAPAGEYTLDEK.I
940	959	3	2256.2	-0.12	1	27.7	28.3	95.00%	R.MKEILSNAEELEQVVQLVGK.S		R.MKEILSNAEELEQVVQLVGK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
154	RTN1_YEAST	12.88%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
236	247	2	1267.67	-0.42	0	55.2	29.1	95.00%	K.LAADVPLEPESK.A		K.LAADVPLEPESK.A
208	216	2	939.58	-0.019	0	45.3	17.7	95.00%	K.LGPISNLVK.S		K.LGPISNLVK.S
219	235	2	1589.79	-0.2	0	77.4	32.2	95.00%	K.TAPVSSTAGPQTASTSK.L		K.TAPVSSTAGPQTASTSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
155	A6ZVR3_YEAS7	15.26%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
611	621	2	1203.65	0.061	1	45.3	29.6	95.00%	R.EAFVSLNIPSK.A		R.EAFVSLNIPSK.A
578	586	2	984.59	-0.42	0	25.1	24.2	94.80%	K.IGDVIIIDK.S		K.IGDVIIIDK.S
216	246	3	3443.59	-1.1	1	69.4	31.1	95.00%	R.QLAVDDINTGHVNCESNPTICEEL GFGDLVK.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.QLAVDDINTGHVNCESNPTICEEL GFGDLVK.I
139	155	2	1919.86	2	1	66.1	34.1	95.00%	R.RESMDPNNLDTDLDSAK.S		R.RESMDPNNLDTDLDSAK.S
443	458	2	1792.92	1.1	2	47.6	30.6	95.00%	K.KYSNPLVTEVDSSNLK.K		K.KYSNPLVTEVDSSNLK.K
433	442	2	1203.59	-0.93	1	33.9	30.9	95.00%	R.NIDAIMDWVK.K		R.NIDAIMDWVK.K
493	505	3	1642.85	0.98	1	30	30.6	95.00%	K.NLLLASWEYEHIR.M		K.NLLLASWEYEHIR.M
140	155	2	1763.75	-1.8	0	76.8	34.2	95.00%	R.ESMDPNNLDTDLDSAK.S		R.ESMDPNNLDTDLDSAK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
156	A7A1B6_YEAS7	14.66%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
154	163	2	1225.58	-0.23	1	57.5	32.5	95.00%	K.YVECSALTQR.G	Carbamidomethyl (+57)	K.YVECSALTQR.G
167	184	2	1952.1	2.2	1	86.1	24.2	95.00%	K.NVFDEAIVAALEPPVIKK.S		K.NVFDEAIVAALEPPVIKK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
157	A6ZN89_YEAS7	10.96%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	19	2	1748.88	1	0	105	31.7	95.00%	M.VNVGPSHAAVAVDASEAR.K		-.MVNVGPSHAAVAVDASEAR.K
513	535	3	2352.08	1.4	1	35.1	33.8	95.00%	R.SAGSVIEQDGSSGMEIENGKDVK .I	Oxidation (+16)	R.SAGSVIEQDGSSGMEIENGKDVK .I
2	20	3	1876.98	1.5	1	60.6	30.4	95.00%	M.VNVGPSHAAVAVDASEARK.R		-.MVNVGPSHAAVAVDASEARK.R
492	512	3	2505.04	1.5	0	51.5	33.8	95.00%	K.TEITVDHTEEDSHNHQNNNDR.S	Deamidation (+1)	K.TEITVDHTEEDSHNHQNNNDR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
158	A6ZZX8_YEAS7	45.73%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	172	2	1351.69	-0.52	1	52.6	32	95.00%	K.QYAQEQGLLFR.E		K.QYAQEQGLLFR.E
92	101	2	1175.57	1.7	0	45.5	31.6	95.00%	Y.DITQEDSLQK.A		R.NANAALVVYDITQEDSLQK.A
62	72	2	1350.62	-0.24	1	70.8	33.2	95.00%	K.FEIWDTAGQER.Y		K.FEIWDTAGQER.Y
127	151	2	2751.14	2.5	0	98.9	33.8	95.00%	K.VDLCQETPSTETSPDSNEGGDE EQK.V	Carbamidomethyl (+57)	K.VDLCQETPSTETSPDSNEGGDE EQK.V
6	16	2	1086.63	-0.19	0	29.6	26.8	95.00%	K.LVLLGDSSVGK.S		K.LVLLGDSSVGK.S
83	101	2	2091.05	1.4	1	117	31.4	95.00%	R.NANAALVVYDITQEDSLQK.A		R.NANAALVVYDITQEDSLQK.A
113	126	2	1532.81	-0.07	1	80.1	30.8	95.00%	K.VGDDDLVIYLLGNK.V		K.VGDDDLVIYLLGNK.V
41	56	2	1752.87	1.1	0	56.9	32.4	95.00%	F.LSQSITIHPNDGNETK.D		R.ESTIGAAFLSQSITIHPNDGNETK. D
122	151	3	3276.46	0.93	1	79.6	33.1	95.00%	Y.LLGNKVDLCQETPSTETSPDSNE GGDEEQK.V	Carbamidomethyl (+57)	K.VGDDDLVIYLLGNKVDLCQETPS TETSPDSNEGGDEEQK.V

63	72	2	1203.55	1.6	1	43.6	32.4	95.00%	F.EIWDTAGQER.Y		K.FEIWDTAGQER.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
159	A6ZVM1_YEAS7	11.03%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
109	126	2	1896.92	-1.3	1	73.7	32.9	95.00%	K.FTNIASSPPSSSNNIFSK.A		K.FTNIASSPPSSSNNIFSK.A
248	261	3	1744.85	-0.17	2	33.8	32.4	95.00%	R.DRESNNELYHVITR.N		R.DRESNNELYHVITR.N
803	817	3	1763.92	2.1	1	34.4	30.1	95.00%	K.VTRPEGAFNQLEYLK.I		K.VTRPEGAFNQLEYLK.I
615	628	4	1614.82	0.081	1	34.8	31	95.00%	R.DRHSISLLHEHSGK.T		R.DRHSISLLHEHSGK.T
629	645	2	2014.01	0.29	1	30	31.5	92.90%	K.TLNYEILQVFPFNSDSK.R		K.TLNYEILQVFPFNSDSK.R
142	155	3	1626.8	2.1	1	28.1	32	95.00%	K.FGSPIELSDQHIER.E		K.FGSPIELSDQHIER.E
487	504	2	2049.06	0.04	2	30.8	30.2	95.00%	R.TSTIPEDLGRIEYLLSDK.T		R.TSTIPEDLGRIEYLLSDK.T
673	689	2	1991.89	1.4	1	63.8	34.1	95.00%	K.IVESNDWLEEETGNMAR.E		K.IVESNDWLEEETGNMAR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
160	A6ZUC1_YEAS7	11.37%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
426	440	2	1527.83	1.8	1	49.5	28.1	95.00%	K.GLVIISGIVHDVSGY.I		K.GLVIISGIVHDVSGYISEHPGGETLIK.T
441	452	2	1279.68	0.92	0	28.1	30.3	91.60%	Y.ISEHPGGETLIK.T		K.GLVIISGIVHDVSGYISEHPGGETLIK.T
376	391	2	1874.94	0.16	1	97.5	31.7	95.00%	K.FSQNAIEEALIQQEQK.K		K.FSQNAIEEALIQQEQK.K
426	452	3	2789.5	-0.46	1	40.5	23.5	95.00%	K.GLVIISGIVHDVSGYISEHPGGETLIK.T		K.GLVIISGIVHDVSGYISEHPGGETLIK.T
400	414	2	1799.9	1.7	1	65.6	31.9	95.00%	K.INWGPVLTDLPMWDK.Q	Oxidation (+16)	K.INWGPVLTDLPMWDK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
161	A6ZU02_YEAS7	8.12%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
478	491	2	1607.89	0.61	1	60	25	95.00%	K.EVEKDAVTNIHLLK.R		K.EVEKDAVTNIHLLK.R
482	491	2	1122.64	0.52	0	48.8	26.4	95.00%	K.DAVTNIHLLK.R		K.DAVTNIHLLK.R
62	75	2	1489.76	1.6	1	104	31.2	95.00%	K.KVDAMGVESTGIQR.I		K.KVDAMGVESTGIQR.I
459	477	2	1960.97	1.5	1	77.4	32.3	95.00%	K.EFPTVTGEINGPELVGSSK.E	Deamidation (+1)	K.EFPTVTGEINGPELVGSSK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
162	YAJ8_YEAST	25.21%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
201	211	2	1248.68	0.39	1	59.9	29.3	95.00%	R.SDPILMAYVLK.A		R.SDPILMAYVLK.A
153	162	3	1294.64	0.41	1	40.3	31.8	95.00%	K.CHEFFTTLIK.E	Carbamidomethyl (+57)	K.CHEFFTTLIK.E
163	188	2	2563.1	1.9	0	80.8	33.8	95.00%	K.EVNSGSHSDSSSNSAEDTQSPVSAGK.T		K.EVNSGSHSDSSSNSAEDTQSPVSAGK.T
189	200	2	1385.66	-0.31	1	48.3	33	95.00%	K.TSNGLNNFYSIR.S	Deamidation (+1)	K.TSNGLNNFYSIR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
163	A6ZUF3_YEAS7	22.91%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
81	97	2	1941	1.7	1	61.9	30.1	95.00%	R.GNVPQYVIDNSPLLHLY.S		R.GNVPQYVIDNSPLLHLYSEEK.Y
273	287	4	1728.03	-0.16	2	17.4	20.9	95.00%	K.LTNEVIKKPLIFSAR.G		K.LTNEVIKKPLIFSAR.G
151	166	2	1793.77	1.3	1	104	33.9	95.00%	R.VSSEGTYMTSLDDFDK.G		R.VSSEGTYMTSLDDFDK.G
57	75	2	2078.02	1.1	0	63.9	32.3	95.00%	K.DILSSTPPLHPSEVTEDNK.S		K.DILSSTPPLHPSEVTEDNK.S
314	326	2	1532.73	1.2	2	53	32.3	95.00%	F.TDRGPLWDPSLNY.Y		R.GTHAHYASVGQHAHDVPFFFMPLSDFTDRGPLWDPSLNYYAYTVTVGEK.M
167	184	3	1995.97	1.8	1	43.1	32.7	95.00%	K.GPDWLLGEQPEYGTGHIK.K		K.GPDWLLGEQPEYGTGHIK.K
347	355	2	1109.56	-0.02	1	36.5	31.7	95.00%	K.MGLEWLSFK.G		K.MGLEWLSFK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
164	A6ZV40_YEAS7	10.80%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
60	73	2	1615.85	-0.52	0	69.3	30.1	95.00%	K.QLGILSCIGLICNR.M	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.QLGILSCIGLICNR.M

6	16	2	1309.7	-0.32	1	74.3	28.4	95.00%	R.TFLSQLNVFNK.E		R.TFLSQLNVFNK.E
17	27	2	1290.57	-0.86	1	44.3	32.9	95.00%	K.ENYQFSSSTTK.K		K.ENYQFSSSTTK.K
542	567	3	2980.39	1.5	1	63.4	31.9	95.00%	K.VYDDTIGDVDTQEDGVIETNIIEHYK.S		K.VYDDTIGDVDTQEDGVIETNIIEHYK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
165	A6ZL51_YEAS7	44.15%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	78	2	1466.63	-0.7	1	61.3	33.4	95.00%	K.YVEPGNAMSGEGEK.L		K.YVEPGNAMSGEGEK.L
155	168	2	1346.66	-1.6	1	57.1	31.7	95.00%	K.APSLFGGMGQTGPK.T		K.APSLFGGMGQTGPK.T
138	150	3	1395.79	0.28	1	24.5	25.4	95.00%	K.IHLFGKPATGDLK.R		K.IHLFGKPATGDLK.R
115	128	2	1623.83	-0.68	1	63.7	30.9	95.00%	K.YTNPLFMQSISPVK.S		K.YTNPLFMQSISPVK.S
79	90	2	1449.78	-0.62	2	44	29.5	95.00%	K.LQVTTVRDYDLK.E		K.LQVTTVRDYDLK.E
173	188	2	1629.79	-1	1	58	32.3	95.00%	K.SIEEAERAGNAGVKAE.-		K.SIEEAERAGNAGVKAE.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
166	A6ZMI1_YEAS7	18.63%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
129	140	2	1486.78	-0.21	1	55.4	30.5	95.00%	K.YFEVILVDPQHK.A		K.YFEVILVDPQHK.A
148	157	2	1330.61	0.15	1	34.5	32.9	95.00%	R.YNWICNPVHK.H	Carbamidomethyl (+57)/ Deamidation (+1)	R.YNWICNPVHK.H
78	93	2	1675.85	-0.9	1	63.7	31.3	95.00%	K.GATYGKPTNQGVNELK.Y		K.GATYGKPTNQGVNELK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
167	B3LP09_YEAS1	12.82%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
411	430	2	2223.08	1.5	0	99.7	32.5	95.00%	Y.NQQQQQQQAQAQAQAQAQAK.V		K.NHQYSSPDHHHHYNQQQQQQQAQAQAQAQAQAK.V
61	77	3	1848.9	2	2	52.8	32.8	95.00%	Y.SGSQSRDDSTIVGLHYK.I		R.LVNGTLPPSLHVSSNLNHNTGNSSASYSGSQSRDDSTIVGLHYK.I
509	524	2	1822.81	-0.77	1	52.7	33.9	95.00%	K.YPYNAQPTANDEQNAK.N		K.YPYNAQPTANDEQNAK.N
431	447	2	1994	0.067	0	93.7	31.3	95.00%	K.VQQQQLQQAQAQQQANR.Y		K.VQQQQLQQAQAQQQANR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
168	A6ZNJ9_YEAS7	21.99%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
246	262	2	1888.89	2.5	1	60	33.6	95.00%	F.ISPTEILQSDANNSNTW.S		R.SSMFISPTEILQSDANNSNTWSQSNESAIYDSLSSTPR.E
172	182	2	1403.61	1.6	1	43.2	33.9	95.00%	R.NLENQYQHDPF.Y		R.NLENQYQHDPFYFQTNINDDESETSSHSDDSDISEK.V
303	315	2	1444.68	2.4	1	36.9	32.8	95.00%	Y.NLSPDSEDRSTPK.S		K.FTDSTNPFNYTSYNLSPDSEDRSTPK.S
326	341	3	1865.97	1.2	1	23.4	30.4	90.20%	K.YRPPSVHLDQLLDGKE.-		K.YRPPSVHLDQLLDGKE.-
272	289	2	1935.93	1.1	1	43.5	32.9	95.00%	Y.DSLSSTPREPGATQILGK.F	Phospho (+80)	R.SSMFISPTEILQSDANNSNTWSQSNESAIYDSLSSTPREPGATQILGK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
169	A6ZS95_YEAS7	13.12%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
249	259	2	1170.66	1.8	0	47.9	27.5	95.00%	Y.EVLSQAGNLLK.Y		K.LPNNFVYMSDVNQLSGFMFHYSKPYEVLSQAGNLLK.Y
16	32	2	1938.93	-0.57	1	71.5	33	95.00%	R.VNSLNAPYQALSYDEQK.A		R.VNSLNAPYQALSYDEQK.A
7	15	2	988.54	2.1	1	38.2	29.5	95.00%	F.GPLTGFLER.V		-.MSSSIFGPLTGFLER.V
208	223	2	1867.86	-0.12	1	63.3	33.5	95.00%	R.TENYFLSIAHTSENDK.L		R.TENYFLSIAHTSENDK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
170	A6ZZX2_YEAS7	45.05%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
136	149	2	1494.76	1.7	1	62.8	31.5	95.00%	R.TNTFTLLTSPDSAK.I		R.TNTFTLLTSPDSAK.I
108	135	3	2735.25	0.92	0	92.7	33.3	95.00%	R.SAGDDNLSGHSVPSSGSAQATTHQTAPR.T		R.SAGDDNLSGHSVPSSGSAQATTHQTAPR.T

22	43	2	2459.99	-0.45	1	102	33.5	95.00%	R.EQQAGYGSQGNANDEYDAEQMR.L		R.EQQAGYGSQGNANDEYDAEQMR.L
28	43	2	1783.71	1.5	1	81.8	33.4	95.00%	Y.GSQGNANDEYDAEQMR.L		R.EQQAGYGSQGNANDEYDAEQMR.L
104	135	4	3264.46	0.22	1	48.5	32.7	95.00%	R.EDERSAGDDNLSGHSVPSSGSAQATTHQTAPR.T		R.EDERSAGDDNLSGHSVPSSGSAQATTHQTAPR.T
55	68	2	1643.81	-0.62	1	60	31.9	95.00%	R.EQELRDIVANTNDK.L		R.EQELRDIVANTNDK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
171	A6ZRM3_YEAS7	14.42%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
149	168	2	2298.15	-0.1	1	72.9	31.1	95.00%	K.LMTPLTFSTETNFIPQDISK.I	Oxidation (+16)	K.LMTPLTFSTETNFIPQDISK.I
109	121	3	1541.86	-0.76	1	27.9	27.5	95.00%	K.VVSYILNHKDQVK.C		K.VVSYILNHKDQVK.C
273	286	2	1578.76	0.18	1	58.9	32.7	95.00%	K.VFYGHDASMGLNLR.R		K.VFYGHDASMGLNLR.R
156	168	2	1478.73	1.2	1	59.8	32.1	95.00%	F.STETNFIPQDISK.I		K.LMTPLTFSTETNFIPQDISK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
172	A6ZX57_YEAS7	43.82%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
146	166	3	2297.14	0.088	1	41	31	95.00%	R.MMARPLTIASDPMSGFFGLQK.K		R.MMARPLTIASDPMSGFFGLQK.K
16	24	3	1054.65	-0.29	0	33.5	20.5	95.00%	K.LNIKPLTTR.L		K.LNIKPLTTR.L
25	35	2	1180.56	0.23	1	39.4	32.3	95.00%	R.LFAGMSPEMAK.K		R.LFAGMSPEMAK.K
88	107	3	2297.09	2.3	1	33.3	32.9	95.00%	K.GQYLVCMDADLQHPPETVPK.L	Carbamidomethyl (+57)	K.GQYLVCMDADLQHPPETVPK.L
2	15	2	1675.84	-0.88	1	36.1	31.8	95.00%	M.SIEYSVIVPAYHEK.L	Acetyl (+42)	-.MSIEYSVIVPAYHEK.L
108	122	3	1742.87	0.45	1	36.2	31.3	95.00%	K.LFESLHDHAFTLGTR.Y		K.LFESLHDHAFTLGTR.Y
36	62	3	2978.38	1.5	2	46.8	32.2	95.00%	K.KTELIFVDDNSQDGSVEEVDALAHQGY.N		K.KTELIFVDDNSQDGSVEEVDALAHQGYNVR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
173	A6ZNG9_YEAS7	34.51%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
19	35	2	1951.98	-0.78	2	61.1	31.5	95.00%	R.GVDLEKLLEMSTEDFVK.L		R.GVDLEKLLEMSTEDFVK.L
25	35	2	1310.65	1.9	1	54.6	32	95.00%	K.LLEMSTEDFVK.L		K.LLEMSTEDFVK.L
65	77	2	1390.76	-1.3	0	61.5	29	95.00%	K.LAAPENEKPAPVR.T		K.LAAPENEKPAPVR.T
82	100	2	2034.06	2.1	1	82.6	30.2	95.00%	R.NMIIVPEMIGSVVGIYNGK.A	Deamidation (+1)	R.NMIIVPEMIGSVVGIYNGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
174	ATG22_YEAS7	16.29%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
512	525	2	1614.78	1.5	0	67.7	32.4	95.00%	R.EAEELSQVLPESER.R		R.EAEELSQVLPESER.R
62	79	2	1982.87	1.3	0	66.7	34.3	95.00%	K.VHDHSIPCLSETGSDSDK.C	Carbamidomethyl (+57)	K.VHDHSIPCLSETGSDSDK.C
281	296	2	1801.86	-0.5	1	58.2	32.9	95.00%	R.SPYPGEQDALGQLNWK.N		R.SPYPGEQDALGQLNWK.N
2	17	2	1862.81	-0.65	1	75.2	34.3	95.00%	M.SYGTINDMNESVTNYR.I		-.MSYGTINDMNESVTNYR.I
189	210	3	2410.15	2.2	1	74.4	32.9	95.00%	K.CQSQGAYEPDKVDSLTTVISGR.G	Carbamidomethyl (+57)	K.CQSQGAYEPDKVDSLTTVISGR.G
200	210	2	1146.62	-0.62	0	57.3	29.5	95.00%	K.VDSLTTVISGR.G		K.VDSLTTVISGR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
175	A6ZPG3_YEAS7	26.61%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
167	181	2	1716.9	2	1	63.4	30.4	95.00%	R.APLEEIVISNDYLNK.D		R.APLEEIVISNDYLNK.D
93	106	2	1651.8	0.89	1	54	32.9	95.00%	R.EQSLDGIFEETKEK.L		R.EQSLDGIFEETKEK.L
53	63	2	1264.57	0.29	1	60.2	31.9	95.00%	R.NETNNIDGNFK.S		R.NETNNIDGNFK.S
145	158	2	1678.79	1.7	1	88.1	33.1	95.00%	R.DVDLIESMKDDIMR.E		R.DVDLIESMKDDIMR.E
220	227	2	905.49	0.091	1	28	28.4	94.30%	R.LELYGPSK.T		R.LELYGPSK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
176	A6ZWS9_YEAS7	17.99%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
6	17	3	1474.73	0.95	1	25.1	32.1	90.30%	K.ILMDSTHFNEIR.S		K.ILMDSTHFNEIR.S
448	460	2	1499.7	-1.3	0	57.8	33.3	95.00%	K.ADIMELLNHSDSR.V		K.ADIMELLNHSDSR.V

95	108	2	1515.82	0.59	0	57.2	29.2	95.00%	K.SVQNLIAELLSSDK.Y		K.SVQNLIAELLSSDK.Y
468	478	2	1211.65	-0.59	1	46.8	28.4	95.00%	K.ATQAIIGYTFK.-		K.ATQAIIGYTFK.-
76	94	4	2196.15	-0.52	1	35.7	28.9	95.00%	K.TLIPLIHLLSTSDNEDCKK.S	Carbamidomethyl (+57)	K.TLIPLIHLLSTSDNEDCKK.S
55	71	2	1703.78	-1.1	1	78.9	33.9	95.00%	K.NIGDGLSSSNNAHSGFK.V		K.NIGDGLSSSNNAHSGFK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
177	A6ZRQ7_YEAS7	31.67%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	76	3	1481.9	0.41	1	42	21.2	95.00%	R.RINELTLLVQKR.F		R.RINELTLLVQKR.F
41	51	3	1255.75	-0.4	1	21	24.8	95.00%	R.VTPTKTEVIIR.A		R.VTPTKTEVIIR.A
226	240	2	1625.76	1.5	0	31.6	33.5	92.10%	Y.RPAEETEAQAEPVEA.-		K.DYRPAEETEAQAEPVEA.-
201	223	2	2458.36	-0.016	1	59.6	23.3	95.00%	K.ALPDAVTIIEPKEEEPILAPSVK.D		K.ALPDAVTIIEPKEEEPILAPSVK.D
28	40	2	1436.68	-0.5	1	73.2	33	95.00%	R.ELAEEGYSGVEVR.V		R.ELAEEGYSGVEVR.V
224	240	2	1903.84	0.3	1	53.2	34	95.00%	K.DYRPAEETEAQAEPVEA.-		K.DYRPAEETEAQAEPVEA.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
178	A7A0Y0_YEAS7	39.37%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
140	153	3	1558.83	0.71	1	37.8	29.5	95.00%	R.TKDSNKDVVVEGLR.R		R.TKDSNKDVVVEGLR.R
83	88	2	757.39	1.1	1	40.1	25.3	95.00%	R.DAFHLR.V		R.DAFHLR.V
186	198	2	1363.66	-0.54	2	51.5	32.2	95.00%	R.EAGEVKDDGAFVK.F		R.EAGEVKDDGAFVK.F
40	69	3	3354.68	0.13	2	79.6	28	95.00%	K.KATVDEFPLCVHLVSNELEQLSSEALEAAR.I	Carbamidomethyl (+57)	K.KATVDEFPLCVHLVSNELEQLSSEALEAAR.I
117	128	3	1219.66	-0.0072	1	31.5	29.7	95.00%	R.GAWGKPHGLAAR.V		R.GAWGKPHGLAAR.V
41	69	3	3226.59	1.4	1	62.3	29.8	95.00%	K.ATVDEFPLCVHLVSNELEQLSSEALEAAR.I	Carbamidomethyl (+57)	K.ATVDEFPLCVHLVSNELEQLSSEALEAAR.I
142	154	3	1485.79	0.13	1	24.1	29.9	92.80%	K.DSNKDVVVEGLRR.A		K.DSNKDVVVEGLRR.A
129	139	2	1245.71	0.15	1	55.6	26.6	95.00%	R.VDIGQIIFSVR.T		R.VDIGQIIFSVR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
179	A6ZKS1_YEAS7	20.63%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
21	38	2	2057.02	1.7	2	106	31.7	95.00%	R.KVWLDPNETSEIAQANSR.N		R.KVWLDPNETSEIAQANSR.N
137	146	2	1120.66	1.5	0	22.7	22.5	91.50%	R.ALVEHIIQAK.A		R.ALVEHIIQAK.A
10	19	2	899.54	-0.46	0	66.1	24.9	95.00%	R.LAASVVGVGK.R		R.LAASVVGVGK.R
136	146	3	1276.76	0.94	1	49.7	20.9	95.00%	K.RALVEHIIQAK.A		K.RALVEHIIQAK.A
24	38	2	1643.78	1.5	0	77.5	32.9	95.00%	W.LDPNETSEIAQANSR.N		K.VWLDPNETSEIAQANSR.N
22	38	2	1928.92	-0.63	1	89.3	33.2	95.00%	K.VWLDPNETSEIAQANSR.N		K.VWLDPNETSEIAQANSR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
180	A6ZSQ1_YEAS7	38.41%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	74	2	2050.19	-0.35	1	115	18.9	95.00%	R.QAINLGQVVLTPLTFALPR.G		R.QAINLGQVVLTPLTFALPR.G
32	42	2	1211.71	1.2	0	60.2	24.3	95.00%	K.LAAIVEIIDQK.K		K.LAAIVEIIDQK.K
110	117	2	921.46	-0.26	1	39.1	31	95.00%	R.AALTDFER.F		R.AALTDFER.F
56	70	2	1612.92	1.5	1	37.5	24.4	95.00%	R.QAINLGQVVLTPLTF.A		R.QAINLGQVVLTPLTFALPR.G
118	124	2	891.5	0.21	1	27.3	30.1	90.60%	R.FQVMVLR.K		R.FQVMVLR.K
94	101	2	905.44	0.42	1	28.9	29.9	93.50%	K.WAASSWAK.K		K.WAASSWAK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
181	A6ZL12_YEAS7	8.37%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
14	23	2	1103.55	-0.29	0	35.4	31.3	95.00%	K.ETSPDSISIR.S		K.ETSPDSISIR.S
24	38	2	1575.68	-0.074	1	96.5	33.6	95.00%	R.SFSAGNNFQSSSSEK.T		R.SFSAGNNFQSSSSEK.T
405	417	2	1447.75	-0.74	1	66	31.3	95.00%	R.LICSLAQQGYAPK.F	Carbamidomethyl (+57)	R.LICSLAQQGYAPK.F
1	13	3	1371.63	-0.14	1	26.9	33.4	91.20%	-.MLSSEDFGSSGKK.E		-.MLSSEDFGSSGKK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
182	A6ZQF2_YEAS7	23.22%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

291	306	2	1683.81	1.6	1	46.8	32.9	95.00%	K.IIIPHDADGNIDASSF.V		K.IIIPHDADGNIDASSFVIANDFYGK.A
83	95	4	1542.89	0.088	1	28.1	23.3	95.00%	R.LIYPHVEHVPVLK.Q		R.LIYPHVEHVPVLK.Q
389	400	2	1350.62	3.1	1	52.7	32.6	95.00%	Y.HYNEGDLAASFK.G		K.VLASQYDASLGQEGESGNGASNGDVYHYNEGDLAASFK.G
114	129	3	1897.02	2	1	59.1	28	95.00%	K.RLILKPEENALTDEEK.K		K.RLILKPEENALTDEEK.K
61	82	3	2263.09	0.71	1	44	32.3	95.00%	R.SAGASYSPSHGLYINEIPASSR.L		R.SAGASYSPSHGLYINEIPASSR.L
261	268	2	915.55	0.31	0	31	27.4	95.00%	K.IMDLALLK.N		K.IMDLALLK.N
269	279	2	1153.64	-0.53	0	24.4	26.5	92.00%	K.NVPVVANSNIK.T		K.NVPVVANSNIK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
183	FET4_YEAST	13.22%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
306	316	2	1370.65	1.9	1	62.2	32.8	95.00%	R.FLVDIFDMDEK.I		R.FLVDIFDMDEK.I
445	454	2	1132.59	-0.46	1	46.1	30.6	95.00%	K.APEINTIGYR.T		K.APEINTIGYR.T
324	340	3	1995.97	-0.96	1	44.5	32.7	95.00%	K.HFNDFETPHPVVTIESK.K		K.HFNDFETPHPVVTIESK.K
4	20	4	1884.97	0.64	1	34.6	29.9	95.00%	K.IAEFLGNPGARPDVHHR.A		K.IAEFLGNPGARPDVHHR.A
248	265	2	1833.81	-1.2	1	98.2	34.2	95.00%	K.DAGNTPPYTGETTGSNPR.L		K.DAGNTPPYTGETTGSNPR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
184	A6ZQA2_YEAS7	20.69%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
78	100	2	2591.19	0.067	1	82.2	33.5	95.00%	R.TDTTYPAGFMDVITLDATNENFR.L		R.TDTTYPAGFMDVITLDATNENFR.L
222	240	3	2115.17	-0.8	1	27.9	25	95.00%	R.LNNVFVIGEQGKPYISLPK.G		R.LNNVFVIGEQGKPYISLPK.G
134	145	2	1326.7	-0.54	2	57.3	29	95.00%	K.KGVPYVVTHDGR.T		K.KGVPYVVTHDGR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
185	CHS3_YEAST	8.41%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
935	945	2	1290.62	-0.94	1	46.8	31.8	95.00%	R.YSDNVTNTLHK.K		R.YSDNVTNTLHK.K
104	118	2	1772.78	-0.73	1	84.8	33.9	95.00%	R.ETDSYLLQDMNTTDK.K		R.ETDSYLLQDMNTTDK.K
598	612	2	1721.84	-0.42	1	50.7	32.6	95.00%	R.NPSTLLPTSSMFWNK.A		R.NPSTLLPTSSMFWNK.A
575	586	2	1368.62	0.067	1	62.5	32.8	95.00%	R.GMTTMTTQNAWK.L		R.GMTTMTTQNAWK.L
286	301	3	1868.92	1.4	1	31.7	32.4	95.00%	F.LFQNVNGNCHNLITPK.S	Deamidation (+1)/ Carbamidomethyl (+57)	K.DASFLFQNVNGNCHNLITPK.S
917	934	2	1985.99	1	1	57	31.6	95.00%	K.GSDGYWVPVLANPDIVER.Y		K.GSDGYWVPVLANPDIVER.Y
686	696	2	1259.7	2.7	0	39.4	28.1	95.00%	K.LLMVVCDGLIK.G	Carbamidomethyl (+57)	K.LLMVVCDGLIK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
186	B3LK87_YEAS1	17.00%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
386	402	2	1913.92	-0.26	0	79.7	33.2	95.00%	K.LQEQSGNMDQNLLPAEK.F		K.LQEQSGNMDQNLLPAEK.F
315	340	3	2734.3	-0.18	1	69.5	32.1	95.00%	R.HPEPSPDPIAVADTTSGSDQSTRLEK.N		R.HPEPSPDPIAVADTTSGSDQSTRLEK.N
372	385	2	1642.83	-0.44	1	52.8	30.9	95.00%	K.NQANIERDILENSK.L		K.NQANIERDILENSK.L
303	314	2	1398.52	0.98	1	44.9	32.7	95.00%	K.SCPGFGNCQCGR.H	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.SCPGFGNCQCGR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
187	A6ZMW0_YEAS7	10.52%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
6	22	3	1792.89	2.2	1	28.8	32.2	95.00%	Y.SVAVGEAANEHETAPRR.N		-.MTEQYSVAVGEAANEHETAPRR.N
485	496	2	1367.7	-0.74	1	60.2	31.2	95.00%	K.LVDVEDLGYFAK.N		K.LVDVEDLGYFAK.N
573	588	2	1912.86	-0.35	1	73.9	34	95.00%	R.SNPYVQNICVYADENK.V	Carbamidomethyl (+57)	R.SNPYVQNICVYADENK.V
677	688	2	1324.74	-0.17	0	47.4	26.4	95.00%	R.DILAAVKPDVER.V		R.DILAAVKPDVER.V

2	21	3	2157.99	-0.092	1	62.5	33.8	95.00%	M.TEQYSVAVGEAANEHETAPR.R		-.MTEQYSVAVGEAANEHETAPR.R
6	21	3	1636.78	1.7	0	40.6	33.1	95.00%	Y.SVAVGEAANEHETAPR.R		-.MTEQYSVAVGEAANEHETAPR.R
532	541	2	1116.55	-0.29	1	41.4	30.2	95.00%	R.TGDIAEWTPK.G		R.TGDIAEWTPK.G
675	688	4	1636.94	0.37	1	46.5	22.6	95.00%	K.RRDILAAVKPDVER.V		K.RRDILAAVKPDVER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
188	A6ZXE9_YEAS7	8.64%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
377	388	2	1330.7	-0.76	0	49.8	30.5	95.00%	R.SLNIDDVDSIIK.N		R.SLNIDDVDSIIK.N
180	192	2	1328.65	-0.6	0	78	32.1	95.00%	R.VGIADTVGCANPR.Q	Carbamidomethyl (+57)	R.VGIADTVGCANPR.Q
234	245	2	1269.73	-0.013	0	44	25.4	95.00%	R.LIDVSVLGIGER.N		R.LIDVSVLGIGER.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
189	YKF4_YEAST	15.04%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
163	196	4	3678.67	1.8	1	31.1	31.3	95.00%	W.AAAVSVDTKHDVPQDSNDNNNEELEAQGQQAQEK.N		K.HVPSKPVSNTTSWAAAVSVDTKHDVPQDSNDNNNEELEAQGQQAQEK.N
257	270	3	1584.87	0.37	1	28.9	28.5	95.00%	K.KTESPLENVAELKK.E		K.KTESPLENVAELKK.E
614	626	2	1426.66	2.8	1	52.8	33.2	95.00%	Y.GQPQYGVAGQYPY.Q		K.QGNNVAAQQYYMYQNQFPGYSYPGMFDSQGYAYGQQYQQLAQNNAQTSGNANQYNFQQGYGQAGANTAAANLTSAAAAAAASPATAHAQPQQQQPYGGSFMPYYAHFYQQSFPYGQPQYGVAGQYPYQLPK.N
475	499	3	2883.37	4.5	0	37.4	32.4	95.00%	Y.AQQQQQHPQPQSQQPQSQQSPQSQK.Q		K.VEISAVISEPPEDQANTVPQPQQQSQQPQQPQQPQQPQQPQQPQQQQPQQPQQPQQQLQQQQQQQQQPVQAQAQAQEEQLSQNYYTQQQQQQYAQQQHQLQQQYLSQQQQYAQQQQQHPQPQSQQPQSQQSPQSQK.Q
637	661	3	2781.23	2.4	0	58.8	33.2	95.00%	Y.QTQNGQEQQSPNQGVAQHSEDSQQK.Q	Deamidation (+1)	K.NNYNYYQTQNGQEQQSPNQGVAQHSEDSQQK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
190	A6ZPF9_YEAS7	31.30%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
28	43	2	1787.92	1.7	1	59.8	30	95.00%	K.TAALRQEIDDTVGIMR.D		K.TAALRQEIDDTVGIMR.D
56	73	2	1891.95	0.78	2	48.6	31.9	95.00%	R.LTSIEDKADNLAISAQGF.K		R.LTSIEDKADNLAISAQGFK.R
63	75	2	1389.74	-0.38	1	59.6	29.5	95.00%	K.ADNLAISAQGFKR.G		K.ADNLAISAQGFKR.G
56	74	2	2020.05	1.7	2	109	30	95.00%	R.LTSIEDKADNLAISAQGFK.R		R.LTSIEDKADNLAISAQGFK.R
63	74	2	1233.63	-0.67	1	49.2	31.5	95.00%	K.ADNLAISAQGFK.R		K.ADNLAISAQGFK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
191	A6ZQP7_YEAS7	42.42%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	40	2	880.54	-0.026	0	41.9	18.4	95.00%	K.IGPLGLSPK.K		K.IGPLGLSPK.K
147	165	2	2073.01	1.8	0	54.3	32.5	95.00%	K.NPHDIIEGINAGEIEIPEN.-		K.NPHDIIEGINAGEIEIPEN.-
100	114	2	1706.9	2	0	72.4	30.1	95.00%	K.HSGNIQLDEIIEIAR.Q		K.HSGNIQLDEIIEIAR.Q
131	142	2	1289.64	-0.064	0	69.4	31.9	95.00%	K.EILGTAQSVGCR.V	Carbamidomethyl (+57)	K.EILGTAQSVGCR.V
17	31	2	1296.7	0.13	0	30	27.4	95.00%	R.AVGGEVGASAALAPK.I		R.AVGGEVGASAALAPK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
192	A7A1A7_YEAS7	18.63%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
172	181	2	1254.6	0.3	1	49.2	32.4	95.00%	K.FYDNSNLINR.E		K.FYDNSNLINR.E

60	74	2	1575.72	-1.6	0	88.5	33.4	95.00%	R.NSAQDLENSPMSVGK.D		R.NSAQDLENSPMSVGK.D
45	59	2	1649.76	-1.2	1	70.2	33.2	95.00%	R.HDNLSSSSSDIIYGR.N		R.HDNLSSSSSDIIYGR.N
17	36	3	1902.97	2.6	1	31.4	30.8	95.00%	K.AKGSGGTSELGGSESTPLLR.G		K.AKGSGGTSELGGSESTPLLR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
193	A6ZQF7_YEAS7	28.26%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
31	43	2	1460.71	-0.44	1	52.3	31.8	95.00%	R.ETAQAINGWELTK.A	Deamidation (+1)	R.ETAQAINGWELTK.A
47	56	2	1285.64	-0.78	1	51.2	31.5	95.00%	K.YLDQVLDHQR.A		K.YLDQVLDHQR.A
112	124	2	1495.81	-0.2	1	61.1	27	95.00%	K.LYVSHIQVNQAPK.Q		K.LYVSHIQVNQAPK.Q
90	105	2	1643.87	1.6	1	92.5	29.5	95.00%	K.FVQGLLQNAAANAEAK.G		K.FVQGLLQNAAANAEAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
194	A6ZSA1_YEAS7	12.34%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
193	219	4	3023.53	-0.48	2	38.8	28.3	95.00%	K.LANVKTDENGKPEQPITIGYISSQEHR.V		K.LANVKTDENGKPEQPITIGYISSQEHR.V
198	212	2	1661.78	1	1	50.9	33.3	95.00%	K.TDENGKPEQPITIGY.I	Deamidation (+1)	K.TDENGKPEQPITIGYISSQEHR.V
234	244	2	1322.6	-1.1	1	57	32.3	95.00%	R.LQDYQNGDLEK.G	Deamidation (+1)	R.LQDYQNGDLEK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
195	YD237_YEAST	21.54%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
171	193	3	2663.27	-1	1	37.1	31.8	95.00%	K.LYTGPLLEILDEVNCQDSDADRK.N	Carbamidomethyl (+57)	K.LYTGPLLEILDEVNCQDSDADRK.N
151	170	3	2209.16	-0.087	1	46.8	27.8	95.00%	K.ILAVGHNEAYLDPVELTLDK.L		K.ILAVGHNEAYLDPVELTLDK.L
351	367	2	1910	-0.17	1	50.2	29.1	95.00%	R.IWGAPTWPANLVETISR.Q		R.IWGAPTWPANLVETISR.Q
282	295	2	1559.86	1.4	1	55.2	27.2	95.00%	R.FAFLDAPLLSLEPK.Y		R.FAFLDAPLLSLEPK.Y
337	346	2	1023.57	-0.6	0	41.4	26.7	95.00%	K.SIIDGAHALK.L		K.SIIDGAHALK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
196	SSO1_YEAST	21.38%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
63	77	3	1793.94	1.1	1	70.9	29.6	95.00%	K.RLLTEVNEEQASHLR.H		K.RLLTEVNEEQASHLR.H
234	251	2	1952.91	1.3	0	89.8	33.6	95.00%	K.NVEDAQLDVEQGVGHTDK.A		K.NVEDAQLDVEQGVGHTDK.A
50	62	3	1568.76	-0.88	1	28.8	32.5	95.00%	K.YDHTINQVDSLHK.R		K.YDHTINQVDSLHK.R
64	77	3	1637.84	1.7	0	39.9	31.4	95.00%	R.LLTEVNEEQASHLR.H		R.LLTEVNEEQASHLR.H
78	93	2	1832.91	1.2	1	76.1	32.1	95.00%	R.HSLDNFVAQATDLQFK.L		R.HSLDNFVAQATDLQFK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
197	B5VE42_YEAST	12.84%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
146	160	2	1574.82	0.25	0	80.9	30.4	95.00%	K.VGQSLSIVSNDELSK.A		K.VGQSLSIVSNDELSK.A
60	70	2	1330.71	-0.021	2	59.7	29.5	95.00%	K.KVNVFNINNNR.Y		K.KVNVFNINNNR.Y
235	249	2	1622.77	-0.48	1	75	32.7	95.00%	K.LQSNGAIQGDSFVCK.N	Carbamidomethyl (+57)	K.LQSNGAIQGDSFVCK.N
61	70	2	1202.62	-0.19	1	43.8	30.6	95.00%	K.VNVFNINNNR.Y		K.VNVFNINNNR.Y
234	249	3	1750.87	-0.086	2	27.6	32.2	94.50%	K.KLQSNGAIQGDSFVCK.N	Carbamidomethyl (+57)	K.KLQSNGAIQGDSFVCK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
198	A7A244_YEAS7	7.66%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
492	500	2	1044.57	-0.5	0	27.4	28.9	92.70%	R.IEDDILVTK.D		R.IEDDILVTK.D
501	518	2	1994.9	0.29	1	68.1	33.6	95.00%	K.DGYENLTGITSDPDEIEK.I		K.DGYENLTGITSDPDEIEK.I
199	212	2	1611.75	0.73	0	68.3	33.4	95.00%	F.TTDLDNVHDENIAR.S		K.ELQDFAIFTTDLDNVHDENIAR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
199	A6ZUM5_YEAS7	15.08%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
39	52	2	1474.8	1.8	0	62.4	29	95.00%	F.NARPDGVHVINVGK.T		R.NVQVHQEPYVFNARPDGVHVINVGK.T
89	101	2	1268.66	-1.3	1	40.1	29.3	95.00%	K.FAAHTGATPIAGR.F		K.FAAHTGATPIAGR.F

28	52	3	2815.45	-1.1	1	22.6	28.2	93.00%	R.NVQVHQEPYVFNARPDGVHVINVGK.T		R.NVQVHQEPYVFNARPDGVHVINVGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
200	A6ZNH7_YEAS7	13.84%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
207	222	2	1828.77	-0.27	1	104	33.9	95.00%	R.QLAAEYFNCGDEADAR.I	Carbamidomethyl (+57)	R.QLAAEYFNCGDEADAR.I
192	206	2	1572.83	-0.64	1	82.2	30.6	95.00%	R.QIPVGYSAADIVANR.Q		R.QIPVGYSAADIVANR.Q
305	313	2	943.5	2.2	0	38.7	29.2	95.00%	Y.GLVQIDGDK.V		K.SSRPFTEIEAIYSTQMSSVFSGGLVYEYSNETNNYGLVQIDGDK.V
34	45	2	1313.56	0.2	1	42	32.4	95.00%	K.GNAFFNSESGER.F		K.GNAFFNSESGER.F
88	102	2	1819.76	-0.97	1	36.2	33.8	95.00%	R.VYTVDNSQDHSHCMK.L	Carbamidomethyl (+57)	R.VYTVDNSQDHSHCMK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
201	HSP72_YEAST	17.84%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
369	384	2	1516.78	1.3	0	48.5	30.7	95.00%	Y.GAAVQAAILTGDESSK.T		R.SINPDEAVAYGAAVQAAILTGDESSK.T
158	169	2	1198.67	-0.44	0	52.4	27.9	95.00%	K.DAGTIAGLNVLR.I		K.DAGTIAGLNVLR.I
548	562	2	1617.78	-1.2	1	29.7	32.1	91.30%	K.NTISEAGDKLEQADK.D		K.NTISEAGDKLEQADK.D
537	547	2	1264.67	-1	1	39.1	30.7	95.00%	K.NQLESIAYSLK.N		K.NQLESIAYSLK.N
55	69	2	1590.74	-1	1	63.7	33.2	95.00%	K.NQAAMNPANTVFDAK.R		K.NQAAMNPANTVFDAK.R
170	185	2	1658.89	-0.44	1	68.9	29.4	95.00%	R.IINEPTAAAIAYGLDK.K		R.IINEPTAAAIAYGLDK.K
111	124	2	1549.78	-1.2	1	62.2	31.7	95.00%	K.NFTPEQISSMVLGK.M		K.NFTPEQISSMVLGK.M
20	34	2	1685.81	1.3	1	57.1	32.6	95.00%	F.SNDRVDIIANDQGNR.T		K.AVGIDLGTTYSCVAHFSNDRVDIIANDQGNR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
202	A6ZRX1_YEAS7	40.83%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
34	67	4	3668.66	1.4	2	61	31.4	95.00%	F.KDEHPGGDEIIMDLGGQDATESFVDIGHSDEALR.L	Oxidation (+16)	K.VYDVSQFKDEHPGGDEIIMDLGGQDATESFVDIGHSDEALR.L
57	67	2	1210.6	1.2	0	79.8	32.5	95.00%	F.VDIGHSDEALR.L		K.DEHPGGDEIIMDLGGQDATESFVDIGHSDEALR.L
6	20	2	1805.77	1.5	1	35.7	34.1	95.00%	Y.SYQEVAEHNGPENFW.I		K.VYSYQEVAEHNGPENFWIIIDDK.V
34	56	3	2460.08	1.2	2	44.8	34.1	95.00%	F.KDEHPGGDEIIMDLGGQDATESF.V		K.VYDVSQFKDEHPGGDEIIMDLGGQDATESFVDIGHSDEALR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
203	B3LMI5_YEAS1	18.98%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
129	139	2	1282.56	1.6	1	47.4	32	95.00%	Y.TGYLDVEDEDK.H		K.ILGIDPNVTQYTGYLDVEDEDK.H
41	52	3	1397.76	0.49	1	40.4	27.6	95.00%	K.FGLNLDLDHLLK.E	Deamidation (+1)	K.FGLNLDLDHLLK.E
449	458	2	1265.59	-0.15	1	29.8	31.9	91.80%	K.DFICNWLGNK.A	Carbamidomethyl (+57)	K.DFICNWLGNK.A
428	444	2	1924.03	1.8	1	26.9	27.5	94.00%	Y.HTAVTDLLNQDLPILVY.A		R.NFLFAGDWMKPYHTAVTDLLNQDLPILVYAGDK.D
481	493	2	1318.66	2	0	53	32.1	95.00%	W.TASITDEVAGEVK.S		R.NWTASITDEVAGEVK.S
93	99	2	907.44	-0.027	1	32.5	31.1	95.00%	K.DWDFVVK.N		K.DWDFVVK.N
297	327	3	3492.41	0.79	1	49.1	32.2	95.00%	Y.NYYEPMACGEGGEPSVLPSEECSAMEDSLER.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.NFNLTSVLIGNGLTDPLTQYNYYEPMACGEGGEPSVLPSEECSAMEDSLER.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
204	A6ZQ99_YEAS7	17.15%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	85	3	2373.12	1.6	1	27.1	33.4	91.80%	Y.THPDFNNQWEVLPPHGSDVGK.G		R.ISSAGQQVTGYTHPDFNNQWEVLPPHGSDVGK.G
106	115	2	1068.56	2.4	1	32.4	28.8	95.00%	Y.LLAHDVASPF.Y		R.HVATDTYLLAHDVASPFYPTNEEITTVTLEEGDGELYPETLFAFQPLK.K

196	216	3	2452.26	-0.45	1	32.5	29.4	95.00%	K.VIDPSNNWVVDEIVNLDEVRK.V		K.VIDPSNNWVVDEIVNLDEVRK.V
54	64	2	1109.54	2.1	1	29.4	32.5	90.00%	R.ISSAGQQVTGY.T		R.ISSAGQQVTGYTHPDFNNQWEV LPPHGSDVGK.G
31	44	4	1646.79	0.87	1	29.5	32.9	95.00%	K.HQDTDAFLHSHLAR.Y		K.HQDTDAFLHSHLAR.Y
196	215	2	2324.17	1.9	1	63.6	30.2	95.00%	K.VIDPSNNWVVDEIVNLDEVR.K		K.VIDPSNNWVVDEIVNLDEVR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
205	YJT8_YEAST	11.46%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
298	310	2	1462.77	2.6	1	76.9	29.4	95.00%	Y.AFQAETIELLNSK.I		K.DTYAFQAETIELLNSK.I
311	320	2	1196.66	0.073	1	54	27.2	95.00%	K.ISQLVTFYAR.I		K.ISQLVTFYAR.I
137	147	2	1194.58	2	1	35.6	32.2	95.00%	Y.DTFVGDLTAEK.Q		R.SSSASSVSSTANENLQLDTYDTF VGDLTAEK.Q
90	104	2	1555.83	1.7	1	71.6	28.5	95.00%	R.ELPTAQTVAAKPSPF.R		R.ELPTAQTVAAKPSPFR.R
31	50	2	2106.98	2.1	1	115	33.5	95.00%	Y.TLQTDELQVGDNEEGFGAGK.S		K.NLIYTLQTDELQVGDNEEGFGAG K.S
90	105	2	1711.93	2.2	1	39.8	28	95.00%	R.ELPTAQTVAAKPSPFR.R		R.ELPTAQTVAAKPSPFR.R
321	336	3	1902.01	2.6	1	28.4	28.6	95.00%	R.ITDRPHNISHSKQELK.S		R.ITDRPHNISHSKQELK.S
353	367	2	1629.83	2.3	0	68.7	30.8	95.00%	K.DMLGLLSQADELTPK.E		K.DMLGLLSQADELTPK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
206	A6ZPF8_YEAS7	7.75%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
205	219	2	1588.83	-0.27	1	41.7	30.6	95.00%	K.ILATNPIMEAFGNAK.T		K.ILATNPIMEAFGNAK.T
581	594	3	1581.81	-0.76	1	26	30.8	94.30%	K.NRDTVSDGHLEVLK.A		K.NRDTVSDGHLEVLK.A
874	890	3	1986.02	-0.14	2	47.1	30.6	95.00%	R.QLKQEHEYNAAVTIQSK.V		R.QLKQEHEYNAAVTIQSK.V
1163	1180	2	2070.11	0.67	0	46	26.7	95.00%	R.LLEDTEILNQEITEGLLK.G		R.LLEDTEILNQEITEGLLK.G
595	610	2	1743.93	0.68	0	53.7	28.8	95.00%	K.ASTNETLINILEGLEK.A		K.ASTNETLINILEGLEK.A
514	537	3	2643.34	-1.3	2	36.5	29.5	95.00%	K.LGILSLLDEESRLPAGSDESWTQ K.L		K.LGILSLLDEESRLPAGSDESWTQ K.L
496	513	2	2195.02	0.32	1	58.1	33.8	95.00%	W.SFIEFNDNQPCIDLIENK.L	Carbamidomethyl (+57)	K.EEIEWSFIEFNDNQPCIDLIENK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
207	A6ZQ10_YEAS7	14.37%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
464	477	2	1280.63	4.1	0	57.2	32.2	95.00%	F.AAGEVSGGVHGANR.L		K.NSESVLSNGIFAAGEVSGGVHGA NR.L
478	491	2	1464.77	0.42	1	43	30.1	95.00%	R.LGGSSLLECVVFGK.T	Carbamidomethyl (+57)	R.LGGSSLLECVVFGK.T
327	336	2	1150.55	-0.44	0	34.4	31.7	95.00%	R.DTVTMEIQSK.C		R.DTVTMEIQSK.C
427	436	2	1082.58	2.6	1	39.9	28.2	95.00%	Y.VGEVTPVVHF.T		K.DISTESTVYVGEVTPVVHFTMGG VK.I
380	395	2	1837.93	0.49	1	79.1	31	95.00%	R.QYDLQTTASELVTELK.S		R.QYDLQTTASELVTELK.S
319	326	2	966.48	0.8	1	29	30.6	92.50%	R.FTNELSTR.D		R.FTNELSTR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
208	AVT7_YEAST	10.82%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
321	346	2	2748.29	0.72	1	53.4	32.7	95.00%	R.ASNLRPISMTVEDPAQPSDALDA TSY.N		R.ASNLRPISMTVEDPAQPSDALDA TSYNEQECLLPNGNFDNGSIESQE NNNDER.G
441	451	2	1098.67	1.7	0	54.1	24.1	95.00%	K.LIGLDSLAIGK.M		K.LIGLDSLAIGK.M
1	16	2	1650.81	-1.1	0	82.5	32.5	95.00%	-.MEATSSALSSTANLVK.T	Acetyl (+42)	-.MEATSSALSSTANLVK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
209	A7A007_YEAS7	19.43%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
232	242	2	1314.64	-0.7	1	44.1	31.8	95.00%	R.FTTVYENNLSK.S		R.FTTVYENNLSK.S
149	176	3	2900.4	-0.83	1	51.2	31.2	95.00%	K.EIGSSGEENKVTDASSLPHVAEL SSTTR.G		K.EIGSSGEENKVTDASSLPHVAEL SSTTR.G
249	264	2	1600.87	1.6	0	108	28.9	95.00%	K.AIVSTGLDLGNATIEK.L		K.AIVSTGLDLGNATIEK.L

159	176	2	1869.95	1.8	0	62.9	30.8	95.00%	K.VTDASSLPHVAELSSTTR.G		K.VTDASSLPHVAELSSTTR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
210	A6ZW77_YEAS7	7.54%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
164	184	2	2237.02	3.6	1	77.2	34.3	95.00%	R.DLEYISSMPHMSGTSGDAAIR.H		R.DLEYISSMPHMSGTSGDAAIR.H
137	153	3	1878.89	-0.099	1	38.1	32.9	95.00%	R.GSNGSFSDHDLLLQYAR.K		R.GSNGSFSDHDLLLQYAR.K
66	78	3	1576.81	0.15	1	26.9	31.1	95.00%	R.MCFENNVVIPVKK.N	Carbamidomethyl (+57)	R.MCFENNVVIPVKK.N
420	427	2	809.51	0.58	0	23	16.3	92.00%	R.AIVIAAPR.N		R.AIVIAAPR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
211	RSP5_YEAST	9.89%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
23	38	2	1750.88	-0.47	1	69.7	31.7	95.00%	R.SPDPFAVLTIDGYQTK.S		R.SPDPFAVLTIDGYQTK.S
138	164	3	2669.23	2.4	0	70.6	33.3	95.00%	K.LPSSSPHSQAPSGHTASSSTNTSSTTR.T		K.LPSSSPHSQAPSGHTASSSTNTSSTTR.T
80	90	2	1202.64	-0.51	1	31.2	30.4	95.00%	K.DQGFLGVVNVR.V		K.DQGFLGVVNVR.V
184	209	3	2561.23	-0.032	0	55.9	32.6	95.00%	R.GTAQAVESTLQSGTTAATNTATTSHR.S		R.GTAQAVESTLQSGTTAATNTATTSHR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
212	A6ZT41_YEAS7	17.18%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
6	24	3	1992.05	0.26	1	41.3	28.4	95.00%	K.SKNQLNTGGVPNGVHNTKK.E		K.SKNQLNTGGVPNGVHNTKK.E
41	52	2	1288.74	1.8	1	53.1	25.2	95.00%	F.TAINTLTKPALF.S		K.LGSASFTAINTLTKPALFSFYDDDITK.N
70	88	2	1955.01	-0.52	0	67.6	30.2	95.00%	K.ALLSNASQLEMVPPSATAR.H		K.ALLSNASQLEMVPPSATAR.H
8	24	2	1776.91	-6.6	1	63.3	31	95.00%	K.NQLNTGGVPNGVHNTKK.E		K.NQLNTGGVPNGVHNTKK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
213	A7A233_YEAS7	25.58%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	134	2	1964	-0.41	0	50.5	31	95.00%	K.TVNEHANDEAQLLLVGNK.S		K.TVNEHANDEAQLLLVGNK.S
71	81	2	1315.65	0.75	1	47	31.6	95.00%	K.LQLWDTAGQER.F		K.LQLWDTAGQER.F
165	178	2	1638.79	-1.6	1	74.2	32.9	95.00%	K.NDDNVNEIFFTLAK.L		K.NDDNVNEIFFTLAK.L
141	152	2	1200.63	-0.6	0	69	29.9	95.00%	R.VVTADQGEALAK.E		R.VVTADQGEALAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
214	A6ZLE8_YEAS7	21.51%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
431	448	4	2066.94	2.7	1	30	33.5	95.00%	K.HHTSELNSSTSEPDSQRR.S		K.HHTSELNSSTSEPDSQRR.S
325	344	2	2141.87	-0.45	1	98.4	34.1	95.00%	K.CNGQDMSEVGNGPGSYDISR.S	Carbamidomethyl (+57)	K.CNGQDMSEVGNGPGSYDISR.S
91	105	2	1897.86	2	1	44.7	33.8	95.00%	K.SRPLNVEEEEEIYEY.S		K.SRPLNVEEEEEIYEYSNELR.D
70	90	2	1956.95	2	0	100	32.4	95.00%	F.LQAGPSDGNAIGTSATAANNK.S		K.QGLSVEDDSPFEGSSSSAGLPSPNTNTNADSTTAFLQAGPSDGNAIGTSATAANNK.S
106	125	2	2357.05	1.4	1	50.8	33.9	95.00%	Y.SNELRDQDRESDEHTADNVK.L		K.SRPLNVEEEEEIYEYSNELRDQDRESDEHTADNVK.L
425	448	4	2694.29	-0.51	1	23.2	31.7	93.90%	K.ASLDLKHHTSELNSSTSEPDSQRR.S		K.ASLDLKHHTSELNSSTSEPDSQRR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
215	A6ZSL1_YEAS7	8.93%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
16	46	4	3541.55	-0.78	1	54.2	32.7	95.00%	K.HVFMGMEHELNPETHNDSNSDSYGLPQLSEK.Y		K.HVFMGMEHELNPETHNDSNSDSYGLPQLSEK.Y
19	38	3	2321.88	1.4	1	46.9	33.5	95.00%	F.MGMEHELNPETHNDSNSDSY.G	Oxidation (+16)	K.HVFMGMEHELNPETHNDSNSDSYGLPQLSEK.Y
607	617	2	1390.64	-0.24	1	50.1	32.7	95.00%	K.DNDPILDWFEK.L		K.DNDPILDWFEK.L

16	38	3	2689.08	1.3	1	36.9	34	95.00%	K.HVFMGMEHELNPETHNDSNSDSY.G		K.HVFMGMEHELNPETHNDSNSDSYGLPQLSEK.Y
1	14	2	1711.82	1.5	1	36.3	33.3	95.00%	-.MESVHSRNPVKEEK.K	Acetyl (+42)/ Deamidation (+1)	-.MESVHSRNPVKEEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
216	A6ZWW2_YEAS7	32.05%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
177	191	2	1577.85	1.3	0	45.2	28.6	95.00%	F.NTSLVPPTLNVPGNR.S		K.DESHTLFNTSLVPPTLNVPGNR.S
129	139	2	1237.62	1.8	2	58.8	31.3	95.00%	K.ALKLEEASQSY.G		K.ALKLEEASQSYGNEEEYFDDEDDDDEDDEDEDDEDDGGMR.K
267	277	2	1215.61	1	0	50	30.5	95.00%	K.DADDNLITAIR.A		K.DADDNLITAIR.A
282	314	4	3769.78	0.62	1	29.9	30.2	95.00%	K.LVQIAEEESDKEIQDLDVIEEQTEADDLSHMAK.S		K.LVQIAEEESDKEIQDLDVIEEQTEADDLSHMAK.S
201	221	2	2116.14	-0.19	1	73.9	27	95.00%	R.ASNILPIAYIPGVTSGLSTDK.L		R.ASNILPIAYIPGVTSGLSTDK.L
241	266	3	2863.35	0.007	0	76.5	32	95.00%	R.SHITLGSSILDGLDDEDDEHNQVLNK.D		R.SHITLGSSILDGLDDEDDEHNQVLNK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
217	B3LU76_YEAS1	29.15%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
147	164	2	1928.89	1.7	1	33.4	33.8	94.30%	K.NSFAELASIEEVHGGSPW.G		K.NSFAELASIEEVHGGSPWGAGTLAGPDGSR.T
50	65	3	1766.89	1.7	0	32.2	31.7	95.00%	K.MNAPQKPEDIPVATEK.T		K.MNAPQKPEDIPVATEK.T
147	176	3	2968.39	-0.81	1	56.4	32	95.00%	K.NSFAELASIEEVHGGSPWGAGTLAGPDGSR.T		K.NSFAELASIEEVHGGSPWGAGTLAGPDGSR.T
33	49	3	1990.03	1.5	1	26.7	30.5	95.00%	K.ADIYRVEETLPDEVLTK.M		K.ADIYRVEETLPDEVLTK.M
37	49	2	1527.82	0.9	1	53.7	28.5	95.00%	Y.RVEETLPDEVLTK.M		K.ADIYRVEETLPDEVLTK.M
24	36	2	1277.66	2.4	2	46.3	30.7	95.00%	K.KGVEAAGGKADIY.R		K.KGVEAAGGKADIYR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
218	A6ZVY2_YEAS7	11.75%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
16	29	2	1576.72	-0.78	0	59.2	33.6	95.00%	K.IETESTTIPNDSDR.S		K.IETESTTIPNDSDR.S
13	29	2	1952.94	1.1	1	74	33.3	95.00%	K.FTKIETESTTIPNDSDR.S		K.FTKIETESTTIPNDSDR.S
546	563	2	2067.97	2	1	101	33.6	95.00%	R.SEIDLDTGCSVENLELFK.A	Carbamidomethyl (+57)	R.SEIDLDTGCSVENLELFK.A
345	357	2	1263.65	1.8	0	43.1	30.3	95.00%	F.VIALSNTGSMGAK.V	Oxidation (+16)	R.LLSGSNSEDISASPFVIALSNTGSMGAK.V
43	63	3	2466.15	-0.84	0	54.5	33.2	95.00%	K.QSNLHVIPEDLENSEQTEQEK.I		K.QSNLHVIPEDLENSEQTEQEK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
219	A6ZR28_YEAS7	34.07%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
21	32	3	1450.81	0.42	2	47.4	26	95.00%	R.KQFVVDVLHPNR.A		R.KQFVVDVLHPNR.A
11	20	2	1109.69	0.25	1	49.1	17.9	95.00%	R.KVISNPLLAR.K		R.KVISNPLLAR.K
12	20	2	981.6	0.28	0	25.8	20.5	95.00%	K.VISNPLLAR.K		K.VISNPLLAR.K
69	83	2	1539.79	0.12	1	37.8	30.2	95.00%	K.SVGFGLVYNSVAEAK.K		K.SVGFGLVYNSVAEAK.K
53	61	2	996.5	0.17	1	47.5	30.4	95.00%	K.DAVSVFGFR.T		K.DAVSVFGFR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
220	TCB3_YEAST	8.54%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1340	1352	2	1358.68	-0.087	0	85	30.8	95.00%	R.SPSNLNSTSVTPR.A		R.SPSNLNSTSVTPR.A
788	801	2	1415.71	1.3	0	41.7	30.8	95.00%	F.AAANSVSEPIGCIK.L	Carbamidomethyl (+57)	K.SIEMTGAFAAANSVSEPIGCIK.L
517	533	2	1860.88	1	0	34.8	33.3	95.00%	Y.IVMTTEDAVPGTDEEVR.T		K.GSDFITNTVDPYIVMTTEDAVPGTDEEVR.T
838	851	2	1647.68	2.3	1	58.3	33.4	95.00%	Y.HSDTDHPIFDNSTY.V		K.SIYHSDTDHPIFDNSTYVPIFSPNQILTLEFHDYQK.I
1339	1352	3	1514.78	2.8	1	28.1	30.1	95.00%	R.RSPSNLNSTSVTPR.A		R.RSPSNLNSTSVTPR.A
389	402	2	1498.81	1.8	0	45	28.2	95.00%	K.TMPILVEDINVAGK.M		K.TMPILVEDINVAGK.M

40	63	4	2678.19	-0.88	1	24.4	33.8	92.30%	R.GSDHAPSGHHQYHQLINHDANDTK.T		R.GSDHAPSGHHQYHQLINHDANDTK.T
1367	1389	3	2328.19	1.1	1	29.4	29.6	95.00%	Y.APVQSASPVVKPTDNTSSSSNKK.D		R.ASLDYDPSVPNTSYAPVQSASPVVKPTDNTSSSSNKK.D
1196	1207	2	1517.76	-0.21	1	58.5	32.1	95.00%	K.NQVIFNVLDWDR.A		K.NQVIFNVLDWDR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
221	EMP47_YEAST	22.47%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	127	2	1060.53	1.8	1	28.1	30.5	91.20%	W.FVQDSNVPR.D		R.SVGYSGQTDGGISFWFVQDSNVPR.D
333	346	2	1637.87	0.36	1	84.1	28.6	95.00%	K.VQQELLSFMTTITK.Q		K.VQQELLSFMTTITK.Q
315	326	2	1313.72	-0.018	0	93	28.3	95.00%	K.ILANDINALETK.L		K.ILANDINALETK.L
139	156	2	1891.02	2.2	0	37.4	27.4	95.00%	Y.DGLQLLVDNNGPLGPTLR.G		K.QLYNGPVNYDGLQLLVDNNGPLGPTLR.G
228	248	2	2223.08	-0.6	1	108	32.6	95.00%	R.IGVTAQNGAVNNNAESFEIFK.M	Deamidation (+1)	R.IGVTAQNGAVNNNAESFEIFK.M
40	53	2	1562.79	-0.46	1	94.9	31.5	95.00%	K.LSSDYSLPDLINAR.K		K.LSSDYSLPDLINAR.K
194	205	2	1436.7	-1.2	1	48.5	32.5	95.00%	R.VTYDLEDDNLLK.V		R.VTYDLEDDNLLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
222	GPA1_YEAST	14.19%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
22	35	2	1641.87	0.052	1	96.2	29.9	95.00%	K.RANDVIEQSLQLEK.Q		K.RANDVIEQSLQLEK.Q
300	314	2	1583.77	-0.64	1	53	32.5	95.00%	K.TTGITETEFNIGSSK.F		K.TTGITETEFNIGSSK.F
179	201	4	2595.11	1.5	1	35.5	34	95.00%	K.SDTDRDAETVTQNEDADRNNSSR.I		K.SDTDRDAETVTQNEDADRNNSSR.I
281	295	2	1770.81	0.23	1	49.7	33.2	95.00%	K.FASPNYVCTDEDILK.G	Carbamidomethyl (+57)	K.FASPNYVCTDEDILK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
223	A6ZSS5_YEAS7	20.73%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	17	2	1718.93	1.4	0	75.2	28.2	95.00%	M.VLVQDLLHPTAASEAR.K		-.MVLVQDLLHPTAASEAR.K
2	18	3	1890.04	7.8	1	29.1	26.2	95.00%	M.VLVQDLLHPTAASEARK.H	Acetyl (+42)/ Deamidation (+1)	-.MVLVQDLLHPTAASEARK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
224	A6ZKL6_YEAS7	26.28%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
121	128	2	1045.47	1.9	1	47.8	31.9	95.00%	K.ECADLWPR.V	Carbamidomethyl (+57)	K.ECADLWPR.V
33	40	2	932.57	-0.12	1	26.9	20.9	95.00%	R.NLYIIAVK.G		R.NLYIIAVK.G
13	32	2	2014.99	0.21	0	81.3	32	95.00%	R.ISLGLPVGAIMNCADNSGAR.N	Carbamidomethyl (+57)	R.ISLGLPVGAIMNCADNSGAR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
225	A6ZXW5_YEAS7	10.23%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
12	33	4	2499.33	0.86	1	36.5	26	95.00%	R.HALLHNDIQTSNNSRPSLVQKK.Y		R.HALLHNDIQTSNNSRPSLVQKK.Y
97	106	2	1235.59	0.89	1	35.7	31.4	95.00%	K.NQEVYSQVNR.I		K.NQEVYSQVNR.I
277	288	2	1252.71	-0.56	0	41	25.1	95.00%	K.LSISHAIAQSVK.I		K.LSISHAIAQSVK.I
12	32	3	2371.23	-0.5	0	35.1	28.9	95.00%	R.HALLHNDIQTSNNSRPSLVQK.K		R.HALLHNDIQTSNNSRPSLVQK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
226	AKR1_YEAST	11.13%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
737	748	2	1380.73	-0.3	1	40.4	29.2	95.00%	K.ALLNGIEVDYFK.L		K.ALLNGIEVDYFK.L
224	235	2	1272.7	2.4	0	44.9	30.1	95.00%	Y.QGDSLTVAELLK.F		R.TSLLWAAYQGDSLTVAELLK.F
242	257	3	1770.89	-0.34	1	25.7	31.3	93.00%	K.IADTEGFTPLHWGTVK.G		K.IADTEGFTPLHWGTVK.G
97	115	3	2149.01	2.1	1	43.3	33	95.00%	K.LLEVNNDGDSTEHITGLHW.A		K.LLEVNNDGDSTEHITGLHWASINNR.L
122	138	2	1788.94	2.3	1	41.9	29.4	95.00%	R.LSVVDFLVSQGADVNAR.A		R.LSVVDFLVSQGADVNAR.A
2	10	2	1068.56	0.25	0	51.9	29.8	95.00%	M.VNELENVPR.A		-.MVNELENVPR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
227	A6ZQC8_YEAS7	6.13%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
151	159	2	1067.64	-0.12	1	30.8	21.5	95.00%	R.ILALLPDWK.C		R.ILALLPDWK.C
76	91	2	1831.91	0.86	2	59.8	31.8	95.00%	W.KGDPTYLPNSPYPEVR.S		R.HSIQEEGLVWKGDPTYLPNSPYPEVR.S
77	91	2	1703.82	-0.25	1	34.9	32.9	95.00%	K.GDPTYLPNSPYPEVR.S		K.GDPTYLPNSPYPEVR.S
404	415	2	1449.73	-1.7	1	52.5	31.8	95.00%	K.ILNEDYSINLEK.Y		K.ILNEDYSINLEK.Y
64	75	2	1547.68	1.4	2	40.8	33.9	95.00%	F.DRHSIQEEGLVW.K	Phospho (+80)	K.FDRHSIQEEGLVWK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
228	A6ZU59_YEAS7	36.61%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
187	203	2	1833.95	-0.54	1	87.1	30.5	95.00%	K.LLQLAGVEDVYTQSNGK.T		K.LLQLAGVEDVYTQSNGK.T
142	157	2	1728.86	-1.3	1	73.2	31.6	95.00%	R.GYWGTNLGQPHSLATK.T		R.GYWGTNLGQPHSLATK.T
50	64	2	1738.99	-0.42	1	46.3	23.3	95.00%	K.ITTIEEIFLHSLPVK.E		K.ITTIEEIFLHSLPVK.E
65	88	3	2767.48	0.11	1	25.2	25	95.00%	K.EFQIIDTLLPGLQDEVMNIKPVQK.Q		K.EFQIIDTLLPGLQDEVMNIKPVQK.Q
231	251	2	2257.11	0.79	1	68.3	32.4	95.00%	W.AEQPLPVSPLDIYSDEASAQK.K		K.AAFVAIGNTYGFLTPNLWAEQPLPVSPLDIYSDEASAQK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
229	A7A001_YEAS7	8.47%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
61	76	3	1822.98	1.2	1	37.9	27.8	95.00%	K.RVKPIEVDPNLSEAEK.V		K.RVKPIEVDPNLSEAEK.V
400	408	2	1017.53	0.47	0	39.7	30.1	95.00%	R.TMVALAEQR.F		R.TMVALAEQR.F
77	87	2	1153.71	-0.36	0	53.7	22.5	95.00%	K.VAIITAQTPLK.H		K.VAIITAQTPLK.H
571	585	2	1770.92	-0.8	1	66.4	29.7	95.00%	R.EVDLDLLKQEIAEEK.A		R.EVDLDLLKQEIAEEK.A
62	76	2	1666.88	1.6	0	38.4	29.3	95.00%	R.VKPIEVDPNLSEAEK.V		R.VKPIEVDPNLSEAEK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
230	A6ZSL9_YEAS7	38.57%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
58	78	2	2261.09	2	0	125	32.3	95.00%	R.QDVIDSLTQICDSNPAISASK.L	Carbamidomethyl (+57)	R.QDVIDSLTQICDSNPAISASK.L
14	27	2	1518.81	0.12	0	77	29.1	95.00%	K.AISLETQTESLLSK.Y		K.AISLETQTESLLSK.Y
155	163	2	1102.58	-0.29	1	45.3	30.8	95.00%	R.LISQAWETR.S		R.LISQAWETR.S
28	44	2	1891.84	-0.42	1	89.7	34.6	95.00%	K.YSTFAQTTSSEQTGQEK.K		K.YSTFAQTTSSEQTGQEK.K
164	179	3	1787.86	0.12	1	32.5	32.9	95.00%	R.SQFHSQSNVLNTANNK.V		R.SQFHSQSNVLNTANNK.V
49	57	2	1012.57	-0.31	0	40.6	24.5	95.00%	K.QLEGILGQR.Q		K.QLEGILGQR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
231	A6ZZH5_YEAS7	13.87%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
230	242	2	1526.76	-0.026	1	43.8	31.8	95.00%	K.HNVDAPIPNFFTR.N		K.HNVDAPIPNFFTR.N
136	147	2	1417.59	1.5	1	59.9	33.1	95.00%	K.WTNDHPSSPSQY.Q		K.WTNDHPSSPSQYQYPSQPALSTSIPSQAPSFSNR.K
68	112	5	4768.36	-0.78	0	32.2	26.5	95.00%	K.KPPLLVNNEAVHASVPDASHTSCNNGTLEVSINNPEPHVVDAVAR.H	Carbamidomethyl (+57)	K.KPPLLVNNEAVHASVPDASHTSCNNGTLEVSINNPEPHVVDAVAR.H
117	131	2	1598.8	-1	0	99.5	31.3	95.00%	R.NPSNSLQLQGGDITR.D		R.NPSNSLQLQGGDITR.D
355	365	2	1140.49	-0.46	1	51	32.1	95.00%	K.VGVDGYGDMGR.I	Oxidation (+16)	K.VGVDGYGDMGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
232	A6ZNP1_YEAS7	18.40%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	201	2	1261.64	1.8	1	37.8	30.8	95.00%	F.AYQQNLIEQR.D		R.DPINNEEFAYQQNLIEQR.D
242	256	2	1677.82	0.88	1	79.4	32.2	95.00%	Y.TTSDNTQLASDELRK.A		K.DLGSVVQQQGVLVDNIEANIYTTSDNTQLASDELRK.A
211	220	2	1148.61	2.1	1	32.9	30.4	95.00%	R.GITELNEVFK.D		R.GITELNEVFK.D
174	191	2	2069.05	2.1	2	29.8	30.7	93.60%	R.IPGSQIVIERDPINNEEF.A		R.IPGSQIVIERDPINNEEFAYQQNLIEQR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
233	A6ZQQ0_YEAS7	14.06%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
170	180	2	1259.73	-0.5	0	26	25	95.00%	R.VNAIEHVIIPR.T		R.VNAIEHVIIPR.T
2	12	2	1331.66	-0.15	2	35.7	31.5	95.00%	M.SGNREQVFPTR.M	Acetyl (+42)	-.MSGNREQVFPTR.M
169	180	3	1415.84	2.6	1	46.4	22	95.00%	R.RVNAIEHVIIPR.T		R.RVNAIEHVIIPR.T
188	200	2	1607.73	0.97	2	57.8	33.8	95.00%	Y.INSELDELDREEF.Y		R.TENTIAYINSELDELDREEFYR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
234	A6ZQ73_YEAS7	7.95%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
235	249	3	1645.87	2.2	2	44.3	30.3	95.00%	K.SIESLADRVGFPLDK.I		K.SIESLADRVGFPLDK.I
41	61	3	2454.22	-0.53	2	76	31.6	95.00%	K.LSETKLPPVLEDEIDDETFHK.S		K.LSETKLPPVLEDEIDDETFHK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
235	A6ZXQ6_YEAS7	17.24%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
180	190	2	1314.68	-0.47	1	85.5	30.4	95.00%	K.KIQDIDDEIAR.L		K.KIQDIDDEIAR.L
150	173	3	2430.09	1.5	1	78.7	34	95.00%	K.KNDSVTAEAAAQSGASKDDHGDEK.N		K.KNDSVTAEAAAQSGASKDDHGDEK.N
151	173	3	2302	1.5	1	60.4	33.7	95.00%	K.NDSVTAEAAAQSGASKDDHGDEK.N		K.NDSVTAEAAAQSGASKDDHGDEK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
236	A6ZLH4_YEAS7	8.57%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
904	928	3	2880.27	-1.5	1	65.9	33.3	95.00%	R.MPTNRIDTPCESEDSDLDTDLTSIR.D	Carbamidomethyl (+57)	R.MPTNRIDTPCESEDSDLDTDLTSIR.D
127	136	2	1073.5	0.37	1	54.1	31.5	95.00%	R.GGGAYYMISR.S		R.GGGAYYMISR.S
735	746	2	1437.7	-0.33	1	34.9	32.5	95.00%	K.TIDLYPIQMCGK.V	Carbamidomethyl (+57)	K.TIDLYPIQMCGK.V
5	31	3	2878.42	-0.2	1	48	30.5	95.00%	R.FYQIPGTHRPSSAISSSNESSSLLSAR.R		R.FYQIPGTHRPSSAISSSNESSSLLSAR.R
869	879	2	1233.66	-0.018	1	29.6	29.7	94.60%	R.FSTIEPQTIAK.Q		R.FSTIEPQTIAK.Q
38	48	2	1384.61	1	1	41.2	32.9	95.00%	Y.FNYQATPECQK.V	Carbamidomethyl (+57)	R.ISQTYFNYQATPECQK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
237	A7A0Y7_YEAS7	5.25%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
104	117	2	1723.86	-0.58	1	67.9	31.9	95.00%	R.IYNSPFQLNMLQEK.E		R.IYNSPFQLNMLQEK.E
148	156	2	924.54	2.6	0	32.5	24.2	95.00%	W.LIDGLPAAR.E		K.NGFFQNWLIDGLPAAR.E
238	249	2	1237.77	1.6	0	36.3	20.6	95.00%	R.VVGVIVEPVSIK.R		R.VVGVIVEPVSIK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
238	A6ZN90_YEAS7	15.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
111	119	2	954.58	0.084	0	24.2	19.4	93.70%	K.IGIVEISPK.G		K.IGIVEISPK.G
25	38	2	1543.86	1.5	2	35	27.2	95.00%	R.QGKLEVPGYVDIVK.T		R.QGKLEVPGYVDIVK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
239	A6ZSR4_YEAS7	23.53%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	48	3	1489.78	0.4	1	38.2	30.9	95.00%	K.SHPFGHALVAGIER.Y		K.SHPFGHALVAGIER.Y
94	107	2	1593.76	-0.76	1	66.9	32.5	95.00%	K.SVVSTETFEQPSQR.E		K.SVVSTETFEQPSQR.E
94	111	2	2050.99	2.3	1	72.8	33.1	95.00%	K.SVVSTETFEQPSQREEAK.K		K.SVVSTETFEQPSQREEAK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
240	VDAC1_YEAST	15.55%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
96	108	2	1341.75	-0.69	0	61.7	28.2	95.00%	K.NELITSLTPGVAK.S		K.NELITSLTPGVAK.S
66	84	2	2060.03	-0.72	1	87	31.8	95.00%	K.QTGLGLTQGWSNTNNLQTK.L		K.QTGLGLTQGWSNTNNLQTK.L
237	248	2	1251.67	-0.084	1	78.6	29	95.00%	K.VSDSGIVTLAYK.Q		K.VSDSGIVTLAYK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
241	A6ZYY5_YEAS7	15.64%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
45	57	2	1460.68	1.6	2	38.6	32.8	95.00%	Y.SDRDFITLGSSTY.R		K.GVNTLENIETLPQQGSIAGVSQGFPNIQEIYSDRDFITLGSSTYR.R
2	13	2	1291.59	8	0	34.5	32.4	95.00%	M.TSSASSPQDLEK.G	Acetyl (+42)/ Deamidation (+1)	-.MTSSASSPQDLEK.G
61	78	2	1945.88	-0.67	1	77.5	34.2	95.00%	R.DLLNALDRGDGEEGNCAK.Y	Carbamidomethyl (+57)	R.DLLNALDRGDGEEGNCAK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
242	A6ZR85_YEAS7	30.25%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
52	66	2	1680.83	1.8	1	43.8	32.6	95.00%	R.DLSEASVYPEYALPK.T		R.DLSEASVYPEYALPK.T
43	51	2	941.53	0.29	0	42.1	25.9	95.00%	R.NIVEAAAVR.D		R.NIVEAAAVR.D
71	82	3	1485.7	0.86	1	42.8	33.3	95.00%	K.LHYCVSCAIHAR.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.LHYCVSCAIHAR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
243	A6ZLE7_YEAS7	8.91%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
295	303	2	1082.54	2.5	1	29.7	31.2	92.80%	F.EIGSLDFFR.S		K.FISNDDGDTYNMCHFWTNFEIGSLDFFR.S
96	104	2	1087.57	0.35	1	35.3	31	95.00%	R.NSDLWNLVK.S		R.NSDLWNLVK.S
348	365	3	2083.95	1.5	1	30.4	33.9	95.00%	F.DGLGFHHPDFTSCPIEQK.I	Carbamidomethyl (+57)	K.SEIHFFDGLGFHHPDFTSCPIEQK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
244	A6ZXF1_YEAS7	18.83%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
488	506	2	2070.88	1.5	1	87.6	34.2	95.00%	Y.YGSLNGDDDDMTNDSALLR.F		R.VATNQEYQHPLSANYISMDSPDVINSSPGHFGMNSGQLLGNTTLYYGSLNGDDDDMTNDSALLR.F
458	473	2	1701.77	2.2	1	75.6	33.7	95.00%	Y.ISMDSPDVINSSPGHF.G		R.VATNQEYQHPLSANYISMDSPDVINSSPGHFGMNSGQLLGNTTLYYGSLNGDDDDMTNDSALLR.F
285	306	3	2472.3	1	1	38	28.1	95.00%	K.LTTLDTGDLSFPIDEEQPILKK.S		K.LTTLDTGDLSFPIDEEQPILKK.S
261	284	3	2737.31	1.7	0	32.5	31.7	95.00%	K.QLHVPDNSQDDTIIMMNPIDNSLK.L		K.QLHVPDNSQDDTIIMMNPIDNSLK.L
221	242	3	2506.21	-0.47	1	25.5	32	91.20%	R.NDSSSISNNVYSSEYHPIKPLR.S		R.NDSSSISNNVYSSEYHPIKPLR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
245	A6ZN11_YEAS7	38.58%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
86	99	2	1496.76	2.1	0	79.6	31.4	95.00%	F.GQPITQADISNPTR.A		R.QSYFSNEEGHVLCDVFGQPITQADISNPTR.A
39	69	3	3400.57	1.4	1	95.2	31.4	95.00%	R.TASVADPILDAVQEAQPFEQAADTFHDNMNR.Q		R.TASVADPILDAVQEAQPFEQAADTFHDNMNR.Q
135	148	2	1537.8	1.6	1	56	30.2	95.00%	R.VRPDFPVFGAAVTY.D		R.VRPDFPVFGAAVTYDANGMPQQVGGASSQMYGEQAVYQPQQHVQTEEK.Q
149	165	2	1739.72	-1.1	1	43.6	33.4	95.00%	Y.DANGMPQQVGGASSQMY.G		R.VRPDFPVFGAAVTYDANGMPQQVGGASSQMYGEQAVYQPQQHVQTEEK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
246	A6ZPF3_YEAS7	6.72%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
49	62	3	1667.89	1.4	2	27.2	28.6	95.00%	R.KDGLHEIYNPLEIK.Q		R.KDGLHEIYNPLEIK.Q
172	182	2	1290.61	-0.25	1	38.6	32	95.00%	K.DTTPWNESLTK.L		K.DTTPWNESLTK.L
197	204	2	928.5	1.6	0	37.8	26.9	95.00%	Y.LDNDAILR.S		R.VIYLDNDAILR.S
50	62	2	1539.8	1.5	1	40.5	30.2	95.00%	K.DGLHEIYNPLEIK.Q		K.DGLHEIYNPLEIK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
247	A6ZLM4_YEAS7	9.75%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
470	485	2	1481.79	1.7	0	43.6	28.9	95.00%	F.INNGIPAGGIATGAEK.N		R.SDYVGFINNGIPAGGIATGAEK.N
206	217	2	1399.7	-0.64	0	28.9	31	91.90%	K.LVEIPNLGCEEK.D	Carbamidomethyl (+57)	K.LVEIPNLGCEEK.D
544	556	2	1528.79	-0.73	1	36.5	30.3	95.00%	K.EVDILNAQQPQFK.Y		K.EVDILNAQQPQFK.Y
92	105	3	1714.87	1.9	1	24.7	30.5	92.70%	Y.FMKPHVESEKLQDK.I		K.QLAVAAFYATNLGSAYVIPQFFQEAFQQEEPIENYLPQLNDDDSSAVAANIPKPHIPYFMKPHVESEKLQDK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
248	A6ZYA1_YEAS7	3.24%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
300	308	2	1055.63	0.75	0	31.9	24.6	95.00%	R.SVLDLLLQR.L		R.SVLDLLLQR.L
550	564	3	1784.86	-0.49	1	36.6	32.5	95.00%	K.LKHDDEVSCEELLAK.I	Carbamidomethyl (+57)	K.LKHDDEVSCEELLAK.I
2	15	2	1580.88	-1.1	0	46.8	25.1	95.00%	M.SLPLKPLTIDSNNK.Q	Acetyl (+42)	-.MSLPLKPLTIDSNNK.Q
78	94	3	1760.99	2	1	39.1	23.8	95.00%	R.RLTSSLSPALPAGVHQK.T		R.RLTSSLSPALPAGVHQK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
249	A6ZQE6_YEAS7	13.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
4	19	2	1628.84	2.1	0	85.8	30.9	95.00%	R.SSVLADALNAINNAEK.T		R.SSVLADALNAINNAEK.T
2	19	2	1885.99	2.3	1	82.9	29	95.00%	M.TRSSVLADALNAINNAEK.T		-.MTRSSVLADALNAINNAEK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
250	A6ZPF1_YEAS7	8.00%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
176	198	3	2467.37	-0.48	1	34.2	22	95.00%	K.AIFTDNSLLPSLIKPVQAAQDVK.Y		K.AIFTDNSLLPSLIKPVQAAQDVK.Y
237	245	2	1084.54	-0.026	1	27.8	30.7	90.40%	K.TFSFDDILK.L		K.TFSFDDILK.L
2	11	2	1060.59	1.2	1	35.5	27.8	95.00%	M.VAQYTVPVGK.A		-.MVAQYTVPVGK.A
620	633	2	1609.75	-1	1	73.9	33.4	95.00%	K.DSSINIENYLEDAK.L		K.DSSINIENYLEDAK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
251	A6ZRQ3_YEAS7	4.94%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
759	782	4	2691.31	-0.097	1	38.9	31.4	95.00%	K.VVRGEDHHHTQVDQSEAHIAGLEK.K		K.VVRGEDHHHTQVDQSEAHIAGLEK.K
670	684	2	1688.71	-1.8	1	66.8	34	95.00%	R.TPDPPSYDESHSTEK.K		R.TPDPPSYDESHSTEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
252	AXL2_YEAST	8.38%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
651	664	2	1512.68	-0.6	1	55.9	33.1	95.00%	R.SSSVYMDSEPAVNK.S		R.SSSVYMDSEPAVNK.S
730	740	2	1191.61	-0.093	1	33.6	31	95.00%	K.SVTPSPYNVTK.H		K.SVTPSPYNVTK.H
620	644	3	2919.37	1.1	2	32.6	32	95.00%	Y.NDQFQSQSKEELLAKPPVQPPESPF.F	Phospho (+80)	R.DSLSGMNTYNDQFQSQSKEELLAKPPVQPPESPFFDPQNR.S
434	442	2	1023.51	2.3	1	41	32	95.00%	Y.FNIIGMDSK.I		K.ANQGSQSQELYFNIIGMDSK.I
188	197	2	1217.63	1.9	1	31.9	31.2	95.00%	Y.NAPLPNWLFF.D		R.SQLYNAPLPNWLFFDSGELK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
253	A6ZUA3_YEAS7	19.26%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
176	196	4	2379.29	0.44	1	31.6	25.7	95.00%	K.YGILSIDDLIHEIITVGPHFK.Q		K.YGILSIDDLIHEIITVGPHFK.Q
159	175	3	1837.01	1.3	1	37.4	25.2	95.00%	K.QRVPLSDNAIIEANLGK.Y		K.QRVPLSDNAIIEANLGK.Y
22	30	2	973.48	2	0	35.2	30	95.00%	K.TAEQVAAER.A		K.TAEQVAAER.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
254	A6ZL34_YEAS7	5.29%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

802	822	3	2146.02	0.7	1	42.1	33.5	95.00%	K.IAVTGGENNENTQAKDDAATK.T		K.IAVTGGENNENTQAKDDAATK.T
603	618	3	1891	1.7	2	23.5	30	91.50%	K.HVVNVQNPPKQEVFEK.I		K.HVVNVQNPPKQEVFEK.I
782	794	2	1340.69	-0.47	0	52.1	30.1	95.00%	K.LLPDGDAVDALSR.K		K.LLPDGDAVDALSR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
255	A6ZLN3_YEAS7	5.92%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
317	336	3	2372.17	-0.84	1	35.5	32.3	95.00%	K.NKEDIQEVDLVRTETEPETK.L		K.NKEDIQEVDLVRTETEPETK.L
293	306	2	1533.72	1.6	0	66.7	33	95.00%	R.NLGTTVSVEDEENK.A		R.NLGTTVSVEDEENK.A
317	328	2	1456.75	-1	1	37.6	30	95.00%	K.NKEDIQEVDLVR.T		K.NKEDIQEVDLVR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
256	A6ZV05_YEAS7	2.20%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1305	1320	2	1769.91	-0.23	1	62	30.6	95.00%	K.ISRPIASQNSLGWNEV.-		K.ISRPIASQNSLGWNEV.-
1261	1272	2	1395.65	-0.29	0	57.4	32.7	95.00%	R.MSVQESITQSMR.I		R.MSVQESITQSMR.I
1260	1272	2	1551.75	-0.84	1	56	32.5	95.00%	K.RMSVQESITQSMR.I		K.RMSVQESITQSMR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
257	YIP8_YEAST	25.00%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
101	112	3	1314.71	-0.15	0	42	29.7	95.00%	R.QLNASMGTLRPK.K		R.QLNASMGTLRPK.K
137	150	2	1675.79	-0.007	1	71.1	32.9	95.00%	R.DPSYSFMYPLTLSR.K		R.DPSYSFMYPLTLSR.K
196	204	2	1112.56	-0.12	1	39.8	29.5	95.00%	R.EFIDSLRPH.-		R.EFIDSLRPH.-
114	129	2	1739.87	-0.35	1	72.9	31.9	95.00%	K.QSTAYTNVPVIFSGEK.V		K.QSTAYTNVPVIFSGEK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
258	A6ZN91_YEAS7	12.90%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
57	66	3	1123.65	0.26	0	41.9	23.1	95.00%	K.INRPPVSVSR.I		K.INRPPVSVSR.I
117	130	2	1501.76	-0.057	0	77	31.3	95.00%	K.AGGECITLDQLAVR.A	Carbamidomethyl (+57)	K.AGGECITLDQLAVR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
259	A6ZTN7_YEAS7	11.25%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
198	221	3	2715.35	-0.74	1	54.4	30.4	95.00%	K.EYRPVDTIPLNDLESTPVMVNSAR.G		K.EYRPVDTIPLNDLESTPVMVNSAR.G
63	80	3	1965.08	2.1	0	33.8	24.3	95.00%	K.HLHGLPILQSPSLTPAER.L		K.HLHGLPILQSPSLTPAER.L
235	250	2	1624.76	4.1	0	77.5	33.2	95.00%	F.SLSSDTTTATATNNNK.R		R.DTLFSLSSDTTTATATNNNK.R
222	234	2	1363.64	2	2	37.4	32.2	95.00%	R.GSPSPSSNRDTLF.S		R.GSPSPSSNRDTLFSLSSDTTTATATNNNK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
260	B3LJM9_YEAS1	12.09%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
411	425	2	1841.88	-0.55	1	65.7	33	95.00%	R.MADQLTDFLIMQNFR.A		R.MADQLTDFLIMQNFR.A
145	158	2	1508.85	1.8	0	27.7	24.4	95.00%	F.TSPPLDGLLLENIK.L		K.DVPEPITEFTSPPLDGLLLENIK.L
181	192	2	1237.55	1.9	0	33.2	32.1	95.00%	R.DLMACAQTGSGK.T	Carbamidomethyl (+57)	R.DLMACAQTGSGK.T
513	530	2	2024.06	2.7	1	65.1	29.6	95.00%	K.GLHEILTEANQEVPSFLK.D		K.GLHEILTEANQEVPSFLK.D
193	206	2	1527.8	0.11	1	36.2	29.3	95.00%	K.TGGFLFPVLSESFK.T		K.TGGFLFPVLSESFK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
261	A6ZW97_YEAS7	20.77%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
190	204	2	1718.86	1.6	1	69.8	31.7	95.00%	R.EFEISPELATVDLEK.H		R.EFEISPELATVDLEK.H
158	165	2	991.53	-0.028	1	46	29.3	95.00%	R.TDFLDIIR.T		R.TDFLDIIR.T
236	246	2	1244.73	1.7	1	59.9	24.6	95.00%	Y.LFLNGISVINR.G		K.LNIDTSAALESIQSPYLFLNGISVINR.G
166	174	2	974.58	-0.13	1	29.1	23.1	95.00%	R.TSPAVLFIK.S		R.TSPAVLFIK.S
75	90	2	1855.86	-0.77	1	86.9	34	95.00%	K.TADSFLSNENELNFQK.V		K.TADSFLSNENELNFQK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
262	B3LLW4_YEAS1	14.97%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
140	150	2	1370.69	-0.67	1	48.3	30.8	95.00%	K.HQEFQNTNIIK.N		K.HQEFQNTNIIK.N
140	164	4	2963.42	1.5	2	40.4	31.1	95.00%	K.HQEFQNTNIIKNPTDDDFPHEAVVR.E		K.HQEFQNTNIIKNPTDDDFPHEAVVR.E
144	164	3	2422.19	0.91	2	52.3	31.5	95.00%	F.QNTNIIKNPTDDDFPHEAVVR.E		K.HQEFQNTNIIKNPTDDDFPHEAVVR.E
151	164	2	1610.73	-1.4	1	48.5	34	95.00%	K.NPTDDDFPHEAVVR.E		K.NPTDDDFPHEAVVR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
263	A6ZR73_YEAS7	16.08%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
356	367	3	1422.7	1.9	0	26	32.8	90.70%	Y.VQLIDGPEEMHR.-		R.ANGETGIIPSNYVQLIDGPEEMHR.-
205	217	2	1533.65	1.6	1	36.6	33.8	95.00%	F.DGYPQQQPSHTNY.V		R.DSGYATQFDGYPQQQPSHTNYVSSTALAGFENTQPNTSEAVNLHLNTLQQHINSASNAK.E
294	304	2	1285.58	1.5	1	38.8	33.4	95.00%	Y.SDIGDDNFIYK.A		K.ETNDNSNNQTNTNIGNTFDTDFSNGNTETTMGDTLGLYSDIGDDNFIYK.A
187	200	2	1627.73	1.5	2	40	33.6	95.00%	Y.QNNVYNDAIRDSGY.A		R.NTTPYQNNVYNDAIRDSGYATQFDGYPQQQPSHTNYVSSTALAGFENTQPNTSEAVNLHLNTLQQHINSASNAK.E
192	204	2	1456.66	1.6	2	52.2	33.5	95.00%	Y.NDAIRDSGYATQF.D		R.NTTPYQNNVYNDAIRDSGYATQFDGYPQQQPSHTNYVSSTALAGFENTQPNTSEAVNLHLNTLQQHINSASNAK.E
182	196	2	1781.83	0.11	1	50.4	33.3	95.00%	R.NTTPYQNNVYNDAIR.D		R.NTTPYQNNVYNDAIR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
264	A6ZLU0_YEAS7	19.23%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
209	233	3	2894.42	3.8	1	38.3	30.6	95.00%	K.VSLLYANETENDILLKDELDEMAEAK.Y		K.VSLLYANETENDILLKDELDEMAEAK.Y
275	292	2	1990	-1.4	1	65.9	31.7	95.00%	R.LLICGPDGMNNLALQYAK.E	Carbamidomethyl (+57)	R.LLICGPDGMNNLALQYAK.E
214	233	3	2319.08	2.4	1	26.8	33.1	91.80%	Y.ANETENDILLKDELDEMAEK.Y		K.VSLLYANETENDILLKDELDEMAEAK.Y
96	112	4	1870.02	-0.31	1	19.5	28.3	93.40%	K.TRLESLDIPAGHHVAVR.V		K.TRLESLDIPAGHHVAVR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
265	A6ZUT8_YEAS7	15.34%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
231	254	2	2557.13	0.31	1	78.3	33.9	95.00%	W.VGETGWPTDGTNFESSYPSVDNAK.Q		K.GSTDITFWVGETGWPTDGTNFESSYPSVDNAK.Q
145	156	2	1191.56	-0.51	0	55.9	31.7	95.00%	R.SVVADISDSDGK.S		R.SVVADISDSDGK.S
129	139	2	1190.58	0.16	0	49.6	31.4	95.00%	R.NDLTASQLSDK.I		R.NDLTASQLSDK.I
128	139	2	1346.68	1.4	1	53.8	31.6	95.00%	Y.RNDLTASQLSDK.I		K.ESTVAGFLVGSEALYRNDLTASQLSDK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
266	A6ZM50_YEAS7	15.17%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	145	3	1095.67	-0.19	0	33.5	19.5	95.00%	K.LKPIEVELR.R		K.LKPIEVELR.R
146	162	2	2064.07	2.2	2	129	29.9	95.00%	R.RVEEITDEIVDELTYLK.N		R.RVEEITDEIVDELTYLK.N
62	67	2	760.46	1.9	1	22.3	23.5	90.80%	K.LNLFVR.D		K.LNLFVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
267	A6ZWH0_YEAS7	27.92%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

139	149	2	1302.71	-0.32	1	42	28.3	95.00%	K.QIVNIPSFMVR.L		K.QIVNIPSFMVR.L
70	78	2	1031.58	-0.42	1	59.2	28.2	95.00%	R.LFEGNALIR.R		R.LFEGNALIR.R
180	197	2	1835.72	-1.1	1	111	33.2	95.00%	R.KAEASGEAADEADEADEE.-		R.KAEASGEAADEADEADEE.-
155	171	3	1781.9	-0.07	1	28.7	31.8	95.00%	K.HIDFAPTSPFGGARPGR.V		K.HIDFAPTSPFGGARPGR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
268	A6ZUW4_YEAS7	42.86%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
70	83	2	1390.69	0.85	1	70.9	32.1	95.00%	Y.FQGGNNELGTAVGK.L		K.VYYFQGGNNELGTAVGK.L
87	105	2	1872.01	1.6	0	94.7	28.2	95.00%	R.VGVVSILEAGDSDILTTLA.-		R.VGVVSILEAGDSDILTTLA.-
41	52	2	1292.82	0.83	0	49.5	13.4	95.00%	K.LIIIAANTPVLR.K		K.LIIIAANTPVLR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
269	HMX1_YEAST	9.46%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
200	211	2	1351.63	2	1	56.7	33	95.00%	F.TFSDLGPTEETR.L		K.GTNFFTFSDLGPTEETR.L
72	89	2	2042.08	0.38	0	107	28.1	95.00%	R.LLNDPVTEEELQTSTILK.Q		R.LLNDPVTEEELQTSTILK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
270	B3LJ36_YEAS1	6.76%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
549	560	3	1415.76	1.1	1	37.7	29.6	95.00%	K.ALKDIDLETDRK.D		K.ALKDIDLETDRK.D
67	79	2	1379.66	-1.3	1	55.7	32.8	95.00%	K.SPLDGSFDTSNLK.R		K.SPLDGSFDTSNLK.R
67	80	2	1535.76	-0.73	1	74.6	32.5	95.00%	K.SPLDGSFDTSNLKR.T		K.SPLDGSFDTSNLKR.T
561	574	2	1641.88	0.84	1	67.8	29.2	95.00%	K.DIDIEIVKQEIAEK.K		K.DIDIEIVKQEIAEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
271	A7A0E6_YEAS7	8.32%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
12	32	3	2272.21	1.9	0	58	28	95.00%	K.KPILAVPEPALADTHSEEISR.S		K.KPILAVPEPALADTHSEEISR.S
271	292	3	2507.28	1.7	2	54.5	29.4	95.00%	R.KVNENWNVEDGHITDVLLGSLR.S		R.KVNENWNVEDGHITDVLLGSLR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
272	B3LJS4_YEAS1	10.26%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
3	33	3	3432.6	-0.34	1	67.1	31.2	95.00%	R.SSYQPVSTTNFEHENAIPTASSSHNLLMSQR.F		R.SSYQPVSTTNFEHENAIPTASSSHNLLMSQR.F
248	258	2	1205.57	-1	1	43.2	31.8	95.00%	K.ENFNPLSSNGK.L		K.ENFNPLSSNGK.L
299	309	2	1226.72	0.078	0	48	25.9	95.00%	K.LVSQQVLIAEK.F		K.LVSQQVLIAEK.F
765	779	2	1771.78	2.1	1	61.3	33.6	95.00%	W.TFPGVMDAIYDDDWK.R		K.NGGNVDFWTFPGVMDAIYDDDWK.R
384	398	2	1477.66	-0.55	0	91.5	33	95.00%	R.LSSGGVTVDDGNSDR.S		R.LSSGGVTVDDGNSDR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
273	A6ZKZ2_YEAS7	23.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	133	2	1855	0.77	0	70.3	27.5	95.00%	R.VQVGDIVTVGQCRPISK.T	Carbamidomethyl (+57)	R.VQVGDIVTVGQCRPISK.T
47	56	2	1095.54	-0.83	1	34.6	31.4	95.00%	K.TAIEGSYIDK.K		K.TAIEGSYIDK.K
58	67	2	1148.6	0.44	1	68.1	30.6	95.00%	K.CPFTGLVSIR.G	Carbamidomethyl (+57)	K.CPFTGLVSIR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
274	A6ZR09_YEAS7	23.14%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
92	102	2	1316.77	1.1	1	57.7	24.6	95.00%	R.AFLIEEQKIVK.K		R.AFLIEEQKIVK.K
44	60	3	1846.88	-0.18	0	49.9	33.4	95.00%	K.CGDCGSALQGISTLRPR.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CGDCGSALQGISTLRPR.Q
92	99	2	976.52	-0.44	1	29	28.9	94.80%	R.AFLIEEQK.I		R.AFLIEEQK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
275	A6ZUG0_YEAS7	10.32%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

78	91	3	1481.86	0.47	0	45	23.8	95.00%	K.AQRPITGASLDLIK.E		K.AQRPITGASLDLIK.E
78	93	3	1767	1.6	1	51.8	24.7	95.00%	K.AQRPITGASLDLIKER.R		K.AQRPITGASLDLIKER.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
276	A6ZTE7_YEAS7	6.45%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
36	45	2	1154.61	1.6	1	33	27.8	95.00%	W.QLANLGPWEK.V		K.ITCTDLVYVFILLFLNTSCVQAVFSDDAFITDWQLANLGPWEK.V
142	149	2	915.5	2.2	0	34.6	30.8	95.00%	Y.LNDQVSIK.N		K.FDLHDWFLLEEGVDNAPSTTILPQSSYLNDQVSIK.N
662	677	3	1896.03	2.9	1	47.4	27.1	95.00%	Y.TPVIPINDNFIITHFR.N		K.EFMATPYTPVIPINDNFIITHFR.N
467	481	2	1588.83	-1.3	0	40.9	30	95.00%	R.ETTNLNTLGITLGDK.S		R.ETTNLNTLGITLGDK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
277	B3LGK8_YEAS1	13.19%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
186	194	2	963.48	1.4	1	59.2	30.2	95.00%	K.YSIQSGGPR.A		K.YSIQSGGPR.A
173	185	2	1392.62	-0.92	0	72	32.6	95.00%	K.GQCTDAALESVDK.Y	Carbamidomethyl (+57)	K.GQCTDAALESVDK.Y
240	254	3	1783.93	1.6	1	50	29.9	95.00%	K.KCLVISDELNHTSIR.T	Carbamidomethyl (+57)	K.KCLVISDELNHTSIR.T
10	38	3	3356.55	1.8	2	44.5	32.1	95.00%	R.VPLCEPEELPDDIQKENEYGTLDSPGHLY.Q	Carbamidomethyl (+57)	R.VPLCEPEELPDDIQKENEYGTLDSPGHLYQVK.S
540	547	2	1058.54	0.069	1	34.6	29.6	95.00%	R.WDIEEVIR.R		R.WDIEEVIR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
278	AGP1_YEAST	10.74%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
92	112	3	2269.06	0.93	1	67.6	33.4	95.00%	R.QAQELEKNESSDNIGANTGHK.S		R.QAQELEKNESSDNIGANTGHK.S
15	48	4	3779.66	1.1	1	56.8	32.1	95.00%	K.NSSTEIHATGQDNEIEYFETGSNDRPSSQPHLGY.E		K.NSSTEIHATGQDNEIEYFETGSNDRPSSQPHLGYEQHNTSAVR.R
430	442	2	1465.78	2	1	46.2	28.9	95.00%	R.LFLTLSEQGYAPK.V		R.LFLTLSEQGYAPK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
279	A7A0K9_YEAS7	11.24%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
28	47	3	2246.14	-0.11	2	57.7	30.9	95.00%	K.KDHLESNAVLACASYINTLK.W	Carbamidomethyl (+57)	K.KDHLESNAVLACASYINTLK.W
444	461	3	2057.99	2	1	31.5	32.9	95.00%	K.ATLINLNTSNNPHDEMFK.V		K.ATLINLNTSNNPHDEMFK.V
647	665	3	2064.09	1.3	1	30.6	28.6	95.00%	F.AHIGNARPNFSNVIENAIK.S		R.DQLIHFDDIMTELTSFAHIGNARPNFSNVIENAIK.S
666	688	2	2409.17	0.1	0	66.6	32.1	95.00%	K.STPPGDSLAVVCCGPPVLVDDVR.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.STPPGDSLAVVCCGPPVLVDDVR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
280	B3LL17_YEAS1	16.46%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
322	344	2	2245.04	3.3	0	61.3	33.3	95.00%	Y.DANGVPGEEMALDGVGGGCTLVK.A	Carbamidomethyl (+57)	K.QPSIRPYDFNNWQESDTGLEIASQMGDDEIIVEGYAEIATYRPLMAHFYDANGVPGEEMALDGVGGGCTLVK.A
142	152	2	1286.73	2	1	48.2	27.5	95.00%	R.ELIELGFITPR.T		R.ELIELGFITPR.T
79	99	3	2448.15	1.8	1	33.4	32.8	95.00%	K.SGWLFNDHVEDIIPEGHIAHY.D		K.SGWLFNDHVEDIIPEGHIAHYDLNK.L
256	265	2	1131.64	-0.37	1	34.9	28.3	95.00%	K.AILAANIYQR.F		K.AILAANIYQR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
281	A6ZPU2_YEAS7	10.85%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
206	217	2	1198.67	-0.44	0	52.4	27.9	95.00%	K.DAGTIAGLNVLR.I		K.DAGTIAGLNVLR.I
218	233	2	1644.87	-0.5	1	60.3	29.3	95.00%	R.IVNEPTAAAIAYGLDK.S		R.IVNEPTAAAIAYGLDK.S
472	484	2	1402.72	1.6	0	57.7	30.9	95.00%	F.STAVDNQPTVMIK.V		K.SQIFSTAVDNQPTVMIK.V
103	117	2	1671.86	-1.1	1	72.9	30.2	95.00%	K.NQVAANPQNTIFDIK.R		K.NQVAANPQNTIFDIK.R
327	344	2	2022.02	0.68	1	101	31.4	95.00%	R.IEIDSFVDGIDLSETLTR.A		R.IEIDSFVDGIDLSETLTR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
282	A6ZW73_YEAS7	10.76%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	64	3	1750.82	1.4	1	29.6	32.8	95.00%	R.VLTHDGTLDNDYFNK.H		R.VLTHDGTLDNDYFNK.H
7	30	4	2618.33	-0.63	2	54	29.8	95.00%	R.TLKSDTDVTSLNASTVSHQSKPFR.Q		R.TLKSDTDVTSLNASTVSHQSKPFR.Q
314	326	3	1378.79	0.22	1	53.1	24.2	95.00%	K.KILDVGNTLAAHK.S		K.KILDVGNTLAAHK.S
82	93	2	1276.68	-0.013	0	43	30.2	95.00%	R.TISGLNMTALTR.V		R.TISGLNMTALTR.V
327	348	4	2579.13	1.3	1	32.8	34	95.00%	K.SNQKPSHSDEQFDQEDHIDAPR.S		K.SNQKPSHSDEQFDQEDHIDAPR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
283	A6ZU67_YEAS7	11.72%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
163	191	3	3028.64	2.2	2	80	23.4	95.00%	R.EKLPFPSGSATATLISVLNGTEILQEVSK.S		R.EKLPFPSGSATATLISVLNGTEILQEVSK.S
428	440	2	1502.76	-0.75	1	33.6	31.4	95.00%	R.LVSRDNEIEVDSK.H		R.LVSRDNEIEVDSK.H
521	551	3	3156.55	-1.1	0	115	29.7	95.00%	R.DRPGSVLMNVVSGGIAEASAQQAGDLMQDLK.T		R.DRPGSVLMNVVSGGIAEASAQQAGDLMQDLK.T
598	609	2	1399.73	0.22	1	43.2	30	95.00%	R.IPTAVVWIDCAR.L	Carbamidomethyl (+57)	R.IPTAVVWIDCAR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
284	A6ZM36_YEAS7	37.67%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	16	2	1781.94	-0.15	1	67.6	28.2	95.00%	M.SLVVQEQGSFQHILR.L	Acetyl (+42)	-.MSLVVQEQGSFQHILR.L
89	108	3	2261.06	-0.26	2	52.7	33.4	95.00%	R.QNDITDGKDYHTLANNVESK.L		R.QNDITDGKDYHTLANNVESK.L
81	88	2	1015.56	1	1	47.3	30.3	95.00%	K.IPAWFLNR.Q		K.IPAWFLNR.Q
57	68	2	1429.71	-1	1	48.4	31.3	95.00%	K.RAGELTQEELER.I		K.RAGELTQEELER.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
285	A6ZNL3_YEAS7	16.93%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
322	338	4	1815.77	3.2	1	26	33.7	94.90%	F.SSNHGPSSGSFEEEHTK.G		K.LYASSFSSNHGPSSGSFEEEHTK.G
352	365	2	1317.67	-0.25	1	94.2	31.1	95.00%	R.ISNGTFINGGPGGK.N		R.ISNGTFINGGPGGK.N
302	315	2	1707.84	0.87	1	35.2	32.9	95.00%	K.EYQEAIKPVEYPDK.L		K.EYQEAIKPVEYPDK.L
38	56	2	2216.85	-0.51	1	72.7	32.9	95.00%	K.ADSYNWQSSSHCNSECSAK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.ADSYNWQSSSHCNSECSAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
286	A6ZU78_YEAS7	26.85%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
116	126	2	1190.75	0.15	1	34.6	15.1	95.00%	K.GRIPNVPVIVK.A		K.GRIPNVPVIVK.A
93	109	2	1692.86	2.2	2	42.3	31.3	95.00%	K.SASKETAPVIDTLAAGY.G		K.SASKETAPVIDTLAAGYGK.I
97	111	2	1504.78	-0.21	1	38.5	31.4	95.00%	K.ETAPVIDTLAAGYGK.I		K.ETAPVIDTLAAGYGK.I
78	87	2	1269.71	0.056	1	24.6	26.5	92.20%	K.LWTLIPEDKR.D		K.LWTLIPEDKR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
287	A6ZZN9_YEAS7	7.40%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
147	154	2	896.55	2.3	0	46	17.4	95.00%	Y.VSLNPIVR.C		K.AHNMGPNEVFVEEEYIDEDDTYVSLNPIVR.C
155	163	2	1155.54	-0.25	1	31.1	32.2	93.40%	R.CTPNLYFNK.G	Carbamidomethyl (+57)	R.CTPNLYFNK.G
171	182	2	1485.62	0.14	1	30.4	33.3	90.30%	R.SEPFCTPYENSR.W	Carbamidomethyl (+57)	R.SEPFCTPYENSR.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
288	A6ZRX9_YEAS7	6.31%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
596	606	3	1359.72	0.96	1	30.3	30.4	95.00%	K.IYVKHDDLTTR.V		K.IYVKHDDLTTR.V
215	235	2	2274.99	0.75	0	85.8	34.4	95.00%	F.TSHESDSINQSSPSSNQDIDK.V		R.QEHQLNDSASSDFTSHESDSINQSSPSSNQDIDK.V

202	235	4	3733.58	-0.55	1	23	31.9	93.10%	R.QEHQLNDSASSDFTSHESDSINQSSPSSNQDIDK.V		R.QEHQLNDSASSDFTSHESDSINQSSPSSNQDIDK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
289	A6ZZN6_YEAS7	24.49%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
364	374	3	1345.67	2	2	30.5	31.5	95.00%	K.INKQDTSLHQY.A		K.INKQDTSLHQYASLVDTEYEPFVMYIINL.-
30	42	2	1494.71	-0.82	1	48.9	32.9	95.00%	K.TDSWFNETLIGGR.A		K.TDSWFNETLIGGR.A
174	200	4	2999.63	0.21	1	30.7	22.5	95.00%	R.SLHDIVKPEDFVLNSEHLTTVLVAVPK.S		R.SLHDIVKPEDFVLNSEHLTTVLVAVPK.S
129	146	2	1988.01	1.2	0	36.7	31.1	95.00%	K.DLITLISNESSQLDADVR.A		K.DLITLISNESSQLDADVR.A
55	81	3	2814.49	1.7	1	76.8	25.8	95.00%	K.IGSLDTLIVESEELSKVDNQIGASIGK.I		K.IGSLDTLIVESEELSKVDNQIGASIGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
290	COS6_YEAST	23.88%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
157	167	2	1275.75	0.92	1	50	23.9	95.00%	R.TTLLEPFSLKK.D		R.TTLLEPFSLKK.D
206	219	2	1525.81	-0.017	1	66.9	28.7	95.00%	K.SWSPVGLEDAKLPK.E		K.SWSPVGLEDAKLPK.E
357	369	2	1544.86	2.1	1	63.7	26.9	95.00%	R.ALSLNVELWPYIK.E		R.ALSLNVELWPYIK.E
291	313	2	2580.22	1	1	96.5	33.1	95.00%	K.MQFLSTIINEQESGANGWDEIAK.K		K.MQFLSTIINEQESGANGWDEIAK.K
113	132	2	2214.99	1.7	1	58.7	34	95.00%	K.NTPSSDPHDWEVVAANLNSY.F		K.NTPSSDPHDWEVVAANLNSYFYENK.A
147	156	2	1185.49	1.4	1	57.9	32.2	95.00%	F.SAMSCQEAFR.T	Carbamidomethyl (+57)	K.YFFFSAMSCQEAFR.T
206	216	2	1187.58	-0.27	1	57.3	31.8	95.00%	K.SWSPVGLEDAK.L		K.SWSPVGLEDAK.L
157	166	2	1147.65	0.15	1	29.8	27.7	95.00%	R.TTLLEPFSLK.K		R.TTLLEPFSLK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
291	A6ZLA4_YEAS7	12.97%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
114	128	3	1677.8	-0.15	1	29.9	32.8	95.00%	K.QSIESCKEGEAVVSR.H	Carbamidomethyl (+57)	K.QSIESCKEGEAVVSR.H
386	411	3	2899.37	-0.58	1	36.1	32	95.00%	K.LISHIHDGQDGGTQDYFERPTDGTLK.A		K.LISHIHDGQDGGTQDYFERPTDGTLK.A
368	385	2	1942.86	-0.41	1	104	33.7	95.00%	K.TGCGEMDLFEILTAGSDK.L	Carbamidomethyl (+57)	K.TGCGEMDLFEILTAGSDK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
292	ATG15_YEAS7	10.00%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
440	453	2	1546.83	1.8	1	62.3	29	95.00%	K.VIDEVLLGYEQAAK.C		K.VIDEVLLGYEQAAK.C
194	201	2	971.48	0.39	1	30.2	29.4	95.00%	R.IPQTGDWR.N		R.IPQTGDWR.N
241	260	2	1919.83	-1.3	0	68.2	34.4	95.00%	K.GTSAQGLPGSGEDETTGNDK.I		K.GTSAQGLPGSGEDETTGNDK.I
417	426	2	1209.57	-0.14	1	44.3	32.7	95.00%	R.VCVYDVVNDK.G	Carbamidomethyl (+57)	R.VCVYDVVNDK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
293	A6ZUT7_YEAS7	3.39%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
148	159	2	1489.66	-1.1	1	73.1	34.1	95.00%	R.MSIETLYDDFEK.N		R.MSIETLYDDFEK.N
666	676	2	1250.63	-0.66	1	53.5	31.9	95.00%	R.DNIIFGSPFNK.E		R.DNIIFGSPFNK.E
729	743	2	1726.84	1.2	1	54.5	32.6	95.00%	K.DIYLFDDVLSAVDSR.V		K.DIYLFDDVLSAVDSR.V
763	774	3	1392.81	-0.14	0	30	23.4	95.00%	R.ILATHQLSLIER.A		R.ILATHQLSLIER.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
294	A6ZPF4_YEAS7	7.30%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
519	538	3	2414.15	1.5	2	25.8	32.7	90.50%	W.NIETHENERLPQGEDFVYPK.T		R.TWWNIETHENERLPQGEDFVYPK.T
420	432	3	1441.77	0.49	0	32.8	28.5	95.00%	K.NLHTHEVPAPISK.S		K.NLHTHEVPAPISK.S
13	21	2	1119.52	0.16	1	31.1	31.5	94.30%	K.STDDDLIWR.R		K.STDDDLIWR.R
99	111	4	1574.76	0.079	1	32.8	33.1	95.00%	R.HEFYHDVHPPLGK.M		R.HEFYHDVHPPLGK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
295	A6ZMY7_YEAS7	8.59%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
181	195	2	1589.85	0.79	1	67	29.3	95.00%	K.GSAPLFGNFLEPLTK.T		K.GSAPLFGNFLEPLTK.T
41	58	3	1933.91	2.1	1	38.5	33.7	95.00%	R.FLSEHPGGDESILDYAGK.D		R.FLSEHPGGDESILDYAGK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
296	A6ZSV7_YEAS7	12.57%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
12	36	3	2768.14	1.6	1	106	33.6	95.00%	W.SDESQTNNDSVNDAYADVNTTHESR.R		-.MTSQEYEPIQWSDESQTNNDSVNDAYADVNTTHESR.R
39	55	2	1833.92	-0.87	0	72.6	31.4	95.00%	R.TTLQPNSTSQSMIGTLR.K		R.TTLQPNSTSQSMIGTLR.K
475	501	3	3020.39	1.6	1	100	32.4	95.00%	K.KPVADRTEDDETIELEEMGIGSSSQER.S		K.KPVADRTEDDETIELEEMGIGSSSQER.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
297	A6ZM02_YEAS7	11.76%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	83	3	2188.06	1.7	1	57.2	32.5	95.00%	R.VVEVCLADLQGSEDHSFRK.V	Carbamidomethyl (+57)	R.VVEVCLADLQGSEDHSFRK.V
65	81	2	1903.87	1.8	1	49.8	33.9	95.00%	R.VVEVCLADLQGSEDHSF.R	Carbamidomethyl (+57)	R.VVEVCLADLQGSEDHSFR.K
203	213	2	1350.74	0.21	1	39.1	27.4	95.00%	K.DIFPLQNIHVR.K		K.DIFPLQNIHVR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
298	A6ZQF9_YEAS7	13.77%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	58	2	2783.31	-2.1	1	33.1	32.3	95.00%	K.ATFSPSGGTVSVPVEWMDNGAYPSLSK.I		K.ATFSPSGGTVSVPVEWMDNGAYPSLSK.I
48	58	2	1181.54	1.6	1	36.8	32.3	95.00%	W.MDNGAYPSLSK.I		K.ATFSPSGGTVSVPVEWMDNGAYPSLSK.I
84	94	2	1245.61	-0.74	0	37.5	32.1	95.00%	K.ITPSELTQDDK.V		K.ITPSELTQDDK.V
35	58	2	2465.15	3	1	68.5	33.1	95.00%	F.SPSGGTVSVPVEWMDNGAYPSLSK.I	Deamidation (+1)	K.ATFSPSGGTVSVPVEWMDNGAYPSLSK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
299	A6ZTK9_YEAS7	5.08%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
7	22	4	1870.95	0.66	1	23.9	31	95.00%	K.SITQHEVERESVSSKR.A		K.SITQHEVERESVSSKR.A
237	246	2	1354.62	1.7	1	33.5	32.9	95.00%	R.YIFNEQELHY.A		R.YIFNEQELHYAR.R
7	21	2	1714.85	-0.3	1	47.5	32.2	95.00%	K.SITQHEVERESVSSK.R		K.SITQHEVERESVSSK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
300	B3LMS1_YEAS1	5.94%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
257	264	2	1101.52	0.35	1	45.6	32.3	95.00%	K.QEIQDWQR.S		K.QEIQDWQR.S
265	285	3	2359.03	2.2	2	29.5	34	94.60%	R.SHGHNRDPESSEETHSGPTLW.Q		R.SHGHNRDPESSEETHSGPTLWQYVTDPSYK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
301	A6ZM38_YEAS7	34.56%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
82	95	2	1590.79	-0.0064	1	69.1	31.9	95.00%	K.DQYVPEVSALDLSR.S		K.DQYVPEVSALDLSR.S
117	128	2	1295.76	-0.39	0	61.9	23.7	95.00%	K.LPLSVINVSAQR.D		K.LPLSVINVSAQR.D
96	111	2	1702.84	-0.71	0	58.6	31.8	95.00%	R.SNGVLNVDNQTSDLVK.S	Deamidation (+1)	R.SNGVLNVDNQTSDLVK.S
112	128	2	1794.08	2.3	1	28	19.4	95.00%	K.SLGLKLPLSVINVSAQR.D		K.SLGLKLPLSVINVSAQR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
302	A6ZXD4_YEAS7	8.37%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
21	43	4	2564.26	-0.69	1	40.2	31.7	95.00%	R.AHQLAQDFNSKQDDTALTSLPHK.N		R.AHQLAQDFNSKQDDTALTSLPHK.N
600	616	2	1973.98	-0.86	1	82.3	31.7	95.00%	K.QNNQAYSSIQNEQILPK.N		K.QNNQAYSSIQNEQILPK.N

4	20	3	1866.92	-0.85	0	64.2	32.3	95.00%	R.SNKPLTQEANSSAHIDR.A		R.SNKPLTQEANSSAHIDR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
303	A6ZT39_YEAS7	12.09%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
330	343	2	1592.83	0.31	1	63.8	30.3	95.00%	R.DLENLLELSYGLSK.A		R.DLENLLELSYGLSK.A
158	173	4	1747.92	0.35	1	20.7	30.1	92.20%	K.ALHISGNKPESNPEKK.T		K.ALHISGNKPESNPEKK.T
137	149	2	1410.76	1.3	1	61.4	27.7	95.00%	R.SFPSLVAVEHLGR.T		R.SFPSLVAVEHLGR.T
352	360	2	1068.49	1.1	1	29.7	32.7	90.20%	R.NYDVISACK.D	Carbamidomethyl (+57)	R.NYDVISACK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
304	A6ZTV6_YEAS7	7.98%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
412	422	2	1194.61	0.16	1	32.9	31.4	95.00%	R.TAVDTVYEAVK.C		R.TAVDTVYEAVK.C
779	788	2	1155.63	0.93	0	35.5	27.2	95.00%	W.ELGSLQERPK.D		K.AVCDSLTEEGEIIWELGSLQERPK.D
289	302	2	1672.88	-0.48	1	35	30.1	95.00%	K.TNQLVPEVLEYNVR.F		K.TNQLVPEVLEYNVR.F
400	411	2	1288.7	-0.084	0	66.5	29.5	95.00%	R.VLSVTSTAQDLR.T		R.VLSVTSTAQDLR.T
29	45	2	1705.81	-0.89	1	50.9	32.9	95.00%	K.IYVAPGNGGTATMDPSR.V		K.IYVAPGNGGTATMDPSR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
305	A6ZU36_YEAS7	29.32%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
92	106	3	1804.95	0.73	1	24.8	29.8	93.90%	R.YVYAHFPINVNIVEK.D		R.YVYAHFPINVNIVEK.D
3	21	2	2160.13	-0.089	1	61.3	28.4	95.00%	K.YIQTEQQIEVPEGVTVSIK.S		K.YIQTEQQIEVPEGVTVSIK.S
175	184	3	1177.61	-0.33	1	29.8	30.6	95.00%	K.FLDGIYVSHK.G		K.FLDGIYVSHK.G
73	84	2	1276.67	-2.2	0	43.1	30.7	95.00%	K.SLVDNMITGVTK.G		K.SLVDNMITGVTK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
306	A6ZMB4_YEAS7	6.52%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
132	141	2	1174.58	0.58	0	48.2	31.2	95.00%	R.QLDESLDSLR.S		R.QLDESLDSLR.S
67	77	2	1263.65	0.69	1	47.7	30.4	95.00%	R.MVGFLNEVVEK.H		R.MVGFLNEVVEK.H
160	170	2	1171.63	-0.2	1	49	29.4	95.00%	K.FIEVNPGIAGR.A		K.FIEVNPGIAGR.A
708	733	4	2817.33	-0.73	1	36.7	32.2	95.00%	K.NGGGGRPHGYQSVGNIEHEEQIAQQR.H		K.NGGGGRPHGYQSVGNIEHEEQIAQQR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
307	A6ZL24_YEAS7	7.52%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
581	587	2	822.44	-0.29	1	28.6	27.9	95.00%	K.SGFPFIR.L		K.SGFPFIR.L
362	378	2	1655.85	0.3	0	61.5	30.5	95.00%	R.GDGTGVGDNVVNQLLAK.M		R.GDGTGVGDNVVNQLLAK.M
425	433	2	1104.62	0.26	1	31.2	28.5	95.00%	R.LQIFDIQTK.K		R.LQIFDIQTK.K
588	602	2	1561.76	-0.78	0	53.8	32	95.00%	R.LISPNELSGMSESAK.I		R.LISPNELSGMSESAK.I
603	611	2	1111.57	0.34	1	31.2	29.7	95.00%	K.IAYIDNTFR.D		K.IAYIDNTFR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
308	A6ZVV4_YEAS7	18.50%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
299	312	2	1421.83	1.8	0	44.5	22.8	95.00%	F.NKPTVLVPTTAGPK.L		R.TVVDVSADTTNPHNPIPIYTVATVFNKPTVLVPTTAGPK.L
313	327	3	1658.98	2	0	39.5	20.4	95.00%	K.LSVISIDHLPSLLPR.E		K.LSVISIDHLPSLLPR.E
274	312	4	4074.17	0.67	1	36.2	26.7	95.00%	R.TVVDVSADTTNPHNPIPIYTVATVFNKPTVLVPTTAGPK.L		R.TVVDVSADTTNPHNPIPIYTVATVFNKPTVLVPTTAGPK.L
334	348	3	1744.99	2	1	33	24.3	95.00%	F.SHDLLPSLELLPQRK.T		R.EASEFFSHDLLPSLELLPQRK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
309	A6ZWJ0_YEAS7	1.13%	100%	1

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
962	978	2	1833.01	2.2	1	93.4	24.8	95.00%	K.IITLLGMQNYAEALVGK.T		K.IITLLGMQNYAEALVGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
310	A6ZTM4_YEAS7	33.86%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	42	2	1205.63	1.5	1	48.4	30.8	95.00%	F.TDEGGYKPVLK.Y		R.EHAFQGTNDLSTVLSPSTFTDEGGYKPVLK.Y
115	127	2	1517.72	1.3	1	35.4	32.8	95.00%	K.MEGGDLEYQHVKI.-		K.MEGGDLEYQHVKI.-
13	31	2	2049.97	2.4	1	45.5	33.4	95.00%	R.EHAFQGTNDLSTVLSPSTF.T		R.EHAFQGTNDLSTVLSPSTFTDEGGYKPVLK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
311	A7A0D8_YEAS7	37.61%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	26	3	2889.31	0.014	1	39.2	33.2	95.00%	M.SSSTPFDPYALSEHDEERPQNVQSK.S	Acetyl (+42)	-.MSSSTPFDPYALSEHDEERPQNVQSK.S
57	75	3	2006.04	1.8	2	28.1	30.2	95.00%	R.LTSIEDKADNLAVSAQGFK.R		R.LTSIEDKADNLAVSAQGFK.R
11	26	2	1865.89	1.8	0	40.7	33.2	95.00%	Y.ALSEHDEERPQNVQSK.S		-.MSSSTPFDPYALSEHDEERPQNVQSK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
312	A6ZLM1_YEAS7	7.14%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	69	2	1619.83	-1.1	1	66.5	31.3	95.00%	K.ATTPNVNDPIYFLR.G		K.ATTPNVNDPIYFLR.G
6	26	3	2414.45	2.2	1	35.5	17.6	95.00%	R.LIDIVKPILPILPEVELPFEK.L		R.LIDIVKPILPILPEVELPFEK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
313	A6ZP14_YEAS7	7.85%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
581	592	2	1265.61	-0.33	1	42.6	32.5	95.00%	K.VESGLFSVDGEK.F		K.VESGLFSVDGEK.F
9	19	2	1170.69	-0.36	0	28.3	25.9	95.00%	R.AILTDEGVLIK.S		R.AILTDEGVLIK.S
593	608	2	1943.99	0.31	1	49.7	30.2	95.00%	K.FPLEPLQVEIMPMLCK.T	Carbamidomethyl (+57)	K.FPLEPLQVEIMPMLCK.T
549	558	2	1129.64	0.25	0	31.7	28.8	95.00%	R.MTPILLSLDK.G		R.MTPILLSLDK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
314	A6ZSD5_YEAS7	10.05%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
101	111	2	1246.53	-0.066	1	45.5	32.6	95.00%	R.GINFDYSGSCK.I	Carbamidomethyl (+57)	R.GINFDYSGSCK.I
90	100	2	1261.49	-0.079	1	75.5	31.5	95.00%	K.FGSMSCSSMPR.G	Oxidation (+16)/ Carbamidomethyl (+57)	K.FGSMSCSSMPR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
315	COS2_YEAST	25.07%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
157	167	2	1275.75	0.92	1	50	23.9	95.00%	R.TTLLEPFSLKK.D		R.TTLLEPFSLKK.D
102	108	2	935.49	1.7	1	31	30.5	95.00%	K.QLIQFCK.E	Carbamidomethyl (+57)	K.QLIQFCK.E
352	367	2	1985.05	0.9	1	55.4	29.1	95.00%	K.SMWPLPLNVELWPYIK.E		K.SMWPLPLNVELWPYIK.E
206	219	2	1525.81	-0.017	1	66.9	28.7	95.00%	K.SWSPVGLEDAKLPK.E		K.SWSPVGLEDAKLPK.E
19	33	3	1813.01	2.7	2	23.5	25.3	95.00%	K.QLESQKIVLPQDLFR.S		K.QLESQKIVLPQDLFR.S
25	33	2	1099.64	-0.29	1	27.9	27.1	95.00%	K.IVLPQDLFR.S		K.IVLPQDLFR.S
206	216	2	1187.58	-0.27	1	57.3	31.8	95.00%	K.SWSPVGLEDAK.L		K.SWSPVGLEDAK.L
157	166	2	1147.65	0.15	1	29.8	27.7	95.00%	R.TTLLEPFSLK.K		R.TTLLEPFSLK.K
109	132	2	2687.21	2.5	1	43.4	33.4	95.00%	K.EITENTPSSDPHDWEVVAANLNSY.L		K.EITENTPSSDPHDWEVVAANLNSYLYENNVWNTK.Y
11	18	2	893.49	-0.02	1	26.5	28.9	91.20%	K.SVDVLSFK.Q		K.SVDVLSFK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
316	B3LI68_YEAS1	6.41%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	21	3	2099.01	-0.091	1	62.7	33	95.00%	M.TDETAHPTQSASKQESAALK.Q		-.MTDETAHPTQSASKQESAALK.Q
172	192	2	2139.93	0.04	0	51	34.2	95.00%	K.ETSDSTSTSTPTPTPSTNDSK.A		K.ETSDSTSTSTPTPTPSTNDSK.A

267	286	3	2170.99	1	1	41.3	33.8	95.00%	K.SAEPEVKQETPAEEGEQGEK.G		K.SAEPEVKQETPAEEGEQGEK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
317	A6ZQX5_YEAS7	9.78%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	201	2	1115.63	-0.11	1	45.3	28	95.00%	R.FNVTVAQLPK.D		R.FNVTVAQLPK.D
50	66	2	1779.94	0.38	0	45.8	29.1	95.00%	F.SINTTPLAPPNATDIQK.F		R.ASSIFSINTTPLAPPNATDIQK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
318	A6ZYP2_YEAS7	6.96%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
367	380	3	1555.78	2.5	1	30.5	31.3	95.00%	F.RVPGVTSISCDTHK.Y	Carbamidomethyl (+57)	K.NLPLLDFRVPGVTSISCDTHK.Y
191	206	3	1884.93	1.7	1	25.5	31.7	91.80%	K.YCVANQLHPDVFPAVR.K	Carbamidomethyl (+57)	K.YCVANQLHPDVFPAVR.K
569	579	2	1250.73	0.15	1	33.6	21.5	95.00%	K.LIVGFLDALYK.L		K.LIVGFLDALYK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
319	A6ZQG2_YEAS7	10.35%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
126	142	2	1758.8	1.7	1	61.4	33.4	95.00%	F.LNHGGEASPCLGNALSY.A	Carbamidomethyl (+57)	K.TADNVTFLNHGGEASPCLGNALSYASSNGTGSASEATVLADGTLISSDQEYIIYSNVSCPK.S
233	240	2	950.53	1.7	0	35.6	25.2	95.00%	W.LLNDHIAR.T		K.NSSSIGYYDLPAIWLLNDHIAR.T
279	294	2	1764.84	2.1	1	57.5	33.1	95.00%	F.HTFQGIEDLGTGIQSY.G		K.NHLYSTFHTFQGIEDLGTGIQSYGYITR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
320	A7A0W1_YEAS7	10.14%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	19	2	2263.11	0.41	1	89.6	31.9	95.00%	-.MDLVLEVADHYVLDDLYAK.V	Acetyl (+42)	-.MDLVLEVADHYVLDDLYAK.V
1	11	2	1345.63	2.6	1	47.8	33.1	95.00%	-.MDLVLEVADHY.V	Acetyl (+42)	-.MDLVLEVADHYVLDDLYAK.V
345	362	2	2121.91	2.1	2	50.8	34.7	95.00%	K.EVEGDDNDRIYENDPNTK.K		K.EVEGDDNDRIYENDPNTK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
321	MKAR_YEAST	9.51%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
116	129	2	1592.8	1.3	2	53.5	32.1	95.00%	K.ILAIDIAEDKESNY.E		K.ILAIDIAEDKESNYESIK.E
116	133	3	2050.05	1.2	2	47.7	30.6	95.00%	K.ILAIDIAEDKESNYESIK.E		K.ILAIDIAEDKESNYESIK.E
64	78	2	1587.73	1.8	2	64.6	33.6	95.00%	K.YCAITGASDGIGKEF.A	Carbamidomethyl (+57)	K.YCAITGASDGIGKEFAR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
322	A6ZP65_YEAS7	20.89%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	19	2	1889.93	1.6	0	45.3	32.4	95.00%	M.SAEPLLPTHNGSQGGEVR.S	Acetyl (+42)	-.MSAEPLLPTHNGSQGGEVR.S
160	172	2	1519.79	2	1	50.5	30.7	95.00%	R.SVGFTEQEIELLR.Q		R.SVGFTEQEIELLR.Q
87	116	3	3269.47	-0.21	1	38.3	32.2	95.00%	K.IAEELTHYFDTANNSNVATGTSVAPEQNNY.Y		K.IAEELTHYFDTANNSNVATGTSVAPEQNNYYIHCIIGTEELTQAELANEDLK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
323	A6ZXE1_YEAS7	29.17%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
13	26	3	1585.9	0.2	1	59	25.1	95.00%	K.SKEQLASQLVDLKK.E		K.SKEQLASQLVDLKK.E
91	103	3	1450.77	0.14	2	65.3	30.3	95.00%	R.ALTKFEASQVTEK.Q		R.ALTKFEASQVTEK.Q
36	43	2	896.54	0.19	0	23.6	18.5	93.00%	K.LSRPSLPK.I		K.LSRPSLPK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
324	A6ZUX1_YEAS7	5.01%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
632	641	2	1274.6	2.5	2	31.4	32.2	93.70%	K.MSYKDFPQLF.N		K.MSYKDFPQLFNGGQATDR.V
472	489	2	1832.91	-0.6	1	62.2	31.9	95.00%	R.TAYSSPSVVLPSQTPDGK.L		R.TAYSSPSVVLPSQTPDGK.L
490	497	2	961.52	0.18	1	41.7	28.3	95.00%	K.LALIDDFR.E		K.LALIDDFR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
325	A6ZXQ3_YEAS7	14.16%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
91	102	2	1261.69	2	1	46.7	28.5	95.00%	F.SYVEPVLVASAK.G		K.NPLFSYVEPVLVASAK.G
87	102	2	1732.94	1.1	1	69.5	28.3	95.00%	K.NPLFSYVEPVLVASAK.G		K.NPLFSYVEPVLVASAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
326	A6ZKM8_YEAS7	7.00%	99%	1

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
165	178	2	1550.76	-1	1	34.9	32.4	95.00%	R.LYACISSRPGQSGR.C	Carbamidomethyl (+57)	R.LYACISSRPGQSGR.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
327	A7A0U9_YEAS7	15.45%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
535	554	2	2285.18	1.4	1	49.4	29.4	95.00%	R.MIEIMLPVFDAPQNLVEQAK.L		R.MIEIMLPVFDAPQNLVEQAK.L
234	249	2	1776.95	1.3	1	65.3	28.6	95.00%	K.LIDLTQFPAFVTPMGK.G		K.LIDLTQFPAFVTPMGK.G
259	273	2	1595.86	-0.25	1	40.5	28.8	95.00%	R.YGGVYVGTLSKPEVK.E		R.YGGVYVGTLSKPEVK.E
155	179	3	2741.51	-0.39	1	35.6	22	95.00%	R.TTYVTQRPVYLGLPANLVDLNVPAK.L		R.TTYVTQRPVYLGLPANLVDLNVPAK.L
199	209	2	1212.74	3	0	30.3	22.5	95.00%	K.EVIDTILALVK.D		K.EVIDTILALVK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
328	A6ZKK0_YEAS7	5.11%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
198	207	2	1149.57	1.8	0	49.3	31.5	95.00%	Y.CTNESIVSLK.F	Carbamidomethyl (+57)	K.HDSSLQIWDMNYHDDSHETINPMFSYCTNESIVSLK.F
32	45	2	1601.78	1.4	1	62	32.3	95.00%	Y.KVDPENESDESIIK.L		R.DEVTHYKVDPENESDESIIK.L
923	938	3	1706.79	-0.47	1	37.7	33	95.00%	K.FNTGSSEAQAADEKPR.H		K.FNTGSSEAQAADEKPR.H
356	368	3	1523.67	2.1	1	35.4	33.3	95.00%	F.VSSVHDTNTMYDR.V		R.DIAADDDNEMNIENLFVSSVHDTNTMYDR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
329	A7A0F5_YEAS7	14.90%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
161	183	3	2562.32	1.9	0	47.3	29.2	95.00%	F.INQQQQLLEQDSHLGALSQSIGR.T		K.DEPLQSQLQSLSQPQPPQPMVSNQELFINQQQQLLEQDSHLGALSQSIGR.T
6	20	2	1777.87	-0.23	1	85.9	32.6	95.00%	K.LGYELDQLSDLVEER.T		K.LGYELDQLSDLVEER.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
330	A6ZZF9_YEAS7	4.24%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
403	417	3	1853.93	2.2	1	27.1	31.8	94.40%	K.SHSHYLEEIETLIQR.I		K.SHSHYLEEIETLIQR.I
145	156	2	1337.67	2.4	1	45.7	32.2	95.00%	Y.SFGSPDILPMFK.D		K.SNPVNFDSFFNQSTHTYSFGSPDILPMFK.D
243	254	2	1444.78	1.9	1	42.8	29.1	95.00%	K.YIDDQIPILIDK.V		K.YIDDQIPILIDK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
331	A6ZLK4_YEAS7	17.59%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
153	162	2	1171.55	-0.19	1	36	31.7	95.00%	K.TGYNFDTLNK.I		K.TGYNFDTLNK.I
163	174	2	1372.8	2	1	34.5	24.2	95.00%	K.IIISLVPESQFK.T		K.IIISLVPESQFK.T
112	124	2	1389.76	1.4	2	32.5	29.1	95.00%	R.AQGTQVILVGNKY.D		R.AQGTQVILVGNKYDLVCEEHSGEVTIPAELQGLPYVAVSAK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
332	A6ZLW3_YEAS7	39.32%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
100	117	2	1975.93	1.4	1	58.7	33.7	95.00%	R.NTGSIEHTMENIFAGKLD.-		R.NTGSIEHTMENIFAGKLD.-
32	59	3	2885.4	-0.63	0	63.6	31.6	95.00%	R.TVQDAKPAPSVATNDPSPEPVPSAPEER.V		R.TVQDAKPAPSVATNDPSPEPVPSAPEER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
333	A7A1T7_YEAS7	11.41%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
253	263	2	1193.67	2.1	0	41.5	24.9	95.00%	Y.ANAPIEEKPLI.-		R.SRPTVIYANAPIEEKPLI.-
38	49	2	1469.69	-0.39	1	52.5	32.9	95.00%	K.IYCAELDLSQMK.V	Carbamidomethyl (+57)	K.IYCAELDLSQMK.V
246	263	2	2010.11	-0.86	1	74.1	24.5	95.00%	R.SRPTVIYANAPIEEKPLI.-		R.SRPTVIYANAPIEEKPLI.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
334	A6ZUK0_YEAS7	5.30%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
161	174	3	1572.72	2	2	31.3	33.6	95.00%	Y.DRGEFHGVDTPTDK.F		K.GDTTTYDRGEFHGVDTPTDK.F
80	91	2	1241.6	-0.73	1	67.2	31.9	95.00%	K.YGSDGLSMTLAK.R		K.YGSDGLSMTLAK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
335	A6ZS93_YEAS7	6.54%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
129	144	3	1823.92	1.9	1	32.6	31.4	95.00%	F.EHRPSILDGSVNEPFK.T		R.QGSSNFISYFDDMSFEHRPSILDGSVNEPFK.T
27	39	2	1523.71	1.8	2	38.9	32.8	95.00%	K.RQSITVDDEGELY.G		K.RQSITVDDEGELYGLDTSGNSPANEHTATTITQNHSVVASNGDVAFIPGTATEGNTEIVTEEVIETDDNMFK.T
387	399	2	1449.7	1.7	0	68.6	32.5	95.00%	F.ELSSQSLSDQTQK.F		K.SCEFCSFELSSQSLSDQTQK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
336	A6ZRM1_YEAS7	10.27%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
424	442	2	1968.95	-0.22	1	37.4	32.9	95.00%	K.SGFDGLLPGDFPESGSIFK.K		K.SGFDGLLPGDFPESGSIFK.K
468	482	2	1780.91	1.8	1	58.7	30.6	95.00%	R.CDYFIDIVAPINLTK.D	Carbamidomethyl (+57)	R.CDYFIDIVAPINLTK.D
393	402	2	1071.55	0.29	0	43.8	28.8	95.00%	K.APVVNVCTGR.E	Carbamidomethyl (+57)	K.APVVNVCTGR.E
497	509	2	1394.65	-0.93	1	74.5	32.6	95.00%	K.LACAAFIDGENSK.I	Carbamidomethyl (+57)	K.LACAAFIDGENSK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
337	A6ZYD0_YEAS7	10.07%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
408	417	2	1191.52	0.069	1	50.1	32.2	95.00%	K.MDDPTVNWSK.E		K.MDDPTVNWSK.E
485	497	2	1421.79	-0.16	1	24.8	27.1	91.50%	R.HINAPFMLPIAAK.M		R.HINAPFMLPIAAK.M
83	98	2	1774.82	0.85	1	74.5	33.7	95.00%	Y.NPQGGYQQQFNPQGGR.G		R.YQGYQAYNAQAQPAGGYYQNYQGYSGYQQGGYQQYNPDAGYQQQYNPQGGYQQYNPQGGYQQQFNPQGGR.G
36	49	2	1543.67	0.98	1	37.2	33.3	95.00%	Y.NAQAQPAGGYYQNY.Q		R.YQGYQAYNAQAQPAGGYYQNYQGYSGYQQGGYQQYNPDAGYQQQYNPQGGYQQYNPQGGYQQQFNPQGGR.G
17	32	2	1855.78	-1	2	43	34	95.00%	Y.SQNGNQQQGNNRYQGY.Q	Deamidation (+1)	-.MSDSNQGNNQQNYQQYSQNGNQQQGNNRYQGYQAYNAQAQPAGGYYQNYQGYSGYQQGGYQQYNPDAGYQQQYNPQGGYQQYNPQGGYQQQFNPQGGR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
338	SEC31_YEAST	3.22%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
747	760	2	1385.71	-0.23	0	35.2	30	95.00%	K.SLPAQNPATATTSK.A		K.SLPAQNPATATTSK.A
505	516	2	1275.67	1.8	0	49.8	30.5	95.00%	F.SLSGNIEQTISK.N		K.EDDGEEFFQQIETNFQPEGDFSLSGNIEQTISK.N
811	825	2	1494.77	3.3	0	78.3	30.7	95.00%	Y.VPATTTSAPVHTEGK.Y		K.NVPVLPTPGMPSTTSIPSMQAPFYGMTPGASANALPPKPYVPATTTSAPVHTEGK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
339	A7A0E2_YEAS7	5.39%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
544	561	2	2057.02	0.38	1	98.8	31.7	95.00%	R.TSSLVEELGQIEYIFSDK.T		R.TSSLVEELGQIEYIFSDK.T
78	88	2	1333.5	1.4	1	44.3	31.8	95.00%	F.MSNNHDDQTSW.N		K.VTNSHANANYIPPSHVLPEETIDLDADDDNIENDVHENPFMSNNHDDQTSWNANR.F
334	346	2	1416.71	1.1	0	57.7	31.7	95.00%	Y.IETANLDGETNLK.I		K.SEEPIPADTIILSSSEPEGLCYIETANLDGETNLK.I
800	830	4	3299.8	1.3	1	20.6	23	95.00%	K.NLILIGATAIEDKLQDGVPETIHTLQEAGIK.I		K.NLILIGATAIEDKLQDGVPETIHTLQEAGIK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
340	A6ZSH5_YEAS7	15.49%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	47	2	1535.8	-0.51	1	55.6	30.3	95.00%	K.YSTVVISCEPIIR.Q	Carbamidomethyl (+57)	K.YSTVVISCEPIIR.Q
17	34	2	1906.87	0.88	1	69.2	33.4	95.00%	Y.GQPASSQDGNAFIPEDFK.Y		-.MSGPPPPYEEQSSHLYGQPASSQDGNAFIPEDFK.Y
2	16	2	1728.77	2.1	1	40.3	33.3	95.00%	M.SGPPPPYEEQSSHLY.G	Acetyl (+42)	-.MSGPPPPYEEQSSHLYGQPASSQDGNAFIPEDFK.Y
34	47	3	1663.9	2.6	2	45.1	27	95.00%	F.KYSTVVISCEPIIR.Q	Carbamidomethyl (+57)	-.MSGPPPPYEEQSSHLYGQPASSQDGNAFIPEDFKYSTVVISCEPIIR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
341	A6ZT43_YEAS7	12.45%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
428	443	2	1935.9	-0.51	1	53.1	33.5	95.00%	K.LDPTSYEAYQHQTQQK.Y		K.LDPTSYEAYQHQTQQK.Y
457	478	3	2805.42	1.8	0	61.2	30	95.00%	K.LQEQQLQEQQLQQQQQQQQQLR.A		K.LQEQQLQEQQLQQQQQQQQQLR.A
479	499	2	2212.06	-1.3	1	79.8	32.4	95.00%	R.ATGQPPSQPQAQTQSQQFGAR.Y		R.ATGQPPSQPQAQTQSQQFGAR.Y
360	367	2	958.49	-0.13	1	37.6	29.6	95.00%	R.GWDLNINK.K		R.GWDLNINK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
342	B3LMC0_YEAS1	3.01%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
199	207	2	1033.59	0.65	1	24.5	26.5	92.00%	R.ILLFNTTGR.N		R.ILLFNTTGR.N
933	943	2	1290.76	0.056	1	49.3	23.5	95.00%	R.LTLDIPVVFFK.C		R.LTLDIPVVFFK.C
607	617	2	1253.55	0.22	1	38.6	32.6	95.00%	R.DTTGDFSENIR.T		R.DTTGDFSENIR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
343	A7A105_YEAS7	8.36%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
310	327	2	2041.97	-0.74	1	60.3	33.3	95.00%	K.TQEIDPTGMSDVFAYIQK.K		K.TQEIDPTGMSDVFAYIQK.K
187	197	2	1319.74	2.1	1	51.3	27.1	95.00%	K.YLSLNDIELLK.T		K.YLSLNDIELLK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
344	A6ZTY9_YEAS7	18.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	110	2	1424.66	1.3	1	49.4	32.9	95.00%	Y.CFLNENTGIETK.D	Carbamidomethyl (+57)	K.GHFQYCFLNENTGIETK.D
80	93	2	1517.73	-1	1	83	32.8	95.00%	R.DTSHGEITLSAPYK.G		R.DTSHGEITLSAPYK.G
145	156	3	1477.78	0.076	2	36.3	30.5	95.00%	R.EVKDEQSYIVIR.E		R.EVKDEQSYIVIR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
345	A6ZTG2_YEAS7	15.23%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

26	48	2	2504.21	0.32	0	95.2	32.6	95.00%	K.LTSAAQSNPNDEQMSTIESLIQK.I		K.LTSAAQSNPNDEQMSTIESLIQK.I
6	25	3	2124.02	-0.046	1	62.1	33	95.00%	K.LISEAESHFSQGNHAEAVAK.L		K.LISEAESHFSQGNHAEAVAK.L
68	84	2	1643.73	-0.011	1	85.3	34	95.00%	R.AAGGGSSFMNTLMADSK.G		R.AAGGGSSFMNTLMADSK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
346	A6ZX25_YEAS7	20.23%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
161	173	2	1340.74	-0.077	1	38.8	27.1	95.00%	R.RTGQVGVPTISQV.-		R.RTGQVGVPTISQV.-
95	116	3	2382.06	-0.48	1	76.3	33.9	95.00%	R.AHSCNNSSYVDSNKITQGSGTR.C	Carbamidomethyl (+57)	R.AHSCNNSSYVDSNKITQGSGTR.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
347	A6ZZV9_YEAS7	32.99%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
38	60	2	2445.15	2	1	101	33.3	95.00%	R.AVSDSSVINQMTDSLGSMFTDIK.N		R.AVSDSSVINQMTDSLGSMFTDIK.N
29	37	2	1057.52	-0.3	0	34.9	31.4	95.00%	R.NINQEIGDR.A		R.NINQEIGDR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
348	A6ZQL2_YEAS7	9.32%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
172	188	3	2034.06	0.054	2	60	29.9	95.00%	R.HETKDPVVNNTHIIVYR.E		R.HETKDPVVNNTHIIVYR.E
160	171	2	1329.74	-0.24	1	64.3	28	95.00%	K.VFGINLNDLVAR.H		K.VFGINLNDLVAR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
349	A6ZRC2_YEAS7	3.44%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
732	749	2	2001.97	0.54	1	54	32.6	95.00%	R.ALSGNSQFYPEEVTFVSK.E		R.ALSGNSQFYPEEVTFVSK.E
872	880	2	980.49	0.49	1	32.2	31.2	95.00%	K.GADSIIYSR.L		K.GADSIIYSR.L
357	383	3	2923.36	2	1	44.4	32.8	95.00%	R.VSADYGRPSLDYDNLEQGAGEANIVDR.S		R.VSADYGRPSLDYDNLEQGAGEANIVDR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
350	A6ZQP1_YEAS7	2.19%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
621	634	2	1689.9	1.6	1	31.3	29.7	95.00%	K.TDLIFDQVRDILDK.L		K.TDLIFDQVRDILDK.L
621	629	2	1105.58	0.072	1	35.8	31.2	95.00%	K.TDLIFDQVR.D		K.TDLIFDQVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
351	A6ZSN7_YEAS7	23.14%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
7	21	2	1883.96	-1.3	1	82	30.7	95.00%	K.EKVEEQEQQQQQIIK.I		K.EKVEEQEQQQQQIIK.I
90	101	2	1386.78	1.3	1	47	27.4	95.00%	R.YIDLEAPVQIVK.R		R.YIDLEAPVQIVK.R
89	101	2	1542.88	1.5	2	34.4	25.6	95.00%	K.RYIDLEAPVQIVK.R		K.RYIDLEAPVQIVK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
352	A6ZMK2_YEAS7	18.88%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
31	45	2	1635.92	-0.56	0	70.5	24.1	95.00%	K.VNGSPITLVEPEILR.F		K.VNGSPITLVEPEILR.F
48	59	2	1357.79	2.7	1	50.4	24.4	95.00%	K.VYEPLLLVGLDK.F		K.VYEPLLLVGLDK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
353	A6ZY37_YEAS7	6.07%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
378	392	2	1557.69	-0.52	1	72	33.3	95.00%	R.SSSPSSSFTVSSNER.S		R.SSSPSSSFTVSSNER.S
320	336	2	1848.74	1.9	1	36.5	34.1	95.00%	R.FSNAGGFTMHNNDSSTF.K	Oxidation (+16)	R.FSNAGGFTMHNNDSSTFK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
354	CSG2_YEAST	10.49%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
78	90	2	1540.67	-1.2	1	67.6	33.6	95.00%	K.MRPMFVSDSDSNR.N		K.MRPMFVSDSDSNR.N

91	120	3	3347.46	-0.087	1	95.6	32.7	95.00%	R.NSQFDNNNSGSVTNEDVDTFSHVLDDPQPR.I		R.NSQFDNNNSGSVTNEDVDTFSHVLDDPQPR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
355	A6ZRQ9_YEAS7	3.93%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
622	633	2	1376.68	-0.3	1	90.1	31.5	95.00%	R.NTVQNNSQGFLR.E		R.NTVQNNSQGFLR.E
557	569	2	1468.65	-0.42	1	35.3	32.8	95.00%	R.NVTAMNGSFQNMR.S		R.NVTAMNGSFQNMR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
356	A6ZZM1_YEAS7	13.81%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	139	2	1544.78	-1.2	0	63.9	30.8	95.00%	K.QSDDATGVAIRPTSK.S		K.QSDDATGVAIRPTSK.S
32	49	2	1945.93	0.31	1	90	32.8	95.00%	R.SGSDLQYLSVYSDNGTLK.L		R.SGSDLQYLSVYSDNGTLK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
357	A6ZV67_YEAS7	13.79%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
36	49	2	1512.81	-0.46	0	72.5	28.4	95.00%	K.VLEQLSGQTPVQSK.A		K.VLEQLSGQTPVQSK.A
73	82	2	1140.61	-0.21	1	30	28.3	95.00%	R.GPKAEEILER.G		R.GPKAEEILER.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
358	B3LH47_YEAS1	5.14%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
438	453	2	1904.95	1.8	1	51.5	31.8	95.00%	Y.HQQAIPQQQLPSQQQF.A		K.SLYVAENDETVPVPFPIEQQSYHQQAIPQQQLPSQQQFAIPPQQHHPQFMVPPSHQQQQAYPPPQMPSQQGYPPQQEHFMAMPPGQSQPQY.-
336	345	2	1176.62	0.52	0	34.8	30.7	95.00%	R.TLVCSDLLTR.G	Carbamidomethyl (+57)	R.TLVCSDLLTR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
359	A6ZYT9_YEAS7	14.23%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
61	76	2	1790.78	1.3	1	71.8	34.6	95.00%	R.SLTDDFGSNVHEPNPY.L		R.SLTDDFGSNVHEPNPYLGNIDEEPDLYYHDEEDGELSR.T
127	147	3	2415	-0.27	2	33.4	34.5	95.00%	R.RYSSVCNSDNEEASQSNTPDR.I	Carbamidomethyl (+57)	R.RYSSVCNSDNEEASQSNTPDR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
360	B3LQX5_YEAS1	7.25%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
111	125	2	1631.78	1.4	1	57.1	32.8	95.00%	F.ASPGGFDDEIVLQER.E		K.HSGILLDSSFASPGGFDDEIVLQER.E
268	277	2	1117.53	-0.096	1	35.7	31.2	95.00%	K.YSIAYESTGK.L		K.YSIAYESTGK.L
470	486	3	1936.01	0.83	1	32.4	30.3	95.00%	R.ITAQTSKPLWSVGTYER.I		R.ITAQTSKPLWSVGTYER.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
361	A6ZRP5_YEAS7	3.98%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
102	128	3	3130.44	1.3	1	41.3	32.3	95.00%	R.QRPPPATAEYNDVFNTNSQQLPSEHQY.N		R.QRPPPATAEYNDVFNTNSQQLPSEHQYNNVPSYPLPSINVIQTTPELIHNGSQTMATPIERPFFNENDYYYNNR.N
116	128	2	1544.69	2.1	1	41	33.9	95.00%	F.NTNSQQLPSEHQY.N		R.QRPPPATAEYNDVFNTNSQQLPSEHQYNNVPSYPLPSINVIQTTPELIHNGSQTMATPIERPFFNENDYYYNNR.N
76	93	2	2051.85	1.7	2	44.2	34	95.00%	Y.NGDDGNNNTINDNERDIY.G		R.YTNQNASMGSFTPVQSLQFPEQSQQTNMLYNGDDGNNNTINDNERDIYGGFVNHHR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
362	A7A0B5_YEAS7	8.05%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
133	149	2	1902.98	-1.1	1	71.7	30.4	95.00%	K.QFPGIAYTIPDLDAQVR.V		K.QFPGIAYTIPDLDAQVR.V
99	117	2	2080.01	-0.46	1	80.3	32.8	95.00%	K.TFDLCSLGQVSLCPLSAGR.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.TFDLCSLGQVSLCPLSAGR.I
736	762	3	2867.4	-0.55	1	28.8	31.7	95.00%	R.TNLAPNNTSTSSLMKPESSLYLGNSNK.S		R.TNLAPNNTSTSSLMKPESSLYLGNSNK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
363	A6ZZI1_YEAS7	11.50%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
489	514	4	3071.33	0.041	2	46.5	33.2	95.00%	R.RVFSTSAIDEDNENEHQDDTEDQIHK.E		R.RVFSTSAIDEDNENEHQDDTEDQIHK.E
460	485	3	2820.26	-1.6	1	67.2	33.5	95.00%	R.THSADRSPLSVQADEADEVHNADNSR.F		R.THSADRSPLSVQADEADEVHNADNSR.F
84	94	3	1373.69	0.0054	1	34.6	31.2	95.00%	R.TEDNYILTLHR.I		R.TEDNYILTLHR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
364	A6ZMQ5_YEAS7	14.00%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
87	98	2	1345.67	-0.54	0	60	31.5	95.00%	K.VEEMNNIIAASR.R		K.VEEMNNIIAASR.R
85	98	2	1544.8	0.37	1	78.1	30.8	95.00%	K.AKVEEMNNIIAASR.R		K.AKVEEMNNIIAASR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
365	A6ZWB1_YEAS7	16.82%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
100	107	2	965.52	0.19	1	36.2	29	95.00%	R.IFLYPSNI.-		R.IFLYPSNI.-
22	31	2	1096.62	-0.015	0	27.1	24.5	95.00%	R.VNNPNVSLIK.I		R.VNNPNVSLIK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
366	A6ZV22_YEAS7	18.60%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
30	39	2	1082.68	-0.2	1	24	19.9	93.50%	R.RVLLSAPLSK.E		R.RVLLSAPLSK.E
49	62	3	1649.96	1.8	1	29.4	21.6	95.00%	K.ALPIRRDDEVLVVR.G		K.ALPIRRDDEVLVVR.G
31	39	2	926.58	1.2	0	27.3	20.8	95.00%	R.VLLSAPLSK.E		R.VLLSAPLSK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
367	A7A1Q4_YEAS7	3.54%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
6	13	2	977.56	2.7	1	50.8	27.9	95.00%	R.VLDLFKPF.E		R.VLDLFKPFESFLPEVIAPER.K
17	25	2	1022.58	2.2	0	39.5	26.7	95.00%	F.LPEVIAPER.K		R.VLDLFKPFESFLPEVIAPER.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
368	A6ZXV4_YEAS7	12.84%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
298	319	4	2664.4	-0.61	1	17.3	27.4	90.60%	R.IKPLEQLTLEPYERDHCIVVGR.Y	Carbamidomethyl (+57)	R.IKPLEQLTLEPYERDHCIVVGR.Y
232	251	3	2235.05	2.7	1	33.4	32.8	95.00%	R.MLIGMVDCVFADVAQPDQAR.I	Carbamidomethyl (+57)	R.MLIGMVDCVFADVAQPDQAR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
369	AKR2_YEAST	7.21%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
212	222	2	1252.58	-0.82	1	30.3	32.6	91.50%	K.FGSTVAWTDNR.G		K.FGSTVAWTDNR.G
270	283	3	1699.81	1.7	1	27.6	33.2	93.00%	K.SLFEQALQHHGYDR.L		K.SLFEQALQHHGYDR.L
610	638	3	3037.45	-0.46	0	28.3	31.8	95.00%	K.GVEDSDMIPEGPSATTITHTISIDGLEPR.N		K.GVEDSDMIPEGPSATTITHTISIDGLEPR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
370	A6ZYY3_YEAS7	34.55%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	62	2	1400.75	-1.1	1	58.9	29.1	95.00%	K.GSLEEIIAEGQKK.F		K.GSLEEIIAEGQKK.F

39	49	2	1201.65	-0.6	0	54.5	28.8	95.00%	R.INELLSSLEGK.G		R.INELLSSLEGK.G
25	49	3	2613.36	2.8	1	46.6	27.7	95.00%	K.AVVESVGAEVDEARINELLSSLEGK.G		K.AVVESVGAEVDEARINELLSSLEGK.G
39	61	3	2456.31	1.8	1	27.3	26.7	95.00%	R.INELLSSLEGKGSLEEIIAEGQK.K		R.INELLSSLEGKGSLEEIIAEGQK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
371	A6ZMK8_YEAS7	14.69%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
118	128	2	1185.64	-0.019	0	55.5	29.5	95.00%	K.LDAALLQEASR.S		K.LDAALLQEASR.S
80	90	2	1209.71	3	0	31.3	21.8	95.00%	F.QNTLLIGLPNK.N		R.IGIDETVPTTITVEDPNEVIQVNFAIESTNKPFQNTLLIGLPNK.N
71	79	2	1005.52	1.9	1	29.8	30.8	93.60%	F.AIESTNKPF.Q		R.IGIDETVPTTITVEDPNEVIQVNFAIESTNKPFQNTLLIGLPNK.N
91	101	2	1319.64	-0.18	1	38.5	31.4	95.00%	K.NLEMAFEPEIK.D		K.NLEMAFEPEIK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
372	A6ZT81_YEAS7	10.76%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
244	255	2	1372.63	0.29	1	60.6	32.9	95.00%	K.IGLDCASSEFFK.D	Carbamidomethyl (+57)	K.IGLDCASSEFFK.D
313	330	2	1853.99	1.9	0	53.3	27.7	95.00%	K.TAGIQIVADDLTVTNPAR.I		K.TAGIQIVADDLTVTNPAR.I
376	392	2	1820.92	1.9	1	48.7	31.7	95.00%	R.SGETEDTFIADLVVGLR.T		R.SGETEDTFIADLVVGLR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
373	VPS41_YEAST	6.25%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
654	674	3	2239.06	-0.76	2	41	33.1	95.00%	R.IEAASEPTASSKEEGSNITYR.T		R.IEAASEPTASSKEEGSNITYR.T
156	166	2	1206.59	0.35	0	43.3	31.9	95.00%	R.SSILCINTDGK.Y	Carbamidomethyl (+57)	R.SSILCINTDGK.Y
640	653	2	1741.81	0.72	1	51.8	33.3	95.00%	K.LFSVEDFEEELETR.I		K.LFSVEDFEEELETR.I
919	934	2	1816.89	1.6	0	30.1	32.4	91.50%	R.GMSDDLQIDNLQDIIK.H		R.GMSDDLQIDNLQDIIK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
374	COS5_YEAST	24.80%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
157	167	2	1275.75	0.92	1	50	23.9	95.00%	R.TTLLEPFSLKK.D		R.TTLLEPFSLKK.D
102	108	2	935.49	1.7	1	31	30.5	95.00%	K.QLIQFCK.E	Carbamidomethyl (+57)	K.QLIQFCK.E
19	33	3	1813.01	2.7	2	23.5	25.3	95.00%	K.QLESQKIVLPQDLFR.S		K.QLESQKIVLPQDLFR.S
354	369	2	2001.08	-0.26	1	39.5	27.9	95.00%	K.SMWLLPLNVELWPYIK.E		K.SMWLLPLNVELWPYIK.E
25	33	2	1099.64	-0.29	1	27.9	27.1	95.00%	K.IVLPQDLFR.S		K.IVLPQDLFR.S
206	219	2	1553.81	-0.2	1	52.8	29.9	95.00%	K.SWSPVGLEDVQLPK.D		K.SWSPVGLEDVQLPK.D
157	166	2	1147.65	0.15	1	29.8	27.7	95.00%	R.TTLLEPFSLK.K		R.TTLLEPFSLK.K
11	18	2	893.49	-0.02	1	26.5	28.9	91.20%	K.SVDVLSFK.Q		K.SVDVLSFK.Q
109	132	2	2673.19	1.6	1	47.2	34	95.00%	K.EVTENTPSSDPHDWEVVAANLNSY.L		K.EVTENTPSSDPHDWEVVAANLNSYLYENK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
375	A6ZNT7_YEAS7	3.79%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
597	616	3	2173.09	2.6	1	26.6	31.2	94.60%	K.DGKGEEIGSTIQTLNDLIDR.S		K.DGKGEEIGSTIQTLNDLIDR.S
575	586	2	1437.65	0.4	1	59.7	33.2	95.00%	K.WNSDYEAVIADR.R		K.WNSDYEAVIADR.R
721	733	2	1549.75	-0.63	0	79.6	32.7	95.00%	R.ITLQCMDVETVNK.D	Carbamidomethyl (+57)	R.ITLQCMDVETVNK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
376	A6ZVQ4_YEAS7	7.46%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
476	499	3	2531.18	1.8	0	37.5	33.2	95.00%	Y.SINPVDGSIIGPVNEEPENDDGHK.S		K.EIFWLGQLYAGQDYSINPVDGSIIGPVNEEPENDDGHK.S
130	147	2	1981.98	2	1	104	32	95.00%	K.FYNVDGVDNTLASLLGER.L		K.FYNVDGVDNTLASLLGER.L
471	499	3	3065.39	0.56	1	66.4	32.9	95.00%	Y.AGQDYSINPVDGSIIGPVNEEPENDDGHK.S		K.EIFWLGQLYAGQDYSINPVDGSIIGPVNEEPENDDGHK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
377	A6ZTP3_YEAS7	13.21%	100%	3								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
49	61	2	1480.79	2.3	1	64.2	29.1	95.00%	R.GIITIEYFDPVSK.S		R.GIITIEYFDPVSK.S	
93	106	2	1570.77	1.8	2	35.2	32.5	95.00%	K.AVIEGKDPNDIHTY.S		K.AVIEGKDPNDIHTYSYR.K	
171	185	3	1602.81	1.8	1	26.2	31.3	93.80%	F.IITTKADGNEELDGK.S		R.LAMAYFGPDSNTSEFIITTKADGNEELDGK.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
378	A7A0L5_YEAS7	5.25%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
160	174	3	1661.78	1.5	0	46.7	33.3	95.00%	K.NADDAHTIPESHLSR.R		K.NADDAHTIPESHLSR.R	
118	137	3	2165.02	2.9	1	34.6	33.2	95.00%	Y.INTQDINHKDNGPPSASSNR.A	Deamidation (+1)	R.SSSQPSHHHSGGTNNNNNNNNNNNSNNNNGNDGGNDDDYDYEMQDYRPSPQSARPTPTYVPQYSVESGAAFPIQEVIPSAYINTQDINHKDNGPPSASSNR.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
379	YM13B_YEAST	11.11%	100%	11								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
297	307	2	1209.65	-0.019	0	43.2	29	95.00%	R.LNNNGIPINNK.V		R.LNNNGIPINNK.V	
131	159	3	3095.41	1	1	28.6	32.6	95.00%	F.TQYPQYVGTHLNTPSPESGNSFPDSSSAK.S		R.MMNTQQANISGWPVYGHPSLMPYPPYQMSPMYAPPGAQSQFTQYPQYVGTHLNTPSPESGNSFPDSSSAK.S	
987	1001	2	1640.82	-1.2	0	49.1	31.3	95.00%	R.EVDPNISESNILPSK.K		R.EVDPNISESNILPSK.K	
471	491	3	2226.08	1.6	0	89	32.9	95.00%	R.SAHHIHSASSNPDINVVDAQK.R		R.SAHHIHSASSNPDINVVDAQK.R	
1713	1730	4	2169.06	0.31	2	28.4	32.2	95.00%	R.LRDEVSGNHLHVCYIETK.K	Carbamidomethyl (+57)	R.LRDEVSGNHLHVCYIETK.K	
331	354	3	2897.27	1.7	1	59.1	33.4	95.00%	R.CIHMTVADLFSDIHSMYEEQQESK.R	Carbamidomethyl (+57)	R.CIHMTVADLFSDIHSMYEEQQESK.R	
1621	1632	2	1318.72	-0.46	1	43.7	29.1	95.00%	K.SQIGNIYLLNGK.V		K.SQIGNIYLLNGK.V	
1	24	3	2598.18	-0.31	0	74.4	33.7	95.00%	-.MESQQLSQHSPISHGSACASVTSK.E	Acetyl (+42)/ Carbamidomethyl (+57)	-.MESQQLSQHSPISHGSACASVTSK.E	
837	850	2	1517.76	1.9	0	44.1	32.1	95.00%	F.GQPVIVNDHNPNSK.I		R.QHAGLAGLDISTLLPFGQPVIVNDHNPNSK.I	
1234	1242	2	1115.51	0.078	1	55.2	31.3	95.00%	R.YDEAITYNK.D		R.YDEAITYNK.D	
958	975	2	1855.84	-0.6	0	47.1	34	95.00%	K.AVSPTDSTPPSTHTEDSK.R		K.AVSPTDSTPPSTHTEDSK.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
380	GAS3_YEAST	7.82%	100%	3								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
234	246	2	1513.7	2	2	36.8	33.1	95.00%	K.VNDDLDISKSDFF.G		K.VNDDLDISKSDFFGLNTYEWCSGTSSWESSGYDK.L	
293	306	2	1513.73	0.12	1	68.2	33.1	95.00%	R.TFDEVSEGLYGGLK.N		R.TFDEVSEGLYGGLK.N	
81	94	2	1580.79	-2	1	77.5	31.7	95.00%	R.DAYAFQQLGVNTVR.I		R.DAYAFQQLGVNTVR.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
381	B3LKB6_YEAS1	12.38%	100%	4								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
80	104	3	2739.45	0.18	1	28.2	26.7	95.00%	K.IFPEEYTLETPTGLVPVATLHSIGR.T		K.IFPEEYTLETPTGLVPVATLHSIGR.T	
65	77	2	1308.67	-0.63	0	42.4	31.5	95.00%	K.APVPDVNAPQSSK.N		K.APVPDVNAPQSSK.N	
380	396	2	1926.83	-0.36	0	86.5	34.2	95.00%	K.IMTEQEAQGVSMGEMMR.A		K.IMTEQEAQGVSMGEMMR.A	
116	137	2	2305.98	1.3	0	102	34.3	95.00%	R.QIDGASSPSSNEDALESDNNEK.G		R.QIDGASSPSSNEDALESDNNEK.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
382	A6ZTH2_YEAS7	30.60%	100%	3								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
66	78	2	1521.7	-0.74	1	34.9	33.5	95.00%	R.NFDIISENSNDVR.G		R.NFDIISENSNDVR.G	

50	65	3	1801.82	0.28	1	47.4	33.7	95.00%	R.LNDSFADDLENGLHSR.N		R.LNDSFADDLENGLHSR.N
91	102	2	1466.63	-0.63	1	52	33.4	95.00%	K.QIMENDNVDFDK.A		K.QIMENDNVDFDK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
383	A6ZVF2_YEAS7	12.79%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	41	2	1185.56	0.35	1	69.8	32.3	95.00%	R.NGYLVYACAR.R	Carbamidomethyl (+57)	R.NGYLVYACAR.R
170	181	3	1439.77	0.62	1	26.9	28.2	95.00%	R.GLHLEMKPFNVR.V		R.GLHLEMKPFNVR.V
182	197	2	1556.84	1.9	0	84.3	28.9	95.00%	R.VINAITGGVATDIADK.R		R.VINAITGGVATDIADK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
384	YNS1_YEAST	6.39%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	16	2	1582.86	7.2	0	89.8	27.8	95.00%	M.PLNIIGTALLDGTDK.I	Acetyl (+42)/ Deamidation (+1)	-.MPLNIIGTALLDGTDK.I
113	123	3	1432.71	-0.67	1	28.7	31.5	95.00%	K.CDLSNLWEIRK.F	Carbamidomethyl (+57)	K.CDLSNLWEIRK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
385	A6ZMV1_YEAS7	11.14%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
188	201	2	1563.78	-1.6	1	69.1	31.7	95.00%	K.NTVSNACLFQIAAR.L	Carbamidomethyl (+57)	K.NTVSNACLFQIAAR.L
324	336	2	1422.74	1.2	1	40.3	31	95.00%	R.MLGLTSVMAPFTR.D		R.MLGLTSVMAPFTR.D
377	400	3	2679.37	0.9	1	25.2	28.9	95.00%	Y.GLGEQMSALEVIQNLLIHDRPAPY.K	Oxidation (+16)	K.QTNDGYYGLGEQMSALEVIQNLLIHDRPAPYK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
386	A6ZXK9_YEAS7	14.77%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	86	3	2309.04	1.6	1	66.2	33.8	95.00%	K.FDLKDTEESLGHDSASASSASR.K		K.FDLKDTEESLGHDSASASSASR.K
69	86	2	1805.77	-0.4	0	68.2	34.1	95.00%	K.DTEESLGHDSASASSASR.K		K.DTEESLGHDSASASSASR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
387	A7A281_YEAS7	14.58%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
161	169	2	1137.55	-0.076	1	32.7	32.7	94.80%	R.IENFISQCK.Q	Carbamidomethyl (+57)	R.IENFISQCK.Q
232	243	2	1349.68	-0.31	1	37	31	95.00%	R.IPASVWNMTFGK.S		R.IPASVWNMTFGK.S
204	225	3	2325.2	1.2	0	24.9	28.7	95.00%	Y.VVEPDGSETLISPDTLDKPSVK.N		R.FSDVYVVEPDGSETLISPDTLDKPSVK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
388	A6ZNC5_YEAS7	6.90%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
277	287	2	1354.6	-0.7	1	65.5	33.1	95.00%	K.CCSDVFNQVVK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CCSDVFNQVVK.S
320	332	2	1446.8	1.9	1	44.2	28	95.00%	K.VVGLSTLPEIYEK.M		K.VVGLSTLPEIYEK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
389	A6ZKR7_YEAS7	9.43%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
20	38	2	1968.01	1.3	1	111	30.7	95.00%	K.ESNFLIDFLMGGVSAAVAK.T		K.ESNFLIDFLMGGVSAAVAK.T
49	59	2	1343.71	-0.38	0	32.1	30.2	95.00%	K.LLIQNQDEMLK.Q		K.LLIQNQDEMLK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
390	A7A0G8_YEAS7	11.42%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
51	62	2	1525.72	-0.39	1	62.5	33.3	95.00%	K.AQIYDDQLQNYR.D		K.AQIYDDQLQNYR.D
108	120	2	1483.79	-0.53	1	45.6	29	95.00%	K.ICIQPEAGGWLIK.A	Carbamidomethyl (+57)	K.ICIQPEAGGWLIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
391	A6ZXK6_YEAS7	21.43%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
109	128	2	2149.08	1.3	1	85.1	31.2	95.00%	R.NVYPSVETPLLQGAAPHDNK.Q		R.NVYPSVETPLLQGAAPHDNK.Q

75	84	2	1266.56	1	1	32.7	32.6	94.80%	Y.YQQGWVDSER.N		R.NAEYVYYYQQGWVDSER.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
392	A6ZZA0_YEAS7	33.57%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
134	143	2	1156.69	-0.28	1	39.1	26.2	95.00%	K.LAEILKPVFQ.-		K.LAEILKPVFQ.-
35	45	3	1227.63	-0.39	0	27.7	30.7	95.00%	K.MVSQETVAHVK.D		K.MVSQETVAHVK.D
118	130	3	1410.75	0.075	1	42.8	28.8	95.00%	K.HIGGNSDLETLKK.N		K.HIGGNSDLETLKK.N
66	79	2	1559.86	0.12	1	37.6	28.2	95.00%	K.ATLSTLFQELNVPK.S		K.ATLSTLFQELNVPK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
393	A6ZQ50_YEAS7	51.09%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
28	36	3	1121.63	-0.17	1	28.7	26.9	95.00%	K.KLEIQQHAR.Y		K.KLEIQQHAR.Y
50	61	2	1369.56	-0.31	1	49.8	32.6	95.00%	R.GAAGIWTCSCCK.K	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GAAGIWTCSCCK.K
63	80	2	1665.87	-1	1	64.9	30.1	95.00%	K.TVAGGAYTVSTAAAATVR.S		K.TVAGGAYTVSTAAAATVR.S
37	44	2	1035.38	1.3	1	30.5	30.3	94.80%	R.YDCSFCGK.K	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.YDCSFCGK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
394	A6ZUK7_YEAS7	6.22%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
198	206	2	1134.59	-0.37	1	39	29.8	95.00%	K.IVDLIYDER.Y		K.IVDLIYDER.Y
514	529	2	1572.77	0.048	0	56.2	32	95.00%	K.NAMQAAEAAVAAATQR.A		K.NAMQAAEAAVAAATQR.A
89	97	2	1017.56	-0.22	1	29	28.5	95.00%	R.IQTGLFSPR.L		R.IQTGLFSPR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
395	A6ZMP4_YEAS7	13.90%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
54	66	2	1584.79	-0.19	1	45.2	31.8	95.00%	R.YENIINQIDAQHK.D		R.YENIINQIDAQHK.D
44	53	2	1100.59	-1.2	0	72.2	29.9	95.00%	K.INSINANLSR.Y		K.INSINANLSR.Y
238	255	3	1966.9	-0.8	0	41.7	34.1	95.00%	K.NVEDAQQDVEQGVGHTNK.A		K.NVEDAQQDVEQGVGHTNK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
396	A6ZKL0_YEAS7	23.85%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	90	3	2060.1	0.34	1	33.9	28.1	95.00%	K.TFLVANVKDLETLTMHTK.T		K.TFLVANVKDLETLTMHTK.T
81	90	2	1187.59	-0.18	0	28.9	31.7	90.50%	K.DLETLTMHTK.T		K.DLETLTMHTK.T
91	103	2	1387.71	-0.66	1	73.9	31	95.00%	K.TYAAEIAHNISAK.N		K.TYAAEIAHNISAK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
397	A6ZM77_YEAS7	5.02%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
362	370	2	1112.63	-0.56	1	41.1	26.7	95.00%	K.IREEQLAVR.N		K.IREEQLAVR.N
284	301	3	2013.92	-0.76	1	42	34.2	95.00%	K.DHIAAGGKPVCVMDAWCK.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.DHIAAGGKPVCVMDAWCK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
398	A6ZU48_YEAS7	6.45%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
79	92	2	1523.69	-1.4	1	49.3	32.8	95.00%	K.SCGVDAMSVDDLKK.L	Carbamidomethyl (+57)	K.SCGVDAMSVDDLKK.L
79	91	2	1395.6	-0.56	0	57.3	32.5	95.00%	K.SCGVDAMSVDDLK.K	Carbamidomethyl (+57)	K.SCGVDAMSVDDLK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
399	A6ZW48_YEAS7	3.58%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
122	135	2	1532.69	-0.73	0	58.9	34	95.00%	K.NIGDNENTATEVEK.A		K.NIGDNENTATEVEK.A
500	514	2	1846.9	-0.12	1	43.9	32.3	95.00%	R.WEVDEPEYILENALK.G		R.WEVDEPEYILENALK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
400	A7A1L9_YEAS7	7.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	75	2	1266.61	-1.3	1	45.5	32.9	95.00%	R.GFLSDLPDFEK.L		R.GFLSDLPDFEK.L
111	122	2	1282.67	-0.34	1	35.2	29.9	95.00%	R.AGAVAPEDIWVR.A		R.AGAVAPEDIWVR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
401	A6ZWW4_YEAS7	6.56%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
332	346	2	1598.74	-0.34	1	38.3	33.4	95.00%	R.LRSSPSASSSSLANR.E	Phospho (+80)	R.LRSSPSASSSSLANR.E
190	199	2	1179.6	0.26	1	58.5	31.8	95.00%	K.ATLLNFVCDK.E	Carbamidomethyl (+57)	K.ATLLNFVCDK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
402	A7A257_YEAS7	1.94%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
643	656	3	1622.8	1.7	1	27.6	32.1	94.60%	Y.SVLNDDHKTDNPIR.S		K.STSAYLEYPLNEEDSSEDEGSMSIYSVLNDDHKTDNPIR.S
370	387	2	1965.89	1.3	0	103	34	95.00%	Y.LLNDDDVQSIMTSGEDSK.L		R.SSNTNPYSHSHSHLHLISQDNHNGTDLHDPVAATDNPQQQNEVYLLNDDDVQSIMTSGEDSK.L
2173	2184	2	1363.71	-0.018	1	44.3	30.6	95.00%	R.ASVWNDTLFLAK.M		R.ASVWNDTLFLAK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
403	B3LLV1_YEAS1	5.03%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
164	173	2	1203.62	1.4	1	33.4	30.4	95.00%	W.YHDLVTDLTK.S		K.DDSFPYDYDEELSLSLSEWYHDLVTDLTK.S
394	415	3	2523.29	1.4	2	36.7	29.7	95.00%	F.ILEKDEIVEIVLNNQDTGTHPF.H		K.VPTLMTVLSSGDQANNSEIYGSNTHTFILEKDEIVEIVLNNQDTGTHPFHLHGHAFQTIQR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
404	A6ZTZ3_YEAS7	1.65%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2373	2389	2	1903.92	2.1	0	95.7	32.4	95.00%	K.TNIVNLVEEEMLGSNDK.L		K.TNIVNLVEEEMLGSNDK.L
2329	2341	2	1352.79	2.3	0	64.7	22.3	95.00%	R.VDPLVIELVTGAK.Q		R.VDPLVIELVTGAK.Q
2158	2171	2	1488.83	-0.68	1	32.5	27.3	95.00%	R.VVNGNFNALSTLLK.K		R.VVNGNFNALSTLLK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
405	A6ZXS1_YEAS7	5.35%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
6	15	3	1303.63	0.24	1	27.4	32.2	94.20%	K.VEHYLSYHTR.L		K.VEHYLSYHTR.L
245	260	2	1912.95	-1.2	1	64.1	32.1	95.00%	K.RLDDQTDVEQSPLLER.S		K.RLDDQTDVEQSPLLER.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
406	A6ZQ25_YEAS7	1.94%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1188	1211	3	2535.21	-0.79	1	34.8	32.6	95.00%	K.ILEANTTDYKPAEQMEAADAGVAK.L		K.ILEANTTDYKPAEQMEAADAGVAK.L
1542	1553	2	1462.79	1.7	1	39.5	28.1	95.00%	R.TQIITEFEEIIK.Y		R.TQIITEFEEIIK.Y
2438	2449	2	1431.69	-1.3	1	36.5	32.4	95.00%	R.FNELDVPEQVDK.L		R.FNELDVPEQVDK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
407	VTH2_YEAST	3.29%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
823	837	2	1748.75	2.7	1	48.7	34	95.00%	K.NCESILSPECHAVAY.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.NCESILSPECHAVAYLTK.D
1495	1517	3	2560.09	1.3	0	67.4	33.9	95.00%	R.GQGSNSEIEQEDVDTSQQEHTSR.T		R.GQGSNSEIEQEDVDTSQQEHTSR.T
394	406	2	1445.75	0.2	1	37.6	30.6	95.00%	K.VSVDNGLTWTNLK.V		K.VSVDNGLTWTNLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
408	A6ZP37_YEAS7	3.34%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
13	21	2	1115.63	-0.49	1	31	28.3	95.00%	R.FLEIPVKNR.A	Deamidation (+1)	R.FLEIPVKNR.A
533	543	2	1324.62	2.1	2	36.7	33.3	95.00%	Y.SEISEEEIRAY.T		K.GMVPYSEISEEEIRAYTLGECFTSGHEYKPESSDDELPELTK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
409	MHP1_YEAST	3.51%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
332	343	3	1280.7	-0.093	0	34.6	26.6	95.00%	K.GRPIPPHPDAPK.L		K.GRPIPPHPDAPK.L
113	133	4	2361.1	0.65	0	32	33.6	95.00%	K.SVVETNLSNVEADSGHHHHHR.H		K.SVVETNLSNVEADSGHHHHHR.H
471	486	4	1746.98	1.3	1	30.7	25.2	95.00%	R.KGEVEVKPNGSVVIHR.L		R.KGEVEVKPNGSVVIHR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
410	A6ZT92_YEAS7	1.61%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1480	1492	2	1480.76	-0.21	1	64	31.1	95.00%	K.IWTTSGDLLNSFK.N		K.IWTTSGDLLNSFK.N
131	142	2	1434.75	0.21	1	56.2	30.8	95.00%	K.NLQAQYETLSLR.T		K.NLQAQYETLSLR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
411	A6ZPD4_YEAS7	19.21%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
62	75	3	1640.95	-0.063	1	20.5	23.5	94.60%	R.LTKVDRETDIVKPK.K		R.LTKVDRETDIVKPK.K
103	117	2	1717.86	0.62	1	53.5	31.5	95.00%	K.INEKPTVVNDYEAAR.A		K.INEKPTVVNDYEAAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
412	A7A1P9_YEAS7	6.09%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
314	334	3	2023.04	0.21	1	49.1	29.8	95.00%	K.TVKKESEVSGSVASGSSTGVK.T		K.TVKKESEVSGSVASGSSTGVK.T
318	334	2	1566.74	0.25	0	91.4	33	95.00%	K.ESEVSGSVASGSSTGVK.T		K.ESEVSGSVASGSSTGVK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
413	A6ZT54_YEAS7	12.47%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
199	233	3	3610.87	4.3	2	48.5	25.3	95.00%	F.HILPIDQSADTTQSNGIIGGPGPVLVPNPGEIKEF.T	Deamidation (+1)	K.EAPGNFHILPIDQSADTTQSNGIIGGPGPVLVPNPGEIKEFTEIR.D
248	270	3	2478.32	-0.24	1	42.8	25.7	95.00%	R.LNKKEEVPEPVAGPIVESSVTEK.S		R.LNKKEEVPEPVAGPIVESSVTEK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
414	A6ZY29_YEAS7	13.91%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
131	140	2	1123.64	0.16	1	34.1	24.8	95.00%	R.TVAVLPPNWK.Y		R.TVAVLPPNWK.Y
10	20	2	1136.58	0.96	1	41.2	30.3	95.00%	K.GISSSAIPYSR.N		K.GISSSAIPYSR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
415	A6ZV68_YEAS7	11.80%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
222	248	3	2906.42	2.1	1	42.9	30.7	95.00%	K.ALLELLDDSPVTPGETRPAYDGYEASK.Q		K.ALLELLDDSPVTPGETRPAYDGYEASK.Q
262	274	2	1405.75	1.4	1	40.3	30.3	95.00%	W.TLDSAQVKPTLSF.K		K.QIIIDAESALNEWTLDSAQVKPTLSFK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
416	A6ZRV2_YEAS7	24.34%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	21	3	2359.2	1.8	2	28.4	30.6	95.00%	M.VELTEIKDDVVQLDEPQFSR.N		-.MVELTEIKDDVVQLDEPQFSR.N
129	145	2	1862.9	-1.4	1	84.9	32.2	95.00%	K.TFDLQSDANNILAQGEK.D		K.TFDLQSDANNILAQGEK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
417	A7A0V2_YEAS7	4.08%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
475	486	2	1413.6	1.1	0	60.9	33.1	95.00%	Y.HDCAADINDEVR.S	Carbamidomethyl (+57)	K.NNFEGMEIYISGTEGNEQDIEIDYIDYHDCAADINDEVR.S
583	598	2	1747.88	-0.46	0	40.7	31.7	95.00%	K.IIEPPAQDPCLEAAPK.K	Carbamidomethyl (+57)	K.IIEPPAQDPCLEAAPK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
418	A6ZRB2_YEAS7	2.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
28	47	2	1942.91	-0.51	0	85.3	33.6	95.00%	K.TTTASTASSSSPSSSSQTIR.N		K.TTTASTASSSSPSSSSQTIR.N
246	264	2	1913.84	1.3	0	74.9	34.1	95.00%	Y.NSSMTAPSSSSSSSSQNLR.N		K.SHGQTVATNYNSSMTAPSSSSSSSQNLR.N
286	305	2	1968.82	-0.72	0	68.4	34	95.00%	K.NDDSSSTTATNSGNDVASAR.S		K.NDDSSSTTATNSGNDVASAR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
419	CASP_YEAST	5.45%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	15	2	1777.83	0.015	1	45.7	33.3	95.00%	-.MDTSVYSHALDIWAK.A	Acetyl (+42)	-.MDTSVYSHALDIWAK.A
236	248	2	1501.77	0.72	0	59.2	31	95.00%	Y.NLVTQELETTQAR.I		R.IAEYNLVTQELETTQAR.I
559	567	2	1095.52	-0.19	1	57.2	31.5	95.00%	R.IDVESQYSR.V		R.IDVESQYSR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
420	A6ZZL6_YEAS7	5.11%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
149	156	2	1061.42	-0.69	1	28.7	31.3	91.00%	R.FFDMMDEK.H		R.FFDMMDEK.H
247	257	2	1224.65	-0.75	1	53.8	29.9	95.00%	K.IGGFVTNLNYK.D		K.IGGFVTNLNYK.D
534	544	2	1329.61	2	1	59.3	33.1	95.00%	F.ILSEYYNDADK.Y		K.ENSITYSTFILSEYYNDADK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
421	A6ZTW2_YEAS7	4.51%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
290	299	2	1219.65	0.15	1	49.8	30.8	95.00%	K.TQDVIQLFEK.D		K.TQDVIQLFEK.D
71	86	3	1761.95	0.23	2	39.5	27.6	95.00%	R.KYDTAVKPVIDDATVK.V		R.KYDTAVKPVIDDATVK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
422	A6ZND5_YEAS7	3.27%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	15	2	1627.88	2	1	87.9	28.8	95.00%	M.SDKIQEEILGLVSR.S	Acetyl (+42)	-.MSDKIQEEILGLVSR.S
118	129	2	1398.61	-0.79	1	41.2	32.9	95.00%	K.ALEDSNYNQMSK.A		K.ALEDSNYNQMSK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
423	A6ZSF8_YEAS7	5.31%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
135	143	2	1135.54	-0.015	1	29	31.6	90.90%	K.TYNTAPQWR.F		K.TYNTAPQWR.F
2	14	2	1478.76	2.8	1	66.7	31.2	95.00%	M.VNFDLGQVGEVFR.R		-.MVNFDLGQVGEVFR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
424	IRC8_YEAST	4.87%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
203	217	2	1631.81	1.9	0	57.7	31.7	95.00%	W.LINELSTNSNTNANK.T		K.SMNGVAWLINELSTNSNTNANK.T
218	231	2	1507.71	-0.34	0	66.3	33.2	95.00%	K.TISSDENSNSSVIR.H		K.TISSDENSNSSVIR.H
305	315	2	1294.69	1.1	1	41.2	29	95.00%	K.SFLNFLALNEK.N		K.SFLNFLALNEK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
425	A6ZRT4_YEAS7	34.11%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
68	84	2	1808.84	1.8	1	46.9	33.4	95.00%	K.DLIDKPDDAATAETTSF.G		K.DLIDKPDDAATAETTSFGWGK.K
2	15	2	1693.77	1.5	1	32.3	33.8	92.80%	M.SEVAETWVDTWMAK.L	Acetyl (+42)	-.MSEVAETWVDTWMAK.L
97	109	2	1547.75	-0.4	1	54.4	31.9	95.00%	R.QQELFENALEEAK.R		R.QQELFENALEEAK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
426	A6ZYE1_YEAS7	9.16%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
176	199	3	2558.25	2.1	1	41.3	31.7	95.00%	R.TVMSLPGNHDIGFGDTVVESSLQR.F		R.TVMSLPGNHDIGFGDTVVESSLQR.F
255	275	3	2559.34	-0.57	1	28.7	27.8	95.00%	R.ILLTHVPLWRDPEQQTCGQLR.E	Carbamidomethyl (+57)	R.ILLTHVPLWRDPEQQTCGQLR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
427	A6ZY59_YEAS7	2.90%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
118	148	3	3330.4	1.2	1	72.3	33.3	95.00%	F.QATPMPNTGGFEDVELDNNEGSNNDSQADHK.L		K.TEIHEHENEVDDDLHSFQATPMPNTGGFEDVELDNNEGSNNDSQADHK.L
855	865	2	1171.59	-0.26	1	30.7	30.8	94.70%	R.QLGYSFVGSSK.S		R.QLGYSFVGSSK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
428	A7A1E2_YEAS7	17.67%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
61	71	2	1315.65	0.75	1	47	31.6	95.00%	R.LQLWDTAGQER.F		R.LQLWDTAGQER.F
126	141	3	1821.83	1.4	1	37.9	33.4	95.00%	K.SDLSDERQISTEEGEK.K		K.SDLSDERQISTEEGEK.K
13	23	2	1145.64	-0.54	1	37.9	27.3	95.00%	K.IVFLGEQGVGK.T		K.IVFLGEQGVGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
429	A6ZZ58_YEAS7	10.27%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	16	2	1920.89	1.5	1	33.8	33.6	95.00%	-.MNNSEDPFQQVVKDTK.E	Acetyl (+42)	-.MNNSEDPFQQVVKDTK.E
22	28	2	892.48	0.43	1	35.5	29.6	95.00%	R.INNYITR.H		R.INNYITR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
430	A7A0T2_YEAS7	6.47%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
141	151	2	1272.69	-0.16	0	32.8	29.8	95.00%	K.NVVNLLNTQMK.N		K.NVVNLLNTQMK.N
209	219	2	1238.57	1.8	0	50.5	32.8	95.00%	F.MTSLLDESSEK.N		K.LTTDTGHAPADDQTQSNHAADLTTYNNSNPFMTSLLDESSEK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
431	YP162_YEAST	10.62%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
263	273	2	1181.56	-1.2	1	35.7	32.6	95.00%	K.DNNISSYGSII.-		K.DNNISSYGSII.-
245	262	2	2010.98	1.3	0	75.7	33.1	95.00%	F.LNDEIPDLSEVSNEVPNK.D		R.LHSESLTITNAENFETNTFLNDEIPDLSEVSNEVPNK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
432	A6ZXZ4_YEAS7	16.67%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
145	162	2	2001.89	2.1	1	95.7	34.1	95.00%	K.NVFAELTNMDEVHGGSPW.G		K.NVFAELTNMDEVHGGSPWGAGTIAGSDGSR.S
175	189	3	1634.86	0.38	0	38.4	30.4	95.00%	R.SPSALELQVHEIQGK.T		R.SPSALELQVHEIQGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
433	A6ZN12_YEAS7	5.38%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
402	415	2	1575.76	-0.26	0	74.5	33.2	95.00%	K.LMDSNNDAVQTLQK.L		K.LMDSNNDAVQTLQK.L
216	227	2	1260.66	2.5	1	38	30.2	95.00%	F.CAAPSVLPAFTK.R	Carbamidomethyl (+57)	K.NYGVGACGPAGFYGNQDVHYTLEYDLAQFFGTQGSVLYGQDFCAAPSVLPAFTK.R
212	227	2	1707.83	1.8	1	53.8	32.8	95.00%	Y.GQDFCAAPSVLPAFTK.R	Carbamidomethyl (+57)	K.NYGVGACGPAGFYGNQDVHYTLEYDLAQFFGTQGSVLYGQDFCAAPSVLPAFTK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
434	A6ZQV0_YEAS7	19.91%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
184	196	2	1408.73	2.5	1	33.3	30.7	95.00%	R.LLGYPVYGDEVGK.V		R.LLGYPVYGDEVGK.V
161	175	2	1448.74	-1.6	1	54.2	31.2	95.00%	K.QSGFGGNLTAALGTR.V		K.QSGFGGNLTAALGTR.V
1	18	2	1833.93	2.8	1	42.9	31.2	95.00%	-.MNGLVLGATGLCGGGFLR.H	Acetyl (+42)/ Carbamidomethyl (+57)	-.MNGLVLGATGLCGGGFLR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
435	A6ZXN6_YEAS7	6.37%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
436	452	2	1835.91	0.32	1	37.8	31.7	95.00%	K.ISDVSGIYPSGNIVMER.L		K.ISDVSGIYPSGNIVMER.L
338	346	2	1256.67	-0.015	1	31.7	28.4	95.00%	R.IENQWLLWR.K		R.IENQWLLWR.K
436	455	2	2193.06	-1.4	1	53.7	32.5	95.00%	K.ISDVSGIYPSGNIVMERLDE.-		K.ISDVSGIYPSGNIVMERLDE.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
436	A6ZMI9_YEAS7	3.37%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
782	799	2	1910.04	1.2	1	71.4	26.3	95.00%	K.TPVFTTGGDYILSLVSIK.D		K.TPVFTTGGDYILSLVSIK.D
5	13	2	1124.52	-0.38	1	32.6	32.4	94.90%	R.YNVFNDTPR.G		R.YNVFNDTPR.G
1048	1065	2	2002.02	0.95	1	34.7	30.8	95.00%	R.ACAANVDQISFLEPINLK.F	Carbamidomethyl (+57)	R.ACAANVDQISFLEPINLK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
437	A6ZXK3_YEAS7	4.07%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
578	594	2	1758.94	0.84	1	69.2	28.8	95.00%	R.AAAPTVVFLDELDSIAK.A		R.AAAPTVVFLDELDSIAK.A
306	322	2	1825.99	1.4	1	68.1	28.6	95.00%	K.NAPAIIFIDEIDSIAPK.R		K.NAPAIIFIDEIDSIAPK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
438	A6ZT16_YEAS7	5.64%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
288	304	2	1999	0.64	0	59	31.3	95.00%	K.IIEEEQEDDALVQDLLK.F		K.IIEEEQEDDALVQDLLK.F
171	186	3	1740.97	1.6	0	35.4	26.6	95.00%	K.ISESDLAVLKPSNQLK.T		K.ISESDLAVLKPSNQLK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
439	A6ZXS0_YEAS7	13.02%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
105	118	2	1729.84	1.5	1	51.8	32.4	95.00%	F.FVLNSDVICEYPFK.E	Carbamidomethyl (+57)	K.DNSPFFVLNSDVICEYPFK.E
225	239	2	1639.89	1.7	1	71.5	27.5	95.00%	K.DFLSGTVLYLNSLAK.R		K.DFLSGTVLYLNSLAK.R
269	286	2	1776.98	1.8	0	26.2	26.9	93.90%	K.IGPDVVIGPNVTIGDGVR.I		K.IGPDVVIGPNVTIGDGVR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
440	A6ZM71_YEAS7	9.88%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
344	363	3	2353.88	0.6	1	44	32.7	95.00%	R.HQHHPNDSNSPSDEDESEMY.E		R.HQHHPNDSNSPSDEDESEMYELDLFNTLQK.D
378	397	2	2146.96	-0.19	1	76.2	34.2	95.00%	K.ALKQDSNDTSDSPQDDQVGK.S		K.ALKQDSNDTSDSPQDDQVGK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
441	A6ZTK7_YEAS7	3.64%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
538	552	2	1662.74	1.5	1	54.5	33.8	95.00%	F.TIGSHGYDNNAIDMR.S		K.NEDNVFTIGSHGYDNNAIDMR.S
577	588	2	1390.66	2	0	35.2	32.5	95.00%	Y.NLLCDICGVAEK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.SVFIGMGPYFPQGYIEPFQNTEIYNLLCDICGVAEK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
442	A6ZSV2_YEAS7	2.68%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
511	525	3	1660.88	1.4	1	33.8	29.5	95.00%	R.GFSIGKPVESDRLEK.A		R.GFSIGKPVESDRLEK.A
513	525	3	1456.79	2.2	1	36.7	28.9	95.00%	F.SIGKPVESDRLEK.A		R.GFSIGKPVESDRLEK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

443	A6ZN84_YEAS7	24.65%	100%	3									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
62	74	2	1445.74	-0.77	0	48.3	30.7	95.00%	K.VIEQPITSETAMK.K		K.VIEQPITSETAMK.K		
101	109	2	1106.59	-0.19	1	31.3	28.9	95.00%	K.ELYEVDVLK.V		K.ELYEVDVLK.V		
126	138	2	1449.71	-0.77	1	87.1	32.4	95.00%	R.LTADYDALDIANR.I		R.LTADYDALDIANR.I		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
444	B5VRB0_YEAST	15.16%	100%	3									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
201	212	2	1414.6	-0.82	1	57.3	33	95.00%	R.NCFICSGSDSLR.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.NCFICSGSDSLR.Y		
31	42	2	1301.7	-0.32	1	53.5	29.9	95.00%	K.ILIDGPYGGIER.D		K.ILIDGPYGGIER.D		
213	225	2	1306.69	-0.54	1	69.8	30.6	95.00%	R.YTVGNSVAGLQAK.V		R.YTVGNSVAGLQAK.V		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
445	A6ZZ10_YEAS7	12.90%	100%	3									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
85	98	2	1671.8	1.2	1	57.4	33.1	95.00%	R.AMPALMELYSIYDR.S		R.AMPALMELYSIYDR.S		
291	308	2	1718.84	-0.65	0	86.5	32.1	95.00%	R.LGTAPATLSQTSGTDSGR.A		R.LGTAPATLSQTSGTDSGR.A		
316	327	2	1303.63	-0.86	1	54.7	31.8	95.00%	R.SGPSNLNQFQGR.G		R.SGPSNLNQFQGR.G		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
446	A7A1R6_YEAS7	17.99%	100%	3									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
38	61	3	2803.18	-1.3	1	47.8	33.8	95.00%	K.SSSTCDSLNQVTCYCEHENSAVK K.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.SSSTCDSLNQVTCYCEHENSAVK K.C		
62	80	2	2130.9	-0.64	1	70.4	33.9	95.00%	K.CLDSICPNNDADAAYSAFK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CLDSICPNNDADAAYSAFK.S		
38	60	3	2675.09	-0.85	1	42.5	33.7	95.00%	K.SSSTCDSLNQVTCYCEHENSAVK .K	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.SSSTCDSLNQVTCYCEHENSAVK .K		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
447	A7A0W2_YEAS7	5.83%	100%	3									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
525	534	2	1195.66	1.1	1	28.4	26.2	95.00%	K.FNFLNSILTK.S		K.FNFLNSILTK.S		
175	184	2	1257.67	0.15	1	32.9	29.6	95.00%	K.SWNQEQLLLK.S		K.SWNQEQLLLK.S		
431	447	2	1900.91	-0.32	1	96.4	33.2	95.00%	K.INDLFQSSYDILDGSSK.N		K.INDLFQSSYDILDGSSK.N		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
448	A6ZSI2_YEAS7	1.96%	100%	3									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
667	678	2	1265.63	-0.4	0	70.7	32.1	95.00%	K.SDVTSIESSLTK.F		K.SDVTSIESSLTK.F		
1143	1154	2	1388.8	-0.43	1	40	25.7	95.00%	K.NAVILNYQTLLK.E		K.NAVILNYQTLLK.E		
1443	1450	2	1018.54	-0.23	1	27.8	28.3	94.10%	R.IIDLFNER.Q		R.IIDLFNER.Q		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
449	A6ZN47_YEAS7	3.85%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
610	622	2	1601.8	-1.2	0	70.2	31.1	95.00%	K.LQCININDLMVNR.N	Carbamidomethyl (+57)	K.LQCININDLMVNR.N		
188	198	2	1154.6	0.15	1	29.6	29.8	94.50%	K.FLYLDGASAAK.T		K.FLYLDGASAAK.T		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
450	B3LNV3_YEAS1	4.98%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		
270	284	2	1694.75	-0.58	0	76.6	33.9	95.00%	R.NTIACTQSEESQATR.G	Carbamidomethyl (+57)	R.NTIACTQSEESQATR.G		
187	203	2	1791.83	0.83	0	74.7	33.5	95.00%	K.TQPAVSANTTNTDTSER.F		K.TQPAVSANTTNTDTSER.F		
Index	AC	Coverage	Scaffold probability	Nb distinct peptides									
451	A6ZKK2_YEAS7	11.16%	100%	2									
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence		

200	210	2	1091.54	-0.38	0	38.1	30.8	95.00%	R.MLSSAGVNSAR.G		R.MLSSAGVNSAR.G
37	49	2	1496.73	-0.48	1	104	32.8	95.00%	K.TLFSSWADSLNTR.A		K.TLFSSWADSLNTR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
452	A6ZQZ3_YEAS7	15.54%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	12	2	1382.71	0.5	1	55.5	30	95.00%	-.MFSLQDVITTTK.T		-.MFSLQDVITTTK.T
56	66	3	1239.66	3.5	0	31.8	28.8	95.00%	R.KPTETTHLSAR.T		R.KPTETTHLSAR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
453	A6ZWP8_YEAS7	4.24%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
552	569	2	2050.88	-0.25	1	43.8	34	95.00%	R.VAGTSNFTNLDDYMMNMK.R		R.VAGTSNFTNLDDYMMNMK.R
589	602	2	1602.81	0.29	1	62.3	31.1	95.00%	R.IPEPLTFTNSEDLK.Q		R.IPEPLTFTNSEDLK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
454	A6ZM44_YEAS7	9.16%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
98	118	2	2226.09	-0.81	0	63.8	32.5	95.00%	R.SVDMTSPLLTNLEAGTHANQK.K		R.SVDMTSPLLTNLEAGTHANQK.K
83	97	2	1665.71	-1.2	0	107	33.6	95.00%	R.ELIMEEEGTGSDSNR.S		R.ELIMEEEGTGSDSNR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
455	A6ZW55_YEAS7	10.00%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
41	56	2	1833.81	-1.1	1	90.2	34.2	95.00%	R.DQLSHESQTAYQQGDK.K		R.DQLSHESQTAYQQGDK.K
106	113	2	960.56	0.08	1	27.5	24.5	95.00%	K.EALFILQK.R		K.EALFILQK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
456	A6ZQ18_YEAS7	5.26%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
225	242	2	2054.03	1.6	1	32.2	31.8	95.00%	R.MLPLPIANPNDFLPEDMK.Q		R.MLPLPIANPNDFLPEDMK.Q
53	77	3	2288.12	2.5	1	101	32.2	95.00%	R.KRPTSPSISGSGSGGNSPSSSAGAR.Q		R.KRPTSPSISGSGSGGNSPSSSAGAR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
457	A6ZSF6_YEAS7	5.06%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
5	13	2	1032.6	-0.025	1	68.4	25.5	95.00%	R.LSLTSLFPR.C		R.LSLTSLFPR.C
308	315	2	1045.52	0.013	0	28.8	30.5	92.50%	R.CLEDQLLR.R	Carbamidomethyl (+57)	R.CLEDQLLR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
458	KHA1_YEAST	3.67%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
478	496	2	1986.09	1.5	0	65.6	26.5	95.00%	R.IGELTTVINTTEAISPSLK.L		R.IGELTTVINTTEAISPSLK.L
620	632	2	1512.77	0.91	1	49.1	30.9	95.00%	K.IPFSSEVIFSTMR.E		K.IPFSSEVIFSTMR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
459	A6ZTX9_YEAS7	37.39%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
62	74	2	1514.78	-1.1	2	64.2	30.2	95.00%	K.IKAQIWDTAGQER.Y		K.IKAQIWDTAGQER.Y
98	107	2	1282.47	2	1	33	31.4	95.00%	K.SSSYENCNHW.L	Carbamidomethyl (+57)	K.SSSYENCNHWLTELR.E
16	26	2	1056.62	0.27	0	32.4	25.5	95.00%	K.IVLIGDSGVGK.S		K.IVLIGDSGVGK.S
153	165	2	1392.64	1.4	0	47.8	32.5	95.00%	F.TETSALNSDNVDK.A		K.NFAMENQMLFTETSALNSDNVDK.A
64	74	2	1273.61	-0.17	1	64.6	32.4	95.00%	K.AQIWDTAGQER.Y		K.AQIWDTAGQER.Y
33	43	2	1329.61	-0.1	1	54.8	33.8	95.00%	R.FTTDEFNIESK.S		R.FTTDEFNIESK.S
113	127	2	1527.75	-1.3	0	74.8	32.7	95.00%	R.ENADDNVAVGLIGNK.S		R.ENADDNVAVGLIGNK.S
44	53	2	1079.56	0.067	1	61.1	29.8	95.00%	K.STIGVEFATR.T		K.STIGVEFATR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
460	A6ZTF3_YEAS7	9.91%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
384	393	2	1105.53	2.6	1	48.8	31.4	95.00%	K.ELVGDALDQF.M		K.ELVGDALDQFMISLPPVPQQEEESSTELASQEQETK.E
144	176	4	3623.57	-2.5	1	45	32.1	95.00%	K.DGFESAVGEEDSKDATSQENGQSTQQQQPPHHR.N		K.DGFESAVGEEDSKDATSQENGQSTQQQQPPHHR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
461	A6ZSX0_YEAS7	6.32%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
72	80	2	1050.54	0.16	1	31.1	30.5	95.00%	R.DFIGLPFDK.C		R.DFIGLPFDK.C
385	409	3	2763.44	1.9	1	58.6	27.7	95.00%	R.LISDYDADELAEALQPVIVNTPHLK.K		R.LISDYDADELAEALQPVIVNTPHLK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
462	A9EDP4_YEAST	4.52%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
324	337	2	1659.82	-0.79	1	94.4	32.2	95.00%	R.NIDIWTVETAQNTR.E		R.NIDIWTVETAQNTR.E
508	521	2	1370.74	-0.81	0	35.6	28.4	95.00%	K.DISASSPNLGGILK.A		K.DISASSPNLGGILK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
463	A7A149_YEAS7	13.92%	99%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
122	145	3	2370.08	0.87	0	28.9	33.7	94.30%	K.EAQADAAAEIAEDAAEAEDAGKPK.T		K.EAQADAAAEIAEDAAEAEDAGKPK.T
171	184	3	1629.86	0.85	1	23.1	30.1	90.30%	K.KVELDAERIETAEK.E		K.KVELDAERIETAEK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
464	A6ZTJ7_YEAS7	3.46%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
849	869	3	2512.98	0.93	2	40.7	33.6	95.00%	Y.VSETSGMHDIDPSDDDRWCEY.I	Carbamidomethyl (+57)	K.LMGNTTRPAILLSYLVVDPGEGNYNTYVSETSGMHDIDPSDDDRWCEYILYK.G
886	897	2	1260.66	-0.48	0	66.6	30.2	95.00%	R.GTITDTELQVGK.F		R.GTITDTELQVGK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
465	A6ZQ13_YEAS7	4.63%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
314	326	2	1490.71	1.9	0	88.9	32.5	95.00%	Y.ASNNNSMIELIER.R	Deamidation (+1)	K.IETSFNDTSYASNNNSMIELIER.R
121	130	2	1150.6	0.43	1	34.4	29.4	95.00%	R.NLNSVLNYSK.F		R.NLNSVLNYSK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
466	A6ZNU4_YEAS7	12.02%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
63	73	2	1336.6	-0.83	1	64.8	32.2	95.00%	K.FNMWDVGGQQR.L		K.FNMWDVGGQQR.L
98	108	2	1410.65	1.3	2	50.3	32.8	95.00%	R.NRMEEAKEELY.S		R.NRMEEAKEELYSIIGEK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
467	A6ZT94_YEAS7	4.59%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
275	289	3	1661.92	0.41	0	31.8	25.7	95.00%	R.GERPIPKPLDGNTLR.C		R.GERPIPKPLDGNTLR.C
387	399	3	1412.85	2.3	0	32.3	18.6	95.00%	K.VTPIVPVPIHVSR.S		K.VTPIVPVPIHVSR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
468	A6ZUP8_YEAS7	2.33%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
140	148	2	1034.6	1.2	1	44.8	24.2	95.00%	K.LSDTLVFLK.D		K.LSDTLVFLK.D
834	847	2	1474.79	2.8	0	49.3	30	95.00%	Y.STQLLADIISEASK.G		R.NEQASSVYSTQLLADIISEASK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
469	A6ZR74_YEAS7	12.28%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
295	330	4	3847.92	0.087	1	27.1	26.7	95.00%	R.ASIHQILQHFAEENVSISATSADEPTVATESSPLIR.D		R.ASIHQILQHFAEENVSISATSADEPTVATESSPLIR.D
331	349	2	2207.05	2.3	1	112	32.9	95.00%	R.DSSLDLNEVIEEESIYQPK.E		R.DSSLDLNEVIEEESIYQPK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
470	A6ZT07_YEAS7	0.83%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1284	1302	3	2129.07	2.3	0	35.7	31	95.00%	K.VLENTLTDIVCELSNANPK.V	Carbamidomethyl (+57)	K.VLENTLTDIVCELSNANPK.V
2796	2807	2	1395.71	-0.17	1	52.6	31.3	95.00%	K.TFLALQNFAESR.K		K.TFLALQNFAESR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
471	A6ZML9_YEAS7	4.53%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
389	414	3	2840.14	1.5	1	42.7	33.8	95.00%	Y.NNLGSNSSTNENDSNDHDSNNDFTTK.S		R.FWDHSTDFTSNSYNNLGSNSSTNENDSNDHDSNNDFTTK.S
100	110	2	1185.6	0.32	0	48.1	30.3	95.00%	R.SAPIVVDDNTR.Y		R.SAPIVVDDNTR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
472	A6ZQR4_YEAS7	4.60%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
315	326	3	1353.64	0.51	1	42.7	33.5	95.00%	R.TGSHFPAFSFEK.H		R.TGSHFPAFSFEK.H
354	364	2	1302.61	1.4	1	32.7	32.6	94.80%	W.HIYEPSSDDLK.H		R.MNYNVIGLPHYVIWHIYEPSSDDLK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
473	A6ZV27_YEAS7	12.61%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
210	218	2	912.54	0.63	0	27.2	24	95.00%	R.ISIPGITGR.A		R.ISIPGITGR.A
20	38	2	1933.98	2.1	1	40.3	30.8	95.00%	R.NQTDLKPFPSAGSASSSIK.T		R.NQTDLKPFPSAGSASSSIK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
474	A6ZUL4_YEAS7	2.75%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
316	328	2	1424.79	1.7	0	23.2	26.3	90.00%	K.LLTPVPSDIDISR.A		K.LLTPVPSDIDISR.A
171	183	2	1326.74	-0.013	0	31.2	26.9	95.00%	R.SDIVGSPVAELLK.S		R.SDIVGSPVAELLK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
475	A6ZTQ1_YEAS7	5.15%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
92	110	2	1971.96	0.54	1	33	32.5	95.00%	R.TDGTAAAGPLDLKPMESLW.S		R.TDGTAAAGPLDLKPMESLWSTAPPPAMAPSPQSTMAPAPAPQQMAPLQPILSMQDLER.Q
722	743	3	2559.35	1.4	2	40.4	27.4	95.00%	R.IIIDEVRDEIFATINEAETLQK.K		R.IIIDEVRDEIFATINEAETLQK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
476	A6ZS90_YEAS7	1.75%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
546	569	3	2818.36	1.5	1	54.4	30.9	95.00%	K.LLETEDFEDNTITTGWLDDLITHK.M		K.LLETEDFEDNTITTGWLDDLITHK.M
899	913	3	1544.9	2.4	0	34.2	24	95.00%	K.LLGAVVEPLADIAHK.Y		K.LLGAVVEPLADIAHK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
477	A7A0G2_YEAS7	19.53%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
30	41	2	1199.69	2.1	1	62.4	27.3	95.00%	Y.APVAISLPAFSK.E		K.STIALPSFFIVLILALVNSVAASSSYAPVAISLPAFSK.E
126	155	4	3393.6	1.2	1	27.3	30.9	95.00%	K.TLTDEHEADVNNDDIIANNAVEEIDRNLNK.I		K.TLTDEHEADVNNDDIIANNAVEEIDRNLNK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
478	A6ZRK5_YEAS7	3.32%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
361	376	2	1665.72	-1.5	1	70.7	33.9	95.00%	Y.SSGSGEYIHSSDINGR.C	Deamidation (+1)	K.DLHPPYSEGCSAVMAVTYSSGSGEYIHSSDINGR.C
270	280	2	1206.48	2.7	1	35	32.1	95.00%	Y.SCSWGPADDGR.H	Carbamidomethyl (+57)	R.ILSGDITTEDEAASLIYGLDVNDIYSCSWGPADDGR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
479	A6ZRY2_YEAS7	13.66%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
252	280	3	3046.41	1.4	1	68.6	32.5	95.00%	K.TQTDRTNIDNSTGQAGQANAQSANTVNNR.V		K.TQTDRTNIDNSTGQAGQANAQSANTVNNR.V
95	109	2	1858.92	2.7	1	73.6	32.3	95.00%	K.SSLDELMTYYQQILR.V		K.SSLDELMTYYQQILR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
480	A7A187_YEAS7	4.96%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
47	57	2	1262.73	0.84	1	48.5	25	95.00%	K.LIELVSFAPFK.G		K.LIELVSFAPFK.G
33	46	2	1624.77	-0.75	1	61	32.9	95.00%	K.EVQEQINDFGAFTK.L		K.EVQEQINDFGAFTK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
481	A6ZZQ1_YEAS7	9.22%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
170	178	2	1014.57	0.29	0	39.7	27.5	95.00%	K.QISLEGLQK.Q		K.QISLEGLQK.Q
131	140	2	1220.6	0.16	1	31.9	31.5	95.00%	K.YQGLINEQEK.Q		K.YQGLINEQEK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
482	A6ZVN8_YEAS7	2.05%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
881	894	3	1617.8	-0.37	1	35.7	31.5	95.00%	R.DVHAYFVPDGVLMR.V		R.DVHAYFVPDGVLMR.V
868	880	2	1518.77	-1	1	49.6	31.9	95.00%	K.TLEQAEELFGQVR.D		K.TLEQAEELFGQVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
483	A6ZTZ0_YEAS7	5.53%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
42	53	2	1316.72	-0.16	0	33.5	29.1	95.00%	R.GTLDETVLQTLK.R		R.GTLDETVLQTLK.R
42	54	3	1472.82	0.14	1	42	28.3	95.00%	R.GTLDETVLQTLKR.D		R.GTLDETVLQTLKR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
484	B3LI87_YEAS1	4.15%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
528	545	3	2056.87	-0.98	0	30.9	34.3	95.00%	K.LSVCTCDNEDHPNQGVGR.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.LSVCTCDNEDHPNQGVGR.G
34	47	2	1486.7	-0.81	0	35.7	33	95.00%	R.QSSSLEPADGQNVR.V		R.QSSSLEPADGQNVR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
485	A6ZUX3_YEAS7	11.49%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
211	223	2	1447.65	-0.64	0	77.5	33.7	95.00%	K.MEAPASVETQEEK.A		K.MEAPASVETQEEK.A
81	94	3	1672.83	-0.12	1	25.9	31	93.80%	K.EINNLKDEIQSENK.A		K.EINNLKDEIQSENK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
486	A6ZW34_YEAS7	4.04%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
701	718	3	1929.94	-0.72	1	26.4	32.3	92.50%	K.ITQQEVSPDRASSSPNSK.S		K.ITQQEVSPDRASSSPNSK.S
610	623	2	1415.74	-0.3	0	73.2	29.7	95.00%	K.SVANELMALGNVAK.D		K.SVANELMALGNVAK.D

Supplementary Table S2: All "Scaffold" validated proteins and peptides identified from solprotSP (*S.pombe*) and from SCVMprot (*S.cerevisiae*) samples

***S.cervisiae* - Chymotrypsin digest of large tryptic peptides (Replicate B)**

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
1	A6ZPV7_YEAS7	55.62%	100%	47								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
540	560	2	2061.93	2.7	1	57.4	33.7	95.00%	Y.GATSAPTSNTNHVVESANAAY.Y	Deamidation (+1)	R.SDNEDNDFDEDDEDDAALVAAM TNAPGNSLDIEESVGYGATSAPTSN TNHVVESANAAYYQR.K	
429	442	2	1679.87	2.8	1	68.4	30.7	95.00%	K.LQTQLGQEPPEWVR.E		K.LQTQLGQEPPEWVR.E	
201	212	2	1513.76	2.6	1	56.7	31.2	95.00%	K.YWVHPDNITELK.L		K.YWVHPDNITELK.L	
74	86	2	1578.85	2.9	1	83.1	28.7	95.00%	R.VKEVQEQVQHTVR.L		R.VKEVQEQVQHTVR.L	
324	348	2	2876.47	0.97	2	74.4	29	95.00%	K.EGKKPMNEIENLEALASEIQYVML K.K		K.EGKKPMNEIENLEALASEIQYVML K.K	
362	371	2	1074.55	3.4	1	46	30.6	95.00%	R.TAFQLPGDAR.V		R.TAFQLPGDAR.V	
401	415	2	1775.88	3.3	1	53.2	31.8	95.00%	R.TDIGVDWPFKQLDDK.D		R.TDIGVDWPFKQLDDK.D	
443	455	2	1402.79	2.8	0	75.3	27.2	95.00%	R.ELVGSHLVEPVPK.F		R.ELVGSHLVEPVPK.F	
327	348	2	2562.32	3.1	1	111	29.3	95.00%	K.KPMNEIENLEALASEIQYVMLK.K		K.KPMNEIENLEALASEIQYVMLK.K	
459	470	2	1326.73	1.3	1	62.2	27.8	95.00%	K.FIHGVATLLNDK.V		K.FIHGVATLLNDK.V	
540	561	2	2225	3.8	1	62.4	34	95.00%	Y.GATSAPTSNTNHVVESANAAYY. Q	Deamidation (+1)	R.SDNEDNDFDEDDEDDAALVAAM TNAPGNSLDIEESVGYGATSAPTSN TNHVVESANAAYYQR.K	
323	344	2	2533.29	6.2	2	48.6	29.5	95.00%	R.KEGKKPMNEIENLEALASEIQY.V		R.KEGKKPMNEIENLEALASEIQYV MLK.K	
401	410	2	1176.59	2.8	1	54.4	31.9	95.00%	R.TDIGVDWPFK.Q		R.TDIGVDWPFK.Q	
598	606	2	1037.52	2.2	1	37.2	31.5	95.00%	K.GTTFDTQIR.A		K.GTTFDTQIR.A	
324	344	2	2405.19	4.5	2	42.3	31.1	95.00%	K.EGKKPMNEIENLEALASEIQY.V		K.EGKKPMNEIENLEALASEIQYVML K.K	
459	476	2	1985.07	3.3	2	36.5	28	95.00%	K.FIHGVATLLNDKVDSIPF.W		K.FIHGVATLLNDKVDSIPFWLPQM DVDIR.K	
471	486	2	1929.96	-0.99	1	32.7	31.4	95.00%	K.VDSIPFWLPQMDVDIR.K		K.VDSIPFWLPQMDVDIR.K	
400	410	2	1332.68	-1.1	2	34.8	31.4	95.00%	R.RTDIGVDWPFK.Q		R.RTDIGVDWPFK.Q	
301	309	3	1156.6	-0.18	2	30	30.4	95.00%	K.ERHVNDFLK.G		K.ERHVNDFLK.G	
411	422	2	1568.74	4	2	42.5	33.6	95.00%	K.QLDDKDICRFPY.A	Carbamidomethyl (+57)	K.QLDDKDICRFPYAVLEVK.L	
327	344	2	2091.03	4.7	1	57.9	32.1	95.00%	K.KPMNEIENLEALASEIQY.V		K.KPMNEIENLEALASEIQYVMLK.K	
477	486	2	1271.64	4.4	1	37.9	31.1	95.00%	F.WLPQMDVDIR.K		K.VDSIPFWLPQMDVDIR.K	
36	58	2	2750.31	5.4	1	112	32.3	95.00%	K.NNGQWTQELETDFLESLEIELDK. V		K.NNGQWTQELETDFLESLEIELDK. V	
567	574	2	871.44	-0.15	0	28.2	28.3	95.00%	R.NAENPISK.K		R.NAENPISK.K	
176	190	3	1416.73	-0.42	1	35.1	30.6	95.00%	R.TSGRPIKGDSSAGGK.Q		R.TSGRPIKGDSSAGGK.Q	
67	72	2	773.38	0.35	1	31.4	26.5	95.00%	K.HSEVFR.R		K.HSEVFR.R	
327	349	3	2690.41	3.4	1	56.7	27.1	95.00%	K.KPMNEIENLEALASEIQYVMLKK. K		K.KPMNEIENLEALASEIQYVMLKK. K	
254	264	3	1280.66	-0.25	1	36.1	31	95.00%	R.LRKDEGAEAHR.L		R.LRKDEGAEAHR.L	
76	86	2	1351.68	-1.3	0	58.5	32	95.00%	K.EVQEQVQHTVR.L		K.EVQEQVQHTVR.L	
598	611	2	1487.78	2.1	1	32	31	95.00%	K.GTTFDTQIRAPPGK.T		K.GTTFDTQIRAPPGK.T	
73	86	3	1734.95	0.18	1	46.1	27.6	95.00%	R.RVKEVQEQVQHTVR.L		R.RVKEVQEQVQHTVR.L	
282	291	3	1257.57	-0.48	2	25.5	32.5	91.10%	K.THREDWTGEK.S		K.THREDWTGEK.S	
420	428	2	1064.59	0.35	1	47.5	27.4	95.00%	R.FPYAVLEVK.L		R.FPYAVLEVK.L	
540	563	2	2508.17	3.5	1	78.9	32.9	95.00%	Y.GATSAPTSNTNHVVESANAAYYQ R.K		R.SDNEDNDFDEDDEDDAALVAAM TNAPGNSLDIEESVGYGATSAPTSN TNHVVESANAAYYQR.K	
141	149	3	1098.7	3.9	1	39.6	21.4	95.00%	F.ILKPVFQVR.L		K.TGFILKPVFQVR.L	
138	149	3	1403.83	3.6	1	58.5	20.4	95.00%	K.TGFILKPVFQVR.L		K.TGFILKPVFQVR.L	
122	129	2	969.49	1	1	47.2	29.4	95.00%	R.LNYTGFQK.I		R.LNYTGFQK.I	

429	455	3	3064.65	4.6	1	41.5	23.9	95.00%	K.LQTQLGQEPPEWVRELVGSHLVEPVPK.F		K.LQTQLGQEPPEWVRELVGSHLVEPVPK.F
374	384	2	1276.67	3.6	0	57.4	30.6	95.00%	R.ISLDTELTMVR.E		R.ISLDTELTMVR.E
167	175	2	1077.58	-0.47	1	46.9	29.2	95.00%	K.ISQLYDIAR.T		K.ISQLYDIAR.T
374	393	2	2324.1	3.3	2	44.6	32.9	95.00%	R.ISLDTELTMVREDNFDGVDR.T		R.ISLDTELTMVREDNFDGVDR.T
20	35	2	1881.93	3.3	1	77.7	32.2	95.00%	Y.ISYDDLKTELEDNLSK.N		R.QYSYYYISYDDLKTELEDNLSK.N
87	118	3	3605.82	6.3	1	62.8	27.2	95.00%	R.LLDSNNPPTQLDFEILEEELSDIIADVHDLAK.F		R.LLDSNNPPTQLDFEILEEELSDIIADVHDLAK.F
487	501	2	1687.97	-1.2	0	24.8	22.1	94.90%	R.KPPLPTNIEITRPGR.S		R.KPPLPTNIEITRPGR.S
218	228	2	1280.73	1.6	1	27.4	24.8	95.00%	K.HLPVLVFNTNK.E		K.HLPVLVFNTNK.E
584	594	2	1322.59	4.1	1	41.4	32.4	95.00%	F.DHYFNGDQISK.I		K.YYEIVAFFDHYFNGDQISK.I
416	428	3	1608.84	3.3	2	52.9	30.8	95.00%	K.DICRFPYAVLEVK.L	Carbamidomethyl (+57)	K.DICRFPYAVLEVK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
2	A6ZPA7_YEAS7	37.86%	100%	37

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
334	352	3	2164.21	3.8	1	67.1	22.9	95.00%	K.ILIAEGWIPRDELATLQAR.L		K.ILIAEGWIPRDELATLQAR.L
32	42	2	1230.71	4	1	62.4	25.7	95.00%	Y.TLGQLGLVQFR.D		R.DSAYTLGQLGLVQFR.D
2	10	2	1133.58	3.3	2	57.1	30.9	95.00%	M.AEKEEAIFR.S	Acetyl (+42)	-.MAEKEEAIFR.S
121	141	2	2522.19	3.3	2	68.5	32.9	95.00%	R.LIQMEDATDQIEVQKNDLEQY.R		R.LIQMEDATDQIEVQKNDLEQYR.F
152	163	2	1346.6	3.3	2	32.8	33.6	94.20%	F.FLKGDNTDSTSY.M		R.FILQSGDEFFLKGDNTDSTSYMDEDMIDANGENIAAAIGASVNYVTGVIAR.D
194	205	2	1470.83	4.2	2	81	27.7	95.00%	R.DKVATLEQILWR.V		R.DKVATLEQILWR.V
353	359	2	788.42	0.095	0	56	30.8	95.00%	R.LGEMIAR.L		R.LGEMIAR.L
196	205	2	1227.7	-0.5	1	59.4	27.3	95.00%	K.VATLEQILWR.V		K.VATLEQILWR.V
360	380	3	2276.22	5	1	39.1	27.2	95.00%	R.LGIDVPSIIQVLDTNHTPPTF.H		R.LGIDVPSIIQVLDTNHTPPTFHR.T
187	193	2	714.44	5.8	0	26.2	29.4	90.40%	Y.VTGVIAR.D		K.GDNTDSTSYMDEDMIDANGENIAAAIGASVNYVTGVIAR.D
723	735	2	1579.73	4.7	1	46.8	33.1	95.00%	F.CLNCVSHTASYLR.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.SHEPLPSTEADASSEDLEAQQLISAMDADDAEEEEVGSGSHGEDFGDIMIHQVIHTIEFCLNCVSHTASYLR.L
11	27	2	1981	-0.36	1	60.9	31.4	95.00%	R.SAEMALVQFYIPQEISR.D		R.SAEMALVQFYIPQEISR.D
121	135	2	1759.87	0.51	0	81.2	31.8	95.00%	R.LIQMEDATDQIEVQK.N		R.LIQMEDATDQIEVQK.N
121	142	2	2678.3	3.5	2	112	31.7	95.00%	R.LIQMEDATDQIEVQKNDLEQYR.F		R.LIQMEDATDQIEVQKNDLEQYR.F
54	60	2	877.47	1.4	1	44.8	29.9	95.00%	R.TFVNEIR.R		R.TFVNEIR.R
360	382	2	2569.37	3	1	61.8	26.8	95.00%	R.LGIDVPSIIQVLDTNHTPPTFHR.T		R.LGIDVPSIIQVLDTNHTPPTFHR.T
28	42	3	1666.87	-0.11	1	59.2	30	95.00%	R.DSAYTLGQLGLVQFR.D		R.DSAYTLGQLGLVQFR.D
240	247	2	881.5	3.6	0	29.3	26.3	95.00%	F.SHGDLIIK.R		K.NAFIVFSHGDLIIK.R
251	270	2	2195.04	3.2	2	133	33.4	95.00%	R.KIAESLDANLYDVDSSNEGR.S		R.KIAESLDANLYDVDSSNEGR.S
234	247	2	1572.87	-0.97	1	46.4	28.4	95.00%	K.NAFIVFSHGDLIIK.R		K.NAFIVFSHGDLIIK.R
386	397	2	1467.59	4.4	1	44.6	32.7	95.00%	K.FTAGFQSICDCY.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.FTAGFQSICDCYGIAQYR.E
290	300	2	1243.59	4	1	34.3	32.8	95.00%	K.TTSTTLESELY.A		K.TTSTTLESELYAIAK.E
21	31	2	1277.63	4.7	2	51.3	31.8	95.00%	Y.IPQEISRDSAY.T		R.SAEMALVQFYIPQEISRDSAYTLGQLGLVQFR.D
209	214	2	724.39	-0.6	1	33	26.5	95.00%	R.GNLFFK.T		R.GNLFFK.T
280	289	2	1164.64	0.25	1	44.1	27.8	95.00%	K.NLSDLYTVLK.T		K.NLSDLYTVLK.T
113	120	2	980.46	-0.024	1	58.5	30.5	95.00%	R.NASYLEER.L		R.NASYLEER.L
100	112	2	1402.71	3.6	1	45.6	31.1	95.00%	Y.VPPSGSVIDDYVR.N		K.YLDGSGELYVPPSGSVIDDYVR.N
305	315	2	1394.65	2.2	1	68.5	32.6	95.00%	K.ELDSWFQDVTR.E		K.ELDSWFQDVTR.E

825	840	2	1525.7	4.1	1	57.3	32.7	95.00%	Y.KDMEVAVASASSSASS.-		K.FFVGEGLPYEPFAFEYKDMEVAVASASSSASS.-
215	226	2	1418.73	2.5	1	67.4	30.5	95.00%	K.TVEIEQPVYDVK.T		K.TVEIEQPVYDVK.T
290	304	2	1626.83	-0.81	1	61.5	30.3	95.00%	K.TTSTTLESELYAIAK.E		K.TTSTTLESELYAIAK.E
252	270	2	2066.95	2.9	1	119	33.6	95.00%	K.IAESLDANLYDVDSSNEGR.S		K.IAESLDANLYDVDSSNEGR.S
334	343	2	1166.69	3.5	1	42.4	21.9	95.00%	K.ILIAEGWIPR.D		K.ILIAEGWIPR.D
144	154	2	1295.68	4.4	1	52.6	30.1	95.00%	F.ILQSGDEFFLK.G		R.FILQSGDEFFLK.G
318	325	2	946.55	-0.031	1	39.5	26.6	95.00%	K.AIFEILNK.S		K.AIFEILNK.S
344	352	2	1015.53	1.3	0	58.2	29.8	95.00%	R.DELATLQAR.L		R.DELATLQAR.L
823	840	2	1817.81	4.6	1	37.8	34.4	95.00%	F.EYKDMEVAVASASSSASS.-		K.FFVGEGLPYEPFAFEYKDMEVAVASASSSASS.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
3	VTC3_YEAST	55.81%	100%	48

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
655	674	2	2133.83	4.1	1	82.7	33.7	95.00%	K.NISENGNDPYSDDTDSASSF.Q		K.NISENGNDPYSDDTDSASSFQLPPGVK.K
821	835	2	1733.93	4.1	1	48.6	28.9	95.00%	R.TLKPIQDFIFNLVGE.-	Deamidation (+1)	R.TLKPIQDFIFNLVGE.-
227	252	3	2927.4	2.6	1	68.5	31.8	95.00%	R.HLPALVYASVPNENDDFVDNLESDVR.V		R.HLPALVYASVPNENDDFVDNLESDVR.V
611	631	2	2451	2.9	0	40.8	34.3	95.00%	R.HVIADLEDHESSDEEGTALPK.K	Phospho (+80)/ Phospho (+80)	R.HVIADLEDHESSDEEGTALPK.K
459	477	2	2301.1	2.9	1	53.3	32.6	95.00%	R.NPENWHRDDIDSNIPNPLR.F		R.NPENWHRDDIDSNIPNPLR.F
806	820	2	1637.88	-0.8	1	64.4	27.3	95.00%	R.ERGLVNVSSQPSLPR.T		R.ERGLVNVSSQPSLPR.T
330	340	2	1329.76	1.3	1	38.9	27.1	95.00%	K.LLDKPDIFLEK.R		K.LLDKPDIFLEK.R
316	323	2	813.47	-0.4	0	28.3	25.2	95.00%	K.ISGAPTLR.L		K.ISGAPTLR.L
101	112	2	1476.66	2.3	0	63.2	33.8	95.00%	K.NTLEECLDEAQR.L	Carbamidomethyl (+57)	K.NTLEECLDEAQR.L
234	252	2	2133.95	3.9	1	121	33.8	95.00%	Y.ASVPNENDDFVDNLESDVR.V		R.HLPALVYASVPNENDDFVDNLESDVR.V
437	453	2	2011	3	1	66.4	31.8	95.00%	R.VTIDSNIMYIREDSLDK.N		R.VTIDSNIMYIREDSLDK.N
63	70	2	984.53	4.3	1	26.3	27.5	93.70%	K.VYTFQISK.Y		K.VYTFQISK.Y
234	258	3	2814.32	4.4	1	38.7	32.6	95.00%	Y.ASVPNENDDFVDNLESDVRVQPEAR.L		R.HLPALVYASVPNENDDFVDNLESDVRVQPEAR.L
487	495	2	1112.56	3.4	1	49	29.5	95.00%	K.FPYSVMEIK.V		K.FPYSVMEIK.V
401	413	2	1609.76	-0.58	1	76.2	33.6	95.00%	R.DFDNIQNFIVEEK.L		R.DFDNIQNFIVEEK.L
143	148	2	715.42	-0.041	0	26.7	28.2	93.20%	K.SLLQVR.L	Deamidation (+1)	K.SLLQVR.L
560	569	2	1235.53	-0.021	1	31.3	32.5	93.60%	K.NPQEAYEEEK.K		K.NPQEAYEEEK.K
611	632	2	2579.09	3.1	1	45.6	34.2	95.00%	R.HVIADLEDHESSDEEGTALPKK.S	Phospho (+80)/ Phospho (+80)	R.HVIADLEDHESSDEEGTALPKK.S
119	126	2	938.52	1.5	1	36	26.9	95.00%	R.LNFTGFIK.I		R.LNFTGFIK.I
176	186	2	1260.57	-0.33	1	33.5	32.7	95.00%	R.SNYDHPNTVSK.S		R.SNYDHPNTVSK.S
437	447	2	1323.68	-0.69	1	55.4	30.8	95.00%	R.VTIDSNIMYIR.E		R.VTIDSNIMYIR.E
48	58	2	1265.58	3	1	54.7	32.4	95.00%	R.NESDFVEALDK.E		R.NESDFVEALDK.E
7	16	2	1201.62	3.3	1	48.5	29.9	95.00%	K.LANDVYPPWK.D		K.LANDVYPPWK.D
512	524	2	1464.76	2.2	0	57	30.6	95.00%	K.DLTNSHLVNEVPK.F		K.DLTNSHLVNEVPK.F
77	86	2	1203.6	-0.44	1	42.5	31.2	95.00%	R.KLDDLEENTK.S		R.KLDDLEENTK.S
194	206	2	1493.72	2	1	57.2	32.6	95.00%	K.LSHFSNLEDASFK.S		K.LSHFSNLEDASFK.S
529	541	2	1377.68	3.8	1	78.7	32.3	95.00%	Y.LQGVASLFGEDDK.Y		K.FSLYLQGVASLFGEDDK.Y
512	528	2	1975.01	3.3	2	30.2	30.9	94.20%	K.DLTNSHLVNEVPKFSLYL.L		K.DLTNSHLVNEVPKFSLYLQGVASLFGEDDK.Y
265	282	2	1849.83	-1.3	0	98.2	34.1	95.00%	K.SNSLSSDGNSNQDVEIGK.S		K.SNSLSSDGNSNQDVEIGK.S
808	820	2	1352.74	0.88	0	41.5	26.8	95.00%	R.GLVNVSSQPSLPR.T		R.GLVNVSSQPSLPR.T
306	312	2	940.44	-0.24	1	33.2	31	95.00%	F.FDLYNNR.L		K.SVIFPQSYDPTITTLYFDNDFFDLYNNR.L
699	705	2	886.47	2.2	1	32.7	29	95.00%	K.VWLANER.T		K.VWLANER.T
210	221	2	1531.72	1.7	1	52.9	33.4	95.00%	K.FWVHDDNIMEVK.A		K.FWVHDDNIMEVK.A
101	118	3	2237	-0.48	2	33.9	34.4	95.00%	K.NTLEECLDEAQRLDNFDR.L	Carbamidomethyl (+57)	K.NTLEECLDEAQRLDNFDR.L
344	358	2	1712.75	3.4	1	79.8	33.8	95.00%	F.TENTETGNSSFEEIR.L		R.TFTENTETGNSSFEEIR.L
17	24	2	1059.45	2	1	53.9	31.7	95.00%	K.DSYIDYER.L		K.DSYIDYER.L

330	341	3	1485.86	4.9	1	27.1	24.7	95.00%	K.LLDKPDIFLEKR.T		K.LLDKPDIFLEKR.T
45	58	2	1637.76	3.6	2	67.4	33.2	95.00%	W.SERNESDFVEALDK.E		R.SSVDSWSERNESDFVEALDK.E
379	386	2	1032.57	3.1	1	38.1	26.6	95.00%	K.NYLINQLR.E		K.NYLINQLR.E
39	47	2	1051.46	-0.11	1	32.8	30.1	95.00%	R.SSVDSWSER.N		R.SSVDSWSER.N
94	100	2	864.43	-0.37	1	30	30.9	94.00%	K.INSEQFK.N		K.INSEQFK.N
655	681	2	2853.26	1.9	1	55.5	33.2	95.00%	K.NISENGNDPYSDDTDSASSFQLPPGVK.K		K.NISENGNDPYSDDTDSASSFQLPPGVK.K
549	559	2	1384.74	3.4	1	28.1	28.7	94.40%	F.WLPDLETDIRK.N		K.YVNILPFWLPDLETDIRK.N
425	436	2	1331.69	3.2	1	47.9	30.8	95.00%	R.TAFQIPGDQSIR.V		R.TAFQIPGDQSIR.V
496	511	2	1993.93	2.8	1	78	33	95.00%	K.VINQDNSQMPNYEWIK.D	Oxidation (+16)	K.VINQDNSQMPNYEWIK.D
464	477	3	1660.83	3.5	1	27.1	31.2	95.00%	W.HRDDIDSNIPNPLR.F		R.NPENWHRDDIDSNIPNPLR.F
342	358	2	1960.87	3.4	1	120	34.2	95.00%	R.TFTENTETGNSSFEEIR.L		R.TFTENTETGNSSFEEIR.L
588	597	2	1122.57	-0.31	1	27.6	30.2	91.40%	R.LSKISVPDGK.T	Phospho (+80)	R.LSKISVPDGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
4	B3LLD7_YEAS1	36.12%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
19	29	2	1220.52	3.7	1	40.2	32.6	95.00%	K.EHLTEGGNMAF.H	Oxidation (+16)	K.EHLTEGGNMAFHNHLNDFAHIEDPLER.R
481	492	2	1085.55	-0.29	0	40.9	30.4	95.00%	R.STAHGISAASGK.V		R.STAHGISAASGK.V
48	64	2	1933.95	5.3	1	81.7	32.4	95.00%	R.LALESIDNEGFGWQQVK.T	Deamidation (+1)	R.LALESIDNEGFGWQQVK.T
47	60	2	1606.77	3.8	2	57	32.5	95.00%	R.RLALESIDNEGFGW.Q	Deamidation (+1)	R.RLALESIDNEGFGWQQVK.T
481	512	3	3160.65	2.5	1	76.7	25.8	95.00%	R.STAHGISAASGKVGAIIAQTALGTLIDHNCAR.D	Carbamidomethyl (+57)	R.STAHGISAASGKVGAIIAQTALGTLIDHNCAR.D
109	131	2	2280.21	-0.97	1	108	27.4	95.00%	K.VSTSVGTVIGQFGFGTLADIVGR.K		K.VSTSVGTVIGQFGFGTLADIVGR.K
284	298	2	1599.81	-0.14	1	70.2	31.1	95.00%	K.LELAAAAQEQDGEKK.I		K.LELAAAAQEQDGEKK.I
7	29	3	2671.23	3.8	2	30.5	32.9	95.00%	K.DTIHVAERSLHKEHLTEGGNMAF.H	Phospho (+80)	K.DTIHVAERSLHKEHLTEGGNMAFHNHLNDFAHIEDPLER.R
298	314	2	1943.9	2.9	1	104	33.8	95.00%	K.KIHDTSDEDMAINGLER.A	Deamidation (+1)	K.KIHDTSDEDMAINGLER.A
276	283	2	949.49	0.31	1	40.6	30.1	95.00%	R.YQLDVNAK.L		R.YQLDVNAK.L
315	328	2	1544.69	-0.81	0	55.2	33.9	95.00%	R.ASTAVESLDNHPPK.A	Phospho (+80)	R.ASTAVESLDNHPPK.A
2	14	3	1496.76	0.76	1	41.9	31.1	95.00%	M.SSVNKDTIHVAER.S	Acetyl (+42)	-.MSSVNKDTIHVAER.S
30	45	2	1955.93	4.4	1	57.7	33.1	95.00%	F.HNHLNDFAHIEDPLER.R		K.EHLTEGGNMAFHNHLNDFAHIEDPLER.R
30	46	4	2112.03	3.5	1	28.4	32.5	95.00%	F.HNHLNDFAHIEDPLERR.R		K.EHLTEGGNMAFHNHLNDFAHIEDPLERR.R
19	45	3	3142.44	3.3	1	41.8	32.4	95.00%	K.EHLTEGGNMAFHNHLNDFAHIEDPLER.R		K.EHLTEGGNMAFHNHLNDFAHIEDPLER.R
299	314	2	1815.8	3.1	0	89	34.4	95.00%	K.IHDTSDEDMAINGLER.A	Deamidation (+1)	K.IHDTSDEDMAINGLER.A
549	569	2	2531.23	3.6	1	103	31.8	95.00%	K.TLEEINELYHDEIDPATLNFR.N		K.TLEEINELYHDEIDPATLNFR.N
493	512	2	2093.11	3.8	0	126	28.5	95.00%	K.VGAIIAQTALGTLIDHNCAR.D	Carbamidomethyl (+57)	K.VGAIIAQTALGTLIDHNCAR.D
572	587	2	1754.77	0.51	0	108	33.4	95.00%	K.NNDIESSSPSQLQHEA.-		K.NNDIESSSPSQLQHEA.-
284	297	2	1471.71	-0.69	0	97.6	32.4	95.00%	K.LELAAAAQEQDGEK.K		K.LELAAAAQEQDGEK.K
315	332	3	1977.93	2.8	2	32.6	33.5	95.00%	R.ASTAVESLDNHPPKASFK.D	Phospho (+80)	R.ASTAVESLDNHPPKASFK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
5	PMA1_YEAST	42.37%	100%	35

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
628	643	2	1586.8	3.8	0	30.6	31.3	94.40%	Y.LVAMTGDGVNDAPSLK.K		R.GYLVAMTGDGVNDAPSLK.K
660	682	3	2328.31	3.9	1	23.9	20.3	95.00%	R.SAADIVFLAPGLSAIIDALKTSR.Q		R.SAADIVFLAPGLSAIIDALKTSR.Q
520	548	3	3253.47	3.9	1	38.3	32.5	95.00%	R.GEGHWEILGVMPCMDPPRDDTAQTVSEAR.H	Carbamidomethyl (+57)	R.GEGHWEILGVMPCMDPPRDDTAQTVSEAR.H
388	414	2	2944.44	4.1	1	78.6	30.7	95.00%	K.LSLHEPYTVEGVSPDDLMLTACLAASR.K	Carbamidomethyl (+57)	K.LSLHEPYTVEGVSPDDLMLTACLAASR.K
457	474	2	1999.08	3.1	1	70.5	27.4	95.00%	K.KVTAVVESPEGERIVCVK.G	Carbamidomethyl (+57)	K.KVTAVVESPEGERIVCVK.G

80	95	2	1764.89	4.6	1	83.7	32	95.00%	Y.LQTDPSYGLTSDEVLK.R		K.TYDDAASESSDDDDIDALIEELQSNHGVDDEDSDNDGPVAAGEARPVPEEYLQTDPSYGLTSDEVLK.R
458	469	2	1271.64	-0.1	0	41.1	31.1	95.00%	K.VTAVVESPEGER.I		K.VTAVVESPEGER.I
175	184	2	1056.63	-0.3	0	53.9	25.9	95.00%	K.TLANTAVVIR.D		K.TLANTAVVIR.D
80	96	2	1920.99	3.9	1	78.8	31	95.00%	Y.LQTDPSYGLTSDEVLKR.R		K.TYDDAASESSDDDDIDALIEELQSNHGVDDEDSDNDGPVAAGEARPVPEEYLQTDPSYGLTSDEVLKR.R
644	659	2	1544.79	3.5	1	108	30.6	95.00%	K.KADTGIAVEGATDAAR.S		K.KADTGIAVEGATDAAR.S
483	501	2	2293.01	-0.099	1	72.7	33.9	95.00%	K.TVEEDHPIPEDVHENYENK.V		K.TVEEDHPIPEDVHENYENK.V
626	644	3	1934.99	3.9	1	23.7	30.8	90.80%	R.GYLVAMTGDGVNDAPSLKK.A		R.GYLVAMTGDGVNDAPSLKK.A
445	456	2	1413.73	-0.66	1	30.9	30.4	95.00%	K.VLEFHPFDPVSK.K		K.VLEFHPFDPVSK.K
584	615	3	3260.52	4	1	119	31.8	95.00%	R.LGLGGGGDMPGSELADFVENADGFAEVFPQHK.Y		R.LGLGGGGDMPGSELADFVENADGFAEVFPQHK.Y
616	625	2	1288.73	3.3	1	44.2	28.1	95.00%	K.YRVVEILQNR.G		K.YRVVEILQNR.G
240	252	2	1455.66	-0.69	1	70.9	33.1	95.00%	K.HYGDQTFSSSTVK.R		K.HYGDQTFSSSTVK.R
899	909	2	1315.55	-0.039	1	80.1	32.1	95.00%	R.SVEDFMAAMQR.V	Oxidation (+16)/ Oxidation (+16)	R.SVEDFMAAMQR.V
395	414	2	2105.02	3.8	0	65.4	32.9	95.00%	Y.TVEGVSPDDLMLTACLAASR.K	Carbamidomethyl (+57)	K.LSLHEPYTVEGVSPDDLMLTACLAASR.K
1	28	3	2809.28	3.2	0	98.9	33.6	95.00%	-.MTDTSSSSSSSSASSVSAHQPTQEKPAK.T		-.MTDTSSSSSSSSASSVSAHQPTQEKPAK.T
457	469	2	1399.74	4.6	1	74.3	29.7	95.00%	K.KVTAVVESPEGER.I		K.KVTAVVESPEGER.I
185	215	2	3258.67	2.7	0	64	27	95.00%	R.DGQLVEIPANEVVPGDILQLEDGTVIPTDGR.I		R.DGQLVEIPANEVVPGDILQLEDGTVIPTDGR.I
216	239	2	2651.31	4.2	1	101	30.8	95.00%	R.IVTEDCFLQIDQSAITGESLAVDK.H	Carbamidomethyl (+57)	R.IVTEDCFLQIDQSAITGESLAVDK.H
483	508	3	3019.43	3.7	1	56.4	31.7	95.00%	K.TVEEDHPIPEDVHENYENKVAELASR.G		K.TVEEDHPIPEDVHENYENKVAELASR.G
87	96	2	1116.62	2.5	1	33.2	29.2	95.00%	Y.GLTSDEVLKR.R		K.TYDDAASESSDDDDIDALIEELQSNHGVDDEDSDNDGPVAAGEARPVPEEYLQTDPSYGLTSDEVLKR.R
386	414	3	3186.58	2.8	2	68.9	29.2	95.00%	K.NKLSLHEPYTVEGVSPDDLMLTACLAASR.K	Carbamidomethyl (+57)	K.NKLSLHEPYTVEGVSPDDLMLTACLAASR.K
660	679	2	1984.13	3.9	1	71.4	21.9	95.00%	R.SAADIVFLAPGLSAIIDALK.T		R.SAADIVFLAPGLSAIIDALK.T
556	566	2	1074.58	3.2	0	57.6	29.2	95.00%	K.MLTGDAVGIAK.E		K.MLTGDAVGIAK.E
618	625	2	969.56	-0.33	0	33.8	24	95.00%	R.VVEILQNR.G		R.VVEILQNR.G
571	583	2	1447.75	2.8	1	85.2	31.4	95.00%	R.QLGLGTNIYNAER.L		R.QLGLGTNIYNAER.L
363	379	2	1803.93	-1.1	0	67.3	31	95.00%	K.LSAIESLAGVEILCSDK.T	Carbamidomethyl (+57)	K.LSAIESLAGVEILCSDK.T
645	659	2	1416.69	1.4	0	87.4	31.9	95.00%	K.ADTGIAVEGATDAAR.S		K.ADTGIAVEGATDAAR.S
626	643	2	1806.89	2.3	1	92.2	32.9	95.00%	R.GYLVAMTGDGVNDAPSLK.K		R.GYLVAMTGDGVNDAPSLK.K
175	215	3	4297.3	3.9	1	54.1	26.6	95.00%	K.TLANTAVVIRDGQLVEIPANEVVPGDILQLEDGTVIPTDGR.I		K.TLANTAVVIRDGQLVEIPANEVVPGDILQLEDGTVIPTDGR.I
388	415	3	3072.53	2.2	1	48.7	29.4	95.00%	K.LSLHEPYTVEGVSPDDLMLTACLAASRK.K	Carbamidomethyl (+57)	K.LSLHEPYTVEGVSPDDLMLTACLAASRK.K
2	28	3	2720.24	1.6	0	58.3	33.3	95.00%	M.TDTSSSSSSSSASSVSAHQPTQEKPAK.T	Acetyl (+42)	-.MTDTSSSSSSSSASSVSAHQPTQEKPAK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
6	A7A234_YEAS7	56.88%	100%	46

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
380	393	2	1723.88	5.2	1	58	31.4	95.00%	R.LEEDFSEIQNFIIK.N		R.LEEDFSEIQNFIIK.N
232	245	2	1588.76	5.1	2	40.3	32.4	95.00%	Y.ANVPSENDDLVNRF.E		R.HLPVLVYANVPSENDDLVNRFESDISNNDEIVGSSSSTSSVEHGLGAR.S
500	515	2	1889	3.6	2	67.9	29.5	95.00%	K.KHGQWLNDLTNSHLVK.E		K.KHGQWLNDLTNSHLVK.E

543	556	2	1724.88	3.4	1	43.2	31.2	95.00%	F.WLPDLETDIRQDPK.Q		K.LDILPFWLPDLETDIRQDPK.Q
94	102	2	1005.49	1.4	1	49.3	30.7	95.00%	K.ALDADAFQR.V		K.ALDADAFQR.V
793	807	3	1837.97	3.3	1	58	29	95.00%	K.SRQELQIQNLEVPER.I		K.SRQELQIQNLEVPER.I
501	515	3	1760.9	2.9	1	60.9	31.4	95.00%	K.HGQWLNDLTNSHLVK.E		K.HGQWLNDLTNSHLVK.E
79	93	3	1682.89	3.3	1	33.8	28.9	95.00%	R.LSHLEKQTDTEAAIK.A		R.LSHLEKQTDTEAAIK.A
7	16	2	1215.63	-0.35	1	33.4	30.2	95.00%	K.LANEVYPPWK.G		K.LANEVYPPWK.G
419	429	2	1247.71	0.79	1	37.2	26	95.00%	R.VTIDSNIVFIK.E		R.VTIDSNIVFIK.E
144	149	2	715.42	-0.031	0	26.7	28.2	93.20%	K.SLLEVR.L		K.SLLEVR.L
793	818	3	3160.71	4	2	27.4	23.2	95.00%	K.SRQELQIQNLEVPERIPEVLRPLQNY.L		K.SRQELQIQNLEVPERIPEVLRPLQNYLFK.L
17	26	2	1142.57	3.8	1	42.1	31.2	95.00%	K.GSYINYEGLK.K		K.GSYINYEGLK.K
469	477	2	1112.56	3.4	1	49	29.5	95.00%	K.FPYSVMEIK.V		K.FPYSVMEIK.V
652	669	2	2049.92	-1.3	0	64.6	34.1	95.00%	K.LMGVDSEEEEIELPPGVK.K	Phospho (+80)	K.LMGVDSEEEEIELPPGVK.K
103	119	2	2021.04	2.8	1	88.5	31.1	95.00%	R.VLEELLSESTELDNFKR.L		R.VLEELLSESTELDNFKR.L
152	166	2	1818.88	0.43	1	52.8	32.4	95.00%	K.ELPSHSEEYSPLLYR.I		K.ELPSHSEEYSPLLYR.I
604	628	3	2824.18	2.7	1	49.7	33.9	95.00%	R.ITSQGDLEADGSSDEETEQEPHSKR.S	Phospho (+80)	R.ITSQGDLEADGSSDEETEQEPHSKR.S
53	63	2	1377.71	3.5	1	52.3	31.2	95.00%	K.FVEELDKELEK.V		K.FVEELDKELEK.V
232	244	2	1441.68	3.2	0	58.8	32.9	95.00%	Y.ANVPSENDDLVNR.F		R.HLPVLVYANVPSENDDLVNR.F
480	496	2	1745.79	2.3	0	87	34.1	95.00%	K.SSLDSSMSASSMISNVK.L	Oxidation (+16)	K.SSLDSSMSASSMISNVK.L
103	118	2	1864.93	-1	1	94.2	32	95.00%	R.VLEELLSESTELDNFK.R		R.VLEELLSESTELDNFK.R
72	78	2	938.43	-0.13	1	31	31.5	94.50%	K.YNNLMER.L		K.YNNLMER.L
524	542	2	2078.07	4.8	2	31.6	30.4	95.00%	F.VQGVASLYGDDEKLDILPF.W		K.FSIFVQGVASLYGDDEKLDILPFWLPDLETDIR.Q
376	390	2	1882.87	4.8	2	44.8	33.5	95.00%	R.DLERLEEDFSEIQNF.I		R.DLERLEEDFSEIQNFIIK.N
191	204	2	1643.76	2	1	85.8	33.1	95.00%	K.FSSIVSNDIDMNFR.S		K.FSSIVSNDIDMNFR.S
167	175	2	1137.65	0.16	1	52	23.1	95.00%	R.ISFLYNILR.S		R.ISFLYNILR.S
308	322	2	1775.91	2.5	1	68.6	30.9	95.00%	R.WTGQLSDKPDIFLEK.K		R.WTGQLSDKPDIFLEK.K
391	401	2	1355.8	4	2	46.3	24.6	95.00%	F.IIKNELQPVFR.T		R.LEEDFSEIQNFIIKNELQPVFR.T
208	219	2	1530.73	3.6	1	61	32.9	95.00%	K.FWVHNDNLMEVK.T		K.FWVHNDNLMEVK.T
407	416	2	1090.53	3.4	1	47.6	30.9	95.00%	R.TAFQIPGDDK.I		R.TAFQIPGDDK.I
436	447	4	1575.8	-0.44	2	26.3	31.2	95.00%	R.ERPIRDPNTWHR.T		R.ERPIRDPNTWHR.T
434	445	2	1553.77	2.8	2	38.4	32.4	95.00%	F.DRERPIRDPNTW.H		K.EDSFDRERPIRDPNTWHR.T
176	190	2	1522.73	0.77	1	87.7	32.7	95.00%	R.SNFNTASEPLASASK.F		R.SNFNTASEPLASASK.F
448	459	2	1269.66	3	0	58.3	29.6	95.00%	R.TDIDANVANPLK.F		R.TDIDANVANPLK.F
687	693	2	886.47	2.2	1	32.7	29	95.00%	K.VWLANER.T		K.VWLANER.T
795	818	3	2917.58	5	2	35.1	23.3	95.00%	R.QELQIQNLEVPERIPEVLRPLQNY.L		R.QELQIQNLEVPERIPEVLRPLQNYLFK.L
103	117	2	1736.85	5.6	1	36.7	33	95.00%	R.VLEELLSESTELDNF.K		R.VLEELLSESTELDNFK.R
795	807	2	1594.84	3.4	0	74.5	29.7	95.00%	R.QELQIQNLEVPER.I		R.QELQIQNLEVPER.I
677	686	2	997.52	0.57	0	34.7	29.5	95.00%	K.NAGPVNVEAK.V		K.NAGPVNVEAK.V
232	272	3	4303.99	4.9	2	60.9	29.1	95.00%	Y.ANVPSENDDLVNRFESDISNNDEIVGSSSSTSSVEHGLGAR.S		R.HLPVLVYANVPSENDDLVNRFESDISNNDEIVGSSSSTSSVEHGLGAR.S
587	603	2	1946.91	3.4	0	61.9	33.5	95.00%	K.EPQHQAAVPVSQEENER.I		K.EPQHQAAVPVSQEENER.I
298	305	2	870.49	-0.83	0	38.2	25.4	95.00%	K.LNSAPTLR.L		K.LNSAPTLR.L
446	459	3	1562.82	4.9	1	72.8	30	95.00%	W.HRTDIDANVANPLK.F		R.DPNTWHRTDIDANVANPLK.F
581	603	3	2658.36	4.5	1	59.2	29.2	95.00%	R.RLSNLKEPQHQAAVPVSQEENER.I		R.RLSNLKEPQHQAAVPVSQEENER.I
582	603	2	2502.26	3.6	1	90.6	30.5	95.00%	R.LSNLKEPQHQAAVPVSQEENER.I		R.LSNLKEPQHQAAVPVSQEENER.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
7	YBT1_YEAST	37.03%	100%	59

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1456	1468	2	1499.84	4.1	2	32.2	27.1	95.00%	R.RSITIIPQDPTLF.S		R.RSITIIPQDPTLFSGTIK.T
118	130	3	1403.72	0.92	0	25.3	31.3	93.10%	K.VNGEPHGTPEIVR.R		K.VNGEPHGTPEIVR.R
1616	1627	2	1490.75	2.9	1	41.6	31.4	95.00%	K.EYDHPYSLLLNK.Q		K.EYDHPYSLLLNK.Q
1457	1473	2	1830.01	-1.1	1	49	26.2	95.00%	R.SITIIPQDPTLFSGTIK.T		R.SITIIPQDPTLFSGTIK.T

1509	1524	2	1709.73	-0.36	0	45.4	34.2	95.00%	R.ETSNEASSTNSENVNK.F		R.ETSNEASSTNSENVNK.F
670	680	2	1321.62	3.1	1	56.9	32	95.00%	R.VQDFLNENDTK.K		R.VQDFLNENDTK.K
228	240	3	1519.83	0.13	1	21	28.1	90.90%	R.SIFIHHINSPISR.K		R.SIFIHHINSPISR.K
1584	1596	2	1471.78	2.6	1	60.5	29.5	95.00%	K.EFQGSTILTIAHR.L		K.EFQGSTILTIAHR.L
901	912	2	1326.72	2.7	0	85.6	28.2	95.00%	R.NAELVVLLEDGR.V		R.NAELVVLLEDGR.V
588	597	2	1216.65	-0.18	0	42.1	30.3	95.00%	R.ENELSLLLMR.S		R.ENELSLLLMR.S
115	130	3	1718.9	3.5	1	31.2	29.8	95.00%	K.SVKVNGEPHGTPEIVR.R	Deamidation (+1)	K.SVKVNGEPHGTPEIVR.R
936	951	2	1748.79	2.1	1	32	33.9	92.60%	K.SSILSRANSSANLAAK.S	Phospho (+80)/ Phospho (+80)	K.SSILSRANSSANLAAK.S
1422	1430	2	1020.6	-0.025	1	44.2	23.5	95.00%	K.STIITALFR.F		K.STIITALFR.F
1365	1389	3	2938.51	4.3	2	62	28.3	95.00%	Y.NEHKEIPPPQWPQDGKIEVNDLSLR.Y		K.EYMEIEQEPYNEHKEIPPPQWPQDGKIEVNDLSLR.Y
1525	1544	2	2123.02	2.9	1	131	32.8	95.00%	K.FLDLSSEISEGGSNLSQGQR.Q		K.FLDLSSEISEGGSNLSQGQR.Q
1599	1615	2	1893.98	3.9	1	33.8	29.7	95.00%	R.SVIDYDKILVMDAGEVK.E		R.SVIDYDKILVMDAGEVK.E
1583	1596	3	1599.87	0.5	2	49	27.7	95.00%	R.KEFQGSTILTIAHR.L		R.KEFQGSTILTIAHR.L
1494	1508	2	1684.88	4.2	0	86.4	29.2	95.00%	R.VNLISEEQLQQGATR.E		R.VNLISEEQLQQGATR.E
1353	1364	2	1556.71	4.6	2	33.5	33.5	95.00%	R.VKEYMEIEQEPY.N		R.VKEYMEIEQEPYNEHK.E
926	935	2	1105.56	-0.84	1	37.5	30.2	95.00%	K.GLFGEDELVK.S		K.GLFGEDELVK.S
1559	1576	2	1923.98	5.1	1	87.1	30.6	95.00%	K.IILLDEATASIDYSSDAK.I		K.IILLDEATASIDYSSDAK.I
1381	1389	2	1057.58	2.8	0	45.4	29.5	95.00%	K.IEVNDLSLR.Y		K.IEVNDLSLR.Y
806	815	2	1101.6	-0.27	1	44.7	30.1	95.00%	K.AVVEACGLKR.D	Carbamidomethyl (+57)	K.AVVEACGLKR.D
665	680	2	1891.93	2.5	2	60.3	32.1	95.00%	K.VSLDRVQDFLNENDTK.K		K.VSLDRVQDFLNENDTK.K
913	925	2	1485.75	2.3	1	63	30.7	95.00%	R.VKDQGDPIDMLQK.G		R.VKDQGDPIDMLQK.G
952	963	2	1282.62	3.2	0	42.4	32.2	95.00%	K.SSTSLSNLPAVK.E	Phospho (+80)	K.SSTSLSNLPAVK.E
1493	1508	2	1840.98	1.2	1	84.6	28.4	95.00%	K.RVNLISEEQLQQGATR.E		K.RVNLISEEQLQQGATR.E
887	900	3	1609.9	2.8	0	31.3	25.3	95.00%	R.TCILVSHNIALTLR.N	Carbamidomethyl (+57)	R.TCILVSHNIALTLR.N
714	720	2	877.46	3.4	1	29.9	31.6	93.00%	K.DLNIEFK.T		K.DLNIEFK.T
915	925	2	1258.59	2.6	0	33.5	32.4	95.00%	K.DQGDPIDMLQK.G		K.DQGDPIDMLQK.G
855	872	2	2024.94	4.5	1	81.2	33.4	95.00%	R.HVLLDDCLSAVDSHTASW.I	Carbamidomethyl (+57)	R.HVLLDDCLSAVDSHTASWIYDNCITGPLMEDR.T
695	705	2	1296.6	4.8	1	61.4	32.9	95.00%	F.AFENSTISWDK.D		R.FAFENSTISWDK.D
65	100	3	4143.89	4.7	1	90.2	29.9	95.00%	K.NPIDELLYSSTDEDEQSPLINNNTITTNYVDNNCTK.D	Carbamidomethyl (+57)	K.NPIDELLYSSTDEDEQSPLINNNTITTNYVDNNCTK.D
778	790	2	1504.74	4.5	1	88.9	31.8	95.00%	Y.CSQAAWLLNDTVK.N	Carbamidomethyl (+57)	R.QELIVDANGTTNSIAYCSQAAWLLNDTVK.N
1606	1621	2	1877.89	3.1	2	53.6	32.9	95.00%	K.ILVMDAGEVKEYDHPY.S		K.ILVMDAGEVKEYDHPYSLLLNK.Q
1633	1649	2	1943.94	4.1	0	85	32.5	95.00%	Y.SMCEHSGELDILIELAK.K	Carbamidomethyl (+57)	K.QSAFYSMCEHSGELDILIELAK.K
549	556	2	901.46	0.53	0	29.2	29.9	94.30%	K.NLAVTDNR.I		K.NLAVTDNR.I
1633	1650	3	2072.04	4.7	1	44.5	31	95.00%	Y.SMCEHSGELDILIELAKK.A	Carbamidomethyl (+57)	K.QSAFYSMCEHSGELDILIELAKK.A
901	914	2	1553.88	2.3	1	61	25	95.00%	R.NAELVVLLEDGRVK.D		R.NAELVVLLEDGRVK.D
427	436	2	1165.66	-0.44	1	29.7	24.3	95.00%	K.SIIISEIYTK.A		K.SIIISEIYTK.A
791	803	2	1535.74	1.9	1	53.3	33	95.00%	K.NNILFNSPFNEAR.Y	Deamidation (+1)	K.NNILFNSPFNEAR.Y
964	979	2	1816.83	-0.67	1	62.2	34	95.00%	K.EQQVSVNNNSSHFEAK.K		K.EQQVSVNNNSSHFEAK.K
1417	1430	3	1434.82	3.1	2	43.7	24	95.00%	R.TGAGKSTIITALFR.F		R.TGAGKSTIITALFR.F
1238	1255	2	2047.07	-1.2	1	68.1	28.9	95.00%	R.SPIYQHFSETLVGVTTIR.A		R.SPIYQHFSETLVGVTTIR.A
560	568	2	1060.57	2.9	1	58.5	29.4	95.00%	K.LNEAFQAIR.I		K.LNEAFQAIR.I
1152	1160	2	1010.48	0.95	1	73.2	32.5	95.00%	R.FFDATPTGR.I		R.FFDATPTGR.I
1486	1492	2	847.48	-0.028	1	26.8	27.4	94.40%	R.QIFEALK.R		R.QIFEALK.R
1441	1453	2	1456.76	2.9	0	76.1	30	95.00%	K.IDNIDISGVDLQR.L		K.IDNIDISGVDLQR.L
1456	1473	2	1986.11	-1.2	2	64.8	25.1	95.00%	R.RSITIIPQDPTLFSGTIK.T		R.RSITIIPQDPTLFSGTIK.T
822	831	2	1031.51	-0.12	0	58.5	29.9	95.00%	K.AGDLTEIGEK.G		K.AGDLTEIGEK.G
1474	1485	2	1470.63	3.2	1	49	32.8	95.00%	K.TNLDPYDEFSDR.Q		K.TNLDPYDEFSDR.Q
1431	1453	2	2608.36	2.8	1	67.6	27.3	95.00%	R.FLEPETGHIKIDNIDISGVDLQR.L		R.FLEPETGHIKIDNIDISGVDLQR.L
1400	1410	2	1180.56	-6.4	1	33.6	32	95.00%	K.NVSFSVDAQSK.I		K.NVSFSVDAQSK.I
681	693	2	1532.76	2	2	49.3	32	95.00%	K.KYDQLTIDPNGNR.F		K.KYDQLTIDPNGNR.F
557	568	2	1429.81	0.82	2	72.4	27.1	95.00%	R.IQKLNEAFQAIR.I		R.IQKLNEAFQAIR.I

901	925	3	2794.47	4.3	1	44.4	26.9	95.00%	R.NAELVVLLEDGRVKDQGDPIDMLQK.G		R.NAELVVLLEDGRVKDQGDPIDMLQK.G
855	886	3	3702.69	3.6	1	66.2	31.7	95.00%	R.HVLLDDCLSAVDSHTASWIYDNCITGPLMEDR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.HVLLDDCLSAVDSHTASWIYDNCITGPLMEDR.T
873	886	2	1711.76	3.5	1	73.6	33.7	95.00%	W.IYDNCITGPLMEDR.T	Carbamidomethyl (+57)/ Oxidation (+16)	R.HVLLDDCLSAVDSHTASWIYDNCITGPLMEDR.T
724	735	2	1140.65	-0.36	0	24.7	25.1	94.60%	K.LNVVIGPTGSGK.T		K.LNVVIGPTGSGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
8	A6ZL63_YEAS7	65.50%	100%	30

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
321	338	2	1892.82	4.2	2	32.3	34.8	91.60%	R.GNVCGDAKNDPPKGCASF.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GNVCGDAKNDPPKGCASFNATVIVLNHPGQISAGYSPVLDCHTAHIACR.F
225	253	3	3318.82	-1.3	2	39.7	21.9	95.00%	K.TLLEAIDAIEQPSRPTDKPLRLPLQDVYK.I		K.TLLEAIDAIEQPSRPTDKPLRLPLQDVYK.I
265	278	2	1475.81	5.2	1	34.4	28.1	95.00%	R.VETGVIKPGMVVTF.A		R.VETGVIKPGMVVTFAPAGVTTEVK.S
402	421	2	2310.13	3.3	1	92	32.1	95.00%	K.FVPSKPMCVEAFSEYPPLGR.F	Carbamidomethyl (+57)	K.FVPSKPMCVEAFSEYPPLGR.F
165	175	2	1340.67	4.5	2	41.8	31.3	95.00%	R.FQEIVKETSNF.I		R.FQEIVKETSNFIK.K
370	376	2	892.46	3	1	38.3	31.5	95.00%	R.FDELLEK.N		R.FDELLEK.N
289	311	3	2565.2	3.1	1	83.7	32.8	95.00%	K.SVEMHHEQLEQGVPGDNVGFNVK.N	Oxidation (+16)	K.SVEMHHEQLEQGVPGDNVGFNVK.N
195	210	2	1823.82	2.7	1	76.8	33.2	95.00%	W.NGDNMIEATTNAPWYK.G		K.TVPFVPISGWNGDNMIEATTNAPWYK.G
185	208	2	2617.23	3.6	1	47.1	32.9	95.00%	K.TVPFVPISGWNGDNMIEATTNAPW.Y	Deamidation (+1)	K.TVPFVPISGWNGDNMIEATTNAPWYK.G
85	96	2	1354.7	2.5	1	66.3	30	95.00%	K.YQVTVIDAPGHR.D		K.YQVTVIDAPGHR.D
86	98	3	1453.74	3.4	2	26.1	31	94.70%	Y.QVTVIDAPGHRDF.I		K.YQVTVIDAPGHRDFIK.N
225	252	3	3190.74	5.6	2	35.5	22.9	95.00%	K.TLLEAIDAIEQPSRPTDKPLRLPLQDVY.K		K.TLLEAIDAIEQPSRPTDKPLRLPLQDVYK.I
394	401	2	759.41	-0.42	0	45.9	29.6	95.00%	K.SGDAALVK.F		K.SGDAALVK.F
147	154	2	883.55	-0.35	0	43.7	19.3	95.00%	R.QLIVAVNK.M		R.QLIVAVNK.M
254	264	2	1024.61	3.2	0	65.4	21.4	95.00%	K.IGGIGTVPVGR.V		K.IGGIGTVPVGR.V
101	129	3	2922.44	-1.4	1	84.5	30.4	95.00%	K.NMITGTSQADCAILIIAGGVGEFEAGISK.D	Carbamidomethyl (+57)	K.NMITGTSQADCAILIIAGGVGEFEAGISK.D
429	437	2	913.56	0.54	0	47.8	23.6	95.00%	R.QTVAVGVIK.S		R.QTVAVGVIK.S
339	355	2	1752.92	3.5	1	79.7	29.4	95.00%	F.NATVIVLNHPGQISAGY.S		K.GCASFNATVIVLNHPGQISAGYSPVLDCHTAHIACR.F
6	20	2	1559.85	2.7	0	82.3	29.1	95.00%	K.SHINVVVIGHVDSGK.S		K.SHINVVVIGHVDSGK.S
254	288	3	3435.93	3.6	2	48.5	23.2	95.00%	K.IGGIGTVPVGRVETGVIKPGMVVTFAPAGVTTEVK.S		K.IGGIGTVPVGRVETGVIKPGMVVTFAPAGVTTEVK.S
265	288	2	2429.33	3	1	76.9	24.3	95.00%	R.VETGVIKPGMVVTFAPAGVTTEVK.S		R.VETGVIKPGMVVTFAPAGVTTEVK.S
86	96	3	1191.64	3.4	0	22.5	28.8	92.50%	Y.QVTVIDAPGHR.D		K.YQVTVIDAPGHR.D
135	146	2	1325.75	-0.022	1	62.4	26.1	95.00%	R.EHALLAFTLGVR.Q		R.EHALLAFTLGVR.Q
334	369	5	3892.86	0.25	1	25.3	29.4	95.00%	K.GCASFNATVIVLNHPGQISAGYSPVLDCHTAHIACR.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GCASFNATVIVLNHPGQISAGYSPVLDCHTAHIACR.F
246	253	2	974.55	3.5	1	30	29.5	95.00%	R.LPLQDVYK.I		R.LPLQDVYK.I
356	369	2	1635.77	3.8	0	87.5	32.7	95.00%	Y.SPVLDCHTAHIACR.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GCASFNATVIVLNHPGQISAGYSPVLDCHTAHIACR.F
101	134	3	3479.72	4.9	1	79.1	28.6	95.00%	K.NMITGTSQADCAILIIAGGVGEFEAGISKDGQTR.E	Carbamidomethyl (+57)	K.NMITGTSQADCAILIIAGGVGEFEAGISKDGQTR.E
225	245	3	2362.29	1.4	0	42	24	95.00%	K.TLLEAIDAIEQPSRPTDKPLR.L		K.TLLEAIDAIEQPSRPTDKPLR.L
356	376	2	2510.22	5	2	79.6	32.4	95.00%	Y.SPVLDCHTAHIACRFDELLEK.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GCASFNATVIVLNHPGQISAGYSPVLDCHTAHIACRFDELLEK.N

289	308	2	2208	3.9	1	55.3	33.5	95.00%	K.SVEMHHEQLEQGVPGDNVGF.N		K.SVEMHHEQLEQGVPGDNVGFNV K.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
9	B5VNN6_YEAST	25.32%	100%	41							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1024	1046	2	2644.27	4.8	1	91.3	32.1	95.00%	R.AYPDLQIAYLDEEPPLTEGEEPR.I		R.AYPDLQIAYLDEEPPLTEGEEPR.I
980	992	2	1400.69	3.5	1	38.5	31.4	95.00%	F.GGNAEGLERELEK.M		R.VENPEIVQMFGGNAEGLERELEK .M
1047	1063	2	1944.94	1	1	69.2	32.3	95.00%	R.IYSALIDGHCEILDNGR.R	Carbamidomethyl (+57)	R.IYSALIDGHCEILDNGR.R
859	869	2	1406.68	0.76	2	40.5	32.5	95.00%	R.EIIREDDQFSR.V		R.EIIREDDQFSR.V
1779	1788	2	1213.72	2.1	1	23.2	24.9	92.70%	R.QIRPPIYSLK.Q		R.QIRPPIYSLK.Q
1139	1154	3	1783.89	0.79	1	68.3	32.1	95.00%	R.YEEQTTNHPVAIVGAR.E		R.YEEQTTNHPVAIVGAR.E
1010	1023	2	1741.92	2.3	1	51.6	29.3	95.00%	K.FKPHELENAEFLLR.A		K.FKPHELENAEFLLR.A
1024	1048	2	2920.42	4.5	2	59.2	31.1	95.00%	R.AYPDLQIAYLDEEPPLTEGEEPRI Y.S		R.AYPDLQIAYLDEEPPLTEGEEPRI YSALIDGHCEILDNGR.R
260	288	3	3253.43	3.8	2	94.6	32.8	95.00%	K.AMEEANPEDTEETLNKIEGDNSL EAADFR.W	Oxidation (+16)	K.AMEEANPEDTEETLNKIEGDNSL EAADFR.W
1117	1138	2	2473.26	4.2	1	85.7	30.3	95.00%	R.SVLAEFEELNVEQVNPYAPGLR.Y		R.SVLAEFEELNVEQVNPYAPGLR.Y
970	992	3	2587.27	3.4	1	48.6	31.4	95.00%	R.VENPEIVQMFGGNAEGLERELEK .M		R.VENPEIVQMFGGNAEGLERELEK .M
367	376	2	1205.61	2.2	1	28.3	31.6	90.00%	R.NQVYEIIDGR.F		R.NQVYEIIDGR.F
775	787	3	1511.8	3.7	1	38.8	27.9	95.00%	K.LLYHQVPSEIEGK.R		K.LLYHQVPSEIEGK.R
1262	1273	2	1248.6	2.9	0	86.4	31.4	95.00%	K.IGAGMGEQMLSR.E		K.IGAGMGEQMLSR.E
893	915	2	2536.18	-0.17	1	85.4	33	95.00%	K.ILAEETAAYEGNENEAEKEDALK. S		K.ILAEETAAYEGNENEAEKEDALK. S
1047	1064	3	2102.03	4	1	47.6	31.9	95.00%	R.IYSALIDGHCEILDNGRR.R	Carbamidomethyl (+57)/ Deamidation (+1)	R.IYSALIDGHCEILDNGRR.R
970	988	2	2088	3.2	1	70.8	33.2	95.00%	R.VENPEIVQMFGGNAEGLER.E		R.VENPEIVQMFGGNAEGLER.E
1010	1020	2	1359.65	3.7	1	39.6	32	95.00%	K.FKPHELENAEF.L		K.FKPHELENAEFLLR.A
1173	1182	2	1168.59	-0.28	1	52.2	31.1	95.00%	K.EQTFGTLFAR.T		K.EQTFGTLFAR.T
1115	1133	2	2248.15	3.5	2	101	30.1	95.00%	K.IRSVLAEFEELNVEQVNPY.A		K.IRSVLAEFEELNVEQVNPYAPGLR .Y
1134	1154	2	2278.19	1.5	2	66.7	29.2	95.00%	Y.APGLRYEEQTTNHPVAIVGAR.E		R.SVLAEFEELNVEQVNPYAPGLRY EEQTTNHPVAIVGAR.E
1049	1064	3	1825.88	3.3	1	34.3	33.2	95.00%	Y.SALIDGHCEILDNGRR.R	Carbamidomethyl (+57)/ Deamidation (+1)	R.IYSALIDGHCEILDNGRR.R
1436	1444	2	1094.62	3.4	1	52.9	25.7	95.00%	R.IPFSILYSR.F		R.IPFSILYSR.F
1095	1114	2	2427.14	3.6	1	121	33	95.00%	R.GEYIQLIDANQDNYLEECLK.I	Carbamidomethyl (+57)	R.GEYIQLIDANQDNYLEECLK.I
1249	1261	2	1425.75	-0.019	1	69.1	29.4	95.00%	R.DLGFGTILNFTTK.I		R.DLGFGTILNFTTK.I
1070	1082	2	1296.71	0.92	0	44.2	27.4	95.00%	R.VQLSGNPILGDGK.S		R.VQLSGNPILGDGK.S
775	788	3	1667.91	3.7	1	39.6	27.5	95.00%	K.LLYHQVPSEIEGKR.T		K.LLYHQVPSEIEGKR.T
331	344	2	1737.78	0.32	1	100	33.9	95.00%	K.CALDYLDSPLCQQR.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CALDYLDSPLCQQR.Q
184	196	2	1623.75	-0.75	1	75.1	32.8	95.00%	R.NMFDHFMVLLDSR.S		R.NMFDHFMVLLDSR.S
823	852	3	3320.69	4.4	1	24.4	27.5	95.00%	F.AQSLSTPIPEPLPVDNMPTFTVLT PHYAER.I		R.ISFFAQSLSTPIPEPLPVDNMPTF TVLTPHYAER.I
1717	1728	2	1383.61	3.3	1	66.4	32.7	95.00%	K.GMGYMAWTQPSR.E		K.GMGYMAWTQPSR.E
200	222	3	2479.17	-0.39	1	49.5	32.3	95.00%	R.MSPDQALISLHADYIGGDTANYK. K		R.MSPDQALISLHADYIGGDTANYK. K
1216	1232	2	1916.93	4.9	1	49.6	32.4	95.00%	K.GLHLNEDIYAGMNAMLR.G		K.GLHLNEDIYAGMNAMLR.G
1155	1172	2	1854.91	3	1	74	33	95.00%	R.EYIFSENSGVLGDVAAGK.E		R.EYIFSENSGVLGDVAAGK.E
1049	1063	2	1668.8	3.5	0	60.3	33	95.00%	Y.SALIDGHCEILDNGR.R	Carbamidomethyl (+57)	R.IYSALIDGHCEILDNGR.R
1520	1527	2	993.5	0.087	1	45.7	31.4	95.00%	R.NSWIGYVR.M		R.NSWIGYVR.M
953	962	2	1174.55	2	1	46.4	31.9	95.00%	R.TISGFMNYSR.A		R.TISGFMNYSR.A
406	422	2	1966.1	2	1	83.6	23.4	95.00%	K.IVLEDGTKLIELPLEER.Y		K.IVLEDGTKLIELPLEER.Y
870	877	2	977.58	3.3	1	51.5	21.6	95.00%	R.VTLLEYLK.Q		R.VTLLEYLK.Q

1191	1203	2	1530.73	4.2	1	42.2	33	95.00%	K.LHYGHPDFINATF.M		K.LHYGHPDFINATFMTTR.G
1117	1133	3	1978.96	6.1	1	42	32.4	95.00%	R.SVLAEFEELNVEQVNPY.A		R.SVLAEFEELNVEQVNPYAPGLR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
10	A6ZY95_YEAS7	31.29%	100%	40

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
620	638	2	2117.05	-1.4	1	36.1	31.5	95.00%	K.NIGDVAINIGDDATFLWQR.K		K.NIGDVAINIGDDATFLWQR.K
1251	1273	2	2569.34	3.2	2	34.2	28.1	95.00%	K.SEAPLIVEGHRPPKEWPSQGDIK.F		K.SEAPLIVEGHRPPKEWPSQGDIK.F
221	231	2	1299.64	-0.32	1	72.8	32.6	95.00%	R.ITFSWMSGLMK.T		R.ITFSWMSGLMK.T
1036	1048	2	1466.73	2.8	1	60.5	32.8	95.00%	R.APMTFFETTPIGR.I		R.APMTFFETTPIGR.I
1349	1364	2	1787.95	3.5	1	35.3	29	95.00%	K.LSIIPQDSQVFEGTVR.E		K.LSIIPQDSQVFEGTVR.E
775	789	3	1632.85	4.2	0	47.2	30.4	95.00%	Y.LLDDPLAAVDEHVAR.H		R.ADTYLLDDPLAAVDEHVAR.H
790	805	2	1777	0.61	0	83.5	24.3	95.00%	R.HLIEHVLGPNGLLHTK.T		R.HLIEHVLGPNGLLHTK.T
1159	1174	2	1825.85	3.1	1	50.7	34.1	95.00%	R.IDNNMSAFYPSINANR.W		R.IDNNMSAFYPSINANR.W
1365	1380	2	1975.94	4.7	1	110	33.7	95.00%	R.ENIDPINQYTDEAIWR.A		R.ENIDPINQYTDEAIWR.A
486	495	2	1141.67	3.6	0	67.1	26.4	95.00%	R.VISEILNNIK.S		R.VISEILNNIK.S
863	875	2	1399.58	-0.44	1	76	33.1	95.00%	K.SNEFGDSSESSVR.E		K.SNEFGDSSESSVR.E
670	682	2	1495.75	-0.73	1	73.1	31.6	95.00%	K.TALLSCMLGDLFR.V	Carbamidomethyl (+57)	K.TALLSCMLGDLFR.V
863	890	3	3066.43	0.49	1	41.4	32.3	95.00%	K.SNEFGDSSESSVRESSIPVEGELEQLQK.L		K.SNEFGDSSESSVRESSIPVEGELEQLQK.L
249	261	2	1537.76	-1.2	1	62.3	32.3	95.00%	R.NFSSEELSQKLEK.N		R.NFSSEELSQKLEK.N
1281	1290	3	1244.72	4.7	1	50.8	25.9	95.00%	R.YRPELDLVLK.H		R.YRPELDLVLK.H
1251	1264	4	1528.84	4	0	24.8	28.3	95.00%	K.SEAPLIVEGHRPPK.E		K.SEAPLIVEGHRPPK.E
1430	1446	2	1800.94	4	0	66.5	29.9	95.00%	K.ILVLDEATAAVDVETDK.V		K.ILVLDEATAAVDVETDK.V
655	664	2	1088.6	-0.72	1	27.5	29	93.20%	K.KGNLTCIVGK.V	Carbamidomethyl (+57)	K.KGNLTCIVGK.V
1380	1388	3	1065.63	3.6	1	37.7	20.3	95.00%	W.RALELSHLK.E		R.ENIDPINQYTDEAIWRALELSHLK.E
876	890	2	1684.85	0.53	0	48.6	31	95.00%	R.ESSIPVEGELEQLQK.L		R.ESSIPVEGELEQLQK.L
1485	1499	2	1618.79	2.6	1	74.9	32.2	95.00%	K.VAEFDSPGQLLSDNK.S		K.VAEFDSPGQLLSDNK.S
1347	1359	2	1510.82	3.4	2	41.8	26.8	95.00%	R.HKLSIIPQDSQVF.E		R.HKLSIIPQDSQVFEGTVR.E
192	206	3	1835.99	-0.81	0	26	26.7	95.00%	K.KPLMPHQHIHQTLTR.R		K.KPLMPHQHIHQTLTR.R
207	218	2	1420.72	3.7	2	31.7	31.7	95.00%	R.RKPNPYDSANIF.S		R.RKPNPYDSANIFSR.I
271	281	2	1289.62	1.9	1	49	31.9	95.00%	K.SNPSLSWAICR.T	Carbamidomethyl (+57)	K.SNPSLSWAICR.T
1322	1343	2	2390.22	5.6	1	48.5	30.5	95.00%	R.MIEASEGNIVIDNIAINEIGLY.D		R.MIEASEGNIVIDNIAINEIGLYDLR.H
771	789	2	2083.03	4.3	1	98	32	95.00%	R.ADTYLLDDPLAAVDEHVAR.H		R.ADTYLLDDPLAAVDEHVAR.H
1458	1467	3	1194.68	-0.5	1	38.8	23.2	95.00%	K.DRTILTIAHR.L		K.DRTILTIAHR.L
1126	1143	2	1975.01	-1.2	1	77.8	31	95.00%	R.SPIYSHFQETLGGLATVR.G		R.SPIYSHFQETLGGLATVR.G
1347	1364	3	2053.1	3.4	2	78.2	27.5	95.00%	R.HKLSIIPQDSQVFEGTVR.E		R.HKLSIIPQDSQVFEGTVR.E
1313	1321	2	1006.58	3.4	1	41.4	24.8	95.00%	K.SSLTLALFR.M		K.SSLTLALFR.M
1460	1467	2	923.55	-1.9	0	32.8	19.6	95.00%	R.TILTIAHR.L		R.TILTIAHR.L
891	905	2	1728.78	2.8	1	45.4	33.7	95.00%	K.LNDLDFGNSDAISLR.R	Phospho (+80)	K.LNDLDFGNSDAISLR.R
2	11	2	1104.54	3.3	1	55.8	31.4	95.00%	M.AGNLVSWACK.L	Carbamidomethyl (+57)	-.MAGNLVSWACK.L
1468	1484	2	1916.01	2.5	1	73.1	28.7	95.00%	R.LNTIMDSDRIIVLDNGK.V		R.LNTIMDSDRIIVLDNGK.V
728	743	2	1718.86	-1.6	0	79.2	31.9	95.00%	K.ACALTIDLAILMDGDK.T	Carbamidomethyl (+57)	K.ACALTIDLAILMDGDK.T
1389	1415	2	2783.32	3.1	0	143	32.2	95.00%	K.EHVLSMSNDGLDAQLTEGGGNLSVGQR.Q		K.EHVLSMSNDGLDAQLTEGGGNLSVGQR.Q
1416	1422	2	872.49	-0.56	0	28.1	29.7	93.00%	R.QLLCLAR.A	Carbamidomethyl (+57)	R.QLLCLAR.A
1381	1388	2	909.52	-7.3	0	35.3	21.3	95.00%	R.ALELSHLK.E		R.ALELSHLK.E
379	388	2	1106.63	-0.37	1	29.1	25.5	95.00%	K.SALTALIYQK.S		K.SALTALIYQK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
11	B3LFI5_YEAS1	51.77%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
355	383	2	3092.49	3.5	1	120	30.9	95.00%	Y.VLEFAENSDTETVLVSTSDHETGGLVTSR.Q		R.EVLAFDEAFQYVLEFAENSDTETVLVSTSDHETGGLVTSR.Q
427	438	2	1511.84	3.5	1	46.2	26	95.00%	K.IENFIKHEILEK.D		K.IENFIKHEILEK.D

172	187	2	1765.82	-1.3	1	65.2	33	95.00%	R.ITDATPASFSSHVDYR.W		R.ITDATPASFSSHVDYR.W
236	249	2	1574.7	3.5	2	49.2	34	95.00%	K.DGRDLIDEAQSNGW.Q		K.DGRDLIDEAQSNGWQYVGDR.K
467	474	2	996.47	1.4	1	33.9	32.3	95.00%	K.LNDMVSFR.A	Oxidation (+16)	K.LNDMVSFR.A
439	466	3	3179.5	5.1	1	49.8	31.7	95.00%	K.DLGIYDYTDSDLETLIHLDDNANAIQDK.L		K.DLGIYDYTDSDLETLIHLDDNANAIQDK.L
113	130	2	1755.84	4.3	2	56.5	33.1	95.00%	R.TRSSDSLVTDSAAGATAF.A		R.TRSSDSLVTDSAAGATAFACALK.S
136	158	2	2448.21	3.4	1	47.6	31.9	95.00%	K.SYNGAIGVDPHHRPCGTVLEAAK.L	Carbamidomethyl (+57)	K.SYNGAIGVDPHHRPCGTVLEAAK.L
159	171	2	1362.79	2.6	1	69.1	22.1	95.00%	K.LAGYLTGLVVTTR.I		K.LAGYLTGLVVTTR.I
187	205	4	2281.17	5.7	2	34.5	30.1	95.00%	Y.RWQEDLIATHQLGEYPLGR.V		R.ITDATPASFSSHVDYRWQEDLIATHQLGEYPLGR.V
206	215	2	1031.54	-0.9	0	57.7	30.7	95.00%	R.VVDLLMGGGR.S	Oxidation (+16)	R.VVDLLMGGGR.S
285	297	2	1620.81	3.2	2	38.2	32.1	95.00%	F.EIDRDEKEYPSLK.E		K.SHGENVTLPFLGLFADNDIPFEIDRDEKEYPSLK.E
329	343	3	1643.78	-0.36	0	26.3	33	91.90%	R.IDHAGHQNDPASQVR.E		R.IDHAGHQNDPASQVR.E
188	205	2	2125.06	0.89	1	74.6	31.3	95.00%	R.WQEDLIATHQLGEYPLGR.V		R.WQEDLIATHQLGEYPLGR.V
1	12	3	1430.67	0.57	0	37.6	33.2	95.00%	-.MMTHTLPSEQTR.L		-.MMTHTLPSEQTR.L
68	86	2	2027.98	-0.76	1	95.4	32.8	95.00%	K.NVIFFVTDGMGPASLSMAR.S	Oxidation (+16)	K.NVIFFVTDGMGPASLSMAR.S
235	249	2	1702.8	3.3	2	52	33.6	95.00%	R.KDGRDLIDEAQSNGW.Q		R.KDGRDLIDEAQSNGWQYVGDR.K
316	328	2	1457.66	-1.5	1	45.5	33.2	95.00%	K.DSNGFFLMVEGSR.I		K.DSNGFFLMVEGSR.I
113	135	2	2299.12	2.6	2	51.4	32.1	95.00%	R.TRSSDSLVTDSAAGATAFACALK.S	Carbamidomethyl (+57)	R.TRSSDSLVTDSAAGATAFACALK.S
115	135	2	2041.96	-1.6	1	110	33.8	95.00%	R.SSDSLVTDSAAGATAFACALK.S	Carbamidomethyl (+57)	R.SSDSLVTDSAAGATAFACALK.S
87	112	3	2981.46	3.9	1	89	30.4	95.00%	R.SFNQHVNDLPIDDILTLDEHFIGSSR.T		R.SFNQHVNDLPIDDILTLDEHFIGSSR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
12	A7A160_YEAS7	53.95%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
12	27	2	1762.88	-0.57	0	96	31.9	95.00%	K.TITLEVESSDTIDNVK.S		K.TITLEVESSDTIDNVK.S
49	59	2	1295.61	4.4	2	31.2	33.1	92.70%	K.QLEDGRTLSDY.N		K.QLEDGRTLSDYNIQK.E
55	72	2	2129.15	2.4	1	75.3	27.5	95.00%	R.TLSDYNIQKESTLHLVLR.L		R.TLSDYNIQKESTLHLVLR.L
64	72	2	1066.62	3.4	0	51.7	23.6	95.00%	K.ESTLHLVLR.L		K.ESTLHLVLR.L
1	6	2	764.43	3.8	1	35.4	25.3	95.00%	-.MQIFVK.T		-.MQIFVK.T
120	136	2	1860.83	2.3	1	85.7	33.9	95.00%	R.ECSNPTCGAGVFLANHK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.ECSNPTCGAGVFLANHK.D
34	42	2	1038.51	-0.21	0	38.7	32.3	95.00%	K.EGIPPDQQR.L		K.EGIPPDQQR.L
55	63	2	1080.55	0.55	1	50	30.7	95.00%	R.TLSDYNIQK.E		R.TLSDYNIQK.E
43	54	2	1345.74	2.5	1	60.8	28.1	95.00%	R.LIFAGKQLEDGR.T		R.LIFAGKQLEDGR.T
30	42	2	1522.77	-0.73	1	32.8	31.8	95.00%	K.IQDKEGIPPDQQR.L		K.IQDKEGIPPDQQR.L
60	72	3	1549.9	4.1	1	49.3	22.5	95.00%	Y.NIQKESTLHLVLR.L		R.TLSDYNIQKESTLHLVLR.L
49	63	2	1778.88	2.1	2	46.8	32.2	95.00%	K.QLEDGRTLSDYNIQK.E		K.QLEDGRTLSDYNIQK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
13	CBPS_YEAST	37.85%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
230	257	3	2908.44	4.3	1	39.6	30.7	95.00%	R.TIVMSLGFDEEASGTLGAASLASFLHER.Y		R.TIVMSLGFDEEASGTLGAASLASFLHER.Y
379	386	2	953.51	4.2	0	44.3	25.7	95.00%	Y.ISNQSHLR.S		K.LVEYISNQSHLR.S
108	119	2	1391.6	2.3	1	53.2	33.5	95.00%	K.NPNPADDPDFYK.H		K.NPNPADDPDFYK.H
419	431	2	1499.78	3	1	49.2	30.2	95.00%	R.INLHSSVAEVFER.N		R.INLHSSVAEVFER.N
533	544	2	1331.77	-0.39	1	55.2	23.7	95.00%	R.FVGSIIDIDLLK.T		R.FVGSIIDIDLLK.T
63	74	2	1433.73	2.9	2	43.2	31.8	95.00%	K.CEKIEPLSPSFK.H	Carbamidomethyl (+57)	K.CEKIEPLSPSFK.H
450	470	2	2397.22	6.1	1	88	29.5	95.00%	K.NGDDYIIPETELGHIDITLLR.E	Deamidation (+1)	K.NGDDYIIPETELGHIDITLLR.E
360	370	3	1258.69	3	2	46.3	28.4	95.00%	K.KTILGAPFCPR.R	Carbamidomethyl (+57)	K.KTILGAPFCPR.R

413	418	2	798.45	-0.79	1	24.3	21.6	94.30%	R.FLINHR.I		R.FLINHR.I
258	278	2	2317.04	5.3	1	131	34	95.00%	R.YGDDGIYSIIDEGEGIMEVDK.D		R.YGDDGIYSIIDEGEGIMEVDK.D
361	370	2	1130.59	2.8	1	29.6	30	94.70%	K.TILGAPFCPR.R	Carbamidomethyl (+57)	K.TILGAPFCPR.R
391	403	2	1314.71	-0.23	0	87.6	29.3	95.00%	R.TTQAVDIINGGVK.A		R.TTQAVDIINGGVK.A
373	386	3	1700.89	4.5	2	54.8	28.8	95.00%	K.DKLVEYISNQSHLR.S		K.DKLVEYISNQSHLR.S
545	564	2	2142.09	3.5	1	77.6	30	95.00%	K.TLHSVNEHVDVPGHLSAIAF.V		K.TLHSVNEHVDVPGHLSAIAFVYEY IVNVNEYA.-
208	229	2	2542.39	4.5	1	75.6	23.9	95.00%	K.NLLIAEFEAIEQLLIDGFKPNR.T		K.NLLIAEFEAIEQLLIDGFKPNR.T
375	386	2	1457.77	2.9	1	59.4	29.8	95.00%	K.LVEYISNQSHLR.S		K.LVEYISNQSHLR.S
75	87	2	1506.76	3.3	1	70.2	31.6	95.00%	K.HSVDTILHDPAFR.N		K.HSVDTILHDPAFR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
14	PPN1_YEAST	30.86%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
623	634	2	1535.67	3	1	50.8	33.2	95.00%	R.YEIEYTSDEKPY.S		R.YEIEYTSDEKPYSMDSLTVGSYL DLAGR.L
184	198	2	1707.82	2.9	1	82.5	33.1	95.00%	R.TEAQIFDMNNIVADK.M		R.TEAQIFDMNNIVADK.M
606	621	2	1918.95	4.8	2	38.9	31.5	95.00%	K.INQELHNSFVESKDIF.R		K.INQELHNSFVESKDIFR.Y
606	614	2	1100.53	2.9	1	35.8	31.7	95.00%	K.INQELHNSF.V		K.INQELHNSFVESK.D
72	83	2	1334.83	3.4	1	36.5	14.8	95.00%	R.LGLTPREPVIIK.D		R.LGLTPREPVIIK.D
645	652	2	919.52	2.8	2	26.3	29.4	90.50%	Y.LDLAGRLY.E		R.YEIEYTSDEKPYSMDSLTVGSYL DLAGRLYENKPAWEK.Y
390	407	2	2119.88	-1.2	0	106	33.9	95.00%	R.VQQGEDSNEEDEETELNR.I		R.VQQGEDSNEEDEETELNR.I
361	374	3	1580.75	3.4	1	31.4	33.2	95.00%	Y.GHMNIDHFIPTDGK.K		R.DIIIGGLYGHMNIDHFIPTDGK.K
533	554	3	2508.15	4.3	0	31.5	33.5	95.00%	K.IMEDSLLEDEMDSSNIEVGINR.E		K.IMEDSLLEDEMDSSNIEVGINR.E
204	233	3	3334.5	3.7	2	32.6	32.6	95.00%	F.SAGNEEDPRDFDVSVIPSLGNND VFPHNMF.A	Oxidation (+16)	K.MTELFSAGNEEDPRDFDVSVIPS LGNNDVFPHNMFALGPTLQTR.E
72	86	2	1677.02	1.3	1	49.9	16.6	95.00%	R.LGLTPREPVIIKDVK.T		R.LGLTPREPVIIKDVK.T
137	153	2	1923.88	4.5	0	98.6	33.6	95.00%	K.AMSGCDSPVILMEETLR.W	Oxidation (+16)/ Carbamidomethyl (+57)	K.AMSGCDSPVILMEETLR.W
361	375	3	1708.84	3.1	1	31.1	32.8	95.00%	Y.GHMNIDHFIPTDGKK.A		R.DIIIGGLYGHMNIDHFIPTDGKK.A
390	416	3	3070.39	4	1	52.2	32.3	95.00%	R.VQQGEDSNEEDEETELNRILDHA MAAK.E		R.VQQGEDSNEEDEETELNRILDHA MAAK.E
234	242	2	955.55	4.4	0	36.4	24.7	95.00%	F.ALGPTLQTR.E		R.DFDVSVIPSLGNNDVFPHNMFAL GPTLQTR.E
606	618	2	1543.76	0.51	1	74.3	31.6	95.00%	K.INQELHNSFVESK.D		K.INQELHNSFVESK.D
635	650	2	1683.82	4.7	1	71.2	32.6	95.00%	Y.SMDSLTVGSYLDLAGR.L		R.YEIEYTSDEKPYSMDSLTVGSYL DLAGR.L
263	274	2	1247.68	0.46	1	31.7	29.8	95.00%	R.SASFLTEVIPGK.L		R.SASFLTEVIPGK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
15	A6ZQR8_YEAS7	31.77%	100%	24

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
710	723	2	1559.86	5.6	1	39.3	27.4	95.00%	K.EVGIVFGETLILDR.A		K.EVGIVFGETLILDR.A
909	929	3	2238.18	3.2	0	52.5	27.5	95.00%	K.AVEEANSKPVEVIKPNGLSEK.K	Deamidation (+1)	K.AVEEANSKPVEVIKPNGLSEK.K
248	260	3	1538.83	3.4	1	24.1	27.1	95.00%	R.TMGIKPYTINVFR.N		R.TMGIKPYTINVFR.N
955	967	2	1323.62	3	1	81.8	32.8	95.00%	K.LGDASCAAPFTSK.L	Carbamidomethyl (+57)	K.LGDASCAAPFTSK.L
489	516	3	2977.48	5.5	2	66.8	29.4	95.00%	K.TGTLTGEDLVFEGLAGISADSENI RHLY.S		K.TGTLTGEDLVFEGLAGISADSENI RHLYSAAEAPESTILVIGAAHALVK.L
806	825	2	2144.92	2.5	1	83.2	34	95.00%	K.DMGYQTLMCGDGTNDVGALK.Q	Carbamidomethyl (+57)	K.DMGYQTLMCGDGTNDVGALK.Q
103	117	2	1599.79	4.5	0	65.3	32	95.00%	Y.TTPNNGSDGIVEIQR.V		K.NVNEATHILIYTTPNNGSDGIVEIQ R.V

669	684	2	1912.02	3.8	1	57.4	27.4	95.00%	F.LIFHCPLKDDAIETIK.M	Carbamidomethyl (+57)	R.DDVESELTFNGFLIFHCPLKDDAIETIK.M
514	537	3	2460.34	2.6	1	59.7	25	95.00%	R.HLYSAAEAPESTILVIGAAHALVK.L		R.HLYSAAEAPESTILVIGAAHALVK.L
672	684	2	1538.78	4.3	1	46.8	30.9	95.00%	F.HCPLKDDAIETIK.M	Carbamidomethyl (+57)	R.DDVESELTFNGFLIFHCPLKDDAIETIK.M
264	282	2	2198.18	2.9	1	56.2	27	95.00%	K.WVALQTNELLPMDLVSITR.T		K.WVALQTNELLPMDLVSITR.T
589	604	2	1600.83	2.7	1	80.6	31.1	95.00%	R.SASIASHNDALFAAVK.G		R.SASIASHNDALFAAVK.G
481	488	2	1055.44	2.9	1	38	30.9	95.00%	R.IDVCCFDK.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.IDVCCFDK.T
514	550	4	3858.97	-0.67	1	44.9	26.1	95.00%	R.HLYSAAEAPESTILVIGAAHALVKLEDGDIVGDPMEK.A		R.HLYSAAEAPESTILVIGAAHALVKLEDGDIVGDPMEK.A
372	383	2	1280.64	1.6	1	75.5	31.6	95.00%	K.TGFETSQGSLVR.V		K.TGFETSQGSLVR.V
489	513	2	2564.28	5.6	1	88.3	31.2	95.00%	K.TGTLTGEDLVFEGLAGISADSENIR.H		K.TGTLTGEDLVFEGLAGISADSENIR.H
930	954	3	2464.29	2.7	0	55.5	28.1	95.00%	K.KPADLASLLLNSAGDAQGDEAPALK.L		K.KPADLASLLLNSAGDAQGDEAPALK.L
283	316	3	3556.81	5.2	0	40.3	26.3	95.00%	R.TAEESAIPCDLILLDGSAIVNEAMLSGESTPLLK.E	Carbamidomethyl (+57)	R.TAEESAIPCDLILLDGSAIVNEAMLSGESTPLLK.E
321	335	2	1697.86	3.3	0	68.5	31	95.00%	K.LRPSEDNLQLDGVDK.I		K.LRPSEDNLQLDGVDK.I
968	979	2	1269.74	3.3	0	75.9	24.7	95.00%	K.LANVSAVTNIIR.Q		K.LANVSAVTNIIR.Q
769	780	2	1307.7	3.8	0	58.9	30	95.00%	Y.ALNALEGHSQLR.D		R.YDIAVTGYALNALEGHSQLR.D
867	887	3	2345.23	-0.82	1	27.4	28.7	95.00%	R.WNQPQPPVPEPIAHLFPPGPK.N		R.WNQPQPPVPEPIAHLFPPGPK.N
92	117	3	2867.44	-0.13	1	41.7	30	95.00%	K.NVNEATHILIYTTPNNGSDGIVEIQR.V		K.NVNEATHILIYTTPNNGSDGIVEIQR.V
345	371	4	2747.5	4.6	1	30.9	24.2	95.00%	K.ALQVTPPEHKSDIPPPPDGGALAIVTK.T		K.ALQVTPPEHKSDIPPPPDGGALAIVTK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
16	KTR1_YEAST	39.44%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
46	57	2	1247.6	0.56	1	77.6	31.6	95.00%	K.YSTVLSSGSGYK.Y		K.YSTVLSSGSGYK.Y
245	270	3	3050.36	4.7	1	51	33.2	95.00%	K.FMEAHPELIHENNMLDFVSDDQGLSY.N		K.FMEAHPELIHENNMLDFVSDDQGLSYNLCHFWSNFEIAALDLWR.S
324	332	3	1152.57	3.9	2	25.8	31.4	93.60%	F.LDRSEIHHF.G		R.WGDAPVHSIGAALFLDRSEIHHFGDIGYYHVPFHSCPIDTSIR.L
310	323	2	1439.73	4.7	1	65.8	31.3	95.00%	R.WGDAPVHSIGAALF.L		R.WGDAPVHSIGAALFLDR.S
83	92	2	1137.6	3.9	1	44.3	30.8	95.00%	R.DLYSLAESIK.S		R.DLYSLAESIK.S
203	213	2	1423.65	1.6	1	55.7	33.1	95.00%	K.LHCDIDYDVFK.F	Carbamidomethyl (+57)	K.LHCDIDYDVFK.F
163	172	2	1185.61	2.5	1	40.8	30	95.00%	R.IIYGDSISYR.H		R.IIYGDSISYR.H
230	243	2	1708.83	1.7	1	41.9	33	95.00%	K.EYEATIPTLWETTR.K		K.EYEATIPTLWETTR.K
310	326	2	1823.94	3.1	1	80.3	30.1	95.00%	R.WGDAPVHSIGAALFLDR.S		R.WGDAPVHSIGAALFLDR.S
73	80	2	905.54	3.9	1	59.6	25.1	95.00%	K.ATFVTLVR.N		K.ATFVTLVR.N
339	352	3	1664.82	4	1	32	32.7	95.00%	Y.HVPFHSCPIDTSIR.L	Carbamidomethyl (+57)	R.SEIHHFGDIGYYHVPFHSCPIDTSIR.L
138	150	2	1730.76	4	1	61.5	34.1	95.00%	K.EHWSFPEWIDEEK.A		K.EHWSFPEWIDEEK.A
81	92	2	1407.74	2.7	2	63.1	29.7	95.00%	R.NRDLYSLAESIK.S		R.NRDLYSLAESIK.S
277	288	2	1433.74	4.9	1	50.3	31.1	95.00%	W.SNFEIAALDLWR.S		K.FMEAHPELIHENNMLDFVSDDQGLSYNLCHFWSNFEIAALDLWR.S
343	352	2	1184.57	4	0	44.3	31.7	95.00%	F.HSCPIDTSIR.L	Carbamidomethyl (+57)	R.SEIHHFGDIGYYHVPFHSCPIDTSIR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
17	A6ZMV7_YEAS7	26.70%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

203	228	3	3013.41	-1.7	1	44.1	31.9	95.00%	R.LSNESQPLLNHDDHDHSHESKKPGHR.S			R.LSNESQPLLNHDDHDHSHESKKPGHR.S
358	383	3	2931.44	3.2	1	85.2	30.6	95.00%	K.IFHQHGIHSATVQPEFVSGDVNEDIR.R			K.IFHQHGIHSATVQPEFVSGDVNEDIR.R
293	309	2	1854.03	3.8	0	104	25.7	95.00%	R.ILLQATPSTISADQIQR.E			R.ILLQATPSTISADQIQR.E
386	411	2	2674.21	2.5	1	89.8	33.7	95.00%	R.FSIIAGGSPSSSQEAFDSHGNTEHGR.K			R.FSIIAGGSPSSSQEAFDSHGNTEHGR.K
420	442	2	2443.02	4.3	0	113	34.1	95.00%	Y.GATTASSNCIVDDAVNCNTSNCL.-	Carbamidomethyl (+57)/Carbamidomethyl (+57)/Carbamidomethyl (+57)		R.SPTAYGATTASSNCIVDDAVNCNTSNCL.-
203	223	2	2438.09	3.5	0	55.4	34.1	95.00%	R.LSNESQPLLNHDDHDHSHESK.K			R.LSNESQPLLNHDDHDHSHESK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
18	B3LPA7_YEAS1	22.42%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
83	107	3	2992.37	-1.1	1	45.7	32.7	95.00%	R.LQVVSHETDINEDEEEAHYEDKHVK.R		R.LQVVSHETDINEDEEEAHYEDKHVK.R
287	300	2	1397.7	3.3	1	31.2	31.4	94.90%	R.NPGAWGPGIISSDK.S		R.NPGAWGPGIISSDK.S
504	513	2	1146.61	2.7	2	29.1	30.1	94.00%	R.GISRDDLPFK.A		R.GISRDDLPFK.A
17	45	3	3352.49	3.1	0	48.3	32.8	95.00%	K.QNNIGEQSMQELPEDQIEHEMEAIDPSNK.T		K.QNNIGEQSMQELPEDQIEHEMEAIDPSNK.T
588	600	2	1585.76	3.3	1	43.6	32.6	95.00%	R.EIEAIIWEDDEPK.N		R.EIEAIIWEDDEPK.N
83	104	3	2628.16	3.5	1	89.1	33.5	95.00%	R.LQVVSHETDINEDEEEAHYEDK.H		R.LQVVSHETDINEDEEEAHYEDK.H
4	12	2	1022.54	2.3	1	55.3	29.3	95.00%	R.FSNIITSNK.W		R.FSNIITSNK.W
576	587	2	1473.75	2.7	1	55.5	31.3	95.00%	W.KLEDIDIDSDRR.E		R.FIWKLEDIDIDSDRR.E
17	49	3	3830.7	2.6	2	44.4	31.4	95.00%	K.QNNIGEQSMQELPEDQIEHEMEAIDPSNKTTPY.S	Oxidation (+16)	K.QNNIGEQSMQELPEDQIEHEMEAIDPSNKTTPYSIDEK.Q
62	82	2	2110.09	4.1	0	114	29.9	95.00%	K.HGSLQGGAIADVNSITNSLTR.L		K.HGSLQGGAIADVNSITNSLTR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
19	ATC2_YEAST	26.17%	100%	26

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
235	251	2	1867.81	-1.1	0	122	34.1	95.00%	K.CEADESSITGESNTIQK.F	Carbamidomethyl (+57)	K.CEADESSITGESNTIQK.F
486	496	2	1326.59	-0.22	1	89.2	32.8	95.00%	K.VFEENCSSSLR.N	Carbamidomethyl (+57)	K.VFEENCSSSLR.N
264	298	4	3854.81	3.4	1	40.1	29.8	95.00%	K.FNSIDSHNHSKPLDIGDVNEDGNKIADCMLISGSR.I	Carbamidomethyl (+57)	K.FNSIDSHNHSKPLDIGDVNEDGNKIADCMLISGSR.I
432	446	2	1602.63	-0.15	0	102	32.7	95.00%	R.SCETMGSATAVCSDK.T	Carbamidomethyl (+57)/Carbamidomethyl (+57)	R.SCETMGSATAVCSDK.T
71	83	2	1432.73	-0.15	1	45.8	31	95.00%	K.NAGISLPEISNYR.K		K.NAGISLPEISNYR.K
71	84	2	1560.83	2	1	31.2	30.4	95.00%	K.NAGISLPEISNYRK.T		K.NAGISLPEISNYRK.T
760	770	2	1161.61	-0.79	0	41.5	30.4	95.00%	R.MVTGDNILTAK.A		R.MVTGDNILTAK.A
447	459	2	1419.74	-0.85	0	52.8	31.2	95.00%	K.TGTLTENVMTVVR.G		K.TGTLTENVMTVVR.G
868	887	2	2165.09	-0.66	1	94.7	30.9	95.00%	R.EASDIILMTDDFSAIVNAIK.W		R.EASDIILMTDDFSAIVNAIK.W
658	679	3	2593.16	3.7	1	57.4	33.7	95.00%	R.NSDDTLEEINEDNKKETDDEIK.N		R.NSDDTLEEINEDNKKETDDEIK.N
574	583	2	1073.61	0.07	0	45.8	27.1	95.00%	K.TETALLSLAR.L		K.TETALLSLAR.L
857	867	2	1106.54	3.4	0	33.6	31.2	95.00%	F.SMGISGTEVAR.E		K.LADVGFSMGISGTEVAR.E
709	726	2	1988.03	4.2	2	106	30	95.00%	R.DKDSPNIAALDLLFNSQK.G		R.DKDSPNIAALDLLFNSQK.G
727	741	2	1591.94	4.4	0	54.3	20.6	95.00%	K.GLILDGLLGIQDPLR.A		K.GLILDGLLGIQDPLR.A
37	46	2	1137.58	-0.63	0	43.1	31.9	95.00%	K.SQLSDLHNPK.S		K.SQLSDLHNPK.S
263	287	4	2779.31	-0.85	2	32.8	32	95.00%	K.KFNSIDSHNHSKPLDIGDVNEDGNK.I		K.KFNSIDSHNHSKPLDIGDVNEDGNK.I
584	597	2	1585.88	-0.38	1	49.8	28.1	95.00%	R.LSLGLQPGELQYLR.D		R.LSLGLQPGELQYLR.D
711	726	2	1744.9	-0.76	1	65.5	30.5	95.00%	K.DSPNIAALDLLFNSQK.G		K.DSPNIAALDLLFNSQK.G
432	459	3	3004.36	-1	1	60.7	33.2	95.00%	R.SCETMGSATAVCSDKTGTLTENVMTVVR.G	Carbamidomethyl (+57)/Carbamidomethyl (+57)	R.SCETMGSATAVCSDKTGTLTENVMTVVR.G
497	513	2	1902.98	-0.49	1	68.7	30.7	95.00%	R.NDLLANIVLNSTAFENR.D		R.NDLLANIVLNSTAFENR.D

831	850	2	1886.91	0.57	0	84.5	33.1	95.00%	K.GMGDVVAVTGDGTNDAPALK.L		K.GMGDVVAVTGDGTNDAPALK.L
264	287	4	2651.22	-0.97	1	31	33	95.00%	K.FNSIDSHNHSKPLDIGDVNEDGNK.I		K.FNSIDSHNHSKPLDIGDVNEDGNK.I
288	298	2	1221.59	3	0	62.1	32.2	95.00%	K.IADCMLISGSR.I	Carbamidomethyl (+57)	K.IADCMLISGSR.I
497	510	2	1503.8	5.1	1	55.4	30.1	95.00%	R.NDLLANIVLNSTAF.E		R.NDLLANIVLNSTAFENR.D
1149	1173	3	2820.21	3.5	2	69.8	33.7	95.00%	K.NHTGKHDDEEALLEESDSPESTAFY.-		K.NHTGKHDDEEALLEESDSPESTAFY.-
252	259	2	946.49	1.2	1	28.5	30.4	92.70%	K.FPVDNSLR.D		K.FPVDNSLR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
20	ADP1_YEAST	21.26%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
430	439	2	1117.64	-0.46	0	45.1	26	95.00%	K.TTLLDILAMK.R		K.TTLLDILAMK.R
76	106	3	3357.41	3.6	2	79.8	33.1	95.00%	Y.TGRCECIEGFAGDDCSLPLCGGLSPDESGNK.D	Carbamidomethyl (+57)/Carbamidomethyl (+57)/Carbamidomethyl (+57)/Carbamidomethyl (+57)	K.QFSECNSYTGRCECIEGFAGDDCSLPLCGGLSPDESGNK.D
68	78	2	1347.55	-0.36	1	44	33.1	95.00%	K.QFSECNSYTGR.C	Carbamidomethyl (+57)	K.QFSECNSYTGR.C
30	39	2	1099.52	4	1	34.3	31.4	95.00%	K.TPFFEGTSSK.N		K.TPFFEGTSSK.N
702	716	2	1689.79	3.2	1	59.5	33.5	95.00%	R.SLLRDEEDVEGTDGR.R		R.SLLRDEEDVEGTDGR.R
657	679	2	2534.15	3.2	1	94.8	33.7	95.00%	R.NISDLEAGTDTNDIDNTIHQTTF.T		R.NISDLEAGTDTNDIDNTIHQTTFTSSDGTTQR.E
774	783	2	1171.66	4.7	0	59.5	28.5	95.00%	F.LQQLSILNSR.S	Deamidation (+1)	K.DSVYYAELSQEIEEVLSEGDEESNVLNGDLPTGQQSAGFLQQLSILNSR.S
259	270	2	1352.57	2.6	1	54.3	32.5	95.00%	K.GPGDFSCDLETR.Q	Carbamidomethyl (+57)	K.GPGDFSCDLETR.Q
245	258	2	1537.79	-1.4	1	45.6	31.2	95.00%	K.GSIDISDFLTETIK.G		K.GSIDISDFLTETIK.G
655	679	2	2803.34	4.6	2	72.8	31.7	95.00%	R.IRNISDLEAGTDTNDIDNTIHQTTF.T		R.IRNISDLEAGTDTNDIDNTIHQTTFTSSDGTTQR.E
538	574	3	4015.05	5.9	1	100	25.2	95.00%	R.VSIACELVTSPLVLFLDEPTSGLDASNANNVIECLVR.L	Carbamidomethyl (+57)/Carbamidomethyl (+57)	R.VSIACELVTSPLVLFLDEPTSGLDASNANNVIECLVR.L
680	690	2	1266.55	4.2	2	59.8	32.3	95.00%	F.TSSDGTTQREW.A		R.NISDLEAGTDTNDIDNTIHQTTFTSSDGTTQREWAHLAAHR.D
171	178	2	897.56	-0.35	0	35.4	19.5	95.00%	K.ILQILNGK.I		K.ILQILNGK.I
702	717	3	1845.89	2.5	1	66.2	32.7	95.00%	R.SLLRDEEDVEGTDGRR.G		R.SLLRDEEDVEGTDGRR.G
582	591	2	1162.69	3.3	0	57.6	22.4	95.00%	R.TLVLSIHQPR.S		R.TLVLSIHQPR.S
79	111	3	3680.61	3.3	1	107	32.3	95.00%	R.CECIEGFAGDDCSLPLCGGLSPDESGNKDRPIR.A	Carbamidomethyl (+57)/Carbamidomethyl (+57)/Carbamidomethyl (+57)/Carbamidomethyl (+57)	R.CECIEGFAGDDCSLPLCGGLSPDESGNKDRPIR.A
296	311	2	1913.8	3.4	1	78.7	34.2	95.00%	K.CESGECVHYSEIPGYK.S	Carbamidomethyl (+57)/Carbamidomethyl (+57)	K.CESGECVHYSEIPGYK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
21	ATC9_YEAST	19.63%	100%	23

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1178	1196	2	2031.87	3.2	1	68.9	34.2	95.00%	K.LDYTVGFCGDGANDCGALK.A	Carbamidomethyl (+57)/Carbamidomethyl (+57)	K.LDYTVGFCGDGANDCGALK.A
1049	1065	2	1820.91	-0.7	0	49	32.1	95.00%	R.TIMCTGDNILTAISVGR.E	Carbamidomethyl (+57)	R.TIMCTGDNILTAISVGR.E
74	90	2	1836.88	3.2	0	82.5	32.7	95.00%	F.QSSNLPSPHSSGNLEQR.G		R.ASFSSTATTSTAATLTSAMVLDQNNSEPYAGATFEAVPSSIVSFHHPHSFQSSNLPSPHSSGNLEQR.G
443	464	2	2488.2	5.7	1	76.2	32.3	95.00%	K.TNNNWIDPDWVDLSTVSNGLTK.G		K.TNNNWIDPDWVDLSTVSNGLTK.G
1094	1106	3	1541.81	3.8	1	23.3	28.8	93.90%	W.RDVNEPDKILDTK.T		R.VYVPSINDTPLHGEPVIVWRDVNEPDKILDTK.T
959	970	2	1315.65	4.2	0	44.6	31.5	95.00%	K.GAPEVISEICNK.S	Carbamidomethyl (+57)	K.GAPEVISEICNK.S

68	90	3	2579.21	3.5	1	61.9	32.9	95.00%	F.HHPHSFQSSNLPSPHSSGNLEQR.G		R.ASFSSTATTSTAATLTSAMVLDQNNSEPYAGATFEAVPSSIVSFHHPHSFQSSNLPSPHSSGNLEQR.G
199	221	3	2438.12	2.2	1	69.8	33.9	95.00%	R.LGENSDTGFVYHSATHSSSSLSR.Y		R.LGENSDTGFVYHSATHSSSSLSR.Y
931	939	2	1126.57	0.5	1	33.5	30.8	95.00%	R.SFEFLSELR.R		R.SFEFLSELR.R
267	287	3	2534.13	3.7	1	39.9	34.2	95.00%	F.SGHDDVHNQHSEYLKPDYHEK.F		R.GSFSGHDDVHNQHSEYLKPDYHEK.F
971	982	2	1375.7	1.7	1	59.4	31.7	95.00%	K.STLPADFEEVLR.C		K.STLPADFEEVLR.C
264	279	2	1814.73	3.6	1	35.4	33.3	95.00%	R.GSFSGHDDVHNQHSEY.L		R.GSFSGHDDVHNQHSEYLKPDYHEK.F
823	835	2	1528.69	1.5	1	64.4	33.7	95.00%	K.FSLNDCSSPLDFK.S	Carbamidomethyl (+57)	K.FSLNDCSSPLDFK.S
809	817	2	1048.56	3.8	1	61.2	30.9	95.00%	K.FGELLSDIR.Q		K.FGELLSDIR.Q
94	109	2	1744.89	2.6	0	79.7	30.8	95.00%	R.LTESEPLVLSSAEQSR.S		R.LTESEPLVLSSAEQSR.S
93	109	2	1900.99	-0.22	1	73.7	29.8	95.00%	R.RLTESEPLVLSSAEQSR.S		R.RLTESEPLVLSSAEQSR.S
1	14	2	1651.78	2.1	0	99.4	33.1	95.00%	-.MDIPSSNQIQHGQR.S	Acetyl (+42)	-.MDIPSSNQIQHGQR.S
1163	1177	2	1825.91	-0.059	1	32	31.7	95.00%	R.MSPDEKHELMIQLQK.L		R.MSPDEKHELMIQLQK.L
1127	1136	2	1063.57	4.9	1	34.8	30	95.00%	Y.TLAVSGDVFR.L		R.ECNYTLAVSGDVFR.L
1113	1126	2	1653.75	3	2	65.1	33.5	95.00%	K.LGNNSVESLRECNY.T	Carbamidomethyl (+57)	K.LGNNSVESLRECNYTLAVSGDVFR.L
210	221	3	1255.6	5.3	0	32.1	32.8	95.00%	Y.HSATHSSSSLSR.Y		R.LGENSDTGFVYHSATHSSSSLSR.Y
851	864	2	1488.75	2.5	1	62.7	32	95.00%	R.SVDGNLLGDPLDFK.M		R.SVDGNLLGDPLDFK.M
760	768	2	1049.54	3.3	1	39.3	31	95.00%	K.GIFCISPTR.L	Carbamidomethyl (+57)	K.GIFCISPTR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
22	XPP_YEAST	43.66%	100%	22

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
443	453	2	1204.72	3.2	0	43.8	20.1	95.00%	F.AIIHSPIDVLK.S		K.MTAQNFAIIHSPIDVLK.S
200	213	2	1859.83	2.7	1	69.2	33.9	95.00%	R.QNEDPITWQEWCVR.E	Carbamidomethyl (+57)	R.QNEDPITWQEWCVR.E
549	565	2	1898.88	4.1	1	103	33.2	95.00%	Y.LCDSGSQFLEGTTDITR.T	Carbamidomethyl (+57)	K.IYLCDSGSQFLEGTTDITR.T
380	397	3	2224.17	2.5	1	43.4	28.3	95.00%	K.INGIEVRPYEQIWEHLTK.I		K.INGIEVRPYEQIWEHLTK.I
261	293	3	3891.02	5.4	1	69.6	25.8	95.00%	K.VELVPVEENLVDSIWPDFETLPERPCNDLLLLK.Y	Carbamidomethyl (+57)	K.VELVPVEENLVDSIWPDFETLPERPCNDLLLLK.Y
398	421	3	2689.28	-1.4	1	42.6	32.3	95.00%	K.ITSQASSAEHEFLIPDSASWQMVR.C		K.ITSQASSAEHEFLIPDSASWQMVR.C
727	740	3	1659.9	2.5	1	29.2	28	95.00%	R.TIVHFLQPQSISYK.W		R.TIVHFLQPQSISYK.W
621	652	6	3467.73	1.4	1	22.1	27.7	90.80%	K.HGTGHGIGSFLNVHEGPMGVGFRPHLMNFPLR.A		K.HGTGHGIGSFLNVHEGPMGVGFRPHLMNFPLR.A
189	199	2	1449.73	2.4	1	55.7	31.4	95.00%	R.QELDYNWTLLR.Q		R.QELDYNWTLLR.Q
162	174	2	1498.67	1.6	1	51.1	33.4	95.00%	R.DLLNFNDDHPDGK.S		R.DLLNFNDDHPDGK.S
708	723	3	1985.99	2.6	2	37	31.6	95.00%	K.LLNEEEKTQINEYHAR.V		K.LLNEEEKTQINEYHAR.V
125	136	2	1462.61	4.5	1	40	33.3	95.00%	Y.IVPSCDEHQSEY.V	Carbamidomethyl (+57)	K.HDLCCYIVPSCDEHQSEYVSLR.D
259	293	3	4076.14	5.5	2	88.9	26.4	95.00%	K.GKVELVPVEENLVDSIWPDFETLPERPCNDLLLLK.Y	Carbamidomethyl (+57)	K.GKVELVPVEENLVDSIWPDFETLPERPCNDLLLLK.Y
36	50	2	1748.78	2.4	0	50.9	34.1	95.00%	F.RPCADCTCSPGLLSR.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GTSASHSPRPFRPCADCTCSPGLLSR.Q
566	585	2	2373.27	4.1	2	50.8	26.5	95.00%	R.TIHLTKPTKEEMDNYTLVLK.G		R.TIHLTKPTKEEMDNYTLVLK.G
145	161	2	1699.84	3.2	1	71.1	31.9	95.00%	R.AFISGFSGSAGVACITR.D	Carbamidomethyl (+57)	R.AFISGFSGSAGVACITR.D
436	453	3	2025.11	1.2	2	32.2	26.3	95.00%	K.KMTAQNFAIIHSPIDVLK.S		K.KMTAQNFAIIHSPIDVLK.S
653	665	2	1424.7	3.2	1	53	32.4	95.00%	R.AGNIISNEPGYYK.D		R.AGNIISNEPGYYK.D
593	609	2	1886.99	-1.3	1	65.6	29.7	95.00%	R.LIFPENTPGFNIDAIAR.Q		R.LIFPENTPGFNIDAIAR.Q
12	24	4	1428.7	-0.26	0	29.8	32	95.00%	R.AHSISHVPGTHMR.G		R.AHSISHVPGTHMR.G
490	497	2	1007.5	2.9	1	33.3	31.6	95.00%	R.EALIDEYR.A		R.EALIDEYR.A
437	453	3	1897.01	-0.26	1	39.6	28.7	95.00%	K.MTAQNFAIIHSPIDVLK.S		K.MTAQNFAIIHSPIDVLK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
23	ATN2_YEAST	22.00%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
784	807	3	2619.29	2.9	1	45.8	31.3	95.00%	K.EASDIVLSDDNFASILNAVEEGRR.M		K.EASDIVLSDDNFASILNAVEEGRR.M
582	595	2	1659.85	-1.1	1	69.7	30.1	95.00%	K.ITPLTDCDVETIRK.N	Carbamidomethyl (+57)	K.ITPLTDCDVETIRK.N
784	806	2	2463.19	4.4	1	138	32.1	95.00%	K.EASDIVLSDDNFASILNAVEEGR.R		K.EASDIVLSDDNFASILNAVEEGR.R
29	45	3	1874.98	3	1	39.3	29.7	95.00%	F.IGTSLTEGLTQDESLRR.L		K.ENNNEEFNAYHTLTTEEAAEFIGTSLTEGLTQDESLRR.L
477	492	2	1696.88	2.2	1	64	29.5	95.00%	K.AHGDPTEIAIQVFATK.M		K.AHGDPTEIAIQVFATK.M
389	413	2	2703.33	4.1	1	104	30.9	95.00%	R.FGTITISNSDDPFNPNEGNVSLIPR.F		R.FGTITISNSDDPFNPNEGNVSLIPR.F
48	63	2	1737.85	3.2	2	79.5	33.1	95.00%	K.AVGENTLGDDTKIDYK.A		K.AVGENTLGDDTKIDYK.A
29	44	2	1718.88	3.8	0	86.4	31.4	95.00%	F.IGTSLTEGLTQDESLR.R		K.ENNNEEFNAYHTLTTEEAAEFIGTSLTEGLTQDESLR.R
124	144	3	2266.18	4.2	1	40.7	29.3	95.00%	K.NLSSPNAHVIRNGKSETINSK.D	Deamidation (+1)	K.NLSSPNAHVIRNGKSETINSK.D
156	165	2	1055.56	-0.5	0	46.8	28	95.00%	K.VGDTIPADLR.L		K.VGDTIPADLR.L
18	45	3	3104.54	4.4	1	87.3	29.6	95.00%	Y.HTLTTEEAAEFIGTSLTEGLTQDESLRR.L		K.ENNNEEFNAYHTLTTEEAAEFIGTSLTEGLTQDESLRR.L
596	606	2	1250.63	2.5	1	48.6	31.9	95.00%	K.NVYSLSNEGLR.V		K.NVYSLSNEGLR.V
353	370	2	1946.97	2.9	1	122	31.2	95.00%	R.KLDSLEALGAVNDICSDK.T	Carbamidomethyl (+57)	R.KLDSLEALGAVNDICSDK.T
751	766	2	1697.74	2.2	1	72	33.7	95.00%	K.FCAMTGDGVNDSPSLK.M	Carbamidomethyl (+57)	K.FCAMTGDGVNDSPSLK.M
171	188	2	1950.95	3.5	1	110	32.5	95.00%	K.NFDTDESLLTGESLPVSK.D		K.NFDTDESLLTGESLPVSK.D
493	504	2	1324.65	2.3	0	32.7	32	95.00%	K.MDLPHNALTGEK.S		K.MDLPHNALTGEK.S
254	264	2	1362.69	-0.74	1	43.3	31.6	95.00%	K.SWLQNTWISTK.K		K.SWLQNTWISTK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
24	B3LFI3_YEAS1	25.79%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
359	375	3	1791.97	0.27	1	29.7	27.1	95.00%	R.WGDAPVHSIAAALFLPK.D		R.WGDAPVHSIAAALFLPK.D
426	435	3	1117.62	4.1	1	22.4	28.7	92.50%	Y.YDAQGLVKPK.N		K.EYYDAQGLVKPK.N
45	65	2	2280.05	2.6	1	85.9	33.4	95.00%	F.DFTSGSISPEQQVISEENDAK.K		R.TQQYIPSSISAAFDFTSGSISPEQQVISEENDAK.K
424	435	2	1409.72	2.8	1	64.2	30.5	95.00%	K.EYYDAQGLVKPK.N		K.EYYDAQGLVKPK.N
105	117	2	1487.69	-5.5	1	76.3	33.3	95.00%	K.TTMDYITPSFANK.A		K.TTMDYITPSFANK.A
123	130	2	980.51	3.2	1	30.8	30	95.00%	K.ACYVTLVR.N	Carbamidomethyl (+57)	K.ACYVTLVR.N
66	88	2	2542.1	4.3	1	86.1	34.2	95.00%	K.KLEQSALNSEASEDSEAMDEESK.A	Oxidation (+16)	K.KLEQSALNSEASEDSEAMDEESK.A
298	317	2	2314.02	4.9	1	92.4	34.1	95.00%	K.NPEYLDENNLMSFLSNDNGK.T	Deamidation (+1)	K.NPEYLDENNLMSFLSNDNGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
25	KTR4_YEAST	35.13%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
382	388	2	799.4	-0.16	1	31.8	27.3	95.00%	R.WGDAPVR.S		R.WGDAPVR.S
406	426	2	2476.03	3.2	1	53.7	33.9	95.00%	R.DIGYHHTPYTNCPTCPADSDR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.DIGYHHTPYTNCPTCPADSDR.C
110	118	2	1055.59	3	0	35.8	26.2	95.00%	F.LLQEISEPK.V		K.QLYEEFLLQEISEPK.V
367	374	2	1102.5	3	1	39.4	32.9	95.00%	K.YMQYLEEK.G		K.YMQYLEEK.G
143	162	2	2366.12	3.7	1	85	32.6	95.00%	R.NSDLEDIISSIQQLEEEYNK.N		R.NSDLEDIISSIQQLEEEYNK.N
440	451	2	1450.59	4.6	1	56.1	32.8	95.00%	W.SDLDNQNCQATW.I	Carbamidomethyl (+57)	K.FTPWSDLDNQNCQATWIR.H
415	435	2	2379.94	3.8	1	33	33.4	94.60%	Y.TNCPTCPADSDRCNGNCVPGK.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Deamidation (+1)/ Carbamidomethyl (+57)	R.DIGYHHTPYTNCPTCPADSDRCNGNCVPGK.F
349	360	2	1480.76	4.2	1	71.9	30.8	95.00%	W.TNFEIVDLDFLR.S		K.NYDYTQGYSTCHFWTNFEIVDLDFLR.S
135	142	2	857.53	-0.6	0	41.8	26.3	95.00%	K.GTILSLVR.N		K.GTILSLVR.N

62	82	2	2357.04	3.5	0	111	34.1	95.00%	K.TESADELPDHDAEVLDSIMDR.L		K.TESADELPDHDAEVLDSIMDR.L
389	398	2	1047.6	-0.12	1	52.3	26.1	95.00%	R.SLALALFADK.S		R.SLALALFADK.S
245	254	3	1269.65	2.7	1	26.9	29.6	95.00%	K.EFYHHPLLSK.Y		K.EFYHHPLLSK.Y
225	240	2	2041.86	0.65	1	111	34.4	95.00%	K.ENIQYAEVESYHNMCR.F	Carbamidomethyl (+57)	K.ENIQYAEVESYHNMCR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
26	A6ZYU5_YEAS7	20.63%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
13	35	2	2494.06	1.1	0	89.1	33.7	95.00%	K.SSENSNADLPSNSSQVMNMPEEK.G		K.SSENSNADLPSNSSQVMNMPEEK.G
279	301	2	2605.3	-1.2	1	87	30.7	95.00%	K.VAPDHPFIQQELEVIEASVEEAR.A		K.VAPDHPFIQQELEVIEASVEEAR.A
534	543	2	1117.55	0.61	1	34	31.2	95.00%	K.SASWVPTSQR.G		K.SASWVPTSQR.G
259	270	2	1362.68	2.5	1	78.6	31.8	95.00%	R.YLVEAGQIDEAR.A		R.YLVEAGQIDEAR.A
515	533	2	2163.07	4.3	1	72	31.8	95.00%	K.GLTLEEVNDMYAEGVLPWK.S		K.GLTLEEVNDMYAEGVLPWK.S
225	233	2	1153.52	2.9	1	49.9	32.5	95.00%	K.NYSNSVQWR.V	Deamidation (+1)	K.NYSNSVQWR.V
36	56	2	2246.05	3.6	1	97.1	33.4	95.00%	K.GVQDDFQAEADQVLTNPNTGK.G		K.GVQDDFQAEADQVLTNPNTGK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
27	BPT1_YEAST	19.44%	100%	22

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1065	1077	2	1468.71	2.8	1	78.5	32.5	95.00%	R.SPMTFFETTPVGR.I		R.SPMTFFETTPVGR.I
1313	1325	2	1480.79	2.4	0	58.9	28.4	95.00%	R.ENLDPVLNNINVK.I		R.ENLDPVLNNINVK.I
1343	1351	2	1006.58	-0.72	1	30.7	24.4	95.00%	K.STLSLALFR.I		K.STLSLALFR.I
389	403	2	1631.86	5.5	0	54.5	29.8	95.00%	K.STGDILNLMSVDVLR.I		K.STGDILNLMSVDVLR.I
1311	1325	2	1799.96	2.3	1	78.4	29	95.00%	K.YRENLDPVLNNINVK.I		K.YRENLDPVLNNINVK.I
1476	1492	2	1848.91	5	0	47.4	32.3	95.00%	K.ILVLDEATASVDMETDK.I		K.ILVLDEATASVDMETDK.I
1360	1373	2	1502.83	5.4	1	85.1	27.5	95.00%	K.IIIDGIDISDIGLF.D		K.IIIDGIDISDIGLFDLR.S
930	950	4	2253.3	0.23	1	18.3	18.6	95.00%	R.ASLATLRPRPFVGAQLDSVKK.T		R.ASLATLRPRPFVGAQLDSVKK.T
1431	1448	2	1946.84	2.1	0	100	34.2	95.00%	R.GDDSNEEDGNVNDILDVK.I		R.GDDSNEEDGNVNDILDVK.I
807	816	2	1160.68	-0.18	1	23.9	25.4	93.30%	K.NIIEYVLIGK.T		K.NIIEYVLIGK.T
1273	1290	2	2115.02	1.8	1	49.2	32.8	95.00%	R.IVEYCELPPEAQSINPEK.R	Carbamidomethyl (+57)	R.IVEYCELPPEAQSINPEK.R
788	806	2	2049.06	4.6	1	96.7	30.3	95.00%	R.ADIYLLDDILSAVDAEVSK.N		R.ADIYLLDDILSAVDAEVSK.N
1410	1423	4	1654.93	-0.95	1	23.5	25.8	95.00%	K.RAVEQAHLKPHLEK.M		K.RAVEQAHLKPHLEK.M
1504	1513	3	1194.68	-0.5	1	38.8	23.2	95.00%	K.DRTILTIAHR.I		K.DRTILTIAHR.I
1449	1461	2	1387.67	0.051	0	66.3	32.7	95.00%	K.INENGSNLSVGQR.Q	Deamidation (+1)	K.INENGSNLSVGQR.Q
1377	1394	3	1924.01	4.4	1	76.3	29.2	95.00%	R.SHLAIIPQDAQAFEGTVK.T		R.SHLAIIPQDAQAFEGTVK.T
1506	1513	2	923.55	-1.9	0	32.8	19.6	95.00%	R.TILTIAHR.I		R.TILTIAHR.I
611	625	2	1759.93	-0.58	1	57.7	29.4	95.00%	R.ALPAIEMNNITFLWK.S		R.ALPAIEMNNITFLWK.S
745	753	2	1056.57	4	0	25.8	28.5	91.20%	K.ACQLLPDLK.I	Carbamidomethyl (+57)	K.ACQLLPDLK.I
1462	1468	2	872.49	-0.56	0	28.1	29.7	93.00%	R.QLLCLAR.A	Carbamidomethyl (+57)	R.QLLCLAR.A
843	862	3	2323.09	4.4	1	52.4	33.4	95.00%	Y.ALENGEIVEQGNYEDVMNRK.N	Oxidation (+16)	K.HSQMIYALENGEIVEQGNYEDVMNRK.N
628	655	3	2976.5	2	1	56.1	29.1	95.00%	K.EVLTSSQSGDNLRTDEESIIGSSQIALK.N		K.EVLTSSQSGDNLRTDEESIIGSSQIALK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
28	PTR2_YEAST	15.14%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
583	601	2	2289.06	-1.2	2	44	34.1	95.00%	K.ANDIEILEPMESLRSTTKY.-	Phospho (+80)	K.ANDIEILEPMESLRSTTKY.-
2	27	4	2911.31	-1.5	2	27.3	33.4	95.00%	M.LNHPSQGSDDAQDEKQGDFPVIEEEK.T		-.MLNHPSQGSDDAQDEKQGDFPVIEEEK.T
2	16	2	1682.71	6.1	0	36.1	33.3	95.00%	M.LNHPSQGSDDAQDEK.Q	Acetyl (+42)/ Deamidation (+1)	-.MLNHPSQGSDDAQDEK.Q
35	48	2	1556.66	0.63	1	54.6	33.4	95.00%	K.DSYVSDDVANSTER.Y		K.DSYVSDDVANSTER.Y

1	27	3	3042.36	2.4	2	58.8	33	95.00%	-.MLNHPSQGSDDAQDEKQGDFPVIEEEK.T		-.MLNHPSQGSDDAQDEKQGDFPVIEEEK.T
17	34	3	2031.06	1.4	1	29.4	29.8	95.00%	K.QGDFPVIEEEKTQAVTLK.D		K.QGDFPVIEEEKTQAVTLK.D
1	16	3	1770.75	-0.61	0	48.8	34.1	95.00%	-.MLNHPSQGSDDAQDEK.Q		-.MLNHPSQGSDDAQDEK.Q
49	72	2	2812.21	3.2	1	55.7	33.7	95.00%	R.YNLSPSPEDEDFEGPTEEEMQTLR.H		R.YNLSPSPEDEDFEGPTEEEMQTLR.H
583	596	2	1628.81	-1.2	0	62.4	31.6	95.00%	K.ANDIEILEPMESLR.S		K.ANDIEILEPMESLR.S
35	49	2	1719.73	3.4	2	83.3	34.2	95.00%	K.DSYVSDDVANSTERY.N		K.DSYVSDDVANSTERYNLSPSPEDEDFEGPTEEEMQTLR.H
50	72	2	2649.15	4.6	1	103	34	95.00%	Y.NLSPSPEDEDFEGPTEEEMQTLR.H		R.YNLSPSPEDEDFEGPTEEEMQTLR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
29	COS2_YEAST	29.82%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
157	167	2	1275.75	3.6	1	33.3	23.7	95.00%	R.TTLLEPFSLKK.D		R.TTLLEPFSLKK.D
352	367	2	1985.05	-0.61	1	45.6	29	95.00%	K.SMWPLPLNVELWPYIK.E		K.SMWPLPLNVELWPYIK.E
206	219	2	1525.82	3.7	1	106	27.5	95.00%	K.SWSPVGLEDAKLPK.E		K.SWSPVGLEDAKLPK.E
19	33	3	1813.01	-0.27	2	23.2	25.5	95.00%	K.QLESQKIVLPQDLFR.S		K.QLESQKIVLPQDLFR.S
25	33	2	1099.64	-0.29	1	24.9	27.1	92.20%	K.IVLPQDLFR.S		K.IVLPQDLFR.S
289	311	2	2608.22	-2.9	1	94.3	33	95.00%	K.MQFLSTIINEQESGANGWDEIAR.K		K.MQFLSTIINEQESGANGWDEIAR.K
206	216	2	1187.59	3.1	1	36.3	31.5	95.00%	K.SWSPVGLEDAK.L		K.SWSPVGLEDAK.L
157	166	2	1147.65	4.2	1	35.1	27.1	95.00%	R.TTLLEPFSLK.K		R.TTLLEPFSLK.K
109	132	2	2687.21	4.7	1	41.3	33.2	95.00%	K.EITENTPSSDPHDWEVVAANLNSY.L		K.EITENTPSSDPHDWEVVAANLNSYLYENNVWNTK.Y
133	142	2	1279.62	3.7	1	46.4	32.1	95.00%	Y.LYENNVWNTK.Y		K.EITENTPSSDPHDWEVVAANLNSYLYENNVWNTK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
30	A6ZWJ5_YEAS7	40.58%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
171	187	2	1857.92	3	0	94.4	32.2	95.00%	R.QAITDSMNGDPELINIK.F		R.QAITDSMNGDPELINIK.F
34	46	2	1582.77	2.9	1	63.2	32.3	95.00%	K.QMSEQYVTPYLPK.S		K.QMSEQYVTPYLPK.S
437	446	2	1211.6	3.7	1	35.4	31	95.00%	K.DKPEGWDRLP.-		K.DKPEGWDRLP.-
410	422	2	1646.63	3.6	1	69.8	32.7	95.00%	Y.NCNCDQGNDFTFR.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.YNNCPLNDDIWNQYNCNCDQGNDFTFR.S
119	128	2	1194.61	0.92	1	60.3	31.7	95.00%	K.ACFVSLITER.D	Carbamidomethyl (+57)	K.ACFVSLITER.D
207	223	2	1713.86	3	0	54.3	31.3	95.00%	K.AAESLISLANVPDGDSR.A		K.AAESLISLANVPDGDSR.A
257	267	2	1465.67	4.4	1	47.2	33.3	95.00%	K.LYCDIDHDLFR.W	Carbamidomethyl (+57)	K.LYCDIDHDLFR.W
154	170	2	1979.99	2.9	1	72.6	32	95.00%	W.VFISQGELDGMKQEMIR.Q		K.NFAYPWVFISQGELDGMKQEMIR.Q
364	380	3	1910.03	-0.51	1	34.6	27.4	95.00%	K.WSDSIIHTIGLSMLLPK.D		K.WSDSIIHTIGLSMLLPK.D
154	165	2	1322.66	3.6	1	59.3	32.6	95.00%	W.VFISQGELDGMK.Q		K.NFAYPWVFISQGELDGMK.Q
119	144	3	3009.53	3.9	1	37.4	29	95.00%	K.ACFVSLITERDSMTQILQSIDEVQVK.F	Carbamidomethyl (+57)	K.ACFVSLITERDSMTQILQSIDEVQVK.F
129	144	2	1832.92	-1.5	0	52.7	31.9	95.00%	R.DSMTQILQSIDEVQVK.F		R.DSMTQILQSIDEVQVK.F
61	72	2	1458.73	-0.5	1	44.3	31.2	95.00%	R.RIQSEQEEAELK.Q		R.RIQSEQEEAELK.Q
423	435	2	1457.61	2.4	1	37	32.6	95.00%	R.SGSCGGHYFDIMK.K	Carbamidomethyl (+57)	R.SGSCGGHYFDIMK.K
277	291	2	1640.78	2.5	1	67.1	33.1	95.00%	F.GFTLSMSEAKEANEK.I		K.VFGFTLSMSEAKEANEK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
31	A7A0C8_YEAS7	51.00%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
217	225	2	1001.55	3.8	0	28	29.5	93.20%	R.TANDVLTIR.E		R.TANDVLTIR.E
397	409	2	1314.75	2.9	0	41.1	27.3	95.00%	K.AIIVLSTSGTTPR.L		K.AIIVLSTSGTTPR.L
313	337	2	2521.18	5.4	0	118	33.2	95.00%	R.AEVSDVGNAILDGADCVMLSGETAK.G	Carbamidomethyl (+57)	R.AEVSDVGNAILDGADCVMLSGETAK.G

7	20	2	1499.84	-0.15	1	34.8	27.2	95.00%	R.LTSLNVVAGSDLRR.T		R.LTSLNVVAGSDLRR.T
31	41	2	1226.66	1.2	0	48.4	27.6	95.00%	K.TNNPETLVALR.K		K.TNNPETLVALR.K
265	281	2	1747.97	-0.53	0	32.5	26.5	95.00%	R.GDLGIEIPAPEVLAVQK.K		R.GDLGIEIPAPEVLAVQK.K
287	306	2	2213.06	4.6	1	41.8	32.3	95.00%	K.SNLAGKPVICATQMLESMTY.N	Carbamidomethyl (+57)	K.SNLAGKPVICATQMLESMTYNPR PTR.A
69	86	2	2000.1	2.4	2	63.7	26.4	95.00%	R.KSEELYPGRPLAIALDTK.G		R.KSEELYPGRPLAIALDTK.G
460	466	2	819.45	-0.16	1	35.5	28.4	95.00%	R.INFGIEK.A		R.INFGIEK.A
414	425	2	1500.83	1.6	1	31.5	28.8	95.00%	K.YRPNCPIILVTR.C	Carbamidomethyl (+57)	K.YRPNCPIILVTR.C
241	264	3	2688.36	3	1	24.5	29.9	94.00%	K.IENQQGVNNFDEILKVTDGVMVA R.G		K.IENQQGVNNFDEILKVTDGVMVA R.G
287	312	4	2934.46	1.8	1	37.3	29.7	95.00%	K.SNLAGKPVICATQMLESMTYNPR PTR.A	Carbamidomethyl (+57)	K.SNLAGKPVICATQMLESMTYNPR PTR.A
92	116	3	2821.29	3.4	1	38.3	33.5	95.00%	R.TGTTTNDVDYPIPPNHEMIFTTDD K.Y		R.TGTTTNDVDYPIPPNHEMIFTTDD K.Y
307	337	3	3242.58	4.9	1	69.9	29.5	95.00%	Y.NPRPTRAEVSDVGNAILDGADCV MLSGETAK.G	Carbamidomethyl (+57)	K.SNLAGKPVICATQMLESMTYNPR PTRAEVSDVGNAILDGADCVMLSG ETAK.G
217	236	3	2184.18	3.3	1	37	25.1	95.00%	R.TANDVLTIREVLGEQGKDVK.I		R.TANDVLTIREVLGEQGKDVK.I
142	161	2	2265.19	4.9	1	34	28.3	95.00%	R.IIYVDDGVLSFQVLEVVDDK.T		R.IIYVDDGVLSFQVLEVVDDK.T
178	200	3	2480.28	3.1	1	23.8	28.4	95.00%	K.GVNLPGTDVDLPALSEKDKEDLR .F		K.GVNLPGTDVDLPALSEKDKEDLR .F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
32	A6ZR26_YEAS7	14.73%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
14	24	2	1250.77	2.5	1	33.7	16.7	95.00%	K.KIALPTRVEPK.V		K.KIALPTRVEPK.V
2	9	2	912.51	3.2	0	42.8	26.5	95.00%	M.SSAPLLQR.T	Acetyl (+42)	-.MSSAPLLQR.T
15	24	2	1122.68	2.6	1	41.8	18.1	95.00%	K.IALPTRVEPK.V		K.IALPTRVEPK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
33	A6ZY55_YEAS7	29.23%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
218	240	2	2327.02	-1.1	0	85.8	34.2	95.00%	R.SDESAHTSSSPEANNSSLPASPR .S		R.SDESAHTSSSPEANNSSLPASPR .S
306	320	2	1603.77	2.7	0	54.9	32.4	95.00%	K.EILDTTDNINSAGNK.S		K.EILDTTDNINSAGNK.S
509	524	2	1737.86	3.6	2	60.3	32.7	95.00%	R.SSGLSQTAINEDNKFK.Q		R.SSGLSQTAINEDNKFK.Q
253	273	3	2337.16	5.1	1	37.1	31.3	95.00%	K.MIDSSLEFDTALIDKAENLGR.F		K.MIDSSLEFDTALIDKAENLGR.F
78	90	2	1436.78	-0.91	1	86.9	28.6	95.00%	R.ILSVESSIIDFSK.G		R.ILSVESSIIDFSK.G
32	47	2	1817.75	2.6	1	74.5	33.9	95.00%	K.VTAYDYDNPNDSGMEK.L		K.VTAYDYDNPNDSGMEK.L
295	305	2	1190.64	2.7	0	44.9	29.4	95.00%	R.IIDDSIISTSK.E		R.IIDDSIISTSK.E
565	572	2	1047.58	3.8	2	43.2	29.5	95.00%	F.QLLLRDQY.K		K.ICLELVHSNELQNDLFQLLLRDQY K.L
431	446	2	1667.91	0.65	0	48.8	27.6	95.00%	K.NISALINSLDPSPISK.I		K.NISALINSLDPSPISK.I
214	240	3	2877.26	3.6	1	57.3	33.2	95.00%	R.SLNRSDESAHTSSSPEANNSSLP ASPR.S	Phospho (+80)	R.SLNRSDESAHTSSSPEANNSSLP ASPR.S
404	414	2	1292.72	2.8	0	46.9	25.7	95.00%	R.NHVVTNDLLLR.D		R.NHVVTNDLLLR.D
549	569	3	2566.36	2.6	1	39	26.3	95.00%	K.ICLELVHSNELQNDLFQLLLR.D	Carbamidomethyl (+57)	K.ICLELVHSNELQNDLFQLLLR.D
447	456	3	1251.68	3.3	1	40.2	28.7	95.00%	K.IALEWIQSHR.L		K.IALEWIQSHR.L
733	746	2	1499.65	4	1	96.3	33.3	95.00%	F.GSQSTSASYDDVQR.Y		K.HPHCSSTNYGSVASFGSQSTSA SYDDVQR.Y
727	746	2	2047.92	3.5	1	129	34.2	95.00%	Y.GSVASFGSQSTSASYDDVQR.Y		K.HPHCSSTNYGSVASFGSQSTSA SYDDVQR.Y
274	285	2	1349.71	3.1	1	60.4	30.1	95.00%	R.FLLSSEDIEGLK.F		R.FLLSSEDIEGLK.F
295	320	3	2776.4	2.4	1	48.4	29.3	95.00%	R.IIDDSIISTSKEILDTTDNINSAGNK. S		R.IIDDSIISTSKEILDTTDNINSAGNK. S
342	353	2	1298.69	1.7	0	55.2	29	95.00%	K.NILPSAVQSNEK.Y		K.NILPSAVQSNEK.Y
574	590	2	1910.89	-0.95	1	63.3	33.4	95.00%	K.LNSDDSLSPDEFFQLGK.D		K.LNSDDSLSPDEFFQLGK.D
327	339	2	1488.76	2.5	1	72.8	31.1	95.00%	K.SFNDLQHTLSLSK.Q		K.SFNDLQHTLSLSK.Q
509	522	2	1462.69	-0.55	0	62.4	31.6	95.00%	R.SSGLSQTAINEDNK.F		R.SSGLSQTAINEDNK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
34	YNL5_YEAST	29.04%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
610	619	2	1143.59	-0.28	1	57.2	30.6	95.00%	K.IVEGGHEIYK.Y		K.IVEGGHEIYK.Y
13	36	3	2773.28	-0.87	1	44.4	32.3	95.00%	R.TGMERTDIDSEHPEAQPLLNNNHR.T		R.TGMERTDIDSEHPEAQPLLNNNHR.T
383	407	3	2598.32	4.2	1	73.7	29.2	95.00%	Y.DRPGYGLSDSPPAPISIAMVAESLR.Y		R.YCLYDRPGYGLSDSPPAPISIAMVAESLR.Y
18	36	3	2199.04	2.6	0	54	33.4	95.00%	R.TDIDSEHPEAQPLLNNNHR.T		R.TDIDSEHPEAQPLLNNNHR.T
37	52	2	1469.72	-1	0	69.6	32.2	95.00%	R.TLGAGSANGPAVNEGR.D		R.TLGAGSANGPAVNEGR.D
563	575	2	1430.7	0.061	0	66.7	31.9	95.00%	R.DVTNNAESLQNVK.T		R.DVTNNAESLQNVK.T
562	575	3	1586.81	5	1	37	31.3	95.00%	Y.RDVTNNAESLQNVK.T		K.FLESVTSSILSYRDVTNNAESLQNVK.T
465	491	3	2734.15	-0.88	1	33.2	33.9	95.00%	R.LLPPGRGDGDDGDDGNGNDGDGRNHDK.T		R.LLPPGRGDGDDGDDGNGNDGDGRNHDK.T
215	235	3	2447.11	2.5	2	78.9	33.7	95.00%	R.RIDDANISTFNENHTNSTENR.D		R.RIDDANISTFNENHTNSTENR.D
588	596	2	1117.53	1.7	1	39.1	31.5	95.00%	K.SALWGDWQR.D		K.SALWGDWQR.D
634	644	2	1186.65	1.3	1	65.2	30.2	95.00%	R.LIGELGKLTED.-		R.LIGELGKLTED.-
439	459	2	2499.26	6.5	1	59	30.6	95.00%	K.NVDIVDSMMLVESWHEELLLK.N		K.NVDIVDSMMLVESWHEELLLK.N
367	375	3	1158.6	3.9	1	23.2	30.6	90.20%	W.IEELYHLDK.I		K.QPIILFEHGGYDTGYLSATWIEELYHLDK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
35	A6ZSR0_YEAS7	25.47%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
354	375	3	2660.42	2.9	1	42.4	25.5	95.00%	K.ELTYDLLQEMPLLNQTIKETLR.M		K.ELTYDLLQEMPLLNQTIKETLR.M
326	346	3	2609.34	4.4	1	48.8	28.5	95.00%	W.ILLHLAERPDVQQELYEEQMR.V		K.MTDQEIANLLIGVLMGGQHTSAATSAWILLHLAERPDVQQELYEEQMR.V
354	371	2	2161.13	-0.46	1	93.2	29	95.00%	K.ELTYDLLQEMPLLNQTIK.E		K.ELTYDLLQEMPLLNQTIK.E
275	289	3	1788.88	4.5	1	26.9	32	94.40%	K.NNDIQDRDLIDSLMK.N		K.NNDIQDRDLIDSLMK.N
127	136	3	1069.6	4.5	1	30.4	26.6	95.00%	Y.AHLTTPVFGK.G		K.LADVSAEAAYAHLTTPVFGK.G
117	136	2	2060.07	3.6	1	66	29.5	95.00%	K.LADVSAEAAYAHLTTPVFGK.G		K.LADVSAEAAYAHLTTPVFGK.G
190	210	2	2298.13	2.4	1	58.2	31.6	95.00%	R.TTGTIDVMVTQPEMTIFTASR.S		R.TTGTIDVMVTQPEMTIFTASR.S
326	341	2	1936.05	4.3	1	39.8	26.5	95.00%	W.ILLHLAERPDVQQELY.E		K.MTDQEIANLLIGVLMGGQHTSAATSAWILLHLAERPDVQQELYEEQMR.V
165	176	2	1409.75	3	1	36.4	29.1	95.00%	K.SYVPLIAEEVYK.Y		K.SYVPLIAEEVYK.Y
455	467	2	1292.65	1.5	1	41.1	31.3	95.00%	K.GVSSPYLPFGGGR.H		K.GVSSPYLPFGGGR.H
260	270	2	1182.64	3	1	53.7	27.9	95.00%	K.AISGTYMSLIK.E		K.AISGTYMSLIK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
36	A6ZR77_YEAS7	29.96%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
173	194	2	2420.05	3.6	1	72	33.8	95.00%	K.SCASSSNNDPNLIYMVDFGMAK.Q	Carbamidomethyl (+57)	K.SCASSSNNDPNLIYMVDFGMAK.Q
439	458	2	2285.03	3.4	1	70.5	33.8	95.00%	K.SQSQTYDSISHTQNSPFVPY.S		K.SQSQTYDSISHTQNSPFVPYSSSK.A
402	411	2	1107.56	-0.74	1	33.7	31.8	95.00%	R.ISSNPQSFTK.Q		R.ISSNPQSFTK.Q
425	438	2	1694.92	3	1	39.4	27.5	95.00%	K.YIPETHSNLQRPIK.S		K.YIPETHSNLQRPIK.S
468	484	3	1978.92	-0.55	1	35	33.8	95.00%	R.SNNEHNLPNHYTNLANK.N		R.SNNEHNLPNHYTNLANK.N
47	64	2	2016.04	2.1	2	56.6	30.6	95.00%	R.DSSIIMANEPVAIKFEPR.H		R.DSSIIMANEPVAIKFEPR.H
467	484	3	2135.03	2.4	2	41.2	32.9	95.00%	K.RSNNEHNLPNHYTNLANK.N		K.RSNNEHNLPNHYTNLANK.N
150	163	2	1735.89	2.6	1	49.5	31.1	95.00%	R.DIKPDNFLISQYQR.I		R.DIKPDNFLISQYQR.I
20	45	3	2764.32	4.3	1	51.5	32.4	95.00%	K.IGEGSFGVIFEGENILHSCQAQTGSK.R	Carbamidomethyl (+57)	K.IGEGSFGVIFEGENILHSCQAQTGSK.R

5	19	2	1591.85	2.6	1	62.9	28.6	95.00%	R.SSQHIVGIHYAVGPK.I		R.SSQHIVGIHYAVGPK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
37	B3LGF8_YEAS1	32.03%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
79	95	2	1817.92	3.7	0	80.3	31	95.00%	K.AVDIDTIDAQPLHEGPK.I		K.AVDIDTIDAQPLHEGPK.I
79	114	3	3934.9	3.4	1	26.4	28.2	95.00%	K.AVDIDTIDAQPLHEGPKIDDSPQDEVNSIKGKPADK.A	Phospho (+80)	K.AVDIDTIDAQPLHEGPKIDDSPQDEVNSIKGKPADK.A
192	214	2	2416.19	3.9	1	54.1	31.3	95.00%	K.SLHIVAPSPEVPVSGDEITSYGY.G		K.SLHIVAPSPEVPVSGDEITSYGYGSIPQSIGDVENGLNPPYVENTSSDELVHDLTR.R
44	70	3	2881.47	-0.14	1	78.1	28	95.00%	R.TSNQIALGNDKIEEINENSPLLSAPSK.Q		R.TSNQIALGNDKIEEINENSPLLSAPSK.Q
44	78	3	3791.96	3.7	1	79.4	26.4	95.00%	R.TSNQIALGNDKIEEINENSPLLSAPSKQEEVSIPK.A		R.TSNQIALGNDKIEEINENSPLLSAPSKQEEVSIPK.A
431	443	2	1518.82	1.8	1	33.3	28.1	95.00%	K.STLYGRPTPTLWK.R		K.STLYGRPTPTLWK.R
145	174	3	3306.52	0.59	1	70.9	32.4	95.00%	R.SVSPLQSITSCNTPMSEHELPVSSSNSFER.A	Carbamidomethyl (+57)	R.SVSPLQSITSCNTPMSEHELPVSSSNSFER.A
705	719	2	1679.75	-0.31	1	101	33.4	95.00%	K.HATESSDWVHESAPK.F		K.HATESSDWVHESAPK.F
79	108	3	3258.6	2.9	1	48.6	29.3	95.00%	K.AVDIDTIDAQPLHEGPKIDDSPQDEVNSIK.G		K.AVDIDTIDAQPLHEGPKIDDSPQDEVNSIK.G
215	247	3	3552.7	4.3	1	83.7	29.7	95.00%	Y.GSIPQSIGDVENGLNPPYVENTSSDELVHDLTR.R	Deamidation (+1)	K.SLHIVAPSPEVPVSGDEITSYGYGSIPQSIGDVENGLNPPYVENTSSDELVHDLTR.R
345	358	2	1378.73	0.37	1	47.8	29.9	95.00%	R.CVTGFGGGSLIALK.S	Carbamidomethyl (+57)	R.CVTGFGGGSLIALK.S
115	144	3	3288.46	-0.32	1	63.9	32.7	95.00%	K.ANEDDLKPPSQHEACGNSALQSSITDFSDR.S	Carbamidomethyl (+57)	K.ANEDDLKPPSQHEACGNSALQSSITDFSDR.S
192	212	2	2196.1	3.8	1	75.8	31	95.00%	K.SLHIVAPSPEVPVSGDEITSY.G		K.SLHIVAPSPEVPVSGDEITSYGYGSIPQSIGDVENGLNPPYVENTSSDELVHDLTR.R
175	191	2	1791.79	-0.11	0	77.9	34	95.00%	R.ADDMPVVQADNQTSSSK.S		R.ADDMPVVQADNQTSSSK.S
173	191	3	2076.95	3.8	1	51.5	33.9	95.00%	F.ERADDMPVVQADNQTSSSK.S		R.SVSPLQSITSCNTPMSEHELPVSSSNSFERADDMPVVQADNQTSSSK.S
55	78	3	2650.38	3.5	1	34.5	27.6	95.00%	K.IEEINENSPLLSAPSKQEEVSIPK.A		K.IEEINENSPLLSAPSKQEEVSIPK.A
213	247	3	3772.78	3.6	1	91	30	95.00%	Y.GYGSIPQSIGDVENGLNPPYVENTSSDELVHDLTR.R	Deamidation (+1)	K.SLHIVAPSPEVPVSGDEITSYGYGSIPQSIGDVENGLNPPYVENTSSDELVHDLTR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
38	A6ZL18_YEAS7	18.34%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
221	233	2	1277.67	2.7	1	65.4	30.7	95.00%	K.YVINLEGTGAGGK.A		K.YVINLEGTGAGGK.A
165	181	2	1659.86	4.7	0	57	30.4	95.00%	Y.GATDDGMGVVSLLANLK.Y		K.NPEEEGLLLSAHFDSVPTGYGATDDGMGVVSLLANLK.Y
746	761	2	1828.98	3.4	1	41.8	28.5	95.00%	R.EGNFLKPMLQDLPSIK.Y		R.EGNFLKPMLQDLPSIK.Y
411	418	2	976.54	4.7	1	28.6	29.3	94.30%	K.LFSNDIIR.S		K.LFSNDIIR.S
816	830	2	1698.95	5.1	1	76.5	26.2	95.00%	R.SPYEPIVAELLLEVK.E		R.SPYEPIVAELLLEVK.E
816	833	3	2098.14	4.5	1	34.7	25.7	95.00%	R.SPYEPIVAELLLEVKENR.A		R.SPYEPIVAELLLEVKENR.A
535	544	3	1188.53	4.8	0	25.1	32.4	90.50%	Y.SSHSQIDMER.D		R.DHHSNYSSHSQIDMER.D
605	616	2	1266.55	-0.33	0	54.1	32.2	95.00%	K.GSNSMEEGLSTR.E		K.GSNSMEEGLSTR.E
873	892	2	2307.11	4	2	47.1	32.7	95.00%	K.SASGINELQLHKLDFDQETY.H		K.SASGINELQLHKLDFDQETYHIGVQWFPK.L
893	901	2	1110.6	3.9	1	41.9	27.7	95.00%	Y.HIGVQWFPK.L		K.LDFDQETYHIGVQWFPK.L
141	164	2	2601.27	2	2	39.5	31.6	95.00%	K.LEGKNPEEEGLLLSAHFDSVPTGY.G		K.LEGKNPEEEGLLLSAHFDSVPTGYGATDDGMGVVSLLANLK.Y
726	745	2	2112.07	1	1	95.7	30.3	95.00%	R.FSQNIDLSQGNAASVHVLGR.E		R.FSQNIDLSQGNAASVHVLGR.E
129	140	2	1398.74	2.4	1	31.1	28.7	95.00%	R.VTYFESSNILVK.L		R.VTYFESSNILVK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
39	A6ZPW7_YEAS7	29.24%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
80	89	2	1186.56	0.14	0	42	32.4	95.00%	R.NIELNADNER.S		R.NIELNADNER.S
48	60	3	1482.8	3	2	49.7	28	95.00%	R.RQSILDHPVGSFK.G		R.RQSILDHPVGSFK.G
14	26	3	1582.86	0.76	2	35.6	27.6	95.00%	K.RSEVHYISIPLNR.G		K.RSEVHYISIPLNR.G
368	388	2	2275.1	4.7	1	58.8	32.5	95.00%	K.SSSPGSLVNPMETSMWPIDLK.H		K.SSSPGSLVNPMETSMWPIDLK.H
135	178	4	4456.08	5.5	1	31.6	28	95.00%	R.VSTASMAIHDDDYGSIQNSTIGDSGSILRPTASLTEMMSGGAGR.R		R.VSTASMAIHDDDYGSIQNSTIGDSGSILRPTASLTEMMSGGAGR.R
180	191	2	1381.66	2.4	1	81.9	32.7	95.00%	R.FTNNDMDSIVVK.R		R.FTNNDMDSIVVK.R
94	113	3	2234.01	1.1	1	34.5	33.8	95.00%	K.ESNDETYDPDTLAPALDGRR.L		K.ESNDETYDPDTLAPALDGRR.L
179	191	2	1537.76	2.5	2	71.4	32.4	95.00%	R.RFTNNDMDSIVVK.R		R.RFTNNDMDSIVVK.R
114	125	2	1296.73	-0.33	0	32.9	26.6	95.00%	R.LSVTLNNAGRPR.I		R.LSVTLNNAGRPR.I
484	512	3	3113.7	3.6	0	78.5	22.9	95.00%	K.TPLNARPIVSVLDVLMNVQHIDEAASAIK.R		K.TPLNARPIVSVLDVLMNVQHIDEAASAIK.R
484	513	5	3269.8	1.5	1	78.5	23.6	95.00%	K.TPLNARPIVSVLDVLMNVQHIDEAASAIKR.R		K.TPLNARPIVSVLDVLMNVQHIDEAASAIKR.R
49	60	2	1326.7	3.1	1	31.9	29.5	95.00%	R.QSILDHPVGSFK.G		R.QSILDHPVGSFK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
40	A6ZSG0_YEAS7	21.37%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
53	62	2	1157.61	2.2	1	35.9	29.6	95.00%	R.YLEGLHEGLK.F		R.YLEGLHEGLK.F
453	472	2	2375.1	1.9	1	72.3	33.4	95.00%	K.YVENSSQSHENEITQQQLNK.N		K.YVENSSQSHENEITQQQLNK.N
713	742	3	3446.61	3.2	1	46.2	31.7	95.00%	K.MIWQLPIADPTSTAPEQQEQNSHDAPNWSR.S		K.MIWQLPIADPTSTAPEQQEQNSHDAPNWSR.S
72	107	4	4035	-0.75	1	29.8	27.1	95.00%	K.RSVSSQSPIVHSSNNTLHHHEHQQHLPPTLESLSSK.S		K.RSVSSQSPIVHSSNNTLHHHEHQQHLPPTLESLSSK.S
131	147	3	1970.74	0.65	0	38.4	32.9	95.00%	R.ELPHDDNDDEDANDDSR.F		R.ELPHDDNDDEDANDDSR.F
20	36	2	1865.99	3.2	1	73.4	28.5	95.00%	R.LKEEVLTPTTSASTPHR.I		R.LKEEVLTPTTSASTPHR.I
20	38	3	2126.14	3.3	2	34.2	26.6	95.00%	R.LKEEVLTPTTSASTPHRIF.S		R.LKEEVLTPTTSASTPHRIFSVDDDPK.E
344	378	4	3703.72	-0.13	1	25.2	30.8	95.00%	R.EDHPAPATESSSLMPPANTTATPLNSNHPSYNSIR.H		R.EDHPAPATESSSLMPPANTTATPLNSNHPSYNSIR.H
37	52	2	1902.94	2.9	1	83.9	32.1	95.00%	R.IFSVDDDPKEIQNDIR.Y		R.IFSVDDDPKEIQNDIR.Y
220	231	2	1353.69	-1.9	0	28.2	30.7	91.70%	R.TAAQDIHETQLK.T		R.TAAQDIHETQLK.T
131	148	2	2117.81	3	2	80.2	32.6	95.00%	R.ELPHDDNDDEDANDDSRF.I		R.ELPHDDNDDEDANDDSRFIIHDSHGHDLLIDEINCQSPSHLENNDQASNASSTESFTLR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
41	A6ZKY2_YEAS7	18.28%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
349	369	2	2284.12	4.7	1	93.7	32.4	95.00%	K.VNQGSLDYLAALGVYQEDMAK.A		K.VNQGSLDYLAALGVYQEDMAK.A
131	143	2	1508.74	5	1	33.5	32.2	95.00%	Y.HLSPQQQPSNNLF.G		R.DNADLPVDPYHLSPQQQPSNNLFGSGR.L
26	35	2	1142.51	1	1	43.9	32.4	95.00%	K.FYANANSNSR.W		K.FYANANSNSR.W
81	93	2	1426.66	3.3	2	43.7	33.4	95.00%	R.DSAHNSPVAPNRY.A		R.DSAHNSPVAPNRYAANLQESPK.R
121	147	3	2965.4	-0.13	1	55.3	32.3	95.00%	R.DNADLPVDPYHLSPQQQPSNNLFGSGR.L		R.DNADLPVDPYHLSPQQQPSNNLFGSGR.L
103	120	3	1968.03	4.6	2	46.5	29.3	95.00%	K.RAGEAVIHLSEGSNLYPR.D		K.RAGEAVIHLSEGSNLYPR.D
246	253	2	883.52	3	0	41.9	24.1	95.00%	K.GLLDTLPR.R		K.GLLDTLPR.R
564	572	2	1130.62	1.9	1	27.5	28.8	93.50%	R.ILCWELVAK.R	Carbamidomethyl (+57)	R.ILCWELVAK.R
93	102	2	1119.56	-0.55	1	34.7	31	95.00%	R.YAANLQESPK.R		R.YAANLQESPK.R
828	840	2	1585.77	2.8	1	61.7	32.6	95.00%	K.QIVETDWPQEVDK.K		K.QIVETDWPQEVDK.K

235	245	2	1220.75	2.4	1	24.2	16.7	94.10%	K.ALLKLDNPIPK.G		K.ALLKLDNPIPK.G
457	472	2	1621.78	2.5	1	99.7	32.5	95.00%	K.VFDMDSNVAGAAGQIK.T		K.VFDMDSNVAGAAGQIK.T
538	548	2	1285.6	2.2	1	55.5	33.2	95.00%	R.SYFLGETQEGR.D		R.SYFLGETQEGR.D
131	147	2	1865.92	3.6	1	101	32.2	95.00%	Y.HLSPQQQPSNNLFGSGR.L		R.DNADLPVDPYHLSPQQQPSNNLFGSGR.L
554	563	2	1182.54	3.3	1	34.5	32.5	95.00%	F.TANMYLAEDR.I		R.DHDVFTANMYLAEDR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
42	A6ZKX6_YEAS7	58.84%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
203	217	2	1628.89	0.17	2	84.2	28.7	95.00%	R.RGPLVVYAEDNGIVK.A		R.RGPLVVYAEDNGIVK.A
145	161	3	1880.05	-1	0	46.4	24.1	95.00%	K.IPEIPLVVSTDLESIQK.T		K.IPEIPLVVSTDLESIQK.T
275	288	2	1525.81	3.1	0	53.1	28.7	95.00%	Y.TLPSHIISTSDVTR.I		K.VGYTLPSHIISTSDVTR.I
221	246	2	2610.43	3.5	0	65.3	23.5	95.00%	R.NVPGVETANVASLNLLQLAPGAHLGR.F		R.NVPGVETANVASLNLLQLAPGAHLGR.F
272	288	2	1844.96	0.7	1	70.1	30	95.00%	K.VGYTLPSHIISTSDVTR.I		K.VGYTLPSHIISTSDVTR.I
347	360	2	1462.81	2.8	1	32.8	27.2	95.00%	K.TGTKPAAVFTETLK.H		K.TGTKPAAVFTETLK.H
289	309	3	2267.24	3.2	1	40.6	24.5	95.00%	R.IINSSEIQSAIRPAGQATQKR.T		R.IINSSEIQSAIRPAGQATQKR.T
289	308	2	2111.14	1.8	0	91.9	27.1	95.00%	R.IINSSEIQSAIRPAGQATQK.R		R.IINSSEIQSAIRPAGQATQK.R
85	95	2	1183.49	-0.58	1	46.1	31.8	95.00%	R.SGQGAFGNMCR.G	Carbamidomethyl (+57)	R.SGQGAFGNMCR.G
258	271	2	1505.74	2.3	1	65.9	31.9	95.00%	K.LDQVWGSETVASSK.V		K.LDQVWGSETVASSK.V
2	26	2	2617.4	4.2	1	65.1	25.7	95.00%	M.SRPQVTVHSLTGEATANALPLPAVF.S	Acetyl (+42)	-.MSRPQVTVHSLTGEATANALPLPAVFSAPIRPDIVHTVFTSVNK.N
120	138	3	1819.02	-0.27	1	24.2	25.1	95.00%	R.YATASAIAATAVASLVLAR.G		R.YATASAIAATAVASLVLAR.G
2	44	4	4579.45	-1.8	1	59.5	28.5	95.00%	M.SRPQVTVHSLTGEATANALPLPAVFSAPIRPDIVHTVFTSVNK.N	Acetyl (+42)	-.MSRPQVTVHSLTGEATANALPLPAVFSAPIRPDIVHTVFTSVNK.N
56	69	3	1443.65	0.074	1	30.2	33.2	95.00%	K.AGHQTSAESWGTGR.A		K.AGHQTSAESWGTGR.A
347	362	3	1714.89	2.7	1	22.8	30.1	90.50%	K.TGTKPAAVFTETLKHD.-		K.TGTKPAAVFTETLKHD.-
204	217	2	1472.79	3.4	1	64.3	28.9	95.00%	R.GPLVVYAEDNGIVK.A		R.GPLVVYAEDNGIVK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
43	A6ZX34_YEAS7	22.64%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
130	143	2	1387.73	2.6	0	60.2	29.8	95.00%	R.AIASSPSLNSNLSK.N		R.AIASSPSLNSNLSK.N
202	232	3	3549.57	3.9	2	54.9	31.9	95.00%	F.GGYPASSFPLMIDEKEEDDYLHNPDPEEEAR.L		R.SPTSSPGNESSASFSSNPFLGEQDFSPFGGYPASSFPLMIDEKEEDDYLHNPDPEEEAR.L
188	201	2	1570.7	4.1	1	35.5	33.2	95.00%	F.SSNPFLGEQDFSPF.G		R.SPTSSPGNESSASFSSNPFLGEQDFSPFGGYPASSFPLMIDEK.E
494	508	2	1572.75	-1	0	92	32.6	95.00%	R.GAPEIDVLEGETDTK.I		R.GAPEIDVLEGETDTK.I
402	420	2	2109.03	-1.9	1	56.3	32.7	95.00%	K.VCFTQGALEISANLPNYGR.V	Carbamidomethyl (+57)	K.VCFTQGALEISANLPNYGR.V
114	129	2	1752.86	1.6	1	46	32.9	95.00%	R.AVSTANDNSFLQPPHR.A		R.AVSTANDNSFLQPPHR.A
476	493	2	2013.87	1.9	0	69.3	34.5	95.00%	K.LSICTCDGEDHPNQGVGR.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.LSICTCDGEDHPNQGVGR.G
304	316	2	1358.66	-0.9	0	51.5	32	95.00%	R.TSLVDPDTPDTAK.T		R.TSLVDPDTPDTAK.T
393	401	2	1049.5	3.4	1	51.8	30	95.00%	R.SGMLQSWNK.V		R.SGMLQSWNK.V
174	187	2	1433.54	3.3	1	34.6	32.5	95.00%	R.SPTSSPGNESSASF.S	Phospho (+80)	R.SPTSSPGNESSASFSSNPFLGEQDFSPFGGYPASSFPLMIDEK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
44	A6ZV88_YEAS7	32.08%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
183	206	2	2780.11	3.4	1	81.8	33.7	95.00%	W.AFEDEDGDDEYATEETLSHHDNNK.G		K.SGDNLTVVINSLGWAFEDEDGDDEYATEETLSHHDNNK.G
138	143	2	705.45	3.8	1	27.6	21.8	95.00%	K.SIVLFK.F		K.SIVLFK.F

117	137	2	2401.12	5.4	1	93.6	33.3	95.00%	F.TVDELPESASDLLYEYSLDDK.S		R.FFANDVSLTVHDDSPLNISQSLSPIMEQFTVDELPESASDLLYEYSLDDK.S
144	152	2	1058.49	-6.2	1	38.5	32.3	95.00%	K.FTSDAYDLK.K		K.FTSDAYDLK.K
29	38	2	1145.53	3.3	1	34.5	32.3	95.00%	K.ESSSFISFDK.E		K.ESSSFISFDK.E
154	168	2	1829.85	4.9	1	38.1	33.7	95.00%	K.LDEFIDSCLSFLEDK.S	Carbamidomethyl (+57)	K.LDEFIDSCLSFLEDK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
45	MAM3_YEAST	31.59%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
427	457	3	3326.52	3.7	0	77.4	32.2	95.00%	K.AADQADESSPLLSPSNSNHPSEHPQQDLNNK.S		K.AADQADESSPLLSPSNSNHPSEHPQQDLNNK.S
391	399	2	1165.55	4.4	0	68.2	32.3	95.00%	F.VDMHQHIMR.Q		K.EPGSSHGAIGVLTLEDVIEELIGEEIVDESDVFVDMHQHIMR.Q
577	608	3	3387.56	0.25	1	42.7	31.8	95.00%	R.NSPDSISIPNSGANHGNENQNVTISTSYQNTK.N		R.NSPDSISIPNSGANHGNENQNVTISTSYQNTK.N
683	691	2	1025.48	2.6	1	34.1	32.6	95.00%	R.SNFTDSLSR.T		R.SNFTDSLSR.T
514	535	3	2380.17	-1.2	1	58.7	31.7	95.00%	K.IITTHTPHSSKEPSPAPHSNDK.S		K.IITTHTPHSSKEPSPAPHSNDK.S
267	277	2	1208.57	4.5	0	53.4	32.5	95.00%	F.TMSADTILDDK.T		R.VEEIMTPIENVFTMSADTILDDK.T
236	251	2	1757.02	-0.41	1	107	22.5	95.00%	R.LTKDEVTIISAVLDLK.A		R.LTKDEVTIISAVLDLK.A
605	619	2	1629.9	3.8	1	29.5	27.8	95.00%	Y.QNTKNGIVESVITVK.G	Deamidation (+1)	R.NSPDSISIPNSGANHGNENQNVTISTSYQNTKNGIVESVITVK.G
358	399	5	4644.26	4.2	1	30.4	27.2	95.00%	K.EPGSSHGAIGVLTLEDVIEELIGEEIVDESDVFVDMHQHIMR.Q		K.EPGSSHGAIGVLTLEDVIEELIGEEIVDESDVFVDMHQHIMR.Q
536	553	2	2011.99	4.1	0	70.8	31.7	95.00%	K.SLSAEEQQLLSDHAELSR.Q		K.SLSAEEQQLLSDHAELSR.Q
470	500	3	3211.69	3.2	0	50.3	25.3	95.00%	R.SNAVLSPTPQVTEHGTIIPSNLASNPLNVNK.S		R.SNAVLSPTPQVTEHGTIIPSNLASNPLNVNK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
46	B3LS12_YEAS1	20.60%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
147	168	3	2347	3.6	1	35.9	34.2	95.00%	Y.SINDNEGVDEGKDANGNPMDEK.S		K.LEYSINDNEGVDEGKDANGNPMDEK.S
712	725	2	1640.81	3.4	0	85.1	32.8	95.00%	R.TTHGELITLDEEQR.L		R.TTHGELITLDEEQR.L
712	740	4	3326.67	0.55	2	34.5	27.9	95.00%	R.TTHGELITLDEEQRLHIDAVNTVWSHANK.D		R.TTHGELITLDEEQRLHIDAVNTVWSHANK.D
393	403	2	1269.68	3.8	1	33.9	28.6	95.00%	W.FLDVSNTIHPK.W		R.SPDFKPVENNYDNSTNVPQEIWFLDVSNTIHPK.W
726	740	2	1703.87	0.05	1	50.6	30.6	95.00%	R.LHIDAVNTVWSHANK.D		R.LHIDAVNTVWSHANK.D
597	616	3	2230.06	3.7	1	85.3	33	95.00%	K.RQEAAVEICSGQIAHMSTDK.K	Carbamidomethyl (+57)	K.RQEAAVEICSGQIAHMSTDK.K
113	122	2	1230.6	3.5	1	55.1	31.1	95.00%	K.HFNELSLTDR.C		K.HFNELSLTDR.C
129	142	2	1683.8	0.77	1	85.9	33.2	95.00%	R.TLYTLDDEWTNSVK.K		R.TLYTLDDEWTNSVK.K
192	207	2	1934.94	-0.098	1	48.7	32.7	95.00%	R.CFMQANPVNIQEIFPK.S	Carbamidomethyl (+57)	R.CFMQANPVNIQEIFPK.S
274	282	2	1029.59	-0.41	1	39.1	29.4	95.00%	K.VLEQGFLPK.F		K.VLEQGFLPK.F
520	533	3	1610.85	-0.18	2	63.7	29.1	95.00%	R.RQHQLEAGLFAVDK.S		R.RQHQLEAGLFAVDK.S
353	364	2	1387.7	4.2	1	46.7	31.1	95.00%	Y.RGDELSQELVDK.L		R.FEGNTLPIQVVYRGDELSQELVDK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
47	B3LNF5_YEAS1	19.28%	100%	20

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
90	99	2	1113.51	-1.2	1	31.8	32.2	94.70%	R.AVATSMYESR.L		R.AVATSMYESR.L
315	328	2	1622.69	3.1	1	82	33.9	95.00%	R.HSMQGEIYEDAMGR.I		R.HSMQGEIYEDAMGR.I
1032	1049	2	1913.05	-0.73	0	90.6	26.8	95.00%	K.IQGLEGIILTNIVSNSDK.V		K.IQGLEGIILTNIVSNSDK.V
907	919	2	1487.68	-1	1	72	33.4	95.00%	R.SLVSSTDFFQDDK.N		R.SLVSSTDFFQDDK.N
1328	1339	2	1201.58	0.34	0	35.4	32.4	95.00%	K.GLSPANAADVCK.K	Carbamidomethyl (+57)	K.GLSPANAADVCK.K
596	611	2	1955.78	-0.054	1	138	33.9	95.00%	K.TCEENDFEDWNLAEGK.C	Carbamidomethyl (+57)	K.TCEENDFEDWNLAEGK.C

31	50	2	2284.13	4.8	1	38.9	31.7	95.00%	K.TIAQDSFEILSFDDSNTLIR.K		K.TIAQDSFEILSFDDSNTLIR.K
211	228	2	1986.92	5	2	70.5	33.5	95.00%	K.TGKDSDLESSDTSIICLF.Q	Carbamidomethyl (+57)	K.TGKDSDLESSDTSIICLFQNMQLIMDEFSSPYTESK.L
229	246	2	2146.97	4.7	1	71	34.2	95.00%	F.QNMQLIMDEFSSPYTESK.L		K.DSDLESSDTSIICLFQNMQLIMDEFSSPYTESK.L
384	395	2	1307.69	1.8	1	47.7	30.2	95.00%	K.GTMIASLYPLSR.R		K.GTMIASLYPLSR.R
709	719	2	1189.57	0.18	0	29.1	31.1	92.50%	K.SVDISCEGVPK.K	Carbamidomethyl (+57)	K.SVDISCEGVPK.K
1143	1155	2	1420.69	3.1	1	75.6	32.3	95.00%	F.TTDGGETWAEVKK.T		K.ECSTFFTTDGGETWAEVKK.T
667	682	2	1908.9	-0.7	1	45.3	33	95.00%	K.CVPDYNLIVLSDVCDK.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CVPDYNLIVLSDVCDK.T
414	426	2	1444.8	2.6	1	89.7	27.9	95.00%	K.ISVDNGLTWTVLK.V		K.ISVDNGLTWTVLK.V
860	880	2	2413.03	3.7	1	118	34.6	95.00%	Y.LTNDGGETFTEMLDNAIHCEF.A	Carbamidomethyl (+57)	K.NCESILSPECHAVAYLTNDGGETFTEMLDNAIHCEFAGSLFK.Y
1431	1451	3	2311.18	3.1	1	32.8	30.1	95.00%	R.LGDDGLIENNNTDRVVNNIVK.S		R.LGDDGLIENNNTDRVVNNIVK.S
1281	1297	2	1997.91	-1.1	1	52.6	33.6	95.00%	K.TDENCFIGNIPLSEFSR.N	Carbamidomethyl (+57)	K.TDENCFIGNIPLSEFSR.N
196	210	2	1611.72	-0.18	1	56.4	33.8	95.00%	R.NENSAISISDCGFAK.T	Carbamidomethyl (+57)	R.NENSAISISDCGFAK.T
887	899	2	1599.68	2.5	1	68.7	33.5	95.00%	K.YPSNEDMVMCQVK.E	Carbamidomethyl (+57)	K.YPSNEDMVMCQVK.E
1267	1279	2	1607.76	2.9	1	65.6	32.8	95.00%	K.SNCLFGHQTEFLR.K	Carbamidomethyl (+57)	K.SNCLFGHQTEFLR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
48	A6ZVP9_YEAS7	42.52%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
164	174	2	954.56	3.5	0	55.4	21	95.00%	R.GVIGVIAGGGR.V		R.GVIGVIAGGGR.V
201	221	2	2158.03	2.5	0	64.3	33.4	95.00%	R.GVAMNPVDHPHGGGNHQHIGK.A		R.GVAMNPVDHPHGGGNHQHIGK.A
129	147	3	2097.07	2.4	1	41.8	30.1	95.00%	R.ASGNYVIIIGHNPDENKTR.V		R.ASGNYVIIIGHNPDENKTR.V
134	147	2	1604.87	5.6	1	45.7	28.2	95.00%	Y.VIIIGHNPDENKTR.V		R.ASGNYVIIIGHNPDENKTR.V
94	123	3	3046.61	4.4	0	31.5	25.4	95.00%	K.ASLNVGNVLPLGSVPEGTIVSNVEEKPGDR.G		K.ASLNVGNVLPLGSVPEGTIVSNVEEKPGDR.G
93	128	4	3642.98	4.2	1	36.9	24.8	95.00%	K.KASLNVGNVLPLGSVPEGTIVSNVEEKPGDRGALAR.A		K.KASLNVGNVLPLGSVPEGTIVSNVEEKPGDRGALAR.A
10	21	3	1260.66	0.078	2	55.2	30	95.00%	R.KGAGSIFTSHTR.L		R.KGAGSIFTSHTR.L
164	181	3	1748.07	1.4	1	20.5	12	95.00%	R.GVIGVIAGGGRVDKPLLK.A		R.GVIGVIAGGGRVDKPLLK.A
129	145	3	1839.91	0.55	1	28.8	31.6	95.00%	R.ASGNYVIIIGHNPDENK.T		R.ASGNYVIIIGHNPDENK.T
199	221	3	2415.18	3.3	1	36.1	32.2	95.00%	K.TRGVAMNPVDHPHGGGNHQHIGK.A		K.TRGVAMNPVDHPHGGGNHQHIGK.A
93	123	3	3174.7	3.9	1	83.2	24.7	95.00%	K.KASLNVGNVLPLGSVPEGTIVSNVEEKPGDR.G		K.KASLNVGNVLPLGSVPEGTIVSNVEEKPGDR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
49	A6ZM61_YEAS7	58.17%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
161	174	2	1561.78	4.7	1	82.1	32.1	95.00%	K.NAINVDTAFEEIAR.S		K.NAINVDTAFEEIAR.S
57	70	2	1606.75	3.2	1	72.5	33.4	95.00%	K.VATMQVWDTAGQER.F	Oxidation (+16)	K.VATMQVWDTAGQER.F
122	135	2	1542.87	4.1	1	75.2	27	95.00%	F.VILGNKIDAEESKK.I		R.DEFLVHANVNSPETFPFVILGNKIDAEESKK.I
122	134	2	1414.77	3.7	1	73.8	28.5	95.00%	F.VILGNKIDAEESK.K		R.DEFLVHANVNSPETFPFVILGNKIDAEESK.K
39	48	2	1035.56	2.9	1	28.6	30	93.40%	K.ATIGADFLTK.E		K.ATIGADFLTK.E
81	101	2	2361.06	-2.7	1	101	33.8	95.00%	R.GADCCVLVYDVTNASSFENIK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GADCCVLVYDVTNASSFENIK.S
148	160	2	1360.76	-0.6	1	63.3	28.1	95.00%	K.SLGDIPLFLTSAK.N		K.SLGDIPLFLTSAK.N
11	21	2	1056.62	2.9	0	27.1	27.3	94.80%	K.VIILGDSGVGK.T		K.VIILGDSGVGK.T
175	198	2	2740.23	2.9	1	123	33.4	95.00%	R.SALQQNQADTEAFEDDYNDAINIR.L		R.SALQQNQADTEAFEDDYNDAINIR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
50	A6ZT96_YEAS7	20.95%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

182	192	2	1056.6	3.7	0	42.8	28.3	95.00%	Y.VAGLVGDGLTR.L		K.MGNGMADYILDENYNLNGLQTV HDYDVYCHYVAGLVGDGLTR.L
2	15	3	1575.92	2.4	1	45.5	21.1	95.00%	M.GKLLQLALHPVEMK.A		-.MGKLLQLALHPVEMK.A
109	120	2	1319.62	7.3	1	29	32.3	90.00%	W.SFDGNAPDVKDR.A		K.WSFDGNAPDVKDR.A
226	235	2	1194.52	0.65	1	49.6	32.1	95.00%	R.DYNEDLVDGR.S		R.DYNEDLVDGR.S
356	365	2	1143.63	2.5	1	26.7	29	92.10%	K.LAVQDPNFLK.L		K.LAVQDPNFLK.L
4	15	2	1390.8	2.7	0	59.8	22.8	95.00%	K.LLQLALHPVEMK.A		K.LLQLALHPVEMK.A
136	150	2	1846.01	2.5	1	81.5	27.6	95.00%	K.LKPEYQEVIKEITEK.M		K.LKPEYQEVIKEITEK.M
373	384	2	1589.68	2.8	1	64.9	33.5	95.00%	K.IEQFMEEMYQDK.L		K.IEQFMEEMYQDK.L
179	192	2	1516.75	4.2	1	54.7	32	95.00%	Y.CHYVAGLVGDGLTR.L	Carbamidomethyl (+57)	K.MGNGMADYILDENYNLNGLQTV HDYDVYCHYVAGLVGDGLTR.L
108	118	2	1234.57	3.1	1	33.7	32	95.00%	K.WSFDGNAPDVK.D		K.WSFDGNAPDVK.D
221	235	2	1791.88	3.4	2	55.5	32.6	95.00%	K.TNIIRDYNEDLVDGR.S		K.TNIIRDYNEDLVDGR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
51	GNP1_YEAST	15.23%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
42	57	2	1909.9	4.2	1	72.1	33.2	95.00%	K.QIGSIEPENEVEYFEK.T		K.QIGSIEPENEVEYFEK.T
11	34	3	2829.14	-1	2	47.1	33.6	95.00%	R.NNEGSSNMNMNRNDLDDVSHY EMK.E	Oxidation (+16)	R.NNEGSSNMNMNRNDLDDVSHY EMK.E
110	122	2	1504.71	-0.28	1	53.5	32.4	95.00%	K.DSSSQLDNELNRK.S		K.DSSSQLDNELNRK.S
86	109	3	2414.11	0.084	1	70.6	33.2	95.00%	R.RAEGSHANSPDSSNSNGTTPIST K.D		R.RAEGSHANSPDSSNSNGTTPIST K.D
110	121	2	1376.62	-0.74	0	37.8	33	95.00%	K.DSSSQLDNELNR.K		K.DSSSQLDNELNR.K
62	78	2	2077.92	-0.44	1	69.1	34.2	95.00%	K.TIENMEYEGEHHASYLR.R		K.TIENMEYEGEHHASYLR.R
11	31	3	2424.97	3.4	2	35.3	33.6	95.00%	R.NNEGSSNMNMNRNDLDDVSHY. E		R.NNEGSSNMNMNRNDLDDVSHY EMK.E
62	76	2	1808.74	3.8	1	66	33.7	95.00%	K.TIENMEYEGEHHASY.L		K.TIENMEYEGEHHASYLR.R
472	478	2	987.42	3.8	1	32.2	31.9	95.00%	K.CFDYIDR.E	Carbamidomethyl (+57)	K.CFDYIDR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
52	A6ZNT9_YEAS7	61.43%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
171	192	3	2514.21	3.3	1	51.1	32.3	95.00%	K.IPLKTAEEQNSASNERESNNQR.V		K.IPLKTAEEQNSASNERESNNQR.V
37	48	2	1302.7	2.8	1	34.1	29.6	95.00%	K.EPTIGAAFLTQR.V		K.EPTIGAAFLTQR.V
171	186	2	1785.89	3.1	1	77.1	32	95.00%	K.IPLKTAEEQNSASNER.E		K.IPLKTAEEQNSASNER.E
156	170	2	1590.79	2.8	1	70.2	31.6	95.00%	K.TGENVNDVFLGIGEK.I		K.TGENVNDVFLGIGEK.I
10	20	2	1068.65	-1.1	0	24	20.5	93.90%	K.LVLLGEAAVGK.S		K.LVLLGEAAVGK.S
58	68	2	1350.62	0.79	1	56.1	33.3	95.00%	K.FEIWDTAGQER.F		K.FEIWDTAGQER.F
112	121	2	1054.64	1.5	0	46.2	22.5	95.00%	K.DIIIALVGNK.I		K.DIIIALVGNK.I
79	97	2	2091.14	3.3	1	85.1	26.1	95.00%	R.NAQAALVVYDVTKPQSFIK.A		R.NAQAALVVYDVTKPQSFIK.A
112	132	3	2311.27	3.3	1	39.7	25.4	95.00%	K.DIIIALVGNKIDMLQEGGERK.V		K.DIIIALVGNKIDMLQEGGERK.V
104	121	3	1977.1	3.3	1	46.4	25.5	95.00%	K.ELHEQASKDIIIALVGNK.I		K.ELHEQASKDIIIALVGNK.I
146	155	2	1111.6	3.4	1	49.4	28	95.00%	K.GLLFFETSAK.T		K.GLLFFETSAK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
53	A6ZS87_YEAS7	15.44%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
74	82	2	984.56	3.2	0	39.1	26.3	95.00%	F.VAALNQELK.K		K.FVAALNQELK.K
43	72	3	3385.6	2.9	1	92.9	30.9	95.00%	K.HHVVEPHDANDENLPLLADASPD DQFYISK.F		K.HHVVEPHDANDENLPLLADASPD DQFYISK.F
115	132	2	2124.09	2.3	1	73.7	29.9	95.00%	K.ATQLFNQQQQHQLQSVAR.N		K.ATQLFNQQQQHQLQSVAR.N
73	82	2	1131.63	2.6	1	55.5	28.3	95.00%	K.FVAALNQELK.K		K.FVAALNQELK.K
100	114	2	1790.84	2.8	1	75.1	33.2	95.00%	Y.NELKDDVMELENTNK.A		K.FYISQETGLIANYNELKDDVMELE NTNK.A
120	132	2	1563.79	4.6	0	53.1	30.9	95.00%	F.NQQQQHQLQSVAR.N		K.ATQLFNQQQQHQLQSVAR.N
755	770	2	1604.88	-0.37	0	63.8	27.8	95.00%	K.AVSSSGLLSTMAQLIK.A		K.AVSSSGLLSTMAQLIK.A
260	272	3	1538.78	3.5	1	41.3	30.9	95.00%	K.FHSHVFNPATINR.I		K.FHSHVFNPATINR.I

334	347	3	1761.9	3.9	2	28.9	31.5	95.00%	R.ELSSHLRDHVVWER.N		R.ELSSHLRDHVVWER.N
860	869	2	1169.64	0.071	1	44.2	27.1	95.00%	R.YLTVGTFITR.G		R.YLTVGTFITR.G
348	359	2	1535.72	0.18	1	38.2	32.9	95.00%	R.NTVWKDMMNLER.K		R.NTVWKDMMNLER.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
54	A6ZM54_YEAS7	36.03%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
181	190	2	1274.52	3	1	50.6	32.6	95.00%	K.MDFEENTFDK.V		K.MDFEENTFDK.V
356	366	2	1324.7	-0.78	1	27.5	29.4	92.70%	K.LFTPMMLFVAR.K		K.LFTPMMLFVAR.K
367	383	2	1844.84	-0.82	0	36.4	34.3	95.00%	R.KPENAETPSQTSQEATQ.-		R.KPENAETPSQTSQEATQ.-
240	253	2	1544.85	3.8	2	73.7	28.2	95.00%	R.KIAYEIELGDGIPK.M		R.KIAYEIELGDGIPK.M
140	157	2	2039.98	3.8	1	69.5	33.1	95.00%	R.FTGCNVIGLNNNDYQIAK.A	Carbamidomethyl (+57)	R.FTGCNVIGLNNNDYQIAK.A
364	383	3	2171.05	2.7	1	49	32.7	95.00%	F.VARKPENAETPSQTSQEATQ.-		K.LFTPMMLFVARKPENAETPSQTSQEATQ.-
226	239	3	1746.77	4.8	2	32	34.1	95.00%	W.VMTDKYDENNPEHR.K		K.VLKPGGTFAVYEWVMTDKYDENNPEHR.K
120	135	2	1540.77	0.85	0	56.6	31.7	95.00%	R.GDLVLDVGCGVGGPAR.E	Carbamidomethyl (+57)	R.GDLVLDVGCGVGGPAR.E
336	353	2	1668.91	4.1	0	70.5	26.7	95.00%	K.EVTAALENAAVGLVAGGK.S		K.EVTAALENAAVGLVAGGK.S
327	353	4	2521.39	4.7	1	28.5	23.4	95.00%	K.LGLAPEGSKEVTAALENAAVGLVAGGK.S		K.LGLAPEGSKEVTAALENAAVGLVAGGK.S
165	175	2	1358.62	2.9	1	36.8	33.1	95.00%	K.YNLSDQMDFVK.G		K.YNLSDQMDFVK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
55	A6ZZF0_YEAS7	17.30%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
176	185	2	1188.7	4	1	67.8	24	95.00%	K.KMSLIDLLTR.R		K.KMSLIDLLTR.R
273	292	2	2279.97	4.2	1	72.8	34.1	95.00%	R.HHHSSESPENYGSNQLSHSF.S		R.HHHSSESPENYGSNQLSHSFSSPLGNDVTENPAALADTQYHPENGSLYPHHHHLETPFSK.L
151	166	2	1634.81	3.4	0	51	32.3	95.00%	Y.ATSSSSVSENDPLITK.D		K.SHSHSHSHSHADSHSNFSNDHDLENAPSEHGYATSSSSVSENDPLITK.D
177	185	2	1060.6	-0.2	0	70.3	27.8	95.00%	K.MSLIDLLTR.R		K.MSLIDLLTR.R
246	264	2	2184.05	4.8	1	39.7	33.2	95.00%	R.GLVCVENNIGYDLENLSLY.R	Carbamidomethyl (+57)	R.GLVCVENNIGYDLENLSLYR.K
246	265	2	2340.14	-1.1	1	95.2	32.4	95.00%	R.GLVCVENNIGYDLENLSLYR.K	Carbamidomethyl (+57)	R.GLVCVENNIGYDLENLSLYR.K
198	218	2	2441.23	-1.8	1	95.1	29.9	95.00%	K.CTPLLQSEQPEYIACVPPVIK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CTPLLQSEQPEYIACVPPVIK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
56	GAS1_YEAST	18.60%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
194	209	2	1793.85	3.5	1	78.8	32.7	95.00%	K.IPVGYSSNDDEDTRVK.M		K.IPVGYSSNDDEDTRVK.M
395	414	2	2152.92	0.9	1	82.8	34.7	95.00%	F.NWICNEVDCSGISANGTAGK.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Deamidation (+1)	K.YWSAATELPPTPNGGLCSCMNAANSCVVSDDVDSDDYETLFNWICNEVDCSGISANGTAGK.Y
215	226	2	1374.55	3.6	2	30.8	31.7	93.90%	F.ACGDDDVKADFY.G	Carbamidomethyl (+57)	K.MTDYFACGDDDVKADFYGINMYEWCGK.S
106	127	3	2286.2	4.6	1	45.7	28.5	95.00%	K.ALNDADIYVIADLAAPATSINR.D		K.ALNDADIYVIADLAAPATSINR.D
194	207	2	1566.68	-0.71	1	74.9	33.2	95.00%	K.IPVGYSSNDDEDTR.V		K.IPVGYSSNDDEDTR.V
261	271	2	1310.56	3.7	1	43.8	32.7	95.00%	F.SEYGCNEVTPR.L	Carbamidomethyl (+57)	K.NLSIPVFFSEYGCNEVTPR.L
114	137	2	2600.32	4.2	2	45.4	29.5	95.00%	Y.VIADLAAPATSINRDDPTWTVDLF.N		K.ALNDADIYVIADLAAPATSINRDDPTWTVDLFNSYK.T
210	222	2	1535.59	0.34	1	71.5	32.4	95.00%	K.MTDYFACGDDDVK.A	Carbamidomethyl (+57)	K.MTDYFACGDDDVK.A
83	90	2	956.58	0.5	1	36.9	24.8	95.00%	K.KLNTNVIR.V		K.KLNTNVIR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
57	YG35_YEAST	18.82%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
805	817	2	1313.73	0.45	0	45.7	28.1	95.00%	K.QNNVVSAVIAATK.N		K.QNNVVSAVIAATK.N

162	189	4	3057.5	4	1	62.1	30.2	95.00%	R.GLQNSSLPELEDGYAGGYQSLRPSHNLR.F		R.GLQNSSLPELEDGYAGGYQSLRPSHNLR.F
716	732	2	1882.85	2.4	1	108	33.6	95.00%	K.NINADNIDYSAAEGFNR.I		K.NINADNIDYSAAEGFNR.I
798	817	3	2155.16	0.88	1	26.5	27.1	95.00%	K.ERLEEGKQNNVVSAVIAATK.N		K.ERLEEGKQNNVVSAVIAATK.N
146	161	2	1770.89	3.5	1	41.2	31.4	95.00%	R.LLLSPASSNVDDDRNR.G		R.LLLSPASSNVDDDRNR.G
923	945	3	2583.36	3.2	1	47	26.7	95.00%	R.LASQSHLLHADNIFFLVETGMLK.A		R.LASQSHLLHADNIFFLVETGMLK.A
55	75	3	2186.11	3.7	1	27.9	30.5	95.00%	F.TGGNSPMINNLSDSKLPISNK.Q		R.SYMSGFFTGGNSPMINNLSDSKLPISNK.Q
891	902	3	1474.78	2.9	1	30.1	30.2	95.00%	K.QYRPDIISEVQK.V		K.QYRPDIISEVQK.V
709	715	2	910.52	0.089	1	34.7	25.5	95.00%	K.YLILDFK.N		K.YLILDFK.N
662	674	2	1493.81	-0.81	1	38.6	28.1	95.00%	K.FLDGIGEQIYVLK.L		K.FLDGIGEQIYVLK.L
1025	1031	2	868.47	4.2	2	29.8	27.8	95.00%	R.FKELLGY.T		R.FKELLGYTLVSA.-
839	849	2	1242.64	2.6	0	36.8	28.9	95.00%	R.NLMSLPTNTPR.N		R.NLMSLPTNTPR.N
850	869	2	2278.17	4.4	1	62.4	30	95.00%	R.NYQILSVAQNVFVNDEQAVK.N		R.NYQILSVAQNVFVNDEQAVK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
58	NCPR_YEAST	42.11%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
484	509	3	2916.49	0.59	1	45.1	28.6	95.00%	R.NIQLAQNNVNIAETNLPVHYDLNGPR.K		R.NIQLAQNNVNIAETNLPVHYDLNGPR.K
254	275	2	2355.26	3.2	1	52.2	26.8	95.00%	R.NADGIQLGPFDLSQPYIAPIVK.S		R.NADGIQLGPFDLSQPYIAPIVK.S
200	219	3	2351.23	4.5	1	56.3	28.1	95.00%	W.KDSILEVLKDELHLDEQEAK.F		K.LGEADDGAGTTDEDYMAWKDSILEVLKDELHLDEQEAK.F
653	664	2	1171.7	3.1	0	42.5	25.1	95.00%	K.GVSTALVGILSR.G		K.GVSTALVGILSR.G
405	413	2	1053.55	3.5	1	40.6	29.1	95.00%	K.YFNIADALK.Y		K.YFNIADALK.Y
326	343	2	2054.1	3.6	1	36	27.2	95.00%	F.NLDPETIFDLKPLDPTVK.V		K.VEQFLSIFNLDPETIFDLKPLDPTVK.V
281	300	3	2279.03	3.6	2	39.4	34.1	95.00%	F.SSNDRNCIHSEFDLSGSNIK.Y	Carbamidomethyl (+57)	R.ELFSSNDRNCIHSEFDLSGSNIK.Y
179	199	2	2213.95	3	2	64.9	34.4	95.00%	R.LGKLGEADDGAGTTDEDYMAWK.K		R.LGKLGEADDGAGTTDEDYMAWK.D
452	483	3	3452.84	2.8	1	37	24.7	95.00%	K.QTVHVTSIVENFPNPELPDAPPVVGVTTNLLR.N		K.QTVHVTSIVENFPNPELPDAPPVVGVTTNLLR.N
421	439	2	2260.1	-1.2	1	59.7	32.4	95.00%	K.WDTVPMQFLVESVPQMTPR.Y		K.WDTVPMQFLVESVPQMTPR.Y
484	503	2	2264.16	2.9	1	126	29.8	95.00%	R.NIQLAQNNVNIAETNLPVHY.D		R.NIQLAQNNVNIAETNLPVHYDLNGPR.K
440	451	2	1349.64	2.4	1	61	32.5	95.00%	R.YYSISSSSLSEK.Q		R.YYSISSSSLSEK.Q
667	678	2	1319.69	2.6	0	37.4	31.3	95.00%	K.SITTDEATELIK.M		K.SITTDEATELIK.M
201	219	3	2223.14	4.8	1	55.5	29.8	95.00%	K.DSILEVLKDELHLDEQEAK.F		K.DSILEVLKDELHLDEQEAK.F
49	59	2	1229.63	1.1	0	54.2	30.5	95.00%	R.DIAQVVTENNK.N		R.DIAQVVTENNK.N
369	384	2	1776.94	-0.18	1	60.3	29.5	95.00%	R.QLFSSLIQFAPNADVK.E		R.QLFSSLIQFAPNADVK.E
227	253	4	3008.48	4.7	1	21.4	30.1	92.70%	Y.TVLNEITDSMSLGEPSAHYLPSHQLNR.N		K.FTSQFQYTVLNEITDSMSLGEPSAHYLPSHQLNR.N
598	611	3	1574.79	3.1	2	53.8	31.6	95.00%	K.KLDGSFEMVVAHSR.L		K.KLDGSFEMVVAHSR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
59	B3LGY9_YEAS1	19.71%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
408	425	2	2113	2.6	1	43	33.3	95.00%	R.LHSHDHKPPVSESSDWQK.E		R.LHSHDHKPPVSESSDWQK.E
9	22	2	1651.84	-0.14	1	67.5	31.1	95.00%	K.RVEQDDPVPELDIK.Q		K.RVEQDDPVPELDIK.Q
510	525	2	1887.94	3.1	1	72.9	32.2	95.00%	W.YVENNSNPLLPEDTKR.I		R.HDLTLWYVENNSNPLLPEDTKR.I
550	569	3	2411.24	3.2	1	31.5	29.5	95.00%	K.NLVEPHVYESQPTSWPFLLR.G		K.NLVEPHVYESQPTSWPFLLR.G
799	812	2	1601.84	3.6	1	62.1	30.1	95.00%	K.MLEEEGANILKVEK.R		K.MLEEEGANILKVEK.R
486	503	2	2021.93	2.4	1	97	33.7	95.00%	K.LPAWGFEQQEVTCASSGR.H	Carbamidomethyl (+57)	K.LPAWGFEQQEVTCASSGR.H
406	425	3	2429.13	-1.2	2	27.7	33.2	93.90%	R.CRLHSHDHKPPVSESSDWQK.E	Carbamidomethyl (+57)	R.CRLHSHDHKPPVSESSDWQK.E

570	579	2	1194.55	3.9	1	30.9	32.1	93.60%	R.GISYWGENNR.N		R.GISYWGENNR.N
799	809	2	1245.63	1.6	0	78	31.9	95.00%	K.MLEEEGANILK.V		K.MLEEEGANILK.V
30	42	2	1370.75	4.8	0	53.5	28	95.00%	F.IVTDPSAELASLR.T		K.QGPVRPFIVTDPSAELASLR.T
23	42	3	2152.16	-0.37	1	46.7	26.3	95.00%	K.QGPVRPFIVTDPSAELASLR.T		K.QGPVRPFIVTDPSAELASLR.T
784	798	3	1699.87	4.3	1	26.9	30.5	95.00%	F.KDTEGNELDPEVVKK.M		K.IFKDTEGNELDPEVVKK.M
472	485	2	1678.76	2.5	1	63.8	33.5	95.00%	R.HAMTGCYLFSHEVK.L	Carbamidomethyl (+57)	R.HAMTGCYLFSHEVK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
60	A7A1A2_YEAS7	14.29%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
663	674	2	1229.67	3.1	0	37.8	29.7	95.00%	R.NAVVQGIDSSLK.I		R.NAVVQGIDSSLK.I
498	509	2	1339.65	-1.3	0	39.8	32.7	95.00%	K.VLSAPNHTVDCK.I	Carbamidomethyl (+57)	K.VLSAPNHTVDCK.I
471	485	2	1826.88	2	2	86.5	33.1	95.00%	R.HRDPNNPDQLTMYVK.A		R.HRDPNNPDQLTMYVK.A
651	662	2	1385.57	3.5	1	40.1	32.9	95.00%	Y.SCGPATFNDDFR.N	Carbamidomethyl (+57)	K.LSELENNNITFYSCGPATFNDDFR.N
510	525	2	1739.97	2.9	1	48.2	26.2	95.00%	K.IFLEGPYGVTVPHIAK.L		K.IFLEGPYGVTVPHIAK.L
51	67	2	1925.9	2.6	1	108	33.8	95.00%	K.NINWLGSVTACAYENSK.S	Carbamidomethyl (+57)	K.NINWLGSVTACAYENSK.S
471	483	2	1599.72	3.2	2	46.8	33.9	95.00%	R.HRDPNNPDQLTMY.V		R.HRDPNNPDQLTMYVK.A
414	427	2	1464.73	0.61	0	67.9	32.5	95.00%	K.TATLSTTDDSNVIK.I		K.TATLSTTDDSNVIK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
61	A6ZNY0_YEAS7	22.80%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
752	769	2	1971.05	3	1	59.1	28.3	95.00%	R.GQVVSEEQRPGTPLFTVK.A		R.GQVVSEEQRPGTPLFTVK.A
633	651	2	2130.02	-0.65	1	63.1	32.7	95.00%	K.IWCFGPDGNGPNLVIDQTK.A	Carbamidomethyl (+57)	K.IWCFGPDGNGPNLVIDQTK.A
786	814	3	3117.47	5.3	1	37.6	31.9	95.00%	R.QATGGQAFPQMVFDHWSTLGSDPLDPTSK.A		R.QATGGQAFPQMVFDHWSTLGSDPLDPTSK.A
712	723	2	1265.67	-0.42	1	36.8	29.9	95.00%	R.ATYAGFLLADPK.I		R.ATYAGFLLADPK.I
635	651	2	1830.86	3	1	63.9	33.3	95.00%	W.CFGPDGNGPNLVIDQTK.A	Carbamidomethyl (+57)	K.IWCFGPDGNGPNLVIDQTK.A
151	162	2	1378.87	2.8	1	55.1	13.2	95.00%	R.IKPVVVINKVDR.A		R.IKPVVVINKVDR.A
724	744	2	2388.21	3.2	1	43.1	30.8	95.00%	K.IQEPVFLVEIQCPEQAVGGIY.S	Carbamidomethyl (+57)	K.IQEPVFLVEIQCPEQAVGGIYSVLNK.K
618	631	2	1626.7	2	1	60.1	33.1	95.00%	R.IMADDYGWDVTDAR.K		R.IMADDYGWDVTDAR.K
33	42	2	1118.6	3.2	0	46.5	29.3	95.00%	K.STLTDSLVQR.A		K.STLTDSLVQR.A
564	578	2	1650.81	3.6	1	64.8	32.5	95.00%	Y.RETVESESSQTALSK.S		K.ISPPVVAYRETVESESSQTALSK.S
353	370	2	1976.92	2.4	1	86.9	33.8	95.00%	R.AEQLYEGPADDANCIAIK.N	Carbamidomethyl (+57)	R.AEQLYEGPADDANCIAIK.N
565	578	2	1494.7	-0.48	0	63.6	32.6	95.00%	R.ETVESESSQTALSK.S		R.ETVESESSQTALSK.S
121	144	3	2572.36	5.2	0	57.8	27.1	95.00%	R.VTDGALVVVDTIEGVCVQTETVLR.Q	Carbamidomethyl (+57)	R.VTDGALVVVDTIEGVCVQTETVLR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
62	A6ZZQ2_YEAS7	16.92%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
146	161	2	1788.92	4.1	1	45.5	30.2	95.00%	R.SLVSDLSPSELESWLK.R		R.SLVSDLSPSELESWLK.R
582	606	2	2590.06	0.46	1	93.4	34.3	95.00%	K.SQAYGATMSNESNANNNNSTSNASR.S	Deamidation (+1)	K.SQAYGATMSNESNANNNNSTSNASR.S
517	534	2	2014.06	3.4	1	64	28.4	95.00%	K.AFGIHPLTTEDIFLGEVR.E		K.AFGIHPLTTEDIFLGEVR.E
381	393	2	1411.78	3	0	53.2	26.5	95.00%	R.IQSGLQDNLLVGR.N		R.IQSGLQDNLLVGR.N
565	579	3	1728.83	-0.81	1	34.2	33.2	95.00%	K.EKQESATLDHESISR.R		K.EKQESATLDHESISR.R
324	339	2	1750.97	4.2	0	68.5	25.4	95.00%	F.SKPIVTNIDVPELGNR.R		R.SQAIQDAEAFHFQYDEDEEDGTSNEDGILFSKPIVTNIDVPELGNR.R
110	126	2	1811.91	2.5	0	56.9	31.6	95.00%	R.EGPQSVSSTVQPQPIMK.F		R.EGPQSVSSTVQPQPIMK.F
48	73	3	3127.5	4.1	1	42.6	31	95.00%	R.RPTQLLHDNLQHNHGQITDFDQIDSW.G		R.RPTQLLHDNLQHNHGQITDFDQIDSWGMLHESDSTSNDIIK.S
394	410	3	2075.04	2	1	24.2	31.3	90.80%	R.NIQYPPHIISNNPEHFR.F		R.NIQYPPHIISNNPEHFR.F

324	340	4	1907.07	4.3	1	41.9	24	95.00%	F.SKPIVTNIDVPELGNRR.V		R.SQAIQDAEAFHFQYDEDEEDGTS NEDGILFSKPIVTNIDVPELGNRR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
63	A6ZQQ8_YEAS7	35.71%	100%	13							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
152	160	2	1033.57	3.9	1	25.2	28	91.10%	K.VAMNYVPIK.A		K.VAMNYVPIK.A
494	507	2	1555.84	-0.57	1	53.3	28.4	95.00%	K.EIGWCLGASLPLLK.A	Carbamidomethyl (+57)	K.EIGWCLGASLPLLK.A
47	80	3	3787.85	4.8	2	64.9	28.4	95.00%	K.TPEDISILPVNDEPGYLQDSKTEQ NYPELADAVK.S		K.TPEDISILPVNDEPGYLQDSKTEQ NYPELADAVK.S
423	432	2	1157.61	3.3	0	26.7	29.9	90.40%	F.TLNELNDLAR.I		R.TRPLGMPLSFTLNELNDLAR.I
245	264	2	2148.08	3.3	1	29.3	31.2	92.60%	F.DLGGGSTQIVFEPTFPINEK.M		K.LPTAAVFDLGGGSTQIVFEPTFPI NEK.M
375	395	3	2383.09	3	1	30.5	33.6	95.00%	K.DAQCQSPPCSFNGVHQPSLVR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.DAQCQSPPCSFNGVHQPSLVR.T
238	264	3	2847.48	2.3	1	34.9	27.7	95.00%	K.LPTAAVFDLGGGSTQIVFEPTFPI NEK.M		K.LPTAAVFDLGGGSTQIVFEPTFPI NEK.M
347	365	2	2154.96	3.9	1	31.6	34.3	91.40%	K.ETYTIDFIGPDEPSGAQCR.F	Carbamidomethyl (+57)	K.ETYTIDFIGPDEPSGAQCR.F
227	237	2	1053.59	3.6	0	50.4	25.9	95.00%	Y.LLGNIGANGPK.L	Deamidation (+1)	K.DYPFPVVEGDGVSIMGGDEEGV FAWITTNYLLGNIGANGPK.L
300	310	2	1184.68	0.49	0	48.4	27.2	95.00%	K.VNSVLVENALK.D		K.VNSVLVENALK.D
37	46	2	1026.57	-0.22	0	31.2	25.1	95.00%	R.TVTPNASIPK.T		R.TVTPNASIPK.T
413	432	3	2257.19	-0.49	1	58.8	29.1	95.00%	R.TRPLGMPLSFTLNELNDLAR.I		R.TRPLGMPLSFTLNELNDLAR.I
366	374	2	1091.59	-1.1	1	26.9	28.5	93.20%	R.FLTDEILNK.D		R.FLTDEILNK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
64	A7A201_YEAS7	42.23%	100%	9							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
11	21	2	1069.65	-0.48	0	24.2	23.6	94.20%	K.LLLIGNSGVGK.S		K.LLLIGNSGVGK.S
171	184	2	1636.73	-0.92	0	58.2	33.5	95.00%	K.ESMSQQNLNETTQK.K		K.ESMSQQNLNETTQK.K
101	108	2	1089.53	4	1	41.9	31.2	95.00%	K.MWLQEIDR.Y		K.MWLQEIDR.Y
130	139	2	1197.6	3.7	2	40.7	31.1	95.00%	R.VVEYDVAKEF.A		R.VVEYDVAKEFADANK.M
59	69	2	1315.65	-0.16	1	49.1	31.4	95.00%	K.LQIWDTAGQER.F		K.LQIWDTAGQER.F
168	184	3	2005.97	-0.28	1	36.2	33	95.00%	R.QIKESMSQQNLNETTQK.K		R.QIKESMSQQNLNETTQK.K
145	167	2	2558.22	4.7	1	150	32.7	95.00%	K.MPFLETSALDSTNVEDAFLTMAR. Q		K.MPFLETSALDSTNVEDAFLTMAR. Q
22	27	2	760.42	-8.9	0	28.8	28.1	95.00%	K.SCLLLR.F	Carbamidomethyl (+57)	K.SCLLLR.F
101	109	2	1252.6	4.4	2	38.2	33.1	95.00%	K.MWLQEIDRY.A		K.MWLQEIDRYATSTVLK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
65	A6ZNV4_YEAS7	45.58%	100%	9							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	152	2	1821.92	3.1	2	72.1	31.4	95.00%	R.TEAVRQDPESSYISIK.V		R.TEAVRQDPESSYISIK.V
77	90	3	1607.87	1.4	1	31.8	28.1	95.00%	R.DKIESNILIHQNGK.L		R.DKIESNILIHQNGK.L
29	42	2	1635.81	-0.75	1	79.9	32.2	95.00%	K.ELSNLIETFAEQSR.V		K.ELSNLIETFAEQSR.V
13	26	2	1591.72	0.81	1	52.5	33.2	95.00%	K.GNSQQEPQFSTNQK.T		K.GNSQQEPQFSTNQK.T
102	112	2	1413.66	-0.98	1	73.2	32.8	95.00%	K.YQSLQQSYNQR.K		K.YQSLQQSYNQR.K
137	148	2	1380.62	3.4	2	48.8	33	95.00%	R.TEAVRQDPESSY.I		R.TEAVRQDPESSYISIK.V
223	247	3	2864.31	2.9	0	49.8	32.7	95.00%	K.EQGEQVTTIDENISHLHDNMQNA NK.Q		K.EQGEQVTTIDENISHLHDNMQNA NK.Q
62	76	2	1821.94	3.4	1	74.1	30.5	95.00%	R.YKIETELIPNCTSVR.D	Carbamidomethyl (+57)	R.YKIETELIPNCTSVR.D
203	222	3	2203.21	-0.67	1	43	25.1	95.00%	R.IHTAVQEVNAIFHQLGSLVK.E		R.IHTAVQEVNAIFHQLGSLVK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
66	RL20_YEAST	41.86%	100%	8							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
100	113	2	1536.77	3.6	1	61.8	32.3	95.00%	R.VAAVETLYQDMAAR.H		R.VAAVETLYQDMAAR.H
147	155	3	1121.64	3.1	2	24	25.7	95.00%	K.DLKFPLPHR.V		K.DLKFPLPHR.V

74	80	2	876.46	0.084	1	30.8	29.2	95.00%	K.NFGVWVR.Y		K.NFGVWVR.Y
54	73	3	2134.14	2.5	1	28.6	27.5	95.00%	K.ASGEIVSINQINEAHPTKVK.N		K.ASGEIVSINQINEAHPTKVK.N
13	23	2	1251.68	0.13	1	30	28.3	95.00%	R.RLPTESVPEPK.L		R.RLPTESVPEPK.L
29	38	2	1090.6	2.2	1	60.7	28.8	95.00%	R.IFASNEVIAK.S		R.IFASNEVIAK.S
54	71	2	1906.97	-0.38	0	70.8	31.3	95.00%	K.ASGEIVSINQINEAHPTK.V		K.ASGEIVSINQINEAHPTK.V
53	71	3	2035.08	4.2	1	59.3	28.7	95.00%	K.KASGEIVSINQINEAHPTK.V		K.KASGEIVSINQINEAHPTK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
67	MNN5_YEAST	21.67%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
332	356	3	2720.28	-0.95	0	78.6	32.6	95.00%	K.HVPLHDLDGTMPDLSSESGQMVIDK.I		K.HVPLHDLDGTMPDLSSESGQMVIDK.I
504	513	2	1115.57	0.16	1	30.2	31.2	93.80%	R.FIGPNGEQVR.G		R.FIGPNGEQVR.G
493	503	2	1400.65	2.8	1	43	33.2	95.00%	K.ADPWTLYHENR.F		K.ADPWTLYHENR.F
78	108	3	3274.43	1.5	1	67	33.1	95.00%	K.LHGAEGCSFANNVAAHDSGHDSDLSYESLSK.C	Carbamidomethyl (+57)	K.LHGAEGCSFANNVAAHDSGHDSDLSYESLSK.C
299	309	2	1220.61	3.2	1	57	31.7	95.00%	R.FVSDDISPVSR.Y		R.FVSDDISPVSR.Y
87	108	3	2316.03	2.5	1	51.5	34.2	95.00%	F.ANNVAAHDSGHDSDLSYESLSK.C		K.LHGAEGCSFANNVAAHDSGHDSDLSYESLSK.C
426	439	2	1675.82	2.4	1	38.3	32.3	95.00%	K.GLALLQHDFEQDYK.Q		K.GLALLQHDFEQDYK.Q
57	77	3	2212.17	4.2	0	37.6	28.6	95.00%	Y.TTLVQAIVENKPADSSPDLSK.L		K.NNFYTTLVQAIVENKPADSSPDLSK.L
53	77	3	2750.39	4.1	1	48.9	29.4	95.00%	K.NNFYTTLVQAIVENKPADSSPDLSK.L		K.NNFYTTLVQAIVENKPADSSPDLSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
68	A6ZQY0_YEAS7	68.61%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
108	127	3	2126.11	4	1	35.5	29.6	95.00%	W.LSELRENADDNVAVGLIGNK.S		K.SSSYENCNHWLSELRENADDNVAVGLIGNK.S
128	134	2	810.43	-1.3	0	48.4	29.3	95.00%	K.SDLAHLR.A		K.SDLAHLR.A
98	107	2	1282.47	3.2	1	31.8	31.7	95.00%	K.SSSYENCNHW.L	Carbamidomethyl (+57)	K.SSSYENCNHWLSELR.E
16	26	2	1056.62	2.9	0	27.1	27.3	94.80%	K.IVLIGDSGVGK.S		K.IVLIGDSGVGK.S
143	165	2	2598.25	3.2	1	107	31.8	95.00%	K.TFAQENQLLFTETSALNSENVDK.A		K.TFAQENQLLFTETSALNSENVDK.A
64	74	2	1273.6	-1.7	1	41.6	32.4	95.00%	K.AQIWDTAGQER.Y		K.AQIWDTAGQER.Y
181	216	3	3605.68	2.7	1	58.2	31.3	95.00%	K.HQMDLGDSSANGNANGASAPNGPTISLTPTPNENKK.A	Deamidation (+1)	K.HQMDLGDSSANGNANGASAPNGPTISLTPTPNENKK.A
145	165	2	2350.14	4.5	1	96	32.4	95.00%	F.AQENQLLFTETSALNSENVDK.A		K.TFAQENQLLFTETSALNSENVDK.A
113	127	2	1527.75	1.2	0	68.2	32.9	95.00%	R.ENADDNVAVGLIGNK.S		R.ENADDNVAVGLIGNK.S
44	53	2	1079.56	3.4	1	61.2	30.1	95.00%	K.STIGVEFATR.T		K.STIGVEFATR.T
166	177	2	1467.77	3.1	1	69.6	29.8	95.00%	K.AFEELINTIYQK.V		K.AFEELINTIYQK.V
85	97	2	1304.74	2.5	1	42.2	26.5	95.00%	R.GAVGALIVYDISK.S		R.GAVGALIVYDISK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
69	PDR5_YEAST	13.63%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
922	938	2	1753.97	-0.98	0	38.4	25.9	95.00%	R.VTMGVITGDILVNGIPR.D		R.VTMGVITGDILVNGIPR.D
1153	1167	2	1829.9	-1.2	1	34.7	32.4	95.00%	R.AVQSELDWMERELPK.K		R.AVQSELDWMERELPK.K
95	109	2	1663.79	3.3	1	37.4	33.1	95.00%	K.LDPNSENFSSAAWVK.N		K.LDPNSENFSSAAWVK.N
412	427	2	1738.84	2.5	1	92	32.9	95.00%	R.QTTADFLTSVTSPSER.T		R.QTTADFLTSVTSPSER.T
368	379	2	1487.64	3.9	1	43	33.8	95.00%	Y.QCSQDAYDLFNK.V	Carbamidomethyl (+57)	K.TQADISNTSATVAIYQCSQDAYDLFNK.V
468	486	3	2122.1	-1.2	1	38.9	29.9	95.00%	R.LLNDDEASREAIKEAHIAK.Q		R.LLNDDEASREAIKEAHIAK.Q
167	204	4	4143.15	-1.7	2	27.8	25.3	95.00%	R.SKETNTFQILKPMDGCLNPGELLVVLGRPGSGCTTLLK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.SKETNTFQILKPMDGCLNPGELLVVLGRPGSGCTTLLK.S
338	349	2	1291.68	2.8	1	31.4	30	95.00%	R.GLDSATALEFIR.A		R.GLDSATALEFIR.A
865	872	2	1044.52	2.6	1	50.3	30.3	95.00%	K.SEAIFHWR.N		K.SEAIFHWR.N

329	337	2	1196.51	3.6	1	30	31.8	92.70%	K.FQCWDNATR.G	Carbamidomethyl (+57)	K.FQCWDNATR.G
49	65	2	1805.86	-0.55	0	104	33	95.00%	R.TLTAQSMQNSTQSAPNK.S		R.TLTAQSMQNSTQSAPNK.S
110	125	2	1838.84	3.3	1	69.2	33.4	95.00%	K.NMAHLSAADPDFYKPY.S		K.NMAHLSAADPDFYKPYSLGCAW K.N
971	982	2	1397.76	3.6	1	53.4	27.6	95.00%	Y.LRQPAEVSIEEK.N		R.FSAYLRQPAEVSIEEK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
70	A7A0U0_YEAS7	9.51%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
401	430	3	3174.6	1.3	1	75.1	28.8	95.00%	K.LMVVHDENGVVRAPADVNAIADE TTPLNSK.H		K.LMVVHDENGVVRAPADVNAIADE TTPLNSK.H
66	79	2	1581.75	2.2	1	52.2	33.3	95.00%	K.LGTITGYDLAENCR.H	Carbamidomethyl (+57)	K.LGTITGYDLAENCR.H
400	412	2	1495.79	3.5	1	65.1	29.3	95.00%	R.KLMVVHDENGVVR.A	Deamidation (+1)	R.KLMVVHDENGVVR.A
413	430	2	1825.91	-0.29	0	82.6	31.7	95.00%	R.APADVNAIADETTPLNSK.H		R.APADVNAIADETTPLNSK.H
401	412	2	1366.71	2.7	0	52.5	30.5	95.00%	K.LMVVHDENGVVR.A		K.LMVVHDENGVVR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
71	A6ZXE9_YEAS7	44.39%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
246	257	2	1198.65	3.6	0	29.1	26.9	95.00%	R.NGITPLGGLMAR.M		R.NGITPLGGLMAR.M
348	368	3	2383.28	3.8	1	29.1	26.2	95.00%	K.ARVDQLNLNLTDDQIKEVTAK.I		K.ARVDQLNLNLTDDQIKEVTAK.I
234	257	3	2451.36	2.6	1	51.3	23.3	95.00%	R.LIDVSVLGIGERNGITPLGGLMAR. M	Deamidation (+1)	R.LIDVSVLGIGERNGITPLGGLMAR. M
350	368	3	2156.14	3.7	1	26.4	28.3	95.00%	R.VDQLNLNLTDDQIKEVTAK.I		R.VDQLNLNLTDDQIKEVTAK.I
135	144	2	1119.62	-0.11	1	28.3	27.2	95.00%	K.SAVEVIEFVK.S		K.SAVEVIEFVK.S
203	233	3	3394.49	3.1	1	42.7	32.5	95.00%	K.SVVSCDIECHFHNDTGCAIANAYT ALEGGAR.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.SVVSCDIECHFHNDTGCAIANAYT ALEGGAR.L
312	331	3	2231.1	4.8	1	27.8	31.3	95.00%	K.AILANPSTYEILDPHDFGMK.R		K.AILANPSTYEILDPHDFGMK.R
160	170	2	1291.7	-0.7	1	28.2	29.1	94.10%	R.SDLVDLLNIYK.T		R.SDLVDLLNIYK.T
377	388	2	1330.7	2.5	0	53.5	29.8	95.00%	R.SLNIDDVDSIIK.N		R.SLNIDDVDSIIK.N
258	267	2	1105.59	3.2	1	40	29.5	95.00%	R.MIVAAPDYVK.S		R.MIVAAPDYVK.S
180	192	2	1328.65	0.46	0	87.7	31.1	95.00%	R.VGIADTVGCANPR.Q	Carbamidomethyl (+57)	R.VGIADTVGCANPR.Q
407	422	2	1667.88	3.6	1	34.2	29.4	95.00%	K.KNDSDVPELATIPAAK.R		K.KNDSDVPELATIPAAK.R
52	73	2	2411.16	4.1	1	117	32.1	95.00%	R.ALDDFGVDYIELTSPVASEQSR.K		R.ALDDFGVDYIELTSPVASEQSR.K
234	245	2	1269.73	1.6	0	67.6	24.9	95.00%	R.LIDVSVLGIGER.N		R.LIDVSVLGIGER.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
72	YA11B_YEAST	11.85%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
439	466	4	3014.45	4.1	0	26.4	31.2	95.00%	K.LTESTVNHTNHSDDELPGHLLLD SGASR.T		K.LTESTVNHTNHSDDELPGHLLLD SGASR.T
987	1001	2	1640.83	2.9	0	57.2	31.1	95.00%	R.EVDPNISESNILPSK.K		R.EVDPNISESNILPSK.K
1050	1075	3	2789.21	0.043	1	48.5	33.7	95.00%	R.HSDSYSENETNHTNVPISSTGGT NNK.T		R.HSDSYSENETNHTNVPISSTGGT NNK.T
331	354	3	2813.39	3.2	1	47.6	31	95.00%	R.HLNMTVAELFLDIHAIYEEQQGSR .N		R.HLNMTVAELFLDIHAIYEEQQGSR .N
471	491	3	2226.08	-0.4	0	86.8	33.2	95.00%	R.SAHHIHSASSNPDINVVDAQK.R		R.SAHHIHSASSNPDINVVDAQK.R
1496	1503	2	893.54	1.6	0	22.9	22.9	92.30%	K.LNVPLNPK.G		K.LNVPLNPK.G
25	39	2	1638.79	0.24	0	32.3	33	94.30%	K.EVHTNQDPLDVSASK.T		K.EVHTNQDPLDVSASK.T
25	45	2	2415.09	2.2	1	65.5	33.6	95.00%	K.EVHTNQDPLDVSASKTEECEK.A	Carbamidomethyl (+57)	K.EVHTNQDPLDVSASKTEECEK.A
1093	1113	3	2202.1	3.9	0	28.5	31.3	95.00%	R.SPSIDASPPENNSSHNIVPIK.T		R.SPSIDASPPENNSSHNIVPIK.T
1621	1632	2	1318.73	3.3	1	51.9	28	95.00%	K.SQIGNIYLLNGK.V		K.SQIGNIYLLNGK.V
308	315	2	989.52	1.9	0	40.9	30.2	95.00%	K.VACQLIMR.G	Carbamidomethyl (+57)	K.VACQLIMR.G

1	24	3	2598.18	-0.65	0	59.5	33.7	95.00%	- .MESQQLSQHSPISHGSACASVTSK .E	Acetyl (+42)/ Carbamidomethyl (+57)	- .MESQQLSQHSPISHGSACASVTSK .E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
73	B3LQG1_YEAS1	18.94%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
51	81	3	3458.67	5	1	64.7	29.8	95.00%	K.EISQSINSANNIQSSDSDLVQHFE SLAQEIR.H		K.EISQSINSANNIQSSDSDLVQHFE SLAQEIR.H
139	151	2	1485.71	3.8	1	38.4	32.8	95.00%	W.SNDEGPERVQDIK.G		K.FPAFIWQTWSNDEGPERVQDIK. G
107	115	2	1011.53	-0.42	0	25.4	28.6	90.20%	K.QTPPEATLR.E		K.QTPPEATLR.E
349	358	2	1129.68	0.16	1	56.3	25.4	95.00%	K.LLSDVLVFPK.F		K.LLSDVLVFPK.F
118	129	2	1407.69	4	1	36.5	32.4	95.00%	R.IAMTFPYDSHVK.F		R.IAMTFPYDSHVK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
74	A6ZXZ5_YEAS7	15.62%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
268	284	2	1788.85	0.66	1	63.6	32.8	95.00%	K.LGYHFGPSDAEAVMAPK.A		K.LGYHFGPSDAEAVMAPK.A
285	303	3	1947.1	3.5	1	21.6	24	95.00%	K.APVASPRPAATPNLSKDKK.K		K.APVASPRPAATPNLSKDKK.K
285	300	2	1575.87	0.42	0	65.1	26.6	95.00%	K.APVASPRPAATPNLSK.D		K.APVASPRPAATPNLSK.D
271	284	2	1455.69	2.9	1	35.2	32.8	95.00%	Y.HFGPSDAEAVMAPK.A		K.LGYHFGPSDAEAVMAPK.A
18	31	2	1524.77	3.1	1	55.6	31	95.00%	K.INPPTGADFHITSR.G		K.INPPTGADFHITSR.G
285	302	2	1819	3.5	1	73.1	27.5	95.00%	K.APVASPRPAATPNLSKDK.K		K.APVASPRPAATPNLSKDK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
75	A6ZSU5_YEAS7	34.32%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
289	305	2	2126.9	3.4	2	63.8	34.3	95.00%	R.KCLEACDEDPDLVQLCY.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.KCLEACDEDPDLVQLCYCLPPTE NDDSANYFTSHPGFK.H
380	394	2	1652.76	2.1	1	69.1	33.3	95.00%	R.GTFQSSGQNCIGIER.V	Carbamidomethyl (+57)	R.GTFQSSGQNCIGIER.V
507	520	2	1572.7	2.9	1	31.7	33.5	92.90%	K.NTDHCVQLANSAPF.G	Carbamidomethyl (+57)	K.NTDHCVQLANSAPFGLGGSVFG ADIK.E
159	176	3	2067.12	5	1	31.5	26.1	95.00%	R.VLASLHDYILNNQDLIAR.V		R.VLASLHDYILNNQDLIAR.V
521	532	2	1119.6	4.4	1	58.5	30.7	95.00%	F.GLGGSVFGADIK.E		K.NTDHCVQLANSAPFGLGGSVFG ADIK.E
572	585	2	1463.71	2.5	1	83.4	32	95.00%	K.FGGEEGLLGLCNAK.S	Carbamidomethyl (+57)	K.FGGEEGLLGLCNAK.S
144	155	2	1354.59	0.94	1	48.9	32.9	95.00%	K.AQSTWGNSDFSR.R		K.AQSTWGNSDFSR.R
395	407	2	1520.81	-1.1	2	71.1	30.1	95.00%	R.VIVSKENYDDLVK.I		R.VIVSKENYDDLVK.I
327	342	3	1823.02	3.1	1	32.6	24.5	95.00%	K.HITFIGSQPVAHYILK.C		K.HITFIGSQPVAHYILK.C
123	140	2	1952.95	4.7	1	45.3	32.7	95.00%	Y.LGSFPSKTEADIDEMVSK.A		R.SVSTNIWNPEEPNFIQCHCPATG QYLGSFPSKTEADIDEMVSK.A
81	94	2	1571.78	3.2	1	50.7	31.1	95.00%	K.FSLPAPEAAQNNWK.G		K.FSLPAPEAAQNNWK.G
369	379	2	1231.66	-0.094	0	52.8	30.1	95.00%	K.NLDALSSIIMR.G		K.NLDALSSIIMR.G
185	200	2	1749.89	-0.86	0	79.6	31.7	95.00%	K.TMLDASMGEILVTLEK.I		K.TMLDASMGEILVTLEK.I
490	504	2	1688.9	-0.54	1	41.5	29.5	95.00%	K.IAQNEVFGPILVMMK.A		K.IAQNEVFGPILVMMK.A
556	571	2	1653.79	3.2	1	38.7	32.8	95.00%	Y.VCQLPFGGINGSGYGK.F	Carbamidomethyl (+57)/ Deamidation (+1)	K.ECNYVANSLQTGNVAINDFATFY VCQLPFGGINGSGYGK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
76	A6ZV40_YEAS7	10.63%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
542	566	3	2852.3	5.4	1	30.1	33	95.00%	K.VYDDTIGDVDTQEDGVIETNIIEHY .K		K.VYDDTIGDVDTQEDGVIETNIIEHY K.S
60	73	2	1615.85	-0.65	0	69	30.1	95.00%	K.QLGILSCIGLICNR.M	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.QLGILSCIGLICNR.M
6	16	2	1309.7	-0.47	1	68.2	28.6	95.00%	R.TFLSQLNVFNK.E		R.TFLSQLNVFNK.E

542	567	3	3060.36	4.2	1	66.1	33	95.00%	K.VYDDTIGDVDTQEDGVIETNIIEHY K.S	Phospho (+80)	K.VYDDTIGDVDTQEDGVIETNIIEHY K.S
527	536	2	1192.55	1.3	1	39.6	32.3	95.00%	K.DVLGEDGFWR.V		K.DVLGEDGFWR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
77	A6ZQN6_YEAS7	10.67%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
603	613	2	1379.69	3.2	2	42.2	31.7	95.00%	F.EIEEKEESFLK.N		K.NTFEIEEKEESFLK.N
1	25	2	2852.38	7.7	1	37.7	32	95.00%	-.MDPGIANHTLPEEFEEVVVPEMLEK.E		-.MDPGIANHTLPEEFEEVVVPEMLEK.E
584	599	2	1740.86	2.5	0	70.6	32.4	95.00%	K.LTDSIALEGNDHLESK.N		K.LTDSIALEGNDHLESK.N
519	530	2	1304.68	2.7	2	39.6	30.6	95.00%	K.RISDPTLAAQAY.G		K.RISDPTLAAQAYGSPFTFITTYTWGTPER.I
581	599	3	2120.06	3.5	1	59.5	31.7	95.00%	R.NHKLTDSIALEGNDHLESK.N		R.NHKLTDSIALEGNDHLESK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
78	B3LH18_YEAS1	11.19%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
26	36	2	1295.72	4.3	1	39.9	26.2	95.00%	R.AAVYDLQYILK.A		R.AAVYDLQYILK.A
181	195	2	1663.83	0.16	2	54.5	32	95.00%	R.ATLPHGKEDHFIDGK.I		R.ATLPHGKEDHFIDGK.I
1	20	4	2133.11	3.9	1	36.8	29.4	95.00%	-.MDATTPLLTVANSHPARNPK.H		-.MDATTPLLTVANSHPARNPK.H
1	17	2	1835.92	2.1	0	91.8	31.8	95.00%	-.MDATTPLLTVANSHPAR.N	Acetyl (+42)	-.MDATTPLLTVANSHPAR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
79	YO092_YEAST	11.36%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
138	162	3	2661.16	2.5	1	58.3	34.1	95.00%	R.IDEEMAAPSSDGNAGDDNLREVNSR.N		R.IDEEMAAPSSDGNAGDDNLREVNSR.N
138	157	2	2075.88	3.4	0	83.8	33.8	95.00%	R.IDEEMAAPSSDGNAGDDNLR.E		R.IDEEMAAPSSDGNAGDDNLR.E
1	10	2	1211.67	0.89	0	40.1	26.3	95.00%	-.MQLVPLELNR.S		-.MQLVPLELNR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
80	A6ZY13_YEAS7	10.26%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
62	78	2	1947.87	3.2	1	86.2	33.9	95.00%	R.AESQRLEEDNDLEDGTK.S		R.AESQRLEEDNDLEDGTK.S
400	412	2	1465.71	2.5	1	67.5	32.9	95.00%	R.LMCSLAQQGYAPK.F	Carbamidomethyl (+57)	R.LMCSLAQQGYAPK.F
26	41	2	1736.87	4	1	71.5	32.4	95.00%	Y.NNFNTSTTASLTPEIK.E		K.SAEFEVTDSALYNNFNTSTTASLTPEIK.E
61	78	2	2103.97	-0.82	1	63.9	34	95.00%	R.RAESQRLEEDNDLEDGTK.S		R.RAESQRLEEDNDLEDGTK.S
29	48	3	2216.06	3.9	1	27.1	32.6	93.90%	F.NTSTTASLTPEIKEHSEESR.N		K.SAEFEVTDSALYNNFNTSTTASLTPEIKEHSEESR.N
26	48	3	2591.22	3	1	44.3	33.4	95.00%	Y.NNFNTSTTASLTPEIKEHSEESR.N		K.SAEFEVTDSALYNNFNTSTTASLTPEIKEHSEESR.N
573	580	2	1021.49	3.4	1	28.9	31.1	92.10%	R.VYDPEIMR.Q		R.VYDPEIMR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
81	A6ZLU9_YEAS7	23.74%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
313	325	2	1424.67	2.5	1	58.6	33.1	95.00%	K.DFGQVIGQGFSDR.H		K.DFGQVIGQGFSDR.H
279	287	2	1159.5	0.85	1	37.4	32.6	95.00%	K.YMDEGYINR.V		K.YMDEGYINR.V
15	26	2	1272.65	3.5	0	32.8	30.2	95.00%	K.AMDNGLSLPISR.N		K.AMDNGLSLPISR.N
135	142	2	979.41	4.7	1	43.6	31.7	95.00%	K.FDDGVQHY.L		K.FDDGVQHYLISQFGSEVLTPK.D
511	526	3	1886.91	3.9	1	60.3	33.2	95.00%	W.HIYEPSDDDLKEIASR.E		R.VGGLPHYTIWHIYEPSDDDLKEIASR.E
201	211	2	1217.65	0.22	1	60	30.4	95.00%	R.NAADVLPLMFK.H		R.NAADVLPLMFK.H
191	200	2	1248.7	1.8	0	43	26.7	95.00%	R.DHILLCIPLR.N	Carbamidomethyl (+57)	R.DHILLCIPLR.N
511	521	2	1330.61	3.5	1	32.2	33.2	94.00%	W.HIYEPSDDDLK.E		R.VGGLPHYTIWHIYEPSDDDLK.E

143	159	2	1904.98	5	1	73.2	30.7	95.00%	Y.LISQFGSEVLTPKDDEK.Y		K.FDDGVQHYLISQFGSEVLTPKDDEK.Y
143	155	2	1417.79	4.4	1	50	27.5	95.00%	Y.LISQFGSEVLTPK.D		K.FDDGVQHYLISQFGSEVLTPK.D
361	378	2	1975.93	4.8	0	77.6	33.7	95.00%	R.DADVELCPGSVIQDLMSK.N	Carbamidomethyl (+57)	R.DADVELCPGSVIQDLMSK.N
389	401	2	1517.79	4.5	1	36.1	30.4	95.00%	W.RPLPTFLGTEQPY.D		K.NYDVIVPNVWRPLPTFLGTEQPYDLNSWMESQEALALAK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
82	NYV1_YEAST	24.11%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
14	27	2	1641.75	2.9	1	72.9	33.9	95.00%	K.NGETISSCFQPFQK.N	Carbamidomethyl (+57)	K.NGETISSCFQPFQK.N
196	202	2	772.47	-3.5	0	22.9	26.2	90.00%	R.VSLLVDK.T		R.VSLLVDK.T
32	46	2	1589.84	4.1	1	36.6	30.3	95.00%	Y.GTITSANEQITPVIF.H		K.NENYGTITSANEQITPVIFHNLIMDMVLPK.V
93	102	2	1208.6	4.6	1	29.1	32.1	90.60%	Y.VCFTLVDMPK.I	Carbamidomethyl (+57)	K.TVYVCFTLVDMPK.I
28	57	3	3401.7	0.56	1	62.1	28.7	95.00%	K.NENYGTITSANEQITPVIFHNLIMDMVLPK.V		K.NENYGTITSANEQITPVIFHNLIMDMVLPK.V
47	57	2	1309.69	4.3	0	51.2	29.1	95.00%	F.HNLIMDMVLPK.V		K.NENYGTITSANEQITPVIFHNLIMDMVLPK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
83	A6ZVM2_YEAS7	14.63%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
314	325	2	1292.68	-0.24	0	78.4	29.7	95.00%	K.HADANVQLVAQK.M		K.HADANVQLVAQK.M
346	360	2	1887.94	5	2	34.1	32.5	95.00%	R.DKEPITWLETQITEW.F		R.DKEPITWLETQITEWFTTALTNSPK.D
239	254	2	1730.84	4.4	1	32.4	32.9	94.40%	F.AFGASFLETMTTTQAR.N		R.ETFAFGASFLETMTTTQAR.N
36	47	2	1412.6	-1.5	1	82.9	32.7	95.00%	K.LDAEEEQSSSYR.S		K.LDAEEEQSSSYR.S
34	47	2	1669.74	-0.91	2	88.8	33.7	95.00%	K.EKLDAEEEQSSSYR.S		K.EKLDAEEEQSSSYR.S
196	204	2	1094.58	2.1	1	56.3	30.1	95.00%	R.LSLLAYCQK.V	Carbamidomethyl (+57)	R.LSLLAYCQK.V
326	345	2	2176.05	2.9	0	130	32.2	95.00%	K.MQQITSSQPTPTSELSSAQR.D		K.MQQITSSQPTPTSELSSAQR.D
797	823	2	2734.28	3.9	1	69.9	32.5	95.00%	R.VTGDAPLPYPIAQVGDDSMDSSDLGSK.A		R.VTGDAPLPYPIAQVGDDSMDSSDLGSK.A
147	165	2	1885.89	3	1	65.7	33.6	95.00%	R.SSSNVDMSTSLYAAGLAGR.S		R.SSSNVDMSTSLYAAGLAGR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
84	A6ZWP0_YEAS7	13.68%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
91	103	2	1443.72	-0.52	0	31.2	31.2	95.00%	K.AQPLISSCPACLK.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.AQPLISSCPACLK.N
79	90	2	1397.77	2.9	1	41.2	27.6	95.00%	K.DQVVALRDNLQK.A		K.DQVVALRDNLQK.A
230	251	4	2648.13	0.41	1	37.1	34.1	95.00%	K.CACSDCQESCPHLKPLKDGVCK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CACSDCQESCPHLKPLKDGVCK.V
918	930	2	1352.66	4.7	0	64.3	33	95.00%	W.INAPSDPCPLGGR.A	Carbamidomethyl (+57)	K.DFMEYLSIWINAPSDPCPLGGR.A
469	489	3	2532.25	-1.1	2	33.2	31.1	95.00%	R.ELQECGKFPVNCLPTFQQPLK.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.ELQECGKFPVNCLPTFQQPLK.T
918	933	2	1683.81	4.8	2	80.8	33	95.00%	W.INAPSDPCPLGGRAPY.S	Carbamidomethyl (+57)	K.DFMEYLSIWINAPSDPCPLGGRAPYSTALVYNETSVSASVFR.T
859	870	2	1581.65	3.2	1	35.8	33.5	95.00%	F.MFLNPQNDQCCR.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.STITEPLANWLDDYFMFLNPQNDQCCR.L
961	971	2	1269.6	3.5	1	44.2	32.8	95.00%	K.DFIQAYSDGVR.I		K.DFIQAYSDGVR.I
33	45	2	1470.73	3	1	28.6	31.4	91.10%	K.SVFGNELPCPVPR.S	Carbamidomethyl (+57)	K.SVFGNELPCPVPR.S
831	841	2	1272.63	1.1	0	59	31.4	95.00%	R.DSLANVLEQER.H		R.DSLANVLEQER.H
185	198	2	1435.72	4	1	44.6	31.9	95.00%	K.FLGDAKPMLGGSPF.Q		K.FLGDAKPMLGGSPFQINYK.Y

873	887	3	1731.84	3	2	45	32.4	95.00%	K.KGTDEVCPPSFPSRR.C	Carbamidomethyl (+57)	K.KGTDEVCPPSFPSRR.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
85	A7A1T6_YEAS7	11.85%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
487	501	2	1744.84	4.5	1	59.7	32.7	95.00%	R.SIVYNNIEGSDFKPY.M		R.SIVYNNIEGSDFKPYMDALNIGK.D
457	464	2	1026.5	3.4	1	35.2	30.5	95.00%	R.LSIFTMCR.A	Carbamidomethyl (+57)	R.LSIFTMCR.A
659	671	2	1508.74	3.4	0	64.2	32.5	95.00%	R.IIEEHESPIDAEK.N		R.IIEEHESPIDAEK.N
201	210	2	1179.66	5.9	2	36.4	25.6	95.00%	K.TKLSPVFELF.A		K.TKLSPVFELFASSK.N
502	521	2	2267.1	4.3	1	70.8	32.8	95.00%	Y.MDALNIGKDDLHLDGELQDR.Q		R.SIVYNNIEGSDFKPYMDALNIGKDDLHLDGELQDR.Q
203	214	2	1323.71	0.13	1	38	28.7	95.00%	K.LSPVFELFASSK.N		K.LSPVFELFASSK.N
477	486	2	1203.54	-1.2	1	33.6	32.5	95.00%	K.SHAVQNMDFR.S		K.SHAVQNMDFR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
86	EF3A_YEAST	20.02%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
320	357	4	3987.02	4.2	1	44.8	26.7	95.00%	R.VGNVGEDDAIPELSHAGDVSTTLQVVNELLKDETVAPR.F		R.VGNVGEDDAIPELSHAGDVSTTLQVVNELLKDETVAPR.F
927	937	3	1173.64	3.2	1	24.3	29.3	94.50%	Y.LDRDSLGALSK.A		K.LVLAAGTWQRPHLIVLDEPTNYLDRDSLGALSK.A
105	127	3	2394.34	-0.66	0	42.8	23.7	95.00%	K.EIQSVASETLISIVNAVNPVAIK.A		K.EIQSVASETLISIVNAVNPVAIK.A
708	732	3	2802.39	2.3	1	40.7	30.5	95.00%	K.STLINVLTGELLPTSGEVYTHENCR.I	Carbamidomethyl (+57)	K.STLINVLTGELLPTSGEVYTHENCR.I
971	987	2	1737.8	0.11	1	79.9	33	95.00%	R.MTPSGHNWVSGQGAGPR.I		R.MTPSGHNWVSGQGAGPR.I
913	937	4	2849.52	4.1	1	23.2	25.3	95.00%	W.QRPHLIVLDEPTNYLDRDSLGALSK.A		K.LVLAAGTWQRPHLIVLDEPTNYLDRDSLGALSK.A
873	893	4	2465.17	0.31	1	39.2	32.9	95.00%	R.KEIEEHCSMLGLDPEIVSHSR.I	Carbamidomethyl (+57)	R.KEIEEHCSMLGLDPEIVSHSR.I
459	469	2	1181.5	-0.8	1	36.2	31.5	95.00%	R.YGICGPNGCGK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.YGICGPNGCGK.S
751	759	2	1178.58	3.2	1	37.4	31.7	95.00%	K.TPSEYIQWR.F		K.TPSEYIQWR.F
296	307	2	1290.62	2.6	1	69.5	31.7	95.00%	K.SNFATIADPEAR.E		K.SNFATIADPEAR.E
874	893	3	2337.08	4.3	0	39	34.1	95.00%	K.EIEEHCSMLGLDPEIVSHSR.I	Carbamidomethyl (+57)	K.EIEEHCSMLGLDPEIVSHSR.I
669	696	3	3247.54	5	1	62.4	30.5	95.00%	K.VTNMEFQYPGTSKPQITDINFQCSLSSR.I	Carbamidomethyl (+57)	K.VTNMEFQYPGTSKPQITDINFQCSLSSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
87	VAC7_YEAST	19.23%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
817	830	3	1474.73	4.5	0	35.2	32	95.00%	Y.GSASNTHELPLHGR.M		K.NDLETKPLISDYGEDEDVDDYDRPNATFNSYYGSASNTHELPLHGR.M
785	812	3	3245.43	3.9	1	58.8	33.1	95.00%	K.NDLETKPLISDYGEDEDVDDYDRPNATF.N		K.NDLETKPLISDYGEDEDVDDYDRPNATFNSYYGSASNTHELPLHGR.M
1079	1104	3	2963.03	-0.34	1	47.7	31.3	95.00%	R.EAKHENDDDDDDDGDDGDDENNTNER.Q		R.EAKHENDDDDDDDGDDGDDENNTNER.Q
460	492	3	3830.86	-2	1	26	27.8	95.00%	K.NLIFPDSSSQQQQQQQQPPKQQQQQQNHGITSK.I		K.NLIFPDSSSQQQQQQQQPPKQQQQQQNHGITSK.I
1062	1071	2	1096.54	0.45	1	54.9	31.2	95.00%	R.NYDVSVSSVK.L		R.NYDVSVSSVK.L
606	643	4	4040.93	2.8	1	66.1	28.2	95.00%	K.VSPHLLSSTSSNGNTISCPNVATNSQELEPNNDISTKK.S	Deamidation (+1)/ Carbamidomethyl (+57)	K.VSPHLLSSTSSNGNTISCPNVATNSQELEPNNDISTKK.S
816	830	2	1637.8	4.1	1	57	32.8	95.00%	Y.YGSASNTHELPLHGR.M		K.NDLETKPLISDYGEDEDVDDYDRPNATFNSYYGSASNTHELPLHGR.M
262	274	2	1471.78	4.8	0	66.9	29.1	95.00%	R.EILLGENLLDDTK.A		R.EILLGENLLDDTK.A

396	425	3	3160.39	3.3	0	80.6	33.3	95.00%	K.NSNADLSASTSNNNAINDDSHESNSEKPTK.A		K.NSNADLSASTSNNNAINDDSHESNSEKPTK.A
688	715	3	3273.52	3.5	1	65.5	32.2	95.00%	R.YSGVPDHVNLEDYIEQPHNYPTMQNSVK.K		R.YSGVPDHVNLEDYIEQPHNYPTMQNSVK.K
813	830	2	2001.94	3.1	1	45.3	33.8	95.00%	F.NSYYGSASNTHELPLHGR.M		K.NDLETKPLISDYGEDEDVDDYDRPNATFNSYYGSASNTHELPLHGR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
88	A6ZL71_YEAS7	29.98%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
145	166	2	2397.17	5.7	1	88.4	32.2	95.00%	R.IYPEEMISTGVSAIDTMNSIAR.G		R.IYPEEMISTGVSAIDTMNSIAR.G
273	289	3	1904.97	-0.46	1	30	31.5	95.00%	R.HVLTILTDMSSYADALR.E		R.HVLTILTDMSSYADALR.E
242	252	2	1254.66	3.9	0	46.9	29.3	95.00%	F.LNLANDPTIER.I		R.TSLFLNLANDPTIER.I
285	295	3	1157.62	4.8	1	48.5	29.7	95.00%	Y.ADALREVSAAR.E		R.HVLTILTDMSSYADALREVSAAR.E
353	362	2	1176.62	3.9	1	57.1	30.6	95.00%	Y.ITEGQIFVDR.Q		R.NGSITQIPILTMPNDDITHPIPDLTGYITEGQIFVDR.Q
49	63	2	1702.89	1.9	1	49.5	30	95.00%	R.YNEIVNLTLPDGTVR.Q		R.YNEIVNLTLPDGTVR.Q
453	466	2	1663.86	-0.25	1	66.6	31.6	95.00%	R.TVFESLDQAWSLLR.I		R.TVFESLDQAWSLLR.I
227	237	2	1322.57	-0.4	1	51.8	32.7	95.00%	K.QDFEENGSLER.T		K.QDFEENGSLER.T
26	43	2	1929.06	-0.94	1	38.4	26.3	95.00%	R.LNYNTVSGVNGPLVILEK.V		R.LNYNTVSGVNGPLVILEK.V
170	189	3	2193.13	-1.3	1	44.1	30	95.00%	K.IPIFSASGLPHNEIAAQICR.Q	Carbamidomethyl (+57)	K.IPIFSASGLPHNEIAAQICR.Q
213	223	2	1131.58	4.9	0	79.5	30.6	95.00%	F.AAMGVNLETAR.F		K.DVHDGHEENFSIVFAAMGVNLETAR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
89	A7A077_YEAS7	22.79%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
359	369	3	1305.64	3	1	33.7	31.4	95.00%	K.LGLSNEDFFHK.V		K.LGLSNEDFFHK.V
390	413	3	2877.39	-1.8	2	26.7	31	95.00%	R.TNCMDCLDRTNVVQSVLAQWVLQK.E	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.TNCMDCLDRTNVVQSVLAQWVLQK.E
271	287	3	1889.03	0.43	1	31.2	28	95.00%	K.YKPNLVLGENSLDATKK.H		K.YKPNLVLGENSLDATKK.H
257	270	2	1602.85	4.4	1	59.6	30	95.00%	R.GSVPIYWAEINNLK.Y		R.GSVPIYWAEINNLK.Y
104	120	4	2042.1	5	1	27.9	27.2	95.00%	R.IDSEEAEYIKLLELHLK.N		R.IDSEEAEYIKLLELHLK.N
453	464	2	1252.65	3.2	2	34.2	31	95.00%	Y.SGTGALKTDFTR.T		K.EFESADVVATGSTWEDNAPLLTSYQNLWADNADAVSVAYSGTGALKTDFTR.T
399	413	2	1711.96	-1.2	1	77.1	25.6	95.00%	R.TNVVQSVLAQWVLQK.E		R.TNVVQSVLAQWVLQK.E
294	308	2	1780.9	-1.7	1	64	31.6	95.00%	K.ELYGDNYLVNLVNQK.G		K.ELYGDNYLVNLVNQK.G
189	207	3	2021.2	-0.59	1	24.7	16.3	95.00%	K.TVDAVLNATPIVLGLITRR.S		K.TVDAVLNATPIVLGLITRR.S
189	206	2	1865.1	-0.54	0	61.6	17.5	95.00%	K.TVDAVLNATPIVLGLITR.R		K.TVDAVLNATPIVLGLITR.R
390	398	2	1183.44	-0.13	0	49.6	31.3	95.00%	R.TNCMDCLDR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.TNCMDCLDR.T
471	483	2	1410.69	2.9	1	101	32.8	95.00%	R.LGAFNDFLNSASR.Y		R.LGAFNDFLNSASR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
90	YOL19_YEAST	27.59%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
376	402	3	3114.36	0.45	1	58.4	33.4	95.00%	R.LLNDIMETSFNEPNDSHINSMSSYNDK.D		R.LLNDIMETSFNEPNDSHINSMSSYNDK.D
490	501	2	1405.73	4	1	49.9	30.6	95.00%	Y.FNVAPNQVPQHR.N		R.TTPAGPDPSNVILQSNPYFNVAPNQVPQHR.N
452	466	2	1940.92	2.1	1	47.7	33.2	95.00%	R.LQPQQQQPQQQYHQY.N		R.LQPQQQQPQQQYHQYNLYQR.T
425	436	2	1258.63	3.3	1	49.8	30.6	95.00%	R.ETAAGPANIRPY.A		R.ETAAGPANIRPYAGQPHPAPLVYPQQR.L
472	501	3	3257.63	3.4	1	69.7	27.8	95.00%	R.TTPAGPDPSNVILQSNPYFNVAPNQVPQHR.N		R.TTPAGPDPSNVILQSNPYFNVAPNQVPQHR.N

540	551	2	1339.66	2.7	1	44.1	32.6	95.00%	R.ATTSLNNPYGFR.-		R.ATTSLNNPYGFR.-
437	451	3	1657.88	5.1	1	39	30.1	95.00%	Y.AGQPHPAPLVYPQQR.L		R.ETAAGPANIRPYAGQPHPAPLVY PQQR.L
425	451	3	2898.49	1.5	1	37.7	27.6	95.00%	R.ETAAGPANIRPYAGQPHPAPLVY PQQR.L		R.ETAAGPANIRPYAGQPHPAPLVY PQQR.L
306	320	2	1586.77	3.3	1	57	32.4	95.00%	R.STSTYSVIESESGLK.N		R.STSTYSVIESESGLK.N
452	463	2	1512.74	2.6	1	32.2	32.8	94.50%	R.LQPQQQQPQQQY.H		R.LQPQQQQPQQQYHQYNLYQR.T
187	202	3	1824.75	0.21	1	26.6	33.9	90.40%	R.SSGSRDDDETEELEEK.G		R.SSGSRDDDETEELEEK.G
472	489	2	1869.92	4.3	1	45.1	32.1	95.00%	R.TTPAGPDPSNVILQSNPY.F		R.TTPAGPDPSNVILQSNPYFNVAP NQVPQHR.N
311	330	3	2139.05	2.6	2	46.9	32.1	95.00%	Y.SVIESESGLKNGSVSNNYVR.N	Deamidation (+1)	R.STSTYSVIESESGLKNGSVSNNY VR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
91	ZRT1_YEAST	16.22%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
155	172	3	2121.03	1.4	1	62	32.8	95.00%	K.YGLSHDHTHDEIKDTVVR.N		K.YGLSHDHTHDEIKDTVVR.N
11	22	2	1387.67	2.8	1	32	32.5	94.40%	K.QWDPSEVTLADK.T		K.QWDPSEVTLADK.T
269	276	2	931.51	-0.57	1	39.5	28	95.00%	R.LSAIEFPR.S		R.LSAIEFPR.S
173	195	3	2332.96	-0.18	0	30.3	34.4	95.00%	R.NTAAVSSENDNENGTANGSHDT K.N	Deamidation (+1)	R.NTAAVSSENDNENGTANGSHDT K.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
92	B3LI54_YEAS1	38.31%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	39	3	3837.02	4.8	1	41.4	24.5	95.00%	M.SAVNVAPELINADNTITYDAIVIGA GVIGPCVATGLAR.K	Acetyl (+42)/ Carbamidomethyl (+57)	- .MSAVNVAPELINADNTITYDAIVIGA GVIGPCVATGLAR.K
2	19	2	1945.97	4.5	1	44.7	31.5	95.00%	M.SAVNVAPELINADNTITY.D	Acetyl (+42)	- .MSAVNVAPELINADNTITYDAIVIGA GVIGPCVATGLAR.K
298	311	2	1519.77	2.8	1	32.4	31.6	95.00%	K.SLRPSFDEAVSQGK.F		K.SLRPSFDEAVSQGK.F
44	56	3	1598.83	4.4	2	37.8	30	95.00%	K.VLIVERDWAMPDR.I		K.VLIVERDWAMPDR.I
218	240	3	2468.22	2.1	1	42	31.2	95.00%	K.ELHPDHVPTVGSSFVGMSLFNAK .N		K.ELHPDHVPTVGSSFVGMSLFNAK .N
314	323	2	1118.56	3.6	1	30.7	30.2	95.00%	R.AMPNSYLPAR.Q		R.AMPNSYLPAR.Q
373	384	3	1547.77	4.5	1	42.7	31.9	95.00%	K.VLDELLDYHFER.K		K.VLDELLDYHFER.K
324	340	2	1892.85	-0.46	0	73.3	34.1	95.00%	R.QNDVTGMCVIGDALNMR.H	Carbamidomethyl (+57)	R.QNDVTGMCVIGDALNMR.H
50	68	3	2126.05	3.8	1	44	31.7	95.00%	R.DWAMPDRIVGELMQPGGVR.A		R.DWAMPDRIVGELMQPGGVR.A
170	189	3	2242.17	2.3	1	50.1	28.6	95.00%	R.VQGNCIEILKDEKNEVVGAK.V	Carbamidomethyl (+57)	R.VQGNCIEILKDEKNEVVGAK.V
341	360	3	2056.16	3.4	0	17.7	24.3	90.50%	R.HPLTGGGMTVGLHDVVLLIK.K		R.HPLTGGGMTVGLHDVVLLIK.K
159	169	2	1241.64	-0.66	0	40.2	30.5	95.00%	R.NITAQEPNVTR.V		R.NITAQEPNVTR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
93	A6ZM72_YEAS7	19.41%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
27	37	2	1339.59	-0.78	0	38	32.8	95.00%	K.LETDESPIQTK.S	Phospho (+80)	K.LETDESPIQTK.S
296	309	2	1492.74	2.8	1	78.6	32.3	95.00%	R.LAGNASWGELFSNK.G		R.LAGNASWGELFSNK.G
95	105	2	1274.58	3.1	1	62.8	32.7	95.00%	K.SDGTYYLSDVR.T		K.SDGTYYLSDVR.T
9	26	2	1924.99	3.5	0	79.9	30.1	95.00%	R.VESGSQQTSIHSTPIVQK.L		R.VESGSQQTSIHSTPIVQK.L
219	227	2	1153.52	2.9	1	49.9	32.5	95.00%	K.DYSNSVQWR.V		K.DYSNSVQWR.V
273	295	2	2562.23	3.9	0	108	32.4	95.00%	K.VTIEDPSIVAEMDTIMANVETER.L		K.VTIEDPSIVAEMDTIMANVETER.L
509	527	2	2220.12	4.3	1	53.7	30.8	95.00%	K.GLTLEEVNEMYVEGVKPWK.S		K.GLTLEEVNEMYVEGVKPWK.S
9	37	3	3166.61	2.3	1	76	27.6	95.00%	R.VESGSQQTSIHSTPIVQKLETDES PIQTK.S		R.VESGSQQTSIHSTPIVQKLETDES PIQTK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

94	A6ZL51_YEAS7	44.15%	100%	7	

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	78	2	1466.63	-0.56	1	67.7	33.4	95.00%	K.YVEPGNAMSGEGEK.L		K.YVEPGNAMSGEGEK.L
155	168	2	1346.67	1.8	1	64.3	31.3	95.00%	K.APSLFGGMGQTGPK.T		K.APSLFGGMGQTGPK.T
138	150	3	1395.79	3.3	1	21.1	24.4	95.00%	K.IHLFGKPATGDLK.R		K.IHLFGKPATGDLK.R
115	128	2	1623.84	2.8	1	63.9	30.8	95.00%	K.YTNPLFMQSISPVK.S		K.YTNPLFMQSISPVK.S
79	90	2	1449.79	2.4	2	36.5	28.1	95.00%	K.LQVTTVRDYDLK.E		K.LQVTTVRDYDLK.E
65	85	2	2264.12	3.8	1	89.5	31.3	95.00%	K.YVEPGNAMSGEGEKLQVTTVR.D		K.YVEPGNAMSGEGEKLQVTTVR.D
173	188	3	1629.8	0.052	1	63.4	32.2	95.00%	K.SIEEAERAGNAGVKAE.-		K.SIEEAERAGNAGVKAE.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
95	A7A1A7_YEAS7	31.68%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
172	181	2	1254.6	3.8	1	49.4	32.1	95.00%	K.FYDNSNLINR.E		K.FYDNSNLINR.E
88	99	2	1349.67	0.57	1	47.6	31.9	95.00%	K.ANLGFFQSVDPR.V		K.ANLGFFQSVDPR.V
8	16	2	984.6	3.2	0	40.2	26.7	95.00%	K.NAVVTLIQK.A		K.NAVVTLIQK.A
19	36	2	1703.84	3.4	0	86.4	31.9	95.00%	K.GSGGTSELGGSESTPLLR.G		K.GSGGTSELGGSESTPLLR.G
37	59	2	2439.11	3.5	2	67.9	34.3	95.00%	R.GSNSNSSRHDNLSSSSSDIIYGR.N		R.GSNSNSSRHDNLSSSSSDIIYGR.N
60	74	2	1575.72	2.6	0	93.5	33.4	95.00%	R.NSAQDLENSPMSVGK.D		R.NSAQDLENSPMSVGK.D
117	129	2	1202.66	4.6	0	79.2	29.1	95.00%	F.ALTAGLSSLGDAK.L		R.VISDLIIGLSDGLTVPFALTAGLSSLGDAK.L
17	36	2	1902.97	3.9	1	131	30.9	95.00%	K.AKGSGGTSELGGSESTPLLR.G		K.AKGSGGTSELGGSESTPLLR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
96	A7A1W6_YEAS7	24.06%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
255	266	2	1369.68	4.6	1	71.6	31.3	95.00%	F.HLAQAQDFEGVR.A		K.LYPLATFHLAQAQDFEGVR.A
248	266	3	2175.11	-0.87	1	30.6	30.5	95.00%	K.LYPLATFHLAQAQDFEGVR.A		K.LYPLATFHLAQAQDFEGVR.A
322	335	2	1715.84	1.1	1	69.3	32.1	95.00%	R.NITWIAECIAQNQR.E	Carbamidomethyl (+57)	R.NITWIAECIAQNQR.E
220	238	2	2042.06	2.9	0	28	29.8	92.70%	R.SINIALNSLQSSDIDPDLK.S		R.SINIALNSLQSSDIDPDLK.S
239	247	2	955.54	1.7	0	33.9	25.7	95.00%	K.SDLLPNIGK.L		K.SDLLPNIGK.L
267	276	2	1168.59	-0.44	1	58.1	31.1	95.00%	R.AALANVYEYR.G		R.AALANVYEYR.G
220	247	3	2979.58	2.2	1	67	24.8	95.00%	R.SINIALNSLQSSDIDPDLKSDLLPNIGK.L		R.SINIALNSLQSSDIDPDLKSDLLPNIGK.L
7	18	2	1331.69	4.3	1	50	30.7	95.00%	F.NIDNGFIEGVVR.G		-.MEGVYFNIDNGFIEGVVR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
97	B3LP09_YEAS1	24.73%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
402	430	5	3320.53	4.4	1	23.4	31.7	90.70%	Y.SSPDHHHHYNQQQQQQQAQAQAQAQAK.V		K.NHQYSSPDHHHHYNQQQQQQQAQAQAQAQAQAK.V
375	390	2	1797.9	2.4	1	39.3	31.9	95.00%	K.KPNLHGYGHPNPPNEK.S		K.KPNLHGYGHPNPPNEK.S
411	430	3	2223.08	4.8	0	59.9	32.5	95.00%	Y.NQQQQQQQAQAQAQAQAQAK.V		K.NHQYSSPDHHHHYNQQQQQQQAQAQAQAQAQAK.V
61	77	3	1848.9	3.6	2	48.2	32.8	95.00%	Y.SGSQSRDDSTIVGLHYK.I		R.LVNGTLPPSLHVSSNLNHNTGNSSASYSGSQSRDDSTIVGLHYK.I
303	319	2	1904.01	-0.63	1	53	28.5	95.00%	R.LTNVYDLAQGLPIQFGR.Y		R.LTNVYDLAQGLPIQFGR.Y
509	524	2	1822.81	-0.77	1	74.3	33.9	95.00%	K.YPYNAQPTANDEQNAK.N		K.YPYNAQPTANDEQNAK.N
340	361	2	2512.2	4.9	1	71.1	32.7	95.00%	R.MLLLSVLDDLGETADGQYDWMK.L		R.MLLLSVLDDLGETADGQYDWMK.L
431	448	3	2157.08	3.5	2	44.1	31.7	95.00%	K.VQQQQLQQAQAQQQANRY.Q		K.VQQQQLQQAQAQQQANRYQLQPDDSHYDEER.E
431	447	2	1994	-0.94	0	81	31.3	95.00%	K.VQQQQLQQAQAQQQANR.Y		K.VQQQQLQQAQAQQQANR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
98	A6ZPF0_YEAS7	14.12%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

393	411	2	2047.01	2.3	0	64.2	32.2	95.00%	R.AGDSQGDHLQNDPLSLRPK.T		R.AGDSQGDHLQNDPLSLRPK.T
213	234	3	2338.05	0.52	1	47.1	34.1	95.00%	K.TPSYSTSSHTIASGGNYTEHNK.R		K.TPSYSTSSHTIASGGNYTEHNK.R
302	322	2	2197.19	1.3	0	78.3	27.1	95.00%	K.ILLQATPSTLSGDQVEGDLLK.I		K.ILLQATPSTLSGDQVEGDLLK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
99	A6ZKW1_YEAS7	12.90%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	80	3	2701.12	0.74	1	51.8	34.1	95.00%	K.YSSSSDAASADDSTPLRDNDEAGNEK.L		K.YSSSSDAASADDSTPLRDNDEAGNEK.L
536	545	2	1283.61	3.1	1	35.5	32.8	95.00%	K.NYDIELENFK.V		K.NYDIELENFK.V
56	80	3	2538.07	3	1	34.8	33.9	95.00%	Y.SSSSDAASADDSTPLRDNDEAGNEK.L		K.YSSSSDAASADDSTPLRDNDEAGNEK.L
136	149	2	1560.77	2.4	0	37.5	32	95.00%	K.CLELSPDEVASLTK.S	Carbamidomethyl (+57)	K.CLELSPDEVASLTK.S
448	458	2	1238.6	3.5	1	64	32.2	95.00%	R.YLNAMESIGNK.Y		R.YLNAMESIGNK.Y
150	165	4	1822.96	3	2	34	29.1	95.00%	K.SHKDYVEHIATLVSPK.G		K.SHKDYVEHIATLVSPK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
100	A6ZNG9_YEAS7	34.51%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
19	35	2	1951.99	5.2	2	96.8	30.7	95.00%	R.GVDLEKLLEMSTEDFVK.L		R.GVDLEKLLEMSTEDFVK.L
25	35	2	1310.65	4.5	1	39.9	31.8	95.00%	K.LLEMSTEDFVK.L		K.LLEMSTEDFVK.L
65	77	2	1390.76	-0.25	0	58.2	28.8	95.00%	K.LAAPENEKPAPVR.T		K.LAAPENEKPAPVR.T
82	100	2	2033.07	-0.84	1	98.2	29.4	95.00%	R.NMIIVPEMIGSVVGIYNGK.A		R.NMIIVPEMIGSVVGIYNGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
101	SNA3_YEAST	40.60%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
93	125	3	3566.54	2.8	1	72.1	32.5	95.00%	R.DLEAHPAEESQAQPPAYDEDDEAGADVPLMDNK.Q		R.DLEAHPAEESQAQPPAYDEDDEAGADVPLMDNK.Q
1	12	3	1601.68	0.14	1	33.7	34.1	95.00%	-.MDRDHINDHDHR.M	Acetyl (+42)	-.MDRDHINDHDHR.M
84	125	3	4485.01	4.4	2	88.8	29.7	95.00%	R.HATAPAVDRDLEAHPAEESQAQPPAYDEDDEAGADVPLMDNK.Q		R.HATAPAVDRDLEAHPAEESQAQPPAYDEDDEAGADVPLMDNK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
102	YNF8_YEAST	31.33%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
299	313	2	1717.86	4.2	2	52.3	31.6	95.00%	K.RQAPSMFLDDVLNGR.E		K.RQAPSMFLDDVLNGR.E
300	316	2	1916.98	4.7	1	54.3	30.5	95.00%	R.QAPSMFLDDVLNGREII.-		R.QAPSMFLDDVLNGREII.-
273	294	2	2214.17	3.2	1	106	28.6	95.00%	K.RNQSSLGLIPVASATSNTSSPK.K		K.RNQSSLGLIPVASATSNTSSPK.K
273	295	3	2342.26	2.3	1	53.8	26	95.00%	K.RNQSSLGLIPVASATSNTSSPKK.A		K.RNQSSLGLIPVASATSNTSSPKK.A
142	157	2	1816.83	3.2	1	82.5	34.1	95.00%	K.HSSSLQSNPFDINDEK.S		K.HSSSLQSNPFDINDEK.S
300	313	2	1561.75	-1.4	1	46	32.6	95.00%	R.QAPSMFLDDVLNGR.E		R.QAPSMFLDDVLNGR.E
218	229	2	1471.69	4.8	1	41.5	33	95.00%	K.DTNIFIDDPFLY.V		K.DTNIFIDDPFLYVGTYLEEEEEEEEER.K
195	209	2	1738.92	4.6	1	74.8	28.9	95.00%	R.SLFISPTLQVSQYEK.S		R.SLFISPTLQVSQYEK.S
230	244	2	1868.79	4.4	1	79.4	33.9	95.00%	Y.VGTYLEEEEEEEER.K		K.DTNIFIDDPFLYVGTYLEEEEEEEEER.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
103	A6ZNR5_YEAS7	21.71%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
285	300	3	1637.73	-0.25	2	39	33.3	95.00%	R.VGKGDDEANGATSFDR.T		R.VGKGDDEANGATSFDR.T
101	116	3	1869.97	3.5	1	29.6	30.5	95.00%	R.SLTTVWAEHLSDEVKR.R		R.SLTTVWAEHLSDEVKR.R
249	266	2	2047.01	3	1	49.1	32.4	95.00%	K.VACIGAWHPAHVMWSVAR.A	Carbamidomethyl (+57)	K.VACIGAWHPAHVMWSVAR.A
202	222	2	2279.14	3.4	1	79.9	30.9	95.00%	K.TVAVDSVFEQNEMIDAIAVTK.G		K.TVAVDSVFEQNEMIDAIAVTK.G

38	50	2	1409.8	4.2	1	43.8	23.7	95.00%	R.SKPVALTSFLGYK.A		R.SKPVALTSFLGYK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
104	YAJ8_YEAST	20.94%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
201	211	2	1248.68	-0.57	1	58.4	29.4	95.00%	R.SDPILMAYVLK.A		R.SDPILMAYVLK.A
163	188	2	2563.09	-0.43	0	80.8	33.7	95.00%	K.EVNSGSHSDSSSNSAEDTQSPVSAGK.T		K.EVNSGSHSDSSSNSAEDTQSPVSAGK.T
189	200	2	1385.66	0.99	1	44	33.2	95.00%	K.TSNGLNNFYSIR.S	Deamidation (+1)	K.TSNGLNNFYSIR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
105	B3LRN6_YEAS1	45.49%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
69	80	2	1289.66	3.8	1	38.2	31.6	95.00%	F.LGLTEEPAADFK.C		K.FYCVRPNAAVVAPGETIQVQVIFLGLTEEPAADFK.C
166	190	3	2780.5	1.8	1	40.5	24.1	95.00%	K.EVPAEPETQPPVQVKKEEVPPVVQK.T		K.EVPAEPETQPPVQVKKEEVPPVVQK.T
125	156	4	3644.81	4	1	25.1	27.5	95.00%	K.YLISPDVHPAQNQNIQENKETVEPVVQDSEPK.E		K.YLISPDVHPAQNQNIQENKETVEPVVQDSEPK.E
100	113	2	1578.76	-0.15	1	66.3	33	95.00%	K.AVADVWSDLEAEFK.Q		K.AVADVWSDLEAEFK.Q
181	190	2	1151.65	-1.1	1	28.1	23.8	95.00%	K.KEEVPPVVQK.T		K.KEEVPPVVQK.T
166	180	2	1646.86	3.7	0	39.1	30.6	95.00%	K.EVPAEPETQPPVQVK.K		K.EVPAEPETQPPVQVK.K
85	99	2	1676.91	4.4	1	42.3	28.3	95.00%	K.FLVITLPSPYDLNGK.A	Deamidation (+1)	K.FLVITLPSPYDLNGK.A
2	14	2	1460.78	4.7	1	43.9	29.4	95.00%	M.SAVEISPDVLVYK.S	Acetyl (+42)	-.MSAVEISPDVLVYK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
106	B5VDM9_YEAST	23.40%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
167	188	2	2226.02	0.25	0	90.1	33.9	95.00%	R.SNAHLSSPTNGAENTQSNTPAK.E	Deamidation (+1)	R.SNAHLSSPTNGAENTQSNTPAK.E
167	198	3	3402.58	4.3	2	56.2	31.5	95.00%	R.SNAHLSSPTNGAENTQSNTPAKEVSNEMVKPY.I	Deamidation (+1)	R.SNAHLSSPTNGAENTQSNTPAKEVSNEMVKPYIFSSDPVLEAYLIK.A
39	47	2	1077.59	4.1	1	30.5	29.2	95.00%	R.SYILNEIAR.C		R.SYILNEIAR.C
199	212	2	1593.87	3.9	1	52.6	27	95.00%	Y.IFSSDPVLEAYLIK.A		K.EVSNEMVKPYIFSSDPVLEAYLIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
107	A6ZNT8_YEAS7	12.59%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
465	480	2	1841.82	3.5	1	75.5	34.1	95.00%	K.VIDNADDEYMALMSQK.T		K.VIDNADDEYMALMSQK.T
653	667	2	1684.97	5.3	1	99.1	22.8	95.00%	K.KVENLTAVITDLLEK.L		K.KVENLTAVITDLLEK.L
2	33	3	3450.6	0.76	1	65.9	31.2	95.00%	M.VSANGDLHLPISNEQCMPENNGSLGFEAPTPR.Q	Carbamidomethyl (+57)	-.MVSANGDLHLPISNEQCMPENNGSLGFEAPTPR.Q
49	70	2	2508.27	4	1	67.2	30.1	95.00%	K.VVPIVYDPNDIVCDHSEILSPK.V	Carbamidomethyl (+57)	K.VVPIVYDPNDIVCDHSEILSPK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
108	A6ZX41_YEAS7	41.63%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
128	137	2	1212.61	0.15	0	68.8	31.2	95.00%	R.NDPQTIEQLR.Q		R.NDPQTIEQLR.Q
2	10	2	1029.52	-0.26	0	37	30.1	95.00%	M.SQQVGNSIR.R	Acetyl (+42)	-.MSQQVGNSIR.R
104	123	2	2338.24	2.6	1	49.3	27.2	95.00%	K.WIAEVLHFCQGVPIILVGCK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.WIAEVLHFCQGVPIILVGCK.V
174	181	2	921.46	0.5	1	35.6	31	95.00%	R.EVFEAATR.A		R.EVFEAATR.A
58	73	2	1879.87	3.6	1	47	33.7	95.00%	R.VELALWDTAGQEDYDR.L		R.VELALWDTAGQEDYDR.L
57	71	2	1764.84	4.6	2	35	32.9	95.00%	R.RVELALWDTAGQEDY.D		R.RVELALWDTAGQEDYDR.L
24	32	2	1079.61	3.5	1	39	25.5	95.00%	K.TCLLIVFSK.G	Carbamidomethyl (+57)	K.TCLLIVFSK.G

90	103	2	1585.79	4	0	77.2	31.7	95.00%	F.SIDLPDSLENVQEK.W		R.LRPLSYPDSNVVLICFSIDLPDSLENVQEK.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
109	A6ZMQ9_YEAS7	58.06%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
167	178	2	1413.68	2.6	1	60.1	32.6	95.00%	R.QTLFQADSYVDK.S		R.QTLFQADSYVDK.S
21	34	2	1453.75	-0.63	0	42.6	29.8	95.00%	K.ASLAEAPSQPLSQR.N		K.ASLAEAPSQPLSQR.N
40	69	3	3472.59	4.9	1	98	31.9	95.00%	K.HVEQQDELFDLLDQMDVEVNNSIGDASER.A		K.HVEQQDELFDLLDQMDVEVNNSIGDASER.A
89	102	3	1612.83	0.68	1	23.6	30.3	91.60%	K.RPLQSLVDSGDRDR.L		K.RPLQSLVDSGDRDR.L
2	13	2	1429.7	-0.75	1	30.8	32.4	93.10%	M.SSLLISYESDFK.T	Acetyl (+42)	-.MSSLLISYESDFK.T
103	129	3	3065.56	3.5	1	42.7	27.4	95.00%	R.LFGDLNASNIDDDQRQQLLSNHAILQK.S		R.LFGDLNASNIDDDQRQQLLSNHAILQK.S
140	156	2	1876.91	5.3	0	62.8	32.6	95.00%	R.IANETEGIGSQIMMDLR.S		R.IANETEGIGSQIMMDLR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
110	A6ZLC2_YEAS7	31.78%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	48	2	1811.83	3.2	2	62.6	33.2	95.00%	R.IGQEVDGEAVGDEFKGY.V		R.IGQEVDGEAVGDEFKGYVFK.I
31	46	2	1747.84	2.9	2	83.1	32.9	95.00%	K.RIGQEVDGEAVGDEFK.G		K.RIGQEVDGEAVGDEFK.G
99	115	2	1647.03	-0.43	0	62.6	13.8	95.00%	R.GAIVGPDLAVLALVIVK.K		R.GAIVGPDLAVLALVIVK.K
15	25	2	1429.7	3.3	1	31.4	31.4	95.00%	K.TFEIDDEHRIR.V		K.TFEIDDEHRIR.V
116	131	2	1743.89	-0.13	1	61.2	30.9	95.00%	K.KGEQELEGLTDTTVPK.R		K.KGEQELEGLTDTTVPK.R
203	214	2	1276.67	3	1	66.2	30.7	95.00%	R.EAAAEYAQLLAK.R		R.EAAAEYAQLLAK.R
116	132	3	1900	3.7	1	39.9	29.5	95.00%	K.KGEQELEGLTDTTVPKR.L		K.KGEQELEGLTDTTVPKR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
111	COS6_YEAST	22.31%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
157	167	2	1275.75	3.6	1	33.3	23.7	95.00%	R.TTLLEPFSLKK.D		R.TTLLEPFSLKK.D
206	219	2	1525.82	3.7	1	106	27.5	95.00%	K.SWSPVGLEDAKLPK.E		K.SWSPVGLEDAKLPK.E
357	369	2	1544.86	-0.59	1	57.8	27.5	95.00%	R.ALSLNVELWPYIK.E		R.ALSLNVELWPYIK.E
291	313	2	2580.22	0.23	1	91.4	33.1	95.00%	K.MQFLSTIINEQESGANGWDEIAK.K		K.MQFLSTIINEQESGANGWDEIAK.K
113	132	2	2214.99	3.5	1	44.6	34	95.00%	K.NTPSSDPHDWEVVAANLNSY.F		K.NTPSSDPHDWEVVAANLNSYFYENK.A
109	132	2	2687.21	-8.8	2	41.3	33.2	95.00%	K.EITKNTPSSDPHDWEVVAANLNSY.F	Deamidation (+1)	K.EITKNTPSSDPHDWEVVAANLNSYFYENK.A
206	216	2	1187.59	3.1	1	36.3	31.5	95.00%	K.SWSPVGLEDAK.L		K.SWSPVGLEDAK.L
157	166	2	1147.65	4.2	1	35.1	27.1	95.00%	R.TTLLEPFSLK.K		R.TTLLEPFSLK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
112	A6ZQK0_YEAS7	7.90%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
544	571	3	3145.62	5	2	45.4	27.6	95.00%	K.VLGTPIDTIITTEDRELFSNAIDEINEK.C		K.VLGTPIDTIITTEDRELFSNAIDEINEK.C
599	615	2	1638.81	3	1	43	32.6	95.00%	R.AAYALGGLGSGFANNEK.E		R.AAYALGGLGSGFANNEK.E
1978	1989	2	1267.75	3.1	0	34	21.2	95.00%	R.IVNVNPLVSSVK.K		R.IVNVNPLVSSVK.K
855	864	2	1050.59	3.9	1	25.3	26.8	93.10%	R.VFAIANAFAK.K		R.VFAIANAFAK.K
2176	2188	3	1644.78	2.9	2	55.4	33.3	95.00%	R.VNEIKEEVDYDHR.A		R.VNEIKEEVDYDHR.A
1152	1166	2	1735.84	-0.12	1	32.8	32.9	95.00%	K.NDLESYLNQAVEVSR.D		K.NDLESYLNQAVEVSR.D
1635	1650	2	1713.96	-1.3	0	31.6	25.8	95.00%	K.TADLASVLLLTSLQNR.S		K.TADLASVLLLTSLQNR.S
1742	1764	3	2492.42	5.4	1	45.4	19.2	95.00%	K.DSLPLLLAAVEEGKLTIDDIVLR.L		K.DSLPLLLAAVEEGKLTIDDIVLR.L
2005	2011	2	790.41	9.5	0	31.1	30.5	95.00%	Y.SDAIVMR.H		R.TLACYSDAIVMR.H
1613	1627	2	1711.92	3.8	1	34.2	28.2	95.00%	K.ITAVAELLNQWPTEK.Q		K.ITAVAELLNQWPTEK.Q
180	198	2	2143.07	6	1	46.7	31	95.00%	R.SAFDVPEWVDPNVQNLVSK.V		R.SAFDVPEWVDPNVQNLVSK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
113	YD237_YEAST	23.33%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
349	367	3	2167.15	-0.19	2	28.1	27.9	95.00%	K.TRIWGAPTWPANLVETISR.Q		K.TRIWGAPTWPANLVETISR.Q
171	193	3	2663.28	2.6	1	38.8	31.7	95.00%	K.LYTGPLLEILDEVNCQDSDADRK.N	Carbamidomethyl (+57)	K.LYTGPLLEILDEVNCQDSDADRK.N
136	150	2	1620.73	2.5	1	92	33.7	95.00%	Y.GASSTEADVWNIDEK.I		K.LPLFEGLAYGASSTEADVWNIDEK.I
151	170	2	2209.17	3.7	1	64.9	27.1	95.00%	K.ILAVGHNEAYLDPVELTLDK.L		K.ILAVGHNEAYLDPVELTLDK.L
351	367	2	1910	-1.2	1	39.7	29.2	95.00%	R.IWGAPTWPANLVETISR.Q		R.IWGAPTWPANLVETISR.Q
282	295	2	1559.86	-1.1	1	46.6	27.7	95.00%	R.FAFLDAPLLSLEPK.Y		R.FAFLDAPLLSLEPK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
114	A6ZZX8_YEAS7	41.88%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
122	153	3	3531.64	3	1	98.1	31.1	95.00%	Y.LLGNKVDLCQETPSTETSPDSNEGGDEEQKVR.A	Carbamidomethyl (+57)	K.VGDDDLVIYLLGNKVDLCQETPSTETSPDSNEGGDEEQKVR.A
162	172	2	1351.69	2.3	1	44.3	31.6	95.00%	K.QYAQEQGLLFR.E		K.QYAQEQGLLFR.E
62	72	2	1350.62	0.79	1	56.1	33.3	95.00%	K.FEIWDTAGQER.Y		K.FEIWDTAGQER.Y
127	151	2	2751.14	3.2	0	82.2	33.6	95.00%	K.VDLCQETPSTETSPDSNEGGDEEQK.V	Carbamidomethyl (+57)	K.VDLCQETPSTETSPDSNEGGDEEQK.V
83	101	2	2091.06	3.3	1	94.3	31.3	95.00%	R.NANAALVVYDITQEDSLQK.A		R.NANAALVVYDITQEDSLQK.A
113	126	2	1532.81	-0.07	1	75.4	30.8	95.00%	K.VGDDDLVIYLLGNK.V		K.VGDDDLVIYLLGNK.V
41	56	2	1752.87	2.4	0	55.1	32.4	95.00%	F.LSQSITIHPNDGNETK.D		R.ESTIGAAFLSQSITIHPNDGNETK.D
122	151	3	3276.47	2.8	1	86.1	33.1	95.00%	Y.LLGNKVDLCQETPSTETSPDSNEGGDEEQK.V	Carbamidomethyl (+57)	K.VGDDDLVIYLLGNKVDLCQETPSTETSPDSNEGGDEEQK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
115	B3RHC6_YEAS1	9.21%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
331	340	2	1113.62	3.5	0	38.9	27.5	95.00%	Y.SQISLGERPK.M		R.QPYSENYHLLGNEQSGAVTHGENVPSSNNNDEDTILYSQISLGERPK.M
352	364	2	1576.81	5.2	1	56.8	31.3	95.00%	K.EVDAIEYLEQQLK.F		K.EVDAIEYLEQQLK.F
301	330	3	3223.48	5.8	1	39.8	32.5	95.00%	Y.HLLGNEQSGAVTHGENVPSSNNNDEDTILY.S		R.QPYSENYHLLGNEQSGAVTHGENVPSSNNNDEDTILYSQISLGERPK.M
292	300	2	1156.52	3.8	2	40.2	32.1	95.00%	R.TRQPYSENY.H		R.TRQPYSENYHLLGNEQSGAVTHGENVPSSNNNDEDTILYSQISLGERPK.M
365	374	2	1175.62	2.3	1	46.1	30.2	95.00%	K.FIDAEIIEAR.K		K.FIDAEIIEAR.K
297	330	3	3716.66	4.5	1	46.9	31.4	95.00%	Y.SENYHLLGNEQSGAVTHGENVPSSNNNDEDTILY.S		R.QPYSENYHLLGNEQSGAVTHGENVPSSNNNDEDTILYSQISLGERPK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
116	FET5_YEAST	19.45%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
485	493	2	1060.51	4.1	2	28.9	31.5	91.50%	R.FRADNPGVW.Y		R.FRADNPGVWYFHCHVDWHLQQGLASVFIEAPVLLQER.E
402	420	3	2238.09	3.9	2	52.9	32.4	95.00%	K.HNDIIEVVLNNYDSGRHPF.H		K.HNDIIEVVLNNYDSGRHPFHLHGHNFQIVQK.S
322	334	2	1579.79	-0.083	1	54.4	32.2	95.00%	R.ATNDFYLEPLIER.D		R.ATNDFYLEPLIER.D
471	484	2	1519.84	2.6	0	40.2	26.5	95.00%	R.DTVVLEPSGHVVLR.F		R.DTVVLEPSGHVVLR.F
512	521	2	1166.67	6	0	30.8	23.4	95.00%	F.IEAPVLLQER.E		R.ADNPGVWYFHCHVDWHLQQGLASVFIEAPVLLQER.E
372	383	2	1229.73	3.2	0	50.7	23.9	95.00%	K.VPTLTTLLTSGK.L		K.VPTLTTLLTSGK.L

534	554	3	2196.07	5.4	1	25.2	31.7	92.20%	K.AADIPVVGNAAGHSNDWFDLK.G		K.AADIPVVGNAAGHSNDWFDLK.G
524	533	2	1280.61	3.8	1	38.2	32.8	95.00%	K.LNENYLDICK.A	Carbamidomethyl (+57)	K.LNENYLDICK.A
159	171	3	1617.78	2.9	1	27.3	31.9	95.00%	R.VITLSDHYHENYK.T		R.VITLSDHYHENYK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
117	AQR1_YEAST	14.16%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
493	504	2	1361.61	4.1	1	41.7	32.8	95.00%	K.SSTASSCFNFVR.C	Carbamidomethyl (+57)	K.SSTASSCFNFVR.C
39	54	2	1749.88	4	1	81.4	32.2	95.00%	K.LNFEGAYINSHGTLSK.T		K.LNFEGAYINSHGTLSK.T
505	517	2	1520.68	-0.69	1	35.4	33.2	95.00%	R.CSLSTIFMGCFAK.M	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.CSLSTIFMGCFAK.M
563	572	2	1158.64	0.25	1	32.1	28.7	95.00%	R.QSWLNTLAVK.A		R.QSWLNTLAVK.A
4	25	3	2677.21	-0.93	1	64.2	33.8	95.00%	R.SNSIYTEDIEMYPTHNEQHLTR.E		R.SNSIYTEDIEMYPTHNEQHLTR.E
298	307	2	1081.67	1.5	1	29.8	19.7	95.00%	R.APIFLLGPVR.R		R.APIFLLGPVR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
118	A6ZYN3_YEAS7	25.61%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
276	289	2	1580.7	0.68	0	44.1	33.5	95.00%	R.IPDEELHPLSDEGM.-		R.IPDEELHPLSDEGM.-
257	275	3	2183.06	3.6	0	48.8	32.8	95.00%	F.KPLMDDSDVTLEEAVTHQR.I		R.IFPPIDDPLPFKPLMDDSDVTLEEAVTHQR.I
245	256	2	1425.77	4.7	2	36.9	27.3	95.00%	R.RIFPPIDDPLPF.K		R.RIFPPIDDPLPFKPLMDDSDVTLEEAVTHQR.I
245	275	4	3590.82	4	2	50.9	26.9	95.00%	R.RIFPPIDDPLPFKPLMDDSDVTLEEAVTHQR.I		R.RIFPPIDDPLPFKPLMDDSDVTLEEAVTHQR.I
132	147	2	1787.91	-2	1	50.4	30.8	95.00%	R.CQPVEGLPLDTLFTAK.D	Carbamidomethyl (+57)	R.CQPVEGLPLDTLFTAK.D
44	56	2	1609.79	4.5	1	64.8	33	95.00%	R.QFYINDLTISHPY.A		R.QFYINDLTISHPYATTER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
119	SMF1_YEAST	17.39%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	19	2	1748.88	2	0	95	31.5	95.00%	M.VNVGPSHAAVAVDASEAR.K		-.MVNVGPSHAAVAVDASEAR.K
35	47	2	1370.7	-0.018	0	35.7	29.7	95.00%	K.DSTVVIEGEAPVR.T		K.DSTVVIEGEAPVR.T
291	297	2	864.46	1.8	1	31.1	28.7	95.00%	R.LLDYDVK.H		R.LLDYDVK.H
513	535	3	2336.09	2.6	1	37.9	33.7	95.00%	R.SAGSVIEQDGSSGMEIENGKDVK.I		R.SAGSVIEQDGSSGMEIENGKDVK.I
22	31	2	1234.62	-0.59	1	33.2	31.7	95.00%	R.NISEEVFELR.D		R.NISEEVFELR.D
2	20	3	1876.98	3.4	1	55.8	30	95.00%	M.VNVGPSHAAVAVDASEARK.R		-.MVNVGPSHAAVAVDASEARK.R
492	512	3	2504.05	-1.2	0	27.4	33.9	92.10%	K.TEITVDHTEEDSHNHQNNNDR.S		K.TEITVDHTEEDSHNHQNNNDR.S
32	47	2	1741.93	2.7	1	59.5	29.1	95.00%	R.DKKDSTVVIEGEAPVR.T		R.DKKDSTVVIEGEAPVR.T
488	512	4	2963.32	2.9	1	33.7	33.7	95.00%	K.SIMKTEITVDHTEEDSHNHQNNNDR.S		K.SIMKTEITVDHTEEDSHNHQNNNDR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
120	A6ZT57_YEAS7	13.49%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
369	377	2	1155.6	3.8	1	40.7	29.7	95.00%	K.SIYQVYLDR.A		K.SIYQVYLDR.A
524	534	2	1380.65	3.9	1	36.2	33.1	95.00%	Y.TAQFVQNPQWY.G		R.IASSIYSEAIQPLNYQDQYQQQEQSPVYNGHTQYPGNGYSGNPQQQGYTAQFVQNPQWYGVPTPQQQQHNHPQTLETIGELPTPAYLAQSASSHSLTSFK.R
240	247	2	1028.46	-0.22	1	30.9	31.6	94.20%	R.FQESESFR.S		R.FQESESFR.S
693	723	3	3308.64	3.8	1	65.4	28.8	95.00%	R.VSGILEETDVVQPPSVGGILPHSGSQDDLRK.Q	Phospho (+80)	R.VSGILEETDVVQPPSVGGILPHSGSQDDLRK.Q

414	429	2	1811.83	-0.68	0	62.3	33.2	95.00%	K.INNNDNIDNNEVPEAK.H		K.INNNDNIDNNEVPEAK.H
638	661	4	2580.31	3.2	1	44.1	30	95.00%	R.QSVVMTNPSDLTAKPSYKPAGSFR.S		R.QSVVMTNPSDLTAKPSYKPAGSFR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
121	ATC1_YEAST	16.53%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
445	466	3	2455.25	4.4	1	61.3	30	95.00%	F.LGNPTDVALLEQLANFEMPDIR.N		R.ETLTIGNLCNNASFSQEHAIFLGNPTDVALLEQLANFEMPDIR.N
553	568	2	1731.91	-0.87	0	63.2	29.9	95.00%	K.LTLSDSSTPLTEDLIK.D		K.LTLSDSSTPLTEDLIK.D
627	655	3	3213.61	3.2	2	72.6	28.6	95.00%	K.LSVLSGDKLDEMSDDQLANVIDHVNIFAR.A		K.LSVLSGDKLDEMSDDQLANVIDHVNIFAR.A
690	699	2	1033.53	2.8	0	76.1	30.8	95.00%	K.LSDIGVSMGR.I		K.LSDIGVSMGR.I
39	54	3	1835.89	4.3	1	29.6	31.9	95.00%	Y.CTLSVDEALEKLDTDK.N	Carbamidomethyl (+57)	R.EILDATAEALSKPSPSLEYCTLSVDEALEKLDTDK.N
235	245	2	1241.62	3.2	1	43.1	31.8	95.00%	R.SCIAYMGTLVK.E	Carbamidomethyl (+57)	R.SCIAYMGTLVK.E
158	178	4	2321.16	2.4	1	43.6	31.1	95.00%	R.CGQESHVLASTLVPGDLVHFR.I	Carbamidomethyl (+57)	R.CGQESHVLASTLVPGDLVHFR.I
219	234	2	1788.87	3.5	1	54.1	32.3	95.00%	K.SSFNDQPNSIVPISER.S		K.SSFNDQPNSIVPISER.S
531	546	2	1722.77	2.4	0	102	33.2	95.00%	K.ATINECANSMASEGLR.V	Carbamidomethyl (+57)	K.ATINECANSMASEGLR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
122	A6ZZX2_YEAS7	57.14%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
136	149	2	1494.76	-1	1	69.3	31.7	95.00%	R.TNTFTLLTSPDSAK.I		R.TNTFTLLTSPDSAK.I
108	135	3	2735.25	-0.18	0	75.4	33.2	95.00%	R.SAGDDNLSGHSVPSSGSAQATTHQTAPR.T		R.SAGDDNLSGHSVPSSGSAQATTHQTAPR.T
157	182	3	2906.57	3	2	42.4	23.4	95.00%	K.KLHSNILNEIFSQSQVNKPGPLTVPF.-		K.KLHSNILNEIFSQSQVNKPGPLTVPF.-
22	43	2	2460	2.8	1	97.6	33.6	95.00%	R.EQQAGYGSQGNANDEYDAEQMR.L		R.EQQAGYGSQGNANDEYDAEQMR.L
28	43	2	1783.71	3.2	1	108	33.3	95.00%	Y.GSQGNANDEYDAEQMR.L		R.EQQAGYGSQGNANDEYDAEQMR.L
55	68	2	1643.82	2.5	1	56.5	31.5	95.00%	R.EQELRDIVANTNDK.L		R.EQELRDIVANTNDK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
123	GLRX6_YEAST	44.16%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
208	219	2	1373.72	0.58	1	51.5	30.8	95.00%	K.LLESLQVWSDGK.F		K.LLESLQVWSDGK.F
85	105	3	2197.17	4.6	1	41.1	28.2	95.00%	K.VGLQQPIASVDDSLSAIKNDK.G		K.VGLQQPIASVDDSLSAIKNDK.G
43	57	2	1544.64	2.4	1	82.2	32.8	95.00%	K.AFSTNMDNMAGGSSR.E		K.AFSTNMDNMAGGSSR.E
70	82	2	1447.67	2.4	0	44	33.4	95.00%	K.GSSEVDEEINEIK.Q		K.GSSEVDEEINEIK.Q
85	102	2	1840	3.9	0	65.6	27	95.00%	K.VGLQQPIASVDDSLSAIK.N		K.VGLQQPIASVDDSLSAIK.N
164	175	2	1438.69	1.9	1	38.9	33.2	95.00%	K.HGHGEELQEYIK.L		K.HGHGEELQEYIK.L
118	133	2	1850.04	-1.2	1	73.8	23.8	95.00%	K.EYSLILDLSPIIIFSK.S		K.EYSLILDLSPIIIFSK.S
181	193	2	1324.75	3.7	0	70.1	25.6	95.00%	R.GTVPNLLVNGVSR.G		R.GTVPNLLVNGVSR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
124	A6ZRM3_YEAS7	20.86%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
149	168	2	2282.16	2	1	111	31.1	95.00%	K.LMTPLTFSTETNFIPQDISK.I		K.LMTPLTFSTETNFIPQDISK.I
109	121	3	1541.86	2.7	1	22	26.3	95.00%	K.VVSYILNHKDQVK.C		K.VVSYILNHKDQVK.C
122	142	3	2450.19	3.6	1	33.6	32.2	95.00%	K.CVLGNHEILVMMAYLNPDFSK.W	Carbamidomethyl (+57)	K.CVLGNHEILVMMAYLNPDFSK.W
273	286	2	1578.76	1.4	1	58	32.7	95.00%	K.VFYGHDASMGLNLR.R		K.VFYGHDASMGLNLR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
125	A6ZZ86_YEAS7	13.87%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
569	584	2	1955	3.1	2	58.4	30.9	95.00%	R.VHELKYEPTQEIIEDI.-		R.VHELKYEPTQEIIEDI.-

288	300	2	1597.76	2.1	2	48.1	33	95.00%	K.RSYTDTSEEIIER.K		K.RSYTDTSEEIIER.K
289	300	2	1441.66	2.6	1	56	33.5	95.00%	R.SYTDTSEEIIER.K		R.SYTDTSEEIIER.K
42	51	2	1224.65	-0.26	0	42.3	30.2	95.00%	K.ITLESHEIQR.A		K.ITLESHEIQR.A
12	38	2	2777.21	2.2	1	104	33.8	95.00%	K.TSQSNVGDAVGNADSVEFNSEHDSPSK.R		K.TSQSNVGDAVGNADSVEFNSEHDSPSK.R
301	315	2	1653.93	2.2	1	74.4	25.2	95.00%	R.KVEELVTLNQSIPGK.N		R.KVEELVTLNQSIPGK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
126	A6ZLA4_YEAS7	25.05%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
263	283	2	1887.96	3.5	0	47	31.3	95.00%	F.AASDGVSGAASAQALGDVTIK.S		R.GSYFVPGSTSNCTFMNNQGGTAGSGVWSSCFGNSISFAASDGVSGAASAQALGDVTIK.S
114	128	3	1677.8	0.024	1	49.8	32.8	95.00%	K.QSIESCKEGEAVVSR.H	Carbamidomethyl (+57)	K.QSIESCKEGEAVVSR.H
386	411	3	2899.38	3.1	1	38.1	32	95.00%	K.LISHIHDGQDGGTQDYFERPTDGTLK.A		K.LISHIHDGQDGGTQDYFERPTDGTLK.A
88	108	2	2308.17	-0.31	1	66	30.3	95.00%	R.GPIELLQFGVYYPNGESNALK.K		R.GPIELLQFGVYYPNGESNALK.K
355	367	2	1574.65	2	1	45.3	33	95.00%	R.TLQYGDASCSCWK.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.TLQYGDASCSCWK.T
368	385	2	1942.88	5.1	1	109	33.8	95.00%	K.TGCGEMDLFEILTAGSDK.L	Carbamidomethyl (+57)	K.TGCGEMDLFEILTAGSDK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
127	A6ZLM5_YEAS7	20.37%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
44	61	2	2092.17	3.3	1	65.6	23.2	95.00%	K.IISLLNVDLFTPCLIFSK.L	Carbamidomethyl (+57)	K.IISLLNVDLFTPCLIFSK.L
225	238	2	1458.67	3.7	1	99.4	33.2	95.00%	R.MNSSFLSSSSIGDK.I		R.MNSSFLSSSSIGDK.I
199	238	3	4596.05	-0.87	2	80.7	29.3	95.00%	R.TPNIDNEELVNEEQEEQELLEENNRMNSSFLSSSSIGDK.I		R.TPNIDNEELVNEEQEEQELLEENNRMNSSFLSSSSIGDK.I
327	335	2	940.61	0.94	0	47.1	20.4	95.00%	K.LLIGSIIGR.M		K.LLIGSIIGR.M
199	224	3	3155.4	0.15	0	53.5	33.1	95.00%	R.TPNIDNEELVNEEQEEQELLEENNR.M		R.TPNIDNEELVNEEQEEQELLEENNR.M
179	198	2	2323.11	1.6	1	53.2	32.6	95.00%	K.WSGENTQHMPPSQVQSLLER.T		K.WSGENTQHMPPSQVQSLLER.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
128	A6ZT03_YEAS7	13.33%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
518	536	2	2149.04	-1.4	1	87.2	32.4	95.00%	K.GLSLEEVNDMYAEGVLPWK.S		K.GLSLEEVNDMYAEGVLPWK.S
262	273	2	1390.73	3.2	1	38.9	30.6	95.00%	R.YLVEAGRIDEAR.A		R.YLVEAGRIDEAR.A
282	304	2	2805.27	1.6	1	83	33.2	95.00%	K.CPPDHPYIQYELETIEASVEEMR.A	Carbamidomethyl (+57)	K.CPPDHPYIQYELETIEASVEEMR.A
228	236	2	1153.52	2.9	1	49.9	32.5	95.00%	K.NYSNSVQWR.V	Deamidation (+1)	K.NYSNSVQWR.V
13	25	2	1508.58	-0.43	1	44.8	32.8	95.00%	K.SNSSNSYELESGR.S	Phospho (+80)	K.SNSSNSYELESGR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
129	ATG27_YEAS7	21.77%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	88	2	1772.92	0.29	1	57.4	30.3	95.00%	K.KNDMLCGLTDVILPGK.D	Carbamidomethyl (+57)	K.KNDMLCGLTDVILPGK.D
119	130	2	1223.56	3.3	1	68.7	32.5	95.00%	K.GATWGANSFDAK.L		K.GATWGANSFDAK.L
89	100	2	1378.7	2.7	1	45.8	31.2	95.00%	K.DAITTQIIDFDK.N		K.DAITTQIIDFDK.N
37	54	2	1948.96	2.4	1	60.3	32.5	95.00%	F.SSLTSTERDTPPSTTIEK.W		K.FSSLTSTERDTPPSTTIEK.W
74	88	2	1644.83	3.8	0	52.8	31.7	95.00%	K.NDMLCGLTDVILPGK.D	Carbamidomethyl (+57)	K.NDMLCGLTDVILPGK.D
36	54	2	2096.03	2.8	1	57.8	32	95.00%	K.FSSLTSTERDTPPSTTIEK.W		K.FSSLTSTERDTPPSTTIEK.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
130	A6ZNJ9_YEAS7	33.14%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

246	262	2	1888.89	3.8	1	57.6	33.7	95.00%	F.ISPTEILQSDANNSNTW.S		R.SSMFISPTEILQSDANNSNTWSQSNESAIYDSLSSTPR.E
172	182	2	1403.62	4	1	40	33.6	95.00%	R.NLENQYQHDPF.Y		R.NLENQYQHDPFYFQTNINDDESETSSHSDDSDISEK.V
242	262	2	2341.06	3.5	1	64.5	33.5	95.00%	R.SSMFISPTEILQSDANNSNTW.S		R.SSMFISPTEILQSDANNSNTWSQSNESAIYDSLSSTPR.E
300	315	3	1795.83	3.8	1	32.4	33.4	95.00%	Y.TSYNLSPDSEDRSTPK.S		K.FTDSTNPFNYTSYNLSPDSEDRSTPK.S
326	341	3	1865.97	4.5	1	24.4	30	93.60%	K.YRPPSVHLDQLLDGKE.-		K.YRPPSVHLDQLLDGKE.-
263	289	3	2915.37	3.6	1	44.2	32.6	95.00%	W.SQSNESAIYDSLSSTPREPGATQILGK.F	Phospho (+80)	R.SSMFISPTEILQSDANNSNTWSQSNESAIYDSLSSTPREPGATQILGK.F
220	241	3	2406.22	4.4	2	26.5	29.3	95.00%	Y.TLGSTSVLNLLNNKTDANDNFR.S		R.MSLYTLGSTSVLNLLNNKTDANDNFR.S
272	289	2	1855.97	2.6	1	47.7	29.4	95.00%	Y.DSLSSTPREPGATQILGK.F		R.SSMFISPTEILQSDANNSNTWSQSNESAIYDSLSSTPREPGATQILGK.F
263	279	2	1840.85	3.1	1	96.1	33.6	95.00%	W.SQSNESAIYDSLSSTPR.E		R.SSMFISPTEILQSDANNSNTWSQSNESAIYDSLSSTPR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
131	A6ZQE5_YEAS7	42.75%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
116	128	2	1414.7	0.62	0	54.4	30.6	95.00%	R.IEDVTPVPSDSTR.K		R.IEDVTPVPSDSTR.K
51	71	2	2179.03	1.7	2	68	33.6	95.00%	K.ADRDESSPYAAMLAAQDVAAK.C		K.ADRDESSPYAAMLAAQDVAAK.C
113	129	3	1869	3.8	1	26.4	27.7	95.00%	R.IGRIEDVTPVPSDSTRK.K		R.IGRIEDVTPVPSDSTRK.K
60	71	2	1158.61	3.9	0	58.5	29.5	95.00%	Y.AAMLAAQDVAAK.C		R.DESSPYAAMLAAQDVAAK.C
113	128	2	1740.91	3.5	1	58.5	29.5	95.00%	R.IGRIEDVTPVPSDSTR.K		R.IGRIEDVTPVPSDSTR.K
10	19	2	1091.54	0.62	1	45.2	30.8	95.00%	R.DNSQVFGVAR.I		R.DNSQVFGVAR.I
94	104	2	1023.55	-0.12	0	50.9	29.9	95.00%	K.TPGPGGQAALR.A		K.TPGPGGQAALR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
132	YJT8_YEAST	9.65%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
298	310	2	1462.77	5.2	1	74.2	29.7	95.00%	Y.AFQAETIELLNSK.I		K.DTYAFQAETIELLNSK.I
311	320	2	1196.66	1.4	1	83.9	25.8	95.00%	K.ISQLVTFYAR.I		K.ISQLVTFYAR.I
31	50	2	2106.98	3.1	1	110	33.5	95.00%	Y.TLQTDELQVGDNEEGFGAGK.S		K.NLIYTLQTDELQVGDNEEGFGAGK.S
397	407	2	1202.67	2.2	1	26.2	28.1	92.70%	K.FTSINNVALPK.L		K.FTSINNVALPK.L
27	50	2	2610.25	3.1	1	68.5	32.3	95.00%	K.NLIYTLQTDELQVGDNEEGFGAGK.S		K.NLIYTLQTDELQVGDNEEGFGAGK.S
353	367	2	1629.84	5	0	62.2	30.6	95.00%	K.DMLGLLSQADELTPK.E		K.DMLGLLSQADELTPK.E
78	89	2	1343.69	1	0	37.4	30.7	95.00%	K.DAGIVEETIELR.E		K.DAGIVEETIELR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
133	A6ZQF7_YEAS7	31.52%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
31	43	2	1459.73	2.7	1	53.3	31.4	95.00%	R.ETAQAINGWELTK.A		R.ETAQAINGWELTK.A
47	56	2	1285.64	1.7	1	50.9	31.4	95.00%	K.YLDQVLDHQR.A		K.YLDQVLDHQR.A
112	124	2	1495.82	1.9	1	64.3	26.8	95.00%	K.LYVSHIQVNQAPK.Q		K.LYVSHIQVNQAPK.Q
114	124	3	1219.67	3.8	0	25	28.8	95.00%	Y.VSHIQVNQAPK.Q		K.LYVSHIQVNQAPK.Q
106	124	3	2081.13	0.4	2	27.8	26.6	95.00%	K.GLDATKLYVSHIQVNQAPK.Q		K.GLDATKLYVSHIQVNQAPK.Q
90	105	2	1643.87	1.5	1	78.4	29.5	95.00%	K.FVQGLLQNAAANAEAK.G		K.FVQGLLQNAAANAEAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
134	YL001_YEAST	7.54%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

400	414	2	1644.75	3.4	1	63.8	33.5	95.00%	Y.APTQIYDSAFCSSAK.R	Carbamidomethyl (+57)	K.IDLEQDFSSLRPIQYAPTQIYDSAFCSSAK.R
836	844	2	984.54	4.2	0	58.6	26.2	95.00%	Y.SVNAIQTPR.D		R.ATTPLIQHSPIIHNPSYSATAHLSPLSQPTFEGSYSVNAIQTPR.D
356	369	2	1635.83	3	1	35.4	31.5	95.00%	K.ITIFVPQASFNEDR.G		K.ITIFVPQASFNEDR.G
247	265	2	2086.16	-0.58	1	58.9	22.6	95.00%	R.TSLLQELIIDDVYGGILPK.E		R.TSLLQELIIDDVYGGILPK.E
523	530	2	930.54	3.5	0	31.4	28	95.00%	K.TALNLLMR.N		K.TALNLLMR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
135	RSP5_YEAST	19.78%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
321	340	2	1973.95	3.5	1	69.5	32.5	95.00%	F.AATGGTTSGLGELPSGWEQR.F		R.TLPGGSSDNSSVTVQVGGGSNIPPVNGAAAAAFAATGGTTSGLGELPSGWEQR.F
91	110	3	2081.02	2.1	0	52	32.1	95.00%	R.VGDVLGHLDEDTATSSGRPR.E		R.VGDVLGHLDEDTATSSGRPR.E
463	474	2	1527.7	-0.67	1	54.1	33.6	95.00%	K.NIFEDAYQEIMR.Q		K.NIFEDAYQEIMR.Q
23	38	2	1750.88	-0.47	1	68.6	31.7	95.00%	R.SPDPFAVLTIDGYQTK.S		R.SPDPFAVLTIDGYQTK.S
721	730	2	1321.53	-0.82	1	36.5	32.8	95.00%	K.CVSEWDNEQR.A	Carbamidomethyl (+57)	K.CVSEWDNEQR.A
138	164	3	2669.23	1.5	0	48	33.3	95.00%	K.LPSSSPHSQAPSGHTASSSTNTSSTTR.T		K.LPSSSPHSQAPSGHTASSSTNTSSTTR.T
259	281	4	2654.3	0.23	1	21.2	31	90.10%	K.RPTLDQTEAERGNQLNANTELER.R		K.RPTLDQTEAERGNQLNANTELER.R
91	116	3	2810.39	2.5	1	24.5	30.5	93.10%	R.VGDVLGHLDEDTATSSGRPREETITR.D		R.VGDVLGHLDEDTATSSGRPREETITR.D
184	209	3	2561.24	3.9	0	63.1	32.4	95.00%	R.GTAQAVESTLQSGTTAATNTATTSHR.S		R.GTAQAVESTLQSGTTAATNTATTSHR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
136	FET4_YEAST	13.77%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
306	316	2	1370.64	-1.9	1	52.2	33	95.00%	R.FLVDIFDMDEK.I		R.FLVDIFDMDEK.I
445	454	2	1132.59	2.7	1	35.9	30.4	95.00%	K.APEINTIGYR.T		K.APEINTIGYR.T
324	340	3	1995.98	4.8	1	38.8	32.5	95.00%	K.HFNDFETPHPVVTIESK.K		K.HFNDFETPHPVVTIESK.K
4	20	3	1884.98	4	1	37	29.7	95.00%	K.IAEFLGNPGARPDVHHR.A		K.IAEFLGNPGARPDVHHR.A
248	265	2	1833.81	-0.4	1	77.2	34.3	95.00%	K.DAGNTPPYTGETTGSNPR.L		K.DAGNTPPYTGETTGSNPR.L
442	454	2	1404.74	3.7	2	40	30.3	95.00%	F.SGKAPEINTIGYR.T		K.EDLELFQELGIECPEEFSGKAPEINTIGYR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
137	A7A0E5_YEAS7	9.22%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
353	383	3	3463.62	0.12	1	57.6	30.8	95.00%	K.NQALGGSLLHSHIQTYPDGSNQQQVTCYGYK.D	Carbamidomethyl (+57)	K.NQALGGSLLHSHIQTYPDGSNQQQVTCYGYK.D
341	352	2	1187.68	2.5	0	40.7	27.3	95.00%	R.DIALGSSVVSIK.N		R.DIALGSSVVSIK.N
106	118	3	1574.77	2.6	1	33.7	33	95.00%	R.HEFYHDVHPPLGK.M		R.HEFYHDVHPPLGK.M
353	380	3	3115.45	3.9	1	45	32.2	95.00%	K.NQALGGSLLHSHIQTYPDGSNQQQVTCY.G	Carbamidomethyl (+57)	K.NQALGGSLLHSHIQTYPDGSNQQQVTCYGYK.D
492	505	2	1574.79	3.9	1	53.5	31.7	95.00%	Y.LAQTGNSLPEWGFR.Q		K.NLEMGCYLAQTGNSLPEWGFR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
138	A6ZQU5_YEAS7	12.79%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
75	85	2	1305.74	4.4	1	54	26.4	95.00%	R.LFDNIIVFPTK.G		R.LFDNIIVFPTK.G
266	285	3	2227.98	3.5	1	58	33.9	95.00%	K.SVHAVHSHADGTSYDEEPYK.I		K.SVHAVHSHADGTSYDEEPYK.I
186	196	2	1248.72	1.2	0	24.5	23.7	94.50%	R.EQIVPILNAPR.T		R.EQIVPILNAPR.T
124	136	2	1489.82	3.7	1	76.7	27.3	95.00%	R.LFLNELGIYPSPK.G		R.LFLNELGIYPSPK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
139	GLRX7_YEAST	27.09%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
130	148	3	2345.21	3.5	1	42.2	29.4	95.00%	Y.VVELDRHEHTKELQDQIEK.V		K.ALLTNSYTFSPSYYVVELDRHEHTKELQDQIEK.V
154	165	2	1212.69	3	0	58.7	25.9	95.00%	R.TVPNVIIGGTSR.G		R.TVPNVIIGGTSR.G
166	176	2	1216.61	2.7	1	45.2	30.9	95.00%	R.GGYTEIAELHK.N		R.GGYTEIAELHK.N
153	165	2	1368.79	2.8	1	33.5	24.4	95.00%	R.RTVPNVIIGGTSR.G		R.RTVPNVIIGGTSR.G
94	105	2	1408.71	2.8	1	37	32	95.00%	K.IMEQSPMIVFSK.T		K.IMEQSPMIVFSK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
140	A6ZSR4_YEAS7	41.18%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
85	93	2	1084.54	-0.11	1	27.9	30.7	91.10%	R.YTLDVEAFK.S		R.YTLDVEAFK.S
35	48	2	1489.79	4.1	1	36.5	30.6	95.00%	K.SHPFGHALVAGIER.Y		K.SHPFGHALVAGIER.Y
94	107	2	1593.77	2.6	1	56.1	32.6	95.00%	K.SVVSTETFEQPSQR.E		K.SVVSTETFEQPSQR.E
94	111	2	2050.99	3.3	1	68.2	33	95.00%	K.SVVSTETFEQPSQREEAK.K		K.SVVSTETFEQPSQREEAK.K
74	84	2	1324.73	2.6	1	36	26.6	95.00%	K.VVNYNHLLPTR.Y		K.VVNYNHLLPTR.Y
35	52	4	1991.08	0.91	2	18.7	26.7	93.90%	K.SHPFGHALVAGIERYPLK.V		K.SHPFGHALVAGIERYPLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
141	A7A244_YEAS7	23.74%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
173	187	2	1696.86	-0.13	1	55.2	31	95.00%	R.VFDIDEALYISDLGK.K		R.VFDIDEALYISDLGK.K
49	66	2	1970.97	3.5	1	56.4	32.4	95.00%	K.EKGEEMGEVANVNEIPVK.I		K.EKGEEMGEVANVNEIPVK.I
101	116	2	1839.84	2.9	2	74.6	33.7	95.00%	F.IAGEELEGNKYCDTNK.D	Carbamidomethyl (+57)	K.ISTAFFIAGEELEGNKYCDTNK.D
469	482	3	1650.88	2.7	1	29.4	28.7	95.00%	K.HPERLEVVDMSVLK.R		K.HPERLEVVDMSVLK.R
81	91	3	1308.79	0.61	1	18.1	20.1	91.50%	R.VKDLLLNRNPK.L		R.VKDLLLNRNPK.L
501	518	2	1994.9	4.2	1	74.7	33.6	95.00%	K.DGYENLTGITSDPDEIEK.I		K.DGYENLTGITSDPDEIEK.I
199	212	2	1611.75	3.6	0	62.7	33.4	95.00%	F.TTDLDNVHDENIAR.S		K.ELQDFAIFTTDLDNVHDENIAR.S
282	302	3	2354.06	4.1	1	27.1	34.2	90.90%	R.SLGYDPICCSGPACGTLHYVK.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.SLGYDPICCSGPACGTLHYVK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
142	A6ZQA2_YEAS7	22.99%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
78	100	2	2591.2	5.5	1	100	33.6	95.00%	R.TDTTYPAGFMDVITLDATNENFR.L		R.TDTTYPAGFMDVITLDATNENFR.L
222	235	2	1576.83	3.7	1	51.7	29.7	95.00%	R.LNNVFVIGEQGKPY.I		R.LNNVFVIGEQGKPYISLPK.G
222	240	2	2115.17	-0.76	1	78	25	95.00%	R.LNNVFVIGEQGKPYISLPK.G		R.LNNVFVIGEQGKPYISLPK.G
180	187	2	863.49	0.1	1	31.3	28.3	95.00%	K.LVYVTGGR.N		K.LVYVTGGR.N
212	221	2	1166.56	3.4	1	31.9	32.1	94.80%	K.DSLDNTFVTR.L		K.DSLDNTFVTR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
143	A7A0C4_YEAS7	24.58%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
245	268	4	2732.42	2.2	1	21	27.9	95.00%	K.TSNLNFNHIINHLSFGKPIQSHSK.L		K.TSNLNFNHIINHLSFGKPIQSHSK.L
234	244	3	1318.6	3.8	1	31.3	32.9	95.00%	Y.GHFHDTSLYDK.T		R.IQGNLHFAPGKPYQNAYGHFHDTSLYDK.T
275	289	2	1491.79	-0.35	1	39.7	30.5	95.00%	K.RHGGAVVATSPLDGR.Q		K.RHGGAVVATSPLDGR.Q
3	14	2	1320.74	3.5	2	25.2	25.3	94.90%	K.RSTLLSLDAFAK.T		K.RSTLLSLDAFAK.T
108	147	3	4129.83	3.8	1	50.2	31	95.00%	R.LNSEGRPVGDATELHVGGNGDGTAPVNNDPNYCGPCYGAK.D	Deamidation (+1)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.LNSEGRPVGDATELHVGGNGDGTAPVNNDPNYCGPCYGAK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
144	A6ZVM1_YEAS7	16.07%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
109	126	2	1896.93	2	1	57.1	32.7	95.00%	K.FTNIASSPPSSSNNIFSK.A		K.FTNIASSPPSSSNNIFSK.A
334	343	2	1015.55	-0.61	0	50.2	29	95.00%	R.ISITASAPEK.S		R.ISITASAPEK.S
248	261	3	1744.85	3.3	2	29.4	32	95.00%	R.DRESNNELYHVITR.N		R.DRESNNELYHVITR.N
317	333	2	1955.98	3.1	0	96.1	32	95.00%	R.VACPLTQNLSENDLINR.I	Carbamidomethyl (+57)	R.VACPLTQNLSENDLINR.I
803	817	3	1763.92	2.3	1	25.6	29.9	95.00%	K.VTRPEGAFNQLEYLK.I		K.VTRPEGAFNQLEYLK.I
615	628	4	1614.83	3.1	1	29.4	30.2	95.00%	R.DRHSISLLHEHSGK.T		R.DRHSISLLHEHSGK.T
629	645	2	2014	-1.7	1	32.2	31.5	95.00%	K.TLNYEILQVFPFNSDSK.R		K.TLNYEILQVFPFNSDSK.R
591	602	2	1240.67	3.5	0	42	27.3	95.00%	Y.QAASPDEIAIVK.F		R.DMILTLAICHNVTPTFEDDELTYQ AASPDEIAIVK.F
735	754	3	2312.24	3.9	1	43	27.3	95.00%	K.YLEHDLELLGLTGVEDKLQK.D		K.YLEHDLELLGLTGVEDKLQK.D
142	155	3	1626.81	4.5	1	38.5	31.6	95.00%	K.FGSPIELSDQHIER.E		K.FGSPIELSDQHIER.E
487	504	2	2049.06	-2.9	2	30.8	30.4	95.00%	R.TSTIPEDLGRIEYLLSDK.T		R.TSTIPEDLGRIEYLLSDK.T
821	836	2	1779.89	-0.11	1	36	32.1	95.00%	R.NACLLIDGESLGMFLK.H	Carbamidomethyl (+57)	R.NACLLIDGESLGMFLK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
145	A6ZQE6_YEAS7	40.77%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
4	19	2	1628.85	5.9	0	78.2	30.2	95.00%	R.SSVLADALNAINNAEK.T		R.SSVLADALNAINNAEK.T
89	97	2	1040.58	3.5	1	26.7	24.7	95.00%	K.WTANLLPAR.Q		K.WTANLLPAR.Q
98	117	3	2237.08	-0.84	1	42.9	32.7	95.00%	R.QFGYVILTTSAGIMDHEEAR.R		R.QFGYVILTTSAGIMDHEEAR.R
2	19	2	1885.98	-1	1	77.8	29	95.00%	M.TRSSVLADALNAINNAEK.T		-.MTRSSVLADALNAINNAEK.T
83	97	2	1695.93	-0.14	2	27.7	26.3	95.00%	K.IGDIEKWTANLLPAR.Q		K.IGDIEKWTANLLPAR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
146	NCB5R_YEAST	32.04%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
183	194	3	1393.76	4.6	1	38.3	27.9	95.00%	F.GNVHEEDILLKK.E		K.VSLVFGNVHEEDILLKK.E
91	102	2	1283.59	-0.87	1	35.3	32.7	95.00%	R.SYTPTSLDGDTK.G		R.SYTPTSLDGDTK.G
37	48	2	1478.76	2.5	2	29.8	31.2	93.30%	K.RNDFQSFPLVEK.T		K.RNDFQSFPLVEK.T
195	208	2	1589.85	2.4	1	37.2	29.2	95.00%	K.ELEALVAMKPSQFK.I		K.ELEALVAMKPSQFK.I
60	80	3	2238.26	4.7	1	32.8	21.9	95.00%	K.FGLPHADDVLGLPIGQHIVIK.A		K.FGLPHADDVLGLPIGQHIVIK.A
147	166	2	2075.04	2.2	1	28.9	31	92.30%	R.SHLGMIAGGTGIAPMYQIMK.A		R.SHLGMIAGGTGIAPMYQIMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
147	B5VE42_YEAST	12.84%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
146	160	2	1574.82	1.8	0	88.2	30.5	95.00%	K.VGQSLSIVSNDELSK.A		K.VGQSLSIVSNDELSK.A
60	70	2	1330.71	1.9	2	63.7	29.5	95.00%	K.KVNVFNINNNR.Y		K.KVNVFNINNNR.Y
235	249	2	1622.78	2.4	1	74.4	32.8	95.00%	K.LQSNGAIQGDSFVCK.N	Carbamidomethyl (+57)	K.LQSNGAIQGDSFVCK.N
61	70	2	1202.62	3.8	1	54.4	30.4	95.00%	K.VNVFNINNNR.Y		K.VNVFNINNNR.Y
234	249	2	1750.87	2.5	2	95.5	32	95.00%	K.KLQSNGAIQGDSFVCK.N	Carbamidomethyl (+57)	K.KLQSNGAIQGDSFVCK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
148	B3LTD0_YEAS1	34.38%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
194	213	3	2015.06	3.1	1	29.1	29.2	95.00%	K.TSAVAALTEVRAEDEAALAK.L		K.TSAVAALTEVRAEDEAALAK.L
81	92	2	1365.69	3	2	32.7	31.8	95.00%	Y.TLDRNTAAETFK.L		K.VPPTIAQFQYTLDRNTAAETFK.L
33	43	2	1157.62	3.3	1	47	29.3	95.00%	K.NFGIGQAVQPK.R		K.NFGIGQAVQPK.R
173	181	2	990.56	3.7	1	28.4	26.4	95.00%	K.MGVPYAIIK.G		K.MGVPYAIIK.G
134	147	3	1612.9	3.3	1	45.2	26.3	95.00%	K.YGLNHVVSLIENKK.A		K.YGLNHVVSLIENKK.A
150	171	3	2450.4	5.6	1	18.1	19.9	91.30%	K.LVLIANDVDPIELVVFLPALCK.K	Carbamidomethyl (+57)	K.LVLIANDVDPIELVVFLPALCK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
149	A7A233_YEAS7	28.37%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	134	2	1964	2.8	0	113	30.6	95.00%	K.TVNEHANDEAQLLLVGNK.S		K.TVNEHANDEAQLLLVGNK.S
71	81	2	1315.65	-0.16	1	49.1	31.4	95.00%	K.LQLWDTAGQER.F		K.LQLWDTAGQER.F

165	178	2	1638.79	-0.51	1	82.5	32.8	95.00%	K.NDDNVNEIFFTLAK.L		K.NDDNVNEIFFTLAK.L
141	152	2	1200.64	0.57	0	50.8	29.6	95.00%	R.VVTADQGEALAK.E		R.VVTADQGEALAK.E
117	140	3	2683.28	-1.3	1	52.3	32	95.00%	K.TVNEHANDEAQLLLVGNKSDMETR.V		K.TVNEHANDEAQLLLVGNKSDMETR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
150	A7A0Y0_YEAS7	24.89%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
140	153	3	1558.83	0.9	1	25.7	29.5	95.00%	R.TKDSNKDVVVEGLR.R		R.TKDSNKDVVVEGLR.R
40	69	3	3354.69	4.6	2	92.8	27.6	95.00%	K.KATVDEFPLCVHLVSNELEQLSSEALEAAR.I	Carbamidomethyl (+57)	K.KATVDEFPLCVHLVSNELEQLSSEALEAAR.I
41	69	3	3226.59	3.2	1	53.9	29.6	95.00%	K.ATVDEFPLCVHLVSNELEQLSSEALEAAR.I	Carbamidomethyl (+57)	K.ATVDEFPLCVHLVSNELEQLSSEALEAAR.I
129	139	2	1245.71	-0.33	1	52.1	26.6	95.00%	R.VDIGQIIFSVR.T		R.VDIGQIIFSVR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
151	B3LJS4_YEAS1	14.22%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
87	104	3	2100.21	2.8	0	22.1	20.9	95.00%	K.ILEPLMENIIHPLLQISK.F		K.ILEPLMENIIHPLLQISK.F
3	33	3	3432.61	2.3	1	85.9	31.2	95.00%	R.SSYQPVSTTNFEHENAIPTASSSHNLLMSQR.F		R.SSYQPVSTTNFEHENAIPTASSSHNLLMSQR.F
248	258	2	1205.57	3.1	1	38.4	31.7	95.00%	K.ENFNPLSSNGK.L		K.ENFNPLSSNGK.L
742	754	2	1472.79	1.4	1	40.2	29.4	95.00%	K.NVLFGPTLIQEDK.S		K.NVLFGPTLIQEDK.S
299	309	2	1226.73	3.2	0	31	25.3	95.00%	K.LVSQQVLIAEK.F		K.LVSQQVLIAEK.F
384	398	2	1477.66	-0.96	0	69.4	33.5	95.00%	R.LSSGGVTVDDGNSDR.S		R.LSSGGVTVDDGNSDR.S
578	593	2	1615.85	2.6	0	39.2	30.3	95.00%	F.LANGIPVSVISSDSTR.N	Deamidation (+1)	R.NAHGNFDISVDNVQHYGDWTPFLANGIPVSVISSDSTR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
152	B3LFU9_YEAS1	18.93%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
287	307	2	2463.19	3.6	2	107	32.1	95.00%	R.ELERELYSPEEDSAAQLVTER.T		R.ELERELYSPEEDSAAQLVTER.T
291	307	2	1935.91	3.3	1	83.2	33.5	95.00%	R.ELYSPEEDSAAQLVTER.T		R.ELYSPEEDSAAQLVTER.T
100	138	4	4322.08	0.13	1	29.7	27.5	95.00%	K.LATVGHEPKPLLPELVENGELLREEEDMIQGGSSAESPR.S	Oxidation (+16)/ Phospho (+80)	K.LATVGHEPKPLLPELVENGELLREEEDMIQGGSSAESPR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
153	A6ZXQ6_YEAS7	17.24%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
180	190	2	1314.68	2.9	1	81.2	30.6	95.00%	K.KIQDIDDEIAR.L		K.KIQDIDDEIAR.L
150	173	2	2430.1	3.2	1	82.2	34	95.00%	K.KNDSVTAEAAAQSGASKDDHGDEK.N		K.KNDSVTAEAAAQSGASKDDHGDEK.N
151	173	3	2302	3.7	1	51.6	33.9	95.00%	K.NDSVTAEAAAQSGASKDDHGDEK.N		K.NDSVTAEAAAQSGASKDDHGDEK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
154	HSP72_YEAST	20.19%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
369	384	2	1516.78	3.8	0	94.9	30.7	95.00%	Y.GAAVQAAILTGDESSK.T		R.SINPDEAVAYGAAVQAAILTGDESSK.T
158	169	2	1198.67	-0.1	0	53.6	27.9	95.00%	K.DAGTIAGLNVLR.I		K.DAGTIAGLNVLR.I
537	547	2	1264.67	2.1	1	31.7	30.2	95.00%	K.NQLESIAYSLK.N		K.NQLESIAYSLK.N
55	69	2	1590.75	0.11	1	56.5	33.2	95.00%	K.NQAAMNPANTVFDAK.R		K.NQAAMNPANTVFDAK.R
170	185	2	1658.89	2.5	1	87.7	28.7	95.00%	R.IINEPTAAAIAYGLDK.K		R.IINEPTAAAIAYGLDK.K
111	124	2	1549.78	-0.72	1	48.9	31.6	95.00%	K.NFTPEQISSMVLGK.M		K.NFTPEQISSMVLGK.M
137	153	2	1893.93	2.7	1	41.2	32.4	95.00%	K.VNDAVVTVPAYFNDSQR.Q		K.VNDAVVTVPAYFNDSQR.Q
20	34	2	1685.81	3.5	1	49.1	32.5	95.00%	F.SNDRVDIIANDQGNR.T		K.AVGIDLGTTYSCVAHFSNDRVDIIANDQGNR.T

35	47	2	1456.69	2.4	1	34.5	33	95.00%	R.TTPSFVGFTDTER.L		R.TTPSFVGFTDTER.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
155	FUI1_YEAST	11.58%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
75	82	2	995.54	3.9	1	29	29.2	94.80%	R.VVEFFEVK.N		R.VVEFFEVK.N
83	98	3	1820.87	2.7	0	26.3	32.6	92.50%	K.NDSTDLADHKPENPIR.T		K.NDSTDLADHKPENPIR.T
236	245	2	1105.59	2.7	1	51.9	30.8	95.00%	K.AIFGTNLNTR.I		K.AIFGTNLNTR.I
109	123	2	1768.9	2.1	1	53.8	31	95.00%	R.STYLYNTDLRPVEAK.R		R.STYLYNTDLRPVEAK.R
112	123	3	1417.76	4.2	1	22.8	29.3	92.20%	Y.LYNTDLRPVEAK.R		R.STYLYNTDLRPVEAK.R
44	68	3	2817.35	-1.2	1	56.5	31.4	95.00%	K.IDANVIEKKDTDSENNITIAQDDEK.V		K.IDANVIEKKDTDSENNITIAQDDEK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
156	A6ZUC1_YEAS7	19.80%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	44	4	4517.28	5.1	1	47.2	26.1	95.00%	M.PTSGTTIELIDDQFPKDDSASSGIVDEVDLTEANILATGLNKK.A		-.MPTSGTTIELIDDQFPKDDSASSGIVDEVDLTEANILATGLNKK.A
376	391	2	1874.94	3	1	88.9	31.4	95.00%	K.FSQNAIEEALIQQEQK.K		K.FSQNAIEEALIQQEQK.K
2	43	4	4389.18	5.1	1	68.1	26.2	95.00%	M.PTSGTTIELIDDQFPKDDSASSGIVDEVDLTEANILATGLNK.K		-.MPTSGTTIELIDDQFPKDDSASSGIVDEVDLTEANILATGLNK.K
426	452	3	2789.51	5	1	74.5	21.7	95.00%	K.GLVIISGIVHDVSGYISEHPGGETLIK.T		K.GLVIISGIVHDVSGYISEHPGGETLIK.T
400	414	2	1783.9	-0.68	1	45.9	31.7	95.00%	K.INWGPVLTDLPMWDK.Q		K.INWGPVLTDLPMWDK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
157	A6ZWS9_YEAS7	16.74%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
95	115	3	2294.16	-0.99	2	27.6	30.6	95.00%	K.SVQNLIAELLSSDKYGDDTVK.F		K.SVQNLIAELLSSDKYGDDTVK.F
6	17	3	1474.73	4.8	1	25.2	32.3	90.90%	K.ILMDSTHFNEIR.S		K.ILMDSTHFNEIR.S
448	460	2	1499.7	-0.21	0	44.9	33.5	95.00%	K.ADIMELLNHSDSR.V		K.ADIMELLNHSDSR.V
95	108	2	1515.82	5.2	0	75.6	28.8	95.00%	K.SVQNLIAELLSSDK.Y		K.SVQNLIAELLSSDK.Y
189	200	2	1442.82	4	1	48.7	26.9	95.00%	R.LLQELAVIPEYR.D		R.LLQELAVIPEYR.D
311	328	2	1951.11	-0.93	0	75.7	23.2	95.00%	K.QLLLLGNALPTVQSLSER.K		K.QLLLLGNALPTVQSLSER.K
444	460	4	1842.9	4.6	1	37.6	32.7	95.00%	K.TGGKADIMELLNHSDSR.V		K.TGGKADIMELLNHSDSR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
158	A6ZUF3_YEAS7	13.49%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
273	287	3	1728.03	2.8	2	27.9	19.8	95.00%	K.LTNEVIKKPLIFSAR.G		K.LTNEVIKKPLIFSAR.G
57	75	2	2078.02	3.1	0	61.7	32.2	95.00%	K.DILSSTPPLHPSEVTEDNK.S		K.DILSSTPPLHPSEVTEDNK.S
55	75	3	2293.15	3.4	1	35.8	31.6	95.00%	W.SKDILSSTPPLHPSEVTEDNK.S		R.AVLVPWLDDDPFEATLLEMGDEPWSKDILSSTPPLHPSEVTEDNK.S
273	284	2	1413.87	3.7	2	31.3	18	95.00%	K.LTNEVIKKPLIF.S		K.LTNEVIKKPLIFSAR.G
167	184	3	1995.98	3.9	1	32.2	32.4	95.00%	K.GPDWLLGEQPEYGTGHIK.K		K.GPDWLLGEQPEYGTGHIK.K
347	355	2	1109.56	-0.2	1	40.7	31.7	95.00%	K.MGLEWLSFK.G		K.MGLEWLSFK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
159	A6ZMK1_YEAS7	32.66%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
158	168	2	1192.55	2.2	1	43.2	32.5	95.00%	R.AVQDNGESAFR.T		R.AVQDNGESAFR.T
46	59	3	1614.01	2.8	0	18.9	13.4	92.90%	K.IAPRPLDLLRPVVR.A		K.IAPRPLDLLRPVVR.A
105	115	2	1332.65	2.5	1	61.1	32.3	95.00%	R.NQEIFDANVQR.L		R.NQEIFDANVQR.L
129	157	3	2952.49	3.9	2	52.5	28.8	95.00%	R.DGKAPEAEQVLSAAATFPIAQPATDVEAR.A		R.DGKAPEAEQVLSAAATFPIAQPATDVEAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
160	RL14A_YEAST	33.33%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	74	2	2050.2	2.6	1	103	18.4	95.00%	R.QAINLGQVVLTPLTFALPR.G		R.QAINLGQVVLTPLTFALPR.G
32	42	2	1211.72	4	0	46	24.2	95.00%	K.LAAIVEIIDQK.K		K.LAAIVEIIDQK.K
110	117	2	921.46	3.4	1	44.3	31.2	95.00%	R.AALTDFER.F		R.AALTDFER.F
56	70	2	1612.93	5.2	1	38.2	24.6	95.00%	R.QAINLGQVVLTPLTF.A		R.QAINLGQVVLTPLTFALPR.G
94	101	2	905.44	4.2	1	32.2	30.2	95.00%	K.WAASSWAK.K		K.WAASSWAK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
161	ATG22_YEAS7	16.29%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
512	525	2	1614.77	0.66	0	67.9	32.6	95.00%	R.EAEELSQVLPESER.R		R.EAEELSQVLPESER.R
62	79	3	1982.87	2.1	0	77.4	34.3	95.00%	K.VHDHSIPCLSETGSDSDK.C	Carbamidomethyl (+57)	K.VHDHSIPCLSETGSDSDK.C
281	296	2	1801.86	-0.73	1	72.2	32.8	95.00%	R.SPYPGEQDALGQLNWK.N		R.SPYPGEQDALGQLNWK.N
2	17	2	1862.81	2.3	1	85.4	34.2	95.00%	M.SYGTINDMNESVTNYR.I		-.MSYGTINDMNESVTNYR.I
189	210	2	2410.15	3.2	1	88.3	32.7	95.00%	K.CQSQGAYEPDKVDSLTTVISGR.G	Carbamidomethyl (+57)	K.CQSQGAYEPDKVDSLTTVISGR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
162	HSP76_YEAST	19.58%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
174	191	2	1728.95	2.3	1	84	27.7	95.00%	R.IINEPTAAAIAYGLGAGK.S		R.IINEPTAAAIAYGLGAGK.S
305	314	2	1166.6	0.65	1	50.4	30.9	95.00%	R.FEDLNAALFK.S		R.FEDLNAALFK.S
544	565	2	2449.29	6.2	2	57	28.1	95.00%	R.QRLESYVASIEQTVTDPVLSSK.L		R.QRLESYVASIEQTVTDPVLSSK.L
456	466	2	1277.65	3	1	43.1	31.4	95.00%	K.ENTLLGEFDLK.N		K.ENTLLGEFDLK.N
115	128	2	1550.8	-0.33	1	36.9	30.6	95.00%	K.TFSPQEISAMVLTK.M		K.TFSPQEISAMVLTK.M
574	603	4	3135.68	3.7	1	37.4	24.3	95.00%	K.IEAALSDALAALQIEDPSADELRKAEVGLK.R		K.IEAALSDALAALQIEDPSADELRKAEVGLK.R
572	597	4	2753.46	4.4	1	56.5	25.9	95.00%	K.SKIEAALSDALAALQIEDPSADELRK.A		K.SKIEAALSDALAALQIEDPSADELRK.A
574	597	3	2538.32	2.7	1	29.1	27.9	95.00%	K.IEAALSDALAALQIEDPSADELRK.A		K.IEAALSDALAALQIEDPSADELRK.A
39	51	2	1477.76	0.046	1	37.6	31.9	95.00%	R.VTPSFVAFTPQER.L		R.VTPSFVAFTPQER.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
163	A6ZUW3_YEAS7	18.06%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
3	12	2	1051.52	1.9	1	28.6	31.3	91.20%	K.VEIDSFSGAK.I		K.VEIDSFSGAK.I
78	91	2	1481.86	2.3	0	48.6	23.1	95.00%	K.AQRPITGASLDLIK.E		K.AQRPITGASLDLIK.E
78	93	3	1767.01	4.1	1	72	24.1	95.00%	K.AQRPITGASLDLIKER.R		K.AQRPITGASLDLIKER.R
1	12	2	1310.66	3.1	2	73.4	31.4	95.00%	-.MKVEIDSFSGAK.I		-.MKVEIDSFSGAK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
164	EMP47_YEAST	18.43%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	127	2	1060.53	4	1	34.5	30.7	95.00%	W.FVQDSNVPR.D		R.SVGYSGQTDGGISFWFVQDSNVPR.D
333	346	2	1637.87	-0.25	1	94.7	29	95.00%	K.VQQELLSFMTTITK.Q		K.VQQELLSFMTTITK.Q
315	326	2	1313.72	2.4	0	81	28	95.00%	K.ILANDINALETK.L		K.ILANDINALETK.L
228	248	2	2222.11	3.9	1	104	31.4	95.00%	R.IGVTAQNGAVNNNAESFEIFK.M		R.IGVTAQNGAVNNNAESFEIFK.M
40	53	2	1562.8	3.4	1	73.7	30.6	95.00%	K.LSSDYSLPDLINAR.K		K.LSSDYSLPDLINAR.K
194	205	2	1436.71	3.5	1	48.1	32.4	95.00%	R.VTYDLEDDNLLK.V		R.VTYDLEDDNLLK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
165	CHS3_YEAST	8.67%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

658	669	2	1456.62	3.6	1	63.5	32.6	95.00%	F.VTCYSEDEEGLR.T	Carbamidomethyl (+57)	K.ATSSPVPGSSLIQSLDSTIIHPDIVQQPPLDFMPYGFPLIHTICFVTCYSEDEEGLR.T
63	85	3	2508.21	4.4	0	35.1	31.7	95.00%	K.TQEQMNHLDVLPSSTGVNPNATR.R		K.TQEQMNHLDVLPSSTGVNPNATR.R
497	511	2	1813.83	1.6	1	92.2	33.9	95.00%	K.HTNDIEDWSNNIQTK.A		K.HTNDIEDWSNNIQTK.A
260	281	2	2338.07	3	1	91.1	34.2	95.00%	R.SGIQDVEVDSDTLYGPWSDAGK.D		R.SGIQDVEVDSDTLYGPWSDAGK.D
917	934	2	1985.98	-1.2	1	53.4	31.9	95.00%	K.GSDGYWVPVLANPDIVER.Y		K.GSDGYWVPVLANPDIVER.Y
686	696	2	1259.7	4.5	0	35.9	27.6	95.00%	K.LLMVVCDGLIK.G	Carbamidomethyl (+57)	K.LLMVVCDGLIK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
166	SSO1_YEAST	26.21%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
63	77	3	1793.95	3.9	1	58.5	29.2	95.00%	K.RLLTEVNEEQASHLR.H		K.RLLTEVNEEQASHLR.H
50	62	3	1568.76	0.27	1	31.9	32.6	95.00%	K.YDHTINQVDSLHK.R		K.YDHTINQVDSLHK.R
78	93	2	1832.91	3.9	1	103	32	95.00%	R.HSLDNFVAQATDLQFK.L		R.HSLDNFVAQATDLQFK.L
206	233	3	3279.57	4.9	1	40.3	30.7	95.00%	K.SMAELTQLFNDMEELVIEQQENVDVIDK.N		K.SMAELTQLFNDMEELVIEQQENVDVIDK.N
46	62	3	2039.99	-0.53	2	49.4	33	95.00%	R.DLDKYDHTINQVDSLHK.R		R.DLDKYDHTINQVDSLHK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
167	A6ZXW5_YEAS7	17.91%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
12	33	5	2499.34	4.1	1	30.6	25.6	95.00%	R.HALLHNDIQTSNNSRPSLVQKK.Y		R.HALLHNDIQTSNNSRPSLVQKK.Y
260	268	2	1153.62	3.6	1	25.6	27.8	92.20%	R.IYNDFITLR.D		R.IYNDFITLR.D
97	106	2	1235.59	-0.083	1	43.9	31.4	95.00%	K.NQEVYSQVNR.I		K.NQEVYSQVNR.I
326	334	2	1046.61	-0.12	1	57.6	25	95.00%	K.SIGELFILR.I		K.SIGELFILR.I
130	142	2	1482.61	-0.52	1	81.8	32.9	95.00%	R.STAYCTASSYNMK.E	Carbamidomethyl (+57)	R.STAYCTASSYNMK.E
46	59	2	1442.67	-1.3	1	53.1	33	95.00%	R.ASYTGSAMINPTSK.Q	Oxidation (+16)	R.ASYTGSAMINPTSK.Q
12	32	3	2371.23	-0.5	0	54.1	28.9	95.00%	R.HALLHNDIQTSNNSRPSLVQK.K		R.HALLHNDIQTSNNSRPSLVQK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
168	A6ZXE1_YEAS7	34.17%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	63	2	1629.85	2.2	0	58.4	29.9	95.00%	K.SIACVLTVINEQQR.E	Carbamidomethyl (+57)	K.SIACVLTVINEQQR.E
13	26	3	1585.91	3.6	1	61.9	24.3	95.00%	K.SKEQLASQLVDLKK.E		K.SKEQLASQLVDLKK.E
91	103	3	1450.77	0.96	2	78.7	30.3	95.00%	R.ALTKFEASQVTEK.Q		R.ALTKFEASQVTEK.Q
15	26	2	1370.78	2.5	1	67.4	27.4	95.00%	K.EQLASQLVDLKK.E		K.EQLASQLVDLKK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
169	MKAR_YEAST	34.29%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
266	278	2	1487.79	3.2	1	27.7	30.7	90.70%	R.SSLMIPNPQQFVK.S		R.SSLMIPNPQQFVK.S
95	115	4	2458.33	4.8	1	22.9	25.5	95.00%	R.TQSKLEALQKELEDQHHVVVK.I		R.TQSKLEALQKELEDQHHVVVK.I
168	187	2	2164.28	-1.9	0	67.3	16.9	95.00%	R.NIITINNTATLLITQIIAPK.I		R.NIITINNTATLLITQIIAPK.I
134	164	3	3460.81	4.8	1	24.6	25	95.00%	K.ELCAQLPITVLVNNVGQSHSIPVPFLETEEK.E	Carbamidomethyl (+57)	K.ELCAQLPITVLVNNVGQSHSIPVPFLETEEK.E
228	243	2	1722.86	-0.76	1	66.2	31.9	95.00%	K.SFLQGWSNSLAGELSK.D		K.SFLQGWSNSLAGELSK.D
116	133	3	2050.05	3.6	2	46.8	30.4	95.00%	K.ILAIDIAEDKESNYESIK.E		K.ILAIDIAEDKESNYESIK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
170	A6ZWC1_YEAS7	21.55%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
144	152	2	1059.61	0.74	1	62.7	26.8	95.00%	K.VFLDIGLQR.T		K.VFLDIGLQR.T
146	152	2	813.47	4.2	0	29.1	26.6	95.00%	F.LDIGLQR.T		K.VFLDIGLQR.T

159	172	2	1353.7	4.4	2	37.6	29.9	95.00%	R.VFGALKGASDGGLY.V		R.VFGALKGASDGGLYVPHSENR.F
225	248	3	2652.23	5.1	1	32.6	32.9	95.00%	K.GYLADDIDADSLEDIYTSAHEAIR.A		K.GYLADDIDADSLEDIYTSAHEAIR.A
180	196	2	2091.98	-0.88	1	61.7	33	95.00%	R.FPGWDFETEEIDPELLR.S		R.FPGWDFETEEIDPELLR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
171	A6ZLU0_YEAS7	24.04%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
179	208	3	3096.75	2.6	0	21.6	22.9	95.00%	K.HLGIVAGGSGITPVLQILNEIITVPEDLTK.V		K.HLGIVAGGSGITPVLQILNEIITVPEDLTK.V
250	259	2	1138.57	3	1	36.9	32.3	95.00%	R.WTGDVGYITK.D		R.WTGDVGYITK.D
275	292	2	1990	-1.2	1	60.2	31.9	95.00%	R.LLICGPDGMNNLALQYAK.E	Carbamidomethyl (+57)	R.LLICGPDGMNNLALQYAK.E
96	112	4	1870.02	-0.74	1	46.1	28.3	95.00%	K.TRLESLDIPAGHHVAVR.V		K.TRLESLDIPAGHHVAVR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
172	A6ZR09_YEAS7	28.93%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
92	102	2	1316.77	0.66	1	33.2	24.4	95.00%	R.AFLIEEQKIVK.K		R.AFLIEEQKIVK.K
44	60	3	1846.89	4.2	0	58.8	32.9	95.00%	K.CGDCGSALQGISTLRPR.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CGDCGSALQGISTLRPR.Q
25	31	2	712.42	-0.46	0	24.7	24.1	94.70%	K.TPGGILR.A		K.TPGGILR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
173	B5VGM1_YEAST	22.89%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
106	126	4	2515.21	5.7	1	23.1	32.2	92.00%	R.VSETPELSPQDVDWILHEHER.R		R.VSETPELSPQDVDWILHEHER.R
127	147	3	2494.96	-0.56	2	46.4	33.9	95.00%	R.RYSSVCNSDNEEASQSNTPDR.I	Carbamidomethyl (+57)/ Phospho (+80)	R.RYSSVCNSDNEEASQSNTPDR.I
77	98	3	2607.13	3.3	1	37.2	34.1	95.00%	Y.LGNIDEEPDLYYHDEEDGELSR.T		R.SLTDDFGSNVHEPNPYLGNIDEEPDLYYHDEEDGELSR.T
128	147	2	2338.86	-2.1	1	78.5	33	95.00%	R.YSSVCNSDNEEASQSNTPDR.I	Carbamidomethyl (+57)/ Phospho (+80)	R.YSSVCNSDNEEASQSNTPDR.I
198	226	3	3199.55	5	1	27.9	31.1	95.00%	R.GSVPTIYQEIDENDSEALAELAHSHVTFK.S		R.GSVPTIYQEIDENDSEALAELAHSHVTFK.S
155	164	2	1344.57	1.2	1	30.5	32.8	92.00%	R.ELEYDEFMNR.L		R.ELEYDEFMNR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
174	A6ZQL2_YEAS7	29.26%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
172	188	3	2034.07	3.6	2	58	29.6	95.00%	R.HETKDPVVNNTHIIVYR.E		R.HETKDPVVNNTHIIVYR.E
160	171	2	1329.74	-0.24	1	37.1	28	95.00%	K.VFGINLNDLVAR.H		K.VFGINLNDLVAR.H
17	41	2	2635.35	2.6	1	51	29.1	95.00%	K.NAPSVPQVDASLDKPLDIDAPPTIY.S		K.NAPSVPQVDASLDKPLDIDAPPTIYSVNLKPEYGTAALNLSADFIR.Q
225	240	3	1826.92	-0.54	1	28.9	31	95.00%	K.SGIIEDLIDWAMLHSK.N		K.SGIIEDLIDWAMLHSK.N
42	62	3	2278.21	4.2	1	20.8	28.1	90.40%	Y.SVNLKPEYGTAALNLSADFIR.Q		K.NAPSVPQVDASLDKPLDIDAPPTIYSVNLKPEYGTAALNLSADFIR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
175	A6ZQR6_YEAS7	47.77%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
69	86	3	2038.05	3.3	1	36.1	29.7	95.00%	K.KLEDLSPSTHNMEVPVVK.R	Oxidation (+16)	K.KLEDLSPSTHNMEVPVVK.R
2	28	3	3110.27	3.1	1	32.1	33.4	95.00%	M.SDEEHTFETADAGSSATYPMQCSALRK.N	Acetyl (+42)/ Phospho (+80)/ Carbamidomethyl (+57)	-.MSDEEHTFETADAGSSATYPMQCSALRK.N
57	68	2	1311.76	-0.015	1	35.4	25.6	95.00%	K.VHLVAIDIFTGK.K		K.VHLVAIDIFTGK.K

115	132	2	1862.86	4	1	58.2	33.9	95.00%	K.APEGELGDSLQTAFDEGK.D		K.APEGELGDSLQTAFDEGK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
176	A6ZSL9_YEAS7	31.39%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
58	78	2	2261.09	3.8	0	125	32.1	95.00%	R.QDVIDSLTQICDSNPAISASK.L	Carbamidomethyl (+57)	R.QDVIDSLTQICDSNPAISASK.L
14	27	2	1518.82	0.78	0	81.2	29.1	95.00%	K.AISLETQTESLLSK.Y		K.AISLETQTESLLSK.Y
155	163	2	1102.58	3.3	1	43.7	30.1	95.00%	R.LISQAWETR.S		R.LISQAWETR.S
28	44	2	1891.84	-0.95	1	100	34.6	95.00%	K.YSTFAQTTSSEQTGQEK.K		K.YSTFAQTTSSEQTGQEK.K
49	78	3	3255.66	5.6	1	37	26.4	95.00%	K.QLEGILGQRQDVIDSLTQICDSNPAISASK.L	Carbamidomethyl (+57)	K.QLEGILGQRQDVIDSLTQICDSNPAISASK.L
49	57	2	1012.57	4	0	23.4	25.3	92.70%	K.QLEGILGQR.Q		K.QLEGILGQR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
177	A7A1B6_YEAS7	14.66%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
154	163	2	1225.58	-0.063	1	57.4	32.5	95.00%	K.YVECSALTQR.G	Carbamidomethyl (+57)	K.YVECSALTQR.G
167	184	2	1952.11	4	1	75.3	24	95.00%	K.NVFDEAIVAALEPPVIKK.S		K.NVFDEAIVAALEPPVIKK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
178	A6ZM36_YEAS7	45.21%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	16	2	1781.95	4.1	1	69.5	28.2	95.00%	M.SLVVQEQGSFQHILR.L	Acetyl (+42)	-.MSLVVQEQGSFQHILR.L
89	108	3	2261.06	2.7	2	33.3	33.2	95.00%	R.QNDITDGKDYHTLANNVESK.L		R.QNDITDGKDYHTLANNVESK.L
81	88	2	1015.56	1.8	1	49	30.3	95.00%	K.IPAWFLNR.Q		K.IPAWFLNR.Q
69	80	3	1470.77	3.6	1	33.8	29.8	95.00%	R.IVQIMQNPTHYK.I		R.IVQIMQNPTHYK.I
17	27	2	1199.65	1.2	0	25.2	28.2	90.50%	R.LLNTNVDGNIK.I		R.LLNTNVDGNIK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
179	A6ZL12_YEAS7	5.91%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
24	38	2	1575.68	-0.074	1	102	33.6	95.00%	R.SFSAGNNFQSSSSEK.T		R.SFSAGNNFQSSSSEK.T
405	417	2	1447.75	3.4	1	51.6	31.2	95.00%	R.LICSLAQQGYAPK.F	Carbamidomethyl (+57)	R.LICSLAQQGYAPK.F
489	496	2	923.46	1.4	1	33.2	30.8	95.00%	R.SLDELGYK.A		R.SLDELGYK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
180	A6ZP92_YEAS7	11.16%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
433	454	2	2362.2	-1	1	68.5	30.8	95.00%	K.ADFLVPGENQVTPSSTPYISLK.V		K.ADFLVPGENQVTPSSTPYISLK.V
179	189	2	1294.64	3	1	61.2	32	95.00%	K.AYESLTDELVR.Q		K.AYESLTDELVR.Q
511	521	2	1310.58	2	1	40.8	32.4	95.00%	R.GSWCCLVSSQK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GSWCCLVSSQK.D
403	414	2	1269.73	2.7	1	34.7	24.7	95.00%	K.IGEVLGIKDQAK.L		K.IGEVLGIKDQAK.L
195	212	3	1888.93	4.3	1	35.8	32.5	95.00%	K.YGHPDGPQSTSHGIALPR.F		K.YGHPDGPQSTSHGIALPR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
181	A6ZS95_YEAS7	18.56%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
249	259	2	1170.67	4.5	0	41.7	27.6	95.00%	Y.EVLSQAGNLLK.Y		K.LPNNFVYMSDVNQLSGFMFHYSKPYEVLSQAGNLLK.Y
73	89	2	1930.99	-0.94	1	32.7	30.7	95.00%	R.GNQIFQSLHSFLANDLK.F		R.GNQIFQSLHSFLANDLK.F
16	32	2	1938.94	2.8	1	94.5	32.5	95.00%	R.VNSLNAPYQALSYDEQK.A		R.VNSLNAPYQALSYDEQK.A
208	223	2	1867.87	3.7	1	74.3	33.1	95.00%	R.TENYFLSIAHTSENDK.L		R.TENYFLSIAHTSENDK.L
2	15	2	1551.79	-0.9	1	59.9	31.3	95.00%	M.SSSIFGPLTGFLER.V	Acetyl (+42)	-.MSSSIFGPLTGFLER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
182	A6ZZH5_YEAS7	17.49%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

230	242	2	1526.77	3.1	1	45.7	31.4	95.00%	K.HNVDAPIPNFFTR.N		K.HNVDAPIPNFFTR.N
148	169	2	2362.16	3.4	1	79.7	32	95.00%	Y.QYPSQPALSTSIPSQAPSFSNR.K		K.WTNDHPSSPSQYQYPSQPALSTSIPSQAPSFSNR.K
148	170	3	2490.26	5	1	24.2	30.1	93.30%	Y.QYPSQPALSTSIPSQAPSFSNRK.R		K.WTNDHPSSPSQYQYPSQPALSTSIPSQAPSFSNRK.R
68	112	5	4769.36	3.3	0	27.9	26.6	95.00%	K.KPPLLVNNEAVHASVPDASHTSCNNGTLEVSINNPEPHVVDAVAR.H	Deamidation (+1)/ Carbamidomethyl (+57)	K.KPPLLVNNEAVHASVPDASHTSCNNGTLEVSINNPEPHVVDAVAR.H
117	131	2	1598.81	2.6	0	88.2	31.4	95.00%	R.NPSNSLQLQGGDITR.D		R.NPSNSLQLQGGDITR.D
583	596	2	1562.77	-0.081	1	47.3	32.7	95.00%	R.ILENWTFPSNASGK.Y		R.ILENWTFPSNASGK.Y
355	365	2	1124.49	0.52	1	51	32.3	95.00%	K.VGVDGYGDMGR.I		K.VGVDGYGDMGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
183	A6ZRQ7_YEAS7	27.08%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	76	3	1481.91	3	1	42.7	19.2	95.00%	R.RINELTLLVQKR.F		R.RINELTLLVQKR.F
201	223	2	2458.37	3.2	1	58.2	23.1	95.00%	K.ALPDAVTIIEPKEEEPILAPSVK.D		K.ALPDAVTIIEPKEEEPILAPSVK.D
28	40	2	1436.68	2.6	1	80.9	32.7	95.00%	R.ELAEEGYSGVEVR.V		R.ELAEEGYSGVEVR.V
224	240	2	1903.85	3.3	1	62.2	33.9	95.00%	K.DYRPAEETEAQAEPVEA.-		K.DYRPAEETEAQAEPVEA.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
184	A6ZSS5_YEAS7	62.20%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	17	2	1718.94	2.7	0	46	28.1	95.00%	M.VLVQDLLHPTAASEAR.K		-.MVLVQDLLHPTAASEAR.K
48	70	3	2451.09	4.1	0	67.6	33.7	95.00%	F.SHAQTAVTCESCSTVLCTPTGGK.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CPGCLNITTVFSHAQTAVTCESCSTVLCTPTGGK.A
2	18	3	1847.03	0.6	1	28	24.9	95.00%	M.VLVQDLLHPTAASEARK.H		-.MVLVQDLLHPTAASEARK.H
37	70	3	3713.67	1.9	1	42.9	31.9	95.00%	K.CPGCLNITTVFSHAQTAVTCESCSTVLCTPTGGK.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CPGCLNITTVFSHAQTAVTCESCSTVLCTPTGGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
185	A6ZU59_YEAS7	21.65%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
142	157	2	1728.86	1.2	1	68.1	31.4	95.00%	R.GYWGTNLGQPHSLATK.T		R.GYWGTNLGQPHSLATK.T
50	64	2	1739	5	1	42.1	22.8	95.00%	K.ITTIEEIFLHSLPVK.E		K.ITTIEEIFLHSLPVK.E
65	88	3	2767.49	3.7	1	23.7	24	95.00%	K.EFQIIDTLLPGLQDEVMNIKPVQK.Q		K.EFQIIDTLLPGLQDEVMNIKPVQK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
186	B3LJW5_YEAS1	20.92%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	131	3	3568.81	4.7	2	40.1	26.3	95.00%	F.DLLNALIEEGHLDPEAPDKLLENSGPDVPFSPK.L		K.SLINFPQEQQQNGSTSTATFDLLNALIEEGHLDPEAPDKLLENSGPDVPFSPK.L
132	140	2	1086.58	3.7	1	37.4	30.2	95.00%	K.LNELLGDWK.H		K.LNELLGDWK.H
8	19	2	1468.69	3.5	1	58.8	33.3	95.00%	K.VSSMQNFEMIQR.E		K.VSSMQNFEMIQR.E
141	164	3	2664.36	2.8	1	34.2	29.3	95.00%	K.HQSGIGQEALRNEDVALIVDEIMK.R		K.HQSGIGQEALRNEDVALIVDEIMK.R
20	32	3	1628.93	0.13	2	34.5	25.5	95.00%	R.ERLPTLYEVLIQR.T		R.ERLPTLYEVLIQR.T
152	164	2	1487.76	5	0	54.3	31.1	95.00%	R.NEDVALIVDEIMK.R		R.NEDVALIVDEIMK.R
99	117	2	2088.05	4.5	0	54	31.3	95.00%	F.DLLNALIEEGHLDPEAPDK.L		K.SLINFPQEQQQNGSTSTATFDLLNALIEEGHLDPEAPDK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

187	A6ZVR3_YEAS7	10.56%		100%		5						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
611	621	2	1203.65	3.7	1	38.1	29.6	95.00%	R.EAFVSLNIPSK.A		R.EAFVSLNIPSK.A	
578	586	2	984.59	1	0	25.3	22.4	95.00%	K.IGDVIIIDK.S		K.IGDVIIIDK.S	
216	246	3	3443.61	4.2	1	64.6	30.8	95.00%	R.QLAVDDINTGHVNCESNPTICEELGFGDLVK.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.QLAVDDINTGHVNCESNPTICEELGFGDLVK.I	
433	442	2	1203.6	0.068	1	29.9	31.1	93.60%	R.NIDAIMDWVK.K		R.NIDAIMDWVK.K	
493	505	3	1642.85	4.1	1	27.1	30.3	95.00%	K.NLLLASWEYEHIR.M		K.NLLLASWEYEHIR.M	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
188	A6ZMI1_YEAS7	20.10%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
82	96	3	1730.91	3.8	2	56.5	29.2	95.00%	Y.GKPTNQGVNELKYQR.S		K.GATYGKPTNQGVNELKYQR.S
129	140	2	1486.79	2.6	1	55.5	30.5	95.00%	K.YFEVILVDPQHK.A		K.YFEVILVDPQHK.A
148	157	2	1330.61	1.1	1	32.8	32.8	95.00%	R.YNWICNPVHK.H	Carbamidomethyl (+57)/ Deamidation (+1)	R.YNWICNPVHK.H
78	93	2	1675.85	-0.66	1	74.7	31.1	95.00%	K.GATYGKPTNQGVNELK.Y		K.GATYGKPTNQGVNELK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
189	OST1_YEAST	10.08%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
114	134	2	2344.27	2.3	1	45.6	25.9	95.00%	R.YGIIQFPNAISPQEEVSLVIK.S		R.YGIIQFPNAISPQEEVSLVIK.S
225	238	4	1616.89	3.6	1	20.5	27.3	95.00%	Y.SHNAPLNQVVNLRR.D		R.FSSNETLAIVYSHNAPLNQVVNLRR.D
159	171	2	1506.77	3.2	2	53.8	31.3	95.00%	W.ETNRLPLSAYDTK.K		K.SFYNTVGIPYPEHVGMSEEQHLLWETNRLPLSAYDTK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
190	A6ZPU2_YEAS7	12.32%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
365	387	3	2442.3	1.8	1	57.7	26.9	95.00%	K.VLQDSGLEKKDVDDIVLVGGSTR.I		K.VLQDSGLEKKDVDDIVLVGGSTR.I
206	217	2	1198.67	-0.1	0	53.6	27.9	95.00%	K.DAGTIAGLNVLR.I		K.DAGTIAGLNVLR.I
218	233	2	1644.88	2.9	1	64.2	29.2	95.00%	R.IVNEPTAAAIAYGLDK.S		R.IVNEPTAAAIAYGLDK.S
103	117	2	1671.86	3.2	1	66	30.4	95.00%	K.NQVAANPQNTIFDIK.R		K.NQVAANPQNTIFDIK.R
327	344	2	2022.02	3.6	1	101	31.3	95.00%	R.IEIDSFVDGIDLSETLTR.A		R.IEIDSFVDGIDLSETLTR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
191	A7A0U9_YEAS7	15.45%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
535	554	2	2285.19	2.3	1	70.3	29.3	95.00%	R.MIEIMLPVFDAPQNLVEQAK.L		R.MIEIMLPVFDAPQNLVEQAK.L
234	249	2	1776.96	4.7	1	64.4	28.3	95.00%	K.LIDLTQFPAFVTPMGK.G		K.LIDLTQFPAFVTPMGK.G
259	273	2	1595.86	-0.13	1	42	28.8	95.00%	R.YGGVYVGTLSKPEVK.E		R.YGGVYVGTLSKPEVK.E
155	179	3	2741.52	2.7	1	33.8	21.8	95.00%	R.TTYVTQRPVYLGLPANLVDLNVPAK.L		R.TTYVTQRPVYLGLPANLVDLNVPAK.L
199	209	2	1212.73	-0.097	0	38	22.9	95.00%	K.EVIDTILALVK.D		K.EVIDTILALVK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
192	A6ZQS1_YEAS7	18.12%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
24	34	2	1038.54	4.4	1	47.5	31	95.00%	F.TSLGAAYGTAK.S		-.MTELCPVYAPFFGAIGCASAIIFTSLGAAYGTAK.S
35	52	2	2005.06	3.1	1	55.3	29.2	95.00%	K.SGVGICATCVLRPDLLFK.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.SGVGICATCVLRPDLLFK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
193	A6ZLD1_YEAS7	23.75%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

140	160	2	2274.18	2.1	1	45.2	29.3	95.00%	R.IVSTEGNVPQTLAPVPYETFI.-		R.IVSTEGNVPQTLAPVPYETFI.-
101	108	3	1136.54	0.11	2	25.3	32.1	91.70%	K.CRQEFLER.V	Carbamidomethyl (+57)	K.CRQEFLER.V
70	78	2	915.54	0.097	0	48.2	26.3	95.00%	K.SSVGVIINK.M		K.SSVGVIINK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
194	A6ZQF2_YEAS7	25.59%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
291	306	2	1683.82	3.5	1	50.2	32.7	95.00%	K.IIIPHDADGNIDASSF.V		K.IIIPHDADGNIDASSFVIANDFYGK.A
16	24	2	1079.51	-0.11	1	28.5	31.9	90.00%	R.SVGSQWFNR.L		R.SVGSQWFNR.L
83	95	4	1542.89	1.1	1	28.3	23.2	95.00%	R.LIYPHVEHVPVLK.Q		R.LIYPHVEHVPVLK.Q
389	400	2	1350.62	2.9	1	90.1	32.6	95.00%	Y.HYNEGDLAASFK.G		K.VLASQYDASLGQEGESGNGASNGDVYHYNEGDLAASFK.G
114	129	3	1897.02	3.9	1	54	28.2	95.00%	K.RLILKPEENALTDEEK.K		K.RLILKPEENALTDEEK.K
61	82	3	2263.09	0.71	1	48	32.3	95.00%	R.SAGASYSPSHGLYINEIPASSR.L		R.SAGASYSPSHGLYINEIPASSR.L
261	268	2	915.55	1.2	0	29.7	27.4	95.00%	K.IMDLALLK.N		K.IMDLALLK.N
316	327	2	1414.79	4.2	1	53.1	27.8	95.00%	K.ALIDYLNDPLLR.N		K.ALIDYLNDPLLR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
195	A6ZQ10_YEAS7	14.17%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
157	173	3	1756.97	0.0023	2	31.2	27.2	95.00%	R.SSGKLPPGFEIVQALSK.K		R.SSGKLPPGFEIVQALSK.K
464	477	2	1280.63	4.1	0	33.4	32.2	95.00%	F.AAGEVSGGVHGANR.L		K.NSESVLSNGIFAAGEVSGGVHGANR.L
478	491	2	1464.76	-0.67	1	39.2	30.3	95.00%	R.LGGSSLLECVVFGK.T	Carbamidomethyl (+57)	R.LGGSSLLECVVFGK.T
427	436	2	1082.58	4.6	1	33.3	28	95.00%	Y.VGEVTPVVHF.T		K.DISTESTVYVGEVTPVVHFTMGGVK.I
380	395	2	1837.94	6.5	1	57.2	30.4	95.00%	R.QYDLQTTASELVTELK.S		R.QYDLQTTASELVTELK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
196	A6ZLM1_YEAS7	7.14%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	69	2	1619.83	2	1	40.5	30.8	95.00%	K.ATTPNVNDPIYFLR.G		K.ATTPNVNDPIYFLR.G
6	26	3	2414.45	3.6	1	44	16.5	95.00%	R.LIDIVKPILPILPEVELPFEK.L		R.LIDIVKPILPILPEVELPFEK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
197	AVT7_YEAST	10.82%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
321	346	2	2748.3	3.6	1	50.4	32.5	95.00%	R.ASNLRPISMTVEDPAQPSDALDATSY.N		R.ASNLRPISMTVEDPAQPSDALDATSYNEQECLLPNGNFDNGSIESQENNNDER.G
441	451	2	1098.67	3.2	0	55.7	24.1	95.00%	K.LIGLDSLAIGK.M		K.LIGLDSLAIGK.M
1	16	2	1650.81	-1.1	0	80.9	32.5	95.00%	-.MEATSSALSSTANLVK.T	Acetyl (+42)	-.MEATSSALSSTANLVK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
198	A6ZU02_YEAS7	8.12%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
478	491	2	1607.89	3.7	1	56.7	23.8	95.00%	K.EVEKDAVTNIHLLK.R		K.EVEKDAVTNIHLLK.R
482	491	2	1122.64	2.5	0	38.2	26.4	95.00%	K.DAVTNIHLLK.R		K.DAVTNIHLLK.R
62	75	2	1489.76	3.1	1	91.9	30.9	95.00%	K.KVDAMGVESTGIQR.I		K.KVDAMGVESTGIQR.I
459	477	2	1959.98	2.5	1	88.9	31.5	95.00%	K.EFPTVTGEINGPELVGSSK.E		K.EFPTVTGEINGPELVGSSK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
199	A6ZRP5_YEAS7	9.11%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

102	128	3	3130.45	5.1	1	39.9	31.9	95.00%	R.QRPPPATAEYNDVFNTNSQQLPSEHQY.N		R.QRPPPATAEYNDVFNTNSQQLPSEHQYNNVPSYPLPSINVIQTTPELIHNGSQTMATPIERPFFNENDYYYNNR.N
418	431	2	1649.78	2.4	1	56.7	32.7	95.00%	R.YQAVTCEPNQLAEK.N	Carbamidomethyl (+57)	R.YQAVTCEPNQLAEK.N
419	431	2	1486.71	2.2	0	39	32.4	95.00%	Y.QAVTCEPNQLAEK.N	Carbamidomethyl (+57)	R.YQAVTCEPNQLAEK.N
642	655	2	1634.87	4.3	1	73.2	29.6	95.00%	K.LLNPLVASQNFEYK.M		K.LLNPLVASQNFEYK.M
335	351	2	1575.78	1.3	0	80.4	31.9	95.00%	F.QANGVPASSSVSSIGSK.E	Deamidation (+1)	K.LQFQANGVPASSSVSSIGSK.E
394	414	2	2383.16	2.9	1	68.7	32.1	95.00%	K.TLLDQYATTTENANTLPNEFK.F		K.TLLDQYATTTENANTLPNEFK.F
709	718	2	1184.52	4.5	1	35.8	32.2	95.00%	F.SSNMYLAEDR.I		K.YFYGEIMENEGFHFFSSNMYLAEDR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
200	A6ZWW2_YEAS7	27.67%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
241	277	4	4060.97	5.9	1	50.3	27.9	95.00%	R.SHITLGSSILDGLDDEDDEHNQVLNKDADDNLITAIR.A		R.SHITLGSSILDGLDDEDDEHNQVLNKDADDNLITAIR.A
48	57	2	1213.52	3.9	0	37	32.3	95.00%	Y.CVMTSLTCDK.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GSDGCVVCDSTASCPVCASGEYCVMTSLTCDK.C
282	314	4	3769.79	5.7	1	35.3	29.7	95.00%	K.LVQIAEEESDKEIQDLDVIEEQTEADDLSHMAK.S		K.LVQIAEEESDKEIQDLDVIEEQTEADDLSHMAK.S
201	221	2	2116.14	-0.19	1	69.1	27	95.00%	R.ASNILPIAYIPGVTSGLSTDK.L		R.ASNILPIAYIPGVTSGLSTDK.L
241	266	3	2863.35	0.32	0	85.8	31.9	95.00%	R.SHITLGSSILDGLDDEDDEHNQVLNK.D		R.SHITLGSSILDGLDDEDDEHNQVLNK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
201	YIL7_YEAST	13.84%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	205	2	1566.83	-0.97	1	44.7	29.2	95.00%	R.NSLFISPTGDILYK.T		R.NSLFISPTGDILYK.T
175	191	2	1966	4.7	1	42.2	31.1	95.00%	F.LSNFERPLFSLASESNR.N		K.DALVSHTNNEKPFLSNFERPLFSLASESNR.N
273	285	2	1466.64	-0.44	0	42.9	32.9	95.00%	K.LLNSPESDGSVNR.N	Phospho (+80)	K.LLNSPESDGSVNR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
202	A6ZSA1_YEAS7	26.30%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
40	67	3	3024.46	2.8	1	42.6	30.9	95.00%	K.YAPDPPITHNVNIGIVFTDPESSEEAGR.L		K.YAPDPPITHNVNIGIVFTDPESSEEAGR.L
193	219	5	3023.54	2.2	2	23.4	28	95.00%	K.LANVKTDENGKPEQPITIGYISSQEHR.V		K.LANVKTDENGKPEQPITIGYISSQEHR.V
234	244	2	1322.6	-0.62	1	39.4	32.3	95.00%	R.LQDYQNGDLEK.G	Deamidation (+1)	R.LQDYQNGDLEK.G
198	219	3	2498.21	2	1	36.6	32.2	95.00%	K.TDENGKPEQPITIGYISSQEHR.V		K.TDENGKPEQPITIGYISSQEHR.V
137	151	2	1768.9	2.8	0	46	30.9	95.00%	K.LPEENHSLIHDRPGR.V		K.LPEENHSLIHDRPGR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
203	ARN2_YEAST	7.22%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	14	2	1675.79	9.1	1	37	33.1	95.00%	-.MIEVPEDNRSSQTK.R	Acetyl (+42)/ Deamidation (+1)	-.MIEVPEDNRSSQTK.R
601	611	2	1314.61	-0.78	1	33	32.7	95.00%	K.EDDPINDWIAK.R		K.EDDPINDWIAK.R
339	348	2	1101.66	0.6	1	27.6	24	95.00%	R.LALVPFAPFK.L		R.LALVPFAPFK.L
536	546	2	1238.68	3.9	1	41.9	26.5	95.00%	F.ILSNPWGTPVR.S		K.LLHYMGDADLATAAYGSPLTFILSNPWGTPVR.S
1	9	2	1101.51	0.065	0	37.9	32.1	95.00%	-.MIEVPEDNR.S		-.MIEVPEDNR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
204	A7A0W1_YEAS7	8.77%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	19	2	2263.12	4.8	1	93.4	31.7	95.00%	-.MDLVLEVADHYVLDDLYAK.V	Acetyl (+42)	-.MDLVLEVADHYVLDDLYAK.V

20	32	2	1291.79	2.3	0	26.6	16.9	95.00%	K.VLPASLAANIPVK.W		K.VLPASLAANIPVK.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
205	A6ZQ73_YEAS7	9.71%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
235	249	3	1645.87	-0.13	2	34.5	30.6	95.00%	K.SIESLADRVGFPLDK.I		K.SIESLADRVGFPLDK.I
41	61	3	2454.23	4	2	57	31	95.00%	K.LSETKLPPVLEDEIDDETFHK.S		K.LSETKLPPVLEDEIDDETFHK.S
409	416	2	912.57	3	0	29.2	24.7	95.00%	R.ALIDLQIK.N		R.ALIDLQIK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
206	B3LKG8_YEAS1	8.88%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
16	30	2	1767.66	-0.81	1	41.6	33.1	95.00%	R.NSSSLDSDHDAYYSK.Q	Phospho (+80)	R.NSSSLDSDHDAYYSK.Q
45	56	2	1388.66	3.7	0	85.6	33.1	95.00%	Y.NIDLEENNVSSR.S		K.EQEIYNIDLEENNVSSR.S
29	44	2	1934.94	3.1	2	36.4	32.6	95.00%	Y.SKQNPDNFPVKEQEIY.N		R.NSSSLDSDHDAYYSKQNPDNFPVKEQEIYNIDLEENNVSSR.S
403	415	2	1372.78	2.5	1	55.2	26.5	95.00%	R.NLYALAIDGKAPK.I		R.NLYALAIDGKAPK.I
31	44	2	1719.82	4.3	2	39.4	32.3	95.00%	K.QNPDNFPVKEQEIY.N		K.QNPDNFPVKEQEIYNIDLEENNVSSR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
207	A6ZUM5_YEAS7	23.41%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
39	52	2	1474.81	3.6	0	74.2	28.8	95.00%	F.NARPDGVHVINVGK.T		R.NVQVHQEPYVFNARPDGVHVINVGK.T
2	27	2	2776.45	2.7	1	55	27	95.00%	M.SLPATFDLTPEDAQLLLAANTHLGAR.N	Acetyl (+42)	-.MSLPATFDLTPEDAQLLLAANTHLGAR.N
120	127	2	911.55	1.6	0	41.2	21	95.00%	R.LVIVTDPR.S		R.LVIVTDPR.S
37	52	2	1720.94	2.9	1	73.9	26.5	95.00%	Y.VFNARPDGVHVINVGK.T		R.NVQVHQEPYVFNARPDGVHVINVGK.T
28	52	3	2815.45	-0.77	1	43.1	28.2	95.00%	R.NVQVHQEPYVFNARPDGVHVINVGK.T		R.NVQVHQEPYVFNARPDGVHVINVGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
208	ERG2_YEAST	19.37%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	46	2	1376.7	2.6	0	59.7	31.1	95.00%	K.TLNEICNSVISK.H	Carbamidomethyl (+57)	K.TLNEICNSVISK.H
47	63	2	1866.91	3.7	0	116	32.4	95.00%	K.HNAAEGLSTEDLLQDVR.D		K.HNAAEGLSTEDLLQDVR.D
64	77	2	1622.74	2.9	1	64.2	33.2	95.00%	R.DALASHYGDEYINR.Y		R.DALASHYGDEYINR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
209	A6ZMW0_YEAS7	10.52%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
485	496	2	1367.7	-0.45	1	62.5	31.2	95.00%	K.LVDVEDLGYFAK.N		K.LVDVEDLGYFAK.N
573	588	2	1912.87	2.3	1	101	34	95.00%	R.SNPYVQNICVYADENK.V	Carbamidomethyl (+57)	R.SNPYVQNICVYADENK.V
2	22	3	2356.1	-0.75	1	61.8	33.3	95.00%	M.TEQYSVAVGEAANEHETAPRR.N	Acetyl (+42)	-.MTEQYSVAVGEAANEHETAPRR.N
532	541	2	1116.55	3.1	1	52.9	30.8	95.00%	R.TGDIAEWTPK.G		R.TGDIAEWTPK.G
675	688	4	1636.94	3.3	1	48.7	22	95.00%	K.RRDILAAVKPDVER.V		K.RRDILAAVKPDVER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
210	A6ZQC8_YEAS7	5.01%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
76	91	2	1831.92	3.4	2	62.4	31.8	95.00%	W.KGDPTYLPNSPYPEVR.S		R.HSIQEEGLVWKGDPTYLPNSPYPEVR.S
404	415	2	1449.74	1.2	1	47	32	95.00%	K.ILNEDYSINLEK.Y		K.ILNEDYSINLEK.Y
64	75	2	1467.72	4.3	2	34.7	32.4	95.00%	F.DRHSIQEEGLVW.K		K.FDRHSIQEEGLVWK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
211	A6ZQQ0_YEAS7	18.75%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	91	2	2658.29	3.8	1	90.4	31.7	95.00%	F.SLAEVSYATGENIGYQVQESVSTAR.F		R.VMQTAAFSLAEVSYATGENIGYQVQESVSTAR.F
170	180	3	1259.74	2.9	0	39.7	22.9	95.00%	R.VNAIEHVIIPR.T		R.VNAIEHVIIPR.T
2	12	2	1331.66	-0.45	2	31.3	31.4	95.00%	M.SGNREQVFPTR.M	Acetyl (+42)	-.MSGNREQVFPTR.M
169	180	3	1415.84	4.1	1	54.3	22	95.00%	R.RVNAIEHVIIPR.T		R.RVNAIEHVIIPR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
212	A6ZNP1_YEAS7	5.21%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
242	256	2	1677.82	3.3	1	95.2	32.2	95.00%	Y.TTSDNTQLASDELRK.A		K.DLGSVVQQQGVLVDNIEANIYTTSDNTQLASDELRK.A
242	255	2	1549.73	3.1	0	104	32.7	95.00%	Y.TTSDNTQLASDELR.K		K.DLGSVVQQQGVLVDNIEANIYTTSDNTQLASDELR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
213	B3LI68_YEAS1	7.98%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
170	192	3	2381.11	-0.25	1	48.8	33	95.00%	K.LKETSDSTSTSTPTPTPSTNDSK.A		K.LKETSDSTSTSTPTPTPSTNDSK.A
2	34	4	3669.67	-0.49	1	52.6	31.3	95.00%	M.TDETAHPTQSASKQESAALKQTGDDQQESQQQR.G	Acetyl (+42)	-.MTDETAHPTQSASKQESAALKQTGDDQQESQQQR.G
2	21	3	2099.01	-0.95	1	64	32.8	95.00%	M.TDETAHPTQSASKQESAALK.Q		-.MTDETAHPTQSASKQESAALK.Q
267	286	2	2170.99	3	1	64.8	33.8	95.00%	K.SAEPEVKQETPAEEGEQGEK.G		K.SAEPEVKQETPAEEGEQGEK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
214	A6ZTN7_YEAS7	11.25%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
198	221	3	2715.36	2.9	1	49.4	29.9	95.00%	K.EYRPVDTIPLNDLESTPVMVNSAR.G		K.EYRPVDTIPLNDLESTPVMVNSAR.G
222	250	3	2970.38	0.64	2	51.1	32.7	95.00%	R.GSPSPSSNRDTLFSLSSDTTTATATNNNK.R		R.GSPSPSSNRDTLFSLSSDTTTATATNNNK.R
63	80	3	1965.08	2.6	0	45.4	23.9	95.00%	K.HLHGLPILQSPSLTPAER.L		K.HLHGLPILQSPSLTPAER.L
235	250	2	1625.74	3.5	0	64.5	33.2	95.00%	F.SLSSDTTTATATNNNK.R	Deamidation (+1)	R.DTLFSLSSDTTTATATNNNK.R
222	234	2	1363.64	3.2	2	47.3	32.3	95.00%	R.GSPSPSSNRDTLF.S		R.GSPSPSSNRDTLFSLSSDTTTATATNNNK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
215	A6ZQF9_YEAS7	21.38%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	58	2	2783.31	-1.4	1	42.4	32.2	95.00%	K.ATFSPSGGTVSVPVEWMDNGAYPSLSK.I		K.ATFSPSGGTVSVPVEWMDNGAYPSLSK.I
84	94	2	1245.61	1.4	0	38.3	32.1	95.00%	K.ITPSELTQDDK.V		K.ITPSELTQDDK.V
63	83	2	2280.1	4.1	1	82.8	32.8	95.00%	F.TFSLCTGPNNNIDCVAVLASK.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.ISTFTFSLCTGPNNNIDCVAVLASK.I
65	83	2	2031.98	3.7	0	55.5	32.3	95.00%	F.SLCTGPNNNIDCVAVLASK.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.ISTFTFSLCTGPNNNIDCVAVLASK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
216	A7A1P9_YEAS7	11.88%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
29	48	3	2308.23	2.6	1	52.8	27.4	95.00%	K.VHVPSIENPFGIELWPIFSK.V		K.VHVPSIENPFGIELWPIFSK.V
317	334	2	1694.83	-0.59	1	97.4	32.9	95.00%	K.KESEVSGSVASGSSTGVK.T		K.KESEVSGSVASGSSTGVK.T

314	334	3	2023.05	4.1	1	53.6	29	95.00%	K.TVKKESEVSGSVASGSSTGVK.T		K.TVKKESEVSGSVASGSSTGVK.T
318	334	2	1566.74	0.12	0	90.3	33.1	95.00%	K.ESEVSGSVASGSSTGVK.T		K.ESEVSGSVASGSSTGVK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
217	TOR1_YEAST	3.12%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1187	1210	3	2535.22	2.1	1	37.4	32.5	95.00%	K.ILEANTTDYKPAEQMEAADAGVAK.L		K.ILEANTTDYKPAEQMEAADAGVAK.L
1937	1955	4	2153.2	4.1	0	19.2	23.3	95.00%	R.IHSPVLVNQAELVSHELIR.V		R.IHSPVLVNQAELVSHELIR.V
1431	1447	3	1907.99	-0.2	1	28.9	30.5	95.00%	R.SLHALGEWEQLSQLAAR.K		R.SLHALGEWEQLSQLAAR.K
1517	1533	3	1949.02	5.9	1	44.3	29.4	95.00%	R.DLLVTEISALINESYNR.A		R.DLLVTEISALINESYNR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
218	A6ZQ79_YEAS7	18.67%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
168	180	2	1338.8	3	0	46.9	21.7	95.00%	R.VNQAIALLTIGAR.E		R.VNQAIALLTIGAR.E
55	65	2	1263.65	3.6	1	56.4	30.6	95.00%	K.DASLVDYVQVR.Q		K.DASLVDYVQVR.Q
186	203	3	1941.08	-1.1	1	34.2	26.1	95.00%	R.NIKTIAETLAEELINAAK.G		R.NIKTIAETLAEELINAAK.G
189	203	2	1585.86	5	0	89.9	28.8	95.00%	K.TIAETLAEELINAAK.G		K.TIAETLAEELINAAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
219	A6ZR28_YEAS7	33.33%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
21	32	3	1450.81	0.62	2	42.4	25.8	95.00%	R.KQFVVDVLHPNR.A		R.KQFVVDVLHPNR.A
12	20	2	981.6	3.5	0	33.3	21.5	95.00%	K.VISNPLLAR.K		K.VISNPLLAR.K
69	83	2	1539.8	3.1	1	26.5	29.7	90.20%	K.SVGFGLVYNSVAEAK.K		K.SVGFGLVYNSVAEAK.K
53	61	2	996.5	-0.43	1	42.8	30	95.00%	K.DAVSVFGFR.T		K.DAVSVFGFR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
220	A7A0Y7_YEAS7	3.90%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
104	117	2	1723.86	-1.3	1	64.7	32.1	95.00%	R.IYNSPFQLNMLQEK.E		R.IYNSPFQLNMLQEK.E
238	249	2	1237.77	1.3	0	41.5	20.6	95.00%	R.VVGVIVEPVSIK.R		R.VVGVIVEPVSIK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
221	A6ZPW0_YEAS7	10.92%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	15	2	1595.89	4.7	2	24	25.3	93.50%	M.SLRLPQNPNAGLFK.Q	Acetyl (+42)	-.MSLRLPQNPNAGLFK.Q
344	359	2	1651.91	2.6	0	72.1	26.2	95.00%	R.LGAPTPEELGLVETVK.T		R.LGAPTPEELGLVETVK.T
441	450	2	1052.66	2.3	0	47.6	20	95.00%	R.TPGLLQLAIK.Q		R.TPGLLQLAIK.Q
388	399	2	1344.63	-0.69	0	72.3	32.7	95.00%	R.GATQNNLDDIER.A		R.GATQNNLDDIER.A
388	409	3	2284.14	4.5	1	27	31.5	95.00%	R.GATQNNLDDIERAIDDGVAAVK.G		R.GATQNNLDDIERAIDDGVAAVK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
222	B3LKQ2_YEAS1	8.30%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
164	184	2	2237.02	3.6	1	119	34.3	95.00%	R.DLEYISSMPHMSGTSGDAAIR.H		R.DLEYISSMPHMSGTSGDAAIR.H
365	375	2	1128.68	2.6	0	28.5	24.8	95.00%	K.ILAILSDTGVK.F		K.ILAILSDTGVK.F
400	419	4	2213.13	0.055	1	54.9	29.7	95.00%	R.ERHPVHDIVGKIEGSEQAGR.A		R.ERHPVHDIVGKIEGSEQAGR.A
352	364	2	1338.72	2.3	0	38.8	28.3	95.00%	K.IPSIPISANQGDK.I		K.IPSIPISANQGDK.I
402	419	3	1927.99	3.7	1	53.1	30.1	95.00%	R.HPVHDIVGKIEGSEQAGR.A		R.HPVHDIVGKIEGSEQAGR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
223	A6ZT02_YEAS7	9.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
524	542	2	2212.15	5.2	1	88.4	29	95.00%	K.GLTLEEVNTLWEEGVLPWK.S		K.GLTLEEVNTLWEEGVLPWK.S

288	310	2	2386.17	4.2	0	115	31.6	95.00%	K.VSADDPAVMAEVEVVQATVEAEK.L		K.VSADDPAVMAEVEVVQATVEAEK.L
311	324	2	1479.74	2.7	1	30.4	32	93.10%	K.LAGNASWGEIFSTK.T		K.LAGNASWGEIFSTK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
224	A6ZUA2_YEAS7	8.88%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
517	531	2	1823.75	3.3	1	50.7	33.6	95.00%	K.EFHALEESENEQAEY.S		K.EFHALEESENEQAEYSNNFDTIEDSR.E
5	26	3	2394.01	2.8	1	54.1	34	95.00%	R.NDNASGGYMQPDQSSNASMHKR.D		R.NDNASGGYMQPDQSSNASMHKR.D
532	544	2	1572.68	4.9	2	51.6	33.1	95.00%	Y.SNNFDTIEDSREF.S		K.EFHALEESENEQAEYSNNFDTIEDSREFSVAASDVELENEHVPWGK.K
5	25	3	2237.91	-0.61	1	32.3	33.7	95.00%	R.NDNASGGYMQPDQSSNASMHK.R		R.NDNASGGYMQPDQSSNASMHK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
225	A6ZN13_YEAS7	7.52%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
100	109	2	1234.6	3.5	1	50.9	31.8	95.00%	K.NDAIENYQLR.V		K.NDAIENYQLR.V
351	361	2	1333.63	4	1	48.7	32.8	95.00%	Y.CNNAQLAPYQR.T	Carbamidomethyl (+57)	R.CLGLIESCYDSQSVWSCVPATIYCNNAQLAPYQR.T
449	458	2	1265.59	0.48	1	34.1	31.9	95.00%	K.DFICNWLGNK.A	Carbamidomethyl (+57)	K.DFICNWLGNK.A
32	40	2	985.54	-3.4	0	40.9	27	95.00%	K.DVLLQAAEK.F		K.DVLLQAAEK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
226	B3LHY2_YEAS1	11.99%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
12	49	4	4276.97	-0.95	1	59.6	29	95.00%	K.HLVDDVLFISPTNDGSEEKPTEVTFQEDEGHDASLHNR.S		K.HLVDDVLFISPTNDGSEEKPTEVTFQEDEGHDASLHNR.S
20	49	3	3338.5	2.5	1	77.7	32.6	95.00%	F.ISPTNDGSEEKPTEVTFQEDEGHDASLHNR.S		K.HLVDDVLFISPTNDGSEEKPTEVTFQEDEGHDASLHNR.S
108	120	2	1258.65	1.2	0	64	30	95.00%	K.SNIGNAEVAGLSK.D		K.SNIGNAEVAGLSK.D
510	522	2	1590.7	-0.63	1	56.5	34.2	95.00%	R.CNELGEPIPYDER.L	Carbamidomethyl (+57)	R.CNELGEPIPYDER.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
227	A6ZM02_YEAS7	17.65%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
188	213	4	3042.7	3.7	2	22.5	21.6	95.00%	K.LIPEVINKEIENATKDIFPLQNIHVR.K		K.LIPEVINKEIENATKDIFPLQNIHVR.K
65	83	3	2188.06	1.9	1	49.5	32.5	95.00%	R.VVEVCLADLQGSEDHSFRK.V	Carbamidomethyl (+57)	R.VVEVCLADLQGSEDHSFRK.V
203	213	2	1350.74	1.4	1	29	27.4	95.00%	K.DIFPLQNIHVR.K		K.DIFPLQNIHVR.K
188	202	2	1709.96	4.7	1	76	24.3	95.00%	K.LIPEVINKEIENATK.D		K.LIPEVINKEIENATK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
228	A6ZMK2_YEAS7	29.37%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
31	45	2	1635.93	4.1	0	53.7	23.4	95.00%	K.VNGSPITLVEPEILR.F		K.VNGSPITLVEPEILR.F
69	82	2	1442.76	-0.0011	1	82	29.4	95.00%	R.VTGGGHVSQVYAIR.Q		R.VTGGGHVSQVYAIR.Q
115	127	3	1494.86	3.4	1	19.5	23.6	93.90%	R.TLLIADSRRPEPK.K		R.TLLIADSRRPEPK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
229	A6ZUT8_YEAS7	15.34%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
145	156	2	1191.56	-0.011	0	89.5	31.7	95.00%	R.SVVADISDSDGK.S		R.SVVADISDSDGK.S
102	110	2	1003.57	3.9	1	32.6	27.7	95.00%	K.AALQTYLPK.I		K.AALQTYLPK.I
128	139	2	1346.68	3.8	1	35.5	31.4	95.00%	Y.RNDLTASQLSDK.I		K.ESTVAGFLVGSEALYRNDLTASQLSDK.I

87	101	2	1673.77	2.5	1	49.9	33.2	95.00%	F.VGVWPTDDSHYAAEK.A		K.VYAASDCNTLQNLGPAAEAEGFTIFVGVWPTDDSHYAAEK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
230	A6ZQG2_YEAS7	10.10%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
233	240	2	950.53	4.2	0	46.7	25	95.00%	W.LLNDHIAR.T		K.NSSSIGYYDLPAIWLLNDHIAR.T
68	80	2	1501.77	1.8	1	53.5	31	95.00%	K.NAPLADYLSVHFR.G		K.NAPLADYLSVHFR.G
276	294	2	2099.99	3.4	1	50.7	33.4	95.00%	Y.STFHTFQGIEDLGTGIQSY.G		K.NHLYSTFHTFQGIEDLGTGIQSYGYITR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
231	B3LQX5_YEAS1	4.66%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
268	277	2	1117.53	0.083	1	41.5	31.6	95.00%	K.YSIAYESTGK.L		K.YSIAYESTGK.L
470	484	2	1650.87	3	1	29.2	30	94.20%	R.ITAQTSKPLWSVGTY.E		R.ITAQTSKPLWSVGTYER.I
470	486	2	1936.01	2.3	1	59.8	30.2	95.00%	R.ITAQTSKPLWSVGTYER.I		R.ITAQTSKPLWSVGTYER.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
232	A6ZKL6_YEAS7	39.42%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
46	63	3	1886.01	0.11	1	41.2	27.6	95.00%	R.LNRLPAASLGDMVMATVK.K		R.LNRLPAASLGDMVMATVK.K
121	128	2	1045.47	-0.19	1	33.1	32.1	95.00%	K.ECADLWPR.V	Carbamidomethyl (+57)	K.ECADLWPR.V
33	40	2	932.57	2.7	1	25.3	23.1	95.00%	R.NLYIIAVK.G		R.NLYIIAVK.G
13	32	2	2014.99	0.21	0	86.8	32	95.00%	R.ISLGLPVGAIMNCADNSGAR.N	Carbamidomethyl (+57)	R.ISLGLPVGAIMNCADNSGAR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
233	A6ZLH4_YEAS7	5.71%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
127	136	2	1073.5	3.3	1	45.5	31.4	95.00%	R.GGGAYYMISR.S		R.GGGAYYMISR.S
5	31	3	2878.42	0.21	1	69.4	30.5	95.00%	R.FYQIPGTHRPSSAISSSNESSSLLSAR.R		R.FYQIPGTHRPSSAISSSNESSSLLSAR.R
693	719	3	3066.61	3.9	1	30	25.6	95.00%	K.VNVQQWVQIVEDLSLMQSNIAIAHGFK.N		K.VNVQQWVQIVEDLSLMQSNIAIAHGFK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
234	A6ZXE6_YEAS7	5.70%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
925	937	2	1645.78	4	1	44.1	32.8	95.00%	K.FYDSNYPEFPVLR.D		K.FYDSNYPEFPVLR.D
446	455	2	1095.61	3.2	0	28.2	26.7	95.00%	R.DLSLLGSHVR.K		R.DLSLLGSHVR.K
89	114	3	2811.53	2.5	1	47	22.9	95.00%	R.TGKPLSVELGPGLMETIYDGIQRPLK.A		R.TGKPLSVELGPGLMETIYDGIQRPLK.A
186	197	2	1305.65	3.5	1	30.6	31.7	93.70%	W.IAPAGEYTLDEK.I		R.GTITWIAPAGEYTLDEK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
235	A6ZNU6_YEAS7	26.84%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	139	4	2593.46	4.2	2	44.2	21.1	95.00%	R.TLTAVHDKILEDLVFPTEIVGKR.V		R.TLTAVHDKILEDLVFPTEIVGKR.V
117	138	3	2437.36	4.8	2	40.7	22.5	95.00%	R.TLTAVHDKILEDLVFPTEIVGK.R		R.TLTAVHDKILEDLVFPTEIVGK.R
8	35	3	3082.63	5.7	1	50.6	25.4	95.00%	K.ILSQAPTELELQVAQAFVELENSSPELK.A		K.ILSQAPTELELQVAQAFVELENSSPELK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
236	A6ZM50_YEAS7	10.90%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
146	162	2	2064.06	-0.74	2	128	30.2	95.00%	R.RVEEITDEIVDELTYLK.N		R.RVEEITDEIVDELTYLK.N
62	67	2	760.46	-0.69	1	26.1	25	95.00%	K.LNLFVR.D		K.LNLFVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
237	A7A288_YEAS7	12.39%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
254	266	2	1516.78	3.1	0	42.7	30.9	95.00%	K.TLIDNLIDTSEQR.D		K.TLIDNLIDTSEQR.D
371	385	2	1727.82	2.4	1	90	33.6	95.00%	K.LYAVEGNDQYVQSSR.S		K.LYAVEGNDQYVQSSR.S
343	364	3	2509.08	-0.9	1	89.2	34.2	95.00%	R.INMLKKEENDSDASCGNDNNNK.N	Carbamidomethyl (+57)	R.INMLKKEENDSDASCGNDNNNK.N
447	458	2	1368.69	-0.087	1	50.9	31.4	95.00%	K.NILGDITFADYK.N		K.NILGDITFADYK.N
82	101	2	2178.04	-0.38	1	82.3	32.7	95.00%	R.FSDISIDNILSDNSDIPSAR.R		R.FSDISIDNILSDNSDIPSAR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
238	AXL2_YEAST	7.17%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
651	664	2	1512.68	0.72	1	59.7	33	95.00%	R.SSSVYMDSEPAVNK.S		R.SSSVYMDSEPAVNK.S
709	729	2	2329.15	3.5	1	69.2	31.5	95.00%	R.DVTMSSLDPWNSNISPSPVRK.S		R.DVTMSSLDPWNSNISPSPVRK.S
730	740	2	1191.61	0.75	1	33.2	30.7	95.00%	K.SVTPSPYNVTK.H		K.SVTPSPYNVTK.H
668	680	2	1419.74	2.2	1	42.4	30.8	95.00%	R.YTGNLSPVSDIVR.D		R.YTGNLSPVSDIVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
239	A6ZLM4_YEAS7	4.08%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
519	527	2	973.53	4.5	1	27.2	29.4	92.20%	K.LIAHSVATY.A		K.LIAHSVATYADSFEGFPK.R
92	105	2	1714.88	2.8	1	55.6	30.7	95.00%	Y.FMKPHVESEKLQDK.I		K.QLAVAAFYATNLGSAYVIPQFFQEAFQQEEPIENYLPQLNDDDSSAVAANIPKPHIPYFMKPHVESEKLQDK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
240	YKF4_YEAST	12.06%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
163	196	3	3678.67	3	1	46.6	31.4	95.00%	W.AAAVSVDTKHDVPQDSNDNNNEELEAQGQQAQEK.N		K.HVPSKPVSNTTSWAAAVSVDTKHDVPQDSNDNNNEELEAQGQQAQEK.N
614	626	2	1426.66	5.5	1	31.6	33.3	93.00%	Y.GQPQYGVAGQYPY.Q		K.QGNNVAAQQYYMYQNQFPGYSYPGMFDSQGYAYGQQYQQLAQNNAQTSGNANQYNFQQGYGQAGANTAAANLTSAAAAAAASPATAHAQPQQQQPYGGSFMPYYAHFYQQSFPYGQPQYGVAGQYPYQLPK.N
475	499	3	2883.37	3.8	0	42.3	32.4	95.00%	Y.AQQQQQHPQPQSQQPQSQQSPQSQK.Q		K.VEISAVISEPPEDQANTVPQPQQQSQQPQQPQQPQQPQQPQQPQQQQQPQQPQQPQQQLQQQQQQQQQPVQAQAQAQEEQLSQNYYTQQQQQQYAQQQHQLQQQYLSQQQQYAQQQQQHPQPQSQQPQSQQSPQSQK.Q
537	553	2	1848.85	6.1	1	49.6	33.8	95.00%	Y.QQLAQNNAQTSGNANQY.N		K.QGNNVAAQQYYMYQNQFPGYSYPGMFDSQGYAYGQQYQQLAQNNAQTSGNANQYNFQQGYGQAGANTAAANLTSAAAAAAASPATAHAQPQQQQPYGGSFMPYYAHFYQQSFPYGQPQYGVAGQYPYQLPK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
241	A6ZXF1_YEAS7	11.52%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

488	506	2	2070.89	5.4	1	121	34.1	95.00%	Y.YGSLNGDDDDMTNDSALLR.F		R.VATNQEYQHPLSANYISMDSPDV INSSPGHFGMNSGQLLGNTTLYYG SLNGDDDDMTNDSALLR.F
285	306	3	2472.31	2.8	1	26.2	27.8	95.00%	K.LTTLDTGDLSFPIDEEQPILKK.S		K.LTTLDTGDLSFPIDEEQPILKK.S
221	242	3	2506.22	3.2	1	40.2	31.8	95.00%	R.NDSSSISNNVYSSEYHPIKPLR.S		R.NDSSSISNNVYSSEYHPIKPLR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
242	A6ZWJ1_YEAS7	9.42%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
328	340	2	1292.66	0.91	0	73.2	30.9	95.00%	K.STSDTASATLLAR.Q		K.STSDTASATLLAR.Q
64	73	3	1281.64	3.9	2	29.6	31.3	95.00%	Y.KTEDIPEHWK.E		K.IIHQTYKTEDIPEHWK.E
146	158	2	1499.89	-0.43	2	34.9	22.8	95.00%	R.KLDPLLAFPAFLR.K		R.KLDPLLAFPAFLR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
243	GPA1_YEAST	17.58%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
22	35	2	1641.87	3.3	1	73.4	29.4	95.00%	K.RANDVIEQSLQLEK.Q		K.RANDVIEQSLQLEK.Q
300	314	2	1583.77	1.9	1	80.7	32.7	95.00%	K.TTGITETEFNIGSSK.F		K.TTGITETEFNIGSSK.F
75	90	2	1863.95	-0.75	1	60.8	31.1	95.00%	R.LQYAQVIWADAIQSMK.I		R.LQYAQVIWADAIQSMK.I
179	201	4	2595.11	3.3	1	38.8	34	95.00%	K.SDTDRDAETVTQNEDADRNNSS R.I		K.SDTDRDAETVTQNEDADRNNSS R.I
281	295	2	1770.82	2.3	1	39.2	33.1	95.00%	K.FASPNYVCTDEDILK.G	Carbamidomethyl (+57)	K.FASPNYVCTDEDILK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
244	A7A0B5_YEAS7	9.58%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
133	149	2	1902.98	-1.1	1	72.1	30.4	95.00%	K.QFPGIAYTIPDLDAQVR.V		K.QFPGIAYTIPDLDAQVR.V
682	693	2	1361.6	2.8	1	64.1	33.3	95.00%	R.LFDDETSSSSFK.Q		R.LFDDETSSSSFK.Q
99	117	2	2080.01	-1.4	1	54.2	33	95.00%	K.TFDLCSLGQVSLCPLSAGR.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.TFDLCSLGQVSLCPLSAGR.I
736	762	3	2867.4	0.91	1	28	31.4	95.00%	R.TNLAPNNTSTSSLMKPESSLYLG NSNK.S		R.TNLAPNNTSTSSLMKPESSLYLG NSNK.S
736	756	2	2254.09	3	1	79.6	33.2	95.00%	R.TNLAPNNTSTSSLMKPESSLY.L		R.TNLAPNNTSTSSLMKPESSLYLG NSNK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
245	A6ZSN7_YEAS7	31.40%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
7	21	2	1883.96	-0.9	1	75	30.8	95.00%	K.EKVEEQEQQQQQIIK.I		K.EKVEEQEQQQQQIIK.I
90	101	2	1386.78	3.7	1	52.3	26.8	95.00%	R.YIDLEAPVQIVK.R		R.YIDLEAPVQIVK.R
33	43	2	1229.66	0.89	0	42.7	29.5	95.00%	K.QLENVSSNIVK.N		K.QLENVSSNIVK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
246	A6ZTV6_YEAS7	12.59%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
620	646	3	2713.39	3	1	30.6	29.2	95.00%	K.INEMAAGDVLLGLASSGVHSNGF SLVR.K		K.INEMAAGDVLLGLASSGVHSNGF SLVR.K
303	332	3	3269.64	4.7	1	51.3	28.3	95.00%	R.FGDPETQAVLSLLDDQTDLAQVF LAAAEHR.L		R.FGDPETQAVLSLLDDQTDLAQVF LAAAEHR.L
500	517	2	1872.96	2.7	1	85.7	30.8	95.00%	F.RQNEDTLLVGATDGVGTK.L		R.RPGADSDIGGFGGLFDLAQAGF RQNEDTLLVGATDGVGTK.L
289	302	2	1672.88	3.3	1	44.8	29.4	95.00%	K.TNQLVPEVLEYNVR.F		K.TNQLVPEVLEYNVR.F
400	411	2	1288.7	4.3	0	41.2	29.1	95.00%	R.VLSVTSTAQDLR.T		R.VLSVTSTAQDLR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
247	A6ZYY5_YEAS7	15.64%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

45	57	2	1460.69	4.6	2	41.2	32.6	95.00%	Y.SDRDFITLGSSTY.R		K.GVNTLENIETLPQQGSIAGVSQG FPNIQEIYSDRDFITLGSSTYR.R
2	13	2	1290.59	-0.91	0	45.7	32.6	95.00%	M.TSSASSPQDLEK.G	Acetyl (+42)	-.MTSSASSPQDLEK.G
61	78	2	1945.88	-0.36	1	59.9	34.1	95.00%	R.DLLNALDRGDGEEGNCAK.Y	Carbamidomethyl (+57)	R.DLLNALDRGDGEEGNCAK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
248	A6ZL34_YEAS7	6.88%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
802	822	2	2146.02	3.4	1	70.8	33.2	95.00%	K.IAVTGGENNENTQAKDDAATK.T		K.IAVTGGENNENTQAKDDAATK.T
696	717	3	2189.08	-0.96	1	30.4	31.7	95.00%	K.AVDNDTAGSAGKKPLATESTEK.R		K.AVDNDTAGSAGKKPLATESTEK.R
724	745	2	2144.15	4	1	33.6	27.4	95.00%	K.VPTVGSYGVAGATLPETIPTSK.N		K.VPTVGSYGVAGATLPETIPTSK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
249	A6ZKM8_YEAS7	14.50%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
165	178	2	1550.76	-0.5	1	55.3	32.3	95.00%	R.LYACISSRPGQSGR.C	Carbamidomethyl (+57)	R.LYACISSRPGQSGR.C
78	92	2	1666.88	3.2	1	42.6	29.2	95.00%	R.IAGVVYHPSNNELVR.T		R.IAGVVYHPSNNELVR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
250	A6ZYA1_YEAS7	5.18%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
300	308	2	1055.63	-0.011	0	42	22.6	95.00%	R.SVLDLLLQR.L		R.SVLDLLLQR.L
550	564	3	1784.87	3.5	1	44.3	32.3	95.00%	K.LKHDDEVSCEELLAK.I	Carbamidomethyl (+57)	K.LKHDDEVSCEELLAK.I
235	256	4	2572.17	-0.81	1	26.3	33.6	95.00%	K.IKMEAEENPSETETNDSHLDRK.K		K.IKMEAEENPSETETNDSHLDRK.K
1472	1482	2	1239.57	4.6	1	32.1	32.5	94.60%	F.NLGSDSEVEYK.C		R.SSVTPTLITFNLGSDSEVEYK.C
2	15	2	1580.88	-0.62	0	30.4	25	95.00%	M.SLPLKPLTIDSNNK.Q	Acetyl (+42)	-.MSLPLKPLTIDSNNK.Q
78	94	3	1761	3.8	1	39.3	22.9	95.00%	R.RLTSSLSPALPAGVHQK.T		R.RLTSSLSPALPAGVHQK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
251	A6ZLZ0_YEAS7	4.84%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
598	614	2	1869.02	-1.4	0	70.2	26.9	95.00%	K.IRPLEELEALLSSGNTK.Q		K.IRPLEELEALLSSGNTK.Q
786	801	3	1914.98	-0.5	1	35.7	30.9	95.00%	R.LQHIQTCLAGDLLFMR.F	Carbamidomethyl (+57)	R.LQHIQTCLAGDLLFMR.F
1026	1043	3	1993.03	3.4	0	31.7	30.2	95.00%	R.KPAEPTKPNNLDATDINR.L		R.KPAEPTKPNNLDATDINR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
252	A6ZX57_YEAS7	20.97%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
146	166	3	2297.14	2.7	1	48	30.6	95.00%	R.MMARPLTIASDPMSGFFGLQK.K		R.MMARPLTIASDPMSGFFGLQK.K
25	35	2	1180.57	2.8	1	40.1	32.1	95.00%	R.LFAGMSPEMAK.K		R.LFAGMSPEMAK.K
108	117	3	1214.58	4.4	1	24.9	32.3	90.20%	K.LFESLHDHAF.T		K.LFESLHDHAFTLGTR.Y
2	15	2	1675.85	3.9	1	46.7	31.1	95.00%	M.SIEYSVIVPAYHEK.L	Acetyl (+42)	-.MSIEYSVIVPAYHEK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
253	A7A0G8_YEAS7	23.74%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
51	62	2	1525.72	2.5	1	58.6	33.4	95.00%	K.AQIYDDQLQNYR.D		K.AQIYDDQLQNYR.D
108	120	2	1483.79	1.8	1	45.6	29.2	95.00%	K.ICIQPEAGGWLIK.A	Carbamidomethyl (+57)	K.ICIQPEAGGWLIK.A
51	61	2	1369.62	4.2	1	48.9	33.2	95.00%	K.AQIYDDQLQNY.R		K.AQIYDDQLQNYR.D
63	89	3	3024.46	5.7	1	38.7	31	95.00%	R.DAGAQDFGVLIDIEETFDDNHLVV HQK.G		R.DAGAQDFGVLIDIEETFDDNHLVV HQK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
254	A6ZYM2_YEAS7	6.67%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
230	243	2	1654.84	2.6	1	76.2	31.5	95.00%	K.FTVFSNLDNTTQLR.L		K.FTVFSNLDNTTQLR.L
425	444	3	2277.28	4.7	0	18	20.8	91.20%	K.EIPIELLQVNDIVEIKPGMK.I		K.EIPIELLQVNDIVEIKPGMK.I
688	702	2	1603.89	4.7	1	70.7	27	95.00%	K.ALNAVVLESEYVLGK.G		K.ALNAVVLESEYVLGK.G
800	817	2	1926.93	4.2	1	58.3	33.2	95.00%	R.EVGISFENVYSDVSPTGK.C		R.EVGISFENVYSDVSPTGK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
255	A6ZPG3_YEAS7	24.89%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
167	181	2	1716.89	-0.88	1	58.2	30.5	95.00%	R.APLEEIVISNDYLNK.D		R.APLEEIVISNDYLNK.D
93	106	2	1651.8	3.8	1	45.5	32.7	95.00%	R.EQSLDGIFEETKEK.L		R.EQSLDGIFEETKEK.L
53	63	2	1264.57	-0.18	1	68.2	31.8	95.00%	R.NETNNIDGNFK.S		R.NETNNIDGNFK.S
145	158	2	1678.8	3.6	1	65.3	33.2	95.00%	R.DVDLIESMKDDIMR.E		R.DVDLIESMKDDIMR.E
141	158	3	2148.07	5	1	35.9	31.4	95.00%	K.ALERDVDLIESMKDDIMR.E		K.ALERDVDLIESMKDDIMR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
256	A6ZW97_YEAS7	17.61%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
190	204	2	1718.86	-0.6	1	62	31.8	95.00%	R.EFEISPELATVDLEK.H		R.EFEISPELATVDLEK.H
158	165	2	991.54	3.8	1	49.9	30.8	95.00%	R.TDFLDIIR.T		R.TDFLDIIR.T
236	246	2	1244.73	4.9	1	58.5	23.7	95.00%	Y.LFLNGISVINR.G		K.LNIDTSAALESIQSPYLFLNGISVINR.G
75	90	2	1855.86	-1.1	1	59.1	34	95.00%	K.TADSFLSNENELNFQK.V		K.TADSFLSNENELNFQK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
257	A6ZKS1_YEAS7	14.29%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
21	38	2	2057.02	2.7	2	104	31.6	95.00%	R.KVWLDPNETSEIAQANSR.N		R.KVWLDPNETSEIAQANSR.N
154	162	2	1001.48	0.46	0	33.1	31.3	95.00%	K.ALNEEAEAR.R		K.ALNEEAEAR.R
22	38	2	1928.92	0.4	1	116	33	95.00%	K.VWLDPNETSEIAQANSR.N		K.VWLDPNETSEIAQANSR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
258	A6ZY37_YEAS7	10.25%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
13	22	2	1209.56	1.4	1	38.7	32.1	95.00%	K.NMYNASLNQR.N		K.NMYNASLNQR.N
1	12	2	1354.73	-0.9	1	38.4	27.5	95.00%	-.MNVIFSLASFVK.N		-.MNVIFSLASFVK.N
378	392	2	1557.69	-0.27	1	80.7	33.2	95.00%	R.SSSPSSSFTVSSNER.S		R.SSSPSSSFTVSSNER.S
320	336	2	1848.74	3.7	1	61.5	34.1	95.00%	R.FSNAGGFTMHNNDSSTF.K	Oxidation (+16)	R.FSNAGGFTMHNNDSSTFK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
259	A6ZU78_YEAS7	20.13%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
116	126	2	1190.75	3	1	26	10.4	95.00%	K.GRIPNVPVIVK.A		K.GRIPNVPVIVK.A
93	111	2	1877.98	3.3	2	84.6	30.2	95.00%	K.SASKETAPVIDTLAAGYGK.I		K.SASKETAPVIDTLAAGYGK.I
97	111	2	1504.78	2.7	1	39	31.1	95.00%	K.ETAPVIDTLAAGYGK.I		K.ETAPVIDTLAAGYGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
260	A6ZM38_YEAS7	35.29%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
81	95	2	1718.89	3.6	2	58.4	30.5	95.00%	R.KDQYVPEVSALDLSR.S		R.KDQYVPEVSALDLSR.S
117	128	2	1295.76	1.8	0	76.2	22.6	95.00%	K.LPLSVINVSAQR.D		K.LPLSVINVSAQR.D
96	111	2	1701.86	2	0	42.2	30.9	95.00%	R.SNGVLNVDNQTSDLVK.S		R.SNGVLNVDNQTSDLVK.S
112	128	2	1794.07	-0.9	1	26.3	20.2	95.00%	K.SLGLKLPLSVINVSAQR.D		K.SLGLKLPLSVINVSAQR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
261	A7A1L9_YEAS7	10.90%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	75	2	1266.61	-0.34	1	44.8	32.8	95.00%	R.GFLSDLPDFEK.L		R.GFLSDLPDFEK.L
111	122	2	1282.67	-0.49	1	38.6	29.9	95.00%	R.AGAVAPEDIWVR.A		R.AGAVAPEDIWVR.A

87	97	2	1289.69	4	1	43.2	29.9	95.00%	F.VFTNEPLTEIK.S		K.GNVGFVFTNEPLTEIK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
262	RTN1_YEAST	16.61%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
186	196	2	1357.56	-0.65	1	39.3	32.3	95.00%	K.TQEFSQMACEK.T	Carbamidomethyl (+57)	K.TQEFSQMACEK.T
236	247	2	1267.67	2.4	0	42.5	28.7	95.00%	K.LAADVPLEPESK.A		K.LAADVPLEPESK.A
208	216	2	939.58	3.4	0	36.8	21.5	95.00%	K.LGPISNLVK.S		K.LGPISNLVK.S
219	235	2	1589.79	-0.45	0	43.7	32.2	95.00%	K.TAPVSSTAGPQTASTSK.L		K.TAPVSSTAGPQTASTSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
263	A6ZNC5_YEAS7	6.61%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
277	287	2	1354.61	3.1	1	58.8	33.3	95.00%	K.CCSDVFNQVVK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CCSDVFNQVVK.S
288	299	2	1250.67	2.6	1	76.2	29.1	95.00%	K.SISIVGSYVGNR.A		K.SISIVGSYVGNR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
264	A6ZN11_YEAS7	47.21%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
86	99	2	1496.76	3.1	0	63.8	31.2	95.00%	F.GQPITQADISNPTR.A		R.QSYFSNEEGHVLCDVFGQPITQADISNPTR.A
39	69	3	3400.58	5	1	102	30.9	95.00%	R.TASVADPILDAVQEAQPFEQAADTFHDNMNR.Q		R.TASVADPILDAVQEAQPFEQAADTFHDNMNR.Q
135	148	2	1537.8	4.9	1	29.8	30	94.80%	R.VRPDFPVFGAAVTY.D		R.VRPDFPVFGAAVTYDANGMPQQVGGASSQMYGEQAVYQPQQHVQTEEK.Q
149	182	3	3735.67	4	1	80.9	31.7	95.00%	Y.DANGMPQQVGGASSQMYGEQAVYQPQQHVQTEEK.Q	Oxidation (+16)	R.VRPDFPVFGAAVTYDANGMPQQVGGASSQMYGEQAVYQPQQHVQTEEK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
265	A6ZU36_YEAS7	43.46%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
125	136	2	1344.71	4.6	2	33.7	30.2	95.00%	R.NVPVRDGVTIEF.S		R.NVPVRDGVTIEFSTNVK.D
3	21	2	2160.14	3.6	1	37.8	28.2	95.00%	K.YIQTEQQIEVPEGVTVSIK.S		K.YIQTEQQIEVPEGVTVSIK.S
175	184	2	1177.62	2.9	1	36.9	30.2	95.00%	K.FLDGIYVSHK.G		K.FLDGIYVSHK.G
73	84	2	1276.67	-0.16	0	69.6	30.7	95.00%	K.SLVDNMITGVTK.G		K.SLVDNMITGVTK.G
137	166	3	3288.61	4.8	1	58.4	29.9	95.00%	F.STNVKDEIVLSGNSVEDVSQNAADLQQICR.V	Carbamidomethyl (+57)	R.DGVTIEFSTNVKDEIVLSGNSVEDVSQNAADLQQICR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
266	A6ZU67_YEAS7	13.79%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
521	551	3	3156.57	5.5	0	73.2	29	95.00%	R.DRPGSVLMNVVSGGIAEASAQQAGDLMQDLK.T		R.DRPGSVLMNVVSGGIAEASAQQAGDLMQDLK.T
598	609	2	1399.73	2.9	1	47.4	30.1	95.00%	R.IPTAVVWIDCAR.L	Carbamidomethyl (+57)	R.IPTAVVWIDCAR.L
163	198	4	3887.08	4	2	24.6	25.3	95.00%	R.EKLPFPSGSATATLISVLNGTEILQEVSKSELLEMR.Q		R.EKLPFPSGSATATLISVLNGTEILQEVSKSELLEMR.Q
388	408	2	2434.22	5	1	77.9	31.1	95.00%	K.AALLNNIIDDTFQSMLLEEER.A		K.AALLNNIIDDTFQSMLLEEER.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
267	A6ZQ50_YEAS7	32.61%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	61	2	1369.56	1.2	1	59.3	32.4	95.00%	R.GAAGIWTCSCCK.K	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GAAGIWTCSCCK.K
63	80	2	1665.87	1.4	1	81.1	30.1	95.00%	K.TVAGGAYTVSTAAAATVR.S		K.TVAGGAYTVSTAAAATVR.S
70	80	2	1046.58	4.8	0	43.5	28.3	95.00%	Y.TVSTAAAATVR.S		K.TVAGGAYTVSTAAAATVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
268	A6ZPF4_YEAS7	10.62%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
519	538	3	2414.16	3.8	2	33.5	32.5	95.00%	W.NIETHENERLPQGEDFVYPK.T		R.TWWNIETHENERLPQGEDFVYPK.T
420	432	3	1441.77	0.07	0	32.5	28.5	95.00%	K.NLHTHEVPAPISK.S		K.NLHTHEVPAPISK.S
479	491	2	1409.7	3	1	44.4	31.9	95.00%	K.NSILGCYLAQSGK.H	Carbamidomethyl (+57)	K.NSILGCYLAQSGK.H
13	21	2	1119.52	3.7	1	40.9	31	95.00%	K.STDDDLIWR.R		K.STDDDLIWR.R
334	345	2	1201.69	0.57	0	34.6	26.6	95.00%	R.DVALGSSIISIK.N		R.DVALGSSIISIK.N
99	111	3	1574.77	2.6	1	33.7	33	95.00%	R.HEFYHDVHPPLGK.M		R.HEFYHDVHPPLGK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
269	A6ZL24_YEAS7	5.01%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
362	378	2	1655.85	1.9	0	58.9	30.4	95.00%	R.GDGTGVGDNVVNQLLAK.M		R.GDGTGVGDNVVNQLLAK.M
588	602	2	1561.77	3.8	0	40.1	31.8	95.00%	R.LISPNELSGMSESAK.I		R.LISPNELSGMSESAK.I
101	106	2	739.39	3.3	1	37.9	29	95.00%	K.AFDLFK.Y		K.AFDLFK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
270	A6ZW48_YEAS7	6.17%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
136	150	2	1755.89	4.5	1	56.7	31	95.00%	K.AVNYPVTVDFTEVFR.K		K.AVNYPVTVDFTEVFR.K
483	488	2	926.39	-0.28	1	34.5	30.5	95.00%	K.CVFCWR.H	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CVFCWR.H
122	135	2	1532.7	-0.34	0	59.5	34.1	95.00%	K.NIGDNENTATEVEK.A		K.NIGDNENTATEVEK.A
500	514	2	1846.9	-0.99	1	63.5	32.3	95.00%	R.WEVDEPEYILENALK.G		R.WEVDEPEYILENALK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
271	B3LH47_YEAS1	6.52%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
438	453	2	1904.95	2.8	1	52.8	31.9	95.00%	Y.HQQAIPQQQLPSQQQF.A		K.SLYVAENDETVPVPFPIEQQSYHQQAIPQQQLPSQQQFAIPPQQHHPQFMVPPSHQQQQAYPPPQMPSQQGYPPQQEHFMAMPPGQSQPQY.-
336	345	2	1176.62	2.7	0	41.3	30.5	95.00%	R.TLVCSDLLTR.G	Carbamidomethyl (+57)	R.TLVCSDLLTR.G
24	30	2	755.46	3.4	0	24.1	20.5	94.10%	K.TALNIPK.K		K.TALNIPK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
272	A6ZTZ3_YEAS7	2.28%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	16	2	1768.93	5.4	1	36.3	29.1	95.00%	M.TAILNWEDISPVLEK.G	Acetyl (+42)	-.MTAILNWEDISPVLEK.G
1211	1226	3	1798.96	3.2	1	21.8	28.6	91.60%	K.FLVDDGGLVDREPIVR.Q		K.FLVDDGGLVDREPIVR.Q
2373	2389	2	1903.93	5.5	0	73.9	32.2	95.00%	K.TNIVNLVEEEMLGSNDK.L		K.TNIVNLVEEEMLGSNDK.L
2329	2341	2	1352.8	5.1	0	24.9	21.5	94.90%	R.VDPLVIELVTGAK.Q		R.VDPLVIELVTGAK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
273	B3LGK8_YEAS1	8.91%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
173	185	2	1392.62	-0.49	0	85.4	32.5	95.00%	K.GQCTDAALESVDK.Y	Carbamidomethyl (+57)	K.GQCTDAALESVDK.Y
10	38	3	3356.55	3.6	2	37.5	31.9	95.00%	R.VPLCEPEELPDDIQKENEYGTLDSPGHLY.Q	Carbamidomethyl (+57)	R.VPLCEPEELPDDIQKENEYGTLDSPGHLYQVK.S
540	547	2	1058.54	1.2	1	29.5	30.4	94.00%	R.WDIEEVIR.R		R.WDIEEVIR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
274	ATG15_YEAS7	10.96%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
440	453	2	1546.83	3.6	1	47.5	28.5	95.00%	K.VIDEVLLGYEQAAK.C		K.VIDEVLLGYEQAAK.C

261	273	2	1641.71	1.7	1	39.1	33.7	95.00%	K.INDNLLFSCCCAR.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.INDNLLFSCCCAR.V
241	260	2	1919.83	-1.2	0	69.8	34.4	95.00%	K.GTSAQGLPGSGEDETTGNDK.I		K.GTSAQGLPGSGEDETTGNDK.I
417	426	2	1209.57	3.5	1	46.4	32.4	95.00%	R.VCVYDVVNDK.G	Carbamidomethyl (+57)	R.VCVYDVVNDK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
275	YIP8_YEAST	25.00%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
101	112	3	1314.71	1.7	0	40.9	29.4	95.00%	R.QLNASMGTLRPK.K		R.QLNASMGTLRPK.K
137	150	2	1675.79	-0.96	1	68.4	32.9	95.00%	R.DPSYSFMYPLTLSR.K		R.DPSYSFMYPLTLSR.K
196	204	2	1112.57	3.1	1	39.7	29.7	95.00%	R.EFIDSLRPH.-		R.EFIDSLRPH.-
114	129	2	1739.87	1	1	39.6	31.7	95.00%	K.QSTAYTNVPVIFSGEK.V		K.QSTAYTNVPVIFSGEK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
276	A6ZNH7_YEAS7	8.88%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
207	222	2	1828.77	2	1	85.5	34	95.00%	R.QLAAEYFNCGDEADAR.I	Carbamidomethyl (+57)	R.QLAAEYFNCGDEADAR.I
192	206	2	1572.83	0.88	1	84.1	30.2	95.00%	R.QIPVGYSAADIVANR.Q		R.QIPVGYSAADIVANR.Q
34	45	2	1313.56	0.96	1	54.5	32.5	95.00%	K.GNAFFNSESGER.F		K.GNAFFNSESGER.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
277	A6ZSD5_YEAS7	10.05%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
101	111	2	1246.53	2.5	1	55.4	32.8	95.00%	R.GINFDYSGSCK.I	Carbamidomethyl (+57)	R.GINFDYSGSCK.I
90	100	2	1245.49	0.33	1	45.2	31.8	95.00%	K.FGSMSCSSMPR.G	Carbamidomethyl (+57)	K.FGSMSCSSMPR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
278	A6ZPF9_YEAS7	34.78%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
28	48	3	2372.22	4.5	1	41.7	29.5	95.00%	K.TAALRQEIDDTVGIMRDNINK.V		K.TAALRQEIDDTVGIMRDNINK.V
33	43	2	1275.62	2.6	0	29.3	31.8	91.70%	R.QEIDDTVGIMR.D		R.QEIDDTVGIMR.D
28	43	3	1787.93	4.7	1	38.4	30	95.00%	K.TAALRQEIDDTVGIMR.D		K.TAALRQEIDDTVGIMR.D
56	74	2	2020.05	1.7	2	86.8	30	95.00%	R.LTSIEDKADNLAISAQGFK.R		R.LTSIEDKADNLAISAQGFK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
279	A6ZV22_YEAS7	27.13%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
92	105	3	1431.79	3.7	0	24.4	28.4	95.00%	K.VNGASVPINLHPSK.L		K.VNGASVPINLHPSK.L
49	62	3	1649.96	3.4	1	26.5	20.8	95.00%	K.ALPIRRDDEVLVVR.G		K.ALPIRRDDEVLVVR.G
80	86	2	805.43	0.97	1	32.2	28.8	95.00%	K.FAVQVDK.V		K.FAVQVDK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
280	A6ZXQ3_YEAS7	24.78%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
51	62	2	1437.81	2.3	1	50.9	25.1	95.00%	R.LAPELNQAIWKR.G		R.LAPELNQAIWKR.G
51	61	2	1281.71	3.1	1	26	26.2	94.80%	R.LAPELNQAIWK.R		R.LAPELNQAIWK.R
87	102	2	1732.94	-0.76	1	49.5	28.6	95.00%	K.NPLFSYVEPVLVASAK.G		K.NPLFSYVEPVLVASAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
281	A7A0F5_YEAS7	21.57%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	20	3	2406.21	5.5	2	30.8	30.4	95.00%	-.MDVLKLGYELDQLSDLVEER.T	Acetyl (+42)	-.MDVLKLGYELDQLSDLVEER.T
161	183	3	2562.33	4.7	0	49.1	28.6	95.00%	F.INQQQQLLEQDSHLGALSQSIGR.T		K.DEPLQSQLQSLSQPQPPQPMVSNQELFINQQQQLLEQDSHLGALSQSIGR.T
42	52	2	1240.74	0.077	0	33.9	25.1	95.00%	R.QLGSILELLQK.C		R.QLGSILELLQK.C
41	52	3	1396.84	0.73	1	25.9	21.8	95.00%	K.RQLGSILELLQK.C		K.RQLGSILELLQK.C
6	20	2	1777.88	3.9	1	98.7	32.3	95.00%	K.LGYELDQLSDLVEER.T		K.LGYELDQLSDLVEER.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
282	A6ZQ99_YEAS7	15.37%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
106	140	3	3909.89	5.2	1	118	28.1	95.00%	Y.LLAHDVASPFYPTNEEITTVTLEEGDGELYPETLF.A		R.HVATDTYLLAHDVASPFYPTNEEITTVTLEEGDGELYPETLFAFQPLK.K
31	44	4	1646.8	3.5	1	38.6	32.6	95.00%	K.HQDTDAFLHSHLAR.Y		K.HQDTDAFLHSHLAR.Y
196	215	2	2324.18	4.5	1	43.3	30.1	95.00%	K.VIDPSNNWVVDEIVNLDEVR.K		K.VIDPSNNWVVDEIVNLDEVR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
283	A6ZTF3_YEAS7	16.82%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
248	267	2	2342.26	-0.68	1	87.1	26.6	95.00%	K.LQQQFYPVQPVLMAINNIAR.Q		K.LQQQFYPVQPVLMAINNIAR.Q
44	63	2	2140.14	4.1	0	26.3	27.9	93.00%	K.LAPTEIPVSTISIEDLDATR.K		K.LAPTEIPVSTISIEDLDATR.K
144	176	3	3623.57	-0.46	1	58.9	31.9	95.00%	K.DGFESAVGEEDSKDATSQENGQSTQQQQPPHHR.N		K.DGFESAVGEEDSKDATSQENGQSTQQQQPPHHR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
284	A6ZT16_YEAS7	10.60%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
288	304	2	1999	-2.4	0	53.1	31.5	95.00%	K.IIEEEQEDDALVQDLLK.F		K.IIEEEQEDDALVQDLLK.F
251	279	3	3327.53	3.8	1	37.8	31.7	95.00%	K.ADLLNEMLESPDSQNWDNETTQELHSALK.V		K.ADLLNEMLESPDSQNWDNETTQELHSALK.V
171	186	3	1740.97	3	0	35.8	26.3	95.00%	K.ISESDLAVLKPSNQLK.T		K.ISESDLAVLKPSNQLK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
285	A6ZT43_YEAS7	15.61%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
368	383	2	1797.9	2.4	1	39.3	31.9	95.00%	K.KPNLHGYGHPNPPNEK.S		K.KPNLHGYGHPNPPNEK.S
296	312	2	1863.95	-1.6	1	69.9	31.6	95.00%	R.STNVYDLAQGLPVQFGR.Y		R.STNVYDLAQGLPVQFGR.Y
457	478	3	2805.42	2.7	0	57.5	30	95.00%	K.LQEQQLQEQQLQQQQQQQQQLR.A		K.LQEQQLQEQQLQQQQQQQQLR.A
479	499	2	2212.06	-0.4	1	66.7	32.5	95.00%	R.ATGQPPSQPQAQTQSQQFGAR.Y		R.ATGQPPSQPQAQTQSQQFGAR.Y
360	367	2	958.49	-0.13	1	34.2	29.6	95.00%	R.GWDLNINK.K		R.GWDLNINK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
286	B3LP77_YEAS1	7.62%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
361	376	2	1665.73	1.7	1	69.1	34	95.00%	Y.SSGSGEYIHSSDINGR.C	Deamidation (+1)	K.DLHPPYSEGCSAVMAVTYSSGSGEYIHSSDINGR.C
409	423	2	1633.89	-1.1	1	57.7	28.1	95.00%	R.DVQYLSILSAVGLEK.N		R.DVQYLSILSAVGLEK.N
333	342	2	1053.59	4.3	0	49.9	26.1	95.00%	Y.SITIGAIDHK.D		R.GDNCNYDGYTNSIYSITIGAIDHK.D
270	290	3	2281.07	5	1	27.5	33.6	93.00%	Y.SCSWGPADDGRHLQGPSDLVK.K	Carbamidomethyl (+57)	R.ILSGDITTEDEAASLIYGLDVNDIYSCSWGPADDGRHLQGPSDLVK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
287	A6ZLE8_YEAS7	20.43%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
431	448	4	2066.94	-0.23	1	25.9	33.7	94.30%	K.HHTSELNSSTSEPDSQRR.S		K.HHTSELNSSTSEPDSQRR.S
325	344	2	2141.88	1.4	1	114	34.1	95.00%	K.CNGQDMSEVGNGPGSYDISR.S	Carbamidomethyl (+57)	K.CNGQDMSEVGNGPGSYDISR.S
70	90	2	1956.95	2.3	0	89.8	32.5	95.00%	F.LQAGPSDGNAIGTSATAANNK.S		K.QGLSVEDDSPFEGSSSSAGLPSPNTNTNADSTTAFLQAGPSDGNAIGTSATAANNK.S
312	324	2	1590.81	0.57	1	58.1	31.5	95.00%	K.GVWQLELQDYVNK.C		K.GVWQLELQDYVNK.C

425	448	4	2694.29	-0.95	1	25.5	31.7	95.00%	K.ASLDLKHHTSELNSSTSEPDSQR R.S		K.ASLDLKHHTSELNSSTSEPDSQR R.S
449	465	2	1675.83	2.4	1	91.4	32.4	95.00%	R.SKDSSVPLIIDSSGSAN.-		R.SKDSSVPLIIDSSGSAN.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
288	MHP1_YEAST	3.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
113	133	3	2361.11	3.9	0	60.1	33.7	95.00%	K.SVVETNLSNVEADSGHHHHHR.H		K.SVVETNLSNVEADSGHHHHHR.H
551	564	2	1386.7	3	0	35.9	31.2	95.00%	R.NIVMAAAEAAAEAR.A		R.NIVMAAAEAAAEAR.A
987	1003	2	1887.93	-1.9	1	58.8	32.7	95.00%	R.LNYFSMLGTELDLASSK.A		R.LNYFSMLGTELDLASSK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
289	A6ZKL0_YEAS7	23.85%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	90	3	2060.11	5.1	1	62.2	27.1	95.00%	K.TFLVANVKDLETLTMHTK.T		K.TFLVANVKDLETLTMHTK.T
81	90	2	1187.59	3.4	0	45.3	31.3	95.00%	K.DLETLTMHTK.T		K.DLETLTMHTK.T
73	80	2	890.53	3.5	1	25.7	28.2	91.70%	K.TFLVANVK.D		K.TFLVANVK.D
91	103	2	1387.71	3.2	1	82.5	30.6	95.00%	K.TYAAEIAHNISAK.N		K.TYAAEIAHNISAK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
290	B3LLW4_YEAS1	23.95%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
140	164	3	2963.43	3.3	2	66.7	31.1	95.00%	K.HQEFQNTNIIKNPTDDDFPHEAV VR.E		K.HQEFQNTNIIKNPTDDDFPHEAV VR.E
2	16	2	1532.84	-0.92	1	42.7	27.8	95.00%	M.ALSLGQFINVGGMVK.D		-.MALSLGQFINVGGMVK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
291	A6ZKZ2_YEAS7	25.64%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
104	116	4	1486.82	0.55	2	25.1	28.5	95.00%	R.HKNVPVHVSPAFR.V		R.HKNVPVHVSPAFR.V
117	133	2	1855	2.3	0	70.7	27.6	95.00%	R.VQVGDIVTVGQCRPISK.T	Carbamidomethyl (+57)	R.VQVGDIVTVGQCRPISK.T
58	67	2	1148.6	2.5	1	39.4	30.6	95.00%	K.CPFTGLVSIR.G	Carbamidomethyl (+57)	K.CPFTGLVSIR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
292	A6ZMQ5_YEAS7	20.00%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
87	98	2	1345.67	2.6	0	64.2	31.2	95.00%	K.VEEMNNIIAASR.R		K.VEEMNNIIAASR.R
57	62	2	741.48	3.7	0	21.7	23.3	90.00%	R.LIDLIR.N		R.LIDLIR.N
85	98	2	1544.8	3	1	89.3	30.2	95.00%	K.AKVEEMNNIIAASR.R		K.AKVEEMNNIIAASR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
293	A6ZRY2_YEAS7	13.66%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
252	280	3	3046.4	-0.58	1	65.9	32.6	95.00%	K.TQTDRTNIDNSTGQAGQANAQS ANTVNNR.V		K.TQTDRTNIDNSTGQAGQANAQS ANTVNNR.V
257	280	2	2445.12	-0.57	0	100	33.6	95.00%	R.TNIDNSTGQAGQANAQSANTVN NR.V		R.TNIDNSTGQAGQANAQSANTVN NR.V
95	109	2	1858.91	-0.43	1	72.6	32.6	95.00%	K.SSLDELMTYYQQILR.V		K.SSLDELMTYYQQILR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
294	A6ZMN0_YEAS7	8.55%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
306	322	2	1951.99	2.4	2	58.8	30.8	95.00%	R.TLFPQCEKGDIVGIGYR.S	Carbamidomethyl (+57)	R.TLFPQCEKGDIVGIGYR.S
244	259	2	1763.83	2.1	1	54.3	33	95.00%	K.IFETDGPLNSDENVSK.G		K.IFETDGPLNSDENVSK.G
75	88	3	1617.79	2.9	1	29.4	31.5	95.00%	R.LITAYYNEHGPGQR.I		R.LITAYYNEHGPGQR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
295	A6ZTE7_YEAS7	7.89%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
342	362	4	2452.2	-0.31	1	24.5	32.1	94.60%	K.NHDELVVFSHDGHYLTIEVTK.D		K.NHDELVVFSHDGHYLTIEVTK.D
142	149	2	915.51	3.9	0	44.3	30.7	95.00%	Y.LNDQVSIK.N		K.FDLHDWFLLEEGVDNAPSTTILPQSSYLNDQVSIK.N
662	677	3	1896.03	4.2	1	68.3	26.8	95.00%	Y.TPVIPINDNFIITHFR.N		K.EFMATPYTPVIPINDNFIITHFR.N
467	481	2	1588.83	-0.58	0	41.1	30.6	95.00%	R.ETTNLNTLGITLGDK.S		R.ETTNLNTLGITLGDK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
296	SNQ2_YEAST	3.80%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1082	1092	2	1326.66	1.3	1	49.3	31.9	95.00%	K.NSATILNYFER.N		K.NSATILNYFER.N
975	998	3	2621.26	5.6	1	36	32.1	95.00%	R.VLGMEEYAEALVGEVGCGLNVEQR.K	Carbamidomethyl (+57)	R.VLGMEEYAEALVGEVGCGLNVEQR.K
285	294	2	1167.63	-0.1	1	29.2	28.6	95.00%	R.DLYATIFGLR.H		R.DLYATIFGLR.H
338	349	2	1237.62	3.1	1	64.3	31.6	95.00%	R.GLDASTALEYAK.A		R.GLDASTALEYAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
297	A7A001_YEAS7	5.15%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
61	76	3	1822.98	2.5	1	56.4	27.6	95.00%	K.RVKPIEVDPNLSEAEK.V		K.RVKPIEVDPNLSEAEK.V
571	585	2	1770.93	3.3	1	70.1	29.5	95.00%	R.EVDLDLLKQEIAEEK.A		R.EVDLDLLKQEIAEEK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
298	A6ZTJ7_YEAS7	3.57%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
849	869	3	2528.98	4.2	2	38.1	33.8	95.00%	Y.VSETSGMHDIDPSDDDRWCEY.I	Oxidation (+16)/ Carbamidomethyl (+57)	K.LMGNTTRPAILLSYLVVDPGEGNYNTYVSETSGMHDIDPSDDDRWCEYILYK.G
886	898	2	1407.73	4.7	2	50.9	30.5	95.00%	R.GTITDTELQVGKF.Q		R.GTITDTELQVGKFQVLSEQVLVEHSDSMYEYGHMSEPEYEDMK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
299	KHA1_YEAST	8.36%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
834	851	2	2059.97	4.2	1	50.6	33.4	95.00%	F.IIGEDLPDESEPFSEEVR.T		K.VPEEAIEKPSFIETVLDVGLSDTALADIEETTFIIGEDLPDESEPFSEEVR.T
478	496	2	1986.09	-1.2	0	76.3	26.9	95.00%	R.IGELTTVINTTEAISPSLK.L		R.IGELTTVINTTEAISPSLK.L
620	632	2	1512.76	-0.81	1	47.3	31.4	95.00%	K.IPFSSEVIFSTMR.E		K.IPFSSEVIFSTMR.E
563	573	2	1158.64	2.9	1	30	28.8	95.00%	K.LTPFEGVGALR.A		K.LTPFEGVGALR.A
643	654	2	1357.75	-0.45	0	45.2	28.8	95.00%	K.MDSTDLILLPLK.G		K.MDSTDLILLPLK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
300	A6ZXS1_YEAS7	3.29%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
246	260	2	1756.85	1.9	0	64.2	32.6	95.00%	R.LDDQTDVEQSPLLER.S		R.LDDQTDVEQSPLLER.S
245	260	2	1912.96	3.1	1	58.3	31.6	95.00%	K.RLDDQTDVEQSPLLER.S		K.RLDDQTDVEQSPLLER.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
301	A6ZR85_YEAS7	22.69%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
52	66	2	1680.83	2.7	1	31.5	32.7	93.70%	R.DLSEASVYPEYALPK.T		R.DLSEASVYPEYALPK.T
71	82	3	1485.7	1.3	1	39.6	33.2	95.00%	K.LHYCVSCAIHAR.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.LHYCVSCAIHAR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
302	B3LU76_YEAS1	25.51%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

50	65	3	1766.89	3.6	0	26	31.5	93.80%	K.MNAPQKPEDIPVATEK.T		K.MNAPQKPEDIPVATEK.T
147	176	3	2968.4	2.1	1	74.5	31.8	95.00%	K.NSFAELASIEEVHGGSPWGAGTLAGPDGSR.T		K.NSFAELASIEEVHGGSPWGAGTLAGPDGSR.T
33	49	2	1990.03	3.7	1	52.3	30.3	95.00%	K.ADIYRVEETLPDEVLTK.M		K.ADIYRVEETLPDEVLTK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
303	A6ZVQ4_YEAS7	9.52%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
130	147	2	1981.98	4	1	67.5	31.8	95.00%	K.FYNVDGVDNTLASLLGER.L		K.FYNVDGVDNTLASLLGER.L
49	61	2	1480.72	0.32	1	76.5	32.8	95.00%	R.TAVESSAFNWIEK.R		R.TAVESSAFNWIEK.R
471	499	3	3065.4	4.5	1	62.5	32.7	95.00%	Y.AGQDYSINPVDGSIIGPVNEEPENDDGHK.S		K.EIFWLGQLYAGQDYSINPVDGSIIGPVNEEPENDDGHK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
304	B3LSP7_YEAS1	13.40%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
41	52	2	1288.74	3.7	1	39.5	25.1	95.00%	F.TAINTLTKPALF.S		K.LGSASFTAINTLTKPALFSFYDDDITK.N
70	88	2	1955.02	2.6	0	64.9	29.9	95.00%	K.ALLSNASQLEMVPPSATAR.H		K.ALLSNASQLEMVPPSATAR.H
130	137	2	877.49	3.6	1	32.8	30.4	95.00%	K.GDIVSFLK.H		K.GDIVSFLK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
305	A6ZTP3_YEAS7	12.58%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
49	61	2	1480.79	3.8	1	64.5	28.9	95.00%	R.GIITIEYFDPVSK.S		R.GIITIEYFDPVSK.S
80	92	3	1400.73	1.9	1	29.8	30.3	95.00%	K.TVNNFAMLAHGVK.A		K.TVNNFAMLAHGVK.A
93	106	2	1570.77	2.5	2	43.8	32.4	95.00%	K.AVIEGKDPNDIHTY.S		K.AVIEGKDPNDIHTYSYR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
306	A6ZPD4_YEAS7	19.21%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
62	75	3	1640.95	3.4	1	37.1	23	95.00%	R.LTKVDRETDIVKPK.K		R.LTKVDRETDIVKPK.K
103	117	2	1717.87	2.6	1	85.7	31.7	95.00%	K.INEKPTVVNDYEAAR.A		K.INEKPTVVNDYEAAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
307	B3LMS1_YEAS1	5.94%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
257	264	2	1101.52	-0.19	1	35.2	32.3	95.00%	K.QEIQDWQR.S		K.QEIQDWQR.S
265	285	3	2359.03	3.5	2	45	34.2	95.00%	R.SHGHNRDPESSEETHSGPTLW.Q		R.SHGHNRDPESSEETHSGPTLWQYVTDPSYK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
308	A6ZLN3_YEAS7	8.54%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
317	336	3	2372.18	3.6	1	30.3	31.7	95.00%	K.NKEDIQEVDLVRTETEPETK.L		K.NKEDIQEVDLVRTETEPETK.L
248	256	2	1116.59	4	1	37.2	30.9	95.00%	K.VLDQDWTLK.L		K.VLDQDWTLK.L
257	262	2	775.46	-0.94	1	23.1	26	91.00%	K.LIDIFR.G		K.LIDIFR.G
293	306	2	1533.71	-0.73	0	63.6	32.8	95.00%	R.NLGTTVSVEDEENK.A		R.NLGTTVSVEDEENK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
309	A6ZZW6_YEAS7	5.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
249	265	2	1829.92	-1	0	46.5	31.2	95.00%	K.VDLMDQGTDVIDILAGR.V		K.VDLMDQGTDVIDILAGR.V
166	184	3	2079.2	2.7	1	19.4	21.1	93.70%	R.IYSPHVLTLTLVDLPGLTK.V		R.IYSPHVLTLTLVDLPGLTK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
310	A6ZLE7_YEAS7	6.44%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
96	104	2	1087.57	0.35	1	31.4	31	95.00%	R.NSDLWNLVK.S		R.NSDLWNLVK.S

325	341	3	1825.94	-0.77	1	33.8	30.4	95.00%	R.WGDAPVHSIAASLFLDK.S		R.WGDAPVHSIAASLFLDK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
311	A6ZUX1_YEAS7	2.65%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
490	497	2	961.52	0.38	1	41.1	28.3	95.00%	K.LALIDDFR.E		K.LALIDDFR.E
708	718	3	1266.78	3.1	1	19.5	17.4	93.90%	R.SIKRPELGLRV.-		R.SIKRPELGLRV.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
312	VTH2_YEAST	3.23%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1494	1517	3	2716.21	4.9	1	87.6	33.4	95.00%	F.RGQGSNSEIEQEDVDTSQQEHTSR.T		K.GATYSSLLHDQLSDEPDGFHEDSNDLSSFRGQGSNSEIEQEDVDTSQQEHTSR.T
394	406	2	1445.76	3.1	1	39.9	30.3	95.00%	K.VSVDNGLTWTNLK.V		K.VSVDNGLTWTNLK.V
1120	1132	2	1435.69	4.2	1	62.6	32.8	95.00%	F.LTTDGGETWTEVK.K		R.LLPYEECSTFLTTDGGETWTEVK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
313	A6ZYD0_YEAS7	6.86%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	16	2	1828.73	3.5	1	34.6	33.9	95.00%	M.SDSNQGNNQQNYQQY.S	Acetyl (+42)	-.MSDSNQGNNQQNYQQYSQNGNQQQGNNR.Y
83	98	2	1774.82	2.6	1	105	33.7	95.00%	Y.NPQGGYQQQFNPQGGR.G		R.YQGYQAYNAQAQPAGGYYQNYQGYSGYQQGGYQQYNPDAGYQQQYNPQGGYQQQYNPQGGYQQQFNPQGGR.G
17	32	2	1855.79	3.5	2	39.8	33.7	95.00%	Y.SQNGNQQQGNNRYQGY.Q	Deamidation (+1)	-.MSDSNQGNNQQNYQQYSQNGNQQQGNNRYQGYQAYNAQAQPAGGYYQNYQGYSGYQQGGYQQYNPDAGYQQQYNPQGGYQQYNPQGGYQQQFNPQGGR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
314	B3LJ36_YEAS1	6.76%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
549	560	3	1415.77	3	1	37.7	29.3	95.00%	K.ALKDIDLETDRK.D		K.ALKDIDLETDRK.D
67	79	2	1379.66	2.6	1	40.6	33	95.00%	K.SPLDGSFDTSNLK.R		K.SPLDGSFDTSNLK.R
67	80	2	1535.76	3	1	52.1	32.4	95.00%	K.SPLDGSFDTSNLKR.T		K.SPLDGSFDTSNLKR.T
561	574	2	1641.89	4	1	70.6	28.8	95.00%	K.DIDIEIVKQEIAEK.K		K.DIDIEIVKQEIAEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
315	A6ZN90_YEAS7	15.28%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
103	110	2	927.58	3	1	21.7	24.2	90.10%	R.KVLQALEK.I		R.KVLQALEK.I
25	38	3	1543.86	1.2	2	45.7	27.1	95.00%	R.QGKLEVPGYVDIVK.T		R.QGKLEVPGYVDIVK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
316	A6ZT39_YEAS7	8.37%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
330	343	2	1592.83	-0.82	1	64.2	30.2	95.00%	R.DLENLLELSYGLSK.A		R.DLENLLELSYGLSK.A
321	329	2	1051.48	4.7	1	32.3	31	95.00%	Y.AYSCDALPR.D	Carbamidomethyl (+57)	K.IYGYIDMHSYSQEILYPYAYSCDALPR.D
137	149	2	1410.77	3.7	1	79.1	26.9	95.00%	R.SFPSLVAVEHLGR.T		R.SFPSLVAVEHLGR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
317	A6ZVG8_YEAS7	7.24%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
345	358	3	1691.87	-0.092	1	29.8	30.9	95.00%	R.ISILCVDNAIHYFK.I	Carbamidomethyl (+57)	R.ISILCVDNAIHYFK.I
758	796	3	4109	3.1	1	50.1	28.4	95.00%	Y.SLHDMADEAGLPVQTEDGEATGTIVLPQPINATSSLFER.Y		K.NIYPDVYSLHDMADEAGLPVQTEDGEATGTIVLPQPINATSSLFER.Y
471	484	2	1688.78	2.3	1	31.1	34.1	90.90%	K.ETAQLLSCQDSFYK.N	Carbamidomethyl (+57)	K.ETAQLLSCQDSFYK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
318	A6ZUT7_YEAS7	3.79%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1068	1085	2	2012.98	-2.2	1	55.5	32.2	95.00%	R.SFVYNNLNEVLGGMDTIK.A		R.SFVYNNLNEVLGGMDTIK.A
148	159	2	1489.66	-1.2	1	63.5	34.2	95.00%	R.MSIETLYDDFEK.N		R.MSIETLYDDFEK.N
729	743	2	1726.85	5	1	91.8	32.5	95.00%	K.DIYLFDDVLSAVDSR.V		K.DIYLFDDVLSAVDSR.V
1221	1231	3	1225.76	3.6	1	32.5	19.5	95.00%	F.AYRPGLPIVLK.N		R.KPEMTPPESWPSMGEIIFENVDFAYRPGLPIVLK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
319	B3LKP8_YEAS1	5.76%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
7	30	4	2618.33	-0.94	2	51.3	29.8	95.00%	R.TLKSDTDVTSLNASTVSHQSKPFR.Q		R.TLKSDTDVTSLNASTVSHQSKPFR.Q
327	348	4	2579.13	0.83	1	34.5	34	95.00%	K.SNQKPSHSDEQFDQEDHIDAPR.S		K.SNQKPSHSDEQFDQEDHIDAPR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
320	A6ZMP4_YEAS7	23.05%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
83	99	2	1999.98	4.7	1	44.4	32.1	95.00%	R.SLDDYISQATDLQYQLK.A		R.SLDDYISQATDLQYQLK.A
54	66	2	1584.79	2.2	1	31.2	31.6	94.70%	R.YENIINQIDAQHK.D		R.YENIINQIDAQHK.D
44	53	2	1100.59	-0.11	0	78.1	28.4	95.00%	K.INSINANLSR.Y		K.INSINANLSR.Y
210	237	3	3293.59	5.9	1	61	30.4	95.00%	K.TMAELTQLFNDMEELVIEQQENVDVIDK.N		K.TMAELTQLFNDMEELVIEQQENVDVIDK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
321	A6ZLW3_YEAS7	39.32%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
100	117	3	1975.94	5.2	1	37.9	33.4	95.00%	R.NTGSIEHTMENIFAGKLD.-		R.NTGSIEHTMENIFAGKLD.-
32	59	3	2885.4	-0.94	0	57.2	31.5	95.00%	R.TVQDAKPAPSVATNDPSPEPVPSAPEER.V		R.TVQDAKPAPSVATNDPSPEPVPSAPEER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
322	A6ZYE1_YEAS7	11.81%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
240	254	3	1728.85	3.9	1	32.5	32.3	95.00%	R.QFLDNFAMGSHPLPR.I		R.QFLDNFAMGSHPLPR.I
176	199	3	2558.25	2.5	1	38.3	31.7	95.00%	R.TVMSLPGNHDIGFGDTVVESSLQR.F		R.TVMSLPGNHDIGFGDTVVESSLQR.F
286	304	2	2215.12	4.1	1	62	30.4	95.00%	K.GHQYQTVIENDISQEILTK.T		K.GHQYQTVIENDISQEILTK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
323	A6ZME5_YEAS7	7.65%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
123	131	2	1035.54	3.6	1	32.1	30.2	95.00%	R.NVTEFSIAR.A		R.NVTEFSIAR.A
284	292	2	1100.66	0.43	1	23.1	25.8	91.30%	K.ILPFELLTR.S		K.ILPFELLTR.S
132	156	3	2446.24	5	0	53.8	30.5	95.00%	R.AICGIGAGGLNAISSIAVSDICTAR.E	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.AICGIGAGGLNAISSIAVSDICTAR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
324	A6ZTG2_YEAS7	15.23%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

26	48	2	2504.2	-2.9	0	131	32.8	95.00%	K.LTSAAQSNPNDEQMSTIESLIQK.I			K.LTSAAQSNPNDEQMSTIESLIQK.I
6	25	3	2124.03	2.6	1	63.6	33	95.00%	K.LISEAESHFSQGNHAEAVAK.L			K.LISEAESHFSQGNHAEAVAK.L
68	84	2	1643.73	3	1	65	33.9	95.00%	R.AAGGGSSFMNTLMADSK.G			R.AAGGGSSFMNTLMADSK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
325	TCB1_YEAST	5.40%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
597	616	3	2173.1	4.8	1	45.9	31	95.00%	K.DGKGEEIGSTIQTLNDLIDR.S		K.DGKGEEIGSTIQTLNDLIDR.S
1000	1018	2	2069	2.9	1	49.3	32.9	95.00%	R.SAENLIASDLNGYSDPYLK.Y		R.SAENLIASDLNGYSDPYLK.Y
575	586	2	1437.66	3	1	61.4	32.9	95.00%	K.WNSDYEAVIADR.R		K.WNSDYEAVIADR.R
721	733	2	1549.75	1.3	0	67.4	32.7	95.00%	R.ITLQCMDVETVNK.D	Carbamidomethyl (+57)	R.ITLQCMDVETVNK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
326	A6ZVY2_YEAS7	8.86%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
546	563	2	2067.98	5.9	1	80.7	33.3	95.00%	R.SEIDLDTGCSVENLELFK.A	Carbamidomethyl (+57)	R.SEIDLDTGCSVENLELFK.A
345	357	2	1247.66	4.6	0	56	30.2	95.00%	F.VIALSNTGSMGAK.V		R.LLSGSNSEDISASPFVIALSNTGSMGAK.V
43	63	2	2466.16	2.5	0	55.6	33.1	95.00%	K.QSNLHVIPEDLENSEQTEQEK.I		K.QSNLHVIPEDLENSEQTEQEK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
327	A6ZRC2_YEAS7	2.10%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
682	691	2	1126.51	-0.26	1	56.1	32.1	95.00%	K.CTINGVSYGR.A	Carbamidomethyl (+57)/ Deamidation (+1)	K.CTINGVSYGR.A
1017	1039	3	2436.2	5.4	2	42	31.3	95.00%	K.TTGDDVKEFGSEPSEIVDALLSK.Y		K.TTGDDVKEFGSEPSEIVDALLSK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
328	A7A0E6_YEAS7	8.12%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
272	292	3	2379.19	4.8	1	43	30.9	95.00%	K.VNENWNVEDGHITDVLLGSLR.S		K.VNENWNVEDGHITDVLLGSLR.S
12	32	3	2272.22	3.9	0	49.3	27.6	95.00%	K.KPILAVPEPALADTHSEEISR.S		K.KPILAVPEPALADTHSEEISR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
329	A6ZMV1_YEAS7	10.70%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
188	201	2	1563.79	2.9	1	67.7	31.2	95.00%	K.NTVSNACLFQIAAR.L	Carbamidomethyl (+57)	K.NTVSNACLFQIAAR.L
324	336	2	1422.74	-1	1	49.9	31.3	95.00%	R.MLGLTSVMAPFTR.D		R.MLGLTSVMAPFTR.D
35	56	2	2434.12	3.5	1	108	33.6	95.00%	K.TSICDATALIQGGMLDYYEGTR.Y	Carbamidomethyl (+57)	K.TSICDATALIQGGMLDYYEGTR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
330	A6ZWH0_YEAS7	23.35%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
139	149	2	1302.72	3.4	1	31.6	27.6	95.00%	K.QIVNIPSFMVR.L		K.QIVNIPSFMVR.L
180	197	2	1835.72	-1.7	1	92.7	33.2	95.00%	R.KAEASGEAADEADEADEE.-		R.KAEASGEAADEADEADEE.-
155	171	3	1781.9	2.8	1	25.1	31.3	92.70%	K.HIDFAPTSPFGGARPGR.V		K.HIDFAPTSPFGGARPGR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
331	B3LLV1_YEAS1	9.91%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
164	173	2	1203.62	3.6	1	33	31.1	95.00%	W.YHDLVTDLTK.S		K.DDSFPYDYDEELSLSLSEWYHDLVTDLTK.S
416	427	3	1443.76	5.5	1	33.4	29.3	95.00%	F.HLHGHAFQTIQR.D		K.DEIVEIVLNNQDTGTHPFHLHGHAFQTIQR.D

394	415	3	2523.3	5	2	41.3	29.1	95.00%	F.ILEKDEIVEIVLNNQDTGTHPF.H		K.VPTLMTVLSSGDQANNSEIYGSN THTFILEKDEIVEIVLNNQDTGTHPF HLHGHAFQTIQR.D
596	614	3	2263.07	5	0	41.3	32.9	95.00%	R.DLHVDPEVLLNEVDENEER.E		R.DLHVDPEVLLNEVDENEER.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
332	A7A105_YEAS7	8.65%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
208	218	2	1284.75	3.5	1	58.5	26.4	95.00%	R.LVDLLHLATYK.D		R.LVDLLHLATYK.D
187	197	2	1319.73	-0.61	1	37.8	27.3	95.00%	K.YLSLNDIELLK.T		K.YLSLNDIELLK.T
284	291	2	931.48	1.1	1	34.2	30.8	95.00%	R.LANPNFEK.Q		R.LANPNFEK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
333	A6ZUA3_YEAS7	20.49%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
176	196	3	2379.29	3.7	1	35.5	24.9	95.00%	K.YGILSIDDLIHEIITVGPHFK.Q		K.YGILSIDDLIHEIITVGPHFK.Q
159	175	2	1837.01	2.7	1	33	25.2	95.00%	K.QRVPLSDNAIIEANLGK.Y		K.QRVPLSDNAIIEANLGK.Y
207	218	2	1225.62	3.2	1	39	30.7	95.00%	K.LSNPSGGWGVPR.K		K.LSNPSGGWGVPR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
334	A6ZRX9_YEAS7	5.61%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
202	235	4	3733.58	-0.44	1	28	31.9	95.00%	R.QEHQLNDSASSDFTSHESDSINQ SSPSSNQDIDK.V		R.QEHQLNDSASSDFTSHESDSINQ SSPSSNQDIDK.V
236	241	2	731.44	3.5	1	31.4	26.9	95.00%	K.VPFLTR.N		K.VPFLTR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
335	A6ZTK4_YEAS7	7.69%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
319	346	3	3074.4	3	2	29.9	32.7	95.00%	R.TYSLHEPTDAVHANIDTAPDGCK ESSIF.H	Carbamidomethyl (+57)	R.TYSLHEPTDAVHANIDTAPDGCK ESSIFHHVFHTK.V
259	277	3	2289.09	2.9	1	34	33.3	95.00%	R.IQDDSENIHHRNENVNSIR.G		R.IQDDSENIHHRNENVNSIR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
336	A6ZZN9_YEAS7	5.36%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
147	154	2	896.55	3.7	0	46.7	20.3	95.00%	Y.VSLNPIVR.C		K.AHNMGPNEVFVEEEYIDEDDTYV SLNPIVR.C
212	224	3	1540.83	2	1	29.1	28.3	95.00%	R.VHLSYVKENPVEK.G		R.VHLSYVKENPVEK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
337	A6ZWW4_YEAS7	13.91%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
143	170	3	2901.5	4.4	1	55.2	27.6	95.00%	Y.VDQLNENNLVSIGDFSTRPALVG GSTAK.K		R.GWGYDTNFTLGICSSPVGEAES QQLSNLTGAFYVDQLNENNLVSIG DFSTRPALVGGSTAK.K
332	346	2	1678.71	-0.64	1	32.3	34.1	92.80%	R.LRSSPSASSSSLANR.E	Phospho (+80)/ Phospho (+80)	R.LRSSPSASSSSLANR.E
190	199	2	1179.6	0.77	1	42.5	31.6	95.00%	K.ATLLNFVCDK.E	Carbamidomethyl (+57)	K.ATLLNFVCDK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
338	A6ZXS3_YEAS7	14.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
183	200	2	1849.09	0.05	0	26.2	17.8	95.00%	K.IPIVPVVVSNTSTLVSPK.Y		K.IPIVPVVVSNTSTLVSPK.Y
244	270	3	2954.47	2	1	39.3	29.8	95.00%	K.EIGYSPAINDTTLPPQAIEYAALQH DK.K		K.EIGYSPAINDTTLPPQAIEYAALQH DK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
339	A6ZWB1_YEAS7	9.35%	99%	1

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

22	31	2	1096.63	1.4	0	22.9	25.7	91.20%	R.VNNPNVSLIK.I		R.VNNPNVSLIK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
340	AKR2_YEAST	3.87%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
270	283	3	1699.81	2.9	1	35.5	32.9	95.00%	K.SLFEQALQHHGYDR.L		K.SLFEQALQHHGYDR.L
223	237	2	1613.78	1	1	38.6	33.3	95.00%	R.GFNALHCALVGGDQR.V	Carbamidomethyl (+57)	R.GFNALHCALVGGDQR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
341	B3LM88_YEAS1	19.92%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
44	66	2	2478.23	5	1	28.6	31.2	91.50%	F.TGPGFYDPVDELLIEPSLPGLSY.S		K.SNQVFTGPGFYDPVDELLIEPSLPGLSYSFTEDGWYEEATYQVSGNPR.N
148	158	2	1203.6	4.1	1	29.1	30.9	92.90%	Y.AVGIDPYHGIY.T		K.EYAVGIDPYHGIYTLQLYQYDGTPMQPLYLAYRPPMMLPTETLNPTSSATSTDDPSSNK.K
121	137	2	1959.83	2.7	1	66.4	34	95.00%	R.QLFSDPCNDDGVSTYSR.Y	Carbamidomethyl (+57)	R.QLFSDPCNDDGVSTYSR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
342	A6ZXK6_YEAS7	31.43%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
109	128	2	2149.09	3.2	1	90	31.2	95.00%	R.NVYPSVETPLLQGAAPHDNK.Q		R.NVYPSVETPLLQGAAPHDNK.Q
85	108	4	2648.29	7	0	23.5	31.1	94.50%	R.NVPSNRPQNSQTPQNRPQQGSSAR.N	Deamidation (+1)	R.NVPSNRPQNSQTPQNRPQQGSSAR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
343	A7A0L5_YEAS7	10.04%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
160	174	3	1661.78	4.2	0	43.6	33.2	95.00%	K.NADDAHTIPESHLSR.R		K.NADDAHTIPESHLSR.R
118	137	3	2165.02	4.7	1	38.2	32.9	95.00%	Y.INTQDINHKDNGPPSASSNR.A	Deamidation (+1)	R.SSSQPSHHHSGGTNNNNNNNNNNNSNNNGNDGGNDDDYDYEMQDYRPSPQSARPTPTYVPQYSVESGAAFPIQEVIPSAYINTQDINHKDNGPPSASSNR.A
181	212	4	3206.38	-0.94	1	33.6	33.4	95.00%	R.ATSNAGHSANTGATNGRTTGAQTNMESNESPR.N	Deamidation (+1)/ Oxidation (+16)	R.ATSNAGHSANTGATNGRTTGAQTNMESNESPR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
344	A6ZT07_YEAS7	0.99%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
77	85	2	1108.53	-1.6	1	30.9	31.8	94.00%	R.NSMLDIFNR.C		R.NSMLDIFNR.C
1429	1437	2	958.49	2.1	0	36.2	30.6	95.00%	F.ATAQQGNIR.I	Deamidation (+1)	K.NEEFATAQQGNIR.I
1284	1302	2	2129.08	5.5	0	33.5	30.8	95.00%	K.VLENTLTDIVCELSNANPK.V	Carbamidomethyl (+57)	K.VLENTLTDIVCELSNANPK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
345	A6ZPF3_YEAS7	2.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
49	62	3	1667.9	4.1	2	36.2	27.9	95.00%	R.KDGLHEIYNPLEIK.Q		R.KDGLHEIYNPLEIK.Q
50	62	2	1539.8	4.5	1	32.3	29.8	95.00%	K.DGLHEIYNPLEIK.Q		K.DGLHEIYNPLEIK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
346	A6ZQP7_YEAS7	27.88%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
147	165	2	2073.01	3.7	0	30.3	32.4	92.30%	K.NPHDIIEGINAGEIEIPEN.-		K.NPHDIIEGINAGEIEIPEN.-
131	142	2	1289.64	-0.22	0	67.4	32.2	95.00%	K.EILGTAQSVGCR.V	Carbamidomethyl (+57)	K.EILGTAQSVGCR.V
17	31	2	1296.71	2.9	0	37.8	27.4	95.00%	R.AVGGEVGASAALAPK.I		R.AVGGEVGASAALAPK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
347	A6ZL13_YEAS7	4.68%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
399	411	2	1379.84	4.2	0	50.4	16.2	95.00%	R.LLLSLAEQGVLPK.C		R.LLLSLAEQGVLPK.C
72	87	3	1924.97	3	1	28.6	31.2	95.00%	K.RQLPPDRNSELESQEK.N		K.RQLPPDRNSELESQEK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
348	A6ZXS0_YEAS7	13.30%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
225	239	2	1639.88	0.36	1	83.1	27.7	95.00%	K.DFLSGTVLYLNSLAK.R		K.DFLSGTVLYLNSLAK.R
306	320	2	1749.83	1.7	1	85.6	32.9	95.00%	K.STIVGWNSTVGQWCR.L	Carbamidomethyl (+57)	K.STIVGWNSTVGQWCR.L
269	286	2	1776.98	2.7	0	36.9	27	95.00%	K.IGPDVVIGPNVTIGDGVR.I		K.IGPDVVIGPNVTIGDGVR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
349	A6ZQX5_YEAS7	16.30%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	201	2	1115.64	3.8	1	50.5	28.4	95.00%	R.FNVTVAQLPK.D		R.FNVTVAQLPK.D
44	66	3	2441.3	1.8	2	20.6	26.5	93.30%	R.RASSIFSINTTPLAPPNATDIQK.F		R.RASSIFSINTTPLAPPNATDIQK.F
67	78	3	1523.63	3.2	1	36.9	33.6	95.00%	K.FTSDEHHFSMMR.N		K.FTSDEHHFSMMR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
350	A6ZT50_YEAS7	6.65%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
13	22	2	1126.64	-1.2	0	30	26.3	95.00%	K.TPLPLCSVIK.S	Carbamidomethyl (+57)	K.TPLPLCSVIK.S
2	12	2	1215.56	3.6	1	43.7	32.9	95.00%	M.AFSDFAAICSK.T	Carbamidomethyl (+57)	-.MAFSDFAAICSK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
351	ERV41_YEAST	12.50%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
113	137	2	2809.45	4.4	1	66.4	28.2	95.00%	K.VNDINEIITPELDEILGEAIPAEFR.E		K.VNDINEIITPELDEILGEAIPAEFR.E
173	182	2	1044.58	0.18	0	60.9	28.3	95.00%	R.VSGELQITAK.S		R.VSGELQITAK.S
238	246	2	990.58	5	1	35.4	26.9	95.00%	Y.TSVVPTLFK.K		K.FNHVINEFSFGDFYPYIDNPLDNT AQFNQDEPLTTYVYYTSVVPTLFK. K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
352	A6ZT94_YEAS7	9.18%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
335	344	2	1235.57	4.3	2	44.4	31.4	95.00%	R.ICAEVDRSTW.T	Carbamidomethyl (+57)	R.ICAEVDRSTWTAFLSVDDTIFSTH DNCFDLSNDQNEGGSGYDFILEST DTTK.V
194	211	2	2043.03	-1.7	1	42.3	30.8	95.00%	R.ASLPNEPICTENLTPFIK.L	Carbamidomethyl (+57)	R.ASLPNEPICTENLTPFIK.L
275	289	3	1661.93	2.4	0	27.3	25.8	95.00%	R.GERPIPKPLDGNTLR.C		R.GERPIPKPLDGNTLR.C
262	274	3	1422.77	4.2	0	29.2	28.2	95.00%	R.IEMVTHVPSALAR.G		R.IEMVTHVPSALAR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
353	A6ZM77_YEAS7	10.41%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
425	452	3	3225.59	6.4	1	23.1	29.5	92.20%	K.GAMLIPTLYPALHDPEVYENPDEF IPER.W		K.GAMLIPTLYPALHDPEVYENPDEF IPER.W
274	283	2	1210.55	-0.24	1	46.4	32.1	95.00%	K.IFENCAQMAK.D	Carbamidomethyl (+57)	K.IFENCAQMAK.D
284	301	3	2013.93	4.6	1	29.9	33.8	95.00%	K.DHIAAGGKPVCVMDAWCK.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.DHIAAGGKPVCVMDAWCK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
354	IRC8_YEAST	4.87%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

203	217	2	1631.82	3.9	0	73.2	31.5	95.00%	W.LINELSTNSNTNANK.T		K.SMNGVAWLINELSTNSNTNANK.T
218	231	2	1587.68	-1.5	0	76.7	34.1	95.00%	K.TISSDENSNSSVIR.H	Phospho (+80)	K.TISSDENSNSSVIR.H
368	378	2	1226.68	2.8	0	28.7	25.5	95.00%	R.INSALLPACLR.V	Carbamidomethyl (+57)	R.INSALLPACLR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
355	A6ZTY6_YEAS7	10.48%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
253	276	3	2693.2	4.7	1	38.2	33.7	95.00%	K.HLTNAHENCQNLINSASTDEAAHF.S	Carbamidomethyl (+57)	K.HLTNAHENCQNLINSASTDEAAHFSYQECENILNLLLSYTR.E
148	159	2	1451.68	1.8	2	47.1	33.1	95.00%	K.NKFDEDLEDVTK.H		K.NKFDEDLEDVTK.H
277	291	2	1857.89	5.2	1	73.6	33.1	95.00%	F.SYQECENILNLLLSY.T	Carbamidomethyl (+57)	K.HLTNAHENCQNLINSASTDEAAHFSYQECENILNLLLSYTR.E
313	324	2	1440.58	2.9	1	43	32.6	95.00%	K.DSYPSCGMNWPK.D	Carbamidomethyl (+57)	K.DSYPSCGMNWPK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
356	A6ZKK0_YEAS7	5.39%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
198	207	2	1149.57	3.1	0	34.4	31.5	95.00%	Y.CTNESIVSLK.F	Carbamidomethyl (+57)	K.HDSSLQIWDMNYHDDSHETINPMFSYCTNESIVSLK.F
32	45	2	1601.78	2.6	1	49.5	32.4	95.00%	Y.KVDPENESDESIIK.L		R.DEVTHYKVDPENESDESIIK.L
923	938	3	1706.79	-0.3	1	27.7	33	94.20%	K.FNTGSSEAQAADEKPR.H		K.FNTGSSEAQAADEKPR.H
893	908	2	1542.72	-0.39	1	89.9	33	95.00%	R.TSSPSSAVSTSAGNYK.N		R.TSSPSSAVSTSAGNYK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
357	A6ZPF1_YEAS7	3.43%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	11	2	1060.59	0.46	1	43.4	26.7	95.00%	M.VAQYTVPVGK.A		-.MVAQYTVPVGK.A
620	633	2	1609.75	2.5	1	49.7	33.6	95.00%	K.DSSINIENYLEDAK.L		K.DSSINIENYLEDAK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
358	A6ZMK8_YEAS7	9.09%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
118	128	2	1185.64	2.2	0	53.3	28.8	95.00%	K.LDAALLQEASR.S		K.LDAALLQEASR.S
71	79	2	1005.52	2.7	1	28.1	30.8	91.40%	F.AIESTNKPF.Q		R.IGIDETVPTTITVEDPNEVIQVNFAIESTNKPFQNTLLIGLPNK.N
118	134	3	1837	4.6	1	28.3	25.9	95.00%	K.LDAALLQEASRSPEPIK.A		K.LDAALLQEASRSPEPIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
359	A6ZSX8_YEAS7	4.24%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
449	463	2	1626.76	2.2	1	34.3	33.4	95.00%	K.TQGYTVADCTAEAIK.A	Carbamidomethyl (+57)	K.TQGYTVADCTAEAIK.A
470	485	3	1854.87	3.6	1	32.6	33.5	95.00%	K.NSPVFSEVHHMISSER.L		K.NSPVFSEVHHMISSER.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
360	A6ZZN6_YEAS7	16.07%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
30	42	2	1494.71	1.6	1	50.2	32.9	95.00%	K.TDSWFNETLIGGR.A		K.TDSWFNETLIGGR.A
7	29	2	2381.27	3.4	1	48.6	27.1	95.00%	Y.TANDFILISLPQNAQPVTAPGSK.T		-.MATALYTANDFILISLPQNAQPVTAPGSK.T
55	81	3	2814.5	4.6	1	20.8	25.5	94.90%	K.IGSLDTLIVESEELSKVDNQIGASIGK.I		K.IGSLDTLIVESEELSKVDNQIGASIGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
361	A7A0E2_YEAS7	1.77%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
544	561	2	2057.02	-1.6	1	75.8	31.9	95.00%	R.TSSLVEELGQIEYIFSDK.T		R.TSSLVEELGQIEYIFSDK.T
99	104	2	728.38	3.9	0	23.7	26.4	91.30%	Y.QPQSLR.A	Deamidation (+1)	R.FDSDAYQPQSLR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
362	A6ZSI2_YEAS7	2.38%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1143	1154	2	1388.81	1.9	1	31.1	24.6	95.00%	K.NAVILNYQTLLK.E		K.NAVILNYQTLLK.E
1415	1433	2	2234.07	4.5	1	94.8	32.7	95.00%	R.INPELDNLTEIDDLNEYSK.Y		R.INPELDNLTEIDDLNEYSK.Y
1443	1450	2	1018.55	0.17	1	39.5	28.2	95.00%	R.IIDLFNER.Q		R.IIDLFNER.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
363	A6ZMI9_YEAS7	3.59%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
782	799	2	1910.03	-2.9	1	47.2	27	95.00%	K.TPVFTTGGDYILSLVSIK.D		K.TPVFTTGGDYILSLVSIK.D
42	52	2	1327.56	-0.24	1	42.1	32.9	95.00%	R.FQYSDDEPAEK.I		R.FQYSDDEPAEK.I
484	502	2	2046.06	2.4	1	29.3	29.8	94.50%	K.ITDGLGNVVDFTSLPEELK.K		K.ITDGLGNVVDFTSLPEELK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
364	A6ZWP8_YEAS7	3.18%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
13	22	2	1095.5	-0.56	1	30.2	32.2	92.50%	R.MSYSSTAPPR.F		R.MSYSSTAPPR.F
589	602	2	1602.82	3.9	1	49.1	30.6	95.00%	R.IPEPLTFTNSEDLK.Q		R.IPEPLTFTNSEDLK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
365	A6ZTY9_YEAS7	12.81%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	110	2	1424.67	3	1	45.5	32.9	95.00%	Y.CFLNENTGIETK.D	Carbamidomethyl (+57)	K.GHFQYCFLNENTGIETK.D
80	93	2	1517.74	2.6	1	59.7	32.4	95.00%	R.DTSHGEITLSAPYK.G		R.DTSHGEITLSAPYK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
366	A6ZR74_YEAS7	12.28%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
295	330	4	3847.93	3.1	1	24.7	26.5	95.00%	R.ASIHQILQHFAEENVSISATSADEPTVATESSPLIR.D		R.ASIHQILQHFAEENVSISATSADEPTVATESSPLIR.D
331	349	2	2207.06	4.1	1	54.4	32.9	95.00%	R.DSSLDLNEVIEEESIYQPK.E		R.DSSLDLNEVIEEESIYQPK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
367	A6ZSP5_YEAS7	6.33%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
549	559	2	1135.6	3.7	1	33.6	29.2	95.00%	K.ANSTTLGGLFR.A		K.ANSTTLGGLFR.A
412	420	2	954.53	2.8	1	32.3	25.2	95.00%	R.SPPGVFPVR.G		R.SPPGVFPVR.G
272	291	3	2391.1	1.3	1	32.7	33.8	95.00%	R.LSLPEYEARDEQPELNMDSR.V		R.LSLPEYEARDEQPELNMDSR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
368	B3LMI6_YEAS1	31.33%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
129	148	2	2277.01	3.4	1	46.8	34	95.00%	Y.VGYDTDSELVQELCADSTIY.H	Carbamidomethyl (+57)	K.GEPGYVAYVGYDTDSELVQELCADSTIYHM.-
102	128	3	3124.48	4.7	2	28.8	31.9	95.00%	F.CIIENDNVPPVHYPIHEDKGEPGYVAY.V	Carbamidomethyl (+57)	R.DYEPNDEHLSFCIIENDNVPPVHYPIHEDKGEPGYVAYVGYDTDSELVQELCADSTIYHM.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
369	A6ZRQ3_YEAS7	4.43%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
759	782	5	2691.31	0.023	1	31.2	31.4	95.00%	K.VVRGEDHHHTQVDQSEAHIAGLEK.K		K.VVRGEDHHHTQVDQSEAHIAGLEK.K
659	669	2	1251.58	2.6	0	34	32	95.00%	R.DCDSLSSLVTR.T	Carbamidomethyl (+57)	R.DCDSLSSLVTR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
370	A6ZZM1_YEAS7	11.72%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
96	105	2	1173.62	4.3	2	27.7	30.3	91.40%	F.SIKDGHLNYK.S		K.EGSESDAATGFSIKDGHLNYK.S
32	49	2	1945.93	0.11	1	97.4	32.8	95.00%	R.SGSDLQYLSVYSDNGTLK.L		R.SGSDLQYLSVYSDNGTLK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
371	YD206_YEAST	7.48%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
443	473	3	3549.76	4.9	1	52.3	27.7	95.00%	R.TQESTNALNSISDVIDNSLLQYERDDIILDR.T		R.TQESTNALNSISDVIDNSLLQYERDDIILDR.T
251	276	4	2912.5	5.1	1	22.4	27.5	95.00%	R.YVRPLGDTQIDEDNAISLDPTRLPSK.S		R.YVRPLGDTQIDEDNAISLDPTRLPSK.S
252	276	3	2749.43	3.2	1	48.5	27.1	95.00%	Y.VRPLGDTQIDEDNAISLDPTRLPSK.S		R.YVRPLGDTQIDEDNAISLDPTRLPSK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
372	A6ZNL3_YEAS7	11.90%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
352	365	2	1317.67	-0.25	1	76.4	31.1	95.00%	R.ISNGTFINGGPGGK.N		R.ISNGTFINGGPGGK.N
339	350	2	1363.6	3.1	1	60.9	32.3	95.00%	K.GQTDINPFDDSR.R		K.GQTDINPFDDSR.R
38	56	3	2216.85	-0.55	1	29.6	32.9	95.00%	K.ADSYNWQSSSHCNSECSAK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.ADSYNWQSSSHCNSECSAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
373	A6ZN47_YEAS7	5.29%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
82	101	3	2137.13	2.6	1	35.4	27.8	95.00%	R.QSPSDIHPVGVSYFPAVIPK.G		R.QSPSDIHPVGVSYFPAVIPK.G
610	622	2	1601.81	2.8	0	65.8	30.9	95.00%	K.LQCININDLMVNR.N	Carbamidomethyl (+57)	K.LQCININDLMVNR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
374	A6ZQV0_YEAS7	13.42%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
184	196	2	1408.72	-0.0055	1	28.2	31	91.10%	R.LLGYPVYGDEVGK.V		R.LLGYPVYGDEVGK.V
1	18	2	1833.92	-0.14	1	30.3	31.4	93.80%	-.MNGLVLGATGLCGGGFLR.H	Acetyl (+42)/ Carbamidomethyl (+57)	-.MNGLVLGATGLCGGGFLR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
375	A6ZYL7_YEAS7	4.32%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
737	748	2	1380.73	-0.88	1	31.5	29.2	95.00%	K.ALLNGIEVDYFK.L		K.ALLNGIEVDYFK.L
224	235	2	1272.7	3.2	0	30.8	30.2	95.00%	Y.QGDSLTVAELLK.F		R.TSLLWAAYQGDSLTVAELLK.F
2	10	2	1068.56	0.25	0	73.1	29.8	95.00%	M.VNELENVPR.A		-.MVNELENVPR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
376	A6ZM19_YEAS7	9.43%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
286	306	2	2125.09	4.1	1	34.3	30	95.00%	K.AAAPGIQLVAGEGFQSPLEDR.F		K.AAAPGIQLVAGEGFQSPLEDR.F
37	53	3	1926.04	-0.62	1	21.5	28.1	91.90%	K.TGLADLMVLRPSIFHEK.E		K.TGLADLMVLRPSIFHEK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
377	A6ZTW2_YEAS7	4.51%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
290	299	2	1219.65	1.3	1	27.7	30.4	91.30%	K.TQDVIQLFEK.D		K.TQDVIQLFEK.D
71	86	3	1761.96	3.5	2	38.7	27.6	95.00%	R.KYDTAVKPVIDDATVK.V		R.KYDTAVKPVIDDATVK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
378	A6ZRM1_YEAS7	6.13%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

424	442	2	1968.94	-2.9	1	29.9	33.2	90.10%	K.SGFDGLLPGDFPESGSIFK.K		K.SGFDGLLPGDFPESGSIFK.K
468	482	2	1780.92	5.7	1	28.9	29.9	94.00%	R.CDYFIDIVAPINLTK.D	Carbamidomethyl (+57)	R.CDYFIDIVAPINLTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
379	A6ZMY7_YEAS7	7.55%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
181	195	2	1589.84	-1.2	1	49.4	30.2	95.00%	K.GSAPLFGNFLEPLTK.T		K.GSAPLFGNFLEPLTK.T
147	160	3	1741.01	0.46	1	24.2	23.7	95.00%	K.FLDLNRPLLMQILR.S		K.FLDLNRPLLMQILR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
380	A6ZT92_YEAS7	1.61%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1480	1492	2	1480.76	-0.62	1	46.6	31.3	95.00%	K.IWTTSGDLLNSFK.N		K.IWTTSGDLLNSFK.N
1310	1321	2	1415.78	-0.15	1	46.3	28.8	95.00%	R.STGLLTEWLQIR.G		R.STGLLTEWLQIR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
381	A6ZYP1_YEAS7	2.40%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
480	495	2	1731.72	0.092	0	62.8	33.3	95.00%	R.SSTINNDSDSLSSPTK.S	Phospho (+80)	R.SSTINNDSDSLSSPTK.S
276	289	2	1684.83	3.8	1	49.3	32.1	95.00%	R.NQSQQPQQQLSPFR.H		R.NQSQQPQQQLSPFR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
382	A6ZVN8_YEAS7	3.34%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
321	351	4	3464.37	-1.4	0	48.3	33.3	95.00%	R.HVDELDHDEATEEHENNDSDNSLPSGDDSSR.I		R.HVDELDHDEATEEHENNDSDNSLPSGDDSSR.I
868	880	2	1518.77	2.2	1	50.2	31.7	95.00%	K.TLEQAEELFGQVR.D		K.TLEQAEELFGQVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
383	A6ZUK7_YEAS7	5.30%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
514	529	3	1572.77	-0.19	0	39.6	32	95.00%	K.NAMQAAEAAVAAATQR.A		K.NAMQAAEAAVAAATQR.A
255	267	2	1526.86	4.3	0	27.3	26.6	95.00%	K.STILPLMQQLEVR.L		K.STILPLMQQLEVR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
384	A7A0W2_YEAS7	4.25%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
175	184	2	1257.67	1.4	1	26.5	29.5	90.80%	K.SWNQEQLLLK.S		K.SWNQEQLLLK.S
431	447	2	1900.9	-0.53	1	83.2	33.3	95.00%	K.INDLFQSSYDILDGSSK.N		K.INDLFQSSYDILDGSSK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
385	A6ZVF2_YEAS7	13.13%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
62	74	2	1517.84	3.5	2	27.6	26.9	95.00%	Y.KLDISKPEEIVTF.S		R.LEPMAQLAIQFGNDSIKPYKLDISKPEEIVTFSGFLR.A
32	41	2	1185.56	3.9	1	43.1	31.9	95.00%	R.NGYLVYACAR.R	Carbamidomethyl (+57)	R.NGYLVYACAR.R
182	197	2	1556.85	2.7	0	62	28.6	95.00%	R.VINAITGGVATDIADK.R		R.VINAITGGVATDIADK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
386	A6ZSL1_YEAS7	8.93%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
16	46	4	3541.57	4.1	1	47.8	32.3	95.00%	K.HVFMGMEHELNPETHNDSNSDSYGLPQLSEK.Y		K.HVFMGMEHELNPETHNDSNSDSYGLPQLSEK.Y
607	617	2	1390.64	-0.53	1	53.7	32.7	95.00%	K.DNDPILDWFEK.L		K.DNDPILDWFEK.L
1	14	2	1711.82	2.4	1	45.3	33.2	95.00%	-.MESVHSRNPVKEEK.K	Acetyl (+42)/ Deamidation (+1)	-.MESVHSRNPVKEEK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
387	B3LJM9_YEAS1	4.64%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

145	158	2	1508.85	4.2	0	25.9	24.3	95.00%	F.TSPPLDGLLLENIK.L		K.DVPEPITEFTSPPLDGLLLENIK.L
193	206	2	1527.8	-0.68	1	37.6	29.4	95.00%	K.TGGFLFPVLSESFK.T		K.TGGFLFPVLSESFK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
388	YP162_YEAST	17.58%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
263	273	2	1181.56	-0.34	1	46.2	32.2	95.00%	K.DNNISSYGSII.-		K.DNNISSYGSII.-
226	262	3	4159.96	-1.7	1	59.5	28.7	95.00%	R.LHSESLTITNAENFETNTFLNDEIPDLSEVSNEVPNK.D		R.LHSESLTITNAENFETNTFLNDEIPDLSEVSNEVPNK.D
245	262	2	2010.98	4.3	0	34.7	32.8	95.00%	F.LNDEIPDLSEVSNEVPNK.D		R.LHSESLTITNAENFETNTFLNDEIPDLSEVSNEVPNK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
389	A6ZMS6_YEAS7	13.26%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	181	3	2119.86	3.8	0	32.2	33.9	95.00%	F.TLNLNDECDACHGSGSADGK.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.QFYSGSSIEFTLNLNDECDACHGSGSADGK.L
200	213	2	1680.76	2.1	0	85.6	33.4	95.00%	R.MGIMTQQIQQMCGR.C	Carbamidomethyl (+57)	R.MGIMTQQIQQMCGR.C
295	310	2	1749.87	-0.47	1	50.7	32.3	95.00%	R.TEVLSAAEALYGGWQR.T		R.TEVLSAAEALYGGWQR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
390	A6ZSV7_YEAS7	9.84%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
502	511	2	1089.57	0.35	1	36	30.7	95.00%	R.SLVSPAPEYK.D		R.SLVSPAPEYK.D
39	55	2	1833.93	3.2	0	36.6	31.1	95.00%	R.TTLQPNSTSQSMIGTLR.K		R.TTLQPNSTSQSMIGTLR.K
475	501	3	3020.4	4.5	1	87.5	32.1	95.00%	K.KPVADRTEDDETIELEEMGIGSSSQER.S		K.KPVADRTEDDETIELEEMGIGSSSQER.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
391	A7A281_YEAS7	13.22%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
199	225	3	2936.46	2.8	1	37	30.1	95.00%	R.FSDVYVVEPDGSETLISPDTLDKPSVK.N		R.FSDVYVVEPDGSETLISPDTLDKPSVK.N
232	243	2	1349.68	2.6	1	48.8	31.5	95.00%	R.IPASVWNMTFGK.S		R.IPASVWNMTFGK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
392	B3LGD6_YEAS1	6.21%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
355	374	2	2176.18	4.1	1	83	26.8	95.00%	K.IPVLLDSGTTISYMPTELVK.M		K.IPVLLDSGTTISYMPTELVK.M
305	321	3	1987.05	-0.69	1	21.6	28.3	91.70%	K.YAGDLYTIPIINTLQHR.G		K.YAGDLYTIPIINTLQHR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
393	A6ZNC2_YEAS7	9.03%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
61	75	2	1694.88	4.1	1	47.8	29.5	95.00%	K.TLAPVYEELGELYAK.K		K.TLAPVYEELGELYAK.K
165	174	2	1150.6	2.9	1	40.7	29.9	95.00%	K.SLSNFIDTVR.S		K.SLSNFIDTVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
394	A6ZM44_YEAS7	9.16%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
98	118	2	2226.1	1.9	0	97.1	32.3	95.00%	R.SVDMTSPLLTNLEAGTHANQK.K		R.SVDMTSPLLTNLEAGTHANQK.K
83	97	2	1665.72	1.6	0	71.5	33.8	95.00%	R.ELIMEEEGTGSDSNR.S		R.ELIMEEEGTGSDSNR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
395	A7A1R6_YEAS7	17.99%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

38	61	3	2803.19	3.5	1	59.5	33.8	95.00%	K.SSSTCDSLNQVTCYCEHENSAVK K.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.SSSTCDSLNQVTCYCEHENSAVK K.C
62	80	2	2130.91	3.1	1	76.1	33.9	95.00%	K.CLDSICPNNDADAAYSAFK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CLDSICPNNDADAAYSAFK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
396	A6ZZ10_YEAS7	8.80%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
268	279	2	1346.64	4.4	1	37.9	31.9	95.00%	F.NNNFANVPSSQR.E		R.ITGAHNETTTFNNNFANVPSSQR.E
291	308	2	1718.84	-0.3	0	113	32	95.00%	R.LGTAPATLSQTSGTDSGR.A		R.LGTAPATLSQTSGTDSGR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
397	A7A1E2_YEAS7	13.02%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
61	71	2	1315.65	-0.16	1	49.1	31.4	95.00%	R.LQLWDTAGQER.F		R.LQLWDTAGQER.F
126	141	2	1821.82	-1.3	1	65.4	33.7	95.00%	K.SDLSDERQISTEEGEK.K		K.SDLSDERQISTEEGEK.K
126	142	3	1949.93	3.7	1	40.6	32.8	95.00%	K.SDLSDERQISTEEGEKK.A		K.SDLSDERQISTEEGEKK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
398	A6ZZA0_YEAS7	16.78%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
134	143	2	1156.69	2	1	40.6	26	95.00%	K.LAEILKPVFQ.-		K.LAEILKPVFQ.-
66	79	2	1559.86	4.3	1	47.2	27.4	95.00%	K.ATLSTLFQELNVPK.S		K.ATLSTLFQELNVPK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
399	A6ZT81_YEAS7	6.41%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
244	255	2	1372.63	0.44	1	73.7	32.9	95.00%	K.IGLDCASSEFFK.D	Carbamidomethyl (+57)	K.IGLDCASSEFFK.D
273	288	2	1892.92	-0.0022	1	52.4	33	95.00%	K.WLTGVELADMYHSLMK.R		K.WLTGVELADMYHSLMK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
400	AGP1_YEAST	5.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
92	112	2	2269.06	2.7	1	66.8	33.4	95.00%	R.QAQELEKNESSDNIGANTGHK.S		R.QAQELEKNESSDNIGANTGHK.S
430	442	2	1465.79	4.4	1	52.2	28.7	95.00%	R.LFLTLSEQGYAPK.V		R.LFLTLSEQGYAPK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
401	A6ZRT4_YEAS7	20.93%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	15	2	1693.77	0.0081	1	38.6	33.6	95.00%	M.SEVAETWVDTWMAK.L	Acetyl (+42)	-.MSEVAETWVDTWMAK.L
97	109	2	1547.75	3.1	1	41.2	32	95.00%	R.QQELFENALEEAK.R		R.QQELFENALEEAK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
402	A6ZP14_YEAS7	6.25%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
581	592	2	1265.62	3	1	30.8	32.4	93.00%	K.VESGLFSVDGEK.F		K.VESGLFSVDGEK.F
9	19	2	1170.69	1.5	0	32.9	25.3	95.00%	R.AILTDEGVLIK.S		R.AILTDEGVLIK.S
593	608	2	1943.99	0.42	1	30.3	30.2	95.00%	K.FPLEPLQVEIMPMLCK.T	Carbamidomethyl (+57)	K.FPLEPLQVEIMPMLCK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
403	A6ZKK2_YEAS7	16.74%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
200	210	2	1091.54	-1.5	0	28.5	30.7	92.10%	R.MLSSAGVNSAR.G		R.MLSSAGVNSAR.G
50	61	2	1389.73	0.069	1	63.1	30.7	95.00%	R.AQDIYQTLPVSR.Q		R.AQDIYQTLPVSR.Q
37	49	2	1496.72	-0.88	1	110	32.7	95.00%	K.TLFSSWADSLNTR.A		K.TLFSSWADSLNTR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
404	B3LRN4_YEAS1	13.90%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
197	217	2	2403.01	2.2	1	51.8	34.3	95.00%	R.DSGYATQFDGYPQQQPSHTNY.V		R.DSGYATQFDGYPQQQPSHTNYVSSTALAGFENTQPNTSEAVNLHLNTLQQR.I	
218	247	3	3239.63	4	1	73.2	28.2	95.00%	Y.VSSTALAGFENTQPNTSEAVNLHLNTLQQR.I		R.DSGYATQFDGYPQQQPSHTNYVSSTALAGFENTQPNTSEAVNLHLNTLQQR.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
405	A6ZMB4_YEAS7	2.47%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
67	77	2	1263.66	2.9	1	39	30.5	95.00%	R.MVGFLNEVVEK.H		R.MVGFLNEVVEK.H	
160	170	2	1171.64	0.82	1	39.3	28.9	95.00%	K.FIEVNPGIAGR.A		K.FIEVNPGIAGR.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
406	YNS1_YEAST	6.39%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
2	16	2	1582.86	6.3	0	81	27.3	95.00%	M.PLNIIGTALLDGTDK.I	Acetyl (+42)/ Deamidation (+1)	-.MPLNIIGTALLDGTDK.I	
113	123	3	1432.72	3.9	1	35.8	31.1	95.00%	K.CDLSNLWEIRK.F	Carbamidomethyl (+57)	K.CDLSNLWEIRK.F	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
407	A6ZSF8_YEAS7	5.31%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
135	143	2	1135.54	1.6	1	30	31.2	93.70%	K.TYNTAPQWR.F		K.TYNTAPQWR.F	
2	14	2	1478.75	-0.42	1	56	32	95.00%	M.VNFDLGQVGEVFR.R		-.MVNFDLGQVGEVFR.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
408	A6ZMS7_YEAS7	5.34%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
293	306	2	1513.73	-0.8	1	53.4	32.9	95.00%	R.TFDEVSEGLYGGLK.D		R.TFDEVSEGLYGGLK.D	
81	94	2	1580.8	2.6	1	77.7	31.5	95.00%	R.DAYAFQQLGVNTVR.I		R.DAYAFQQLGVNTVR.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
409	A7A187_YEAS7	4.96%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
47	57	2	1262.73	-0.42	1	49.3	25	95.00%	K.LIELVSFAPFK.G		K.LIELVSFAPFK.G	
33	46	2	1624.78	2.8	1	56	32.9	95.00%	K.EVQEQINDFGAFTK.L		K.EVQEQINDFGAFTK.L	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
410	A7A0K9_YEAS7	5.48%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
631	646	2	1923.9	5.1	1	32.3	33.4	93.70%	R.DQLIHFDDIMTELTSF.A		R.DQLIHFDDIMTELTSFAHIGNARPNFSNVIENAIK.S	
666	688	2	2409.18	4.3	0	78.3	31.9	95.00%	K.STPPGDSLAVVCCGPPVLVDDVR.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.STPPGDSLAVVCCGPPVLVDDVR.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
411	A6ZML9_YEAS7	4.66%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
389	414	3	2840.14	2.9	1	49.7	33.6	95.00%	Y.NNLGSNSSTNENDSNDHDSNNDFTTK.S		R.FWDHSTDFTSNSYNNLGSNSSTNENDSNDHDSNNDFTTK.S	
278	289	2	1410.72	-0.71	0	27.5	30.5	90.70%	K.LSQNLAQEQPQR.V		K.LSQNLAQEQPQR.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
412	A6ZN84_YEAS7	18.31%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
62	74	2	1445.75	2.8	0	41.3	30.6	95.00%	K.VIEQPITSETAMK.K		K.VIEQPITSETAMK.K	

126	138	2	1449.71	-1.5	1	61.3	32.4	95.00%	R.LTADYDALDIANR.I		R.LTADYDALDIANR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
413	A6ZV20_YEAS7	13.25%	100%	20

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
878	888	2	1406.68	0.76	2	40.5	32.5	95.00%	R.EIIREDDQFSR.V		R.EIIREDDQFSR.V
1798	1807	2	1213.72	2.1	1	23.2	24.9	92.70%	R.QIRPPIYSLK.Q		R.QIRPPIYSLK.Q
1029	1042	2	1741.92	2.3	1	51.6	29.3	95.00%	K.FKPHELENAEFLLR.A		K.FKPHELENAEFLLR.A
794	806	3	1511.8	3.7	1	38.8	27.9	95.00%	K.LLYHQVPSEIEGK.R		K.LLYHQVPSEIEGK.R
1136	1157	3	2469.29	5.2	1	50	27.9	95.00%	R.SVLAEFEELGIEQIHPYTPGLK.Y		R.SVLAEFEELGIEQIHPYTPGLK.Y
1281	1292	2	1248.6	2.9	0	86.4	31.4	95.00%	K.IGAGMGEQMLSR.E		K.IGAGMGEQMLSR.E
1029	1039	2	1359.65	3.7	1	39.6	32	95.00%	K.FKPHELENAEF.L		K.FKPHELENAEFLLR.A
1192	1201	2	1168.59	-0.28	1	52.2	31.1	95.00%	K.EQTFGTLFAR.T		K.EQTFGTLFAR.T
1153	1173	3	2252.16	3.8	2	41.3	29.5	95.00%	Y.TPGLKYEDQSTNHPVAIVGAR.E		R.SVLAEFEELGIEQIHPYTPGLKYE DQSTNHPVAIVGAR.E
1455	1463	2	1094.62	3.4	1	52.9	25.7	95.00%	R.IPFSILYSR.F		R.IPFSILYSR.F
1114	1133	2	2427.14	3.6	1	121	33	95.00%	R.GEYIQLIDANQDNYLEECLK.I	Carbamidomethyl (+57)	R.GEYIQLIDANQDNYLEECLK.I
1268	1280	2	1425.75	-0.019	1	69.1	29.4	95.00%	R.DLGFGTILNFTTK.I		R.DLGFGTILNFTTK.I
1089	1101	2	1296.71	0.92	0	44.2	27.4	95.00%	R.VQLSGNPILGDGK.S		R.VQLSGNPILGDGK.S
794	807	3	1667.91	3.7	1	39.6	27.5	95.00%	K.LLYHQVPSEIEGKR.T		K.LLYHQVPSEIEGKR.T
842	871	3	3320.69	4.4	1	24.4	27.5	95.00%	F.AQSLSTPIPEPLPVDNMPTFTVLT PHYAER.I		R.ISFFAQSLSTPIPEPLPVDNMPTF TVLTPHYAER.I
1174	1191	2	1854.91	3	1	74	33	95.00%	R.EYIFSENSGVLGDVAAGK.E		R.EYIFSENSGVLGDVAAGK.E
1539	1546	2	993.5	0.087	1	45.7	31.4	95.00%	R.NSWIGYVR.M		R.NSWIGYVR.M
972	981	2	1174.55	2	1	46.4	31.9	95.00%	R.TISGFMNYSR.A		R.TISGFMNYSR.A
889	896	2	977.58	3.3	1	51.5	21.6	95.00%	R.VTLLEYLK.Q		R.VTLLEYLK.Q
1210	1222	2	1530.73	4.2	1	42.2	33	95.00%	K.LHYGHPDFINATF.M		K.LHYGHPDFINATFMTTR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
414	A6ZW55_YEAS7	19.17%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
41	56	3	1833.81	-0.36	1	43.9	34.3	95.00%	R.DQLSHESQTAYQQGDK.K		R.DQLSHESQTAYQQGDK.K
192	221	3	3268.41	4.8	1	37.3	32.8	95.00%	Y.NAQPHPQYNNNGGQPQGQAQN YNNSGNDNK.D	Deamidation (+1)	K.GNSGVLVLELQGVQMQMDGPAV NAPTNQYNAQPHPQYNNNGGQPQ GQAQNYNNSGNDNK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
415	B5VJB7_YEAST	22.18%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
33	65	3	3299.69	4.6	0	73.9	27.6	95.00%	F.QNTVGSSNTGNDNNLGVAPDPL PVGILHALSTK.G		K.NANNGGGFYQPSAQFAVPQGS MSFQNTVGSSNTGNDNNLGVAPD PLPVGILHALSTK.G
66	87	4	2531.32	4.7	1	21.2	28	95.00%	K.GYPHEPPLLEEIGINFDHIITK.T		K.GYPHEPPLLEEIGINFDHIITK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
416	A6ZQ13_YEAS7	4.63%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
314	326	2	1490.71	3.9	0	36	32.3	95.00%	Y.ASNNNSMIELIER.R	Deamidation (+1)	K.IETSFNDTSYASNNNSMIELIER.R
121	130	2	1150.6	4.1	1	38.4	29.7	95.00%	R.NLNSVLNYSK.F		R.NLNSVLNYSK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
417	A7A171_YEAS7	12.04%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
6	40	4	3839.78	5.1	1	29.9	30.1	95.00%	F.LFTSESVGEGHPDKICDQVSDAIL DACLAEDPHSK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	- .MAGTFLFTSESVGEGHPDKICDQV SDAILDACLAEDPHSK.V
328	338	2	1260.65	3.1	0	38.9	31.1	95.00%	K.SDEEIIDIISK.N		K.SDEEIIDIISK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
418	A6ZM25_YEAS7	7.47%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
416	437	2	2524.22	3.9	1	64.3	32.2	95.00%	Y.SISVDLTNQEYELDMIAQNVSR.S		K.IAPYSISVDLTNQEYELDMIAQNVSR.S
400	410	2	1254.59	3.5	1	66.6	32.4	95.00%	K.GFQDFEQLGSK.K		K.GFQDFEQLGSK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
419	A6ZZL6_YEAS7	3.75%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
247	257	2	1224.65	3.3	1	45.1	29	95.00%	K.IGGFVTNLNYK.D		K.IGGFVTNLNYK.D
534	544	2	1329.61	3.8	1	41.8	32.8	95.00%	F.ILSEYYNDADK.Y		K.ENSITYSTFILSEYYNDADK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
420	A6ZZ58_YEAS7	20.09%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	16	2	1920.89	0.48	1	57.3	33.5	95.00%	-.MNNSEDPFQQVVKDTK.E	Acetyl (+42)	-.MNNSEDPFQQVVKDTK.E
29	57	3	3353.56	5.7	1	98.3	31.4	95.00%	R.HNTAGDDDQEEEIQDILKDVEETIVDLDR.S		R.HNTAGDDDQEEEIQDILKDVEETIVDLDR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
421	A6ZWX4_YEAS7	3.38%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
503	517	3	1683.8	4.7	2	29.9	33.2	95.00%	Y.RGGIWEEQDPEAAAR.A		K.ESLVVPFMDDIVFYPTPNEVYRGGIWEEQDPEAAAR.A
463	473	2	1220.68	3.3	1	27.5	27.8	94.70%	K.LSYNVVTNAIK.S		K.LSYNVVTNAIK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
422	A6ZR56_YEAS7	10.80%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
194	208	3	1795.98	5.1	1	36.1	27.4	95.00%	K.VISLEEILDPEDRIR.A		K.VISLEEILDPEDRIR.A
138	149	2	1441.7	3.3	1	41.2	32.2	95.00%	R.NSISYNTFQNVR.F		R.NSISYNTFQNVR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
423	A6ZSH5_YEAS7	10.10%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
17	34	2	1906.88	3.4	1	49	33.6	95.00%	Y.GQPASSQDGNAFIPEDFK.Y		-.MSGPPPPYEEQSSHLYGQPASSQDGNAFIPEDFK.Y
36	47	2	1372.74	4.5	0	51	30	95.00%	Y.STVVISCEPIIR.Q	Carbamidomethyl (+57)	K.YSTVVISCEPIIR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
424	A6ZXC2_YEAS7	4.84%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
282	288	2	862.49	3.2	1	32.1	28.9	95.00%	F.LNVLNYK.V		R.VSCDEVTETEAPSNPFLNVLNYK.V
322	332	2	1268.53	3.3	2	41.5	31.8	95.00%	Y.YGMADHESGRF.S		R.ASSSDGIYIAHPYYGMADHESGRFSYVSSYNESTESSIEETSSSASTITRPNIQQINSFLR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
425	A6ZU48_YEAS7	17.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
131	147	3	1844.91	3.5	2	42.9	31.9	95.00%	K.AGKFPTPVSHNDDLYGK.V		K.AGKFPTPVSHNDDLYGK.V
55	76	3	2593.2	4	1	27.7	33.5	93.50%	K.LPNCPRPNMSICIFGDAFDVDR.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.LPNCPRPNMSICIFGDAFDVDR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

426	A6ZND5_YEAS7	3.52%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
2	15	2	1627.88	-0.66	1	58.4	29.1	95.00%	M.SDKIQEEILGLVSR.S	Acetyl (+42)	-.MSDKIQEEILGLVSR.S	
469	482	2	1687.79	-0.95	1	46.4	33.5	95.00%	K.NVQTDSLDYMIFSR.F		K.NVQTDSLDYMIFSR.F	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
427	A6ZLI8_YEAS7	7.84%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
189	201	2	1350.72	4.3	1	47	29.1	95.00%	R.ELASGLSFPVGFK.N		R.ELASGLSFPVGFK.N	
121	136	2	1786.89	1.8	1	71.2	31.8	95.00%	K.GLINDPDVNNTFNINK.G		K.GLINDPDVNNTFNINK.G	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
428	A6ZUG8_YEAS7	3.22%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
858	869	2	1359.7	-0.6	1	40	30.8	95.00%	R.AWDIKQTLDSLA.-		R.AWDIKQTLDSLA.-	
635	650	2	1874.92	-1.9	1	71.3	32.3	95.00%	K.EWNILIQEAMDSVATR.L		K.EWNILIQEAMDSVATR.L	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
429	B3LMC0_YEAS1	2.14%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
933	943	2	1290.76	-0.41	1	42.3	23.5	95.00%	R.LTLDIPVVFFK.C		R.LTLDIPVVFFK.C	
607	617	2	1253.55	0.38	1	55.2	32.4	95.00%	R.DTTGDFSENIR.T		R.DTTGDFSENIR.T	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
430	A7A0I6_YEAS7	2.02%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
797	804	2	914.56	2.8	1	30.3	27.7	95.00%	K.IGLWSVLK.S		K.IGLWSVLK.S	
814	829	2	1813.99	-0.51	1	75.8	26.8	95.00%	K.LTLPVSFNEPTSLLQR.V		K.LTLPVSFNEPTSLLQR.V	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
431	A6ZXZ4_YEAS7	17.17%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
73	79	2	802.47	2.9	1	27.2	26	95.00%	F.LFGIPTR.F		K.ALGGAPKPNYPIATQDTLTEYDAF LFGIPTR.F	
163	189	3	2664.36	3.3	1	51.5	29.4	95.00%	W.GAGTIAGSDGSRSPSALELQVH EIQGK.T		K.NVFAELTNMDEVHGGSPWGAGT IAGSDGSRSPSALELQVHEIQGK.T	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
432	A6ZXD4_YEAS7	5.87%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
21	43	4	2564.26	0.72	1	29.2	31.7	95.00%	R.AHQLAQDFNSKQDDTALTSLPHK .N		R.AHQLAQDFNSKQDDTALTSLPHK .N	
4	20	3	1866.92	-0.37	0	74.8	32.4	95.00%	R.SNKPLTQEANSSAHIDR.A		R.SNKPLTQEANSSAHIDR.A	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
433	A6ZQR0_YEAS7	5.79%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
52	60	2	1212.51	3.2	2	38.6	31.5	95.00%	Y.CLNNCDVRY.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VEAATFCNATQACPEDKPCCSQ YGECGTGQYCLNNCDVRYSFSHD SCMPVPICK.S	
272	289	2	1943.83	3.9	1	67.1	33.6	95.00%	W.SGGEINWDASDISNPGYY.Y		K.VDISIWPGGNSTNAPGTIAWSGG EINWDASDISNPGYYYAIVNEVNITC YDPPSDTK.K	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
434	A6ZRY5_YEAS7	15.26%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
8	22	2	1624.91	3.7	0	66.3	26.3	95.00%	K.ILSQAPSELELQVAK.T		K.ILSQAPSELELQVAK.T	

125	138	2	1575.83	3.5	1	54.9	30.6	95.00%	K.VLEDMVFPTEIVGK.R		K.VLEDMVFPTEIVGK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
435	COS5_YEAST	20.89%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
157	167	2	1275.75	3.6	1	33.3	23.7	95.00%	R.TTLLEPFSLKK.D		R.TTLLEPFSLKK.D
19	33	3	1813.01	-0.27	2	23.2	25.5	95.00%	K.QLESQKIVLPQDLFR.S		K.QLESQKIVLPQDLFR.S
354	369	2	2001.08	-0.26	1	27.3	27.9	94.40%	K.SMWLLPLNVELWPYIK.E		K.SMWLLPLNVELWPYIK.E
25	33	2	1099.64	-0.29	1	24.9	27.1	92.20%	K.IVLPQDLFR.S		K.IVLPQDLFR.S
206	219	2	1553.81	3.3	1	69.3	28.8	95.00%	K.SWSPVGLEDVQLPK.D		K.SWSPVGLEDVQLPK.D
157	166	2	1147.65	4.2	1	35.1	27.1	95.00%	R.TTLLEPFSLK.K		R.TTLLEPFSLK.K
109	132	2	2673.2	5.4	1	64.8	33.9	95.00%	K.EVTENTPSSDPHDWEVVAANLN SY.L		K.EVTENTPSSDPHDWEVVAANLN SYLYENK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
436	A7A1K8_YEAS7	21.79%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
45	61	3	1778.96	2.3	2	25.4	27.5	95.00%	K.VRGSSSLYTLVINDAGK.A		K.VRGSSSLYTLVINDAGK.A
47	61	2	1523.79	2.6	1	60.8	30.7	95.00%	R.GSSSLYTLVINDAGK.A		R.GSSSLYTLVINDAGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
437	A7A0T2_YEAS7	5.00%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
203	219	2	1911.86	4.2	1	31.5	34.1	91.60%	Y.NNSNPFMTSLLDESSEK.N		K.LTTDTGHAPADDQTQSNHAADLT TYNNSNPFMTSLLDESSEK.N
209	219	2	1238.58	4.1	0	38	32.6	95.00%	F.MTSLLDESSEK.N		K.LTTDTGHAPADDQTQSNHAADLT TYNNSNPFMTSLLDESSEK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
438	A6ZP61_YEAS7	2.90%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
191	205	2	1653.83	3.1	1	29.1	31.8	91.20%	R.LLGQDSDPGLYFTTK.E		R.LLGQDSDPGLYFTTK.E
253	264	2	1424.73	-1.1	1	42.4	31.2	95.00%	K.LIFGTNLESEFR.H		K.LIFGTNLESEFR.H

Supplementary Table S2: All "Scaffold" validated proteins and peptides identified from solprotSP (*S.pombe*) and from SCVMprot (*S.cerevisiae*) samples

***S.cervisiae* - Asp-N digest of large tryptic peptides (Replicate A)**

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
1	VTC3_YEAST	28.14%	100%	29

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
158	166	2	1168.58	-0.36	1	30.2	29.4	95.00%	S.EEYSPLLYR.I		K.ELPFNNSEEYSPLLYR.I
669	681	2	1331.67	-0.61	0	55.2	28.5	95.00%	T.DSASSFQLPPGVK.K		K.NISENGNDPYSDDTDSASSFQLPPGVK.K
7	16	2	1201.61	-0.85	1	43.6	28.4	95.00%	K.LANDVYPPWK.D		K.LANDVYPPWK.D
149	157	2	1060.55	-0.88	1	27.1	28.3	94.30%	R.LKELPFNNS.E		R.LKELPFNNSEEYSPLLYR.I
512	524	2	1464.76	-0.9	1	57.6	27	95.00%	K.DLTNSHLVNEVPK.F		K.DLTNSHLVNEVPK.F
440	448	2	1139.53	-0.98	1	41.1	31.1	95.00%	I.DSNIMYIRE.D		R.VTIDSNIMYIREDSLDK.N
403	411	2	1090.53	-0.48	1	27.3	29.2	93.20%	F.DNIQNFIVE.E		R.DFDNIQNFIVEEK.L
808	820	2	1352.74	0.73	0	52.5	24.4	95.00%	R.GLVNVSSQPSLPR.T		R.GLVNVSSQPSLPR.T
117	126	2	1210.64	0.37	1	45.7	27.2	95.00%	F.DRLNFTGFIK.I	Deamidation (+1)	R.LDNFDRLNFTGFIK.I
365	372	2	1041.56	0.061	0	30.6	25.8	95.00%	K.FINNFIFK.N		K.FINNFIFK.N
542	551	2	1260.69	-0.096	0	45.2	25.8	95.00%	K.YVNILPFWLP.D		K.YVNILPFWLPDLETDIR.K
440	447	2	1010.48	-0.9	0	48.6	30.5	95.00%	I.DSNIMYIR.E		R.VTIDSNIMYIR.E
699	705	2	886.47	-0.031	1	25.2	26.4	94.30%	K.VWLANER.T		K.VWLANER.T
806	820	2	1637.88	-0.19	1	75.7	23.2	95.00%	R.ERGLVNVSSQPSLPR.T		R.ERGLVNVSSQPSLPR.T
827	835	2	1052.52	-0.69	1	28.4	30	93.80%	Q.DFIFNLVGE.-		R.TLKPIQDFIFNLVGE.-
316	323	2	813.47	-0.4	0	31.9	25.3	95.00%	K.ISGAPTLR.L		K.ISGAPTLR.L
63	70	2	984.53	-0.21	0	27.3	25.6	95.00%	K.VYTFQISK.Y		K.VYTFQISK.Y
227	240	2	1523.76	-3.9	1	60.2	29.4	95.00%	R.HLPALVYASVPNEN.D	Deamidation (+1)	R.HLPALVYASVPNENDDFVDNLESDVR.V
167	175	2	1202.63	0.24	1	55.8	27.3	95.00%	R.ISYLYEFLR.S		R.ISYLYEFLR.S
643	649	2	763.42	1	0	26.4	27.9	93.90%	K.TNAAFLK.I		K.TNAAFLK.I
487	495	2	1112.56	0.34	1	34.3	28.6	95.00%	K.FPYSVMEIK.V		K.FPYSVMEIK.V
641	649	2	1038.59	0.16	1	34.2	22.5	95.00%	K.FKTNAAFLK.I		K.FKTNAAFLK.I
143	148	2	715.42	1.1	0	25.5	28.7	91.20%	K.SLLQVR.L	Deamidation (+1)	K.SLLQVR.L
379	386	2	1032.57	0.38	0	33.9	24.1	95.00%	K.NYLINQLR.E		K.NYLINQLR.E
132	142	2	1296.68	-2.1	1	37.4	27.6	95.00%	H.DKLHPNYPSVK.S		K.HDKLHPNYPSVK.S
119	126	2	938.52	0.61	0	38.3	24.7	95.00%	R.LNFTGFIK.I		R.LNFTGFIK.I
425	436	2	1331.68	-0.39	1	43	28.1	95.00%	R.TAFQIPGDQSIR.V		R.TAFQIPGDQSIR.V
591	597	2	714.39	2.1	1	25.8	27.6	93.40%	K.ISVPDGK.T		K.ISVPDGK.T
437	447	2	1323.69	0.67	1	43.8	27.7	95.00%	R.VTIDSNIMYIR.E		R.VTIDSNIMYIR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
2	A6ZPV7_YEAS7	34.26%	100%	29

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
623	629	2	884.44	0.083	1	24.6	27	92.50%	K.VYFATER.T		K.VYFATER.T
535	563	3	3044.37	-0.78	1	78.4	27.4	95.00%	E.ESVGYGATSAPTSNTNHVVESANAAYYQR.K	Deamidation (+1)	R.SDNEDNDFDEDDEDDAALVAAMTNAPGNSLDIEESVGYGATSAPTSNTNHVVESANAAYYQR.K
336	348	2	1493.78	-1.3	1	76.2	26.8	95.00%	L.EALASEIQYVMLK.K		K.KPMNEIENLEALASEIQYVMLK.K
535	553	2	1889.87	-0.74	0	59.8	29.2	95.00%	E.ESVGYGATSAPTSNTNHVV.E		R.SDNEDNDFDEDDEDDAALVAAMTNAPGNSLDIEESVGYGATSAPTSNTNHVVESANAAYYQR.K
362	371	2	1074.55	0.99	1	43.2	29	95.00%	R.TAFQLPGDAR.V		R.TAFQLPGDAR.V
76	86	2	1351.69	1	1	51.3	29.5	95.00%	K.EVQEQVQHTVR.L		K.EVQEQVQHTVR.L
443	455	2	1402.78	-0.086	1	69.7	24.5	95.00%	R.ELVGSHLVEPVPK.F		R.ELVGSHLVEPVPK.F
420	428	2	1064.59	2	1	47.2	25.5	95.00%	R.FPYAVLEVK.L		R.FPYAVLEVK.L
357	368	2	1399.69	-0.87	1	29.4	29.7	95.00%	R.SFYNRTAFQLPG.D		R.SFYNRTAFQLPGDAR.V
459	468	2	1083.61	-0.85	0	36.1	24.6	95.00%	K.FIHGVATLLN.D		K.FIHGVATLLNDK.V
416	425	2	1252.63	-0.55	1	27.4	29.3	93.30%	K.DICRFPYAVL.E	Carbamidomethyl (+57)	K.DICRFPYAVLEVK.L
138	149	2	1403.83	-1.4	0	41.4	16.4	95.00%	K.TGFILKPVFQVR.L		K.TGFILKPVFQVR.L

516	531	2	1514.74	-1.3	0	99.6	29.5	95.00%	D.DAALVAAMTNAPGNSL.D		R.SDNEDNDFDEDDEDDAALVAAM TNAPGNSLDIEESVGYGATSAPTSN TNHVVESANAAYYQR.K
122	129	2	969.49	-0.013	0	43.3	27.6	95.00%	R.LNYTGFQK.I		R.LNYTGFQK.I
137	149	2	1531.92	-1.6	1	22.8	15.9	92.90%	K.KTGFILKPVFQVR.L		K.KTGFILKPVFQVR.L
167	175	2	1077.58	0.45	1	41.3	27.4	95.00%	K.ISQLYDIAR.T		K.ISQLYDIAR.T
274	280	2	878.45	-0.26	1	28.8	29.9	94.30%	T.DTIFVER.K		R.WYGGMSTDTIFVER.K
598	606	2	1037.52	0.65	1	36.2	29.6	95.00%	K.GTTFDTQIR.A		K.GTTFDTQIR.A
312	320	2	1069.54	-0.76	1	34.7	28.2	95.00%	K.YTVDQVFAK.M		K.YTVDQVFAK.M
3	9	2	816.41	0.46	1	28.5	28	95.00%	K.FGEHLSK.S		K.FGEHLSK.S
341	348	2	1022.55	-1.3	0	34.5	28.6	95.00%	S.EIQYVMLK.K		K.KPMNEIENLEALASEIQYVMLK.K
119	129	3	1359.69	-0.14	1	24.3	28.5	95.00%	K.FSRLNYTGFQK.I		K.FSRLNYTGFQK.I
377	384	2	963.47	-0.85	1	29.1	29.7	95.00%	L.DTELTMVR.E		R.ISLDTELTMVR.E
515	531	2	1645.76	-0.14	1	91.2	30.2	95.00%	E.DDAALVAAMTNAPGNSL.D	Oxidation (+16)	R.SDNEDNDFDEDDEDDAALVAAM TNAPGNSLDIEESVGYGATSAPTSN TNHVVESANAAYYQR.K
487	501	2	1687.97	0.69	1	23.7	16.8	94.10%	R.KPPLPTNIEITRPGR.S		R.KPPLPTNIEITRPGR.S
584	594	2	1323.57	-1.7	1	60.5	30.4	95.00%	F.DHYFNGDQISK.I	Deamidation (+1)	K.YYEIVAFFDHYFNGDQISK.I
218	228	2	1280.72	-1.5	0	24.2	21.7	94.70%	K.HLPVLVFNTNK.E		K.HLPVLVFNTNK.E
341	349	2	1150.64	-2	1	33.2	24.3	95.00%	S.EIQYVMLKK.K		K.KPMNEIENLEALASEIQYVMLKK. K
567	574	2	871.44	2.4	1	28.3	26.2	95.00%	R.NAENPISK.K		R.NAENPISK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
3	B3LLD7_YEAS1	14.48%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
481	506	3	2407.34	-0.24	1	19.3	18.9	95.00%	R.STAHGISAASGKVGAIIAQTALGT LI.D		R.STAHGISAASGKVGAIIAQTALGT LIDHNCAR.D
35	40	2	730.33	-1.1	1	32.5	29.9	95.00%	N.DFAHIE.D		K.EHLTEGGNMAFHNHLNDFAHIED PLER.R
481	492	2	1085.55	3	0	53.4	28.1	95.00%	R.STAHGISAASGK.V		R.STAHGISAASGK.V
23	34	2	1339.57	-1.3	0	39	30.4	95.00%	T.EGGNMAFHNHLN.D		K.EHLTEGGNMAFHNHLNDFAHIED PLER.R
109	126	2	1739.91	-0.64	0	48.8	25.2	95.00%	K.VSTSVGTVIGQFGFGTLA.D		K.VSTSVGTVIGQFGFGTLADIVGR. K
109	131	2	2280.21	0.78	1	108	22.5	95.00%	K.VSTSVGTVIGQFGFGTLADIVGR. K		K.VSTSVGTVIGQFGFGTLADIVGR. K
562	569	2	932.47	-1.5	0	43.3	28.9	95.00%	I.DPATLNFR.N		K.TLEEINELYHDEIDPATLNFR.N
19	34	2	1819.8	-1.3	1	99	29.9	95.00%	K.EHLTEGGNMAFHNHLN.D		K.EHLTEGGNMAFHNHLNDFAHIED PLER.R
493	512	2	2093.1	-0.95	1	119	23.4	95.00%	K.VGAIIAQTALGTLIDHNCAR.D	Carbamidomethyl (+57)	K.VGAIIAQTALGTLIDHNCAR.D
493	506	2	1339.81	-0.53	0	76.1	17	95.00%	K.VGAIIAQTALGTLI.D		K.VGAIIAQTALGTLIDHNCAR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
4	YBT1_YEAST	15.65%	100%	27

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
78	94	2	1934.92	-2.3	1	52.8	28.7	95.00%	E.DEQSPLINNNTITTNYV.D		K.NPIDELLYSSTDEDEQSPLINNNTI TTNYVDNNCTK.D
1616	1627	2	1490.74	0.26	1	44.7	29.1	95.00%	K.EYDHPYSLLLNK.Q		K.EYDHPYSLLLNK.Q
1457	1473	2	1830.01	-0.44	1	57.2	21.6	95.00%	R.SITIIPQDPTLFSGTIK.T		R.SITIIPQDPTLFSGTIK.T
1618	1627	2	1198.63	-1.3	0	35.1	27	95.00%	Y.DHPYSLLLNK.Q		K.EYDHPYSLLLNK.Q
228	240	3	1519.83	0.73	0	25.5	25.1	95.00%	R.SIFIHHINSPISR.K		R.SIFIHHINSPISR.K
1584	1596	2	1471.78	-0.15	0	57.2	26.4	95.00%	K.EFQGSTILTIAHR.L		K.EFQGSTILTIAHR.L
588	597	2	1216.65	0.15	1	34.8	27.6	95.00%	R.ENELSLLLMR.S		R.ENELSLLLMR.S
964	976	2	1488.66	-1.5	0	56.1	30.6	95.00%	K.EQQVSVNNNSSHF.E		K.EQQVSVNNNSSHFEAK.K
427	436	2	1165.66	-0.61	1	36.2	21.5	95.00%	K.SIIISEIYTK.A		K.SIIISEIYTK.A
791	803	2	1535.73	-1.4	1	64.7	29.6	95.00%	K.NNILFNSPFNEAR.Y	Deamidation (+1)	K.NNILFNSPFNEAR.Y
964	979	2	1816.83	-0.89	1	67.9	30.1	95.00%	K.EQQVSVNNNSSHFEAK.K		K.EQQVSVNNNSSHFEAK.K

1417	1430	3	1434.82	-0.42	1	27.4	21.7	95.00%	R.TGAGKSTIITALFR.F		R.TGAGKSTIITALFR.F
1642	1649	2	913.55	-1.1	1	21.7	22.2	90.80%	L.DILIELAK.K		K.QSAFYSMCEHSGELDILIELAK.K
936	951	2	1748.78	-0.79	1	41	29.9	95.00%	K.SSILSRANSSANLAAK.S	Phospho (+80)/ Phospho (+80)	K.SSILSRANSSANLAAK.S
1422	1430	2	1020.6	0.17	0	49.3	18.8	95.00%	K.STIITALFR.F		K.STIITALFR.F
1238	1245	2	977.46	-0.83	0	41.1	29.1	95.00%	R.SPIYQHFS.E		R.SPIYQHFSETLVGVTTIR.A
1238	1255	2	2047.07	-1.2	1	79.8	25.6	95.00%	R.SPIYQHFSETLVGVTTIR.A		R.SPIYQHFSETLVGVTTIR.A
560	568	2	1060.57	-0.69	1	56.9	28.9	95.00%	K.LNEAFQAIR.I		K.LNEAFQAIR.I
1152	1160	2	1010.48	0.36	1	38.1	31	95.00%	R.FFDATPTGR.I		R.FFDATPTGR.I
1464	1473	2	1077.57	-0.58	0	34.9	27	95.00%	Q.DPTLFSGTIK.T		R.SITIIPQDPTLFSGTIK.T
1583	1596	3	1599.87	-0.061	1	46.9	23.5	95.00%	R.KEFQGSTILTIAHR.L		R.KEFQGSTILTIAHR.L
1486	1492	2	847.48	1.2	1	31.5	25.5	95.00%	R.QIFEALK.R		R.QIFEALK.R
1400	1410	2	1180.57	0.41	1	30.9	30.3	95.00%	K.NVSFSVDAQSK.I		K.NVSFSVDAQSK.I
767	786	2	2169.96	-1.1	0	73.1	30	95.00%	V.DANGTTNSIAYCSQAAWLLN.D	Deamidation (+1)/ Carbamidomethyl (+57)	R.QELIVDANGTTNSIAYCSQAAWLLNDTVK.N
952	963	2	1202.65	-0.011	0	49.2	26.8	95.00%	K.SSTSLSNLPAVK.E		K.SSTSLSNLPAVK.E
1246	1255	2	1087.62	-0.94	0	48.6	25.7	95.00%	S.ETLVGVTTIR.A		R.SPIYQHFSETLVGVTTIR.A
887	900	3	1609.9	0.4	0	39.1	21.2	95.00%	R.TCILVSHNIALTLR.N	Carbamidomethyl (+57)	R.TCILVSHNIALTLR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
5	PMA1_YEAST	15.80%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
445	451	2	887.45	-0.6	1	41	30.9	95.00%	K.VLEFHPF.D		K.VLEFHPFDPVSK.K
185	194	2	1054.53	-0.017	1	31.8	28.7	95.00%	R.DGQLVEIPAN.E		R.DGQLVEIPANEVVPGDILQLEDGTVIPTDGR.I
175	184	2	1056.63	-1.6	0	89.4	24.8	95.00%	K.TLANTAVVIR.D		K.TLANTAVVIR.D
3	23	2	2023.86	-0.49	0	77.4	30.5	95.00%	T.DTSSSSSSSSASSVSAHQPTQ.E		-.MTDTSSSSSSSSASSVSAHQPTQEKPAK.T
2	23	2	2124.9	-1.3	1	89.5	30	95.00%	M.TDTSSSSSSSSASSVSAHQPTQ.E		-.MTDTSSSSSSSSASSVSAHQPTQEKPAK.T
502	508	2	744.41	1.4	1	34.7	30.6	95.00%	K.VAELASR.G		K.VAELASR.G
663	675	2	1327.77	-0.54	0	44.3	21.9	95.00%	A.DIVFLAPGLSAII.D		R.SAADIVFLAPGLSAIIDALK.T
556	566	2	1074.57	-0.48	1	68.1	27.7	95.00%	K.MLTGDAVGIAK.E		K.MLTGDAVGIAK.E
618	625	2	969.56	1.7	1	36.1	23.7	95.00%	R.VVEILQNR.G		R.VVEILQNR.G
571	583	2	1447.74	0.68	1	84.7	28.6	95.00%	R.QLGLGTNIYNAER.L		R.QLGLGTNIYNAER.L
265	271	2	807.39	-0.16	0	27.9	28.7	94.70%	G.DNTFVGR.A		R.GEGFMVVTATGDNTFVGR.A
240	252	2	1455.66	-0.55	1	74.8	30.7	95.00%	K.HYGDQTFSSSTVK.R		K.HYGDQTFSSSTVK.R
605	615	3	1273.61	-1.4	1	24.4	30.7	94.50%	A.DGFAEVFPQHK.Y		R.LGLGGGGDMPGSELADFVENADGFAEVFPQHK.Y
475	482	2	843.52	1.5	0	25.8	24.2	95.00%	K.GAPLFVLK.T		K.GAPLFVLK.T
3	28	3	2577.18	0.089	1	46.5	28.5	95.00%	T.DTSSSSSSSSASSVSAHQPTQEKPAK.T		-.MTDTSSSSSSSSASSVSAHQPTQEKPAK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
6	A6ZPA7_YEAS7	20.71%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
13	27	2	1822.93	-0.99	1	68.5	26.4	95.00%	A.EMALVQFYIPQEISR.D		R.SAEMALVQFYIPQEISR.D
170	193	2	2346.18	-1.8	1	109	26	95.00%	I.DANGENIAAAIGASVNYVTGVIAR.D	Deamidation (+1)	K.GDNTDSTSYMDEDMIDANGENIAAAIGASVNYVTGVIAR.D
209	214	2	724.39	0.78	0	31.3	25.6	95.00%	R.GNLFFK.T		R.GNLFFK.T
280	289	2	1164.64	0.25	1	44.7	24.8	95.00%	K.NLSDLYTVLK.T		K.NLSDLYTVLK.T
196	205	2	1227.7	-0.014	1	46.3	23.7	95.00%	K.VATLEQILWR.V		K.VATLEQILWR.V
395	403	2	1144.5	-1.2	0	53	30.8	95.00%	C.DCYGIAQYR.E	Carbamidomethyl (+57)	K.FTAGFQSICDCYGIAQYR.E
234	242	2	990.49	-0.83	0	41	28.6	95.00%	K.NAFIVFSHG.D		K.NAFIVFSHGDLIIK.R
11	23	2	1495.74	-0.61	1	49.2	29.4	95.00%	R.SAEMALVQFYIPQ.E		R.SAEMALVQFYIPQEISR.D
54	60	2	877.47	0.31	1	39.4	29.2	95.00%	R.TFVNEIR.R		R.TFVNEIR.R

360	371	2	1265.76	-0.4	1	43.2	17.5	95.00%	R.LGIDVPSIIQVL.D	R.LGIDVPSIIQVLDTNHTPPTFHR.T
334	343	2	1166.68	-1.3	1	63.1	19.6	95.00%	K.ILIAEGWIPR.D	K.ILIAEGWIPR.D
71	77	2	932.5	0.74	0	24.4	28	90.20%	R.YFYSLLK.K	R.YFYSLLK.K
383	394	2	1372.64	-1	1	68.2	29.9	95.00%	R.TNKFTAGFQSIC.D	Carbamidomethyl (+57) R.TNKFTAGFQSICDCYGIAQYR.E
318	325	2	946.55	-0.031	1	49.3	24.3	95.00%	K.AIFEILNK.S	K.AIFEILNK.S
344	352	2	1015.53	-0.71	1	33.4	27.9	95.00%	R.DELATLQAR.L	R.DELATLQAR.L
386	403	2	2155.94	-1	1	106	29.4	95.00%	K.FTAGFQSICDCYGIAQYR.E	Carbamidomethyl (+57)/ Carbamidomethyl (+57) K.FTAGFQSICDCYGIAQYR.E
809	817	2	1027.5	-0.12	1	25.8	28.8	91.40%	K.FFVGEGLPY.E	K.FFVGEGLPYEPFAFEYK.D
28	42	3	1666.87	-0.83	0	61.1	26.8	95.00%	R.DSAYTLGQLGLVQFR.D	R.DSAYTLGQLGLVQFR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
7	B5VNN6_YEAST	20.15%	100%	35

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	66	2	1427.56	-1.5	1	44.1	30.3	95.00%	A.DMYGQQPPNESY.D		- .MNTDQQPYQGQTDYTQGPDNGQ SQEQDYDQYGQPLYPSQADGYYD PNVAAGTEADMYGQQPPNESYDQ DYTNGEYYGQPPNMAAQDGENFS DFSSYGPPGTPGYDSYGGQYTPS QMSYGEPNSSGTSTPIYGNYDPNAI AMALPNEPYPAWTADSQSPVSIEQI EDIFIDLTNR.L
392	405	2	1692.85	-1.6	1	42.5	29	95.00%	D.DLNQLFWYPEGIAK.I		K.IVGYDDLNQLFWYPEGIAK.I
1779	1788	2	1213.72	-1.8	0	35.2	21.3	95.00%	R.QIRPPIYSLK.Q		R.QIRPPIYSLK.Q
837	850	2	1605.75	-0.14	0	47.5	29.5	95.00%	V.DNMPTFTVLTPHYA.E		R.ISFFAQSLSTPIPEPLPVDNMPTF TVLTPHYAER.I
920	929	2	1258.6	-0.95	0	36	29.3	95.00%	D.DLPFYCIGFK.S	Carbamidomethyl (+57)	K.SQIDDLPFYCIGFK.S
1124	1138	2	1697.87	-2.1	1	66.4	25.8	95.00%	E.ELNVEQVNPYAPGLR.Y		R.SVLAEFEELNVEQVNPYAPGLR.Y
919	929	2	1373.63	-0.43	1	62.2	29.9	95.00%	I.DDLPFYCIGFK.S	Carbamidomethyl (+57)	K.SQIDDLPFYCIGFK.S
1702	1712	2	1246.57	-1.9	0	48.5	30.4	95.00%	N.DHANTAFWTGK.W		K.NDHANTAFWTGK.W
1262	1273	2	1248.6	-0.33	1	89.3	29.8	95.00%	K.IGAGMGEQMLSR.E		K.IGAGMGEQMLSR.E
135	145	2	1125.55	0.95	0	28.3	29.4	94.40%	Y.DPNAIAMALPN.E		- .MNTDQQPYQGQTDYTQGPDNGQ SQEQDYDQYGQPLYPSQADGYYD PNVAAGTEADMYGQQPPNESYDQ DYTNGEYYGQPPNMAAQDGENFS DFSSYGPPGTPGYDSYGGQYTPS QMSYGEPNSSGTSTPIYGNYDPNAI AMALPNEPYPAWTADSQSPVSIEQI EDIFIDLTNR.L
1197	1207	2	1315.62	-1	0	41.7	30	95.00%	P.DFINATFMTTR.G		K.LHYGHPDFINATFMTTR.G
1083	1094	2	1476.71	-0.48	1	28	30	93.10%	K.SDNQNHALIFYR.G		K.SDNQNHALIFYR.G
1222	1232	2	1253.59	-0.73	0	58.3	31	95.00%	E.DIYAGMNAMLR.G		K.GLHLNEDIYAGMNAMLR.G
135	153	2	2056.96	-0.56	1	47.8	29.4	95.00%	Y.DPNAIAMALPNEPYPAWTA.D	Oxidation (+16)	- .MNTDQQPYQGQTDYTQGPDNGQ SQEQDYDQYGQPLYPSQADGYYD PNVAAGTEADMYGQQPPNESYDQ DYTNGEYYGQPPNMAAQDGENFS DFSSYGPPGTPGYDSYGGQYTPS QMSYGEPNSSGTSTPIYGNYDPNAI AMALPNEPYPAWTADSQSPVSIEQI EDIFIDLTNR.L
1173	1182	2	1168.59	-0.8	0	48.2	29	95.00%	K.EQTFGTLFAR.T		K.EQTFGTLFAR.T

92	104	2	1343.57	0.21	0	49.2	30.6	95.00%	S.DFSSYGPPGTPGY.D		-.MNTDQQPYQGQTDYTQGPDNGQSQEQDYDQYGQPLYPSQADGYYDPNVAAGTEADMYGQQPPNESYDQDYTNGEYYGQPPNMAAQDGENFSDFSSYGPPGTPGYDSYGGQYTPSQMSYGEPNSSGTSTPIYGNYDPNAIAMALPNEPYPAWTADSQSPVSIEQIEDIFIDLTNR.L
69	85	2	1934.76	-0.27	1	61.9	29.7	95.00%	Q.DYTNGEYYGQPPNMAAQ.D	Deamidation (+1)/ Oxidation (+16)	-.MNTDQQPYQGQTDYTQGPDNGQSQEQDYDQYGQPLYPSQADGYYDPNVAAGTEADMYGQQPPNESYDQDYTNGEYYGQPPNMAAQDGENFSDFSSYGPPGTPGYDSYGGQYTPSQMSYGEPNSSGTSTPIYGNYDPNAIAMALPNEPYPAWTADSQSPVSIEQIEDIFIDLTNR.L
658	670	2	1628.71	-0.52	1	64.8	30.5	95.00%	R.CTGEYWWGAVLCK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.CTGEYWWGAVLCK.V
837	852	2	1890.89	-1.8	1	75.4	28.9	95.00%	V.DNMPTFTVLTPHYAER.I		R.ISFFAQSLSTPIPEPLPVDNMPTFTVLTPHYAER.I
166	174	2	1105.58	0.79	1	40.6	28.9	95.00%	E.DIFIDLTNR.L		-.MNTDQQPYQGQTDYTQGPDNGQSQEQDYDQYGQPLYPSQADGYYDPNVAAGTEADMYGQQPPNESYDQDYTNGEYYGQPPNMAAQDGENFSDFSSYGPPGTPGYDSYGGQYTPSQMSYGEPNSSGTSTPIYGNYDPNAIAMALPNEPYPAWTADSQSPVSIEQIEDIFIDLTNR.L
1191	1207	2	2019.96	-0.61	1	60.7	28.6	95.00%	K.LHYGHPDFINATFMTTR.G		K.LHYGHPDFINATFMTTR.G
1436	1444	2	1094.61	-0.2	0	48.5	23.9	95.00%	R.IPFSILYSR.F		R.IPFSILYSR.F
789	799	2	1265.68	-1.4	1	50.8	27.1	95.00%	R.TLRAPTFFVSQ.D		R.TLRAPTFFVSQDDNNFETEFFPR.D
120	134	2	1585.69	-0.38	0	35.2	30.3	95.00%	G.EPNSSGTSTPIYGNY.D		-.MNTDQQPYQGQTDYTQGPDNGQSQEQDYDQYGQPLYPSQADGYYDPNVAAGTEADMYGQQPPNESYDQDYTNGEYYGQPPNMAAQDGENFSDFSSYGPPGTPGYDSYGGQYTPSQMSYGEPNSSGTSTPIYGNYDPNAIAMALPNEPYPAWTADSQSPVSIEQIEDIFIDLTNR.L
105	119	2	1655.64	-1.3	0	70.8	30.2	95.00%	Y.DSYGGQYTPSQMSYG.E	Oxidation (+16)	-.MNTDQQPYQGQTDYTQGPDNGQSQEQDYDQYGQPLYPSQADGYYDPNVAAGTEADMYGQQPPNESYDQDYTNGEYYGQPPNMAAQDGENFSDFSSYGPPGTPGYDSYGGQYTPSQMSYGEPNSSGTSTPIYGNYDPNAIAMALPNEPYPAWTADSQSPVSIEQIEDIFIDLTNR.L
1249	1261	2	1425.75	-1.4	0	81.5	26.5	95.00%	R.DLGFGTILNFTTK.I		R.DLGFGTILNFTTK.I
1140	1154	2	1620.82	-1.5	1	79.7	27.9	95.00%	Y.EEQTTNHPVAIVGAR.E		R.YEEQTTNHPVAIVGAR.E
1070	1082	2	1296.7	-0.0085	1	62.1	25	95.00%	R.VQLSGNPILGDGK.S		R.VQLSGNPILGDGK.S
1167	1182	2	1709.87	-1.1	1	80.4	27.1	95.00%	G.DVAAGKEQTFGTLFAR.T		R.EYIFSENSGVLGDVAAGKEQTFGTLFAR.T
1717	1728	2	1383.61	-0.15	0	66	31.1	95.00%	K.GMGYMAWTQPSR.E		K.GMGYMAWTQPSR.E

203	211	2	966.51	-0.53	0	45	26.7	95.00%	P.DQALISLHA.D		R.MSPDQALISLHADYIGGDTANYK.K
1520	1527	2	993.5	-0.11	0	40.9	28.6	95.00%	R.NSWIGYVR.M		R.NSWIGYVR.M
953	962	2	1174.54	-0.35	0	46.5	30.6	95.00%	R.TISGFMNYSR.A		R.TISGFMNYSR.A
870	877	2	977.58	-0.012	1	44.9	16.6	95.00%	R.VTLLEYLK.Q		R.VTLLEYLK.Q
1155	1166	2	1313.61	-0.7	1	40.2	30.1	95.00%	R.EYIFSENSGVLG.D		R.EYIFSENSGVLGDVAAGK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
8	A7A234_YEAS7	24.03%	100%	23

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
158	166	2	1168.58	-0.36	1	30.2	29.4	95.00%	S.EEYSPLLYR.I		K.ELPSHSEEYSPLLYR.I
225	238	2	1550.81	0.38	1	74.2	27.1	95.00%	R.HLPVLVYANVPSEN.D		R.HLPVLVYANVPSENDDLVNR.F
422	430	2	1063.55	-1.1	1	33.3	28	95.00%	I.DSNIVFIKE.D		R.VTIDSNIVFIKEDSFDR.E
394	401	2	1001.53	2	1	29.4	28.9	95.00%	K.NELQPVFR.T		K.NELQPVFR.T
383	393	2	1352.7	-1.7	1	64	28	95.00%	E.DFSEIQNFIIK.N		R.LEEDFSEIQNFIIK.N
501	515	3	1760.9	0.52	1	40.8	27	95.00%	K.HGQWLNDLTNSHLVK.E		K.HGQWLNDLTNSHLVK.E
483	496	2	1442.64	-1.4	0	72	30.2	95.00%	L.DSSMSASSMISNVK.L		K.SSLDSSMSASSMISNVK.L
386	394	2	1117.61	-1.3	1	39.7	26.9	95.00%	S.EIQNFIIKN.E		R.LEEDFSEIQNFIIKNELQPVFR.T
7	16	2	1215.63	0.47	1	45.5	27.3	95.00%	K.LANEVYPPWK.G		K.LANEVYPPWK.G
144	149	2	715.42	1.1	1	25.5	28.7	91.20%	K.SLLEVR.L		K.SLLEVR.L
483	499	2	1780.87	-1.4	1	50	28.1	95.00%	L.DSSMSASSMISNVKLPK.K		K.SSLDSSMSASSMISNVKLPK.K
451	462	2	1356.75	-0.91	1	23.2	23.8	93.40%	I.DANVANPLKFLR.G		R.TDIDANVANPLKFLR.G
17	26	2	1142.56	-0.36	1	45.8	28.8	95.00%	K.GSYINYEGLK.K		K.GSYINYEGLK.K
469	477	2	1112.56	0.34	1	34.3	28.6	95.00%	K.FPYSVMEIK.V		K.FPYSVMEIK.V
306	313	2	959.52	-1.2	1	28.6	27.5	95.00%	R.LRWTGQLS.D		R.LRWTGQLSDKPDIFLEK.K
480	496	2	1745.78	-0.92	1	76.4	31	95.00%	K.SSLDSSMSASSMISNVK.L	Oxidation (+16)	K.SSLDSSMSASSMISNVK.L
72	78	2	938.43	0.94	1	35.9	31.2	95.00%	K.YNNLMER.L		K.YNNLMER.L
436	447	2	1575.8	-1.1	1	28.2	27.9	95.00%	R.ERPIRDPNTWHR.T		R.ERPIRDPNTWHR.T
176	190	2	1522.73	-0.41	1	102	29.5	95.00%	R.SNFNTASEPLASASK.F		R.SNFNTASEPLASASK.F
687	693	2	886.47	-0.031	1	25.2	26.4	94.30%	K.VWLANER.T		K.VWLANER.T
275	283	2	1094.56	-1	0	27.3	29.3	93.10%	F.DPLINTLYF.D		R.SFDPLINTLYFDNEHFELYNDK.L
298	305	2	870.49	1.7	0	25.7	24.4	95.00%	K.LNSAPTLR.L		K.LNSAPTLR.L
386	393	2	1003.57	-0.52	0	35.7	24.4	95.00%	S.EIQNFIIK.N		R.LEEDFSEIQNFIIK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
9	A6ZL63_YEAS7	35.59%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
197	210	2	1652.75	-1	1	64.7	30.2	95.00%	G.DNMIEATTNAPWYK.G		K.TVPFVPISGWNGDNMIEATTNAPWYK.G
411	421	2	1264.61	-0.98	1	38.7	30.4	95.00%	V.EAFSEYPPLGR.F		K.FVPSKPMCVEAFSEYPPLGR.F
360	370	2	1386.59	-1.3	1	40.2	30.7	95.00%	L.DCHTAHIACRF.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GCASFNATVIVLNHPGQISAGYSPVLDCHTAHIACRFDELLEK.N
85	96	2	1354.7	-0.6	1	61.9	27	95.00%	K.YQVTVIDAPGHR.D		K.YQVTVIDAPGHR.D
394	401	2	759.41	1.7	1	40.5	29.4	95.00%	K.SGDAALVK.F		K.SGDAALVK.F
254	264	2	1024.61	1.8	0	68.3	20.2	95.00%	K.IGGIGTVPVGR.V		K.IGGIGTVPVGR.V
429	437	2	913.56	-0.34	0	45.5	22.6	95.00%	R.QTVAVGVIK.S		R.QTVAVGVIK.S
6	20	2	1559.84	-0.0025	1	81.3	25.4	95.00%	K.SHINVVVIGHVDSGK.S		K.SHINVVVIGHVDSGK.S
241	249	2	1078.65	-1.4	1	32.4	20.1	95.00%	T.DKPLRLPLQ.D		K.TLLEAIDAIEQPSRPTDKPLRLPLQDVYK.I
185	196	2	1272.65	-1	0	39.3	28.7	95.00%	K.TVPFVPISGWNG.D		K.TVPFVPISGWNGDNMIEATTNAPWYK.G
334	369	5	3892.85	-0.78	1	21.2	24.8	95.00%	K.GCASFNATVIVLNHPGQISAGYSPVLDCHTAHIACR.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GCASFNATVIVLNHPGQISAGYSPVLDCHTAHIACR.F
246	253	2	974.54	-0.0093	1	40.2	25.5	95.00%	R.LPLQDVYK.I		R.LPLQDVYK.I
265	285	2	2073.12	-1.4	1	54.9	22.9	95.00%	R.VETGVIKPGMVVTFAPAGVTT.E		R.VETGVIKPGMVVTFAPAGVTTEVK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
10	A6ZZ70_YEAS7	34.28%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
191	199	2	966.51	-0.43	0	36.5	26.5	95.00%	E.DLIATHQLG.E		R.WQEDLIATHQLGEYPLGR.V
302	309	2	799.48	-0.03	1	33.6	26.6	95.00%	K.VALGALEK.A		K.VALGALEK.A
449	456	2	952.52	-1.4	1	48.7	24.5	95.00%	S.DLETLIHL.D		K.DLGIYDYTESDLETLIHLDDNANAIQDK.L
467	474	2	980.48	1.5	1	30.4	31.3	94.60%	K.LNDMVSFR.A		K.LNDMVSFR.A
191	205	2	1681.88	-2	1	56.4	25.8	95.00%	E.DLIATHQLGEYPLGR.V		R.WQEDLIATHQLGEYPLGR.V
136	154	2	2049.97	-1.9	1	37.4	29.7	95.00%	K.SYNGAIGVDPHHRPCGTVL.E	Deamidation (+1)/ Carbamidomethyl (+57)	K.SYNGAIGVDPHHRPCGTVLEAAK.L
159	171	2	1362.79	-0.15	0	81.9	20	95.00%	K.LAGYLTGLVVTTR.I		K.LAGYLTGLVVTTR.I
549	557	2	1074.5	-0.66	1	39.8	29.5	95.00%	T.EIASEVQHY.D		K.HTSDFDATEIASEVQHYDEYYHELTN.-
373	383	2	1170.57	2	1	27.8	29.7	93.20%	S.DHETGGLVTSR.Q		R.EVLAFDEAFQYVLEFAENSDTETVLVSTSDHETGGLVTSR.Q
488	498	2	1297.66	-1.7	1	40.2	27.9	95.00%	V.DVNIYAYANKK.A		R.AQIGWTTHGHSAVDVNIYAYANKK.A
475	487	2	1363.66	-1.4	0	51.3	29.4	95.00%	R.AQIGWTTHGHSAV.D		R.AQIGWTTHGHSAVDVNIYAYANK.K
488	497	2	1169.57	-1	0	57.5	29.5	95.00%	V.DVNIYAYANK.K		R.AQIGWTTHGHSAVDVNIYAYANK.K
206	215	2	1015.55	1.6	1	58.9	28.5	95.00%	R.VVDLLMGGGR.S		R.VVDLLMGGGR.S
122	135	2	1352.64	-1.4	0	82.4	30.8	95.00%	T.DSAAGATAFACALK.S	Carbamidomethyl (+57)	R.SSDSLVTDSAAGATAFACALK.S
1	12	3	1430.66	-0.061	1	39.2	30.5	95.00%	-.MMTHTLPSEQTR.L		-.MMTHTLPSEQTR.L
68	86	2	2027.98	-1.7	1	104	28.5	95.00%	K.NVIFFVTDGMGPASLSMAR.S	Oxidation (+16)	K.NVIFFVTDGMGPASLSMAR.S
316	328	2	1458.64	-1.5	1	63.3	30.7	95.00%	K.DSNGFFLMVEGSR.I	Deamidation (+1)	K.DSNGFFLMVEGSR.I
75	86	2	1191.54	-0.94	0	72.1	30.2	95.00%	T.DGMGPASLSMAR.S		K.NVIFFVTDGMGPASLSMAR.S
174	184	2	1117.5	-1.9	0	37.8	30.3	95.00%	T.DATPASFSSHV.D		R.ITDATPASFSSHVDYR.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
11	A6ZY95_YEAS7	13.20%	100%	20

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1333	1343	2	1233.62	-0.98	1	29.9	28.8	95.00%	I.DNIAINEIGLY.D		R.MIEASEGNIVIDNIAINEIGLYDLR.H
1400	1415	2	1600.78	-1.3	1	103	29.4	95.00%	L.DAQLTEGGGNLSVGQR.Q		K.EHVLSMSNDGLDAQLTEGGGNLSVGQR.Q
1036	1048	2	1466.72	-0.78	1	61.7	29.3	95.00%	R.APMTFFETTPIGR.I		R.APMTFFETTPIGR.I
790	805	3	1777	-0.45	1	52.9	19.3	95.00%	R.HLIEHVLGPNGLLHTK.T		R.HLIEHVLGPNGLLHTK.T
486	495	2	1141.67	0.25	1	47.6	23.7	95.00%	R.VISEILNNIK.S		R.VISEILNNIK.S
1134	1143	2	1015.57	-1.1	0	57.7	26.3	95.00%	Q.ETLGGLATVR.G		R.SPIYSHFQETLGGLATVR.G
192	206	3	1835.99	-0.32	0	32.5	23.1	95.00%	K.KPLMPHQHIHQTLTR.R		K.KPLMPHQHIHQTLTR.R
271	281	2	1289.62	0.94	0	53.4	29.6	95.00%	K.SNPSLSWAICR.T	Carbamidomethyl (+57)	K.SNPSLSWAICR.T
1458	1467	3	1194.68	-0.25	1	39.9	20.3	95.00%	K.DRTILTIAHR.L		K.DRTILTIAHR.L
1126	1143	2	1975.01	-1.6	1	82	26.3	95.00%	R.SPIYSHFQETLGGLATVR.G		R.SPIYSHFQETLGGLATVR.G
1313	1321	2	1006.58	1.5	0	51.4	23.4	95.00%	K.SSLTLALFR.M		K.SSLTLALFR.M
1460	1467	2	923.56	0.52	0	30.7	18.9	95.00%	R.TILTIAHR.L		R.TILTIAHR.L
630	638	2	1150.54	-0.72	1	54.2	30.5	95.00%	G.DDATFLWQR.K		K.NIGDVAINIGDDATFLWQR.K
2	11	2	1146.55	-0.31	0	39.1	29.9	95.00%	M.AGNLVSWACK.L	Acetyl (+42)/ Carbamidomethyl (+57)	-.MAGNLVSWACK.L
1291	1301	3	1341.75	0.22	1	27	24.1	95.00%	K.HINIHIKPNEK.V		K.HINIHIKPNEK.V
709	717	2	1147.58	-0.89	1	27.6	28.5	94.60%	K.ENILFGHRY.D		K.ENILFGHRYDAEFYEK.T
1274	1280	2	900.41	2.6	0	33.3	29.2	95.00%	K.FNNYSTR.Y		K.FNNYSTR.Y
1381	1388	2	909.53	-0.46	1	33.8	19.5	95.00%	R.ALELSHLK.E		R.ALELSHLK.E
379	388	2	1106.63	0.35	0	24.6	22	95.00%	K.SALTALIYQK.S		K.SALTALIYQK.S
242	248	2	903.52	-1.2	1	22.4	24.9	92.10%	A.DLYKLPR.N		K.YLVEADLYKLPR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
12	B3LSE9_YEAS1	23.84%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
756	766	2	1315.61	-0.7	1	64.5	30.5	95.00%	G.DDNVHFQNSLK.F		R.FLLMHGTGDDNVHFQNSLK.F
258	264	2	868.47	-1.3	0	34.3	25.7	95.00%	G.DYLAFLK.I		K.AAWWSPTGDYLAFLK.I
404	417	2	1591.8	-0.38	0	29	28.1	95.00%	V.DILPIGGYNHLAYF.E		R.NESSNGGWWEITHNTLFIPANETFDRPHNGYVDILPIGGYNHLAYFENSNSSHYK.T
206	218	2	1527.79	-1.1	1	48.8	26.8	95.00%	Q.DNNIYIYSAISKK.T		K.SSSSFEEIGNEVALAIWSPNSNDIAYVQDNNIYIYSAISKK.T
699	710	2	1380.65	-0.15	1	47.4	30.8	95.00%	K.YGMSVAPVTDWR.F		K.YGMSVAPVTDWR.F
587	606	2	2299.1	-1.2	0	67.1	28	95.00%	S.DHYPVFFFAYGGPNSQQVVK.T		K.DILVNSYEILPNDFDETLSDHYPVFFFAYGGPNSQQVVK.T
206	217	2	1399.7	-1.1	0	47.5	28.3	95.00%	Q.DNNIYIYSAISK.K		K.SSSSFEEIGNEVALAIWSPNSNDIAYVQDNNIYIYSAISK.K
793	803	2	1318.67	-0.54	1	44	29.3	95.00%	R.YHNANVIVFDK.L		R.YHNANVIVFDK.L
86	93	2	1074.51	-0.38	1	27	29.3	92.80%	K.YHELQWIS.D		K.YHELQWISDNK.I
720	728	2	1181.48	-1.3	1	34.9	30.2	95.00%	R.YMHTPQENF.D	Oxidation (+16)	R.YMHTPQENFDGYVESSVHNVTALAQANR.F
166	177	2	1449.66	-0.83	1	49.1	30.9	95.00%	R.HSTFGSYFVYDK.S		R.HSTFGSYFVYDK.S
258	265	2	981.55	-1.2	1	44	23.7	95.00%	G.DYLAFLKI.D		K.AAWWSPTGDYLAFLKIDESEVGEFIIPYYVQDEK.D
327	346	2	2113.14	0.61	1	87.6	22.5	95.00%	K.DGSLLITEVTWVGNGNVLVK.T		K.DGSLLITEVTWVGNGNVLVK.T
334	346	2	1414.74	-1.2	0	49	27.4	95.00%	T.EVTWVGNGNVLVK.T	Deamidation (+1)	K.DGSLLITEVTWVGNGNVLVK.T
297	312	2	1815.86	-0.12	1	72.5	29.2	95.00%	K.SGTPNPHAELWVYSMK.D		K.SGTPNPHAELWVYSMK.D
381	395	2	1745.86	-1.7	1	33.4	28.6	95.00%	W.EITHNTLFIPANETF.D		R.NESSNGGWWEITHNTLFIPANETFDRPHNGYVDILPIGGYNHLAYFENSNSSHYK.T
72	78	2	792.45	0.98	0	26	25.4	95.00%	K.VSFSVVR.N		K.VSFSVVR.N
226	236	2	1168.54	0.56	0	58.8	29.8	95.00%	N.DGSSFLFNGKP.D	Deamidation (+1)	R.AVTNDGSSFLFNGKPDWVYEEEVFEDDK.A
250	264	2	1724.86	-0.65	1	61.2	28.4	95.00%	K.AAWWSPTGDYLAFLK.I		K.AAWWSPTGDYLAFLK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
13	A6ZVC8_YEAS7	30.47%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
64	72	2	1066.61	0.45	0	62.5	21.3	95.00%	K.ESTLHLVLR.L		K.ESTLHLVLR.L
58	72	2	1827.98	-0.22	1	57	24.2	95.00%	S.DYNIQKESTLHLVLR.L		R.TLSDYNIQKESTLHLVLR.L
1	6	2	764.43	-0.41	0	35.4	27.4	95.00%	-.MQIFVK.T		-.MQIFVK.T
39	48	2	1174.64	-1	1	24.6	26.2	93.80%	P.DQQRLIFAGK.Q		K.EGIPPDQQRLIFAGK.Q
34	42	2	1038.51	0.94	1	39.5	30.2	95.00%	K.EGIPPDQQR.L		K.EGIPPDQQR.L
55	63	2	1080.55	-0.0048	1	50.4	28.4	95.00%	R.TLSDYNIQK.E		R.TLSDYNIQK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
14	B3LS03_YEAS1	31.83%	100%	20

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
39	50	2	1338.64	-1.1	1	45.8	29.7	95.00%	K.DQLDFYSGGPLK.A		K.DQLDFYSGGPLK.A
59	65	2	871.45	-0.48	0	25.4	27.2	93.40%	S.DNLNLQR.S		K.ALTTLVYSDNLNLQR.S
300	317	2	1954.09	-0.55	1	51.5	20	95.00%	K.LIQSDSIPLVLASVACIR.N	Carbamidomethyl (+57)	K.LIQSDSIPLVLASVACIR.N
331	340	3	1114.65	-0.55	0	19.5	24.1	95.00%	V.DAGFLKPLVR.L		R.NISIHPLNEGLIVDAGFLKPLVR.L
304	317	2	1512.83	-1.5	0	32.6	23.2	95.00%	S.DSIPLVLASVACIR.N	Carbamidomethyl (+57)	K.LIQSDSIPLVLASVACIR.N
161	174	3	1448.87	-0.066	1	39.8	15.1	95.00%	K.HKIATSGALIPLTK.L		K.HKIATSGALIPLTK.L
349	359	2	1312.65	-1.7	0	58.8	28.7	95.00%	E.EIQCHAVSTLR.N	Carbamidomethyl (+57)	K.DSEEIQCHAVSTLR.N
138	156	2	2132.99	-1.4	1	93.8	29.2	95.00%	G.DNVEVQCNAVGCITNLATR.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.LLIVEMGGLEPLINQMMGDNVEVQCNAVGCITNLATR.D
267	276	2	1158.65	-0.51	1	29.5	25.9	95.00%	R.VKCQATLALR.N	Carbamidomethyl (+57)	R.VKCQATLALR.N
163	174	2	1183.72	-0.35	0	66.9	19.8	95.00%	K.IATSGALIPLTK.L		K.IATSGALIPLTK.L
269	276	2	931.49	1.1	0	44.2	29.8	95.00%	K.CQATLALR.N	Carbamidomethyl (+57)	K.CQATLALR.N

565	578	2	1758.93	-0.79	0	49.2	25.6	95.00%	L.ELYNITQQILQFLH.-		K.NPGSNNNPSSNDNNSNNNDTGSEHQPVEDASLELYNITQQILQFLH.-
223	237	2	1716.8	-0.38	0	56.1	29.8	95.00%	P.DVQYYCTTALSNIAV.D	Carbamidomethyl (+57)	K.ELVNAGAVPVLVSLLSSTDPDVQYYCTTALSNIAVDEANR.K
186	197	2	1228.59	-0.66	0	59.9	30.5	95.00%	R.NATGALLNMTHS.E		R.NATGALLNMTHSEENR.K
88	97	2	1152.67	-1	0	38.7	17.5	95.00%	L.EPILILLQSQ.D		R.EVLEPILILLQSQDPQIQVAACAALGNLAVNNENK.L
42	50	2	982.47	-1.5	0	30.2	29.9	95.00%	L.DFYSGGPLK.A		K.DQLDFYSGGPLK.A
256	266	2	1206.59	-0.023	1	52	30.3	95.00%	K.LVSLMDSPSSR.V	Oxidation (+16)	K.LVSLMDSPSSR.V
186	198	2	1357.63	-1.5	1	66.6	30.8	95.00%	R.NATGALLNMTHSE.E		R.NATGALLNMTHSEENR.K
203	220	2	1768	0.33	0	52.2	21.7	95.00%	K.ELVNAGAVPVLVSLLSST.D		K.ELVNAGAVPVLVSLLSSTDPDVQYYCTTALSNIAVDEANR.K
203	222	2	1980.08	0.2	1	56.7	20.8	95.00%	K.ELVNAGAVPVLVSLLSSTDP.D		K.ELVNAGAVPVLVSLLSSTDPDVQYYCTTALSNIAVDEANR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
15	CBPS_YEAST	14.93%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
184	191	2	950.43	-0.66	0	30.3	30	95.00%	K.FPPFSGHY.D		K.FPPFSGHYDPETDFVWGR.G
279	290	2	1302.68	1.7	1	59.6	27.9	95.00%	K.DVFVATPINAEK.G		K.DVFVATPINAEK.G
522	528	2	972.47	0.61	0	33.8	29.5	95.00%	K.YYWNLSK.N		K.YYWNLSK.N
361	370	2	1130.59	-0.36	0	32	28.8	95.00%	K.TILGAPFCPR.R	Carbamidomethyl (+57)	K.TILGAPFCPR.R
159	169	2	1277.71	-1.6	0	53.4	23.7	95.00%	P.DLKPLLLMAHQ.D		K.VNELGLLYTWEGSDPDLKPLLLMAHQDVVPVNNETLSSWK.F
391	403	2	1314.72	1.4	1	74.9	25.1	95.00%	R.TTQAVDIINGGVK.A		R.TTQAVDIINGGVK.A
554	566	2	1387.71	-1	0	36.6	27.7	95.00%	V.DVPGHLSAIAFVY.E		K.TLHSVNEHVDVPGHLSAIAFVYEYIVNVNEYA.-
375	386	2	1457.76	0.27	1	60.3	26.8	95.00%	K.LVEYISNQSHLR.S		K.LVEYISNQSHLR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
16	A6ZTJ2_YEAS7	18.97%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
88	100	2	1389.59	-1.4	1	43.3	30.8	95.00%	G.DDCSLPLCGGLSP.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.CECIEGFAGDDCSLPLCGGLSPDESGNK.D
430	439	2	1117.64	0.43	1	41.3	23.6	95.00%	K.TTLLDILAMK.R		K.TTLLDILAMK.R
68	78	2	1347.55	-0.21	1	62.4	31.3	95.00%	K.QFSECNSYTGR.C	Carbamidomethyl (+57)	K.QFSECNSYTGR.C
30	39	2	1099.52	0.88	1	36.6	28.8	95.00%	K.TPFFEGTSSK.N		K.TPFFEGTSSK.N
860	873	2	1681.8	-0.71	0	38.6	29.2	95.00%	R.SNNYYSPLAYYISK.I		R.SNNYYSPLAYYISK.I
200	210	2	1317.55	-1	1	33.7	31.3	95.00%	I.DQLESFYCGLS.D	Carbamidomethyl (+57)	K.IPQITFACDKPNQECNFQFWIDQLESFYCGLSDCAFEYDLEQNTSHYK.C
289	295	2	848.46	-1.3	0	37.8	26.3	95.00%	G.DPYITLK.C		K.FSEPSMNDLILTVFGDPYITLK.C
561	574	2	1573.75	-1.6	1	70.3	29.3	95.00%	L.DASNANNVIECLVR.L	Carbamidomethyl (+57)	R.VSIACELVTSPLVLFLDEPTSGLDASNANNVIECLVR.L
641	651	2	1161.57	-0.71	1	44.2	29.1	95.00%	I.DITFEAGPQGK.R		R.NEGYICPDNYNIADYLIDITFEAGPQGK.R
689	697	2	1089.55	-0.85	0	31	29.6	95.00%	R.EWAHLAAHR.D		R.EWAHLAAHR.D
171	178	2	897.56	-0.12	0	27	18.1	95.00%	K.ILQILNGK.I		K.ILQILNGK.I
51	64	2	1770.72	-2.1	0	28.9	31.3	92.50%	N.DTCPPCFNCMLPIF.E	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GNDTCPPCFNCMLPIFECK.Q
683	697	3	1747.85	-1.5	1	37.2	28.5	95.00%	S.DGTTQREWAHLAAHR.D		R.NISDLEAGTDTNDIDNTIHQTTFTSSDGTTQREWAHLAAHR.D
763	783	2	2272.18	-0.88	0	93.7	24.1	95.00%	G.DLPTGQQSAGFLQQLSILNSR.S		K.DSVYYAELSQEIEEVLSEGDEESNVLNGDLPTGQQSAGFLQQLSILNSR.S
671	682	2	1350.6	-2.1	0	61.1	30.9	95.00%	I.DNTIHQTTFTSS.D		R.NISDLEAGTDTNDIDNTIHQTTFTSSDGTTQR.E

300	311	2	1480.67	-0.19	1	46	29.7	95.00%	G.ECVHYSEIPGYK.S	Carbamidomethyl (+57)	K.CESGECVHYSEIPGYK.S
543	553	2	1229.73	0.96	0	29.5	20.9	95.00%	C.ELVTSPLVLFL.D		R.VSIACELVTSPLVLFLDEPTSGLD ASNANNVIECLVR.L
51	67	2	2187.89	-1.3	1	45.8	29.9	95.00%	N.DTCPPCFNCMLPIFECK.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GNDTCPPCFNCMLPIFECK.Q
669	682	2	1578.71	-1.8	1	35.2	30.9	95.00%	N.DIDNTIHQTTFTSS.D		R.NISDLEAGTDTNDIDNTIHQTTFT SSDGTTQR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
17	ATC2_YEAST	16.03%	100%	18

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
498	513	2	1788.94	-0.8	1	68.2	25.8	95.00%	N.DLLANIVLNSTAFENR.D		R.NDLLANIVLNSTAFENR.D
290	298	2	1037.46	-1.2	0	39.8	30.4	95.00%	A.DCMLISGSR.I	Carbamidomethyl (+57)	K.IADCMLISGSR.I
432	444	2	1359.51	-1.2	1	64.7	29.9	95.00%	R.SCETMGSATAVCS.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.SCETMGSATAVCSDK.T
71	83	2	1432.73	1.2	1	27.9	27.8	95.00%	K.NAGISLPEISNYR.K		K.NAGISLPEISNYR.K
498	510	2	1389.75	-0.73	0	43.7	26.6	95.00%	N.DLLANIVLNSTAF.E		R.NDLLANIVLNSTAFENR.D
760	770	2	1161.61	0.59	1	34.2	28.7	95.00%	R.MVTGDNILTAK.A		R.MVTGDNILTAK.A
447	459	2	1419.74	1.7	1	64.5	27.5	95.00%	K.TGTLTENVMTVVR.G		K.TGTLTENVMTVVR.G
574	583	2	1073.61	2.3	1	62.8	24.7	95.00%	K.TETALLSLAR.L		K.TETALLSLAR.L
877	887	2	1191.61	-1.2	1	69.2	28.5	95.00%	T.DDFSAIVNAIK.W		R.EASDIILMTDDFSAIVNAIK.W
853	867	2	1524.72	-1.7	1	29.2	30	94.70%	A.DVGFSMGISGTEVAR.E		K.LADVGFSMGISGTEVAR.E
37	46	2	1137.58	2	1	31.9	28.7	95.00%	K.SQLSDLHNPK.S		K.SQLSDLHNPK.S
584	597	2	1585.88	-1.6	1	55.8	23	95.00%	R.LSLGLQPGELQYLR.D		R.LSLGLQPGELQYLR.D
54	64	2	1303.64	-0.32	1	47.4	29.4	95.00%	R.LFGYESNSLFK.Y		R.LFGYESNSLFK.Y
711	726	2	1744.9	0.39	1	75.9	26.3	95.00%	K.DSPNIAALDLLFNSQK.G		K.DSPNIAALDLLFNSQK.G
15	29	2	1685.71	-4.3	1	47	30.8	95.00%	N.ENNKPSYTGNENGVY.D	Deamidation (+1)	R.QDENSALLANNENNKPSYTGNE NGVYDNFK.L
288	298	2	1221.58	-0.068	1	81.2	30.1	95.00%	K.IADCMLISGSR.I	Carbamidomethyl (+57)	K.IADCMLISGSR.I
497	510	2	1503.79	-0.61	1	44.5	27.4	95.00%	R.NDLLANIVLNSTAF.E		R.NDLLANIVLNSTAFENR.D
252	259	2	946.49	0.6	1	26.9	30.2	90.90%	K.FPVDNSLR.D		K.FPVDNSLR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
18	A6ZYU5_YEAS7	12.35%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
534	543	2	1117.55	-0.1	0	39.7	30	95.00%	K.SASWVPTSQR.G		K.SASWVPTSQR.G
1	12	2	1387.66	-0.5	1	48.4	29.8	95.00%	-.MNSTPDLISPQK.S	Acetyl (+42)/ Oxidation (+16)	-.MNSTPDLISPQK.S
282	290	2	1125.54	-0.73	1	28	30	93.10%	P.DHPFIQQEL.E		K.VAPDHPFIQQELEVIEASVEEAR. A
225	233	2	1153.52	0.85	0	47.9	30.8	95.00%	K.NYSNSVQWR.V	Deamidation (+1)	K.NYSNSVQWR.V
302	320	2	1954.96	-2.5	1	49.6	28.2	95.00%	R.AAGSASWGELFTGKPAMFK.R		R.AAGSASWGELFTGKPAMFK.R
523	533	2	1307.62	-1.5	1	60.8	30	95.00%	N.DMYAEGVLPWK.S		K.GLTLEEVNDMYAEGVLPWK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
19	B3LFI3_YEAS1	25.57%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
359	375	2	1791.97	0.15	1	28.6	23.6	95.00%	R.WGDAPVHSIAAALFLPK.D		R.WGDAPVHSIAAALFLPK.D
349	358	2	1254.54	-1.5	1	34.7	30.8	95.00%	L.DHQGGFFYER.W		R.EYFDTLDHQGGFFYER.W
108	117	2	1154.56	-0.54	0	29	28.9	95.00%	M.DYITPSFANK.A		K.TTMDYITPSFANK.A
303	313	2	1282.55	-1.2	1	38	29.9	95.00%	L.DENNLMSFLSN.D		K.NPEYLDENNLMSFLSNDNGK.T
424	435	2	1409.72	-0.15	1	58.7	27.7	95.00%	K.EYYDAQGLVKPK.N		K.EYYDAQGLVKPK.N
105	117	2	1487.7	0.86	1	75.5	30	95.00%	K.TTMDYITPSFANK.A		K.TTMDYITPSFANK.A
226	233	2	1089.5	1.4	0	38.4	29.9	95.00%	R.YQSGFFWR.H		R.YQSGFFWR.H
413	423	2	1308.54	-1.5	0	54.8	30.8	95.00%	N.DFTFQGYSCGK.E	Carbamidomethyl (+57)	K.EVYNSNNCECDQGNDFTFQGYS CGK.E
383	391	2	1097.49	-1.4	0	35.3	30.6	95.00%	S.DIGYHHPPY.D		K.IHYFSDIGYHHPPYDNCPLDK.E
361	375	3	1548.87	-0.65	0	37	21.6	95.00%	G.DAPVHSIAAALFLPK.D		R.WGDAPVHSIAAALFLPK.D

281	292	2	1404.69	-1	0	34.9	28.2	95.00%	Y.EVTIPTLWQTSM.D		K.VYGFTVSIHEYEVTIPTLWQTSMDFIK.K
151	160	2	1309.69	0.054	1	25.7	26.8	94.30%	K.KFPYPWVFLN.D		K.KFPYPWVFLNDEPFTEEFK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
20	PPN1_YEAST	12.91%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
417	428	2	1319.69	-2	0	46.7	27.9	95.00%	K.EVFLMGAKPSNK.E		K.EVFLMGAKPSNK.E
581	595	2	1687.89	-0.55	0	55.8	25.5	95.00%	Y.ELGPAYVPQLFTPTR.F		K.YELGPAYVPQLFTPTR.F
544	554	2	1202.59	-1.4	1	51.8	28.4	95.00%	M.DSSNIEVGINR.E		K.IMEDSLLEDEMDSSNIEVGINR.E
482	500	2	2067.08	0.23	0	83.6	24.1	95.00%	R.YSIVNIGGSVIPTFNPSFR.I		R.YSIVNIGGSVIPTFNPSFR.I
226	242	2	1942.97	-1.2	0	75.4	26.8	95.00%	N.DVFPHNMFALGPTLQTR.E		R.DFDVSVIPSLGNNDVFPHNMFALGPTLQTR.E
263	274	2	1247.68	0.62	1	34.2	26.8	95.00%	R.SASFLTEVIPGK.L		R.SASFLTEVIPGK.L
580	595	2	1850.95	-1.5	1	56.5	25.9	95.00%	K.YELGPAYVPQLFTPTR.F		K.YELGPAYVPQLFTPTR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
21	A6ZX34_YEAS7	23.19%	100%	16

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
130	143	2	1387.73	-0.011	0	60.9	26.4	95.00%	R.AIASSPSLNSNLSK.N		R.AIASSPSLNSNLSK.N
658	669	2	1351.64	-0.72	0	44.3	30	95.00%	R.IYQPSNAISVTC.D	Carbamidomethyl (+57)	R.IYQPSNAISVTCDPSDYPTYDYIQSHLNAFQNANLTTWEDAGYTFPK.N
47	58	2	1222.53	-1.2	0	74.5	30.6	95.00%	N.DNAGLTNPFMGS.D		R.NLTETHNFSSTNLDTDGTGDDHDGAPLSSSPSFGQQNDNSTNDNAGLTNPFMGSDEESNAR.D
594	607	2	1634.81	-0.38	1	67.4	28.5	95.00%	R.WFVGDTPTYTIHAK.A		R.WFVGDTPTYTIHAK.A
27	41	2	1490.66	-1.6	0	68.5	30.8	95.00%	H.DGAPLSSSPSFGQQN.D		R.NLTETHNFSSTNLDTDGTGDDHDGAPLSSSPSFGQQNDNSTNDNAGLTNPFMGSDEESNAR.D
153	161	2	1061.56	-1.2	1	38	28.3	95.00%	F.DRYPLVGSR.V		K.NDILSPPEFDRYPLVGSR.V
66	81	2	1676.73	-0.83	1	52.8	30.8	95.00%	R.DGESLSSSVHYQPQGS.D		R.DGESLSSSVHYQPQGSDSSLLHDNSR.L
130	144	2	1501.77	-1.5	1	77.6	27.3	95.00%	R.AIASSPSLNSNLSKN.D		R.AIASSPSLNSNLSKNDILSPPEFDR.Y
8	17	2	1148.51	-0.8	0	30.5	30.2	95.00%	T.ETHNFSSTNL.D		R.NLTETHNFSSTNLDTDGTGDDHDGAPLSSSPSFGQQNDNSTNDNAGLTNPFMGSDEESNAR.D
697	704	2	897.42	-1.5	0	28.6	30.6	93.00%	E.DAGYTFPK.N		R.IYQPSNAISVTCDPSDYPTYDYIQSHLNAFQNANLTTWEDAGYTFPK.N
114	129	2	1752.85	-0.64	1	40	28.4	95.00%	R.AVSTANDNSFLQPPHR.A		R.AVSTANDNSFLQPPHR.A
197	213	2	1847.84	-0.62	0	60.7	30.5	95.00%	Q.DFSPFGGYPASSFPLMI.D	Oxidation (+16)	R.SPTSSPGNESSASFSSNPFLGEQDFSPFGGYPASSFPLMIDEK.E
393	401	2	1049.5	-0.0072	0	40.2	30.1	95.00%	R.SGMLQSWNK.V		R.SGMLQSWNK.V
608	618	2	1234.62	-0.67	1	26.1	29	91.60%	K.ALHPDGNIGWR.R		K.ALHPDGNIGWR.R
120	129	2	1209.59	-0.6	0	40.3	30.1	95.00%	N.DNSFLQPPHR.A		R.AVSTANDNSFLQPPHR.A
5	17	2	1476.68	-1.2	1	49.1	30.1	95.00%	R.NLTETHNFSSTNL.D		R.NLTETHNFSSTNLDTDGTGDDHDGAPLSSSPSFGQQNDNSTNDNAGLTNPFMGSDEESNAR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
22	A6ZMV7_YEAS7	26.02%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
293	309	2	1854.02	-1	1	106	21.7	95.00%	R.ILLQATPSTISADQIQR.E		R.ILLQATPSTISADQIQR.E
293	304	2	1213.69	-0.59	0	61.7	24.2	95.00%	R.ILLQATPSTISA.D		R.ILLQATPSTISADQIQR.E

414	430	2	1754.82	-0.62	1	78.3	29.8	95.00%	K.RSPTAYGATTASSNCIV.D	Carbamidomethyl (+57)	K.RSPTAYGATTASSNCIVDDAVNCNTSNCL.-
193	202	2	1139.63	-0.71	0	39.8	26	95.00%	G.EVLPQSVVNR.L		R.LVLYVGVAGLISNVVGLFLFHDHGSDSLHSHSHGSVESGNNDLDIESNATHSHSHASLPNDNLAIDEDAISSPGPSGQIGEVLPQSVVNR.L
386	401	2	1583.75	-0.71	1	34.5	29.8	95.00%	R.FSIIAGGSPSSSQEAF.D		R.FSIIAGGSPSSSQEAFDSHGNTEHGR.K
431	442	2	1381.52	-1.8	1	59.4	29.8	95.00%	V.DDAVNCNTSNCL.-	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.SPTAYGATTASSNCIVDDAVNCNTSNCL.-
415	430	2	1598.72	-1.6	0	70.2	29.6	95.00%	R.SPTAYGATTASSNCIV.D	Carbamidomethyl (+57)	R.SPTAYGATTASSNCIVDDAVNCNTSNCL.-
415	431	2	1713.75	-1	1	59.4	30.1	95.00%	R.SPTAYGATTASSNCIVD.D	Carbamidomethyl (+57)	R.SPTAYGATTASSNCIVDDAVNCNTSNCL.-
180	202	2	2306.18	-2.3	1	66.4	23.4	95.00%	E.DAISSPGPSGQIGEVLPQSVVNR.L		R.LVLYVGVAGLISNVVGLFLFHDHGSDSLHSHSHGSVESGNNDLDIESNATHSHSHASLPNDNLAIDEDAISSPGPSGQIGEVLPQSVVNR.L
358	376	2	2090.03	-0.96	1	39.3	27.6	95.00%	K.IFHQHGIHSATVQPEFVSG.D		K.IFHQHGIHSATVQPEFVSGDVNEDIR.R
203	213	2	1251.61	-0.26	1	51.5	30.8	95.00%	R.LSNESQPLLNH.D	Deamidation (+1)	R.LSNESQPLLNHDDHDHSHESK.K
432	442	2	1266.49	-1.8	0	45.4	30.4	95.00%	D.DAVNCNTSNCL.-	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.SPTAYGATTASSNCIVDDAVNCNTSNCL.-
386	398	2	1236.6	-0.49	0	30.3	30	95.00%	R.FSIIAGGSPSSSQ.E		R.FSIIAGGSPSSSQEAFDSHGNTEHGR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
23	A7A0C8_YEAS7	28.40%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
72	83	2	1311.75	-1.2	0	25.2	23	95.00%	E.ELYPGRPLAIAL.D		K.SEELYPGRPLAIALDTK.G
287	301	2	1601.82	-1.9	0	49.8	26.6	95.00%	K.SNLAGKPVICATQML.E	Carbamidomethyl (+57)	K.SNLAGKPVICATQMLESMTYNPRPTR.A
217	225	2	1001.55	-0.022	1	39	26.7	95.00%	R.TANDVLTIR.E		R.TANDVLTIR.E
50	61	2	1498.63	-0.14	1	38.7	31	95.00%	R.MNFSHGSYEYHK.S		R.MNFSHGSYEYHK.S
487	500	2	1340.67	-1	0	30.5	29	95.00%	K.AGAGHSNTLQVSTV.-		K.AGAGHSNTLQVSTV.-
397	409	2	1314.75	0.29	0	41.9	23.1	95.00%	K.AIIVLSTSGTTPR.L		K.AIIVLSTSGTTPR.L
31	41	2	1226.66	-0.27	1	53.6	26.1	95.00%	K.TNNPETLVALR.K		K.TNNPETLVALR.K
370	391	2	2222.09	-1.6	1	35	26.8	95.00%	R.NCTPKPTSTTETVAASAVAAVF.E	Carbamidomethyl (+57)	R.NCTPKPTSTTETVAASAVAAVFEQK.A
414	425	2	1500.82	-0.66	0	49.1	23.9	95.00%	K.YRPNCPIILVTR.C	Carbamidomethyl (+57)	K.YRPNCPIILVTR.C
327	337	2	1209.54	-1.4	1	60	30.8	95.00%	A.DCVMLSGETAK.G	Carbamidomethyl (+57)	R.AEVSDVGNAILDGADCVMLSGETAK.G
287	312	3	2934.45	-1.2	1	37.2	24.9	95.00%	K.SNLAGKPVICATQMLESMTYNPRPTR.A	Carbamidomethyl (+57)	K.SNLAGKPVICATQMLESMTYNPRPTR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
24	KTR1_YEAST	18.83%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
46	57	2	1247.6	-0.076	0	69.9	29.6	95.00%	K.YSTVLSSGSGYK.Y		K.YSTVLSSGSGYK.Y
83	92	2	1137.59	-0.012	1	42.2	27.5	95.00%	R.DLYSLAESIK.S		R.DLYSLAESIK.S
163	172	2	1185.6	-0.0046	1	45	28.7	95.00%	R.IIYGDSISYR.H		R.IIYGDSISYR.H
364	375	2	1531.64	-0.9	0	35	30.6	95.00%	K.DFTWHSYSCTTK.F	Carbamidomethyl (+57)	K.DFTWHSYSCTTK.F
334	347	2	1703.78	-0.28	0	37.2	30.5	95.00%	G.DIGYYHVPFHSCPI.D	Carbamidomethyl (+57)	R.SEIHHFGDIGYYHVPFHSCPIDTSIR.L
73	80	2	905.53	1.5	0	43.1	22	95.00%	K.ATFVTLVR.N		K.ATFVTLVR.N
177	184	2	1051.48	0.16	1	30.8	30.4	95.00%	R.FESGFFYR.H		R.FESGFFYR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
25	ATC9_YEAST	13.32%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
921	930	3	1152.6	-1.4	0	27.2	27.6	95.00%	N.DPHNFLGVVR.S		R.ENTFTDNDPHNFLGVVR.S
1049	1065	2	1820.91	-0.37	1	66.2	27.5	95.00%	R.TIMCTGDNILTAISVGR.E	Carbamidomethyl (+57)	R.TIMCTGDNILTAISVGR.E
454	464	2	1134.58	-1.3	0	29.8	29.1	95.00%	V.DLSTVSNGLTK.G	Deamidation (+1)	K.TNNNWIDPDWVDLSTVSNGLTK.G
204	221	3	1937.88	-1.4	0	58.1	29.8	95.00%	S.DTGFVYHSATHSSSSLSR.Y		R.LGENSDTGFVYHSATHSSSSLSR.Y
652	665	2	1396.79	-0.8	0	70	22.6	95.00%	R.IAPGQTAALAMVVR.T		R.IAPGQTAALAMVVR.T
625	638	2	1587.74	-1.1	1	69.7	30	95.00%	C.DDFQSTQISSFVSK.S		K.FPATEETMYQLCDDFQSTQISSFVSK.S
1055	1065	2	1157.64	-0.1	0	75.7	27	95.00%	G.DNILTAISVGR.E		R.TIMCTGDNILTAISVGR.E
600	612	2	1362.67	-1.7	1	80.8	28.9	95.00%	N.ESMLTGESVPVSK.F		K.FWTTISSSELVPGDIYEVSDPNITILPCDSILLSSDCIVNESMLTGESVPVSK.F
288	300	2	1695.81	-0.53	0	63.2	29	95.00%	K.FYPQYAPNLHYQR.F		K.FYPQYAPNLHYQR.F
153	163	2	1223.62	-1.6	1	41.2	28.4	95.00%	Q.DRIYGTGLSSR.R		R.FFTQEQISNAEGASTLENTDYDMAWDATPAYEQDRIYGTGLSSR.R
639	649	2	1296.68	-0.48	0	35.5	26.9	95.00%	K.SFLYNGTNIIR.A		K.SFLYNGTNIIR.A
1170	1177	2	1001.56	-0.51	0	34	27.2	95.00%	H.ELMIQLQK.L		K.HELMIQLQK.L
1	14	2	1651.77	-0.58	1	92.7	29.6	95.00%	-.MDIPSSNQIQHGQR.S	Acetyl (+42)	-.MDIPSSNQIQHGQR.S
1152	1162	2	1277.7	-0.87	0	35	26	95.00%	N.EILLNSSIYAR.M		R.DENEIPEEYLNEILLNSSIYAR.M
760	768	2	1049.53	0.86	0	36.2	30.2	95.00%	K.GIFCISPTR.L	Carbamidomethyl (+57)	K.GIFCISPTR.L
414	425	2	1368.77	0.42	0	26.2	22.2	95.00%	N.EINPNVPILITF.E		R.QWYNRPLSTVLPFENYPNPSYEPNDINLSHHHANEINPNVPILITFEYR.Y
1113	1122	2	1087.56	0.26	1	90.7	28	95.00%	K.LGNNSVESLR.E		K.LGNNSVESLR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
26	A6ZQR8_YEAS7	12.59%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
362	371	2	943.53	-0.66	0	43.8	28.1	95.00%	P.DGGALAIVTK.T		K.SDIPPPPDGGALAIVTK.T
955	967	2	1323.61	-0.15	1	58.7	30.5	95.00%	K.LGDASCAAPFTSK.L	Carbamidomethyl (+57)	K.LGDASCAAPFTSK.L
118	132	2	1729.87	-0.12	1	63.3	26.6	95.00%	R.VTEAGSLQTFFQFQK.K		R.VTEAGSLQTFFQFQK.K
762	780	3	2027.04	-0.49	1	29.1	26.3	95.00%	Y.DIAVTGYALNALEGHSQLR.D		R.YDIAVTGYALNALEGHSQLR.D
520	537	2	1818.02	-1.3	1	79.8	20.8	95.00%	A.EAPESTILVIGAAHALVK.L		R.HLYSAAEAPESTILVIGAAHALVK.L
589	604	2	1600.82	-0.27	1	70.8	27.6	95.00%	R.SASIASHNDALFAAVK.G		R.SASIASHNDALFAAVK.G
933	943	2	1072.58	-0.67	0	82.5	28.3	95.00%	A.DLASLLLNSAG.D		K.KPADLASLLLNSAGDAQGDEAPALK.L
304	316	2	1374.7	-1.5	1	64.6	28.2	95.00%	N.EAMLSGESTPLLK.E		R.TAEESAIPCDLILLDGSAIVNEAMLSGESTPLLK.E
792	805	2	1602.9	-1.4	1	57.7	22.5	95.00%	R.VSPSQKEFLLNTLK.D		R.VSPSQKEFLLNTLK.D
372	383	2	1280.64	-0.56	1	71.7	29.6	95.00%	K.TGFETSQGSLVR.V		K.TGFETSQGSLVR.V
968	979	2	1269.74	0.14	0	69.8	21.3	95.00%	K.LANVSAVTNIIR.Q		K.LANVSAVTNIIR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
27	YBS4_YEAST	17.93%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
221	233	2	1277.66	1.2	1	64	27.8	95.00%	K.YVINLEGTGAGGK.A		K.YVINLEGTGAGGK.A
834	842	2	1083.5	-0.089	1	25.8	29.4	90.10%	R.ACTLTFESR.H	Carbamidomethyl (+57)	R.ACTLTFESR.H
63	77	2	1719.88	-0.064	0	92.1	26.7	95.00%	G.DLQIITASFHPYTSK.E		K.EDEHPEFNDLLETAWGDLQIITASFHPYTSK.E
168	181	2	1430.74	-0.22	1	74.4	26.8	95.00%	T.DDGMGVVSLLANLK.Y		K.NPEEEGLLLSAHFDSVPTGYGATDDGMGVVSLLANLK.Y
746	755	2	1191.59	-0.95	0	33.2	29.1	95.00%	R.EGNFLKPMLQ.D	Oxidation (+16)	R.EGNFLKPMLQDLPSIK.Y
731	745	2	1522.78	-1.3	0	55.9	26.5	95.00%	I.DLSQGNAASVHVLGR.E		R.FSQNIDLSQGNAASVHVLGR.E

782	802	2	2221.03	-1	0	58	29.3	95.00%	Y.DGMQPNLLSTNGNTNISSMVK.V	Deamidation (+1)	K.YSSTHINCTSVTNGMELCMYDG MQPNLLSTNGNTNISSMVK.V
169	181	2	1315.72	-0.24	0	74.2	25.7	95.00%	D.DGMGVVSLLANLK.Y		K.NPEEEGLLLSAHFDSVPTGYGAT DDGMGVVSLLANLK.Y
726	745	3	2112.07	-0.46	1	78.8	26.4	95.00%	R.FSQNIDLSQGNAASVHVLGR.E		R.FSQNIDLSQGNAASVHVLGR.E
287	296	2	1237.62	-0.83	1	47.4	28.7	95.00%	R.GWDVAFYKPR.N		R.GWDVAFYKPR.N
569	583	2	1499.65	-1.9	1	78.4	30.4	95.00%	Q.DDNVSTTSAGPSHNV.D		R.DGQENLEQPQDQLTSSQDDQAS IQDDNVSTTSAGPSHNVDEDHGMD SSSQQHDER.V
129	140	2	1398.74	-0.0082	1	36.6	26.4	95.00%	R.VTYFESSNILVK.L		R.VTYFESSNILVK.L
254	269	2	1905.86	-0.058	0	79.3	29.8	95.00%	K.ENPFGNSIYQQGFYSR.Y		K.ENPFGNSIYQQGFYSR.Y
888	901	2	1746.83	-1.1	1	54.1	29.6	95.00%	F.DQETYHIGVQWFPK.L		K.LDFDQETYHIGVQWFPK.L
42	47	2	712.41	-2.3	1	21.3	24.8	90.10%	K.LNLPKE.D		K.LNLPKEDEHPEFNDLLETAWGDL QIITASFHPYTSK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
28	ATN2_YEAST	10.54%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
399	413	2	1667.82	-2.2	1	31.3	28.7	95.00%	D.DPFNPNEGNVSLIPR.F		R.FGTITISNSDDPFNPNEGNVSLIP R.F
27	39	2	1394.69	-0.94	1	63.6	29.4	95.00%	A.EFIGTSLTEGLTQ.D		K.ENNNEEFNAYHTLTTEEAAEFIGT SLTEGLTQDESLR.R
565	577	2	1575.67	-1.9	0	48	30.3	95.00%	F.ESIISCCSSWYGK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GAFESIISCCSSWYGK.D
454	468	2	1676.91	-1.3	1	85.1	24.1	95.00%	K.WLETATLANIATVFK.D		K.WLETATLANIATVFK.D
426	434	2	1032.56	-0.89	0	28.8	26	95.00%	G.DVGILQNFK.D		R.FSPYEYSHNEDGDVGILQNFK.D
596	606	2	1250.63	-0.17	1	44	30.4	95.00%	K.NVYSLSNEGLR.V		K.NVYSLSNEGLR.V
513	529	2	1858.84	-1.5	1	53.5	31.1	95.00%	N.DQSSLSQHNEKPGSAQF.E		K.STNQSNENDQSSLSQHNEKPGS AQFEHIAEFPFDSTVK.R
254	264	2	1362.69	-0.0057	0	52.6	28.5	95.00%	K.SWLQNTWISTK.K		K.SWLQNTWISTK.K
124	134	2	1206.65	-0.51	0	30.2	27.8	95.00%	K.NLSSPNAHVIR.N		K.NLSSPNAHVIR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
29	KTR4_YEAST	26.51%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
443	453	2	1404.62	-0.91	0	52.8	30.9	95.00%	L.DNQNCQATWIR.H	Carbamidomethyl (+57)	K.FTPWSDLDNQNCQATWIR.H
337	351	2	1925.77	-1.5	0	54.6	30.5	95.00%	Y.DYTQGYSTCHFWTNF.E	Carbamidomethyl (+57)	K.NYDYTQGYSTCHFWTNFEIVDLD FLR.S
382	388	2	799.4	1.1	1	22.3	25.1	91.70%	R.WGDAPVR.S		R.WGDAPVR.S
163	172	2	1234.56	-1.1	0	31.9	30.3	95.00%	K.NFGYPYTFLN.D		K.NFGYPYTFLNDEEFTDEFK.D
399	405	2	931.47	-0.13	0	31.6	29.2	95.00%	K.SSIHWFR.D		K.SSIHWFR.D
271	281	2	1417.67	-0.57	1	65.6	29.4	95.00%	K.INYDVFQFMNK.N		K.INYDVFQFMNK.N
375	381	2	890.39	0.43	1	33.5	30.1	95.00%	K.GGFYYER.W		K.GGFYYER.W
406	422	2	2002.83	-1.5	0	55.5	29.7	95.00%	R.DIGYHHTPYTNCPTCPA.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.DIGYHHTPYTNCPTCPADSDR.C
135	142	2	857.53	-0.6	0	30.8	24.5	95.00%	K.GTILSLVR.N		K.GTILSLVR.N
389	398	2	1047.6	-0.12	1	49.9	23.1	95.00%	R.SLALALFADK.S		R.SLALALFADK.S
245	254	3	1269.65	0.081	0	29.2	27.2	95.00%	K.EFYHHPLLSK.Y		K.EFYHHPLLSK.Y
148	157	2	1144.6	-1.1	1	55.6	27.9	95.00%	E.DIISSIQQLE.E		R.NSDLEDIISSIQQLEEEYNK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
30	A6ZSR0_YEAS7	20.75%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
123	136	2	1503.77	-1.2	0	57	28	95.00%	A.EAAYAHLTTPVFGK.G		K.LADVSAEAAYAHLTTPVFGK.G
235	252	2	2160.12	-0.16	1	50.6	25	95.00%	K.GFTPINFVFPNLPLEHYR.K		K.GFTPINFVFPNLPLEHYR.K
358	371	2	1654.89	-1.2	1	53.6	23.3	95.00%	Y.DLLQEMPLLNQTIK.E		K.ELTYDLLQEMPLLNQTIK.E
195	210	2	1824.87	-1.6	1	53.3	29	95.00%	I.DVMVTQPEMTIFTASR.S		R.TTGTIDVMVTQPEMTIFTASR.S
505	518	2	1463.73	-0.7	0	60.3	28.4	95.00%	P.DFTSMVTLPTGPAK.I		K.TVPPPDFTSMVTLPTGPAK.I

455	467	2	1292.65	0.76	0	57.2	29.3	95.00%	K.GVSSPYLPFGGGR.H		K.GVSSPYLPFGGGR.H
137	146	2	1179.53	0.098	1	29.4	30.7	94.10%	K.GVIYDCPNSR.L	Carbamidomethyl (+57)	K.GVIYDCPNSR.L
260	270	2	1182.63	-0.43	0	43.6	25.7	95.00%	K.AISGTYMSLIK.E		K.AISGTYMSLIK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
31	XPP_YEAST	20.29%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
380	388	2	1060.55	-1.1	1	33	28.3	95.00%	K.INGIEVRPY.E	Deamidation (+1)	K.INGIEVRPYEQIWEHLTK.I
437	449	2	1441.74	-1.8	0	76	28	95.00%	K.MTAQNFAIIHSPI.D		K.MTAQNFAIIHSPIDVLK.S
68	77	2	1120.58	-0.37	1	25.7	29	90.90%	R.SSSMLLNELK.G		R.SSSMLLNELK.G
578	585	2	964.52	-1.5	0	40.7	27.3	95.00%	M.DNYTLVLK.G		K.EEMDNYTLVLK.G
360	371	2	1423.66	-1.3	1	35.6	30.2	95.00%	E.DETILFTNNPFN.D		R.GSDIDYNPVFFSYVAINEDETILFTNNPFNDDISEYFK.I
593	604	2	1360.7	-0.76	1	44.1	27.9	95.00%	R.LIFPENTPGFNI.D		R.LIFPENTPGFNIDAIAR.Q
145	161	2	1699.83	-0.94	0	71.5	28.2	95.00%	R.AFISGFSGSAGVACITR.D	Carbamidomethyl (+57)	R.AFISGFSGSAGVACITR.D
422	435	2	1434.68	-0.49	0	74.3	29.3	95.00%	R.CLNTSTNANGAIAK.K	Carbamidomethyl (+57)/ Deamidation (+1)	R.CLNTSTNANGAIAK.K
75	93	2	1757.75	-1.4	1	98.1	30.9	95.00%	N.ELKGAGGGSSAGNGSVYSC.D	Deamidation (+1)/ Carbamidomethyl (+57)	R.SSSMLLNELKGAGGGSSAGNGSVYSCDSLCAVNR.E
653	665	2	1424.69	-0.0086	1	27.1	29.9	91.80%	R.AGNIISNEPGYYK.D		R.AGNIISNEPGYYK.D
12	24	4	1428.7	-0.26	0	32.1	29.3	95.00%	R.AHSISHVPGTHMR.G		R.AHSISHVPGTHMR.G
437	453	3	1897.01	-0.1	1	45.2	23.8	95.00%	K.MTAQNFAIIHSPIDVLK.S		K.MTAQNFAIIHSPIDVLK.S
40	50	2	1264.55	-0.91	0	38.8	30.3	95.00%	A.DCTCSPGLLSR.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GTSASHSPRPFRPCADCTCSPGLLSR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
32	A6ZR77_YEAS7	20.61%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
278	295	2	2111.09	-2.2	1	62.6	24.9	95.00%	P.DDLLLNNAIPYQFATYLK.Y		K.LNPDDLLLNNAIPYQFATYLK.Y
402	411	2	1107.55	-1.3	0	39.2	29.8	95.00%	R.ISSNPQSFTK.Q		R.ISSNPQSFTK.Q
445	462	2	1979.92	-1.3	0	66.9	29.4	95.00%	Y.DSISHTQNSPFVPYSSSK.A		K.SQSQTYDSISHTQNSPFVPYSSSK.A
468	484	3	1978.92	-0.85	1	43.5	29.9	95.00%	R.SNNEHNLPNHYTNLANK.N		R.SNNEHNLPNHYTNLANK.N
150	163	2	1735.89	-1.2	1	46.3	26.7	95.00%	R.DIKPDNFLISQYQR.I		R.DIKPDNFLISQYQR.I
5	19	3	1591.85	-0.55	0	47.7	25.4	95.00%	R.SSQHIVGIHYAVGPK.I		R.SSQHIVGIHYAVGPK.I
30	45	3	1757.8	-2	1	28.1	29.9	95.00%	F.EGENILHSCQAQTGSK.R	Carbamidomethyl (+57)	K.IGEGSFGVIFEGENILHSCQAQTGSK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
33	A6ZM54_YEAS7	24.28%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
356	366	2	1340.7	-0.55	0	32.9	27.4	95.00%	K.LFTPMMLFVAR.K	Oxidation (+16)	K.LFTPMMLFVAR.K
26	34	2	906.48	-0.12	0	49.7	28.8	95.00%	K.TGLSALMSK.N		K.TGLSALMSK.N
82	93	2	1458.63	-1.3	0	33.1	30.9	95.00%	Y.EYGWGSSFHFSR.F		R.LEDYNEATHSYYNVVTDFYEYGWGSSFHFSR.F
296	308	2	1555.82	0.5	0	61.4	25.4	95.00%	K.YVQNLANLATFFR.T		K.YVQNLANLATFFR.T
140	157	2	2039.97	-0.087	1	71.7	28.8	95.00%	R.FTGCNVIGLNNNDYQIAK.A	Carbamidomethyl (+57)	R.FTGCNVIGLNNNDYQIAK.A
191	202	2	1358.66	-6.4	1	48.2	29.3	95.00%	K.VYAIEATCHAPK.L	Carbamidomethyl (+57)	K.VYAIEATCHAPK.L
140	151	2	1321.61	-0.82	0	43.3	30.8	95.00%	R.FTGCNVIGLNNN.D	Carbamidomethyl (+57)	R.FTGCNVIGLNNNDYQIAK.A
336	353	2	1668.9	-1.3	1	92	23.2	95.00%	K.EVTAALENAAVGLVAGGK.S		K.EVTAALENAAVGLVAGGK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
34	A6ZL71_YEAS7	25.34%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
170	181	2	1251.66	-0.98	0	56.2	27.2	95.00%	K.IPIFSASGLPHN.E		K.IPIFSASGLPHNEIAAQICR.Q
459	466	2	987.51	-0.63	0	40.8	27.5	95.00%	L.DQAWSLLR.I		R.TVFESLDQAWSLLR.I
15	25	2	1243.67	-0.42	1	49.2	27.8	95.00%	K.AVEQGFNVKPR.L		K.AVEQGFNVKPR.L
368	381	2	1524.86	-1.4	0	32.2	21.8	95.00%	K.GIYPPINVLPSLSR.L		K.GIYPPINVLPSLSR.L

348	360	2	1454.73	-1.7	1	33.5	28.9	95.00%	P.DLTGYITEGQIFV.D		R.NGSITQIPILTMPNDDITHPIPDLTGYITEGQIFVDR.Q
326	339	2	1497.79	-0.87	0	46.2	26.2	95.00%	R.NGSITQIPILTMPN.D		R.NGSITQIPILTMPNDDITHPIPDLTGYITEGQIFVDR.Q
75	86	2	1219.64	-0.91	1	40.9	27.8	95.00%	R.AIVQVFEGTSGI.D		R.AIVQVFEGTSGIDVK.K
26	43	2	1930.03	-3.3	1	89.4	23.1	95.00%	R.LNYNTVSGVNGPLVILEK.V	Deamidation (+1)	R.LNYNTVSGVNGPLVILEK.V
264	272	2	1171.55	-0.95	1	46.9	30	95.00%	A.EYLAYQTER.H		R.LALTTAEYLAYQTER.H
133	144	2	1316.64	-0.86	0	41.3	29.5	95.00%	L.DINGSPINPYAR.I	Deamidation (+1)	K.VFAEDYLDINGSPINPYAR.I
170	189	2	2193.13	-1.5	1	71.4	24.5	95.00%	K.IPIFSASGLPHNEIAAQICR.Q	Carbamidomethyl (+57)	K.IPIFSASGLPHNEIAAQICR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
35	A6ZV88_YEAS7	24.53%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	113	2	1615.78	-0.93	1	40.8	29.4	95.00%	H.DDSPLNISQSLSPIM.E		R.FFANDVSLTVHDDSPLNISQSLSPIMEQFTVDELPESASDLLYEYSLDDK.S
138	143	2	705.44	0.11	0	27.5	18.3	95.00%	K.SIVLFK.F		K.SIVLFK.F
88	98	2	1249.6	-0.83	1	61.4	29.4	95.00%	R.FFANDVSLTVH.D	Deamidation (+1)	R.FFANDVSLTVHDDSPLNISQSLSPIMEQFTVDELPESASDLLYEYSLDDK.S
171	185	2	1676.84	-1.4	1	33.8	28.7	95.00%	G.DNLTVVINSLGWAFE.D		K.SGDNLTVVINSLGWAFEDEDGDDEYATEETLSHHDNNK.G
29	38	2	1145.53	2.9	1	29.9	30.1	95.00%	K.ESSSFISFDK.E		K.ESSSFISFDK.E
127	134	2	1014.49	-0.4	1	31.7	29.2	95.00%	S.DLLYEYSL.D		R.FFANDVSLTVHDDSPLNISQSLSPIMEQFTVDELPESASDLLYEYSLDDK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
36	A6ZWJ5_YEAS7	19.51%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
37	46	2	1236.64	-1.1	0	24.7	28.1	90.70%	S.EQYVTPYLPK.S		K.QMSEQYVTPYLPK.S
306	313	2	997.49	0.37	1	26.5	29.8	91.00%	K.FISENNFK.S		K.FISENNFK.S
34	46	2	1582.77	-0.5	1	68.5	28.9	95.00%	K.QMSEQYVTPYLPK.S		K.QMSEQYVTPYLPK.S
119	128	2	1194.61	0.088	1	59.7	29.4	95.00%	K.ACFVSLITER.D	Carbamidomethyl (+57)	K.ACFVSLITER.D
423	435	2	1457.61	0.084	1	35.1	30.3	95.00%	R.SGSCGGHYFDIMK.K	Carbamidomethyl (+57)	R.SGSCGGHYFDIMK.K
148	161	2	1669.81	-0.73	1	43.8	28.9	95.00%	K.NFAYPWVFISQGEL.D		K.NFAYPWVFISQGELDGMK.Q
129	138	2	1134.56	-0.88	0	38.5	29.4	95.00%	R.DSMTQILQSI.D		R.DSMTQILQSIDEVQVK.F
403	413	2	1500.54	-1.4	1	63.1	29.5	95.00%	N.DDIWNQYNCNC.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.YNNCPLNDDIWNQYNCNCDQGNDFTFR.S
180	187	2	940.52	-0.98	1	40.9	24.9	95.00%	G.DPELINIK.F		R.QAITDSMNGDPELINIK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
37	YA11B_YEAST	7.69%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
439	450	2	1339.59	-7.4	1	28.9	30.2	94.10%	K.LTESTVNHTNHS.D	Deamidation (+1)	K.LTESTVNHTNHSDDELPGHLLLDSGASR.T
560	568	2	1163.53	-1.8	1	29.8	30.1	95.00%	K.YGDFYWVSK.K		K.YGDFYWVSK.K
452	460	2	1005.55	-0.92	1	25.2	26.5	94.20%	D.DELPGHLLL.D		K.LTESTVNHTNHSDDELPGHLLLDSGASR.T
295	307	3	1521.76	-1.7	1	21.1	29	91.20%	I.DRLNNNGIHINNK.V	Deamidation (+1)	K.VTNIIDRLNNNGIHINNK.V
1621	1632	2	1318.72	-0.46	0	43.7	25.8	95.00%	K.SQIGNIYLLNGK.V		K.SQIGNIYLLNGK.V
308	315	2	989.52	0.32	0	31.3	29.6	95.00%	K.VACQLIMR.G	Carbamidomethyl (+57)	K.VACQLIMR.G
1168	1178	2	1212.56	-1.5	0	48.9	30.2	95.00%	G.DSNAYTTINSK.K		K.ELPPINSHQTNSSLGGIGDSNAYTTINSK.K
671	681	2	1235.67	-0.99	0	41	27.1	95.00%	T.DIFGPVHNLPK.S		K.YQNSYEPFQYLHTDIFGPVHNLPK.S
1	24	3	2598.18	-0.31	1	74.4	28.8	95.00%	-.MESQQLSQHSPISHGSACASVTSK.E	Acetyl (+42)/ Carbamidomethyl (+57)	-.MESQQLSQHSPISHGSACASVTSK.E

1610	1620	2	1304.57	-1.5	0	43.7	31.7	95.00%	S.DASYGNQPYYK.S		K.LVAISDASYGNQPYYK.S
1023	1037	2	1620.83	-1.5	0	54.1	27.6	95.00%	K.LNVPLLAPMSQSNTH.E		K.LNVPLLAPMSQSNTHESSHASK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
38	B3LPA7_YEAS1	10.31%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
287	300	2	1397.69	-0.8	1	35.5	29.2	95.00%	R.NPGAWGPGIISSDK.S		R.NPGAWGPGIISSDK.S
4	13	2	1208.62	-0.1	1	35.2	29.3	95.00%	R.FSNIITSNKW.D		R.FSNIITSNKWDEK.Q
41	51	2	1221.59	-1.5	1	31.9	29.7	95.00%	I.DPSNKTTPYSI.D		K.QNNIGEQSMQELPEDQIEHEMEAIDPSNKTTPYSIDEK.Q
72	82	2	1218.62	-1.2	0	60.6	29	95.00%	A.DVNSITNSLTR.L		K.HGSLQGGAIADVNSITNSLTR.L
4	12	2	1022.54	0.18	0	29.1	27.2	95.00%	R.FSNIITSNK.W		R.FSNIITSNK.W
435	441	2	869.44	1.7	0	27.7	26.5	95.00%	K.QFGYVTR.Q		K.QFGYVTR.Q
62	82	2	2110.08	-0.67	1	120	25.7	95.00%	K.HGSLQGGAIADVNSITNSLTR.L		K.HGSLQGGAIADVNSITNSLTR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
39	A6ZUD9_YEAS7	15.73%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
805	817	2	1313.73	0.3	0	28	24.7	95.00%	K.QNNVVSAVIAATK.N		K.QNNVVSAVIAATK.N
146	156	2	1114.59	-0.55	1	32.5	27.1	95.00%	R.LLLSPASSNVD.D		R.LLLSPASSNVDDDR.N
957	967	2	1259.55	-1	0	44.2	30.7	95.00%	Y.EIFSNGTCFGK.I	Deamidation (+1)/ Carbamidomethyl (+57)	K.ATYELPQGTLYEIFSNGTCFGK.I
651	661	2	1358.68	-0.59	1	42.2	29.1	95.00%	R.STVYRDYVQTK.F		R.STVYRDYVQTK.F
48	66	2	2022.88	-2	0	86.3	30.1	95.00%	R.SYMSGFFTGGNSPMINNLS.D		R.SYMSGFFTGGNSPMINNLSDSK.L
821	830	2	1071.57	1.3	1	35.6	26.3	95.00%	K.IDTIGNGLNR.G		K.IDTIGNGLNR.G
637	650	2	1547.77	-0.91	1	27.8	28.9	94.40%	K.LQTINGEYNGNVAR.S		K.LQTINGEYNGNVAR.S
1025	1036	2	1339.74	-1.7	1	40.7	25.9	95.00%	R.FKELLGYTLVSA.-		R.FKELLGYTLVSA.-
173	189	3	1889.91	-1.1	0	43	28.3	95.00%	E.DGYAGGYQSLRPSHNLR.F		R.GLQNSSLPELEDGYAGGYQSLRPSHNLR.F
709	715	2	910.52	-0.13	1	25.1	22.7	95.00%	K.YLILDFK.N		K.YLILDFK.N
850	863	2	1607.83	-0.5	0	65.4	26.6	95.00%	R.NYQILSVAQNVFVN.D		R.NYQILSVAQNVFVNDEQAVK.N
878	890	2	1466.88	1.1	1	25	13.6	95.00%	D.DEPVLPILLFALK.Q		K.DDEPVLPILLFALK.Q
839	849	2	1242.64	-0.099	0	35.1	27.6	95.00%	R.NLMSLPTNTPR.N		R.NLMSLPTNTPR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
40	B3LS12_YEAS1	11.68%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
473	479	2	890.49	0.65	1	36.2	26	95.00%	R.YETLLPR.N		R.YETLLPR.N
685	700	2	1708.74	-0.73	0	88.8	30.7	95.00%	R.ASAGACGGYIWCATHK.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.ASAGACGGYIWCATHK.T
603	614	2	1332.58	-1.3	0	37.5	31.7	95.00%	V.EICSGQIAHMST.D	Carbamidomethyl (+57)	R.QEAAVEICSGQIAHMSTDK.K
726	740	2	1703.87	-1.1	1	58.5	27.1	95.00%	R.LHIDAVNTVWSHANK.D		R.LHIDAVNTVWSHANK.D
78	91	2	1588.84	0.49	1	66.6	25.5	95.00%	V.DTIPVSPLELVPFY.D		K.VLIEAFGSPEVDPVDTIPVSPLELVPFYDQSIDTK.R
729	740	2	1340.65	-1.1	0	63.2	29.7	95.00%	I.DAVNTVWSHANK.D		R.LHIDAVNTVWSHANK.D
274	282	2	1029.59	-0.022	1	30.5	25.8	95.00%	K.VLEQGFLPK.F		K.VLEQGFLPK.F
451	457	2	842.43	-0.024	0	23.8	25.6	93.50%	K.TGTVFYR.E		K.TGTVFYR.E
373	381	2	1125.5	-0.21	1	40.5	30.9	95.00%	P.DFKPVENNY.D	Deamidation (+1)	R.SPDFKPVENNYDNSTNVPQEIWFLDVSNTIHPK.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
41	YNL5_YEAST	9.63%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
444	453	2	1233.52	-0.66	1	40.3	30.7	95.00%	V.DSMMLVESWH.E		K.NVDIVDSMMLVESWHEELLLK.N
37	52	2	1469.72	-0.9	1	82.9	29.1	95.00%	R.TLGAGSANGPAVNEGR.D		R.TLGAGSANGPAVNEGR.D

297	310	2	1582.87	-1.1	1	51.3	22.9	95.00%	R.LTHKLPITVQSPSY.E		R.LTHKLPITVQSPSYEAFHYVDAAK.T
563	575	2	1430.7	-0.5	1	77.2	29.4	95.00%	R.DVTNNAESLQNVK.T		R.DVTNNAESLQNVK.T
588	596	2	1117.53	1.9	1	34.2	29.5	95.00%	K.SALWGDWQR.D		K.SALWGDWQR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
42	PDR5_YEAST	10.26%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
180	204	3	2625.36	-0.54	1	23.1	23.1	95.00%	M.DGCLNPGELLVVLGRPGSGCTTLLK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.ETNTFQILKPMDGCLNPGELLVVLGRPGSGCTTLLK.S
285	297	2	1434.69	-1.5	0	63.5	29	95.00%	A.EVAMATYGLSHTR.N		R.ESYANHLAEVAMATYGLSHTR.N
945	957	2	1588.76	-1.9	1	41	29.6	95.00%	R.SIGYCQQQDLHLK.T	Carbamidomethyl (+57)	R.SIGYCQQQDLHLK.T
873	881	2	1165.58	0.022	1	27.9	30.5	92.30%	R.NLCYEVQIK.A	Carbamidomethyl (+57)	R.NLCYEVQIK.A
436	445	3	1117.66	-0.44	1	26.3	20.3	95.00%	K.KGIHIPQTPK.E		K.KGIHIPQTPK.E
67	84	2	1852.88	-0.93	1	31.3	30	95.00%	S.DAQSIFSSGVEGVNPIFS.D		K.SDAQSIFSSGVEGVNPIFSDPEAPGYDPK.L
120	132	3	1633.76	-0.83	0	23.2	29.1	95.00%	P.DFYKPYSLGCAWK.N	Carbamidomethyl (+57)	K.NMAHLSAADPDFYKPYSLGCAWK.N
142	155	2	1595.82	-1.2	0	67.8	28.1	95.00%	A.DVAYQSTVVNIPYK.I		K.NLSASGASADVAYQSTVVNIPYK.I
329	337	2	1196.5	-0.24	1	41.3	30.2	95.00%	K.FQCWDNATR.G	Carbamidomethyl (+57)	K.FQCWDNATR.G
49	65	2	1805.86	-0.99	0	112	29.3	95.00%	R.TLTAQSMQNSTQSAPNK.S		R.TLTAQSMQNSTQSAPNK.S
96	109	2	1550.7	-1.2	1	93.8	30.6	95.00%	L.DPNSENFSSAAWVK.N		K.LDPNSENFSSAAWVK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
43	HIP1_YEAST	10.78%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
31	42	2	1341.67	-0.31	1	56	29.2	95.00%	K.ESTTFVTELTSK.T		K.ESTTFVTELTSK.T
43	52	2	1051.52	-0.4	1	39.1	29.1	95.00%	K.TDSAFPLSSK.D		K.TDSAFPLSSK.D
44	52	2	950.47	-0.76	0	30.2	29.1	95.00%	T.DSAFPLSSK.D		K.TDSAFPLSSK.D
268	282	2	1533.72	-1.4	0	64.6	30.1	95.00%	H.DPGAFVGHSSGTQFK.G		K.YWHDPGAFVGHSSGTQFK.G
486	497	2	1332.69	-0.69	1	31	28.3	95.00%	L.DELPFISQTGVK.G		R.SLDELPFISQTGVK.G
400	412	3	1440.7	-0.18	0	40.7	29.6	95.00%	R.CMVAMAHIGNLPK.F	Carbamidomethyl (+57)	R.CMVAMAHIGNLPK.F
265	282	3	2019.92	-0.44	1	21.8	29.8	91.00%	K.YWHDPGAFVGHSSGTQFK.G		K.YWHDPGAFVGHSSGTQFK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
44	A7A1A2_YEAS7	12.10%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
478	485	2	996.5	-0.1	0	29.8	30.7	94.60%	P.DQLTMYVK.A		R.DPNNPDQLTMYVK.A
663	674	2	1229.66	-0.49	1	43.2	26.4	95.00%	R.NAVVQGIDSSLK.I		R.NAVVQGIDSSLK.I
498	509	2	1339.65	-0.96	1	48	29.8	95.00%	K.VLSAPNHTVDCK.I	Carbamidomethyl (+57)	K.VLSAPNHTVDCK.I
453	470	2	2188.04	-0.1	1	100	27.9	95.00%	K.SAWFYSFQSHPFTVLSER.H		K.SAWFYSFQSHPFTVLSER.H
510	525	3	1739.96	-0.29	1	58.5	21.2	95.00%	K.IFLEGPYGVTVPHIAK.L		K.IFLEGPYGVTVPHIAK.L
51	67	2	1925.89	-0.35	1	122	29.6	95.00%	K.NINWLGSVTACAYENSK.S	Carbamidomethyl (+57)	K.NINWLGSVTACAYENSK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
45	GNP1_YEAST	3.62%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
418	431	2	1441.77	-1.4	0	71.9	25.7	95.00%	K.ASPYVIAVSSHGVR.V		K.ASPYVIAVSSHGVR.V
123	132	2	1081.57	1.7	1	34.2	26.8	95.00%	K.SSYITVDGIK.Q		K.SSYITVDGIK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
46	A6ZY55_YEAS7	10.47%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
673	685	2	1511.74	-0.48	1	55.1	29.7	95.00%	R.NSPPDYGFILFSR.N		R.NSPPDYGFILFSR.N
361	373	2	1314.67	-1.3	1	55.4	28.5	95.00%	L.DTVGNEGSPLLLT.D		K.YVSISILDTVGNEGSPLLLTDDNINQHPNMIVSSTAEDTCIVMCHVGGLR.N

583	590	2	982.48	-0.94	1	39	30.4	95.00%	P.DEFFQLGK.D		K.LNSDDSLSPDEFFQLGK.D
598	610	2	1300.63	-0.47	0	61.5	29.4	95.00%	F.DLTGPINNSQGSV.D		R.LEEEFDLTGPINNSQGSVDSGR.R
404	414	2	1292.72	0.064	1	48.2	22.6	95.00%	R.NHVVTNDLLLR.D		R.NHVVTNDLLLR.D
342	353	2	1298.68	-0.63	1	30.8	27	95.00%	K.NILPSAVQSNEK.Y		K.NILPSAVQSNEK.Y
391	403	3	1516.69	-1.2	0	34	30.4	95.00%	E.DTCIVMCHVGGLR.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.YVSISILDTVGNEGSPLLLTDDNINQHPNMIVSSTAEDTCIVMCHVGGLR.N
562	569	2	1016.6	-0.41	0	27.5	22.1	95.00%	N.DLFQLLLR.D		K.ICLELVHSNELQNDLFQLLLR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
47	A6ZNT9_YEAS7	43.33%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
37	48	2	1302.69	-0.71	0	59.7	26.8	95.00%	K.EPTIGAAFLTQR.V		K.EPTIGAAFLTQR.V
112	122	2	1167.72	-0.27	1	26.6	17.5	95.00%	K.DIIIALVGNKI.D		K.DIIIALVGNKIDMLQEGGER.K
10	20	2	1068.65	-0.019	1	27.6	17.3	95.00%	K.LVLLGEAAVGK.S		K.LVLLGEAAVGK.S
112	121	2	1054.64	-1.3	0	30.6	21.1	95.00%	K.DIIIALVGNK.I		K.DIIIALVGNK.I
79	97	2	2091.14	-0.53	1	79.3	20.3	95.00%	R.NAQAALVVYDVTKPQSFIK.A		R.NAQAALVVYDVTKPQSFIK.A
69	78	2	1217.59	0.15	0	44.1	28.5	95.00%	R.FASLAPMYYR.N		R.FASLAPMYYR.N
162	170	2	976.52	-1.2	1	33.3	27.3	95.00%	N.DVFLGIGEK.I		K.TGENVNDVFLGIGEK.I
1	9	2	1037.51	0.87	0	34.2	30.5	95.00%	-.MNTSVTSIK.L	Acetyl (+42)/ Oxidation (+16)	-.MNTSVTSIK.L
146	155	2	1111.59	-0.21	1	48.5	25.7	95.00%	K.GLLFFETSAK.T		K.GLLFFETSAK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
48	A6ZSG0_YEAS7	6.83%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
713	720	2	970.53	-0.32	0	22.4	26	90.10%	K.MIWQLPIA.D		K.MIWQLPIADPTSTAPEQQEQNSHDAPNWSR.S
345	378	3	3574.69	2.9	1	36.4	25.8	95.00%	E.DHPAPATESSSLMPPANTTATPLNSNHPSYNSIR.H		R.EDHPAPATESSSLMPPANTTATPLNSNHPSYNSIR.H
73	91	3	2066.98	-2	0	33.6	28.5	95.00%	R.SVSSQSPIVHSSNNTLHHH.E		R.SVSSQSPIVHSSNNTLHHHEHQQHLPPTLESLSSK.S
72	91	4	2224.07	-1.9	1	38.1	28.2	95.00%	K.RSVSSQSPIVHSSNNTLHHH.E	Deamidation (+1)	K.RSVSSQSPIVHSSNNTLHHHEHQQHLPPTLESLSSK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
49	A6ZKX6_YEAS7	33.15%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
294	309	3	1752.96	-1.7	1	55.3	23.1	95.00%	S.EIQSAIRPAGQATQKR.T		R.IINSSEIQSAIRPAGQATQKR.T
33	44	2	1358.72	-0.89	0	50.5	27.6	95.00%	P.DIVHTVFTSVNK.N		-.MSRPQVTVHSLTGEATANALPLPAVFSAPIRPDIVHTVFTSVNK.N
221	246	4	2610.43	0.51	1	45	19.9	95.00%	R.NVPGVETANVASLNLLQLAPGAHLGR.F		R.NVPGVETANVASLNLLQLAPGAHLGR.F
272	288	2	1844.96	-0.49	1	58	25.3	95.00%	K.VGYTLPSHIISTSDVTR.I		K.VGYTLPSHIISTSDVTR.I
294	308	2	1596.86	-1.9	0	51.4	24.8	95.00%	S.EIQSAIRPAGQATQK.R		R.IINSSEIQSAIRPAGQATQK.R
347	360	3	1462.8	-1	1	28.5	23.6	95.00%	K.TGTKPAAVFTETLK.H		K.TGTKPAAVFTETLK.H
289	308	2	2111.13	-0.098	1	66.7	21.5	95.00%	R.IINSSEIQSAIRPAGQATQK.R		R.IINSSEIQSAIRPAGQATQK.R
85	95	2	1183.49	-0.074	0	27.7	29.7	93.10%	R.SGQGAFGNMCR.G	Carbamidomethyl (+57)	R.SGQGAFGNMCR.G
120	138	2	1819.02	-1.1	0	57.7	21.8	95.00%	R.YATASAIAATAVASLVLAR.G		R.YATASAIAATAVASLVLAR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
50	MAM3_YEAST	19.41%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
514	533	3	2137.05	-1.1	1	50.9	26.8	95.00%	K.IITTHTPHSSKEPSPAPHSN.D		K.IITTHTPHSSKEPSPAPHSNDK.S
257	270	2	1581.74	-1.1	1	41.2	29.7	95.00%	E.EIMTPIENVFTMSA.D		R.VEEIMTPIENVFTMSADTILDDK.T
609	619	2	1158.65	0.32	1	41.5	25.8	95.00%	K.NGIVESVITVK.G	Deamidation (+1)	K.NGIVESVITVK.G

683	691	2	1025.48	0.46	1	29.9	31.7	93.50%	R.SNFTDSLSR.T		R.SNFTDSLSR.T
580	608	3	3089.42	-1.8	1	30.5	27.5	95.00%	P.DSISIPNSGANHGNENQNVTISTSYQNTK.N		R.NSPDSISIPNSGANHGNENQNVTISTSYQNTK.N
282	289	2	926.46	0.074	0	27.1	25.8	95.00%	K.IFNSGFSR.I		K.IFNSGFSR.I
470	500	3	3211.68	-1.5	1	45.8	21.2	95.00%	R.SNAVLSPTPQVTEHGTIIPSNLASNPLNVNK.S		R.SNAVLSPTPQVTEHGTIIPSNLASNPLNVNK.S
358	372	2	1465.74	-1.9	1	27.4	28.5	94.40%	K.EPGSSHGAIGVLTLE.D		K.EPGSSHGAIGVLTLEDVIEELIGEEIVDESDVFVDMHQHIMR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
51	A6ZSU5_YEAS7	20.19%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
380	394	2	1652.76	-1.3	1	43.1	29.9	95.00%	R.GTFQSSGQNCIGIER.V	Carbamidomethyl (+57)	R.GTFQSSGQNCIGIER.V
314	326	2	1469.65	-1.9	0	62	30.2	95.00%	D.DSANYFTSHPGFK.H		K.CLEACDEDPDLVQLCYCLPPTENDDSANYFTSHPGFK.H
144	155	2	1354.59	-0.24	1	44.4	30.9	95.00%	K.AQSTWGNSDFSR.R		K.AQSTWGNSDFSR.R
313	326	2	1584.68	-2	1	53.7	29.5	95.00%	N.DDSANYFTSHPGFK.H		K.CLEACDEDPDLVQLCYCLPPTENDDSANYFTSHPGFK.H
327	342	3	1823.01	-1.4	0	30	22	95.00%	K.HITFIGSQPVAHYILK.C		K.HITFIGSQPVAHYILK.C
509	529	2	2102.98	-1.5	0	80.6	28.9	95.00%	T.DHCVQLANSAPFGLGGSVFGA.D	Carbamidomethyl (+57)	K.NTDHCVQLANSAPFGLGGSVFGADIK.E
81	94	2	1571.77	-0.4	1	49.4	29.3	95.00%	K.FSLPAPEAAQNNWK.G		K.FSLPAPEAAQNNWK.G
369	379	2	1247.66	0.78	1	62.4	27.5	95.00%	K.NLDALSSIIMR.G	Oxidation (+16)	K.NLDALSSIIMR.G
347	358	2	1197.7	-0.51	1	31.2	23.2	95.00%	K.SLTPVVVELGGK.D		K.SLTPVVVELGGK.D
490	504	2	1688.9	-1	1	57.6	24.7	95.00%	K.IAQNEVFGPILVMMK.A		K.IAQNEVFGPILVMMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
52	A6ZZQ2_YEAS7	17.85%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
9	25	2	1923.9	-0.65	1	31.9	29.6	95.00%	K.DEGVPLLSPYSSSPQLR.K	Phospho (+80)	K.DEGVPLLSPYSSSPQLR.K
582	606	2	2589.07	-1.9	1	108	29	95.00%	K.SQAYGATMSNESNANNNNSTSNASR.S		K.SQAYGATMSNESNANNNNSTSNASR.S
449	467	3	2049.96	-2	1	28.2	29.7	95.00%	Q.DNSAGHIKTHPNSPTPGIK.A	Phospho (+80)	K.FQDLFVASIYSQDNSAGHIKTHPNSPTPGIK.A
299	307	2	1126.47	-0.11	1	28.5	30.5	93.20%	Q.DAEAFHFQY.D		R.SQAIQDAEAFHFQYDEDEEDGTSNEDGILFSKPIVTNIDVPELGNR.R
193	208	2	1669.75	-1	0	60.2	30.8	95.00%	V.DALMNHVNNNASTGVN.D		R.QSNANNDVVIDVDALMNHVNNNASTGVNDNSK.R
381	393	2	1411.78	-0.78	1	59.6	25.2	95.00%	R.IQSGLQDNLLVGR.N		R.IQSGLQDNLLVGR.N
110	126	2	1811.91	0.28	0	41.8	26.9	95.00%	R.EGPQSVSSTVQPQPIMK.F		R.EGPQSVSSTVQPQPIMK.F
394	410	3	2075.03	0.0005	1	28.5	27	95.00%	R.NIQYPPHIISNNPEHFR.F		R.NIQYPPHIISNNPEHFR.F
319	331	2	1415.8	-1.3	0	45.7	23.4	95.00%	E.DGILFSKPIVTNI.D		R.SQAIQDAEAFHFQYDEDEEDGTSNEDGILFSKPIVTNIDVPELGNR.R
481	494	2	1448.68	-1.5	1	38	30.1	95.00%	K.NPSTLSSMSVANIE.D		K.NPSTLSSMSVANIEDVPPFWLDVSNPTEEEMK.I
468	480	2	1344.73	0.89	1	55.6	27	95.00%	K.AETVSQLQGLTAK.N		K.AETVSQLQGLTAK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
53	NCPR_YEAST	21.71%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
305	317	2	1504.77	-1	1	55.9	28.1	95.00%	G.DHLAVWPSNPLEK.V		K.YSTGDHLAVWPSNPLEK.V
422	439	2	2074.02	-0.73	1	40.5	27.3	95.00%	W.DTVPMQFLVESVPQMTPR.Y		K.WDTVPMQFLVESVPQMTPR.Y
653	664	2	1171.69	0.074	0	31.5	22.2	95.00%	K.GVSTALVGILSR.G		K.GVSTALVGILSR.G
264	275	2	1342.75	-1	0	21.7	23.6	90.80%	F.DLSQPYIAPIVK.S		R.NADGIQLGPFDLSQPYIAPIVK.S
405	413	2	1053.55	0.26	1	23.9	26.4	92.30%	K.YFNIADALK.Y		K.YFNIADALK.Y

318	327	2	1208.64	0.23	1	39.6	26.9	95.00%	K.VEQFLSIFNL.D	K.VEQFLSIFNLDPETIFDLKPLDPTVK.V
147	157	2	1265.54	-1.3	0	38.8	30.4	95.00%	R.YNMFGLGNSTY.E	R.YNMFGLGNSTYEFFNGAAK.K
470	483	2	1450.81	-1.2	0	42.4	21.3	95.00%	P.DAPPVVGVTTNLLR.N	K.QTVHVTSIVENFPNPELPDAPPVVGVTTNLLR.N
234	253	3	2238.05	-0.89	1	33.5	28.5	95.00%	T.DSMSLGEPSAHYLPSHQLNR.N	K.FTSQFQYTVLNEITDSMSLGEPSAHYLPSHQLNR.N
440	451	2	1349.63	-0.22	1	70.5	30	95.00%	R.YYSISSSSLSEK.Q	R.YYSISSSSLSEK.Q
49	59	2	1229.63	-0.012	1	78.6	28	95.00%	R.DIAQVVTENNK.N	R.DIAQVVTENNK.N
240	253	3	1647.81	-0.66	0	30.5	28.4	95.00%	G.EPSAHYLPSHQLNR.N	K.FTSQFQYTVLNEITDSMSLGEPSAHYLPSHQLNR.N
147	165	2	2129.95	-0.1	1	86.4	30.4	95.00%	R.YNMFGLGNSTYEFFNGAAK.K	R.YNMFGLGNSTYEFFNGAAK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
54	COS1_YEAST	21.78%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
102	108	2	935.49	1.7	0	31	29.2	95.00%	K.QLIQFCK.E	Carbamidomethyl (+57)	K.QLIQFCK.E
357	369	2	1544.86	0.83	1	48.5	22.7	95.00%	R.ALSLNVELWPYIK.E		R.ALSLNVELWPYIK.E
143	156	2	1828.81	0.87	1	75.3	30.6	95.00%	K.YFFFNAMVCQEAFR.T	Carbamidomethyl (+57)	K.YFFFNAMVCQEAFR.T
185	192	2	953.5	-0.027	0	33.2	27.5	95.00%	E.EALGVYFR.E		K.DSVPYIEEALGVYFR.E
25	33	2	1099.64	-0.29	1	27.9	23.9	95.00%	K.IVLPQDLFR.S		K.IVLPQDLFR.S
123	134	2	1354.68	-0.82	0	42.3	29.2	95.00%	W.EVVAANLNSYLY.E		K.EVTENTPSSDPHDWEVVAANLNSYLYENK.A
121	134	2	1655.78	-1.1	1	39.7	30.4	95.00%	H.DWEVVAANLNSYLY.E		K.EVTENTPSSDPHDWEVVAANLNSYLYENK.A
157	166	2	1147.65	0.15	1	29.8	23.8	95.00%	R.TTLLEPFSLK.K		R.TTLLEPFSLK.K
11	18	2	893.49	-0.02	1	26.5	26.4	95.00%	K.SVDVLSFK.Q		K.SVDVLSFK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
55	B3LNF5_YEAS1	7.17%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
687	698	2	1277.81	-1.3	1	21.4	11.1	90.20%	K.TVPVKPLQLVKGD.K		K.TVPVKPLQLVKGDK.C
1032	1047	2	1669.92	-0.96	1	49.6	21.8	95.00%	K.IQGLEGIILTNIVSNS.D		K.IQGLEGIILTNIVSNSDK.V
1367	1379	3	1335.62	0.25	1	41.1	29.6	95.00%	K.LDAPSSPHACPGK.E	Carbamidomethyl (+57)	K.LDAPSSPHACPGK.E
566	576	2	1263.63	-0.032	0	31.4	29.1	95.00%	K.FILNGFTLAHM.D	Deamidation (+1)	K.FILNGFTLAHMDGTTNFIYAIDFSTAFNDK.T
126	136	2	1330.63	-0.81	1	45.6	29.8	95.00%	R.GCYIETHPLNK.N	Carbamidomethyl (+57)	R.GCYIETHPLNK.N
1486	1495	2	1060.52	-1	0	32	29	95.00%	R.TGPSYSSLIH.D		R.TGPSYSSLIHDQFLDEADDLLAGHDEDANDLSSFMDQGSNFEIEEDDVPTLEEEHTSYTDQPTTTDVPDALPEGNEENIDRPDSTAPSNENQ.-
508	520	2	1407.7	-1.7	0	45	29.4	95.00%	G.DYGNVIVAIPYNA.D		K.LAFDFPCLYAVGDYGNVIVAIPYNADEDDDPQSEFYYSLDQGK.T
1267	1279	2	1607.75	-1.1	1	62.2	30	95.00%	K.SNCLFGHQTEFLR.K	Carbamidomethyl (+57)	K.SNCLFGHQTEFLR.K
873	886	2	1607.74	-1.6	1	68.8	30.7	95.00%	L.DNAIHCEFAGSLFK.Y	Carbamidomethyl (+57)	K.NCESILSPECHAVAYLTNDGGETFTEMLDNAIHCEFAGSLFK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
56	A7A201_YEAS7	24.27%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
11	21	2	1070.63	0.63	0	40	24.2	95.00%	K.LLLIGNSGVGK.S	Deamidation (+1)	K.LLLIGNSGVGK.S
72	79	2	989.48	0.9	0	25.5	29	90.50%	R.TITSSYYR.G		R.TITSSYYR.G
168	179	2	1418.68	-2.1	1	30.8	29.7	95.00%	R.QIKESMSQQNLN.E		R.QIKESMSQQNLNETTQK.K
160	167	2	923.45	-1	0	36.1	30.4	95.00%	E.DAFLTMAR.Q		K.MPFLETSALDSTNVEDAFLTMAR.Q
171	184	2	1636.74	-0.79	1	67.2	30.5	95.00%	K.ESMSQQNLNETTQK.K		K.ESMSQQNLNETTQK.K
22	27	2	760.43	1.9	0	25.1	27.2	93.10%	K.SCLLLR.F	Carbamidomethyl (+57)	K.SCLLLR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
57	A6ZT96_YEAS7	15.32%	100%	6								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
161	173	2	1516.68	-1.6	1	72.9	30.2	95.00%	L.DENYNLNGLQTVH.D	Deamidation (+1)	K.MGNGMADYILDENYNLNGLQTV HDYDVYCHYVAGLVGDGLTR.L	
212	220	2	1051.54	-0.87	0	27.4	29.3	93.20%	Y.ESMGLFLQK.T		K.FANESLYSNEQLYESMGLFLQK.T	
176	192	2	1893.9	-2.5	1	67.2	29	95.00%	Y.DVYCHYVAGLVGDGLTR.L	Carbamidomethyl (+57)	K.MGNGMADYILDENYNLNGLQTV HDYDVYCHYVAGLVGDGLTR.L	
356	365	2	1143.63	1.1	1	31.8	25.9	95.00%	K.LAVQDPNFLK.L		K.LAVQDPNFLK.L	
4	15	2	1390.8	-1.3	1	54.2	20.1	95.00%	K.LLQLALHPVEMK.A		K.LLQLALHPVEMK.A	
366	372	2	814.49	1.1	0	34.4	26.1	95.00%	K.LNIQISK.I		K.LNIQISK.I	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
58	A6ZQK0_YEAS7	9.17%	100%	16								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
325	337	3	1398.67	0.24	0	33.2	30.7	95.00%	R.GHNIPCTSTISGR.C	Carbamidomethyl (+57)	R.GHNIPCTSTISGR.C	
599	615	2	1638.8	-0.26	1	58.3	29.1	95.00%	R.AAYALGGLGSGFANNEK.E		R.AAYALGGLGSGFANNEK.E	
412	427	2	1744.97	-1.5	1	30	19.6	95.00%	K.YTQVLKPIAFPGGLLE.D		K.YTQVLKPIAFPGGLLEDNVK.A	
1551	1564	2	1385.78	-0.08	1	32.1	23.5	95.00%	R.SISGPVITDVASLK.A		R.SISGPVITDVASLK.A	
752	762	2	1208.71	-0.35	1	32.9	18.1	95.00%	K.LGLNIPLNEVK.N		K.LGLNIPLNEVK.N	
855	864	2	1050.59	0.82	0	45.4	25.1	95.00%	R.VFAIANAFAK.K		R.VFAIANAFAK.K	
352	366	2	1661.84	-1.1	0	37.9	27.4	95.00%	V.DTLTSGWKPLFVNAN.D		R.CYITSQNHGFAVDVDTLTSGWKP LFVNANDDSNEGIYHSELPYFSVQF HPESTPGPR.D	
999	1007	2	1076.51	-1	0	44.9	30.2	95.00%	F.DWCAVTAVR.T	Carbamidomethyl (+57)	R.IGSSVEFDWCAVTAVR.T	
619	635	2	1891.93	-0.62	1	70.5	28	95.00%	V.DLCNVAFSSSPQVLVEK.S	Carbamidomethyl (+57)	K.ELVDLCNVAFSSSPQVLVEK.S	
2000	2011	2	1398.66	-0.7	1	34.5	30.5	95.00%	R.TLACYSDAIVMR.H	Carbamidomethyl (+57)	R.TLACYSDAIVMR.H	
1311	1318	2	976.51	-0.033	0	23.7	26.2	92.30%	K.VPQFSFPR.L		K.VPQFSFPR.L	
1242	1253	2	1363.75	-0.38	0	27.9	24.6	95.00%	K.ITGPYNIQFIAK.D		K.ITGPYNIQFIAK.D	
116	124	2	1124.51	-0.9	1	36.6	31.4	95.00%	T.DEYSHYLAK.S		R.IHIAGLVISHYTDEYSHYLAK.S	
978	991	3	1503.71	-1.1	1	34.7	29.6	95.00%	F.DDHGVMVLGSGVYR.I		K.QIDTVAAEFPAYTNYLYMTYNAD SHDLSFDDHGVMVLGSGVYR.I	
1635	1650	2	1713.96	-0.12	1	35.6	21	95.00%	K.TADLASVLLLTSLQNR.S		K.TADLASVLLLTSLQNR.S	
189	198	2	1112.58	-0.55	0	34.1	27.2	95.00%	V.DPNVQNLVSK.V		R.SAFDVPEWVDPNVQNLVSK.V	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
59	A6ZPW7_YEAS7	14.78%	100%	7								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
157	178	2	2193.05	-0.28	1	45.8	27.3	95.00%	G.DSGSILRPTASLTEMMSGGAGR. R		R.VSTASMAIHDDDYGSIQNSTIGDS GSILRPTASLTEMMSGGAGR.R	
113	125	3	1452.83	0.063	1	26.7	22.3	95.00%	R.RLSVTLNNAGRPR.I		R.RLSVTLNNAGRPR.I	
53	67	3	1598.81	-1	1	43.6	27.9	95.00%	L.DHPVGSFKGVNSLSR.F		R.QSILDHPVGSFKGVNSLSR.F	
114	125	2	1296.73	-0.021	0	34.5	23	95.00%	R.LSVTLNNAGRPR.I		R.LSVTLNNAGRPR.I	
135	143	2	915.45	-1	0	39.1	29.8	95.00%	R.VSTASMAIH.D		R.VSTASMAIHDDDYGSIQNSTIGDS GSILRPTASLTEMMSGGAGR.R	
368	385	2	1918.88	-1.2	1	29.1	30.1	94.50%	K.SSSPGSLVNPMETSMWPI.D		K.SSSPGSLVNPMETSMWPIDLK.H	
15	26	3	1426.76	0.22	1	27.2	25.9	95.00%	R.SEVHYISIPLNR.G		R.SEVHYISIPLNR.G	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
60	BPT1_YEAST	7.18%	100%	11								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
1065	1077	2	1468.7	-4	1	48.9	30.2	95.00%	R.SPMTFFETTPVGR.I		R.SPMTFFETTPVGR.I	
824	836	2	1415.86	-0.5	0	51.6	8.45	95.00%	K.TIILTTNTVSILK.H		K.TIILTTNTVSILK.H	
1343	1351	2	1006.58	0.67	0	29	22.8	95.00%	K.STLSLALFR.I		K.STLSLALFR.I	
1316	1325	2	1124.62	-1.6	0	39.2	25.4	95.00%	L.DPVLNNINVK.I		R.ENLDPVLNNINVK.I	
1523	1532	2	1098.64	1.1	1	25.1	23.3	95.00%	K.IIVLDQGSVR.E		K.IIVLDQGSVR.E	
807	816	2	1160.68	-0.53	1	46.3	19.3	95.00%	K.NIIEYVLIGK.T		K.NIIEYVLIGK.T	
1504	1513	3	1194.68	-0.25	1	39.9	20.3	95.00%	K.DRTILTIAHR.I		K.DRTILTIAHR.I	

1449	1461	2	1386.69	0.64	1	63.5	29.5	95.00%	K.INENGSNLSVGQR.Q		K.INENGSNLSVGQR.Q
1506	1513	2	923.56	0.52	0	30.7	18.9	95.00%	R.TILTIAHR.I		R.TILTIAHR.I
611	625	2	1759.93	-0.36	1	57.2	25.1	95.00%	R.ALPAIEMNNITFLWK.S		R.ALPAIEMNNITFLWK.S
745	753	2	1056.56	0.77	1	27	27.6	95.00%	K.ACQLLPDLK.I	Carbamidomethyl (+57)	K.ACQLLPDLK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
61	A6ZQQ8_YEAS7	15.83%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
413	428	2	1801.94	-1.3	1	62.4	26.1	95.00%	R.TRPLGMPLSFTLNELN.D		R.TRPLGMPLSFTLNELNDLAR.I
494	507	2	1555.84	-0.31	0	58	23.8	95.00%	K.EIGWCLGASLPLLK.A	Carbamidomethyl (+57)	K.EIGWCLGASLPLLK.A
413	425	2	1445.77	-1.1	0	42.7	26.4	95.00%	R.TRPLGMPLSFTLN.E		R.TRPLGMPLSFTLNELNDLAR.I
375	395	3	2384.06	-1.8	0	39.5	29.7	95.00%	K.DAQCQSPPCSFNGVHQPSLVR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Deamidation (+1)	K.DAQCQSPPCSFNGVHQPSLVR.T
126	135	2	1094.49	-1.6	1	27.7	30.1	92.60%	F.DMLEPGLSSF.D		K.FDMLEPGLSSFDTDSVGAANSLDPLLK.V
300	310	2	1184.68	-0.013	1	65	25.2	95.00%	K.VNSVLVENALK.D		K.VNSVLVENALK.D
37	46	2	1026.57	0.76	0	26.8	24	95.00%	R.TVTPNASIPK.T		R.TVTPNASIPK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
62	B3LGF8_YEAS1	11.46%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
163	172	2	1065.5	-1.2	0	26.7	29.6	91.60%	H.ELPVSSSNSF.E		R.SVSPLQSITSCNTPMSEHELPVSSSNSFER.A
145	162	2	1973.88	-1.2	1	82.4	29.8	95.00%	R.SVSPLQSITSCNTPMSEH.E	Carbamidomethyl (+57)	R.SVSPLQSITSCNTPMSEHELPVSSSNSFER.A
207	222	2	1685.77	-2.3	1	46.2	30	95.00%	G.DEITSYGYGSIPQSIG.D		K.SLHIVAPSPEVPVSGDEITSYGYGSIPQSIGDVENGLNPPYVENTSSDELVHDLTR.R
192	206	2	1487.8	-1.8	1	41.6	25.7	95.00%	K.SLHIVAPSPEVPVSG.D		K.SLHIVAPSPEVPVSGDEITSYGYGSIPQSIGDVENGLNPPYVENTSSDELVHDLTR.R
163	174	2	1350.64	-1.4	1	48	29.8	95.00%	H.ELPVSSSNSFER.A		R.SVSPLQSITSCNTPMSEHELPVSSSNSFER.A
431	444	3	1674.92	-1.6	1	26.9	22.7	95.00%	K.STLYGRPTPTLWKR.F		K.STLYGRPTPTLWKR.F
127	139	2	1336.59	-1.6	0	34.5	30.5	95.00%	H.EACGNSALQSSIT.D	Carbamidomethyl (+57)	K.ANEDDLKPPSQHEACGNSALQSSITDFSDR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
63	B3LH18_YEAS1	4.87%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	17	2	1662.87	-1.8	0	84.1	26.6	95.00%	M.DATTPLLTVANSHPAR.N		-.MDATTPLLTVANSHPAR.N
2	20	2	2002.06	-2.2	1	62.8	23.7	95.00%	M.DATTPLLTVANSHPARNPK.H		-.MDATTPLLTVANSHPARNPK.H
1	20	2	2175.11	-1.6	1	41.3	25.3	95.00%	-.MDATTPLLTVANSHPARNPK.H	Acetyl (+42)	-.MDATTPLLTVANSHPARNPK.H
1	17	2	1793.91	-1.6	1	86.2	27.6	95.00%	-.MDATTPLLTVANSHPAR.N		-.MDATTPLLTVANSHPAR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
64	A6ZM61_YEAS7	15.87%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
151	160	2	1103.62	-0.39	0	57.5	22.6	95.00%	G.DIPLFLTSAK.N		K.SLGDIPLFLTSAK.N
39	48	2	1035.56	-0.22	1	43.9	26.3	95.00%	K.ATIGADFLTK.E		K.ATIGADFLTK.E
148	160	2	1360.76	0.42	1	49.8	22.6	95.00%	K.SLGDIPLFLTSAK.N		K.SLGDIPLFLTSAK.N
71	80	2	1186.62	1.7	0	41	27.9	95.00%	R.FQSLGVAFYR.G		R.FQSLGVAFYR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
65	A7A0Z7_YEAS7	30.43%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
14	27	2	1642.73	-1.2	1	73.2	31.2	95.00%	K.NGETISSCFQPFQK.N	Deamidation (+1)/ Carbamidomethyl (+57)	K.NGETISSCFQPFQK.N

52	57	2	701.38	-1.3	0	32.3	31.3	95.00%	M.DMVLPK.V		K.NENYGTITSANEQITPVIFHNLIMDMVLPK.V
144	165	2	2180.9	-1.8	0	119	30.2	95.00%	R.NQTLNSSGNGQSSNGNGQNTIS.D	Deamidation (+1)/ Deamidation (+1)/ Deamidation (+1)	R.NQTLNSSGNGQSSNGNGQNTISDIGDATEDQIK.D
28	38	2	1182.51	-1.4	1	46	30.4	95.00%	K.NENYGTITSAN.E		K.NENYGTITSANEQITPVIFHNLIMDMVLPK.V
39	51	2	1569.82	-1	0	24.9	26.8	93.30%	N.EQITPVIFHNLIM.D	Oxidation (+16)	K.NENYGTITSANEQITPVIFHNLIMDMVLPK.V
122	132	2	1194.66	-0.76	0	51.1	23.2	95.00%	N.ELLSSHVGQIL.D		R.ILSGLQEYESNATNELLSSHVGQILDSFHEELVEYR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
66	A6ZKY2_YEAS7	8.41%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
128	147	2	2241.05	-2.2	0	66.2	28.8	95.00%	V.DPYHLSPQQQPSNNLFGSGR.L		R.DNADLPVDPYHLSPQQQPSNNLFGSGR.L
594	602	2	1079.52	-1.2	1	37.4	30.3	95.00%	E.DVSEFISQR.R		K.EATGETDVPEDVSEFISQR.R
246	253	2	883.51	0.085	1	27.4	23.6	95.00%	K.GLLDTLPR.R		K.GLLDTLPR.R
223	232	2	1069.55	0.074	1	38.8	28.3	95.00%	R.MVSDLPPPSK.K		R.MVSDLPPPSK.K
564	572	2	1130.62	0.63	1	28.2	26.9	95.00%	R.ILCWELVAK.R	Carbamidomethyl (+57)	R.ILCWELVAK.R
93	102	2	1119.56	0.34	1	46.1	29.1	95.00%	R.YAANLQESPK.R		R.YAANLQESPK.R
49	63	2	1601.78	-1.5	0	66.8	28.8	95.00%	Y.DQSNVFQGLPASPSR.A		R.WANPSEESLEDSYDQSNVFQGLPASPSR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
67	A6ZWP0_YEAS7	8.97%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
91	103	2	1443.72	-0.66	0	51.6	28	95.00%	K.AQPLISSCPACLK.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.AQPLISSCPACLK.N
961	971	2	1269.6	0.46	1	46.9	30.5	95.00%	K.DFIQAYSDGVR.I		K.DFIQAYSDGVR.I
104	116	2	1614.67	-0.79	0	49.4	30.6	95.00%	K.NFNNLFCHFTCAA.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.NFNNLFCHFTCAADQGR.F
33	45	2	1470.73	-0.68	1	34.2	28.9	95.00%	K.SVFGNELPCPVPR.S	Carbamidomethyl (+57)	K.SVFGNELPCPVPR.S
185	203	3	2082.06	-0.24	1	28	26.9	95.00%	K.FLGDAKPMLGGSPFQINYK.Y		K.FLGDAKPMLGGSPFQINYK.Y
476	489	2	1687.87	-2.8	0	44	27.1	95.00%	K.FPVNCLPTFQQPLK.T	Carbamidomethyl (+57)	K.FPVNCLPTFQQPLK.T
188	203	2	1764.88	-1.5	0	53.6	27.9	95.00%	G.DAKPMLGGSPFQINYK.Y		K.FLGDAKPMLGGSPFQINYK.Y
161	177	2	1671.79	-0.85	1	88.4	29.7	95.00%	K.FSATNGYAMDLIGGGAK.N		K.FSATNGYAMDLIGGGAK.N
104	120	2	2070.88	-0.71	1	61	30.3	95.00%	K.NFNNLFCHFTCAADQGR.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.NFNNLFCHFTCAADQGR.F
188	204	3	1927.95	-1.3	1	24.1	28	95.00%	G.DAKPMLGGSPFQINYKY.D		K.FLGDAKPMLGGSPFQINYKYDLANEEK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
68	YIL7_YEAST	23.27%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
179	187	2	1018.54	-0.91	0	24	26.8	91.90%	F.ERPLFSLAS.E		K.DALVSHTNNEKPFLSNFERPLFSLASESNR.N
290	298	2	956.57	1.8	0	24	26.1	93.00%	K.GNLLVVQSK.R		K.GNLLVVQSK.R
218	227	2	1128.66	-1.4	0	34.6	22.5	95.00%	R.LLQKPVIMTS.D		R.LLQKPVIMTSDNVSTNSLVSTISSSSASSLDNGNEK.E
117	127	2	1345.57	-1.1	0	45.3	30.9	95.00%	K.MFSTQHTQFYG.D		K.MFSTQHTQFYGDSPYMDYPAK.E
179	191	2	1504.76	-1.2	1	37.8	27.4	95.00%	F.ERPLFSLASESNR.N		K.DALVSHTNNEKPFLSNFERPLFSLASESNR.N
192	205	2	1566.83	0.18	1	43.7	24.8	95.00%	R.NSLFISPTGDILYK.T		R.NSLFISPTGDILYK.T
162	178	3	1931.94	-1.3	1	20.8	28.5	91.60%	K.DALVSHTNNEKPFLSNF.E		K.DALVSHTNNEKPFLSNFERPLFSLASESNR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
69	AQR1_YEAST	14.16%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
282	292	2	1140.69	-0.72	0	31	22.6	95.00%	R.TIAGNLSIKPK.R		R.TIAGNLSIKPK.R
493	504	2	1361.6	-0.43	0	49.4	31	95.00%	K.SSTASSCFNFVR.C	Carbamidomethyl (+57)	K.SSTASSCFNFVR.C
42	54	2	1375.67	-1.6	0	49.2	28.9	95.00%	F.EGAYINSHGTLSK.T		K.LNFEGAYINSHGTLSK.T
39	54	2	1749.87	0.22	1	75.5	28.6	95.00%	K.LNFEGAYINSHGTLSK.T		K.LNFEGAYINSHGTLSK.T
78	88	2	1230.61	-0.82	1	60.3	28.6	95.00%	V.DPTQQITAETK.A		K.VDPTQQITAETK.A
505	517	2	1520.68	-0.69	0	60.3	30.1	95.00%	R.CSLSTIFMGCFAK.M	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.CSLSTIFMGCFAK.M
563	572	2	1158.64	-0.27	0	29.8	26.3	95.00%	R.QSWLNTLAVK.A		R.QSWLNTLAVK.A
298	307	2	1081.67	0.25	0	30.5	16.2	95.00%	R.APIFLLGPVR.R		R.APIFLLGPVR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
70	VAC7_YEAST	11.93%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1141	1150	2	1271.62	-0.18	1	29.4	29.4	95.00%	K.YEVPFFNTQK.S		K.YEVPFFNTQK.S
774	784	2	1453.64	-1.4	0	36.2	30.3	95.00%	N.DIHSMFYYNHK.N		K.FPHGLNFYGDNNVIEEENNGDSSNVNRPQHTNLQHEFIPEDNESDENDIHSMFYYNHK.N
1031	1046	2	1586.85	-0.64	1	36.3	25.4	95.00%	N.DISGGNIETVLLGTAK.K		K.ILQITTNLSLVEESANNDISGGNIETVLLGTAK.K
806	823	2	2000.86	-1.9	0	85.7	30.3	95.00%	Y.DRPNATFNSYYGSASNTH.E		K.NDLETKPLISDYGEDEDVDDYDRPNATFNSYYGSASNTHELPLHGR.M
786	794	2	1014.56	-0.51	1	27.9	26.8	95.00%	N.DLETKPLIS.D		K.NDLETKPLISDYGEDEDVDDYDRPNATFNSYYGSASNTHELPLHGR.M
898	910	2	1553.72	-0.91	0	45.3	30.1	95.00%	N.DIVGYSPHNFYSR.K		R.TNNSIMNGSIHMNGNDDVTHSNINNNDIVGYSPHNFYSR.K
699	715	2	2062.94	-2.2	1	56	29.6	95.00%	E.DYIEQPHNYPTMQNSVK.K		R.YSGVPDHVNLEDYIEQPHNYPTMQNSVK.K
293	303	2	1192.59	-1.3	1	27.8	29.2	94.10%	N.DGLRIPNHSNA.D		K.NAPANSTTHDNGPVANDGLRIPNHSNADDNENNNK.M
400	412	2	1319.59	-1.7	0	37.6	30.7	95.00%	A.DLSASTSNNNAIN.D		K.NSNADLSASTSNNNAINDDSHESNSEKPTK.A
54	74	2	2196.06	-2	1	42.2	27.5	95.00%	V.DDSVATANTTSNVVQHNLPTI.D		R.EIVDDSVATANTTSNVVQHNLPTIDNNLMDSDATSHNQDHWHSDINR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
71	MNN5_YEAST	11.95%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
504	513	2	1115.57	-0.38	1	40.2	29.1	95.00%	R.FIGPNGEQVR.G		R.FIGPNGEQVR.G
100	108	2	1040.5	-1.2	1	32.9	29.1	95.00%	S.DLSYESLSK.C		K.LHGAEGCSFANNVAAHDSGHDSDLSYESLSK.C
53	69	2	1921.98	-0.59	1	60.2	25.9	95.00%	K.NNFYTTLVQAIVENKPA.D	Deamidation (+1)	K.NNFYTTLVQAIVENKPADSSPDLSK.L
278	295	2	1890.02	-1.4	0	30.4	22.5	95.00%	R.VTPPAFYNIIGSSINIGK.R		R.VTPPAFYNIIGSSINIGK.R
78	93	2	1653.73	-1	1	93.8	30.8	95.00%	K.LHGAEGCSFANNVAAH.D	Carbamidomethyl (+57)	K.LHGAEGCSFANNVAAHDSGHDSDLSYESLSK.C
82	93	2	1275.53	-1	0	41	31.2	95.00%	A.EGCSFANNVAAH.D	Carbamidomethyl (+57)	K.LHGAEGCSFANNVAAHDSGHDSDLSYESLSK.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
72	A6ZQY0_YEAS7	18.83%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
116	127	2	1213.63	-1.3	1	51.8	27.6	95.00%	A.DDNVAVGLIGNK.S		R.ENADDNVAVGLIGNK.S
16	26	2	1056.62	0.27	1	32.4	24.6	95.00%	K.IVLIGDSGVGK.S		K.IVLIGDSGVGK.S
169	177	2	1120.61	-1.3	0	31.8	25.6	95.00%	E.ELINTIYQK.V		K.AFEELINTIYQK.V

44	53	2	1079.56	0.067	1	61.1	27.8	95.00%	K.STIGVEFATR.T		K.STIGVEFATR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
73	A6ZS87_YEAS7	8.28%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
115	132	2	2124.08	-1.5	0	80.6	26.3	95.00%	K.ATQLFNQQQQHQLQSVAR.N		K.ATQLFNQQQQHQLQSVAR.N
353	359	2	907.39	0.2	1	30.1	29.8	95.00%	K.DMMNLER.K		K.DMMNLER.K
73	82	2	1131.63	2.1	1	50.5	25.7	95.00%	K.FVAALNQELK.K		K.FVAALNQELK.K
755	770	2	1604.88	-1.7	0	61.8	22.9	95.00%	K.AVSSSGLLSTMAQLIK.A		K.AVSSSGLLSTMAQLIK.A
341	347	2	939.45	-1.7	1	24.1	27.7	90.20%	R.DHVVWER.N		R.DHVVWER.N
3	18	2	1892.9	-0.96	1	52	28.9	95.00%	K.FSHSLQFNSVPEWSTK.Y		K.FSHSLQFNSVPEWSTK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
74	A6ZKW1_YEAS7	14.41%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
83	98	2	1920.91	-0.38	1	63.5	29.5	95.00%	K.SFYNNVFNFLMVDSPK.G		K.SFYNNVFNFLMVDSPK.G
153	165	2	1470.77	-0.89	1	52.5	26.8	95.00%	K.DYVEHIATLVSPK.G		K.DYVEHIATLVSPK.G
352	364	2	1420.68	-1.6	1	60.5	30.1	95.00%	P.DVSTESGQLMINK.T		K.DLSDVPLSDLDGTIPDVSTESGQLMINK.T
448	458	2	1238.6	-0.25	1	51	30.6	95.00%	R.YLNAMESIGNK.Y		R.YLNAMESIGNK.Y
429	439	3	1210.55	-1.4	0	42.8	31.3	95.00%	E.DGFHGVAMLQH.D		R.TGVEGYHDEDGFHGVAMLQHDFVQDYGR.Y
496	507	2	1480.72	-0.76	1	47.3	29.2	95.00%	V.DVMFIHSNFPKF.D		K.NHVDVMFIHSNFPKFDPYDLSK.S
546	555	2	1236.62	-1.4	1	46	30	95.00%	K.VLNEYVCVNK.N	Carbamidomethyl (+57)	K.VLNEYVCVNK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
75	GAS1_YEAST	7.51%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	127	2	1127.59	-1.2	0	53	27.1	95.00%	A.DLAAPATSINR.D		K.ALNDADIYVIADLAAPATSINR.D
415	424	2	1192.52	0.27	0	36	30.3	95.00%	K.YGAYSFCTPK.E	Carbamidomethyl (+57)	K.YGAYSFCTPK.E
425	437	2	1678.79	-0.25	1	47.9	29.8	95.00%	K.EQLSFVMNLYYEK.S	Oxidation (+16)	K.EQLSFVMNLYYEK.S
83	90	2	956.58	2.2	1	40.2	21.3	95.00%	K.KLNTNVIR.V		K.KLNTNVIR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
76	A6ZT57_YEAS7	14.31%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
369	377	2	1155.59	-0.17	1	51.3	28.3	95.00%	K.SIYQVYLDR.A		K.SIYQVYLDR.A
647	661	3	1636.86	-0.98	0	23.6	26.1	95.00%	S.DLTAKPSYKPAGSFR.S		R.QSVVMTNPSDLTAKPSYKPAGSFR.S
701	719	2	1887.93	-1.9	1	25.8	27.9	93.10%	T.DVVQPPSVGGILPHSGSQD.D		R.VSGILEETDVVQPPSVGGILPHSGSQDDLR.K
476	491	2	1795.9	-2	1	44.5	28.7	95.00%	R.IASSIYSEAIQPLNYQ.D		R.IASSIYSEAIQPLNYQDQYQQQEQSPVYNGHTQYPGNGYSGNPQQQGYTAQFVQNPQWYGVPTPQQQQHNHPQTLETIGELPTPAYLAQSASSHSLTSFK.R
610	623	2	1705.74	-0.76	0	48.8	30.7	95.00%	N.DAYYAPQQQGQYMK.F	Oxidation (+16)	R.LNGTALNPVDHPEMFYSPTNDAYYAPQQQGQYMK.F
599	609	2	1336.54	-1.4	1	45	30.4	95.00%	V.DHPEMFYSPTN.D		R.LNGTALNPVDHPEMFYSPTNDAYYAPQQQGQYMK.F
483	491	2	1074.53	-0.38	0	36	29.1	95.00%	S.EAIQPLNYQ.D		R.IASSIYSEAIQPLNYQDQYQQQEQSPVYNGHTQYPGNGYSGNPQQQGYTAQFVQNPQWYGVPTPQQQQHNHPQTLETIGELPTPAYLAQSASSHSLTSFK.R
638	661	3	2580.3	-1.4	1	29.9	25.2	95.00%	R.QSVVMTNPSDLTAKPSYKPAGSFR.S		R.QSVVMTNPSDLTAKPSYKPAGSFR.S
402	413	2	1336.73	-1.4	0	57.4	24.3	95.00%	V.DNIVQNPLPSIK.I		R.VDNIVQNPLPSIK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
77	A6ZRM3_YEAS7	27.61%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
278	286	2	975.48	-1.5	0	30.2	29.9	95.00%	H.DASMGLNLR.R		K.VFYGHDASMGLNLR.R
293	306	2	1593.78	-1.9	1	34.2	28.6	95.00%	L.DTACIKNNLLSSMK.V	Carbamidomethyl (+57)	K.GLDTACIKNNLLSSMK.V
218	235	3	1991.98	-1	0	22.8	28.2	95.00%	G.DFMKPNQIPGVSSLSNMK.Y		K.LSQLAEHCSMAIELDLDITGDILFGAHAGMVPGDFMKPNQIPGVSSLSNMK.Y
37	51	2	1564.94	-1.2	0	25.6	15.4	95.00%	R.LSPPVSLLPTISTLK.K		R.LSPPVSLLPTISTLK.K
109	121	3	1541.86	-0.76	1	27.9	22.4	95.00%	K.VVSYILNHKDQVK.C		K.VVSYILNHKDQVK.C
149	164	2	1838.91	-1.2	1	49.8	28.8	95.00%	K.LMTPLTFSTETNFIPQ.D		K.LMTPLTFSTETNFIPQDISK.I
273	286	2	1578.76	0.18	1	58.9	30	95.00%	K.VFYGHDASMGLNLR.R		K.VFYGHDASMGLNLR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
78	A6ZPF0_YEAS7	15.95%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
302	313	2	1199.67	-1.4	0	26.5	24.1	95.00%	K.ILLQATPSTLSG.D		K.ILLQATPSTLSGDQVEGDLLK.I
213	234	4	2338.04	-1.7	1	52	28.7	95.00%	K.TPSYSTSSHTIASGGNYTEHNK.R		K.TPSYSTSSHTIASGGNYTEHNK.R
404	411	2	924.54	-1.5	0	24.8	22.8	95.00%	N.DPLSLRPK.T		R.AGDSQGDHLQNDPLSLRPK.T
412	424	2	1328.63	-0.88	0	49.2	30.7	95.00%	K.TYGTGISGSTCLI.D	Carbamidomethyl (+57)	K.TYGTGISGSTCLIDDAADCNTADCLEDH.-
213	230	2	1829.8	-1.3	0	43.6	31	95.00%	K.TPSYSTSSHTIASGGNYT.E		K.TPSYSTSSHTIASGGNYTEHNK.R
371	385	2	1731.89	-1.3	1	63	26.8	95.00%	R.YGIHSATLQPEFITR.E		R.YGIHSATLQPEFITR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
79	A6ZVP9_YEAS7	15.75%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
74	92	2	2093.06	-1.4	1	68.4	26.1	95.00%	E.EIFIANEGVHTGQFIYAGK.K		R.EEIFIANEGVHTGQFIYAGK.K
201	221	3	2158.03	0.47	1	44.3	28.1	95.00%	R.GVAMNPVDHPHGGGNHQHIGK.A		R.GVAMNPVDHPHGGGNHQHIGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
80	A6ZT03_YEAS7	14.04%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
41	59	2	1950.96	-0.83	1	73.2	27.6	95.00%	H.DNLSESQVQPAVAPPNTGK.G		K.NESFHDNLSESQVQPAVAPPNTGK.G
313	324	3	1423.73	-1.1	0	24.7	28.2	95.00%	G.ELFTGKPAMFQR.T		R.AAGTASWGELFTGKPAMFQR.T
1	12	2	1387.66	-0.5	1	48.4	29.8	95.00%	-.MNSTPDLISPQK.S	Acetyl (+42)/ Oxidation (+16)	-.MNSTPDLISPQK.S
305	324	2	2125.04	-2	1	95.9	27.8	95.00%	R.AAGTASWGELFTGKPAMFQR.T		R.AAGTASWGELFTGKPAMFQR.T
228	236	2	1153.52	0.85	0	47.9	30.8	95.00%	K.NYSNSVQWR.V	Deamidation (+1)	K.NYSNSVQWR.V
537	545	2	959.51	0.5	0	44.9	29.3	95.00%	K.SASWVPVSK.R		K.SASWVPVSK.R
45	59	2	1521.78	-1.5	0	28.1	28.2	95.00%	S.ESQVQPAVAPPNTGK.G		K.NESFHDNLSESQVQPAVAPPNTGK.G
526	536	2	1307.62	-1.5	1	60.8	30	95.00%	N.DMYAEGVLPWK.S		K.GLSLEEVNDMYAEGVLPWK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
81	A6ZZF0_YEAS7	14.71%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
177	185	2	1060.6	0.17	1	48.3	24.9	95.00%	K.MSLIDLLTR.R		K.MSLIDLLTR.R
246	256	2	1236.58	-0.38	1	38.5	29.8	95.00%	R.GLVCVENNIGY.D	Carbamidomethyl (+57)	R.GLVCVENNIGYDLENLSLYR.K
267	272	2	722.37	-0.59	0	23.7	27	91.00%	K.NFLSSR.H		K.NFLSSR.H
278	298	2	2249.98	-0.45	1	57.3	29.7	95.00%	S.ESPENYGSNQLSHSFSSPLGN.D		R.HHHSSESPENYGSNQLSHSFSSPLGNDVTENPAALADTQYHPENGSLYPHHHHLETPFSK.L

257	265	2	1121.57	-1.5	1	39.7	29	95.00%	Y.DLENLSLYR.K		R.GLVCVENNIGYDLENLSLYR.K
309	326	3	2181.96	-2	1	35.8	29.1	95.00%	A.DTQYHPENGSLYPHHHHL.E	Deamidation (+1)	R.HHHSSESPENYGSNQLSHSFSSPLGNDVTENPAALADTQYHPENGSLYPHHHHLETPFSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
82	A6ZNR5_YEAS7	14.21%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
304	315	2	1294.6	-0.87	0	43.2	30.1	95.00%	K.TITPMGGFVHYG.E	Oxidation (+16)	K.TITPMGGFVHYGEIK.N
249	266	3	2047	-1	0	22.6	28	95.00%	K.VACIGAWHPAHVMWSVAR.A	Carbamidomethyl (+57)	K.VACIGAWHPAHVMWSVAR.A
180	191	2	1274.63	-1.4	1	51.7	28.9	95.00%	A.EIQLNGGSISEK.V	Deamidation (+1)	K.AHLAEIQLNGGSISEK.V
38	50	2	1409.79	-1.2	0	47.7	22.9	95.00%	R.SKPVALTSFLGYK.A		R.SKPVALTSFLGYK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
83	YOL19_YEAST	29.58%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
502	529	3	2950.53	-1.5	0	45.8	23.9	95.00%	R.NPVPGVGFAPNPLPNQSPITQGYKPAYK.R		R.NPVPGVGFAPNPLPNQSPITQGYKPAYK.R
472	501	3	3257.62	-0.24	1	80.1	22.8	95.00%	R.TTPAGPDPSNVILQSNPYFNVAPNQVPQHR.N		R.TTPAGPDPSNVILQSNPYFNVAPNQVPQHR.N
540	551	2	1339.65	-0.018	0	37.3	29.5	95.00%	R.ATTSLNNPYGFR.-		R.ATTSLNNPYGFR.-
203	214	2	1336.67	-0.31	1	36.9	29.4	95.00%	K.GMLLNDPYLSSK.S		K.GMLLNDPYLSSK.S
452	471	3	2615.26	-1.5	0	32.7	26.5	95.00%	R.LQPQQQQPQQQYHQYNLYQR.T		R.LQPQQQQPQQQYHQYNLYQR.T
425	451	3	2898.49	-0.86	0	44.5	22.9	95.00%	R.ETAAGPANIRPYAGQPHPAPLVYPQQR.L		R.ETAAGPANIRPYAGQPHPAPLVYPQQR.L
239	251	2	1418.7	-0.87	1	33.9	28.5	95.00%	G.DNFKNGTNITVVP.D	Deamidation (+1)	R.TNLLGDNFKNGTNITVVPDIISHNQDPK.L
390	400	2	1253.5	-2.3	0	27.2	30.5	90.80%	N.DSHINSMSSYN.D		R.LLNDIMETSFNEPNDSHINSMSSYNDK.D
403	412	2	1106.56	-0.91	0	40.2	30.2	95.00%	K.DSTLTSISQR.G		K.DSTLTSISQR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
84	A7A052_YEAS7	3.66%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
321	333	2	1438.72	-1.6	1	45.3	29.1	95.00%	F.DFNAAKPSVHPEK.N		K.FDFNAAKPSVHPEK.N
574	582	2	953.52	-0.76	0	33.7	25.1	95.00%	F.DLNPISAPK.A		K.YNDTEEEMNAMDYEEEDEFDLNPISAPK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
85	A6ZQR6_YEAS7	22.93%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
29	35	2	776.44	-0.31	0	30.2	26.6	95.00%	K.NGFVVIK.S	Deamidation (+1)	K.NGFVVIK.S
57	68	2	1311.75	-0.32	1	66.2	22.9	95.00%	K.VHLVAIDIFTGK.K		K.VHLVAIDIFTGK.K
12	27	2	1713.74	-1.2	0	49.8	30.1	95.00%	A.DAGSSATYPMQCSALR.K	Carbamidomethyl (+57)	-.MSDEEHTFETADAGSSATYPMQCSALR.K
12	28	2	1841.84	-1.3	1	93.8	30.5	95.00%	A.DAGSSATYPMQCSALRK.N	Carbamidomethyl (+57)	-.MSDEEHTFETADAGSSATYPMQCSALRK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
86	B3LQG1_YEAS1	17.17%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
130	140	2	1395.66	-1.2	0	28.5	30.3	93.40%	K.FPAFIWQTWSN.D		K.FPAFIWQTWSNDEGPER.V
68	78	2	1285.63	-0.71	1	58.5	30.1	95.00%	S.DLVQHFESLAQ.E		K.EISQSINSANNIQSSDSDLVQHFESLAQEIR.H
340	348	3	1109.6	-0.18	0	20.7	25	95.00%	K.LFHNLNQPK.L		K.LFHNLNQPK.L
349	358	2	1129.68	0.16	1	52	20	95.00%	K.LLSDVLVFPK.F		K.LLSDVLVFPK.F

51	65	2	1590.75	-0.88	0	65.4	29.8	95.00%	K.EISQSINSANNIQSS.D		K.EISQSINSANNIQSSDSDLVQHFESLAQEIR.H
118	129	3	1407.69	0.72	1	30.8	29.5	95.00%	R.IAMTFPYDSHVK.F		R.IAMTFPYDSHVK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
87	EF3A_YEAST	11.11%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	44	2	1442.7	-1.2	1	43.4	29	95.00%	S.EVASFLNGNIIEH.D	Deamidation (+1)	R.HEIASEVASFLNGNIIEHDVPEHFFGELAK.G
708	723	2	1613.89	-1.1	1	33.7	23.2	95.00%	K.STLINVLTGELLPTSG.E		K.STLINVLTGELLPTSGEVYTHENCR.I
829	842	2	1700.81	-1.8	1	42.9	29.1	95.00%	R.WVPMMSVDNAWIPR.G		R.WVPMMSVDNAWIPR.G
971	987	3	1737.8	-0.45	0	64.7	30	95.00%	R.MTPSGHNWVSGQGAGPR.I		R.MTPSGHNWVSGQGAGPR.I
686	696	2	1325.6	-1.2	0	64.9	31.2	95.00%	T.DINFQCSLSSR.I	Carbamidomethyl (+57)	K.VTNMEFQYPGTSKPQITDINFQCSLSSR.I
510	520	2	1184.57	-1.2	1	42.1	29.5	95.00%	L.DFVFESGVGTK.E		R.TVYVEHDIDGTHSDTSVLDFVFESGVGTK.E
279	289	2	1183.66	-0.95	0	50.7	24.3	95.00%	E.DPQVIAPFLGK.L		K.LVEDPQVIAPFLGK.L
266	275	2	1149.56	2.9	1	47	30.2	95.00%	K.SAVIIDNMCK.L	Carbamidomethyl (+57)	K.SAVIIDNMCK.L
813	825	2	1496.7	-0.86	1	33.6	29.4	95.00%	Y.ECSFLLGENIGMK.S	Carbamidomethyl (+57)	K.NTYEYECSFLLGENIGMK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
88	A6ZVM2_YEAS7	10.86%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
314	325	2	1292.68	-0.86	1	78.3	26.9	95.00%	K.HADANVQLVAQK.M		K.HADANVQLVAQK.M
48	63	2	1913.91	-0.05	0	74.6	28.7	95.00%	R.SWMPSVSVYQTAFQQR.E		R.SWMPSVSVYQTAFQQR.E
354	370	2	1965.97	-1.7	1	85.7	28	95.00%	L.ETQITEWFTTALTNSPK.D		K.EPITWLETQITEWFTTALTNSPK.D
326	338	2	1420.65	-1.5	0	60.9	30.2	95.00%	K.MQQITSSQPTPTS.E	Oxidation (+16)	K.MQQITSSQPTPTSELSSAQR.D
152	165	2	1411.68	-0.86	0	52.2	30.3	95.00%	V.DMSTSLYAAGLAGR.S		R.SSSNVDMSTSLYAAGLAGR.S
876	885	2	1175.59	-1.5	0	28.1	29.1	94.50%	T.DFQRPTVNTV.D		R.SIPWAHATDFQRPTVNTVDDR.S
196	204	2	1094.58	-0.25	0	39.6	27.4	95.00%	R.LSLLAYCQK.V	Carbamidomethyl (+57)	R.LSLLAYCQK.V
326	345	2	2176.04	0.14	1	114	27.5	95.00%	K.MQQITSSQPTPTSELSSAQR.D		K.MQQITSSQPTPTSELSSAQR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
89	B3LI54_YEAS1	11.49%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
222	240	3	1991.98	-0.45	0	41.9	28.2	95.00%	P.DHVPTVGSSFVGMSLFNAK.N		K.ELHPDHVPTVGSSFVGMSLFNAK.N
241	253	3	1328.66	-1	0	21.5	28.5	93.30%	K.NPAPMHGHVILGS.D		K.NPAPMHGHVILGSDHMPILVYQISPEETR.I
218	240	4	2468.22	0.38	1	21.6	26	95.00%	K.ELHPDHVPTVGSSFVGMSLFNAK.N		K.ELHPDHVPTVGSSFVGMSLFNAK.N
314	323	2	1118.55	0.16	0	34.8	29.8	95.00%	R.AMPNSYLPAR.Q		R.AMPNSYLPAR.Q
159	169	2	1241.64	-0.34	1	47.5	28	95.00%	R.NITAQEPNVTR.V		R.NITAQEPNVTR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
90	YO092_YEAST	13.64%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
124	138	2	1720.88	-0.7	1	63	26.2	95.00%	N.EQQPLLNSQGQPNRI.D		K.SSDGLSLLFVVLWLAGDVFNLMGAVMQHLLSTMIILAAYYTVADIILLGQCLWYDNEEKPAVDPIHLSPANPINENVLHDVFNEQQPLLNSQGQPNRIDEEMAAPSSDGNAGDDNLR.E

103	119	2	1878.96	-0.92	1	43.2	26.6	95.00%	V.DPIHLSPANPINENVLH.D		K.SSDGLSLLFVVLWLAGDVFNLMGAVMQHLLSTMIILAAYYTVADIILLGQCLWYDNEEKPAVDPIHLSPANPINENVLHDVFNEQQPLLNSQGQPNR.I
1	10	2	1211.67	0.23	1	30.4	24.1	95.00%	-.MQLVPLELNR.S		-.MQLVPLELNR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
91	B5VDM9_YEAST	15.32%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
189	202	2	1628.77	-1.7	1	28	29.8	93.50%	K.EVSNEMVKPYIFSS.D		K.EVSNEMVKPYIFSSDPVLEAYLIK.A
167	188	2	2226.01	-0.64	1	89.7	29.2	95.00%	R.SNAHLSSPTNGAENTQSNTPAK.E	Deamidation (+1)	R.SNAHLSSPTNGAENTQSNTPAK.E
193	202	2	1199.59	-1.5	0	26	29.2	91.00%	N.EMVKPYIFSS.D		K.EVSNEMVKPYIFSSDPVLEAYLIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
92	A6ZLH4_YEAS7	13.48%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1069	1084	2	1708.9	0.34	1	38.6	24.9	95.00%	S.DLIFSTLPVPALGTHE.D		K.SSDLIFSTLPVPALGTHEDHDASLQYVEDLDIWLEGLPPCMLINSQTMTVTTAL.-
127	136	2	1073.5	0.37	0	54.1	29.7	95.00%	R.GGGAYYMISR.S		R.GGGAYYMISR.S
735	746	2	1437.7	-0.33	1	34.9	28.8	95.00%	K.TIDLYPIQMCGK.V	Carbamidomethyl (+57)	K.TIDLYPIQMCGK.V
5	31	3	2878.42	-0.52	1	62.3	26.4	95.00%	R.FYQIPGTHRPSSAISSSNESSSLLSAR.R		R.FYQIPGTHRPSSAISSSNESSSLLSAR.R
964	981	2	2003.04	-2.1	0	38.3	24.7	95.00%	S.DVSTQSLRPVFSSNTLPR.T		K.NLQSDVSTQSLRPVFSSNTLPR.T
704	719	3	1743.9	-0.85	0	32	26.4	95.00%	E.DLSLMQSNIAIAHGFK.N		K.VNVQQWVQIVEDLSLMQSNIAIAHGFK.N
1047	1058	2	1306.69	-1.1	0	41.2	28	95.00%	N.DLPSTAQHLVLN.D		K.DSLVTAMQNLGFNDLPSTAQHLVLNDVMTQMSK.S
33	48	2	1976.89	-1.5	1	73.4	29.8	95.00%	R.ISQTYFNYQATPECQK.V	Carbamidomethyl (+57)	R.ISQTYFNYQATPECQK.V
1034	1046	2	1408.66	-1.1	0	46.7	30.2	95.00%	K.DSLVTAMQNLGFN.D		K.DSLVTAMQNLGFNDLPSTAQHLVLNDVMTQMSK.S
869	879	2	1233.66	-0.018	1	29.6	26.9	95.00%	R.FSTIEPQTIAK.Q		R.FSTIEPQTIAK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
93	G3P3_YEAST	13.25%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
79	90	2	1255.58	-0.57	0	46.9	30.5	95.00%	R.DPANLPWGSSNV.D		R.DPANLPWGSSNVDIAIDSTGVFK.E
144	160	2	1818.89	-1.8	0	67.6	28	95.00%	K.IVSNASCTTNCLAPLAK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.IVSNASCTTNCLAPLAK.V
199	213	2	1373.71	-0.23	0	53.4	27.9	95.00%	R.TASGNIIPSSTGAAK.A		R.TASGNIIPSSTGAAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
94	A6ZX41_YEAS7	41.63%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
129	137	2	1098.57	-1.2	1	43.9	27.9	95.00%	N.DPQTIEQLR.Q		R.NDPQTIEQLR.Q
2	10	2	1029.52	2.1	0	26	28.7	91.90%	M.SQQVGNSIR.R	Acetyl (+42)	-.MSQQVGNSIR.R
104	123	3	2338.23	-0.74	1	25.6	22.4	95.00%	K.WIAEVLHFCQGVPIILVGCK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.WIAEVLHFCQGVPIILVGCK.V
139	153	2	1543.71	-1.6	1	46.7	30	95.00%	Q.EGQQPVTSQEGQSVA.D		R.QEGQQPVTSQEGQSVADQIGATGYYECSAK.T
174	181	2	921.46	1.4	1	32.1	30.1	95.00%	R.EVFEAATR.A		R.EVFEAATR.A
154	167	2	1561.67	-1.6	1	90	31.3	95.00%	A.DQIGATGYYECSAK.T	Carbamidomethyl (+57)	R.QEGQQPVTSQEGQSVADQIGATGYYECSAK.T

33	44	2	1381.69	-0.45	1	35.1	29.1	95.00%	K.GQFPEVYVPTVF.E		K.GQFPEVYVPTVFENYVADVEVDGR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
95	A6ZXE6_YEAS7	8.78%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
89	102	2	1397.76	-1.4	1	41.3	24.5	95.00%	R.TGKPLSVELGPGLM.E		R.TGKPLSVELGPGLMETIYDGIQRPLK.A
208	219	3	1520.74	-0.063	1	27.7	29.5	95.00%	K.SDFTLYHTWPVR.V		K.SDFTLYHTWPVR.V
2	9	2	842.43	0.47	1	41.8	27.7	95.00%	M.AGAIENAR.K	Acetyl (+42)	-.MAGAIENAR.K
356	367	3	1445.71	0.37	1	26.1	29.2	95.00%	K.FTCNATHELVVR.T	Carbamidomethyl (+57)	K.FTCNATHELVVR.T
446	455	2	1095.6	-0.29	0	48.3	25.2	95.00%	R.DLSLLGSHVR.K		R.DLSLLGSHVR.K
242	263	2	2312.03	-2.5	0	70.4	28.8	95.00%	L.DALFPCVQGGTTCIPGAFGCGK.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VLDALFPCVQGGTTCIPGAFGCGK.T
769	784	3	1716.89	-1.4	1	36.5	27.2	95.00%	K.RTTLVANTSNMPVAAR.E	Oxidation (+16)	K.RTTLVANTSNMPVAAR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
96	A7A0E5_YEAS7	10.28%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
353	383	3	3463.62	-0.75	1	111	25.8	95.00%	K.NQALGGSLLHSHIQTYPDGSNQQQVTCYGYK.D	Carbamidomethyl (+57)	K.NQALGGSLLHSHIQTYPDGSNQQQVTCYGYK.D
426	438	3	1369.75	0.44	0	27	24.9	95.00%	R.NLHTHPVAAPVSK.T		R.NLHTHPVAAPVSK.T
353	369	2	1834.93	-1	0	54.5	26.2	95.00%	K.NQALGGSLLHSHIQTYP.D		K.NQALGGSLLHSHIQTYPDGSNQQQVTCYGYK.D
384	393	2	1311.56	-0.11	1	42.3	30.1	95.00%	K.DANNEWFFNR.E		K.DANNEWFFNR.E
341	352	2	1187.68	-0.34	0	45.5	23.6	95.00%	R.DIALGSSVVSIK.N		R.DIALGSSVVSIK.N
406	417	2	1440.72	-2.2	1	34.4	28.1	95.00%	T.DIEYLKPGTSYR.L		R.GLPSWSENETDIEYLKPGTSYR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
97	A6ZZE8_YEAS7	8.51%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
403	413	2	1275.62	-0.94	0	62.2	29.7	95.00%	R.HIPYVTQGQSF.D		R.HIPYVTQGQSFDDEISLGGFSK.V
347	364	2	2067.93	-1.2	0	51.8	29.1	95.00%	T.ENYSPCVGTPISQAHFYV.D	Carbamidomethyl (+57)	R.NPFSTDSENYISTCTENYSPCVGTPISQAHFYVDYR.I
403	414	2	1390.65	-1	1	42.3	30.4	95.00%	R.HIPYVTQGQSFD.D		R.HIPYVTQGQSFDDEISLGGFSK.V
415	424	2	1051.52	-0.12	1	48.1	29.1	95.00%	D.DEISLGGFSK.V		R.HIPYVTQGQSFDDEISLGGFSK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
98	A6ZLU9_YEAS7	16.26%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
313	325	2	1424.67	0.13	1	30.7	30.2	95.00%	K.DFGQVIGQGFSDR.H		K.DFGQVIGQGFSDR.H
402	410	2	1108.45	-1.4	1	29	29.8	94.80%	Y.DLNSWMESQ.E		K.NYDVIVPNVWRPLPTFLGTEQPYDLNSWMESQEALALAK.T
381	401	2	2440.28	-1.6	1	36.1	22.8	95.00%	Y.DVIVPNVWRPLPTFLGTEQPY.D		K.NYDVIVPNVWRPLPTFLGTEQPYDLNSWMESQEALALAK.T
15	26	2	1272.65	-0.57	1	38	28.7	95.00%	K.AMDNGLSLPISR.N		K.AMDNGLSLPISR.N
201	211	2	1217.65	0.22	1	35.4	27.5	95.00%	R.NAADVLPLMFK.H		R.NAADVLPLMFK.H
456	466	2	1014.57	-1.1	0	38.5	28	95.00%	L.DGVGGVSILAK.A		R.DAEGDPNEAVDLDGVGGVSILAK.A
191	200	2	1248.7	0.41	0	24.9	23.5	95.00%	R.DHILLCIPLR.N	Carbamidomethyl (+57)	R.DHILLCIPLR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
99	A6ZNY0_YEAS7	11.88%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

93	103	2	1205.63	-0.93	1	27.7	27.8	95.00%	K.TDGNSFLINLI.D		K.TDGNSFLINLIDSPGHVDFSSEVTAALR.V
799	809	2	1226.56	-1.1	1	34.8	30.5	95.00%	F.DHWSTLGSDPL.D		R.QATGGQAFPQMVFDHWSTLGSDPLDPTSK.A
2	10	2	1065.53	1	1	38.7	29.2	95.00%	M.VAFTVDQMR.S		-.MVAFTVDQMR.S
244	253	2	1209.58	0.055	1	34.4	30.7	95.00%	R.LWGDSFFNPK.T		R.LWGDSFFNPK.T
151	160	3	1107.74	-0.26	1	32.5	10.8	95.00%	R.IKPVVVINKV.D		R.IKPVVVINKVDR.A
712	723	2	1265.66	-3.6	1	53.3	27.8	95.00%	R.ATYAGFLLADPK.I		R.ATYAGFLLADPK.I
446	459	2	1412.7	-0.49	1	34.3	28.6	95.00%	I.DDCPAGNIIGLVGI.D	Carbamidomethyl (+57)	R.FVEPIDDCPAGNIIGLVGIDQFLLK.T
33	42	2	1118.59	0.17	1	40.3	27.9	95.00%	K.STLTDSLVQR.A		K.STLTDSLVQR.A
757	769	2	1500.79	-2.2	1	31.6	26	95.00%	S.EEQRPGTPLFTVK.A		R.GQVVSEEQRPGTPLFTVK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
100	A6ZYN3_YEAS7	7.61%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
252	260	2	1056.57	-0.6	0	27	26.8	95.00%	D.DPLPFKPLM.D		R.IFPPIDDPLPFKPLMDDSDVTLEEAVTHQR.I
49	61	2	1502.74	-0.94	1	48.7	28.8	95.00%	N.DLTISHPYATTER.V		R.QFYINDLTISHPYATTER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
101	A6ZNV4_YEAS7	22.97%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
143	152	2	1137.55	-1.4	1	61.9	30.6	95.00%	Q.DPESSYISIK.V		R.QDPESSYISIK.V
187	196	2	1285.64	-2	1	61.8	29.4	95.00%	L.DFQTIIHQER.S		K.VNEQSPLLHNEGQHQLQLQEEQEQQQQGLSQEELDFQTIIHQER.S
13	26	2	1591.72	0.94	1	72.6	30.5	95.00%	K.GNSQQEPQFSTNQK.T		K.GNSQQEPQFSTNQK.T
102	112	2	1413.66	-0.41	0	69.7	30.1	95.00%	K.YQSLQQSYNQR.K		K.YQSLQQSYNQR.K
203	222	3	2203.21	0.28	1	67.6	18.6	95.00%	R.IHTAVQEVNAIFHQLGSLVK.E		R.IHTAVQEVNAIFHQLGSLVK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
102	A6ZXE9_YEAS7	11.92%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
236	245	2	1043.56	-0.78	1	39.5	26.6	95.00%	I.DVSVLGIGER.N		R.LIDVSVLGIGER.N
216	233	2	1809.83	-1.5	1	110	29.3	95.00%	N.DTGCAIANAYTALEGGAR.L	Carbamidomethyl (+57)	K.SVVSCDIECHFHNDTGCAIANAYTALEGGAR.L
258	267	2	1105.58	0.35	1	25.2	28.7	90.50%	R.MIVAAPDYVK.S		R.MIVAAPDYVK.S
180	192	2	1328.65	-0.6	1	78	30	95.00%	R.VGIADTVGCANPR.Q	Carbamidomethyl (+57)	R.VGIADTVGCANPR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
103	A7A077_YEAS7	14.13%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
257	270	2	1602.84	0.24	1	59.1	26.8	95.00%	R.GSVPIYWAEINNLK.Y		R.GSVPIYWAEINNLK.Y
446	459	2	1337.68	-1.1	0	62.1	28.2	95.00%	A.DAVSVAYSGTGALK.T		K.EFESADVVATGSTWEDNAPLLTSYQNLWADNADAVSVAYSGTGALK.T
429	442	2	1604.78	-1.2	0	27.7	28.9	94.30%	E.DNAPLLTSYQNLWA.D		K.EFESADVVATGSTWEDNAPLLTSYQNLWADNADAVSVAYSGTGALK.T
399	413	2	1711.96	-1.5	0	59.1	21.6	95.00%	R.TNVVQSVLAQWVLQK.E		R.TNVVQSVLAQWVLQK.E
298	308	2	1318.69	-0.84	0	35.5	28.9	95.00%	G.DNYLVNLVNQK.G		K.ELYGDNYLVNLVNQK.G
397	413	3	1983.09	-0.69	1	28.9	22.3	95.00%	L.DRTNVVQSVLAQWVLQK.E		R.TNCMDCLDRTNVVQSVLAQWVLQK.E
294	308	2	1780.9	-0.34	1	61.6	27.6	95.00%	K.ELYGDNYLVNLVNQK.G		K.ELYGDNYLVNLVNQK.G
175	188	2	1612.85	-0.38	1	55.1	26.2	95.00%	R.IDSFIQPVIYGYAK.T		R.IDSFIQPVIYGYAK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
104	GLRX7_YEAST	11.82%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
154	165	2	1212.68	-0.76	0	73.1	25.1	95.00%	R.TVPNVIIGGTSR.G		R.TVPNVIIGGTSR.G
94	105	2	1424.7	-0.58	1	69.7	29.1	95.00%	K.IMEQSPMIVFSK.T	Oxidation (+16)	K.IMEQSPMIVFSK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
105	B3LGY9_YEAS1	3.06%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
472	482	2	1322.55	-0.74	0	34.9	30.9	95.00%	R.HAMTGCYLFSH.E	Carbamidomethyl (+57)	R.HAMTGCYLFSHEVK.L
326	336	2	1128.65	-0.9	0	68.5	24.4	95.00%	A.DVGIGSIISLR.H		K.IPQNVVADVGIGSIISLR.H
472	485	3	1678.76	-0.033	1	31.3	30.5	95.00%	R.HAMTGCYLFSHEVK.L	Carbamidomethyl (+57)	R.HAMTGCYLFSHEVK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
106	A6ZMQ9_YEAS7	16.59%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
115	129	2	1790.97	-2.2	1	64	22.9	95.00%	D.DQRQQLLSNHAILQK.S		R.LFGDLNASNIDDDQRQQLLSNHAILQK.S
89	95	2	811.49	-1	0	23.1	19.9	93.30%	K.RPLQSLV.D		K.RPLQSLVDSGDR.D
118	129	2	1391.79	-0.72	0	46.3	21.5	95.00%	R.QQLLSNHAILQK.S		R.QQLLSNHAILQK.S
21	34	2	1453.75	-0.49	1	51.8	27.4	95.00%	K.ASLAEAPSQPLSQR.N		K.ASLAEAPSQPLSQR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
107	A6ZXZ5_YEAS7	17.50%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
95	110	3	1943.93	2	1	36.4	28.8	95.00%	K.YNHVQTSTQKEHPGYR.Q		K.YNHVQTSTQKEHPGYR.Q
268	275	2	876.41	-1.2	0	29.5	29.9	95.00%	K.LGYHFGPS.D		K.LGYHFGPSDAEAVMAPK.A
285	300	2	1575.87	-1.5	0	59.3	22	95.00%	K.APVASPRPAATPNLSK.D		K.APVASPRPAATPNLSK.D
18	31	2	1524.77	-0.55	1	71.2	28.4	95.00%	K.INPPTGADFHITSR.G		K.INPPTGADFHITSR.G
285	302	3	1818.99	-0.28	1	22.7	23.1	95.00%	K.APVASPRPAATPNLSKDK.K		K.APVASPRPAATPNLSKDK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
108	A6ZNH7_YEAS7	13.43%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	206	2	1572.83	-0.64	1	82.2	26.2	95.00%	R.QIPVGYSAADIVANR.Q		R.QIPVGYSAADIVANR.Q
253	269	2	1987.93	-0.79	1	70.1	29.8	95.00%	Q.DYSVPVFLSEFGCNQVK.S	Carbamidomethyl (+57)	K.LYQDYSVPVFLSEFGCNQVK.S
134	143	2	1182.59	-0.77	0	27.5	29	93.90%	A.DYLQNVFATI.D		R.YDPACSYNADYLQNVFATIDTFADYDNVLGFFAGNEVINSVNTTNTATYVK.A
236	247	2	1289.61	-1.9	0	54.1	29.4	95.00%	G.ESSFVVSGYSTK.M		R.IDMFGVNDYSWCGESSFVVSGYSTK.M
114	124	2	1159.58	-0.79	0	29.9	29	95.00%	L.DVNTPTSAISR.Y		K.LLQENGIYLILDVNTPTSAISR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
109	RL20_YEAST	19.19%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	12	3	1346.71	0.078	1	29.9	27	95.00%	M.AHFKEYQVIGR.R		-.MAHFKEYQVIGR.R
29	38	2	1090.6	-0.39	1	57.7	26.1	95.00%	R.IFASNEVIAK.S		R.IFASNEVIAK.S
54	65	2	1243.64	-1.3	1	33.7	28	95.00%	K.ASGEIVSINQIN.E		K.ASGEIVSINQINEAHPTK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
110	A7A1W6_YEAS7	22.32%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
248	260	2	1471.78	-1.4	0	28.8	26.4	95.00%	K.LYPLATFHLAQAQ.D		K.LYPLATFHLAQAQDFEGVR.A
9	18	2	1105.54	-0.58	1	70.1	29.4	95.00%	I.DNGFIEGVVR.G	Deamidation (+1)	-.MEGVYFNIDNGFIEGVVR.G
322	335	2	1715.84	-0.46	1	69.2	28.8	95.00%	R.NITWIAECIAQNQR.E	Carbamidomethyl (+57)	R.NITWIAECIAQNQR.E
220	231	2	1245.65	-1.4	0	86.3	28.5	95.00%	R.SINIALNSLQSS.D		R.SINIALNSLQSSDIDPDLK.S
267	276	2	1168.59	-0.44	1	57.4	29	95.00%	R.AALANVYEYR.G		R.AALANVYEYR.G
19	36	2	2128	-1.6	1	126	29.3	95.00%	R.GYRNGLLSNNQYINLTQC.D	Deamidation (+1)/ Carbamidomethyl (+57)	R.GYRNGLLSNNQYINLTQCDTLEDLK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
111	A6ZM72_YEAS7	9.61%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
296	309	2	1492.73	-0.69	1	87.2	29.8	95.00%	R.LAGNASWGELFSNK.G		R.LAGNASWGELFSNK.G
9	26	3	1924.98	-1.9	1	51.5	26.1	95.00%	R.VESGSQQTSIHSTPIVQK.L		R.VESGSQQTSIHSTPIVQK.L
219	227	2	1153.52	0.77	0	47.9	30.8	95.00%	K.DYSNSVQWR.V		K.DYSNSVQWR.V
517	527	2	1364.68	-0.67	1	60.8	28.8	95.00%	N.EMYVEGVKPWK.S		K.GLTLEEVNEMYVEGVKPWK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
112	B3LKQ2_YEAS1	12.01%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
233	255	3	2643.24	-1.1	1	55.8	28.4	95.00%	N.EENFNPMSHNGQLNNIPVIYANK.A	Deamidation (+1)	K.DDTEGFDIPLNEENFNPMSHNGQLNNIPVIYANK.A
547	569	2	2484.28	-0.93	0	65.3	24.1	95.00%	G.DWTPYLAQGIPVAIISSPGVMNR.E		K.VDNVHQFGDWTPYLAQGIPVAIISSPGVMNR.E
164	179	2	1710.72	-0.94	1	45.8	30.7	95.00%	R.DLEYISSMPHMSGTSG.D		R.DLEYISSMPHMSGTSGDAAIR.H
420	427	2	809.51	0.58	0	23	16.7	93.20%	R.AIVIAAPR.N		R.AIVIAAPR.N
146	153	2	990.55	-0.92	0	32.9	26.2	95.00%	H.DLLLQYAR.K		R.GSNGSFSDHDLLLQYAR.K
282	297	2	1890.88	-2.2	1	33.6	29.3	95.00%	G.DYVFQQMLTAQEYGAK.A		K.ASLDDMASMQDQGLLNGDFILLVHYGDYVFQQMLTAQEYGAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
113	NCB5R_YEAST	25.00%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
220	230	2	1195.59	-0.59	0	37.3	29.9	95.00%	E.DWTGGVGYITK.D		R.EDWTGGVGYITK.D
195	208	2	1589.85	-0.27	1	40	25.6	95.00%	K.ELEALVAMKPSQFK.I		K.ELEALVAMKPSQFK.I
49	59	2	1307.65	-0.0036	0	57	29.5	95.00%	K.TILTHNTSMYK.F		K.TILTHNTSMYK.F
147	166	2	2075.04	-0.72	0	51.6	27	95.00%	R.SHLGMIAGGTGIAPMYQIMK.A		R.SHLGMIAGGTGIAPMYQIMK.A
66	80	2	1615.93	-1.9	1	44	19.6	95.00%	A.DDVLGLPIGQHIVIK.A		K.FGLPHADDVLGLPIGQHIVIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
114	A6ZP92_YEAS7	9.35%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
199	212	2	1434.72	-2	0	77.4	28.5	95.00%	P.DGPQSTSHGIALPR.F		K.YGHPDGPQSTSHGIALPR.F
494	508	2	1737.91	-0.42	0	31.7	25.8	95.00%	K.QPLVPYSFAPFFPTK.R		K.QPLVPYSFAPFFPTK.R
511	521	2	1310.57	-0.56	0	35.3	30.4	95.00%	R.GSWCCLVSSQK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GSWCCLVSSQK.D
486	493	2	925.4	-1.5	0	28.3	30.2	93.30%	R.DPFAMMSK.Q		R.DPFAMMSK.Q
195	212	4	1888.92	0.76	1	23.8	28.3	95.00%	K.YGHPDGPQSTSHGIALPR.F		K.YGHPDGPQSTSHGIALPR.F
525	534	2	1166.73	2.5	1	25.6	12	95.00%	K.ILQTPIIIEK.L		K.ILQTPIIIEK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
115	A6ZLM5_YEAS7	12.18%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
179	196	2	2037.95	-2.2	1	56.4	29.1	95.00%	K.WSGENTQHMPPSQVQSLL.E		K.WSGENTQHMPPSQVQSLLER.T
225	238	2	1458.66	-0.97	1	107	30.3	95.00%	R.MNSSFLSSSSIGDK.I		R.MNSSFLSSSSIGDK.I
327	335	2	940.61	0.51	0	44.5	18.8	95.00%	K.LLIGSIIGR.M		K.LLIGSIIGR.M
51	61	2	1339.68	-1	0	34.7	27.8	95.00%	V.DLFTPCLIFSK.L	Carbamidomethyl (+57)	K.IISLLNVDLFTPCLIFSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
116	AVT7_YEAST	11.02%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
17	31	2	1536.85	-1.2	0	56.9	22	95.00%	K.TIVGAGTLAIPYSFK.S		K.TIVGAGTLAIPYSFK.S
321	332	2	1316.67	-1.1	1	38.4	28.5	95.00%	R.ASNLRPISMTVE.D		R.ASNLRPISMTVEDPAQPSDALDATSYNEQECLLPNGNFDNGSIESQENNNDER.G
441	451	2	1098.67	0.26	1	49.5	21.6	95.00%	K.LIGLDSLAIGK.M		K.LIGLDSLAIGK.M

1	16	2	1650.81	-1.1	1	82.5	28.6	95.00%	-.MEATSSALSSTANLVK.T	Acetyl (+42)	-.MEATSSALSSTANLVK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
117	AXL2_YEAST	11.30%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
730	740	2	1191.61	-0.093	0	33.6	29	95.00%	K.SVTPSPYNVTK.H		K.SVTPSPYNVTK.H
630	645	2	1794.95	-2.7	1	27.6	25.5	95.00%	E.ELLAKPPVQPPESPFF.D		K.EELLAKPPVQPPESPFFDPQNR.S
174	183	2	1201.56	-1.2	1	38.1	30.3	95.00%	N.EESIVSYYGR.S		R.SMFTNEESIVSYYGR.S
751	769	2	1901.82	-0.49	1	71.1	30.2	95.00%	Q.DSQSGKNGITPTTMSTSSS.D	Deamidation (+1)/ Oxidation (+16)	R.HLQNIQDSQSGKNGITPTTMSTSSSDDFVPVK.D
716	729	2	1595.8	-1	1	53.1	28.6	95.00%	L.DPWNSNISPSPVRK.S		R.DVTMSSLDPWNSNISPSPVRK.S
585	593	2	955.61	-0.75	1	31	18.9	95.00%	R.LAALNTLKL.D		R.LAALNTLKLDNHSATESDISSVDEK.R
184	197	2	1708.86	1.3	0	32.7	28	95.00%	R.SQLYNAPLPNWLFF.D		R.SQLYNAPLPNWLFFDSGELK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
118	A6ZX57_YEAS7	28.46%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	65	2	1242.61	-1.4	0	51	29.6	95.00%	V.DALAHQGYNVR.I		K.TELIFVDDNSQDGSVEEVDALAHQGYNVR.I
200	212	2	1390.76	-0.38	1	36.1	24.4	95.00%	R.VAIGEVPFTFGVR.T		R.VAIGEVPFTFGVR.T
156	166	2	1225.58	-1.1	0	43.3	30.6	95.00%	S.DPMSGFFGLQK.K		R.MMARPLTIASDPMSGFFGLQK.K
146	166	3	2297.14	0.088	1	41	27.4	95.00%	R.MMARPLTIASDPMSGFFGLQK.K		R.MMARPLTIASDPMSGFFGLQK.K
16	24	3	1054.65	-0.29	0	33.5	17.2	95.00%	K.LNIKPLTTR.L		K.LNIKPLTTR.L
25	35	2	1180.56	0.23	1	39.4	30.8	95.00%	R.LFAGMSPEMAK.K		R.LFAGMSPEMAK.K
97	107	2	1259.65	-2.4	1	27.4	28.1	94.90%	A.DLQHPPETVPK.L		K.GQYLVCMDADLQHPPETVPK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
119	VDAC1_YEAST	37.81%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
96	108	2	1341.75	-0.69	1	61.7	24.3	95.00%	K.NELITSLTPGVAK.S		K.NELITSLTPGVAK.S
51	61	2	1129.56	0.33	1	26.2	29.3	91.20%	K.DGPLSTNVEAK.L		K.DGPLSTNVEAK.L
109	124	2	1799.92	-1.2	0	64.5	26.8	95.00%	K.SAVLNTTFTQPFFTAR.G		K.SAVLNTTFTQPFFTAR.G
165	174	2	1163.57	0.5	0	49.9	29.1	95.00%	R.YAMALSYFAK.D		R.YAMALSYFAK.D
66	84	2	2060.03	-0.72	0	87	26.5	95.00%	K.QTGLGLTQGWSNTNNLQTK.L		K.QTGLGLTQGWSNTNNLQTK.L
191	205	2	1696.86	-1.3	0	62.3	27.6	95.00%	V.DFFQNVNAFLQVGAK.A		K.DYSLGATLNNEQITTVDFFQNVNAFLQVGAK.A
85	95	2	1201.67	-0.52	1	34.6	24.5	95.00%	K.LEFANLTPGLK.N		K.LEFANLTPGLK.N
237	248	2	1251.67	-0.084	1	78.6	26.4	95.00%	K.VSDSGIVTLAYK.Q		K.VSDSGIVTLAYK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
120	HSP76_YEAST	11.75%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
174	191	2	1728.94	-0.94	1	84.5	23.6	95.00%	R.IINEPTAAAIAYGLGAGK.S		R.IINEPTAAAIAYGLGAGK.S
437	451	2	1780.84	-0.96	1	55.3	29.1	95.00%	S.DNQTTVQFPVYQGER.V		R.TFTTVSDNQTTVQFPVYQGER.V
502	513	2	1217.64	-0.59	0	69.6	28.8	95.00%	K.SSNITISNAVGR.L		K.SSNITISNAVGR.L
144	157	2	1563.8	-1.2	1	27.2	27.8	95.00%	K.AVITVPAYFNDAQR.Q		K.AVITVPAYFNDAQR.Q
39	51	2	1478.74	-2.3	1	34.5	29.2	95.00%	R.VTPSFVAFTPQER.L	Deamidation (+1)	R.VTPSFVAFTPQER.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
121	A6ZQU5_YEAS7	8.84%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
75	85	2	1305.73	0.74	1	40.3	23.7	95.00%	R.LFDNIIVFPTK.G		R.LFDNIIVFPTK.G
77	85	2	1045.58	-1.1	0	41.1	26.5	95.00%	F.DNIIVFPTK.G		R.LFDNIIVFPTK.G

77	88	2	1287.72	-2.1	1	26.4	25.9	95.00%	F.DNIIVFPTKGGK.N		R.LFDNIIVFPTKGGK.N
186	196	2	1248.72	-0.58	0	48.6	22.3	95.00%	R.EQIVPILNAPR.T		R.EQIVPILNAPR.T
149	161	2	1480.79	-1.7	1	39.5	26.6	95.00%	S.EELVVSSNHLLNK.Y		R.DYFSPSSEELVVSSNHLLNK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
122	B3LTD0_YEAS1	10.94%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
33	43	2	1157.62	2.7	0	41	27.7	95.00%	K.NFGIGQAVQPK.R		K.NFGIGQAVQPK.R
194	204	2	1116.61	-0.56	1	64.5	27.1	95.00%	K.TSAVAALTEVR.A		K.TSAVAALTEVR.A
52	57	2	848.42	-0.5	1	29.6	28	95.00%	K.WPEYVR.L		K.WPEYVR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
123	A6ZMK1_YEAS7	12.06%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
46	59	3	1614.01	0.8	1	23.1	10.4	95.00%	K.IAPRPLDLLRPVVR.A		K.IAPRPLDLLRPVVR.A
82	91	2	963.52	1.5	0	28.5	26.9	95.00%	K.AAGLTAAYAR.T		K.AAGLTAAYAR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
124	YIP8_YEAST	38.24%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
101	112	3	1314.71	-0.15	0	42	26.8	95.00%	R.QLNASMGTLRPK.K		R.QLNASMGTLRPK.K
137	150	2	1675.79	-0.007	0	71.1	30.2	95.00%	R.DPSYSFMYPLTLSR.K		R.DPSYSFMYPLTLSR.K
196	204	2	1112.56	-0.12	1	39.8	28	95.00%	R.EFIDSLRPH.-		R.EFIDSLRPH.-
158	174	2	1705.77	-1	1	97.1	30.6	95.00%	R.SASTSNLSSSTENTALH.E		R.SASTSNLSSSTENTALHEEIK.L
114	129	2	1739.87	-0.35	1	72.9	28.2	95.00%	K.QSTAYTNVPVIFSGEK.V		K.QSTAYTNVPVIFSGEK.V
186	195	2	1256.61	-1.7	1	39.2	29.4	95.00%	N.DFTNYTVNKR.E		K.LDDPYENDFTNYTVNKR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
125	A6ZZX2_YEAS7	31.32%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
136	149	2	1494.76	1.7	1	62.8	27.8	95.00%	R.TNTFTLLTSPDSAK.I		R.TNTFTLLTSPDSAK.I
111	135	3	2600.12	-0.62	1	86.4	28.9	95.00%	G.DDNLSGHSVPSSGSAQATTHQTAPR.T	Phospho (+80)	R.SAGDDNLSGHSVPSSGSAQATTHQTAPR.T
165	182	2	1987.04	-1.2	0	49.4	24.8	95.00%	N.EIFSQSQVNKPGPLTVPF.-		K.LHSNILNEIFSQSQVNKPGPLTVPF.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
126	A6ZQE5_YEAS7	39.13%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
33	42	2	1088.58	-1.4	1	39.6	29.1	95.00%	T.DLSGKETIAR.V		R.IYASFNDTFVHVTDLSGKETIAR.V
10	19	2	1091.54	0.44	0	47.3	29.7	95.00%	R.DNSQVFGVAR.I		R.DNSQVFGVAR.I
54	66	2	1352.59	-0.9	1	32.9	30.9	95.00%	R.DESSPYAAMLAAQ.D		R.DESSPYAAMLAAQDVAAK.C
94	104	2	1023.55	1.4	0	39	25.1	95.00%	K.TPGPGGQAALR.A		K.TPGPGGQAALR.A
74	83	2	1051.6	-0.21	0	23.1	21.4	93.20%	K.EVGITAVHVK.I		K.EVGITAVHVK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
127	A6ZY13_YEAS7	7.78%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
21	41	2	2286.1	-1.8	1	70.4	27.5	95.00%	T.DSALYNNFNTSTTASLTPEIK.E		K.SAEFEVTDSALYNNFNTSTTASLTPEIK.E
400	412	2	1465.71	-0.047	0	74.9	29.5	95.00%	R.LMCSLAQQGYAPK.F	Carbamidomethyl (+57)	R.LMCSLAQQGYAPK.F
269	281	2	1250.55	-0.67	1	65.6	30.3	95.00%	R.DPGSFAEGSGATR.F		R.DPGSFAEGSGATR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
128	A6ZNT8_YEAS7	5.04%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
176	190	2	1694.75	-1.2	0	65	30.9	95.00%	T.DMHCTTVIGSSGFQR.C	Carbamidomethyl (+57)	R.YVINENDEDQEPLNALELATDMHCTTVIGSSGFQR.C

125	133	2	1060.53	0.4	0	31.9	29.4	95.00%	R.NLASQQLCK.L	Carbamidomethyl (+57)	R.NLASQQLCK.L
471	480	2	1214.53	-1.3	1	34.5	31.1	95.00%	D.DEYMALMSQK.T		K.VIDNADDEYMALMSQK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
129	CHS3_YEAST	8.67%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
53	62	2	1281.58	-1.9	0	29.4	30.4	94.50%	P.DNPHFYYAQK.T		R.LNNPDNPHFYYAQK.T
919	929	2	1229.61	-0.75	0	26.3	29.1	91.80%	S.DGYWVPVLANP.D		K.GSDGYWVPVLANPDIVER.Y
720	735	2	1698.84	-1.9	1	49.1	27.9	95.00%	P.DEVKPYSYVAVASGSK.R		K.TTPEIALGMMDDFVTPPDEVKPYSYVAVASGSK.R
935	945	2	1290.62	-0.94	1	46.8	29.8	95.00%	R.YSDNVTNTLHK.K		R.YSDNVTNTLHK.K
598	612	2	1721.84	-1.9	0	58.7	27.8	95.00%	R.NPSTLLPTSSMFWNK.A		R.NPSTLLPTSSMFWNK.A
560	574	2	1607.67	-0.25	0	69.5	31.1	95.00%	L.DTSMSSSLQSSGSYR.G	Oxidation (+16)	K.MFQFNESVIDLDTSMSSSLQSSGSYR.G
575	586	2	1368.62	0.067	0	62.5	30.5	95.00%	R.GMTTMTTQNAWK.L		R.GMTTMTTQNAWK.L
686	696	2	1259.7	0.018	1	26.7	25.4	95.00%	K.LLMVVCDGLIK.G	Carbamidomethyl (+57)	K.LLMVVCDGLIK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
130	A6ZYM2_YEAS7	6.18%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
200	208	2	1072.52	-1.4	1	30.5	29.1	95.00%	S.DDMHTLTIK.Y		K.SIEISDDMHTLTIK.Y
768	778	2	1342.65	-1.7	0	36.4	29.9	95.00%	H.DSYATVQYLQR.N		K.HDSYATVQYLQR.N
81	100	2	2112.98	-1	0	101	28.8	95.00%	K.EGLLSVQGMTCGSCVSTVTK.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.EGLLSVQGMTCGSCVSTVTK.Q
71	80	2	1063.54	-1.1	1	48	29.9	95.00%	R.DSEITAISTK.E		R.DSEITAISTK.E
629	640	2	1253.67	0.71	0	23.5	26.2	92.10%	K.TGTLTTGFMVVK.K		K.TGTLTTGFMVVK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
131	A6ZU02_YEAS7	5.87%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
482	491	2	1122.64	0.52	0	48.8	23.4	95.00%	K.DAVTNIHLLK.R		K.DAVTNIHLLK.R
64	75	2	1262.59	-1.6	1	53	30.3	95.00%	V.DAMGVESTGIQR.I		K.VDAMGVESTGIQR.I
466	477	2	1228.63	-0.99	1	50	27.5	95.00%	G.EINGPELVGSSK.E		K.EFPTVTGEINGPELVGSSK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
132	A7A0Y7_YEAS7	7.65%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
141	156	2	1817.92	-0.018	1	84.4	27.1	95.00%	K.NGFFQNWLIDGLPAAR.E		K.NGFFQNWLIDGLPAAR.E
104	115	2	1466.72	-1.2	0	26.5	29.3	91.80%	R.IYNSPFQLNMLQ.E		R.IYNSPFQLNMLQEK.E
104	117	2	1723.86	-0.58	1	67.9	28.3	95.00%	R.IYNSPFQLNMLQEK.E		R.IYNSPFQLNMLQEK.E
214	222	2	1136.53	-0.2	0	40	30.1	95.00%	Y.ELPYFANHF.D		K.TYELPYFANHFDIMIEYHDR.G
238	249	2	1237.77	1.6	1	36.3	17.3	95.00%	R.VVGVIVEPVSIK.R		R.VVGVIVEPVSIK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
133	A6ZXW5_YEAS7	10.00%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
97	106	2	1235.59	0.89	1	35.7	29.7	95.00%	K.NQEVYSQVNR.I		K.NQEVYSQVNR.I
277	288	2	1252.71	-0.56	0	41	21.5	95.00%	K.LSISHAIAQSVK.I		K.LSISHAIAQSVK.I
12	32	3	2371.23	-0.5	1	35.1	23.7	95.00%	R.HALLHNDIQTSNNSRPSLVQK.K		R.HALLHNDIQTSNNSRPSLVQK.K
18	32	2	1685.87	-2.4	0	62.8	25.9	95.00%	N.DIQTSNNSRPSLVQK.K		R.HALLHNDIQTSNNSRPSLVQK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
134	A6ZQF7_YEAS7	22.83%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
31	43	2	1460.71	-0.44	1	52.3	28.8	95.00%	R.ETAQAINGWELTK.A	Deamidation (+1)	R.ETAQAINGWELTK.A
112	124	2	1495.81	-0.2	0	61.1	24.2	95.00%	K.LYVSHIQVNQAPK.Q		K.LYVSHIQVNQAPK.Q
90	105	2	1643.86	-0.8	1	85.7	25	95.00%	K.FVQGLLQNAAANAEAK.G		K.FVQGLLQNAAANAEAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
135	A7A0K9_YEAS7	12.50%	100%	6								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
444	456	2	1407.71	-1.6	0	61.7	28.8	95.00%	K.ATLINLNTSNNPH.D		K.ATLINLNTSNNPHDEMFK.V	
132	144	2	1426.69	-0.99	1	69	28.7	95.00%	E.DYGSIESLSTSIR.V		K.FSNISLEQYYSSLNNASSHALEDYGSIESLSTSIR.V	
551	566	2	1558.87	-0.72	0	65.6	22.2	95.00%	F.DHLLLLSGGTGLPGPL.D		K.FDHLLLLSGGTGLPGPLDHAIK.L	
671	684	2	1484.73	-1.6	0	25.1	28.2	91.30%	G.DSLAVVCCGPPVLV.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.STPPGDSLAVVCCGPPVLVDDVR.N	
534	547	2	1465.76	-0.83	1	73.8	27.2	95.00%	R.VAIEGPYGPSNLHL.D		R.VAIEGPYGPSNLHLDK.F	
29	47	3	2118.04	-1.1	1	64	27.3	95.00%	K.DHLESNAVLACASYINTLK.W	Carbamidomethyl (+57)	K.DHLESNAVLACASYINTLK.W	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
136	YL001_YEAST	13.46%	100%	7								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
485	496	2	1391.74	-0.3	1	26.8	25.8	95.00%	K.ELNLLDLPSNHK.G		K.ELNLLDLPSNHK.G	
551	563	2	1377.73	-0.14	0	82.3	27.2	95.00%	K.NLYGNSVSIGVQK.I		K.NLYGNSVSIGVQK.I	
801	844	4	4728.39	-1.5	1	27.5	24.1	95.00%	R.ATTPLIQHSPIIHNPSYSATAHLSPLSQPTFEGSYSVNAIQTPR.D		R.ATTPLIQHSPIIHNPSYSATAHLSPLSQPTFEGSYSVNAIQTPR.D	
302	312	2	1203.63	-0.52	1	41.9	28.3	95.00%	R.IFEIGVVHGFS.D		R.IFEIGVVHGFSDLDFLR.T	
523	530	2	930.53	-0.13	0	41.6	25.7	95.00%	K.TALNLLMR.N		K.TALNLLMR.N	
589	600	2	1398.73	-0.8	0	37.4	26.9	95.00%	S.DIFFNQGVIHPI.D		K.ESIIIEESSDIFFNQGVIHPIDQLDFPVDLEISLK.E	
390	405	2	1897.95	-1.4	0	35.9	27.2	95.00%	Q.DFSSLRPIQYAPTQIY.D		K.IDLEQDFSSLRPIQYAPTQIYDSAFCSSAK.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
137	EMP47_YEAST	13.03%	100%	5								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
221	227	2	812.38	0.95	0	26	29.1	91.30%	R.FPSGSYR.I		R.FPSGSYR.I	
173	184	2	1405.56	-1.2	0	29.9	31	94.50%	Y.DQSFASCLMGYQ.D	Carbamidomethyl (+57)	K.IYDQSFASCLMGYQDSSVPSTIR.V	
146	156	2	1153.57	-0.99	0	38.2	29.9	95.00%	V.DNNGPLGPTLR.G	Deamidation (+1)	K.QLYNGPVNYDGLQLLVDNNGPLGPTLR.G	
333	346	2	1637.87	0.36	1	84.1	24.6	95.00%	K.VQQELLSFMTTITK.Q		K.VQQELLSFMTTITK.Q	
228	241	2	1341.66	-1.9	0	53.5	29.3	95.00%	R.IGVTAQNGAVNNNA.E		R.IGVTAQNGAVNNNAESFEIFK.M	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
138	A6ZSQ1_YEAS7	24.64%	100%	3								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
56	74	2	2050.19	-0.35	0	115	15.3	95.00%	R.QAINLGQVVLTPLTFALPR.G		R.QAINLGQVVLTPLTFALPR.G	
118	124	2	891.5	0.21	0	27.3	26.9	95.00%	R.FQVMVLR.K		R.FQVMVLR.K	
94	101	2	905.44	0.42	0	28.9	29.5	95.00%	K.WAASSWAK.K		K.WAASSWAK.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
139	A6ZL12_YEAS7	6.24%	100%	3								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
14	23	2	1103.55	-0.29	1	35.4	30	95.00%	K.ETSPDSISIR.S		K.ETSPDSISIR.S	
24	38	2	1575.68	-0.074	1	96.5	30.1	95.00%	R.SFSAGNNFQSSSSEK.T		R.SFSAGNNFQSSSSEK.T	
405	417	2	1447.75	-0.74	0	66	28.2	95.00%	R.LICSLAQQGYAPK.F	Carbamidomethyl (+57)	R.LICSLAQQGYAPK.F	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
140	A6ZYY5_YEAS7	12.36%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
19	41	2	2426.2	-1.9	1	82.8	26.1	95.00%	L.ENIETLPQQGSIAGVSQGFPNIQ.E		K.GVNTLENIETLPQQGSIAGVSQGFPNIQEIYSDR.D	
48	58	2	1258.62	-0.17	0	71.4	29.1	95.00%	R.DFITLGSSTYR.R		R.DFITLGSSTYR.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
141	A6ZWJ1_YEAS7	9.42%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
328	340	2	1292.66	-0.015	1	89.4	28.8	95.00%	K.STSDTASATLLAR.Q		K.STSDTASATLLAR.Q
347	357	2	1323.68	0.27	1	42.5	28.4	95.00%	R.KDSNTNIVLLK.S	Phospho (+80)	R.KDSNTNIVLLK.S
348	357	2	1115.62	-0.46	0	31.1	26.6	95.00%	K.DSNTNIVLLK.S		K.DSNTNIVLLK.S
148	159	2	1386.8	-0.68	1	26.7	21	95.00%	L.DPLLAFPAFLRK.T		K.LDPLLAFPAFLRK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
142	A7A1Z8_YEAS7	10.61%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
390	401	2	1360.73	-1.3	1	49.9	26.3	95.00%	R.IYGDNINAQLLK.H		R.IYGDNINAQLLK.H
471	484	2	1519.84	-0.34	1	41.6	24.6	95.00%	R.DTVVLEPSGHVVLR.F		R.DTVVLEPSGHVVLR.F
372	383	2	1229.72	-0.58	0	25.8	20.8	95.00%	K.VPTLTTLLTSGK.L		K.VPTLTTLLTSGK.L
536	548	2	1249.6	-1.4	0	61.3	29.2	95.00%	A.DIPVVGNAAGHSN.D		K.AADIPVVGNAAGHSNDWFDLK.G
418	432	4	1837.95	0.18	0	17.2	26.4	95.00%	R.HPFHLHGHNFQIVQK.S		R.HPFHLHGHNFQIVQK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
143	RTN1_YEAST	8.81%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
208	216	2	939.58	-0.019	0	45.3	17.2	95.00%	K.LGPISNLVK.S		K.LGPISNLVK.S
219	235	2	1589.79	-0.2	0	77.4	29.1	95.00%	K.TAPVSSTAGPQTASTSK.L		K.TAPVSSTAGPQTASTSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
144	A6ZV05_YEAS7	5.23%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1305	1320	2	1769.91	-0.35	1	70.4	26.7	95.00%	K.ISRPIASQNSLGWNEV.-		K.ISRPIASQNSLGWNEV.-
1261	1272	2	1395.65	-0.29	1	57.4	30	95.00%	R.MSVQESITQSMR.I		R.MSVQESITQSMR.I
1278	1289	2	1354.54	-1.6	1	51.2	30.4	95.00%	M.DDSYYGHGLTNN.D		R.IQNWMDDSYYGHGLTNNDSTPTR.H
1041	1058	2	1982.01	-0.72	1	36.1	26.1	95.00%	K.SSAQIFGYLPEALNTPFK.N		K.SSAQIFGYLPEALNTPFK.N
1123	1133	2	1151.62	-1.2	0	28.1	26.6	95.00%	V.DSSIPLTGLLH.D		K.SMAAMVDSSIPLTGLLHDSNSNSGGSSDGSSSSNSNSGSSGSGSNSNSGVSSSSGNSYQDAGTLEYSSK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
145	A7A233_YEAS7	8.84%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
124	134	2	1198.65	-1.1	1	66.9	26	95.00%	N.DEAQLLLVGNK.S		K.TVNEHANDEAQLLLVGNK.S
171	178	2	967.54	-0.76	0	35.3	25.1	95.00%	N.EIFFTLAK.L		K.NDDNVNEIFFTLAK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
146	A7A1A7_YEAS7	5.90%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
172	181	2	1254.6	0.3	1	49.2	30.1	95.00%	K.FYDNSNLINR.E		K.FYDNSNLINR.E
196	204	2	1050.56	-1.2	1	34.2	25.1	95.00%	S.DETIVSFIK.D		R.EIEDILLEINPNFSDETIVSFIK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
147	A6ZU19_YEAS7	5.89%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
386	395	2	1252.56	-0.7	1	27	30.5	90.50%	K.LWCLDSMSNK.L	Carbamidomethyl (+57)	K.LWCLDSMSNK.L
648	655	2	970.5	-1.1	0	28	26.7	95.00%	I.DHVNIFAR.A		K.LDEMSDDQLANVIDHVNIFAR.A
690	699	2	1033.52	0.28	1	54.7	28.8	95.00%	K.LSDIGVSMGR.I		K.LSDIGVSMGR.I
27	36	2	1027.55	-0.61	0	29.1	25.8	95.00%	A.EALSKPSPSL.E		R.EILDATAEALSKPSPSLEYCTLSVDETLEK.L
235	245	2	1241.61	-0.38	0	36.4	29.4	95.00%	R.SCIAYMGTLVK.E	Carbamidomethyl (+57)	R.SCIAYMGTLVK.E

27	43	2	1879.92	-1.6	1	38.7	28.6	95.00%	A.EALSKPSPSLEYCTLSV.D	Carbamidomethyl (+57)	R.EILDATAEALSKPSPSLEYCTLSVDETLEK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
148	B3LP09_YEAS1	12.09%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
375	390	4	1797.89	-0.43	1	21.2	28.2	95.00%	K.KPNLHGYGHPNPPNEK.S		K.KPNLHGYGHPNPPNEK.S
398	430	4	3862.74	0.91	1	21.2	26.3	95.00%	K.NHQYSSPDHHHHYNQQQQQQQAQAQAQAQAQAK.V		K.NHQYSSPDHHHHYNQQQQQQQAQAQAQAQAQAK.V
405	430	4	3049.39	-1.7	0	34.5	27.6	95.00%	P.DHHHHYNQQQQQQQAQAQAQAQAQAK.V		K.NHQYSSPDHHHHYNQQQQQQQAQAQAQAQAQAK.V
431	447	2	1994	0.067	0	93.7	25.6	95.00%	K.VQQQQLQQAQAQQQANR.Y		K.VQQQQLQQAQAQQQANR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
149	A6ZMI1_YEAS7	19.61%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
148	157	2	1330.61	0.15	0	34.5	31.1	95.00%	R.YNWICNPVHK.H	Carbamidomethyl (+57)/ Deamidation (+1)	R.YNWICNPVHK.H
115	128	2	1715.81	-0.81	1	68.8	29.4	95.00%	R.VLNSYWVNQDSTYK.Y		R.VLNSYWVNQDSTYK.Y
78	93	2	1675.85	-0.9	1	63.7	28.4	95.00%	K.GATYGKPTNQGVNELK.Y		K.GATYGKPTNQGVNELK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
150	FCY2_YEAST	3.56%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
63	72	2	1126.57	1.9	1	41.1	28	95.00%	K.FFASLNAETK.G		K.FFASLNAETK.G
156	164	2	991.55	0.19	0	49.3	26.4	95.00%	R.YLVGNVTAR.I		R.YLVGNVTAR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
151	A7A288_YEAS7	9.67%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
306	315	2	1103.54	-1	0	48.5	30.1	95.00%	P.DHLPNPVGQQ.D		R.DHHYEYYSGVETVEDANNNYELETSGNNNNANQDTTTVPDHLPNPVGQQDSFNPMEPQFFAEETPLEIEK.R
316	327	2	1444.6	-1.1	1	29.7	30.4	94.80%	Q.DSFNPMEPQFFA.E	Oxidation (+16)	R.DHHYEYYSGVETVEDANNNYELETSGNNNNANQDTTTVPDHLPNPVGQQDSFNPMEPQFFAEETPLEIEK.R
191	207	2	1942.98	0.46	1	85.8	26.1	95.00%	R.ITAYNVADGFNLNQLYK.F		R.ITAYNVADGFNLNQLYK.F
60	75	2	1680.86	-2	0	76.1	27.7	95.00%	R.SSAIGPSPLQSFTHPR.R		R.SSAIGPSPLQSFTHPR.R
488	496	2	1089.62	0.99	1	46	23.1	95.00%	R.IFNDIVTLR.S		R.IFNDIVTLR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
152	A6ZUC1_YEAS7	7.25%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
48	59	2	1209.61	-0.69	0	28.1	29.6	93.80%	R.IVNGFGSLMGSK.E	Deamidation (+1)	R.IVNGFGSLMGSK.E
33	44	2	1270.72	-1.1	1	32	23.6	95.00%	T.EANILATGLNKK.A		K.DDSASSGIVDEVDLTEANILATGLNKK.A
426	435	2	1006.62	-0.41	0	53.1	14	95.00%	K.GLVIISGIVH.D		K.GLVIISGIVHDVSGYISEHPGGETLIK.T
30	43	2	1471.79	-2.3	1	97.8	25.1	95.00%	V.DLTEANILATGLNK.K		K.DDSASSGIVDEVDLTEANILATGLNK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
153	ARN2_YEAST	2.67%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
586	592	2	817.43	-0.89	1	37.5	29.7	95.00%	E.DFAQKLP.D		R.LTEDFAQKLPDR.E
339	348	2	1101.66	0.056	0	27.7	18	95.00%	R.LALVPFAPFK.L		R.LALVPFAPFK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
154	A6ZV40_YEAS7	6.27%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
60	73	2	1615.85	-0.52	0	69.3	25.8	95.00%	K.QLGILSCIGLICNR.M	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.QLGILSCIGLICNR.M
6	16	2	1309.7	-0.32	0	74.3	26.1	95.00%	R.TFLSQLNVFNK.E		R.TFLSQLNVFNK.E
17	27	2	1290.57	-0.86	0	44.3	30.6	95.00%	K.ENYQFSSSTTK.K		K.ENYQFSSSTTK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
155	A6ZZH5_YEAS7	12.14%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
230	242	2	1526.76	-0.026	1	43.8	28.3	95.00%	K.HNVDAPIPNFFTR.N		K.HNVDAPIPNFFTR.N
136	169	3	3761.73	-0.66	1	61	26.3	95.00%	K.WTNDHPSSPSQYQYPSQPALST SIPSQAPSFSNR.K		K.WTNDHPSSPSQYQYPSQPALST SIPSQAPSFSNR.K
96	107	2	1332.67	-1.1	1	39.8	28.8	95.00%	L.EVSINNPEPHVV.D		K.KPPLLVNNEAVHASVPDASHTSC NNGTLEVSINNPEPHVVDAVAR.H
279	288	2	1148.57	-1.3	1	38.5	28.7	95.00%	L.ETESTQLVSR.E		R.NFIEFLTLYGHFAGEDLSEEEEEE EETEEEPEEEALETESTQLVSR.E
139	169	3	3360.56	-1.4	0	51.5	27.6	95.00%	N.DHPSSPSQYQYPSQPALSTSIPS QAPSFSNR.K		K.WTNDHPSSPSQYQYPSQPALST SIPSQAPSFSNR.K
233	242	2	1176.59	-1.4	0	27.1	29.3	92.90%	V.DAPIPNFFTR.N		K.HNVDAPIPNFFTR.N
117	131	2	1598.8	-1	1	99.5	28.3	95.00%	R.NPSNSLQLQGGDITR.D		R.NPSNSLQLQGGDITR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
156	A6ZS21_YEAS7	18.79%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
271	292	2	2214.16	-2.3	1	111	24.8	95.00%	K.RNQSSLGLIPVASATSNTSSPK.K		K.RNQSSLGLIPVASATSNTSSPK.K
177	186	2	1058.5	-0.31	0	39	30.1	95.00%	E.DAASPFNPIQ.D		K.SYMQDDWDSMSQLESSQYEDA ASPFNPIQDPFTDNR.R
195	209	2	1738.91	-1.1	1	64.9	25.3	95.00%	R.SLFISPTLQVSQYEK.S		R.SLFISPTLQVSQYEK.S
122	133	2	1377.59	-0.59	1	49.4	31.5	95.00%	R.FTMTNSYANDSK.N		R.FTMTNSYANDSK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
157	A6ZZW6_YEAS7	10.51%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
594	605	2	1233.73	-1	1	38.8	22	95.00%	K.LAALESPPPVLK.A		K.LAALESPPPVLK.A
166	184	3	2079.2	-0.13	1	20	12.6	95.00%	R.IYSPHVLTLTLVDLPGLTK.V		R.IYSPHVLTLTLVDLPGLTK.V
28	42	2	1514.79	-1.1	0	51.1	27.1	95.00%	I.DLPQITVVGSQSSGK.S		K.LQDALAPLGGGSQSPIDLPQITVV GSQSSGK.S
389	400	2	1232.6	-0.095	1	80.3	29.3	95.00%	K.ELSSQELSGGAR.I		K.ELSSQELSGGAR.I
150	165	2	1583.86	-0.32	0	57.7	24.3	95.00%	K.VTGANSGISSVPINLR.I		K.VTGANSGISSVPINLR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
158	A6ZU59_YEAS7	10.63%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
78	88	2	1299.68	-1.5	1	58.2	27.2	95.00%	Q.DEVMNIKPVQK.Q		K.EFQIIDTLLPGLQDEVMNIKPVQK. Q
142	157	2	1728.86	-1.3	0	73.2	27.5	95.00%	R.GYWGTNLGQPHSLATK.T		R.GYWGTNLGQPHSLATK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
159	A6ZL51_YEAS7	21.81%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
155	168	2	1346.66	-1.6	0	57.1	29	95.00%	K.APSLFGGMGQTGPK.T		K.APSLFGGMGQTGPK.T
138	147	2	1039.58	-0.8	0	32.6	20.8	95.00%	K.IHLFGKPATG.D		K.IHLFGKPATGDLK.R
138	150	3	1395.79	0.28	1	24.5	21.6	95.00%	K.IHLFGKPATGDLK.R		K.IHLFGKPATGDLK.R
115	128	2	1623.83	-0.68	0	63.7	27.6	95.00%	K.YTNPLFMQSISPVK.S		K.YTNPLFMQSISPVK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
160	YAJ8_YEAST	14.10%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
201	211	2	1248.68	0.39	1	59.9	25.9	95.00%	R.SDPILMAYVLK.A		R.SDPILMAYVLK.A
153	162	3	1294.64	0.41	1	40.3	28.7	95.00%	K.CHEFFTTLIK.E	Carbamidomethyl (+57)	K.CHEFFTTLIK.E
189	200	2	1385.66	-0.31	0	48.3	30.7	95.00%	K.TSNGLNNFYSIR.S	Deamidation (+1)	K.TSNGLNNFYSIR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
161	A7A0B5_YEAS7	10.34%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
706	729	2	2564.24	0.9	0	84	26.8	95.00%	T.EQPVQPTSAVMGTGGSFLSPQYQR.A		K.QNSSPFDASEVTEQPVQPTSAVMGTGGSFLSPQYQR.A
37	47	2	1303.63	-0.59	0	31	29.7	95.00%	K.HLQTTSLLTCM.D	Carbamidomethyl (+57)	K.HLQTTSLLTCMDNSQLTASFFDVK.F
99	117	2	2080.01	-0.46	1	80.3	27.5	95.00%	K.TFDLCSLGQVSLCPLSAGR.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.TFDLCSLGQVSLCPLSAGR.I
736	762	3	2867.39	-1.2	1	49	25.7	95.00%	R.TNLAPNNTSTSSLMKPESSLYLGNSNK.S		R.TNLAPNNTSTSSLMKPESSLYLGNSNK.S
101	117	2	1831.89	-1.7	0	69.8	28.5	95.00%	F.DLCSLGQVSLCPLSAGR.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.TFDLCSLGQVSLCPLSAGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
162	B3LGB1_YEAS1	10.22%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
440	456	2	1783.88	-0.62	1	42.3	28.9	95.00%	K.TDVVFMPVSGYSGANLK.D		K.TDVVFMPVSGYSGANLK.D
485	497	2	1421.78	-0.87	0	41.1	23.5	95.00%	R.HINAPFMLPIAAK.M		R.HINAPFMLPIAAK.M
562	573	2	1259.68	-0.42	0	24.9	26.6	93.50%	E.DISPGFVLTSPK.N		K.GVEEEDISPGFVLTSPK.N
421	432	2	1437.67	-0.68	0	31.9	30.6	95.00%	Y.DQCVSNVSNFLR.A	Carbamidomethyl (+57)	R.YDQCVSNVSNFLR.A
220	235	2	1659.73	-2.1	1	52.1	30.1	95.00%	K.ISESTHNTNNANVTSA.D	Deamidation (+1)	K.ISESTHNTNNANVTSADALIK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
163	SSO1_YEAST	8.97%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
166	182	2	1829.94	-1.4	0	74.2	26.7	95.00%	S.DVGGQQIFSQALLNANR.R		R.QYMIIQPEATEDEVEAAISDVGGQQIFSQALLNANR.R
166	183	3	1986.04	-1.1	1	24.3	25.5	95.00%	S.DVGGQQIFSQALLNANRR.G		R.QYMIIQPEATEDEVEAAISDVGGQQIFSQALLNANRR.G
32	39	2	956.44	-0.66	0	31.2	29.8	95.00%	H.DFVGFMNK.I		-.MSYNNPYQLETPFEESYELDEGSSAIGAEGHDFVGFMNK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
164	A6ZWS9_YEAS7	9.62%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
468	478	2	1211.65	-0.59	0	46.8	25.9	95.00%	K.ATQAIIGYTFK.-		K.ATQAIIGYTFK.-
55	71	2	1703.78	-1.1	1	78.9	30.6	95.00%	K.NIGDGLSSSNNAHSGFK.V		K.NIGDGLSSSNNAHSGFK.V
311	328	2	1951.11	-1	1	80.4	18.2	95.00%	K.QLLLLGNALPTVQSLSER.K		K.QLLLLGNALPTVQSLSER.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
165	A6ZLE7_YEAS7	7.67%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
96	104	2	1087.57	0.35	1	35.3	29.1	95.00%	R.NSDLWNLVK.S		R.NSDLWNLVK.S
315	324	2	1163.49	-0.63	1	43.2	30.9	95.00%	L.DSSGGFFYER.W		R.EYFDYLDSSGGFFYER.W
379	390	2	1559.67	0.13	1	28.4	30.2	93.40%	K.DVTWTPDYFCTR.K	Carbamidomethyl (+57)	K.DVTWTPDYFCTR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
166	A7A1T6_YEAS7	4.89%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

487	496	2	1094.52	-0.65	1	56.5	30.3	95.00%	R.SIVYNNIEGS.D		R.SIVYNNIEGSDFKPYMDALNIGK.D
520	530	3	1342.68	-1.4	1	32.9	28	95.00%	Q.DRQHMYVPAVK.A		K.DDLHLDGELQDRQHMYVPAVK.A
203	214	2	1323.71	-0.78	1	58.9	26.2	95.00%	K.LSPVFELFASSK.N		K.LSPVFELFASSK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
167	A6ZLM1_YEAS7	10.82%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	69	2	1619.83	-1.1	1	66.5	27.7	95.00%	K.ATTPNVNDPIYFLR.G		K.ATTPNVNDPIYFLR.G
402	410	2	989.5	-1.2	0	44.2	28.6	95.00%	K.DQGITLMGR.R		K.DQGITLMGR.R
63	69	2	922.49	-0.79	0	27.6	28.2	95.00%	N.DPIYFLR.G		K.ATTPNVNDPIYFLR.G
209	225	2	1838.98	-1.4	1	80.4	24.5	95.00%	D.DQTEAQGALINLIQGLR.S		K.VGEDDQTEAQGALINLIQGLR.S
8	20	2	1444.89	-0.99	1	26.7	10.8	95.00%	I.DIVKPILPILPEV.E		R.LIDIVKPILPILPEVELPFEK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
168	B3LRN6_YEAS1	11.48%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
199	212	2	1512.75	0.33	0	37.2	28.6	95.00%	K.QTSNSTPAPQNQIK.E		K.QTSNSTPAPQNQIK.E
130	143	3	1633.78	-1.2	1	26.9	29.2	95.00%	P.DVHPAQNQNIQENK.E		K.YLISPDVHPAQNQNIQENK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
169	RSP5_YEAST	9.02%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
712	720	2	1249.61	-1.3	1	34.8	29.4	95.00%	S.DEVIQWFWK.C		R.GYQESDEVIQWFWK.C
138	164	3	2669.22	-1.2	0	73.3	27.9	95.00%	K.LPSSSPHSQAPSGHTASSSTNTSSTTR.T		K.LPSSSPHSQAPSGHTASSSTNTSSTTR.T
80	90	2	1202.64	-0.51	0	31.2	27.4	95.00%	K.DQGFLGVVNVR.V		K.DQGFLGVVNVR.V
184	209	3	2561.23	-0.032	1	55.9	27.3	95.00%	R.GTAQAVESTLQSGTTAATNTATTSHR.S		R.GTAQAVESTLQSGTTAATNTATTSHR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
170	A6ZM36_YEAS7	23.97%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	16	2	1781.94	-1.3	1	70.6	25.4	95.00%	M.SLVVQEQGSFQHILR.L	Acetyl (+42)	-.MSLVVQEQGSFQHILR.L
81	88	2	1015.56	1	0	47.3	28.8	95.00%	K.IPAWFLNR.Q		K.IPAWFLNR.Q
97	108	2	1390.63	-1.7	1	43.8	30.8	95.00%	K.DYHTLANNVESK.L	Deamidation (+1)	K.DYHTLANNVESK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
171	GLRX6_YEAST	19.05%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
43	57	2	1560.63	-0.54	1	86.9	30.1	95.00%	K.AFSTNMDNMAGGSSR.E	Oxidation (+16)	K.AFSTNMDNMAGGSSR.E
118	133	2	1850.04	-1.1	1	64.7	19	95.00%	K.EYSLILDLSPIIIFSK.S		K.EYSLILDLSPIIIFSK.S
181	193	2	1324.75	-0.69	0	47.4	22.8	95.00%	R.GTVPNLLVNGVSR.G		R.GTVPNLLVNGVSR.G
124	133	2	1131.65	-1.2	0	40.8	21.4	95.00%	L.DLSPIIIFSK.S		K.EYSLILDLSPIIIFSK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
172	B3LFU9_YEAS1	7.26%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
298	307	2	1088.54	-1.5	1	66.5	30.1	95.00%	E.DSAAQLVTER.T		R.ELYSPEEDSAAQLVTER.T
126	138	2	1413.56	-1.9	1	64.7	30.4	95.00%	E.DMIQGGSSAESPR.S	Phospho (+80)	R.EEEDMIQGGSSAESPR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
173	A6ZZN9_YEAS7	10.71%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
144	154	2	1275.68	-0.72	0	51.6	27.7	95.00%	D.DTYVSLNPIVR.C		K.AHNMGPNEVFVEEEYIDEDDTYVSLNPIVR.C
143	154	2	1390.71	-0.37	1	36.7	28.6	95.00%	E.DDTYVSLNPIVR.C		K.AHNMGPNEVFVEEEYIDEDDTYVSLNPIVR.C

230	241	2	1411.67	-0.73	1	52.3	30.5	95.00%	R.DIPATFFSSEWI.D		R.DIPATFFSSEWIDNVNGLMPVEVR.D
155	163	2	1155.54	-0.25	0	31.1	29.9	95.00%	R.CTPNLYFNK.G	Carbamidomethyl (+57)	R.CTPNLYFNK.G
188	196	2	1235.6	0.15	0	27.5	29.5	93.20%	K.TYFVTWYTR.F		K.TYFVTWYTR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
174	HSP72_YEAST	12.52%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
170	183	2	1415.76	-1.2	1	50.2	26.3	95.00%	R.IINEPTAAAIAYGL.D		R.IINEPTAAAIAYGLDK.K
158	169	2	1198.67	-0.44	0	52.4	26.1	95.00%	K.DAGTIAGLNVLR.I		K.DAGTIAGLNVLR.I
537	547	2	1264.67	-1	1	39.1	27.9	95.00%	K.NQLESIAYSLK.N		K.NQLESIAYSLK.N
8	21	2	1570.67	-1.5	0	68.1	30.6	95.00%	I.DLGTTYSCVAHFSN.D	Carbamidomethyl (+57)	K.AVGIDLGTTYSCVAHFSNDR.V
55	69	2	1590.74	-1	1	63.7	29.9	95.00%	K.NQAAMNPANTVFDAK.R		K.NQAAMNPANTVFDAK.R
111	124	2	1549.78	-1.2	1	62.2	28.4	95.00%	K.NFTPEQISSMVLGK.M		K.NFTPEQISSMVLGK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
175	A6ZWC1_YEAS7	7.07%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
144	152	2	1059.61	0.17	1	70.8	24	95.00%	K.VFLDIGLQR.T		K.VFLDIGLQR.T
197	208	2	1387.62	-0.57	0	41.4	30.7	95.00%	R.SYIFGGHVSQYM.E		R.SYIFGGHVSQYMEELADDDEER.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
176	B3LJM9_YEAS1	12.09%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
417	425	2	1182.58	-0.7	0	28	29.1	94.40%	T.DFLIMQNFR.A		R.MADQLTDFLIMQNFR.A
150	158	2	1013.57	-1.3	1	24.2	24.6	94.70%	L.DGLLLENIK.L		K.DVPEPITEFTSPPLDGLLLENIK.L
181	192	2	1237.55	1.9	0	33.2	30.1	95.00%	R.DLMACAQTGSGK.T	Carbamidomethyl (+57)	R.DLMACAQTGSGK.T
493	512	2	2054	-1.7	1	73.1	28	95.00%	R.AGNTGLATAFFNSENSNIVK.G		R.AGNTGLATAFFNSENSNIVK.G
313	321	2	1091.51	-1.4	1	30	29.4	95.00%	L.DMGFEPQIR.H		R.MLDMGFEPQIR.H
193	206	2	1527.8	0.11	1	36.2	25.7	95.00%	K.TGGFLFPVLSESFK.T		K.TGGFLFPVLSESFK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
177	A6ZWW2_YEAS7	14.79%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
269	277	2	1029.55	-0.61	1	68.4	27.6	95.00%	A.DDNLITAIR.A		K.DADDNLITAIR.A
199	219	2	2130.17	-1.5	1	62.8	20.9	95.00%	R.TRASNILPIAYIPGVTSGLST.D		R.TRASNILPIAYIPGVTSGLSTDK.L
170	191	2	2407.21	-0.8	1	98.2	27	95.00%	K.DESHTLFNTSLVPPTLNVPGNR.S		K.DESHTLFNTSLVPPTLNVPGNR.S
201	221	2	2116.14	-0.19	1	73.9	20.8	95.00%	R.ASNILPIAYIPGVTSGLSTDK.L		R.ASNILPIAYIPGVTSGLSTDK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
178	A6ZNJ9_YEAS7	14.08%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
255	271	2	1899.78	-1.3	1	62.4	30.6	95.00%	S.DANNSNTWSQSNESAIY.D		R.SSMFISPTEILQSDANNSNTWSQSNESAIYDSLSSTPR.E
272	289	2	1855.96	-1.8	1	37	25.8	95.00%	Y.DSLSSTPREPGATQILGK.F		R.SSMFISPTEILQSDANNSNTWSQSNESAIYDSLSSTPREPGATQILGK.F
242	254	2	1454.7	0.19	1	46.2	29.7	95.00%	R.SSMFISPTEILQS.D	Oxidation (+16)	R.SSMFISPTEILQSDANNSNTWSQSNESAIYDSLSSTPR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
179	A7A0C4_YEAS7	6.75%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
351	366	2	1755.87	0.21	1	56.3	27.6	95.00%	R.GGIPGMFVFFEMSPLK.V		R.GGIPGMFVFFEMSPLK.V
275	286	2	1163.64	-0.45	1	24.5	25	95.00%	K.RHGGAVVATSPL.D		K.RHGGAVVATSPLDGR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
180	A6ZLC2_YEAS7	17.37%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	115	2	1647.03	-0.31	1	55.7	6.02	95.00%	R.GAIVGPDLAVLALVIVK.K		R.GAIVGPDLAVLALVIVK.K
3	14	2	1319.67	-0.39	0	56.7	29.4	95.00%	K.LNISYPVNGSQK.T	Deamidation (+1)	K.LNISYPVNGSQK.T
203	214	2	1276.67	1.9	1	58.7	28.2	95.00%	R.EAAAEYAQLLAK.R		R.EAAAEYAQLLAK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
181	A6ZTE7_YEAS7	6.97%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
34	45	2	1455.71	-1.3	1	32.7	29.5	95.00%	T.DWQLANLGPWEK.V		K.ITCTDLVYVFILLFLNTSCVQAVFSDDAFITDWQLANLGPWEK.V
669	677	2	1161.59	-1.1	0	43.6	29.5	95.00%	N.DNFIITHFR.N		K.EFMATPYTPVIPINDNFIITHFR.N
467	481	2	1588.83	-1.3	1	40.9	26.2	95.00%	R.ETTNLNTLGITLGDK.S		R.ETTNLNTLGITLGDK.S
128	143	2	1719.83	-1.7	0	65.1	28.7	95.00%	V.DNAPSTTILPQSSYLN.D		K.FDLHDWFLLEEGVDNAPSTTILPQSSYLNDQVSIK.N
466	479	2	1501.81	-1.6	1	29.4	25.3	95.00%	K.RETTNLNTLGITLG.D		K.RETTNLNTLGITLGDK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
182	B5VQ30_YEAST	4.51%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
514	524	2	1171.63	-0.018	1	32.5	26.9	95.00%	K.AMDLLASNLPK.A		K.AMDLLASNLPK.A
858	873	2	1900.91	-1.2	1	64.4	28.5	95.00%	Y.DYPAVSAQCPELWIPR.D	Carbamidomethyl (+57)	R.VNDFDISHAYDYPAVSAQCPELWIPR.D
874	880	2	796.37	-1.5	0	32.6	31.8	95.00%	R.DPFGFSK.L		R.DPFGFSK.L
196	204	2	1031.6	1.9	0	34	22.6	95.00%	R.TVLFQTVPK.Q		R.TVLFQTVPK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
183	A6ZUM5_YEAS7	21.03%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
102	113	2	1402.69	-0.09	0	54.8	29.6	95.00%	R.FTPGSFTNYITR.S		R.FTPGSFTNYITR.S
135	147	2	1388.75	-1.2	0	38.2	26.3	95.00%	K.EASYVNIPVIALT.D		K.EASYVNIPVIALTDLDSPSEFVDVAIPCNNR.G
89	101	2	1268.66	-1.3	0	40.1	27.1	95.00%	K.FAAHTGATPIAGR.F		K.FAAHTGATPIAGR.F
13	27	2	1562.85	-1.8	0	75.2	23.8	95.00%	E.DAQLLLAANTHLGAR.N		-.MSLPATFDLTPEDAQLLLAANTHLGAR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
184	ATG22_YEAS7	6.25%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
8	17	2	1227.52	-1.1	1	49.3	30.6	95.00%	N.DMNESVTNYR.I		-.MSYGTINDMNESVTNYR.I
64	75	2	1301.55	-0.83	1	74.5	30.7	95.00%	H.DHSIPCLSETGS.D	Carbamidomethyl (+57)	K.VHDHSIPCLSETGSDSDK.C
201	210	2	1047.56	-0.87	0	35.3	28.3	95.00%	V.DSLTTVISGR.G		K.VDSLTTVISGR.G
200	210	2	1146.62	-0.62	1	57.3	26.6	95.00%	K.VDSLTTVISGR.G		K.VDSLTTVISGR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
185	B3LQ13_YEAS1	13.51%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
167	181	2	1621.77	-1.1	0	87.5	28.9	95.00%	R.IQTGSSGSYFVYGTR.A		R.IQTGSSGSYFVYGTR.A
39	55	2	1649.77	-1.9	0	52	29.7	95.00%	K.NPITHASPGVGSNAQNS.D		K.NPITHASPGVGSNAQNSDIAEAPQVFHPSYQSLVNVPSESPRPDQTSGSNPAVGLLHNAEDK.A
579	588	2	1128.55	-1.8	0	25.6	29.1	90.30%	Y.DSTLHPFANK.T		K.NAIDEPIGSYSTSPMVLPSTPSTIPFHAHNQSNSNPVYYDSTLHPFANK.T

82	98	2	1708.8	-2.2	1	70.4	29.3	95.00%	P.DQTSGSNPAVGLLHNAE.D		K.NPITHASPGVGSNAQNSDIAEAP QVFHPSYQSLVNVPSESPRPDQTS GSNPAVGLLHNAEDK.A
59	81	3	2564.26	-0.93	1	31.7	26.8	95.00%	A.EAPQVFHPSYQSLVNVPSESPRP .D		K.NPITHASPGVGSNAQNSDIAEAP QVFHPSYQSLVNVPSESPRPDQTS GSNPAVGLLHNAEDK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
186	B5VE42_YEAST	7.95%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
60	70	2	1330.71	-0.021	1	59.7	25.6	95.00%	K.KVNVFNINNNR.Y		K.KVNVFNINNNR.Y
235	249	2	1622.77	-0.48	1	75	29.2	95.00%	K.LQSNGAIQGDSFVCK.N	Carbamidomethyl (+57)	K.LQSNGAIQGDSFVCK.N
61	70	2	1202.62	-0.19	0	43.8	28.8	95.00%	K.VNVFNINNNR.Y		K.VNVFNINNNR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
187	A6ZLZ0_YEAS7	6.64%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
727	740	2	1272.7	-0.72	0	73.1	26.1	95.00%	K.AINAGGGATTVLTK.D		K.AINAGGGATTVLTK.D
786	801	3	1914.98	0.13	1	30	26.4	95.00%	R.LQHIQTCLAGDLLFMR.F	Carbamidomethyl (+57)	R.LQHIQTCLAGDLLFMR.F
524	535	2	1374.71	-0.58	1	40.9	27.7	95.00%	R.IHTSYTADQLVK.T		R.IHTSYTADQLVK.T
804	817	2	1456.64	0.27	1	36	30.8	95.00%	R.TTTGDAMGMNMISK.G		R.TTTGDAMGMNMISK.G
67	80	2	1818.76	-0.92	1	71.8	30.5	95.00%	K.DSNTLFQECSHYYR.D	Carbamidomethyl (+57)	K.DSNTLFQECSHYYR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
188	B3LMA9_YEAS1	5.56%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
283	293	3	1070.59	-0.46	0	32	25.8	95.00%	K.SGGIFGVLHGK.S		K.SGGIFGVLHGK.S
496	504	2	981.48	0.1	0	36.4	29.6	95.00%	R.GLSSNYQTI.-		R.GLSSNYQTI.-
84	91	2	963.49	0.71	1	32.4	30.3	95.00%	K.ILDMYGPR.V		K.ILDMYGPR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
189	A6ZNP1_YEAS7	18.75%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
221	233	2	1340.73	-0.66	0	58.8	25.5	95.00%	K.DLGSVVQQQGVLV.D		K.DLGSVVQQQGVLVDNIEANIYTTS DNTQLASDELR.K
39	55	2	1891.99	-1.4	0	29.7	25.2	95.00%	F.EINGQISTLQQFTATLK.S	Deamidation (+1)	K.EEVAAELFEINGQISTLQQFTATL K.S
174	183	2	1110.64	-1.5	1	60.1	21.4	95.00%	R.IPGSQIVIER.D		R.IPGSQIVIER.D
118	131	2	1702.79	-0.18	1	57.7	30	95.00%	R.DVSYSFQEFQGIQR.Q		R.DVSYSFQEFQGIQR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
190	A7A244_YEAS7	6.92%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
401	416	2	1729.8	-1.8	0	37.3	29.8	95.00%	R.ASCAFYPHGLGHMLGL.D	Carbamidomethyl (+57)	R.ASCAFYPHGLGHMLGLDVHDVG GNPNYDDPDPMFR.Y
282	302	3	2354.05	-0.12	1	22.4	29.6	93.00%	R.SLGYDPICCSGPACGTLHYVK.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.SLGYDPICCSGPACGTLHYVK.N
286	302	2	1933.84	-2.5	0	63.3	30.3	95.00%	Y.DPICCSGPACGTLHYVK.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.SLGYDPICCSGPACGTLHYVK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
191	A6ZM69_YEAS7	9.49%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
407	419	2	1490.84	-1.5	0	29.5	21	95.00%	E.DNQNIPLVPLLQK.E		K.NATSSIIESEYLFLVDGGEDNQNI PLVPLLQK.E
237	247	2	1195.6	0.33	0	46.7	29.7	95.00%	R.GGVGYTWSTLR.E		R.GGVGYTWSTLR.E

547	558	2	1379.67	-1.4	0	51.4	30.3	95.00%	S.DFLGCVGCAIIR.R	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.NGFEAATMGNFTDDSDFLGCVG CAIIR.R
441	451	2	1222.59	-0.99	0	49.3	30.2	95.00%	P.DGASLVNTYQR.Q		R.ELDVIFALDNSADTDDYWPDGAS LVNTYQR.Q
492	507	2	1901.03	-1.2	1	49	23.3	95.00%	T.DLEYIPPLIVYIPNSR.H		R.NLTDLEYIPPLIVYIPNSR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
192	A6ZQF2_YEAS7	12.80%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
83	95	4	1542.89	0.088	1	28.1	18.4	95.00%	R.LIYPHVEHVPVLK.Q		R.LIYPHVEHVPVLK.Q
61	82	3	2263.09	0.71	1	44	28	95.00%	R.SAGASYSPSHGLYINEIPASSR.L		R.SAGASYSPSHGLYINEIPASSR.L
261	268	2	915.55	0.31	1	31	24.1	95.00%	K.IMDLALLK.N		K.IMDLALLK.N
269	279	2	1153.64	-0.53	0	24.4	24.1	95.00%	K.NVPVVANSNIK.T		K.NVPVVANSNIK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
193	B3LPM2_YEAS1	7.92%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
102	119	3	2127.01	-1.4	1	42.1	28.9	95.00%	K.IFTVEHQNTWFSSFATGR.S		K.IFTVEHQNTWFSSFATGR.S
2	15	2	1551.79	-1.3	1	52.6	28.2	95.00%	M.SSSIFGPLTGFLER.V	Acetyl (+42)	-.MSSSIFGPLTGFLER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
194	FET4_YEAST	7.25%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
445	454	2	1132.59	-0.46	1	46.1	28.2	95.00%	K.APEINTIGYR.T		K.APEINTIGYR.T
4	15	2	1240.65	-1.7	1	60.5	27.3	95.00%	K.IAEFLGNPGARP.D		K.IAEFLGNPGARPDVHHR.A
248	265	2	1833.81	-1.2	1	98.2	30.3	95.00%	K.DAGNTPPYTGETTGSNPR.L		K.DAGNTPPYTGETTGSNPR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
195	B3LQX5_YEAS1	9.15%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
280	292	2	1414.78	-1.2	0	30.8	24.3	95.00%	R.INNPFTASTLLPK.L		R.INNPFTASTLLPK.L
189	201	2	1527.72	-0.8	1	35.4	30.4	95.00%	I.DEYGNFLPSFIVQ.D		R.GIQSYFLLPSINDNIDEYGNFLPSF IVQDK.L
268	277	2	1117.53	-0.096	1	35.7	28.7	95.00%	K.YSIAYESTGK.L		K.YSIAYESTGK.L
470	486	2	1936	-0.99	1	56.9	25.1	95.00%	R.ITAQTSKPLWSVGTYER.I		R.ITAQTSKPLWSVGTYER.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
196	A6ZPF3_YEAS7	12.63%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
219	231	2	1515.74	-0.74	0	26.5	29	92.30%	K.FAAPLTYWFLSNS.D		K.FAAPLTYWFLSNSDLEK.S
172	182	2	1290.61	-0.25	1	38.6	29.6	95.00%	K.DTTPWNESLTK.L		K.DTTPWNESLTK.L
473	486	2	1700.82	-0.29	0	58.1	29	95.00%	C.DLWNSVYASYIQSR.E		K.LEHQACDLWNSVYASYIQSR.E
208	218	2	1397.72	-1	1	27.8	27.1	95.00%	L.DELFFLPNYIK.F		R.SSLDELFFLPNYIK.F
399	411	2	1583.8	-0.5	1	43.5	27.8	95.00%	R.HYSIIYNDVLGYK.T		R.HYSIIYNDVLGYK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
197	A6ZKL6_YEAS7	33.58%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
13	26	2	1414.73	-1.4	0	52.3	27	95.00%	R.ISLGLPVGAIMNCA.D	Carbamidomethyl (+57)	R.ISLGLPVGAIMNCADNSGAR.N
121	128	2	1045.47	1.9	1	47.8	30.2	95.00%	K.ECADLWPR.V	Carbamidomethyl (+57)	K.ECADLWPR.V
33	40	2	932.57	-0.12	0	26.9	18.5	95.00%	R.NLYIIAVK.G		R.NLYIIAVK.G
13	32	2	2014.99	0.21	1	81.3	27.8	95.00%	R.ISLGLPVGAIMNCADNSGAR.N	Carbamidomethyl (+57)	R.ISLGLPVGAIMNCADNSGAR.N
46	55	2	1010.59	-0.92	1	25.9	19.8	95.00%	R.LNRLPAASLG.D		R.LNRLPAASLGDMVMATVK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
198	A6ZUF3_YEAS7	8.35%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

288	301	3	1471.67	1.4	0	25.8	31.1	95.00%	R.GTHAHYASVGQHAH.D		R.GTHAHYASVGQHAHDVPFFFMP LSDFTDR.G
321	336	2	1818.87	-0.99	1	80.6	29.4	95.00%	W.DPSLNYYAYTVTVGEK.M		R.GPLWDPSLNYYAYTVTVGEK.M
347	355	2	1109.56	-0.02	1	36.5	28.8	95.00%	K.MGLEWLSFK.G		K.MGLEWLSFK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
199	YD237_YEAST	9.49%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
286	295	2	1081.6	-0.3	1	24.4	22.8	95.00%	L.DAPLLSLEPK.Y		R.FAFLDAPLLSLEPK.Y
351	367	2	1910	-1.4	1	55.5	24.2	95.00%	R.IWGAPTWPANLVETISR.Q		R.IWGAPTWPANLVETISR.Q
337	346	2	1023.57	-0.6	1	41.4	23.4	95.00%	K.SIIDGAHALK.L		K.SIIDGAHALK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
200	A6ZR85_YEAS7	27.73%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	66	2	1365.68	-1.6	1	31.5	29.5	95.00%	S.EASVYPEYALPK.T		R.DLSEASVYPEYALPK.T
43	51	2	941.53	0.29	1	42.1	24.9	95.00%	R.NIVEAAAVR.D		R.NIVEAAAVR.D
71	82	3	1485.7	0.86	0	42.8	30	95.00%	K.LHYCVSCAIHAR.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.LHYCVSCAIHAR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
201	A6ZKM8_YEAS7	18.50%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
165	178	2	1550.76	-1	0	34.9	29.3	95.00%	R.LYACISSRPGQSGR.C	Carbamidomethyl (+57)	R.LYACISSRPGQSGR.C
187	194	2	1039.53	-0.22	1	42.3	28.2	95.00%	G.EELAFYLR.R		R.CDGYILEGEELAFYLR.R
78	92	2	1666.88	-1.3	1	27	25.6	95.00%	R.IAGVVYHPSNNELVR.T		R.IAGVVYHPSNNELVR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
202	A6ZQP7_YEAS7	33.33%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	40	2	880.54	-0.026	0	41.9	15.4	95.00%	K.IGPLGLSPK.K		K.IGPLGLSPK.K
131	142	2	1289.64	-0.064	0	69.4	29.4	95.00%	K.EILGTAQSVGCR.V	Carbamidomethyl (+57)	K.EILGTAQSVGCR.V
17	31	2	1296.7	0.13	1	30	25	95.00%	R.AVGGEVGASAALAPK.I		R.AVGGEVGASAALAPK.I
68	86	2	1812.03	-1	0	32.2	19.5	95.00%	R.QAAASVVPSASSLVITALK.E		R.QAAASVVPSASSLVITALK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
203	A6ZM77_YEAS7	8.18%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
425	437	2	1395.76	-0.44	0	26.6	24.3	95.00%	K.GAMLIPTLYPALH.D		K.GAMLIPTLYPALHDPEVYENPDEF IPER.W
248	260	2	1545.88	-1.3	0	24.1	21.2	94.60%	L.ELVNFPIIIPYTK.T		K.IADDYYLVTAALELVNFPIIIPYTK.T
284	296	2	1353.65	-2.1	0	63.7	30.4	95.00%	K.DHIAAGGKPVCVM.D	Carbamidomethyl (+57)	K.DHIAAGGKPVCVMDAWCK.L
284	301	3	2013.92	-0.76	1	42	29.8	95.00%	K.DHIAAGGKPVCVMDAWCK.L	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.DHIAAGGKPVCVMDAWCK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
204	A6ZQ99_YEAS7	11.14%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
82	96	3	1646.92	-1.7	1	40.7	21.4	95.00%	S.DVGKGQAVLLNQHIR.L		R.ISSAGQQVTGYTHPDFNNQWEV LPPHGSDVGKGQAVLLNQHIR.L
35	44	2	1165.6	-1.2	0	32	28.8	95.00%	T.DAFLHSHLAR.Y		K.HQDTDAFLHSHLAR.Y
54	67	2	1444.69	-1.3	0	89.1	29.6	95.00%	R.ISSAGQQVTGYTHP.D		R.ISSAGQQVTGYTHPDFNNQWEV LPPHGSDVGK.G
20	30	2	1325.72	-0.011	1	23.4	26	92.30%	K.TVNYFDIITIK.H		K.TVNYFDIITIK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
205	AGP1_YEAST	5.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
389	402	3	1425.77	-0.76	0	26.7	24.2	95.00%	K.ASPYVIAVASHGVR.V		K.ASPYVIAVASHGVR.V
38	57	3	2278.08	-1.6	1	52.1	28.2	95.00%	N.DRPSSQPHLGYEQHNTSAVR.R		K.NSSTEIHATGQDNEIEYFETGSNDRPSSQPHLGYEQHNTSAVR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
206	B3LL17_YEAS1	5.32%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
142	152	2	1286.72	-0.49	1	52.8	23.7	95.00%	R.ELIELGFITPR.T		R.ELIELGFITPR.T
256	265	2	1131.64	-0.37	0	34.9	25.2	95.00%	K.AILAANIYQR.F		K.AILAANIYQR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
207	A6ZU67_YEAS7	4.97%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
521	544	2	2313.14	-1.3	1	70.5	27	95.00%	R.DRPGSVLMNVVSGGIAEASAQQAG.D		R.DRPGSVLMNVVSGGIAEASAQQAGDLMQDLK.T
521	536	2	1570.81	-1.2	0	59.2	26.9	95.00%	R.DRPGSVLMNVVSGGIA.E		R.DRPGSVLMNVVSGGIAEASAQQAGDLMQDLK.T
598	609	2	1399.73	0.22	1	43.2	26.9	95.00%	R.IPTAVVWIDCAR.L	Carbamidomethyl (+57)	R.IPTAVVWIDCAR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
208	A6ZT43_YEAS7	13.38%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
368	383	4	1797.89	-0.43	1	21.2	28.2	95.00%	K.KPNLHGYGHPNPPNEK.S		K.KPNLHGYGHPNPPNEK.S
464	478	2	1937.96	-2	0	66.2	27.6	95.00%	Q.EQQLQQQQQQQQLR.A		K.LQEQQLQEQQLQQQQQQQQLR.A
301	312	2	1299.69	-1.3	0	48.1	27.1	95.00%	Y.DLAQGLPVQFGR.Y		R.STNVYDLAQGLPVQFGR.Y
479	499	2	2212.06	-1.3	0	79.8	28	95.00%	R.ATGQPPSQPQAQTQSQQFGAR.Y		R.ATGQPPSQPQAQTQSQQFGAR.Y
360	367	2	958.49	-0.13	1	37.6	27.3	95.00%	R.GWDLNINK.K		R.GWDLNINK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
209	A6ZT41_YEAS7	12.37%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
70	88	2	1955.01	-0.52	1	67.6	25.5	95.00%	K.ALLSNASQLEMVPPSATAR.H		K.ALLSNASQLEMVPPSATAR.H
8	24	2	1776.91	-6.6	1	63.3	26.3	95.00%	K.NQLNTGGVPNGVHNTKK.E		K.NQLNTGGVPNGVHNTKK.E
79	88	2	1057.52	-0.78	0	41.1	29.3	95.00%	L.EMVPPSATAR.H		K.ALLSNASQLEMVPPSATAR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
210	A7A1C4_YEAS7	4.60%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
742	749	2	921.53	0.094	0	24.3	22.4	94.80%	K.YIALSSIR.E		K.YIALSSIR.E
389	402	2	1387.68	-0.65	0	39.1	29.9	95.00%	M.DSVANAQMAAQAVL.D		K.QHYSATPTAFVTMDSVANAQMAAQAVLDPR.V
375	388	2	1580.76	-1.6	1	52.2	29.1	95.00%	R.KQHYSATPTAFVTM.D		R.KQHYSATPTAFVTMDSVANAQMAAQAVLDPR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
211	A6ZSR4_YEAS7	15.44%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	48	2	1489.78	-1.2	1	41.3	26.9	95.00%	K.SHPFGHALVAGIER.Y		K.SHPFGHALVAGIER.Y
127	133	2	955.46	1.8	0	26.9	29.7	91.90%	K.NQWFFSK.L		K.NQWFFSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
212	YJT8_YEAST	6.92%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
311	320	2	1196.66	0.073	0	54	24.7	95.00%	K.ISQLVTFYAR.I		K.ISQLVTFYAR.I
90	105	2	1711.92	-1.9	0	59.2	23.6	95.00%	R.ELPTAQTVAAKPSPFR.R		R.ELPTAQTVAAKPSPFR.R
302	310	2	1045.56	-1.4	1	30.2	27.3	95.00%	A.ETIELLNSK.I		K.DTYAFQAETIELLNSK.I

222	235	2	1652.82	-1.4	0	70	27.7	95.00%	E.DNTALLHHSQYNIK.S		K.IGVIEYDIDDDTLFNEPIASTNDEVPPLDLDDDEDDDEFYDDQSNIEDNTALLHHSQYNIK.S
185	196	2	1320.62	-2	1	48.4	29.9	95.00%	D.DTLFNEPIASTN.D		K.IGVIEYDIDDDTLFNEPIASTNDEVPPLDLDDDEDDDEFYDDQSNIEDNTALLHHSQYNIK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
213	A6ZQR0_YEAS7	7.73%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
36	56	2	2569.94	-1.5	1	57.3	28.3	95.00%	E.DKPCCSQYGECGTGQYCLNNC.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VEAATFCNATQACPEDKPCCSQYGECGTGQYCLNNCDVR.Y
65	74	2	1205.52	-1.4	0	27.7	30.7	91.50%	H.DSCMPVPICK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.YSFSHDSCMPVPICK.S
60	74	2	1826.78	-1.1	1	62.4	30.7	95.00%	R.YSFSHDSCMPVPICK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.YSFSHDSCMPVPICK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
214	A6ZWW4_YEAS7	13.39%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
75	85	2	1188.6	-1.1	0	59.1	29.5	95.00%	I.DLSQLSSTPNK.L		K.SENDEDLFCAVTNPVTGSYIDLSQLSSTPNK.L
60	74	2	1655.79	-0.71	0	63	30.3	95.00%	E.DLFCAVTNPVTGSYI.D	Carbamidomethyl (+57)	K.SENDEDLFCAVTNPVTGSYIDLSQLSSTPNK.L
332	346	2	1598.74	-0.34	1	38.3	30.2	95.00%	R.LRSSPSASSSSLANR.E	Phospho (+80)	R.LRSSPSASSSSLANR.E
190	199	2	1179.6	0.26	1	58.5	30.1	95.00%	K.ATLLNFVCDK.E	Carbamidomethyl (+57)	K.ATLLNFVCDK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
215	A6ZT92_YEAS7	5.07%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1132	1145	2	1594.83	-0.89	1	29	26.8	95.00%	K.HTEPLQLPLNSSFL.D		K.HTEPLQLPLNSSFLDYSR.E
2	18	2	1995.06	4.7	1	37.4	24.1	95.00%	M.PEIYGPQPLKPLNTVMR.H	Acetyl (+42)/ Deamidation (+1)	-.MPEIYGPQPLKPLNTVMR.H
1480	1492	2	1480.76	-0.21	1	64	27.6	95.00%	K.IWTTSGDLLNSFK.N		K.IWTTSGDLLNSFK.N
1443	1465	3	2668.16	-1.5	0	35.2	28.9	95.00%	V.DQNVTSQYGSQQKPTTMTCMQVH.E	Carbamidomethyl (+57)	R.SEDPVESFVDQNVTSQYGSQQKPTTMTCMQVHEHAPIIATGTK.Q
131	142	2	1434.75	0.21	1	56.2	27.7	95.00%	K.NLQAQYETLSLR.T		K.NLQAQYETLSLR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
216	ATG27_YEAS7	7.75%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	130	2	1223.56	0.55	1	42	30.5	95.00%	K.GATWGANSFDAK.L		K.GATWGANSFDAK.L
142	150	2	1058.47	-0.68	1	28.2	31.1	91.70%	Q.DELTSHTWA.D		K.QDELTSHTWADK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
217	A6ZTN7_YEAS7	7.45%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
63	80	4	1965.08	-0.7	1	40.5	20.8	95.00%	K.HLHGLPILQSPSLTPAER.L		K.HLHGLPILQSPSLTPAER.L
47	62	2	1661.86	-1	1	65.2	26.7	95.00%	I.DVSSTASIVPVPHEPK.H		R.FVSILSLFGCAATLVTAHDDMDMDMDMDMDMDMNIDTTTSQSIDVSSTASIVPVPHEPK.H
209	221	2	1417.69	-1.4	1	54	30.2	95.00%	N.DLESTPVMVNSAR.G		K.EYRPVDTIPLNDLESTPVMVNSAR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
218	A6ZQ10_YEAS7	8.58%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
478	491	2	1464.77	0.42	1	43	26	95.00%	R.LGGSSLLECVVFGK.T	Carbamidomethyl (+57)	R.LGGSSLLECVVFGK.T
327	336	2	1150.55	-0.44	1	34.4	30.1	95.00%	R.DTVTMEIQSK.C		R.DTVTMEIQSK.C
276	286	2	1239.62	-1.2	0	38.3	28.2	95.00%	M.DQVQVHPTGFI.D		K.LGAELIDMDQVQVHPTGFIDPNDR.E
319	326	2	966.48	0.8	1	29	29	95.00%	R.FTNELSTR.D		R.FTNELSTR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
219	A6ZR28_YEAS7	25.19%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
11	20	2	1109.69	0.25	1	49.1	13.4	95.00%	R.KVISNPLLAR.K		R.KVISNPLLAR.K
12	20	2	981.6	0.28	0	25.8	18.3	95.00%	K.VISNPLLAR.K		K.VISNPLLAR.K
69	83	2	1539.79	0.12	1	37.8	27	95.00%	K.SVGFGLVYNSVAEAK.K		K.SVGFGLVYNSVAEAK.K
53	61	2	996.5	0.17	0	47.5	29	95.00%	K.DAVSVFGFR.T		K.DAVSVFGFR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
220	B3LJW5_YEAS1	10.34%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
79	98	2	2198.01	-1.6	1	67.3	29.4	95.00%	K.SLINFPQEQQQNGSTSTATF.D	Deamidation (+1)	K.SLINFPQEQQQNGSTSTATFDLLNALIEEGHLDPEAPDK.L
378	390	2	1410.74	-2.1	0	28.8	26.9	95.00%	T.DHVPMILAVFGGR.R		K.NAGNDEGDASSGTDHVPMILAVFGGR.R
8	19	2	1468.68	-0.55	1	44.5	29.8	95.00%	K.VSSMQNFEMIQR.E		K.VSSMQNFEMIQR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
221	A6ZVM1_YEAS7	3.65%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
109	126	2	1896.92	-1.3	0	73.7	28.5	95.00%	K.FTNIASSPPSSSNNIFSK.A		K.FTNIASSPPSSSNNIFSK.A
827	836	2	1095.53	-0.93	1	39.9	31.1	95.00%	I.DGESLGMFLK.H		R.NACLLIDGESLGMFLK.H
42	55	2	1567.78	-2	1	48.9	28.6	95.00%	L.DSLQINNNPEPLSK.H		K.QNLFNSNNNQHANSVDSFDLHLDDSFDAALDSLQINNNPEPLSK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
222	A6ZPF1_YEAS7	6.00%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
180	195	2	1692.94	-0.95	0	26.5	21.4	95.00%	T.DNSLLPSLIKPVQAAQ.D		K.AIFTDNSLLPSLIKPVQAAQDVK.Y
263	278	2	1817.76	-2.3	1	62.7	30.6	95.00%	D.DLCCIMYTSGSTGEPK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.DDLCCIMYTSGSTGEPK.G
2	11	2	1060.59	1.2	0	35.5	25.2	95.00%	M.VAQYTVPVGK.A		-.MVAQYTVPVGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
223	B3LK87_YEAS1	6.65%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
122	136	2	1829.77	-1	0	71.5	31.2	95.00%	M.DMSMGMNYYLTPTYK.N	Oxidation (+16)	K.TLASTMSSMASMSMGSSSMSGMSMSMSSTPTSSASAQTTSDSSMSGMSGMSSSDNSSSSGMDMDMSMGMNYYLTPTYK.N
303	314	2	1398.52	0.98	0	44.9	30.8	95.00%	K.SCPGFGNCQCGR.H	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.SCPGFGNCQCGR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
224	B3LHY2_YEAS1	4.31%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
108	120	2	1258.65	0.7	1	69.9	27.8	95.00%	K.SNIGNAEVAGLSK.D		K.SNIGNAEVAGLSK.D
306	315	2	1319.66	-2	0	47.7	29.8	95.00%	F.EWFQVWQAVK.D		K.FEWFQVWQAVK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
225	A6ZSL9_YEAS7	15.25%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
155	163	2	1102.58	-0.29	1	45.3	29.3	95.00%	R.LISQAWETR.S		R.LISQAWETR.S
164	179	3	1787.86	0.12	0	32.5	29.5	95.00%	R.SQFHSQSNVLNTANNK.V		R.SQFHSQSNVLNTANNK.V
49	57	2	1012.57	-0.31	1	40.6	24	95.00%	K.QLEGILGQR.Q		K.QLEGILGQR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
226	A7A1B6_YEAS7	10.99%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
154	163	2	1225.58	-0.23	1	57.5	30.7	95.00%	K.YVECSALTQR.G	Carbamidomethyl (+57)	K.YVECSALTQR.G
134	144	3	1242.67	2.2	1	21.5	27.1	95.00%	R.LRPITSEQGSR.L		R.LRPITSEQGSR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
227	A6ZMP4_YEAS7	12.20%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
170	186	2	1887.94	-1.8	0	75.4	27.5	95.00%	N.DVNGQQIFSQALLNANR.R	Deamidation (+1)	R.QYTIIQPEATDEEVEAAINDVNGQQIFSQALLNANR.R
35	43	2	1085.48	-0.95	1	41.1	30.5	95.00%	S.DDFVAFMNK.I		-.MSNANPYENNNPYAENYEMQEDLNNAPTGHSDGSDDFVAFMNK.I
44	53	2	1100.59	-1.2	0	72.2	28.5	95.00%	K.INSINANLSR.Y		K.INSINANLSR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
228	A6ZM44_YEAS7	5.34%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
98	109	2	1289.65	-1.2	1	39.5	28.8	95.00%	R.SVDMTSPLLTNL.E		R.SVDMTSPLLTNLEAGTHANQK.K
100	118	2	2039.99	-0.69	1	78.3	27.9	95.00%	V.DMTSPLLTNLEAGTHANQK.K		R.SVDMTSPLLTNLEAGTHANQK.K
100	109	2	1103.55	-0.92	0	38.9	29.8	95.00%	V.DMTSPLLTNL.E		R.SVDMTSPLLTNLEAGTHANQK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
229	A6ZW73_YEAS7	5.88%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
82	93	2	1276.68	-0.013	0	43	27.3	95.00%	R.TISGLNMTALTR.V		R.TISGLNMTALTR.V
400	416	2	1907.9	-1.2	1	66	28.8	95.00%	L.ENYAPNMILSQSTGVER.R		K.DIEGHSLLENYAPNMILSQSTGVER.R
13	30	3	1972.99	-1.4	0	30.6	26.7	95.00%	T.DVTSLNASTVSHQSKPFR.Q		K.SDTDVTSLNASTVSHQSKPFR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
230	A6ZR09_YEAS7	14.05%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
44	60	3	1846.88	-0.18	1	49.9	29.7	95.00%	K.CGDCGSALQGISTLRPR.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CGDCGSALQGISTLRPR.Q
46	60	3	1629.82	-1.3	0	20.9	27	94.80%	G.DCGSALQGISTLRPR.Q	Carbamidomethyl (+57)	K.CGDCGSALQGISTLRPR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
231	A6ZYL7_YEAS7	5.10%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
36	47	2	1276.65	-1.3	1	35.5	28.5	95.00%	G.DSNEITSLASLK.A		R.ASTLTNEEQTVDPSNNDSQEDISLGDSNEITSLASLK.A
244	257	2	1586.77	-1.5	1	48.7	29.1	95.00%	A.DTEGFTPLHWGTVK.G		K.IADTEGFTPLHWGTVK.G
646	658	2	1324.73	-1.8	0	24.4	22.2	95.00%	N.DTVLAPVPGSTIR.K		K.SIGPDGLSFNENFNTTPEGFAPSIDPGEESNDTVLAPVPGSTIR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

232	A6ZXD4_YEAS7	8.81%		100%		4						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
69	82	2	1533.81	-1.4	1	57.5	26.1	95.00%	S.DATVVLPLSEHTPR.L		R.DSDATVVLPLSEHTPR.L	
33	43	2	1196.6	-1.8	1	32.8	28.8	95.00%	Q.DDTALTSLPHK.N		K.QDDTALTSLPHK.N	
600	616	2	1973.98	-0.86	1	82.3	27.7	95.00%	K.QNNQAYSSIQNEQILPK.N		K.QNNQAYSSIQNEQILPK.N	
659	676	2	1669.76	-4.6	0	49.1	30.7	95.00%	S.DNIAANKPSSGGGQNSPG.D		R.TDPNISDNIAANKPSSGGGQNSPGDMAVA.-	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
233	A7A0U9_YEAS7	12.08%	100%	5								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
494	505	2	1297.7	-0.94	0	40.6	26.2	95.00%	W.DHLSLLPTFGAK.D		K.AQYNEIQGWDHLSLLPTFGAK.D	
234	249	2	1776.95	-1.2	1	54.2	24.2	95.00%	K.LIDLTQFPAFVTPMGK.G		K.LIDLTQFPAFVTPMGK.G	
259	273	2	1595.85	-1.6	1	57.5	24.9	95.00%	R.YGGVYVGTLSKPEVK.E		R.YGGVYVGTLSKPEVK.E	
155	172	2	2004.1	-1.5	0	43.4	20.1	95.00%	R.TTYVTQRPVYLGLPANLV.D		R.TTYVTQRPVYLGLPANLVDLNVPAK.L	
155	179	3	2741.51	-0.39	1	35.6	16.2	95.00%	R.TTYVTQRPVYLGLPANLVDLNVPAK.L		R.TTYVTQRPVYLGLPANLVDLNVPAK.L	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
234	PSS_YEAST	14.13%	100%	3								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
192	201	2	1115.63	-0.11	0	45.3	25.1	95.00%	R.FNVTVAQLPK.D		R.FNVTVAQLPK.D	
7	16	2	1187.52	-0.87	1	28.2	30.6	92.60%	E.DFAPQEFPHT.D		-.MVESDEDFAPQEFPHTDTDVIVNEHR.D	
44	62	2	1957.03	-0.78	1	23.7	25.2	93.90%	R.RASSIFSINTTPLAPPNAT.D		R.RASSIFSINTTPLAPPNATDIQK.F	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
235	B3LJS4_YEAS1	4.70%	100%	3								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
327	342	2	1673.86	-1.4	0	46.7	26.7	95.00%	I.DVVQSKPVGLPQYSTG.D		K.AVIFISEPYGENIDVVQSKPVGLPQYSTGDASGLNWDGSPVEEK.D	
248	258	2	1205.57	-1	0	43.2	30	95.00%	K.ENFNPLSSNGK.L		K.ENFNPLSSNGK.L	
299	309	2	1226.72	0.078	1	48	22.2	95.00%	K.LVSQQVLIAEK.F		K.LVSQQVLIAEK.F	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
236	A6ZYA1_YEAS7	2.36%	100%	3								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
300	308	2	1055.63	0.75	1	31.9	21.5	95.00%	R.SVLDLLLQR.L		R.SVLDLLLQR.L	
2	15	2	1580.88	-1.1	1	46.8	21.7	95.00%	M.SLPLKPLTIDSNNK.Q	Acetyl (+42)	-.MSLPLKPLTIDSNNK.Q	
78	94	3	1760.99	-0.85	1	52.8	19.9	95.00%	R.RLTSSLSPALPAGVHQK.T		R.RLTSSLSPALPAGVHQK.T	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
237	A6ZTY6_YEAS7	12.81%	100%	6								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
58	65	2	1146.54	-0.025	1	28.3	29.5	94.30%	S.DLEYFFWK.F		R.SEDADEQDSSDLEYFFWK.F	
127	140	2	1506.69	-1.5	1	71.4	29.9	95.00%	I.DQPTGTGFSVEQNK.D		K.GDLLFIDQPTGTGFSVEQNK.D	
76	92	2	1872.88	-3.1	0	26.1	28.8	92.10%	V.DRPLIIWLNGGPGCSSM.D	Deamidation (+1)/ Carbamidomethyl (+57)	K.FTNNDSNGNVDRPLIIWLNGGPGCSSMDGALVESGPFR.V	
226	241	2	1839.87	-0.88	1	104	29.9	95.00%	I.DPNTQSLSYLPFAMEK.K		K.ALLIGNGWIDPNTQSLSYLPFAMEK.K	
22	31	2	1052.57	-0.69	1	25.8	23.9	95.00%	Y.ELLPGLSEVP.D		K.VAYELLPGLSEVPDPSNIPQMHAGHIPLR.S	
313	324	2	1440.58	0.64	0	42	30.7	95.00%	K.DSYPSCGMNWPK.D	Carbamidomethyl (+57)	K.DSYPSCGMNWPK.D	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
238	A6ZRP5_YEAS7	6.54%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
663	682	2	2177.08	-1.8	1	70	27.9	95.00%	K.TTESNFGFITVLPGAFSAYR.F		K.TTESNFGFITVLPGAFSAYR.F
216	231	2	1808.81	-1.7	0	41.9	29.8	95.00%	H.DQPFGYNNGYHGLQAK.D	Deamidation (+1)	R.TSPSIASSSDGYADQEARPILEQPNNNMNSGNIPQYHDQPFGYNNGYHGLQAK.D
91	101	2	1313.63	-1.2	0	39.9	30.3	95.00%	R.DIYGGFVNHHR.Q		R.DIYGGFVNHHR.Q
642	652	2	1214.66	-1.1	0	31.3	26.1	95.00%	K.LLNPLVASQNF.E		K.LLNPLVASQNFEYK.M
200	215	2	1855.79	-1.5	0	49.7	30.1	95.00%	L.EQPNNNMNSGNIPQYH.D		R.TSPSIASSSDGYADQEARPILEQPNNNMNSGNIPQYHDQPFGYNNGYHGLQAK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
239	A6ZLK4_YEAS7	24.12%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
140	152	2	1373.75	-1.4	0	26.3	25.5	95.00%	A.ELQGLPYVAVSAK.T		K.YDLVCEEHSGEVTIPAELQGLPYVAVSAK.T
153	162	2	1171.55	-0.19	1	36	29.9	95.00%	K.TGYNFDTLNK.I		K.TGYNFDTLNK.I
163	174	2	1372.79	-1.5	1	60.5	21.2	95.00%	K.IIISLVPESQFK.T		K.IIISLVPESQFK.T
112	124	2	1389.76	-1.2	1	44.3	25.4	95.00%	R.AQGTQVILVGNKY.D		R.AQGTQVILVGNKYDLVCEEHSGEVTIPAELQGLPYVAVSAK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
240	A6ZMS7_YEAS7	7.63%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
274	288	2	1724.84	-1.3	1	64.5	28.8	95.00%	E.DAVIPLIFSEYGCNK.N	Carbamidomethyl (+57)	K.LNSTFEDAVIPLIFSEYGCNK.N
223	233	2	1310.59	-0.44	1	29.4	30.8	94.00%	K.YLQCNSLDGNK.V	Carbamidomethyl (+57)	K.YLQCNSLDGNK.V
81	94	2	1580.79	-2	0	77.5	27.7	95.00%	R.DAYAFQQLGVNTVR.I		R.DAYAFQQLGVNTVR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
241	A7A0F5_YEAS7	13.73%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
158	168	2	1372.73	-1.6	0	46.4	27.4	95.00%	Q.ELFINQQQQLL.E		K.DEPLQSQLQSLSQPQPPQPMVSNQELFINQQQQLLEQDSHLGALSQSIGR.T
42	52	2	1240.74	0.24	1	21.7	21.2	90.80%	R.QLGSILELLQK.C		R.QLGSILELLQK.C
171	183	2	1339.68	-0.53	0	60.9	27.8	95.00%	Q.DSHLGALSQSIGR.T		K.DEPLQSQLQSLSQPQPPQPMVSNQELFINQQQQLLEQDSHLGALSQSIGR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
242	A6ZYE1_YEAS7	9.78%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
255	264	3	1246.75	-1.5	0	25.9	17.1	95.00%	R.ILLTHVPLWR.D		R.ILLTHVPLWR.D
317	330	2	1702.75	-0.86	0	68.9	30.5	95.00%	H.DHCQISHSYPFQGK.T	Carbamidomethyl (+57)	K.TQPEILFSGDDHDHCQISHSYPFQGK.T
363	376	2	1454.67	-1.7	1	59.9	30.3	95.00%	S.DLTMVNAGGEYASK.T		K.SCAMNMGISRPAIQLLSLYNPSDLTMVNAGGEYASK.T
190	199	2	1132.57	-0.36	1	44.4	28.8	95.00%	G.DTVVESSLQR.F		R.TVMSLPGNHDIGFGDTVVESSLQR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
243	A6ZPF9_YEAS7	11.30%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
64	74	2	1162.6	-1.1	0	46.4	29.2	95.00%	A.DNLAISAQGFK.R		K.ADNLAISAQGFK.R
63	74	2	1233.63	-0.67	1	49.2	28.5	95.00%	K.ADNLAISAQGFK.R		K.ADNLAISAQGFK.R
64	75	2	1318.7	-1.4	1	45.7	27.9	95.00%	A.DNLAISAQGFKR.G		K.ADNLAISAQGFKR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
244	A6ZWH0_YEAS7	18.78%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
139	149	2	1302.71	-0.32	0	42	25.3	95.00%	K.QIVNIPSFMVR.L		K.QIVNIPSFMVR.L
70	78	2	1031.58	-0.42	1	59.2	25.2	95.00%	R.LFEGNALIR.R		R.LFEGNALIR.R
155	171	3	1781.89	-0.91	1	34.5	27.8	95.00%	K.HIDFAPTSPFGGARPGR.V		K.HIDFAPTSPFGGARPGR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
245	A6ZRQ3_YEAS7	4.18%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
255	269	2	1638.77	-0.076	0	73.6	29.8	95.00%	R.SGSFSSQLGNFFFSK.N		R.SGSFSSQLGNFFFSK.N
162	179	2	1859.96	-1.1	0	23.9	25.8	93.30%	R.AIPSLSSSIPYSVPNSNK.D		R.AIPSLSSSIPYSVPNSNK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
246	B3LML0_YEAS1	7.84%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
338	357	2	1950.97	-1.2	0	35.2	27.2	95.00%	E.DVSASPFVIALSNTGSMGAK.V		R.LLSGSNSEDVSASPFVIALSNTGSMGAK.V
252	265	4	1661.84	0.55	1	35	27.5	95.00%	K.YWHDPGAFAKPVFK.N		K.YWHDPGAFAKPVFK.N
570	581	2	1485.78	-1.5	0	35.9	25.9	95.00%	E.EQLIASKPFYYK.I		K.EAEEQLIASKPFYYK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
247	A6ZL24_YEAS7	4.62%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
581	587	2	822.44	-0.29	0	28.6	25.9	95.00%	K.SGFPFIR.L		K.SGFPFIR.L
369	378	2	1112.62	-0.19	0	28.9	24.4	95.00%	G.DNVVNQLLAK.M		R.GDGTGVGDNVVNQLLAK.M
425	433	2	1104.62	0.26	1	31.2	25	95.00%	R.LQIFDIQTK.K		R.LQIFDIQTK.K
603	611	2	1111.57	0.34	1	31.2	27.6	95.00%	K.IAYIDNTFR.D		K.IAYIDNTFR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
248	A6ZN90_YEAS7	18.06%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
111	119	2	954.58	0.084	1	24.2	18.6	94.70%	K.IGIVEISPK.G		K.IGIVEISPK.G
8	24	2	1927.94	0.72	1	65.4	28	95.00%	R.DVAAQDFINAYASFLQR.Q		R.DVAAQDFINAYASFLQR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
249	A6ZKS1_YEAS7	16.40%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	146	2	1120.66	1.5	1	22.7	20	92.60%	R.ALVEHIIQAK.A		R.ALVEHIIQAK.A
10	19	2	899.54	-0.46	0	66.1	24	95.00%	R.LAASVVGVGK.R		R.LAASVVGVGK.R
118	128	3	1415.76	0.23	1	21.4	26.4	95.00%	K.HLYHVLYKESK.G		K.HLYHVLYKESK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
250	A6ZSL1_YEAS7	4.47%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
36	46	2	1235.6	-1.2	1	38.3	28.9	95.00%	S.DSYGLPQLSEK.Y		K.HVFMGMEHELNPETHNDSNSDSYGLPQLSEK.Y
535	551	2	2074.96	-1.1	1	50	29.2	95.00%	Y.ESPYTFIETYTWGTPQR.N		R.MGDVALATTAYESPYTFIETYTWGTPQR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
251	A6ZTY9_YEAS7	11.33%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
63	71	2	1108.55	-2.2	1	28.9	29.1	95.00%	G.DFIIYGPER.H		R.NPQSSSQLTGDFIIYGPER.H
80	93	2	1517.73	-1	1	83	29.6	95.00%	R.DTSHGEITLSAPYK.G		R.DTSHGEITLSAPYK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
252	A6ZTV6_YEAS7	7.61%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

320	329	2	1017.55	-0.32	0	56.6	25.3	95.00%	T.DLAQVFLAAA.E		R.FGDPETQAVLSLLDDQTDLAQVFLAAAEHR.L
231	252	2	2085.09	-1.8	0	64.9	24.8	95.00%	K.GLNTGGMGAYAPAPVATPSLLK.T		K.GLNTGGMGAYAPAPVATPSLLK.T
400	411	2	1288.7	-0.084	1	66.5	26.3	95.00%	R.VLSVTSTAQDLR.T		R.VLSVTSTAQDLR.T
29	45	2	1705.81	-0.89	1	50.9	29.6	95.00%	K.IYVAPGNGGTATMDPSR.V		K.IYVAPGNGGTATMDPSR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
253	A6ZQL2_YEAS7	12.54%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
176	188	2	1538.82	-2	0	60.2	24.7	95.00%	K.DPVVNNTHIIVYR.E		K.DPVVNNTHIIVYR.E
206	219	2	1579.73	-1.3	1	52	30.4	95.00%	T.DENLVMSVTTVGCR.R	Carbamidomethyl (+57)	R.ETPIALISLAPNMTLSTDENLVMSVTTVGCR.R
160	171	2	1329.74	-0.24	1	64.3	24.3	95.00%	K.VFGINLNDLVAR.H		K.VFGINLNDLVAR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
254	A6ZUW4_YEAS7	27.62%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
41	52	2	1292.82	0.83	0	49.5	7.78	95.00%	K.LIIIAANTPVLR.K		K.LIIIAANTPVLR.K
67	83	2	1815.88	-0.33	1	86.2	28.4	95.00%	K.VYYFQGGNNELGTAVGK.L		K.VYYFQGGNNELGTAVGK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
255	A6ZP14_YEAS7	3.21%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
505	514	2	1170.59	-1	0	28.7	27.9	95.00%	T.DNLTIFYTGK.M		K.MDSELTDNLTIFYTGK.M
549	558	2	1129.64	0.25	1	31.7	25.4	95.00%	R.MTPILLSLDK.G		R.MTPILLSLDK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
256	B3LU76_YEAS1	9.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
81	92	2	1422.67	-2	0	54.1	29.9	95.00%	R.FGNLPAQWSAFW.D		R.FGNLPAQWSAFWDK.T
81	94	2	1665.79	-0.74	1	56.2	29.7	95.00%	R.FGNLPAQWSAFWDK.T		R.FGNLPAQWSAFWDK.T
71	80	2	1121.59	-0.92	0	46.5	28.6	95.00%	Y.DAFLFGVPTR.F		K.TLLEYDAFLFGVPTR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
257	A6ZY37_YEAS7	5.12%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
320	331	2	1295.53	-1.3	0	64.9	30.4	95.00%	R.FSNAGGFTMHNN.D		R.FSNAGGFTMHNNDSSTFK.L
378	392	2	1557.69	-0.52	1	72	31	95.00%	R.SSSPSSSFTVSSNER.S		R.SSSPSSSFTVSSNER.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
258	A6ZSD5_YEAS7	10.05%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
101	111	2	1246.53	-0.066	1	45.5	30.4	95.00%	R.GINFDYSGSCK.I	Carbamidomethyl (+57)	R.GINFDYSGSCK.I
90	100	2	1261.49	-0.079	0	75.5	29.7	95.00%	K.FGSMSCSSMPR.G	Oxidation (+16)/ Carbamidomethyl (+57)	K.FGSMSCSSMPR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
259	A6ZMN0_YEAS7	7.27%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
428	439	2	1189.56	-2.1	0	50.3	30.1	95.00%	S.DNIAAGSTTNLN.D		K.DTLLESGGEDNDFDEDFSDGDSDNIAAGSTTNLNDDIIIR.N
200	211	2	1395.68	-1.9	1	52.3	29.8	95.00%	P.DMPNHTVIVENK.T		R.QYIQEEGAYAWEFSPNPDMPNHTVIVENK.T
149	164	2	1824.93	-1.3	1	51.3	26.6	95.00%	K.QNPPFLLNQGLLQQSE.D		K.QNPPFLLNQGLLQQSEDSNPDATR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
260	VTH1_YEAST	3.68%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
202	210	2	1093.56	-0.63	0	55	29.4	95.00%	N.DASILCLFR.N	Carbamidomethyl (+57)	K.SSEDSDLGGNDASILCLFR.N
1263	1275	2	1538.75	-0.78	1	28.2	28.4	95.00%	K.CFIGNIPLSEFSR.N	Carbamidomethyl (+57)	K.CFIGNIPLSEFSR.N
524	533	2	1279.66	-2	0	24.4	26.5	93.00%	Y.DLIMPIYPYR.L		K.TWGEYDLIMPIYPYR.L
394	406	2	1445.75	0.2	1	37.6	27	95.00%	K.VSVDNGLTWTNLK.V		K.VSVDNGLTWTNLK.V
488	499	2	1466.76	0.33	0	39.9	26.3	95.00%	G.DLGNIIMYIPYR.S		R.LVHNSTGLYTTGDLGNIIMYIPYR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
261	A6ZLI0_YEAS7	4.51%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
230	240	2	1230.6	-0.5	1	37.6	28.9	95.00%	R.WLVSHGFVSEA.E		R.WLVSHGFVSEAETALFK.L
67	77	2	1254.6	-1	1	37.2	29.9	95.00%	Y.DDTWVGQHGLK.Q		R.FEAPDENISYDDTWVGQHGLK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
262	A6ZKZ2_YEAS7	17.31%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	133	2	1855	-0.52	1	47.2	23.5	95.00%	R.VQVGDIVTVGQCRPISK.T	Carbamidomethyl (+57)	R.VQVGDIVTVGQCRPISK.T
58	67	2	1148.6	0.44	0	68.1	28	95.00%	K.CPFTGLVSIR.G	Carbamidomethyl (+57)	K.CPFTGLVSIR.G
121	133	2	1471.78	-1.7	0	58.3	26.4	95.00%	G.DIVTVGQCRPISK.T	Carbamidomethyl (+57)	R.VQVGDIVTVGQCRPISK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
263	A6ZQG2_YEAS7	10.35%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
286	299	2	1542.76	-2.1	0	43.8	28.6	95.00%	E.DLGTGIQSYGYITR.N		K.NHLYSTFHTFQGIEDLGTGIQSYGYITR.N
28	40	2	1418.67	-1.7	1	77.2	30.4	95.00%	K.LDFTNVGFTGSYV.D		K.LDFTNVGFTGSYVDVNK.F
191	204	2	1433.68	0.14	0	38.4	29.7	95.00%	R.SGIPAYYGYGGTTK.M		R.SGIPAYYGYGGTTK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
264	A6ZQC8_YEAS7	4.88%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
151	159	2	1067.64	-0.12	1	30.8	21.4	95.00%	R.ILALLPDWK.C		R.ILALLPDWK.C
78	91	2	1646.79	-1.9	1	55.3	28.9	95.00%	G.DPTYLPNSPYPEVR.S		K.GDPTYLPNSPYPEVR.S
383	398	2	1816.83	-2.1	1	51.4	30.3	95.00%	K.YMPVISGSTYDNTQNK.Y		K.YMPVISGSTYDNTQNK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
265	TCB3_YEAST	3.37%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1340	1352	2	1358.68	-0.087	0	85	29	95.00%	R.SPSNLNSTSVTPR.A		R.SPSNLNSTSVTPR.A
1339	1352	3	1514.78	2.8	1	28.1	27.7	95.00%	R.RSPSNLNSTSVTPR.A		R.RSPSNLNSTSVTPR.A
1244	1257	2	1625.81	-1.4	1	43.7	28.6	95.00%	K.LQGSFNPEYIKPSF.D		K.LQGSFNPEYIKPSFDIVK.G
101	124	3	2439.32	-1.4	1	21.9	20.5	95.00%	K.TNQLPGPNPQGSIGAVPLEGLRPK.E		K.TNQLPGPNPQGSIGAVPLEGLRPK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
266	A6ZT81_YEAS7	6.64%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
61	79	2	1944.02	-2	0	48.1	25.1	95.00%	K.GVMNAVNNVNNVIAAAFVK.A		K.GVMNAVNNVNNVIAAAFVK.A
321	330	2	1100.54	-1.7	1	50.4	29	95.00%	A.DDLTVTNPAR.I		K.TAGIQIVADDLTVTNPAR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
267	A6ZU78_YEAS7	17.45%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
116	126	2	1190.75	-1.4	1	46.1	13.6	95.00%	K.GRIPNVPVIVK.A		K.GRIPNVPVIVK.A
97	111	2	1504.78	-0.21	1	38.5	27.6	95.00%	K.ETAPVIDTLAAGYGK.I		K.ETAPVIDTLAAGYGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
268	B3LLW4_YEAS1	15.57%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
140	150	2	1370.69	-0.67	1	48.3	28.6	95.00%	K.HQEFQNTNIIK.N		K.HQEFQNTNIIK.N	
2	16	2	1574.85	-2	0	63.5	25.7	95.00%	M.ALSLGQFINVGGMVK.D	Acetyl (+42)	-.MALSLGQFINVGGMVK.D	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
269	A6ZN13_YEAS7	3.20%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
449	458	2	1265.59	-0.15	0	29.8	29.8	95.00%	K.DFICNWLGNK.A	Carbamidomethyl (+57)	K.DFICNWLGNK.A	
93	99	2	907.44	-0.027	1	32.5	29.7	95.00%	K.DWDFVVK.N		K.DWDFVVK.N	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
270	A6ZXF1_YEAS7	6.58%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
443	460	2	2064.96	-0.96	1	42.6	29.1	95.00%	R.VATNQEYQHPLSANYISM.D		R.VATNQEYQHPLSANYISMDSPDV INSSPGHFGMNSGQLLGNTTLYYG SLNGDDDDMTNDSALLR.F	
307	324	2	2056.95	-0.78	1	53.5	29.5	95.00%	K.SFGYTWAVPNENTQNTTK.S		K.SFGYTWAVPNENTQNTTK.S	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
271	A6ZT39_YEAS7	7.44%	100%	3								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
137	149	2	1410.76	-1.4	1	61.5	24.8	95.00%	R.SFPSLVAVEHLGR.T		R.SFPSLVAVEHLGR.T	
217	226	2	1159.63	-0.37	0	31.5	26.9	95.00%	L.DFLVIPVFNP.D		K.YLDDLDFLVIPVFNPDGYAYTWS HDR.L	
352	360	2	1068.49	1.1	1	29.7	31.1	94.00%	R.NYDVISACK.D	Carbamidomethyl (+57)	R.NYDVISACK.D	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
272	A6ZM19_YEAS7	6.45%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
305	316	2	1356.7	-1.2	1	24.8	28.3	90.40%	E.DRFTASTFTAIK.T		K.AAAPGIQLVAGEGFQSPLEDRFT ASTFTAIK.T	
96	109	2	1693.88	-1.2	1	49.7	26.4	95.00%	I.DQLWPGQLVVPEWK.L		K.SIHPGYLSEGGCLMFHYEADNEE NLEELNDSKPLIDQLWPGQLVVPE WK.L	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
273	A6ZXE1_YEAS7	15.00%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
36	43	2	896.54	0.19	0	23.6	16.3	94.00%	K.LSRPSLPK.I		K.LSRPSLPK.I	
13	22	2	1101.6	-1.1	1	45.6	28.1	95.00%	K.SKEQLASQLV.D		K.SKEQLASQLVDLK.K	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
274	A6ZKL0_YEAS7	17.69%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
81	90	2	1187.58	-2	1	38.8	29.7	95.00%	K.DLETLTMHTK.T		K.DLETLTMHTK.T	
91	103	2	1387.71	-0.66	1	73.9	27.7	95.00%	K.TYAAEIAHNISAK.N		K.TYAAEIAHNISAK.N	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
275	A6ZMB4_YEAS7	3.26%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
708	725	3	1835.83	-1.7	1	27.8	29.8	95.00%	K.NGGGGRPHGYQSVGNIEH.E	Deamidation (+1)	K.NGGGGRPHGYQSVGNIEHEEQI AQQR.H	
160	170	2	1171.63	-0.2	1	49	27.6	95.00%	K.FIEVNPGIAGR.A		K.FIEVNPGIAGR.A	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
276	A6ZYJ7_YEAS7	6.62%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	

262	274	2	1426.69	-0.77	0	68.3	28.7	95.00%	Q.DCGGFNLGSFLIK.N	Carbamidomethyl (+57)	R.DDIPYVDYSEEMEFLITQDCGGF NLGSFLIK.N
354	366	2	1485.65	-1.1	0	57.5	30	95.00%	H.DFVVNMAGCNFGR.D	Carbamidomethyl (+57)	K.DHDFVVNMAGCNFGR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
277	A6ZM38_YEAS7	12.50%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
117	128	2	1295.76	-0.39	0	61.9	20.5	95.00%	K.LPLSVINVSAQR.D		K.LPLSVINVSAQR.D
112	128	3	1794.07	0.4	1	22.5	10.8	95.00%	K.SLGLKLPLSVINVSAQR.D		K.SLGLKLPLSVINVSAQR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
278	A7A0Y0_YEAS7	13.12%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
83	88	2	757.39	1.1	0	40.1	24.8	95.00%	R.DAFHLR.V		R.DAFHLR.V
117	128	3	1219.66	-0.0072	0	31.5	26.8	95.00%	R.GAWGKPHGLAAR.V		R.GAWGKPHGLAAR.V
129	139	2	1245.71	0.15	1	55.6	24.3	95.00%	R.VDIGQIIFSVR.T		R.VDIGQIIFSVR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
279	A6ZNU6_YEAS7	10.00%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
166	175	2	1197.6	-0.43	1	26.7	28.7	93.00%	K.LESFQAVYNK.L		K.LESFQAVYNK.L
36	44	2	1100.63	-0.85	1	23.9	24.3	94.40%	K.AELRPLQFK.S		K.AELRPLQFK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
280	A6ZZX8_YEAS7	9.40%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	172	2	1351.69	-0.52	1	52.6	29.2	95.00%	K.QYAQEQGLLFR.E		K.QYAQEQGLLFR.E
6	16	2	1086.63	-0.19	1	29.6	24.5	95.00%	K.LVLLGDSSVGK.S		K.LVLLGDSSVGK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
281	A6ZQQ0_YEAS7	8.59%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
170	180	2	1259.73	-0.5	1	26	20.9	95.00%	R.VNAIEHVIIPR.T		R.VNAIEHVIIPR.T
2	12	2	1331.66	-0.15	1	35.7	29.4	95.00%	M.SGNREQVFPTR.M	Acetyl (+42)	-.MSGNREQVFPTR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
282	A6ZSI2_YEAS7	2.32%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1143	1154	2	1388.8	-0.43	0	40	22.6	95.00%	K.NAVILNYQTLLK.E		K.NAVILNYQTLLK.E
1595	1610	2	1793.04	-0.73	1	48.5	15.7	95.00%	K.QIGVENLQTLSPLILR.T		K.QIGVENLQTLSPLILR.T
728	737	2	1263.62	-0.86	1	32.8	28.6	95.00%	K.DEIIPCIYNK.A	Carbamidomethyl (+57)	K.DEIIPCIYNK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
283	ATC4_YEAST	1.18%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1480	1487	2	954.55	-0.76	1	38.2	23.3	95.00%	R.INEIRPLT.D		R.INEIRPLTDFK.E
855	865	2	1171.59	-0.26	0	30.7	29.2	95.00%	R.QLGYSFVGSSK.S		R.QLGYSFVGSSK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
284	A6ZMV1_YEAS7	5.90%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
188	201	2	1563.78	-1.6	0	69.1	28.4	95.00%	K.NTVSNACLFQIAAR.L	Carbamidomethyl (+57)	K.NTVSNACLFQIAAR.L
324	336	2	1422.74	-0.86	0	44.9	27.8	95.00%	R.MLGLTSVMAPFTR.D		R.MLGLTSVMAPFTR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
285	B5VMB7_YEAST	5.35%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	45	2	1319.56	-0.12	0	35.9	30.4	95.00%	K.NYQVCAGMYSK.E	Carbamidomethyl (+57)	K.NYQVCAGMYSK.E
134	150	2	1856.91	-1	1	67.3	27.7	95.00%	R.SLANPIMTFSQNEVGLH.D		R.SLANPIMTFSQNEVGLHDTR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
286	A7A0Y2_YEAS7	11.07%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
181	188	2	972.49	1	1	28.8	28.6	95.00%	F.ENIVEQNK.I		R.GNAQLDYILEMGQQSFENIVEQNK.I
1	10	2	1201.59	0.1	0	31.1	29.2	95.00%	-.MNALYNHAVK.Q	Acetyl (+42)	-.MNALYNHAVK.Q
13	21	2	1098.58	-0.19	1	24.5	26.4	93.20%	K.NQLQQELAR.F		K.NQLQQELAR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
287	B3LRN4_YEAS1	11.17%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	174	3	1474.8	-1.4	1	55.4	24.3	95.00%	K.GIRPSPLENSLHR.A		K.GIRPSPLENSLHR.A
182	192	2	1326.58	-1.6	0	72.2	30.7	95.00%	R.NTTPYQNNVYN.D		R.NTTPYQNNVYNDAIR.D
235	247	3	1534.82	-0.38	0	25.3	25.3	95.00%	S.EAVNLHLNTLQQR.I		R.DSGYATQFDGYPQQQPSHTNYVSSTALAGFENTQPNTSEAVNLHLNTLQQR.I
182	196	2	1781.83	0.11	1	50.4	29.6	95.00%	R.NTTPYQNNVYNDAIR.D		R.NTTPYQNNVYNDAIR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
288	PIN2_YEAST	23.05%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
260	278	2	2249.98	-2.3	1	49.5	29.7	95.00%	R.SPYPTENYQSYQGYKPNQS.D		R.SPYPTENYQSYQGYKPNQSDR.Y
238	259	3	2486.09	-1.1	0	60.8	28.6	95.00%	Y.DNNNINNNLQGNSYNTPSSNHR.S		R.NSFIQNAANTGSNNAHVASQSPIFDISDYGENYYYDNNNINNNLQGNSYNTPSSNHR.S
203	226	2	2488.17	-2.2	0	71.6	28.5	95.00%	R.NSFIQNAANTGSNNAHVASQSPIF.D		R.NSFIQNAANTGSNNAHVASQSPIFDISDYGENYYYDNNNINNNLQGNSYNTPSSNHR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
289	A6ZUG0_YEAS7	9.03%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
78	87	2	1012.57	-1.6	0	39	26.1	95.00%	K.AQRPITGASL.D		K.AQRPITGASLDLIK.E
78	91	3	1481.86	0.47	1	45	19.8	95.00%	K.AQRPITGASLDLIK.E		K.AQRPITGASLDLIK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
290	A7A001_YEAS7	3.32%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
400	408	2	1017.53	0.47	1	39.7	28.6	95.00%	R.TMVALAEQR.F		R.TMVALAEQR.F
77	87	2	1153.71	-0.36	0	53.7	19.3	95.00%	K.VAIITAQTPLK.H		K.VAIITAQTPLK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
291	B3LH47_YEAS1	7.11%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
74	84	2	1154.63	-0.72	1	31.1	25.8	95.00%	Q.EEAIPVAITGR.D		R.ELLMGIFEAGFEKPSPIQEEAIPVAITGR.D
336	345	2	1176.62	0.52	1	34.8	27.6	95.00%	R.TLVCSDLLTR.G	Carbamidomethyl (+57)	R.TLVCSDLLTR.G
492	506	2	1762.74	-0.81	0	32.9	30.8	95.00%	Q.EHFMAMPPGQSQPQY.-	Oxidation (+16)	K.SLYVAENDETVPVPFPIEQQSYHQQAIPQQQLPSQQQFAIPPQQHHPQFMVPPSHQQQQAYPPPQMPSQQGYPPQQEHFMAMPPGQSQPQY.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
292	A6ZW34_YEAS7	5.42%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
288	302	2	1709.87	-0.71	1	30.2	27.1	95.00%	R.AENVLYGNSNTLIFR.G		R.AENVLYGNSNTLIFR.G

755	768	2	1472.65	-1.6	0	50.4	30.9	95.00%	E.DAASSTQMHAMPAR.D		R.QESEANNGLINAYEDEQFSLMEPSILEDAASSTQMHAMPAR.D
610	623	2	1415.74	-0.3	1	73.2	26.6	95.00%	K.SVANELMALGNVAK.D		K.SVANELMALGNVAK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
293	A7A0G8_YEAS7	9.59%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	62	2	1050.47	-1.4	1	47.5	29.9	95.00%	Y.DDQLQNYR.D		K.AQIYDDQLQNYR.D
108	120	2	1483.79	-0.53	1	45.6	25.9	95.00%	K.ICIQPEAGGWLIK.A	Carbamidomethyl (+57)	K.ICIQPEAGGWLIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
294	A6ZN47_YEAS7	8.33%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
610	622	2	1601.8	-1.2	1	70.2	27.9	95.00%	K.LQCININDLMVNR.N	Carbamidomethyl (+57)	K.LQCININDLMVNR.N
86	101	2	1737.94	-1.3	0	35.5	23.7	95.00%	S.DIHPVGVSYFPAVIPK.G		R.QSPSDIHPVGVSYFPAVIPK.G
515	526	2	1426.7	-0.64	1	43	28.1	95.00%	N.DLLIPEVYSFMT.D		K.VNDLLIPEVYSFMTDNTTSSDLIK.N
188	198	2	1154.6	0.15	1	29.6	27.2	95.00%	K.FLYLDGASAAK.T		K.FLYLDGASAAK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
295	A6ZSX8_YEAS7	3.42%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
237	249	2	1436.83	-1.5	0	38.9	20.7	95.00%	R.GVYIPVSYLSLVK.F		R.GVYIPVSYLSLVK.F
42	53	2	1431.7	-0.99	0	43.3	29.3	95.00%	N.DPPSTFTQWLLQ.D		R.ESWEYLTPQQAANDPPSTFTQWLLQDPK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
296	A6ZUT7_YEAS7	2.44%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
666	676	2	1250.63	-0.66	0	53.5	30.3	95.00%	R.DNIIFGSPFNK.E		R.DNIIFGSPFNK.E
1219	1231	2	1487.85	-0.96	0	27.6	20.5	95.00%	V.DFAYRPGLPIVLK.N		R.KPEMTPPESWPSMGEIIFENVDFAYRPGLPIVLK.N
763	774	3	1392.81	-0.14	1	30	20.5	95.00%	R.ILATHQLSLIER.A		R.ILATHQLSLIER.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
297	B3LMC0_YEAS1	3.30%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
199	207	2	1033.59	0.65	0	24.5	22.2	95.00%	R.ILLFNTTGR.N		R.ILLFNTTGR.N
933	943	2	1290.76	0.056	1	49.3	18.4	95.00%	R.LTLDIPVVFFK.C		R.LTLDIPVVFFK.C
173	186	2	1557.8	-0.92	1	40.8	27.7	95.00%	E.DPSKEPITALFLNN.D		R.IIYEDPSKEPITALFLNNDATACFAATTSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
298	FRE7_YEAST	6.45%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
577	588	2	1414.6	-0.82	1	57.3	30.6	95.00%	R.NCFICSGSDSLR.Y	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.NCFICSGSDSLR.Y
345	359	2	1747.83	-0.69	1	58.1	29.7	95.00%	K.DVEMAYSPGQHIFVR.T		K.DVEMAYSPGQHIFVR.T
589	601	2	1306.69	-0.54	0	69.8	28	95.00%	R.YTVGNSVAGLQAK.V		R.YTVGNSVAGLQAK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
299	A6ZLB9_YEAS7	9.98%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
330	343	2	1699.83	-0.84	1	49.8	28.6	95.00%	K.NPSFYMFTPENLIK.A		K.NPSFYMFTPENLIK.A
354	368	2	1594.73	-1.1	1	51.2	29.8	95.00%	F.DEVYTAPALGFPNAM.E		R.EFDEVYTAPALGFPNAMEYYK.A
164	179	2	1596.9	-0.88	0	86.3	21.5	95.00%	V.DLPLVVILHGLAGGSH.E		R.EVDLPLVVILHGLAGGSHEPIIR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
300	A6ZU36_YEAS7	19.37%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
92	106	3	1804.95	0.73	1	24.8	24.9	95.00%	R.YVYAHFPINVNIVEK.D		R.YVYAHFPINVNIVEK.D
175	184	3	1177.61	-0.33	1	29.8	27.8	95.00%	K.FLDGIYVSHK.G		K.FLDGIYVSHK.G
73	84	2	1276.67	-2.2	1	43.1	28.1	95.00%	K.SLVDNMITGVTK.G		K.SLVDNMITGVTK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
301	A6ZRQ9_YEAS7	3.93%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
622	633	2	1376.68	-0.3	0	90.1	29.1	95.00%	R.NTVQNNSQGFLR.E		R.NTVQNNSQGFLR.E
557	569	2	1468.65	-0.42	0	35.3	30.2	95.00%	R.NVTAMNGSFQNMR.S		R.NVTAMNGSFQNMR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
302	A6ZWB1_YEAS7	16.82%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
100	107	2	965.52	0.19	0	36.2	27.4	95.00%	R.IFLYPSNI.-		R.IFLYPSNI.-
22	31	2	1096.62	-0.015	0	27.1	22.6	95.00%	R.VNNPNVSLIK.I		R.VNNPNVSLIK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
303	A6ZM50_YEAS7	11.85%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
97	107	2	1428.61	-1.5	1	51.3	30.9	95.00%	F.DVCFENQAQYR.G	Carbamidomethyl (+57)	R.VAFTAPSSTAFDVCFENQAQYR.G
30	37	2	1015.48	-0.78	1	40.9	30.3	95.00%	T.DPEQVCIR.D	Carbamidomethyl (+57)	-.MQVLQLWLTTLISLVVAVQGLHFDIAASTDPEQVCIR.D
62	67	2	760.46	1.9	0	22.3	20.6	92.10%	K.LNLFVR.D		K.LNLFVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
304	A6ZZN6_YEAS7	8.42%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
10	29	2	2095.13	-1.1	0	38.2	22.4	95.00%	N.DFILISLPQNAQPVTAPGSK.T		-.MATALYTANDFILISLPQNAQPVTAPGSK.T
99	111	2	1499.77	-2.6	1	32.2	27.9	95.00%	R.TLPINNMPVPEYL.E		R.TLPINNMPVPEYLENFQWQTR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
305	A6ZW55_YEAS7	15.00%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
3	16	2	1339.72	-1.9	0	36.5	25.9	95.00%	K.GTGGVVVGTQNPVR.D		K.GTGGVVVGTQNPVR.D
106	113	2	960.56	0.08	0	27.5	21.6	95.00%	K.EALFILQK.R		K.EALFILQK.R
41	54	2	1590.69	-1.3	1	37.8	30.8	95.00%	R.DQLSHESQTAYQQG.D		R.DQLSHESQTAYQQGDK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
306	A6ZQ25_YEAS7	1.05%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1733	1745	2	1419.74	-1.1	0	36	27.7	95.00%	P.DAILGSYLLATHF.D		R.NTNPDAILGSYLLATHFDK.N
2159	2171	2	1468.79	0.67	0	21.9	25.1	91.10%	L.DIQQYPAIPLSPK.S		R.HLDIQQYPAIPLSPK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
307	B3LKB6_YEAS1	4.82%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	77	2	1308.67	-0.63	1	42.4	29.2	95.00%	K.APVPDVNAPQSSK.N		K.APVPDVNAPQSSK.N
88	104	2	1746.96	-1.6	0	57	21.5	95.00%	L.ETPTGLVPVATLHSIGR.T		K.IFPEEYTLETPTGLVPVATLHSIGR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
308	A6ZRC2_YEAS7	2.23%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1502	1517	2	1862.93	1	0	24.1	27.4	91.00%	Q.DLLQSPQFQQAQTFGR.G		K.ETQDLLQSPQFQQAQTFGR.G
872	880	2	980.49	0.49	1	32.2	29.1	95.00%	K.GADSIIYSR.L		K.GADSIIYSR.L
169	178	2	1224.62	-0.41	0	25.1	28.7	90.20%	R.TVYYNMPLPK.D		R.TVYYNMPLPK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
309	A6ZSV7_YEAS7	4.92%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
502	511	2	1089.57	0.17	1	25.9	27.8	93.30%	R.SLVSPAPEYK.D		R.SLVSPAPEYK.D
39	55	2	1833.92	-0.87	0	72.6	26.9	95.00%	R.TTLQPNSTSQSMIGTLR.K		R.TTLQPNSTSQSMIGTLR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
310	MHP1_YEAST	1.72%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
332	343	3	1280.7	-0.093	1	34.6	25.3	95.00%	K.GRPIPPHPDAPK.L		K.GRPIPPHPDAPK.L
53	64	2	1317.66	-0.1	1	32.5	28.9	95.00%	M.DTARPPVFETSV.D		K.ANSVAPDIQMDTARPPVFETSVD SSSSILSSNDK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
311	A6ZRZ3_YEAS7	3.48%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
262	271	2	1148.62	0.52	0	22.8	26.1	90.80%	R.NYVNSNVVLK.A		R.NYVNSNVVLK.A
594	606	2	1405.79	-0.5	0	33.2	21.3	95.00%	K.VISSSVQPLNHLI.D		K.VISSSVQPLNHLIDR.T
725	742	3	2109.02	-1	1	46	28.4	95.00%	G.DDHNLGSLNIQTQNIYHK.D		K.VSIDCFGIDTNGDDHNLGSLNIQT QNIYHK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
312	A6ZQS1_YEAS7	11.25%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	47	2	1388.69	-2.6	0	30.6	28.7	95.00%	K.SGVGICATCVLRP.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.SGVGICATCVLRPDLLFK.N
35	52	2	2005.05	-0.88	1	39.9	24.9	95.00%	K.SGVGICATCVLRPDLLFK.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.SGVGICATCVLRPDLLFK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
313	A6ZL13_YEAS7	4.04%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
571	581	2	1218.65	-0.67	1	39.6	27.1	95.00%	R.NIFVSPSLTEI.D		R.NIFVSPSLTEIDK.V
11	24	3	1610.74	-0.8	1	22.1	29.9	91.40%	K.EASPAQYSHSLHER.T		K.EASPAQYSHSLHER.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
314	YHA8_YEAST	6.54%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
544	554	2	1135.6	0.33	0	36	27.3	95.00%	K.ANSTTLGGLFR.A		K.ANSTTLGGLFR.A
521	535	2	1574.7	-1.6	0	44.1	30.6	95.00%	Q.DTFPHNAPASSPAYT.D		R.TTQDTFPHNAPASSPAYTDDAHS LR.K
587	601	2	1568.85	-1.4	1	57.5	24.5	95.00%	R.ITANNVAGIVNLNKE.D		R.ITANNVAGIVNLNKEDLDSTTR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
315	A6ZXS3_YEAS7	11.22%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
253	268	2	1766.88	-0.74	1	38	27.8	95.00%	N.DTTLPPQAIEYAALQH.D		K.EIGYSPAINDTTLPPQAIEYAALQH DK.K
183	200	2	1849.09	-1.5	0	69.4	12.3	95.00%	K.IPIVPVVVSNTSTLVSPK.Y		K.IPIVPVVVSNTSTLVSPK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
316	A6ZZC9_YEAS7	13.50%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

34	50	2	1863.88	0.42	1	91.3	29.7	95.00%	R.SSVGQFMTFFAETVASR.T		R.SSVGQFMTFFAETVASR.T
24	33	2	1244.58	-0.99	1	38.2	30.1	95.00%	K.DLSQFGFFER.S		K.DLSQFGFFER.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
317	A6ZSH5_YEAS7	9.43%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
9	23	2	1646.71	-1.6	1	46.5	30.7	95.00%	Y.EEQSSHLYGQPASSQ.D		-.MSGPPPPYEEQSSHLYGQPASSQDGNAFIPEDFK.Y
35	47	2	1535.8	-0.51	1	55.6	27.1	95.00%	K.YSTVVISCEPIIR.Q	Carbamidomethyl (+57)	K.YSTVVISCEPIIR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
318	A6ZYP2_YEAS7	4.24%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
548	561	2	1323.67	-0.38	0	67.8	28.7	95.00%	P.DGTSALYGVAGSVK.T		K.SESNSKPSPDGTSALYGVAGSVK.T
569	579	2	1250.73	0.15	1	33.6	18.3	95.00%	K.LIVGFLDALYK.L		K.LIVGFLDALYK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
319	A6ZKX1_YEAS7	6.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
116	125	2	1164.61	-0.34	1	44.5	28.4	95.00%	R.SVDSIYQVVR.C		R.SVDSIYQVVR.C
99	115	3	1655.84	-0.37	1	36.6	27	95.00%	K.GASAGEGLGNAFLSHIR.S		K.GASAGEGLGNAFLSHIR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
320	A7A0L8_YEAS7	1.27%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
499	508	2	1107.64	-1.5	1	26.2	23.4	95.00%	E.DKGPVLQVPR.E		R.QELYDAIEFDENEDKGPVLQVPR.E
435	452	2	1872.86	-3.4	1	58	29.8	95.00%	E.DSPTPTASSNIEPQTSNK.S		K.LGMSEDSPTPTASSNIEPQTSNK.S
3051	3062	2	1369.72	-1.5	1	36.1	26.2	95.00%	N.DEYLSHVILPGK.E		K.TVNGGVFMNDEYLSHVILPGK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
321	A6ZM15_YEAS7	7.95%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
284	291	2	966.53	0.48	0	52.2	24.5	95.00%	K.GINFFTIR.K		K.GINFFTIR.K
90	105	3	1909.94	-0.84	0	29.5	28	95.00%	V.DNFNTHINVPHQFISK.R		K.DGSDTCTSNLAPAYPISPVDNFNTHINVPHQFISK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
322	A6ZNC5_YEAS7	5.46%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
304	311	2	967.48	-0.56	1	27.5	30	92.30%	R.EALDFFAR.G		R.EALDFFAR.G
277	287	2	1354.6	-0.7	1	65.5	30.7	95.00%	K.CCSDVFNQVVK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CCSDVFNQVVK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
323	A6ZT50_YEAS7	6.96%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
13	22	2	1126.64	0.72	0	24.7	24.1	95.00%	K.TPLPLCSVIK.S	Carbamidomethyl (+57)	K.TPLPLCSVIK.S
39	50	2	1305.74	-1.2	0	61.6	23.9	95.00%	F.DPLNLNVGVLPR.C		K.THLILSNSTIIHDFDPLNLNVGVLPR.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
324	A7A027_YEAS7	2.29%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

7	23	5	1893.01	-1.1	1	30.2	23.7	95.00%	A.DHNAAKPIPHVPQASRR.Y		-.MSAPAADHNAAKPIPHVPQASRR.Y
7	22	4	1736.91	-0.85	0	23.4	26.8	95.00%	A.DHNAAKPIPHVPQASR.R		-.MSAPAADHNAAKPIPHVPQASR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
325	A6ZQ50_YEAS7	41.30%	100%	3							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	61	2	1369.56	-0.31	0	49.8	30.5	95.00%	R.GAAGIWTCSCCK.K	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GAAGIWTCSCCK.K
63	80	2	1665.87	-1	0	64.9	26.7	95.00%	K.TVAGGAYTVSTAAAATVR.S		K.TVAGGAYTVSTAAAATVR.S
37	44	2	1035.38	1.3	1	30.5	27.9	95.00%	R.YDCSFCGK.K	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.YDCSFCGK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
326	A6ZRY2_YEAS7	8.39%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
260	286	3	2775.23	-2.2	1	88.1	28.3	95.00%	I.DNSTGQAGQANAQSANTVNNRVNNNSK.A	Deamidation (+1)/ Deamidation (+1)	R.TNIDNSTGQAGQANAQSANTVNNRVNNNSK.A
260	280	2	2116.95	-0.33	0	58.7	29.6	95.00%	I.DNSTGQAGQANAQSANTVNNR.V		R.TNIDNSTGQAGQANAQSANTVNNR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
327	CASP_YEAST	6.48%	100%	3							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	15	2	1777.83	0.015	1	45.7	29.2	95.00%	-.MDTSVYSHALDIWAK.A	Acetyl (+42)	-.MDTSVYSHALDIWAK.A
102	113	2	1353.71	-1.6	1	34.5	26.8	95.00%	P.DPQPLLQSSLEK.L		K.LSEAPDPQPLLQSSLEK.L
479	495	2	1770.93	-1	1	63.2	24.9	95.00%	E.DGELSGNQSTILPIVTK.Q		K.MSPTSSIIGIPEDGELSGNQSTILPIVTK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
328	A6ZSF8_YEAS7	5.07%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
135	143	2	1135.54	-0.015	0	29	29.3	95.00%	K.TYNTAPQWR.F		K.TYNTAPQWR.F
210	221	2	1302.66	-1.5	0	51	29.4	95.00%	H.DATGINCKPLSK.N	Carbamidomethyl (+57)	R.GEDASYETVHDATGINCKPLSK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
329	AKR2_YEAST	3.87%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
615	632	2	1882.93	-1.2	1	30.9	27.9	95.00%	S.DMIPEGPSATTITHTISI.D		K.GVEDSDMIPEGPSATTITHTISIDGLEPR.N
212	222	2	1252.58	-0.82	1	30.3	30.8	95.00%	K.FGSTVAWTDNR.G		K.FGSTVAWTDNR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
330	A6ZLM4_YEAS7	4.79%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
353	366	2	1388.71	-1.1	1	87.4	27.5	95.00%	N.DDGSGTISLLNVAK.Q		K.HGDPDNIVALGAHSDSVEEGPGINDDGSGTISLLNVAK.Q
544	556	2	1528.79	-0.73	1	36.5	26.7	95.00%	K.EVDILNAQQPQFK.Y		K.EVDILNAQQPQFK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
331	A6ZZQ1_YEAS7	14.08%	100%	2							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
170	178	2	1014.57	0.29	1	39.7	27.3	95.00%	K.QISLEGLQK.Q		K.QISLEGLQK.Q

79	98	2	1929.97	-1.6	0	126	26.3	95.00%	N.DNSGSIGSSAVTPIQALASR.A			R.VSLYHNDNSGSIGSSAVTPIQALASR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
332	IRC8_YEAST	2.92%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
675	687	3	1484.68	-0.87	0	24.9	30.1	95.00%	T.DPINYSFGHGHNK.N		K.LSLSNISDTMSPYEGSTTDPINYSFGHGHNK.N
305	315	2	1294.69	1.1	1	41.2	26.9	95.00%	K.SFLNFLALNEK.N		K.SFLNFLALNEK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
333	KHA1_YEAST	3.67%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
647	654	2	923.61	-0.89	0	29.3	10	95.00%	T.DLILLPLK.G		K.MDSTDLILLPLK.G
863	873	2	1283.61	-0.95	1	27.5	30.1	92.20%	F.DTLIVHHFSSE.-		R.FDTLIVHHFSSE.-
620	632	2	1512.77	0.91	1	49.1	27.9	95.00%	K.IPFSSEVIFSTMR.E		K.IPFSSEVIFSTMR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
334	B3LM88_YEAS1	4.69%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
76	86	2	1220.58	-0.42	0	47.8	30.1	95.00%	E.EATYQVSGNPR.N		K.SNQVFTGPGFYDPVDELLIEPSLPGLSYSFTEDGWYEEATYQVSGNPR.N
75	86	2	1349.62	-1.6	1	72.8	30.4	95.00%	Y.EEATYQVSGNPR.N		K.SNQVFTGPGFYDPVDELLIEPSLPGLSYSFTEDGWYEEATYQVSGNPR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
335	A6ZN12_YEAS7	5.38%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
80	93	2	1551.82	-1.3	1	46.2	25	95.00%	K.SLQAQKPNLSPQEI.D		K.SLQAQKPNLSPQEIDALIEDWEPEPLVDPSATDEQSWR.V
235	250	2	1781.93	-1.2	1	66.6	25.9	95.00%	A.DDQVSLPVQNALQLSR.S		R.GDVIVADDQVSLPVQNALQLSR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
336	A6ZVF2_YEAS7	7.41%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	41	2	1185.56	0.35	0	69.8	30.2	95.00%	R.NGYLVYACAR.R	Carbamidomethyl (+57)	R.NGYLVYACAR.R
170	181	3	1439.77	0.62	1	26.9	24.4	95.00%	R.GLHLEMKPFNVR.V		R.GLHLEMKPFNVR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
337	A7A0W2_YEAS7	3.15%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
525	534	2	1195.66	1.1	0	28.4	23.8	95.00%	K.FNFLNSILTK.S		K.FNFLNSILTK.S
175	184	2	1257.67	0.15	1	32.9	27.1	95.00%	K.SWNQEQLLLK.S		K.SWNQEQLLLK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
338	A6ZZA0_YEAS7	24.48%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
134	143	2	1156.69	-0.28	1	39.1	22.5	95.00%	K.LAEILKPVFQ.-		K.LAEILKPVFQ.-
35	45	3	1227.63	-0.39	1	27.7	28	95.00%	K.MVSQETVAHVK.D		K.MVSQETVAHVK.D
66	79	2	1559.86	0.12	1	37.6	24.4	95.00%	K.ATLSTLFQELNVPK.S		K.ATLSTLFQELNVPK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
339	A6ZUK7_YEAS7	4.57%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
514	529	2	1572.77	0.048	1	56.2	28.4	95.00%	K.NAMQAAEAAVAAATQR.A		K.NAMQAAEAAVAAATQR.A
89	97	2	1017.56	-0.22	0	29	26.5	95.00%	R.IQTGLFSPR.L		R.IQTGLFSPR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
340	A6ZN11_YEAS7	11.17%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
127	134	2	969.45	-1.3	0	26.3	29.6	90.80%	L.ETPTYGFR.V		R.SFEYAVSGDPVWAQQLETPTYGFR.V
135	148	2	1537.79	-0.48	1	38.5	26.8	95.00%	R.VRPDFPVFGAAVTY.D		R.VRPDFPVFGAAVTYDANGMPQQVGGASSQMYGEQAVYQPQQHVQTEEK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
341	A6ZYY3_YEAS7	21.82%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
63	85	2	1789.86	-1.9	0	84.7	29.2	95.00%	K.FATVPTGGASSAAAGAAGAAAGG.D		K.FATVPTGGASSAAAGAAGAAAGGDAAEEEK.E
62	85	2	1917.95	-1.1	1	78.5	28.5	95.00%	K.KFATVPTGGASSAAAGAAGAAAGG.D		K.KFATVPTGGASSAAAGAAGAAAGGDAAEEEK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
342	A6ZRM1_YEAS7	3.42%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
483	491	2	1084.54	0.16	0	36.2	29.4	95.00%	K.DVFNPLHLM.D		K.DVFNPLHLMDNWNK.L
393	402	2	1071.55	0.29	0	43.8	27.7	95.00%	K.APVVNVCTGR.E	Carbamidomethyl (+57)	K.APVVNVCTGR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
343	A6ZPU2_YEAS7	6.01%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
206	217	2	1198.67	-0.44	0	52.4	26.1	95.00%	K.DAGTIAGLNVLR.I		K.DAGTIAGLNVLR.I
218	231	2	1401.75	-1	1	38.3	26.7	95.00%	R.IVNEPTAAAIAYGL.D		R.IVNEPTAAAIAYGLDK.S
103	117	2	1671.86	-1.1	1	72.9	26.1	95.00%	K.NQVAANPQNTIFDIK.R		K.NQVAANPQNTIFDIK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
344	A7A0I6_YEAS7	3.12%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
814	829	2	1813.99	-0.62	1	49.4	21.3	95.00%	K.LTLPVSFNEPTSLLQR.V		K.LTLPVSFNEPTSLLQR.V
170	182	2	1456.73	-2.6	1	35	28.5	95.00%	R.DFGHLESILSSPR.N		R.DFGHLESILSSPR.N
1167	1174	2	1056.47	0.92	1	32.3	29.7	95.00%	K.FNGEYWNK.R		K.FNGEYWNK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
345	A6ZZ46_YEAS7	2.84%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
593	600	2	1070.45	0.077	0	30.4	30.9	95.00%	S.DSQWFQNF.D		K.LGTIFNSDSQWFQNFDEQVLKPVFLDNVSPSLQDSATQSPADFSSQNH.-
601	610	2	1186.66	-1.1	1	67.3	25.2	95.00%	F.DEQVLKPVFL.D		K.LGTIFNSDSQWFQNFDEQVLKPVFLDNVSPSLQDSATQSPADFSSQNH.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
346	A6ZY29_YEAS7	13.91%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
131	140	2	1123.64	0.16	0	34.1	22.8	95.00%	R.TVAVLPPNWK.Y		R.TVAVLPPNWK.Y
10	20	2	1136.58	0.96	0	41.2	28.7	95.00%	K.GISSSAIPYSR.N		K.GISSSAIPYSR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
347	A6ZQR4_YEAS7	4.60%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
299	309	2	1028.59	-0.99	0	57.5	24.8	95.00%	L.DGIGGVSILAK.A		R.DPNGNPEDEMELDGIGGVSILAK.A

315	326	3	1353.64	0.51	1	42.7	31	95.00%	R.TGSHFPAFSFEK.H		R.TGSHFPAFSFEK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
348	A6ZVJ1_YEAS7	6.38%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
447	457	2	1333.48	-3	1	52.6	29.3	95.00%	F.DEGYNFGCGCR.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.NALQSQENLNTFDEGYNFGCGCR.C
298	308	3	1386.71	-0.37	1	24.6	28.5	95.00%	R.WVNFPWDAKPK.L		R.WVNFPWDAKPK.L
356	366	2	1501.61	-0.79	0	29.5	30.6	94.40%	E.DYNLCHFWSNF.E	Carbamidomethyl (+57)	K.VPMLEDSLEGEDYNLCHFWSNFEIAPVDLFDNEIYNAYFK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
349	A7A0T2_YEAS7	7.94%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
141	151	2	1272.69	-0.16	0	32.8	27.1	95.00%	K.NVVNLLNTQMK.N		K.NVVNLLNTQMK.N
198	213	2	1829.85	0.76	0	35.7	29.5	95.00%	A.DLTTYNNSNPFMTSLL.D		K.LTTDTGHAPADDQTQSNHAADLTTYNNSNPFMTSLLDESSEK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
350	A6ZND7_YEAS7	9.01%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
306	317	2	1340.71	-0.77	1	40.5	27.3	95.00%	A.DEPARPLGVQFL.D		R.GSSTTPTNTSNAGDDEPGADEPARPLGVQFLDTFR.R
244	260	2	1569.82	-0.47	0	102	26.4	95.00%	R.ANVAIAANAATNTAAAR.A		R.ANVAIAANAATNTAAAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
351	A6ZRA2_YEAS7	6.44%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
230	238	2	1204.53	-0.35	1	38	30.2	95.00%	R.GAWYFENYR.F		R.GAWYFENYR.F
376	392	2	1814.82	-1.9	1	42.7	29.6	95.00%	Y.ELPEQTTSHSSSQNVAT.D		K.MENINFNEDGEINVQENYELPEQTTSHSSSQNVATDK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
352	A6ZPA8_YEAS7	7.95%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
239	255	2	1846.11	-0.98	0	37.8	12.8	95.00%	R.VINATPTMVIPPLILVR.L		R.VINATPTMVIPPLILVR.L
16	24	2	1159.53	0.34	1	40.4	30.1	95.00%	R.YDLSTYWGR.I		R.YDLSTYWGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
353	A6ZW91_YEAS7	8.06%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
263	273	2	1181.56	-1.2	0	35.7	31.2	95.00%	K.DNNISSYGSII.-		K.DNNISSYGSII.-
226	236	2	1184.6	-0.94	1	29.5	27.8	95.00%	R.LHSESLTITNA.E		R.LHSESLTITNAENFETNTFLNDEIPDLSEISNEVPNK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
354	B3LGD6_YEAS1	6.88%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
360	374	2	1640.8	-0.92	1	34.8	29.5	95.00%	L.DSGTTISYMPTELVK.M		K.IPVLLDSGTTISYMPTELVK.M
308	321	2	1695.93	-1.8	0	40.3	22.5	95.00%	G.DLYTIPIINTLQHR.G		K.YAGDLYTIPIINTLQHR.G
260	271	2	1475.71	0.13	0	28	29.7	93.70%	K.SYTYNNFPMVLK.N		K.SYTYNNFPMVLK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
355	A6ZT07_YEAS7	0.59%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1947	1956	2	1177.65	1.8	1	33.7	25.5	95.00%	L.DVLTPVLHER.M		K.QSLDVLTPVLHER.M
2796	2807	2	1395.71	-0.17	1	52.6	28.2	95.00%	K.TFLALQNFAESR.K		K.TFLALQNFAESR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
356	B3LQV1_YEAS1	8.94%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
245	255	2	1265.64	-1.9	1	33.5	29.8	95.00%	K.DFIQEHVPGPK.E		K.DFIQEHVPGPK.E
281	296	2	1732.9	0.8	1	59.2	26.7	95.00%	K.DQGELIGILNNLGYSK.D		K.DQGELIGILNNLGYSK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
357	A6ZNH0_YEAS7	29.25%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
38	48	2	1088.61	0.81	1	38.5	25.4	95.00%	K.VSSVLSALEGK.S		K.VSSVLSALEGK.S
61	80	2	1536.79	-0.93	0	71.3	27.9	95.00%	K.LAAVPAAGPASAGGAAAASG.D		K.LAAVPAAGPASAGGAAAASGDA AAEEEK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
358	A7A0S3_YEAS7	8.70%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
39	48	2	1102.6	-1.7	1	36.6	26.7	95.00%	K.LGNFESPVLK.E		K.LGNFESPVLK.E
177	192	2	1793.87	-2	0	56.5	28.6	95.00%	V.DTGLQPQHPHYVSTSK.I		K.LLGVDMQSSVDTGLQPQHPHYV STSK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
359	A6ZQV0_YEAS7	14.29%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
161	175	2	1448.74	-1.6	0	54.2	28	95.00%	K.QSGFGGNLTAALGTR.V		K.QSGFGGNLTAALGTR.V
1	18	2	1833.92	-2.4	0	118	27.2	95.00%	-.MNGLVLGATGLCGGGFLR.H	Acetyl (+42)/ Carbamidomethyl (+57)	-.MNGLVLGATGLCGGGFLR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
360	A6ZM68_YEAS7	3.82%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
409	420	2	1305.77	-0.39	0	35.4	17.3	95.00%	E.DGQNLPLVPLIK.K		R.NYTSSIVDADDLFLVDGGEDGQN LPLVPLIK.K
409	421	3	1433.86	-0.9	1	27.1	14.1	95.00%	E.DGQNLPLVPLIKK.E		R.NYTSSIVDADDLFLVDGGEDGQN LPLVPLIKK.E
547	560	2	1594.76	-1.6	0	37.8	30.2	95.00%	D.DSNFLGCIGCAIIR.R	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.NGFEAATMGNFTDDSNFLGCIGC AIIR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
361	A6ZTK7_YEAS7	4.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
594	604	2	1234.58	-0.66	0	45.2	29.4	95.00%	N.DGTGMLMNQLR.E		R.NSNDGTGMLMNQLR.E
349	361	2	1496.83	-1.2	0	27.4	22.8	95.00%	N.ERPQLILGYVPNV.D		K.IIEYVDMSTLNERPQLILGYVPNV DAFGHK.H
534	544	2	1208.55	-0.67	0	38.3	30.1	95.00%	E.DNVFTIGSHGY.D		K.NEDNVFTIGSHGYDNNAIDMR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
362	A6ZRC1_YEAS7	2.25%	99%	1

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	68	2	1376.73	-1.5	0	78.6	27	95.00%	Y.DIFSPIGSVSSIR.V		K.QAATGSESQSVENSSASLYVGDL EPSVSEAHLYDIFSPIGSVSSIR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
363	A6ZY70_YEAS7	3.57%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
243	255	2	1379.81	-1.3	1	59.2	16	95.00%	R.VVGVIVNPVSIER.S		R.VVGVIVNPVSIER.S
100	110	2	1338.66	-1.2	0	54.6	28.7	95.00%	R.IYNSPFQLNML.E		R.IYNSPFQLNMLEEK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
364	A6ZZQ6_YEAS7	8.91%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	73	2	1794.91	-2.6	0	39.5	27.9	95.00%	K.SPIILQTSNGGAAYFAGK.G	Deamidation (+1)	K.SPIILQTSNGGAAYFAGK.G
195	208	2	1758.88	-2.6	1	34.7	27.7	95.00%	E.DLYTKPEQVYNVYK.A		K.EDLYTKPEQVYNVYK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
365	B3LKX9_YEAS1	13.50%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
135	145	2	1501.66	-1.8	1	53.5	31	95.00%	A.DEYFVWNYNPR.T		K.AQLEADEYFVWNYNPR.T
2	27	3	2341.18	-1.7	0	45.3	25.1	95.00%	M.SAVGPGSNAGASVNGGSATAIATLLR.N	Acetyl (+42)/ Deamidation (+1)	-.MSAVGPGSNAGASVNGGSATAIATLLR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
366	A6ZV22_YEAS7	15.50%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
20	29	2	1127.53	0.33	1	28.1	29.8	93.50%	K.AYFTAPSSER.R		K.AYFTAPSSER.R
30	39	2	1082.68	-0.2	1	24	15.1	94.50%	R.RVLLSAPLSK.E		R.RVLLSAPLSK.E
31	39	2	926.58	1.2	0	27.3	19.9	95.00%	R.VLLSAPLSK.E		R.VLLSAPLSK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
367	A7A281_YEAS7	7.12%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
161	169	2	1137.55	-0.076	1	32.7	31.1	95.00%	R.IENFISQCK.Q	Carbamidomethyl (+57)	R.IENFISQCK.Q
232	243	2	1349.68	-0.31	0	37	28.4	95.00%	R.IPASVWNMTFGK.S		R.IPASVWNMTFGK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
368	A6ZKK2_YEAS7	11.16%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
200	210	2	1091.54	-0.38	0	38.1	29.6	95.00%	R.MLSSAGVNSAR.G		R.MLSSAGVNSAR.G
37	49	2	1496.73	-0.48	1	104	29.6	95.00%	K.TLFSSWADSLNTR.A		K.TLFSSWADSLNTR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
369	A6ZQZ3_YEAS7	15.54%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	12	2	1382.71	0.5	1	55.5	27.4	95.00%	-.MFSLQDVITTTK.T		-.MFSLQDVITTTK.T
56	66	3	1239.66	3.5	1	31.8	25.6	95.00%	R.KPTETTHLSAR.T		R.KPTETTHLSAR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
370	A6ZPX0_YEAS7	4.00%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
173	186	2	1546.72	-0.8	1	45.5	29.7	95.00%	F.DPAAFTENVFHSGR.S		K.LGNQMSDVVNFDPAAFTENVFHSGR.S
63	74	2	1493.7	-1	1	47.2	30.1	95.00%	G.DEFTLSMPHVYR.I		R.EGDEFTLSMPHVYR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
371	A6ZTV9_YEAS7	12.11%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
63	72	2	1169.68	-0.42	0	23.5	24.7	93.90%	K.NQITVLQVQK.A		K.NQITVLQVQK.A
178	190	2	1564.69	-2.4	1	34.7	30.6	95.00%	R.IAHYNNGLQWFSD.-	Deamidation (+1)	R.IAHYNNGLQWFSD.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
372	A6ZSX0_YEAS7	4.28%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
72	80	2	1050.54	0.16	1	31.1	29.2	95.00%	R.DFIGLPFDK.C		R.DFIGLPFDK.C
396	409	2	1557.89	-1.9	0	21.8	21	91.00%	A.EALQPVIVNTPHLK.K		R.LISDYDADELAEALQPVIVNTPHLK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
373	A6ZX16_YEAS7	9.67%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
194	206	2	1375.65	-2	0	31.3	30.5	95.00%	I.DPSITTMNPAMAK.T		K.EFIDPSITTMNPAMAK.T	
222	237	2	1808.93	-0.72	1	39.6	25.5	95.00%	K.TAITTLPISNMEYLSR.F		K.TAITTLPISNMEYLSR.F	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
374	A6ZZ10_YEAS7	8.80%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
291	308	2	1718.84	-0.65	1	86.5	28.3	95.00%	R.LGTAPATLSQTSGTDSGR.A		R.LGTAPATLSQTSGTDSGR.A	
316	327	2	1303.63	-0.86	0	54.7	29.7	95.00%	R.SGPSNLNQFQGR.G		R.SGPSNLNQFQGR.G	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
375	A6ZNC2_YEAS7	8.66%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
165	174	2	1150.6	-0.19	1	45.1	29	95.00%	K.SLSNFIDTVR.S		K.SLSNFIDTVR.S	
101	114	2	1592.93	-0.21	1	35	15.8	95.00%	T.DLPGFPIIELVKPR.T		K.DDTPINFLEVNCEFFGPTLCTDLP GFPIIELVKPR.T	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
376	A6ZTG3_YEAS7	3.71%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
338	345	2	968.46	-0.94	0	46.8	30.8	95.00%	P.DSQITSYR.N		R.SPILEYNNTPLDANDSVNNLGNT TPDSQITSYR.N	
429	439	2	1164.58	0.42	1	38.2	28.5	95.00%	K.YNGEASVQLGK.T		K.YNGEASVQLGK.T	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
377	A6ZNA6_YEAS7	4.93%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
62	72	2	1177.6	-0.43	0	40.1	28.9	95.00%	K.SPVSTSTMQIK.S		K.SPVSTSTMQIK.S	
16	34	2	1960.87	1.6	0	33.2	30.5	95.00%	R.LSHFFPSYTNSSGMGAAST.D		R.LSHFFPSYTNSSGMGAASTDQS STQGEELHHR.K	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
378	A6ZYK3_YEAS7	3.98%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
587	601	2	1539.68	-1.8	0	84.5	30.9	95.00%	V.DPVSSGTPYSSNSSR.F		R.GLHGPSAASSSPVISANNFVDPV SSGTPYSSNSSR.F	
527	544	2	1820.83	0.16	0	46.4	30.4	95.00%	K.QVYSGPSGTPTSGNNNNK.S		K.QVYSGPSGTPTSGNNNNK.S	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
379	A6ZX15_YEAS7	5.93%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
460	477	2	1837.83	-0.81	1	99	30	95.00%	E.DSQNSSLSSATVSGQNEK.S		R.DYYQWGVDTDALHTTCNGANSA SETNPTEDSQNSSLSSATVSGQNE K.S	
84	94	2	1271.63	0.21	1	51.7	28.9	95.00%	K.FIGNLDSFGFR.N		K.FIGNLDSFGFR.N	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
380	A6ZLI8_YEAS7	8.11%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
189	201	2	1350.72	-0.61	0	36	26.5	95.00%	R.ELASGLSFPVGFK.N		R.ELASGLSFPVGFK.N	
213	229	3	1882.82	-0.25	0	29.9	30.5	95.00%	V.DACQAAAHSHHFMGVTK.H	Carbamidomethyl (+57)/ Oxidation (+16)	K.NGTDGTLSVAVDACQAAAHSHH FMGVTK.H	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
381	A6ZMV4_YEAS7	11.78%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
219	239	2	2108.14	-1.2	1	89.9	23.7	95.00%	K.IGASALGGGLSAWNQPIEVIR.V		K.IGASALGGGLSAWNQPIEVIR.V	
145	160	2	1593.78	-0.51	0	43.4	28.7	95.00%	K.SASAGGVPQSSWSVFK.N		K.SASAGGVPQSSWSVFK.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
382	A6ZXU5_YEAS7	7.10%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
130	153	5	2683.37	0.1	0	34	24.7	95.00%	R.TGHTVPHLPHSIHNPINYIHQGSK.D		R.TGHTVPHLPHSIHNPINYIHQGSK.D	
208	227	2	1973.85	-2.3	1	54.3	30.4	95.00%	M.DSQASTPGSVELQHNSSSGS.D		K.HFMDSQASTPGSVELQHNSSSGSDDTSSR.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
383	A6ZMI9_YEAS7	1.65%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
5	13	2	1124.52	-0.38	1	32.6	30.8	95.00%	R.YNVFNDTPR.G		R.YNVFNDTPR.G	
244	256	2	1495.75	-1.1	1	27.1	28.6	94.00%	K.ILPENTAMFNPLH.E		K.ILPENTAMFNPLHESYCLPMDTNLFK.I	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
384	A7A100_YEAS7	2.27%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
67	75	2	1016.49	0.45	1	29	30.1	94.40%	K.QGKEQAAQR.Q	Deamidation (+1)/ Deamidation (+1)	K.QGKEQAAQR.Q	
995	1011	3	1769.78	-0.21	0	28	30.7	95.00%	L.DSQLSSSYHSTASSASR.N		K.AMDLQNSLDSQLSSSYHSTASSASR.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
385	A6ZV27_YEAS7	11.26%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
210	218	2	912.54	0.63	0	27.2	23.6	95.00%	R.ISIPGITGR.A		R.ISIPGITGR.A	
23	38	2	1590.82	-0.77	0	36.8	27.1	95.00%	T.DLKPFPSAGSASSSIK.T		R.NQTDLKPFPSAGSASSSIK.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
386	SNQ2_YEAST	1.67%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
1082	1092	2	1326.66	-0.7	1	47.8	29.3	95.00%	K.NSATILNYFER.N		K.NSATILNYFER.N	
446	459	2	1742.79	-1.8	1	26.1	29.6	90.40%	F.ETYWLNSPEFAQMK.K		R.TAEEFETYWLNSPEFAQMK.K	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
387	A6ZP32_YEAS7	6.86%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
405	417	3	1473.79	-1.1	1	27.3	24.9	95.00%	C.DLIHPTPLEVGQR.F		K.EVEDHSMQVMPGDNVEMECDLIHPTPLEVGQR.F	
202	218	2	1786.87	-1.3	1	34	28.5	95.00%	G.DNAPIIMGSALCALEGR.Q	Carbamidomethyl (+57)	R.ELLNEYGFDGDNAPIIMGSALCALEGR.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
388	PAT1_YEAST	5.65%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
53	77	3	2287.02	-1.1	0	56.8	29.2	95.00%	F.DFGNPHSSGSSGNAIGGNGVGATAR.S	Deamidation (+1)	K.GYGEHELEENDYLNDETFGDNVQVGTDFDFGNPHSSGSSGNAIGGNGVGATAR.S	
432	451	2	1739.82	-1.2	0	118	29.8	95.00%	V.DLASSGSSSTGSSAAAVASK.Q		K.DVTDSLTNVDLASSGSSSTGSSAAAVASK.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
389	A6ZWX4_YEAS7	2.99%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
277	288	2	1235.62	-0.83	0	48.8	28.9	95.00%	L.DPNVSANAAHLK.T		K.NSNSLSTGLLDPNVSANAAHLK.T	
256	266	2	1399.68	-0.71	0	53.1	29.9	95.00%	E.DWYYQLINASK.N		K.EDWYYQLINASK.N	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
390	A6ZQK2_YEAS7	3.89%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
225	233	2	898.49	-4.5	0	25.3	24.9	95.00%	K.LPPGGMSLK.M		K.LPPGGMSLK.M
189	205	4	1935.05	-0.4	0	14.7	23	93.40%	R.RPLSTQHPTRPNVAPHK.A		R.RPLSTQHPTRPNVAPHK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
391	A6ZS90_YEAS7	1.52%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1133	1147	2	1639.86	-1.1	0	48.6	25.2	95.00%	K.FQLPSAAFSTFPTVK.S		K.FQLPSAAFSTFPTVK.S
1746	1764	2	1932.1	0.044	1	43.2	15.3	95.00%	R.AIQVEGQPIILTGAPAINK.M		R.AIQVEGQPIILTGAPAINK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
392	INP54_YEAST	5.99%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
214	226	2	1455.68	-1.9	0	70.3	30.3	95.00%	Y.DPTTNYSSTTTLR.R		R.VTSTYDPTTNYSSTTTLR.R
312	321	3	1177.62	-1.9	0	20.3	26.9	94.10%	S.DHQPVNLTVR.L		R.SNALLFSDHQPVNLTVR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
393	A6ZZS0_YEAS7	5.79%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
388	403	2	1549.68	-3.4	1	51.2	31.1	95.00%	L.DKPAPYTAENGGSSVG.D	Deamidation (+1)	R.ALDKPAPYTAENGGSSVGDGAA GTQAQPTNLAPLNITK.G
45	54	2	1207.51	-1.2	0	27.4	30.7	90.70%	M.DYYTGNQYGK.T		R.FTNAVELDLDNYESLQNATSLIAY GLMDYYTGNQYGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
394	A6ZNT6_YEAS7	6.29%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	110	2	1332.62	-0.39	1	29.1	30	94.70%	K.SSNSDTSIFFTK.V		K.SSNSDTSIFFTK.V
335	344	2	1159.64	0.32	0	26.1	25.8	95.00%	K.SPAYPFPLLR.L		K.SPAYPFPLLR.L

Supplementary Table S2: All "Scaffold" validated proteins and peptides identified from solprotSP (*S.pombe*) and from SCVMprot (*S.cerevisiae*) samples

***S.cervisiae* - Asp-N digest of large tryptic peptides (Replicate B)**

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
1	A6ZPV7_YEAS7	29.40%	100%	24

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	72	2	773.38	0.35	1	31.4	27.8	95.00%	K.HSEVFR.R		K.HSEVFR.R
336	348	2	1493.79	5.1	1	56	26.6	95.00%	L.EALASEIQYVMLK.K		K.KPMNEIENLEALASEIQYVMLK.K
535	553	2	1889.89	6.6	0	36.2	29	95.00%	E.ESVGYGATSAPTSNTNHVV.E		R.SDNEDNDFDEDDEDDAALVAAM TNAPGNSLDIEESVGYGATSAPTSN TNHVVESANAAYYQR.K
362	371	2	1074.55	3.4	1	46	29	95.00%	R.TAFQLPGDAR.V		R.TAFQLPGDAR.V
76	86	2	1351.68	-1.3	1	58.5	29.7	95.00%	K.EVQEQVQHTVR.L		K.EVQEQVQHTVR.L
443	455	2	1402.79	5.2	1	83.1	23.2	95.00%	R.ELVGSHLVEPVPK.F		R.ELVGSHLVEPVPK.F
420	428	2	1064.59	0.35	1	47.5	25.3	95.00%	R.FPYAVLEVK.L		R.FPYAVLEVK.L
459	468	2	1083.61	5.6	0	22.6	23.6	93.70%	K.FIHGVATLLN.D		K.FIHGVATLLNDK.V
416	425	2	1252.64	6.8	1	28.4	28.8	95.00%	K.DICRFPYAVL.E	Carbamidomethyl (+57)	K.DICRFPYAVLEVK.L
138	149	3	1403.83	3.6	0	58.5	14.1	95.00%	K.TGFILKPVFQVR.L		K.TGFILKPVFQVR.L
516	531	2	1514.75	6.9	0	99.7	28.6	95.00%	D.DAALVAAMTNAPGNSL.D		R.SDNEDNDFDEDDEDDAALVAAM TNAPGNSLDIEESVGYGATSAPTSN TNHVVESANAAYYQR.K
122	129	2	969.49	1	0	47.2	27.8	95.00%	R.LNYTGFQK.I		R.LNYTGFQK.I
459	470	2	1326.73	1.3	1	62.2	25	95.00%	K.FIHGVATLLNDK.V		K.FIHGVATLLNDK.V
137	149	3	1531.92	0.52	1	26.7	14.1	95.00%	K.KTGFILKPVFQVR.L		K.KTGFILKPVFQVR.L
79	88	2	1221.69	5.2	1	24.9	22.7	95.00%	Q.EQVQHTVRLL.D		K.EVQEQVQHTVRLLDSNNPPTQL DFEILEEELSDIIADVHDLAK.F
167	175	2	1077.58	-0.47	1	46.9	26.8	95.00%	K.ISQLYDIAR.T		K.ISQLYDIAR.T
598	606	2	1037.52	2.2	1	37.2	30.1	95.00%	K.GTTFDTQIR.A		K.GTTFDTQIR.A
312	320	2	1069.54	-1.3	1	24.5	28.2	91.50%	K.YTVDQVFAK.M		K.YTVDQVFAK.M
119	129	2	1359.7	2.6	1	40	28.3	95.00%	K.FSRLNYTGFQK.I		K.FSRLNYTGFQK.I
515	531	2	1629.78	8.5	1	105	29.3	95.00%	E.DDAALVAAMTNAPGNSL.D		R.SDNEDNDFDEDDEDDAALVAAM TNAPGNSLDIEESVGYGATSAPTSN TNHVVESANAAYYQR.K
487	501	2	1687.98	4.8	1	42.9	17.1	95.00%	R.KPPLPTNIEITRPGR.S		R.KPPLPTNIEITRPGR.S
218	228	2	1280.73	1.6	0	27.4	21.5	95.00%	K.HLPVLVFNTNK.E		K.HLPVLVFNTNK.E
584	594	2	1323.58	4.7	1	76.3	30.6	95.00%	F.DHYFNGDQISK.I	Deamidation (+1)	K.YYEIVAFFDHYFNGDQISK.I
567	574	2	871.44	-0.15	1	28.2	26.9	95.00%	R.NAENPISK.K		R.NAENPISK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
2	VTC3_YEAST	30.18%	100%	30

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
669	681	2	1331.68	5.8	0	26.6	28.1	95.00%	T.DSASSFQLPPGVK.K		K.NISENGNDPYSDDTDSASSFQLP PGVK.K
7	16	2	1201.62	3.3	1	48.5	27.6	95.00%	K.LANDVYPPWK.D		K.LANDVYPPWK.D
149	157	2	1060.56	5	1	25.4	28.5	92.70%	R.LKELPFNNS.E		R.LKELPFNNSEEYSPLLYR.I
512	524	2	1464.76	3.3	1	59.5	26.6	95.00%	K.DLTNSHLVNEVPK.F		K.DLTNSHLVNEVPK.F
500	511	2	1523.68	5.2	1	28.9	30.5	94.80%	Q.DNSQMPNYEWIK.D		K.VINQDNSQMPNYEWIK.D
469	477	2	1024.54	5.6	0	36	27.7	95.00%	I.DSNIPNPLR.F		R.DDIDSNIPNPLR.F
440	448	2	1139.54	6	1	45.5	30.5	95.00%	I.DSNIMYIRE.D		R.VTIDSNIMYIREDSLDK.N
808	820	2	1352.75	5.6	0	58.7	22.7	95.00%	R.GLVNVSSQPSLPR.T		R.GLVNVSSQPSLPR.T
117	126	2	1209.66	5.7	1	48.5	24.8	95.00%	F.DRLNFTGFIK.I		R.LDNFDRLNFTGFIK.I
365	372	2	1041.57	3.5	0	37.6	25.4	95.00%	K.FINNFIFK.N		K.FINNFIFK.N
542	551	2	1260.7	6.7	0	34.8	25.6	95.00%	K.YVNILPFWLP.D		K.YVNILPFWLPDLETDIR.K
699	705	2	886.47	2.2	1	32.7	29.9	95.00%	K.VWLANER.T		K.VWLANER.T
806	820	2	1637.88	-0.8	1	64.4	23.5	95.00%	R.ERGLVNVSSQPSLPR.T		R.ERGLVNVSSQPSLPR.T
316	323	2	813.47	-0.4	0	28.3	25.3	95.00%	K.ISGAPTLR.L		K.ISGAPTLR.L
63	70	2	984.53	4.3	0	26.3	26.5	95.00%	K.VYTFQISK.Y		K.VYTFQISK.Y

227	240	2	1522.79	6.1	1	31.5	26.7	95.00%	R.HLPALVYASVPNEN.D		R.HLPALVYASVPNENDDFVDNLESDVR.V
167	175	2	1202.63	-0.096	1	70.6	27.9	95.00%	R.ISYLYEFLR.S		R.ISYLYEFLR.S
365	373	2	1156.6	6	1	26.4	28.4	94.40%	K.FINNFIFKN.D	Deamidation (+1)	K.FINNFIFKNDPSYK.N
307	315	2	1147.64	6.1	1	24.7	23.3	95.00%	F.DLYNNRLLK.I		K.SVIFPQSYDPTITTLYFDNDFFDLYNNRLLK.I
487	495	2	1112.56	3.4	1	49	28	95.00%	K.FPYSVMEIK.V		K.FPYSVMEIK.V
641	649	2	1038.58	-6	1	28.3	24.3	95.00%	K.FKTNAAFLK.I		K.FKTNAAFLK.I
143	148	2	715.42	-0.041	0	26.7	28.6	94.50%	K.SLLQVR.L	Deamidation (+1)	K.SLLQVR.L
379	386	2	1032.57	3.1	0	38.1	22.3	95.00%	K.NYLINQLR.E		K.NYLINQLR.E
132	142	2	1296.69	5.5	1	59.9	25.5	95.00%	H.DKLHPNYPSVK.S		K.HDKLHPNYPSVK.S
94	100	2	864.43	-0.37	1	30	30.5	95.00%	K.INSEQFK.N		K.INSEQFK.N
119	126	2	938.52	1.5	0	36	24.7	95.00%	R.LNFTGFIK.I		R.LNFTGFIK.I
425	436	2	1331.69	3.2	1	47.9	27.6	95.00%	R.TAFQIPGDQSIR.V		R.TAFQIPGDQSIR.V
176	186	2	1260.57	-0.33	1	33.5	30.9	95.00%	R.SNYDHPNTVSK.S		R.SNYDHPNTVSK.S
437	447	2	1323.68	-0.69	1	55.4	28	95.00%	R.VTIDSNIMYIR.E		R.VTIDSNIMYIR.E
363	372	2	1240.7	-0.35	1	27.7	24.5	95.00%	K.AKFINNFIFK.N		K.AKFINNFIFK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
3	A6ZPA7_YEAS7	22.02%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
234	247	2	1572.87	-0.97	1	46.4	23.8	95.00%	K.NAFIVFSHGDLIIK.R		K.NAFIVFSHGDLIIK.R
170	193	2	2345.21	5.9	1	137	24.4	95.00%	I.DANGENIAAAIGASVNYVTGVIAR.D		K.GDNTDSTSYMDEDMIDANGENIAAAIGASVNYVTGVIAR.D
209	214	2	724.39	-0.6	0	33	24.7	95.00%	R.GNLFFK.T		R.GNLFFK.T
280	289	2	1164.64	0.25	1	44.1	24.8	95.00%	K.NLSDLYTVLK.T		K.NLSDLYTVLK.T
353	359	2	788.42	0.095	1	56	31.1	95.00%	R.LGEMIAR.L		R.LGEMIAR.L
196	205	2	1227.7	-0.5	1	59.4	23.7	95.00%	K.VATLEQILWR.V		K.VATLEQILWR.V
206	214	3	1092.65	1.1	1	19.6	18.6	95.00%	R.VLRGNLFFK.T		R.VLRGNLFFK.T
372	382	3	1321.62	5	0	26.8	29.9	95.00%	L.DTNHTPPTFHR.T		R.LGIDVPSIIQVLDTNHTPPTFHR.T
395	403	2	1144.51	8.1	0	38.7	30.6	95.00%	C.DCYGIAQYR.E	Carbamidomethyl (+57)	K.FTAGFQSICDCYGIAQYR.E
234	242	2	990.5	6	0	32.4	29.4	95.00%	K.NAFIVFSHG.D		K.NAFIVFSHGDLIIK.R
54	60	2	877.47	1.4	1	44.8	28.4	95.00%	R.TFVNEIR.R		R.TFVNEIR.R
360	371	2	1265.77	7	1	31.1	16.5	95.00%	R.LGIDVPSIIQVL.D		R.LGIDVPSIIQVLDTNHTPPTFHR.T
334	343	2	1166.69	6.2	1	73.1	18.9	95.00%	K.ILIAEGWIPR.D		K.ILIAEGWIPR.D
383	394	2	1372.65	5.1	1	74.4	30.1	95.00%	R.TNKFTAGFQSIC.D	Carbamidomethyl (+57)	R.TNKFTAGFQSICDCYGIAQYR.E
318	325	2	946.55	-0.031	1	39.5	24.3	95.00%	K.AIFEILNK.S		K.AIFEILNK.S
344	352	2	1015.53	1.3	1	58.2	28	95.00%	R.DELATLQAR.L		R.DELATLQAR.L
386	403	2	2155.95	2.7	1	93.4	29.4	95.00%	K.FTAGFQSICDCYGIAQYR.E	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.FTAGFQSICDCYGIAQYR.E
519	536	2	2138	7.3	1	52.8	28.3	95.00%	L.DWAWHGTENALLFSNSYK.M		K.GESITATSVGTYPIGLDWAWHGTENALLFSNSYK.M
28	42	3	1666.88	6.7	0	74.8	25.5	95.00%	R.DSAYTLGQLGLVQFR.D		R.DSAYTLGQLGLVQFR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
4	B3LLD7_YEAS1	14.99%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
481	492	2	1085.55	-0.29	0	40.9	27.5	95.00%	R.STAHGISAASGK.V		R.STAHGISAASGK.V
276	283	2	949.49	0.31	1	40.6	29.2	95.00%	R.YQLDVNAK.L		R.YQLDVNAK.L
109	126	2	1739.92	6.1	0	61.5	24.9	95.00%	K.VSTSVGTVIGQFGFGTLA.D		K.VSTSVGTVIGQFGFGTLADIVGR.K
109	131	2	2280.21	-0.97	1	108	22.7	95.00%	K.VSTSVGTVIGQFGFGTLADIVGR.K		K.VSTSVGTVIGQFGFGTLADIVGR.K
19	34	2	1820.8	3.9	1	65.3	30.1	95.00%	K.EHLTEGGNMAFHNHLN.D	Deamidation (+1)	K.EHLTEGGNMAFHNHLNDFAHIEDPLER.R
306	314	2	1018.48	5.5	1	28.1	30.4	94.00%	E.DMAINGLER.A	Deamidation (+1)	K.IHDTSDEDMAINGLER.A
493	512	2	2093.11	0.0086	1	119	23.1	95.00%	K.VGAIIAQTALGTLIDHNCAR.D	Carbamidomethyl (+57)	K.VGAIIAQTALGTLIDHNCAR.D

493	506	2	1339.82	7.4	0	92	16.4	95.00%	K.VGAIIAQTALGTLI.D		K.VGAIIAQTALGTLIDHNCAR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
5	YBT1_YEAST	16.80%	100%	28

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
78	94	2	1934.93	5.6	1	44.3	28.6	95.00%	E.DEQSPLINNNTITTNYV.D		K.NPIDELLYSSTDEDEQSPLINNNTITTNYVDNNCTK.D
1616	1627	2	1490.75	2.9	1	41.6	28.8	95.00%	K.EYDHPYSLLLNK.Q		K.EYDHPYSLLLNK.Q
549	556	2	901.46	0.53	1	29.2	28.3	95.00%	K.NLAVTDNR.I		K.NLAVTDNR.I
1457	1473	2	1830.01	-1.1	1	49	21.8	95.00%	R.SITIIPQDPTLFSGTIK.T		R.SITIIPQDPTLFSGTIK.T
1618	1627	2	1198.64	5.9	0	31	26.7	95.00%	Y.DHPYSLLLNK.Q		K.EYDHPYSLLLNK.Q
866	874	2	1078.48	6.6	0	28.3	30.5	94.10%	V.DSHTASWIY.D		R.HVLLDDCLSAVDSHTASWIYDNCITGPLMEDR.T
228	240	3	1519.83	0.13	0	21	25	95.00%	R.SIFIHHINSPISR.K		R.SIFIHHINSPISR.K
1584	1596	2	1471.79	5.3	0	62.2	24.5	95.00%	K.EFQGSTILTIAHR.L		K.EFQGSTILTIAHR.L
588	597	2	1216.65	-0.18	1	42.1	27.6	95.00%	R.ENELSLLLMR.S		R.ENELSLLLMR.S
964	976	2	1488.67	5.4	0	42.2	30.2	95.00%	K.EQQVSVNNNSSHF.E		K.EQQVSVNNNSSHFEAK.K
683	693	2	1242.59	5.6	1	41.6	30.4	95.00%	Y.DQLTIDPNGNR.F	Deamidation (+1)	K.YDQLTIDPNGNR.F
427	436	2	1165.66	-0.44	1	29.7	22.1	95.00%	K.SIIISEIYTK.A		K.SIIISEIYTK.A
791	803	2	1534.76	5.9	1	62.1	28.8	95.00%	K.NNILFNSPFNEAR.Y		K.NNILFNSPFNEAR.Y
964	979	2	1816.85	6.2	1	66.4	29.9	95.00%	K.EQQVSVNNNSSHFEAK.K		K.EQQVSVNNNSSHFEAK.K
1417	1430	3	1434.82	3.1	1	43.7	20.7	95.00%	R.TGAGKSTIITALFR.F		R.TGAGKSTIITALFR.F
936	951	2	1748.79	2.1	1	32	30.1	95.00%	K.SSILSRANSSANLAAK.S	Phospho (+80)/ Phospho (+80)	K.SSILSRANSSANLAAK.S
1422	1430	2	1020.6	-0.025	0	44.2	18.8	95.00%	K.STIITALFR.F		K.STIITALFR.F
1238	1255	2	2047.07	-1.2	1	68.1	25.6	95.00%	R.SPIYQHFSETLVGVTTIR.A		R.SPIYQHFSETLVGVTTIR.A
560	568	2	1060.57	2.9	1	58.5	27.1	95.00%	K.LNEAFQAIR.I		K.LNEAFQAIR.I
1152	1160	2	1010.48	0.95	1	73.2	31.1	95.00%	R.FFDATPTGR.I		R.FFDATPTGR.I
1464	1473	2	1077.58	5.4	0	43.3	28.6	95.00%	Q.DPTLFSGTIK.T		R.SITIIPQDPTLFSGTIK.T
1583	1596	3	1599.87	0.5	1	49	23.1	95.00%	R.KEFQGSTILTIAHR.L		R.KEFQGSTILTIAHR.L
1486	1492	2	847.48	-0.028	1	26.8	25.5	95.00%	R.QIFEALK.R		R.QIFEALK.R
1400	1410	2	1180.56	-6.4	1	33.6	30.4	95.00%	K.NVSFSVDAQSK.I		K.NVSFSVDAQSK.I
952	963	2	1282.62	3.2	0	42.4	29.5	95.00%	K.SSTSLSNLPAVK.E	Phospho (+80)	K.SSTSLSNLPAVK.E
887	900	3	1609.9	2.8	0	31.3	20.9	95.00%	R.TCILVSHNIALTLR.N	Carbamidomethyl (+57)	R.TCILVSHNIALTLR.N
714	720	2	877.46	3.4	1	29.9	30.9	95.00%	K.DLNIEFK.T		K.DLNIEFK.T
724	735	2	1140.65	-0.36	0	24.7	25	95.00%	K.LNVVIGPTGSGK.T		K.LNVVIGPTGSGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
6	A7A234_YEAS7	24.03%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
480	496	2	1745.79	2.3	1	87	30.8	95.00%	K.SSLDSSMSASSMISNVK.L	Oxidation (+16)	K.SSLDSSMSASSMISNVK.L
72	78	2	938.43	-0.13	1	31	31	95.00%	K.YNNLMER.L		K.YNNLMER.L
167	175	2	1137.65	0.16	0	52	22.4	95.00%	R.ISFLYNILR.S		R.ISFLYNILR.S
225	238	2	1550.82	6.3	1	65.4	26	95.00%	R.HLPVLVYANVPSEN.D		R.HLPVLVYANVPSENDDLVNR.F
422	430	2	1063.56	7.5	1	41.7	28.1	95.00%	I.DSNIVFIKE.D		R.VTIDSNIVFIKEDSFDR.E
337	344	2	957.59	4.7	1	21	21.2	90.90%	F.DLTKLQLK.Q		K.SEFDLTKLQLK.Q
383	393	2	1352.71	6.3	1	56	27.7	95.00%	E.DFSEIQNFIIK.N		R.LEEDFSEIQNFIIK.N
501	515	3	1760.9	2.9	1	60.9	26.8	95.00%	K.HGQWLNDLTNSHLVK.E		K.HGQWLNDLTNSHLVK.E
483	496	2	1458.64	5.8	0	57.7	31	95.00%	L.DSSMSASSMISNVK.L	Oxidation (+16)	K.SSLDSSMSASSMISNVK.L
436	447	2	1575.8	-0.98	1	27.1	28	95.00%	R.ERPIRDPNTWHR.T		R.ERPIRDPNTWHR.T
176	190	2	1522.73	0.77	1	87.7	29.6	95.00%	R.SNFNTASEPLASASK.F		R.SNFNTASEPLASASK.F
687	693	2	886.47	2.2	1	32.7	29.9	95.00%	K.VWLANER.T		K.VWLANER.T
7	16	2	1215.63	-0.35	1	33.4	27.9	95.00%	K.LANEVYPPWK.G		K.LANEVYPPWK.G
419	429	2	1247.71	0.79	1	37.2	21.9	95.00%	R.VTIDSNIVFIK.E		R.VTIDSNIVFIK.E
144	149	2	715.42	-0.031	1	26.7	28.6	94.50%	K.SLLEVR.L		K.SLLEVR.L
449	459	2	1168.62	6.6	1	53.1	27.4	95.00%	T.DIDANVANPLK.F		R.TDIDANVANPLK.F
17	26	2	1142.57	3.8	1	42.1	29.3	95.00%	K.GSYINYEGLK.K		K.GSYINYEGLK.K
469	477	2	1112.56	3.4	1	49	28	95.00%	K.FPYSVMEIK.V		K.FPYSVMEIK.V
677	686	2	997.52	0.57	1	34.7	27	95.00%	K.NAGPVNVEAK.V		K.NAGPVNVEAK.V
538	545	2	999.55	6.9	0	34.2	26.4	95.00%	L.DILPFWLP.D		K.LDILPFWLPDLETDIR.Q

298	305	2	870.49	-0.83	0	38.2	24.6	95.00%	K.LNSAPTLR.L		K.LNSAPTLR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
7	PMA1_YEAST	12.64%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
445	451	2	887.46	6.4	1	41.1	30	95.00%	K.VLEFHPF.D		K.VLEFHPFDPVSK.K
175	184	2	1056.64	6.5	0	89.4	21.4	95.00%	K.TLANTAVVIR.D		K.TLANTAVVIR.D
2	23	2	2124.92	7.2	1	47.6	30.2	95.00%	M.TDTSSSSSSSSASSVSAHQPTQ.E		-.MTDTSSSSSSSSASSVSAHQPTQEKPAK.T
663	675	2	1327.79	7.3	0	35.2	20.5	95.00%	A.DIVFLAPGLSAII.D		R.SAADIVFLAPGLSAIIDALK.T
556	566	2	1074.58	3.2	1	57.6	27.6	95.00%	K.MLTGDAVGIAK.E		K.MLTGDAVGIAK.E
618	625	2	969.56	-0.33	1	33.8	22.9	95.00%	R.VVEILQNR.G		R.VVEILQNR.G
571	583	2	1447.75	2.8	1	85.2	28.3	95.00%	R.QLGLGTNIYNAER.L		R.QLGLGTNIYNAER.L
240	252	2	1455.66	-0.69	1	70.9	30.7	95.00%	K.HYGDQTFSSSTVK.R		K.HYGDQTFSSSTVK.R
605	615	2	1273.62	6.1	1	42.1	29	95.00%	A.DGFAEVFPQHK.Y		R.LGLGGGGDMPGSELADFVENADGFAEVFPQHK.Y
475	482	2	843.52	0.085	0	23.4	24.3	94.80%	K.GAPLFVLK.T		K.GAPLFVLK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
8	A6ZY95_YEAS7	15.58%	100%	24

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	206	3	1835.99	-0.81	0	26	23.2	95.00%	K.KPLMPHQHIHQTLTR.R		K.KPLMPHQHIHQTLTR.R
221	231	2	1299.64	-0.32	0	72.8	29.8	95.00%	R.ITFSWMSGLMK.T		R.ITFSWMSGLMK.T
271	281	2	1289.62	1.9	0	49	29.5	95.00%	K.SNPSLSWAICR.T	Carbamidomethyl (+57)	K.SNPSLSWAICR.T
1458	1467	3	1194.68	-0.5	1	38.8	20.3	95.00%	K.DRTILTIAHR.L		K.DRTILTIAHR.L
1400	1415	2	1600.79	5.6	1	107	29.1	95.00%	L.DAQLTEGGGNLSVGQR.Q		K.EHVLSMSNDGLDAQLTEGGGNLSVGQR.Q
1036	1048	2	1466.73	5.6	1	63.1	29	95.00%	R.APMTFFETTPIGR.I		R.APMTFFETTPIGR.I
1126	1143	2	1975.01	-1.2	1	77.8	26.1	95.00%	R.SPIYSHFQETLGGLATVR.G		R.SPIYSHFQETLGGLATVR.G
1126	1133	2	977.47	6.1	0	43.5	29.8	95.00%	R.SPIYSHFQ.E		R.SPIYSHFQETLGGLATVR.G
1313	1321	2	1006.58	3.4	0	41.4	23.3	95.00%	K.SSLTLALFR.M		K.SSLTLALFR.M
1347	1354	2	934.57	6.5	1	30	16.1	95.00%	R.HKLSIIPQ.D		R.HKLSIIPQDSQVFEGTVR.E
1460	1467	2	923.55	-1.9	0	32.8	18.9	95.00%	R.TILTIAHR.L		R.TILTIAHR.L
630	638	2	1150.55	7.4	1	39.5	29.8	95.00%	G.DDATFLWQR.K		K.NIGDVAINIGDDATFLWQR.K
2	11	2	1104.54	3.3	0	55.8	29.7	95.00%	M.AGNLVSWACK.L	Carbamidomethyl (+57)	-.MAGNLVSWACK.L
790	805	2	1777	0.61	1	83.5	19.3	95.00%	R.HLIEHVLGPNGLLHTK.T		R.HLIEHVLGPNGLLHTK.T
1159	1174	2	1825.85	3.1	1	50.7	30	95.00%	R.IDNNMSAFYPSINANR.W		R.IDNNMSAFYPSINANR.W
709	717	2	1147.58	5.9	1	39.8	27.6	95.00%	K.ENILFGHRY.D		K.ENILFGHRYDAEFYEK.T
486	495	2	1141.67	3.6	1	67.1	23.6	95.00%	R.VISEILNNIK.S		R.VISEILNNIK.S
670	682	2	1495.75	-0.73	1	73.1	28.3	95.00%	K.TALLSCMLGDLFR.V	Carbamidomethyl (+57)	K.TALLSCMLGDLFR.V
1416	1422	2	872.49	-0.56	0	28.1	29	95.00%	R.QLLCLAR.A	Carbamidomethyl (+57)	R.QLLCLAR.A
1381	1388	2	909.52	-7.3	1	35.3	20.5	95.00%	R.ALELSHLK.E		R.ALELSHLK.E
379	388	2	1106.63	-0.37	0	29.1	21.8	95.00%	K.SALTALIYQK.S		K.SALTALIYQK.S
242	248	2	903.52	4.5	1	22.1	25.3	92.50%	A.DLYKLPR.N		K.YLVEADLYKLPR.N
655	664	2	1088.6	-0.72	1	27.5	25.9	95.00%	K.KGNLTCIVGK.V	Carbamidomethyl (+57)	K.KGNLTCIVGK.V
1134	1143	2	1015.57	4.4	0	42.8	26.2	95.00%	Q.ETLGGLATVR.G		R.SPIYSHFQETLGGLATVR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
9	B5VNN6_YEAST	16.95%	100%	30

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

55	66	2	1427.58	6.3	1	49.6	30.5	95.00%	A.DMYGQQPPNESY.D		-.MNTDQQPYQGQTDYTQGPDNGQSQEQDYDQYGQPLYPSQADGYYDPNVAAGTEADMYGQQPPNESYDQDYTNGEYYGQPPNMAAQDGENFSDFSSYGPPGTPGYDSYGGQYTPSQMSYGEPNSSGTSTPIYGNYDPNAIAMALPNEPYPAWTADSQSPVSIEQIEDIFIDLTNR.L
135	153	2	2040.98	6.7	1	45.4	28.9	95.00%	Y.DPNAIAMALPNEPYPAWTA.D		-.MNTDQQPYQGQTDYTQGPDNGQSQEQDYDQYGQPLYPSQADGYYDPNVAAGTEADMYGQQPPNESYDQDYTNGEYYGQPPNMAAQDGENFSDFSSYGPPGTPGYDSYGGQYTPSQMSYGEPNSSGTSTPIYGNYDPNAIAMALPNEPYPAWTADSQSPVSIEQIEDIFIDLTNR.L
69	85	2	1934.77	6.1	1	48.7	30	95.00%	Q.DYTNGEYYGQPPNMAAQ.D	Deamidation (+1)/ Oxidation (+16)	-.MNTDQQPYQGQTDYTQGPDNGQSQEQDYDQYGQPLYPSQADGYYDPNVAAGTEADMYGQQPPNESYDQDYTNGEYYGQPPNMAAQDGENFSDFSSYGPPGTPGYDSYGGQYTPSQMSYGEPNSSGTSTPIYGNYDPNAIAMALPNEPYPAWTADSQSPVSIEQIEDIFIDLTNR.L
92	104	2	1343.58	7.2	0	39.4	30.1	95.00%	S.DFSSYGPPGTPGY.D		-.MNTDQQPYQGQTDYTQGPDNGQSQEQDYDQYGQPLYPSQADGYYDPNVAAGTEADMYGQQPPNESYDQDYTNGEYYGQPPNMAAQDGENFSDFSSYGPPGTPGYDSYGGQYTPSQMSYGEPNSSGTSTPIYGNYDPNAIAMALPNEPYPAWTADSQSPVSIEQIEDIFIDLTNR.L
1173	1182	2	1168.59	-0.28	0	52.2	29	95.00%	K.EQTFGTLFAR.T		K.EQTFGTLFAR.T
1779	1788	2	1213.72	2.1	0	23.2	20.8	94.60%	R.QIRPPIYSLK.Q		R.QIRPPIYSLK.Q
320	330	2	1450.67	2.8	1	42	30.4	95.00%	R.FTAECLCFIYK.C	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.FTAECLCFIYK.C
837	850	2	1605.76	7.1	0	36	29.1	95.00%	V.DNMPTFTVLTPHYA.E		R.ISFFAQSLSTPIPEPLPVDNMPTFTVLTPHYAER.I
837	852	2	1906.9	6.1	1	90.7	28.8	95.00%	V.DNMPTFTVLTPHYAER.I	Oxidation (+16)	R.ISFFAQSLSTPIPEPLPVDNMPTFTVLTPHYAER.I
166	174	2	1105.59	8.2	1	28.7	28.7	95.00%	E.DIFIDLTNR.L		-.MNTDQQPYQGQTDYTQGPDNGQSQEQDYDQYGQPLYPSQADGYYDPNVAAGTEADMYGQQPPNESYDQDYTNGEYYGQPPNMAAQDGENFSDFSSYGPPGTPGYDSYGGQYTPSQMSYGEPNSSGTSTPIYGNYDPNAIAMALPNEPYPAWTADSQSPVSIEQIEDIFIDLTNR.L
1191	1207	2	2019.97	2.4	1	79.1	28.3	95.00%	K.LHYGHPDFINATFMTTR.G		K.LHYGHPDFINATFMTTR.G
789	799	2	1265.68	6.3	1	42.9	25.6	95.00%	R.TLRAPTFFVSQ.D		R.TLRAPTFFVSQDDNNFETEFFPR.D
1436	1444	2	1094.62	3.4	0	52.9	24.4	95.00%	R.IPFSILYSR.F		R.IPFSILYSR.F

105	119	2	1655.65	7.2	0	41.7	29.9	95.00%	Y.DSYGGQYTPSQMSYG.E	Oxidation (+16)	- .MNTDQQPYQGQTDYTQGPDNGQ SQEQDYDQYGQPLYPSQADGYYD PNVAAGTEADMYGQQPPNESYDQ DYTNGEYYGQPPNMAAQDGENFS DFSSYGPPGTPGYDSYGGQYTPS QMSYGEPNSSGTSTPIYGNYDPNAI AMALPNEPYPAWTADSQSPVSIEQI EDIFIDLTNR.L
1140	1154	2	1620.83	5.4	1	68.3	27.3	95.00%	Y.EEQTTNHPVAIVGAR.E		R.YEEQTTNHPVAIVGAR.E
1249	1261	2	1425.75	-0.019	0	69.1	26.5	95.00%	R.DLGFGTILNFTTK.I		R.DLGFGTILNFTTK.I
1070	1082	2	1296.71	0.92	1	44.2	24.9	95.00%	R.VQLSGNPILGDGK.S		R.VQLSGNPILGDGK.S
1167	1182	2	1709.88	4.9	1	76.9	26.8	95.00%	G.DVAAGKEQTFGTLFAR.T		R.EYIFSENSGVLGDVAAGKEQTFG TLFAR.T
1717	1728	2	1383.61	3.3	0	66.4	31.2	95.00%	K.GMGYMAWTQPSR.E		K.GMGYMAWTQPSR.E
919	929	2	1373.64	6.8	1	41.1	30.2	95.00%	I.DDLPFYCIGFK.S	Carbamidomethyl (+57)	K.SQIDDLPFYCIGFK.S
293	301	2	1086.55	3.5	1	25.1	28.5	92.10%	K.MNQLSPLER.V		K.MNQLSPLER.V
200	211	2	1281.65	5.3	1	55.8	28.6	95.00%	R.MSPDQALISLHA.D		R.MSPDQALISLHADYIGGDTANYK. K
203	211	2	966.52	5.9	0	42.1	27	95.00%	P.DQALISLHA.D		R.MSPDQALISLHADYIGGDTANYK. K
1262	1273	2	1248.6	2.9	1	86.4	29.7	95.00%	K.IGAGMGEQMLSR.E		K.IGAGMGEQMLSR.E
1520	1527	2	993.5	0.087	0	45.7	29.9	95.00%	R.NSWIGYVR.M		R.NSWIGYVR.M
953	962	2	1174.55	2	0	46.4	30.5	95.00%	R.TISGFMNYSR.A		R.TISGFMNYSR.A
135	145	2	1141.55	6.8	0	29.3	29.8	95.00%	Y.DPNAIAMALPN.E	Oxidation (+16)	- .MNTDQQPYQGQTDYTQGPDNGQ SQEQDYDQYGQPLYPSQADGYYD PNVAAGTEADMYGQQPPNESYDQ DYTNGEYYGQPPNMAAQDGENFS DFSSYGPPGTPGYDSYGGQYTPS QMSYGEPNSSGTSTPIYGNYDPNAI AMALPNEPYPAWTADSQSPVSIEQI EDIFIDLTNR.L
870	877	2	977.58	3.3	1	51.5	19.7	95.00%	R.VTLLEYLK.Q		R.VTLLEYLK.Q
1247	1261	3	1638.88	1.3	1	17.7	24.2	93.90%	K.GRDLGFGTILNFTTK.I		K.GRDLGFGTILNFTTK.I
819	836	2	1942.06	6.1	1	54.7	22.1	95.00%	R.ISFFAQSLSTPIPEPLPV.D		R.ISFFAQSLSTPIPEPLPVDNMPTF TVLTPHYAER.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
10	A6ZL63_YEAS7	40.83%	100%	17

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
197	210	2	1652.76	6.3	1	66	30	95.00%	G.DNMIEATTNAPWYK.G		K.TVPFVPISGWNGDNMIEATTNAP WYK.G
394	401	2	759.41	-0.42	1	45.9	29.5	95.00%	K.SGDAALVK.F		K.SGDAALVK.F
147	155	2	1014.6	5.9	1	24.4	22.6	95.00%	R.QLIVAVNKM.D		R.QLIVAVNKMDSVK.W
147	154	2	883.55	-0.35	0	43.7	20	95.00%	R.QLIVAVNK.M		R.QLIVAVNK.M
254	264	2	1024.61	3.2	0	65.4	19.8	95.00%	K.IGGIGTVPVGR.V		K.IGGIGTVPVGR.V
298	311	2	1458.72	5.5	1	33.9	28.8	95.00%	L.EQGVPGDNVGFNVK.N		K.SVEMHHEQLEQGVPGDNVGFNV K.N
429	437	2	913.56	0.54	0	47.8	22.6	95.00%	R.QTVAVGVIK.S		R.QTVAVGVIK.S
6	20	2	1559.85	2.7	1	82.3	24.9	95.00%	K.SHINVVVIGHVDSGK.S		K.SHINVVVIGHVDSGK.S
241	249	2	1078.66	5.1	1	22.8	17.2	94.00%	T.DKPLRLPLQ.D		K.TLLEAIDAIEQPSRPTDKPLRLPLQ DVYK.I
360	370	2	1386.6	5.5	1	39.8	30.8	95.00%	L.DCHTAHIACRF.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GCASFNATVIVLNHPGQISAGYSP VLDCHTAHIACRFDELLEK.N
135	146	2	1325.75	-0.022	0	62.4	24	95.00%	R.EHALLAFTLGVR.Q		R.EHALLAFTLGVR.Q
185	196	2	1272.66	6.8	0	28.9	28.8	95.00%	K.TVPFVPISGWNG.D		K.TVPFVPISGWNGDNMIEATTNAP WYK.G

334	369	5	3892.86	0.25	1	25.3	24.9	95.00%	K.GCASFNATVIVLNHPGQISAGYSPVLDCHTAHIACR.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GCASFNATVIVLNHPGQISAGYSPVLDCHTAHIACR.F
246	253	2	974.55	3.5	1	30	26.7	95.00%	R.LPLQDVYK.I		R.LPLQDVYK.I
360	369	3	1239.53	7.1	0	25.5	30.3	95.00%	L.DCHTAHIACR.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GCASFNATVIVLNHPGQISAGYSPVLDCHTAHIACR.F
85	96	2	1354.7	2.5	1	66.3	27.1	95.00%	K.YQVTVIDAPGHR.D		K.YQVTVIDAPGHR.D
265	285	2	2073.13	6.4	1	34.1	21.2	95.00%	R.VETGVIKPGMVVTFAPAGVTT.E		R.VETGVIKPGMVVTFAPAGVTTEVK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
11	B3LFI5_YEAS1	31.63%	100%	19

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
373	383	2	1170.57	7.5	1	41.5	29	95.00%	S.DHETGGLVTSR.Q		R.EVLAFDEAFQYVLEFAENSDTETVLVSTSDHETGGLVTSR.Q
191	199	2	966.52	5.8	0	33.9	27	95.00%	E.DLIATHQLG.E		R.WQEDLIATHQLGEYPLGR.V
488	498	2	1297.67	4.8	1	38.9	26.8	95.00%	V.DVNIYAYANKK.A		R.AQIGWTTHGHSAVDVNIYAYANKK.A
475	487	2	1363.67	5.1	0	50.2	29.5	95.00%	R.AQIGWTTHGHSAV.D		R.AQIGWTTHGHSAVDVNIYAYANK.K
488	497	2	1169.58	4.6	0	40.7	29.4	95.00%	V.DVNIYAYANK.K		R.AQIGWTTHGHSAVDVNIYAYANK.K
449	456	2	952.53	6.4	1	49	25.2	95.00%	S.DLETLIHL.D		K.DLGIYDYTDSDLETLIHLDDNANAIQDK.L
206	215	2	1031.54	-0.9	1	57.7	28.4	95.00%	R.VVDLLMGGGR.S	Oxidation (+16)	R.VVDLLMGGGR.S
122	135	2	1352.65	4.9	0	86.7	30.7	95.00%	T.DSAAGATAFACALK.S	Carbamidomethyl (+57)	R.SSDSLVTDSAAGATAFACALK.S
467	474	2	996.47	1.4	1	33.9	30.2	95.00%	K.LNDMVSFR.A	Oxidation (+16)	K.LNDMVSFR.A
191	205	2	1681.89	5	1	59.7	25.4	95.00%	E.DLIATHQLGEYPLGR.V		R.WQEDLIATHQLGEYPLGR.V
1	12	3	1430.67	0.57	1	37.6	30.6	95.00%	-.MMTHTLPSEQTR.L		-.MMTHTLPSEQTR.L
68	86	2	2027.98	-0.76	1	95.4	28.5	95.00%	K.NVIFFVTDGMGPASLSMAR.S	Oxidation (+16)	K.NVIFFVTDGMGPASLSMAR.S
316	328	2	1458.65	5.8	1	84.4	30.7	95.00%	K.DSNGFFLMVEGSR.I	Deamidation (+1)	K.DSNGFFLMVEGSR.I
136	154	2	2049	5	1	47.6	28.8	95.00%	K.SYNGAIGVDPHHRPCGTVL.E	Carbamidomethyl (+57)	K.SYNGAIGVDPHHRPCGTVLEAAK.L
75	86	2	1191.54	5.3	0	45.5	30.3	95.00%	T.DGMGPASLSMAR.S		K.NVIFFVTDGMGPASLSMAR.S
174	184	2	1117.51	6.9	0	34.5	29.9	95.00%	T.DATPASFSSHV.D		R.ITDATPASFSSHVDYR.W
172	184	2	1331.64	5.5	1	49.9	30	95.00%	R.ITDATPASFSSHV.D		R.ITDATPASFSSHVDYR.W
475	497	2	2515.23	2.8	1	35.9	26.5	95.00%	R.AQIGWTTHGHSAVDVNIYAYANK.K		R.AQIGWTTHGHSAVDVNIYAYANK.K
159	171	2	1362.79	2.6	0	69.1	18.9	95.00%	K.LAGYLTGLVVTTR.I		K.LAGYLTGLVVTTR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
12	A7A160_YEAS7	33.55%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
55	63	2	1080.55	0.55	1	50	29	95.00%	R.TLSDYNIQK.E		R.TLSDYNIQK.E
64	72	2	1066.62	3.4	0	51.7	20.9	95.00%	K.ESTLHLVLR.L		K.ESTLHLVLR.L
119	136	3	2016.94	5.3	1	50.3	29.4	95.00%	R.RECSNPTCGAGVFLANHK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.RECSNPTCGAGVFLANHK.D
58	72	2	1827.99	4.9	1	78.9	23.5	95.00%	S.DYNIQKESTLHLVLR.L		R.TLSDYNIQKESTLHLVLR.L
1	6	2	764.43	3.8	0	35.4	22.1	95.00%	-.MQIFVK.T		-.MQIFVK.T
120	136	2	1860.83	2.3	0	85.7	29.6	95.00%	R.ECSNPTCGAGVFLANHK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.ECSNPTCGAGVFLANHK.D
34	42	2	1038.51	-0.21	1	38.7	31.3	95.00%	K.EGIPPDQQR.L		K.EGIPPDQQR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
13	B3LSE9_YEAS1	28.24%	100%	23

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
327	346	2	2113.14	-2.2	1	85.6	21.9	95.00%	K.DGSLLITEVTWVGNGNVLVK.T		K.DGSLLITEVTWVGNGNVLVK.T
756	766	2	1315.62	4.9	1	63.2	30	95.00%	G.DDNVHFQNSLK.F		R.FLLMHGTGDDNVHFQNSLK.F

258	264	2	868.47	5.8	0	27	25.3	95.00% G.DYLAFLK.I		K.AAWWSPTGDYLAFLK.I
404	417	2	1591.81	4.9	0	25.5	27.2	94.70% V.DILPIGGYNHLAYF.E		R.NESSNGGWWEITHNTLFIPANETFDRPHNGYVDILPIGGYNHLAYFENSNSSHYK.T
496	502	2	840.47	-0.26	0	36.9	24.8	95.00% R.FGLLTYK.G		R.FGLLTYK.G
206	218	2	1527.8	5.7	1	34.2	25.7	95.00% Q.DNNIYIYSAISKK.T		K.SSSSFEEIGNEVALAIWSPNSNDIAYVQDNNIYIYSAISKK.T
297	312	2	1815.86	0.21	1	69.8	29.2	95.00% K.SGTPNPHAELWVYSMK.D		K.SGTPNPHAELWVYSMK.D
699	710	2	1380.65	3	1	28.9	31	94.20% K.YGMSVAPVTDWR.F		K.YGMSVAPVTDWR.F
587	606	2	2299.12	6.6	0	81.1	26.8	95.00% S.DHYPVFFFAYGGPNSQQVVK.T		K.DILVNSYEILPNDFDETLSDHYPVFFFAYGGPNSQQVVK.T
206	217	2	1399.71	6.1	0	68	27.7	95.00% Q.DNNIYIYSAISK.K		K.SSSSFEEIGNEVALAIWSPNSNDIAYVQDNNIYIYSAISK.K
793	803	2	1318.66	-3.4	1	25.6	28.9	92.30% R.YHNANVIVFDK.L		R.YHNANVIVFDK.L
449	455	2	898.49	-0.022	0	23.9	24.9	95.00% R.LYFISTR.K		R.LYFISTR.K
72	78	2	792.45	3	0	43.9	25.3	95.00% K.VSFSVVR.N		K.VSFSVVR.N
226	236	2	1167.56	5.9	0	42.1	30	95.00% N.DGSSFLFNGKP.D		R.AVTNDGSSFLFNGKPDWVYEEEVFEDDK.A
654	672	2	2039.02	0.048	1	72.2	26.9	95.00% R.DQISAASLYGSLTFVDPQK.I		R.DQISAASLYGSLTFVDPQK.I
396	403	2	957.44	6.4	0	28.6	30.4	94.70% F.DRPHNGYV.D	Deamidation (+1)	R.NESSNGGWWEITHNTLFIPANETFDRPHNGYVDILPIGGYNHLAYFENSNSSHYK.T
353	360	2	932.56	6.8	0	32.7	19.8	95.00% S.DILTVFLI.D		R.SSDILTVFLIDTIAK.T
166	177	2	1449.66	4	1	35.4	30.7	95.00% R.HSTFGSYFVYDK.S		R.HSTFGSYFVYDK.S
250	264	2	1724.86	-0.072	1	46.6	28.4	95.00% K.AAWWSPTGDYLAFLK.I		K.AAWWSPTGDYLAFLK.I
258	265	2	981.56	6.3	1	27	23.2	95.00% G.DYLAFLKI.D		K.AAWWSPTGDYLAFLKIDESEVGEFIIPYYVQDEK.D
158	165	2	1003.48	0.58	0	34.1	30	95.00% R.TNSVQNWR.H		R.TNSVQNWR.H
554	562	3	1062.59	6.3	1	26	26.5	95.00% K.SFRELNLGK.D		K.SFRELNLGK.D
351	360	2	1106.63	7.8	1	58.5	21.9	95.00% R.SSDILTVFLI.D		R.SSDILTVFLIDTIAK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
14	CBPS_YEAST	22.57%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
361	370	2	1130.59	2.8	0	29.6	27.6	95.00%	K.TILGAPFCPR.R	Carbamidomethyl (+57)	K.TILGAPFCPR.R
159	169	2	1277.73	6.6	0	52.5	22.4	95.00%	P.DLKPLLLMAHQ.D		K.VNELGLLYTWEGSDPDLKPLLLMAHQDVVPVNNETLSSWK.F
391	403	2	1314.71	-0.23	1	87.6	25.8	95.00%	R.TTQAVDIINGGVK.A		R.TTQAVDIINGGVK.A
554	566	2	1387.72	5.6	0	36.7	27.4	95.00%	V.DVPGHLSAIAFVY.E		K.TLHSVNEHVDVPGHLSAIAFVYEYIVNVNEYA.-
279	290	2	1302.69	6.3	1	64.2	27.4	95.00%	K.DVFVATPINAEK.G		K.DVFVATPINAEK.G
375	386	2	1457.77	5.3	1	63.4	26.2	95.00%	K.LVEYISNQSHLR.S		K.LVEYISNQSHLR.S
337	352	2	1787.86	6.7	1	41.2	29	95.00%	F.DNPIYGLLTCAAEHSK.S	Carbamidomethyl (+57)	K.GYVDFEVSILGHGGHSSVPPDHTTIGIASELITEFEANPFDYEFEFDNPIYGLLTCAAEHSK.S
471	485	2	1564.79	6.5	1	32	28.4	95.00%	R.ELEPAPLSPSSGPVW.D		R.ELEPAPLSPSSGPVWDILAGTIQDVFENGVLQNNEEFYVTTGLFSGNTDTK.Y
360	370	3	1258.69	3	1	46.3	25.7	95.00%	K.KTILGAPFCPR.R	Carbamidomethyl (+57)	K.KTILGAPFCPR.R
413	418	2	798.45	-0.79	0	24.3	23.6	95.00%	R.FLINHR.I		R.FLINHR.I
522	528	2	972.47	-0.0068	0	34.1	29.5	95.00%	K.YYWNLSK.N		K.YYWNLSK.N
505	518	2	1563.72	6.7	1	63.4	30.2	95.00%	N.EEFYVTTGLFSGNT.D		R.ELEPAPLSPSSGPVWDILAGTIQDVFENGVLQNNEEFYVTTGLFSGNTDTK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
15	ADP1_YEAST	22.40%	100%	21

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
689	697	3	1089.55	6.2	0	29.7	29.1	95.00%	R.EWAHLAAHR.D		R.EWAHLAAHR.D

538	553	2	1759.99	6.3	1	41.8	20	95.00%	R.VSIACELVTSPLVLFL.D	Carbamidomethyl (+57)	R.VSIACELVTSPLVLFLDEPTSGLDASNANNVIECLVR.L
430	439	2	1117.64	-0.46	1	45.1	23.5	95.00%	K.TTLLDILAMK.R		K.TTLLDILAMK.R
171	178	2	897.56	-0.35	0	35.4	18.1	95.00%	K.ILQILNGK.I		K.ILQILNGK.I
68	78	2	1347.55	-0.36	1	44	31.3	95.00%	K.QFSECNSYTGR.C	Carbamidomethyl (+57)	K.QFSECNSYTGR.C
683	697	3	1747.86	5	1	44.4	28.5	95.00%	S.DGTTQREWAHLAAHR.D		R.NISDLEAGTDTNDIDNTIHQTTFTSSDGTTQREWAHLAAHR.D
30	39	2	1099.52	4	1	34.3	29.8	95.00%	K.TPFFEGTSSK.N		K.TPFFEGTSSK.N
860	873	2	1681.8	1.5	0	38.8	29.3	95.00%	R.SNNYYSPLAYYISK.I		R.SNNYYSPLAYYISK.I
200	210	2	1317.56	7.1	1	29.9	31.2	95.00%	I.DQLESFYCGLS.D	Carbamidomethyl (+57)	K.IPQITFACDKPNQECNFQFWIDQLESFYCGLSDCAFEYDLEQNTSHYK.C
592	600	2	1145.58	-0.28	1	39.1	28.9	95.00%	R.SNIFYLFDK.L		R.SNIFYLFDK.L
289	295	2	848.47	5	0	40.2	28.5	95.00%	G.DPYITLK.C		K.FSEPSMNDLILTVFGDPYITLK.C
763	783	2	2272.19	5.3	0	67.5	23.6	95.00%	G.DLPTGQQSAGFLQQLSILNSR.S		K.DSVYYAELSQEIEEVLSEGDEESNVLNGDLPTGQQSAGFLQQLSILNSR.S
582	591	2	1162.69	3.3	0	57.6	18.6	95.00%	R.TLVLSIHQPR.S		R.TLVLSIHQPR.S
138	147	2	1135.53	6.2	1	27.1	30.2	92.60%	C.DAFMPDPSIK.G	Oxidation (+16)	R.AQNDTCHCDNGWGGINCDVCQEDFVCDAFMPDPSIK.G
179	186	2	948.48	6.5	0	26.7	28.3	94.90%	K.IPQITFAC.D	Carbamidomethyl (+57)	K.IPQITFACDKPNQECNFQFWIDQLESFYCGLSDCAFEYDLEQNTSHYK.C
51	67	2	2187.91	6	1	66.3	29.9	95.00%	N.DTCPPCFNCMLPIFECK.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GNDTCPPCFNCMLPIFECK.Q
234	244	2	1218.58	1.4	1	26.2	29.6	92.20%	K.CVPDTVLCGAK.G	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CVPDTVLCGAK.G
669	682	2	1579.71	5.6	1	42.3	30.5	95.00%	N.DIDNTIHQTTFTSS.D	Deamidation (+1)	R.NISDLEAGTDTNDIDNTIHQTTFTSSDGTTQR.E
561	574	2	1573.76	6	1	82.6	29.6	95.00%	L.DASNANNVIECLVR.L	Carbamidomethyl (+57)	R.VSIACELVTSPLVLFLDEPTSGLDASNANNVIECLVR.L
281	288	2	876.5	5.9	0	28.6	26.9	95.00%	N.DLILTVFG.D		K.FSEPSMNDLILTVFGDPYITLK.C
641	651	2	1161.57	5.3	1	50.6	29.7	95.00%	I.DITFEAGPQGK.R		R.NEGYICPDNYNIADYLIDITFEAGPQGK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
16	PPN1_YEAST	20.03%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
581	595	2	1687.9	6.7	0	48	24.2	95.00%	Y.ELGPAYVPQLFTPTR.F		K.YELGPAYVPQLFTPTR.F
544	554	2	1202.6	5.1	1	79.1	28.4	95.00%	M.DSSNIEVGINR.E		K.IMEDSLLEDEMDSSNIEVGINR.E
323	334	3	1302.75	3	0	17.4	21.6	93.20%	K.VWLSGHVPPIAK.N		K.VWLSGHVPPIAK.N
482	500	2	2067.08	-0.73	0	63.3	24.5	95.00%	R.YSIVNIGGSVIPTFNPSFR.I		R.YSIVNIGGSVIPTFNPSFR.I
226	242	2	1958.98	5.7	0	81	27.3	95.00%	N.DVFPHNMFALGPTLQTR.E	Oxidation (+16)	R.DFDVSVIPSLGNNDVFPHNMFALGPTLQTR.E
72	83	2	1334.84	5.1	1	24.3	11.5	95.00%	R.LGLTPREPVIIK.D		R.LGLTPREPVIIK.D
353	365	2	1414.74	6.6	0	43	27.3	95.00%	R.DIIIGGLYGHMNI.D		R.DIIIGGLYGHMNIDHFIPTDGK.K
215	242	3	3039.53	5.8	1	25.3	24	95.00%	F.DVSVIPSLGNNDVFPHNMFALGPTLQTR.E	Deamidation (+1)	R.DFDVSVIPSLGNNDVFPHNMFALGPTLQTR.E
512	523	2	1441.66	5.9	1	48.7	30.7	95.00%	N.DSNFAVSEYKPW.D		R.IWEYNITDIVNDSNFAVSEYKPWDEFFESLNK.I
263	274	2	1247.68	0.46	1	31.7	26.8	95.00%	R.SASFLTEVIPGK.L		R.SASFLTEVIPGK.L
580	595	2	1850.95	-1.7	1	46.2	25.9	95.00%	K.YELGPAYVPQLFTPTR.F		K.YELGPAYVPQLFTPTR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
17	A6ZMV7_YEAS7	26.02%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

386	401	2	1583.76	5.9	1	53.9	30	95.00%	R.FSIIAGGSPSSSQEAF.D		R.FSIIAGGSPSSSQEAFDSHGNTEHGR.K
431	442	2	1381.53	5.6	1	67.7	30.5	95.00%	V.DDAVNCNTSNCL.-	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.SPTAYGATTASSNCIVDDAVNCNTSNCL.-
415	430	2	1598.73	6.4	0	45.3	30.3	95.00%	R.SPTAYGATTASSNCIV.D	Carbamidomethyl (+57)	R.SPTAYGATTASSNCIVDDAVNCNTSNCL.-
415	431	2	1713.76	4.2	1	42.9	29.5	95.00%	R.SPTAYGATTASSNCIVD.D	Carbamidomethyl (+57)	R.SPTAYGATTASSNCIVDDAVNCNTSNCL.-
180	202	2	2306.2	4.6	1	77	23.9	95.00%	E.DAISSPGPSGQIGEVLPQSVVNR.L		R.LVLYVGVAGLISNVVGLFLFHDHGSDSLHSHSHGSVESGNNDLDIESNATHSHSHASLPNDNLAIDEDAISSPGPSGQIGEVLPQSVVNR.L
293	309	2	1854.03	3.8	1	104	21	95.00%	R.ILLQATPSTISADQIQR.E		R.ILLQATPSTISADQIQR.E
293	304	2	1213.7	6.3	0	24.1	23.1	95.00%	R.ILLQATPSTISA.D		R.ILLQATPSTISADQIQR.E
358	376	2	2090.05	5.7	1	61.2	26.4	95.00%	K.IFHQHGIHSATVQPEFVSG.D		K.IFHQHGIHSATVQPEFVSGDVNEDIR.R
414	430	2	1754.83	5	1	65.8	29.5	95.00%	K.RSPTAYGATTASSNCIV.D	Carbamidomethyl (+57)	K.RSPTAYGATTASSNCIVDDAVNCNTSNCL.-
203	213	2	1250.63	5.8	1	53	30	95.00%	R.LSNESQPLLNH.D		R.LSNESQPLLNHDDHDHSHESK.K
432	442	2	1266.5	6	0	45.4	30.6	95.00%	D.DAVNCNTSNCL.-	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.SPTAYGATTASSNCIVDDAVNCNTSNCL.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides							
18	ATC9_YEAST	15.90%	100%	18							
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
414	428	2	1816.98	6.6	1	39.8	24.2	95.00%	N.EINPNVPILITFEYR.Y		R.QWYNRPLSTVLPFENYPNPSYEPNDINLSHHHANEINPNVPILITFEYR.Y
1082	1094	2	1517.81	5.6	1	34.7	26.2	95.00%	N.DTPLHGEPVIVWR.D		R.VYVPSINDTPLHGEPVIVWR.D
1049	1065	2	1820.91	-0.7	1	49	27.5	95.00%	R.TIMCTGDNILTAISVGR.E	Carbamidomethyl (+57)	R.TIMCTGDNILTAISVGR.E
454	464	2	1134.58	4.8	0	33.2	29	95.00%	V.DLSTVSNGLTK.G	Deamidation (+1)	K.TNNNWIDPDWVDLSTVSNGLTK.G
579	587	2	1041.53	8	0	25.7	27.9	94.20%	S.DPNITILPC.D	Carbamidomethyl (+57)	K.FWTTISSSELVPGDIYEVSDPNITILPCDSILLSSDCIVNESMLTGESVPVSK.F
58	90	4	3595.74	6.2	1	23	25.4	95.00%	F.EAVPSSIVSFHHPHSFQSSNLPSPHSSGNLEQR.G		R.ASFSSTATTSTAATLTSAMVLDQNNSEPYAGATFEAVPSSIVSFHHPHSFQSSNLPSPHSSGNLEQR.G
288	300	2	1695.82	2.1	0	67.8	28.8	95.00%	K.FYPQYAPNLHYQR.F		K.FYPQYAPNLHYQR.F
204	221	2	1937.89	3.8	0	87	29.8	95.00%	S.DTGFVYHSATHSSSSLSR.Y		R.LGENSDTGFVYHSATHSSSSLSR.Y
153	163	2	1223.63	6.1	1	39	28.1	95.00%	Q.DRIYGTGLSSR.R		R.FFTQEQISNAEGASTLENTDYDMAWDATPAYEQDRIYGTGLSSR.R
1170	1177	2	1001.56	5.9	0	46.4	26.4	95.00%	H.ELMIQLQK.L		K.HELMIQLQK.L
1	14	2	1651.78	2.1	1	99.4	29.5	95.00%	-.MDIPSSNQIQHGQR.S	Acetyl (+42)	-.MDIPSSNQIQHGQR.S
45	57	2	1412.59	7.1	1	35.9	30.7	95.00%	L.DQNNSEPYAGATF.E		R.ASFSSTATTSTAATLTSAMVLDQNNSEPYAGATFEAVPSSIVSFHHPHSFQSSNLPSPHSSGNLEQR.G
625	638	2	1587.75	7	1	80.1	29.3	95.00%	C.DDFQSTQISSFVSK.S		K.FPATEETMYQLCDDFQSTQISSFVSK.S
792	805	2	1482.78	5.2	1	35.7	26.5	95.00%	L.DVLGVQISEPNGVR.G	Deamidation (+1)	K.TGTLTEDGLDVLGVQISEPNGVR.G
760	768	2	1049.54	3.3	0	39.3	29.6	95.00%	K.GIFCISPTR.L	Carbamidomethyl (+57)	K.GIFCISPTR.L
919	930	2	1381.68	5.7	1	52.2	29.3	95.00%	T.DNDPHNFLGVVR.S		R.ENTFTDNDPHNFLGVVR.S
1055	1065	2	1157.65	6.3	0	29.8	25.4	95.00%	G.DNILTAISVGR.E		R.TIMCTGDNILTAISVGR.E

1113	1122	2	1087.57	6	1	98.9	29.2	95.00%	K.LGNNSVESLR.E		K.LGNNSVESLR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
19	B3LFI3_YEAS1	26.92%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
123	130	2	980.51	3.2	0	30.8	27.9	95.00%	K.ACYVTLVR.N	Carbamidomethyl (+57)	K.ACYVTLVR.N
226	233	2	1089.5	-0.11	0	44.2	30.1	95.00%	R.YQSGFFWR.H		R.YQSGFFWR.H
413	423	2	1308.55	5.4	0	28.8	31.1	94.00%	N.DFTFQGYSCGK.E	Carbamidomethyl (+57)	K.EVYNSNNCECDQGNDFTFQGYSCGK.E
359	375	3	1791.97	0.27	1	29.7	23.6	95.00%	R.WGDAPVHSIAAALFLPK.D		R.WGDAPVHSIAAALFLPK.D
349	358	2	1254.55	5.4	1	35.6	30.9	95.00%	L.DHQGGFFYER.W		R.EYFDTLDHQGGFFYER.W
383	391	2	1097.5	5.2	0	37.7	30.5	95.00%	S.DIGYHHPPY.D		K.IHYFSDIGYHHPPYDNCPLDK.E
361	375	2	1548.88	6.1	0	72.2	20	95.00%	G.DAPVHSIAAALFLPK.D		R.WGDAPVHSIAAALFLPK.D
338	345	2	1031.48	6.1	1	36.5	30	95.00%	R.SPAYREYF.D		R.SPAYREYFDTLDHQGGFFYER.W
424	435	2	1409.72	2.8	1	64.2	27.3	95.00%	K.EYYDAQGLVKPK.N		K.EYYDAQGLVKPK.N
105	117	2	1487.69	-5.5	1	76.3	30.1	95.00%	K.TTMDYITPSFANK.A		K.TTMDYITPSFANK.A
212	221	2	1193.54	-0.17	1	52.2	29.9	95.00%	K.YIYGGSESYR.H		K.YIYGGSESYR.H
32	44	2	1411.71	6.7	0	33.4	28.5	95.00%	R.TQQYIPSSISAAF.D		R.TQQYIPSSISAAFDFTSGSISPEQQVISEENDAK.K
427	435	2	954.56	6.3	0	21	24	91.00%	Y.DAQGLVKPK.N		K.EYYDAQGLVKPK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
20	KTR1_YEAST	23.41%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
46	57	2	1247.6	0.56	0	77.6	29.5	95.00%	K.YSTVLSSGSGYK.Y		K.YSTVLSSGSGYK.Y
364	375	2	1531.65	5.5	0	52.2	30.8	95.00%	K.DFTWHSYSCTTK.F	Carbamidomethyl (+57)	K.DFTWHSYSCTTK.F
334	347	2	1703.79	5.8	0	38.8	30.7	95.00%	G.DIGYYHVPFHSCPI.D	Carbamidomethyl (+57)	R.SEIHHFGDIGYYHVPFHSCPIDTSIR.L
73	80	2	905.54	3.9	0	59.6	22.6	95.00%	K.ATFVTLVR.N		K.ATFVTLVR.N
312	324	2	1309.71	6.6	0	44.9	25	95.00%	G.DAPVHSIGAALFL.D		R.WGDAPVHSIGAALFLDR.S
83	92	2	1137.6	3.9	1	44.3	27.8	95.00%	R.DLYSLAESIK.S		R.DLYSLAESIK.S
334	352	2	2276.08	5.6	1	81.3	28.3	95.00%	G.DIGYYHVPFHSCPIDTSIR.L	Carbamidomethyl (+57)	R.SEIHHFGDIGYYHVPFHSCPIDTSIR.L
163	172	2	1185.61	2.5	1	40.8	28.6	95.00%	R.IIYGDSISYR.H		R.IIYGDSISYR.H
177	184	2	1051.48	-0.034	1	38.6	30.3	95.00%	R.FESGFFYR.H		R.FESGFFYR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
21	A6ZL18_YEAS7	18.44%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
297	311	3	1809.93	0.79	1	27.5	25.6	95.00%	R.NLYHTIKDSIQYTSK.A		R.NLYHTIKDSIQYTSK.A
221	233	2	1277.67	2.7	1	65.4	27.9	95.00%	K.YVINLEGTGAGGK.A		K.YVINLEGTGAGGK.A
63	77	2	1719.89	6.3	0	86.8	26.1	95.00%	G.DLQIITASFHPYTSK.E		K.EDEHPEFNDLLETAWGDLQIITASFHPYTSK.E
168	181	2	1430.75	6.6	1	94.5	27	95.00%	T.DDGMGVVSLLANLK.Y		K.NPEEEGLLLSAHFDSVPTGYGATDDGMGVVSLLANLK.Y
411	418	2	976.54	4.7	1	28.6	26.4	95.00%	K.LFSNDIIR.S		K.LFSNDIIR.S
746	755	2	1175.61	5.8	0	34.5	28.3	95.00%	R.EGNFLKPMLQ.D		R.EGNFLKPMLQDLPSIK.Y
731	745	2	1522.79	5.5	0	59.8	26.1	95.00%	I.DLSQGNAASVHVLGR.E		R.FSQNIDLSQGNAASVHVLGR.E
782	802	2	2221.05	4.4	0	63.2	28.7	95.00%	Y.DGMQPNLLSTNGNTNISSMVK.V	Deamidation (+1)	K.YSSTHINCTSVTNGMELCMYDGMQPNLLSTNGNTNISSMVK.V
169	181	2	1315.73	6.4	0	77.4	25.5	95.00%	D.DGMGVVSLLANLK.Y		K.NPEEEGLLLSAHFDSVPTGYGATDDGMGVVSLLANLK.Y
726	745	2	2112.07	1	1	95.7	26.4	95.00%	R.FSQNIDLSQGNAASVHVLGR.E		R.FSQNIDLSQGNAASVHVLGR.E
247	269	2	2752.34	5.4	1	81.4	25.6	95.00%	K.IYQQSVKENPFGNSIYQQGFYSR.Y		K.IYQQSVKENPFGNSIYQQGFYSR.Y
569	583	2	1579.62	4.8	1	49.2	30	95.00%	Q.DDNVSTTSAGPSHNV.D	Phospho (+80)	R.DGQENLEQPQDQFTSSQDDQASIQDDNVSTTSAGPSHNVDEDHGMDSSSQQHDER.V

129	140	2	1398.74	2.4	1	31.1	26.3	95.00%	R.VTYFESSNILVK.L		R.VTYFESSNILVK.L
254	269	2	1905.87	0.89	0	61.7	29.6	95.00%	K.ENPFGNSIYQQGFYSR.Y		K.ENPFGNSIYQQGFYSR.Y
888	901	2	1746.85	6.7	1	44.5	29.4	95.00%	F.DQETYHIGVQWFPK.L		K.LDFDQETYHIGVQWFPK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
22	ATC2_YEAST	12.53%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
498	513	2	1789.93	5.8	1	55.1	25.7	95.00%	N.DLLANIVLNSTAFENR.D	Deamidation (+1)	R.NDLLANIVLNSTAFENR.D
37	46	2	1137.58	-0.63	1	43.1	29.9	95.00%	K.SQLSDLHNPK.S		K.SQLSDLHNPK.S
584	597	2	1585.88	-0.38	1	49.8	23.1	95.00%	R.LSLGLQPGELQYLR.D		R.LSLGLQPGELQYLR.D
54	64	2	1303.65	3.2	1	46.6	29.5	95.00%	R.LFGYESNSLFK.Y		R.LFGYESNSLFK.Y
711	726	2	1744.9	-0.76	1	65.5	26.6	95.00%	K.DSPNIAALDLLFNSQK.G		K.DSPNIAALDLLFNSQK.G
432	444	2	1359.52	5.1	1	33.1	29.4	95.00%	R.SCETMGSATAVCS.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.SCETMGSATAVCSDK.T
71	83	2	1432.73	-0.15	1	45.8	27.7	95.00%	K.NAGISLPEISNYR.K		K.NAGISLPEISNYR.K
760	770	2	1161.61	-0.79	1	41.5	28.8	95.00%	R.MVTGDNILTAK.A		R.MVTGDNILTAK.A
447	459	2	1419.75	5.2	1	63.1	26.5	95.00%	K.TGTLTENVMTVVR.G		K.TGTLTENVMTVVR.G
288	298	2	1221.59	3	1	62.1	30.2	95.00%	K.IADCMLISGSR.I	Carbamidomethyl (+57)	K.IADCMLISGSR.I
497	510	2	1503.8	6.4	1	50.1	26.6	95.00%	R.NDLLANIVLNSTAF.E		R.NDLLANIVLNSTAFENR.D
574	583	2	1073.61	0.07	1	45.8	24.5	95.00%	K.TETALLSLAR.L		K.TETALLSLAR.L
252	259	2	946.49	1.2	1	28.5	30.2	94.80%	K.FPVDNSLR.D		K.FPVDNSLR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
23	KTR4_YEAST	23.92%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
406	424	2	2204.9	4.6	1	40.6	30.9	95.00%	R.DIGYHHTPYTNCPTCPADS.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.DIGYHHTPYTNCPTCPADSDR.C
443	453	2	1404.63	6.5	0	52.2	30.6	95.00%	L.DNQNCQATWIR.H	Carbamidomethyl (+57)	K.FTPWSDLDNQNCQATWIR.H
382	388	2	799.4	-0.16	1	31.8	25.9	95.00%	R.WGDAPVR.S		R.WGDAPVR.S
271	281	2	1417.67	-0.43	1	70.4	29.4	95.00%	K.INYDVFQFMNK.N		K.INYDVFQFMNK.N
406	422	2	2002.84	4.5	0	48.8	30	95.00%	R.DIGYHHTPYTNCPTCPA.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.DIGYHHTPYTNCPTCPADSDR.C
375	381	2	890.39	2	1	32.1	30.1	95.00%	K.GGFYYER.W		K.GGFYYER.W
135	142	2	857.53	-0.6	0	41.8	24.5	95.00%	K.GTILSLVR.N		K.GTILSLVR.N
389	398	2	1047.6	-0.12	1	52.3	23.1	95.00%	R.SLALALFADK.S		R.SLALALFADK.S
245	254	2	1269.66	4.2	0	52.9	27.1	95.00%	K.EFYHHPLLSK.Y		K.EFYHHPLLSK.Y
148	157	2	1144.61	6.4	1	42.3	28.2	95.00%	E.DIISSIQQLE.E		R.NSDLEDIISSIQQLEEEYNK.N
337	354	2	2266.98	6.4	1	41.3	29.9	95.00%	Y.DYTQGYSTCHFWTNFEIV.D	Carbamidomethyl (+57)	K.NYDYTQGYSTCHFWTNFEIVDLD FLR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
24	A6ZYU5_YEAS7	10.76%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
225	233	2	1153.52	2.9	0	49.9	31	95.00%	K.NYSNSVQWR.V	Deamidation (+1)	K.NYSNSVQWR.V
302	320	2	1954.96	1.1	1	71.4	27.9	95.00%	R.AAGSASWGELFTGKPAMFK.R		R.AAGSASWGELFTGKPAMFK.R
534	543	2	1117.55	0.61	0	34	29.7	95.00%	K.SASWVPTSQR.G		K.SASWVPTSQR.G
310	320	2	1267.67	5.6	0	25.1	26.3	95.00%	G.ELFTGKPAMFK.R		R.AAGSASWGELFTGKPAMFK.R
1	12	2	1371.67	2.8	1	27.7	29.6	94.40%	-.MNSTPDLISPQK.S	Acetyl (+42)	-.MNSTPDLISPQK.S
523	533	2	1307.63	8.2	1	28	30	94.30%	N.DMYAEGVLPWK.S		K.GLTLEEVNDMYAEGVLPWK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
25	B3LPA7_YEAS1	11.62%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
287	300	2	1397.7	3.3	1	31.2	28.5	95.00%	R.NPGAWGPGIISSDK.S		R.NPGAWGPGIISSDK.S
83	90	2	911.48	5.3	1	22.9	27	90.80%	R.LQVVSHET.D		R.LQVVSHETDINEDEEEAHYEDK.H
4	13	2	1208.63	6	1	55	28.4	95.00%	R.FSNIITSNKW.D		R.FSNIITSNKWDEK.Q
4	12	2	1022.54	2.3	0	55.3	27.6	95.00%	R.FSNIITSNK.W		R.FSNIITSNK.W
435	441	2	869.44	0.097	0	23	26.1	92.70%	K.QFGYVTR.Q		K.QFGYVTR.Q

41	51	2	1221.59	5.5	1	36.3	29.8	95.00%	I.DPSNKTTPYSI.D		K.QNNIGEQSMQELPEDQIEHEMEAIDPSNKTTPYSIDEK.Q
72	82	2	1219.61	6	0	45.6	29.7	95.00%	A.DVNSITNSLTR.L	Deamidation (+1)	K.HGSLQGGAIADVNSITNSLTR.L
62	82	2	2110.08	3.1	1	113	24.7	95.00%	K.HGSLQGGAIADVNSITNSLTR.L		K.HGSLQGGAIADVNSITNSLTR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
26	A6ZQR8_YEAS7	12.76%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
588	596	2	941.47	4.5	1	28.1	25.8	95.00%	K.RSASIASHN.D		K.RSASIASHNDALFAAVK.G
589	604	2	1600.83	2.7	1	80.6	27.5	95.00%	R.SASIASHNDALFAAVK.G		R.SASIASHNDALFAAVK.G
248	260	3	1538.83	3.4	0	24.1	24.2	95.00%	R.TMGIKPYTINVFR.N		R.TMGIKPYTINVFR.N
955	967	2	1323.62	3	1	81.8	30.4	95.00%	K.LGDASCAAPFTSK.L	Carbamidomethyl (+57)	K.LGDASCAAPFTSK.L
699	709	2	1163.64	5.4	0	42.8	24.8	95.00%	G.DNPLTAVHVAK.E		R.SIMITGDNPLTAVHVAK.E
118	132	2	1729.87	-0.82	1	58	26.8	95.00%	R.VTEAGSLQTFFQFQK.K		R.VTEAGSLQTFFQFQK.K
792	805	2	1602.91	5.2	1	69	20	95.00%	R.VSPSQKEFLLNTLK.D		R.VSPSQKEFLLNTLK.D
762	780	2	2027.06	5.8	1	108	25.7	95.00%	Y.DIAVTGYALNALEGHSQLR.D		R.YDIAVTGYALNALEGHSQLR.D
372	383	2	1280.64	1.6	1	75.5	29.4	95.00%	K.TGFETSQGSLVR.V		K.TGFETSQGSLVR.V
798	805	2	976.56	3.7	0	22.5	26.1	91.80%	K.EFLLNTLK.D		K.EFLLNTLK.D
580	587	2	926.49	4.4	0	22.7	26.5	91.50%	R.FQFSSALK.R		R.FQFSSALK.R
968	979	2	1269.74	3.3	0	75.9	20.5	95.00%	K.LANVSAVTNIIR.Q		K.LANVSAVTNIIR.Q
867	887	3	2345.23	-0.82	1	27.4	22.9	95.00%	R.WNQPQPPVPEPIAHLFPPGPK.N		R.WNQPQPPVPEPIAHLFPPGPK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
27	A6ZSR0_YEAS7	25.09%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
195	210	2	1840.88	5.7	1	64	29.5	95.00%	I.DVMVTQPEMTIFTASR.S	Oxidation (+16)	R.TTGTIDVMVTQPEMTIFTASR.S
500	518	2	1955.01	-0.99	1	26.8	25.6	95.00%	K.TVPPPDFTSMVTLPTGPAK.I		K.TVPPPDFTSMVTLPTGPAK.I
417	430	2	1786.83	5.9	1	73.9	30.5	95.00%	R.DEYFPNAHQFNIHR.W		R.DEYFPNAHQFNIHR.W
505	518	2	1479.74	6.1	0	42.8	28.9	95.00%	P.DFTSMVTLPTGPAK.I	Oxidation (+16)	K.TVPPPDFTSMVTLPTGPAK.I
123	136	2	1503.78	5.3	0	47.6	27.4	95.00%	A.EAAYAHLTTPVFGK.G		K.LADVSAEAAYAHLTTPVFGK.G
235	252	2	2160.11	-2	1	53.7	25.1	95.00%	K.GFTPINFVFPNLPLEHYR.K		K.GFTPINFVFPNLPLEHYR.K
358	371	2	1654.91	7.3	1	50.8	23.2	95.00%	Y.DLLQEMPLLNQTIK.E		K.ELTYDLLQEMPLLNQTIK.E
119	136	2	1875.95	5	1	84.7	27.7	95.00%	A.DVSAEAAYAHLTTPVFGK.G		K.LADVSAEAAYAHLTTPVFGK.G
455	467	2	1292.65	1.5	0	41.1	29	95.00%	K.GVSSPYLPFGGGR.H		K.GVSSPYLPFGGGR.H
137	146	2	1179.53	0.27	1	28.4	30.7	94.00%	K.GVIYDCPNSR.L	Carbamidomethyl (+57)	K.GVIYDCPNSR.L
260	270	2	1182.64	3	0	53.7	25.7	95.00%	K.AISGTYMSLIK.E		K.AISGTYMSLIK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
28	XPP_YEAST	26.70%	100%	15

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
25	50	3	2873.31	-0.53	1	22.1	28.1	95.00%	R.GTSASHSPRPFRPCADCTCSPGLLSR.Q	Carbamidomethyl (+57)/Carbamidomethyl (+57)/Carbamidomethyl (+57)	R.GTSASHSPRPFRPCADCTCSPGLLSR.Q
578	585	2	964.53	4.3	0	28.3	28.1	95.00%	M.DNYTLVLK.G		K.EEMDNYTLVLK.G
360	371	2	1423.67	7	1	39.1	30.1	95.00%	E.DETILFTNNPFN.D		R.GSDIDYNPVFFSYVAINEDETILFTNNPFNDDISEYFK.I
436	449	2	1569.84	5.1	1	42.6	25.6	95.00%	K.KMTAQNFAIIHSPI.D		K.KMTAQNFAIIHSPIDVLK.S
145	161	2	1699.84	3.2	0	71.1	28.3	95.00%	R.AFISGFSGSAGVACITR.D	Carbamidomethyl (+57)	R.AFISGFSGSAGVACITR.D
346	359	2	1676.78	6	1	39.2	30.2	95.00%	I.DYNPVFFSYVAINE.D		R.GSDIDYNPVFFSYVAINEDETILFTNNPFNDDISEYFK.I
94	106	2	1477.69	5.5	1	39.4	30.2	95.00%	C.DSLCAVNREVNTT.D	Carbamidomethyl (+57)	K.GAGGGSSAGNGSVYSCDSLCAVNREVNTTDR.L
727	740	3	1659.9	2.5	0	29.2	23.7	95.00%	R.TIVHFLQPQSISYK.W		R.TIVHFLQPQSISYK.W
653	665	2	1424.7	3.2	1	53	29.4	95.00%	R.AGNIISNEPGYYK.D		R.AGNIISNEPGYYK.D
621	652	6	3467.73	1.4	1	22.1	24	93.50%	K.HGTGHGIGSFLNVHEGPMGVGFRPHLMNFPLR.A		K.HGTGHGIGSFLNVHEGPMGVGFRPHLMNFPLR.A
12	24	4	1428.7	-0.26	0	29.8	29.3	95.00%	R.AHSISHVPGTHMR.G		R.AHSISHVPGTHMR.G

413	421	2	1078.49	6	0	40.2	29.8	95.00%	P.DSASWQMVR.C		K.ITSQASSAEHEFLIPDSASWQMVR.C
437	453	3	1897.01	-0.26	1	39.6	23.9	95.00%	K.MTAQNFAIIHSPIDVLK.S		K.MTAQNFAIIHSPIDVLK.S
40	50	2	1264.56	5.6	0	38.2	30.2	95.00%	A.DCTCSPGLLSR.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GTSASHSPRPFRPCADCTCSPGLLSR.Q
551	561	2	1140.5	6.5	1	34	31.3	95.00%	C.DSGSQFLEGTT.D		K.IYLCDSGSQFLEGTTDITR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
29	A6ZX34_YEAS7	21.39%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
402	420	2	2109.03	-1.9	1	56.3	27.6	95.00%	K.VCFTQGALEISANLPNYGR.V	Carbamidomethyl (+57)	K.VCFTQGALEISANLPNYGR.V
66	81	2	1676.74	6.2	1	39.3	30.6	95.00%	R.DGESLSSSVHYQPQGS.D		R.DGESLSSSVHYQPQGSDSSLLHDNSR.L
130	144	2	1501.78	5.4	1	53.9	27	95.00%	R.AIASSPSLNSNLSKN.D		R.AIASSPSLNSNLSKNDILSPPEFDR.Y
697	704	2	897.43	6.3	0	27.5	31.2	91.40%	E.DAGYTFPK.N		R.IYQPSNAISVTCDPSDYPTYDYIQSHLNAFQNANLTTWEDAGYTFPK.N
130	143	2	1387.73	2.6	0	60.2	26.4	95.00%	R.AIASSPSLNSNLSK.N		R.AIASSPSLNSNLSK.N
114	129	2	1752.86	1.6	1	46	28.6	95.00%	R.AVSTANDNSFLQPPHR.A		R.AVSTANDNSFLQPPHR.A
658	669	2	1352.64	5.6	0	41.5	31	95.00%	R.IYQPSNAISVTC.D	Deamidation (+1)/ Carbamidomethyl (+57)	R.IYQPSNAISVTCDPSDYPTYDYIQSHLNAFQNANLTTWEDAGYTFPK.N
197	213	2	1831.86	6.3	0	80	29.6	95.00%	Q.DFSPFGGYPASSFPLMI.D		R.SPTSSPGNESSASFSSNPFLGEQDFSPFGGYPASSFPLMIDEK.E
393	401	2	1049.5	3.4	0	51.8	29.4	95.00%	R.SGMLQSWNK.V		R.SGMLQSWNK.V
120	129	2	1209.6	5.7	0	40.3	30.2	95.00%	N.DNSFLQPPHR.A		R.AVSTANDNSFLQPPHR.A
594	607	2	1634.81	0.72	1	59.7	28.4	95.00%	R.WFVGDTPTYTIHAK.A		R.WFVGDTPTYTIHAK.A
5	17	2	1476.69	5.7	1	50.4	30.1	95.00%	R.NLTETHNFSSTNL.D		R.NLTETHNFSSTNLDTDGTGDDHDGAPLSSSPSFGQQNDNSTNDNAGLTNPFMGSDEESNAR.D
27	41	2	1490.67	7	0	61.2	31	95.00%	H.DGAPLSSSPSFGQQN.D		R.NLTETHNFSSTNLDTDGTGDDHDGAPLSSSPSFGQQNDNSTNDNAGLTNPFMGSDEESNAR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
30	A6ZPW7_YEAS7	18.94%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
114	125	2	1296.73	-0.33	0	32.9	23	95.00%	R.LSVTLNNAGRPR.I		R.LSVTLNNAGRPR.I
157	178	2	2193.06	5.2	1	53.7	27	95.00%	G.DSGSILRPTASLTEMMSGGAGR.R		R.VSTASMAIHDDDYGSIQNSTIGDSGSILRPTASLTEMMSGGAGR.R
133	143	2	1186.58	5.5	1	37	29.3	95.00%	N.DRVSTASMAIH.D		R.ITNLANNDRVSTASMAIHDDDYGSIQNSTIGDSGSILRPTASLTEMMSGGAGR.R
274	283	2	1041.52	6.3	0	43.8	28.6	95.00%	A.DLGYAAFGTK.G		R.CLDTDPTLISYADLGYAAFGTK.G
496	504	2	1067.55	6.9	0	38.4	27.1	95.00%	L.DVLMNVQHI.D		K.TPLNARPIVSVLDVLMNVQHIDEAASAIK.R
368	385	2	1918.89	6.4	1	32.2	29.7	95.00%	K.SSSPGSLVNPMETSMWPI.D		K.SSSPGSLVNPMETSMWPIDLK.H
113	125	3	1452.83	1.3	1	16.8	22.3	91.70%	R.RLSVTLNNAGRPR.I		R.RLSVTLNNAGRPR.I
15	26	2	1426.76	2.9	1	22.4	25.6	92.60%	R.SEVHYISIPLNR.G		R.SEVHYISIPLNR.G
53	67	2	1598.82	4.8	1	63.8	26.7	95.00%	L.DHPVGSFKGVNSLSR.F		R.QSILDHPVGSFKGVNSLSR.F
49	60	2	1326.7	3.1	1	31.9	27.2	95.00%	R.QSILDHPVGSFK.G		R.QSILDHPVGSFK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
31	YNL5_YEAST	14.29%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

588	596	2	1117.53	1.7	1	39.1	29	95.00%	K.SALWGDWQR.D		K.SALWGDWQR.D
426	433	2	877.47	6	0	25.4	29.4	91.10%	Y.DLGGLFTR.V		K.GPFTTVGYDLGGLFTR.V
347	357	2	1272.66	6.4	1	26.8	28.6	94.60%	K.QPIILFEHGGY.D		K.QPIILFEHGGYDTGYLSATWIEELYHLDK.I
37	52	2	1469.73	5.4	1	75.5	29.2	95.00%	R.TLGAGSANGPAVNEGR.D		R.TLGAGSANGPAVNEGR.D
418	433	2	1699.86	-1.2	1	75.6	27.9	95.00%	K.GPFTTVGYDLGGLFTR.V		K.GPFTTVGYDLGGLFTR.V
563	575	2	1430.7	0.061	1	66.7	29.4	95.00%	R.DVTNNAESLQNVK.T		R.DVTNNAESLQNVK.T
391	407	2	1752.92	6.2	1	62.5	25.8	95.00%	S.DSPPAPISIAMVAESLR.Y		R.YCLYDRPGYGLSDSPPAPISIAMVAESLR.Y
321	330	2	1254.58	6.2	0	35.3	30.5	95.00%	K.TYQLHITCYG.D	Carbamidomethyl (+57)	K.TYQLHITCYGDVFDQENNTDLSENK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
32	ATN2_YEAST	11.37%	100%	10

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
454	468	2	1676.92	6.5	1	64.7	22.1	95.00%	K.WLETATLANIATVFK.D		K.WLETATLANIATVFK.D
426	434	2	1032.57	5.9	0	45.5	26.2	95.00%	G.DVGILQNFK.D		R.FSPYEYSHNEDGDVGILQNFK.D
596	606	2	1250.63	2.5	1	48.6	30.3	95.00%	K.NVYSLSNEGLR.V		K.NVYSLSNEGLR.V
721	732	2	1319.79	6.1	1	52.4	17.5	95.00%	V.DDLPVLPLVIAR.C		K.AIAQEVGILPTNLYHYSQEIVDSMVMTGSQFDGLSEEEVDDLPVLPLVIAR.C
722	732	2	1204.76	6.2	0	42.8	14.1	95.00%	D.DLPVLPLVIAR.C		K.AIAQEVGILPTNLYHYSQEIVDSMVMTGSQFDGLSEEEVDDLPVLPLVIAR.C
562	577	2	1850.8	2.9	1	60	30	95.00%	K.GAFESIISCCSSWYGK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.GAFESIISCCSSWYGK.D
27	39	2	1394.7	6.2	1	83	28.4	95.00%	A.EFIGTSLTEGLTQ.D		K.ENNNEEFNAYHTLTTEEAAEFIGTSLTEGLTQDESLR.R
513	529	2	1938.82	4.7	1	43.4	30.3	95.00%	N.DQSSLSQHNEKPGSAQF.E	Phospho (+80)	K.STNQSNENDQSSLSQHNEKPGSAQFEHIAEFPFDSTVK.R
254	264	2	1362.69	-0.74	0	43.3	28.7	95.00%	K.SWLQNTWISTK.K		K.SWLQNTWISTK.K
662	681	3	2142.07	-0.88	1	21.5	27	95.00%	K.FHQAGINVHMLTGDFVGTAK.A		K.FHQAGINVHMLTGDFVGTAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
33	A6ZY55_YEAS7	17.15%	100%	14

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
447	456	3	1251.68	3.3	1	40.2	26.3	95.00%	K.IALEWIQSHR.L		K.IALEWIQSHR.L
598	614	2	1715.82	5.1	1	91.3	29.5	95.00%	F.DLTGPINNSQGSVDSGR.R		R.LEEEFDLTGPINNSQGSVDSGR.R
673	685	2	1511.74	-0.88	1	38.9	29.8	95.00%	R.NSPPDYGFILFSR.N		R.NSPPDYGFILFSR.N
342	353	2	1298.69	1.7	1	55.2	26.3	95.00%	K.NILPSAVQSNEK.Y		K.NILPSAVQSNEK.Y
391	403	2	1532.7	6.8	0	39.6	31.2	95.00%	E.DTCIVMCHVGGLR.N	Carbamidomethyl (+57)/ Oxidation (+16)/ Carbamidomethyl (+57)	K.YVSISILDTVGNEGSPLLLTDDNINQHPNMIVSSTAEDTCIVMCHVGGLR.N
361	373	2	1314.68	6.9	1	42.8	27.7	95.00%	L.DTVGNEGSPLLLT.D		K.YVSISILDTVGNEGSPLLLTDDNINQHPNMIVSSTAEDTCIVMCHVGGLR.N
562	569	2	1016.61	6.5	0	29.7	22.1	95.00%	N.DLFQLLLR.D		K.ICLELVHSNELQNDLFQLLLR.D
327	339	2	1488.76	2.5	1	72.8	28.3	95.00%	K.SFNDLQHTLSLSK.Q		K.SFNDLQHTLSLSK.Q
583	590	2	982.48	6.8	1	27.7	30.2	93.70%	P.DEFFQLGK.D		K.LNSDDSLSPDEFFQLGK.D
330	339	2	1140.62	4.4	0	42.1	25.8	95.00%	N.DLQHTLSLSK.Q		K.SFNDLQHTLSLSK.Q
485	501	2	1814.98	6.6	1	53	22.1	95.00%	L.DESITIGNVSTLPFPIL.E		R.FISADNGDIYLIALDESITIGNVSTLPFPILEIK.K
598	610	2	1300.63	6.1	0	33	29.5	95.00%	F.DLTGPINNSQGSV.D		R.LEEEFDLTGPINNSQGSVDSGR.R
404	414	2	1292.72	2.8	1	46.9	21.7	95.00%	R.NHVVTNDLLLR.D		R.NHVVTNDLLLR.D
57	70	2	1679.86	5.9	1	70.8	26.8	95.00%	F.DQEFQNVNLFVSLK.I		K.LLNQCSVAFDQEFQNVNLFVSLK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
34	COS2_YEAST	16.62%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
25	33	2	1099.64	-0.29	1	24.9	23.9	95.00%	K.IVLPQDLFR.S		K.IVLPQDLFR.S
352	367	2	1985.05	-0.61	1	45.6	24.3	95.00%	K.SMWPLPLNVELWPYIK.E		K.SMWPLPLNVELWPYIK.E
121	134	2	1655.79	6.8	1	79.1	30.2	95.00%	H.DWEVVAANLNSYLY.E		K.EITENTPSSDPHDWEVVAANLNSYLYENNVWNTK.Y
157	166	2	1147.65	4.2	1	35.1	23.5	95.00%	R.TTLLEPFSLK.K		R.TTLLEPFSLK.K
143	156	2	1828.8	-0.88	1	75.4	30.6	95.00%	K.YFFFNAMVCQEAFR.T	Carbamidomethyl (+57)	K.YFFFNAMVCQEAFR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
35	A6ZR77_YEAS7	24.43%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
445	462	2	1979.93	5.6	0	67.4	29.1	95.00%	Y.DSISHTQNSPFVPYSSSK.A		K.SQSQTYDSISHTQNSPFVPYSSSK.A
278	295	2	2111.11	5.3	1	74.9	23.9	95.00%	P.DDLLLNNAIPYQFATYLK.Y		K.LNPDDLLLNNAIPYQFATYLK.Y
349	360	3	1308.63	0.3	0	21.5	30.1	90.50%	R.ANLHGYGNPNPR.V		R.ANLHGYGNPNPR.V
468	484	3	1978.92	-0.55	1	35	29.9	95.00%	R.SNNEHNLPNHYTNLANK.N		R.SNNEHNLPNHYTNLANK.N
402	411	2	1107.56	-0.74	0	33.7	29.7	95.00%	R.ISSNPQSFTK.Q		R.ISSNPQSFTK.Q
425	438	2	1694.92	3.8	1	52.2	23.9	95.00%	K.YIPETHSNLQRPIK.S		K.YIPETHSNLQRPIK.S
150	163	2	1735.9	5.7	1	53.6	26.2	95.00%	R.DIKPDNFLISQYQR.I		R.DIKPDNFLISQYQR.I
219	228	2	1224.57	3.2	0	26.5	30.6	90.80%	R.YMSINTHFGR.E		R.YMSINTHFGR.E
5	19	2	1591.85	2.6	0	62.9	24.9	95.00%	R.SSQHIVGIHYAVGPK.I		R.SSQHIVGIHYAVGPK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
36	B3LS12_YEAS1	11.15%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
726	740	2	1703.87	0.05	1	50.6	27.2	95.00%	R.LHIDAVNTVWSHANK.D		R.LHIDAVNTVWSHANK.D
78	91	2	1588.85	6.5	1	63	24.8	95.00%	V.DTIPVSPLELVPFY.D		K.VLIEAFGSPEVDPVDTIPVSPLELVPFYDQSIDTK.R
729	740	2	1340.65	5.7	0	68	29.1	95.00%	I.DAVNTVWSHANK.D		R.LHIDAVNTVWSHANK.D
7	12	2	789.45	3.9	0	22.1	25.3	92.50%	R.FILNQR.S		R.FILNQR.S
178	185	2	1042.46	6.1	1	31.5	29.7	95.00%	Y.DMFQAFER.I		K.YDMFQAFER.I
192	207	2	1934.94	-0.098	1	48.7	28.3	95.00%	R.CFMQANPVNIQEIFPK.S	Carbamidomethyl (+57)	R.CFMQANPVNIQEIFPK.S
274	282	2	1029.59	-0.41	1	39.1	25.8	95.00%	K.VLEQGFLPK.F		K.VLEQGFLPK.F
100	107	2	933.5	4.2	0	25	27.9	92.90%	R.SSSWLINK.K		R.SSSWLINK.K
373	381	2	1124.52	6.2	1	28.5	31.4	92.90%	P.DFKPVENNY.D		R.SPDFKPVENNYDNSTNVPQEIWFLDVSNTIHPK.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
37	A6ZR26_YEAS7	17.05%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	9	2	912.51	3.2	0	42.8	24.1	95.00%	M.SSAPLLQR.T	Acetyl (+42)	-.MSSAPLLQR.T
14	20	2	797.51	-0.037	1	20.7	18.3	90.30%	K.KIALPTR.V		K.KIALPTR.V
25	31	2	881.44	1.8	1	27.1	28.6	94.90%	K.VFFANER.T		K.VFFANER.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
38	B3LNF5_YEAS1	9.51%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
90	99	2	1113.51	-1.2	1	31.8	30.6	95.00%	R.AVATSMYESR.L		R.AVATSMYESR.L
566	576	2	1263.64	6.1	0	35.1	29.2	95.00%	K.FILNGFTLAHM.D	Deamidation (+1)	K.FILNGFTLAHMDGTTNFIYAIDFSTAFNDK.T
384	395	2	1307.69	1.8	0	47.7	26.7	95.00%	K.GTMIASLYPLSR.R		K.GTMIASLYPLSR.R
1070	1079	3	1299.72	5.1	1	19.1	26	94.60%	S.DWNFLKPPKR.D		K.ITFNEGSDWNFLKPPKR.D
508	520	2	1407.71	6.5	0	35.5	28.8	95.00%	G.DYGNVIVAIPYNA.D		K.LAFDFPCLYAVGDYGNVIVAIPYNADEDDDPQSEFYYSLDQGK.T
823	833	2	1232.63	3.3	1	24	28.1	90.90%	R.QLGMPLDFNAK.A		R.QLGMPLDFNAK.A
1328	1339	2	1201.58	0.34	1	35.4	29.8	95.00%	K.GLSPANAADVCK.K	Carbamidomethyl (+57)	K.GLSPANAADVCK.K

414	426	2	1445.79	5.9	1	97.1	25.7	95.00%	K.ISVDNGLTWTVLK.V	Deamidation (+1)	K.ISVDNGLTWTVLK.V
221	235	2	1825.89	7.3	0	30.4	28.7	95.00%	S.DTSIICLFQNMQLIM.D	Carbamidomethyl (+57)	K.DSDLESSDTSIICLFQNMQLIMDEFSSPYTESK.L
1032	1047	2	1669.94	6.1	1	45.4	18.4	95.00%	K.IQGLEGIILTNIVSNS.D		K.IQGLEGIILTNIVSNSDK.V
1267	1279	2	1607.76	2.9	1	65.6	29.6	95.00%	K.SNCLFGHQTEFLR.K	Carbamidomethyl (+57)	K.SNCLFGHQTEFLR.K
873	886	2	1607.75	5.3	1	70.8	30	95.00%	L.DNAIHCEFAGSLFK.Y	Carbamidomethyl (+57)	K.NCESILSPECHAVAYLTNDGGETFTEMLDNAIHCEFAGSLFK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
39	A6ZWJ5_YEAS7	19.06%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
34	46	2	1582.77	2.9	1	63.2	28.7	95.00%	K.QMSEQYVTPYLPK.S		K.QMSEQYVTPYLPK.S
119	128	2	1194.61	0.92	1	60.3	29	95.00%	K.ACFVSLITER.D	Carbamidomethyl (+57)	K.ACFVSLITER.D
423	435	2	1457.61	2.4	1	37	30.6	95.00%	R.SGSCGGHYFDIMK.K	Carbamidomethyl (+57)	R.SGSCGGHYFDIMK.K
148	161	2	1669.83	7.1	1	44.3	28.8	95.00%	K.NFAYPWVFISQGEL.D		K.NFAYPWVFISQGELDGMK.Q
129	138	2	1134.57	6.7	0	26	30	91.00%	R.DSMTQILQSI.D		R.DSMTQILQSIDEVQVK.F
231	238	2	1092.52	1.4	0	40.2	30.6	95.00%	R.YFAGFFWR.H		R.YFAGFFWR.H
364	380	3	1910.03	-0.51	1	34.6	22.4	95.00%	K.WSDSIIHTIGLSMLLPK.D		K.WSDSIIHTIGLSMLLPK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
40	A6ZUD9_YEAS7	14.96%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
805	817	2	1313.73	0.45	0	45.7	24.7	95.00%	K.QNNVVSAVIAATK.N		K.QNNVVSAVIAATK.N
146	156	2	1114.59	6.6	1	53.6	28.1	95.00%	R.LLLSPASSNVD.D		R.LLLSPASSNVDDDR.N
957	967	2	1259.56	5.1	0	30.2	31.3	95.00%	Y.EIFSNGTCFGK.I	Deamidation (+1)/ Carbamidomethyl (+57)	K.ATYELPQGTLYEIFSNGTCFGK.I
910	920	2	1487.7	-1.1	0	55.5	30.2	95.00%	K.FWAQLCPYFTR.R	Carbamidomethyl (+57)	K.FWAQLCPYFTR.R
933	945	2	1525.79	6.3	1	74.8	26	95.00%	A.DNIFFLVETGMLK.A		R.LASQSHLLHADNIFFLVETGMLK.A
48	69	2	2353.03	-0.9	1	82	29.1	95.00%	R.SYMSGFFTGGNSPMINNLSDSK.L		R.SYMSGFFTGGNSPMINNLSDSK.L
48	66	2	2022.9	7.9	0	66.9	29.5	95.00%	R.SYMSGFFTGGNSPMINNLS.D		R.SYMSGFFTGGNSPMINNLSDSK.L
709	715	2	910.52	0.089	1	34.7	22.7	95.00%	K.YLILDFK.N		K.YLILDFK.N
850	863	2	1607.84	7	0	46.2	26	95.00%	R.NYQILSVAQNVFVN.D		R.NYQILSVAQNVFVNDEQAVK.N
878	890	2	1466.89	7.1	1	52.4	13.8	95.00%	D.DEPVLPILLFALK.Q		K.DDEPVLPILLFALK.Q
839	849	2	1242.64	2.6	0	36.8	27.4	95.00%	R.NLMSLPTNTPR.N		R.NLMSLPTNTPR.N
1025	1036	2	1339.74	3.9	1	36.5	24.6	95.00%	R.FKELLGYTLVSA.-		R.FKELLGYTLVSA.-
173	189	2	1889.92	5.2	0	44.7	27.9	95.00%	E.DGYAGGYQSLRPSHNLR.F		R.GLQNSSLPELEDGYAGGYQSLRPSHNLR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
41	BPT1_YEAST	7.83%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
62	71	3	1177.65	2.4	1	19.5	25.4	95.00%	R.FKNFPTLPSK.I		R.FKNFPTLPSK.I
807	816	2	1160.68	-0.18	1	23.9	21.8	95.00%	K.NIIEYVLIGK.T		K.NIIEYVLIGK.T
1065	1077	2	1468.71	2.8	1	78.5	30	95.00%	R.SPMTFFETTPVGR.I		R.SPMTFFETTPVGR.I
684	696	2	1388.69	1	0	24.6	28.1	92.10%	K.AILGQLPCMSGSR.D	Carbamidomethyl (+57)	K.AILGQLPCMSGSR.D
1504	1513	3	1194.68	-0.5	1	38.8	20.3	95.00%	K.DRTILTIAHR.I		K.DRTILTIAHR.I
1313	1325	2	1480.79	2.4	1	58.9	26.2	95.00%	R.ENLDPVLNNINVK.I		R.ENLDPVLNNINVK.I
1343	1351	2	1006.58	-0.72	0	30.7	22.9	95.00%	K.STLSLALFR.I		K.STLSLALFR.I
1449	1461	2	1387.67	0.051	1	66.3	30.2	95.00%	K.INENGSNLSVGQR.Q	Deamidation (+1)	K.INENGSNLSVGQR.Q
1506	1513	2	923.55	-1.9	0	32.8	18.9	95.00%	R.TILTIAHR.I		R.TILTIAHR.I
611	625	2	1759.93	-0.58	1	57.7	25.1	95.00%	R.ALPAIEMNNITFLWK.S		R.ALPAIEMNNITFLWK.S
745	753	2	1056.57	4	1	25.8	26.8	95.00%	K.ACQLLPDLK.I	Carbamidomethyl (+57)	K.ACQLLPDLK.I
1316	1325	2	1124.63	5.3	0	43.3	24.6	95.00%	L.DPVLNNINVK.I		R.ENLDPVLNNINVK.I
1462	1468	2	872.49	-0.56	0	28.1	29	95.00%	R.QLLCLAR.A	Carbamidomethyl (+57)	R.QLLCLAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

42	GAS1_YEAST	7.16%		100%		4						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
117	127	2	1127.6	5.6	0	42.3	26.7	95.00%	A.DLAAPATSINR.D		K.ALNDADIYVIADLAAPATSINR.D	
83	90	2	956.58	0.5	1	36.9	21.3	95.00%	K.KLNTNVIR.V		K.KLNTNVIR.V	
391	401	2	1423.65	6.2	1	48.5	30.7	95.00%	Y.ETLFNWICNEV.D	Carbamidomethyl (+57)	K.YWSAATELPPTPNGGLCSCMNAANSCVVSDDVDSDDYETLFNWICNEVDCSGISANGTAGK.Y	
415	424	2	1192.52	-0.24	0	35.4	30.4	95.00%	K.YGAYSFCTPK.E	Carbamidomethyl (+57)	K.YGAYSFCTPK.E	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
43	NCPR_YEAST	25.47%		100%		12						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
305	317	2	1504.78	6.4	1	52.1	27.6	95.00%	G.DHLAVWPSNPLEK.V		K.YSTGDHLAVWPSNPLEK.V	
470	483	2	1450.82	6.4	0	55.1	20.9	95.00%	P.DAPPVVGVTTNLLR.N		K.QTVHVTSIVENFPNPELPDAPPVVGVTTNLLR.N	
422	439	3	2074.04	6.1	1	28.4	26.6	95.00%	W.DTVPMQFLVESVPQMTPR.Y		K.WDTVPMQFLVESVPQMTPR.Y	
234	253	2	2238.06	5.6	1	85.5	28.1	95.00%	T.DSMSLGEPSAHYLPSHQLNR.N		K.FTSQFQYTVLNEITDSMSLGEPSAHYLPSHQLNR.N	
484	503	2	2264.17	6.4	1	113	24.1	95.00%	R.NIQLAQNNVNIAETNLPVHY.D		R.NIQLAQNNVNIAETNLPVHYDLNGPR.K	
440	451	2	1349.64	2.4	1	61	29.9	95.00%	R.YYSISSSSLSEK.Q		R.YYSISSSSLSEK.Q	
49	59	2	1229.63	1.1	1	54.2	27.3	95.00%	R.DIAQVVTENNK.N		R.DIAQVVTENNK.N	
653	664	2	1171.7	3.1	0	42.5	19.6	95.00%	K.GVSTALVGILSR.G		K.GVSTALVGILSR.G	
369	384	2	1776.94	-0.18	1	60.3	24.7	95.00%	R.QLFSSLIQFAPNADVK.E		R.QLFSSLIQFAPNADVK.E	
264	275	2	1342.76	6.2	0	49.5	23.8	95.00%	F.DLSQPYIAPIVK.S		R.NADGIQLGPFDLSQPYIAPIVK.S	
147	165	2	2130.95	5.5	1	82.6	29.9	95.00%	R.YNMFGLGNSTYEFFNGAAK.K	Deamidation (+1)	R.YNMFGLGNSTYEFFNGAAK.K	
405	413	2	1053.55	3.5	1	40.6	26.9	95.00%	K.YFNIADALK.Y		K.YFNIADALK.Y	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
44	A6ZKY2_YEAS7	11.11%		100%		9						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
128	147	2	2241.07	4	0	84.8	28.8	95.00%	V.DPYHLSPQQQPSNNLFGSGR.L		R.DNADLPVDPYHLSPQQQPSNNLFGSGR.L	
26	35	2	1142.51	1	0	43.9	30.7	95.00%	K.FYANANSNSR.W		K.FYANANSNSR.W	
49	63	2	1601.79	5.5	0	68.5	28.2	95.00%	Y.DQSNVFQGLPASPSR.A		R.WANPSEESLEDSYDQSNVFQGLPASPSR.A	
482	495	2	1668.85	-0.67	1	57.2	28	95.00%	K.LFNPLVASQNFEYK.I		K.LFNPLVASQNFEYK.I	
594	602	2	1079.53	5.4	1	52.1	30	95.00%	E.DVSEFISQR.R		K.EATGETDVPEDVSEFISQR.R	
81	98	2	1923.93	5	1	61.9	28.1	95.00%	R.DSAHNSPVAPNRYAANLQ.E		R.DSAHNSPVAPNRYAANLQESPK.R	
246	253	2	883.52	3	1	41.9	24.3	95.00%	K.GLLDTLPR.R		K.GLLDTLPR.R	
564	572	2	1130.62	1.9	1	27.5	26.9	95.00%	R.ILCWELVAK.R	Carbamidomethyl (+57)	R.ILCWELVAK.R	
93	102	2	1119.56	-0.55	1	34.7	29.2	95.00%	R.YAANLQESPK.R		R.YAANLQESPK.R	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
45	A7A0C8_YEAS7	15.60%		100%		7						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
287	301	2	1601.84	6.2	0	44.6	26.2	95.00%	K.SNLAGKPVICATQML.E	Carbamidomethyl (+57)	K.SNLAGKPVICATQMLESMTYNPRPTR.A	
460	466	2	819.45	-0.16	1	35.5	26.3	95.00%	R.INFGIEK.A		R.INFGIEK.A	
217	225	2	1001.55	3.8	1	28	26.8	95.00%	R.TANDVLTIR.E		R.TANDVLTIR.E	
414	425	2	1500.83	5.6	0	36.8	23.4	95.00%	K.YRPNCPIILVTR.C	Carbamidomethyl (+57)	K.YRPNCPIILVTR.C	
397	409	2	1314.75	2.9	0	41.1	22.4	95.00%	K.AIIVLSTSGTTPR.L		K.AIIVLSTSGTTPR.L	
287	312	4	2934.46	1.8	1	37.3	25.1	95.00%	K.SNLAGKPVICATQMLESMTYNPRPTR.A	Carbamidomethyl (+57)	K.SNLAGKPVICATQMLESMTYNPRPTR.A	
31	41	2	1226.66	1.2	1	48.4	25.2	95.00%	K.TNNPETLVALR.K		K.TNNPETLVALR.K	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
46	A6ZV88_YEAS7	16.23%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
159	166	2	969.42	5.6	1	27.6	30.8	92.60%	I.DSCLSFLE.D	Carbamidomethyl (+57)	K.LDEFIDSCLSFLEDK.S
138	143	2	705.45	3.8	0	27.6	18.3	95.00%	K.SIVLFK.F		K.SIVLFK.F
88	98	2	1249.61	6.4	1	29.4	29.2	95.00%	R.FFANDVSLTVH.D	Deamidation (+1)	R.FFANDVSLTVHDDSPLNISQSLSP IMEQFTVDELPESASDLLYEYSLDD K.S
29	38	2	1145.53	3.3	1	34.5	30.2	95.00%	K.ESSSFISFDK.E		K.ESSSFISFDK.E
127	134	2	1014.5	6.9	1	33.9	29.1	95.00%	S.DLLYEYSL.D		R.FFANDVSLTVHDDSPLNISQSLSP IMEQFTVDELPESASDLLYEYSLDD K.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
47	A6ZNT9_YEAS7	39.05%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
112	121	2	1054.64	1.5	0	46.2	21	95.00%	K.DIIIALVGNK.I		K.DIIIALVGNK.I
79	97	2	2091.14	0.43	1	59.6	19.8	95.00%	R.NAQAALVVYDVTKPQSFIK.A		R.NAQAALVVYDVTKPQSFIK.A
37	48	2	1302.7	2.8	0	34.1	26.2	95.00%	K.EPTIGAAFLTQR.V		K.EPTIGAAFLTQR.V
69	78	2	1217.59	3.4	0	39.5	28.4	95.00%	R.FASLAPMYYR.N		R.FASLAPMYYR.N
112	122	2	1167.73	7.3	1	40	16	95.00%	K.DIIIALVGNKI.D		K.DIIIALVGNKIDMLQEGGER.K
162	170	2	976.53	5.8	1	25.5	28.5	92.90%	N.DVFLGIGEK.I		K.TGENVNDVFLGIGEK.I
146	155	2	1111.6	3.4	1	49.4	26.8	95.00%	K.GLLFFETSAK.T		K.GLLFFETSAK.T
10	20	2	1068.65	-1.1	1	24	18.9	95.00%	K.LVLLGEAAVGK.S		K.LVLLGEAAVGK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
48	A7A0Z7_YEAS7	23.72%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
116	132	2	1810.92	6.5	1	46.5	26.2	95.00%	Y.ESNATNELLSSHVGQIL.D		R.ILSGLQEYESNATNELLSSHVGQI LDSFHEELVEYR.N
14	27	2	1641.75	2.9	1	72.9	30.2	95.00%	K.NGETISSCFQPFQK.N	Carbamidomethyl (+57)	K.NGETISSCFQPFQK.N
196	202	2	772.47	-3.5	1	22.9	26.1	92.40%	R.VSLLVDK.T		R.VSLLVDK.T
144	165	2	2180.92	6.4	0	113	30.3	95.00%	R.NQTLNSSGNGQSSNGNGQNTIS. D	Deamidation (+1)/ Deamidation (+1)/ Deamidation (+1)	R.NQTLNSSGNGQSSNGNGQNTIS DIGDATEDQIK.D
122	132	2	1194.67	6.4	0	57.6	22.6	95.00%	N.ELLSSHVGQIL.D		R.ILSGLQEYESNATNELLSSHVGQI LDSFHEELVEYR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
49	A6ZS87_YEAS7	11.41%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
755	770	2	1604.88	-0.37	0	63.8	23.1	95.00%	K.AVSSSGLLSTMAQLIK.A		K.AVSSSGLLSTMAQLIK.A
260	272	3	1538.78	3.5	0	41.3	26.8	95.00%	K.FHSHVFNPATINR.I		K.FHSHVFNPATINR.I
860	869	2	1169.64	0.071	0	44.2	24.2	95.00%	R.YLTVGTFITR.G		R.YLTVGTFITR.G
115	132	2	2124.09	4.2	0	75.4	25.4	95.00%	K.ATQLFNQQQQHQLQSVAR.N		K.ATQLFNQQQQHQLQSVAR.N
73	82	2	1131.63	2.6	1	55.5	25.7	95.00%	K.FVAALNQELK.K		K.FVAALNQELK.K
226	237	2	1397.69	5	1	51.5	29.7	95.00%	K.DFIELNQTGFSK.I		K.DFIELNQTGFSK.I
341	347	2	939.46	-0.025	1	25.9	27.4	95.00%	R.DHVVWER.N		R.DHVVWER.N
3	18	2	1892.91	2.6	1	57	28.8	95.00%	K.FSHSLQFNSVPEWSTK.Y		K.FSHSLQFNSVPEWSTK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
50	A6ZZF0_YEAS7	9.15%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
257	265	2	1121.58	5.4	1	42.4	28.5	95.00%	Y.DLENLSLYR.K		R.GLVCVENNIGYDLENLSLYR.K
309	326	2	2181.97	4.4	1	60.8	28.6	95.00%	A.DTQYHPENGSLYPHHHHL.E	Deamidation (+1)	R.HHHSSESPENYGSNQLSHSFSS PLGNDVTENPAALADTQYHPENGS LYPHHHHLETPFSK.L
177	185	2	1060.6	-0.2	1	70.3	24.9	95.00%	K.MSLIDLLTR.R		K.MSLIDLLTR.R
299	308	2	999.49	6.5	1	41.1	28.5	95.00%	N.DVTENPAALA.D		R.HHHSSESPENYGSNQLSHSFSS PLGNDVTENPAALADTQYHPENGS LYPHHHHLETPFSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
51	A6ZVM2_YEAS7	13.08%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
314	325	2	1292.68	-0.24	1	78.4	26.8	95.00%	K.HADANVQLVAQK.M		K.HADANVQLVAQK.M
838	852	2	1744.77	5	1	81.6	30.5	95.00%	H.DNNPHSFAEPMPAYR.G		K.AFSSLNDIPITPSHDNNPHSFAEPMPAYR.G
800	811	2	1239.66	6.2	0	26.3	25.8	95.00%	G.DAPLPYPIAQVG.D		R.VTGDAPLPYPIAQVGDDSMDSSDLGSK.A
48	67	2	2325.12	-1.6	1	51.8	28.4	95.00%	R.SWMPSVSVYQTAFQQREPGK.S		R.SWMPSVSVYQTAFQQREPGK.S
48	63	2	1913.91	-1.2	0	71.3	28.7	95.00%	R.SWMPSVSVYQTAFQQR.E		R.SWMPSVSVYQTAFQQR.E
196	204	2	1094.58	2.1	0	56.3	27.6	95.00%	R.LSLLAYCQK.V	Carbamidomethyl (+57)	R.LSLLAYCQK.V
326	345	2	2176.05	2	1	113	27.6	95.00%	K.MQQITSSQPTPTSELSSAQR.D		K.MQQITSSQPTPTSELSSAQR.D
152	165	2	1411.68	4.9	0	49.1	29.8	95.00%	V.DMSTSLYAAGLAGR.S		R.SSSNVDMSTSLYAAGLAGR.S
147	165	2	1885.89	3	1	65.7	29.6	95.00%	R.SSSNVDMSTSLYAAGLAGR.S		R.SSSNVDMSTSLYAAGLAGR.S
876	886	2	1290.63	5.2	1	31.1	29.8	95.00%	T.DFQRPTVNTVD.D		R.SIPWAHATDFQRPTVNTVDDR.S
876	885	2	1175.6	5.7	0	41.9	28.7	95.00%	T.DFQRPTVNTV.D		R.SIPWAHATDFQRPTVNTVDDR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
52	PDR5_YEAST	9.46%	100%	12

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	84	2	1852.9	6.6	1	39.9	28.3	95.00%	S.DAQSIFSSGVEGVNPIFS.D		K.SDAQSIFSSGVEGVNPIFSDPEAPGYDPK.L
120	132	3	1633.77	6.9	0	30.5	29.2	95.00%	P.DFYKPYSLGCAWK.N	Carbamidomethyl (+57)	K.NMAHLSAADPDFYKPYSLGCAWK.N
922	938	2	1753.97	-0.98	1	38.4	20.8	95.00%	R.VTMGVITGDILVNGIPR.D		R.VTMGVITGDILVNGIPR.D
967	972	2	755.4	2.2	0	21.2	24.7	91.40%	R.FSAYLR.Q		R.FSAYLR.Q
142	155	2	1595.83	5.5	0	59	27.6	95.00%	A.DVAYQSTVVNIPYK.I		K.NLSASGASADVAYQSTVVNIPYK.I
329	337	2	1196.51	3.6	1	30	30.2	95.00%	K.FQCWDNATR.G	Carbamidomethyl (+57)	K.FQCWDNATR.G
285	297	2	1450.7	5.4	0	40.5	29.6	95.00%	A.EVAMATYGLSHTR.N	Oxidation (+16)	R.ESYANHLAEVAMATYGLSHTR.N
49	65	2	1805.86	-0.55	0	104	29.2	95.00%	R.TLTAQSMQNSTQSAPNK.S		R.TLTAQSMQNSTQSAPNK.S
49	66	2	1892.9	4.9	1	91.3	28.8	95.00%	R.TLTAQSMQNSTQSAPNKS.D		R.TLTAQSMQNSTQSAPNKSDAQSIFSSGVEGVNPIFSDPEAPGYDPK.L
96	109	2	1550.71	6.6	1	75.6	30.5	95.00%	L.DPNSENFSSAAWVK.N		K.LDPNSENFSSAAWVK.N
945	957	2	1588.77	-0.099	1	25.5	29.6	90.70%	R.SIGYCQQQDLHLK.T	Carbamidomethyl (+57)	R.SIGYCQQQDLHLK.T
865	872	2	1044.52	2.6	1	50.3	29.6	95.00%	K.SEAIFHWR.N		K.SEAIFHWR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
53	A6ZQQ8_YEAS7	27.80%	100%	13

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
197	205	2	1021.48	7.1	1	32.2	30.1	95.00%	K.DYPFPVVEG.D		K.DYPFPVVEGDGVSIMGGDEEGVFAWITTNYLLGNIGANGPK.L
152	160	2	1033.57	3.9	0	25.2	24.6	95.00%	K.VAMNYVPIK.A		K.VAMNYVPIK.A
126	135	2	1094.5	6.3	1	29	30.5	94.90%	F.DMLEPGLSSF.D		K.FDMLEPGLSSFDTDSVGAANSLDPLLK.V
413	428	2	1801.95	6.5	1	57.8	24.6	95.00%	R.TRPLGMPLSFTLNELN.D		R.TRPLGMPLSFTLNELNDLAR.I
494	507	2	1555.84	-0.57	0	53.3	23.8	95.00%	K.EIGWCLGASLPLLK.A	Carbamidomethyl (+57)	K.EIGWCLGASLPLLK.A
413	425	2	1445.78	6.6	0	39.6	26.3	95.00%	R.TRPLGMPLSFTLN.E		R.TRPLGMPLSFTLNELNDLAR.I
375	395	3	2384.08	7	0	37.7	29.7	95.00%	K.DAQCQSPPCSFNGVHQPSLVR.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Deamidation (+1)	K.DAQCQSPPCSFNGVHQPSLVR.T
300	310	2	1184.68	0.49	1	48.4	25.2	95.00%	K.VNSVLVENALK.D		K.VNSVLVENALK.D
112	121	2	1101.55	7.3	0	24.1	28.2	90.80%	F.DVCTSPPTLL.D	Carbamidomethyl (+57)	K.FDVCTSPPTLLDEK.F

106	111	2	805.45	6.7	1	25.3	22.6	95.00%	R.VHIYKF.D		R.VHIYKFDVCTSPPTLLDEK.F
37	46	2	1026.57	-0.22	0	31.2	24.5	95.00%	R.TVTPNASIPK.T		R.TVTPNASIPK.T
136	146	2	1048.47	6.4	1	41.6	30.2	95.00%	F.DTDSVGAANSL.D		K.FDMLEPGLSSFDTDSVGAANSLDPLLK.V
278	294	2	2046.98	5.2	1	58.1	28.6	95.00%	G.DENYTLYQFSHLGYGLK.E		K.FGDENYTLYQFSHLGYGLK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
54	A6ZM54_YEAS7	16.19%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
356	366	2	1324.7	-0.78	0	27.5	26.2	95.00%	K.LFTPMMLFVAR.K		K.LFTPMMLFVAR.K
296	308	2	1555.81	-0.14	0	55.9	25.8	95.00%	K.YVQNLANLATFFR.T		K.YVQNLANLATFFR.T
140	157	2	2039.98	2.9	1	65.8	28.7	95.00%	R.FTGCNVIGLNNNDYQIAK.A	Carbamidomethyl (+57)	R.FTGCNVIGLNNNDYQIAK.A
336	353	2	1668.91	6	1	73.9	22.8	95.00%	K.EVTAALENAAVGLVAGGK.S		K.EVTAALENAAVGLVAGGK.S
354	366	3	1539.83	-0.13	1	31.4	25.3	95.00%	K.SKLFTPMMLFVAR.K		K.SKLFTPMMLFVAR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
55	A6ZT96_YEAS7	7.88%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
161	173	2	1516.69	6.6	1	70.3	30	95.00%	L.DENYNLNGLQTVH.D	Deamidation (+1)	K.MGNGMADYILDENYNLNGLQTVHDYDVYCHYVAGLVGDGLTR.L
356	365	2	1143.63	2.5	1	26.7	25.9	95.00%	K.LAVQDPNFLK.L		K.LAVQDPNFLK.L
4	15	2	1390.8	2.7	1	59.8	20.3	95.00%	K.LLQLALHPVEMK.A		K.LLQLALHPVEMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
56	A7A1A2_YEAS7	14.58%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
453	470	2	2188.04	-0.1	1	95.7	27.9	95.00%	K.SAWFYSFQSHPFTVLSER.H		K.SAWFYSFQSHPFTVLSER.H
663	674	2	1229.67	3.1	1	37.8	25.2	95.00%	R.NAVVQGIDSSLK.I		R.NAVVQGIDSSLK.I
510	525	2	1739.97	4.8	1	53.9	20.6	95.00%	K.IFLEGPYGVTVPHIAK.L		K.IFLEGPYGVTVPHIAK.L
498	509	2	1339.65	-1.3	1	39.8	29.9	95.00%	K.VLSAPNHTVDCK.I	Carbamidomethyl (+57)	K.VLSAPNHTVDCK.I
51	67	2	1925.9	2.6	1	108	29.3	95.00%	K.NINWLGSVTACAYENSK.S	Carbamidomethyl (+57)	K.NINWLGSVTACAYENSK.S
473	485	2	1533.72	5.3	1	45.8	30.2	95.00%	R.DPNNPDQLTMYVK.A		R.DPNNPDQLTMYVK.A
562	573	2	1533.8	-0.53	1	36.3	26.8	95.00%	K.FYWIVNDLSHLK.W		K.FYWIVNDLSHLK.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
57	A6ZSG0_YEAS7	5.18%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
193	204	2	1368.68	4.3	1	53.2	28.3	95.00%	Q.DAINETHPFGIR.I		R.QDAINETHPFGIR.I
175	189	2	1612.74	6.1	1	53.6	30.1	95.00%	N.DQASNASSTESFTLR.E		R.FIIHDSHGHDLLIDEINCQSPSHLENNDQASNASSTESFTLR.E
73	91	3	2067.98	4.5	0	21.5	28.4	94.70%	R.SVSSQSPIVHSSNNTLHHH.E	Deamidation (+1)	R.SVSSQSPIVHSSNNTLHHHEHQQHLPPTLESLSSK.S
72	91	4	2223.11	7.4	1	20.9	27.5	95.00%	K.RSVSSQSPIVHSSNNTLHHH.E		K.RSVSSQSPIVHSSNNTLHHHEHQQHLPPTLESLSSK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
58	A7A201_YEAS7	24.27%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
11	21	2	1069.65	-0.48	0	24.2	21.3	95.00%	K.LLLIGNSGVGK.S		K.LLLIGNSGVGK.S
36	46	2	1256.64	6	1	28.7	28	95.00%	N.DYISTIGVDFK.I		R.FSDDTYTNDYISTIGVDFK.I
160	167	2	923.46	5.3	0	35.2	28.6	95.00%	E.DAFLTMAR.Q		K.MPFLETSALDSTNVEDAFLTMAR.Q
171	184	2	1636.73	-0.92	1	58.2	30.5	95.00%	K.ESMSQQNLNETTQK.K		K.ESMSQQNLNETTQK.K
22	27	2	760.42	-8.9	0	28.8	26.8	95.00%	K.SCLLLR.F	Carbamidomethyl (+57)	K.SCLLLR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
59	B3LH18_YEAS1	7.54%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
26	36	2	1295.72	4.3	1	39.9	23.7	95.00%	R.AAVYDLQYILK.A		R.AAVYDLQYILK.A

2	17	2	1662.87	3	0	23.5	25.9	93.80%	M.DATTPLLTVANSHPAR.N		-.MDATTPLLTVANSHPAR.N
1	20	2	2175.12	4.9	1	57.4	23.9	95.00%	-.MDATTPLLTVANSHPARNPK.H	Acetyl (+42)	-.MDATTPLLTVANSHPARNPK.H
1	17	2	1835.92	2.1	1	91.8	27.3	95.00%	-.MDATTPLLTVANSHPAR.N	Acetyl (+42)	-.MDATTPLLTVANSHPAR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
60	A6ZWP0_YEAS7	10.68%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
91	103	2	1443.72	-0.52	0	31.2	27.9	95.00%	K.AQPLISSCPACLK.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.AQPLISSCPACLK.N
79	90	2	1397.77	2.9	1	41.2	24.2	95.00%	K.DQVVALRDNLQK.A		K.DQVVALRDNLQK.A
188	203	2	1764.9	6	0	62.5	26.9	95.00%	G.DAKPMLGGSPFQINYK.Y		K.FLGDAKPMLGGSPFQINYK.Y
104	120	2	2070.88	2.2	1	84	30.4	95.00%	K.NFNNLFCHFTCAADQGR.F	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.NFNNLFCHFTCAADQGR.F
961	971	2	1269.6	3.5	1	44.2	30.3	95.00%	K.DFIQAYSDGVR.I		K.DFIQAYSDGVR.I
1092	1105	2	1534.87	6.4	1	74.1	20.7	95.00%	R.VLYSLNTIGESVIK.G		R.VLYSLNTIGESVIK.G
104	116	2	1615.67	6.5	0	29.7	30.6	95.00%	K.NFNNLFCHFTCAA.D	Deamidation (+1)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.NFNNLFCHFTCAADQGR.F
33	45	2	1470.73	3	1	28.6	28.7	95.00%	K.SVFGNELPCPVPR.S	Carbamidomethyl (+57)	K.SVFGNELPCPVPR.S
188	204	2	1927.96	6.2	1	51.4	27.6	95.00%	G.DAKPMLGGSPFQINYKY.D		K.FLGDAKPMLGGSPFQINYKYDLANEEK.E
444	463	2	2304.09	6.1	1	79.8	28.5	95.00%	E.DSTCVIESFTQYFQGALPNK.D	Carbamidomethyl (+57)	R.TEQIFVVNETGPVLSYETLHWWFDVENFITEELQSSENIGYQDLCFRPTEDSTCVIESFTQYFQGALPNK.D
436	443	2	1036.47	6.1	1	29.2	29.7	95.00%	Q.DLCFRPTE.D	Carbamidomethyl (+57)	R.TEQIFVVNETGPVLSYETLHWWFDVENFITEELQSSENIGYQDLCFRPTEDSTCVIESFTQYFQGALPNK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
61	EF3A_YEAST	14.56%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
337	350	2	1557.87	5.6	1	54.2	22.2	95.00%	G.DVSTTLQVVNELLK.D		R.VGNVGEDDAIPELSHAGDVSTTLQVVNELLK.D
669	685	2	1939.95	5.8	1	47.3	27.6	95.00%	K.VTNMEFQYPGTSKPQIT.D		K.VTNMEFQYPGTSKPQITDINFQCSLSSR.I
829	842	2	1700.82	-0.54	1	29.2	29	95.00%	R.WVPMMSVDNAWIPR.G		R.WVPMMSVDNAWIPR.G
459	469	2	1181.5	-0.8	0	36.2	29.2	95.00%	R.YGICGPNGCGK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.YGICGPNGCGK.S
751	759	2	1178.58	3.2	1	37.4	29.4	95.00%	K.TPSEYIQWR.F		K.TPSEYIQWR.F
430	443	2	1646.72	5.6	1	47.5	30.7	95.00%	E.DLCNCEFSLAYGAK.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.AVDNIPVGPNFDDEEDEGEDLCNCEFSLAYGAK.I
510	520	2	1184.58	6	1	29.2	29.9	95.00%	L.DFVFESGVGTK.E		R.TVYVEHDIDGTHSDTSVLDFVFESGVGTK.E
279	289	2	1183.67	5.8	0	33.1	24.4	95.00%	E.DPQVIAPFLGK.L		K.LVEDPQVIAPFLGK.L
105	127	3	2394.34	-0.66	1	42.8	16.4	95.00%	K.EIQSVASETLISIVNAVNPVAIK.A		K.EIQSVASETLISIVNAVNPVAIK.A
971	987	2	1737.8	0.11	0	79.9	30.1	95.00%	R.MTPSGHNWVSGQGAGPR.I		R.MTPSGHNWVSGQGAGPR.I
686	696	2	1325.61	5	0	36	30.8	95.00%	T.DINFQCSLSSR.I	Carbamidomethyl (+57)	K.VTNMEFQYPGTSKPQITDINFQCSLSSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
62	A6ZSU5_YEAS7	23.91%	100%	11

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
380	394	2	1652.76	2.1	1	69.1	29.8	95.00%	R.GTFQSSGQNCIGIER.V	Carbamidomethyl (+57)	R.GTFQSSGQNCIGIER.V
590	603	2	1554.87	5.1	0	37.9	22	95.00%	F.DTLPFVSTQIPKPL.D		K.SVCFDTLPFVSTQIPKPLDYPIR.N

550	571	2	2398.11	4.7	0	83.7	29	95.00%	N.DFATFYVCQLPFGGINGSGYGK.F	Carbamidomethyl (+57)/ Deamidation (+1)	K.ECNYVANSLQTGNVAINDFATFYVCQLPFGGINGSGYGK.F
327	342	3	1823.02	3.1	0	32.6	20.6	95.00%	K.HITFIGSQPVAHYILK.C		K.HITFIGSQPVAHYILK.C
314	326	2	1469.67	5.2	0	59.5	30.1	95.00%	D.DSANYFTSHPGFK.H		K.CLEACDEDPDLVQLCYCLPPTENDDSANYFTSHPGFK.H
144	155	2	1354.59	0.94	1	48.9	30.9	95.00%	K.AQSTWGNSDFSR.R		K.AQSTWGNSDFSR.R
509	529	2	2103	6.1	0	98	28.7	95.00%	T.DHCVQLANSAPFGLGGSVFGA.D	Carbamidomethyl (+57)	K.NTDHCVQLANSAPFGLGGSVFGADIK.E
81	94	2	1571.78	3.2	1	50.7	28	95.00%	K.FSLPAPEAAQNNWK.G		K.FSLPAPEAAQNNWK.G
369	379	2	1231.66	-0.094	1	52.8	27.3	95.00%	K.NLDALSSIIMR.G		K.NLDALSSIIMR.G
313	326	2	1584.69	6.4	1	65.9	30.2	95.00%	N.DDSANYFTSHPGFK.H		K.CLEACDEDPDLVQLCYCLPPTENDDSANYFTSHPGFK.H
490	504	2	1688.9	-0.54	1	41.5	24.7	95.00%	K.IAQNEVFGPILVMMK.A		K.IAQNEVFGPILVMMK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
63	A6ZKW1_YEAS7	17.25%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
47	59	2	1498.67	5.3	1	31	30.2	95.00%	R.YVQSYSNKYSSSS.D		R.YVQSYSNKYSSSSDAASADDSTPLR.D
448	458	2	1238.6	3.5	1	64	30.5	95.00%	R.YLNAMESIGNK.Y		R.YLNAMESIGNK.Y
227	236	2	1234.64	0.58	1	24.8	28.1	92.40%	K.CIYVSDILPR.E	Carbamidomethyl (+57)	K.CIYVSDILPR.E
251	265	2	1602.94	7.5	1	55.8	18.3	95.00%	K.SLALIASSFENLLLL.D		K.SLALIASSFENLLLLDADNFPIKPLDNIFNEEPYVSTGLVMWPDFWR.R
83	98	2	1920.91	-0.9	1	68.3	29.6	95.00%	K.SFYNNVFNFLMVDSPK.G		K.SFYNNVFNFLMVDSPK.G
496	507	2	1480.73	5.3	1	42.8	29.3	95.00%	V.DVMFIHSNFPKF.D		K.NHVDVMFIHSNFPKFDPYDLSK.S
153	165	2	1470.78	5.9	1	56.5	26.4	95.00%	K.DYVEHIATLVSPK.G		K.DYVEHIATLVSPK.G
352	364	2	1420.69	5	1	76.6	29.5	95.00%	P.DVSTESGQLMINK.T		K.DLSDVPLSDLDGTIPDVSTESGQLMINK.T
496	506	2	1333.66	6.5	0	31.1	29.1	95.00%	V.DVMFIHSNFPK.F		K.NHVDVMFIHSNFPK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
64	RL20_YEAST	26.74%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
100	108	2	992.52	5.4	1	39.7	29.5	95.00%	R.VAAVETLYQ.D		R.VAAVETLYQDMAAR.H
147	155	3	1121.64	3.1	1	24	22.6	95.00%	K.DLKFPLPHR.V		K.DLKFPLPHR.V
29	38	2	1090.6	2.2	1	60.7	25.9	95.00%	R.IFASNEVIAK.S		R.IFASNEVIAK.S
74	80	2	876.46	0.084	0	30.8	28.2	95.00%	K.NFGVWVR.Y		K.NFGVWVR.Y
2	12	3	1346.72	4.8	1	25.7	26.1	95.00%	M.AHFKEYQVIGR.R		-.MAHFKEYQVIGR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
65	B3LGF8_YEAS1	11.59%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
345	358	2	1378.73	0.37	0	47.8	27.5	95.00%	R.CVTGFGGGSLIALK.S	Carbamidomethyl (+57)	R.CVTGFGGGSLIALK.S
431	443	2	1518.82	1.8	0	33.3	25.1	95.00%	K.STLYGRPTPTLWK.R		K.STLYGRPTPTLWK.R
145	162	2	1973.89	6	1	41.2	29.9	95.00%	R.SVSPLQSITSCNTPMSEH.E	Carbamidomethyl (+57)	R.SVSPLQSITSCNTPMSEHELPVSSSNSFER.A
207	222	2	1685.79	6	1	40.2	29.4	95.00%	G.DEITSYGYGSIPQSIG.D		K.SLHIVAPSPEVPVSGDEITSYGYGSIPQSIGDVENGLNPPYVENTSSDELVHDLTR.R
192	206	2	1487.81	6.4	1	33.6	24.4	95.00%	K.SLHIVAPSPEVPVSG.D		K.SLHIVAPSPEVPVSGDEITSYGYGSIPQSIGDVENGLNPPYVENTSSDELVHDLTR.R
163	174	2	1350.65	5.9	1	42.7	29.5	95.00%	H.ELPVSSSNSFER.A		R.SVSPLQSITSCNTPMSEHELPVSSSNSFER.A
431	444	3	1674.92	0.54	1	30.5	22.5	95.00%	K.STLYGRPTPTLWKR.F		K.STLYGRPTPTLWKR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
66	A6ZVP9_YEAS7	17.32%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
164	174	2	954.56	3.5	0	55.4	18.4	95.00%	R.GVIGVIAGGGR.V		R.GVIGVIAGGGR.V
10	21	3	1260.66	0.078	1	55.2	27.3	95.00%	R.KGAGSIFTSHTR.L		R.KGAGSIFTSHTR.L
201	221	2	2158.02	-0.33	1	50.1	28.3	95.00%	R.GVAMNPVDHPHGGGNHQHIGK.A		R.GVAMNPVDHPHGGGNHQHIGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
67	A7A077_YEAS7	18.78%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
298	308	2	1318.7	6.7	0	51.6	28.2	95.00%	G.DNYLVNLVNQK.G		K.ELYGDNYLVNLVNQK.G
257	270	2	1602.84	-0.88	1	59	26.8	95.00%	R.GSVPIYWAEINNLK.Y		R.GSVPIYWAEINNLK.Y
446	459	2	1337.69	5.3	0	57.9	27.8	95.00%	A.DAVSVAYSGTGALK.T		K.EFESADVVATGSTWEDNAPLLTSYQNLWADNADAVSVAYSGTGALK.T
294	308	2	1780.9	-1.7	1	64	27.6	95.00%	K.ELYGDNYLVNLVNQK.G		K.ELYGDNYLVNLVNQK.G
175	188	2	1612.85	-1.4	1	43.4	26.1	95.00%	R.IDSFIQPVIYGYAK.T		R.IDSFIQPVIYGYAK.T
189	206	2	1865.1	-0.54	1	61.6	15.1	95.00%	K.TVDAVLNATPIVLGLITR.R		K.TVDAVLNATPIVLGLITR.R
429	442	2	1604.79	6.2	0	34.5	29	95.00%	E.DNAPLLTSYQNLWA.D		K.EFESADVVATGSTWEDNAPLLTSYQNLWADNADAVSVAYSGTGALK.T
399	413	2	1711.96	-1.2	0	77.1	21.6	95.00%	R.TNVVQSVLAQWVLQK.E		R.TNVVQSVLAQWVLQK.E
471	483	2	1410.69	2.9	1	101	29.6	95.00%	R.LGAFNDFLNSASR.Y		R.LGAFNDFLNSASR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
68	A6ZZQ2_YEAS7	16.00%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
9	25	2	1923.91	5.3	1	41.8	29.1	95.00%	K.DEGVPLLSPYSSSPQLR.K	Phospho (+80)	K.DEGVPLLSPYSSSPQLR.K
582	606	2	2590.06	0.46	1	93.4	29.3	95.00%	K.SQAYGATMSNESNANNNNSTSNASR.S	Deamidation (+1)	K.SQAYGATMSNESNANNNNSTSNASR.S
110	126	2	1811.91	2.6	0	49.8	26.4	95.00%	R.EGPQSVSSTVQPQPIMK.F		R.EGPQSVSSTVQPQPIMK.F
449	467	3	1970.01	5.9	1	23.5	26.8	95.00%	Q.DNSAGHIKTHPNSPTPGIK.A		K.FQDLFVASIYSQDNSAGHIKTHPNSPTPGIK.A
394	410	3	2075.04	2	1	24.2	26.7	95.00%	R.NIQYPPHIISNNPEHFR.F		R.NIQYPPHIISNNPEHFR.F
319	331	2	1415.81	5.3	0	48.2	22.4	95.00%	E.DGILFSKPIVTNI.D		R.SQAIQDAEAFHFQYDEDEEDGTSNEDGILFSKPIVTNIDVPELGNR.R
193	208	2	1669.76	5.7	0	37.9	30.7	95.00%	V.DALMNHVNNNASTGVN.D		R.QSNANNDVVIDVDALMNHVNNNASTGVNDNSK.R
381	393	2	1411.78	3	1	53.2	24.8	95.00%	R.IQSGLQDNLLVGR.N		R.IQSGLQDNLLVGR.N
419	436	3	1863.98	6.3	0	17	24.6	92.20%	L.DSTVHSPTISGLLQPGQK.F		R.VDLDSTVHSPTISGLLQPGQK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
69	MAM3_YEAST	10.06%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
470	500	3	3211.7	6	1	37.8	20.3	95.00%	R.SNAVLSPTPQVTEHGTIIPSNLASNPLNVNK.S		R.SNAVLSPTPQVTEHGTIIPSNLASNPLNVNK.S
358	372	2	1465.75	5.6	1	40.5	27.4	95.00%	K.EPGSSHGAIGVLTLE.D		K.EPGSSHGAIGVLTLEDVIEELIGEEIVDESDVFVDMHQHIMR.Q
683	691	2	1025.48	2.6	1	34.1	30.9	95.00%	R.SNFTDSLSR.T		R.SNFTDSLSR.T
408	423	4	1979.01	-0.025	1	34.2	25.8	95.00%	K.RHITSYLHHLYTSSHK.E		K.RHITSYLHHLYTSSHK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
70	A6ZM61_YEAS7	21.15%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
39	48	2	1035.56	2.9	1	28.6	27.7	95.00%	K.ATIGADFLTK.E		K.ATIGADFLTK.E
148	160	2	1360.76	-0.6	1	63.3	23.7	95.00%	K.SLGDIPLFLTSAK.N		K.SLGDIPLFLTSAK.N
11	21	2	1056.62	2.9	1	27.1	24.6	95.00%	K.VIILGDSGVGK.T		K.VIILGDSGVGK.T
71	80	2	1186.61	-1.7	0	41.4	28.3	95.00%	R.FQSLGVAFYR.G		R.FQSLGVAFYR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
71	A6ZX41_YEAS7	35.89%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
139	153	2	1543.72	5.9	1	28.9	29.9	95.00%	Q.EGQQPVTSQEGQSVA.D		R.QEGQQPVTSQEGQSVADQIGATGYYECSAK.T
174	181	2	921.46	0.5	1	35.6	30.1	95.00%	R.EVFEAATR.A		R.EVFEAATR.A
2	10	2	1029.52	-0.26	0	37	28.7	95.00%	M.SQQVGNSIR.R	Acetyl (+42)	-.MSQQVGNSIR.R
154	167	2	1561.68	5.9	1	78	31.3	95.00%	A.DQIGATGYYECSAK.T	Carbamidomethyl (+57)	R.QEGQQPVTSQEGQSVADQIGATGYYECSAK.T
24	32	2	1079.61	3.5	0	39	21.6	95.00%	K.TCLLIVFSK.G	Carbamidomethyl (+57)	K.TCLLIVFSK.G
104	123	2	2338.24	2.6	1	49.3	22.1	95.00%	K.WIAEVLHFCQGVPIILVGCK.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.WIAEVLHFCQGVPIILVGCK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
72	MNN5_YEAST	10.58%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
504	513	2	1115.57	0.16	1	30.2	28.5	95.00%	R.FIGPNGEQVR.G		R.FIGPNGEQVR.G
78	93	2	1653.74	4.5	1	89.2	30.7	95.00%	K.LHGAEGCSFANNVAAH.D	Carbamidomethyl (+57)	K.LHGAEGCSFANNVAAHDSGHDSDLSYESLSK.C
100	108	2	1040.51	6.9	1	30.5	28.8	95.00%	S.DLSYESLSK.C		K.LHGAEGCSFANNVAAHDSGHDSDLSYESLSK.C
160	169	2	1187.63	5	0	23	27.5	90.00%	K.YSVLAYTMIK.K		K.YSVLAYTMIK.K
53	69	3	1921.01	7	1	62	24.8	95.00%	K.NNFYTTLVQAIVENKPA.D		K.NNFYTTLVQAIVENKPADSSPDLSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
73	B3LGY9_YEAS1	6.85%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
570	579	2	1194.55	3.9	1	30.9	29.8	95.00%	R.GISYWGENNR.N		R.GISYWGENNR.N
558	569	2	1459.75	6	0	30	27.6	95.00%	Y.ESQPTSWPFLLR.G		K.NLVEPHVYESQPTSWPFLLR.G
23	32	2	1112.64	5.1	0	22.8	23.8	94.00%	K.QGPVRPFIVT.D		K.QGPVRPFIVTDPSAELASLR.T
472	485	2	1678.76	2.5	1	63.8	30.5	95.00%	R.HAMTGCYLFSHEVK.L	Carbamidomethyl (+57)	R.HAMTGCYLFSHEVK.L
33	42	2	1057.55	6.4	1	53.9	28.6	95.00%	T.DPSAELASLR.T		K.QGPVRPFIVTDPSAELASLR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
74	A6ZNV4_YEAS7	19.43%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
13	26	2	1591.72	0.81	1	52.5	30.6	95.00%	K.GNSQQEPQFSTNQK.T		K.GNSQQEPQFSTNQK.T
187	196	2	1285.65	5.1	1	62.7	27.9	95.00%	L.DFQTIIHQER.S		K.VNEQSPLLHNEGQHQLQLQEEQEQQQQGLSQEELDFQTIIHQER.S
102	112	2	1413.66	-0.98	0	73.2	30	95.00%	K.YQSLQQSYNQR.K		K.YQSLQQSYNQR.K
203	222	3	2203.21	-0.67	1	43	19.4	95.00%	R.IHTAVQEVNAIFHQLGSLVK.E		R.IHTAVQEVNAIFHQLGSLVK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
75	A6ZNR5_YEAS7	14.47%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
304	315	2	1278.62	6.4	0	32.5	29.8	95.00%	K.TITPMGGFVHYG.E		K.TITPMGGFVHYGEIK.N
249	266	2	2047.01	3	0	49.1	27.8	95.00%	K.VACIGAWHPAHVMWSVAR.A	Carbamidomethyl (+57)	K.VACIGAWHPAHVMWSVAR.A
180	191	2	1274.64	4.9	1	32.3	29	95.00%	A.EIQLNGGSISEK.V	Deamidation (+1)	K.AHLAEIQLNGGSISEK.V
248	266	4	2175.1	2.9	1	66.2	25.5	95.00%	R.KVACIGAWHPAHVMWSVAR.A	Carbamidomethyl (+57)	R.KVACIGAWHPAHVMWSVAR.A
38	50	2	1409.79	0.48	0	41.5	21.4	95.00%	R.SKPVALTSFLGYK.A		R.SKPVALTSFLGYK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
76	A6ZV40_YEAS7	4.36%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
6	16	2	1309.7	-0.47	0	68.2	26.4	95.00%	R.TFLSQLNVFNK.E		R.TFLSQLNVFNK.E

60	73	2	1615.85	-0.65	0	69	25.8	95.00%	K.QLGILSCIGLICNR.M	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.QLGILSCIGLICNR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
77	B3LQG1_YEAS1	14.90%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
130	140	2	1395.67	6.6	0	30.2	30.1	95.00%	K.FPAFIWQTWSN.D		K.FPAFIWQTWSNDEGPER.V
107	115	2	1011.53	-0.42	1	25.4	26.3	95.00%	K.QTPPEATLR.E		K.QTPPEATLR.E
349	358	2	1129.68	0.16	1	56.3	20	95.00%	K.LLSDVLVFPK.F		K.LLSDVLVFPK.F
51	65	2	1590.76	5.7	0	68.4	29.5	95.00%	K.EISQSINSANNIQSS.D		K.EISQSINSANNIQSSDSDLVQHFESLAQEIR.H
51	67	2	1792.82	5.1	1	44.6	30.5	95.00%	K.EISQSINSANNIQSSDS.D		K.EISQSINSANNIQSSDSDLVQHFESLAQEIR.H
118	129	2	1407.69	0.63	1	33	29.5	95.00%	R.IAMTFPYDSHVK.F		R.IAMTFPYDSHVK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
78	A6ZXE9_YEAS7	12.38%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
216	233	2	1809.84	5.9	1	104	28.7	95.00%	N.DTGCAIANAYTALEGGAR.L	Carbamidomethyl (+57)	K.SVVSCDIECHFHNDTGCAIANAYTALEGGAR.L
246	257	2	1198.65	3.6	0	29.1	26.1	95.00%	R.NGITPLGGLMAR.M		R.NGITPLGGLMAR.M
258	267	2	1105.59	3.2	1	40	27.5	95.00%	R.MIVAAPDYVK.S		R.MIVAAPDYVK.S
180	192	2	1328.65	0.46	1	87.7	29.2	95.00%	R.VGIADTVGCANPR.Q	Carbamidomethyl (+57)	R.VGIADTVGCANPR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
79	YO092_YEAST	8.77%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1	10	2	1211.67	0.89	1	40.1	24.1	95.00%	-.MQLVPLELNR.S		-.MQLVPLELNR.S
103	119	2	1878.97	7.2	1	27.4	25.5	95.00%	V.DPIHLSPANPINENVLH.D		K.SSDGLSLLFVVLWLAGDVFNLMGAVMQHLLSTMIILAAYYTVADIILLGQCLWYDNEEKPAVDPIHLSPANPINENVLHDVFNEQQPLLNSQGQPNR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
80	YJ12B_YEAST	6.61%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
268	283	2	1676.84	5.6	0	39.9	28.9	95.00%	N.DIVTLANLQYNGSTPA.D	Deamidation (+1)	K.MQSDTQEANDIVTLANLQYNGSTPADAFETK.V
829	843	2	1611.9	5.6	0	27.1	23	95.00%	L.DISTLLPFGQPVIVN.D		R.QHAGLAGLDISTLLPFGQPVIVNDHNPNSK.I
308	315	2	989.52	1.9	0	40.9	28.9	95.00%	K.VACQLIMR.G	Carbamidomethyl (+57)	K.VACQLIMR.G
1	24	3	2638.2	4.6	1	56.9	28.1	95.00%	-.MESQQLSQHSHISHGSACASVTSK.E	Acetyl (+42)/ Carbamidomethyl (+57)	-.MESQQLSQHSHISHGSACASVTSK.E
560	568	2	1163.53	2.7	1	33.5	30	95.00%	K.YGDFYWVSK.K		K.YGDFYWVSK.K
1496	1503	2	893.54	1.6	0	22.9	21.7	94.20%	K.LNVPLNPK.G		K.LNVPLNPK.G
784	807	3	2803.42	2.6	1	58.3	24.8	95.00%	R.TQLQCSGLPNHLWFSAIEFSTIVR.N	Carbamidomethyl (+57)	R.TQLQCSGLPNHLWFSAIEFSTIVR.N
1621	1632	2	1318.73	3.3	0	51.9	24.9	95.00%	K.SQIGNIYLLNGK.V		K.SQIGNIYLLNGK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
81	A6ZXZ5_YEAS7	10.00%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
18	31	2	1524.77	3.1	1	55.6	27.8	95.00%	K.INPPTGADFHITSR.G		K.INPPTGADFHITSR.G
285	300	2	1575.87	0.42	0	65.1	22.4	95.00%	K.APVASPRPAATPNLSK.D		K.APVASPRPAATPNLSK.D
285	302	2	1819	-0.077	1	64.8	23.4	95.00%	K.APVASPRPAATPNLSKDK.K		K.APVASPRPAATPNLSKDK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

82	A6ZQY0_YEAS7	23.77%		100%		5						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
116	127	2	1213.64	5.4	1	37.3	27.2	95.00%	A.DDNVAVGLIGNK.S		R.ENADDNVAVGLIGNK.S	
44	53	2	1079.56	3.4	1	61.2	28.4	95.00%	K.STIGVEFATR.T		K.STIGVEFATR.T	
128	134	2	810.43	-1.3	1	48.4	25.2	95.00%	K.SDLAHLR.A		K.SDLAHLR.A	
16	26	2	1056.62	2.9	1	27.1	24.6	95.00%	K.IVLIGDSGVGK.S		K.IVLIGDSGVGK.S	
85	97	2	1304.74	2.5	1	42.2	22.9	95.00%	R.GAVGALIVYDISK.S		R.GAVGALIVYDISK.S	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
83	A6ZT57_YEAS7	15.40%		100%		10						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
701	718	2	1772.92	6.7	0	31.4	26.6	95.00%	T.DVVQPPSVGGILPHSGSQ.D		R.VSGILEETDVVQPPSVGGILPHSGSQDDLR.K	
369	377	2	1155.6	3.8	1	40.7	28.1	95.00%	K.SIYQVYLDR.A		K.SIYQVYLDR.A	
610	623	2	1689.75	5.2	0	46.8	31.3	95.00%	N.DAYYAPQQQGQYMK.F		R.LNGTALNPVDHPEMFYSPTNDAYYAPQQQGQYMK.F	
647	661	2	1636.87	5.2	0	60.4	25.1	95.00%	S.DLTAKPSYKPAGSFR.S		R.QSVVMTNPSDLTAKPSYKPAGSFR.S	
217	235	3	2157.98	-0.59	1	21.9	29.6	92.70%	R.NASQTSLHPDNFSNCTPIR.A	Carbamidomethyl (+57)	R.NASQTSLHPDNFSNCTPIR.A	
701	719	2	1967.91	6.9	1	37.3	29.5	95.00%	T.DVVQPPSVGGILPHSGSQD.D	Phospho (+80)	R.VSGILEETDVVQPPSVGGILPHSGSQDDLR.K	
476	491	2	1795.91	6	1	26.2	27.9	94.80%	R.IASSIYSEAIQPLNYQ.D		R.IASSIYSEAIQPLNYQDQYQQQEQSPVYNGHTQYPGNGYSGNPQQQGYTAQFVQNPQWYGVPTPQQQQHNHPQTLETIGELPTPAYLAQSASSHSLTSFK.R	
483	491	2	1074.54	7.1	0	25	28.9	91.20%	S.EAIQPLNYQ.D		R.IASSIYSEAIQPLNYQDQYQQQEQSPVYNGHTQYPGNGYSGNPQQQGYTAQFVQNPQWYGVPTPQQQQHNHPQTLETIGELPTPAYLAQSASSHSLTSFK.R	
638	661	4	2580.31	3.2	1	44.1	23.9	95.00%	R.QSVVMTNPSDLTAKPSYKPAGSFR.S		R.QSVVMTNPSDLTAKPSYKPAGSFR.S	
402	413	2	1336.74	5.2	0	52	23.4	95.00%	V.DNIVQNPLPSIK.I		R.VDNIVQNPLPSIK.I	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
84	A6ZNT8_YEAS7	9.33%		100%		5						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
218	229	2	1396.76	6.7	0	41.3	24.6	95.00%	A.EVSLISHFNPVR.L		K.DDSLAEVSLISHFNPVR.L	
74	84	2	1178.54	-0.25	1	25.9	29.8	91.10%	K.LAYEACGGNPK.D	Carbamidomethyl (+57)	K.LAYEACGGNPK.D	
198	212	2	1688.89	5.7	1	72.5	25	95.00%	R.GWIVQNGLDPTTFIK.D	Deamidation (+1)	R.GWIVQNGLDPTTFIK.D	
471	480	2	1214.54	4.9	1	45.4	31.3	95.00%	D.DEYMALMSQK.T		K.VIDNADDEYMALMSQK.T	
176	190	2	1694.76	5	0	71.1	30.3	95.00%	T.DMHCTTVIGSSGFQR.C	Carbamidomethyl (+57)	R.YVINENDEDQEPLNALELATDMHCTTVIGSSGFQR.C	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
85	B3LP09_YEAS1	13.92%		100%		4						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
405	430	3	3049.42	4.9	0	61.7	27.9	95.00%	P.DHHHHYNQQQQQQQAQAQAQAQAQAK.V		K.NHQYSSPDHHHHYNQQQQQQQAQAQAQAQAQAK.V	
375	390	3	1797.9	6.1	1	36.4	27.5	95.00%	K.KPNLHGYGHPNPPNEK.S		K.KPNLHGYGHPNPPNEK.S	
303	319	2	1904.01	-0.63	1	53	23	95.00%	R.LTNVYDLAQGLPIQFGR.Y		R.LTNVYDLAQGLPIQFGR.Y	
431	447	2	1994	-0.94	0	81	25.8	95.00%	K.VQQQQLQQAQAQQQANR.Y		K.VQQQQLQQAQAQQQANR.Y	
Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
86	VAC7_YEAST	12.70%		100%		10						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
1062	1071	2	1096.54	0.45	1	54.9	29	95.00%	R.NYDVSVSSVK.L		R.NYDVSVSSVK.L	

786	794	2	1014.57	7.2	1	27.6	28.6	95.00%	N.DLETKPLIS.D		K.NDLETKPLISDYGEDEDVDDYDR PNATFNSYYGSASNTHELPLHGR. M
898	910	2	1553.73	5	0	42.5	29.7	95.00%	N.DIVGYSPHNFYSR.K		R.TNNSIMNGSIHMNGNDDVTHSNI NNNDIVGYSPHNFYSR.K
573	582	2	1099.48	7.5	1	29.9	30.7	95.00%	M.DVQSVDSYTS.D		K.QEPPHQLQQQQPPMDVQSVDS YTSDNPDSNVIAK.S
699	715	2	2062.95	4.6	1	55.7	29.3	95.00%	E.DYIEQPHNYPTMQNSVK.K		R.YSGVPDHVNLEDYIEQPHNYPTM QNSVK.K
1031	1046	2	1586.86	6.4	1	48.9	24	95.00%	N.DISGGNIETVLLGTAK.K		K.ILQITTNLSLVEESANNDISGGNIE TVLLGTAK.K
249	261	3	1552.82	5.6	1	35.8	25.2	95.00%	K.IIERPTMHVTNSR.E		K.IIERPTMHVTNSR.E
841	861	2	2410.11	5.1	1	73.9	28.7	95.00%	Y.DFMVGNNTGNNNQLNEYTPLR. M		R.SNNDYYDFMVGNNTGNNNQLNE YTPLR.M
54	74	2	2196.08	7.1	1	29.8	26.1	95.00%	V.DDSVATANTTSNVVQHNLPTI.D		R.EIVDDSVATANTTSNVVQHNLPTI DNNLMDSDATSHNQDHWHSDINR. A
806	823	2	2000.87	6.1	0	67.6	30.2	95.00%	Y.DRPNATFNSYYGSASNTH.E		K.NDLETKPLISDYGEDEDVDDYDR PNATFNSYYGSASNTHELPLHGR. M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
87	A7A1A7_YEAS7	15.84%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
172	181	2	1254.6	3.8	1	49.4	29.3	95.00%	K.FYDNSNLINR.E		K.FYDNSNLINR.E
88	99	2	1349.67	0.57	1	47.6	29.3	95.00%	K.ANLGFFQSVDPR.V		K.ANLGFFQSVDPR.V
64	74	2	1175.55	4.7	1	37.8	30.2	95.00%	Q.DLENSPMSVGK.D		R.NSAQDLENSPMSVGK.D
8	16	2	984.6	3.2	0	40.2	23.2	95.00%	K.NAVVTLIQK.A		K.NAVVTLIQK.A
196	204	2	1050.57	6.6	1	41.7	26	95.00%	S.DETIVSFIK.D		R.EIEDILLEINPNFSDETIVSFIK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
88	AQR1_YEAST	12.29%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
39	54	2	1749.88	5.7	1	81.3	27.8	95.00%	K.LNFEGAYINSHGTLSK.T		K.LNFEGAYINSHGTLSK.T
78	88	2	1230.62	5.8	1	57.5	28.8	95.00%	V.DPTQQITAETK.A		K.VDPTQQITAETK.A
505	517	2	1520.68	-0.69	0	35.4	30.1	95.00%	R.CSLSTIFMGCFAK.M	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.CSLSTIFMGCFAK.M
563	572	2	1158.64	0.25	0	32.1	26.1	95.00%	R.QSWLNTLAVK.A		R.QSWLNTLAVK.A
493	504	2	1361.61	4.1	0	41.7	30	95.00%	K.SSTASSCFNFVR.C	Carbamidomethyl (+57)	K.SSTASSCFNFVR.C
298	307	2	1081.67	1.5	0	29.8	16.2	95.00%	R.APIFLLGPVR.R		R.APIFLLGPVR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
89	A6ZLH4_YEAS7	10.62%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
964	981	2	2003.05	4.9	0	49.8	24	95.00%	S.DVSTQSLRPVFSSNTLPR.T		K.NLQSDVSTQSLRPVFSSNTLPR.T
1069	1084	2	1708.91	5.4	1	52.2	24.4	95.00%	S.DLIFSTLPVPALGTHE.D		K.SSDLIFSTLPVPALGTHEDHDASL QYVEDLDIWLEGLPPCMLINSQTMT VTTAL.-
127	136	2	1073.5	3.3	0	45.5	29.6	95.00%	R.GGGAYYMISR.S		R.GGGAYYMISR.S
244	262	2	2097.96	5.8	1	37	29.5	95.00%	R.SPFTEGGISYTGPSWQTFH.D		R.SPFTEGGISYTGPSWQTFHDNLL PHLTK.G
33	48	2	1976.89	0.17	1	66	29.9	95.00%	R.ISQTYFNYQATPECQK.V	Carbamidomethyl (+57)	R.ISQTYFNYQATPECQK.V
5	31	3	2878.42	0.21	1	69.4	26.4	95.00%	R.FYQIPGTHRPSSAISSSNESSSLL SAR.R		R.FYQIPGTHRPSSAISSSNESSSLL SAR.R
1034	1046	2	1408.68	6.6	0	68.2	30.1	95.00%	K.DSLVTAMQNLGFN.D		K.DSLVTAMQNLGFNDLPSTAQHLV LNDVMTQMSK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

90	A7A0E5_YEAS7	8.56%		100%		6						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
384	393	2	1311.56	-0.41	1	26.7	30.5	91.50%	K.DANNEWFFNR.E		K.DANNEWFFNR.E	
370	383	2	1646.71	3.8	0	95	30.4	95.00%	P.DGSNQQQVTCYGYK.D	Carbamidomethyl (+57)	K.NQALGGSLLHSHIQTYPDGSNQQQVTCYGYK.D	
341	352	2	1187.68	2.5	0	40.7	23	95.00%	R.DIALGSSVVSIK.N		R.DIALGSSVVSIK.N	
406	417	2	1440.73	5.5	1	36	27.5	95.00%	T.DIEYLKPGTSYR.L		R.GLPSWSENETDIEYLKPGTSYR.L	
353	383	3	3463.62	0.12	1	57.6	26	95.00%	K.NQALGGSLLHSHIQTYPDGSNQQQVTCYGYK.D	Carbamidomethyl (+57)	K.NQALGGSLLHSHIQTYPDGSNQQQVTCYGYK.D	
353	369	2	1834.94	5.9	0	27.1	25.8	95.00%	K.NQALGGSLLHSHIQTYP.D		K.NQALGGSLLHSHIQTYPDGSNQQQVTCYGYK.D	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
91	B5VDM9_YEAST	19.57%		100%		3						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
189	202	2	1628.79	6.1	1	27.6	29.4	94.60%	K.EVSNEMVKPYIFSS.D		K.EVSNEMVKPYIFSSDPVLEAYLIK.A	
167	188	2	2226.02	0.25	1	90.1	29.3	95.00%	R.SNAHLSSPTNGAENTQSNTPAK.E	Deamidation (+1)	R.SNAHLSSPTNGAENTQSNTPAK.E	
203	212	2	1159.66	6.7	1	66.8	23.6	95.00%	S.DPVLEAYLIK.A		K.EVSNEMVKPYIFSSDPVLEAYLIK.A	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
92	A6ZZX2_YEAS7	21.43%		100%		2						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
136	149	2	1494.76	-1	1	69.3	27.9	95.00%	R.TNTFTLLTSPDSAK.I		R.TNTFTLLTSPDSAK.I	
111	135	3	2520.17	5.7	1	87	27.5	95.00%	G.DDNLSGHSVPSSGSAQATTHQTAPR.T		R.SAGDDNLSGHSVPSSGSAQATTHQTAPR.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
93	YAJ8_YEAST	9.83%		100%		2						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
201	211	2	1248.68	-0.57	1	58.4	26	95.00%	R.SDPILMAYVLK.A		R.SDPILMAYVLK.A	
189	200	2	1385.66	0.99	0	44	30.9	95.00%	K.TSNGLNNFYSIR.S	Deamidation (+1)	K.TSNGLNNFYSIR.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
94	A6ZLU9_YEAS7	14.02%		100%		6						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
313	325	2	1424.67	2.5	1	58.6	29.9	95.00%	K.DFGQVIGQGFSDR.H		K.DFGQVIGQGFSDR.H	
201	211	2	1217.65	0.22	1	60	27.5	95.00%	R.NAADVLPLMFK.H		R.NAADVLPLMFK.H	
191	200	2	1248.7	1.8	0	43	23.2	95.00%	R.DHILLCIPLR.N	Carbamidomethyl (+57)	R.DHILLCIPLR.N	
381	401	2	2440.29	5.8	1	33.1	21.8	95.00%	Y.DVIVPNVWRPLPTFLGTEQPY.D		K.NYDVIVPNVWRPLPTFLGTEQPYDLNSWMESQEALALAK.T	
15	26	2	1272.65	3.5	1	32.8	28	95.00%	K.AMDNGLSLPISR.N		K.AMDNGLSLPISR.N	
240	247	2	907.48	5.6	0	29.5	28.1	95.00%	L.DALIAYSR.Q		K.HLMNLTYPHELIDLAFLVSDCSEGDTTLDALIAYSR.Q	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
95	A6ZT03_YEAS7	12.46%		100%		5						
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
41	59	2	1950.97	4.4	1	42.8	27	95.00%	H.DNLSESQVQPAVAPPNTGK.G		K.NESFHDNLSESQVQPAVAPPNTGK.G	
228	236	2	1153.52	2.9	0	49.9	31	95.00%	K.NYSNSVQWR.V	Deamidation (+1)	K.NYSNSVQWR.V	
1	12	2	1371.67	2.8	1	27.7	29.6	94.40%	-.MNSTPDLISPQK.S	Acetyl (+42)	-.MNSTPDLISPQK.S	
305	324	2	2125.05	4.6	1	84.6	27.3	95.00%	R.AAGTASWGELFTGKPAMFQR.T		R.AAGTASWGELFTGKPAMFQR.T	
526	536	2	1307.63	8.2	1	28	30	94.30%	N.DMYAEGVLPWK.S		K.GLSLEEVNDMYAEGVLPWK.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
96	A7A1T6_YEAS7	6.96%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
457	464	2	1026.5	3.4	0	35.2	28.2	95.00%	R.LSIFTMCR.A	Carbamidomethyl (+57)	R.LSIFTMCR.A
440	456	3	2073.1	3.6	1	18.2	23.5	94.70%	K.EMTPSILEYLHIPVIYR.L		K.EMTPSILEYLHIPVIYR.L
203	214	2	1323.71	0.13	1	38	26.1	95.00%	K.LSPVFELFASSK.N		K.LSPVFELFASSK.N
477	486	2	1203.54	-1.2	1	33.6	30.5	95.00%	K.SHAVQNMDFR.S		K.SHAVQNMDFR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
97	B3LJS4_YEAS1	9.64%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
327	342	2	1673.87	5.3	0	41.4	26.5	95.00%	I.DVVQSKPVGLPQYSTG.D		K.AVIFISEPYGENIDVVQSKPVGLPQYSTGDASGLNWDGSPVEEK.D
520	531	2	1316.7	5	1	46.4	26.5	95.00%	I.DISQLGIPFAEK.Y		K.DEIYSLIDISQLGIPFAEK.Y
248	258	2	1205.57	3.1	0	38.4	29.8	95.00%	K.ENFNPLSSNGK.L		K.ENFNPLSSNGK.L
742	752	2	1229.67	5.3	1	36.6	26.2	95.00%	K.NVLFGPTLIQE.D		K.NVLFGPTLIQEDK.S
573	589	2	1802.92	5.9	0	67.9	26.8	95.00%	G.DWTPFLANGIPVSVISS.D	Deamidation (+1)	R.NAHGNFDISVDNVQHYGDWTPFLANGIPVSVISSDSTR.N
299	309	2	1226.73	3.2	1	31	20.3	95.00%	K.LVSQQVLIAEK.F		K.LVSQQVLIAEK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
98	A6ZL71_YEAS7	14.89%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
348	360	2	1454.74	5.7	1	49.3	28.6	95.00%	P.DLTGYITEGQIFV.D		R.NGSITQIPILTMPNDDITHPIPDLTGYITEGQIFVDR.Q
326	339	2	1497.8	6.3	0	32.1	25.4	95.00%	R.NGSITQIPILTMPN.D		R.NGSITQIPILTMPNDDITHPIPDLTGYITEGQIFVDR.Q
26	43	2	1929.06	-0.94	1	38.4	20.3	95.00%	R.LNYNTVSGVNGPLVILEK.V		R.LNYNTVSGVNGPLVILEK.V
133	144	2	1316.64	5.1	0	29.5	28.5	95.00%	L.DINGSPINPYAR.I	Deamidation (+1)	K.VFAEDYLDINGSPINPYAR.I
170	189	3	2193.15	6.3	1	45	23.2	95.00%	K.IPIFSASGLPHNEIAAQICR.Q	Carbamidomethyl (+57)	K.IPIFSASGLPHNEIAAQICR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
99	A6ZL51_YEAS7	32.45%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
138	147	2	1039.59	5.9	0	22.5	22.3	93.60%	K.IHLFGKPATG.D		K.IHLFGKPATGDLK.R
138	150	3	1395.79	3.3	1	21.1	21.2	95.00%	K.IHLFGKPATGDLK.R		K.IHLFGKPATGDLK.R
155	168	2	1346.67	1.8	0	64.3	28.3	95.00%	K.APSLFGGMGQTGPK.T		K.APSLFGGMGQTGPK.T
115	128	2	1623.84	5.5	0	65.2	26.6	95.00%	K.YTNPLFMQSISPVK.S		K.YTNPLFMQSISPVK.S
1	20	5	2435.18	-4.4	1	18.1	27.5	91.00%	-.MNPQVSNIIIMLVMMQLSRR.I	Acetyl (+42)/ Deamidation (+1)/ Deamidation (+1)/ Deamidation (+1)/ Oxidation (+16)/ Deamidation (+1)	-.MNPQVSNIIIMLVMMQLSRR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
100	A6ZQS1_YEAS7	31.87%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	34	3	3423.7	2.8	1	51.2	23.3	95.00%	M.TELCPVYAPFFGAIGCASAIIFTSLGAAYGTAK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	-.MTELCPVYAPFFGAIGCASAIIFTSLGAAYGTAK.S
35	52	2	2005.06	3.1	1	55.3	24.5	95.00%	K.SGVGICATCVLRPDLLFK.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.SGVGICATCVLRPDLLFK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
101	A6ZQR6_YEAS7	33.76%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
57	68	2	1311.76	-0.015	1	35.4	22.9	95.00%	K.VHLVAIDIFTGK.K		K.VHLVAIDIFTGK.K

12	27	2	1713.75	5.2	0	54.9	29.9	95.00%	A.DAGSSATYPMQCSALR.K	Carbamidomethyl (+57)	- .MSDEEHTFETADAGSSATYPMQCSALR.K
97	105	2	1026.46	6.9	0	38.2	30.6	95.00%	D.DGFLSLMNM.D		R.NEYQLLDIDDGFLSLMNMDGDTK.D
72	86	2	1651.83	5.3	1	74.4	27.5	95.00%	E.DLSPSTHNMEVPVVK.R		K.LEDLSPSTHNMEVPVVK.R
12	28	2	1841.85	4.6	1	89.7	30.2	95.00%	A.DAGSSATYPMQCSALRK.N	Carbamidomethyl (+57)	- .MSDEEHTFETADAGSSATYPMQCSALRK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
102	A6ZRM3_YEAS7	31.60%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
278	286	2	975.49	4.3	0	31.1	30.6	95.00%	H.DASMGLNLR.R		K.VFYGHDASMGLNLR.R
293	306	2	1593.79	3.8	1	44.8	28.6	95.00%	L.DTACIKNNLLSSMK.V	Carbamidomethyl (+57)	K.GLDTACIKNNLLSSMK.V
205	217	2	1283.64	5.9	0	27.4	29.3	94.50%	G.DILFGAHAGMVPG.D		K.LSQLAEHCSMAIELDLDITGDILFGAHAGMVPGDFMKPNQIPGVSSLSNMK.Y
218	235	3	1992	7.3	0	24.6	27.3	95.00%	G.DFMKPNQIPGVSSLSNMK.Y		K.LSQLAEHCSMAIELDLDITGDILFGAHAGMVPGDFMKPNQIPGVSSLSNMK.Y
37	51	2	1564.95	6.1	0	34.2	11.8	95.00%	R.LSPPVSLLPTISTLK.K		R.LSPPVSLLPTISTLK.K
149	164	2	1838.93	7.8	1	53.5	27.9	95.00%	K.LMTPLTFSTETNFIPQ.D		K.LMTPLTFSTETNFIPQDISK.I
109	121	2	1541.86	2.1	1	22.8	22.5	94.00%	K.VVSYILNHKDQVK.C		K.VVSYILNHKDQVK.C
273	286	2	1578.76	1.4	1	58	29.9	95.00%	K.VFYGHDASMGLNLR.R		K.VFYGHDASMGLNLR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
103	A6ZQU5_YEAS7	11.16%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
77	85	2	1045.59	5.4	0	43.1	27.1	95.00%	F.DNIIVFPTK.G		R.LFDNIIVFPTK.G
75	85	2	1305.73	-0.18	1	40.6	23.8	95.00%	R.LFDNIIVFPTK.G		R.LFDNIIVFPTK.G
348	357	2	1191.61	7.9	1	39.2	29	95.00%	P.DRHGVFTFLT.D		R.LTLSPSGNDSETQYYTTGEFILPDRHGVFTFLTDYR.K
186	196	2	1248.72	1.2	0	24.5	20.1	95.00%	R.EQIVPILNAPR.T		R.EQIVPILNAPR.T
183	196	3	1647.92	5.6	1	29.2	20.6	95.00%	L.ENREQIVPILNAPR.T		K.SEDFVFGESSAALLENREQIVPILNAPR.T
124	136	2	1489.83	5.6	1	55.1	23.6	95.00%	R.LFLNELGIYPSPK.G		R.LFLNELGIYPSPK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
104	A6ZM72_YEAS7	9.61%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
296	309	2	1492.74	2.8	1	78.6	29.5	95.00%	R.LAGNASWGELFSNK.G		R.LAGNASWGELFSNK.G
9	26	2	1924.98	-0.57	1	68.3	25.7	95.00%	R.VESGSQQTSIHSTPIVQK.L		R.VESGSQQTSIHSTPIVQK.L
219	227	2	1153.52	2.9	0	49.9	31	95.00%	K.DYSNSVQWR.V		K.DYSNSVQWR.V
517	527	2	1364.69	6.1	1	32.2	29.1	95.00%	N.EMYVEGVKPWK.S		K.GLTLEEVNEMYVEGVKPWK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
105	GLRX7_YEAST	12.32%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
94	105	2	1424.72	8	1	49.1	27.6	95.00%	K.IMEQSPMIVFSK.T	Oxidation (+16)	K.IMEQSPMIVFSK.T
154	165	2	1212.69	3	0	58.7	24.1	95.00%	R.TVPNVIIGGTSR.G		R.TVPNVIIGGTSR.G
153	165	2	1368.79	2.8	1	33.5	20.6	95.00%	R.RTVPNVIIGGTSR.G		R.RTVPNVIIGGTSR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
106	YOL19_YEAST	21.23%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
425	451	3	2898.49	1.5	0	37.7	22.7	95.00%	R.ETAAGPANIRPYAGQPHPAPLVYPQQR.L		R.ETAAGPANIRPYAGQPHPAPLVYPQQR.L

472	501	3	3257.64	6.2	1	72.7	22.5	95.00%	R.TTPAGPDPSNVILQSNPYFNVAPNQVPQHR.N		R.TTPAGPDPSNVILQSNPYFNVAPNQVPQHR.N
502	529	3	2950.55	5.8	0	40.6	22.2	95.00%	R.NPVPGVGFAPNPLPNQSPITQGYKPAYK.R		R.NPVPGVGFAPNPLPNQSPITQGYKPAYK.R
540	551	2	1339.66	2.7	0	44.1	29.8	95.00%	R.ATTSLNNPYGFR.-		R.ATTSLNNPYGFR.-
452	471	2	2615.27	4	0	44.1	26.3	95.00%	R.LQPQQQQPQQQYHQYNLYQR.T		R.LQPQQQQPQQQYHQYNLYQR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
107	A6ZP92_YEAS7	11.01%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
511	521	2	1310.58	2	0	40.8	30	95.00%	R.GSWCCLVSSQK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GSWCCLVSSQK.D
199	212	2	1434.73	4.2	0	59.3	28.4	95.00%	P.DGPQSTSHGIALPR.F		K.YGHPDGPQSTSHGIALPR.F
494	508	2	1737.91	-0.54	0	25.2	25.8	95.00%	K.QPLVPYSFAPFFPTK.R		K.QPLVPYSFAPFFPTK.R
195	212	3	1888.93	4.3	1	35.8	27.9	95.00%	K.YGHPDGPQSTSHGIALPR.F		K.YGHPDGPQSTSHGIALPR.F
434	454	2	2291.18	5.5	1	46.6	24.7	95.00%	A.DFLVPGENQVTPSSTPYISLK.V		K.ADFLVPGENQVTPSSTPYISLK.V
565	572	2	960.5	6	1	25.6	29.7	90.80%	N.DWEIGTIK.I		K.FDINDWEIGTIK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
108	A6ZPF0_YEAS7	7.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
399	411	3	1531.82	5.4	1	20.3	25.8	95.00%	G.DHLQNDPLSLRPK.T		R.AGDSQGDHLQNDPLSLRPK.T
213	234	4	2338.06	6	1	64.8	29.6	95.00%	K.TPSYSTSSHTIASGGNYTEHNK.R		K.TPSYSTSSHTIASGGNYTEHNK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
109	A6ZNY0_YEAS7	3.80%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
712	723	2	1265.67	-0.42	1	36.8	27.2	95.00%	R.ATYAGFLLADPK.I		R.ATYAGFLLADPK.I
33	42	2	1118.6	3.2	1	46.5	27.3	95.00%	K.STLTDSLVQR.A		K.STLTDSLVQR.A
244	253	2	1209.58	1.7	1	38.1	30.6	95.00%	R.LWGDSFFNPK.T		R.LWGDSFFNPK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
110	A7A1W6_YEAS7	17.39%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
322	335	2	1715.84	1.1	1	69.3	28.7	95.00%	R.NITWIAECIAQNQR.E	Carbamidomethyl (+57)	R.NITWIAECIAQNQR.E
19	36	2	2128.01	5.9	1	117	28.8	95.00%	R.GYRNGLLSNNQYINLTQC.D	Deamidation (+1)/ Carbamidomethyl (+57)	R.GYRNGLLSNNQYINLTQCDTLEDLK.L
239	247	2	955.54	1.7	1	33.9	25.3	95.00%	K.SDLLPNIGK.L		K.SDLLPNIGK.L
267	276	2	1168.59	-0.44	1	58.1	29	95.00%	R.AALANVYEYR.G		R.AALANVYEYR.G
76	84	3	1253.62	3	1	27.8	28.6	95.00%	K.LYHEFNYIR.D		K.LYHEFNYIR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
111	B3LI54_YEAS1	12.90%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
222	240	2	1991.99	6.7	0	61.3	27.5	95.00%	P.DHVPTVGSSFVGMSLFNAK.N		K.ELHPDHVPTVGSSFVGMSLFNAK.N
218	240	3	2468.22	2.1	1	42	26.2	95.00%	K.ELHPDHVPTVGSSFVGMSLFNAK.N		K.ELHPDHVPTVGSSFVGMSLFNAK.N
314	323	2	1118.56	3.6	0	30.7	28.9	95.00%	R.AMPNSYLPAR.Q		R.AMPNSYLPAR.Q
341	360	3	2056.16	3.4	1	17.7	19.3	93.80%	R.HPLTGGGMTVGLHDVVLLIK.K		R.HPLTGGGMTVGLHDVVLLIK.K
159	169	2	1241.64	-0.66	1	40.2	28	95.00%	R.NITAQEPNVTR.V		R.NITAQEPNVTR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
112	A6ZSR4_YEAS7	23.53%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	48	2	1489.79	4.8	1	61.6	26.2	95.00%	K.SHPFGHALVAGIER.Y		K.SHPFGHALVAGIER.Y

74	84	2	1324.73	2.6	0	36	23.5	95.00%	K.VVNYNHLLPTR.Y		K.VVNYNHLLPTR.Y
127	133	2	955.46	0.078	0	28.4	29	95.00%	K.NQWFFSK.L		K.NQWFFSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
113	ECM33_YEAS7	12.12%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
162	172	2	1330.71	1.9	1	63.7	26.1	95.00%	K.KVNVFNINNNR.Y		K.KVNVFNINNNR.Y
163	172	2	1202.62	3.8	0	54.4	28.5	95.00%	K.VNVFNINNNR.Y		K.VNVFNINNNR.Y
337	351	2	1622.78	2.4	1	74.4	29.2	95.00%	K.LQSNGAIQGDSFVCK.N	Carbamidomethyl (+57)	K.LQSNGAIQGDSFVCK.N
173	185	2	1459.69	6.6	1	59.1	30.2	95.00%	R.YLNSFQSSLESVS.D		R.YLNSFQSSLESVSDSLQFSSNGDNTTLAFDNLVWANNITLR.D
62	74	2	1286.68	6.4	1	34.7	27.6	95.00%	G.DLGSAALASIQEI.D		K.ISGCSTIVGNLTITGDLGSAALASIQEIDGSLTIFNSSSLSSFSADSIK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
114	A6ZMQ9_YEAS7	13.36%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
21	34	2	1453.75	-0.63	1	42.6	27.3	95.00%	K.ASLAEAPSQPLSQR.N		K.ASLAEAPSQPLSQR.N
115	129	2	1790.99	5.7	1	35.7	22	95.00%	D.DQRQQLLSNHAILQK.S		R.LFGDLNASNIDDDQRQQLLSNHAILQK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
115	A7A0Y7_YEAS7	12.74%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
67	79	2	1808.77	3	1	84.3	30.4	95.00%	K.ENFLYSYDYYYNR.F		K.ENFLYSYDYYYNR.F
141	156	2	1817.92	-0.46	1	63.4	27.1	95.00%	K.NGFFQNWLIDGLPAAR.E		K.NGFFQNWLIDGLPAAR.E
212	222	2	1400.65	6.7	1	34.6	30.7	95.00%	K.TYELPYFANHF.D		K.TYELPYFANHFDIMIEYHDR.G
238	249	2	1237.77	1.3	1	41.5	17.3	95.00%	R.VVGVIVEPVSIK.R		R.VVGVIVEPVSIK.R
104	117	2	1723.86	-1.3	1	64.7	28.4	95.00%	R.IYNSPFQLNMLQEK.E		R.IYNSPFQLNMLQEK.E
37	55	3	2233.14	5.6	0	24.7	25.2	95.00%	N.DNIPLLVNHLTPSMNYQHK.D		R.ENDNIPLLVNHLTPSMNYQHK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
116	AXL2_YEAST	8.63%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
716	729	2	1595.81	5.2	1	63.4	27.9	95.00%	L.DPWNSNISPSPVRK.S		R.DVTMSSLDPWNSNISPSPVRK.S
730	740	2	1191.61	0.75	0	33.2	28.3	95.00%	K.SVTPSPYNVTK.H		K.SVTPSPYNVTK.H
668	680	2	1419.74	2.2	1	42.4	27.5	95.00%	R.YTGNLSPVSDIVR.D		R.YTGNLSPVSDIVR.D
751	769	2	1885.83	6.5	1	78.3	30.4	95.00%	Q.DSQSGKNGITPTTMSTSSS.D	Deamidation (+1)	R.HLQNIQDSQSGKNGITPTTMSTSSSDDFVPVK.D
184	197	2	1708.87	7.6	0	41	27.5	95.00%	R.SQLYNAPLPNWLFF.D		R.SQLYNAPLPNWLFFDSGELK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
117	A6ZM36_YEAS7	39.73%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	16	2	1781.94	-1.3	1	65.7	25.4	95.00%	M.SLVVQEQGSFQHILR.L	Acetyl (+42)	-.MSLVVQEQGSFQHILR.L
81	88	2	1015.56	1.8	0	49	28.8	95.00%	K.IPAWFLNR.Q		K.IPAWFLNR.Q
69	80	3	1470.77	3.6	0	33.8	26.8	95.00%	R.IVQIMQNPTHYK.I		R.IVQIMQNPTHYK.I
97	108	2	1389.66	4.4	1	50.2	29.8	95.00%	K.DYHTLANNVESK.L		K.DYHTLANNVESK.L
17	27	2	1199.65	1.2	1	25.2	26	95.00%	R.LLNTNVDGNIK.I		R.LLNTNVDGNIK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
118	A6ZQF7_YEAS7	22.83%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
112	124	2	1495.82	5.3	0	66.8	22.8	95.00%	K.LYVSHIQVNQAPK.Q		K.LYVSHIQVNQAPK.Q
31	43	2	1459.73	2.7	1	53.3	28.3	95.00%	R.ETAQAINGWELTK.A		R.ETAQAINGWELTK.A
90	105	2	1643.87	5.5	1	88.8	24.2	95.00%	K.FVQGLLQNAAANAEAK.G		K.FVQGLLQNAAANAEAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
119	A7A0U9_YEAS7	15.99%	100%	8

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
202	209	2	871.54	6.4	0	42.7	23.8	95.00%	I.DTILALVK.D		K.EVIDTILALVK.D
155	172	2	2004.12	6.4	0	25.3	19.1	95.00%	R.TTYVTQRPVYLGLPANLV.D		R.TTYVTQRPVYLGLPANLVDLNVPAK.L
494	505	2	1297.71	6.1	0	28.1	25.6	95.00%	W.DHLSLLPTFGAK.D		K.AQYNEIQGWDHLSLLPTFGAK.D
155	179	3	2741.52	2.7	1	33.8	17.3	95.00%	R.TTYVTQRPVYLGLPANLVDLNVPAK.L		R.TTYVTQRPVYLGLPANLVDLNVPAK.L
234	249	2	1776.95	-0.97	1	52.8	24.1	95.00%	K.LIDLTQFPAFVTPMGK.G		K.LIDLTQFPAFVTPMGK.G
259	273	2	1595.86	4.8	1	51.7	23.9	95.00%	R.YGGVYVGTLSKPEVK.E		R.YGGVYVGTLSKPEVK.E
199	209	2	1212.73	-0.097	1	38	19.2	95.00%	K.EVIDTILALVK.D		K.EVIDTILALVK.D
544	554	2	1211.62	4.9	1	43.7	28.3	95.00%	F.DAPQNLVEQAK.L		R.MIEIMLPVFDAPQNLVEQAK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
120	YD237_YEAST	9.49%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
351	367	2	1910.02	6.4	1	48.7	23.3	95.00%	R.IWGAPTWPANLVETISR.Q		R.IWGAPTWPANLVETISR.Q
286	295	2	1081.61	5.4	1	25.4	22.9	95.00%	L.DAPLLSLEPK.Y		R.FAFLDAPLLSLEPK.Y
171	180	2	1130.67	6.8	1	31.1	20.6	95.00%	K.LYTGPLLEIL.D		K.LYTGPLLEILDEVNCQDSDADR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
121	A6ZQK0_YEAS7	5.42%	100%	9

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2000	2011	2	1398.67	2.4	1	29.2	30.6	95.00%	R.TLACYSDAIVMR.H	Carbamidomethyl (+57)	R.TLACYSDAIVMR.H
1599	1610	3	1398.87	5.9	1	17	6.99	92.30%	K.VTALFLPLRELK.N		K.VTALFLPLRELK.N
599	615	2	1638.81	3	1	43	28.8	95.00%	R.AAYALGGLGSGFANNEK.E		R.AAYALGGLGSGFANNEK.E
1551	1564	2	1385.78	3.1	1	23.2	22.4	94.60%	R.SISGPVITDVASLK.A		R.SISGPVITDVASLK.A
1978	1989	2	1267.75	3.1	0	34	19.3	95.00%	R.IVNVNPLVSSVK.K		R.IVNVNPLVSSVK.K
855	864	2	1050.59	3.9	0	25.3	24.8	95.00%	R.VFAIANAFAK.K		R.VFAIANAFAK.K
1635	1650	2	1713.96	-1.3	1	31.6	20.6	95.00%	K.TADLASVLLLTSLQNR.S		K.TADLASVLLLTSLQNR.S
189	198	2	1112.59	5.4	0	28.6	26.8	95.00%	V.DPNVQNLVSK.V		R.SAFDVPEWVDPNVQNLVSK.V
619	635	2	1891.95	6.2	1	44.5	27.5	95.00%	V.DLCNVAFSSSPQVLVEK.S	Carbamidomethyl (+57)	K.ELVDLCNVAFSSSPQVLVEK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
122	A6ZQA2_YEAS7	14.18%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
222	240	2	2115.17	-0.76	1	78	17.7	95.00%	R.LNNVFVIGEQGKPYISLPK.G		R.LNNVFVIGEQGKPYISLPK.G
180	187	2	863.49	0.1	0	31.3	25.4	95.00%	K.LVYVTGGR.N		K.LVYVTGGR.N
212	221	2	1166.56	3.4	1	31.9	30.1	95.00%	K.DSLDNTFVTR.L		K.DSLDNTFVTR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
123	A6ZLM5_YEAS7	9.60%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
44	61	2	2092.17	3.3	1	65.6	18.3	95.00%	K.IISLLNVDLFTPCLIFSK.L	Carbamidomethyl (+57)	K.IISLLNVDLFTPCLIFSK.L
225	238	2	1458.67	3.7	1	99.4	30.2	95.00%	R.MNSSFLSSSSIGDK.I		R.MNSSFLSSSSIGDK.I
327	335	2	940.61	0.94	0	47.1	18.8	95.00%	K.LLIGSIIGR.M		K.LLIGSIIGR.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
124	HSP72_YEAST	13.15%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
111	124	2	1549.78	-0.72	1	48.9	28.2	95.00%	K.NFTPEQISSMVLGK.M		K.NFTPEQISSMVLGK.M
170	183	2	1415.77	6.1	1	56.6	25.8	95.00%	R.IINEPTAAAIAYGL.D		R.IINEPTAAAIAYGLDK.K
158	169	2	1198.67	-0.1	0	53.6	26.1	95.00%	K.DAGTIAGLNVLR.I		K.DAGTIAGLNVLR.I
537	547	2	1264.67	2.1	1	31.7	27.5	95.00%	K.NQLESIAYSLK.N		K.NQLESIAYSLK.N

392	409	2	1757.93	5.7	1	28.8	24.4	95.00%	L.DVAPLSLGIETAGGVMTK.L		K.TQDLLLLDVAPLSLGIETAGGVMTK.L
55	69	2	1590.75	0.11	1	56.5	29.9	95.00%	K.NQAAMNPANTVFDAK.R		K.NQAAMNPANTVFDAK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
125	A6ZU59_YEAS7	13.78%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
78	88	2	1299.69	4.8	1	45.8	27.1	95.00%	Q.DEVMNIKPVQK.Q		K.EFQIIDTLLPGLQDEVMNIKPVQK.Q
142	157	2	1728.86	1.2	0	68.1	27.2	95.00%	R.GYWGTNLGQPHSLATK.T		R.GYWGTNLGQPHSLATK.T
187	194	2	841.5	6.4	1	30.8	27	95.00%	K.LLQLAGVE.D		K.LLQLAGVEDVYTQSNGK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
126	YL001_YEAST	12.30%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
302	312	2	1203.64	7	1	51.6	26.9	95.00%	R.IFEIGVVHGFS.D		R.IFEIGVVHGFSDLDFLR.T
523	530	2	930.54	3.5	0	31.4	25.9	95.00%	K.TALNLLMR.N		K.TALNLLMR.N
589	600	2	1398.74	6.3	0	51.7	26.4	95.00%	S.DIFFNQGVIHPI.D		K.ESIIIEESSDIFFNQGVIHPIDQLDFPVDLEISLK.E
801	844	4	4728.39	-1.5	1	29.6	24.1	95.00%	R.ATTPLIQHSPIIHNPSYSATAHLSPLSQPTFEGSYSVNAIQTPR.D		R.ATTPLIQHSPIIHNPSYSATAHLSPLSQPTFEGSYSVNAIQTPR.D
390	405	2	1897.97	6.2	0	33.5	26.2	95.00%	Q.DFSSLRPIQYAPTQIY.D		K.IDLEQDFSSLRPIQYAPTQIYDSAFCSSAK.R
370	384	3	1737.92	5.1	1	18.2	25.7	93.40%	R.GYTKPSLLYHFVEGK.I		R.GYTKPSLLYHFVEGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
127	A6ZZH5_YEAS7	15.46%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
230	242	2	1526.77	3.1	1	45.7	27.8	95.00%	K.HNVDAPIPNFFTR.N		K.HNVDAPIPNFFTR.N
68	83	3	1683.94	6.8	1	22.1	21.2	95.00%	K.KPPLLVNNEAVHASVP.D		K.KPPLLVNNEAVHASVPDASHTSCNNGTLEVSINNPEPHVVDAVAR.H
139	169	3	3360.58	4.9	0	61.1	26.7	95.00%	N.DHPSSPSQYQYPSQPALSTSIPSQAPSFSNR.K		K.WTNDHPSSPSQYQYPSQPALSTSIPSQAPSFSNR.K
233	242	2	1176.6	6.2	0	31.7	28.5	95.00%	V.DAPIPNFFTR.N		K.HNVDAPIPNFFTR.N
117	131	2	1598.81	2.6	1	88.2	27.9	95.00%	R.NPSNSLQLQGGDITR.D		R.NPSNSLQLQGGDITR.D
21	38	2	1670.76	4.6	0	66.2	30.4	95.00%	K.NNNGGSTGISHASGSPLT.D	Deamidation (+1)	K.NNNGGSTGISHASGSPLTDGNGGNSNGNSR.S
583	596	2	1562.77	-0.081	1	47.3	29	95.00%	R.ILENWTFPSNASGK.Y		R.ILENWTFPSNASGK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
128	A7A244_YEAS7	11.40%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
131	143	2	1407.68	6.9	0	40.4	29.8	95.00%	V.DIPASAILFNCST.D	Carbamidomethyl (+57)	R.YFYHLSGVDIPASAILFNCSTDK.L
401	416	2	1729.82	6.4	0	25.4	29.5	90.90%	R.ASCAFYPHGLGHMLGL.D	Carbamidomethyl (+57)	R.ASCAFYPHGLGHMLGLDVHDVGGNPNYDDPDPMFR.Y
282	302	3	2354.05	1	1	24.3	29.6	95.00%	R.SLGYDPICCSGPACGTLHYVK.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.SLGYDPICCSGPACGTLHYVK.N
286	302	2	1933.86	4.5	0	75	30.3	95.00%	Y.DPICCSGPACGTLHYVK.N	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.SLGYDPICCSGPACGTLHYVK.N
157	167	2	1216.62	6.2	0	26.8	29	94.20%	E.DVIWSGMPLSL.D		K.LTLFLPNIDEEDVIWSGMPLSLDEAMR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
129	A6ZY13_YEAS7	5.63%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

21	41	2	2286.11	5.2	1	105	27.7	95.00%	T.DSALYNNFNTSTTASLTPEIK.E		K.SAEFEVTDSALYNNFNTSTTASLTPEIK.E
400	412	2	1465.71	2.5	0	67.5	29.5	95.00%	R.LMCSLAQQGYAPK.F	Carbamidomethyl (+57)	R.LMCSLAQQGYAPK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
130	A6ZU19_YEAS7	5.47%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
507	516	2	1215.64	2.9	1	24.7	28	92.20%	R.ILEYSTSYLK.S		R.ILEYSTSYLK.S
23	36	2	1385.71	5.7	1	35.7	27.4	95.00%	L.DATAEALSKPSPSL.E		R.EILDATAEALSKPSPSLEYCTLSVDETLEK.L
27	43	2	1879.94	6.4	1	36.4	27.9	95.00%	A.EALSKPSPSLEYCTLSV.D	Carbamidomethyl (+57)	R.EILDATAEALSKPSPSLEYCTLSVDETLEK.L
690	699	2	1033.53	2.8	1	76.1	29.1	95.00%	K.LSDIGVSMGR.I		K.LSDIGVSMGR.I
235	245	2	1241.62	3.2	0	43.1	29.4	95.00%	R.SCIAYMGTLVK.E	Carbamidomethyl (+57)	R.SCIAYMGTLVK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
131	HSP76_YEAST	9.79%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
437	451	2	1780.85	5.8	1	41.6	28.4	95.00%	S.DNQTTVQFPVYQGER.V		R.TFTTVSDNQTTVQFPVYQGER.V
174	191	2	1728.95	2.3	1	84	23.4	95.00%	R.IINEPTAAAIAYGLGAGK.S		R.IINEPTAAAIAYGLGAGK.S
115	128	2	1550.8	-0.33	1	36.9	27.5	95.00%	K.TFSPQEISAMVLTK.M		K.TFSPQEISAMVLTK.M
39	51	2	1478.75	4.9	1	50.7	28.5	95.00%	R.VTPSFVAFTPQER.L	Deamidation (+1)	R.VTPSFVAFTPQER.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
132	A6ZXW5_YEAS7	17.67%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
12	32	3	2371.23	-0.5	1	54.1	23.7	95.00%	R.HALLHNDIQTSNNSRPSLVQK.K		R.HALLHNDIQTSNNSRPSLVQK.K
18	32	2	1685.88	5.2	0	62.3	25.4	95.00%	N.DIQTSNNSRPSLVQK.K		R.HALLHNDIQTSNNSRPSLVQK.K
260	268	2	1153.62	3.6	1	25.6	26	95.00%	R.IYNDFITLR.D		R.IYNDFITLR.D
97	106	2	1235.59	-0.083	1	43.9	29.8	95.00%	K.NQEVYSQVNR.I		K.NQEVYSQVNR.I
326	334	2	1046.61	-0.12	1	57.6	21	95.00%	K.SIGELFILR.I		K.SIGELFILR.I
130	142	2	1482.61	-0.52	0	81.8	30.9	95.00%	R.STAYCTASSYNMK.E	Carbamidomethyl (+57)	R.STAYCTASSYNMK.E
46	59	2	1442.67	-1.3	0	53.1	30.5	95.00%	R.ASYTGSAMINPTSK.Q	Oxidation (+16)	R.ASYTGSAMINPTSK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
133	YIL7_YEAST	11.01%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	205	2	1566.83	-0.97	1	44.7	24.9	95.00%	R.NSLFISPTGDILYK.T		R.NSLFISPTGDILYK.T
218	227	2	1128.66	6.2	0	32.5	22	95.00%	R.LLQKPVIMTS.D		R.LLQKPVIMTSDNVSTNSLVSTISSSSASSLDNGNEK.E
117	127	2	1361.58	5.9	0	40.7	31	95.00%	K.MFSTQHTQFYG.D	Oxidation (+16)	K.MFSTQHTQFYGDSPYMDYPAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
134	AVT7_YEAST	7.96%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
321	332	2	1332.68	5.4	1	43.4	28.1	95.00%	R.ASNLRPISMTVE.D	Oxidation (+16)	R.ASNLRPISMTVEDPAQPSDALDATSYNEQECLLPNGNFDNGSIESQENNNDER.G
441	451	2	1098.67	3.2	1	55.7	20.4	95.00%	K.LIGLDSLAIGK.M		K.LIGLDSLAIGK.M
1	16	2	1650.81	-1.1	1	80.9	28.6	95.00%	-.MEATSSALSSTANLVK.T	Acetyl (+42)	-.MEATSSALSSTANLVK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
135	CHS3_YEAST	6.70%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
892	911	2	2314.02	-0.28	1	80.2	28.9	95.00%	K.AFESVFGSVTCLPGCFSMYR.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.AFESVFGSVTCLPGCFSMYR.I

71	85	2	1526.78	5.4	0	48	27.4	95.00%	L.DVLPSSTGVNPNATR.R		K.TQEQMNHLDVLPSSTGVNPNATR.R
720	735	2	1698.86	5.2	1	47.2	27.2	95.00%	P.DEVKPYSYVAVASGSK.R		K.TTPEIALGMMDDFVTPPDEVKPYSYVAVASGSK.R
855	866	2	1332.65	5.2	1	48.4	29.1	95.00%	K.DPLIMGLCGETK.I	Carbamidomethyl (+57)	K.DPLIMGLCGETK.I
598	612	2	1721.84	-1.1	0	29.3	27.8	95.00%	R.NPSTLLPTSSMFWNK.A		R.NPSTLLPTSSMFWNK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
136	A6ZS21_YEAS7	14.97%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
271	292	2	2214.17	4.1	1	126	23.4	95.00%	K.RNQSSLGLIPVASATSNTSSPK.K		K.RNQSSLGLIPVASATSNTSSPK.K
177	186	2	1058.51	6.5	0	41.6	30.3	95.00%	E.DAASPFNPIQ.D		K.SYMQDDWDSMSQLESSQYEDAASPFNPIQDPFTDNR.R
195	209	2	1738.92	5.5	1	64.5	24.9	95.00%	R.SLFISPTLQVSQYEK.S		R.SLFISPTLQVSQYEK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
137	A6ZX57_YEAS7	25.09%	100%	7

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
25	35	2	1180.57	2.8	1	40.1	30.4	95.00%	R.LFAGMSPEMAK.K		R.LFAGMSPEMAK.K
97	107	2	1259.66	5.1	1	23.4	27.2	91.30%	A.DLQHPPETVPK.L		K.GQYLVCMDADLQHPPETVPK.L
146	155	2	1089.57	5.6	0	45.1	28.2	95.00%	R.MMARPLTIAS.D		R.MMARPLTIASDPMSGFFGLQK.K
55	65	2	1242.62	5.5	0	33	28.7	95.00%	V.DALAHQGYNVR.I		K.TELIFVDDNSQDGSVEEVDALAHQGYNVR.I
200	212	2	1390.77	6.2	1	52.8	23.5	95.00%	R.VAIGEVPFTFGVR.T		R.VAIGEVPFTFGVR.T
156	166	2	1225.59	5.6	0	60.7	30.4	95.00%	S.DPMSGFFGLQK.K		R.MMARPLTIASDPMSGFFGLQK.K
146	166	3	2297.14	2.7	1	48	27.1	95.00%	R.MMARPLTIASDPMSGFFGLQK.K		R.MMARPLTIASDPMSGFFGLQK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
138	NCB5R_YEAST	21.13%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
220	230	2	1195.59	5.1	0	46.9	29.7	95.00%	E.DWTGGVGYITK.D		R.EDWTGGVGYITK.D
195	208	2	1589.86	5	1	38.7	25.5	95.00%	K.ELEALVAMKPSQFK.I		K.ELEALVAMKPSQFK.I
147	166	2	2075.04	2.2	0	28.9	26.2	95.00%	R.SHLGMIAGGTGIAPMYQIMK.A		R.SHLGMIAGGTGIAPMYQIMK.A
66	80	2	1615.94	5.9	1	33.2	17.9	95.00%	A.DDVLGLPIGQHIVIK.A		K.FGLPHADDVLGLPIGQHIVIK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
139	A7A0C4_YEAS7	15.90%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
351	366	2	1755.87	-2	1	38.8	27.7	95.00%	R.GGIPGMFVFFEMSPLK.V		R.GGIPGMFVFFEMSPLK.V
245	268	4	2732.42	2.2	0	21	22.7	95.00%	K.TSNLNFNHIINHLSFGKPIQSHSK.L		K.TSNLNFNHIINHLSFGKPIQSHSK.L
136	147	2	1400.56	5.5	0	47.2	30.2	95.00%	N.DPNYCGPCYGAK.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.LNSEGRPVGDATELHVGGNGDGTAPVNNDPNYCGPCYGAK.D
294	307	4	1796.85	5	1	25.8	29.8	95.00%	P.DRNTHFHQFSYFAK.I		R.QVFPDRNTHFHQFSYFAK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
140	GLRX6_YEAST	19.05%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
43	57	2	1544.64	2.4	1	82.2	30	95.00%	K.AFSTNMDNMAGGSSR.E		K.AFSTNMDNMAGGSSR.E
118	133	2	1850.04	-1.2	1	73.8	19	95.00%	K.EYSLILDLSPIIIFSK.S		K.EYSLILDLSPIIIFSK.S
181	193	2	1324.75	3.7	0	70.1	22.9	95.00%	R.GTVPNLLVNGVSR.G		R.GTVPNLLVNGVSR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
141	A6ZYN3_YEAS7	10.03%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

251	260	2	1171.6	7	1	30.1	27.2	95.00%	I.DDPLPFKPLM.D		R.IFPPIDDPLPFKPLMDDSDVTLEEAVTHQR.I
158	163	2	719.4	3.4	1	20.7	24.4	90.20%	R.LLDGFR.T		R.LLDGFR.T
252	260	2	1056.57	6.4	0	26.4	26.7	95.00%	D.DPLPFKPLM.D		R.IFPPIDDPLPFKPLMDDSDVTLEEAVTHQR.I
49	61	2	1502.74	5.3	1	44.9	28.5	95.00%	N.DLTISHPYATTER.V		R.QFYINDLTISHPYATTER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
142	ATG27_YEAS7	8.12%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	130	2	1223.56	3.3	1	68.7	30.4	95.00%	K.GATWGANSFDAK.L		K.GATWGANSFDAK.L
89	98	2	1135.59	9	1	31	29.1	95.00%	K.DAITTQIIDF.D		K.DAITTQIIDFDK.N
89	96	2	873.49	7	0	27.1	29.8	93.30%	K.DAITTQII.D		K.DAITTQIIDFDK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
143	A6ZL12_YEAS7	4.60%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
24	38	2	1575.68	-0.074	1	102	30.1	95.00%	R.SFSAGNNFQSSSSEK.T		R.SFSAGNNFQSSSSEK.T
405	417	2	1447.75	-1	0	51.1	28.3	95.00%	R.LICSLAQQGYAPK.F	Carbamidomethyl (+57)	R.LICSLAQQGYAPK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
144	RL14A_YEAST	24.64%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	74	2	2050.2	2.6	0	103	15.3	95.00%	R.QAINLGQVVLTPLTFALPR.G		R.QAINLGQVVLTPLTFALPR.G
94	101	2	905.44	4.2	0	32.2	29.6	95.00%	K.WAASSWAK.K		K.WAASSWAK.K
118	124	2	891.5	3.6	0	24.4	26	94.80%	R.FQVMVLR.K		R.FQVMVLR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
145	A7A233_YEAS7	15.81%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
189	211	3	2175.09	5.1	1	21	26.6	95.00%	K.LVGVGNGKEGNISINSGSGNSSK.S	Deamidation (+1)	K.LVGVGNGKEGNISINSGSGNSSK.S
124	134	2	1198.66	5.4	1	68.9	26.1	95.00%	N.DEAQLLLVGNK.S		K.TVNEHANDEAQLLLVGNK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
146	EMP47_YEAST	10.34%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
221	227	2	812.38	-0.52	0	26.1	29.8	91.60%	R.FPSGSYR.I		R.FPSGSYR.I
146	156	2	1153.58	5.6	0	38.4	29.3	95.00%	V.DNNGPLGPTLR.G	Deamidation (+1)	K.QLYNGPVNYDGLQLLVDNNGPLGPTLR.G
333	346	2	1637.87	-0.25	1	94.7	25.1	95.00%	K.VQQELLSFMTTITK.Q		K.VQQELLSFMTTITK.Q
228	241	2	1342.66	5.9	0	51.8	29.5	95.00%	R.IGVTAQNGAVNNNA.E	Deamidation (+1)	R.IGVTAQNGAVNNNAESFEIFK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
147	A6ZWS9_YEAS7	5.65%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
449	457	2	1070.51	6.2	1	38.3	29.9	95.00%	A.DIMELLNHS.D		K.ADIMELLNHSDSR.V
311	328	2	1951.11	-0.93	1	75.7	17.3	95.00%	K.QLLLLGNALPTVQSLSER.K		K.QLLLLGNALPTVQSLSER.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
148	FET4_YEAST	7.25%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
445	454	2	1132.59	2.7	1	35.9	27.7	95.00%	K.APEINTIGYR.T		K.APEINTIGYR.T
248	265	2	1833.81	-0.4	1	77.2	30.2	95.00%	K.DAGNTPPYTGETTGSNPR.L		K.DAGNTPPYTGETTGSNPR.L
4	15	2	1240.66	5.7	1	64.7	26.3	95.00%	K.IAEFLGNPGARP.D		K.IAEFLGNPGARPDVHHR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
149	B3LQX5_YEAS1	12.09%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
244	261	2	2061.05	-1.8	0	38.8	25.7	95.00%	K.SNSIFSIGLTTVPYPYFR.V		K.SNSIFSIGLTTVPYPYFR.V
268	277	2	1117.53	0.083	1	41.5	29.1	95.00%	K.YSIAYESTGK.L		K.YSIAYESTGK.L
470	486	2	1936.01	4.8	1	62.6	24.3	95.00%	R.ITAQTSKPLWSVGTYER.I		R.ITAQTSKPLWSVGTYER.I
146	156	2	1323.61	3	0	27.9	30.5	93.40%	K.EFQMMSPPMVK.D		K.EFQMMSPPMVK.D
172	185	2	1621.86	6	1	32.2	26.4	95.00%	K.DRGIQSYFLLPSIN.D		K.DRGIQSYFLLPSINDNIDEYGNFLPSFIVQDK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
150	A6ZLA4_YEAS7	9.67%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
302	319	2	1988.86	4.8	1	34.5	29.9	95.00%	G.DCGYYREGIPAYHGFGGA.D	Carbamidomethyl (+57)	K.SGNEFMIFSGEECSGNNGDCGYYREGIPAYHGFGGADK.I
308	321	3	1417.67	3.5	1	24.2	29.7	95.00%	R.EGIPAYHGFGGADK.I		R.EGIPAYHGFGGADK.I
341	351	2	1270.68	6.8	0	54.5	26	95.00%	Q.DMPAIWLLNAK.I		K.IFVFEFSMPSDTSGSAYNQDMPAIWLLNAK.I
355	367	2	1574.65	2	1	45.3	30.1	95.00%	R.TLQYGDASCSCWK.T	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.TLQYGDASCSCWK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
151	B3RHC6_YEAS1	2.94%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
228	236	2	996.6	5.7	1	33.8	19.6	95.00%	R.LSGIPIELR.D		R.LSGIPIELR.D
375	388	2	1580.77	5.7	1	47.1	29	95.00%	R.KQHYSATPTAFVTM.D		R.KQHYSATPTAFVTMDSVANAQMAAQAVLDPR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
152	YIP8_YEAST	38.24%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
101	112	3	1314.71	1.7	0	40.9	26.3	95.00%	R.QLNASMGTLRPK.K		R.QLNASMGTLRPK.K
137	150	2	1675.8	6.1	0	72.7	30	95.00%	R.DPSYSFMYPLTLSR.K		R.DPSYSFMYPLTLSR.K
196	204	2	1112.57	3.1	1	39.7	27.6	95.00%	R.EFIDSLRPH.-		R.EFIDSLRPH.-
158	174	2	1705.79	5.7	1	39.8	30.7	95.00%	R.SASTSNLSSSTENTALH.E		R.SASTSNLSSSTENTALHEEIK.L
114	129	2	1739.87	1	1	39.6	28	95.00%	K.QSTAYTNVPVIFSGEK.V		K.QSTAYTNVPVIFSGEK.V
186	195	2	1256.62	5.9	1	29.4	28.7	95.00%	N.DFTNYTVNKR.E		K.LDDPYENDFTNYTVNKR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
153	A7A0B5_YEAS7	7.66%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	132	2	1536.78	3.9	1	38.5	28.6	95.00%	I.DVMSTQVIESSITK.Q		R.IDVMSTQVIESSITK.Q
99	117	2	2080.01	-1.4	1	54.2	27.6	95.00%	K.TFDLCSLGQVSLCPLSAGR.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.TFDLCSLGQVSLCPLSAGR.I
736	762	3	2867.4	0.91	1	28	25.4	95.00%	R.TNLAPNNTSTSSLMKPESSLYLGNSNK.S		R.TNLAPNNTSTSSLMKPESSLYLGNSNK.S
101	117	2	1831.9	3.6	0	27.7	28.3	95.00%	F.DLCSLGQVSLCPLSAGR.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.TFDLCSLGQVSLCPLSAGR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
154	A6ZQE5_YEAS7	22.46%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
33	42	2	1088.59	5.9	1	45	27.6	95.00%	T.DLSGKETIAR.V		R.IYASFNDTFVHVTDLSGKETIAR.V
94	104	2	1023.55	-0.12	0	50.9	26.7	95.00%	K.TPGPGGQAALR.A		K.TPGPGGQAALR.A
10	19	2	1091.54	0.62	0	45.2	29.7	95.00%	R.DNSQVFGVAR.I		R.DNSQVFGVAR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
155	A6ZMW0_YEAS7	4.61%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

28	43	2	1773.94	5.2	0	60.8	25.6	95.00%	K.DQPLIRPINSSASTLY.E		K.DQPLIRPINSSASTLYEFALECFTK.G
263	278	2	1684.75	5.1	0	78.9	30.9	95.00%	E.DPACIMYTSGSTGTPK.G	Carbamidomethyl (+57)	K.DEVELHFPKPEDPACIMYTSGSTGTPK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
156	A6ZKQ4_YEAS7	3.91%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
236	245	2	1105.59	2.7	0	51.9	28.2	95.00%	K.AIFGTNLNTR.I		K.AIFGTNLNTR.I
326	334	2	1043.61	1.6	0	22.5	23.8	93.60%	K.TVLAWSVIR.A		K.TVLAWSVIR.A
69	74	2	787.44	3.5	0	26.9	31	90.90%	K.VSWLQR.V		K.VSWLQR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
157	A6ZTE7_YEAS7	8.82%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
669	677	2	1161.6	5.7	0	50.5	29.1	95.00%	N.DNFIITHFR.N		K.EFMATPYTPVIPINDNFIITHFR.N
582	596	3	1722.91	4.9	0	25.1	25.3	95.00%	Y.DPLTGHINKPQFQTK.Q		R.LSNSSDNFSYDPLTGHINKPQFQTK.Q
467	481	2	1588.83	-0.58	1	41.1	26.4	95.00%	R.ETTNLNTLGITLGDK.S		R.ETTNLNTLGITLGDK.S
128	143	2	1719.84	6.3	0	34.1	27.6	95.00%	V.DNAPSTTILPQSSYLN.D		K.FDLHDWFLLEEGVDNAPSTTILPQSSYLNDQVSIK.N
34	45	2	1455.72	5.9	1	34.1	29.3	95.00%	T.DWQLANLGPWEK.V		K.ITCTDLVYVFILLFLNTSCVQAVFSDDAFITDWQLANLGPWEK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
158	A6ZXE1_YEAS7	20.00%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	63	2	1629.86	5.6	1	65.9	25.3	95.00%	K.SIACVLTVINEQQR.E	Carbamidomethyl (+57)	K.SIACVLTVINEQQR.E
13	22	2	1101.61	5.4	1	42.5	27	95.00%	K.SKEQLASQLV.D		K.SKEQLASQLVDLK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
159	A6ZS95_YEAS7	10.89%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
16	28	2	1438.72	5.9	0	37.7	29.1	95.00%	R.VNSLNAPYQALSY.D		R.VNSLNAPYQALSYDEQK.A
73	89	2	1930.99	-0.94	1	32.7	26.3	95.00%	R.GNQIFQSLHSFLANDLK.F		R.GNQIFQSLHSFLANDLK.F
2	15	2	1551.8	7.3	1	74.5	27.3	95.00%	M.SSSIFGPLTGFLER.V	Acetyl (+42)	-.MSSSIFGPLTGFLER.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
160	RSP5_YEAST	6.55%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
138	164	3	2669.25	6.9	0	52.5	28.3	95.00%	K.LPSSSPHSQAPSGHTASSSTNTSSTTR.T		K.LPSSSPHSQAPSGHTASSSTNTSSTTR.T
184	209	3	2561.23	1	1	54.3	27.5	95.00%	R.GTAQAVESTLQSGTTAATNTATTSHR.S		R.GTAQAVESTLQSGTTAATNTATTSHR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
161	A6ZNH7_YEAS7	8.68%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	206	2	1572.83	0.88	1	84.1	26.1	95.00%	R.QIPVGYSAADIVANR.Q		R.QIPVGYSAADIVANR.Q
253	269	2	1987.95	7.1	1	32.4	29.1	95.00%	Q.DYSVPVFLSEFGCNQVK.S	Carbamidomethyl (+57)	K.LYQDYSVPVFLSEFGCNQVK.S
134	143	2	1182.6	5.3	0	39	28.3	95.00%	A.DYLQNVFATI.D		R.YDPACSYNADYLQNVFATIDTFADYDNVLGFFAGNEVINSVNTTNTATYVK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
162	A7A288_YEAS7	4.08%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
198	207	2	1210.61	6	0	28.5	29.2	95.00%	A.DGFNLNQLYK.F		R.ITAYNVADGFNLNQLYK.F
191	207	2	1942.98	-1.3	1	87.6	26.4	95.00%	R.ITAYNVADGFNLNQLYK.F		R.ITAYNVADGFNLNQLYK.F

306	315	2	1103.54	5.9	0	28.2	30.3	94.10%	P.DHLPNPVGQQ.D		R.DHHYEYYSGVETVEDANNNYELETSGNNNNANQDTTTVPDHLPNPVGQQDSFNPMEPQFFAEETPLEIEK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
163	ADH1_YEAST	15.23%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
123	132	2	1086.47	7.2	0	43.1	31.2	95.00%	H.DGSFQQYATA.D		K.WLNGSCMACEYCELGNESNCPHADLSGYTHDGSFQQYATADAVQAAHIPQGTDLAQVAPILCAGITVYK.A
133	144	2	1206.61	6.1	0	62.1	29.1	95.00%	A.DAVQAAHIPQGT.D		K.WLNGSCMACEYCELGNESNCPHADLSGYTHDGSFQQYATADAVQAAHIPQGTDLAQVAPILCAGITVYK.A
288	299	2	1250.67	2.6	0	76.2	26.6	95.00%	K.SISIVGSYVGNR.A		K.SISIVGSYVGNR.A
304	311	2	967.48	-0.15	1	26.8	30	92.50%	R.EALDFFAR.G		R.EALDFFAR.G
277	287	2	1354.61	3.1	1	58.8	31	95.00%	K.CCSDVFNQVVK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CCSDVFNQVVK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
164	A6ZQE6_YEAS7	15.38%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
9	19	2	1171.59	5	1	56.1	29.3	95.00%	A.DALNAINNAEK.T		R.SSVLADALNAINNAEK.T
89	97	2	1040.58	3.5	0	26.7	25.7	95.00%	K.WTANLLPAR.Q		K.WTANLLPAR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
165	A6ZR09_YEAS7	19.83%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
44	60	3	1846.89	5.5	1	64.1	29.1	95.00%	K.CGDCGSALQGISTLRPR.Q	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CGDCGSALQGISTLRPR.Q
25	31	2	712.42	-0.46	0	24.7	23.2	95.00%	K.TPGGILR.A		K.TPGGILR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
166	A6ZWW2_YEAS7	16.99%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
170	191	2	2407.23	6.7	1	85.7	25	95.00%	K.DESHTLFNTSLVPPTLNVPGNR.S		K.DESHTLFNTSLVPPTLNVPGNR.S
241	250	2	1026.58	6.2	0	24.2	25.6	95.00%	R.SHITLGSSIL.D		R.SHITLGSSILDGLDDEDDEHNQVLNK.D
269	277	2	1029.55	6.6	1	55.2	28	95.00%	A.DDNLITAIR.A		K.DADDNLITAIR.A
201	219	2	1873.03	6.6	0	35.7	21.9	95.00%	R.ASNILPIAYIPGVTSGLST.D		R.ASNILPIAYIPGVTSGLSTDK.L
201	221	2	2116.16	6.4	1	71.6	21	95.00%	R.ASNILPIAYIPGVTSGLSTDK.L		R.ASNILPIAYIPGVTSGLSTDK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
167	A6ZZE8_YEAS7	4.68%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
403	413	2	1275.63	5.3	0	41.5	29.1	95.00%	R.HIPYVTQGQSF.D		R.HIPYVTQGQSFDDEISLGGFSK.V
403	414	2	1470.63	5.3	1	41.2	30.2	95.00%	R.HIPYVTQGQSFD.D	Phospho (+80)	R.HIPYVTQGQSFDDEISLGGFSK.V
415	424	2	1051.52	5	1	51.2	30.1	95.00%	D.DEISLGGFSK.V		R.HIPYVTQGQSFDDEISLGGFSK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
168	A6ZU02_YEAS7	1.90%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
482	491	2	1122.65	6	0	46	23.3	95.00%	K.DAVTNIHLLK.R		K.DAVTNIHLLK.R

482	492	2	1278.75	5.2	1	23.6	18.8	95.00%	K.DAVTNIHLLKR.K		K.DAVTNIHLLKR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
169	TOR1_YEAST	1.50%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2158	2170	2	1468.8	5.8	0	39.3	24.9	95.00%	L.DIQQYPAIPLSPK.S		R.HLDIQQYPAIPLSPK.S
2059	2071	2	1457.77	5.8	0	45	26.2	95.00%	L.DLQHVSPQLLATH.D		R.QIPQLQTLDLQHVSPQLLATHDLELAVPGTYFPGKPTIR.I
2093	2103	2	1252.67	-0.26	1	22.9	26	92.70%	K.FEPLFSVISSK.Q		K.FEPLFSVISSK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
170	A6ZLC2_YEAS7	17.37%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
99	115	2	1647.03	-0.43	1	62.6	6.02	95.00%	R.GAIVGPDLAVLALVIVK.K		R.GAIVGPDLAVLALVIVK.K
3	14	2	1319.68	3.8	0	27.1	29.2	94.30%	K.LNISYPVNGSQK.T	Deamidation (+1)	K.LNISYPVNGSQK.T
203	214	2	1276.67	3	1	66.2	28	95.00%	R.EAAAEYAQLLAK.R		R.EAAAEYAQLLAK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
171	A6ZQG2_YEAS7	12.63%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
73	80	2	1035.52	6.4	0	33.3	29.4	95.00%	A.DYLSVHFR.G		K.NAPLADYLSVHFR.G
191	204	2	1433.69	2.4	0	37.9	28.9	95.00%	R.SGIPAYYGYGGTTK.M		R.SGIPAYYGYGGTTK.M
286	299	2	1542.77	3.8	0	49	27.9	95.00%	E.DLGTGIQSYGYITR.N		K.NHLYSTFHTFQGIEDLGTGIQSYGYITR.N
227	235	2	1053.59	6.2	0	27.5	22.3	95.00%	Y.DLPAIWLLN.D		K.NSSSIGYYDLPAIWLLNDHIAR.T
68	80	2	1501.77	1.8	1	53.5	27.5	95.00%	K.NAPLADYLSVHFR.G		K.NAPLADYLSVHFR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
172	A6ZUF3_YEAS7	7.28%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
321	336	2	1818.88	6.3	1	101	28.7	95.00%	W.DPSLNYYAYTVTVGEK.M		R.GPLWDPSLNYYAYTVTVGEK.M
347	355	2	1109.56	-0.2	1	40.7	28.8	95.00%	K.MGLEWLSFK.G		K.MGLEWLSFK.G
370	378	3	1306.63	3.6	1	21.3	29.9	90.40%	R.QKWCPFQWK.Y	Carbamidomethyl (+57)	R.QKWCPFQWK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
173	A6ZNJ9_YEAS7	9.09%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
272	289	2	1935.94	5.2	1	46.2	28.6	95.00%	Y.DSLSSTPREPGATQILGK.F	Phospho (+80)	R.SSMFISPTEILQSDANNSNTWSQSNESAIYDSLSSTPREPGATQILGK.F
242	254	2	1454.71	6.6	1	39.4	29.4	95.00%	R.SSMFISPTEILQS.D	Oxidation (+16)	R.SSMFISPTEILQSDANNSNTWSQSNESAIYDSLSSTPR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
174	A6ZUM5_YEAS7	28.97%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
28	42	2	1796.91	5.2	1	55	27.8	95.00%	R.NVQVHQEPYVFNARP.D		R.NVQVHQEPYVFNARPDGVHVINVGK.T
34	52	3	2110.11	5.6	1	18.8	22.9	95.00%	Q.EPYVFNARPDGVHVINVGK.T		R.NVQVHQEPYVFNARPDGVHVINVGK.T
102	113	2	1402.69	0.19	0	26.7	29.5	93.20%	R.FTPGSFTNYITR.S		R.FTPGSFTNYITR.S
120	127	2	911.55	1.6	1	41.2	21	95.00%	R.LVIVTDPR.S		R.LVIVTDPR.S
135	147	2	1388.76	6.4	0	45.9	25.2	95.00%	K.EASYVNIPVIALT.D		K.EASYVNIPVIALTDLDSPSEFVDVAIPCNNR.G
13	27	2	1562.86	5.2	0	64.9	23.9	95.00%	E.DAQLLLAANTHLGAR.N		-.MSLPATFDLTPEDAQLLLAANTHLGAR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
175	A7A1Z8_YEAS7	4.18%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
471	484	2	1519.84	2.6	1	40.2	23.8	95.00%	R.DTVVLEPSGHVVLR.F		R.DTVVLEPSGHVVLR.F
372	383	2	1229.73	3.2	0	50.7	20.9	95.00%	K.VPTLTTLLTSGK.L		K.VPTLTTLLTSGK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
176	A6ZTV6_YEAS7	8.48%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
627	646	3	2028.08	7	0	38.9	22.8	95.00%	G.DVLLGLASSGVHSNGFSLVR.K	Deamidation (+1)	K.INEMAAGDVLLGLASSGVHSNGFSLVR.K
231	252	2	2085.11	5.9	0	21.4	23.8	91.80%	K.GLNTGGMGAYAPAPVATPSLLK.T		K.GLNTGGMGAYAPAPVATPSLLK.T
504	517	2	1345.72	5.8	1	51.6	27.1	95.00%	E.DTLLVGATDGVGTK.L		R.QNEDTLLVGATDGVGTK.L
400	411	2	1288.7	4.3	1	41.2	25.9	95.00%	R.VLSVTSTAQDLR.T		R.VLSVTSTAQDLR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
177	B3LKQ2_YEAS1	8.05%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
365	375	2	1128.68	2.6	1	28.5	21.1	95.00%	K.ILAILSDTGVK.F		K.ILAILSDTGVK.F
352	364	2	1338.72	2.3	1	38.8	25.4	95.00%	K.IPSIPISANQGDK.I		K.IPSIPISANQGDK.I
547	569	2	2484.3	5.5	0	81.3	23.3	95.00%	G.DWTPYLAQGIPVAIISSPGVMNR.E		K.VDNVHQFGDWTPYLAQGIPVAIISSPGVMNR.E
282	297	2	1890.89	6	1	51	28.6	95.00%	G.DYVFQQMLTAQEYGAK.A		K.ASLDDMASMQDQGLLNGDFILLVHYGDYVFQQMLTAQEYGAK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
178	A6ZRY2_YEAS7	9.32%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
257	280	2	2445.12	-0.57	1	100	28.7	95.00%	R.TNIDNSTGQAGQANAQSANTVNNR.V		R.TNIDNSTGQAGQANAQSANTVNNR.V
260	286	3	2773.29	6.4	1	67.3	27.6	95.00%	I.DNSTGQAGQANAQSANTVNNRVNNNSK.A		R.TNIDNSTGQAGQANAQSANTVNNRVNNNSK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
179	A6ZVR3_YEAS7	2.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
611	621	2	1203.65	3.7	0	38.1	26.8	95.00%	R.EAFVSLNIPSK.A		R.EAFVSLNIPSK.A
165	173	2	1004.56	6.3	1	32.8	27.2	95.00%	F.DFLELIAGK.A		K.SESQYLEGFDFLELIAGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
180	COS6_YEAST	15.75%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
121	134	2	1689.78	6.2	1	27.6	30.3	93.40%	H.DWEVVAANLNSYFY.E		K.NTPSSDPHDWEVVAANLNSYFYENK.A
357	369	2	1544.86	-0.59	1	57.8	23.4	95.00%	R.ALSLNVELWPYIK.E		R.ALSLNVELWPYIK.E
25	33	2	1087.6	-0.48	1	22.9	26.5	91.90%	K.TVLPQDLFR.S		K.TVLPQDLFR.S
143	156	2	1789.76	-0.95	1	41.7	30.4	95.00%	K.YFFFSAMSCQEAFR.T	Carbamidomethyl (+57)	K.YFFFSAMSCQEAFR.T
157	166	2	1147.65	4.2	1	35.1	23.5	95.00%	R.TTLLEPFSLK.K		R.TTLLEPFSLK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
181	A6ZLD1_YEAS7	11.25%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
121	129	2	912.54	0.32	0	20.9	23.6	90.80%	K.AQGVAVQLK.R		K.AQGVAVQLK.R
70	78	2	915.54	0.097	0	48.2	23.8	95.00%	K.SSVGVIINK.M		K.SSVGVIINK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
182	B5VDK9_YEAST	14.51%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

158	168	2	1372.75	7.3	0	31.1	25.8	95.00%	Q.ELFINQQQQLL.E		K.DEPLQSQLQSQSQPQPPQPMVSNQELFINQQQQLLEQDSHLGALSQSIGR.T
42	52	2	1240.74	0.077	1	33.9	21.2	95.00%	R.QLGSILELLQK.C		R.QLGSILELLQK.C
158	170	2	1629.85	7.6	1	27.6	25.6	95.00%	Q.ELFINQQQQLLEQ.D		K.DEPLQSQLQSQSQPQPPQPMVSNQELFINQQQQLLEQDSHLGALSQSIGR.T
171	183	2	1339.69	6.9	0	61	27	95.00%	Q.DSHLGALSQSIGR.T		K.DEPLQSQLQSQSQPQPPQPMVSNQELFINQQQQLLEQDSHLGALSQSIGR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
183	A6ZKL6_YEAS7	33.58%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
13	26	2	1414.74	5.8	0	51.2	27	95.00%	R.ISLGLPVGAIMNCA.D	Carbamidomethyl (+57)	R.ISLGLPVGAIMNCADNSGAR.N
121	128	2	1045.47	-0.19	1	33.1	30.6	95.00%	K.ECADLWPR.V	Carbamidomethyl (+57)	K.ECADLWPR.V
33	40	2	932.57	2.7	0	25.3	20.4	95.00%	R.NLYIIAVK.G		R.NLYIIAVK.G
13	32	2	2014.99	0.21	1	86.8	27.8	95.00%	R.ISLGLPVGAIMNCADNSGAR.N	Carbamidomethyl (+57)	R.ISLGLPVGAIMNCADNSGAR.N
46	55	2	1010.59	6	1	30.6	21.1	95.00%	R.LNRLPAASLG.D		R.LNRLPAASLGDMVMATVK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
184	A6ZLM1_YEAS7	6.33%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	69	2	1619.83	2	1	40.5	27.4	95.00%	K.ATTPNVNDPIYFLR.G		K.ATTPNVNDPIYFLR.G
402	410	2	989.5	5.2	0	54.6	29.4	95.00%	K.DQGITLMGR.R		K.DQGITLMGR.R
70	77	2	920.42	0.32	1	26.4	30.3	91.30%	R.GVFGCEPR.T	Carbamidomethyl (+57)	R.GVFGCEPR.T
63	69	2	922.5	6.1	0	29.4	27.8	95.00%	N.DPIYFLR.G		K.ATTPNVNDPIYFLR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
185	B3LTD0_YEAS1	12.89%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
33	43	2	1157.62	3.3	0	47	27.2	95.00%	K.NFGIGQAVQPK.R		K.NFGIGQAVQPK.R
134	146	3	1484.81	6.7	1	26.3	23.9	95.00%	K.YGLNHVVSLIENK.K		K.YGLNHVVSLIENK.K
173	181	2	990.56	3.7	0	28.4	22.9	95.00%	K.MGVPYAIIK.G		K.MGVPYAIIK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
186	A6ZR28_YEAS7	24.44%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
12	20	2	981.6	3.5	0	33.3	18.1	95.00%	K.VISNPLLAR.K		K.VISNPLLAR.K
69	83	2	1539.8	5.7	1	73.2	26.2	95.00%	K.SVGFGLVYNSVAEAK.K		K.SVGFGLVYNSVAEAK.K
53	61	2	996.5	-0.43	0	42.8	28.7	95.00%	K.DAVSVFGFR.T		K.DAVSVFGFR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
187	A7A0K9_YEAS7	10.67%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
444	456	2	1407.72	5.8	0	54.5	27.9	95.00%	K.ATLINLNTSNNPH.D		K.ATLINLNTSNNPHDEMFK.V
132	144	2	1426.7	6.4	1	64.1	28.2	95.00%	E.DYGSIESLSTSIR.V		K.FSNISLEQYYSSLNNASSHALEDYGSIESLSTSIR.V
551	566	2	1558.88	6.1	0	38.4	20.7	95.00%	F.DHLLLLSGGTGLPGPL.D		K.FDHLLLLSGGTGLPGPLDHAIK.L
29	47	2	2118.05	5.6	1	93.4	26.6	95.00%	K.DHLESNAVLACASYINTLK.W	Carbamidomethyl (+57)	K.DHLESNAVLACASYINTLK.W
534	547	2	1465.77	6.3	1	37.5	25.9	95.00%	R.VAIEGPYGPSNLHL.D		R.VAIEGPYGPSNLHLDK.F
550	566	2	1705.95	6.1	1	31.3	20.8	95.00%	K.FDHLLLLSGGTGLPGPL.D		K.FDHLLLLSGGTGLPGPLDHAIK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
188	A6ZKM8_YEAS7	14.50%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
78	92	2	1666.89	5.5	1	32.7	24.6	95.00%	R.IAGVVYHPSNNELVR.T		R.IAGVVYHPSNNELVR.T

165	178	2	1550.76	-0.5	0	55.3	29.3	95.00%	R.LYACISSRPGQSGR.C	Carbamidomethyl (+57)	R.LYACISSRPGQSGR.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
189	A6ZPF3_YEAS7	12.22%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
399	411	2	1583.8	2.4	1	41.1	27.3	95.00%	R.HYSIIYNDVLGYK.T		R.HYSIIYNDVLGYK.T
288	300	2	1365.71	6.6	0	33.8	27.2	95.00%	Q.DIISSTSSLSPLF.D		K.GQMIYNHLPSLPHSLYLNSNNIAQ DIISSTSSLSPLFDFQSSK.K
473	486	2	1700.83	6.8	0	56.2	28.8	95.00%	C.DLWNSVYASYIQSR.E		K.LEHQACDLWNSVYASYIQSR.E
208	218	2	1397.73	6.6	1	40.6	26.7	95.00%	L.DELFFLPNYIK.F		R.SSLDELFFLPNYIK.F
54	62	2	1117.61	6.2	1	34.3	27.6	95.00%	H.EIYNPLEIK.Q		K.DGLHEIYNPLEIK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
190	A6ZLE7_YEAS7	7.92%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
96	104	2	1087.57	0.35	1	31.4	29.1	95.00%	R.NSDLWNLVK.S		R.NSDLWNLVK.S
327	339	2	1339.72	7	0	27.9	26.6	95.00%	G.DAPVHSIAASLFL.D		R.WGDAPVHSIAASLFLDK.S
315	324	2	1163.5	6.1	1	37.4	31.4	95.00%	L.DSSGGFFYER.W		R.EYFDYLDSSGGFFYER.W

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
191	A6ZUA3_YEAS7	15.16%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
165	175	2	1156.61	4.9	1	68.2	26.1	95.00%	S.DNAIIEANLGK.Y		R.VPLSDNAIIEANLGK.Y
207	218	2	1225.62	3.2	0	39	28.4	95.00%	K.LSNPSGGWGVPR.K		K.LSNPSGGWGVPR.K
183	196	3	1617.9	6.6	1	56	21.6	95.00%	D.DLIHEIITVGPHFK.Q		K.YGILSIDDLIHEIITVGPHFK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
192	A6ZQL2_YEAS7	12.54%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
176	188	2	1538.83	5.4	0	65.8	23.9	95.00%	K.DPVVNNTHIIVYR.E		K.DPVVNNTHIIVYR.E
160	171	2	1329.74	-0.24	1	37.1	24.3	95.00%	K.VFGINLNDLVAR.H		K.VFGINLNDLVAR.H
206	219	2	1579.74	5.3	1	51.1	30.2	95.00%	T.DENLVMSVTTVGCR.R	Carbamidomethyl (+57)	R.ETPIALISLAPNMTLSTDENLVMS VTTVGCR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
193	A6ZY37_YEAS7	11.57%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
320	331	2	1295.54	6.2	0	95.2	30.7	95.00%	R.FSNAGGFTMHNN.D		R.FSNAGGFTMHNNDSSTFK.L
1	12	2	1354.73	-0.9	0	38.4	24	95.00%	-.MNVIFSLASFVK.N		-.MNVIFSLASFVK.N
271	282	3	1320.68	-0.52	1	23	28.4	95.00%	R.VDSHLGTHLNTK.G		R.VDSHLGTHLNTK.G
13	22	2	1209.56	1.4	0	38.7	30.5	95.00%	K.NMYNASLNQR.N		K.NMYNASLNQR.N
378	392	2	1557.69	-0.27	1	80.7	31	95.00%	R.SSSPSSSFTVSSNER.S		R.SSSPSSSFTVSSNER.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
194	A6ZSS5_YEAS7	41.46%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
37	70	3	3713.67	1.9	1	42.9	26.4	95.00%	K.CPGCLNITTVFSHAQTAVTCESC STVLCTPTGGK.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CPGCLNITTVFSHAQTAVTCESC STVLCTPTGGK.A
57	70	2	1495.67	5.3	0	70.5	30.2	95.00%	C.ESCSTVLCTPTGGK.A	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.CPGCLNITTVFSHAQTAVTCESC STVLCTPTGGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
195	A6ZMI1_YEAS7	19.61%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
115	128	2	1715.82	2.2	1	80.2	29.1	95.00%	R.VLNSYWVNQDSTYK.Y		R.VLNSYWVNQDSTYK.Y
78	93	2	1675.85	-0.66	1	74.7	28.2	95.00%	K.GATYGKPTNQGVNELK.Y		K.GATYGKPTNQGVNELK.Y

148	157	2	1330.61	1.1	0	32.8	31	95.00%	R.YNWICNPVHK.H	Carbamidomethyl (+57)/ Deamidation (+1)	R.YNWICNPVHK.H		

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
196	A6ZVM1_YEAS7	2.43%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
109	126	2	1896.93	2	0	57.1	28.4	95.00%	K.FTNIASSPPSSSNNIFSK.A		K.FTNIASSPPSSSNNIFSK.A
334	343	2	1015.55	-0.61	1	50.2	27.9	95.00%	R.ISITASAPEK.S		R.ISITASAPEK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
197	B3LSP9_YEAS1	17.47%	100%	6

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
368	383	3	1797.9	6.1	1	36.4	27.5	95.00%	K.KPNLHGYGHPNPPNEK.S		K.KPNLHGYGHPNPPNEK.S
464	478	2	1937.98	5.2	0	65.6	27.1	95.00%	Q.EQQLQQQQQQQQQLR.A		K.LQEQQLQEQQLQQQQQQQQLR.A
296	312	2	1863.95	-1.6	1	69.9	27.1	95.00%	R.STNVYDLAQGLPVQFGR.Y		R.STNVYDLAQGLPVQFGR.Y
43	59	2	1685.74	6.4	0	62.4	30.6	95.00%	R.SSMTATTAANSNSNSSR.D		R.SSMTATTAANSNSNSSR.D
479	499	2	2212.06	-0.4	0	66.7	28.5	95.00%	R.ATGQPPSQPQAQTQSQQFGAR.Y		R.ATGQPPSQPQAQTQSQQFGAR.Y
360	367	2	958.49	-0.13	1	34.2	27.3	95.00%	R.GWDLNINK.K		R.GWDLNINK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
198	A6ZWC1_YEAS7	10.77%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
144	152	2	1059.61	0.74	1	62.7	24.4	95.00%	K.VFLDIGLQR.T		K.VFLDIGLQR.T
197	208	2	1387.63	6.1	0	43.2	30.6	95.00%	R.SYIFGGHVSQYM.E		R.SYIFGGHVSQYMEELADDDEER.F
238	248	2	1274.63	4.5	1	53.9	28.9	95.00%	E.DIYTSAHEAIR.A		K.GYLADDIDADSLEDIYTSAHEAIR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
199	A6ZYJ7_YEAS7	8.91%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
113	121	2	1234.55	-0.75	1	26.9	29.9	92.70%	R.WSFWNQDPR.I		R.WSFWNQDPR.I
262	274	2	1426.7	6.7	0	85.9	28.5	95.00%	Q.DCGGFNLGSFLIK.N	Carbamidomethyl (+57)	R.DDIPYVDYSEEMEFLITQDCGGFNLGSFLIK.N
354	366	2	1485.66	5.7	0	72.9	29.9	95.00%	H.DFVVNMAGCNFGR.D	Carbamidomethyl (+57)	K.DHDFVVNMAGCNFGR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
200	A6ZXE6_YEAS7	3.45%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
446	455	2	1095.61	3.2	0	28.2	25.2	95.00%	R.DLSLLGSHVR.K		R.DLSLLGSHVR.K
769	784	3	1700.91	5	1	34.1	23.9	95.00%	K.RTTLVANTSNMPVAAR.E		K.RTTLVANTSNMPVAAR.E
832	842	2	1165.58	5.2	0	29	29.9	95.00%	A.DQGFPAYLGAK.L		R.LGEMPADQGFPAYLGAK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
201	A6ZRP5_YEAS7	6.45%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
663	682	2	2177.08	-1.8	1	66.4	27.9	95.00%	K.TTESNFGFITVLPGAFSAYR.F		K.TTESNFGFITVLPGAFSAYR.F
509	520	2	1310.66	6	0	31.3	28.7	95.00%	R.SLALLSSLGCYQ.D	Carbamidomethyl (+57)	R.SLALLSSLGCYQDGFAK.D
247	257	2	1342.62	5.5	1	54.2	30.2	95.00%	G.DDYQINSYLGR.N		R.GDDYQINSYLGR.N
642	655	2	1634.88	5.1	1	65.6	25.3	95.00%	K.LLNPLVASQNFEYK.M		K.LLNPLVASQNFEYK.M
216	231	2	1808.82	5.2	0	57	29.3	95.00%	H.DQPFGYNNGYHGLQAK.D	Deamidation (+1)	R.TSPSIASSSDGYADQEARPILEQPNNNMNSGNIPQYHDQPFGYNNGYHGLQAK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
202	A6ZWW4_YEAS7	13.39%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

60	74	2	1655.8	6.7	0	50	29.9	95.00%	E.DLFCAVTNPVTGSYI.D	Carbamidomethyl (+57)	K.SENDEDLFCAVTNPVTGSYIDLSQLSSTPNK.L
75	85	2	1188.61	5.8	0	52.4	29.5	95.00%	I.DLSQLSSTPNK.L		K.SENDEDLFCAVTNPVTGSYIDLSQLSSTPNK.L
332	346	2	1678.71	-0.64	1	32.3	30.8	95.00%	R.LRSSPSASSSSLANR.E	Phospho (+80)/ Phospho (+80)	R.LRSSPSASSSSLANR.E
190	199	2	1179.6	0.77	1	42.5	29.8	95.00%	K.ATLLNFVCDK.E	Carbamidomethyl (+57)	K.ATLLNFVCDK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
203	A6ZLU0_YEAS7	8.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
275	292	2	1990.01	6.4	1	65.9	25.6	95.00%	R.LLICGPDGMNNLALQYAK.E	Carbamidomethyl (+57)	R.LLICGPDGMNNLALQYAK.E
250	259	2	1138.57	3	1	36.9	29.6	95.00%	R.WTGDVGYITK.D		R.WTGDVGYITK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
204	A6ZSL9_YEAS7	8.07%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
155	163	2	1102.58	3.3	1	43.7	28.2	95.00%	R.LISQAWETR.S		R.LISQAWETR.S
49	57	2	1012.57	4	1	23.4	25.2	94.60%	K.QLEGILGQR.Q		K.QLEGILGQR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
205	A6ZSD5_YEAS7	10.05%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
101	111	2	1246.53	2.5	1	55.4	30.5	95.00%	R.GINFDYSGSCK.I	Carbamidomethyl (+57)	R.GINFDYSGSCK.I
90	100	2	1245.49	0.33	0	45.2	30.4	95.00%	K.FGSMSCSSMPR.G	Carbamidomethyl (+57)	K.FGSMSCSSMPR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
206	KHA1_YEAST	3.67%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
620	632	2	1512.77	5.8	1	71.4	28	95.00%	K.IPFSSEVIFSTMR.E		K.IPFSSEVIFSTMR.E
647	654	2	923.61	6.7	0	25.7	14.3	95.00%	T.DLILLPLK.G		K.MDSTDLILLPLK.G
563	573	2	1158.64	2.9	1	30	25.8	95.00%	K.LTPFEGVGALR.A		K.LTPFEGVGALR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
207	A7A105_YEAS7	10.09%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
284	291	2	931.48	1.1	1	34.2	30.2	95.00%	R.LANPNFEK.Q		R.LANPNFEK.Q
210	218	2	1072.6	5.2	0	26.5	26.6	95.00%	V.DLLHLATYK.D		R.LVDLLHLATYK.D
119	134	2	1821.93	5.7	1	59.7	26.5	95.00%	K.EVFTNPLEAVTNPTYK.I		K.EVFTNPLEAVTNPTYK.I
208	218	2	1284.75	3.5	1	58.5	21.3	95.00%	R.LVDLLHLATYK.D		R.LVDLLHLATYK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
208	A6ZMN0_YEAS7	7.64%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
200	211	2	1395.69	4.4	1	65.3	29.4	95.00%	P.DMPNHTVIVENK.T		R.QYIQEEGAYAWEFSPNPDMPNHTVIVENK.T
149	164	2	1824.95	6.1	1	65.1	26.2	95.00%	K.QNPPFLLNQGLLQQSE.D		K.QNPPFLLNQGLLQQSEDSNPDATR.E
75	88	3	1617.79	2.9	1	29.4	28.4	95.00%	R.LITAYYNEHGPGQR.I		R.LITAYYNEHGPGQR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
209	A6ZMK2_YEAS7	16.78%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
48	57	2	1114.67	7.3	1	48.1	19.2	95.00%	K.VYEPLLLVGL.D		K.VYEPLLLVGLDK.F
69	82	2	1442.76	-0.0011	0	82	26.5	95.00%	R.VTGGGHVSQVYAIR.Q		R.VTGGGHVSQVYAIR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
210	B3LHY2_YEAS1	3.75%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

43	49	2	811.4	5.6	0	34.7	26.1	95.00%	H.DASLHNR.S		K.HLVDDVLFISPTNDGSEEKPTEVTFQEDEGHDASLHNR.S
108	120	2	1258.65	1.2	1	64	27.3	95.00%	K.SNIGNAEVAGLSK.D		K.SNIGNAEVAGLSK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
211	A6ZWJ1_YEAS7	12.04%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
328	340	2	1292.66	0.91	1	73.2	28.7	95.00%	K.STSDTASATLLAR.Q		K.STSDTASATLLAR.Q
347	357	2	1323.68	2.8	1	26.2	28.2	94.20%	R.KDSNTNIVLLK.S	Phospho (+80)	R.KDSNTNIVLLK.S
237	247	2	1346.64	3.4	0	29.5	30.1	95.00%	K.MHSYSFFSITK.G		K.MHSYSFFSITK.G
148	158	2	1258.72	6.6	0	23.1	23.2	94.40%	L.DPLLAFPAFLR.K		K.LDPLLAFPAFLR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
212	A6ZKZ2_YEAS7	25.64%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
104	116	4	1486.82	0.55	1	25.1	23.8	95.00%	R.HKNVPVHVSPAFR.V		R.HKNVPVHVSPAFR.V
58	67	2	1148.6	2.5	0	39.4	27.8	95.00%	K.CPFTGLVSIR.G	Carbamidomethyl (+57)	K.CPFTGLVSIR.G
117	133	2	1855	2.3	1	70.7	23.1	95.00%	R.VQVGDIVTVGQCRPISK.T	Carbamidomethyl (+57)	R.VQVGDIVTVGQCRPISK.T
121	133	2	1471.79	5.4	0	53.4	24.6	95.00%	G.DIVTVGQCRPISK.T	Carbamidomethyl (+57)	R.VQVGDIVTVGQCRPISK.T
106	116	3	1221.67	3.8	0	17.3	25.6	91.60%	K.NVPVHVSPAFR.V		K.NVPVHVSPAFR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
213	A6ZQ73_YEAS7	9.05%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
409	416	2	912.57	3	1	29.2	22.7	95.00%	R.ALIDLQIK.N		R.ALIDLQIK.N
259	274	3	1742.83	3.4	0	21.2	29.5	91.60%	R.SSHSNAYFTGLPFTSK.R		R.SSHSNAYFTGLPFTSK.R
424	440	3	2034.95	5.3	1	35	28.9	95.00%	V.DPLYSSYHYSHPTLAER.L		K.NLSTMNVDPLYSSYHYSHPTLAER.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
214	A6ZMS7_YEAS7	8.02%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
121	133	2	1423.64	5.8	1	57.2	30.7	95.00%	L.DVNSGNYGESLNR.A		K.CMTIFNNAGIYAILDVNSGNYGESLNR.A
274	288	2	1724.85	6	1	70.9	28.4	95.00%	E.DAVIPLIFSEYGCNK.N	Carbamidomethyl (+57)	K.LNSTFEDAVIPLIFSEYGCNK.N
81	94	2	1580.8	2.6	0	77.7	27.5	95.00%	R.DAYAFQQLGVNTVR.I		R.DAYAFQQLGVNTVR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
215	A6ZTP3_YEAS7	16.04%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
130	140	2	1178.6	5	0	37.6	29	95.00%	P.DVGPFTVYGPK.F		K.YIQGGVVVPDVGPFTVYGPK.F
130	141	2	1325.67	6.1	1	34	28.6	95.00%	P.DVGPFTVYGPKF.D		K.YIQGGVVVPDVGPFTVYGPKFDDENFYLK.H
251	263	2	1435.74	6	1	79.9	27.5	95.00%	G.DVSVGSTLENIFR.N		R.NGDVSVGSTLENIFR.N
67	79	2	1480.79	6.1	1	23.3	26.6	92.40%	A.DLTFELYGTVVPK.T		K.EADLTFELYGTVVPK.T
80	92	3	1400.73	1.9	0	29.8	27.5	95.00%	K.TVNNFAMLAHGVK.A		K.TVNNFAMLAHGVK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
216	A6ZNP1_YEAS7	14.24%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
39	55	2	1892	6.3	0	57	24.1	95.00%	F.EINGQISTLQQFTATLK.S	Deamidation (+1)	K.EEVAAELFEINGQISTLQQFTATLK.S
174	183	2	1110.65	5	1	58.7	20.8	95.00%	R.IPGSQIVIER.D		R.IPGSQIVIER.D
118	131	2	1702.8	0.76	1	71.4	30.1	95.00%	R.DVSYSFQEFQGIQR.Q		R.DVSYSFQEFQGIQR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
217	A6ZUC1_YEAS7	5.29%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

30	43	2	1471.8	6	1	76.8	24.5	95.00%	V.DLTEANILATGLNK.K		K.DDSASSGIVDEVDLTEANILATGLNK.K
470	482	3	1425.68	3.2	1	23.5	30	95.00%	R.HSNAAQNVLADMR.V		R.HSNAAQNVLADMR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
218	A6ZU78_YEAS7	17.45%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
116	126	2	1190.75	3	1	26	10.4	95.00%	K.GRIPNVPVIVK.A		K.GRIPNVPVIVK.A
103	111	2	894.45	6.7	0	29.4	30.5	95.00%	I.DTLAAGYGK.I		K.ETAPVIDTLAAGYGK.I
97	111	2	1504.78	2.7	1	39	27.4	95.00%	K.ETAPVIDTLAAGYGK.I		K.ETAPVIDTLAAGYGK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
219	A6ZN13_YEAS7	3.57%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
32	40	2	985.54	-3.4	1	40.9	27	95.00%	K.DVLLQAAEK.F		K.DVLLQAAEK.F
449	458	2	1265.59	0.48	0	34.1	29.9	95.00%	K.DFICNWLGNK.A	Carbamidomethyl (+57)	K.DFICNWLGNK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
220	A6ZQF2_YEAS7	12.32%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
16	24	2	1079.51	-0.11	0	28.5	29.6	95.00%	R.SVGSQWFNR.L		R.SVGSQWFNR.L
261	268	2	915.55	1.2	1	29.7	24.1	95.00%	K.IMDLALLK.N		K.IMDLALLK.N
83	95	4	1542.89	1.1	1	28.3	18.1	95.00%	R.LIYPHVEHVPVLK.Q		R.LIYPHVEHVPVLK.Q
61	82	2	2263.1	4.7	1	128	28	95.00%	R.SAGASYSPSHGLYINEIPASSR.L		R.SAGASYSPSHGLYINEIPASSR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
221	MKAR_YEAST	14.12%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
266	278	2	1487.79	3.2	0	27.7	26.7	95.00%	R.SSLMIPNPQQFVK.S		R.SSLMIPNPQQFVK.S
228	243	2	1722.87	6.5	1	66.5	27.6	95.00%	K.SFLQGWSNSLAGELSK.D		K.SFLQGWSNSLAGELSK.D
168	187	2	2164.28	-1.9	0	67.3	13.2	95.00%	R.NIITINNTATLLITQIIAPK.I		R.NIITINNTATLLITQIIAPK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
222	RTN1_YEAST	8.81%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
208	216	2	939.58	3.4	0	36.8	19.5	95.00%	K.LGPISNLVK.S		K.LGPISNLVK.S
219	235	2	1589.79	-0.45	0	43.7	29.1	95.00%	K.TAPVSSTAGPQTASTSK.L		K.TAPVSSTAGPQTASTSK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
223	A6ZM19_YEAS7	9.43%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
305	316	2	1356.71	5.1	1	31.2	26.7	95.00%	E.DRFTASTFTAIK.T		K.AAAPGIQLVAGEGFQSPLEDRFTASTFTAIK.T
96	109	2	1693.89	6.2	1	54.9	25.6	95.00%	I.DQLWPGQLVVPEWK.L		K.SIHPGYLSEGGCLMFHYEADNEENLEELNDSKPLIDQLWPGQLVVPEWK.L
257	268	2	1569.67	5.3	1	59.1	30.4	95.00%	Y.DDYQTNYYNYVI.D		R.ATYDDYQTNYYNYVIDK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
224	A6ZN47_YEAS7	7.69%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
610	622	2	1601.81	2.8	1	65.8	27.7	95.00%	K.LQCININDLMVNR.N	Carbamidomethyl (+57)	K.LQCININDLMVNR.N
86	101	2	1737.96	6.3	0	52.4	23.1	95.00%	S.DIHPVGVSYFPAVIPK.G		R.QSPSDIHPVGVSYFPAVIPK.G
82	101	3	2137.13	2.6	1	35.4	25.1	95.00%	R.QSPSDIHPVGVSYFPAVIPK.G		R.QSPSDIHPVGVSYFPAVIPK.G
474	488	2	1790.9	6.4	0	47.7	28	95.00%	K.DFAVYQYVSPYQALK.T		K.DFAVYQYVSPYQALK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
225	A6ZQ79_YEAS7	10.67%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
168	180	2	1338.8	3	0	46.9	17.1	95.00%	R.VNQAIALLTIGAR.E		R.VNQAIALLTIGAR.E
55	65	2	1263.65	3.6	1	56.4	27.7	95.00%	K.DASLVDYVQVR.Q		K.DASLVDYVQVR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
226	A6ZTN7_YEAS7	7.45%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
63	80	3	1965.08	2.6	1	45.4	18.6	95.00%	K.HLHGLPILQSPSLTPAER.L		K.HLHGLPILQSPSLTPAER.L
47	62	2	1661.87	5	1	66.4	25.9	95.00%	I.DVSSTASIVPVPHEPK.H		R.FVSILSLFGCAATLVTAHDDMDMDMDMDMDMDMNIDTTTSQSIDVSSTASIVPVPHEPK.H
209	221	2	1417.69	4.6	1	72.2	29.7	95.00%	N.DLESTPVMVNSAR.G		K.EYRPVDTIPLNDLESTPVMVNSAR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
227	A6ZYE1_YEAS7	10.59%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
240	254	3	1728.85	3.9	1	32.5	28.4	95.00%	R.QFLDNFAMGSHPLPR.I		R.QFLDNFAMGSHPLPR.I
317	330	2	1702.76	5.8	0	76.2	30.3	95.00%	H.DHCQISHSYPFQGK.T	Carbamidomethyl (+57)	K.TQPEILFSGDDHDHCQISHSYPFQGK.T
296	304	2	1045.57	5.8	1	23.5	27.5	90.80%	N.DISQEILTK.T		K.GHQYQTVIENDISQEILTK.T
363	376	2	1454.68	6	1	51.3	30	95.00%	S.DLTMVNAGGEYASK.T		K.SCAMNMGISRPAIQLLSLYNPSDLTMVNAGGEYASK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
228	A6ZV05_YEAS7	5.30%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1305	1320	2	1769.91	2.7	1	66.3	26.6	95.00%	K.ISRPIASQNSLGWNEV.-		K.ISRPIASQNSLGWNEV.-
1134	1175	3	3807.46	6.3	1	19	26.7	93.00%	H.DSNSNSGGSSDGSSSSNSNSGSSGSGSNSNSGVSSSSGNSYQ.D		K.SMAAMVDSSIPLTGLLHDSNSNSGGSSDGSSSSNSNSGSSGSGSNSNSGVSSSSGNSYQDAGTLEYSSK.S
1278	1289	2	1354.55	5.3	1	45.2	30.5	95.00%	M.DDSYYGHGLTNN.D		R.IQNWMDDSYYGHGLTNNDSTPTR.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
229	A6ZSI2_YEAS7	4.46%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1143	1154	2	1388.81	1.9	0	31.1	20.2	95.00%	K.NAVILNYQTLLK.E		K.NAVILNYQTLLK.E
1595	1610	2	1793.05	6	1	35.2	15.9	95.00%	K.QIGVENLQTLSPLILR.T		K.QIGVENLQTLSPLILR.T
58	70	2	1522.77	5.6	0	65.3	27.8	95.00%	P.DFALPFVLACQSR.N	Carbamidomethyl (+57)	R.HPDFALPFVLACQSR.N
373	391	2	2193.15	5.5	1	23.8	22.8	95.00%	K.ECIVLLNSPEYITFLAPSK.V	Carbamidomethyl (+57)	K.ECIVLLNSPEYITFLAPSK.V
1493	1505	2	1500.68	6	0	41.3	31.2	95.00%	F.DFSCIFGSTTNPR.F	Carbamidomethyl (+57)	K.LSSFDFSCIFGSTTNPR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
230	A6ZM50_YEAS7	8.06%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
97	107	2	1428.62	5.2	1	53.3	30.4	95.00%	F.DVCFENQAQYR.G	Carbamidomethyl (+57)	R.VAFTAPSSTAFDVCFENQAQYR.G
62	67	2	760.46	-0.69	0	26.1	22.9	95.00%	K.LNLFVR.D		K.LNLFVR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
231	A6ZZW6_YEAS7	6.39%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
28	42	2	1514.8	5.5	0	55.4	26.3	95.00%	I.DLPQITVVGSQSSGK.S		K.LQDALAPLGGGSQSPIDLPQITVVGSQSSGK.S
579	589	2	1180.56	0.053	0	39.4	30.5	95.00%	K.SGFFGGFFSTK.N		K.SGFFGGFFSTK.N
166	184	3	2079.2	2.7	1	19.4	13.4	95.00%	R.IYSPHVLTLTLVDLPGLTK.V		R.IYSPHVLTLTLVDLPGLTK.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
232	A6ZQQ0_YEAS7	12.11%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	12	2	1331.66	-0.45	1	31.3	29.4	95.00%	M.SGNREQVFPTR.M	Acetyl (+42)	-.MSGNREQVFPTR.M
119	127	2	1033.57	4.8	1	24	25.4	95.00%	N.DFRLTGLGR.G		R.QENVSGVYLSQFESYIDPEINDFRLTGLGR.G
170	180	3	1259.74	2.9	1	39.7	19	95.00%	R.VNAIEHVIIPR.T		R.VNAIEHVIIPR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
233	B3LKG8_YEAS1	3.12%	99%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
403	412	2	1076.59	2.9	1	23.1	26.5	92.10%	R.NLYALAIDGK.A		R.NLYALAIDGK.A
563	571	2	1190.59	6.4	1	25.6	29.2	91.80%	V.DLYTFKEIY.D		K.STDVDLYTFKEIYDR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
234	A6ZT92_YEAS7	3.79%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1493	1510	2	1783.86	-0.6	0	26.4	29.2	93.10%	K.NSHNNGVTSTLAATGIPK.S	Deamidation (+1)/ Deamidation (+1)/ Deamidation (+1)	K.NSHNNGVTSTLAATGIPK.S
1480	1492	2	1480.76	-0.62	1	46.6	27.8	95.00%	K.IWTTSGDLLNSFK.N		K.IWTTSGDLLNSFK.N
283	298	2	1982.94	5.6	1	30.4	29.2	95.00%	A.DLFSCCLTCPIEISIR.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.DDEEGNHDVAAPSPTSAYQDCFQLASCTSDELLLMSPELPADLFSCCLTCPIEISIR.I
1310	1321	2	1415.78	-0.15	1	46.3	25.4	95.00%	R.STGLLTEWLQIR.G		R.STGLLTEWLQIR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
235	A6ZTY6_YEAS7	10.32%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
127	140	2	1506.7	5.8	1	75.8	29.8	95.00%	I.DQPTGTGFSVEQNK.D		K.GDLLFIDQPTGTGFSVEQNK.D
93	103	2	1146.57	5.2	1	41.8	29.4	95.00%	M.DGALVESGPFR.V		K.FTNNDSNGNVDRPLIIWLNGGPGCSSMDGALVESGPFR.V
76	92	2	1872.9	6.1	0	52.4	27.8	95.00%	V.DRPLIIWLNGGPGCSSM.D	Deamidation (+1)/ Carbamidomethyl (+57)	K.FTNNDSNGNVDRPLIIWLNGGPGCSSMDGALVESGPFR.V
58	65	2	1146.55	6.9	1	34.3	29.6	95.00%	S.DLEYFFWK.F		R.SEDADEQDSSDLEYFFWK.F
313	324	2	1440.58	2.9	0	43	30.5	95.00%	K.DSYPSCGMNWPK.D	Carbamidomethyl (+57)	K.DSYPSCGMNWPK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
236	A6ZL34_YEAS7	2.43%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
45	54	2	1212.62	6.7	0	45.8	28.3	95.00%	H.DLQTSYAFIR.I		R.LNIHSIIEPGHDLQTSYAFIR.I
58	70	2	1505.8	7	0	43.5	26.5	95.00%	Q.DNAKPLFSFLQNL.D		R.IHQDNAKPLFSFLQNLDFIESIIPYHDTELSDDLHK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
237	B3LJW5_YEAS1	10.34%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
8	19	2	1468.69	3.5	1	58.8	30.4	95.00%	K.VSSMQNFEMIQR.E		K.VSSMQNFEMIQR.E
79	98	2	2198.03	5.7	1	61.1	29.2	95.00%	K.SLINFPQEQQQNGSTSTATF.D	Deamidation (+1)	K.SLINFPQEQQQNGSTSTATFDLLNALIEEGHLDPEAPDK.L
378	390	3	1410.75	7.2	0	33.5	24.5	95.00%	T.DHVPMILAVFGGR.R		K.NAGNDEGDASSGTDHVPMILAVFGGR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
238	A6ZQ50_YEAS7	32.61%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
50	61	2	1369.56	1.2	0	59.3	30	95.00%	R.GAAGIWTCSCCK.K	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.GAAGIWTCSCCK.K
63	80	2	1665.87	1.4	0	81.1	26.4	95.00%	K.TVAGGAYTVSTAAAATVR.S		K.TVAGGAYTVSTAAAATVR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
239	A6ZPF9_YEAS7	10.43%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
64	74	2	1162.6	5.1	0	28.7	28.5	95.00%	A.DNLAISAQGFK.R		K.ADNLAISAQGFK.R
64	75	2	1318.7	-3.1	1	29	28.1	95.00%	A.DNLAISAQGFKR.G		K.ADNLAISAQGFKR.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
240	LCB4_YEAST	6.41%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
293	305	2	1508.76	5.8	1	41.6	28.4	95.00%	G.DGIPYEVINGLYR.R	Deamidation (+1)	K.YDTIACASGDGIPYEVINGLYR.R
36	47	2	1366.66	6.8	0	37.1	30.1	95.00%	G.DSLSLLSCLSCL.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.SGDSLSLLSCLSCLDDGTLSSDG GSFDEDDSLELLPLNTTIPFNR.I
34	47	2	1510.71	6.2	1	50.2	29.5	95.00%	R.SGDSLSLLSCLSCL.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.SGDSLSLLSCLSCLDDGTLSSDG GSFDEDDSLELLPLNTTIPFNR.I
66	78	2	1526.86	6.4	0	23	23.1	94.40%	L.ELLPLNTTIPFNR.I		R.SGDSLSLLSCLSCLDDGTLSSDG GSFDEDDSLELLPLNTTIPFNR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
241	B3LFU9_YEAS1	7.26%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
126	138	2	1333.6	5.9	1	59.4	30.7	95.00%	E.DMIQGGSSAESPR.S		R.EEEDMIQGGSSAESPR.S
298	307	2	1088.55	5.3	1	44.4	29.3	95.00%	E.DSAAQLVTER.T		R.ELYSPEEDSAAQLVTER.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
242	AGP1_YEAST	6.95%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
430	442	2	1465.79	5.4	1	80.8	25.9	95.00%	R.LFLTLSEQGYAPK.V		R.LFLTLSEQGYAPK.V
38	57	3	2278.1	5.1	1	61.4	27.9	95.00%	N.DRPSSQPHLGYEQHNTSAVR.R		K.NSSTEIHATGQDNEIEYFETGSND RPSSQPHLGYEQHNTSAVR.R
81	91	2	1132.58	4.6	0	37.8	27.9	95.00%	N.DLTSAISPSSR.Q		R.ADQGPQDEVEATQMNDLTSAISP SSR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
243	A6ZT16_YEAS7	7.01%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
455	472	2	1878.93	6.6	0	54.7	28.1	95.00%	F.DLLMGFNPTTGTTTAPAR.T	Oxidation (+16)	K.NGDSNAASQIHPSHVSAPLQQSS GALTNEINLIDFNDLDEAPSQGNNN TNGTGTPAAAETSVNDLLGDLTDLS ISNPSTANQASFGLGGDIVLGSSQP APPVTTTNNSNNTLDLLGLSTPQLP TNSQAVNSSGFDLLMGFNPTTGTT TAPAR.T
410	432	3	2339.18	6.4	0	21.2	25.1	95.00%	G.DIVLGSSQPAPPVTTTNNSNNTL. D		K.NGDSNAASQIHPSHVSAPLQQSS GALTNEINLIDFNDLDEAPSQGNNN TNGTGTPAAAETSVNDLLGDLTDLS ISNPSTANQASFGLGGDIVLGSSQP APPVTTTNNSNNTLDLLGLSTPQLP TNSQAVNSSGFDLLMGFNPTTGTT TAPAR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
244	A6ZKL0_YEAS7	23.85%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
81	90	2	1187.59	3.4	1	45.3	29.7	95.00%	K.DLETLTMHTK.T		K.DLETLTMHTK.T
73	80	2	890.53	3.5	0	25.7	25.4	95.00%	K.TFLVANVK.D		K.TFLVANVK.D
91	103	2	1387.71	3.2	1	82.5	27.6	95.00%	K.TYAAEIAHNISAK.N		K.TYAAEIAHNISAK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
245	ATG15_YEAS7	5.19%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
261	273	2	1641.71	1.7	1	39.1	30.7	95.00%	K.INDNLLFSCCCAR.V	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.INDNLLFSCCCAR.V
274	287	2	1792.82	0.095	1	47.6	30.5	95.00%	R.VSYLWTTVCDCYVK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VSYLWTTVCDCYVK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
246	B3LQ13_YEAS1	11.53%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
82	98	2	1708.81	5.3	1	57.8	29	95.00%	P.DQTSGSNPAVGLLHNAE.D		K.NPITHASPGVGSNAQNSDIAEAP QVFHPSYQSLVNVPSESPRPDQTS GSNPAVGLLHNAEDK.A
39	55	2	1729.75	5.2	0	63	30.4	95.00%	K.NPITHASPGVGSNAQNS.D	Phospho (+80)	K.NPITHASPGVGSNAQNSDIAEAP QVFHPSYQSLVNVPSESPRPDQTS GSNPAVGLLHNAEDK.A
543	578	3	3933.84	5.2	1	60.3	25.3	95.00%	I.DEPIGSYSTSPMVLPSTPSTIPFHA HNQSNSNPVYY.D		K.NAIDEPIGSYSTSPMVLPSTPSTIP FHAHNQSNSNPVYYDSTLHPFANK. T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
247	B3LS15_YEAS1	18.61%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
143	156	3	1570.94	3.1	1	17	13.4	92.10%	K.HTIILRPGPLLGER.T		K.HTIILRPGPLLGER.T
1	18	2	1833.93	6	0	119	26.3	95.00%	-.MNGLVLGATGLCGGGFLR.H	Acetyl (+42)/ Carbamidomethyl (+57)	-.MNGLVLGATGLCGGGFLR.H
92	102	2	1183.66	5.4	0	40.5	24.4	95.00%	H.DLNLQLAQAAK.E		K.IDHDLNLQLAQAAK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
248	A6ZWH0_YEAS7	14.21%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
139	149	2	1302.72	3.4	0	31.6	24.5	95.00%	K.QIVNIPSFMVR.L		K.QIVNIPSFMVR.L
155	171	3	1781.91	6.2	1	41.9	26.9	95.00%	K.HIDFAPTSPFGGARPGR.V		K.HIDFAPTSPFGGARPGR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
249	A6ZPF4_YEAS7	6.37%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
420	432	3	1441.77	0.07	1	32.5	26	95.00%	K.NLHTHEVPAPISK.S		K.NLHTHEVPAPISK.S
479	491	2	1409.7	3	0	44.4	28.5	95.00%	K.NSILGCYLAQSGK.H	Carbamidomethyl (+57)	K.NSILGCYLAQSGK.H
377	386	2	1325.59	5.2	1	35.5	31	95.00%	S.DANNEWFFQR.I		K.NQALGGALLHSHVQPFPEGSEQ QQVTVYGYSDANNEWFFQR.I
334	345	2	1201.69	0.57	0	34.6	21.9	95.00%	R.DVALGSSIISIK.N		R.DVALGSSIISIK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
250	A6ZXS3_YEAS7	13.20%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
183	200	2	1849.09	0.05	0	26.2	11.1	95.00%	K.IPIVPVVVSNTSTLVSPK.Y		K.IPIVPVVVSNTSTLVSPK.Y
150	159	2	1174.62	3.1	1	25.5	27.6	94.20%	R.ALWVFPEGTR.S		R.ALWVFPEGTR.S
213	224	2	1355.81	4.7	1	25.3	19.6	95.00%	R.ILKPISTENLTK.D		R.ILKPISTENLTK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
251	A6ZLZ0_YEAS7	2.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
727	740	2	1272.7	-0.25	0	23.3	26.1	93.20%	K.AINAGGGATTVLTK.D		K.AINAGGGATTVLTK.D
786	801	3	1914.98	-0.5	1	35.7	26.5	95.00%	R.LQHIQTCLAGDLLFMR.F	Carbamidomethyl (+57)	R.LQHIQTCLAGDLLFMR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
252	A6ZRX9_YEAS7	2.95%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
31	45	2	1738.88	0.97	1	58.2	28.1	95.00%	R.RAQSTVLNSNPFYSR.K		R.RAQSTVLNSNPFYSR.K
236	241	2	731.44	3.5	0	31.4	22.4	95.00%	K.VPFLTR.N		K.VPFLTR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
253	A6ZM77_YEAS7	9.29%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
274	283	2	1210.55	-0.24	1	46.4	30.4	95.00%	K.IFENCAQMAK.D	Carbamidomethyl (+57)	K.IFENCAQMAK.D
425	437	2	1395.77	5.9	0	35.5	22.9	95.00%	K.GAMLIPTLYPALH.D		K.GAMLIPTLYPALHDPEVYENPDEFIPER.W
173	186	2	1603.84	6.5	1	54.3	26.6	95.00%	K.QALAQYLPSLEQIM.D		K.QALAQYLPSLEQIMDK.Y
284	296	2	1353.66	4.7	0	38.3	30	95.00%	K.DHIAAGGKPVCVM.D	Carbamidomethyl (+57)	K.DHIAAGGKPVCVMDAWCK.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
254	A6ZSP5_YEAS7	10.44%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
368	378	2	1238.67	6.7	1	27.7	23.6	95.00%	S.DLGEPVPFIPR.S		R.SLNSLLSIPSSVVTSDNATMESDLGEPVPFIPR.S
549	559	2	1135.6	3.7	0	33.6	27.4	95.00%	K.ANSTTLGGLFR.A		K.ANSTTLGGLFR.A
4	23	3	2131.08	6.6	1	38.7	26.3	95.00%	D.DSNYLTPHETALAVVATAMK.K		-.MVDDSNYLTPHETALAVVATAMK.K
412	420	2	954.53	2.8	0	32.3	25.3	95.00%	R.SPPGVFPVR.G		R.SPPGVFPVR.G
592	606	2	1568.86	5.8	1	44.7	23.1	95.00%	R.ITANNVAGIVNLNKE.D		R.ITANNVAGIVNLNKEDLDSIPR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
255	A6ZQ10_YEAS7	7.39%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
276	289	2	1565.76	5.6	1	34.7	29.6	95.00%	M.DQVQVHPTGFIDPN.D		K.LGAELIDMDQVQVHPTGFIDPNDR.E
478	491	2	1464.76	-0.67	1	39.2	26.3	95.00%	R.LGGSSLLECVVFGK.T	Carbamidomethyl (+57)	R.LGGSSLLECVVFGK.T
407	415	2	1057.6	6.7	0	43.9	25.4	95.00%	F.DRPLIINAF.D		K.DTFDRPLIINAFDK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
256	A6ZYM2_YEAS7	3.49%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
230	243	2	1654.84	2.6	1	76.2	28.1	95.00%	K.FTVFSNLDNTTQLR.L		K.FTVFSNLDNTTQLR.L
768	778	2	1342.66	5.3	0	46.4	29.3	95.00%	H.DSYATVQYLQR.N		K.HDSYATVQYLQR.N
71	80	2	1063.55	6.2	1	37.8	28.8	95.00%	R.DSEITAISTK.E		R.DSEITAISTK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
257	B3LTT3_YEAS1	5.42%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
356	366	2	1501.62	6.4	0	33.4	30.7	95.00%	E.DYNLCHFWSNF.E	Carbamidomethyl (+57)	K.VPMLEDSLEGEDYNLCHFWSNFEIAR.V
298	308	3	1386.71	3.5	1	25.6	27.7	95.00%	R.WVNFPWDAKPK.L		R.WVNFPWDAKPK.L
209	214	2	1001.44	-0.016	1	26.5	30.5	90.90%	K.YEWYWR.I		K.YEWYWR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
258	A6ZM69_YEAS7	5.72%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
237	247	2	1195.6	3.2	0	30.2	29.6	95.00%	R.GGVGYTWSTLR.E		R.GGVGYTWSTLR.E
547	558	2	1379.68	5.8	0	59	29.7	95.00%	S.DFLGCVGCAIIR.R	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.NGFEAATMGNFTDDSDFLGCVGCAIIR.R
437	451	2	1783.83	6.6	1	33	29.6	95.00%	D.DYWPDGASLVNTYQR.Q		R.ELDVIFALDNSADTDDYWPDGASLVNTYQR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
259	A6ZLN3_YEAS7	2.26%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
257	262	2	775.46	-0.94	1	23.1	23.7	94.50%	K.LIDIFR.G		K.LIDIFR.G
263	269	2	844.41	2.2	0	29.3	29.8	95.00%	R.GPSFYFK.S		R.GPSFYFK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
260	A6ZR85_YEAS7	21.01%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
43	51	2	941.53	0.5	1	21.1	24.9	91.20%	R.NIVEAAAVR.D		R.NIVEAAAVR.D
71	82	3	1485.7	1.3	0	39.6	30.1	95.00%	K.LHYCVSCAIHAR.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.LHYCVSCAIHAR.I
67	82	4	1991.95	3.6	1	22.5	29.1	95.00%	K.TYNKLHYCVSCAIHAR.I	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	K.TYNKLHYCVSCAIHAR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
261	A6ZXQ3_YEAS7	23.89%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
51	61	2	1281.71	3.1	1	26	23.5	95.00%	R.LAPELNQAIWK.R		R.LAPELNQAIWK.R
87	102	2	1732.94	-0.76	1	49.5	23.6	95.00%	K.NPLFSYVEPVLVASAK.G		K.NPLFSYVEPVLVASAK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
262	IRC8_YEAST	9.37%	100%	5

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
675	687	2	1484.69	6	0	39.4	30.1	95.00%	T.DPINYSFGHGHNK.N		K.LSLSNISDTMSPYEGSTTDPINYSFGHGHNK.N
383	393	2	1261.57	6.3	1	61.8	30.7	95.00%	K.MISPQQSTQNE.D		K.MISPQQSTQNEDSYQATPLIPQVEVDDDFYVGDILMTNELQDIPQVPR.I
552	571	2	2134.05	5.8	1	25	26.2	95.00%	E.DASQLIESSLNQNNLSSTTI.D		K.TSDTISELDEYLHDPSIQEEDASQLIESSLNQNNLSSTTIDNGPK.D
196	217	3	2378.13	6.6	1	20	28	92.20%	K.SMNGVAWLINELSTNSNTNANK.T	Deamidation (+1)	K.SMNGVAWLINELSTNSNTNANK.T
368	378	2	1226.68	2.8	0	28.7	24.4	95.00%	R.INSALLPACLR.V	Carbamidomethyl (+57)	R.INSALLPACLR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
263	A6ZQ99_YEAS7	5.35%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
35	44	3	1165.61	6	0	22.7	28	95.00%	T.DAFLHSHLAR.Y		K.HQDTDAFLHSHLAR.Y
54	67	2	1444.7	5.2	0	90.8	29	95.00%	R.ISSAGQQVTGYTHP.D		R.ISSAGQQVTGYTHPDFNNQWEVLPPHGSDVGK.G

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
264	A6ZVQ4_YEAS7	6.35%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
303	317	2	1808.85	5.5	0	51.3	28.7	95.00%	L.DTNFANTYISFFQNK.W		R.VYLVDCSTVLDTNFANTYISFFQNK.W
75	85	2	1312.72	1.7	0	40.4	23.9	95.00%	R.LSAYFLPFLSR.S		R.LSAYFLPFLSR.S
460	473	2	1666.85	6	1	45.8	27.7	95.00%	G.DKEIFWLGQLYAGQ.D		R.CVYGDKEIFWLGQLYAGQDYSINPVDGSIIGPVNEEPENDDGHK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
265	AKR2_YEAST	5.47%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
241	252	2	1396.71	6.1	1	44.5	28.5	95.00%	C.DLILSGANFYER.N		R.VICDLILSGANFYER.N
83	96	2	1683.79	5.6	1	45	30.3	95.00%	I.DELSGLHWACINNR.F	Carbamidomethyl (+57)	R.IDELSGLHWACINNR.F
223	237	2	1613.78	1	1	38.6	29.5	95.00%	R.GFNALHCALVGGDQR.V	Carbamidomethyl (+57)	R.GFNALHCALVGGDQR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
266	B3LR14_YEAS1	8.42%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
230	241	2	1411.68	6.6	1	56.9	30.3	95.00%	R.DIPATFFSSEWI.D		R.DIPATFFSSEWIDNDNGLMPVEVR.D
188	196	2	1235.6	-1.3	0	28.8	29.9	95.00%	K.TYFVTWYTR.F		K.TYFVTWYTR.F
143	154	2	1390.72	6	1	34.5	28	95.00%	E.DDTYVSLNPIVR.C		K.AHNMGPNEVFVEEEYIDEDDTYVSLNPIVR.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
267	PSS_YEAST	14.13%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
192	201	2	1115.64	3.8	0	50.5	24.9	95.00%	R.FNVTVAQLPK.D		R.FNVTVAQLPK.D
7	16	2	1187.53	5.5	1	29.2	30.4	95.00%	E.DFAPQEFPHT.D		-.MVESDEDFAPQEFPHTDTDVIVNEHR.D
44	62	2	1957.04	5.8	1	20.6	23.9	90.10%	R.RASSIFSINTTPLAPPNAT.D		R.RASSIFSINTTPLAPPNATDIQK.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
268	A6ZMP4_YEAS7	9.15%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
170	186	2	1887.96	6.2	0	64.9	26.8	95.00%	N.DVNGQQIFSQALLNANR.R	Deamidation (+1)	R.QYTIIQPEATDEEVEAAINDVNGQQIFSQALLNANR.R
44	53	2	1100.59	-0.11	0	78.1	27.4	95.00%	K.INSINANLSR.Y		K.INSINANLSR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
269	A6ZT50_YEAS7	10.44%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
13	22	2	1126.64	-1.2	0	30	23.9	95.00%	K.TPLPLCSVIK.S	Carbamidomethyl (+57)	K.TPLPLCSVIK.S
2	12	2	1215.56	3.6	1	43.7	30.5	95.00%	M.AFSDFAAICSK.T	Carbamidomethyl (+57)	-.MAFSDFAAICSK.T
39	50	2	1305.75	6.3	0	55.6	21.3	95.00%	F.DPLNLNVGVLPR.C		K.THLILSNSTIIHDFDPLNLNVGVLPR.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
270	A6ZV20_YEAS7	12.82%	100%	22

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
5	20	2	1672.66	3.6	1	29.1	30.8	94.70%	N.DPNLNGQYYSNGDGTG.D	Deamidation (+1)/ Deamidation (+1)	-.MSYNDPNLNGQYYSNGDGTGDGNYPTYQVTQDQSAYDEYGQPIYTQNQLDDGYYDPNEQYVDGTQFPQGQDPSQDQGPYNNDASYYNQPPNMMNPSSQDGENFSDFSSYGPPSGTYPNDQYTPSQMSYPDQDGSSGASTPYGNGVVNGNGQYYDPNAIEMALPNDPYPAWTADPQSPLPIEQIEDIFIDLTNK.F
1192	1201	2	1168.59	-0.28	0	52.2	29	95.00%	K.EQTFGTLFAR.T		K.EQTFGTLFAR.T
1798	1807	2	1213.72	2.1	0	23.2	20.8	94.60%	R.QIRPPIYSLK.Q		R.QIRPPIYSLK.Q
856	869	2	1605.76	7.1	0	36	29.1	95.00%	V.DNMPTFTVLTPHYA.E		R.ISFFAQSLSTPIPEPLPVDNMPTFTVLTPHYAER.I
856	871	2	1906.9	6.1	1	90.7	28.8	95.00%	V.DNMPTFTVLTPHYAER.I	Oxidation (+16)	R.ISFFAQSLSTPIPEPLPVDNMPTFTVLTPHYAER.I

37	49	2	1567.73	6.8	1	48.6	29.9	95.00%	Y.DEYGQPIYTQNQL.D		- .MSYNDPNLNGQYYSNGDGTGDG NYPTYQVTQDQSAYDEYGQPIYTQ NQLDDGYYDPNEQYVDGTQFPQG QDPSQDQGPYNNDASYYNQPPNM MNPSSQDGENFSDFSSYGPPSGT YPNDQYTPSQMSYPDQDGSSGAS TPYGNGVVNGNGQYYDPNAIEMAL PNDPYPAWTADPQSPLPIEQIEDIFI DLTNK.F
1210	1226	2	2019.97	2.4	1	79.1	28.3	95.00%	K.LHYGHPDFINATFMTTR.G		K.LHYGHPDFINATFMTTR.G
808	818	2	1265.68	6.3	1	42.9	25.6	95.00%	R.TLRAPTFFVSQ.D		R.TLRAPTFFVSQDDNNFETEFFPR. D
1455	1463	2	1094.62	3.4	0	52.9	24.4	95.00%	R.IPFSILYSR.F		R.IPFSILYSR.F
1160	1173	3	1463.76	6.5	0	21	27.4	95.00%	E.DQSTNHPVAIVGAR.E		K.YEDQSTNHPVAIVGAR.E
1268	1280	2	1425.75	-0.019	0	69.1	26.5	95.00%	R.DLGFGTILNFTTK.I		R.DLGFGTILNFTTK.I
1089	1101	2	1296.71	0.92	1	44.2	24.9	95.00%	R.VQLSGNPILGDGK.S		R.VQLSGNPILGDGK.S
1186	1201	2	1709.88	4.9	1	76.9	26.8	95.00%	G.DVAAGKEQTFGTLFAR.T		R.EYIFSENSGVLGDVAAGKEQTFG TLFAR.T
938	948	2	1373.64	6.8	1	41.1	30.2	95.00%	I.DDLPFYCIGFK.S	Carbamidomethyl (+57)	K.SQIDDLPFYCIGFK.S
105	118	2	1487.63	5.6	0	32.4	30.4	95.00%	S.DFSSYGPPSGTYPN.D		- .MSYNDPNLNGQYYSNGDGTGDG NYPTYQVTQDQSAYDEYGQPIYTQ NQLDDGYYDPNEQYVDGTQFPQG QDPSQDQGPYNNDASYYNQPPNM MNPSSQDGENFSDFSSYGPPSGT YPNDQYTPSQMSYPDQDGSSGAS TPYGNGVVNGNGQYYDPNAIEMAL PNDPYPAWTADPQSPLPIEQIEDIFI DLTNK.F
1281	1292	2	1248.6	2.9	1	86.4	29.7	95.00%	K.IGAGMGEQMLSR.E		K.IGAGMGEQMLSR.E
1539	1546	2	993.5	0.087	0	45.7	29.9	95.00%	R.NSWIGYVR.M		R.NSWIGYVR.M
972	981	2	1174.55	2	0	46.4	30.5	95.00%	R.TISGFMNYSR.A		R.TISGFMNYSR.A
889	896	2	977.58	3.3	1	51.5	19.7	95.00%	R.VTLLEYLK.Q		R.VTLLEYLK.Q
1266	1280	3	1638.88	1.3	1	17.7	24.2	93.90%	K.GRDLGFGTILNFTTK.I		K.GRDLGFGTILNFTTK.I
838	855	2	1942.06	6.1	1	54.7	22.1	95.00%	R.ISFFAQSLSTPIPEPLPV.D		R.ISFFAQSLSTPIPEPLPVDNMPTF TVLTPHYAER.I
219	230	2	1295.66	6.5	1	33	27.7	95.00%	R.MSPEQALLSLHA.D		R.MSPEQALLSLHADYIGGDTANYK. K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
271	A6ZWB1_YEAS7	17.76%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
100	107	2	965.53	3.7	0	25.9	27.6	94.70%	R.IFLYPSNI.-		R.IFLYPSNI.-
22	32	2	1211.67	-4.7	1	22.2	24.1	93.30%	R.VNNPNVSLIKI.E	Deamidation (+1)/ Deamidation (+1)	R.VNNPNVSLIKIEGVATPQDAQFYL GK.R
22	31	2	1096.63	1.4	0	22.9	23.6	94.30%	R.VNNPNVSLIK.I		R.VNNPNVSLIK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
272	A6ZYL7_YEAS7	4.19%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
646	658	2	1324.74	6.6	0	21.5	22.8	91.90%	N.DTVLAPVPGSTIR.K		K.SIGPDGLSFNENFNTTPEGFAPSI DPGEESNDTVLAPVPGSTIR.K
646	661	3	1705.99	6	1	18.2	17.3	94.70%	N.DTVLAPVPGSTIRKPR.T		K.SIGPDGLSFNENFNTTPEGFAPSI DPGEESNDTVLAPVPGSTIRKPR.T
282	297	2	1916.89	6.9	1	31.3	29.3	95.00%	K.DCFAIAQEMNTVYSLR.E	Carbamidomethyl (+57)	K.DCFAIAQEMNTVYSLR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
273	A6ZN12_YEAS7	5.38%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
80	93	2	1551.83	5.5	1	31.6	24.6	95.00%	K.SLQAQKPNLSPQEI.D		K.SLQAQKPNLSPQEIDALIEDWEP EPLVDPSATDEQSWR.V	
198	213	2	1729.84	5.4	0	26.1	27.8	94.70%	Y.DLAQFFGTQGSVLYGQ.D		K.NYGVGACGPAGFYGNQDVHYTL EYDLAQFFGTQGSVLYGQDFCAAP SVLPAFTK.R	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
274	TCB3_YEAST	1.68%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
1081	1092	2	1341.67	5.5	1	26.4	27.8	95.00%	D.DVISETSYSTLK.L		K.DSDDVISETSYSTLK.L	
1244	1257	2	1625.82	5.6	1	47.3	28.4	95.00%	K.LQGSFNPEYIKPSF.D		K.LQGSFNPEYIKPSFDIVK.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
275	A6ZYA1_YEAS7	2.36%	100%	3								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
2	15	2	1580.88	-0.62	1	30.4	21.4	95.00%	M.SLPLKPLTIDSNNK.Q	Acetyl (+42)	-.MSLPLKPLTIDSNNK.Q	
300	308	2	1055.63	-0.011	1	42	21	95.00%	R.SVLDLLLQR.L		R.SVLDLLLQR.L	
78	94	3	1761	4.8	1	56.6	19.1	95.00%	R.RLTSSLSPALPAGVHQK.T		R.RLTSSLSPALPAGVHQK.T	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
276	A6ZV22_YEAS7	25.58%	100%	4								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
92	105	3	1431.79	3.7	0	24.4	24.7	95.00%	K.VNGASVPINLHPSK.L		K.VNGASVPINLHPSK.L	
90	105	3	1689.92	5.9	1	37.5	23.9	95.00%	K.EKVNGASVPINLHPSK.L	Deamidation (+1)	K.EKVNGASVPINLHPSK.L	
20	29	2	1127.52	0.15	1	28.4	29.8	95.00%	K.AYFTAPSSER.R		K.AYFTAPSSER.R	
80	86	2	805.43	0.97	1	32.2	27.6	95.00%	K.FAVQVDK.V		K.FAVQVDK.V	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
277	A6ZMY7_YEAS7	7.55%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
181	195	2	1589.85	5.7	1	77	25.5	95.00%	K.GSAPLFGNFLEPLTK.T		K.GSAPLFGNFLEPLTK.T	
147	160	3	1741.01	0.46	1	24.2	17.2	95.00%	K.FLDLNRPLLMQILR.S		K.FLDLNRPLLMQILR.S	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
278	A6ZZX8_YEAS7	9.40%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
116	126	2	1261.7	6.5	1	30.1	25.2	95.00%	D.DDLVIYLLGNK.V		K.VGDDDLVIYLLGNK.V	
162	172	2	1351.69	2.3	1	44.3	28.3	95.00%	K.QYAQEQGLLFR.E		K.QYAQEQGLLFR.E	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
279	A6ZMQ5_YEAS7	15.00%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
57	62	2	741.48	3.7	1	21.7	24.1	92.30%	R.LIDLIR.N		R.LIDLIR.N	
5	13	2	885.53	0.091	0	21.5	25.3	91.40%	K.TGIAIGLNK.G		K.TGIAIGLNK.G	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
280	A6ZM38_YEAS7	12.50%	100%	2								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
112	128	2	1794.07	-0.9	1	26.3	13.6	95.00%	K.SLGLKLPLSVINVSAQR.D		K.SLGLKLPLSVINVSAQR.D	
117	128	2	1295.76	1.8	0	76.2	17.7	95.00%	K.LPLSVINVSAQR.D		K.LPLSVINVSAQR.D	

Index	AC	Coverage	Scaffold probability	Nb distinct peptides								
281	A6ZRZ3_YEAS7	4.58%	100%	4								
Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence	
594	606	2	1405.8	5.6	0	37	20.4	95.00%	K.VISSSVQPLNHLI.D		K.VISSSVQPLNHLIDR.T	
642	653	2	1293.68	2	0	36.8	26.8	95.00%	K.SVGYTTPIGMLR.V		K.SVGYTTPIGMLR.V	
373	383	2	1138.7	3	1	20.7	19.5	90.20%	K.TGLPIGVLEIK.V		K.TGLPIGVLEIK.V	

725	742	3	2109.04	6.6	1	37	27.6	95.00%	G.DDHNLGSLNIQTQNIYHK.D		K.VSIDCFGIDTNGDDHNLGSLNIQTQNIYHK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
282	A6ZU67_YEAS7	4.97%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
521	544	2	2313.15	6.5	1	79.3	26.1	95.00%	R.DRPGSVLMNVVSGGIAEASAQQAG.D		R.DRPGSVLMNVVSGGIAEASAQQAGDLMQDLK.T
598	609	2	1399.73	2.9	1	47.4	27.2	95.00%	R.IPTAVVWIDCAR.L	Carbamidomethyl (+57)	R.IPTAVVWIDCAR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
283	A6ZUT7_YEAS7	1.69%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1219	1231	2	1487.86	6.2	0	24.7	18.9	95.00%	V.DFAYRPGLPIVLK.N		R.KPEMTPPESWPSMGEIIFENVDFAYRPGLPIVLK.N
763	774	3	1392.82	6.3	1	59.7	16.5	95.00%	R.ILATHQLSLIER.A		R.ILATHQLSLIER.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
284	A6ZLI8_YEAS7	10.00%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
189	201	2	1350.73	5.7	0	59.5	26.6	95.00%	R.ELASGLSFPVGFK.N		R.ELASGLSFPVGFK.N
29	52	2	2460.36	5.5	1	56	17.2	95.00%	Y.DPLASPALLQVQIPATPTSLETAK.R		R.ILGYDPLASPALLQVQIPATPTSLETAK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
285	A6ZKX1_YEAS7	12.44%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
80	91	2	1286.66	5.7	1	28.7	28.4	95.00%	K.TASEVPAHLTVY.D		K.TASEVPAHLTVYDIAGLTK.G
116	125	2	1164.62	2.9	1	22.8	27.2	90.10%	R.SVDSIYQVVR.C		R.SVDSIYQVVR.C
329	338	2	976.51	4.9	0	38.8	28.3	95.00%	K.APQAAGVIHN.D		K.APQAAGVIHNDLMNTFILAQVMK.C
99	115	3	1655.85	6.2	1	20.3	26.3	95.00%	K.GASAGEGLGNAFLSHIR.S		K.GASAGEGLGNAFLSHIR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
286	A6ZPU2_YEAS7	7.77%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
218	231	2	1401.76	6.5	1	28.4	25.8	95.00%	R.IVNEPTAAAIAYGL.D		R.IVNEPTAAAIAYGLDK.S
103	117	2	1671.86	3.2	1	66	26.4	95.00%	K.NQVAANPQNTIFDIK.R		K.NQVAANPQNTIFDIK.R
251	262	2	1291.67	6.6	1	41.7	27.8	95.00%	F.DVSLLSIENGVF.E		K.EHQIIVYDLGGGTFDVSLLSIENGVFEVQATSGDTHLGGEDFDYK.I
206	217	2	1198.67	-0.1	0	53.6	26.1	95.00%	K.DAGTIAGLNVLR.I		K.DAGTIAGLNVLR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
287	A6ZTY9_YEAS7	11.33%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
80	93	2	1517.74	2.6	1	59.7	29.8	95.00%	R.DTSHGEITLSAPYK.G		R.DTSHGEITLSAPYK.G
63	71	2	1108.56	6.6	1	32.5	29	95.00%	G.DFIIYGPER.H		R.NPQSSSQLTGDFIIYGPER.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
288	A6ZU95_YEAS7	5.00%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
396	408	2	1630.72	1.7	1	49.3	30.5	95.00%	R.CVDNNYSSLAFWR.A	Carbamidomethyl (+57)	R.CVDNNYSSLAFWR.A
2	16	2	1583.92	8	1	46	20.5	95.00%	M.SLISILSPLITSEGL.D	Acetyl (+42)	-.MSLISILSPLITSEGLDSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
289	A6ZSL4_YEAS7	3.30%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	63	2	962.47	0.6	1	27	30.9	91.30%	R.FMEVPQGR.H		R.FMEVPQGR.H
532	541	2	1158.64	6.4	1	31.5	25.7	95.00%	H.DGLIVTEWVK.K		K.ITYLHDGLIVTEWVK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
290	ERV41_YEAST	11.65%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
173	182	2	1044.58	0.18	1	60.9	26	95.00%	R.VSGELQITAK.S		R.VSGELQITAK.S
228	246	2	2235.15	5.5	1	61.8	25.3	95.00%	Q.DEPLTTYVYYTSVVPTLFK.K		K.FNHVINEFSFGDFYPYIDNPLDNTAQFNQDEPLTTYVYYTSVVPTLFK.K
216	227	2	1375.61	5.9	1	38.7	31.3	95.00%	I.DNPLDNTAQFNQ.D		K.FNHVINEFSFGDFYPYIDNPLDNTAQFNQDEPLTTYVYYTSVVPTLFK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
291	A6ZXF1_YEAS7	5.85%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
271	284	2	1603.81	7.7	1	60.3	27.8	95.00%	D.DTIIMMNPIDNSLK.L		K.QLHVPDNSQDDTIIMMNPIDNSLK.L
307	324	2	2056.96	3.1	1	52.4	29.4	95.00%	K.SFGYTWAVPNENTQNTTK.S		K.SFGYTWAVPNENTQNTTK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
292	A6ZN11_YEAS7	15.23%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
119	134	2	1906.93	6.4	1	76.8	28.1	95.00%	G.DPVWAQQLETPTYGFR.V		R.SFEYAVSGDPVWAQQLETPTYGFR.V
135	148	2	1537.8	6	1	55.9	26.7	95.00%	R.VRPDFPVFGAAVTY.D		R.VRPDFPVFGAAVTYDANGMPQQVGGASSQMYGEQAVYQPQQHVQTEEK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
293	A6ZVN8_YEAS7	3.79%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
904	915	2	1425.74	6	0	60.4	26.9	95.00%	R.NYVQTMFVPVTK.D		R.NYVQTMFVPVTK.D
403	429	3	2939.55	4.8	1	20.2	21.3	95.00%	F.DDLIAAQQNAINRPNAPVFIPPPAQNR.A		R.AQNEFDDLIAAQQNAINRPNAPVFIPPPAQNR.A
67	77	2	1320.65	6.7	1	46.5	30	95.00%	H.ESCLLEWVASK.N	Carbamidomethyl (+57)	K.YMHESCLLEWVASK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
294	A7A0E6_YEAS7	3.87%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
12	23	2	1217.75	6	1	42.6	15.8	95.00%	K.KPILAVPEPALA.D		K.KPILAVPEPALADTHSEEISR.S
285	292	2	871.52	5.3	0	22.8	26.9	90.80%	T.DVLLGSLR.S		K.VNENWNVEDGHITDVLLGSLR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
295	B3LM88_YEAS1	15.62%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
39	52	2	1526.71	6.7	1	30.8	30.5	95.00%	K.SNQVFTGPGFYDPV.D		K.SNQVFTGPGFYDPVDELLIEPSLPGLSYSFTEDGWYEEATYQVSGNPR.N
75	86	2	1349.63	5.2	1	59.7	30.4	95.00%	Y.EEATYQVSGNPR.N		K.SNQVFTGPGFYDPVDELLIEPSLPGLSYSFTEDGWYEEATYQVSGNPR.N
152	165	2	1772.85	6.6	0	27.1	29.4	93.90%	I.DPYHGIYTLQLYQY.D		K.EYAVGIDPYHGIYTLQLYQYDGTPMQPLYLAYRPPMMLPTETLNPTSSATSTDDPSSNK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
296	A6ZSV7_YEAS7	8.01%	100%	4

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence

73	88	3	1572.74	6.2	0	29.8	30.3	95.00%	M.DPGNYSTAVAAGSAHR.Y		R.FIGPGLMVSVSYMDPGNYSTAVAAGSAHR.Y
39	56	3	1962.03	5	1	22.4	25.5	95.00%	R.TTLQPNSTSQSMIGTLRK.Y		R.TTLQPNSTSQSMIGTLRK.Y
502	511	2	1089.57	0.35	1	36	28.3	95.00%	R.SLVSPAPEYK.D		R.SLVSPAPEYK.D
39	55	2	1833.93	3.2	0	36.6	26.3	95.00%	R.TTLQPNSTSQSMIGTLR.K		R.TTLQPNSTSQSMIGTLR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
297	ATC4_YEAST	1.12%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
727	736	2	1126.51	-0.26	0	56.1	30.7	95.00%	K.CTINGVSYGR.A	Carbamidomethyl (+57)/ Deamidation (+1)	K.CTINGVSYGR.A
1480	1487	2	954.56	6.4	1	32.6	24	95.00%	R.INEIRPLT.D		R.INEIRPLTDFK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
298	VTH1_YEAST	2.52%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
851	864	2	1621.77	6.5	1	52	28.8	95.00%	L.DNAIHCEFAGTLFK.Y	Carbamidomethyl (+57)	K.DGGETFTEMLDNAIHCEFAGTLFK.Y
394	406	2	1445.76	3.1	1	39.9	27.1	95.00%	K.VSVDNGLTWTNLK.V		K.VSVDNGLTWTNLK.V
488	499	2	1466.77	6.9	0	22.4	26.7	90.40%	G.DLGNIIMYIPYR.S		R.LVHNSTGLYTTGDLGNIIMYIPYR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
299	A6ZMV1_YEAS7	7.86%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
188	201	2	1563.79	2.9	0	67.7	27.9	95.00%	K.NTVSNACLFQIAAR.L	Carbamidomethyl (+57)	K.NTVSNACLFQIAAR.L
386	394	2	1077.63	6.6	0	36.6	23.3	95.00%	L.EVIQNLLIH.D		K.QTNDGYYGLGEQMSALEVIQNLLIHDRPAPYK.E
324	336	2	1422.74	-1	0	49.9	27.8	95.00%	R.MLGLTSVMAPFTR.D		R.MLGLTSVMAPFTR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
300	A6ZM15_YEAS7	15.89%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
255	283	3	2913.39	5	1	26.9	26	95.00%	E.DMQQSASIVGPSSNANPVTATAATENQPK.G		K.EQATDPILTATGPEDMQQSASIVGPSSNANPVTATAATENQPK.G
60	70	2	1410.64	-0.27	1	48.2	30.4	95.00%	R.WTFWGACLQDK.D	Carbamidomethyl (+57)	R.WTFWGACLQDK.D
284	291	2	966.53	0.9	0	35.3	24.5	95.00%	K.GINFFTIR.K		K.GINFFTIR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
301	A6ZR74_YEAS7	4.24%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
295	305	3	1263.68	7	0	23	27.3	95.00%	R.ASIHQILQHFA.E		R.ASIHQILQHFAEENVSISATSADEPTVATESSPLIR.D
66	73	2	851.45	2.5	0	24.6	27.1	93.60%	R.ASFSALTR.L		R.ASFSALTR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
302	B3LH47_YEAS1	3.36%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
336	345	2	1176.62	2.7	1	41.3	27.6	95.00%	R.TLVCSDLLTR.G	Carbamidomethyl (+57)	R.TLVCSDLLTR.G
24	30	2	755.46	3.4	0	24.1	20.4	95.00%	K.TALNIPK.K		K.TALNIPK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
303	A7A0I6_YEAS7	3.12%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
797	804	2	914.56	2.8	0	30.3	23	95.00%	K.IGLWSVLK.S		K.IGLWSVLK.S
170	182	2	1456.74	6.2	1	47.3	27.7	95.00%	R.DFGHLESILSSPR.N		R.DFGHLESILSSPR.N
814	829	2	1813.99	-0.51	1	75.8	21.3	95.00%	K.LTLPVSFNEPTSLLQR.V		K.LTLPVSFNEPTSLLQR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
304	A6ZMI9_YEAS7	2.39%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
782	799	2	1910.03	-2.9	1	47.2	22.4	95.00%	K.TPVFTTGGDYILSLVSIK.D		K.TPVFTTGGDYILSLVSIK.D
953	966	2	1580.82	6.1	1	36.1	25.6	95.00%	V.DLALFGSPPFILEY.D		K.EEVCQGMEGTVDLALFGSPPFILEYDLMAPNGHISTK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
305	A6ZSF8_YEAS7	5.07%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
135	143	2	1135.54	1.6	0	30	29.2	95.00%	K.TYNTAPQWR.F		K.TYNTAPQWR.F
210	221	2	1302.67	5.7	0	49	28.9	95.00%	H.DATGINCKPLSK.N	Carbamidomethyl (+57)	R.GEDASYETVHDATGINCKPLSK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
306	A7A187_YEAS7	4.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
47	57	2	1262.73	-0.42	1	49.3	22	95.00%	K.LIELVSFAPFK.G		K.LIELVSFAPFK.G
267	277	2	1367.6	5	1	31.4	30.2	95.00%	T.DMENVCVFAQR.V	Carbamidomethyl (+57)	R.ISMGQDISETDMENVCVFAQR.V

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
307	A6ZMS6_YEAS7	9.28%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
200	213	2	1680.76	2.1	0	85.6	29.7	95.00%	R.MGIMTQQIQQMCGR.C	Carbamidomethyl (+57)	R.MGIMTQQIQQMCGR.C
90	110	2	1722.78	4.7	1	98.2	30.6	95.00%	A.DAVKNGGGGGGPGGPGAGGFH.D	Deamidation (+1)	K.IYDQFGADAVKNGGGGGGPGGPGAGGFHDPFDIFER.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
308	SNQ2_YEAST	1.40%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
285	294	2	1167.63	-0.1	0	29.2	25.7	95.00%	R.DLYATIFGLR.H		R.DLYATIFGLR.H
1082	1092	2	1326.66	1.3	1	49.3	29.7	95.00%	K.NSATILNYFER.N		K.NSATILNYFER.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
309	B3LSP7_YEAS1	9.28%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
70	88	2	1955.02	2.6	1	64.9	25.1	95.00%	K.ALLSNASQLEMVPPSATAR.H		K.ALLSNASQLEMVPPSATAR.H
130	137	2	877.49	3.6	1	32.8	27.7	95.00%	K.GDIVSFLK.H		K.GDIVSFLK.H

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
310	A6ZYD0_YEAS7	2.19%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
483	497	3	1692.93	7.3	1	31	22.4	95.00%	V.DRHINAPFMLPIAAK.M		K.ECPWYTGPTLLEYLDTMNHVDRHINAPFMLPIAAK.M
485	497	2	1421.79	3.1	0	21.7	23.8	92.30%	R.HINAPFMLPIAAK.M		R.HINAPFMLPIAAK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
311	B3LGD6_YEAS1	5.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
305	321	3	1987.05	-0.69	1	21.6	23.8	95.00%	K.YAGDLYTIPIINTLQHR.G		K.YAGDLYTIPIINTLQHR.G
360	374	2	1640.81	5.5	1	32.9	29.2	95.00%	L.DSGTTISYMPTELVK.M		K.IPVLLDSGTTISYMPTELVK.M

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
312	A7A1E2_YEAS7	9.30%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
74	81	2	947.55	3.6	0	20.8	24.3	90.50%	R.SLIPSYIR.D		R.SLIPSYIR.D
114	125	2	1372.71	6.6	1	47.8	28.1	95.00%	G.DENVILCIVGNK.S	Carbamidomethyl (+57)	R.GDENVILCIVGNK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
313	A6ZUV7_YEAS7	8.33%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
365	376	2	1379.79	5.5	1	41.9	21.5	95.00%	S.DILLINPNLNKN.D		R.YNSDILLINPNLNKNDEEGSESATTPAK.D
205	220	3	1927.06	0.004	1	24.3	20.7	95.00%	K.SWLNNIIDLNKPIPYK.N		K.SWLNNIIDLNKPIPYK.N
350	361	2	1525.77	5.2	1	47.7	28.6	95.00%	S.DIIFEYMNNVLR.Y		K.NVDGSDIMNWTGPGIFSDIIFEYMNNVLR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
314	A6ZPW0_YEAS7	4.23%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	15	2	1595.89	8.6	1	27.1	21.1	95.00%	M.SLRLPQNPNAGLFK.Q	Acetyl (+42)	-.MSLRLPQNPNAGLFK.Q
441	450	2	1052.66	2.3	0	47.6	17.8	95.00%	R.TPGLLQLAIK.Q		R.TPGLLQLAIK.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
315	A6ZRQ3_YEAS7	3.80%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
129	147	3	1859.86	4.3	0	28.8	29.1	95.00%	N.DQGTAGLSSHGGSFAAQNR.I		R.FGSLINDQGTAGLSSHGGSFAAQNR.I
659	669	2	1251.58	2.6	1	34	30.1	95.00%	R.DCDSLSSLVTR.T	Carbamidomethyl (+57)	R.DCDSLSSLVTR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
316	A6ZW34_YEAS7	5.04%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
755	768	2	1472.66	5.6	0	58.4	30.6	95.00%	E.DAASSTQMHAMPAR.D		R.QESEANNGLINAYEDEQFSLMEPSILEDAASSTQMHAMPAR.D
97	108	2	1408.7	6.2	0	27.3	28.4	95.00%	K.QFCPVHPGNIQI.D	Carbamidomethyl (+57)	K.QFCPVHPGNIQIDSIEYIAEK.Y
610	623	2	1415.75	3	1	54.3	25.8	95.00%	K.SVANELMALGNVAK.D		K.SVANELMALGNVAK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
317	B3LJM9_YEAS1	7.12%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
417	425	2	1182.59	6.7	0	40.4	28.7	95.00%	T.DFLIMQNFR.A		R.MADQLTDFLIMQNFR.A
493	512	2	2054.02	5.1	1	83.5	27.4	95.00%	R.AGNTGLATAFFNSENSNIVK.G		R.AGNTGLATAFFNSENSNIVK.G
193	206	2	1527.8	-0.68	1	37.6	26	95.00%	K.TGGFLFPVLSESFK.T		K.TGGFLFPVLSESFK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
318	A6ZYY3_YEAS7	21.82%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
63	85	2	1789.87	5.7	0	51.7	28.7	95.00%	K.FATVPTGGASSAAAGAAGAAAGGG.D		K.FATVPTGGASSAAAGAAGAAAGGDAAEEEK.E
62	85	2	1917.96	4.8	1	67.2	28.2	95.00%	K.KFATVPTGGASSAAAGAAGAAAGG.D		K.KFATVPTGGASSAAAGAAGAAAGGDAAEEEK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
319	A6ZQP7_YEAS7	16.36%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
131	142	2	1289.64	-0.22	0	67.4	29.7	95.00%	K.EILGTAQSVGCR.V	Carbamidomethyl (+57)	K.EILGTAQSVGCR.V
17	31	2	1296.71	2.9	1	37.8	24.3	95.00%	R.AVGGEVGASAALAPK.I		R.AVGGEVGASAALAPK.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
320	A6ZM68_YEAS7	2.12%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
546	560	2	1709.8	6.1	1	45.5	29.2	95.00%	T.DDSNFLGCIGCAIIR.R	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.NGFEAATMGNFTDDSNFLGCIGCAIIR.R
547	560	2	1594.77	5.3	0	39.7	29.8	95.00%	D.DSNFLGCIGCAIIR.R	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.NGFEAATMGNFTDDSNFLGCIGCAIIR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
321	B3LT28_YEAS1	2.47%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
774	784	2	1295.63	6.1	1	26.4	29.1	93.30%	K.QSFGILMQELM.E		K.QSFGILMQELMELNSGAK.G
175	184	2	1257.67	1.4	1	26.5	26.5	95.00%	K.SWNQEQLLLK.S		K.SWNQEQLLLK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
322	A6ZKK2_YEAS7	16.74%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
200	210	2	1091.54	-1.5	0	28.5	29.4	95.00%	R.MLSSAGVNSAR.G		R.MLSSAGVNSAR.G
37	49	2	1496.72	-0.88	1	110	29.6	95.00%	K.TLFSSWADSLNTR.A		K.TLFSSWADSLNTR.A
50	61	2	1389.73	0.069	1	63.1	27.9	95.00%	R.AQDIYQTLPVSR.Q		R.AQDIYQTLPVSR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
323	A6ZME5_YEAS7	7.65%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
123	131	2	1035.54	3.6	1	32.1	28	95.00%	R.NVTEFSIAR.A		R.NVTEFSIAR.A
284	292	2	1100.66	0.43	1	23.1	18.8	94.50%	K.ILPFELLTR.S		K.ILPFELLTR.S
132	156	3	2446.23	1.5	1	38.9	26	95.00%	R.AICGIGAGGLNAISSIAVSDICTAR.E	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.AICGIGAGGLNAISSIAVSDICTAR.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
324	A6ZMB4_YEAS7	1.24%	100%	1

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
160	170	2	1171.64	0.82	1	39.3	27	95.00%	K.FIEVNPGIAGR.A		K.FIEVNPGIAGR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
325	A6ZY70_YEAS7	4.32%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	152	2	1776.89	-2	1	32.2	27.9	95.00%	K.SGFFQNWLVDGLPAAR.K		K.SGFFQNWLVDGLPAAR.K
243	255	2	1379.82	4.5	1	54	15.4	95.00%	R.VVGVIVNPVSIER.S		R.VVGVIVNPVSIER.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
326	A6ZZA0_YEAS7	16.78%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
66	79	2	1559.87	6.4	1	54.8	23.1	95.00%	K.ATLSTLFQELNVPK.S		K.ATLSTLFQELNVPK.S
134	143	2	1156.69	2	1	40.6	22.2	95.00%	K.LAEILKPVFQ.-		K.LAEILKPVFQ.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
327	A6ZT07_YEAS7	0.48%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2516	2524	2	1063.56	7.1	1	37.3	27.9	95.00%	N.DLELSNFVK.G		K.NIYCLSPPSILQEYLPENAEMVTEVNDLELSNFVK.G
77	85	2	1108.53	-1.6	1	30.9	30	95.00%	R.NSMLDIFNR.C		R.NSMLDIFNR.C

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
328	INP54_YEAST	10.94%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
74	85	2	1362.68	0.89	1	34.3	28.7	95.00%	R.ITTTAVNCLNEK.V	Carbamidomethyl (+57)	R.ITTTAVNCLNEK.V
214	226	2	1455.69	5.1	0	46.8	29.8	95.00%	Y.DPTTNYSSTTTLR.R		R.VTSTYDPTTNYSSTTTLR.R
305	321	3	1910.01	3.1	1	17.7	24.1	93.90%	R.SNALLFSDHQPVNLTVR.L		R.SNALLFSDHQPVNLTVR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
329	A6ZXN6_YEAS7	5.93%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
403	420	2	2198.06	5.5	0	52.2	27.8	95.00%	N.DTLPVYQPANYQHQYSFK.L		K.FDASLPTEEIYAFVELQLHDMLNSENDTLPVYQPANYQHQYSFK.L
338	346	2	1256.67	-0.81	1	41.9	26.8	95.00%	R.IENQWLLWR.K		R.IENQWLLWR.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
330	A6ZZC9_YEAS7	13.50%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
34	50	2	1863.88	-0.98	1	94.9	29.9	95.00%	R.SSVGQFMTFFAETVASR.T		R.SSVGQFMTFFAETVASR.T
24	33	2	1244.58	-1.2	1	40.8	31.3	95.00%	K.DLSQFGFFER.S		K.DLSQFGFFER.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
331	A6ZXS0_YEAS7	8.31%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
225	239	2	1639.88	0.36	0	83.1	23.5	95.00%	K.DFLSGTVLYLNSLAK.R		K.DFLSGTVLYLNSLAK.R
306	320	2	1749.83	1.7	0	85.6	29.6	95.00%	K.STIVGWNSTVGQWCR.L	Carbamidomethyl (+57)	K.STIVGWNSTVGQWCR.L

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
332	A6ZRQ9_YEAS7	3.93%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
622	633	2	1376.68	0.43	0	63.7	29.5	95.00%	R.NTVQNNSQGFLR.E		R.NTVQNNSQGFLR.E
557	569	2	1468.66	3	0	27.4	30	93.50%	R.NVTAMNGSFQNMR.S		R.NVTAMNGSFQNMR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
333	A6ZNC2_YEAS7	8.66%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
165	174	2	1150.6	2.9	1	40.7	27.7	95.00%	K.SLSNFIDTVR.S		K.SLSNFIDTVR.S
101	114	2	1592.94	6.2	1	56.9	12.8	95.00%	T.DLPGFPIIELVKPR.T		K.DDTPINFLEVNCEFFGPTLCTDLP GFPIIELVKPR.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
334	B3LMC0_YEAS1	2.43%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
933	943	2	1290.76	-0.41	1	42.3	18.4	95.00%	R.LTLDIPVVFFK.C		R.LTLDIPVVFFK.C
173	186	2	1557.81	6.1	1	53.4	26.5	95.00%	E.DPSKEPITALFLNN.D		R.IIYEDPSKEPITALFLNNDATACFA ATTSR.I

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
335	A6ZPF1_YEAS7	3.71%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
180	195	2	1692.95	6	0	48.4	18.9	95.00%	T.DNSLLPSLIKPVQAAQ.D		K.AIFTDNSLLPSLIKPVQAAQDVK.Y
2	11	2	1060.59	0.46	0	43.4	24.4	95.00%	M.VAQYTVPVGK.A		-.MVAQYTVPVGK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
336	A6ZRA2_YEAS7	6.44%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
230	238	2	1204.53	-0.35	1	45.4	30.2	95.00%	R.GAWYFENYR.F		R.GAWYFENYR.F
376	392	2	1814.84	6.3	1	44.4	29.8	95.00%	Y.ELPEQTTSHSSSQNVAT.D		K.MENINFNEDGEINVQENYELPEQ TTSHSSSQNVATDK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
337	A6ZNH0_YEAS7	29.25%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
38	48	2	1088.61	3.8	1	34.9	24.9	95.00%	K.VSSVLSALEGK.S		K.VSSVLSALEGK.S
61	80	2	1536.8	4	0	34.4	27.3	95.00%	K.LAAVPAAGPASAGGAAAASG.D		K.LAAVPAAGPASAGGAAAASGDA AAEEEK.E

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
338	A6ZZQ1_YEAS7	14.08%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
170	178	2	1014.57	3	1	34.5	28.1	95.00%	K.QISLEGLQK.Q		K.QISLEGLQK.Q
79	98	2	1929.99	5.6	0	74.6	25.1	95.00%	N.DNSGSIGSSAVTPIQALASR.A		R.VSLYHNDNSGSIGSSAVTPIQALA SR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
339	B5VMB7_YEAST	6.69%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
175	182	2	965.51	3.2	0	31.2	28.9	95.00%	K.FNAVVNFR.N		K.FNAVVNFR.N
134	150	2	1856.92	6.4	1	68.3	27.2	95.00%	R.SLANPIMTFSQNEVGLH.D		R.SLANPIMTFSQNEVGLHDTR.Y
83	92	2	1153.59	7	1	28.8	28.4	95.00%	Q.DFEHLGVQLP.D		K.ISGLSDESDPGLVVAIYDFQDFEHLGVQLPDEEMYYICDDYAIDIGICEEENR.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
340	A6ZPF8_YEAS7	2.03%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
205	219	2	1588.84	6.3	1	51	25.5	95.00%	K.ILATNPIMEAFGNAK.T		K.ILATNPIMEAFGNAK.T
1543	1559	2	1917	4.8	1	24.8	25.4	95.00%	F.DQVEAYIPAWLSLPSTK.R		K.FDQVEAYIPAWLSLPSTK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
341	A6ZND7_YEAS7	9.01%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
306	317	2	1340.72	6.7	1	37	27	95.00%	A.DEPARPLGVQFL.D		R.GSSTTPTNTSNAGDDEPGADEPARPLGVQFLDTFR.R
244	260	2	1569.83	2.8	0	26.1	26.5	95.00%	R.ANVAIAANAATNTAAAR.A		R.ANVAIAANAATNTAAAR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
342	FAB1_YEAST	1.27%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
59	73	2	1608.92	5.8	0	76.3	18	95.00%	T.DLVTNPILSNISVPK.I		K.KPSLHIMSTSTTSTTTDLVTNPILSNISVPK.I
1553	1566	2	1562.8	5.4	1	50	27.1	95.00%	R.TNEPQNAVTITTFK.D		R.TNEPQNAVTITTFK.D

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
343	A6ZZN6_YEAS7	8.42%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
10	29	2	2095.15	6.6	0	26.8	19.9	95.00%	N.DFILISLPQNAQPVTAPGSK.T		-.MATALYTANDFILISLPQNAQPVTAPGSK.T
129	141	2	1431.76	6.4	1	52.3	27.3	95.00%	K.DLITLISNESSQL.D		K.DLITLISNESSQLDADVR.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
344	A6ZW55_YEAS7	11.67%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
3	16	2	1339.73	4.4	0	61.5	27	95.00%	K.GTGGVVVGTQNPVR.D		K.GTGGVVVGTQNPVR.D
41	54	2	1590.7	5.2	1	37.4	30.8	95.00%	R.DQLSHESQTAYQQG.D		R.DQLSHESQTAYQQGDK.K

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
345	A7A0V2_YEAS7	4.37%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
646	662	2	1910.98	5.9	1	55	26.6	95.00%	R.DHAEYLSQVWVLAAGPR.G		R.DHAEYLSQVWVLAAGPR.G
674	686	2	1385.64	5.7	1	32.4	30.3	95.00%	T.DGGLHFHGESFAL.-		R.WATDGGLHFHGESFAL.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
346	A6ZS90_YEAS7	1.84%	100%	3

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
1133	1147	2	1639.87	5.2	0	37	24.4	95.00%	K.FQLPSAAFSTFPTVK.S		K.FQLPSAAFSTFPTVK.S
736	752	3	1943.99	-6.1	1	17	25.7	90.10%	K.MQMPLVSQENGIVQLLK.Q	Oxidation (+16)/ Deamidation (+1)	K.MQMPLVSQENGIVQLLK.Q
1068	1076	2	1055.62	-6.9	1	21.4	23.2	91.70%	P.DLNILKDLI.D		R.SEPDLNILKDLIDSNYVVFDVLLQFLTHQDPVVTAAAAQVYIR.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
347	A6ZQR0_YEAS7	6.65%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
65	74	2	1205.53	5.8	0	33.5	30.5	95.00%	H.DSCMPVPICK.S	Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.YSFSHDSCMPVPICK.S
36	56	2	2569.95	5.6	1	52.2	28.4	95.00%	E.DKPCCSQYGECGTGQYCLNNC.D	Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)/ Carbamidomethyl (+57)	R.VEAATFCNATQACPEDKPCCSQYGECGTGQYCLNNCDVR.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
348	PIN2_YEAST	16.31%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
238	259	3	2487.09	4.1	0	69.8	29.8	95.00%	Y.DNNNINNNLQGNSYNTPSSNHR.S	Deamidation (+1)	R.NSFIQNAANTGSNNAHVASQSPIFDISDYGENYYYDNNNINNNLQGNSYNTPSSNHR.S
203	226	2	2488.19	6.6	0	76.3	27.8	95.00%	R.NSFIQNAANTGSNNAHVASQSPIF.D		R.NSFIQNAANTGSNNAHVASQSPIFDISDYGENYYYDNNNINNNLQGNSYNTPSSNHR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
349	A6ZVG8_YEAS7	3.02%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
345	358	3	1691.87	-0.092	1	29.8	27.6	95.00%	R.ISILCVDNAIHYFK.I	Carbamidomethyl (+57)	R.ISILCVDNAIHYFK.I
471	484	2	1688.78	2.3	1	31.1	30.1	95.00%	K.ETAQLLSCQDSFYK.N	Carbamidomethyl (+57)	K.ETAQLLSCQDSFYK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
350	A6ZV27_YEAS7	11.26%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
210	218	2	912.54	3.5	0	25	24.7	95.00%	R.ISIPGITGR.A		R.ISIPGITGR.A
23	38	2	1590.83	3.1	0	55	26.9	95.00%	T.DLKPFPSAGSASSSIK.T		R.NQTDLKPFPSAGSASSSIK.T

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
351	A6ZKK0_YEAS7	2.41%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
260	268	2	1045.53	7.2	1	29.6	29.1	95.00%	D.DGTLAIWDR.R		K.LNPFNDWQFSTYGDDGTLAIWDR.R
893	908	2	1542.72	-0.39	0	89.9	29.9	95.00%	R.TSSPSSAVSTSAGNYK.N		R.TSSPSSAVSTSAGNYK.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
352	A6ZQ18_YEAS7	4.52%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
500	511	3	1537.73	6.1	0	30.5	29.6	95.00%	Y.DNFINHQNPHFR.D		R.EFEVSYDNFINHQNPHFR.D
53	77	3	2288.11	-1.2	1	122	27.1	95.00%	R.KRPTSPSISGSGSGGNSPSSSAGAR.Q		R.KRPTSPSISGSGSGGNSPSSSAGAR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
353	A6ZX15_YEAS7	5.93%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
460	477	2	1837.84	5.3	1	77.1	29.5	95.00%	E.DSQNSSLSSATVSGQNEK.S		R.DYYQWGVDTDALHTTCNGANSASETNPTEDSQNSSLSSATVSGQNEK.S
84	94	2	1271.63	3.5	1	61.5	28.9	95.00%	K.FIGNLDSFGFR.N		K.FIGNLDSFGFR.N

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
354	A6ZWX4_YEAS7	2.86%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
256	266	2	1399.69	5.7	0	60.2	29.6	95.00%	E.DWYYQLINASK.N		K.EDWYYQLINASK.N
463	473	2	1220.68	3.3	0	27.5	25.9	95.00%	K.LSYNVVTNAIK.S		K.LSYNVVTNAIK.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
355	A6ZZF9_YEAS7	2.39%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
211	223	2	1518.74	6.7	1	30.2	29.4	95.00%	R.QDGNVFFLHLLGC.D	Carbamidomethyl (+57)	R.QDGNVFFLHLLGCDTAGHSYRPYSAEYYDNVK.Y
76	84	2	1092.6	3.4	1	24.2	26.2	94.40%	K.TEFLAPFIR.S		K.TEFLAPFIR.S

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
356	B3LUC5_YEAS1	2.91%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
137	152	2	1583.9	6.2	1	44	21.3	95.00%	R.ATVAAIASSEVPTVIR.I		R.ATVAAIASSEVPTVIR.I
1048	1062	2	1515.71	6.8	1	28.5	30.1	94.90%	N.DDNAVAGTVNYAGLH.D		R.MLTTEMQASGTVDVTEDVSLSSEVISALNVEITSLPNPVAPPQTIAAPLNNNSNTNIVNDDNAVAGTVNYAGLHDEL.-

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
357	B3LFK7_YEAS1	1.21%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
499	506	2	983.54	3.8	1	30.4	25.9	95.00%	K.DDIIWLPL.D		K.DDIIWLPLDFETNGK.R
500	506	2	868.51	1.4	0	28.7	22.7	95.00%	D.DIIWLPL.D		K.DDIIWLPLDFETNGK.R

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
358	A6ZZQ6_YEAS7	8.91%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
56	73	2	1794.92	4.7	0	32.4	27.1	95.00%	K.SPIILQTSNGGAAYFAGK.G	Deamidation (+1)	K.SPIILQTSNGGAAYFAGK.G
195	208	2	1758.89	5.6	1	47.5	27	95.00%	E.DLYTKPEQVYNVYK.A		K.EDLYTKPEQVYNVYK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
359	A6ZTK7_YEAS7	2.96%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
420	431	2	1382.75	6.2	1	44	25.7	95.00%	S.DIVVPSNVIIWE.D		R.NLTSFTNLVIVSDHGMSDIVVPSNVIIWEDLLDK.K
144	153	2	1118.55	6	1	27.4	29.6	94.00%	R.VLSHFGSPEF.D		R.VLSHFGSPEFDPYVK.Y

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
360	B3LGN4_YEAS1	12.63%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
49	63	2	1497.79	4.9	1	43.3	26	95.00%	K.ALGGAPKPDYPIATQ.D		K.ALGGAPKPDYPIATQDTLTEYDAFLFGIPTR.F
70	79	2	1135.61	6.9	0	25.9	26.2	95.00%	Y.DAFLFGIPTR.F		K.ALGGAPKPDYPIATQDTLTEYDAFLFGIPTR.F

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
361	A6ZSV2_YEAS7	3.93%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
220	228	2	1115.63	6.4	1	39.8	25.8	95.00%	C.DVITWKELI.D		K.LIIVCDDPIESLQFDANCDVITWKELIDGFTK.D
161	173	3	1390.78	6	0	18	21.8	94.40%	R.TGSIPHFLPAVPR.Q		R.TGSIPHFLPAVPR.Q

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
362	B3LKX9_YEAS1	13.14%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
2	27	3	2341.2	6.3	0	44.7	24.7	95.00%	M.SAVGPGSNAGASVNGGSATAIATLLR.N	Acetyl (+42)/ Deamidation (+1)	-.MSAVGPGSNAGASVNGGSATAIATLLR.N
120	129	2	1168.63	5.2	0	41.7	26	95.00%	K.DFPHLIVSNK.A		K.DFPHLIVSNK.A

Index	AC	Coverage	Scaffold probability	Nb distinct peptides
363	A6ZTM4_YEAS7	18.90%	100%	2

Start	End	charge	Mr(expt)	ppm	MC	Ion score	Identity score	Scaffold probability	Sequence	Modification	Extended sequence
33	42	2	1104.59	5.7	1	30.1	28.4	95.00%	T.DEGGYKPVLK.Y		R.EHAFQGTNDLSTVLSPSTFTDEGGYKPVLK.Y
7	20	2	1557.76	6.3	1	30.8	28.9	95.00%	L.DASLLREHAFQGTN.D		-.MIPAPLDASLLREHAFQGTNDLSTVLSPSTFTDEGGYKPVLK.Y

Supplementary Table S3: Phosphoproteins with the corresponding phosphopeptides and localized phosphosites from solprotSP (*S.pombe*) and from SKMel (human melanoma) samples
(*) Phosphorylated amino acid **X** is displayed as **X#**

***S.pombe* - Trypsin - Whole tryptic digest**

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
1	sp|P78958|G3P1_SCHPO	5041	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
235	248	2	1547.7854	0.0006	0	34.72	R.VPTPDVSVVDLTVK.L	Phospho (ST)	120.85	VPT#PDVSVVDLTVK	92.17						--N----------
201	215	2	1423.672	0.0013	0	14.11	R.GASANIIPSSTGAAK.A	Phospho (ST)	52.58	GAS#ANIIPSSTGAAK	45.89						--N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
2	sp|P40370|ENO11_SCHPO	4694	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
415	432	3	1895.8324	0.0022	0	23.44	R.IEEELGSEGVYAGAHAGK.Y	Phospho (ST)	55.6	IEEELGS#EGVYAGAHAGK	19.53						------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
3	sp|O60101|PGK_SCHPO	2594	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
359	378	2	1997.9126	-0.0003	0	51.08	K.TCEAGNVVIVGGGDTATVAK.K	Phospho (ST)	177.69	TCEAGNVVIVGGGDTAT#VAK	28.5						----------N---
151	169	3	2099.9701	0.0023	0	57.56	K.SLTSLGDIFVNDAFGTAHR.A	Phospho (ST)	83.32	S#LTSLGDIFVNDAFGTAHR	21.3						N----------
348	358	2	1288.5564	0.0008	1	25.09	K.GTKSMLDACVK.T	Phospho (ST)	70.75	GTKS#MLDACVK	21.3						---Y-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
4	sp|Q92345|PDC2_SCHPO	2457	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
228	237	2	1029.454	0.0008	0	14.7	R.AAGAESAFVK.L	Phospho (ST)	58.72	AAGAES#AFVK	1000						-----Y----
556	569	2	1433.6318	0.0019	0	33.12	K.AVASANARPPTADN.-	Phospho (ST)	103.23	AVASANARPPT#ADN	57.73						----------N---

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
5	sp|Q10208|KPYK_SCHPO	2443	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
76	93	2	1950.0236	0.001	1	44.36	R.KASATNPLFPLAIALDTK.G	Phospho (ST)	104.88	KAS#ATNPLFPLAIALDTK	32.85						--N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
6	sp|O74173|EF1B_SCHPO	1174	2	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
2	13	2	1289.5542	0.0002	0	55.37	M.GFSDLTSDAGLK.Q	Phospho (ST)	125.17	GFSDLTS#DAGLK	22.85						
74	106	3	3605.4472	0.0106	0	25.83	K.EVSAYGPEGAAAAEEDEIDLFGSDEEEDPEAER.I	Phospho (ST)	101.34	EVSAYGPEGAAAAEEDEIDLFGS#DEEEDPEAER	69.94						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
7	sp|O14273|YET4_SCHPO	1055	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
190	216	3	2846.2354	-0.0018	0	33.85	R.NDEQLGNSPASITSKPATTSAAQPSSK.V	2 Phospho (ST)	101.28	NDEQLGNS#PAS#ITSKPATTSAAQPSSK	28.14	34.28					-------Y--Y----------
517	535	2	1749.7958	0.0024	0	44.03	K.QASAPSSPGTTSAAVPGGK.K	Phospho (ST)	99.69	QASAPSS#PGTTSAAVPGGK	20.35						------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
8	sp|O42914|YBI8_SCHPO	935	4	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
34	42	2	1089.4984	0.0016	1	14.22	K.RSDSPPVPR.E	Phospho (ST)	58.78	RSDS#PPVPR	32.85						---Y-----
35	42	2	933.3962	0.0005	0	31.69	R.SDSPPVPR.E	Phospho (ST)	55.54	SDS#PPVPR	28.8						--Y-----
140	175	3	3797.5762	0.0031	0	81.19	R.GWGDLVNSAANPDVAENEGNTPSGAQTPAAEEENVK.T	2 Phospho (ST)	172.93	GWGDLVNSAANPDVAENEGNTPS#GAQT#PAAEEENVK	36.01	20.65					----------Y---Y---------
95	112	3	1897.8544	0	1	16.9	R.ANNAAHPVDATGAPSNRR.N	Phospho (ST)	14.81	ANNAAHPVDATGAPS#NRR	26.66						----------N---

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
9	sp|O94497|YBS7_SCHPO	870	4	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
293	315	3	2611.1047	-0.0015	0	32.27	K.SDPVTDVDESQTIDEQSIPEAEK.G	Phospho (ST)	135.58	SDPVTDVDESQTIDEQS#IPEAEK	72.09						----------N------
510	528	2	1935.7894	0.0031	1	39.26	K.SPSGTKSPASGETSEAGVK.E	2 Phospho (ST)	92.38	SPSGTKS#PAS#GETSEAGVK	51.64	29.64					------Y--N---------
210	218	2	1026.4396	0.0014	0	32.14	K.GASLEDLSR.S	Phospho (ST)	75.38	GAS#LEDLSR	75.77						--N------
147	158	2	1240.6066	0.0003	0	48.35	K.ASSNLSLASLAK.T	Phospho (ST)	89.52	ASSNLSLAS#LAK	21.11						--------N---

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
10	sp|P36580|ALF_SCHPO	711	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
285	300	2	1905.8522	0.0013	0	62.04	K.VNIDTDTQFAYVEGVR.D	Phospho (ST)	184.55	VNIDT#DTQFAYVEGVR	33.7						------N---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
11	sp|O42938|K6PF_SCHPO	678	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
160	183	2	2576.1674	0.0015	1	42.33	K.SEESGAASNLESGLATPVVETLKK.A	2 Phospho (ST)	121.58	SEESGAASNLES#GLAT#PVVETLKK	45	74.2					----------Y---Y--------
160	182	2	2448.0714	0.0005	0	56.05	K.SEESGAASNLESGLATPVVETLK.K	2 Phospho (ST)	170.08	SEESGAASNLES#GLAT#PVVETLK	71.24	96.14					----------Y---Y-------
159	182	3	2496.2041	0.0045	1	41.24	K.KSEESGAASNLESGLATPVVETLK.K	Phospho (ST)	129.4	KSEESGAASNLESGLAT#PVVETLK	42.8						----------Y-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
12	sp|P31209|PABP_SCHPO	634	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
9	30	3	2357.9875	0.0015	0	32.69	K.QADAAVESDVNTNNEAVESSTK.E	Phospho (ST)	127.5	QADAAVES#DVNTNNEAVESSTK	58.55						-------N----------
634	653	2	2300.0234	-0.0015	0	50.75	R.VNEAIGVLQEFVDQEPGFTE.-	Phospho (ST)	144.48	VNEAIGVLQEFVDQEPGFT#E	1000						----------N-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
13	sp|Q10193|SRP1_SCHPO	630	4	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
170	197	3	3213.2842	0.0012	1	28.98	R.SPSPVSFAPQKSPVENETETNVDNGDTK.I	3 Phospho (ST)	140.37	S#PS#PVSFAPQKS#PVENETETNVDNGDTK	29.93	30.66	25.3				--Y--N-----Y----------
198	235	4	4151.8029	-0.0011	1	21.45	K.ISESNEKSGTEVEQQSAPNSNGNEEVNNLEPVGQNESK.Q	Phospho (ST)	57.62	ISESNEKSGT#EVEQQSAPNSNGNEEVNNLEPVGQNESK	19.88						-------N----------
181	197	2	1927.7678	-0.0006	0	59.68	K.SPVENETETNVDNGDTK.I	Phospho (ST)	138.6	S#PVENETETNVDNGDTK	72.08						Y----------
170	180	2	1223.5592	0.0005	0	33.27	R.SPSPVSFAPQK.S	Phospho (ST)	90.39	SPS#PVSFAPQK	24.21						--Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
14	sp|O36025|MPD2_SCHPO	520	4	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
140	160	3	2324.0326	0.0215	0	31.9	K.NANTSFTNAFSNEGISPGFLR.D	Deamidated (NQ); Phospho (ST)	111.33	NANTSFTNAFSNEGIS#PGFLR	75						----------N-----
161	177	2	1849.7396	-0.0045	0	73.29	R.DCFPSSNSITTGTASPK.L	Deamidated (NQ); Phospho (ST)	131.61	DCFPSSNSITTGTAS#PK	21.3						----------Y--
507	522	2	1964.7972	0.0038	0	83.57	K.ANSLSEISYNQQSECR.S	Phospho (ST)	147.56	ANS#LSEISYNQQSECR	33.68						--Y----------
317	328	2	1408.6488	0.0002	0	19.85	R.DTDSPLNILVDK.A	Phospho (ST)	50.7	DTDS#PLNILVDK	24.75						---Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
15	sp|P87228|SERA_SCHPO	520	5	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
9	37	4	3294.5357	0.0051	1	26.67	R.GNVEDSLNKLSLSPPDNNSSFLSNHFQVR.K	Phospho (ST)	91.68	GNVEDSLNKLSLS#PPDNNSSFLSNHFQVR	58.21						----------N----------
285	298	2	1463.7288	0.0016	0	24.46	R.GTVVDIPALVDASK.S	Phospho (ST)	48.3	GT#VVDIPALVDASK	55.13						-N----------
18	37	3	2338.0792	0.0049	0	43.95	K.LSLSPPDNNSSFLSNHFQVR.K	Phospho (ST)	51.78	LSLS#PPDNNSSFLSNHFQVR	25.92						---N----------
186	194	2	1172.4698	0.0013	0	18.29	K.VSSGCWEIR.G	Phospho (ST)	91.36	VSS#GCWEIR	32.4						--N------
84	94	2	1332.516	0.0004	0	22.18	K.TSMSEDDLVEK.I	Phospho (ST)	76.67	TSMS#EDDLVEK	42.65						---Y-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
16	sp|P87147|NACA_SCHPO	499	4	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
119	127	2	1217.487	0.0018	0	20.76	K.IEESFEQEK.A	Phospho (ST)	76.4	IEES#FEQEK	1000						---Y-----
119	137	2	2202.9594	0.0025	1	59.84	K.IEESFEQEKAVDETGVDAK.D	Phospho (ST)	126.48	IEES#FEQEKAVDETGVDAK	111.69						---Y----------
100	118	2	2011.8274	0.0016	0	41.34	K.EEAAITEESGDAQPADTAK.I	Phospho (ST)	86.98	EEAAITEES#GDAQPADTAK	55.25						--------N----------
94	118	3	2670.1516	-0.0029	1	40.15	K.QATETKEEAAITEESGDAQPADTAK.I	Phospho (ST)	101.39	QATETKEEAAITEES#GDAQPADTAK	36.59						----------N---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
17	sp|O74511|EKC1_SCHPO	456	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
407	423	2	2028.7034	0.0003	0	33.16	R.DLVMSDEDDDDSTFSDK.N	Oxidation (M); Phospho (ST)	63.48	DLVMS#DEDDDDSTFSDK	52.93						----Y----------
732	746	2	1832.7344	0.0018	1	70.84	R.RLSFESANDSDQDNR.D	Phospho (ST)	153.29	RLS#FESANDSDQDNR	39.2						--N----------
706	727	2	2510.9314	0.0008	0	49.5	R.ELSHNSSSNDEDDGNDEDPLSR.E	Phospho (ST)	145.51	ELSHNSSS#NDEDDGNDEDPLSR	21.51						-------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
18	sp|O13351|PMT3_SCHPO	438	2	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
15	39	4	2747.3001	-0.0014	0	16.36	K.SAITPTTGDTSQQDVKPSTEHINLK.V	Phospho (ST)	61.5	SAIT#PTTGDTSQQDVKPSTEHINLK	33.47						
2	14	2	1521.5286	0.0014	0	47.21	M.SESPSANISDADK.S	Acetyl (Protein N-term); 2 Phospho (ST)	80.86	S#ES#PSANISDADK	33.47	24.75					

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
19	sp|O14027|PDX1_SCHPO	414	4	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
178	189	2	1483.5958	0.0017	0	20.83	K.SMSPDELYTYAK.E	Phospho (ST)	83.46	S#MSPDELYTYAK	27.7						Y----------
281	290	2	1214.5444	0.0013	1	22.79	R.SVSSLEEKEK.L	Phospho (ST)	61.5	SVSS#LEEKEK	26.38						---N------
176	189	2	1726.7544	0.002	1	47.94	R.VKSMSPDELYTYAK.E	Oxidation (M); Phospho (ST)	49.49	VKS#MSPDELYTYAK	24.75						--Y----------
2	12	2	1268.6014	0.0001	1	25.92	M.SAEIKGSTQVK.A	Acetyl (Protein N-term); Phospho (ST)	30.89	S#AEIKGSTQVK	50.22						N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
20	sp|Q9Y7I8|YOI1_SCHPO	405	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
68	87	3	2486.008	0.0037	1	32.28	K.VQEEVKEESEDEEEDPAMLR.A	Oxidation (M); Phospho (ST)	68.28	VQEEVKEES#EDEEEDPAMLR	1000						--------Y----------
55	65	3	1431.628	-0.0003	1	25.91	R.TFSEDERLEVK.N	Phospho (ST)	73.02	TFS#EDERLEVK	24.76						--Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
21	sp|Q9UT19|METE_SCHPO	405	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
393	404	2	1364.6344	0.0008	0	42.5	R.AESPITNVEAVR.E	Phospho (ST)	81.23	AES#PITNVEAVR	46.24						--N---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
22	sp|O14081|TPSX_SCHPO	379	4	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?

175	186	2	1404.5742	-0.0002	0	53.46	R.SLSFSMNGTPQR.R	Deamidated (NQ); Phospho (ST)	58.06	SLS#FSMNGTPQR	24.75							--Y---------
160	170	3	1467.6166	0.0022	1	32.06	R.RHDSELEEFAR.R	Phospho (ST)	98.44	RHDS#ELEEFAR	1000							---Y-------
143	156	2	1570.7098	-0.0042	0	15.55	R.HQSPPPSSVLASQR.H	Deamidated (NQ); Phospho (ST)	46.98	HQS#PPPSSVLASQR	46.68							--Y----------
100	120	3	2344.048	0.0008	0	15.29	K.TPSSDSPSLENSLSNLNDLFK.S	Phospho (ST)	73.58	TPSSDSPSLENS#LSNLNDLFK	30.17							----------N---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
23	sp|P40998|THI2_SCHPO	377	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
23	38	3	1751.8291	0.0014	1	37.63	K.TAHNTVVKSEMGALSK.A	Phospho (ST)	80.46	TAHNTVVKS#EMGALSK	27.13						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
24	sp|Q9P6L9|YKQ7_SCHPO	374	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
643	666	3	2461.114	0.0017	0	40.76	K.GDTSPNSVEQGIEPQAASVVGSPR.S	Phospho (ST)	107.67	GDTSPNSVEQGIEPQAASVVGS#PR	72.77						----------N--
667	682	2	1739.835	0.0008	0	67.88	R.SSLVSNNSLEEGALLK.N	Phospho (ST)	126.33	SSLVS#NNSLEEGALLK	35.82						----N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
25	sp|O13637|SEC31_SCHPO	360	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
945	971	4	2872.3993	0.0084	0	16.01	R.VPPVQQPSHPNPYTPVAPQSPVAAASR.I	Deamidated (NQ); Phospho (ST)	35.35	VPPVQQPSHPNPYTPVAPQS#PVAAASR	35.33						----------N-------
901	930	3	2934.4474	0.0024	0	18.05	R.TSSVSTLPPPPPTASMTASAPAIASPPPPK.V	Phospho (ST)	68.89	TSSVSTLPPPPPTASMTASAPAIAS#PPPPK	65.69						----------N-----
885	900	2	1640.7026	0.0009	0	62.11	R.SPFPGASSAQPAAMSR.T	Phospho (ST)	81.69	SPFPGASSAQPAAMS#R	41.03						----------N-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
26	sp|TRYP_PIG|	358	2	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
98	107	2	1124.5244	0.0018	0	32.86	K.LSSPATLNSR.V	Phospho (ST)	80.64	LSSPATLNS#R	31.87						
108	115	2	921.4692	0.0008	0	28.44	R.VATVSLPR.S	Phospho (ST)	70.63	VATVS#LPR	30.7						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
27	sp|O42854|YFHH_SCHPO	349	7	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
482	522	4	4592.0269	0.0057	1	16.09	K.DSSSTSTQPTEQSNAQQAPSPKEEERPLPSEPSQNQPAEYR.D	Phospho (ST)	67.66	DSSSTSTQPTEQSNAQQAPS#PKEEERPLPSEPSQNQPAEYR	21.55						----------N----------
658	688	3	3095.4772	-0.004	1	20.74	K.VIDGIDPPKEAGAGATADVESAANSPITPPR.T	Phospho (ST)	46.15	VIDGIDPPKEAGAGATADVESAANSPIT#PPR	78.69						----------N---
711	734	3	2743.171	0.0001	1	52.84	R.ISEVTEDSIDEDKQNEVDPSTSAR.A	Phospho (ST)	126.38	ISEVTEDS#IDEDKQNEVDPSTSAR	48.16						-------N----------
482	503	3	2354.9896	0.0032	0	32.74	K.DSSSTSTQPTEQSNAQQAPSPK.E	Phospho (ST)	64.04	DSSSTSTQPTEQSNAQQAPS#PK	39.56						----------N--
1254	1279	3	2547.1066	0.0005	0	37.67	R.SSVPSPHSNASPSPTSSSMASAAPAR.T	Phospho (ST)	74.74	SSVPSPHSNASPS#PTSSSMASAAPAR	25.88						----------Y----------
472	503	3	3369.4492	0.001	1	32.65	K.STTNDSSPPKDSSSTSTQPTEQSNAQQAPSPK.E	Phospho (ST)	109.18	STTNDSSPPKDSSSTSTQPTEQSNAQQAPS#PK	52.54						----------N--
139	161	3	2548.1998	0.0039	0	20.78	K.IVDVDTLSAPFGNDSNSRPHSLK.N	Phospho (ST)	103.2	IVDVDTLSAPFGNDSNSRPHS#LK	26.1						----------N------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
28	sp|O74653|POB1_SCHPO	343	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
424	437	2	1584.7062	-0.001	0	54.25	R.FDSNEPSATSPILK.R	Phospho (ST)	143.61	FDSNEPSATS#PILK	24.44						---------Y----
220	243	3	2651.2483	0.0003	0	19.08	R.TPNDSSPLPYIENRPASSLAVSEK.I	Phospho (ST)	37.66	TPNDSS#PLPYIENRPASSLAVSEK	27.31						-----Y----------
424	438	2	1740.8076	-0.0007	1	17.71	R.FDSNEPSATSPILKR.S	Phospho (ST)	57.93	FDSNEPSATS#PILKR	19.33						---------Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
29	sp|O94740|CDC37_SCHPO	334	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
231	251	2	2369.9414	0.0031	0	70.15	K.NPVNENESEDEEGLSLSEDGK.K	Phospho (ST)	222.72	NPVNENES#EDEEGLSLSEDGK	147.63						-------Y----------
231	252	2	2498.0374	0.0041	1	71.64	K.NPVNENESEDEEGLSLSEDGKK.F	Phospho (ST)	119.75	NPVNENES#EDEEGLSLSEDGKK	78.66						-------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
30	sp|O74417|YJL4_SCHPO	322	4	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
300	312	2	1481.6002	0.0033	0	15.51	K.TSTPNMSNNPSPR.V	Phospho (ST)	41.89	TSTPNMSNNPS#PR	25.31						----------Y--
313	340	3	2933.4553	0.0017	1	48.74	R.VANTVVSPAPIPTIGSATIDKDAEGFQR.V	Phospho (ST)	69.34	VANTVVS#PAPIPTIGSATIDKDAEGFQR	23.75						------N----------
433	447	3	1663.8343	0.0008	1	42.71	K.AVKSPEISAPPGLYR.G	Phospho (ST)	111.16	AVKS#PEISAPPGLYR	49.5						---Y----------
240	261	3	2177.0206	0.0018	0	22.05	R.SAAQAMATVVPSVSTPGGTPPR.F	Oxidation (M); Phospho (ST)	41.75	SAAQAMATVVPSVSTPGGT#PPR	27.51						----------Y---

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
31	sp|O74887|TSA1_SCHPO	305	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
2	13	2	1421.696	0.0005	0	28.16	M.SLQIGKPAPDFK.G	Acetyl (Protein N-term); Phospho (ST)	38.91	S#LQIGKPAPDFK	1000						N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
32	sp|O43024|YGVA_SCHPO	303	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
344	365	2	2239.9854	0.0009	0	54.36	K.SQDSATPANVETTPSTATSAPK.K	Phospho (ST)	102.54	SQDSATPANVETT#PSTATSAPK	21.51						----------N---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
33	sp|Q9USH9|YJQ1_SCHPO	289	4	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
46	75	3	3447.5002	0.0123	1	54.89	K.ASAFNSDNDSNYDLKPEDDEVDEEVVPVKK.K	Phospho (ST)	122.29	AS#AFNSDNDSNYDLKPEDDEVDEEVVPVKK	19.16						-----Y----------
86	112	4	3191.3521	0.0066	1	26.95	K.ANAFEAFADEQSVEEEEEEDSEKPVRK.N	Phospho (ST)	98.47	ANAFEAFADEQS#VEEEEEEDSEKPVRK	49.46						----------Y----------
158	176	2	2075.8034	-0.0021	1	85.95	K.SKDDGSEALDDGDIESSEK.D	Phospho (ST)	146.71	SKDDGS#EALDDGDIESSEK	44.21						-----Y----------
46	74	3	3319.3972	0.0043	0	54.88	K.ASAFNSDNDSNYDLKPEDDEVDEEVVPVK.K	Phospho (ST)	185.33	ASAFNS#DNDSNYDLKPEDDEVDEEVVPVK	30.64						-----Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
34	sp|P78780|DHAS_SCHPO	282	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
319	328	2	1272.6118	0.0004	1	27.32	R.IRSDSIFDIK.F	Phospho (ST)	86.82	IRSDS#IFDIK	42.65						----Y-----
321	328	2	1003.4272	0.0009	0	35.57	R.SDSIFDIK.F	Phospho (ST)	111.47	SDS#IFDIK	33.76						--Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
35	sp|O74354|DNT1_SCHPO	277	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
146	167	3	2560.2514	0.0039	1	34.86	K.KNFVEAIDANSPGFVYRPTSIR.D	Phospho (ST)	70.44	KNFVEAIDANS#PGFVYRPTSIR	27.72						----------N----------
271	282	3	1419.7177	0.0014	0	14.11	K.YLVEHSPAALIK.E	Phospho (ST)	45.33	YLVEHS#PAALIK	25.47						-----N------
235	254	2	2179.9074	0.0015	0	79.86	R.ANFFSINDASSDSSSDAPLR.T	Phospho (ST)	215.15	ANFFSINDASSDSS#SDAPLR	28.87						----------N-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
36	sp|Q10074|YAN9_SCHPO	270	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
163	171	2	1129.5294	0.0013	0	32.07	K.VSDPNLHLR.S	Phospho (ST)	34	VS#DPNLHLR	1000						-N-------
14	26	2	1484.5588	0.002	0	42.13	R.SNENFASGSYSSR.R	Phospho (ST)	108.06	S#NENFASGSYSSR	67.97						N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
37	sp|O13771|YE99_SCHPO	264	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
230	257	3	3218.3602	0.0042	0	41.7	K.MYNEGVILGEDEAMEEEALSEAEENIPK.K	Phospho (ST)	130.43	MYNEGVILGEDEAMEEEALS#EAEENIPK	88.92						----------N--------
279	293	2	1801.7384	0.0018	1	49.98	K.RDELESSGTESDLER.D	Phospho (ST)	107.61	RDELESS#GTESDLER	19.33						----------N----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
38	sp|Q9Y7N0|YCK2_SCHPO	264	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
237	249	3	1371.6916	0.0004	0	25.24	K.AASPAVLPEGKPR.R	Phospho (ST)	42.85	AAS#PAVLPEGKPR	1000						--Y----------
498	521	3	2725.2388	0.0008	0	16.38	R.YVCKPDADSSEPASPVLMPTKPEK.K	Phospho (ST)	67.07	YVCKPDADSSEPAS#PVLMPTKPEK	39.69						----------Y----------
12	48	4	4078.6949	0.0052	1	32.4	K.AETKDEIANDGSPQLNGDNNIQSSDGHNDENEESLSR.K	Phospho (ST)	58.92	AETKDEIANDGS#PQLNGDNNIQSSDGHNDENEESLSR	41.89						----------N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
39	sp|O14062|RS12A_SCHPO	262	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
2	34	3	3662.6722	0.011	0	30.34	M.SEQGDQIEQVDVVEEVEVEAAAPETVSVEDALK.E	Acetyl (Protein N-term); Phospho (ST)	23.59	S#EQGDQIEQVDVVEEVEVEAAAPETVSVEDALK	21.32						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
40	sp|O74463|YQC1_SCHPO	260	8	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
495	510	2	1641.7152	0.0018	0	26.93	R.SDTASPETIAGLGDTK.N	Phospho (ST)	84.65	SDTAS#PETIAGLGDTK	20.91						----Y----------
275	286	2	1392.5602	0.001	0	65.93	R.CSSTDTLSSLSR.L	Phospho (ST)	124.8	CSS#TDTLSSLSR	22.85						--N---------
495	523	3	3011.3752	0.0031	1	55.65	R.SDTASPETIAGLGDTKNDPVVSTNNSVSR.I	Phospho (ST)	121.66	SDTAS#PETIAGLGDTKNDPVVSTNNSVSR	25.11						----Y----------
360	374	3	1893.7579	0.0015	0	17.57	K.VDLNHQMDVSDEEQR.F	Phospho (ST)	71.55	VDLNHQMDVS#DEEQR	1000						---------N-----
125	138	2	1542.676	0.0012	0	15.43	K.QMGANQISPSLSSK.T	Oxidation (M); Phospho (ST)	45.28	QMGANQIS#PSLSSK	24.75						-------N------
295	307	2	1397.7332	0.0013	0	25.73	K.ASLPLQSPPLAPK.T	Phospho (ST)	64.26	ASLPLQS#PPLAPK	37.11						------N------
375	395	2	2316.1034	-0.0004	0	35.27	R.FLSTPLGSFDESILGSSPINR.L	Phospho (ST)	103.41	FLSTPLGSFDESILGSS#PINR	24.44						----------N----
341	359	2	1961.9156	0.0021	0	33.67	R.SNSYAGAFPSVVSASLPTK.V	Phospho (ST)	109.62	SNSYAGAFPSVVSAS#LPTK	22.62						----------Y------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
41	sp|Q9Y7M8|YNTB_SCHPO	252	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
54	66	2	1542.7008	0.0001	0	43.84	K.GPPSFVTPEYIEK.Q	Phospho (ST)	65.42	GPPS#FVTPEYIEK	34.55						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
42	sp|O60184|CYC8_SCHPO	246	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
885	901	2	1772.8214	0.0021	1	73.02	K.KLENSTVVSGSPSSSSK.S	Phospho (ST)	123.26	KLENSTVVSGS#PSSSSK	20.05						----------Y------

986	996	2	1309.5804	0.0002	1	34.36	K.SESLPKSPEEK.S	Phospho (ST)	85.22	SESLPKS#PEEK	65.02						------Y----			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
43	sp|Q9UU99|YJX4_SCHPO	242	4	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
556	564	2	1119.5016	0.0015	1	34.36	K.SKASFEFPK.E	Phospho (ST)	72.8	SKAS#FEFPK	30.04						---Y-----
408	422	2	1683.749	0.0026	0	56.79	K.ASLVENSQTQSSTPR.K	Phospho (ST)	153.9	ASLVENSQTQSST#PR	32.4						----------N--
216	245	4	3219.4645	0.0036	1	20.42	K.SPDAVAYSSETVSDEKQPTEHPVSANVPAK.S	Phospho (Y)	129.91	SPDAVAYSSETVS#DEKQPTEHPVSANVPAK	33.45						------N----------
948	959	2	1381.6494	0.0004	1	27.45	K.KEDSIPVAQSTK.A	Phospho (ST)	66.36	KEDS#IPVAQSTK	47.61						---N-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
44	sp|P58234|RS19A_SCHPO	225	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
134	144	2	1361.5662	0.0023	0	65.08	R.IAYSLLEEESE.-	Phospho (ST)	178.71	IAYSLLEEES#E	173.24						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
45	sp|Q10475|IF4G_SCHPO	223	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
441	461	3	2239.9963	0.0005	0	40.05	R.SGSQVSDQVVESPNSSTLSPR.N	Phospho (ST)	119.75	SGSQVSDQVVESPNSSTLS#PR	27.14						----------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
46	sp|Q9Y7Z8|MYO1_SCHPO	217	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
359	376	2	2049.0394	-0.0014	1	47.72	R.RGSVYEVPLNPTQALAVR.D	Phospho (ST)	126.34	RGS#VYEVPLNPTQALAVR	28.5						--Y----------
1205	1217	2	1529.5682	0.0011	1	15.91	R.ASAVRGSDEEEDW.-	Phospho (ST)	59.74	ASAVRGS#DEEEDW	21.61						------Y------
780	787	2	1030.496	0	1	41.58	R.RYSILGSR.K	Phospho (ST)	38.73	RYS#ILGSR	26.38						--Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
47	sp|Q9P7E8|APP1_SCHPO	214	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
353	367	2	1791.8806	0.0025	1	39.04	K.NVENPVSHHLKSPVR.T	Phospho (ST)	88.17	NVENPVSHHLKS#PVR	61.12						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
48	sp|O14250|PSA1_SCHPO	213	2	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
4	18	2	1774.6962	0.0014	0	58.96	R.NQYDGDATTWSPQGR.L	Phospho (ST)	145.54	NQYDGDATTWS#PQGR	45.71						
249	272	2	2512.0214	0.0015	0	97.84	R.AAAEEPQAPTAEAILDSADAMETD.-	Oxidation (M); Phospho (ST)	101.78	AAAEEPQAPTAEAILDSADAMET#D	40.07						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
49	sp|Q9UUA1|YJX1_SCHPO	210	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
408	425	5	2191.0091	0.0032	1	21.85	K.FLSENTKPEDSSIHKHSR.D	Phospho (ST)	65.66	FLSENTKPEDSSIHKHS#R	28.28						----------N-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
50	sp|O14319|CUE5_SCHPO	207	2	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
370	388	3	2071.8835	0	1	29.39	K.DSTSVEAEKTETDEPAVGK.G	Phospho (ST)	78.46	DSTSVEAEKT#ETDEPAVGK	19.69						
407	424	3	2042.8333	0.0016	1	26.86	K.NADSEANLEEKSDVGEEK.E	Phospho (ST)	63.2	NADSEANLEEKS#DVGEEK	48.65						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
51	sp|O74448|PIN1_SCHPO	207	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
47	66	3	2241.022	0.0018	0	52.58	K.FIANELQESVTPTEASNSPK.I	Phospho (ST)	111.03	FIANELQESVT#PTEASNSPK	38.95						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
52	sp|P28758|SODC_SCHPO	206	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
98	116	2	2063.9954	0.0026	0	34.37	K.TTFSDSVISLFGANSIIGR.T	Phospho (ST)	111.18	TTFSDS#VISLFGANSIIGR	21.3						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
53	sp|Q10251|IF2P_SCHPO	204	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
70	87	2	2066.8294	-0.0023	0	64.92	K.NQVSDDESQELESPQGPK.E	Deamidated (NQ); Phospho (ST)	110.74	NQVS#DDESQELESPQGPK	58.09						---Y----------
115	132	3	2132.9173	0.0022	1	30.64	K.KVEEDDEPQEIESPQGPK.E	Phospho (ST)	149.73	KVEEDDEPQEIES#PQGPK	1000						----------Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
54	sp|O14327|PAB2_SCHPO	201	2	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
2	12	2	1370.5248	0.001	0	42.74	M.SDQDALDTQEK.E	Acetyl (Protein N-term); Phospho (ST)	51.32	S#DQDALDTQEK	51.02						
2	18	2	2113.9154	0.0029	1	75.4	M.SDQDALDTQEKELLEMK.E	Acetyl (Protein N-term); Phospho (ST)	55.2	S#DQDALDTQEKELLEMK	39.63						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
55	sp|O74766|PUT2_SCHPO	197	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
388	405	2	1853.866	0.0001	0	55.46	K.VLESAASDSEIEVLAGGK.A	Phospho (ST)	181.55	VLESAAS#DSEIEVLAGGK	28.76						---Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
56	sp|P50998|AMPD_SCHPO	194	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
97	106	2	1138.5514	0.0019	0	18.23	R.RPSVSASTVR.N	Phospho (ST)	42.04	RPS#VSASTVR	24.75						--Y-------
784	799	2	1763.7076	0.0003	0	57.33	K.YDAMTGTSDPLSASPR.T	Oxidation (M); Phospho (ST)	85.95	YDAMTGTSDPLSAS#PR	26.53						----------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
57	sp|O13936|SPT5_SCHPO	190	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
35	51	2	1783.712	-0.0028	0	66.14	R.ASPNGSDLLNDDSEAAK.I	Deamidated (NQ); Phospho (ST)	103.88	AS#PNGSDLLNDDSEAAK	25.37						-Y---------------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
58	sp|P50519|HSP9_SCHPO	189	2	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
40	59	3	2231.923	0.001	1	45.42	K.VASAFTSDEDKSTSQEAHDK.A	Phospho (ST)	98.18	VASAFTSDEDKS#TSQEAHDK	38.66						
29	39	2	1261.5602	0.0011	1	24.52	K.AKESITGAYDK.V	Phospho (ST)	83.52	AKES#ITGAYDK	40.71						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
59	sp|O74975|PCY1_SCHPO	184	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
62	78	2	1993.8882	0.0001	0	64.22	K.SLEEISQSVSPVEEEPR.D	Phospho (ST)	211.79	SLEEISQSVS#PVEEEPR	64.79						---------N-------
337	345	2	1140.4618	0.0018	0	26.37	R.SSSHYDLPR.V	Phospho (ST)	60.21	SSS#HYDLPR	21.3						-N-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
60	sp|Q9HGL2|YHLA_SCHPO	176	2	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
856	865	2	1081.5064	0.0008	0	29.65	R.GSPVLSDLSK.L	Phospho (ST)	53.29	GS#PVLSDLSK	49.6						
759	776	2	1894.8174	0.0004	0	41.99	R.SPSLNSNNSSAHASTVSR.N	Phospho (ST)	76.09	SPSLNS#NNSSAHASTVSR	20.26						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
61	sp|P08094|RLA2_SCHPO	174	2	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
96	110	2	1843.604	0.0021	0	21.53	K.EEEESDEDMGFGLFD.-	Oxidation (M); Phospho (ST)	51.61	EEEES#DEDMGFGLFD	1000						
92	110	2	2300.8214	0.0023	1	48	K.EEAKEEEESDEDMGFGLFD.-	Oxidation (M); Phospho (ST)	42.62	EEAKEEEES#DEDMGFGLFD	1000						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
62	sp|P30821|P25_SCHPO	172	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
179	189	2	1339.5666	0.001	0	63.04	R.NVSDDELEIAR.I	Phospho (ST)	181.18	NVS#DDELEIAR	1000						--Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
63	sp|P19117|IPYR_SCHPO	172	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
281	289	2	1148.4952	0.0009	0	20.13	K.WFYISGSPL.-	Phospho (ST)	73.29	WFYISGS#PL	43.03						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
64	sp|O13735|FAT1_SCHPO	169	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
509	524	2	1788.7314	0.0012	0	44.18	K.AESSEDTSEIESLQGK.L	Phospho (ST)	109.67	AESSEDTSEIES#LQGK	72.42						----------N----
593	608	2	1871.7962	0.0024	0	78.41	K.GGLANFENDSLEELER.L	Phospho (ST)	147.74	GGLANFENDS#LEELER	1000						---------Y------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
65	sp|O74500|NUP60_SCHPO	161	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
112	136	3	2790.2596	0.0024	0	24.97	R.DTSAQATPSIVEQSPNQMLANFFSK.K	Phospho (ST)	120.42	DTSAQATPSIVEQS#PNQMLANFFSK	60.96						----------N----------
687	700	3	1683.742	0.0027	1	23.52	K.TDKQGSLEEEPFPK.F	Phospho (ST)	67.88	TDKQGS#LEEEPFPK	20.65						-----N-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
66	sp|O59797|YCO6_SCHPO	159	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
15	36	3	2315.9296	0.0013	0	19.82	K.MSAAPTPHNTPSGTSAPNFGAK.A	Oxidation (M); 2 Phospho (ST)	37.27	MSAAPT#PHNT#PSGTSAPNFGAK	32.81	40.34					-----Y-----Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
67	sp|P78820|ACAC_SCHPO	158	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
1176	1189	2	1773.8452	0.0002	1	29.22	R.RLQSVSDLSWYVNK.T	Phospho (ST)	80.91	RLQS#VSDLSWYVNK	21.3						---Y----------
1177	1189	2	1617.7444	0.0005	0	53.44	R.LQSVSDLSWYVNK.T	Phospho (ST)	142.71	LQS#VSDLSWYVNK	33.7						--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
68	sp|Q9USU9|TOA1_SCHPO	156	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
78	101	2	2515.2714	0.0032	0	70.28	R.TDSLDVTAPAVANSPILNNIAAIR.A	Phospho (ST)	170.05	TDSLDVTAPAVANS#PILNNIAAIR	92.26						----------N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
69	sp|Q10268|MAC1_SCHPO	153	4	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
496	513	3	2067.808	0.0006	0	31.83	R.NNSSNNLHAQGGMPMNMR.G	Oxidation (M); Phospho (ST)	16.42	NNS#SNNLHAQGGMPMNMR	19.84						--N----------
622	639	2	1902.8112	0.0003	0	32.8	R.SNSSTDLFGQSGIPGNSR.G	Phospho (ST)	103.16	S#NSSTDLFGQSGIPGNSR	20.35						N----------
470	484	2	1678.7126	-0.0007	0	56.74	R.NNSSNDLHAQAGMLK.N	Phospho (ST)	157.33	NNS#SNDLHAQAGMLK	26.38						--N----------
573	590	3	2029.8271	0.0023	0	26.04	R.NNSSNDLHAHGGMPVNMR.G	Phospho (ST)	60.59	NNS#SNDLHAHGGMPVNMR	39.56						--N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
70	sp|Q09826|SDS23_SCHPO	150	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
322	335	2	1754.7512	0.0009	0	51.23	R.LWLVQSPSCPPSPK.N	2 Phospho (ST)	147.52	LWLVQSPS#CPPS#PK	42.65	79.31					-------Y---Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
71	sp|Q9Y7X7|YGRB_SCHPO	149	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
9	18	2	1286.5556	0.0013	0	19.07	K.NSLENENFLK.E	Phospho (ST)	46.69	NS#LENENFLK	1000						-Y--------
1	18	2	2191.9734	0.0027	1	34.65	-.METTVSAKNSLENENFLK.E	Acetyl (Protein N-term); Oxidation (M); Phospho (ST)	44.23	METTVSAKNS#LENENFLK	20.17						---N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
72	sp|O13759|CSX1_SCHPO	144	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
30	59	3	3207.5032	0.0025	1	40.53	K.MSASNSDVNAPISPVVDEGKSELVSPTLER.L	Phospho (ST)	87.16	MSASNSDVNAPIS#PVVDEGKSELVSPTLER	34.23						----------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
73	sp|O74526|KJ45_SCHPO	144	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
247	259	3	1489.7662	0.0008	1	40.87	R.KKPSPLSPNSSIR.N	Phospho (ST)	81.94	KKPSPLS#PNSSIR	31.81						------Y------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
74	sp|O14340|YB35_SCHPO	143	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
693	705	2	1555.6786	0.002	0	42.33	R.QESLPSQQTTETK.H	Phospho (ST)	87.78	QES#LPSQQTTETK	35.82						--N----------
888	904	2	1893.8748	0.0028	0	18.04	K.SVSSELTHASKPSLDEK.T	Phospho (ST)	50.1	SVSSELTHASKPS#LDEK	39.63						----------N----
378	398	2	2393.9014	-0.0019	0	78.48	K.FTQSNASGNSGWDDNESDIDR.A	Phospho (ST)	197.32	FTQSNASGNS#GWDDNESDIDR	31.87						---------N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
75	sp|O60129|FKH2_SCHPO	141	4	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
372	386	2	1586.6344	-0.0004	0	67.39	K.DVGSPSTAETSAEEK.Q	Phospho (ST)	104.63	DVGS#PSTAETSAEEK	30.7						---Y----------
332	344	2	1426.7486	0.0014	0	31.06	R.EGSPSLPIPILPK.M	Phospho (ST)	103.1	EGS#PSLPIPILPK	30.83						--Y----------
624	639	2	1951.9402	-0.0002	1	29.16	K.EKSPQQYIQVPQSNVK.S	Phospho (ST)	67.63	EKS#PQQYIQVPQSNVK	26.42						--Y----------
319	329	2	1174.6006	0.0008	0	24.32	R.SPSSPVPLLAK.K	Phospho (ST)	70.59	SPSS#PVPLLAK	24.44						---Y-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
76	sp|Q9HDX7|YK1D_SCHPO	141	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
57	65	2	1137.475	0.0007	0	18.79	R.SFSSFQDLK.G	Phospho (ST)	98.16	SFSS#FQDLK	22.85						--N------
121	134	2	1554.7534	-0.0007	1	28.18	K.SSVEATISPLKDTK.S	Phospho (ST)	76.81	SSVEATIS#PLKDTK	24.84						-------Y------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
77	sp|P40381|SWI6_SCHPO	140	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
223	242	2	2266.9874	0.0033	0	65.94	K.ESNESEDIQIAETPSNVTPK.K	Phospho (ST)	173.16	ESNESEDIQIAETPSNVT#PK	68.23						----------Y--
18	33	2	1841.7638	-0.0003	0	43.54	R.SVIDDDSEPELPSMTK.E	Phospho (ST)	153.36	SVIDDDS#EPELPSMTK	53.39						------Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
78	sp|Q10414|MU161_SCHPO	138	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
317	328	3	1415.6212	0.0018	0	29.49	K.SESHSALNNLHK.S	Phospho (ST)	117.95	SES#HSALNNLHK	20.17						--Y---------
277	290	2	1706.7996	0.0008	1	28.82	K.RASEDQIIPQQTNK.F	Phospho (ST)	49.23	RAS#EDQIIPQQTNK	31.11						--N----------
278	290	2	1551.677	-0.0047	0	38.56	R.ASEDQIIPQQTNK.F	Deamidated (NQ); Phospho (ST)	55.9	AS#EDQIIPQQTNK	59.56						-N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
79	sp|Q09717|RANG_SCHPO	138	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
58	80	2	2570.1614	0.0037	0	38.92	K.KPAEGDEDAEPASPEVHFEPIVK.L	Phospho (ST)	162.55	KPAEGDEDAEPAS#PEVHFEPIVK	1000						----------Y----------
49	80	4	3459.5445	0.009	1	27.99	K.SGASTNDEKKPAEGDEDAEPASPEVHFEPIVK.L	Phospho (ST)	93.52	SGASTNDEKKPAEGDEDAEPAS#PEVHFEPIVK	80.9						----------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
80	sp|P56329|IF2B_SCHPO	136	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
40	57	2	1887.6646	0.0003	0	56.01	K.DGPEASSAGATDEDDSER.K	Phospho (ST)	130.19	DGPEASS#AGATDEDDSER	22.85						------N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
81	sp|Q09756|HXK1_SCHPO	132	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
2	12	2	1489.6156	0.0017	0	32.25	M.SLHDAYHWPSR.T	Acetyl (Protein N-term); Phospho (ST)	44.99	S#LHDAYHWPSR	46.68						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
82	sp|Q9UUE6|SYKC_SCHPO	132	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?

2	14	2	1509.673	0.0018	0	45.35	M.SEEQVNGVTQAVK.A	Acetyl (Protein N-term); Phospho (ST)	33.4	S#EEQVNGVTQAVK	31.51									

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
83	sp|Q09822|CDC15_SCHPO	130	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
772	783	3	1372.663	0.0017	1	17.87	R.SVSPNPLGPNRR.S	Phospho (ST)	28.35	SVS#PNPLGPNRR	28.34						--Y---------
634	646	2	1395.629	0.0008	0	17.25	R.NTSIASDIDGVPK.K	Phospho (ST)	63.59	NTSIAS#DIDGVPK	45.2						-----Y-------
604	618	2	1641.713	-0.0004	0	37.64	R.QSTSVDDEAPVSLSK.T	Phospho (ST)	71.92	QSTSVDDEAPVSLS#K	21.3						----------N-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
84	sp|O94733|YQ61_SCHPO	123	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
128	144	2	2064.8334	0.0012	0	62.32	R.QFCNVVGYDMPTPGEQK.E	Oxidation (M); Phospho (ST)	57.42	QFCNVVGYDMPT#PGEQK	27.99						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
85	sp|Q9P7V5|SEC7B_SCHPO	118	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
40	57	2	2116.7894	0.0002	0	49.35	K.IINDSDNEDDENGMDLGR.V	Oxidation (M); Phospho (ST)	63.23	IINDS#DNEDDENGMDLGR	1000						----Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
86	sp|Q9P7B2|RS8B_SCHPO	117	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
60	74	2	1648.6782	0.0012	0	61.49	R.LDSGNFSWGSEGVSK.K	Phospho (ST)	136.85	LDS#GNFSWGSEGVSK	105.5						--Y----------
60	75	3	1776.7735	0.0015	1	16.85	R.LDSGNFSWGSEGVSKK.T	Phospho (ST)	53.4	LDS#GNFSWGSEGVSKK	43.77						--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
87	sp|O74452|SCW1_SCHPO	114	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
1	18	2	1998.9734	-0.0002	0	63.03	-.MFVGSPSAIEKPLSLSSK.T	Acetyl (Protein N-term); Phospho (ST)	58.87	MFVGS#PSAIEKPLSLSSK	24.75						----N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
88	sp|O13370|DED1_SCHPO	113	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
2	18	2	1940.8364	0	0	48.49	M.SDNVQQQVDSVGSVTEK.L	Acetyl (Protein N-term); Phospho (ST)	54.06	S#DNVQQQVDSVGSVTEK	23.13						N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
89	sp|Q9US06|PAF1_SCHPO	113	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
385	404	3	2297.992	0.002	0	57.61	R.SVEGSLNEELSEEEKPAESR.E	Phospho (ST)	149.55	SVEGSLNEELS#EEEKPAESR	103.58						----------N---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
90	sp|Q9C104|GDE1_SCHPO	112	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
1065	1076	2	1462.5514	0.0014	0	18.89	R.ALNQYDESLESD.-	Phospho (ST)	111.76	ALNQYDESLES#D	79.13						----------N-
521	544	3	2614.1257	-0.0002	0	37.96	R.SPSFAASRPSSVDFMSQSTDSLSK.N	Oxidation (M); Phospho (ST)	30.85	S#PSFAASRPSSVDFMSQSTDSLSK	24.44						--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
91	sp|Q09864|HSP60_SCHPO	111	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
68	79	2	1394.6506	0.0024	0	26.18	R.NVLIDQPFGSPK.I	Deamidated (NQ); Phospho (ST)	57.16	NVLIDQPFGS#PK	1000						---------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
92	sp|O14031|OPT_SCHPO	110	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
5	14	2	1124.524	0.0014	0	26.36	R.NSASIPTSIR.K	Phospho (ST)	64.44	NS#ASIPTSIR	28.76						-N--------
16	36	2	2170.9274	0.0007	0	78.44	K.TSENEVSGDETPAGVGNLSTK.T	Phospho (ST)	196.45	TSENEVS#GDETPAGVGNLSTK	62.59						------N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
93	sp|Q9UT53|NMAH_SCHPO	108	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
19	45	3	3148.2922	-0.0013	0	58.96	R.NSSSSNVIQYSDEFSPDEDWLNEHAAK.E	Phospho (ST)	131.32	NSSSSNVIQYSDEFS#PDEDWLNEHAAK	46.43						----------Y----------
51	58	3	1076.5609	0.0005	1	19.1	R.IRRPSVNR.A	Phospho (ST)	34.33	IRRPS#VNR	1000						----N---
77	94	2	2053.8914	0	0	22.5	R.EADVASLGEVMDLEEVPR.G	Oxidation (M); Phospho (ST)	20.57	EADVAS#LGEVMDLEEVPR	1000						-----Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
94	sp|O14029|SEC16_SCHPO	108	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
561	578	3	1842.853	0.0017	0	29.85	K.SSASPPANAPIVSSDVHK.N	Phospho (ST)	101.74	SSAS#PPANAPIVSSDVHK	27.03						---N----------
1	19	2	2309.9354	-0.0004	1	38.44	-.MDIESDHEPKESSVDLEGR.H	Acetyl (Protein N-term); Oxidation (M); Phospho (ST)	45.61	MDIES#DHEPKESSVDLEGR	29.56						----N----------
177	195	3	2279.0281	0.0035	0	17.53	K.EIYDNDETIPKPPSPEVEK.I	Phospho (ST)	68.21	EIYDNDETIPKPPS#PEVEK	55.46						----------N-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
95	sp|O74536|SNF1_SCHPO	107	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?

359		380	3	2646.1618	-0.0038	1	29.39	K.RVDSFLSVSPPAFSEYTSELQK.K	2 Phospho (ST)	83.09	RVDS#FLSVS#PPAFSEYTSELQK	20.9	24.15					------N-N----------
360		380	2	2410.0994	0.0013	0	65.54	R.VDSFLSVSPPAFSEYTSELQK.K	Phospho (ST)	119.28	VDSFLSVS#PPAFSEYTSELQK	45.27						-------N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
96	sp|O74428|YQ5C_SCHPO	107	2	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
261	270	2	1123.5396	0.001	0	48.55	R.GNSLSLLANR.K	Phospho (ST)	82.36	GNS#LSLLANR	21.3						
90	103	3	1699.8064	0.0021	1	25.87	K.QRSLNDLHELNGPK.H	Phospho (ST)	54.8	QRS#LNDLHELNGPK	1000						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
97	sp|P41887|HSP90_SCHPO	106	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
440	458	2	2279.0234	-0.0011	0	57.32	R.YNSLNSPDDLISLEDYITK.M	Phospho (ST)	174	YNSLNSPDDLIS#LEDYITK	78.69						----------N-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
98	sp|Q10164|RGA2_SCHPO	105	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
269	283	2	1716.7732	0.0013	0	60.43	R.SDNLSPLSLNTSSFR.R	Phospho (ST)	112.75	SDNLS#PLSLNTSSFR	26.78						----N----------
133	147	2	1738.6744	0.0021	0	62.42	R.ANSPQSDSYSSPYEK.G	Phospho (ST)	142.24	ANS#PQSDSYSSPYEK	64.54						--N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
99	sp|O42923|CIP1_SCHPO	104	5	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
391	405	2	1744.7192	0.001	0	25.94	K.NTSVSQSQPASPNLR.F	2 Phospho (ST)	72.04	NTSVSQS#QPAS#PNLR	25.31	45.55					------Y---Y----
80	105	3	2694.1903	0.0052	0	31.27	R.AASPAPSDSFPTFGYSQLGGLENSSK.G	Phospho (ST)	144.31	AAS#PAPSDSFPTFGYSQLGGLENSSK	19.24						--N----------
55	68	2	1458.6766	0.0011	1	29.4	R.KTSGSGSSAPLYPK.W	Phospho (ST)	107.13	KTS#GSGSSAPLYPK	20.35						--N----------
461	471	2	1217.5344	0.0015	0	23.21	K.ASTLSSPFNSK.N	Phospho (ST)	58.13	ASTLSS#PFNSK	19.33						-----Y-----
446	460	2	1785.8188	0.0003	1	46.71	R.SIDDKIYGNESPLQK.A	Phospho (ST)	132.03	SIDDKIYGNES#PLQK	44.37						----------Y----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
100	sp|Q09747|DBP5_SCHPO	104	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
11	24	2	1730.665	-0.0022	0	40.79	K.TDWASLDSDEEVQR.I	Deamidated (NQ); Phospho (ST)	61.7	TDWASLDS#DEEVQR	27.03						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
101	sp|O43059|YGT6_SCHPO	104	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
411	426	3	1806.8056	0.0006	0	14.75	K.ASPFNKPNSVHSEASR.N	Phospho (ST)	46.55	ASPFNKPNS#VHSEASR	25.88						--------N-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
102	sp|O74864|RLA0_SCHPO	103	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
265	312	5	4780.0281	0.007	0	21.62	K.AFLADPSAFVVAAAPAAAAGGEAEAPAAEAAAEEEEESDEDMGFGLFD.-	Oxidation (M); Phospho (ST)	40.31	AFLADPSAFVVAAAPAAAAGGEAEAPAAEAAAEEEEES#DEDMGFGLFD	37.83						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
103	sp|O74871|YCW3_SCHPO	102	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
131	148	3	2039.9074	0.0025	1	18.8	K.QSVSNEVSSPDVAKEQEK.L	Phospho (ST)	64.43	QSVSNEVSS#PDVAKEQEK	32.85						--------Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
104	sp|Q09794|PYR1_SCHPO	101	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
1880	1906	3	2769.3202	0.0005	0	42.55	K.VSALMSPGLPHAAPSLAEAFGQAPENK.A	Phospho (ST)	118.28	VSALMSPGLPHAAPS#LAEAFGQAPENK	24.95						-----Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
105	sp|Q9USX3|RAD60_SCHPO	100	2	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
70	100	3	3448.4812	-0.0027	1	60.12	R.QSTILDADEGNQDVSDTTPNACLNEGRHSPK.S	Phospho (ST)	93.98	QSTILDADEGNQDVSDTTPNACLNEGRHS#PK	22.06						
101	117	2	1957.8986	0.0018	0	59.79	K.SAISCVTQPVSPVYNTR.A	Phospho (ST)	161.34	SAISCVTQPVS#PVYNTR	26.79						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
106	sp|P56287|EI2BE_SCHPO	100	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
499	524	3	3038.2492	0.0077	1	53.41	R.DSANTINSEDFDEGDFNKEAQQSLER.A	Phospho (ST)	155.84	DSANTINS#EDFDEGDFNKEAQQSLER	51.71						-------Y----------
499	516	2	2096.7854	0.0007	0	66.4	R.DSANTINSEDFDEGDFNK.E	Phospho (ST)	200.66	DSANTINS#EDFDEGDFNK	86.62						-------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
107	sp|Q9USS2|PPK29_SCHPO	98	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
461	491	3	3356.4322	0.0004	0	46.74	K.FSASEVTEDNGSPNAGLDADNVDVEEVVNQR.Y	Phospho (ST)	179.66	FSASEVTEDNGS#PNAGLDADNVDVEEVVNQR	42.44						----------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
108	sp|O14224|GDIR_SCHPO	98	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
2	32	3	3511.5082	0.0029	0	59.83	M.SVNNEVSADQHNPELEDDTFEHGPPVSLGEK.K	Acetyl (Protein N-term); Phospho (ST)	89.27	S#VNNEVSADQHNPELEDDTFEHGPPVSLGEK	23.1						N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
109	sp|O13734|SGO2_SCHPO	98	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
233	242	2	1294.5606	0.0012	0	16.37	K.NHEYEIVSPK.S	Phospho (ST)	78.96	NHEYEIVS#PK	44.28						-------Y--
330	345	2	1725.8172	-0.0013	0	34.52	R.ANSLDSAVLLVQSSNK.S	Deamidated (NQ); Phospho (ST)	63.59	ANS#LDSAVLLVQSSNK	29.64						--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
110	sp|P40371|PP2C1_SCHPO	97	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
32	50	3	2120.9209	0.0011	0	16.14	K.NASDHSADGETRPIAIEMK.D	Phospho (ST)	47.6	NASDHS#ADGETRPIAIEMK	22.31						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
111	sp|Q9C0U7|VPS5_SCHPO	96	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
28	50	3	2504.0596	0.0004	0	34.47	K.TDQEPSAEGVEEESPNVQASPPK.T	Phospho (ST)	113.39	TDQEPSAEGVEEESPNVQAS#PPK	64.24						----------N---
28	58	3	3459.5482	0.0014	1	63.71	K.TDQEPSAEGVEEESPNVQASPPK.THIYTSPR.K	Phospho (ST)	112.41	TDQEPSAEGVEEESPNVQAS#PPKTHIYTSPR	25.13						----------N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
112	sp|Q10289|FAS2_SCHPO	95	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
604	613	2	1274.4976	0.0008	0	15.4	K.SVDGNWEFNK.S	Phospho (ST)	31.48	S#VDGNWEFNK	1000						Y---------
1412	1420	2	1154.4764	0.0007	0	44.99	R.SQIGEWAER.E	Phospho (ST)	59.88	S#QIGEWAER	1000						Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
113	sp|O13792|SUB2_SCHPO	95	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
2	38	4	4196.8029	0.0072	0	42.18	M.ASAQEDLIDYEEEEELVQDQPAQEITPAADTAENGEK.S	Acetyl (Protein N-term); Phospho (ST)	48.08	ASAQEDLIDYEEEEELVQDQPAQEIT#PAADTAENGEK	19.69						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
114	sp|Q9UT28|NNT1_SCHPO	93	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
2	26	3	2901.2572	0.0037	0	37.41	M.ADNDFEGFGIFEEPEGFRPSTPPPK.E	Acetyl (Protein N-term); Phospho (ST)	40.73	ADNDFEGFGIFEEPEGFRPST#PPPK	21.51						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
115	sp|Q8TFG6|PPK18_SCHPO	92	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
316	327	2	1354.6534	0.0001	0	15.5	R.LLSPASEVFNAK.T	Phospho (ST)	66.31	LLS#PASEVFNAK	42.44						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
116	sp|Q09741|SPEE_SCHPO	92	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
2	12	2	1371.68	0.0001	0	42.52	M.SVQELSHPLIK.D	Acetyl (Protein N-term); Phospho (ST)	55.48	S#VQELSHPLIK	58.55						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
117	sp|O94489|EF3_SCHPO	91	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
766	777	2	1448.5538	0.0008	0	59.5	R.FQSGEDLEAMDK.A	Phospho (ST)	99.83	FQS#GEDLEAMDK	1000						--Y---------
1038	1047	2	1126.4448	0.0017	0	20.8	K.AGLEVSDDEL.-	Phospho (ST)	91.72	AGLEVS#DDEL	1000						-----Y----
1037	1047	2	1254.5398	0.0018	1	32.84	R.KAGLEVSDDEL.-	Phospho (ST)	98.74	KAGLEVS#DDEL	1000						------Y----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
118	sp|O43120|UAP2_SCHPO	90	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
359	367	2	1174.4342	0.0011	0	15.12	K.FADWLENSN.-	Phospho (ST)	36.42	FADWLENS#N	1000						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
119	sp|P36600|KAPR_SCHPO	90	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
102	120	2	2161.9734	0.002	1	59.09	R.RQSVSTESMNPSAFALETK.R	Phospho (ST)	121.3	RQS#VSTESMNPSAFALETK	35.82						--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
120	sp|A0ZWU1|EAF1_SCHPO	89	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
233	251	2	2010.7214	0	0	88.71	R.DYASSAQAEGISSASEDED.-	Phospho (ST)	232.84	DYASSAQAEGISS#ASEDED	38.42						----------N------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
121	sp|O60079|UBP12_SCHPO	86	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
37	48	2	1285.579	-0.0012	0	58.08	K.SISLGDASEISK.N	Phospho (ST)	77.64	SIS#LGDASEISK	24.21						--Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
122	sp|O94684|TFB3_SCHPO	85	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?

231		256	3	2798.3296		0.0033	0	45.92	R.SSSILLSDVQQVAEDTTPFSPLAGEK.D	Phospho (ST)		169.23	SSSILLSDVQQVAEDTTPFS#PLAGEK	76.29							

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
123	sp|O74927|MTHR2_SCHPO	85	1	Not annotated																	
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		
330	354	4	2848.4137		0.0017	1	17.39	K.RLSLDEPAELHNQVVVPSQQPVADK.S	Phospho (ST)		79.28	RLS#LDEPAELHNQVVVPSQQPVADK	62.47								

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
124	sp|Q09729|YA4C_SCHPO	84	2	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		
489	506	3	2060.0563		-0.0005	0	17.76	R.IEHLSRPPSPGIVTPPQR.T	Phospho (ST)		89.54	IEHLSRPPS#PGIVTPPQR	40.07						--------Y---------		
447	458	2	1368.5938		0.0016	0	50.33	R.NPSETSLADLSR.V	Phospho (ST)		120.64	NPS#ETSLADLSR	30.7						--N--------		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
125	sp|P87142|YDMC_SCHPO	82	2	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		
82	91	2	1216.4884		0.0011	0	26.46	R.NADNSVTNFR.D	Phospho (ST)		102.61	NADNS#VTNFR	30.7						----Y-----		
488	513	3	3197.3032		0.0059	1	59.74	K.VEPEPIDEEEAFSDDEEEEPEEIKER.I	Phospho (ST)		141	VEPEPIDEEEAFS#DDEEEEPEEIKER	1000						----------Y----------		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
126	sp|P36582|PCK1_SCHPO	81	1	Not annotated																	
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		
949	973	3	2933.3134		-0.0021	0	48.43	R.DLNNFDEEFTSACPTLTPVNTVLTR.Q	Phospho (ST)		153.52	DLNNFDEEFTSACPTLT#PVNTVLTR	30.34								

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
127	sp|O42939|UBA2_SCHPO	81	1	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		
606	618	3	1594.7479		0.0015	1	40	K.RRPSNDTLTQEAK.S	Phospho (ST)		83.36	RRPS#NDTLTQEAK	50.22						---N---------		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
128	sp|O14164|EIF3C_SCHPO	78	1	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		
7	24	2	1906.6704		0.0003	0	55.51	K.GGSSDSDAESVDSSEENR.L	Phospho (ST)		114.83	GGSSDS#DAESVDSSEENR	37.41						-----Y----------		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
129	sp|Q9UTN2|YII1_SCHPO	78	1	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		
222	240	2	1970.8826		-0.0007	0	64.74	K.ISSDPSSPSTQTTINSAAK.S	Phospho (ST)		157.15	ISSDPSS#PSTQTTINSAAK	21.24						------Y----------		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
130	sp|O74960|SLBR2_SCHPO	77	2	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		
334	351	2	1879.8574		0.001	0	16.99	R.IASESSDAVPQQTAVQVA.-	Phospho (ST)		87.42	IAS#ESSDAVPQQTAVQVA	28.5						--N----------		
249	284	4	4057.8869		-0.0012	0	20.38	R.QIVMDAEHALSSWVPSQPAVNFVKPQIEDDAQSDAR.S	Phospho (ST)		62.67	QIVMDAEHALSSWVPSQPAVNFVKPQIEDDAQS#DAR	20.92						----------N---		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
131	sp|P79058|YF9G_SCHPO	76	2	Not annotated																	
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		
60	71	2	1499.632		-0.0013	1	44.99	R.KYFDSGDYALNK.A	Phospho (ST)		133.53	KYFDS#GDYALNK	26.79								
61	71	2	1371.5392		0.0009	0	41.29	K.YFDSGDYALNK.A	Phospho (ST)		116.45	YFDS#GDYALNK	35.82								

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
132	sp|Q9C0X8|RRP12_SCHPO	75	1	Not annotated																	
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		
1075	1101	3	3130.4092		0	0	74.57	R.LLINDSDEDELIEDSLANAQQHAEVNR.T	Phospho (ST)		170.26	LLINDS#DEDELIEDSLANAQQHAEVNR	80.75								

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
133	sp|O13868|ELOF1_SCHPO	74	1	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		
86	107	3	2651.0455		0.002	1	38.91	K.EVDNINDQEAYSPEAAYEEEKE.-	Phospho (ST)		171.13	EVDNINDQEAYS#PEAAYEEEKE	57.75						----------Y----------		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
134	sp|Q10496|YDG9_SCHPO	74	1	Not annotated																	
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		
203	214	2	1535.643		0.0025	0	24.65	K.SVHEFNEPNDLR.Q	Phospho (ST)		77.38	S#VHEFNEPNDLR	1000								

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
135	sp|Q9UTL2|KLP8_SCHPO	73	1	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		
274	287	2	1608.6328		0.0024	0	36.95	R.NESISSFESSSNNK.S	Phospho (ST)		120.59	NESISS#FESSSNNK	24.44						-----Y--------		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
136	sp|Q9Y7U0|YCJE_SCHPO	73	2	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		
865	885	3	2517.0439		-0.0007	1	17.83	R.NGFGDVDEQDATEVYRHSIER.I	Deamidated (NQ); Phospho (ST)		42.95	NGFGDVDEQDATEVYRHS#IER	25.17						----------N---		

562		589	3	2961.3985		-0.0024	0	33.29	R.APQAPSVLSPVVTASEGDFELDGITPER.Q	Phospho (ST)		89.37	APQAPSVLS#PVVTASEGDFELDGITPER	23.53							--------N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
137	sp|Q10324|YD6C_SCHPO	72	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
199	215	3	1981.8808	0.0025	0	26.49	R.NFSDGPIVTNLETDQPR.I	Phospho (ST)	116.06	NFS#DGPIVTNLETDQPR	46.94						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
138	sp|O14093|VPS54_SCHPO	71	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
481	495	2	1546.6878	0.0003	0	71.2	R.SLSAASLSSLSDSSR.R	Phospho (ST)	109.38	SLS#AASLSSLSDSSR	24.26						--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
139	sp|P78789|YC63_SCHPO	71	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
37	66	3	3348.3172	0.0028	0	36.05	R.AQSMISIAADDLNQEGEMSDDNQQEGGNNR.T	2 Oxidation (M); Phospho (ST)	20.46	AQSMISIAADDLNQEGEMS#DDNQQEGGNNR	22.81						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
140	sp|O74343|YH2X_SCHPO	69	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
2	11	2	1302.525	0.0009	0	22.84	M.SQENHVDVPR.K	Acetyl (Protein N-term); Deamidated (NQ); Phospho (ST)	41.26	S#QENHVDVPR	1000						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
141	sp|O74895|RL15A_SCHPO	68	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
180	191	2	1550.6644	-0.0023	0	35.38	R.FNNSPQHATWLR.H	Deamidated (NQ); Phospho (ST)	50.1	FNNS#PQHATWLR	42.07						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
142	sp|O13774|GCH1_SCHPO	67	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
6	14	2	1185.5442	0.0012	1	29.76	K.KDYIDSPLR.M	Phospho (ST)	77.99	KDYIDS#PLR	38.72						-----N---
7	14	2	1057.4494	0.0013	0	26.17	K.DYIDSPLR.M	Phospho (ST)	63.4	DYIDS#PLR	53.6						----N---

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
143	sp|Q9P7S5|UBP7_SCHPO	67	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
493	498	2	795.3894	0.0003	0	19.67	R.SLDILR.L	Phospho (ST)	45.75	S#LDILR	1000						Y-----
333	348	2	1912.8496	0.0007	0	66.68	R.SLQLSPCLTDDEQLSK.S	Phospho (ST)	142.82	SLQLS#PCLTDDEQLSK	37.82						----Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
144	sp|O13956|TSR1_SCHPO	67	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
430	442	2	1558.5926	0.0003	0	34.13	K.IDSDEEETIDDAK.S	Phospho (ST)	100.74	IDS#DEEETIDDAK	46.44						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
145	sp|P87157|YB0G_SCHPO	66	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
313	330	2	1912.8778	0	0	65.6	R.TVAADNNSLLQATTESAK.S	Phospho (ST)	191.45	TVAADNNS#LLQATTESAK	62.08						-------Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
146	sp|Q9UTN3|CID14_SCHPO	65	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
159	174	2	1980.6906	0.0008	0	65.44	K.FDWNSDEDEDSVSNDK.S	Phospho (ST)	179.84	FDWNS#DEDEDSVSNDK	85.86						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
147	sp|O94667|RTF1_SCHPO	65	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
450	486	3	3652.7782	0.0165	0	65.33	R.LSAAATATPMSAPTSVLTGTSPQPSPSLSTSIMSTPK.L	Phospho (ST)	149.91	LSAAATATPMSAPTSVLTGTS#PQPSPSLSTSIMSTPK	24.75						----------N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
148	sp|Q09818|YAC4_SCHPO	65	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
355	363	2	1107.5334	0.0009	0	57.92	K.LSPSVLQER.L	Phospho (ST)	57.41	LS#PSVLQER	51.64						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
149	sp|Q9URT9|GSK31_SCHPO	65	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
175	189	2	1798.8334	0.001	0	53.1	K.VLVPSEPNVSYICSR.Y	Phospho (Y)	166.57	VLVPSEPNVSY#ICSR	24.44						----------Y----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
150	sp|O94311|YH56_SCHPO	65	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
81	97	2	1862.8058	0.0011	0	49.14	K.ELSPNTDNQNTPAGPTK.H	Phospho (ST)	98.93	ELS#PNTDNQNTPAGPTK	27.03						--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
151	sp|Q09915|SPT6_SCHPO	65	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?

131	160	3	3659.4592	0.0048	1	64.78	R.GRDQEETLENIFSEEEEEEENEVDDEAPNR.T	Phospho (ST)	238.99	GRDQEETLENIFS#EEEEEEENEVDDEAPNR	80.3							----------Y----------		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
152	sp|O59787|SRP72_SCHPO	65	1	Not annotated																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?			
2	14	2	1704.7004	0.0013	0	64.72	M.SNHEEEIEELAQR.I	Acetyl (Protein N-term); Phospho (ST)	66.35	S#NHEEEIEELAQR	1000									

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
153	sp|Q9Y7Y1|SGM1_SCHPO	64	2	Not annotated																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?			
410	431	3	2464.141	-0.0001	1	40.41	R.KFSLYESEAISPTSGTPSNLEK.G	Phospho (ST)	108.98	KFSLYESEAIS#PTSGTPSNLEK	33.85									
356	372	2	2023.8894	0.0007	0	35.95	R.NALENFLDNLPSPSEER.S	Phospho (ST)	75.17	NALENFLDNLPS#PSEER	21.3									

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
154	sp|Q92375|TRXB_SCHPO	63	1	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?			
296	322	3	2973.2812	0.0039	0	24.73	R.QAITSAGSGCQAALLAMHYLEELEDTD.-	Phospho (ST)	82.11	QAITSAGSGCQAALLAMHYLEELEDT#D	119.76							----------N-		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
155	sp|Q96WV9|CDK9_SCHPO	63	1	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?			
210	218	2	1163.4692	0.001	0	38.54	R.EYTGCVVTR.W	Phospho (ST)	103.76	EYT#GCVVTR	26.38							--Y------		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
156	sp|P41878|RPN11_SCHPO	63	1	Not annotated																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?			
258	270	3	1591.7629	0.0022	0	19.64	R.VQNEVTLSPEQLR.I	Phospho (ST)	44.95	VQNEVTLS#PEQLR	37.25									

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
157	sp|P87126|CWC2_SCHPO	62	1	Not annotated																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?			
2	15	2	1711.7206	0.0017	0	62.1	M.SENGLEQEVTVEEK.N	Acetyl (Protein N-term); Phospho (ST)	55.54	S#ENGLEQEVTVEEK	37.01									

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
158	sp|O14259|YFP2_SCHPO	62	1	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?			
229	248	2	2266.0534	0	1	44.69	K.KLTPTTSPINSTSLSFVDAK.K	2 Phospho (ST)	143.96	KLT#PTTS#PINSTSLSFVDAK	30.7	28.87						----NN----------		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
159	sp|O13964|YE44_SCHPO	61	1	Not annotated																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?			
106	121	2	1918.7674	0.0019	1	61.45	K.EDVRESPVDTFMENAT.-	Phospho (ST)	131.99	EDVRES#PVDTFMENAT	30.1									

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
160	sp|Q02953|HSF_SCHPO	61	1	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?			
585	597	2	1453.665	0.0014	0	43.73	K.SVNPSLMTVSSPR.Q	Phospho (ST)	93.25	SVNPSLMTVSS#PR	38.42							----------N--		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
161	sp|O13736|SLA1_SCHPO	60	3	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?			
218	230	2	1478.7068	0.0011	0	31.26	R.AVSPEIPPTYTPK.Q	Phospho (ST)	91.06	AVS#PEIPPTYTPK	63.42							--N----------		
459	467	2	1074.487	0.0011	0	38.67	K.LPSDSALHR.L	Phospho (ST)	60.51	LPS#DSALHR	30.7							--N------		
447	458	2	1237.54	-0.0013	0	20.83	R.EIAAASGSPMPK.L	Phospho (ST)	70.64	EIAAASGS#PMPK	21.3							-------Y----		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
162	sp|O14233|RNA14_SCHPO	60	1	Not annotated																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?			
1	21	2	2386.9854	0.0019	1	53.65	-.MNSDDNVEADASSNIIKDSPK.I	Acetyl (Protein N-term); Oxidation (M); Phospho (ST)	75.14	MNSDDNVEADASSNIIKDS#PK	54.87									

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
163	sp|O13791|SLT1_SCHPO	60	1	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?			
357	376	3	2235.9859	0.0021	0	16.17	K.QPSPPVAEHFSNETFSASPK.G	Phospho (ST)	44.32	QPSPPVAEHFSNETFSAS#PK	24.24							----------N--		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
164	sp|P56286|IF2A_SCHPO	59	1	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?			
290	306	2	1889.6356	0.0033	0	58.81	K.ENAEISGDEEDDQSGSE.-	Phospho (ST)	190.82	ENAEIS#GDEEDDQSGSE	121.99							-----Y----------		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
165	sp|Q10411|SPO15_SCHPO	59	1	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?			
45	69	3	2756.1412	0.0002	1	42.88	R.ASTGQLAEDGDTSSQHEDSSEELKR.Q	Phospho (ST)	94.84	ASTGQLAEDGDTSS#QHEDSSEELKR	28.5							----------N----------		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
166	sp|O74874|CCR4_SCHPO	59	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
300	317	2	2043.8274	0.0004	0	58.65	K.LVSDDDDDVNDNVSTSVR.D	Phospho (ST)	127.02	LVS#DDDDDVNDNVSTSVR	146.9						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
167	sp|O75005|SYV_SCHPO	58	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
67	77	2	1284.6002	0	0	35.14	K.IASPVAEYVEK.T	Phospho (ST)	93.4	IAS#PVAEYVEK	52.52						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
168	sp|Q09904|NU124_SCHPO	57	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
373	388	2	1819.8968	0	1	26.89	R.ILEPIIASPKDNTSDK.G	Phospho (ST)	127.47	ILEPIIAS#PKDNTSDK	46.05						-------Y--------
373	382	2	1159.6262	0.0009	0	22.38	R.ILEPIIASPK.D	Phospho (ST)	85.18	ILEPIIAS#PK	1000						-------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
169	sp|O94704|YC54_SCHPO	57	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
133	149	2	1657.7326	0.0018	0	57.04	R.GISPSSAQSSAAVSSSR.K	Phospho (ST)	89.94	GIS#PSSAQSSAAVSSSR	37.41						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
170	sp|P40375|MAOX_SCHPO	57	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
15	23	2	1035.5124	0.001	0	18.74	K.GVTLLNSPR.Y	Phospho (ST)	60.88	GVTLLNS#PR	40.46						------N--
439	452	2	1498.7888	-0.002	0	36.93	K.ALIATGSPLPPLNR.N	Phospho (ST)	104.57	ALIATGS#PLPPLNR	21.3						------Y-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
171	sp|Q9P7F8|GET3_SCHPO	57	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
2	20	2	2223.0714	0.0003	0	56.56	M.SFDPLPGTLENLLEQTSLK.W	Acetyl (Protein N-term); Phospho (ST)	62.32	S#FDPLPGTLENLLEQTSLK	22.1						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
172	sp|O74504|YJD1_SCHPO	56	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
579	597	3	2183.9947	0	1	37.78	K.IVEERSIDEVSQSNTPSSK.Q	Phospho (ST)	112.59	IVEERS#IDEVSQSNTPSSK	49.59						-----N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
173	sp|O14048|UBX2_SCHPO	56	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
285	300	3	1952.8009	0	0	55.95	K.SQKPVEAMSEDEQMHK.A	Phospho (ST)	122.86	SQKPVEAMS#EDEQMHK	65.68						--------N-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
174	sp|O94563|YGD4_SCHPO	55	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
156	171	2	1994.7726	0.0023	0	29.84	R.EAEESDDELLNYTVCK.K	Deamidated (NQ); Phospho (ST)	46.31	EAEES#DDELLNYTVCK	32.45						----N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
175	sp|O74942|CYP9_SCHPO	55	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
2	19	3	2056.8595	0.0017	1	34.4	M.MDGASPVDRDVSPVGLPK.K	Acetyl (Protein N-term); Oxidation (M); 2 Phospho (ST)	38.2	MDGAS#PVDRDVS#PVGLPK	1000						----N------Y------
11	19	2	990.4788	0.0001	0	21.57	R.DVSPVGLPK.K	Phospho (ST)	58.63	DVS#PVGLPK	1000						--Y------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
176	sp|O43058|SEP1_SCHPO	55	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
443	454	2	1437.6656	0.0003	1	29.83	K.RSNSIDFPTPPK.A	Phospho (ST)	71.54	RSNS#IDFPTPPK	26.22						-N----------
424	434	2	1218.6266	0.0006	0	14.32	R.LPSLPSSPTIK.N	Phospho (ST)	46.77	LPS#LPSSPTIK	37.54						--N--------
444	454	2	1281.5654	0.0012	0	40.09	R.SNSIDFPTPPK.A	Phospho (ST)	85.45	SNS#IDFPTPPK	19.84						--Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
177	sp|O94326|YGK8_SCHPO	54	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
28	40	2	1602.5884	0.002	0	16.58	R.SQSPPGEQSAYHR.E	2 Phospho (ST)	51.36	S#QS#PPGEQSAYHR	36.4	34.55					Y-Y----------
27	40	3	1758.6889	0.0013	1	16.19	R.RSQSPPGEQSAYHR.E	2 Phospho (ST)	70.75	RS#QS#PPGEQSAYHR	70.93	49.85					-Y-Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
178	sp|Q9UT09|AROG_SCHPO	53	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
2	21	3	2398.0141	0.0026	0	25.33	M.SPVFLPSGETYDQEHLDDNR.V	Phospho (ST)	45.64	S#PVFLPSGETYDQEHLDDNR	28.93						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
179	sp|P42657|RAD25_SCHPO	53	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
244	261	2	1926.801	0.0015	0	40.67	K.EEAPAAAAAASENEHPEPK.E	Phospho (ST)	47.43	EEAPAAAAAS#ENEHPEPK	1000						--------Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
180	sp|O74793|YOUB_SCHPO	53	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?

157		166	2	1147.4962		0.0012	0	44.82	K.ASGFFVEPSK.L	Phospho (ST)		75.14	AS#GFFVEPSK		101.96					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
181	sp|Q07538|PRP4_SCHPO		53	1	Phosphoprotein															
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
82		96	2	1643.7286		-0.0005	0	52.56	K.LDVTNSTTSDSPSIK.S	Phospho (ST)		97.02	LDVTNSTTSDS#PSIK		21.24						----------Y----
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
182	sp|Q9C0U9|YQD3_SCHPO		52	2	Phosphoprotein															
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
10		22	2	1519.6936		0.0017	1	21.38	R.TASISSKEGYEIR.Q	Phospho (ST)		79.33	TASISS#KEGYEIR		19.33						-----N-------
37		59	3	2601.1375		0.0004	0	42.89	K.ENAVDTTIAKPFDSDEDIADVEK.A	Phospho (ST)		136.96	ENAVDTTIAKPFDS#DEDIADVEK		87.59						----------N---------
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
183	sp|O13789|YEOB_SCHPO		52	1	Not annotated															
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
29		44	2	1782.6952		0.0007	0	52.09	R.DTSTSSFTNPTDSSTR.L	Phospho (ST)		131.11	DTSTSS#FTNPTDSSTR		20.35						
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
184	sp|Q09697|RGA8_SCHPO		52	2	Phosphoprotein															
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
762		777	2	1750.7158		-0.0017	1	29.94	K.IVNEAVASRDSSLSGS.-	2 Phospho (ST)		73.33	IVNEAVAS#RDSS#LSGS		26.79	24.44					-------N-----N--
676		691	3	1782.8149		-0.0001	0	30.72	R.STDVSPTRPDSISSVR.S	Phospho (ST)		72.99	STDVS#PTRPDSISSVR		20.17						----Y----------
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
185	sp|Q9UT17|YFYB_SCHPO		52	1	Phosphoprotein															
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
168		181	2	1599.7662		0.0005	1	44.18	K.KTSPNSGYITSPLR.H	Phospho (ST)		107.85	KTS#PNSGYITSPLR		21.51						-N----------
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
186	sp|O13796|YKY1_SCHPO		52	1	Phosphoprotein															
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
105		123	2	2186.9214		-0.0001	1	47.02	R.DLDNQSSDNEKLEGLESSK.N	Phospho (ST)		142.12	DLDNQSS#DNEKLEGLESSK		26.38						------Y----------
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
187	sp|P50530|SCK1_SCHPO		51	2	Phosphoprotein															
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
8		41	4	3768.7105		0.0016	1	43.29	K.LHRSSNSENTNQASPSTIQSHSTQPVLSNDHSTK.V	Phospho (ST)		58.87	LHRSS#NSENTNQASPSTIQSHSTQPVLSNDHSTK		21.77						----N----------
115		123	2	1159.4738		0.0006	0	19.84	R.TPPSSCYIR.H	Phospho (ST)		58.52	T#PPSSCYIR		43.13						N--------
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
188	sp|O94441|YPP1_SCHPO		51	1	Phosphoprotein															
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
630		642	2	1514.651		0.0009	0	47.37	K.EGSSDELSTLLER.S	Phospho (ST)		95.54	EGS#SDELSTLLER		20.35						---Y---------
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
189	sp|Q9P783|RRB1_SCHPO		51	1	Phosphoprotein															
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
154		177	3	2911.0699		-0.0007	0	42.16	K.TQHDENDDASDNSDVEEDPILEHK.S	2 Phospho (ST)		108.33	TQHDENDDAS#DNS#DVEEDPILEHK		43.96	55.04					---------Y--Y----------
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
190	sp|Q8WZK0|YHRA_SCHPO		50	1	Not annotated															
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
559		589	3	3633.6082		0.0013	0	50.35	R.LLLEEEDEEPQGYSPNPQKPKPAMEENDAEK.T	Phospho (ST)		156.74	LLLEEEDEEPQGYS#PNPQKPKPAMEENDAEK		24.21						
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
191	sp|O94601|YC8E_SCHPO		50	1	Not annotated															
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
290		314	2	2723.1554		0.0027	0	39.93	R.GTYDAEIDSPYSALAASPPPEDYSK.K	Phospho (ST)		153.54	GTYDAEIDSPYSALAAS#PPPEDYSK		56.04						
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
192	sp|Q10175|FKBPH_SCHPO		50	2	Phosphoprotein															
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
172		202	4	3633.6373		0.0028	1	17.55	R.IEELNSDEEDAEQAEEEILEKPVPKDEVAEK.H	Phospho (ST)		104.28	IEELNS#DEEDAEQAEEEILEKPVPKDEVAEK		1000						-----Y----------
172		196	3	2962.3297		0.0078	0	34.94	R.IEELNSDEEDAEQAEEEILEKPVPK.D	Phospho (ST)		76.77	IEELNS#DEEDAEQAEEEILEKPVPK		1000						-----Y----------
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
193	sp|O74503|UAF30_SCHPO		50	1	Not annotated															
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
51		66	2	1919.7852		-0.0007	1	38.56	K.CFDETAAPSEKESLEK.Q	Phospho (ST)		106.89	CFDETAAPS#EKESLEK		31.27						
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
194	sp|Q9HDV9|GCSH_SCHPO		50	1	Phosphoprotein															
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
141		150	2	1208.6054		0.0001	1	28.28	K.IKLSSPDELK.S	Phospho (ST)		79.36	IKLSS#PDELK		24.44						----N-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
195	sp|O74502|MSH6_SCHPO	49	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
135	152	3	2097.8986	-0.0005	1	30.7	R.TSVKQEPDSEEEIDSPTK.K	Phospho (ST)	95.29	TSVKQEPDS#EEEIDSPTK	46.28						--------N---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
196	sp|O74904|RL35_SCHPO	47	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
10	24	3	1892.902	0.0027	1	24.27	R.KQSQENLAEQLQELR.Q	Phospho (ST)	107.14	KQS#QENLAEQLQELR	1000						--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
197	sp|Q10253|MUG64_SCHPO	47	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
99	116	2	1930.9804	0.004	0	47.23	R.NLGNLTPLEQTPLASVGK.N	Phospho (ST)	141.28	NLGNLT#PLEQTPLASVGK	63.94						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
198	sp|Q9UUJ6|NED1_SCHPO	47	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
278	293	3	1808.8252	0.0005	1	48.2	K.KFAEVYGHSPPASPSR.T	Phospho (ST)	90.11	KFAEVYGHS#PPASPSR	26.99						--------Y-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
199	sp|P78795|EIF3G_SCHPO	47	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
147	165	2	2014.9634	0.0022	0	25.26	K.SIIGPVDEPPLDASPVSSR.A	Phospho (ST)	73.51	SIIGPVDEPPLDAS#PVSSR	24.15						----------Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
200	sp|Q9P7M9|RIB1_SCHPO	47	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
30	62	4	3710.8113	0.0064	1	31.45	K.RLPIDDVQCVNSPMLSPALDIEPKPNVVGTAER.L	Deamidated (NQ); Phospho (ST)	71.16	RLPIDDVQCVNS#PMLSPALDIEPKPNVVGTAER	39.77						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
201	sp|O94432|YHKF_SCHPO	46	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
24	50	3	3048.3112	0.0027	1	46.34	K.VESASGNQETSNVTPTKENEGYEELEK.S	Phospho (ST)	119.76	VESASGNQETSNVT#PTKENEGYEELEK	24.15						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
202	sp|O59813|YCT3_SCHPO	46	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
542	554	2	1352.661	0.0022	0	34.19	K.AASIAEGSITQII.-	Phospho (ST)	107.46	AASIAEGS#ITQII	23.34						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
203	sp|P28189|RS13_SCHPO	45	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
28	39	2	1366.6388	0.0007	0	31.27	K.ADADSVVEQILK.F	Phospho (ST)	103.3	ADADS#VVEQILK	1000						----Y-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
204	sp|O42861|YFC1_SCHPO	45	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
203	227	3	2978.0236	0.0043	1	44.79	R.KTYEPEADDDSNDDMYSDDDSNADR.W	Oxidation (M); Phospho (ST)	86.75	KTYEPEADDDS#NDDMYSDDDSNADR	37.4						----------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
205	sp|P36627|BYR3_SCHPO	45	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
162	179	2	2047.8354	-0.0026	0	33.43	K.CNQPGHIAVNCTSPVIEA.-	2 Deamidated (NQ); Phospho (ST)	41.4	CNQPGHIAVNCTS#PVIEA	24.44						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
206	sp|O74407|SYDC_SCHPO	44	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
7	16	2	1209.5656	0.0015	0	17.01	K.QVENLSLEAK.N	Phospho (ST)	58.95	QVENLS#LEAK	1000						-----N----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
207	sp|P87058|LAH1_SCHPO	44	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
59	69	2	1344.5854	0.0004	0	44.32	K.DLSFDEAEVLK.Q	Phospho (ST)	84.86	DLS#FDEAEVLK	1000						--Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
208	sp|O13870|NOT3_SCHPO	44	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
417	427	2	1277.545	0.0009	0	37.01	K.WDSLGHTASPK.M	Phospho (ST)	78.05	WDSLGHTAS#PK	36.83						--------Y--
354	368	2	1599.7314	0.0021	0	15.81	K.VASPETPNATHTAPK.V	Phospho (ST)	66.55	VAS#PETPNATHTAPK	32.44						--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
209	sp|O94321|MPR1_SCHPO	43	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
45	58	3	1548.7216	0.0018	1	24.25	R.ARSPSGSAIPHAYR.V	Phospho (ST)	64.08	ARS#PSGSAIPHAYR	27.12						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
210	sp|Q9P6P7|YKCG_SCHPO	42	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
295	309	2	1490.7134	0.0004	0	27.06	R.GSTPASATVPISPAR.G	Phospho (ST)	78.88	GSTPASATVPIS#PAR	50.72						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
211	sp|O74418|SNUT3_SCHPO	42	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
114	129	3	1810.7893	0.0006	1	42.02	R.RDGVSPFSPEGEGLER.K	Phospho (ST)	90.5	RDGVSPFS#PEGEGLER	52.62						-------Y--------
136	154	3	2231.0104	-0.0003	1	15.4	K.LQAPSPKEEEERPVDQGDK.M	Phospho (ST)	58.86	LQAPS#PKEEEERPVDQGDK	1000						----Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
212	sp|O13923|CORO_SCHPO	42	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
551	562	2	1351.6394	0.001	0	41.19	K.DISAVNLADLNK.R	Phospho (ST)	100.81	DIS#AVNLADLNK	1000						--Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
213	sp|O94342|YHM9_SCHPO	41	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
21	37	2	1935.8834	0.0008	0	41.44	R.QVSEPSVEEPIEASVTR.Y	Phospho (ST)	75.73	QVS#EPSVEEPIEASVTR	37.54						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
214	sp|Q9P7R0|ARO1_SCHPO	41	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
481	493	2	1443.639	-0.0004	0	31.96	K.EELYLGNAGTAAR.F	Phospho (ST)	90.91	EELYLGNAGT#AAR	60.46						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
215	sp|Q9P3T8|TBCC_SCHPO	41	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
10	15	2	844.4026	-0.0069	1	16.52	R.KEFLTK.L	Phospho (ST)	24.52	KEFLT#K	1000						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
216	sp|P15567|PUR6_SCHPO	41	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
30	41	2	1351.6218	0.0012	0	41.36	K.CIILDAANSPAK.Q	Phospho (ST)	111.97	CIILDAANS#PAK	1000						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
217	sp|O59740|MOD5P_SCHPO	41	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
39	51	2	1349.6346	0.0006	0	41.22	R.NVGTSAPSTPAIR.R	Phospho (ST)	84.97	NVGTS#APSTPAIR	28.87						----Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
218	sp|Q9URT2|YJU3_SCHPO	41	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
689	709	3	2395.1539	0.002	1	17.11	K.ISEKQENNVAETILEVTSSPK.S	Phospho (ST)	53.53	ISEKQENNVAETILEVTSS#PK	38.42						----------Y--
693	709	2	1937.8986	0.0004	0	40.55	K.QENNVAETILEVTSSPK.S	Phospho (ST)	112.67	QENNVAETILEVTSS#PK	22.85						----------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
219	sp|Q10328|YD73_SCHPO	40	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
932	942	2	1385.581	0.0012	1	36.85	K.LRGQQFSPDMQ.-	Phospho (ST)	102.01	LRGQQFS#PDMQ	1000						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
220	sp|Q9USL4|NUP61_SCHPO	40	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
13	29	3	2002.7923	0.0017	1	26.48	K.DQDDSDDDRHGPVEVPK.E	Phospho (ST)	81.83	DQDDS#DDDRHGPVEVPK	1000						----Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
221	sp|Q9USJ3|YJ23_SCHPO	39	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
586	602	2	1849.8584	0.0013	0	34.51	R.LGNVIESNVVSPDGTNR.I	Phospho (ST)	90.74	LGNVIESNVVS#PDGTNR	24.15						----------Y------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
222	sp|O60182|RFC1_SCHPO	39	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
39	53	2	1713.7324	-0.0021	0	39.29	R.IVLSDDEDGTIENSK.V	Phospho (ST)	111.48	IVLS#DDEDGTIENSK	47.97						---N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
223	sp|Q9P789|YN8E_SCHPO	39	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
519	533	3	1685.8264	0.0014	1	16.01	R.LRGSPIHNQPVSSSK.S	Phospho (ST)	35.36	LRGS#PIHNQPVSSSK	37.49						---N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
224	sp|O59817|EFR3_SCHPO	39	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
759	767	2	1095.4972	0.0011	0	31.84	R.SPSEINLTR.Q	Phospho (ST)	93.76	SPS#EINLTR	51.66						--N------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
225	sp|P13681|PP11_SCHPO	39	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
2	14	2	1579.6776	0.001	0	38.8	M.SNPDVDLDSIIDR.L	Acetyl (Protein N-term); Phospho (ST)	50.65	S#NPDVDLDSIIDR	45.81						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
226	sp|O14079|YEAE_SCHPO	39	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
46	56	2	1278.597	0.0001	0	15.22	R.QGSDQVIPLSR.F	Phospho (ST)	42.06	QGS#DQVIPLSR	57.73						--N--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
227	sp|Q9UTE3|SEB1_SCHPO	39	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
359	388	4	3186.5913	0.005	1	21.4	R.RSPSPSHLSIPSTLPPADGVPKPTPDGFPR.R	Phospho (ST)	55.38	RS#PSPSHLSIPSTLPPADGVPKPTPDGFPR	26.79						-N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
228	sp|Q9UUI7|TPSY_SCHPO	38	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
108	116	2	1127.502	0.0008	0	22.8	R.SSPLYTQPR.S	Phospho (ST)	56.27	SS#PLYTQPR	33.17						-Y-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
229	sp|Q10069|MU151_SCHPO	38	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
34	48	3	1748.8243	0.001	1	21.02	K.IPNSPKAEVDTELEK.K	Phospho (ST)	98.37	IPNS#PKAEVDTELEK	107.13						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
230	sp|O94548|YCD9_SCHPO	38	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
115	133	3	2336.0713	0.0027	1	38.08	K.TVNEINKSQEFQEHVETPK.Q	Phospho (ST)	88.18	TVNEINKS#QEFQEHVETPK	36.7						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
231	sp|O94451|PLI1_SCHPO	38	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
479	492	2	1607.7308	0.0004	0	38.08	R.NVQSPNIDTAISNR.S	Phospho (ST)	104.18	NVQS#PNIDTAISNR	35.28						---N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
232	sp|O14339|RL17A_SCHPO	38	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
4	13	2	1145.5016	0.0011	0	25.8	R.YSASPALETK.C	Phospho (ST)	70.97	YSAS#PALETK	30.83						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
233	sp|O14026|SET2_SCHPO	38	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
592	618	3	3068.3332	0.0012	1	37.73	R.RLSNSDTPSETTTPNNEQEQVSNQANK.V	Phospho (ST)	92.84	RLSNS#DTPSETTTPNNEQEQVSNQANK	21.24						--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
234	sp|P40387|TPS1_SCHPO	38	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
501	513	2	1418.6134	0.0022	1	25.04	R.TKSAQVLSMNSSS.-	Phospho (ST)	86.9	TKS#AQVLSMNSSS	19.84						--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
235	sp|O42851|YFHE_SCHPO	37	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
2	13	2	1439.6348	0.0015	0	30	M.THTPSFDLSDIK.S	Phospho (ST)	75.72	THTPS#FDLSDIK	29.85						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
236	sp|O59732|CHR1_SCHPO	37	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
220	233	2	1525.7026	0.0002	0	36.84	R.VTNEANASAISLEK.A	Phospho (ST)	113.65	VTNEANASAIS#LEK	37.54						----------Y---

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
237	sp|Q9UTM5|YIJ1_SCHPO	36	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
278	288	2	1160.4862	-0.0001	0	36.49	K.SFSDAVAAASR.A	Phospho (ST)	80.55	S#FSDAVAAASR	24.21						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
238	sp|Q9Y7Z6|YP02_SCHPO	36	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
362	381	3	2337.9229	-0.0005	1	36.15	K.DDTADIHELGESDDDDNVKR.R	Phospho (ST)	118.56	DDTADIHELGES#DDDDNVKR	66.94						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
239	sp|Q9P6P3|PPK15_SCHPO	36	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
54	71	3	2050.99	-0.0011	1	15.2	R.RVSPHGSYISPLEAMTVK.L	Phospho (ST)	64.43	RVS#PHGSYISPLEAMTVK	26.35						--Y----------
286	295	2	1338.5864	0.0008	0	23.47	R.QTVYTYIQSR.F	Deamidated (NQ); Phospho (Y)	52.23	QTVYTY#IQSR	22.85						-----Y----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
240	sp|Q10160|RMI1_SCHPO	35	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
118	143	3	2936.1847	0.0014	0	35.38	R.LVHDESGDEEQNDDDGLTEAQDAVQK.G	Phospho (ST)	135.65	LVHDES#GDEEQNDDDGLTEAQDAVQK	56.73						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
241	sp|O74964|RSC1_SCHPO	35	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
145	157	2	1454.608	0.0002	0	35.19	R.NPEYSVSPPNGSK.F	Phospho (ST)	104.55	NPEYSVS#PPNGSK	26.22						------N------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
242	sp|Q9US22|RL15B_SCHPO	35	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
180	191	2	1566.6588	-0.0028	0	22.76	R.YNNSPQHATWLR.H	Deamidated (NQ); Phospho (ST)	59.66	YNNS#PQHATWLR	30.15						---Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
243	sp|O43078|SUR2_SCHPO	34	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
130	141	2	1309.593	0.0016	0	23.57	R.GAQSEVNLSTPK.Q	Phospho (ST)	78.76	GAQS#EVNLSTPK	43.65						---N--------
177	201	3	2569.2103	0.0002	0	32.86	R.SPPLKPEDPFASFNSSASAIAAASK.S	Phospho (ST)	106.93	S#PPLKPEDPFASFNSSASAIAAASK	34.5						Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
244	sp|P40377|MCM2_SCHPO	34	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
157	183	3	3002.3722	0.0037	0	34.18	R.IYDEYSPNVGALDESGELPLESIADVK.A	Phospho (ST)	162.02	IYDEYS#PNVGALDESGELPLESIADVK	27.7						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
245	sp|P87233|PHF1_SCHPO	34	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
2	11	2	1320.5398	0.0011	1	34.04	M.SQKNFFDEGK.S	Acetyl (Protein N-term); Phospho (ST)	51.36	S#QKNFFDEGK	1000						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
246	sp|O94438|RS3A2_SCHPO	34	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
245	252	2	908.3894	0.0002	0	15.68	K.DVAPLESV.-	Phospho (ST)	56.47	DVAPLES#V	1000						------Y-
242	252	2	1234.622	0.001	1	26.83	K.VVKDVAPLESV.-	Phospho (ST)	125.72	VVKDVAPLES#V	1000						---------Y-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
247	sp|P87159|NIF1_SCHPO	33	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
65	78	2	1686.7726	0.0005	1	33.19	R.AMMSKSEDNLQILK.E	Phospho (ST)	109.39	AMMSKS#EDNLQILK	51.64						-----Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
248	sp|P78831|GHT5_SCHPO	33	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
532	546	2	1844.724	-0.0014	0	33.12	R.AKPESSYHDQEEQFA.-	Phospho (ST)	99.56	AKPES#SYHDQEEQFA	20.35						----N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
249	sp|Q09715|TUP11_SCHPO	33	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
606	614	2	1064.4594	0.0015	0	20.97	R.IWSIDPASP.-	Phospho (ST)	61.35	IWSIDPAS#P	72.25						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
250	sp|O74969|GHT2_SCHPO	32	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
505	513	2	1146.4602	0.0008	0	32.43	R.GESVEYVER.A	Phospho (ST)	66.03	GES#VEYVER	30.66						--Y------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
251	sp|Q9Y808|YN91_SCHPO	32	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
945	958	2	1523.7242	0.001	0	27.48	K.NSLSPSNILSLDGK.F	Phospho (ST)	60.9	NSLS#PSNILSLDGK	28.5						---Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
252	sp|Q9UUG2|YFT6_SCHPO	32	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
288	298	2	1253.6642	0.001	0	24.95	K.TLSQSVLVLSK.D	Phospho (ST)	74.14	TLS#QSVLVLSK	30.7						--Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
253	sp|Q09330|MLO3_SCHPO	32	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
2	18	2	1982.926	-0.0011	0	31.68	M.SMELDQSLDAIIASKPK.G	Acetyl (Protein N-term); Oxidation (M); Phospho (ST)	55.6	S#MELDQSLDAIIASKPK	28.35						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
254	sp|Q92355|SEN1_SCHPO	31	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
834	860	4	3165.4901	0.0034	1	31.15	R.KPTFNEVKPANLLAEDLSDNEDDIDRK.Q	Phospho (ST)	112.12	KPTFNEVKPANLLAEDLS#DNEDDIDRK	40.31						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
255	sp|O74499|LSM7_SCHPO	31	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
22	30	2	1139.5608	0.0021	1	30.62	R.KESILDLSR.Y	Phospho (ST)	73.69	KES#ILDLSR	67.86						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
256	sp|O13827|YEEB_SCHPO	30	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
191	207	3	2005.8538	0.0012	1	14.64	R.FKGSPDMQSTDLDNLMK.E	Phospho (ST)	69.82	FKGS#PDMQSTDLDNLMK	27.21						---Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
257	sp|O36027|WSP1_SCHPO	30	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
384	398	2	1519.7556	0.0008	0	22.91	R.AVSNPPAPPPAIPGR.S	Phospho (ST)	50.03	AVS#NPPAPPPAIPGR	1000						--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
258	sp|Q9P6I5|KGUA_SCHPO	30	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
2	12	2	1183.5498	0.0013	0	22.3	M.TPQLSSSVASK.L	Phospho (ST)	32.2	T#PQLSSSVASK	41.54						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
259	sp|O14064|BIR1_SCHPO	30	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
495	503	2	1154.5494	0.0009	0	29.87	K.ILQTNFSPR.S	Phospho (ST)	74.42	ILQTNFS#PR	27.99						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
260	sp|O13672|RL8_SCHPO	30	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
33	43	2	1268.5818	0.0016	0	27.47	R.SFGIGQDIQPK.R	Phospho (ST)	101.78	S#FGIGQDIQPK	1000						Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
261	sp|O75000|RL12_SCHPO	30	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
32	40	2	960.5056	0.0011	0	24.39	K.IGPLGLSPK.K	Phospho (ST)	61.27	IGPLGLS#PK	1000						------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
262	sp|P07799|TOP1_SCHPO	30	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
95	113	3	2210.0536	0.0028	1	29.62	K.TAVVKEEEDFNEIAKPSPK.H	Phospho (ST)	49.54	TAVVKEEEDFNEIAKPS#PK	71.93						----------N--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
263	sp|Q09948|RSC4_SCHPO	30	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
263	282	3	2145.9235	0.0019	0	29.58	K.HEPEETPASPTPSVSASTSR.E	Phospho (ST)	67.47	HEPEETPAS#PTPSVSASTSR	34.28						--------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
264	sp|O74490|IST1_SCHPO	29	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
255	264	2	1169.5124	0.0007	0	29.43	K.APSFEELAAR.L	Phospho (ST)	73.09	APS#FEELAAR	1000						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
265	sp|Q09889|YC9F_SCHPO	29	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
581	590	2	1183.5978	0.0017	1	28.7	R.KSLSSTNLVR.R	Phospho (ST)	47.55	KSLS#STNLVR	23.34						---Y------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
266	sp|Q09897|CHR3_SCHPO	28	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
154	165	2	1316.6754	0.0014	0	28.51	R.QASPILPSPSLK.L	Phospho (ST)	48.15	QAS#PILPSPSLK	31.34						--N---------
465	489	3	2715.2938	0.0033	0	17.67	R.ADSTPISHNLAVTPSFSPIPQQSNK.S	Phospho (ST)	93.38	ADSTPISHNLAVTPSFS#PIPQQSNK	21.08						----------N--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
267	sp|O42924|EAF7_SCHPO	28	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
191	203	2	1476.687	0.0009	0	27.52	R.SISPVTEQPQSPK.I	Phospho (ST)	94.29	SISPVTEQPQS#PK	46.49						---------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
268	sp|Q9P6R7|VTS1_SCHPO	27	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
671	681	2	1306.5454	0.0012	0	23.17	K.NQSSESLTSFK.G	Phospho (ST)	46.32	NQS#SESLTSFK	21.51						--Y--------
247	265	2	1954.9056	0.0019	0	28.32	K.ALAFSSIEPPASSASTSPR.N	Phospho (ST)	102.24	ALAFSSIEPPASSASTS#PR	38.42						----------N--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
269	sp|O14216|SLD2_SCHPO	27	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
93	101	2	1156.5182	0.0017	0	26.73	R.NDYLQVTPK.T	Phospho (ST)	82.57	NDYLQVT#PK	82.9						------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
270	sp|O13845|RSD1_SCHPO	26	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
460	476	2	1961.9112	0.0017	0	24.67	R.EAAPLSPTEEESRPITR.D	Phospho (ST)	45.19	EAAPLS#PTEEESRPITR	24.75						-----Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
271	sp|Q9USU7|YHHB_SCHPO	26	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
294	307	2	1473.643	0.0008	0	26.4	K.SSMSSSITTPPTAK.V	Phospho (ST)	85.08	SSMSSSITT#PPTAK	19.33						--------Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
272	sp|Q09781|RS3A1_SCHPO	26	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?

242		252	2	1207.574		0.0003	0	19.1	K.VISDVAPLESV.-	Phospho (ST)		61.56	VISDVAPLES#V		66.68					

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
273	sp|P40383|XRN1_SCHPO	26	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
1232	1254	3	2520.2311	0.0009	0	25.8	R.LVTKPTSTFPSPPSPPSSSVWNK.R	Phospho (ST)	52.95	LVTKPTSTFPSPPS#PPSSSVWNK	20.57						

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
274	sp|Q9UTQ8|YL35_SCHPO	25	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
70	86	3	2135.8675	0.0035	1	20.16	K.MQLMEQDDSIESDDKLK.V	2 Oxidation (M); Phospho (ST)	11.98	MQLMEQDDS#IESDDKLK	19.16						--------N--------
321	339	2	2047.9114	-0.0025	0	15.51	K.EFPPSNIDSSPQSPLPGSL.-	Phospho (ST)	56.11	EFPPSNIDSSPQS#PLPGSL	24.24						----------Y------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
275	sp|O59804|CH10_SCHPO	25	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
29	38	2	1141.5422	0.0002	0	25.38	K.TASGIFLPEK.S	Phospho (ST)	72.74	TAS#GIFLPEK	30.7						--N-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
276	sp|Q1MTM9|YFN1_SCHPO	25	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
213	222	2	1132.5536	0.0007	0	16.24	K.NLVLDPASPK.S	Phospho (ST)	53.91	NLVLDPAS#PK	1000						-------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
277	sp|O75011|NAK1_SCHPO	25	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
539	558	3	2145.0739	0.002	0	24.67	K.SISPSILHKPSLESASSTPK.I	Phospho (ST)	75.51	SIS#PSILHKPSLESASSTPK	28.52						--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
278	sp|Q09815|PPK5_SCHPO	25	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
675	682	2	1108.497	0.0016	0	24.67	K.VYTYLQSR.F	Phospho (Y)	85.23	VYTY#LQSR	26.38						---Y----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
279	sp|O59746|YN2B_SCHPO	24	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?
39	50	2	1529.6046	0.0011	0	24.38	R.FTENENDLSPER.A	Phospho (ST)	88.49	FTENENDLS#PER	105.4						--------N---

Supplementary Table S2 Phosphoproteins with the corresponding phosphopeptides and localized phosphosites from solprotSB (*S.pombe*) and from SKMel (human melanoma) samples
(*) Phosphorylated amino acid **X** is displayed as **X#**

***S.pombe* - Glu-C digest of large tryptic peptides**

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
1	sp|P78958|G3P1_SCHPO	503	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
173	186	2	1538.7186	0.0022	0	37.18	E.GLMTTVHATTATQK.T	Phospho (ST)	59.66	GLMTTVHATTAT#QK	25.48						----------N--	K.VINDTFGIEEGLMTTVHATTATQKTVDGPSK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
2	sp|P36597|THI3_SCHPO	370	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
37	56	2	2061.0454	0.006	0	43.03	E.VAILEPTNPSDVTALIGSGK.V	Phospho (ST)	147.53	VAILEPTNPS#DVTALIGSGK	20.91							R.EGIEVAILEPTNPSDVTALIGSGKVDMGLK.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
3	sp|O14362|YB4H_SCHPO	261	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
70	102	3	3362.6212	0.0068	0	60.15	R.ANSVTNLPNSSNTSQVGLNNISPAPVGYVPGSK.T	Phospho (ST)	166.75	ANS#VTNLPNSSNTSQVGLNNISPAPVGYVPGSK	22.65						----------N----------	R.ANSVTNLPNSSNTSQVGLNNISPAPVGYVPGSKTNELANNSMEMQEISPNGSASLPPPVSESWR.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
4	sp|P87228|SERA_SCHPO	208	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
18	37	3	2339.0695	0.0112	0	56.35	K.LSLSPPDNNSSFLSNHFQVR.K	Deamidated (NQ); Phospho (ST)	91.25	LSLS#PPDNNSSFLSNHFQVR	19.19						---N----------	K.LSLSPPDNNSSFLSNHFQVRK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
5	sp|O74960|SLBR2_SCHPO	202	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
300	314	2	1780.717	0.0018	0	21.71	E.QVTHLQDDVQSDTSE.I	Phospho (ST)	68.91	QVTHLQDDVQS#DTSE	30.7						----------N----	R.SWNEYEAQGEPVPVEQVTHLQDDVQSDTSEIIENEPGMHPHVHAER.M
291	314	3	2687.1646	0.0046	1	43.75	E.AQGEPVPVEQVTHLQDDVQSDTSE.I	Phospho (ST)	145.86	AQGEPVPVEQVTHLQDDVQS#DTSE	22.84						----------N----	R.SWNEYEAQGEPVPVEQVTHLQDDVQSDTSEIIENEPGMHPHVHAER.M
277	288	2	1472.5232	0.0027	1	31.28	E.DDAQSDARSWNE.Y	Phospho (ST)	91.42	DDAQSDARS#WNE	34.98						--------N---	R.QIVMDAEHALSSWVPSQPAVNFVKPQIEDDAQSDARSWNEYEAQGEPVPVEQVTHLQDDVQSDTSEIIENEPGMHPHVHAER.M

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
6	sp|O14273|YET4_SCHPO	185	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
556	593	3	3629.7112	0.0014	1	39.05	K.HAAGSGSATTIPSPGSATTKPTPGSATTKPTPVSATEE.H	Phospho (ST)	75.98	HAAGSGS#ATTIPSPGSATTKPTPGSATTKPTPVSATEE	24.75						------N----------	K.HAAGSGSATTIPSPGSATTKPTPGSATTKPTPVSATEEHAAGTTKPAPAAGATATAENETADGK.A
328	341	2	1473.651	0.001	1	25.14	E.ESPIALGQGGVTHE.A	Phospho (ST)	60.11	ES#PIALGQGGVTHE	96.71						-N----------	K.EINTTHDQAAATTTAAVASASTTATAESHAVADGIMNDNVLESIGENVQQETVFEDASDIPHADVIPHTTTVTVEEESPIALGQGGVTHEATTSAR.A
170	183	2	1521.626	0.0025	0	19.61	K.STATTQSADYVVAE.H	Phospho (ST)	96.45	STATTQS#ADYVVAE	21.3						------N------	K.STATTQSADYVVAEHFAPQR.N

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
7	sp|Q9USW1|YHZ3_SCHPO	153	2	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
490	506	2	1859.7936	-0.0042	0	44.02	E.NKPSSSPVFFNGPVSSE.K	Deamidated (NQ); Phospho (ST)	59.8	NKPSSS#PVFFNGPVSSE	21.51							K.FTIPSKPAPVNASRPMMPQQSNNSEASIPSTTPQSPSVVSNGENKPSSSPVFFNGPVSSEK.E
472	489	2	1836.8152	0.001	0	47.55	E.ASIPSTTPQSPSVVSNGE.N	Phospho (ST)	147.98	ASIPSTTPQS#PSVVSNGE	23.34							K.FTIPSKPAPVNASRPMMPQQSNNSEASIPSTTPQSPSVVSNGENKPSSSPVFFNGPVSSEK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
8	sp|Q9Y7N0|YCK2_SCHPO	147	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
18	41	3	2590.0246	0.0041	0	34.14	E.IANDGSPQLNGDNNIQSSDGHNDE.N	Phospho (ST)	140.08	IANDGS#PQLNGDNNIQSSDGHNDE	136.39						-----N----------	K.DEIANDGSPQLNGDNNIQSSDGHNDENEESLSR.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
9	sp|O13637|SEC31_SCHPO	115	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
945	971	3	2871.4141	0.0072	0	33.21	R.VPPVQQPSHPNPYTPVAPQSPVAAASR.I	Phospho (ST)	117.82	VPPVQQPSHPNPYTPVAPQS#PVAAASR	36.19						----------N-------	R.VPPVQQPSHPNPYTPVAPQSPVAAASRISSSPNMPPSNPYTPIAVASSTVNPAHTYKPHGGSQIVPPPK.Q

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
10	sp|P36580|ALF_SCHPO	114	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
306	318	2	1605.6808	0.0023	1	46.07	K.YKDYLMTPVGNPE.G	Phospho (ST)	178.97	YKDYLMT#PVGNPE	86.62						------Y------	K.YKDYLMTPVGNPEGADKPNK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
11	sp|O14360|NAF1_SCHPO	106	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
219	231	2	1437.6242	0.0032	1	33.71	E.SMAPSTPPKTVNE.L	Phospho (ST)	91.1	SMAPST#PPKTVNE	32.4						-----N-------	K.SDAESMAPSTPPKTVNELPEQIYEKPEIVLQPNSLIEPLGK.I

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
12	sp|Q09871|YAG7_SCHPO	105	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
224	239	2	1822.7636	0.0014	1	26.28	E.QAVGQPIEQQSISDDE.A	Phospho (ST)	101.83	QAVGQPIEQQSIS#DDE	30.7							R.VDNFFAAPLPSEQAEELIEDDYAEQPEQAVGQPIEQQSISDDEAR.Q

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
13	sp|O94497|YBS7_SCHPO	104	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
282	301	2	2171.8974	0.0045	1	35.49	E.SDNICGLTAGKSDPVTDVDE.S	Phospho (ST)	139	SDNICGLTAGKS#DPVTDVDE	44.37						----------N--------	R.STADLTESDNICGLTAGKSDPVTDVDESQTIDEQSIPEAEK.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
14	sp|O74463|YQC1_SCHPO	92	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
375	385	2	1291.5402	0.0029	0	43.36	R.FLSTPLGSFDE.S	Phospho (ST)	64.21	FLSTPLGS#FDE	22.87						-------N---	R.FLSTPLGSFDESILGSSPINR.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
15	sp|O14289|LEUC_SCHPO	82	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
675	689	2	1778.797	-0.0158	0	23.27	K.FSVDLVNQTITYGDK.Q	Phospho (Y)	117.96	FSVDLVNQTITY#GDK	28.87						----------N---	K.FSVDLVNQTITYGDKQVK.F

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
16	sp|O74504|YJD1_SCHPO	82	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
171	190	2	2168.9934	0.0209	0	14.18	E.INDSSDVSLSDLPSTNVTPK.K	Deamidated (NQ); Phospho (ST)	85.16	INDSSDVSLSDLPSTNVT#PK	29.64						----------N--	R.LEDAVISLVEADSQESDTESLPEINDSSDVSLSDLPSTNVTPKK.T

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
17	sp|O42938|K6PF_SCHPO	81	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
163	179	2	1760.7318	0.0048	1	22.17	E.SGAASNLESGLATPVVE.T	2 Phospho (ST)	79.46	SGAASNLES#GLAT#PVVE	21.77	49.5					--------Y---Y----	K.SEESGAASNLESGLATPVVETLK.K
171	179	2	951.4338	0.0024	0	17.14	E.SGLATPVVE.T	Phospho (ST)	46.16	QSIS#IPVE	24.75						Y--------	K.SEESGAASNLESGLATPVVETLK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
18	sp|Q9USP9|YHP4_SCHPO	73	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
97	114	2	2036.8594	0.001	1	32.75	E.VSRYSPTSSMIPATNSME.T	Phospho (ST)	102.28	VSRYS#PTSSMIPATNSME	24.44						----N----------	K.SYLEGASNMPSTGMVTEEVSRYSPTSSMIPATNSMETNFNNSLPAVGK.T

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
19	sp|P19117|IPYR_SCHPO	73	2	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
269	280	2	1309.6466	0.0035	0	18.13	E.LAPAPVDPSVHK.W	Phospho (ST)	71.96	LAPAPVDPS#VHK	1000							K.SDFSLVNVSVTGSVANDPSVSSTIPPAQELAPAPVDPSVHKWFYISGSPL.-
24	42	2	2192.9834	0.0055	1	47.43	K.NGTPISSWHDIPLYANAEK.T	Deamidated (NQ); Phospho (ST)	87.48	NGT#PISSWHDIPLYANAEK	22.61							K.NGTPISSWHDIPLYANAEKTILNMVVEIPR.W

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
20	sp|O74417|YJL4_SCHPO	72	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
240	261	2	2161.0274	0.0036	0	55.05	R.SAAQAMATVVPSVSTPGGTPPR.F	Phospho (ST)	174.65	SAAQAMATVVPSVSTPGGT#PPR	39.8						----------Y---	R.SAAQAMATVVPSVSTPGGTPPRFASPALTVESMVHAAPSTTTSSR.F

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
21	sp|O43024|YGVA_SCHPO	66	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
652	677	3	2982.2743	0	0	15.96	E.LGYASNTSQQYQQTSHPAYTTMSPIE.Y	Phospho (ST)	114.35	LGYASNTSQQYQQTSHPAYTTMS#PIE	57.89						----------N---	R.SANSPFDNFQHIDHSTELGYASNTSQQYQQTSHPAYTTMSPIEYGQAAPAAHYYNER.N

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
22	sp|Q9C0V4|YOM2_SCHPO	65	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
69	81	2	1312.6046	0.0022	0	25.65	E.VSVGSSIASPSSR.I	Phospho (ST)	82.82	VSVGSSIAS#PSSR	24.84							R.STSSQLNQPSNYHMHSSLHEEVSVGSSIASPSSRIPDK.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
23	sp|Q9UUE2|CSX2_SCHPO	65	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
216	242	3	2830.429	0.0024	0	54.22	E.ISDAPPLSGNVDPLPINSPPLTNPVAR.D	Phospho (ST)	157.42	ISDAPPLSGNVDPLPINS#PPLTNPVAR	46.03						----------N---------	K.TFQFYVTESDQDSTPATPFPMPMHLAEETATSPEISDAPPLSGNVDPLPINSPPLTNPVARDIDQTEPEDGPLFR.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
24	sp|O74452|SCW1_SCHPO	62	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence

1	18	2	2014.9734	0.0048	1	35.53	-.MFVGSPSAIEKPLSLSSK.T	Acetyl (Protein N-term); Oxidation (M); Phospho (ST)	46.21	MFVGS#PSAIEKPLSLSSK	23.34						----N----------	-.MFVGSPSAIEKPLSLSSKTK.V

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
25	sp|Q9P7K3|YJN2_SCHPO	57	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
45	60	2	1713.7782	0.0019	0	35.29	E.LATSNLPSPAHPPFGE.L	Phospho (ST)	98.96	LATSNLPS#PAHPPFGE	63.77						-------N--------	R.QCSADSLSNSSMQFDLSGLNTPVGELATSNLPSPAHPPFGELHQESR.T

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
26	sp|Q9Y808|YN91_SCHPO	57	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
867	879	2	1364.6608	0.002	1	38.05	E.IPSSVSPGTIAKE.E	Phospho (ST)	86.79	IPSSVS#PGTIAKE	21.3						-----N-------	K.DSVVNTPDVIMSSVDEIPSSVSPGTIAKEEGMAK.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
27	sp|O94312|YH57_SCHPO	56	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
474	489	3	1802.8504	0.0052	1	20.81	E.SKPTPSPPAEQLTDQK.Q	Phospho (ST)	62.63	SKPTPS#PPAEQLTDQK	24.81							K.QLSTDASQTQDASIANENETEIASLDEGSESKPTPSPPAEQLTDQKQNEDNEDK.V

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
28	sp|O36025|MPD2_SCHPO	54	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
153	160	2	925.4446	0.0024	0	19.85	E.GISPGFLR.D	Phospho (ST)	74.17	GIS#PGFLR	1000						--N-----	K.NANTSFTNAFSNEGISPGFLRDCFPSSNSITTGTASPK.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
29	sp|Q9C0U7|VPS5_SCHPO	54	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
41	58	3	2059.9663	-0.0065	1	40.25	E.SPNVQASPPKTHIYTSPR.K	Deamidated (NQ); Phospho (ST)	76.64	SPNVQAS#PPKTHIYTSPR	19.35						------N----------	K.TDQEPSAEGVEEESPNVQASPPKTHIYTSPRK.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
30	sp|Q9USS2|PPK29_SCHPO	49	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
795	808	2	1615.6064	0.0025	0	49.21	R.SSSSFHNPDLTDTE.I	Phospho (ST)	146.08	SSSS#FHNPDLTDTE	22.85						---N---------	R.SSSSFHNPDLTDTEIQETSFNNDLRPVASIQSAETSR.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
31	sp|O14081|TPSX_SCHPO	49	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
110	120	2	1343.6152	0.003	0	28.99	E.NSLSNLNDLFK.S	Phospho (ST)	78.97	NS#LSNLNDLFK	45.71						-N---------	K.TPSSDSPSLENSLSNLNDLFKSR.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
32	sp|Q10187|UCP6_SCHPO	48	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
549	561	2	1430.731	0.0028	0	47.77	E.LAGIIHSPTVSTR.S	Phospho (ST)	113.62	LAGIIHS#PTVSTR	28.5						------N------	K.NFIAEDNEYFDDELAGIIHSPTVSTRSSSR.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
33	sp|O42923|CIP1_SCHPO	46	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
80	101	2	2277.9874	0.0043	0	46.99	R.AASPAPSDSFPTFGYSQLGGLE.N	Phospho (ST)	200.29	AAS#PAPSDSFPTFGYSQLGGLE	26.79						------Y---------------	R.AASPAPSDSFPTFGYSQLGGLENSSK.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
34	sp|Q09794|PYR1_SCHPO	41	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
1880	1897	2	1842.8612	0.0026	0	16.18	K.VSALMSPGLPHAAPSLAE.A	Oxidation (M); Phospho (ST)	10.75	VSALMS#PGLPHAAPSLAE	20.65						-----Y----------	K.VSALMSPGLPHAAPSLAEAFGQAPENK.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
35	sp|O74942|CYP9_SCHPO	41	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
2	19	2	1960.8976	0.0011	1	40.68	M.MDGASPVDRDVSPVGLPK.K	Acetyl (Protein N-term); Phospho (ST)	19.87	MDGASPVDRDVS#PVGLPK	34.33						----------Y------	-.MMDGASPVDRDVSPVGLPKK.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
36	sp|O42854|YFHH_SCHPO	38	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
678	688	2	1189.5508	0.0016	0	26.84	E.SAANSPITPPR.T	Phospho (ST)	92.45	SAANSPIT#PPR	30.66						-------N---	K.EAGAGATADVESAANSPITPPRTWHSPDFTSK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
37	sp|P52822|RL5A_SCHPO	36	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
165	186	3	2409.0856	0.0065	1	35.5	K.GASDGGLFIPHSPNRFPGFDIE.T	Phospho (ST)	114.05	GASDGGLFIPHS#PNRFPGFDIE	53.41						----------N----------	K.GASDGGLFIPHSPNRFPGFDIETEELDDETLR.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
38	sp|Q9P6P3|PPK15_SCHPO	35	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
54	66	2	1520.7064	0.004	1	34.8	R.RVSPHGSYISPLE.A	Phospho (ST)	91.65	RVS#PHGSYISPLE	26.43						--Y----------	R.VSPHGSYISPLEAMTVK.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
39	sp|P78795|EIF3G_SCHPO	35	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
147	165	2	2014.9654	0.0042	0	34.66	K.SIIGPVDEPPLDASPVSSR.A	Phospho (ST)	80.54	SIIGPVDEPPLDAS#PVSSR	34.46						----------Y-----	K.SIIGPVDEPPLDASPVSSRASGALGEK.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
40	sp|O74354|DNT1_SCHPO	34	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
214	234	3	2488.033	0.0038	0	33.65	E.DDNHQSFNSSLTPSQPTTYNR.A	Phospho (ST)	115.24	DDNHQSFNSSLT#PSQPTTYNR	46.68						----------N---------	K.ADGIVNLSVTQEEDDNHQSFNSSLTPSQPTTYNRANFFSINDASSDSSSDAPLR.T

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
41	sp|Q10280|GAF1_SCHPO	33	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
119	138	2	2141.9614	0.0023	0	32.6	K.LNPIPAYSVPADTTGSSLME.F	Phospho (ST)	130.73	LNPIPAYS#VPADTTGSSLME	38.42						-------N----------	K.LNPIPAYSVPADTTGSSLMEFNYIQR.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
42	sp|P36583|PCK2_SCHPO	32	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
979	992	2	1602.8672	0.0039	1	32.26	R.ELPVLTPVNSILTK.E	Phospho (ST)	94.11	ELPVLT#PVNSILTK	23.64						-----Y--------	R.ELPVLTPVNSILTKEMQQHFEGFSYSCEDDKPSTTDNA.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
43	sp|O13759|CSX1_SCHPO	31	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
52	59	2	993.4912	0.0017	1	27.84	E.LVSPTLER.L	Phospho (ST)	77.79	LVS#PTLER	42.65						--Y-----	K.SELVSPTLERLVAPFNCSPSSTPLQDVAGVGSK.M

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
44	sp|O43078|SUR2_SCHPO	31	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
177	201	3	2569.2133	0.0032	1	31.05	R.SPPLKPEDPFASFNSSASAIAAASK.S	Phospho (ST)	84.26	S#PPLKPEDPFASFNSSASAIAAASK	19.36						Y----------	R.SPPLKPEDPFASFNSSASAIAAASKSAAASASALSSDTGR.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
45	sp|O74304|WIN1_SCHPO	30	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
121	147	3	2858.4202	0.0099	0	30.38	R.AYAVSPSDTSNLLHPPTSSSSIPIPIK.N	Phospho (ST)	88.01	AYAVS#PSDTSNLLHPPTSSSSIPIPIK	22.84						----N----------	R.AYAVSPSDTSNLLHPPTSSSSIPIPIKNAGHSNLDHPIRPSLQSSISSNR.I

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
46	sp|P28748|SPI1_SCHPO	30	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
186	199	2	1772.7356	-0.0037	0	19.65	E.VQVDQQLLAQYQQE.M	4 Deamidated (NQ); Phospho (Y)	1.72	VQVDQQLLAQY#QQE	1000						----------N---	K.LVGNPNLEFVASPALAPPEVQVDQQLLAQYQQEMNEAAAMPLPDEDDADL.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
47	sp|O13791|SLT1_SCHPO	29	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
304	321	2	1977.8516	0.006	1	28.57	E.ALLSTGQYSVVSSDEDVE.S	Phospho (ST)	119.4	ALLSTGQYSVVSS#DEDVE	28.87						----------N-----	R.NPLEALLSTGQYSVVSSDEDVESVR.D

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
48	sp|P36582|PCK1_SCHPO	28	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
814	829	2	1821.7358	0.0044	0	28.42	E.NMLLGNTTSTFCGTPE.F	Phospho (ST)	130.7	NMLLGNTTST#FCGTPE	26.38							K.ENMLLGNTTSTFCGTPEFMAPEILLEQQYSK.D

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
49	sp|P36623|PMGY_SCHPO	28	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
23	36	2	1669.777	0.0018	1	28.2	K.LNLFTGWKDPALSE.T	Phospho (ST)	61.54	LNLFTGWKDPALS#E	61.72						----------N-	K.LNLFTGWKDPALSETGIK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
50	sp|O74345|UCP3_SCHPO	28	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
251	260	2	1125.4744	0.0001	0	27.53	R.AASPTLNPFE.Q	Phospho (ST)	66.28	AAS#PTLNPFE	23.34							R.AASPTLNPFEQMMAMTNQGMSVSPGVETTSSPFFTAPVEPNQPLQPLRPSMTGPVPSSMGSEATLNMPSTYGIDSNLYTNSNSSSIVQNPLQPAR.T

Supplementary Table S2 Phosphoproteins with the corresponding phosphopeptides and localized phosphosites from solprotSR *S.pombe*) and from SKMel (human melanoma) samples
(*) Phosphorylated amino acid **X** is displayed as **X#**

***S.pombe* - Chymotrypsin digest of large tryptic peptides**

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
1	sp|O74173|EF1B_SCHPO	653	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
79	106	3	3056.1982	0.0051	1	40.61	Y.GPEGAAAAEEDEIDLFGSDEEEDPEAER.I	Phospho (ST)	146.14	GPEGAAAAEEDEIDLFGS#DEEEDPEAER	1000							K.EVSAYGPEGAAAAEEDEIDLFGSDEEEDPEAERIK.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
2	sp|Q10193|SRP1_SCHPO	466	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
177	197	2	2352.9974	0.0016	1	24.27	F.APQKSPVENETETNVDNGDTK.I	Deamidated (NQ); Phospho (ST)	58.05	APQKS#PVENETETNVDNGDTK	34.4						----------N---------	R.SPSPVSFAPQKSPVENETETNVDNGDTKISESNEK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
3	sp|O42914|YBI8_SCHPO	351	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
142	175	3	3474.5092	0.0032	0	60.8	W.GDLVNSAANPDVAENEGNTPSGAQTPAAEEENVK.T	Phospho (ST)	200.9	GDLVNSAANPDVAENEGNTPSGAQT#PAAEEENVK	56.02						----------Y----------	R.GWGDLVNSAANPDVAENEGNTPSGAQTPAAEEENVKTLDEYLSER.K
140	175	3	3717.6112	0.0044	1	107.55	R.GWGDLVNSAANPDVAENEGNTPSGAQTPAAEEENVK.T	Phospho (ST)	192.48	GWGDLVNSAANPDVAENEGNTPSGAQT#PAAEEENVK	47.61						----------Y----------	R.GWGDLVNSAANPDVAENEGNTPSGAQTPAAEEENVKTLDEYLSER.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
4	sp|P42656|RAD24_SCHPO	270	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
240	267	3	2704.1242	-0.0007	0	61.01	Y.SAAAAGGNTEGAQENAPSNAPEGEAEPK.A	Phospho (ST)	158.25	SAAAAGGNTEGAQENAPS#NAPEGEAEPK	46.39						----------N----------	R.DNLTLWTSDAEYSAAAAGGNTEGAQENAPSNAPEGEAEPKADA.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
5	sp|O42938|K6PF_SCHPO	267	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
160	182	2	2368.1094	0.0048	0	88.17	K.SEESGAASNLESGLATPVVETLK.K	Phospho (ST)	175.31	SEESGAASNLESGLAT#PVVETLK	72.42						----------Y-------	K.SEESGAASNLESGLATPVVETLKK.A
159	182	3	2496.2035	0.0039	1	28.08	K.KSEESGAASNLESGLATPVVETLK.K	Phospho (ST)	81.55	KSEESGAASNLESGLAT#PVVETLK	42.4						----------Y-------	K.SEESGAASNLESGLATPVVETLKK.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
6	sp|P40370|ENO11_SCHPO	190	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
33	44	2	1237.5754	0.001	0	22.15	R.AIVPSGASTGIW.E	Phospho (ST)	66.38	AIVPSGAS#TGIW	20.35						-------N----	R.AIVPSGASTGIWEALEMR.D

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
7	sp|O13637|SEC31_SCHPO	183	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
972	984	2	1485.586	0.0014	0	16.21	R.ISSSPNMPPSNPY.T	Oxidation (M); Phospho (ST)	28.49	ISSSPNMPPS#NPY	26.79						-N----------	R.ISSSPNMPPSNPYTPIAVASSTVNPAHTYKPHGGSQIVPPPK.Q
958	971	2	1431.6776	0.0018	0	58.07	Y.TPVAPQSPVAAASR.I	Deamidated (NQ); Phospho (ST)	65.58	TPVAPQS#PVAAASR	38.28						------N-------	R.VPPVQQPSHPNPYTPVAPQSPVAAASRISSSPNMPPSNPYTPIAVASSTVNPAHTYKPHGGSQIVPPPK.Q

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
8	sp|P78958|G3P1_SCHPO	174	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
296	309	2	1540.716	-0.0014	1	35.33	F.DASAGIQLSPQFVK.L	Deamidated (NQ); Phospho (ST)	58.91	DASAGIQLS#PQFVK	64.26						--------N-----	K.GVLGYTEDAVVSTDFCGDNHSSIFDASAGIQLSPQFVKLVSWYDNEWGYSR.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
9	sp|Q11118|WOS2_SCHPO	157	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
155	184	3	3084.2242	0.0038	0	66.42	F.GNLGGAGAGEDASDSEPELEEEEEVGSNEK.K	Phospho (ST)	175.03	GNLGGAGAGEDASDS#EPELEEEEEVGSNEK	25.78							R.WVDEDEQEAQPEVSPFGAGGMPDLSALGGMGGMDFSQFGNLGGAGAGEDASDSEPELEEEEEVGSNEKK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
10	sp|O42854|YFHH_SCHPO	155	5	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
658	688	3	3095.4862	0.005	1	17.81	K.VIDGIDPPKEAGAGATADVESAANSPITPPR.T	Phospho (ST)	61.74	VIDGIDPPKEAGAGATADVESAANSPIT#PPR	49.15						----------N---	K.VIDGIDPPKEAGAGATADVESAANSPITPPRTWHSPDFTSK.S
711	734	3	2743.1734	0.0025	1	33.2	R.ISEVTEDSIDEDKQNEVDPSTSAR.A	Phospho (ST)	125.23	ISEVTEDS#IDEDKQNEVDPSTSAR	24.3						-------N---------	R.ISEVTEDSIDEDKQNEVDPSTSARALPPPGLR.F
893	914	4	2426.1857	0.0014	1	19.46	F.QGHPTISNVATPPLKQDVTESK.A	Phospho (ST)	67.67	QGHPTISNVAT#PPLKQDVTESK	54.65						----------N----------	R.NVVPVSIVTSGGRPALPDEMASPSSSIGHPLPSPPPADFNSLNVDFYEPHSYLESPAPEPQPSYEEESFNATVIHAPTPSTATFQGHPTISNVATPPLKQDVTESKASPVADASATHQSSTGLTQEITQLGSNMR.L
667	688	3	2160.9694	0.0005	0	16.74	K.EAGAGATADVESAANSPITPPR.T	Phospho (ST)	83.31	EAGAGATADVESAANSPIT#PPR	72.77						----------N---	K.EAGAGATADVESAANSPITPPRTWHSPDFTSK.S
657	688	4	3223.5781	0.0019	2	23.09	R.KVIDGIDPPKEAGAGATADVESAANSPITPPR.T	Phospho (ST)	78.54	KVIDGIDPPKEAGAGATADVESAANSPIT#PPR	37						----------N---	K.VIDGIDPPKEAGAGATADVESAANSPITPPRTWHSPDFTSK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
11	sp|Q9Y7I8|YOI1_SCHPO	152	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
68	87	3	2486.0077	0.0034	1	24.45	K.VQEEVKEESEDEEEDPAMLR.A	Oxidation (M); Phospho (ST)	49.83	VQEEVKEES#EDEEEDPAMLR	1000						--------Y----------	K.VQEEVKEESEDEEEDPAMLRADPK.E
66	87	3	2712.1477	0.0004	2	30.14	K.NKVQEEVKEESEDEEEDPAMLR.A	Phospho (ST)	101.22	NKVQEEVKEES#EDEEEDPAMLR	1000						----------Y----------	K.NKVQEEVKEESEDEEEDPAMLRADPK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
12	sp|P87147|NACA_SCHPO	151	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
119	137	2	2202.9594	0.0025	2	54.79	K.IEESFEQEKAVDETGVDAK.D	Phospho (ST)	99.24	IEES#FEQEKAVDETGVDAK	79.25						---Y--------------	K.IEESFEQEKAVDETGVDAKDIELVMAQANVSR.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
13	sp|Q09717|RANG_SCHPO	149	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
58	80	3	2570.1625	0.0047	1	39.49	K.KPAEGDEDAEPASPEVHFEPIVK.L	Phospho (ST)	111.61	KPAEGDEDAEPAS#PEVHFEPIVK	1000						----------Y----------	K.KPAEGDEDAEPASPEVHFEPIVKLSAVETK.T
49	80	3	3459.5362	0.0007	2	59.04	K.SGASTNDEKKPAEGDEDAEPASPEVHFEPIVK.L	Phospho (ST)	153.73	SGASTNDEKKPAEGDEDAEPAS#PEVHFEPIVK	127.24						----------Y----------	K.SGASTNDEKKPAEGDEDAEPASPEVHFEPIVKLSAVETK.T

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
14	sp|O36025|MPD2_SCHPO	127	5	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
351	369	2	1984.8084	0.0025	0	14.03	R.EHSAVNSPAAAMSPSTAMF.S	Phospho (ST)	79.92	EHSAVNSPAAAMS#PSTAMF	30.7						----------N------	R.EHSAVNSPAAAMSPSTAMFSSEAFPQHLASLIPPALLHWLYK.D
150	160	2	1255.5624	0.0026	1	38.28	F.SNEGISPGFLR.D	Phospho (ST)	96.89	SNEGIS#PGFLR	106.09						-----N-----	K.NANTSFTNAFSNEGISPGFLRDCFPSSNSITTGTASPK.L
742	754	3	1430.7916	0.0018	1	38.21	W.ANKPAALKSPLIK.K	Deamidated (NQ); Phospho (ST)	79.32	ANKPAALKS#PLIK	1000						--------N----	K.ASTPALASGSIWGSPSVINAWANKPAALKSPLIKK.N
42	65	3	2477.1367	0.0044	0	28.31	F.TKPTATNGVDSPTSSHIDPSVSAK.L	Deamidated (NQ); Phospho (ST)	41.08	TKPTATNGVDS#PTSSHIDPSVSAK	24.15						----------N----------	K.ANNSSSSTTGAFPQLTSFTKPTATNGVDSPTSSHIDPSVSAKLDSQR.K
146	160	2	1688.7574	0.0015	2	40.53	F.TNAFSNEGISPGFLR.D	Phospho (ST)	87.77	TNAFSNEGIS#PGFLR	90.66						---------N-----	K.NANTSFTNAFSNEGISPGFLRDCFPSSNSITTGTASPK.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
15	sp|P87228|SERA_SCHPO	120	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
18	29	2	1356.562	0.0022	0	57.69	K.LSLSPPDNNSSF.L	Phospho (ST)	114.38	LSLS#PPDNNSSF	24.75						---N--------	K.LSLSPPDNNSSFLSNHFQVR.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
16	sp|Q10169|DSK2_SCHPO	111	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
282	313	3	2992.4116	0.0076	0	58.13	F.GAGLGDAGLGAGLGGAASPPAPAQDTRPPEER.Y	Phospho (ST)	95.83	GAGLGDAGLGAGLGGAAS#PPAPAQDTRPPEER	48.08							R.QMAQLHQQMGAAGIDPMSLMGGGLGGAGLGGLGGAGLGGFGGANATAGIAGAAPVDQTAAANTIQNLLNNLGGAGFGAGLGDAGLGAGLGGAASPPAPAQDTRPPEERYAEQLSQLNEMGFVDFER.N

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
17	sp|P78871|RST2_SCHPO	108	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
434	453	3	2264.0161	0.001	0	23.12	Y.AHVNSPLGTEQYPSEAYPPK.G	Phospho (ST)	81.27	AHVNS#PLGTEQYPSEAYPPK	19.59							R.QSCISPSGTNFSPSCYSPESLMQQPLTLSPSSIPSGLPTYAHVNSPLGTEQYPSEAYPPKGYVDMEGR.I

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
18	sp|Q9USH9|YJQ1_SCHPO	105	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
90	112	3	2788.1623	0.0023	2	63.09	F.EAFADEQSVEEEEEEDSEKPVRK.N	Phospho (ST)	127.22	EAFADEQS#VEEEEEEDSEKPVRK	127.86						--------Y----------	K.ANAFEAFADEQSVEEEEEEDSEKPVRKNK.K
90	111	3	2660.0698	0.0048	1	33.87	F.EAFADEQSVEEEEEEDSEKPVR.K	Phospho (ST)	87.62	EAFADEQS#VEEEEEEDSEKPVR	90.14						--------Y----------	K.ANAFEAFADEQSVEEEEEEDSEKPVRK.N
93	112	3	2441.0161	0.0042	1	40.81	F.ADEQSVEEEEEEDSEKPVRK.N	Phospho (ST)	93.41	ADEQS#VEEEEEEDSEKPVRK	75.3						----Y----------	K.ANAFEAFADEQSVEEEEEEDSEKPVRKNK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
19	sp|O74448|PIN1_SCHPO	96	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
47	66	3	2241.0211	0.0009	1	33.8	K.FIANELQESVTPTEASNSPK.I	Phospho (ST)	94.03	FIANELQESVT#PTEASNSPK	32.69							K.FIANELQESVTPTEASNSPKIR.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
20	sp|Q10251|IF2P_SCHPO	87	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
28	44	2	1982.8142	0.0037	0	20.38	Y.LDNTSQDSPQNDELAEK.S	Phospho (ST)	70.47	LDNTSQDS#PQNDELAEK	37.54						--------N---------	K.SGYADWEDDLGEDISGQNEYLDNTSQDSPQNDELAEKSENLAVSSEK.T
115	132	3	2132.9194	0.0043	1	24.24	K.KVEEDDEPQEIESPQGPK.E	Phospho (ST)	130.23	KVEEDDEPQEIES#PQGPK	1000						----------Y-----	K.VEEDDEPQEIESPQGPKELTAVTELDDDEFDYKPK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
21	sp|O14273|YET4_SCHPO	80	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
170	185	2	1805.753	0.0021	1	32.42	K.STATTQSADYVVAEHF.A	Phospho (ST)	81.18	STATTQS#ADYVVAEHF	23.62						------N--------	K.STATTQSADYVVAEHFAPQR.N

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
22	sp|O74975|PCY1_SCHPO	78	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
62	78	3	1993.8901	0.002	0	14.54	K.SLEEISQSVSPVEEEPR.D	Phospho (ST)	41.83	SLEEISQSVS#PVEEEPR	31.51						---------N-------	K.SLEEISQSVSPVEEEPRDVR.F

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
23	sp|P40371|PP2C1_SCHPO	74	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
32	50	3	2120.9221	0.0023	0	15.85	K.NASDHSADGETRPIAIEMK.D	Phospho (ST)	62.72	NASDHS#ADGETRPIAIEMK	30.95							K.NASDHSADGETRPIAIEMKDSK.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
24	sp|O74962|PANK_SCHPO	74	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
77	96	2	2172.8094	0.0053	0	74.42	Y.VCESSSPSSSSSSISEAENY.T	Phospho (ST)	177.6	VCESSS#PSSSSSSISEAENY	28.87						-----Y----------	K.VMYYVCESSSPSSSSSSISEAENYTGGR.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
25	sp|P78795|EIF3G_SCHPO	72	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
147	165	3	2014.9642	0.0029	0	40.81	K.SIIGPVDEPPLDASPVSSR.A	Phospho (ST)	117.58	SIIGPVDEPPLDAS#PVSSR	29.93						----------Y-----	K.SIIGPVDEPPLDASPVSSRASGALGEK.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
26	sp|Q09868|CIP2_SCHPO	71	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
2	17	2	1823.8488	0.0034	0	26.78	M.AEGTSQRPLTPLSQAF.L	Acetyl (Protein N-term); Phospho (ST)	49.61	AEGTSQRPLT#PLSQAF	28.35							-.MAEGTSQRPLTPLSQAFLSTNTLSPASSPLTFHSEAASLR.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
27	sp|P42657|RAD25_SCHPO	64	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
239	261	3	2455.0687	0.0035	1	42.21	Y.NQSAKEEAPAAAAASENEHPEPK.E	Phospho (ST)	83.77	NQS#AKEEAPAAAAASENEHPEPK	63.72						--N----------	R.DNLTLWTSDAEYNQSAKEEAPAAAAASENEHPEPKESTTDTVK.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
28	sp|O74463|YQC1_SCHPO	62	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
345	359	2	1510.7454	0.0022	0	62.22	Y.AGAFPSVVSASLPTK.V	Phospho (ST)	128.42	AGAFPSVVSAS#LPTK	48.87						----------Y----	R.SNSYAGAFPSVVSASLPTKVDLNHQMDVSDEEQR.F

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
29	sp|O74535|CPSFX_SCHPO	62	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
31	50	3	2353.0741	0.0015	1	47.92	Y.SGKPEFINLSPDLEENLDEK.L	Phospho (ST)	133.77	SGKPEFINLS#PDLEENLDEK	75.02							K.TSENPPHTSNEYSGKPEFINLSPDLEENLDEKLMSAFPGLEPHVFQHSQSPLSHK.D

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
30	sp|O74803|RHP23_SCHPO	62	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
357	368	2	1504.5528	0.0021	1	27.16	Y.LFEHGHESEDEP.-	Phospho (ST)	67.31	LFEHGHES#EDEP	1000						-------Y----	K.NEELAANYLFEHGHESEDEP.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
31	sp|O74960|SLBR2_SCHPO	60	4	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
271	286	3	1923.8389	0.0025	1	24.56	F.VKPQIEDDAQSDARSW.N	Phospho (ST)	67.97	VKPQIEDDAQSDARS#W	51.79						----------N-	R.QIVMDAEHALSSWVPSQPAVNFVKPQIEDDAQSDARSWNEYEAQGEPVPVEQVTHLQDDVQSDTSEIIENEPGMHPHVHAER.M
271	289	3	2329.9891	0.0039	2	22.54	F.VKPQIEDDAQSDARSWNEY.E	Phospho (ST)	128.29	VKPQIEDDAQSDARS#WNEY	42.14						----------N----	R.QIVMDAEHALSSWVPSQPAVNFVKPQIEDDAQSDARSWNEYEAQGEPVPVEQVTHLQDDVQSDTSEIIENEPGMHPHVHAER.M
271	284	2	1650.7292	0.0042	0	22.93	F.VKPQIEDDAQSDAR.S	Phospho (ST)	56.9	VKPQIEDDAQS#DAR	1000						----------N---	R.QIVMDAEHALSSWVPSQPAVNFVKPQIEDDAQSDARSWNEYEAQGEPVPVEQVTHLQDDVQSDTSEIIENEPGMHPHVHAER.M
334	351	2	1879.8612	0.0048	0	19.17	R.IASESSDAVPQQTAVQVA.-	Phospho (ST)	91.18	IAS#ESSDAVPQQTAVQVA	33.7						--N----------	R.IASESSDAVPQQTAVQVA.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
32	sp|Q02953|HSF_SCHPO	59	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
555	572	2	1958.8662	0.004	0	58.95	F.TNISNLTSPIEASNGNTF.G	Phospho (ST)	146.48	TNISNLTS#PIEASNGNTF	32.4						-------N---------	K.IDDAGFSANSPTNLNLPVSSDLDSVLNIPPNEDVFPDSNPVFDEFTNISNLTSPIEASNGNTFGSNPVSLPNQQK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
33	sp|O13759|CSX1_SCHPO	57	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence

30	59	3	3207.5092	0.0085	1	53.42	K.MSASNSDVNAPISPVVDEGKSELVSPTLER.L	Phospho (ST)	100.76	MSASNSDVNAPISPVVDEGKSELVS#PTLER	21.18						----------Y-----	K.MSASNSDVNAPISPVVDEGKSELVSPTLERLVAPFNCSPSSTPLQDVAGVGSK.M
65	82	2	1882.8158	0.0026	0	25.35	F.NCSPSSTPLQDVAGVGSK.M	Phospho (ST)	98.93	NCS#PSSTPLQDVAGVGSK	24.75						--Y----------	R.LVAPFNCSPSSTPLQDVAGVGSKMSDTLWMGDLEPWMDATFIQQLWASLNEPVNVK.V

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
34	sp|O74500|NUP60_SCHPO	57	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
454	470	2	1780.8312	0.0028	0	28.61	K.APSATTDKPSPPVSSIF.S	Phospho (ST)	94.85	APSATTDKPS#PPVSSIF	32.07						---------N-------	K.APSATTDKPSPPVSSIFSFNAPSAASTKPSPAVSSTFSFNAPTTTPSATSFSIINK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
35	sp|O74653|POB1_SCHPO	56	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
626	645	2	1968.0014	0.0046	0	30.37	F.VAPSPAASLPASPPVGTELK.T	Phospho (ST)	84.42	VAPSPAASLPAS#PPVGTELK	22.16						----------N--------	K.LGNTFVAPSPAASLPASPPVGTELKTRPTLR.S
230	243	3	1579.7632	0.0025	0	27.4	Y.IENRPASSLAVSEK.I	Phospho (ST)	85.88	IENRPASSLAVS#EK	58.55						----------Y--	R.TPNDSSPLPYIENRPASSLAVSEKIQNVPNWSTEEVVEWLMNAGLGSVAPNFAENEITGEILLGLDSNVLK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
36	sp|O74417|YJL4_SCHPO	55	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
313	338	2	2649.2934	-0.0004	1	31.13	R.VANTVVSPAPIPTIGSATIDKDAEGF.Q	Phospho (ST)	90.98	VANTVVS#PAPIPTIGSATIDKDAEGF	21.3						---N----------	R.VANTVVSPAPIPTIGSATIDKDAEGFQR.V
313	340	3	2933.4586	0.005	2	38.54	R.VANTVVSPAPIPTIGSATIDKDAEGFQR.V	Phospho (ST)	59.01	VANTVVS#PAPIPTIGSATIDKDAEGFQR	39.77						------N----------	R.VANTVVSPAPIPTIGSATIDKDAEGFQRVLAMLGR.Q

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
37	sp|Q09729|YA4C_SCHPO	54	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
362	376	2	1605.7422	0.0023	0	53.82	Y.SNLDTPLPSGATTPR.R	Phospho (ST)	123.72	SNLDTPLPSGATT#PR	32.4						----------Y--	R.LYDGLSYSNLDTPLPSGATTPRR.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
38	sp|Q09826|SDS23_SCHPO	50	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
324	335	2	1376.6056	0.0009	0	17.75	W.LVQSPSCPPSPK.N	Deamidated (NQ); Phospho (ST)	68.16	LVQSPS#CPPSPK	20.26						-----Y------	R.LWLVQSPSCPPSPKNNAHLSPGSMGGVK.V

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
39	sp|O94601|YC8E_SCHPO	49	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
301	314	2	1511.6566	0.0022	1	34.79	Y.SALAASPPPEDYSK.K	Phospho (ST)	114.18	SALAAS#PPPEDYSK	60.43							R.GTYDAEIDSPYSALAASPPPEDYSKK.N

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
40	sp|P40381|SWI6_SCHPO	47	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
223	242	2	2266.9854	0.0013	0	42.28	K.ESNESEDIQIAETPSNVTPK.K	Phospho (ST)	118.31	ESNESEDIQIAETPSNVT#PK	53.2						----------Y--	K.ESNESEDIQIAETPSNVTPKK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
41	sp|O14029|SEC16_SCHPO	44	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
177	195	2	2279.0274	0.0029	1	38.72	K.EIYDNDETIPKPPSPEVEK.I	Phospho (ST)	61.78	EIYDNDETIPKPPS#PEVEK	42.12						----------N-----	K.EIYDNDETIPKPPSPEVEKIETSTSVENAYITNSQYNDTLDMEDQTSDLITTFEHENEDHEVHEVPSIHGMEGTFETVNLTSEAGNEK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
42	sp|Q9P6L9|YKQ7_SCHPO	43	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
643	666	3	2461.1146	0.0023	0	24.7	K.GDTSPNSVEQGIEPQAASVVGSPR.S	Phospho (ST)	108.3	GDTSPNSVEQGIEPQAASVVGS#PR	68.07						----------N--	K.GDTSPNSVEQGIEPQAASVVGSPRSSLVSNNSLEEGALLK.N

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
43	sp|Q09146|HBA1_SCHPO	43	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
128	143	2	1702.7628	0.0025	1	42.63	K.ESAAKPAASVSPFSQF.A	Phospho (ST)	133.74	ESAAKPAASVS#PFSQF	30.7							K.ESAAKPAASVSPFSQFASFSNASSPFSNVSTASSEPK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
44	sp|O74313|YOG8_SCHPO	41	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
34	49	3	1814.848	0.0028	0	41.15	Y.LASPSSPIDQVHDELK.H	Phospho (ST)	86.33	LASPSS#PIDQVHDELK	24.75							R.HEPEMLSEYPSLMFEHSYLASPSSPIDQVHDELKHSQK.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
45	sp|P87142|YDMC_SCHPO	40	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
488	513	3	3197.2972	-0.0001	2	39.91	K.VEPEPIDEEEAFSDDEEEEPEEIKER.I	Phospho (ST)	129.54	VEPEPIDEEEAFS#DDEEEEPEEIKER	1000						----------Y----------	K.VEPEPIDEEEAFSDDEEEEPEEIKERIAIPK.T

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
46	sp|Q9UUI7|TPSY_SCHPO	38	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
60	80	2	2363.0054	0.0026	1	29.85	K.SESGQATPVLTPQLEGMNDYF.S	Phospho (ST)	131.93	SESGQATPVLT#PQLEGMNDYF	82.9						----------N----------	K.SESGQATPVLTPQLEGMNDYFSLGPSK.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
47	sp|Q9C0U7|VPS5_SCHPO	37	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
28	50	3	2504.0641	0.0049	0	37.09	K.TDQEPSAEGVEEESPNVQASPPK.T	Phospho (ST)	141.43	TDQEPSAEGVEEESPNVQAS#PPK	72.17						----------N---	K.TDQEPSAEGVEEESPNVQASPPKTHIYTSPR.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
48	sp|O13868|ELOF1_SCHPO	37	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
86	102	2	2006.7814	0.0032	1	36.96	K.EVDNINDQEAYSPEAAY.E	Phospho (ST)	128.77	EVDNINDQEAYS#PEAAY	38.42						----------Y-----	K.EVDNINDQEAYSPEAAYEEEK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
49	sp|Q10496|YDG9_SCHPO	36	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
185	207	3	2679.1975	0.0022	2	36.27	R.DLDETGNLAPEDLKDEVKSVHEFK.N	Phospho (ST)	117.12	DLDETGNLAPEDLKDEVKS#VHEF	104.45							R.DLDETGNLAPEDLKDEVKSVHEFNEPNDLR.Q

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
50	sp|P36580|ALF_SCHPO	36	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
262	275	2	1558.658	0.0015	2	31.91	F.VFHGGSGSSVNEFR.T	Phospho (ST)	132.79	VFHGGS#GSSVNEFR	21.99						-----N--------	K.TTNDKPVFFVFHGGSGSSVNEFRTGIK.C

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
51	sp|O13779|YF2E_SCHPO	35	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
137	148	2	1383.5612	0.0017	0	35.32	R.DQPSPLAEVSDF.A	Phospho (ST)	70.42	DQPS#PLAEVSDF	68.07						---N--------	R.DQPSPLAEVSDFAISSPHVYPK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
52	sp|Q9USU9|TOA1_SCHPO	35	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
200	211	2	1316.6506	0.0017	0	35.3	F.GGLLLPNQNSPK.K	Phospho (ST)	74.37	GGLLLPNQNS#PK	1000						---------N--	R.AVQQMDTFAQQHGNSNYYSPPTPSLPQSATNISFDSSAIPNVQSNPNNTAPFPSYSSNSLQLPTNQTADSPIINDHSTANVTSTGQEHAPDSSSTNSFGGLLLPNQNSPKK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
53	sp|O94255|CAN_SCHPO	34	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
8	34	4	3002.4009	0.0027	2	34.37	R.RIEEIDHQDEIIDREASTASPVSGAGK.I	Phospho (ST)	97.88	RIEEIDHQDEIIDREASTAS#PVSGAGK	19.55						----------Y-------	R.IEEIDHQDEIIDREASTASPVSGAGKIDQNGEIK.D

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
54	sp|O43024|YGVA_SCHPO	34	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
663	678	2	1932.799	0.0026	1	14.52	Y.QQTSHPAYTTMSPIEY.G	Phospho (ST)	74.34	QQTSHPAYTTMS#PIEY	33.7						----------N----	R.SANSPFDNFQHIDHSTELGYASNTSQQYQQTSHPAYTTMSPIEYGQAAPAAHYYNER.N
581	592	2	1334.5558	0.0015	0	31.67	Y.SPATHGISPQPY.A	Deamidated (NQ); Phospho (ST)	55.7	SPATHGIS#PQPY	26.42						---N--------	K.QSAGYGGIYSPATHGISPQPYAGASLIPPSTGAAFNNETASSNAGETTALPYSSR.F

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
55	sp|Q10364|SCK2_SCHPO	34	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
67	92	3	2880.2233	0.0033	1	33.56	F.ASDQSTVGNRNSNDILPEVDHEPSGY.L	Phospho (ST)	179.04	ASDQSTVGNRNS#NDILPEVDHEPSGY	29.24							R.SPLASIQTNQPVEEGEGGSLPSVSNLGPSSIDHPMEEFASDQSTVGNRNSNDILPEVDHEPSGYLK.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
56	sp|O74964|RSC1_SCHPO	32	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
612	621	2	1151.5384	0.0008	0	20.57	K.STSPIPARPF.Y	Phospho (ST)	95.15	STS#PIPARPF	30.7						--N-------	K.STSPIPARPFYAQSGSLQSLNTTQHSHQISGGHSGR.M

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
57	sp|Q9USZ4|RPA34_SCHPO	31	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
176	193	3	1956.8863	0.0033	0	31.41	F.RPIGDAVGPESEPEAEPK.S	Phospho (ST)	80.2	RPIGDAVGPES#EPEAEPK	1000						----------N-------	R.QHFRPIGDAVGPESEPEAEPKSGIK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
58	sp|P40998|THI2_SCHPO	31	2	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
39	49	2	1371.5282	0.0011	1	17.09	K.AYPTYSLDESF.S	Phospho (ST)	80.31	AYPTYS#LDESF	38.42							K.AYPTYSLDESFSFAPIR.E
50	61	2	1428.678	0.0018	2	24.41	F.SFAPIRESTVSR.A	Phospho (ST)	38.25	SFAPIRES#TVSR	24.81							K.AYPTYSLDESFSFAPIRESTVSRAMTR.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
59	sp|O94435|MUG35_SCHPO	31	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
139	150	2	1423.604	0.002	0	28.93	R.DVSPVSHSEKPY.W	Phospho (ST)	46.74	DVS#PVSHSEKPY	30.66						--Y---------	R.DVSPVSHSEKPYWDR.Y

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
60	sp|O14306|YE8A_SCHPO	30	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
134	141	2	921.4946	0.001	0	29.77	F.VSVSPLLK.R	Phospho (ST)	60.35	VSVS#PLLK	51.64						---N----	R.LPSDSSESHVATPSSPTISNSFVS VSPLLKRPQQK.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
61	sp|O14109|YEJC_SCHPO	29	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
57	68	2	1365.587	0.0017	2	29.24	F.ALSSSKSPEYAF.S	Phospho (ST)	107.39	ALSSSKS#PEYAF	30.83							R.CQEDLFALSSSKSPEYAFSLTQQ SPFGPLDQSSSR.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
62	sp|P36600|KAPR_SCHPO	28	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
102	115	2	1619.6664	0.0014	1	28.13	R.RQSVSTESMNPSAF.A	Phospho (ST)	82.39	RQS#VSTESMNPSAF	24.84						--Y----------	R.QSVSTESMNPSAFALETK.R

Supplementary Table S2 Phosphoproteins with the corresponding phosphopeptides and localized phosphosites from solprotSP *S.pombe*) and from SKMel (human melanoma) samples
(*) Phosphorylated amino acid **X** is displayed as **X#**

***S.pombe* - Asp-N digest of large tryptic peptides**

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
1	sp|P78958|G3P1_SCHPO	261	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
296	309	2	1540.7164	-0.001	0	21.75	F.DASAGIQLSPQFVK.L	Deamidated (NQ); Phospho (ST)	88.19	DASAGIQLS#PQFVK	78.01						--------N-----	K.GVLGYTEDAVVSTDFCGDNHSSIFDASAGIQLSPQFVKLVSWYDNEWGYSR.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
2	sp|O74429|VIP1_SCHPO	257	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
719	735	2	1797.704	0.0051	0	35.39	T.DSNGNLVGMTGANTNHT.E	Oxidation (M); Phospho (ST)	34.94	DS#NGNLVGMTGANTNHT	23.73						-Y----------	R.TDSNGNLVGMTGANTNHTERPLEK.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
3	sp|Q10169|DSK2_SCHPO	169	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
287	305	2	1656.7528	0.002	0	25.3	G.DAGLGAGLGGAASPPAPAQ.D	Phospho (ST)	89.92	DAGLGAGLGGAAS#PPAPAQ	1000							R.QMAQLHQQMGAAGIDPMSLMGGGLGGAGLGGLGGAGLGGFGGANNATAGIAGAAPVDQTAAANTIQNLLNNLGGAGFGAGLGDAGLGAGLGGAASPPAPAQDTRPPEER.Y

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
4	sp|O14081|TPSX_SCHPO	144	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
104	116	2	1468.6108	0.0026	1	18.9	S.DSPSLENSLSNLN.D	Phospho (ST)	72.19	DSPSLENS#LSNLN	21.3						-------N-----	K.TPSSDSPSLENSLSNLNDLFK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
5	sp|O14273|YET4_SCHPO	126	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
327	340	2	1474.6322	-0.0018	1	14.38	E.EESPIALGQGGVTH.E	Deamidated (NQ); Phospho (ST)	15	EES#PIALGQGGVTH	20.07						--N----------	K.EINTTHDQAAATTTAAVASASTTATAESHAVADGIMNDNVLESIGENVQQETVFEDASDIPHADVIPHTTTVTVEEESPIALGQGGVTHEATTSAR.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
6	sp|O13774|GCH1_SCHPO	121	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
15	28	2	1519.604	0.001	0	23.1	R.MQPASLSGASTPTI.D	2 Phospho (ST)	95.38	MQPASLS#GAST#PTI	20.91	32.4					------N---Y---	R.MQPASLSGASTPTIDLDGLSWPCQGTQR.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
7	sp|O60101|PGK_SCHPO	118	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
383	397	2	1479.626	0.0018	1	21.65	K.EDALSHVSTGGGASL.E	Phospho (ST)	39.75	EDALSHVSTGGGAS#L	22.16						----------N-	K.EDALSHVSTGGGASLELLEGK.A
384	397	2	1350.583	0.0014	0	22.09	E.DALSHVSTGGGASL.E	Phospho (ST)	30.29	DALSHVSTGGGAS#L	31.11						----------N-	K.EDALSHVSTGGGASLELLEGK.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
8	sp|Q9UUI7|TPSY_SCHPO	101	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
60	73	2	1506.7002	0.0035	1	23.75	K.SESGQATPVLTPQL.E	Phospho (ST)	60.99	S#ESGQATPVLTPQL	22.65						--N----------	K.SESGQATPVLTPQLEGMNDYFSLGPSK.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
9	sp|Q9USW1|YHZ3_SCHPO	98	3	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
489	507	3	2115.9535	0.0021	1	30.53	G.ENKPSSSPVFFNGPVSSEK.E	Phospho (ST)	52.98	ENKPSSS#PVFFNGPVSSEK	23.34							K.FTIPSKPAPVNASRPMMPQQSNNSEASIPSTTPQSPSVVSNGENKPSSSPVFFNGPVSSEKEPILDNFNVFK.N
489	505	2	1858.8164	0.0026	0	28.56	G.ENKPSSSPVFFNGPVSS.E	Phospho (ST)	70.23	ENKPSSS#PVFFNGPVSS	28.87							K.FTIPSKPAPVNASRPMMPQQSNNSEASIPSTTPQSPSVVSNGENKPSSSPVFFNGPVSSEK.E
471	488	2	1836.815	0.0008	0	58.4	S.EASIPSTTPQSPSVVSNG.E	Phospho (ST)	180.69	EASIPSTTPQS#PSVVSNG	28.5							K.FTIPSKPAPVNASRPMMPQQSNNSEASIPSTTPQSPSVVSNGENKPSSSPVFFNGPVSSEK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
10	sp|Q9Y7Y1|SGM1_SCHPO	83	2	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
415	429	2	1568.662	0.0014	1	43.28	Y.ESEAISPTSGTPSNL.E	Phospho (ST)	121.62	ESEAIS#PTSGTPSNL	24.75							K.FSLYESEAISPTSGTPSNLEK.G
417	431	2	1609.7248	0.0012	1	62.29	S.EAISPTSGTPSNLEK.G	Phospho (ST)	69.12	EAIS#PTSGTPSNLEK	30.7							K.FSLYESEAISPTSGTPSNLEKGAGNVPDVSLLEQLATTIR.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
11	sp|O74526|KJ45_SCHPO	79	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
76	97	3	2517.0898	0.0025	1	21.21	T.DSMAHVPGNNSPLQTPQKSPPR.Q	2 Phospho (ST)	75.67	DSMAHVPGNNS#PLQTPQKS#PPR	39.81	25.59					---------N-------Y---	R.VNHTTDSMAHVPGNNSPLQTPQKSPPRQK.H

76	93	3	2000.8621	-0.0042	0	24.87	T.DSMAHVPGNNSPLQTPQK.S	Deamidated (NQ); Phospho (ST)	49.28	DSMAHVPGNNS#PLQTPQK	27.17						----------N-------	R.VNHTTDSMAHVPGNNSPLQTPQKSPPR.Q

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
12	sp|Q9UT81|UBX3_SCHPO	74	1	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence			
162	178	2	1770.7588	0.0014	0	50.57	Q.DSGPSSLASSWASVGQR.L	Phospho (ST)	101.63	DSGPSSLASS#WASVGQR	21.51						---------N-------	R.QHTISPLDEQDSGPSSLASSWASVGQRLGTENEASGSTTPVTQSGPPR.E			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
13	sp|O94577|YQ74_SCHPO	69	1	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence			
2	17	2	1720.7466	0.0009	0	21.19	M.AGVSPVVNHPYTTNSG.D	Acetyl (Protein N-term); Phospho (ST)	20.58	AGVS#PVVNHPYTTNSG	32.44						---N----------	-.MAGVSPVVNHPYTTNSGDFIELGMEPAQK.V			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
14	sp|Q9P7I0|YIT2_SCHPO	67	1	Not annotated																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence			
34	43	2	1171.5042	0.002	0	36.34	G.DGVSFINNAR.D	Phospho (ST)	56.05	DGVS#FINNAR	1000							R.SNNVDMLEEVVHQQEGDGVSFINNARDSLGNDCVHVCTK.Y			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
15	sp|O42854|YFHH_SCHPO	65	3	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence			
675	688	2	1612.656	0.0025	1	17.63	A.DVESAANSPITPPR.T	2 Phospho (ST)	48.21	DVESAANS#PIT#PPR	28.28	44.72					-------N--N---	K.EAGAGATADVESAANSPITPPRTWHSPDFTSK.S			
482	503	3	2354.9869	0.0005	1	18.03	K.DSSSTSTQPTEQSNAQQAPSPK.E	Phospho (ST)	65.38	DSSSTSTQPTEQSNAQQAPS#PK	35.19						----------N--	K.DSSSTSTQPTEQSNAQQAPSPKEEERPLPSEPSQNQPAEYR.D			
826	845	2	2068.8834	0.0022	1	20.21	P.DEMASPSSSIGHPLPSPPPA.D	Oxidation (M); Phospho (ST)	54.17	DEMASPSSSIGHPLPS#PPPA	35.63						----------N----	R.NVVPVSIVTSGGRPALPDEMASPSSSIGHPLPSPPPADFNSLNVDFYEPHSYLESPAPEPQPSYEEESFNATVIHAPTPSTATFQGHPTISNVATPPLK.Q			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
16	sp|O43071|PRP17_SCHPO	64	1	Not annotated																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence			
155	169	2	1601.6414	0.0015	1	63.87	K.GPWAGYGSEQSSSPL.E	Phospho (ST)	177.67	GPWAGYGSEQSSS#PL	32.4							K.GPWAGYGSEQSSSPLEYSEYEEVESLDVK.S			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
17	sp|Q9C0V4|YOM2_SCHPO	62	1	Not annotated																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence			
67	81	2	1570.6884	0.0009	1	39.35	H.EEVSVGSSIASPSSR.I	Phospho (ST)	91.56	EEVSVGSSIAS#PSSR	24.75							R.STSSQLNQPSNYHMHSSLHEEVSVGSSIASPSSRIPDK.A			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
18	sp|Q10422|YDC1_SCHPO	55	1	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence			
49	60	2	1350.5656	0.0017	0	27.52	S.DAGSIAMNVHQL.D	Oxidation (M); Phospho (ST)	23.98	DAGS#IAMNVHQL	1000						---N--------	K.DAGETDSDAGSIAMNVHQLDTAGEPLQSMNEDEVDPNNESTALDK.K			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
19	sp|P36616|DSK1_SCHPO	54	1	Not annotated																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence			
227	249	3	2409.0697	0	1	37.35	Q.DALQHIEAPATTSSPTSNTSSSK.T	Phospho (ST)	108.23	DALQHIEAPATTSS#PTSNTSSSK	34.55							R.ECGIIHTDLKPENVLICIDQDALQHIEAPATTSSPTSNTSSSKTR.N			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
20	sp|O13771|YE99_SCHPO	52	1	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence			
20	37	2	2020.7834	0.008	1	19.17	T.DSMESGQQQNMVSSTPSI.D	Oxidation (M); Phospho (ST)	45.34	DSMESGQQQNMVSSTPS#I	48.59						----------N-	R.MSSPSLETDSMESGQQQNMVSSTPSIDMNESDCSGTGTPSEER.I			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
21	sp|O74360|RGA4_SCHPO	50	2	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence			
263	279	2	1880.8334	0.0029	1	42.21	C.DSFHSGSSIPIEPVSSR.Q	Phospho (ST)	94.98	DS#FHSGSSIPIEPVSSR	22.61						-N----------	R.SANASPFDSCDSFHSGSSIPIEPVSSRQSSVVNNNSVQQPVAYHAFVQSPTENGTLPQLPK.N			
179	188	2	1083.4612	0.0015	0	26.92	S.DSPSSVLSGR.M	Phospho (ST)	43.21	DS#PSSVLSGR	30.7						-N--------	R.NIAQTAENTSLTGQNQGFQNPHFIASDSPSSVLSGRMQNTSSPTNSLRPQLK.V			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
22	sp|Q9C104|GDE1_SCHPO	48	1	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence			
521	532	2	1271.556	0.0013	0	15.31	R.SPSFAASRPSSV.D	Phospho (ST)	72.32	SPS#FAASRPSSV	24.21						--Y---------	R.SPSFAASRPSSVDFMSQSTDSLSK.N			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
23	sp|Q9HGL2|YHLA_SCHPO	46	1	Not annotated																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence			

397	416	2	2149.9714	0.0033	0	31.59	L.DATPFSPTLAPQHTSSNATK.H	Phospho (ST)	102.85	DATPFS#PTLAPQHTSSNATK	30.7							R.VTSGTEDLLSLDATPFSPTLAPQHTSSNATKHSAPPVTK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
24	sp|O13923|CORO_SCHPO	43	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
494	507	2	1559.6926	0.0018	1	32.11	K.SFPKPASSPVTFSE.D	Phospho (ST)	92.7	SFPKPASS#PVTFSE	26.79						-------Y------	K.SFPKPASSPVTFSEDVK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
25	sp|Q9Y7U0|YCJE_SCHPO	43	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
562	578	2	1688.8048	0.0026	1	41.63	R.APQAPSVLSPVVTASEG.D	Phospho (ST)	132.3	APQAPSVLS#PVVTASEG	50.72						--------N--------	R.APQAPSVLSPVVTASEGDFELDGITPER.Q
451	460	2	1237.5502	0.001	0	19.64	K.NYSPPVQPTR.D	Phospho (ST)	60.81	NYS#PPVQPTR	38.42						--N-------	K.NYSPPVQPTRDDEVSQEDAR.V

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
26	sp|Q10475|IF4G_SCHPO	43	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
230	255	3	2605.1806	0.0036	0	29.1	K.GPRPTTSASNTNTSPANGAPTNKPST.D	Phospho (ST)	91.26	GPRPTTSASNTNTS#PANGAPTNKPST	45.71						----------N----------	K.GPRPTTSASNTNTSPANGAPTNKPSTDINTTDPATQTTQVSASNSPALSGSSTPSNTSSR.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
27	sp|P40235|HHP1_SCHPO	41	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
352	365	2	1582.6788	0.0012	0	41.27	N.DPSATGAQYINRPN.-	Phospho (ST)	101.74	DPS#ATGAQYINRPN	30.7							K.GGDINTTVPVINDPSATGAQYINRPN.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
28	sp|O42958|PAT1_SCHPO	41	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
49	61	2	1374.583	0.0014	1	41.07	N.DETFGVSAGSIGR.D	Phospho (ST)	93.41	DETFGVSAGS#IGR	35.41							K.ENMFPNEGQLEEDGIDFEETYDDLGNQLNEAGDELNDETFGVSAGSIGRDFDFSGTTAQASAQLEDEQYQINQQNIFAKPVKPASSELPQVSR.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
29	sp|P87228|SERA_SCHPO	41	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
13	23	2	1250.5822	0.0027	1	19	E.DSLNKLSLSPP.D	Deamidated (NQ); Phospho (ST)	55.88	DSLNKLSLS#PP	42.65						--------N--	R.GNVEDSLNKLSLSPPDNNSSFLSNHFQVR.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
30	sp|O94488|MBO1_SCHPO	40	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
134	150	2	1940.8528	0.0011	1	35.57	D.DEQLSPVLTANQGFQSQ.E	Phospho (ST)	122.07	DEQLS#PVLTANQGFQSQ	24.15						----N----------	R.LNDNITTDDEQLSPVLTANQGFQSQEQYEEDSYNNYDYTSDPSSPNYISSSLDQLPHLDDEDDLQLTPIK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
31	sp|O74504|YJD1_SCHPO	40	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
214	227	2	1387.6046	0.0026	0	22.91	P.DSPNPPAATPATVA.D	Phospho (ST)	69.86	DS#PNPPAATPATVA	60.54						-N----------	K.TTTQIDVQTNIVTPPITVTAVPDSPNPPAATPATVADNDDLSIVSSDSGNTTAPR.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
32	sp|Q9USU9|TOA1_SCHPO	38	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
192	211	2	2142.9474	0.0004	0	17.09	P.DSSSTNSFGGLLLPNQNSPK.K	Deamidated (NQ); Phospho (ST)	46.27	DSSSTNSFGGLLLPNQNS#PK	75.84						----------N--	R.AVQQMDTFAQQHGNSNYYSPPTPSLPQSATNISFDSSAIPNVQSNPNNTAPFPSYSSNSLQLPTNQTADSPIINDHSTANVTSTGQEHAPDSSSTNSFGGLLLPNQNSPKK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
33	sp|Q10203|YBX5_SCHPO	38	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
96	114	2	1840.848	0.0025	0	38.27	K.STLSSTPTAGSNLLGTSPA.E	Phospho (ST)	130.41	STLSSTPTAGSNLLGTS#PA	38.42							K.STLSSTPTAGSNLLGTSPAEPASGLVGSSGFGSSMLGSSLPGNATSNFGSQASTSLLHPR.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
34	sp|O14012|RRP17_SCHPO	38	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
149	160	2	1455.6212	0.0012	1	30.76	K.EGFVTPRISPPP.D	2 Phospho (ST)	72.91	EGFVT#PRIS#PPP	1000							K.EGFVTPRISPPPDVPLRPHKPK.N

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
35	sp|O36025|MPD2_SCHPO	36	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
93	117	3	2563.1485	0.0005	0	36.02	K.NPTVSSTTSSANPAIVSNGGSPFYK.N	Deamidated (NQ); Phospho (ST)	52.45	NPTVSSTTSSANPAIVSNGGS#PFYK	22.88						----------N----	K.NPTVSSTTSSANPAIVSNGGSPFYKNPVVANNPSSTFDMSTNLFNSK.N

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
36	sp|Q9P7M9|RIB1_SCHPO	34	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
35	48	2	1609.6894	0.0013	0	31.62	D.DVQCVNSPMLSPAL.D	Phospho (ST)	83.6	DVQCVNS#PMLSPAL	40.34							R.LPIDDVQCVNSPMLSPALDIEPKPNVVGTAER.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
37	sp|O13905|YF3E_SCHPO	33	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
287	297	2	1259.5554	0.0007	1	19.86	K.GLQIETQPASH.D	Phospho (ST)	79.53	GLQIETQPAS#H	39.8						---------N-	K.GLQIETQPASHDGEVDGEVK.E
109	118	2	1208.5356	0.0031	1	25.35	L.DQALQISPKE.D	Deamidated (NQ); Phospho (ST)	77.98	DQALQIS#PKE	1000						------N---	K.VEETAGSFWSGFGSTVNGFLDQALQISPKEDDVSTPTHEASSSVFLNR.H

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
38	sp|P08965|MEI2_SCHPO	33	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
145	159	2	1673.6844	0.0023	0	32.87	S.ESPPQNGIQSYISSS.E	Deamidated (NQ); Phospho (ST)	58.6	ES#PPQNGIQSYISSS	44.15							R.QPLSTWQQNISVLSESPPQNGIQSYISSSEQAAQALTR.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
39	sp|Q1MTN9|RLF2_SCHPO	32	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
27	37	2	1198.5134	0.0016	0	31.88	T.DITSLSVSSPN.E	Phospho (ST)	77.35	DITSLSVSS#PN	38.42							K.GNELCSSSTDITSLSVSSPNESVIHSSHSASEADEYVCK.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
40	sp|O94358|YHOA_SCHPO	32	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
383	397	2	1634.7574	0.0022	0	31.81	K.ELSPQATLNSPIQSA.E	Phospho (ST)	80.17	ELS#PQATLNSPIQSA	46.68						--N----------	K.ELSPQATLNSPIQSAEAGNVELK.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
41	sp|Q09746|YB65_SCHPO	31	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
492	505	2	1607.7116	0.0037	0	31.18	M.DSSSIYQTSLSNVK.T	Phospho (ST)	116.6	DSSSIYQTS#LSNVK	19.33							R.NTYTDDMDSSSIYQTSLSNVKTEETTPAEPASK.V

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
42	sp|O94497|YBS7_SCHPO	31	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
283	293	2	1214.501	0.0008	1	32.58	S.DNICGLTAGKS.D	Phospho (ST)	114.63	DNICGLTAGKS#	67.94						----------N	R.STADLTESDNICGLTAGKSDPVTDVDESQTIDEQSIPEAEK.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
43	sp|Q9P6R7|VTS1_SCHPO	30	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
170	184	2	1598.7456	0.0016	0	30.43	G.DSPSLSSSLPSLTTK.S	Phospho (ST)	66.05	DS#PSLSSSLPSLTTK	24.21						-N----------	K.GDSPSLSSSLPSLTTKSNLSGNLNMVTPASTQGPAFSSK.H

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
44	sp|Q9C102|GLT1_SCHPO	30	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
505	513	2	1029.4276	0.0009	1	19.43	V.DSLIESTSV.D	Phospho (ST)	46.74	DSLIESTS#V	22.85							R.SWLDQELIDMNSIVDSLIESTSVDLTPIVDDVPLADDK.T

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
45	sp|O42938|K6PF_SCHPO	30	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
170	182	2	1422.7018	0.0011	1	26.63	L.ESGLATPVVETLK.K	Phospho (ST)	58.51	ESGLAT#PVVETLK	44.78						-----Y-------	K.SEESGAASNLESGLATPVVETLKK.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
46	sp|O74354|DNT1_SCHPO	30	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
214	234	3	2488.0327	0.0035	1	30.19	E.DDNHQSFNSSLTPSQPTTYNR.A	Phospho (ST)	106.29	DDNHQSFNSSLT#PSQPTTYNR	55.91						----------N--------	K.ADGIVNLSVTQEEDDNHQSFNSSLTPSQPTTYNRANFFSINDASSDSSSDAPLR.T

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
47	sp|O43078|SUR2_SCHPO	28	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
147	163	2	1759.7322	0.0021	0	21.5	K.HSPPSTSTSSIVSSSYG.D	Phospho (ST)	78.26	HS#PPSTSTSSIVSSSYG	19.19						-N----------	K.HSPPSTSTSSIVSSSYGDAPSYLAPSKPNR.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
48	sp|Q09818|YAC4_SCHPO	28	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
280	295	2	1746.7588	0.0015	0	27.84	E.EANSSPAAQNQHITTV.D	Phospho (ST)	60.08	EANSS#PAAQNQHITTV	20.35							K.TPLEEANSSPAAQNQHITTVDHVHPQVSMTPSLSTNNTATSVPAPYSSAASVNVVPGHATTILHHEESSALPPTAAWAK.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
49	sp|Q10074|YAN9_SCHPO	28	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
48	62	2	1647.7524	0.002	1	24.22	K.LNISPSESNLPNNVA.E	Phospho (ST)	93.32	LNISPSES#NLPNNVA	51.64						-------N-------	K.LNISPSESNLPNNVAENTTDTPVNYGSIR.D

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
50	sp|Q9UUG2|YFT6_SCHPO	27	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
84	94	2	1378.5824	0.0019	0	27.37	S.DYTSFLNQSPK.K	Phospho (ST)	79.74	DYTSFLNQS#PK	60.04						--------N--	R.IENLHSETFPSDYTSFLNQSPKK.N

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
51	sp|O14029|SEC16_SCHPO	27	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
444	454	2	1211.4962	0.0004	1	26.78	P.DISSSPLSPTE.D	Phospho (ST)	49.74	DISSSPLS#PTE	23.62						-------N---	K.LENPDISSSPLSPTEDLFPNDPEEENLFSAALGLNSNTGSQPSETQSKPSIDPSESITVTDNQDSLLFSQLTNNALQAENATK.V

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
52	sp|P52890|ATF1_SCHPO	26	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
74	85	2	1285.5968	0.0013	0	16.44	S.DGVTPSFVGSLK.L	Phospho (ST)	28.54	DGVT#PSFVGSLK	37.41							-.MSPSPVNTSTEPASVAAVSNGNATASSTQVPENNQSDSFAPPSNNSQQNQQSSTIAPNGGAGSVANANPADQSDGVTPSFVGSLKLDYEPNPFEHSFGSTASVGQGNPSLNR.N

Supplementary Table S2 Phosphoproteins with the corresponding phosphopeptides and localized phosphosites from solprotSILAC (*S.pombe*) and from SKMel (human melanoma) samples
(*) Phosphorylated amino acid **X** is displayed as **X#**

***S.pombe* - Formic acid digest of large tryptic peptides**

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
1	sp|P78958|G3P1_SCHPO	2707	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
297	309	2	1425.6928	0.0024		0	22.78	D.ASAGIQLSPQFVK.L	Deamidated (NQ); Phospho (ST)	30.55	ASAGIQLS#PQFVK	38.52						--------N-----	K.GVLGYTEDAVVSTDFCGDNHSSIFDASAGIQLSPQFVKLVSWYDNEWGYSR.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
2	sp|O42914|YBI8_SCHPO	596	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
144	175	3	3382.4272	0.0033		1	75.97	D.LVNSAANPDVAENEGNTPSGAQTPAAEEENVK.T	2 Phospho (ST)	189.52	LVNSAANPDVAENEGNTPS#GAQT#PAAEEENVK	25.31	75.64					----------Y---Y--------	R.GWGDLVNSAANPDVAENEGNTPSGAQTPAAEEENVKTLDEYLSER.K
153	175	2	2501.9934	0.0099		0	29.94	D.VAENEGNTPSGAQTPAAEEENVK.T	Deamidated (NQ); 2 Phospho (ST)	81.52	VAENEGNTPS#GAQT#PAAEEENVK	37.41	39.55					---------Y---Y--------	R.GWGDLVNSAANPDVAENEGNTPSGAQTPAAEEENVKTLDEYLSER.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
3	sp|Q11118|WOS2_SCHPO	520	3	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
169	185	2	2040.8434	0.0023		1	50.47	D.SEPELEEEEEVGSNEKK.E	Phospho (ST)	46.87	S#EPELEEEEEVGSNEKK	37.15							R.WVDEDEQEAQPEVSPFGAGGMPDLSALGGMGGMDFSQFGNLGGAGAGEDASDSEPELEEEEEVGSNEKK.E-R.WVDEDEQEAQPEVSPFGAGGMPDLSALGGMGGMDFSQFGNLGGAGAGEDASDSEPELEEEEEVGSNEK.K
151	168	2	1778.682	0.0036		1	65.01	D.FSQFGNLGGAGAGEDASD.S	Phospho (ST)	150.56	FSQFGNLGGAGAGEDAS#D	178.38							
169	184	2	1912.7518	0.0056		0	61.58	D.SEPELEEEEEVGSNEK.K	Phospho (ST)	158.53	S#EPELEEEEEVGSNEK	148.26							R.WVDEDEQEAQPEVSPFGAGGMPDLSALGGMGGMDFSQFGNLGGAGAGEDASDSEPELEEEEEVGSNEKK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
4	sp|P40370|ENO11_SCHPO	501	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
415	432	3	1895.8333	0.0031		0	27.15	R.IEEELGSEGVYAGAHAGK.Y	Phospho (ST)	69.97	IEEELGS#EGVYAGAHAGK	60.31						------Y----------	R.IEEELGSEGVYAGAHAGKYIK.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
5	sp|O42938|K6PF_SCHPO	361	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
160	183	4	2496.2057	0.0061		1	25.05	K.SEESGAASNLESGLATPVVETLKK.A	Phospho (ST)	54.91	SEESGAASNLES#GLATPVVETLKK	22.19						----------Y----------	K.SEESGAASNLESGLATPVVETLKKATTSDKPAGVK.K
160	182	3	2368.1107	0.006		0	52.62	K.SEESGAASNLESGLATPVVETLK.K	Phospho (ST)	224.71	SEESGAASNLESGLAT#PVVETLK	68.26						---------------Y-------	K.SEESGAASNLESGLATPVVETLKK.A
159	182	3	2496.2044	0.0048		1	24.96	K.KSEESGAASNLESGLATPVVETLK.K	Phospho (ST)	102.69	KSEESGAASNLESGLAT#PVVETLK	42.56						---------------Y-------	K.SEESGAASNLESGLATPVVETLKK.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
6	sp|Q9UT81|UBX3_SCHPO	248	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
179	199	2	2164.9674	0.0037		0	75.47	R.LGTENEASGSTTPVTQSGPPR.E	Phospho (ST)	154.18	LGTENEAS#GSTTPVTQSGPPR	24.75						-------Y----------	R.LGTENEASGSTTPVTQSGPPRENPPTESQPEKPLR.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
7	sp|O74960|SLBR2_SCHPO	201	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
308	330	3	2707.177	0.0072		1	52.8	D.VQSDTSEIIENEPGMHPHVHAER.M	Oxidation (M); Phospho (ST)	26.52	VQS#DTSEIIENEPGMHPHVHAER	24.84						--N----------	R.SWNEYEAQGEPVPVEQVTHLQDDVQSDTSEIIENEPGMHPHVHAERMSR.I
285	306	3	2634.1351	0.0075		0	30.17	R.SWNEYEAQGEPVPVEQVTHLQD.D	Phospho (ST)	94.8	S#WNEYEAQGEPVPVEQVTHLQD	30.82						N----------	R.SWNEYEAQGEPVPVEQVTHLQDDVQSDTSEIIENEPGMHPHVHAER.M

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
8	sp|O14273|YET4_SCHPO	195	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
190	216	3	2766.2749	0.004		1	48.26	R.NDEQLGNSPASITSKPATTSAAQPSSK.V	Phospho (ST)	132.4	NDEQLGNSPAS#ITSKPATTSAAQPSSK	23.29						----------Y----------	R.NDEQLGNSPASITSKPATTSAAQPSSKVEENMAK.A
348	367	2	2141.9194	0.004		0	48.2	R.ASASGIPGAFEEVQQTVQED.L	Phospho (ST)	156.42	AS#ASGIPGAFEEVQQTVQED	20.35						-N----------	R.ASASGIPGAFEEVQQTVQEDLPHPTAETVEIAR.F

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
9	sp|Q9Y7Z8|MYO1_SCHPO	194	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
359	376	2	2049.0454	0.0046		1	55.25	R.RGSVYEVPLNPTQALAVR.D	Phospho (ST)	129.75	RGS#VYEVPLNPTQALAVR	42.65						--Y----------	R.GSVYEVPLNPTQALAVRDALSMAIYNCLFDWIVER.V

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
10	sp|Q9UT19|METE_SCHPO	187	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
434	449	2	1826.925	0.0031		0	43.14	K.LPLFPTTTIGSFPQTK.E	Phospho (ST)	77.9	LPLFPTTTIGS#FPQTK	34.46						----------N-----	K.LPLFPTTTIGSFPQTKEIR.V

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
11	sp|P87228|SERA_SCHPO	186	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
18	37	3	2339.065	0.0067	1	44.5	K.LSLSPPDNNSSFLSNHFQVR.K	Deamidated (NQ); Phospho (ST)	77.86	LSLS#PPDNNSSFLSNHFQVR	19.19						---N----------	K.LSLSPPDNNSSFLSNHFQVRK.S
14	24	2	1249.6	0.0045	1	15.1	D.SLNKLSLSPPD.N	Phospho (ST)	57.82	SLNKLSLS#PPD	24.75						-------N---	R.GNVEDSLNKLSLSPPDNNSSFLSNHFQVR.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
12	sp|O43125|CSH3_SCHPO	176	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
44	67	2	2390.2154	0.002	0	56.33	D.GPASPVTAPAAQPVESSVPLPLPK.R	Deamidated (NQ); Phospho (ST)	75.86	GPAS#PVTAPAAQPVESSVPLPLPK	36.83							R.SALDWVHANIHLQDGPASPVTAPAAQPVESSVPLPLPKR.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
13	sp|O13637|SEC31_SCHPO	155	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
945	971	4	2872.4033	0.0124	0	16.48	R.VPPVQQPSHPNPYTPVAPQSPVAAASR.I	Deamidated (NQ); Phospho (ST)	42.62	VPPVQQPSHPNPYTPVAPQS#PVAAASR	19.73						----------N-------	R.VPPVQQPSHPNPYTPVAPQSPVAAASRISSSPNMPPSNPYTPIAVASSTVNPAHTYKPHGGSQIVPPPK.Q
901	930	3	2934.4534	0.0084	0	14.11	R.TSSVSTLPPPPPTASMTASAPAIASPPPPK.V	Phospho (ST)	47.42	TSSVSTLPPPPPTASMTASAPAIAS#PPPPK	31.71						----------N-----	R.TSSVSTLPPPPPTASMTASAPAIASPPPPKVGETYHPPTASGTR.V

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
14	sp|O14081|TPSX_SCHPO	137	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
105	120	2	1856.8578	0.0022	1	77.81	D.SPSLENSLSNLNDLFK.S	Phospho (ST)	169.42	SPSLENS#LSNLNDLFK	30.83						------N--------	K.TPSSDSPSLENSLSNLNDLFKSR.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
15	sp|O74448|PIN1_SCHPO	130	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
47	66	3	2241.0232	0.003	0	52.86	K.FIANELQESVTPTEASNSPK.I	Phospho (ST)	117.6	FIANELQESVT#PTEASNSPK	30.82							K.FIANELQESVTPTEASNSPKIR.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
16	sp|P87216|VIPI_SCHPO	126	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
225	254	3	3035.3662	0.0054	1	27.84	K.NQAEGTASPASSTPTAPAEKEPTAPTTESK.T	Phospho (ST)	79.92	NQAEGTASPAS#STPTAPAEKEPTAPTTESK	30.53						-------Y----------	K.NQAEGTASPASSTPTAPAEKEPTAPTTESKTTE.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
17	sp|O74452|SCW1_SCHPO	102	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
1	18	2	2014.9714	0.0028	0	53.32	-.MFVGSPSAIEKPLSLSSK.T	Acetyl (Protein N-term); Oxidation (M); Phospho (ST)	69.46	MFVGS#PSAIEKPLSLSSK	24.75						----N----------	-.MFVGSPSAIEKPLSLSSKTK.V
47	65	4	2195.9293	0.0051	1	14.05	D.DECHALHMSPQAIHSQAGK.A	Phospho (ST)	54.4	DECHALHMS#PQAIHSQAGK	60.5						--------N---------	R.GSSLVPTGILNGDDECHALHMSPQAIHSQAGKAESDGLPTYASVEK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
18	sp|O74975|PCY1_SCHPO	97	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
62	78	2	1994.8734	0.0013	0	48.27	K.SLEEISQSVSPVEEEPR.D	Deamidated (NQ); Phospho (ST)	79.79	SLEEISQSVS#PVEEEPR	37.41						---------N-------	K.SLEEISQSVSPVEEEPRDVR.F

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
19	sp|P31209|PABP_SCHPO	96	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
12	30	2	2043.8654	0.0021	1	18.14	D.AAVESDVNTNNEAVESSTK.E	Phospho (ST)	52.2	AAVES#DVNTNNEAVESSTK	21.08						----N----------	K.QADAAVESDVNTNNEAVESSTKEESSNTPSTETQPEK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
20	sp|O60176|YG41_SCHPO	87	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
62	85	3	2579.0272	0.0041	0	41.8	D.PISPNMASNESGNSENTSNYGSSR.D	Phospho (ST)	140.57	PIS#PNMASNESGNSENTSNYGSSR	29.09						--Y----------	K.SNDEPVQSQDPISPNMASNESGNSENTSNYGSSRDENVYQK.T

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
21	sp|Q9US06|PAF1_SCHPO	84	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
385	404	2	2297.9934	0.0035	0	66.93	R.SVEGSLNEELSEEEKPAESR.E	Phospho (ST)	91.9	SVEGSLNEELS#EEEKPAESR	63.63						----------N---------	R.SVEGSLNEELSEEEKPAESREQLESAEQTNGVKPETQAQNMSASESQANSPAPPVEEGNTQPSPVEQLQNEED.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
22	sp|O74864|RLA0_SCHPO	83	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
270	303	3	3235.3762	0.0045	0	56.11	D.PSAFVVAAAPAAAAGGEAEAPAAEAAAEEEEESD.E	Phospho (ST)	202.72	PSAFVVAAAPAAAAGGEAEAPAAEAAAEEEEES#D	259.09							K.AFLADPSAFVVAAAPAAAAGGEAEAPAAEAAAEEEEESDEDMGFGLFD.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
23	sp|O36025|MPD2_SCHPO	82	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence

285	295	2	1326.598	0.0011	1	45.51	D.NLADFSQSPLR.R	Phospho (ST)	103.65	NLADFSQS#PLR	37.41						-------N---	R.AGSDTFPDLNTSSSNQPGGEPNVASANTHSLEILSSSAYHPSGSSNGISAGLTQSVASPVGQVDNLADFSQSPLRR.G
140	160	2	2323.0294	0.0024	0	39.68	K.NANTSFTNAFSNEGISPGFLR.D	Phospho (ST)	102.43	NANTSFTNAFSNEGIS#PGFLR	43.7						----------N-----	K.NANTSFTNAFSNEGISPGFLRDCFPSSNSITTGTASPK.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
24	sp|Q10074|YAN9_SCHPO	80	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
48	67	2	2207.9614	0.0031	0	35.08	K.LNISPSESNLPNNVAENTTD.T	Phospho (ST)	105.19	LNIS#PSESNLPNNVAENTTD	25.48						---N----------	K.LNISPSESNLPNNVAENTTDTPVNYGSIR.D

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
25	sp|Q9UUE2|CSX2_SCHPO	77	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
228	242	3	1664.8681	0.003	0	44.46	D.PLPINSPPLTNPVAR.D	Phospho (ST)	111.34	PLPINS#PPLTNPVAR	79.11						-----N---------	K.TFQFYVTESDQDSTPATPFPMPMHLAEETATSPEISDAPPLSGNVDPLPINSPPLTNPVARDIDQTEPEDGPLFR.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
26	sp|P40976|LYS2_SCHPO	75	2	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
912	921	2	1103.5504	0.0016	0	40.81	D.IGGHSILATR.L	Phospho (ST)	101.41	IGGHS#ILATR	72.42							K.ASFFDIGGHSILATRLIFELR.K
907	921	2	1670.7846	0.0029	1	34.31	K.ASFFDIGGHSILATR.L	Phospho (ST)	87.13	ASFFDIGGHS#ILATR	72.42							K.ASFFDIGGHSILATRLIFELR.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
27	sp|Q09717|RANG_SCHPO	74	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
66	80	2	1728.8152	0.0029	0	20.17	D.AEPASPEVHFEPIVK.L	Phospho (ST)	60.12	AEPAS#PEVHFEPIVK	1000						----Y----------	K.KPAEGDEDAEPASPEVHFEPIVKLSAVETK.T

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
28	sp|Q9USU9|TOA1_SCHPO	64	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
83	101	3	1984.0558	0.0051	0	20.07	D.VTAPAVANSPILNNIAAIR.A	Phospho (ST)	73.55	VTAPAVANS#PILNNIAAIR	24.37						--------N----------	R.TDSLDVTAPAVANSPILNNIAAIRAVQQMDTFAQQHGNSNYYSPPTPSLPQSATNISFDSSAIPNVQSNPNNTAPFPSYSSNSLQLPTNQTADSPIINDHSTANVTSTGQEHAPDSSSTNSFGGLLLPNQNSPK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
29	sp|P36623|PMGY_SCHPO	63	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
32	40	2	994.4748	0.0012	0	37.78	D.PALSETGIK.E	Phospho (ST)	53.84	PALS#ETGIK	37.41						---N-----	K.DPALSETGIKEAK.L
32	43	2	1322.6498	0.0016	1	34.09	D.PALSETGIKEAK.L	Phospho (ST)	50.4	PALS#ETGIKEAK	30.7						---N--------	K.DPALSETGIKEAKLGGER.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
30	sp|Q9USH9|YJQ1_SCHPO	63	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
136	148	2	1560.6114	0.0035	1	25.72	D.LSLDEEESESSEK.S	Phospho (ST)	74.55	LS#LDEEESESSEK	53.41						-Y----------	K.NAFDALADDMDDLSLDEEESESSEKSK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
31	sp|Q10475|IF4G_SCHPO	56	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
441	461	2	2239.9974	0.0016	1	46.98	R.SGSQVSDQVVESPNSSTLSPR.N	Phospho (ST)	151.86	SGSQVSDQVVESPNSSTLS#PR	42.65						----------Y--	R.SGSQVSDQVVESPNSSTLSPRNGFAPIVK.Q

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
32	sp|O74417|YJL4_SCHPO	55	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
240	261	2	2161.0314	0.0076	0	55.46	R.SAAQAMATVVPSVSTPGGTPPR.F	Phospho (ST)	105.91	SAAQAMATVVPSVSTPGGT#PPR	24.15						----------Y---	R.SAAQAMATVVPSVSTPGGTPPRFASPALTVESMVHAAPSTTTSSR.F

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
33	sp|O94601|YC8E_SCHPO	49	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
298	314	2	1858.8054	0.0029	1	49.48	D.SPYSALAASPPPEDYSK.K	Phospho (ST)	145.18	SPYSALAAS#PPPEDYSK	38.52							R.GTYDAEIDSPYSALAASPPPEDYSKK.N

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
34	sp|P36600|KAPR_SCHPO	48	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
102	120	2	2161.9754	0.004	1	35.41	R.RQSVSTESMNPSAFALETK.R	Phospho (ST)	81.71	RQS#VSTESMNPSAFALETK	21.3						--Y----------	R.QSVSTESMNPSAFALETKR.T

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
35	sp|O74803|RHP23_SCHPO	48	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
348	366	3	2310.9448	0.0018	1	27.9	D.KNEELAANYLFEHGHESED.E	Phospho (ST)	41.12	KNEELAANYLFEHGHES#ED	49.84						----------Y--	K.NEELAANYLFEHGHESEDEP.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
36	sp|O14319|CUE5_SCHPO	47	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
198	217	3	2310.1033	0.0028	1	47.12	R.RSTAATLESAYEERPPSLPR.R	Phospho (ST)	62.08	RSTAATLESAYEERPPS#LPR	50.58							R.STAATLESAYEERPPSLPRR.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
37	sp|Q9HDV9|GCSH_SCHPO	47	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
127	140	2	1714.7292	0.0019	1	21.32	D.KVSSSPEEEGWICK.I	Phospho (ST)	87.51	KVSSS#PEEEGWICK	24.44						----Y---------	K.VSSSPEEEGWICKIK.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
38	sp|O94740|CDC37_SCHPO	47	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
231	249	2	2184.8234	0.0015	1	46.66	K.NPVNENESEDEEGLSLSED.G	Phospho (ST)	194.66	NPVNENES#EDEEGLSLSED	111.09						-------Y----------	K.NPVNENESEDEEGLSLSEDGK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
39	sp|Q10253|MUG64_SCHPO	44	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
99	116	2	1930.9814	0.005	0	43.85	R.NLGNLTPLEQTPLASVGK.N	Phospho (ST)	95.57	NLGNLT#PLEQTPLASVGK	37.11							R.NLGNLTPLEQTPLASVGKNLEEK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
40	sp|O74504|YJD1_SCHPO	43	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
215	228	2	1387.6044	0.0024	0	26.69	D.SPNPPAATPATVAD.N	Phospho (ST)	88.18	S#PNPPAATPATVAD	47.61						N----------	K.TTTQIDVQTNIVTPPITVTAVPDSPNPPAATPATVADNDDLSIVSSDSGNTTAPR.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
41	sp|Q9P6R7|VTS1_SCHPO	42	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
247	265	2	1954.9072	0.0035	0	27.57	K.ALAFSSIEPPASSASTSPR.N	Phospho (ST)	119.3	ALAFSSIEPPASSASTS#PR	32.4						----------N--	K.ALAFSSIEPPASSASTSPRNTPTPSNNGTSINANVTSSLTSNSTGK.T

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
42	sp|P40383|XRN1_SCHPO	39	2	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
1232	1255	3	2676.337	0.0057	1	37.35	R.LVTKPTSTFPSPPSPPSSSVWNKR.E	Phospho (ST)	100.56	LVTKPTSTFPSPPS#PPSSSVWNKR	52.62							R.LVTKPTSTFPSPPSPPSSSVWNKREHHPKPFSLHQVPPPESLIHK.S
1232	1254	3	2520.2368	0.0066	0	21.39	R.LVTKPTSTFPSPPSPPSSSVWNK.R	Phospho (ST)	63.68	LVTKPTSTFPSPPS#PPSSSVWNK	34.55							R.LVTKPTSTFPSPPSPPSSSVWNKR.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
43	sp|P52890|ATF1_SCHPO	39	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
75	85	2	1170.5698	0.0012	0	39	D.GVTPSFVGSLK.L	Phospho (ST)	60.87	GVT#PSFVGSLK	42.65							-.MSPSPVNTSTEPASVAAVSNGNATASSTQVPENNQSDSFAPPSNNSQQNQQSSTIAPNGGAGSVANANPADQSDGVTPSFVGSLKLDYEPNPFEHSFGSTASVGQGNPSLNR.N

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
44	sp|O74511|EKC1_SCHPO	35	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
459	474	2	1905.728	0.0054	1	23.74	D.SPMSEAEPVSEEEYKD.V	Phospho (ST)	125.39	S#PMSEAEPVSEEEYKD	33.7						Y----------	K.DNLNLTTTDSPMSEAEPVSEEEYKDVMETAK.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
45	sp|O94548|YCD9_SCHPO	33	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
115	133	3	2336.0725	0.0039	1	33.34	K.TVNEINKSQEFQEHVETPK.Q	Phospho (ST)	70.58	TVNEINKS#QEFQEHVETPK	31.5							K.TVNEINKSQEFQEHVETPKQSNWLGGFWSTASAAVR.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
46	sp|Q09826|SDS23_SCHPO	31	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
322	335	2	1674.7898	0.0058	0	30.99	R.LWLVQSPSCPPSPK.N	Phospho (ST)	102.14	LWLVQSPSCPPS#PK	34.98						----------Y--	R.LWLVQSPSCPPSPKNNAHLSPGSMGGVK.V

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
47	sp|Q9UTE9|TIM10_SCHPO	30	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
9	34	3	3197.3032	0.0126	1	17.78	K.NNQTINPQNIAMAEQEVEMMSDIFNR.L	Deamidated (NQ); 2 Phospho (ST)	15.64	NNQT#INPQNIAMAEQEVEMMS#DIFNR	1000							K.NNQTINPQNIAMAEQEVEMMSDIFNRLVMTCHK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
48	sp|O42923|CIP1_SCHPO	27	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
80	105	3	2695.1632	-0.0059	1	17.48	R.AASPAPSDSFPTFGYSQLGGLENSSK.G	Deamidated (NQ); Phospho (ST)	60.59	AAS#PAPSDSFPTFGYSQLGGLENSSK	20.57						--N----------	R.AASPAPSDSFPTFGYSQLGGLENSSKGSALFNSANSIGTPYLSSR.N

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
49	sp|Q9USW1|YHZ3_SCHPO	26	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
389	414	3	2907.3535	0.0036	1	15.33	D.GNTSSPSKEEEKPSTEPEKPSVVTQR.K	Phospho (ST)	94.03	GNTSS#PSKEEEKPSTEPEKPSVVTQR	22.62							K.VDGNTSSPSKEEEKPSTEPEKPSVVTQRK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
50	sp|P09627|PMA1_SCHPO	26	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Extended tryptic sequence
44	53	2	1244.5282	0.0069	0	25.96	D.ALIEELFSED.V	Phospho (ST)	78.91	ALIEELFS#ED	1000						--------N--	K.HAPEQQAPPPQQPAHAAAPAQDDEPDDDIDALIEELFSEDVQEEQEDNDDAPAAGEAK.A

Supplementary Table S3: Phosphoproteins with the corresponding phosphopeptides and localized phosphosites from solprotSB (*S. pombe*) and from SKMel (human melanoma) samples
(*) Phosphorylated amino acid **X** is displayed as **X#**

***Human melanoma* - Trypsin - Whole tryptic digest**

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
1	sp|Q13283|G3BP1_HUMAN	1001	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
133	159	3	3295.3372	0.013	0	42.35	R.YQDEVFGGFVTEPQEESEEEVEEPEER.Q	Phospho (ST)	116.25	YQDEVFGGFVTEPQEES#EEEVEEPEER	66.42						----------Y----------	----------Y----------
248	257	2	1192.5212	0.0047	0	28.41	R.TFSWASVTSK.N	Phospho (ST)	50.82	TFSWAS#VTSK	22.62						-----N----	-----N----
230	247	2	1964.8796	0.0068	0	85.71	K.SSSPAPADIAQTVQEDLR.T	Deamidated (NQ); Phospho (ST)	137.42	SSS#PAPADIAQTVQEDLR	19.21						--Y----------	--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
2	sp|P05387|RLA2_HUMAN	981	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
99	115	2	2124.6914	0.0119	1	20.38	K.KEESEESDDDMGFGLFD.-	Oxidation (M); 2 Phospho (ST)	24.89	KEES#EES#DDDM!GFGLFD	1000						---Y--Y----------	---Y--Y----------
62	94	3	2853.3991	0.0082	0	29.34	K.LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK.K	Phospho (ST)	117.1	LASVPAGGAVAVSAAPGS#AAPAAGSAPAAAEEK	27.68						----------Y----------	----------Y----------
3	21	2	1947.9404	0.0062	0	32.71	R.YVASYLLAALGGNSSPSAK.D	Phospho (ST)	133.95	YVASYLLAALGGNSS#PSAK	22.85						----------Y----	----------Y----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
3	sp|P67809|YBOX1_HUMAN	750	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
102	118	2	1874.7882	0.0059	0	83.26	R.SVGDGETVEFDVVEGEK.G	Phospho (ST)	128.48	S#VGDGETVEFDVVEGEK	46.2						Y----------	Y----------
305	324	2	1976.7706	0.007	0	38.27	K.AADPPAENSSAPEAEQGGAE.-	Phospho (ST)	170.55	AADPPAENSS#APEAEQGGAE	28.87						---------Y----------	---------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
4	sp|Q09666|AHNK_HUMAN	694	15	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
133	149	3	1898.8345	0.0086	1	33.94	R.LKSEDGVEGDLGETQSR.T	Phospho (ST)	128.08	LKS#EDGVEGDLGETQSR	113.55						--N----------	--N----------
29	45	2	1911.8426	0.0063	0	37.08	R.DDGVFVQEVTQNSPAAR.T	Phospho (ST)	125.41	DDGVFVQEVTQNS#PAAR	64.54						----------Y----	----------N----
711	721	2	1313.6316	0.0048	1	20.02	K.VKGEYDVTVPK.L	Phospho (Y)	78.72	VKGEY#DVTVPK	26.79						----Y------	----N------
208	225	2	1801.7706	0.0058	0	25.32	R.LPSGSGAASPTGSAVDIR.A	2 Phospho (ST)	82.47	LPS#GSGAASPTGSAVDIR	24.84	22.01					--Y-----Y---------	--N-----N---------
500	513	2	1584.7142	0.0036	0	42.19	K.ISMQDVDLSLGSPK.L	Oxidation (M); Phospho (ST)	67.46	ISMQDVDLSLGS#PK	43.47						----------Y--	----------N--
5748	5767	4	1996.9037	0.0047	1	47.13	K.ASLGSLEGEAEAEASSPKGK.F	Phospho (ST)	71.99	ASLGSLEGEAEAEASS#PKGK	20.91						----------Y----	----------N----
4906	4915	2	1151.5334	0.0037	0	33.05	K.MPSLEISAPK.V	Phospho (ST)	98.77	MPS#LEISAPK	71.24						--N-------	--N-------
829	842	2	1613.722	0.006	1	35.25	K.GPNVKGEYDVTMPK.V	Phospho (Y)	126.52	GPNVKGEY#DVTMPK	37.54						-------Y------	-------N------
5102	5112	3	1263.6313	0.0049	1	15.82	K.FKAEAPLPSPK.L	Phospho (ST)	56.63	FKAEAPLPS#PK	1000						--------Y--	--------N--
5726	5740	2	1412.625	0.0066	0	14.68	K.GGVTGSPEASISGSK.G	Phospho (ST)	48.48	GGVTGS#PEASISGSK	38.66						-----Y---------	-----N---------
569	582	2	1552.727	0.0063	0	51.32	R.ISMSEVDLNVAAPK.V	Phospho (ST)	109.55	IS#MSEVDLNVAAPK	25.91						-Y----------	-N----------
3415	3428	2	1635.7978	0.0036	1	22.56	K.VSMPDVELNLKSPK.V	Phospho (ST)	60.77	VSMPDVELNLKS#PK	73.72						----------N--	----------N--
5748	5765	2	1811.7888	0.0063	0	73.97	K.ASLGSLEGEAEAEASSPK.G	Phospho (ST)	110.6	ASLGS#LEGEAEAEASSPK	22.84						-----Y----------	-----N----------
172	181	2	1229.5266	0.005	0	14.92	K.DIDISSPEFK.I	Phospho (ST)	58.03	DIDISS#PEFK	21.51						-----Y----	-----N----
2386	2399	3	1688.8258	0.0049	1	29.74	K.ISMPDLDLHLKSPK.A	Oxidation (M); Phospho (ST)	39.94	ISMPDLDLHLKS#PK	47.37						----------Y--	----------N--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
5	sp|P08670|VIME_HUMAN	647	4	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
37	50	3	1574.7508	0.0054	0	22.05	R.TYSLGSALRPSTSR.S	Phospho (Y)	78.39	TY#SLGSALRPSTSR	33.68						-Y----------	-Y----------
425	440	2	1903.9116	0.0076	1	27.14	R.ETNLDSLPLVDTHSKR.T	Phospho (ST)	53.08	ETNLDS#LPLVDTHSKR	24.15						-----Y----------	-----Y----------
425	439	2	1747.807	0.0041	0	34	R.ETNLDSLPLVDTHSK.R	Phospho (ST)	87.46	ETNLDS#LPLVDTHSK	32.07						-----Y----------	-----Y----------
51	64	2	1507.6744	0.0036	0	28.72	R.SLYASSPGGVYATR.S	Phospho (ST)	72.38	SLYAS#SPGGVYATR	19.05						----Y---------	----Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
6	sp|Q15149|PLEC1_HUMAN	643	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
4384	4401	2	1833.8206	0.0061	0	93.89	R.SSSVGSSSSYPISPAVSR.T	Phospho (ST)	147.85	SSS#VGSSSSYPISPAVSR	24.98						--Y----------	--Y----------
4402	4428	3	2967.376	0.0122	0	44.97	R.TQLASWSDPTEETGPVAGILDTETLEK.V	Phospho (ST)	153.47	TQLAS#WSDPTEETGPVAGILDTETLEK	22.84						----N----------	----Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
7	sp|P06748|NPM_HUMAN	626	5	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
102	134	4	3700.6217	0.013	1	22.01	R.LKCGSGPVHISGQHLVAVEEDAESEDEEEEDVK.L	Phospho (ST)	77.06	LKCGSGPVHISGQHLVAVEEDAES#EDEEEEDVK	43.62						----------Y---------	----------Y---------
104	134	3	3459.4492	0.0195	0	33.56	K.CGSGPVHISGQHLVAVEEDAESEDEEEEDVK.L	Phospho (ST)	74.79	CGSGPVHISGQHLVAVEEDAES#EDEEEEDVK	54.35						----------Y---------	----------Y---------
46	73	3	3008.4292	0.009	1	57.67	R.TVSLGAGAKDELHIVEAEAMNYEGSPIK.V	Phospho (ST)	149.88	TVSLGAGAKDELHIVEAEAMNYEGS#PIK	78.31						----------Y---	----------Y---
104	141	5	4157.8806	0.0182	1	46.7	K.CGSGPVHISGQHLVAVEEDAESEDEEEEDVKLLSISGK.R	Phospho (ST)	76.63	CGSGPVHISGQHLVAVEEDAES#EDEEEEDVKLLSISGK	32.16						----------Y----------	----------Y----------
1	24	3	3044.2282	0.0147	0	22.92	-.MEDSMDMDMSPLRPQNYLFGCELK.A	Acetyl (Protein N-term); Oxidation (M); Phospho (ST)	43.13	MEDS#MDMDMSPLRPQNYLFGCELK	21.59						---Y----------	---Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
8	sp|O75822|EIF3J_HUMAN	555	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
234	258	3	2934.1051	0.0125	1	60.58	K.ATMKDDLADYGGYDGGYVQDYEDFM.-	Oxidation (M); Phospho (Y)	47.1	ATMKDDLADYGGYDGGYVQDY#EDFM	23.84						----------Y----	----------N----
2	27	2	2714.1594	0.0097	1	56.59	M.AAAAAAAGDSDSWDADAFSVEDPVRK.V	Acetyl (Protein N-term); Phospho (ST)	71.97	AAAAAAAGDS#DSWDADAFSVEDPVRK	21.3						---------Y----------	---------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
9	sp|Q13263|TIF1B_HUMAN	542	4	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
473	483	2	1200.4894	0.0049	0	23.46	R.SGEGEVSGLMR.K	Phospho (ST)	86.92	S#GEGEVSGLMR	72.67						Y----------	Y----------
2	32	2	2664.1894	0.0118	1	100.51	M.AASAAAASAAAASAASGSPGPGEGSAGGEKR.S	Acetyl (Protein N-term); Phospho (ST)	73.91	AASAAAASAAAASAASGS#PGPGEGSAGGEKR	24.84						----------Y----------	----------Y----------
471	483	2	1443.6222	0.0045	1	33.37	R.SRSGEGEVSGLMR.K	Phospho (ST)	89.14	SRS#GEGEVSGLMR	27.7						--Y----------	--Y----------

2	31	3	2508.085	0.0085	0	50.95	M.AASAAAASAAAASAASGSPGPGEGSAGGEK.R	Acetyl (Protein N-term); Phospho (ST)	90.65	AASAAAASAAAASAASGS#PGPGEGSAGGEK	23.38						----------Y----------	----------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
10	sp|Q15185|TEBP_HUMAN	541	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				
108	122	2	1970.6238	0.0089	0	59.35	K.DWEDDSDEDMSNFDR.F	Oxidation (M); Phospho (ST)	65.96	DWEDDS#DEDMSNFDR	28.35						-----Y---------	-----Y---------					

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
11	sp|P23528|COF1_HUMAN	510	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				
2	13	2	1223.586	0.0062	0	26.96	M.ASGVAVSDGVIK.V	Acetyl (Protein N-term); Phospho (ST)	27.47	AS#GVAVSDGVIK	21.27						-Y----------	-N----------					

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
12	sp|P04792|HSPB1_HUMAN	501	3	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				
38	75	4	4172.0389	0.0192	0	17.37	R.LPEEWSQWLGGSSWPGYVRPLPPAAIESPAVAAPAYSR.A	Phospho (ST)	76.25	LPEEWSQWLGGSSWPGYVRPLPAAIES#PAVAAPAYSR	24.41						----------Y----------	----------Y----------					
13	20	2	1040.4156	0.004	0	15.78	R.GPSWDPFR.D	Phospho (ST)	104.08	GPS#WDPFR	1000						--Y-----	--Y-----					
80	89	2	1155.5228	0.0056	0	46.57	R.QLSSGVSEIR.H	Deamidated (NQ); Phospho (ST)	67.85	QLS#SGVSEIR	24.44						---Y------	---Y------					

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
13	sp|Q14247|SRC8_HUMAN	490	5	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				
132	147	2	1864.8298	0.0054	1	42.29	R.VDQSAVGFEYQGKTEK.H	Phospho (Y)	121.53	VDQSAVGFEY#QGKTEK	76.73						---------Y------	---------Y------					
415	428	2	1669.673	0.0053	0	46.82	R.LPSSPVYEDAASFK.A	Phospho (ST); Phospho (Y)	153.69	LPSS#PVY#EDAASFK	22.85	67.77					---Y--Y-------	---Y--Y-------					
435	454	2	2313.8974	0.0073	0	80.01	R.GPVSGTEPEPVYSMEAADYR.E	2 Phospho (Y)	135.87	GPVSGTEPEPVY#SMEAADY#R	28.87	57.18					----------Y------Y-	----------Y------Y-					
317	336	2	2344.0014	0.0084	1	71.06	R.MDKNASTFEDVTQVSSAYQK.T	Oxidation (M); Phospho (Y)	99.6	MDKNASTFEDVTQVSSAY#QK	30.83						----------Y--	----------Y--					
320	336	3	1953.8446	0.0089	0	25.35	K.NASTFEDVTQVSSAYQK.T	Phospho (Y)	119.38	NASTFEDVTQVSSAY#QK	46.68						----------Y--	----------Y--					

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
14	sp|P46821|MAP1B_HUMAN	475	4	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				
1052	1070	2	2019.8914	0.0088	0	32.83	K.AAEAGGAEEQYGFLTTPTK.Q	Phospho (Y)	89.08	AAEAGGAEEQY#GFLTTPTK	54.64						----------Y---------	----------Y---------					
1932	1945	2	1817.6748	0.0063	0	43.51	K.TPEDGDYSYEIIEK.T	2 Phospho (Y)	135.93	TPEDGDY#S#YEIIEK	30.83	24.44					------Y-Y-----	------Y-Y-----					
1811	1833	3	2488.0465	0.0099	0	21.24	K.TATCHSSSSPPIDAASAEPYGFR.A	Phospho (Y)	93.12	TATCHSSSSPPIDAASAEPY#GFR	37.23						----------Y---	----------Y---					
1317	1344	3	3044.3692	0.004	0	14.33	K.TLEVVSPSQSVTGSAGHTPYYQSPTDEK.S	Phospho (Y)	43.01	TLEVVSPSQSVTGSAGHTPYY#QSPTDEK	32.46						----------Y-------	----------N-------					

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
15	sp|P16401|H15_HUMAN	453	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				
2	21	2	2102.9854	0.0082	1	43.44	M.SETAPAETATPAPVEKSPAK.K	Acetyl (Protein N-term); Phospho (ST)	42.38	SETAPAETATPAPVEKS#PAK	20.98						----------Y---	----------N---					

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
16	sp|Q8IYB3|SRRM1_HUMAN	448	5	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				
763	788	4	2790.4217	0.0111	1	17.73	K.KPPAPPSPVQSQSPSTNWSPAVPVKK.A	Phospho (ST)	83.25	KPPAPPS#PVQSQSPSTNWSPAVPVKK	49.64						------Y----------	------Y----------					
595	602	2	1096.5128	0.0062	1	21.36	R.RYSPPIQR.R	Deamidated (NQ); Phospho (ST)	69.34	RYS#PPIQR	28.87						--Y-----	--Y-----					
870	885	2	2023.7654	0.0107	1	47.53	K.KETESEAEDNLDDLEK.H	2 Phospho (ST)	172	KET#ES#EAEDNLDDLEK	1000						--Y-Y----------	--Y-Y----------					
218	229	2	1432.6902	0.0052	1	14.61	K.EKTPELPEPSVK.V	Phospho (ST)	40.21	EKT#PELPEPSVK	47.25						--Y---------	--Y---------					
247	263	3	1976.992	0.006	1	32.4	K.VPKPEPIPEPKEPSPEK.N	Phospho (ST)	97.56	VPKPEPIPEPKEPS#PEK	1000						----------Y---	----------Y---					

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
17	sp|Q8NHW5|RLA0L_HUMAN	416	2	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				
302	317	2	2010.6094	0.0092	0	14.48	K.EESEESDEDMGFGLFD.-	Oxidation (M); 2 Phospho (ST)	40.9	EES#EES#DEDM!GFGLFD	1000						--Y--Y----------	--Y--Y----------					
298	317	2	2437.8534	0.0101	1	37.09	K.VEAKEESEESDEDMGFGLFD.-	Oxidation (M); 2 Phospho (ST)	75.29	VEAKEES#EES#DEDM!GFGLFD	1000						------Y--Y----------	------Y--Y----------					

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
18	sp|P49006|MRP_HUMAN	374	4	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				
100	107	2	986.4994	0.0044	1	21.12	K.LSGLSFKR.N	Phospho (ST)	44.36	LSGLS#FKR	49.62						----Y---	----Y---					
158	195	3	3704.5252	0.0129	0	86.56	K.GAEASAASEEEAGPQATEPSTPSSGPESGPTPASAEQNE.-	Phospho (ST)	164.15	GAEASAASEEEAGPQATEPST#PSGPESGPTPASAEQNE	22.01						----------Y----------	----------Y----------					
91	95	2	735.3376	0.002	1	14.59	K.KFSFK.K	Phospho (ST)	47.62	KFS#FK	1000						--Y--	--Y--					
11	35	4	2488.0953	0.0086	1	18.21	R.GDVTAEEAAGASPAKANGQENGHVK.S	Deamidated (NQ); Phospho (ST)	13.27	GDVTAEEAAGAS#PAKANGQENGHVK	19.61						----------Y----------	----------Y----------					

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
19	sp|A6NK07|IF2BL_HUMAN	364	3	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				
103	124	3	2566.1119	0.0085	0	19.26	K.IESDVQEPTEPEDDLDIMLGNK.K	Phospho (ST)	100.45	IESDVQEPT#EPEDDLDIMLGNK	25.66						--------Y----------	--------N----------					
2	15	2	1722.6928	0.0047	1	17.78	M.SGDEMIFDPTMSKK.K	Acetyl (Protein N-term); Oxidation (M); Phospho (ST)	28.34	S#GDEMIFDPTMSKK	28.83						Y----------	N----------					
2	14	2	1610.594	0.0059	0	22.64	M.SGDEMIFDPTMSK.K	Acetyl (Protein N-term); 2 Oxidation (M); Phospho (ST)	3.95	S#GDEMIFDPTMSK	20.27						Y----------	N----------					

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
20	sp|Q16666|IF16_HUMAN	342	4	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				
768	785	2	2168.9134	0.0121	1	33.01	K.KDILNPDSSMETSPDFFF.-	Phospho (ST)	143.87	KDILNPDSS#METSPDFFF	32.4						--------N---------	--------N---------					
144	165	2	2283.9574	0.0073	0	69.13	K.VSEEQTQPPSPAGAGMSTAMGR.S	Oxidation (M); Phospho (ST)	59.12	VSEEQTQPPS#PAGAGMSTAMGR	24.77						---------Y----------	---------Y----------					
769	785	2	2040.8154	0.0091	0	33.74	K.DILNPDSSMETSPDFFF.-	Phospho (ST)	115.03	DILNPDSS#METSPDFFF	20.35						--------N---------	--------N---------					
101	116	2	1655.7342	0.0051	0	36.12	K.EVDATSPAPSTSSTVK.T	Phospho (ST)	52.68	EVDATS#PAPSTSSTVK	20.35						-----Y----------	-----Y----------					

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
21	sp|P14618|KPYM_HUMAN	332	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
33	43	2	1276.6106	0.0042	0	32.96	R.LDIDSPPITAR.N	Phospho (ST)	64.23	LDIDS#PPITAR	23.64						----N------	----N------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
22	sp|P48681|NEST_HUMAN	328	10	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1406	1436	3	3377.2342	0.0105	1	102.5	R.DGESDGFADEEESGEEGEEDQEEGREPGAGR.W	Phospho (ST)	163.05	DGESDGFADEEES#GEEGEEDQEEGREPGAGR	41.74						----------Y----------	----------Y----------
768	789	3	2602.2823	0.0109	1	17.62	R.SLGEQDQMTLRPPEKVDLEPLK.S	Phospho (ST)	44.39	S#LGEQDQMTLRPPEKVDLEPLK	39.3						Y----------	Y----------
331	342	3	1521.7387	0.0046	1	18.35	K.LELQFPRTPEGR.R	Phospho (ST)	81.94	LELQFPRT#PEGR	1000						-------Y----	-------Y----
578	587	2	1255.5632	0.0048	0	35	R.SLEEDLETLK.S	Phospho (ST)	85.48	S#LEEDLETLK	89.38						Y---------	Y---------
768	782	3	1823.8195	0.007	0	17.75	R.SLGEQDQMTLRPPEK.V	Oxidation (M); Phospho (ST)	28.11	S#LGEQDQMTLRPPEK	34.2						Y----------	Y----------
916	933	2	2215.9734	0.0101	1	41.9	R.NLEEEENLGKGEYQESLR.S	Phospho (Y)	139.71	NLEEEENLGKGEY#QESLR	68.23						----------N-----	----------Y-----
673	694	3	2586.2428	0.0102	1	32.48	K.ENQEPLRSPEVGDEEALRPLTK.E	Phospho (ST)	74.67	ENQEPLRS#PEVGDEEALRPLTK	99.62						-------Y----------	-------Y----------
452	480	3	3065.3722	0.0107	0	40.64	R.QEASTGQSPEDHASLAPPLSPDHSSLEAK.D	Phospho (ST)	76.54	QEASTGQSPEDHASLAPPLS#PDHSSLEAK	21.26						----------Y---------	----------Y---------
548	558	2	1311.601	0.0052	0	40.1	K.SLGEEIQESLK.T	Phospho (ST)	66.48	S#LGEEIQESLK	74.42						Y----------	Y----------
743	756	2	1782.823	0.0082	1	17.37	K.SLRSLEEQDQETLR.T	Phospho (ST)	67.65	SLRS#LEEQDQETLR	19.19						---Y----------	---Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
23	sp|P60981|DEST_HUMAN	309	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
2	13	2	1412.5702	0.0059	0	28.79	M.ASGVQVADEVCR.I	Acetyl (Protein N-term); Deamidated (NQ); Phospho (ST)	11.74	A!S#GVQ!VADEVCR	1000						-Y----------	-N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
24	sp|Q71U36|TBA1A_HUMAN	304	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
423	451	3	3315.2842	0.0145	1	68.55	R.EDMAALEKDYEEVGVDSVEGEGEEEGEEY.-	Phospho (Y)	188.65	EDMAALEKDYEEVGVDSVEGEGEEEGEEY#	134.38						----------N	----------Y

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
25	sp|P27816|MAP4_HUMAN	289	7	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1139	1152	2	1641.7206	0.0072	0	46.11	R.EAQTLDSQIQETSI.-	Phospho (ST)	132.39	EAQTLDS#QIQETSI	64.62						------N-------	------N-------
45	63	3	2202.9994	0.0061	1	38.26	K.TDYIPLLDVDEKTGNSESK.K	Phospho (Y)	130.98	TDY#IPLLDVDEKTGNSESK	42.65						--N----------	--Y----------
45	56	2	1499.6856	0.006	0	38.95	K.TDYIPLLDVDEK.T	Phospho (Y)	148.42	TDY#IPLLDVDEK	19.84						--N---------	--Y---------
277	290	2	1642.7588	0.0064	1	16.66	K.DMESPTKLDVTLAK.D	Oxidation (M); Phospho (ST)	43.71	DMES#PTKLDVTLAK	37.41						---Y---------	---Y---------
505	532	3	3185.4652	0.0086	1	26.23	K.DMSPLSETEMALGKDVTPPPETEVVLIK.N	2 Phospho (ST)	93.68	DMS#PLSETEMALGKDVT#PPPETEVVLIK	20.63	44.12					--Y----------Y----------	--Y----------Y----------
1071	1087	3	1669.8244	0.0055	0	21.74	K.VGSLDNVGHLPAGGAVK.T	Phospho (ST)	46.16	VGS#LDNVGHLPAGGAVK	1000						--Y----------	--Y----------
505	518	2	1587.6614	0.0053	0	29.23	K.DMSPLSETEMALGK.D	Phospho (ST)	90.25	DMS#PLSETEMALGK	44.73						--Y----------	--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
26	sp|Q8WWM7|ATX2L_HUMAN	282	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
582	599	2	1911.8574	0.0038	0	32.97	K.EVDGLLTSEPMGSPVSSK.T	Phospho (ST)	98.67	EVDGLLTSEPMGS#PVSSK	53.16						----------Y-----	----------Y-----
107	122	2	1826.8076	0.0088	0	62.81	K.GPPQSPVFEGVYNNSR.M	Phospho (ST)	150.58	GPPQS#PVFEGVYNNSR	79.71						----Y----------	----Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
27	sp|P02545|LMNA_HUMAN	279	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
628	644	2	1645.7158	0.0061	0	55.52	R.SVGGSGGGSFGDNLVTR.S	Phospho (ST)	63.83	SVGGSGGGS#FGDNLVTR	34.28						--------Y--------	--------Y--------
645	654	2	1172.5272	0.0046	0	33.82	R.SYLLGNSSPR.T	Phospho (ST)	96.11	SYLLGNSS#PR	21.51						-------Y--	-------Y--
387	397	2	1400.6268	0.0054	1	19.28	R.LRLSPSPTSQR.S	2 Phospho (ST)	72.79	LRLS#PS#PTSQR	37.11	26.79					---Y-Y-----	---Y-Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
28	sp|O15061|SYNEM_HUMAN	275	8	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1173	1185	2	1427.6974	0.0052	0	30.83	R.HVTLGPGQSPLSR.E	Phospho (ST)	93.39	HVTLGPGQS#PLSR	43.47						--------Y----	--------Y----
1044	1064	2	2014.8694	0.0062	0	62.19	R.SPAPGSPDEEGGAEAPAAGIR.F	Phospho (ST)	135.65	SPAPGS#PDEEGGAEAPAAGIR	23.64						-----Y----------	-----Y----------
1548	1565	2	2271.9434	0.0073	0	65.02	K.VALLYLDNEEEENDGHWF.-	Phospho (Y)	233.46	VALLY#LDNEEEENDGHWF	1000						----N----------	----N----------
649	667	2	2164.8914	0.0077	0	46.93	K.QFTQSPETEASADSFPDTK.V	Phospho (ST)	105.7	QFTQS#PETEASADSFPDTK	26.79						----Y----------	----N----------
692	710	3	2160.9814	0.0098	0	14.05	K.LTEDVDVSDEAGLDYLLSK.D	Phospho (Y)	71.32	LTEDVDVSDEAGLDY#LLSK	41.54						----------N----	----------N----
1042	1064	3	2378.995	0.0057	1	37.93	R.QRSPAPGSPDEEGGAEAPAAGIR.F	2 Phospho (ST)	65.13	QRS#PAPGS#PDEEGGAEAPAAGIR	1000						--Y----Y----------	--Y----Y----------
595	609	2	1492.709	0.0055	1	18.33	K.GLQTPVKDAGGGTGR.E	Phospho (ST)	44.27	GLQT#PVKDAGGGTGR	57.28						---Y----------	---Y----------
427	436	2	1233.5846	0.0052	0	27.49	R.TFSPTYGLLR.N	Phospho (ST)	60.34	TFS#PTYGLLR	30.7						--Y-------	--Y-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
29	sp|Q12888|TP53B_HUMAN	273	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1614	1626	2	1423.6652	0.0057	0	21.21	K.AADISLDNLVEGK.R	Phospho (ST)	61.3	AADIS#LDNLVEGK	1000						----Y--------	----Y--------
372	387	2	1810.8204	0.0066	0	29.52	R.STPFIVPSSPTEQEGR.Q	Phospho (ST)	124.34	STPFIVPSS#PTEQEGR	20.35						--------Y-------	--------Y-------
349	371	2	2485.1474	0.0101	0	79.01	R.SLVQDSLSTNSSDLVAPSPDAFR.S	Phospho (ST)	183.99	SLVQDSLSTNSSDLVAPS#PDAFR	122.64						----------Y-----	----------Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
30	sp|Q92625|ANS1A_HUMAN	253	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
566	578	2	1457.696	0.0045	0	46.25	R.VGYLTGLPTTNSR.S	Phospho (Y)	157.57	VGY#LTGLPTTNSR	76.83						--N----------	--N----------
825	843	3	2256.139	0.0086	0	28.83	R.IIASLADRPYEEPPQKPPR.F	Phospho (Y)	97.56	IIASLADRPY#EEPPQKPPR	38.48						---------N---------	---------N---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
31	sp|Q9NYF8|BCLF1_HUMAN	248	5	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?

655	663	2	1080.5254	0.0038	0	21.48	R.IDISPSTLR.K	Phospho (ST)	70.28	IDIS#PSTLR	21.3							---Y-----	---Y-----
394	412	3	2431.9153	0.0075	1	45.43	K.FNDSEGDDTEETEDYRQFR.K	Phospho (ST)	89.3	FNDS#EGDDTEETEDYRQFR	49.59							---Y----------	---Y----------
414	429	3	1753.822	0.0071	1	16.84	K.SVLADQGKSFATASHR.N	Phospho (ST)	37.28	SVLADQGKS#FATASHR	20.95							--------N-------	--------Y-------
394	409	2	2000.6894	0.0098	0	33.68	K.FNDSEGDDTEETEDYR.Q	Phospho (ST)	95.62	FNDS#EGDDTEETEDYR	38.19							---Y----------	---Y----------
205	224	2	2159.9254	0.0094	0	21.31	K.SSATSGDIWPGLSAYDNSPR.S	Phospho (ST)	107.98	SSATSGDIWPGLSAYDNS#PR	32.46							----------Y--	----------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
32	sp|O60841|IF2P_HUMAN	239	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
206	224	3	2112.8722	0.0085	0	28.76	K.NKPGPNIESGNEDDDASFK.I	Phospho (ST)	55.1	NKPGPNIES#GNEDDDASFK	50.36						--------Y----------	--------Y----------
106	122	2	2079.7874	0.0081	1	34.48	K.QSFDDNDSEELEDKDSK.S	Phospho (ST)	73.57	QSFDDNDS#EELEDKDSK	25.88						-------Y---------	-------Y---------
131	148	2	2233.8234	0.0071	1	31.58	K.VEMYSGSDDDDDFNKLPK.K	2 Phospho (ST)	157.28	VEMYS#GS#DDDDDFNKLPK	22.85	49.62					----Y-Y----------	----Y-Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
33	sp|Q15365|PCBP1_HUMAN	232	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
161	177	3	2054.9626	0.0096	0	26.13	K.QICLVMLETLSQSPQGR.V	Oxidation (M); Phospho (ST)	34.09	QICLVMLETLSQS#PQGR	31.51						----------Y----	----------Y----
178	200	3	2554.1515	0.0095	0	39.87	R.VMTIPYQPMPASSPVICAGGQDR.C	Phospho (ST)	135.88	VMTIPYQPMPAS#SPVICAGGQDR	22.62						----------Y----------	----------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
34	sp|Q96N67|DOCK7_HUMAN	231	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
882	893	2	1376.6984	0.0059	0	23.43	R.SAVRPASLNLNR.S	Phospho (ST)	58.46	SAVRPAS#LNLNR	34.51						------Y-----	------Y-----
927	937	2	1225.517	0.0042	0	32.51	R.SNSWVNTGGPK.A	Phospho (ST)	58.12	SNS#WVNTGGPK	33.68						--Y--------	--Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
35	sp|P34932|HSP74_HUMAN	228	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
74	84	2	1318.5536	0.0054	0	23.38	R.AFSDPFVEAEK.S	Phospho (ST)	78.08	AFS#DPFVEAEK	1000						--Y--------	--Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
36	sp|P08238|HS90B_HUMAN	216	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
250	265	2	1816.6948	0.0061	1	64.15	K.IEDVGSDEEDDSGKDK.K	Phospho (ST)	90.4	IEDVGS#DEEDDSGKDK	72.77						-----Y----------	-----N----------
250	263	2	1573.572	0.0052	0	32.23	K.IEDVGSDEEDDSGK.D	Phospho (ST)	84.48	IEDVGS#DEEDDSGK	45.03						-----Y---------	-----N---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
37	sp|Q9C0C2|TB182_HUMAN	214	5	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
427	442	2	1913.86	0.008	1	41.22	R.RFSEGVLQSPSQDQEK.L	Phospho (ST)	82.81	RFS#EGVLQSPSQDQEK	65.61						--Y----------	--Y----------
663	683	2	2349.9954	0.0058	1	26.19	R.TEAQDLCRASPEPPGPESSSR.W	Phospho (ST)	103.56	TEAQDLCRAS#PEPPGPESSSR	29.56						---------Y----------	---------Y----------
836	847	2	1588.626	0.0065	0	49.24	R.SQEADVQDWEFR.K	Phospho (ST)	149.45	S#QEADVQDWEFR	1000						Y----------	Y----------
1618	1632	2	1845.7146	0.0076	0	33.59	R.VPSSDEEVVEEPQSR.R	2 Phospho (ST)	147.83	VPS#S#DEEVVEEPQSR	197.74	212.96					--YY----------	--YY----------
1708	1723	2	1726.7612	0.0049	0	23.86	K.SSGSEGSSPNWLQALK.L	Phospho (ST)	75.94	SSGSEGSS#PNWLQALK	19.33						-------Y-------	-------Y-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
38	sp|P40763|STAT3_HUMAN	214	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
710	729	3	2389.0663	0.0145	0	45.2	K.FICVTPTTCSNTIDLPMSPR.T	Phospho (ST)	109	FICVTPTTCSNTIDLPMS#PR	114.03						----------Y--	----------Y--
686	707	3	2581.0987	0.0043	0	25.52	K.YCRPESQEHPEADPGSAAPYLK.T	Phospho (Y)	103.32	YCRPESQEHPEADPGSAAPY#LK	41.17						----------Y--	----------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
39	sp|Q9UQ80|PA2G4_HUMAN	213	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
2	20	2	2239.9834	0.0101	0	54.7	M.SGEDEQQEQTIAEDLVVTK.Y	Acetyl (Protein N-term); Phospho (ST)	42.39	S#GEDEQQEQTIAEDLVVTK	19.66						Y----------	Y----------
377	394	2	1916.722	0.006	0	52.68	K.TAENATSGETLEENEAGD.-	Phospho (ST)	146.33	TAENATSGET#LEENEAGD	31.87						---------Y--------	---------Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
40	sp|P61978|HNRPK_HUMAN	213	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
104	139	4	4134.0069	0.0161	0	14.44	K.IIPTLEEGLQLPSPTATSQLPLESDAVECLNYQHYK.G	Phospho (ST)	77.61	IIPTLEEGLQLPS#PTATSQLPLESDAVECLNYQHYK	35.28						----------N----------	----------Y----------
279	286	2	1077.3514	0.004	0	15.62	R.DYDDMSPR.R	Phospho (ST)	48.58	DYDDMS#PR	39.8						-----Y--	-----Y--
103	139	4	4262.0989	0.0131	1	18.55	K.KIIPTLEEGLQLPSPTATSQLPLESDAVECLNYQHYK.G	Phospho (ST)	71.89	KIIPTLEEGLQLPS#PTATSQLPLESDAVECLNYQHYK	19.27						----------Y----------	----------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
41	sp|Q9H3N1|TMX1_HUMAN	209	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
234	254	2	2516.9934	0.0132	1	87.94	K.KVEEEQEADEEDVSEEEAESK.E	Phospho (ST)	170.71	KVEEEQEADEEDVS#EEEAESK	71.24						----------Y-------	----------Y-------
270	280	2	1154.5262	0.0042	1	19.7	R.SLGPSLATDKS.-	Phospho (ST)	50.99	S#LGPSLATDKS	42.69						Y----------	Y----------
235	254	2	2388.8954	0.0101	0	79.01	K.VEEEQEADEEDVSEEEAESK.E	Phospho (ST)	182.03	VEEEQEADEEDVS#EEEAESK	74.33						----------Y-------	----------Y-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
42	sp|P05455|LA_HUMAN	208	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
364	384	4	2405.9509	0.0112	1	28.63	K.FASDDEHDEHDENGATGPVKR.A	Deamidated (NQ); Phospho (ST)	64.31	FAS#DDEHDEHDENGATGPVKR	65.47						--Y----------	--Y----------
364	383	3	2249.8438	0.0051	0	35.71	K.FASDDEHDEHDENGATGPVK.R	Deamidated (NQ); Phospho (ST)	49.96	FAS#DDEHDEHDENGATGPVK	56.59						--Y----------	--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
43	sp|Q13838|UAP56_HUMAN	204	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
2	33	3	3471.4522	0.016	1	78.09	M.AENDVDNELLDYEDDEVETAAGGDGAEAPAKK.D	Acetyl (Protein N-term); Phospho (Y)	155.18	AENDVDNELLDY#EDDEVETAAGGDGAEAPAKK	92.11						----------N----------	----------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
44	sp|Q9UKY7|CDV3_HUMAN	204	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
238	251	2	1755.806	-0.002	0	32.32	K.LQLDNQYAVLENQK.S	Deamidated (NQ); Phospho (Y)	94.57	LQLDNQ!Y#AVLENQK	1000						------Y-------	------Y-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
45	sp|P19338|NUCL_HUMAN	201	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
555	567	3	1474.6987	0.0058	1	15.9	R.LELQGPRGSPNAR.S	Deamidated (NQ); Phospho (ST)	24.24	LELQGPRGS#PN!AR	1000						--------Y----	--------Y----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
46	sp|Q14678|KANK1_HUMAN	199	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
323	337	2	1690.7192	-0.0007	0	47.82	R.SYSAGNASQLEQLSR.A	Deamidated (NQ); Phospho (ST)	84.22	SYS#AGNASQLEQLSR	19.33						--Y----------	--Y----------
184	209	3	2616.175	0.007	0	43.79	R.LASFGGMGTTSSLPSFVGSGNHNPAK.H	Oxidation (M); Phospho (ST)	54.66	LAS#FGGMGTTSSLPSFVGSGNHNPAK	30.14						--N-------------------	--N-------------------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
47	sp|Q9H1E3|NUCKS_HUMAN	199	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
9	28	3	2444.9728	0.0082	1	38.94	R.KVVDYSQFQESDDADEDYGR.D	Phospho (ST)	152.04	KVVDYSQFQES#DDADEDYGR	38.81						----------Y---------	----------Y---------
10	28	2	2316.8774	0.0078	0	62.6	K.VVDYSQFQESDDADEDYGR.D	Phospho (ST)	199.09	VVDYSQFQES#DDADEDYGR	89.35						----------Y---------	----------Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
48	sp|Q5SNT6|FA21B_HUMAN	197	5	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
196	208	2	1499.6818	0.0049	0	19.81	R.SRPTSFADELAAR.I	Phospho (ST)	93.13	SRPTS#FADELAAR	28.87						----Y--------	----Y--------
711	734	3	2899.3309	0.0111	1	29.83	K.TVLSLFDEEEDKMEDQNIIQAPQK.E	Phospho (ST)	106.07	TVLS#LFDEEEDKMEDQNIIQAPQK	32.17						----Y----------	----Y----------
258	277	2	2053.8774	0.0104	0	58.59	K.LTDEDFSPFGSGGGLFSGGK.G	Phospho (ST)	121.7	LTDEDFS#PFGSGGGLFSGGK	24.15						------Y------------	------Y------------
448	467	2	2256.9034	0.0087	0	71.79	K.GLFSDEEDSEDLFSSQSASK.L	Phospho (ST)	176.17	GLFS#DEEDSEDLFSSQSASK	72.14						---Y---------------	---Y---------------
525	552	3	3234.3652	0.0108	0	44.31	K.ASALLFSSDEEDQWNIPASQTHLASDSR.S	2 Phospho (ST)	106.17	ASALLFS#S#DEEDQWNIPASQTHLASDSR	38.19	43.27					------YY------------------	------YY------------------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
49	sp|Q9BQG0|MBB1A_HUMAN	195	5	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1255	1275	3	2171.9893	0.0045	0	45.61	K.NQKPSQVNGAPGSPTEPAGQK.Q	Deamidated (NQ); Phospho (ST)	58.41	NQKPSQVNGAPGS#PTEPAGQK	26.42						----------Y---------	----------Y---------
769	801	3	3622.5352	0.0137	0	55.12	K.ALGGEDSENEEELGDEAMMALDQSLASLFAEQK.L	Oxidation (M); Phospho (ST)	102.5	ALGGEDS#ENEEELGDEAMMALDQSLASLFAEQK	65.13						------Y----------------------	------Y----------------------
1254	1275	3	2300.0833	0.0035	1	23.21	K.KNQKPSQVNGAPGSPTEPAGQK.Q	Deamidated (NQ); Phospho (ST)	50.39	KNQKPSQVNGAPGS#PTEPAGQK	24.15						----------Y---------	----------Y---------
5	25	3	2217.9544	0.007	0	15.42	R.DPAQPMSPGEATQSGARPADR.Y	Phospho (ST)	50.07	DPAQPMS#PGEATQSGARPADR	47.99						------Y------------	------Y------------
1	25	3	2763.1828	0.0086	1	28.91	-.MESRDPAQPMSPGEATQSGARPADR.Y	Acetyl (Protein N-term); Phospho (ST)	64.85	MESRDPAQPMS#PGEATQSGARPADR	33.07						----------Y------------	----------Y------------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
50	sp|P46937|YAP1_HUMAN	195	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
107	124	2	1859.8566	0.0039	0	58.12	R.QASTDAGTAGALTPQHVR.A	Phospho (ST)	72.5	QAS#TDAGTAGALTPQHVR	24.44						--Y---------------	--Y---------------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
51	sp|O95817|BAG3_HUMAN	195	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
498	534	4	4017.9309	0.0204	0	33.29	K.AIDVPGQVQVYELQPSNLEADQPLQAIMEMGAVAADK.G	Phospho (Y)	124.86	AIDVPGQVQVY#ELQPSNLEADQPLQAIMEMGAVAADK	57.55						----------N----------	----------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
52	sp|P41236|IPP2_HUMAN	190	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
116	136	3	2579.9866	0.0077	1	21.05	R.IQEQESSGEEDSDLSPEEREK.K	2 Phospho (ST)	91.32	IQEQES#S#GEEDSDLSPEEREK	25.38	27.72					-----YY-----------	-----YN-----------
116	134	2	2322.8474	0.0061	0	42.09	R.IQEQESSGEEDSDLSPEER.E	2 Phospho (ST)	139.55	IQEQES#S#GEEDSDLSPEER	34.97	42.81					-----YY-----------	-----YN-----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
53	sp|Q9Y4E1|FA21C_HUMAN	187	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
536	557	2	2484.0314	0.0097	0	92.31	K.GLFSDEEDSEDLFSSQSASNLK.G	Phospho (ST)	186.75	GLFS#DEEDSEDLFSSQSASNLK	50.15						---Y---------------	---Y---------------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
54	sp|Q7Z417|NUFP2_HUMAN	180	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
570	581	2	1377.7434	0.0053	1	16.41	K.RTSPQVLGSILK.S	Phospho (ST)	79.75	RTS#PQVLGSILK	24.44						--Y---------	--Y---------
650	659	2	1275.498	0.0059	0	28.73	R.NDSWGSFDLR.A	Phospho (ST)	72.15	NDS#WGSFDLR	44.73						-----N----	-----N----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
55	sp|Q7Z5J4|RAI1_HUMAN	180	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1348	1366	3	1944.9013	0.0071	1	34.76	K.APGASPGNPLSPSLSDKDR.G	Phospho (ST)	46.18	APGASPGNPLS#PSLSDKDR	28.83						----------Y---------	----------Y---------
1370	1390	2	1990.9438	0.0077	0	76.47	K.GAGGSPVGVEEGLVNVGTGQK.L	Phospho (ST)	108.2	GAGGS#PVGVEEGLVNVGTGQK	131.39						----Y---------------	----Y---------------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
56	sp|Q13428|TCOF_HUMAN	176	5	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?

147	158	2	1321.6806	0.0052	1	60.91	K.TVANLLSGKSPR.K	Phospho (ST)	102.54	TVANLLSGKS#PR	20.91						---------Y--	---------Y--
1094	1120	3	2680.2661	0.0068	0	51.68	R.TQPSSGVDSAVGTLPATSPQSTSVQAK.G	Phospho (ST)	155.46	TQPSSGVDSAVGTLPATS#PQSTSVQAK	38.66						-----------------Y---------	-----------------Y---------
1348	1357	2	1121.5276	0.0046	1	17.95	R.KLSGDQPAAR.T	Phospho (ST)	33.79	KLS#GDQPAAR	1000						--Y-------	--Y-------
1225	1238	2	1441.675	0.0049	0	31.5	K.LDSSPSVSSTLAAK.D	Phospho (ST)	84.55	LDSS#PSVSSTLAAK	19.33						---Y----------	---Y----------
368	383	2	1635.7682	0.0065	1	34.66	K.TSQVGAASAPAKESPR.K	Phospho (ST)	36.57	TSQVGAASAPAKES#PR	20.62						-------------Y--	-------------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
57	sp|Q16637|SMN_HUMAN	176	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
24	41	2	2015.8454	0.0093	0	49.85	R.GTGQSDDSDIWDDTALIK.A	Phospho (ST)	140.44	GTGQS#DDSDIWDDTALIK	37.68						-------Y----------	-------Y----------
23	41	2	2251.9114	0.0079	1	52.12	R.RGTGQSDDSDIWDDTALIK.A	2 Phospho (ST)	183.49	RGTGQS#DDS#DIWDDTALIK	27.69	79.36					-----Y--Y----------	-----Y--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
58	sp|Q9UQ35|SRRM2_HUMAN	172	6	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1324	1334	2	1361.5708	0.0056	0	22.49	R.ENSFGSPLEFR.N	Phospho (ST)	64.31	ENSFGS#PLEFR	27.14						-----Y-----	-----Y-----
871	882	2	1474.574	0.0053	0	29	R.SCFESSPDPELK.S	Phospho (ST)	104.42	SCFESS#PDPELK	22.85						-----Y------	-----Y------
1101	1111	2	1212.5432	0.0045	0	46.9	R.SSSPVTELASR.S	Phospho (ST)	105.71	SSS#PVTELASR	33.17						--Y--------	--Y--------
1119	1128	2	1145.487	0.0043	0	29.64	R.GEFSASPMLK.S	Phospho (ST)	87.12	GEFSAS#PMLK	43.03						-----Y----	-----Y----
2044	2051	2	1058.4712	0.0038	1	17.06	R.SRSPLAIR.R	2 Phospho (ST)	33.81	S#RS#PLAIR	1000						Y-Y-----	Y-Y-----
2261	2274	2	1437.6382	0.006	0	19.33	R.TPAAAAAMNLASPR.T	Deamidated (NQ); Oxidation (M); Phospho (ST)	19.21	TPAAAAAMNLAS#PR	20.15						-----------Y--	-----------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
59	sp|P36507|MP2K2_HUMAN	170	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
210	231	3	2469.0781	0.0075	0	29.74	K.LCDFGVSGQLIDSMANSFVGTR.S	Oxidation (M); Phospho (ST)	86.09	LCDFGVSGQLIDSMANS#FVGTR	34.55						----------------Y-----	----------------Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
60	sp|P54105|ICLN_HUMAN	170	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
207	237	3	3536.4202	0.0115	1	57.85	R.TEDSIRDYEDGMEVDTTPTVAGQFEDADVDH.-	Phospho (Y)	205.97	TEDSIRDY#EDGMEVDTTPTVAGQFEDADVDH	19.27						-------N-----------------------	-------Y-----------------------
86	113	3	3393.3592	0.0135	1	55.73	K.FEEESKEPVADEEEEDSDDDVEPITEFR.F	Phospho (ST)	156.7	FEEESKEPVADEEEEDS#DDDVEPITEFR	62.92						----------------Y-----------	----------------Y-----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
61	sp|Q9BTT0|AN32E_HUMAN	169	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
224	254	3	3737.4022	0.0114	1	112.78	K.EEIQDEEDDDDYVEEGEEEEEEEGGLRGEK.R	Phospho (Y)	160.19	EEIQDEEDDDDY#VEEGEEEEEEEGGLRGEK	1000						-----------Y-------------------	-----------Y-------------------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
62	sp|Q00839|HNRPU_HUMAN	167	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
269	300	3	3913.6672	0.0183	1	20.16	R.AKSPQPPVEEEDEHFDDTVVCLDTYNCDLHFK.I	Phospho (ST)	97.74	AKS#PQPPVEEEDEHFDDTVVCLDTYNCDLHFK	44.3						--Y-----------------------------	--Y-----------------------------
38	69	3	3221.4082	0.015	0	19.33	R.LQAALDDEEAGGRPAMEPGNGSLDLGGDSAGR.S	Oxidation (M); Phospho (ST)	30.23	LQAALDDEEAGGRPAMEPGNGS#LDLGGDSAGR	37.24						--------------------Y----------	--------------------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
63	sp|Q05655|KPCD_HUMAN	167	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
650	669	2	2267.0054	0.0085	0	41.52	K.NLIDSMDQSAFAGFSFVNPK.F	Phospho (ST)	121.51	NLIDSMDQSAFAGFS#FVNPK	87.27						--------------Y-----	--------------N-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
64	sp|P49736|MCM2_HUMAN	165	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
83	110	3	3141.4012	0.0098	0	26.99	R.AIPELDAYEAEGLALDDEDVEELTASQR.E	Phospho (ST)	132.68	AIPELDAYEAEGLALDDEDVEELTAS#QR	42.28						------------------------Y--	------------------------Y--
134	150	3	2100.907	0.0069	1	34.97	R.GLLYDSDEEDEERPARK.R	Phospho (ST)	82.46	GLLYDS#DEEDEERPARK	28.28						-----Y-----------	-----Y-----------
134	149	2	1972.8126	0.0075	0	40.54	R.GLLYDSDEEDEERPAR.K	Phospho (ST)	105.31	GLLYDS#DEEDEERPAR	28.5						-----Y----------	-----Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
65	sp|P16949|STMN1_HUMAN	164	4	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
14	27	3	1703.7877	0.008	1	25.91	K.RASGQAFELILSPR.S	2 Phospho (ST)	72.19	RAS#GQAFELILS#PR	1000						--Y--------Y--	--N--------N--
30	41	2	1405.6594	0.0064	0	26.78	K.ESVPEFPLSPPK.K	Phospho (ST)	80.09	ESVPEFPLS#PPK	90.02						--------Y---	--------N---
15	27	2	1547.6832	0.0047	0	18.8	R.ASGQAFELILSPR.S	2 Phospho (ST)	50.21	AS#GQAFELILS#PR	1000						-Y--------Y--	-N--------N--
28	41	3	1620.7867	0.0067	1	27.51	R.SKESVPEFPLSPPK.K	Phospho (ST)	89.33	SKESVPEFPLS#PPK	114.16						----------Y---	----------N---

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
66	sp|P54578|UBP14_HUMAN	164	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
142	157	2	1718.7748	0.005	0	62.28	R.ASGEMASAQYITAALR.D	Phospho (ST)	101.85	AS#GEMASAQYITAALR	41.72						-Y--------------	-N--------------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
67	sp|Q92974|ARHG2_HUMAN	164	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
682	706	3	2516.1139	0.0071	0	27.68	R.EPALPLEPDSGGNTSPGVTANGEAR.T	Deamidated (NQ); Phospho (ST)	64.03	EPALPLEPDSGGNTS#PGVTANGEAR	24.24						--------------Y----------	--------------Y----------
886	904	3	2109.0025	0.0093	0	22.34	R.SLPAGDALYLSFNPPQPSR.G	Phospho (Y)	84.76	SLPAGDALY#LSFNPPQPSR	26.42						--------Y----------	--------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
68	sp|Q9UKA4|AKA11_HUMAN	159	4	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
442	451	2	1199.527	0.0047	0	23.4	R.EDSGLFSPIR.S	Phospho (ST)	67.31	EDSGLFS#PIR	31.27						--N-------	--N-------
1240	1254	2	1806.7516	0.0038	0	15.21	R.SVSPTFLNPSDENLK.T	2 Phospho (ST)	69.26	S#VS#PTFLNPSDENLK	20.91	24.75					Y-Y------------	Y-Y------------
18	28	2	1351.5754	0.0057	0	58.26	K.SFSEDVFQSVK.S	Phospho (ST)	109.32	S#FSEDVFQSVK	27.7						Y----------	N----------
17	28	2	1479.6698	0.0052	1	27.29	K.KSFSEDVFQSVK.S	Phospho (ST)	53.53	KS#FSEDVFQSVK	30.7						-Y----------	-N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
69	sp|Q9BQE3|TBA1C_HUMAN	159	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
423	449	3	3061.1182	0.0115	1	53.52	R.EDMAALEKDYEEVGADSADGEDEGEEY.-	Oxidation (M); Phospho (Y)	64.97	EDMAALEKDYEEVGADSADGEDEGEEY#	24.37						----------N	----------Y

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
70	sp|P63172|DYLT1_HUMAN	157	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1	22	2	2624.1354	0.0114	0	72.95	-.MEDYQAAEETAFVVDEVSNIVK.E	Acetyl (Protein N-term); Oxidation (M); Phospho (Y)	112.43	MEDY#QAAEETAFVVDEVSNIVK	61.28							

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
71	sp|P29692|EF1D_HUMAN	153	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
144	175	4	3656.5313	0.015	1	47.64	K.KPATPAEDDEDDDIDLFGSDNEEEDKEAAQLR.E	Phospho (ST)	87.06	KPATPAEDDEDDDIDLFGS#DNEEEDKEAAQLR	65.47						----------Y----------	----------N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
72	sp|Q9UNF1|MAGD2_HUMAN	150	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
138	171	3	3657.5782	0.0078	0	81.83	K.AQETEAAPSQAPADEPEPESAAAQSQENQDTRPK.V	Phospho (ST)	118	AQETEAAPSQAPADEPEPES#AAAQSQENQDTRPK	23.9						----------Y----------	----------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
73	sp|P43307|SSRA_HUMAN	150	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
241	270	3	3470.5612	0.0128	1	46.65	K.VEMGTSSQNDVDMSWIPQETLNQINKASPR.R	Oxidation (M); Phospho (ST)	61.71	VEMGTSSQNDVDMSWIPQETLNQINKAS#PR	20.47						----------Y--	----------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
74	sp|O94804|STK10_HUMAN	149	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
429	443	2	1591.7048	0.0057	0	42.99	K.QVAEQGGDLSPAANR.S	Phospho (ST)	86.91	QVAEQGGDLS#PAANR	1000						---------Y-----	---------Y-----
941	955	2	1725.682	0.0016	0	38.49	K.LSEEAECPNPSTPSK.A	Deamidated (NQ); Phospho (ST)	53.53	LSEEAECPNPST#PSK	21.51						----------Y---	----------Y---

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
75	sp|Q9NTI5|PDS5B_HUMAN	145	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1356	1373	2	1955.844	0.008	0	57.55	R.AESPESSAIESTQSTPQK.G	Phospho (ST)	143.83	AES#PESSAIESTQSTPQK	37.54						--Y--------------	--N--------------
1152	1169	2	1873.7578	0.0065	0	61.2	R.METVSNASSSSNPSSPGR.I	Phospho (ST)	127.99	METVSNASSSSNPSS#PGR	28.87						------------Y---	------------N---

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
76	sp|Q5H9R7|SAPS3_HUMAN	144	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
609	626	3	2218.8655	0.0075	0	43.17	R.IQQFDDGGSDEEDIWEEK.H	Phospho (ST)	156.55	IQQFDDGGS#DEEDIWEEK	1000						---------Y---------	---------Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
77	sp|P78324|SHPS1_HUMAN	143	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
418	435	2	2142.9814	0.0093	0	82.89	R.EITQDTNDITYADLNLPK.G	Phospho (ST)	164.44	EITQDTNDITY#ADLNLPK	28.87						---------N--------	---------N--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
78	sp|O94885|SASH1_HUMAN	143	4	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
405	416	2	1454.5564	0.0027	0	30.89	R.TCSFGGFDLTNR.S	Deamidated (NQ); Phospho (ST)	35.53	TCS#FGGFDLTNR	27.7						--N---------	--Y---------
88	108	3	2447.2126	0.0069	1	38.97	R.RVSQDLEVEKPDASPTSLQLR.S	Phospho (ST)	73.7	RVS#QDLEVEKPDASPTSLQLR	79.34						--Y----------------	--Y----------------
813	820	2	1010.466	0.004	0	27.38	R.SLPVSICR.S	Phospho (ST)	53.41	S#LPVSICR	33.47						N-------	Y-------
921	930	2	1204.5344	0.0033	0	15.89	R.GLSPPQCLPR.N	Deamidated (NQ); Phospho (ST)	35.76	GLS#PPQ!CLPR	1000						--N-------	--N-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
79	sp|Q14980|NUMA1_HUMAN	143	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
154	176	3	2533.1275	0.0079	0	27.49	K.APVPSTCSSTFPEELSPPSHQAK.R	Phospho (ST)	75.95	APVPSTCSSTFPEELS#PPSHQAK	29.58						--------------Y-------	--------------Y-------
1744	1762	2	2002.9074	0.0077	0	58.33	R.TQPDGTSVPGEPASPISQR.L	Phospho (ST)	143.66	TQPDGTSVPGEPAS#PISQR	46.24						------------Y-----	------------Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
80	sp|Q13501|SQSTM_HUMAN	142	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
266	281	2	1892.7866	0.0061	1	36.62	R.SRLTPVSPESSSTEEK.S	2 Phospho (ST)	130.12	SRLT#PVS#PESSSTEEK	34.16	35.82					---Y--Y---------	---Y--Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
81	sp|Q7Z6Z7|HUWE1_HUMAN	142	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1902	1915	2	1576.6106	0.0064	0	51.03	R.GSGTASDDEFENLR.I	Phospho (ST)	94.78	GSGTAS#DDEFENLR	48.87						-----Y--------	-----Y--------
1366	1377	2	1550.551	0.0059	0	41.19	R.DLSMSEEDQMMR.A	Phospho (ST)	106.66	DLS#MSEEDQMMR	42.65						--Y---------	--Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
82	sp|Q86W92|LIPB1_HUMAN	141	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
599	616	3	2194.8949	0.0071	1	20.51	R.SQSTTFNPDDMSEPEFKR.G	Phospho (ST)	51.04	SQS#TTFNPDDMSEPEFKR	21.75						--Y---------------	--Y---------------
570	583	2	1589.719	0.0064	0	21.72	R.NSPFQIPPPSPDSK.K	Phospho (ST)	92.47	NSPFQIPPPS#PDSK	49.62						----------Y----	----------Y----
950	970	3	2621.0941	0.0101	1	55.31	R.LYEEDDLDRLEQMEDSEGTVR.Q	Phospho (Y)	205.51	LY#EEDDLDRLEQMEDSEGTVR	165.98						-N------------------	-Y------------------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
83	sp|O15541|R113A_HUMAN	138	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?

78		101	2	2803.1134		0.0097	0	51.7	K.AAYGDLSSEEEEENEPESLGVVYK.S	Phospho (ST); Phospho (Y)	155.05	AAYGDLS#S#EEEEENEPESLGVVYK	27.73	22.61					--Y----Y----------	--Y----Y----------
2		20	2	2259.0734		0.0088	1	70.5	M.AEQLSPGKAVDQVCTFLFK.K	Acetyl (Protein N-term); Phospho (ST)	61.01	AEQLS#PGKAVDQVCTFLFK	66.18						----Y----------	----N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
84	sp|Q66I50|GG12F_HUMAN	138	2	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
17	50	3	3953.7232	0.0219	0	29.49	R.YVQPPEMIGPMRPEQFSDEVEPATPEEGEPATQR.Q	Deamidated (NQ); 2 Oxidation (M); Phospho (ST)	50.83	YVQPPEMIGPMRPEQFSDEVEPAT#PEEGEPATQR	32.59							
16	50	4	4109.8189	0.0165	1	27.96	R.RYVQPPEMIGPMRPEQFSDEVEPATPEEGEPATQR.Q	Deamidated (NQ); 2 Oxidation (M); Phospho (ST)	47.06	RYVEPPEMIGPMRPEQFSDEVEPAT#PEEGEPATQR	31.99							

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
85	sp|P35221|CTNA1_HUMAN	137	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
634	651	3	2237.8639	0.0113	0	32.26	R.TPEELDDSDFETEDFDVR.S	Phospho (ST)	125.96	TPEELDDS#DFETEDFDVR	21.49						N----------	Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
86	sp|P55081|MFAP1_HUMAN	136	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
44	65	3	2849.1298	0.0118	1	31.95	K.RPDYAPMESSDEEDEEFQFIKK.A	2 Phospho (ST)	118.98	RPDYAPMES#S#DEEDEEFQFIKK	44.12	39.77					--------YY----------	--------YY----------
258	280	3	2720.1106	0.0092	0	32	R.SLAALDALNTDDENDEEEYEAWK.V	Phospho (ST)	143.14	SLAALDALNT#DDENDEEEYEAWK	33.21						---------Y----------	---------Y----------
107	126	2	2360.9574	0.0124	0	43.87	K.IVEPEVVGESDSEVEGDAWR.M	2 Phospho (ST)	166.41	IVEPEVVGES#DS#EVEGDAWR	1000						---------Y-Y--------	---------Y-Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
87	sp|O95218|ZRAB2_HUMAN	135	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
147	166	3	2418.9043	0.0084	1	24.75	K.EVEDKESEGEEEDEDEDLSK.Y	Phospho (ST)	96.5	EVEDKES#EGEEEDEDEDLSK	107.07						------Y----------	------Y----------
110	129	2	2544.0074	0.0109	1	53.55	R.ENVEYIEREESDGEYDEFGR.K	Phospho (ST)	67.91	ENVEYIEREES#DGEYDEFGR	30.85						---------Y---------	---------Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
88	sp|Q99549|MPP8_HUMAN	135	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
44	63	2	2237.8614	0.0089	0	84.7	R.GAEAFGDSEEDGEDVFEVEK.I	Phospho (ST)	194.27	GAEAFGDS#EEDGEDVFEVEK	1000						-------Y----------	-------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
89	sp|Q9H0H5|RGAP1_HUMAN	133	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
203	218	2	1653.7668	0.0058	0	45.48	R.SIGSAVDQGNESIVAK.T	Phospho (ST)	93.3	S#IGSAVDQGNESIVAK	21.3						Y----------	Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
90	sp|Q6PKG0|LARP1_HUMAN	131	4	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
766	778	2	1539.7026	0.0056	0	21.96	R.SLPTTVPESPNYR.N	Phospho (ST)	50.47	S#LPTTVPESPNYR	19.16						Y----------	Y----------
524	539	3	1791.9082	0.0062	1	27.69	R.AVTPVPTKTEEVSNLK.T	Phospho (ST)	73.38	AVT#PVPTKTEEVSNLK	45.94						--Y----------	--Y----------
74	114	4	3762.7465	0.0118	1	35.24	R.ESPRPLQLPGAEGPAISDGEEGGGEPGAGGGAAGAAGAGRR.D	Phospho (ST)	70.36	ESPRPLQLPGAEGPAIS#DGEEGGGEPGAGGGAAGAAGAGRR	90.14						----------Y----------	----------Y----------
74	113	3	3606.6472	0.0136	0	60.62	R.ESPRPLQLPGAEGPAISDGEEGGGEPGAGGGAAGAAGAGR.R	Phospho (ST)	135.41	ESPRPLQLPGAEGPAIS#DGEEGGGEPGAGGGAAGAAGAGR	78.3						----------Y----------	----------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
91	sp|Q66K74|MAP1S_HUMAN	131	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
654	660	2	864.4498	0.0029	0	18.03	R.LSLSPLR.G	Phospho (ST)	48.02	LSLS#PLR	42.65						---Y---	---Y---
749	769	3	2076.937	0.007	1	56.52	R.KAVPMAPAPASPGSSNDSSAR.S	Phospho (ST)	105.91	KAVPMAPAPAS#PGSSNDSSAR	38.52						----------Y----------	----------Y----------
623	645	3	2641.288	0.0102	1	21.35	K.ALELPLAASSIPRPRTPSPESHR.S	2 Phospho (ST)	79.78	ALELPLAAS#S#IPRPRTPSPESHR	37.49	42.17					--------NN----------	--------YN----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
92	sp|Q70E73|RAPH1_HUMAN	130	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
520	535	2	1840.7804	0.0037	0	80.63	R.TESAYDWTSLSSSSIK.S	Phospho (Y)	189.91	TESAY#DWTSLSSSSIK	42.65						----N----------	----N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
93	sp|Q9Y2W1|TR150_HUMAN	128	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
236	245	2	1095.5002	0.0041	0	37.35	R.ASAVSELSPR.E	Phospho (ST)	112.83	ASAVSELS#PR	27.03						-------Y--	-------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
94	sp|P49023|PAXI_HUMAN	127	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
111	123	2	1613.6832	0.007	0	37.79	R.VGEEEHVYSFPNK.Q	Phospho (Y)	146.5	VGEEEHVY#SFPNK	32.4						-------Y-----	-------Y-----
94	110	2	1843.7474	0.0067	0	44.92	K.TSSVSNPQDSVGSPCSR.V	Phospho (ST)	114.26	TSSVSNPQDSVGS#PCSR	64.54						----------Y----	----------Y----
76	93	3	2026.9225	0.0075	0	17.17	R.FIHQQPQSSSPVYGSSAK.T	Phospho (Y)	84.17	FIHQQPQSSSPVY#GSSAK	19.16						----------Y-----	----------Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
95	sp|P13861|KAP2_HUMAN	126	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
71	93	2	2632.0554	0.0088	1	42.78	R.VADAKGDSESEEDEDLEVPVPSR.F	2 Phospho (ST)	123.89	VADAKGDS#ES#EEDEDLEVPVPSR	110.93	103.54					-------Y-Y----------	-------N-N----------
97	117	2	2590.0254	0.0088	1	39.41	R.RVSVCAETYNPDEEEEDTDPR.V	Phospho (ST)	141.18	RVS#VCAETYNPDEEEEDTDPR	65.33						--Y----------	--N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
96	sp|P13693|TCTP_HUMAN	126	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?

39		85	4	4936.2429		0.0195	0	70.06	R.TEGNIDDSLIGGNASAEGPEGEGTESTVITGVDIVMNHHLQETSFTK.E	Phospho (ST)	67.94	TEGNIDDS#LIGGNASAEGPEGEGTESTVITGVDIVMNHHLQETSFTK	24.64							-------Y----------	-------Y----------
																						-	-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
97	sp|P18583|SON_HUMAN	126	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1687	1699	2	1451.6974	0.0066	0	36.75	K.ESDQTLAALLSPK.E	Phospho (ST)	55.8	ESDQTLAALLS#PK	57.78						-Y----------	-N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
98	sp|Q13765|NACA_HUMAN	123	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
145	179	4	3939.7377	0.0107	0	29.42	K.VQGEAVSNIQENTQTPTVQEESEEEEVDETGVEVK.D	Phospho (ST)	105.33	VQGEAVSNIQENTQTPTVQEES#EEEEVDETGVEVK	26.38						----------Y----------	----------N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
99	sp|Q14157|UBP2L_HUMAN	122	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
27	37	2	1378.6178	-0.0063	0	19.77	K.QRPQATAEQIR.L	2 Deamidated (NQ); Phospho (ST)	12.04	Q!RPQAT#AEQ!IR	1000						-----N-----	-----N-----
439	459	2	2039.0034	0.0058	0	37.44	K.SPAVATSTAAPPPPSSPLPSK.S	Phospho (ST)	123.79	SPAVATSTAAPPPPSS#PLPSK	20.35						--------------Y-----	--------------Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
100	sp|Q92609|TBCD5_HUMAN	121	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
535	549	2	1645.6816	0.0067	0	53.89	K.NISSSPSVESLPGGR.E	2 Phospho (ST)	105.85	NISSSPS#VES#LPGGR	31.86	33.81					------Y--Y-----	------Y--Y-----
520	529	2	1211.5292	0.0035	0	16.44	K.SESMPVQLNK.G	Phospho (ST)	48.33	SES#MPVQLNK	21.75						--Y-------	--Y-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
101	sp|Q16655|MAR1_HUMAN	119	2	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
107	118	2	1351.5754	0.0058	0	43.92	K.LSAEQSPPPYSP.-	Phospho (ST)	93.4	LSAEQSPPPYS#P	32.4							
92	106	2	1764.7438	0.0009	0	34.58	K.NCEPVVPNAPPAYEK.L	Deamidated (NQ); Phospho (Y)	83.73	N!CEPVVPNAPPAY#EK	1000							

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
102	sp|P60174|TPIS_HUMAN	119	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
19	33	3	1621.8505	0.0065	1	16.68	R.KQSLGELIGTLNAAK.V	Phospho (ST)	63.94	KQS#LGELIGTLNAAK	60.47						--Y----------	--N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
103	sp|O60716|CTND1_HUMAN	118	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
216	233	2	2052.7914	0.0064	0	53.13	R.HYEDGYPGGSDNYGSLSR.V	Phospho (Y)	147.62	HYEDGYPGGSDNY#GSLSR	26.22						----------Y-----	----------Y-----
152	180	3	3065.4652	0.0122	0	63.27	R.TVQPVAMGPDGLPVDASSVSNNYIQTLGR.D	Phospho (Y)	160.44	TVQPVAMGPDGLPVDASSVSNNY#IQTLGR	19.55						----------Y------	----------Y------
250	264	3	1776.8374	0.0065	1	20.67	R.APSRQDVYGPQPQVR.V	Phospho (Y)	133.51	APSRQDVY#GPQPQVR	42.64						-------Y-------	-------Y-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
104	sp|Q9Y6G9|DC1L1_HUMAN	117	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
193	211	2	2346.0034	0.0081	1	51.7	R.DFQEYVEPGEDFPASPQRR.N	Phospho (ST)	112.62	DFQEYVEPGEDFPAS#PQRR	123.41						----------Y----	----------Y----
505	523	2	2044.8714	0.0071	0	29.97	R.KPVTVSPTTPTSPTEGEAS.-	2 Phospho (ST)	110.12	KPVTVSPTT#PTS#PTEGEAS	26.15	20.35					--------Y-Y-------	--------Y-Y-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
105	sp|Q9H6F5|CCD86_HUMAN	116	4	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
11	27	3	1863.9148	0.0056	0	18.8	R.LGGLRPESPESLTSVSR.T	Phospho (ST)	64.48	LGGLRPES#PESLTSVSR	54.48						-------Y--------	-------Y--------
31	53	2	2634.2054	0.0092	1	30.76	R.ALVEFESNPEETREPGSPPSVQR.A	Phospho (ST)	104.35	ALVEFESNPEETREPGS#PPSVQR	38.7						---------------Y------	---------------Y------
10	27	3	2020.0183	0.008	1	14.75	R.RLGGLRPESPESLTSVSR.T	Phospho (ST)	19.27	RLGGLRPES#PESLTSVSR	28.57						--------Y---------	--------Y---------
72	94	3	2462.0668	0.004	0	32.37	R.LQQGAGLESPQGQPEPGAASPQR.Q	2 Phospho (ST)	135.53	LQQGAGLES#PQGQPEPGAAS#PQR	1000						--------Y---------Y---	--------Y---------Y---

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
106	sp|Q8NC51|PAIRB_HUMAN	116	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
388	408	2	2182.9374	0.0067	1	35.53	R.TDKSSASAPDVDDPEAFPALA.-	Phospho (ST)	141.41	TDKSS#ASAPDVDDPEAFPALA	20.35						----Y----------	----Y----------
217	236	3	2164.9489	0.0062	1	30.29	R.GGSGSHNWGTVKDELTESPK.Y	Phospho (ST)	62.17	GGSGSHNWGTVKDELTES#PK	22.01						----------Y--	----------Y--
17	32	2	2022.8514	0.0015	0	42.33	R.FDQLFDDESDPFEVLK.A	Phospho (ST)	112.42	FDQLFDDES#DPFEVLK	1000						--------Y-------	--------Y-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
107	sp|Q92769|HDAC2_HUMAN	113	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
373	405	4	3696.5453	0.0107	1	15.8	R.MLPHAPGVQMQAIPEDAVHEDSGDEDGEDPDKR.I	2 Oxidation (M); Phospho (ST)	17.91	M!LPHAPGVQM!QAIPEDAVHEDS#GDEDGEDPDKR	1000						----------Y----------	----------Y----------
415	433	2	2316.7954	0.0075	1	42.73	R.IACDEEFSDSEDEGEGGRR.N	2 Phospho (ST)	105.3	IACDEEFS#DS#EDEGEGGRR	1000						--------Y-Y---------	--------Y-Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
108	sp|Q04637|IF4G1_HUMAN	112	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1225	1235	2	1200.6202	0.0047	0	26.55	R.EAALPPVSPLK.A	Phospho (ST)	65.93	EAALPPVS#PLK	1000						-------Y---	-------Y---
1073	1096	4	2622.3069	0.0114	1	23.03	K.ITKPGSIDSNNQLFAPGGRLSWGK.G	Phospho (ST)	107.69	ITKPGSIDSNNQLFAPGGRLS#WGK	93.25						----------Y---	----------Y---

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
109	sp|Q9NYB0|TE2IP_HUMAN	112	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
195	208	2	1540.7262	0.0088	0	54.18	K.YLLGDAPVSPSSQK.L	Phospho (ST)	145.39	YLLGDAPVS#PSSQK	21.3						--------Y-----	--------Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
110	sp|P40818|UBP8_HUMAN	110	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
716	732	3	2059.9207	0.0108		1	16.86	R.SYSSPDITQAIQEEEKR.K	Phospho (ST)	67.78	SYS#SPDITQAIQEEEKR	21.75						--Y----------	--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
111	sp|Q13459|MYO9B_HUMAN	110	4	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1391	1413	3	2320.1023	0.0075		1	51.57	K.KKPGDASSLPDAGLSPGSQVDSK.S	Phospho (ST)	134.13	KKPGDASSLPDAGLS#PGSQVDSK	28.4						----------Y---------	----------Y---------
1260	1275	2	1737.6954	0.0055		0	15.72	R.VSPPAPGSAPETPEDK.S	2 Phospho (ST)	59.98	VSPPAPGS#APET#PEDK	30.09	52.74					-------Y---Y----	-------Y---Y----
1043	1051	2	1135.4668	0.0048		0	22.04	K.SFSQMISEK.Q	Phospho (ST)	58.65	S#FSQMISEK	27.7						N--------	N--------
1284	1299	3	1806.8173	0.0024		0	22.07	R.VQEKPDSPGGSTQIQR.Y	Deamidated (NQ); Phospho (ST)	72.02	VQEKPDS#PGGSTQIQR	28.14						------Y---------	------Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
112	sp|P35579|MYH9_HUMAN	110	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1938	1960	2	2253.8994	0.0084		1	70.95	K.GAGDGSDEEVDGKADGAEAKPAE.-	Phospho (ST)	141.05	GAGDGS#DEEVDGKADGAEAKPAE	1000						-----Y----------	-----N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
113	sp|P52943|CRIP2_HUMAN	109	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
66	97	3	3289.6522	0.0138		0	76.86	K.GVNIGGAGSYIYEKPLAEGPQVTGPIEVPAAR.A	Phospho (Y)	207.14	GVNIGGAGSYIY#EKPLAEGPQVTGPIEVPAAR	27.69						----------Y----------	----------Y----------
187	205	2	2076.9214	0.0061		1	50.22	K.GVNTGAVGSYIYDRDPEGK.V	Phospho (Y)	110.69	GVNTGAVGSYIY#DRDPEGK	21.3						----------N-------	----------Y-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
114	sp|P23588|IF4B_HUMAN	108	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
593	611	2	2154.7874	0.0084		0	61.42	K.YAALSVDGEDENEGEDYAE.-	Phospho (Y)	198.72	YAALSVDGEDENEGEDY#AE	176.33						----------N--	----------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
115	sp|Q13085|ACACA_HUMAN	107	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
77	86	2	1137.529	0.0037		0	20.19	R.SSMSGLHLVK.Q	Phospho (ST)	69.66	SSMS#GLHLVK	30.83						---Y------	---Y------
19	38	2	2354.0054	0.0087		0	53.04	R.FIIGSVSEDNSEDEISNLVK.L	2 Phospho (ST)	151.25	FIIGS#VSEDNS#EDEISNLVK	22.01	40.34					----Y-----Y---------	----Y-----Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
116	sp|O00567|NOP56_HUMAN	106	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
562	578	2	1935.796	0.0057		1	14.41	K.FSKEEPVSSGPEEAVGK.S	2 Phospho (ST)	61.18	FSKEEPVS#S#GPEEAVGK	50.22	47.25					-------YY--------	-------NY--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
117	sp|P42166|LAP2A_HUMAN	103	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
61	86	3	2729.1472	0.0101		1	63.21	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	2 Phospho (ST)	174.14	GPPDFS#S#DEEREPTPVLGSGAAAAGR	64.35	69.45					-----YY----------	-----YN----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
118	sp|P60468|SC61B_HUMAN	103	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
47	57	2	1203.478	0.0037		0	24.86	R.TTSAGTGGMWR.F	Phospho (ST)	50.57	TTS#AGTGGMWR	32.4						--N--------	--Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
119	sp|Q96K21|ZFY19_HUMAN	102	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
351	366	2	1926.7418	0.0051		0	101.87	R.LPDSDDDEDEETAIQR.V	Phospho (ST)	171.02	LPDS#DDDEDEETAIQR	126.6						---Y----------	---Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
120	sp|Q8N9T8|KRI1_HUMAN	102	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
172	193	2	2318.9514	0.0087		0	63.4	R.AFVEDSEDEDGAGEGGSSLLQK.R	Phospho (ST)	172.56	AFVEDS#EDEDGAGEGGSSLLQK	120.92						-----Y----------	-----Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
121	sp|Q9H6Z4|RANB3_HUMAN	102	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
331	346	2	1804.8774	0.0054		1	15.47	R.VLSPPKLNEVSSDANR.E	Phospho (ST)	41.41	VLS#PPKLNEVSSDANR	29.38						--Y----------	--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
122	sp|Q13153|PAK1_HUMAN	101	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
163	198	3	3887.7352	0.0089		0	65.47	K.AVSETPAVPPVSEDEDDDDDDATPPPVIAPRPEHTK.S	Phospho (ST)	151.34	AVSETPAVPPVS#EDEDDDDDDATPPPVIAPRPEHTK	87.58						----------N----------	----------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
123	sp|Q92785|REQU_HUMAN	100	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
157	178	3	2720.0887	0.0097		0	29.16	R.ILEPDDFLDDLDDEDYEEDTPK.R	Phospho (ST)	184.89	ILEPDDFLDDLDDEDY#EEDTPK	37.06						----------Y--	----------Y--
138	152	2	1729.7252	0.0056		0	44.28	R.VDDDSLGEFPVTNSR.A	Phospho (ST)	141.67	VDDDS#LGEFPVTNSR	86.63						----Y----------	----Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
124	sp|P31948|STIP1_HUMAN	99	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
14	32	2	2145.9754	0.0101		0	66.66	K.ALSVGNIDDALQCYSEAIK.L	Phospho (ST)	103.81	ALS#VGNIDDALQCYSEAIK	101.19						--Y----------	--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
125	sp|Q13177|PAK2_HUMAN	99	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
2	17	2	1842.797	-0.0066		0	28.95	M.SDNGELEDKPPAPPVR.M	Acetyl (Protein N-term); Deamidated (NQ); Phospho (ST)	40.49	S!#DN!GELEDKPPAPPVR	1000						Y----------	Y----------

161		191	3	3394.5172		0.0082	0	68	K.GTEAPAVVTEEEDDDEETAPPVIAPRPDHTK.S	Phospho (ST)		121.12	GTEAPAVVT#EEEDDDEETAPPVIAPRPDHTK	48.38							--------Y----------	--------Y----------
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
126	sp|Q15417|CNN3_HUMAN		98	2	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?			
257		265	2	1018.4358		0.0051	0	51.94	K.GMSVYGLGR.Q	Phospho (Y)		101.05	GMSVY#GLGR	43.03						----Y----		----Y----			
319		329	2	1445.5082		0.0058	0	20.11	R.DYQYSDQGIDY.-	Phospho (ST)		78.92	DYQYS#DQGIDY	22.85						----Y------		----Y------			
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
127	sp|O00410|IPO5_HUMAN		98	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?			
815		841	3	3382.4002		0.0116	1	59.18	K.RQDEDYDEQVEESLQDEDDNDVYILTK.V	Phospho (Y)		224.87	RQDEDY#DEQVEESLQDEDDNDVYILTK	107.65						-----N----------		-----Y----------			
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
128	sp|Q9NRY5|F1142_HUMAN		98	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?			
205		213	2	1080.5396		0.0068	0	22.09	R.NATLSQVLR.E	Phospho (ST)		86.93	NATLS#QVLR	52.75						----N----		----N----			
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
129	sp|Q96GM8|TOE1_HUMAN		98	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?			
2		22	2	1926.7922		0.0078	0	58.76	M.AADSDDGAVSAPAASDGGVSK.S	Phospho (ST)		118.55	AADS#DDGAVSAPAASDGGVSK	71.75						---Y----------		---Y----------			
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
130	sp|Q9Y5J1|UTP18_HUMAN		97	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?			
115		131	2	2060.7334		0.0086	0	49.75	R.VQEHEDSGDSEVENEAK.G	2 Phospho (ST)		129.82	VQEHEDS#GDS#EVENEAK	1000						------Y--Y-------		------Y--Y-------			
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
131	sp|P50402|EMD_HUMAN		96	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?			
89		103	2	2081.7034		0.0066	0	50.03	K.GYNDDYYEESYFTTR.T	2 Phospho (Y)		153.59	GYNDDY#Y#EESYFTTR	40.46	65.16					-----NY---------		-----YY---------			
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
132	sp|Q96TA1|NIBL1_HUMAN		96	3	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?			
673		692	2	2126.9894		0.0092	0	17.39	K.AAPEASSPPASPLQHLLPGK.A	2 Phospho (ST)		88.86	AAPEASS#PPAS#PLQHLLPGK	24.44	49.62					------Y---Y---------		------Y---Y---------			
608		641	3	3720.6982		0.0133	0	69.01	K.QVVSVVQDEEVGLPFEASPESPPPASPDGVTEIR.G	2 Phospho (ST)		166.73	QVVSVVQDEEVGLPFEASPES#PPPAS#PDGVTEIR	48.83	23.84					----------Y----Y---------		----------Y----Y---------			
642		672	3	3096.5872		0.0227	0	40.81	R.GLLAQGLRPESPPPAGPLLNGAPAGESPQPK.A	Deamidated (NQ); Phospho (ST)		125.84	GLLAQGLRPES#PPPAGPLLNGAPAGESPQPK	102.85						----------Y----------		----------Y----------			
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
133	sp|Q66PJ3|AR6P4_HUMAN		96	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?			
271		286	2	1782.725		0.0054	0	44.26	R.SAGEEEDGPVLTDEQK.S	Phospho (ST)		111.07	S#AGEEEDGPVLTDEQK	56.47						Y----------		Y----------			
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
134	sp|O00505|IMA3_HUMAN		96	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?			
50		67	2	2115.8614		0.0093	0	42.9	R.NVPQEESLEDSDVDADFK.A	Phospho (ST)		144.6	NVPQEESLEDS#DVDADFK	63.63						----------Y--------		----------Y--------			
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
135	sp|Q92890|UFD1_HUMAN		95	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?			
290		301	2	1376.6178		0.0053	0	53.52	R.FVAFSGEGQSLR.K	Phospho (ST)		100.6	FVAFSGEGQS#LR	43.65						---------Y--		---------Y--			
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
136	sp|Q08J23|NSUN2_HUMAN		95	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?			
738		767	3	3173.2702		0.0267	0	40.99	R.AGEPNSPDAEEANSPDVTAGCDPAGVHPPR.-	2 Phospho (ST)		134.05	AGEPNS#PDAEEANS#PDVTAGCDPAGVHPPR	87.39	33.62					-----Y-------Y----------		-----N-------N----------			
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
137	sp|Q9UKX7|NUP50_HUMAN		95	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?			
207		229	2	2477.1034		0.0076	1	22.23	R.NSESESNKVAAETQSPSLFGSTK.L	Phospho (ST)		77.98	NSESESNKVAAETQS#PSLFGSTK	22.01						------------Y--------		------------Y--------			
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
138	sp|Q13067|GAGE3_HUMAN		95	2	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?			
17		51	3	4060.8682		0.0168	1	28.72	R.RYVQPPEVIGPMRPEQFSDEVEPATPEEGEPATQR.Q	Oxidation (M); Phospho (ST)		72.44	RYVQPPEVIGPMRPEQFSDEVEPAT#PEEGEPATQR	47.21						----------N----------		----------N----------			
18		51	3	3904.7662		0.0159	0	33.44	R.YVQPPEVIGPMRPEQFSDEVEPATPEEGEPATQR.Q	Oxidation (M); Phospho (ST)		55.44	YVQPPEVIGPMRPEQFSDEVEPAT#PEEGEPATQR	22.16						----------N----------		----------N----------			
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
139	sp|O75396|SC22B_HUMAN		94	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?			
134		147	2	1665.7784		0.0061	0	74.3	R.NLGSINTELQDVQR.I	Phospho (ST)		138.84	NLGS#INTELQDVQR	30.66						---Y----------		---N----------			
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
140	sp|Q86UE4|LYRIC_HUMAN		94	3	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?			
293		314	3	2312.0752		0.0066	1	18.44	K.LSSQISAGEEKWNSVSPASAGK.R	Phospho (ST)		73.53	LSSQIS#AGEEKWNSVSPASAGK	24.66						-----Y----------		-----Y----------			
492		504	2	1438.7004		0.0048	0	37.61	K.TISTSDPAEVLVK.N	Phospho (ST)		89.58	TIS#TSDPAEVLVK	26.38						--N----------		--Y----------			

344	370	3	2984.3197	0.012	0	54.3	R.SIFSGIGSTAEPVSQSTTSDYQWDVSR.N	Phospho (Y)	156.7	SIFSGIGSTAEPVSQSTTSDY#QWDVSR	24.76						----------N------	----------N------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
141	sp|Q9H3Z4|DNJC5_HUMAN	94	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
8	24	3	1884.8947	0.0077	0	37.94	R.SLSTSGESLYHVLGLDK.N	Phospho (ST)	79.09	SLS#TSGESLYHVLGLDK	39.56						---Y----------	---Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
142	sp|O60504|VINEX_HUMAN	93	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
520	532	2	1534.655	0.0063	0	38	R.LCDDGPQLPTSPR.L	Phospho (ST)	87.15	LCDDGPQLPTS#PR	22.85						----------Y--	----------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
143	sp|P37840|SYUA_HUMAN	92	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
33	43	2	1259.6212	0.005	1	21.99	K.TKEGVLYVGSK.T	Phospho (Y)	100.89	TKEGVLY#VGSK	49.62						------N----	------Y----
35	43	2	1030.4766	0.003	0	16.42	K.EGVLYVGSK.T	Phospho (Y)	36.02	EGVLY#VGSK	26.79						----N----	----Y----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
144	sp|Q8IWX8|CHERP_HUMAN	91	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
902	908	2	922.3978	0.0029	0	14.9	K.SYSFIAR.M	Phospho (ST)	58.21	SYS#FIAR	32.4						--Y----	--Y----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
145	sp|Q13671|RIN1_HUMAN	90	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
28	54	4	2841.3305	0.011	0	24.81	R.EKPAQDPLYDVPNASGGQAGGPQRPGR.V	Phospho (Y)	47.94	EKPAQDPLY#DVPNASGGQAGGPQRPGR	34.77						--------Y----------	--------Y----------
249	280	3	3269.6752	0.0167	0	14.33	R.VSTETSSPLSPPAVPPPPVPVLPGAVPSQTER.L	Phospho (ST)	74.11	VSTETSSPLS#PPAVPPPPVPVLPGAVPSQTER	28.13						---------Y----------	---------Y----------
609	616	2	1097.4948	0.0042	0	29.05	R.SLSLWEQR.R	Phospho (ST)	87.22	SLS#LWEQR	30.7						--N-----	--N-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
146	sp|Q13439|GOGA4_HUMAN	90	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
2146	2157	2	1392.6384	0.0058	0	42.5	K.NVYATTVGTPYK.G	Phospho (Y)	126.82	NVY#ATTVGTPYK	48.87						--N---------	--Y---------
69	77	2	1112.5306	0.0039	0	22.82	R.VPSVESLFR.S	Phospho (ST)	79.64	VPS#VESLFR	45.2						--Y------	--Y------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
147	sp|P22626|ROA2_HUMAN	89	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
239	266	3	2574.004	0.0053	0	41.58	R.GFGDGYNGYGGGPGGGNFGGSPGYGGGR.G	Phospho (ST)	115.41	GFGDGYNGYGGGPGGGNFGGS#PGYGGGR	45.02						----------Y-------	----------Y-------
214	228	2	1456.5944	0.0059	0	22.28	R.GGGGNFGPGPGSNFR.G	Phospho (ST)	64.14	GGGGNFGPGPGS#NFR	1000						----------Y---	----------Y---

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
148	sp|Q9BTC0|DIDO1_HUMAN	88	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1454	1477	4	2613.3013	0.0101	1	33.38	R.RNSVERPAEPVAGAATPSLVEQQK.M	Phospho (ST)	83.02	RNS#VERPAEPVAGAATPSLVEQQK	45.19						--------------Y--------	--------------Y--------
1040	1052	2	1498.675	0.0046	0	18.67	R.SPPEGDTTLFLSR.L	Phospho (ST)	50.49	S#PPEGDTTLFLSR	47.64						Y----------	Y----------
885	926	4	4402.9389	0.0216	1	43.49	K.SKHDSSAPDPAPDSADEVMPEAVPEVASEPGLESASHPNVDR.T	Phospho (ST)	90.78	SKHDSSAPDPAPDS#ADEVMPEAVPEVASEPGLESASHPNVDR	42.95						------------Y--------------------------	------------Y--------------------------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
149	sp|Q92841|DDX17_HUMAN	88	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
490	508	3	2350.9375	0.0067	1	18.84	R.TTSSANNPNLMYQDECDRR.L	Phospho (ST)	54.45	TTS#SANNPNLMYQDECDRR	20.35						---N----------	---N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
150	sp|P55196|AFAD_HUMAN	87	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1229	1237	2	1168.4878	0.0037	0	17.43	R.EYFTFPASK.S	Phospho (Y)	38.74	EY#FTFPASK	26.53						-Y-------	-N-------
1797	1807	2	1301.571	0.0058	0	49.92	R.LFSQGQDVSNK.V	Phospho (ST)	96.32	LFS#QGQDVSNK	53.29						--N--------	--N--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
151	sp|P06454|PTMA_HUMAN	86	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
2	15	2	1545.6502	0.0055	0	25.12	M.SDAAVDTSSEITTK.D	Acetyl (Protein N-term); Phospho (ST)	36.24	S#DAAVDTSSEITTK	40.87						Y----------	N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
152	sp|Q8N122|RPTOR_HUMAN	86	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
868	894	3	2671.2313	0.0074	0	54.88	K.GVHIHQAGGSPPASSTSSSSLTNDVAK.Q	Phospho (ST)	128.34	GVHIHQAGGS#PPASSTSSSSLTNDVAK	57.52						---------Y----------	---------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
153	sp|Q6Y7W6|PERQ2_HUMAN	86	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
17	35	2	1938.9158	0.0054	0	41.66	R.ALSSGGSITSPPLSPALPK.Y	2 Phospho (ST)	110.03	ALSSGGSITS#PPLS#PALPK	32.4	42.81					---------Y---Y-----	---------Y---Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
154	sp|Q15154|PCM1_HUMAN	85	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
107	115	2	1186.506	0.0041	0	26.59	R.INFSDLDQR.S	Phospho (ST)	117.6	INFS#DLDQR	1000						---N-----	---N-----
88	102	2	1848.7718	0.0044	0	50.27	R.YMSQMSVPEQAELEK.L	Phospho (ST)	132.75	YMSQMS#VPEQAELEK	35.82						-----Y---------	-----N---------
60	74	2	1593.708	0.0045	0	48.9	R.VTNDISPESSPGVGR.R	Phospho (ST)	108.27	VTNDIS#PESSPGVGR	26.79						-----Y---------	-----N---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
155	sp|Q8NE71|ABCF1_HUMAN	85	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
224	255	4	3530.3693	0.0052	1	23	K.AEQGSEEEGEGEEEEEEGGESK ADDPYAHLSK.K	Phospho (ST)	95.99	AEQGS#EEEGEGEEEEEEGGESK ADDPYAHLSK	82.11						-----Y----------	-----Y----------
103	121	2	2332.9714	0.0084	1	31.89	K.KLSVPTSDEEDEVPAPKPR.G	3 Phospho (ST)	70.26	KLS#VPT#S#DEEDEVPAPKPR	1000						--Y--YY----------	--Y--YY----------
223	245	3	2560.954	0.009	1	31.69	K.KAEQGSEEEGEGEEEEEEGGESK.A	Phospho (ST)	134.09	KAEQGS#EEEGEGEEEEEEGGESK	162.49						-----Y----------	-----Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
156	sp|Q13541|4EBP1_HUMAN	85	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
20	51	3	3362.5672	0.0086	1	30.91	R.RVVLGDGVQLPPGDYSTTPGGT LFSTTPGGTR.I	2 Phospho (ST)	129.69	RVVLGDGVQLPPGDYSTT#PGGTL FSTT#PGGTR	32.44	26.38					----------Y---Y----------	----------N---N----------
107	118	2	1391.501	0.0058	0	32.4	R.AGGEESQFEMDI.-	Phospho (ST)	88.35	AGGEES#QFEMDI	1000						-----Y------	-----N------
106	118	2	1547.6018	0.0055	1	28.74	K.RAGGEESQFEMDI.-	Phospho (ST)	57.78	RAGGEES#QFEMDI	1000						------Y------	------N------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
157	sp|Q8NDC0|MISSL_HUMAN	84	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
2	18	2	1934.8424	0.0126	0	32.38	M.SDEFSLADALPEHSPAK.T	Acetyl (Protein N-term); Phospho (ST)	38.22	SDEFSLADALPEHS#PAK	55.58						----------Y---	----------N---

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
158	sp|O95747|OXSR1_HUMAN	84	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
331	351	2	2554.8894	0.0085	0	57.27	K.TEDGGWEWSDDEFDEESEEGK .A	Phospho (ST)	176.95	TEDGGWEWS#DDEFDEESEEGK	67.79						---------Y----------	---------Y----------
331	358	3	3294.3262	0.0112	1	48.63	K.TEDGGWEWSDDEFDEESEEGK AAISQLR.S	Phospho (ST)	97.98	TEDGGWEWS#DDEFDEESEEGK AAISQLR	70.86						---------Y----------	---------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
159	sp|P10644|KAP0_HUMAN	84	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
75	92	3	2055.958	0.0066	1	15.61	R.TDSREDEISPPPPNPVVK.G	Phospho (ST)	58.85	TDSREDEIS#PPPPNPVVK	20.27						N----------	Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
160	sp|P22314|UBA1_HUMAN	83	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
11	43	3	3430.6162	0.0264	1	25.8	R.RVSGPDPKPGSNCSPAQSVLSE VPSVPTNGMAK.N	Deamidated (NQ); Phospho (ST)	50.9	RVS#GPDPKPGSNCSPAQSVLSEV PSVPTNGMAK	21.82						--Y----------	--Y----------
44	57	2	1605.622	0.0025	0	48.17	K.NGSEADIDEGLYSR.Q	Deamidated (NQ); Phospho (ST)	74.29	NGS#EADIDEGLYSR	84.7						--Y----------	--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
161	sp|Q96T23|RSF1_HUMAN	83	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1300	1323	3	2843.1664	0.0098	1	39.75	R.LHRIETDEEESCDNAHGDANQP AR.D	Phospho (ST)	90.43	LHRIET#DEEESCDNAHGDANQPA R	19.98						-----Y----------	-----N----------
1343	1356	2	1718.6612	0.0053	0	46.12	R.IESDEEEDFENVGK.V	Phospho (ST)	153.87	IES#DEEEDFENVGK	1000						--Y----------	--N----------
613	640	3	3089.3662	0.0126	0	19.15	K.STLESEKPGSPEAAETSPPSNIID HCEK.L	Phospho (ST)	68.28	STLESEKPGS#PEAAETSPPSNIID HCEK	21.77						---------Y----------	---------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
162	sp|Q9UGP4|LIMD1_HUMAN	81	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
294	307	2	1534.726	0.0046	0	46.85	R.TPSVSAPLALSCPR.Q	Phospho (ST)	85.26	TPS#VSAPLALSCPR	27.73						--Y----------	--Y----------
1	13	2	1605.6658	0.0025	1	22.36	-.MDKYDDLGLEASK.F	Acetyl (Protein N-term); Phospho (Y)	55.7	MDKY#DDLGLEASK	75.53						---N---------	---N---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
163	sp|O76021|RL1D1_HUMAN	81	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
357	374	3	2046.9958	0.0083	1	22.66	K.ATNESEDEIPQLVPIGKK.T	Phospho (ST)	93.35	ATNES#EDEIPQLVPIGKK	48.83						----Y----------	----Y----------
357	373	2	1919.8698	-0.0066	0	22.51	K.ATNESEDEIPQLVPIGK.K	Deamidated (NQ); Phospho (ST)	62.47	ATNES#EDEIPQLVPIGK	19.73						----Y----------	----Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
164	sp|O95425|SVIL_HUMAN	81	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
236	247	2	1428.6322	0.0036	1	19.67	R.DSSFTEVPRSPK.H	Phospho (ST)	54.9	DSSFTEVPRS#PK	47.64						---------Y--	---------Y--
850	867	2	2069.9714	0.0044	0	64.39	R.YQTQPVTLGEVEQVQSGK.L	Phospho (ST)	205.75	YQT#QPVTLGEVEQVQSGK	48.59						--Y---------------	--Y---------------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
165	sp|P54727|RD23B_HUMAN	81	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
145	173	3	3024.3682	0.0121	0	45.92	K.QEKPAEKPAETPVATSPTATDST SGDSSR.S	Phospho (ST)	77.91	QEKPAEKPAETPVATS#PTATDST SGDSSR	26.49						--------------Y------------	--------------Y------------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
166	sp|Q14671|PUM1_HUMAN	80	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
75	87	2	1700.6614	0.0073	0	80.4	R.SQDDAMVDYFFQR.Q	Phospho (Y)	185.66	SQDDAMVDY#FFQR	114.6						--------N----	--------Y----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
167	sp|Q8WXI9|P66B_HUMAN	80	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
479	498	2	2063.0354	0.0055	0	49.45	R.LQQQAALSPTTAPAVSSVSK.Q	Phospho (ST)	149.79	LQQQAALS#PTTAPAVSSVSK	23.34						-------Y----------	-------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
168	sp|P52948|NUP98_HUMAN	80	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
604	616	2	1567.7216	0.0073	0	43.8	K.NLNNSNLFSPVNR.D	Phospho (ST)	106.19	NLNNS#NLFSPVNR	26.92						----Y--------	----Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
169	sp|O95639|CPSF4_HUMAN	80	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
200	217	2	2053.9494	0.0065	0	79.55	R.SSSLIQLTSQNSSPNQQR.T	Phospho (ST)	167.34	SSS#LIQLTSQNSSPNQQR	19.21						Y----------	N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
170	sp|Q15019|SEPT2_HUMAN	80	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
210	229	4	2516.0489	0.0109	1	20.17	K.IYHLPDAESDEDEDFKEQTR.L	Phospho (ST)	71.72	IYHLPDAES#DEDEDFKEQTR	39.37						--------Y----------	--------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
171	sp|Q9Y2J2|E41L3_HUMAN	79	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
953	967	2	1544.7164	0.0041	0	40.65	K.TETISFGSVSPGGVK.L	Phospho (ST)	97.25	TETISFGSVS#PGGVK	24.75						---------Y-----	---------Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
172	sp|P08559|ODPA_HUMAN	79	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
289	302	2	1751.6234	0.007	0	16.08	R.YHGHSMSDPGVSYR.T	2 Phospho (ST)	72.42	YHGHS#MSDPGVS#YR	26.53	19.33					----Y------Y--	----Y------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
173	sp|Q96ST3|SIN3A_HUMAN	79	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
829	853	3	2832.1531	0.0111	1	21.67	R.GDLSDVEEEEEEEMDVDEATGAVKK.H	Phospho (ST)	48.91	GDLS#DVEEEEEEEMDVDEATGAVKK	79.86						---Y----------	---Y----------
829	852	2	2704.0574	0.0105	0	76.12	R.GDLSDVEEEEEEEMDVDEATGAVK.K	Phospho (ST)	164.06	GDLS#DVEEEEEEEMDVDEATGAVK	199.13						---Y----------	---Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
174	sp|Q9Y2K7|KDM2A_HUMAN	79	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
844	877	3	3772.4212	0.0072	1	78.72	R.TPQRGDEEGLGGEEEEEEEEEEEDDSAEEGGAAR.L	Phospho (ST)	176.56	TPQRGDEEGLGGEEEEEEEEEEDDS#AEEGGAAR	158.46						----------Y---------	----------Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
175	sp|Q15424|SAFB1_HUMAN	78	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
307	348	3	4390.9342	0.0183	0	78.31	R.TDCEPVGLEPAVEQSSAASELAEASSEELAEAPTEAPSPEAR.D	Phospho (ST)	187.43	TDCEPVGLEPAVEQSSAASELAEASSEELAEAPTEAPS#PEAR	51.71						----------Y----	----------Y----
601	609	2	1087.536	0.0046	1	18.65	R.SVVSFDKVK.E	Phospho (ST)	45.31	SVVS#FDKVK	35.82						---Y-----	---Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
176	sp|Q9ULW0|TPX2_HUMAN	78	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
728	740	2	1433.686	0.0057	0	27.61	K.SSDQPLTVPVSPK.F	Phospho (ST)	87.87	SSDQPLTVPVS#PK	59.3						----------Y--	----------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
177	sp|Q15029|U5S1_HUMAN	78	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1	31	3	3717.4852	0.0139	1	78.06	-.MDTDLYDEFGNYIGPELDSDEDDDELGRETK.D	Acetyl (Protein N-term); Phospho (ST)	69.66	MDTDLYDEFGNYIGPELDS#DEDDDELGRETK	43.97						----------Y----------	----------N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
178	sp|Q13610|PWP1_HUMAN	78	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
41	67	3	2934.1435	0.0089	1	40.94	K.EKLQEEGGGSDEEETGSPSEDGMQSAR.T	Oxidation (M); Phospho (ST)	101	EKLQEEGGGS#DEEETGSPSEDGMQSAR	97.6						---------Y----------	---------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
179	sp|Q5T200|ZC3HD_HUMAN	78	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
980	995	2	1867.7336	0.0058	0	36.39	R.GNIETTSEDGQVFSPK.K	2 Phospho (ST)	120.56	GNIETTS#EDGQVFS#PK	20.35	126.6					------Y------Y--	------Y------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
180	sp|Q99733|NP1L4_HUMAN	78	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
2	19	2	1939.7894	0.0058	0	58.84	M.ADHSFSDGVPSDSVEAAK.N	Acetyl (Protein N-term); Phospho (ST)	49.48	ADHS#FSDGVPSDSVEAAK	30.7						---Y----------	---Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
181	sp|Q14573|ITPR3_HUMAN	78	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
932	953	2	2268.0874	0.0087	1	77.09	R.KQSVFSAPSLSAGASAAEPLDR.S	Phospho (ST)	108.09	KQS#VFSAPSLSAGASAAEPLDR	35.82						--Y----------	--Y----------
1830	1841	2	1273.5752	0.0049	0	20.85	R.VASFSIPGSSSR.Y	Phospho (ST)	64.26	VAS#FSIPGSSSR	24.75						--Y---------	--Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
182	sp|O00264|PGRC1_HUMAN	78	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
48	67	2	2114.8474	0.0045	0	46.94	R.GDQPAASGDSDDDEPPPLPR.L	Phospho (ST)	126.07	GDQPAASGDS#DDDEPPPLPR	42.44						---------Y----------	---------N----------
45	67	3	2483.104	0.0074	1	21.96	K.IVRGDQPAASGDSDDDEPPPLPR.L	Phospho (ST)	86.28	IVRGDQPAASGDS#DDDEPPPLPR	25.13						----------Y----------	----------N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
183	sp|P50479|PDLI4_HUMAN	77	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
9	16	2	982.4096	0.0034	0	23.47	R.GPSPWGFR.L	Phospho (ST)	98.94	GPS#PWGFR	1000						--N-----	--N-----
102	117	2	1844.8362	0.0057	0	31.87	R.IHIDPEIQDGSPTTSR.R	Phospho (ST)	122.87	IHIDPEIQDGS#PTTSR	21.99						----------Y-----	----------Y-----
310	326	3	1924.9414	0.0078	0	19.48	R.VKPPEGYDVVAVYPNAK.V	Phospho (Y)	100.56	VKPPEGY#DVVAVYPNAK	131.22						------Y----------	------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
184	sp|O75691|UTP20_HUMAN	76	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1732	1753	2	2138.8634	-0.0007	0	52.84	K.SLSDNGQPGTPDPADSGGTSAK.E	Deamidated (NQ); Phospho (ST)	69.74	SLSDNGQPGT#PDPADSGGTSAK	23.84						---------Y----------	---------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
185	sp|Q15139|KPCD1_HUMAN	76	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
742	756	2	1650.8444	0.0062	0	42.33	R.SVVGTPAYLAPEVLR.N	Phospho (ST)	104.76	S#VVGTPAYLAPEVLR	49.62						Y----------	Y----------
904	912	2	1036.536	0.0043	1	20.85	K.ALGERVSIL.-	Phospho (ST)	51.55	ALGERVS#IL	1000						------Y--	------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
186	sp|Q9BZG1|RAB34_HUMAN	76	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
239	252	2	1619.7134	0.0055	0	49.53	R.INSDDSNLYLTASK.K	Phospho (Y)	135.7	INSDDSNLY#LTASK	36.45						--------N-----	--------Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
187	sp|Q9UNZ2|NSF1C_HUMAN	76	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
77	101	3	3032.2042	0.0097	1	20.6	R.DLIHDQDEDEEEEEGQRFYAGGSER.S	Phospho (Y)	99.94	DLIHDQDEDEEEEEGQRFY#AGGSER	45.54						----------N------	----------Y------
157	173	2	1855.8406	0.0054	1	67.1	R.LGAAPEEESAYVAGEKR.Q	Phospho (Y)	160.8	LGAAPEEESAY#VAGEKR	24.75						----------Y------	----------Y------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
188	sp|Q86V48|LUZP1_HUMAN	76	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
655	672	3	2010.9106	0.0071	0	29.56	R.EKPDSDDDLDIASLVTAK.L	Phospho (ST)	89.47	EKPDS#DDDLDIASLVTAK	73.48						----Y----------	----Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
189	sp|Q9NZ63|CI078_HUMAN	75	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
141	154	2	1814.7606	0.0061	0	61.25	K.NAEDCLYELPENIR.V	Phospho (Y)	192.09	NAEDCLY#ELPENIR	1000						------Y-------	------Y-------
250	265	3	1886.8588	0.0064	1	15.1	R.VGDTEKPEPERSPPNR.K	Phospho (ST)	72.73	VGDTEKPEPERS#PPNR	55.58						---Y----------	---Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
190	sp|P00558|PGK1_HUMAN	74	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
200	216	3	1847.9617	0.0071	0	32.72	K.ALESPERPFLAILGGAK.V	Phospho (ST)	91.68	ALES#PERPFLAILGGAK	1000						---Y----------	---Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
191	sp|P55265|DSRAD_HUMAN	74	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
596	613	2	1922.8374	0.0075	0	43.13	K.TAESQTPTPSATSFFSGK.S	Phospho (ST)	104.17	TAESQT#PTPSATSFFSGK	24.75						-----Y----------	-----Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
192	sp|Q6PD62|CTR9_HUMAN	74	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
914	933	2	2306.9214	0.011	0	55.33	K.GGEFDEFVNDDTDDDLPISK.K	Phospho (ST)	204.45	GGEFDEFVNDDT#DDDLPISK	90.91						----------Y--------	----------Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
193	sp|P28715|ERCC5_HUMAN	74	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
373	386	2	1462.65	0.0047	0	43.23	R.NAPAAVDEGSISPR.T	Phospho (ST)	150.27	NAPAAVDEGSIS#PR	30.83						----------Y--	----------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
194	sp|P42224|STAT1_HUMAN	74	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
717	736	2	2400.0654	0.0098	0	75.63	R.LQTTDNLLPMSPEEFDEVSR.I	Phospho (ST)	155.92	LQTTDNLLPMS#PEEFDEVSR	95.37						---------Y---------	---------Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
195	sp|SUMO1_HUMAN|	74	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
2	17	3	1868.8102	0.0061	1	34.52	M.SDQEAKPSTEDLGDKK.E	Acetyl (Protein N-term); Phospho (ST)	45.04	S#DQEAKPSTEDLGDKK	24.18						Y----------	N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
196	sp|P49792|RBP2_HUMAN	74	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
2893	2924	4	3669.6385	0.0138	0	16.66	K.VGEDEDGSDEEVVHNEDIHFEPIVSLPEVEVK.S	Phospho (ST)	82.01	VGEDEDGS#DEEVVHNEDIHFEPIVSLPEVEVK	46.71						--------Y----------	--------Y----------
946	957	2	1353.6364	0.0035	0	39.55	R.FESPATGILSPR.G	Phospho (ST)	102.28	FESPATGILS#PR	54.64						---------Y--	---------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
197	sp|O95183|VAMP5_HUMAN	73	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
41	53	2	1564.6532	0.0052	0	45.12	R.SDQLLDMSSTFNK.T	Phospho (ST)	153.37	SDQLLDMS#STFNK	20.35						-------Y-----	-------Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
198	sp|Q9UBW7|ZMYM2_HUMAN	73	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
295	312	3	1943.9764	0.0046	1	36.87	R.NQKQPGVDSLSPVASLPK.Q	Phospho (ST)	111.65	NQKQPGVDSLS#PVASLPK	25.87						---------Y--------	---------Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
199	sp|A0MZ66|SHOT1_HUMAN	73	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
506	518	2	1386.6512	0.0047	0	24.33	K.SMPVLGSVSSVTK.T	Oxidation (M); Phospho (ST)	23.98	S#MPVLGSVSSVTK	35.78						Y----------	Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
200	sp|P55072|TERA_HUMAN	73	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
773	806	3	3299.2912	0.0111	0	31.09	R.FPSGNQGGAGPSQGSGGGTGGSVYTEDNDDDLYG.-	Phospho (ST)	89.69	FPSGNQGGAGPSQGSGGGTGGSVYTEDNDDDLY#G	25.84						----------N---------	----------N---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
201	sp|Q9NR30|DDX21_HUMAN	73	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
114	131	3	2118.9799	0.0077	1	38.75	K.VTKNEEPSEEEIDAPKPK.K	Phospho (ST)	72.15	VTKNEEPS#EEEIDAPKPK	30.4							-------Y----------	-------Y----------
117	131	2	1790.7692	0.0082	0	29.18	K.NEEPSEEEIDAPKPK.K	Phospho (ST)	119.43	NEEPS#EEEIDAPKPK	1000							----Y----------	----Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
202	sp|Q9BWU0|NADAP_HUMAN	73	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
457	474	2	2375.8474	0.0095	0	72.77	K.NWEDEDFYDSDDDTFLDR.T	Phospho (ST)	231.27	NWEDEDFYDS#DDDTFLDR	57.75							---------Y--------	---------Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
203	sp|Q01831|XPC_HUMAN	72	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
869	898	3	3047.1772	0.0106	0	72.44	K.SEAAAPHTDAGGGLSSDEEEGTSSQAEAAR.I	2 Phospho (ST)	129.72	SEAAAPHTDAGGGLS#S#DEEEGTSSQAEAAR	49.52	50.72						-------------YY-------------	-------------YY-------------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
204	sp|Q8WWQ0|PHIP_HUMAN	72	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1313	1322	2	1289.5372	0.0043	0	38.6	R.AQSYDIQAWK.K	Deamidated (NQ); Phospho (ST)	42.37	AQS#YDIQAWK	28.87							--Y-------	--Y-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
205	sp|O60664|PLIN3_HUMAN	72	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
123	140	2	1915.9028	0.0067	1	61.01	K.ELVSSKVSGAQEMVSSAK.D	Phospho (ST)	69.96	ELVSSKVS#GAQEMVSSAK	54.95							-------Y----------	-------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
206	sp|P55884|EIF3B_HUMAN	71	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
142	174	3	3674.5672	0.0111	0	60.66	R.ALENGDADEPSFSDPEDFVDDVSEEELLGDVLK.D	Phospho (ST)	177.81	ALENGDADEPSFS#DPEDFVDDVSEEELLGDVLK	24.24							----------Y----------	----------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
207	sp|P28290|SSFA2_HUMAN	71	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
737	749	2	1477.7594	0.0053	0	36.45	R.SQSLPTTLLSPVR.V	Phospho (ST)	74.6	SQS#LPTTLLSPVR	21.75							--Y----------	--Y----------
87	102	2	1712.792	0.0051	0	44.96	R.TPLGASLDEQSSSTLK.G	Phospho (ST)	91.13	TPLGAS#LDEQSSSTLK	57.41							-----Y----------	-----Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
208	sp|Q14155|ARHG7_HUMAN	71	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
517	525	2	1125.462	0.0055	0	29.99	R.MSGFIYQGK.L	Oxidation (M); Phospho (ST)	43.79	MS#GFIYQGK	46.68							-Y-------	-Y-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
209	sp|Q9C004|SPY4_HUMAN	71	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
45	65	2	2351.0814	0.0132	0	72.04	K.TSHVENDYIDNPSLALTTGPK.R	Phospho (Y)	219.31	TSHVENDY#IDNPSLALTTGPK	72.08							-------Y----------	-------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
210	sp|Q9NR12|PDLI7_HUMAN	71	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
196	233	3	4032.8782	0.0098	0	70.61	R.TEAPAPASSTPQEPWPGPTAPSPTSRPPWAVDPAFAER.Y	Phospho (ST)	127.07	TEAPAPASSTPQEPWPGPTAPS#PTSRPPWAVDPAFAER	24.65							----------N----------	----------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
211	sp|Q06210|GFPT1_HUMAN	71	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
259	271	2	1603.6894	0.0054	0	45.97	R.VDSTTCLFPVEEK.A	Phospho (ST)	121.32	VDS#TTCLFPVEEK	21.51							--Y----------	--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
212	sp|P09651|ROA1_HUMAN	70	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
4	14	3	1378.6186	0.0056	1	29.43	K.SESPKEPEQLR.K	Phospho (ST)	96.23	SES#PKEPEQLR	25.37							--Y--------	--Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
213	sp|Q9Y3T9|NOC2L_HUMAN	70	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
663	684	3	2767.0684	0.0108	1	17.2	K.QFKDLFDLNSSEEDDTEGFSER.G	2 Phospho (ST)	55.72	QFKDLFDLNS#S#EEDDTEGFSER	28.57	25.41						---------YY----------	---------YY----------
666	684	2	2363.8454	0.0099	0	47.68	K.DLFDLNSSEEDDTEGFSER.G	2 Phospho (ST)	211.83	DLFDLNS#S#EEDDTEGFSER	89.12	80.68						------YY----------	------YY----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
214	sp|Q9H9C1|CN133_HUMAN	70	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
117	135	2	2056.9554	0.0088	0	51.54	R.TRPGSFQSLSDALSDTPAK.S	Phospho (ST)	119.17	TRPGS#FQSLSDALSDTPAK	19.52							----Y----------	----Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
215	sp|Q9H0B6|KLC2_HUMAN	70	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
580	588	2	1073.4838	0.0044	0	23.18	R.ASSLNFLNK.S	Deamidated (NQ); Phospho (ST)	90.64	ASS#LNFLNK	32.4							--Y------	--Y------
427	439	2	1601.6118	0.0043	0	39.45	R.DSAPYGEYGSWYK.A	Phospho (ST)	93.37	DSAPYGEY#GSWYK	26.22							---------N---	---------N---

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
216	sp|Q9H6Y2|WDR55_HUMAN	69	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
4	27	3	2802.0349	0.0079	0	54.19	R.TCEERPAEDGSDEEDPDSMEAPTR.I	Phospho (ST)	182.64	TCEERPAEDGS#DEEDPDSMEAPTR	73.51							----------Y----------	----------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
217	sp|Q13547|HDAC1_HUMAN	69	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
414	432	2	2316.8314	0.0184		1	25.97	R.IACEEEFSDSEEEGEGGRK.N	2 Phospho (ST)	102.28	IACEEEFS#DS#EEEGEGGRK	1000						--------Y-Y---------	--------Y-Y---------
372	404	4	3742.5789	0.0137		1	26.27	R.MLPHAPGVQMQAIPEDAIPEESGDEDEDDPDKR.I	2 Oxidation (M); Phospho (ST)	24.14	M!LPHAPGVQM!QAIPEDAIPEES#GDEDEDDPDKR	1000						----------Y----------	----------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
218	sp|P36871|PGM1_HUMAN	69	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
108	130	2	2285.1274	0.0069		0	57.16	K.AIGGIILTASHNPGGPNGDFGIK.F	Phospho (ST)	132.51	AIGGIILTAS#HNPGGPNGDFGIK	32.85						---------Y----------	---------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
219	sp|O60343|TBCD4_HUMAN	69	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
586	594	2	1088.4584	0.0045		0	27.82	R.LGSVDSFER.S	Phospho (ST)	52.82	LGS#VDSFER	31.87						--Y------	--Y------
584	594	2	1301.5798	0.0033		1	19.32	R.GRLGSVDSFER.S	Phospho (ST)	33.61	GRLGS#VDSFER	35.82						----Y------	----Y------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
220	sp|P16070|CD44_HUMAN	69	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
695	715	4	2332.1325	0.0079		1	31.58	R.KPSGLNGEASKSQEMVHLVNK.E	Phospho (ST)	80.59	KPSGLNGEASKS#QEMVHLVNK	20.57						--Y----------	--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
221	sp|Q00526|CDK3_HUMAN	68	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
10	20	2	1344.5464	0.0061		0	29.34	K.IGEGTYGVVYK.A	Phospho (ST); Phospho (Y)	81.47	IGEGT#Y#GVVYK	56.63	48.99					----YY-----	----YY-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
222	sp|Q13435|SF3B2_HUMAN	68	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
279	298	2	2147.9554	0.0083		1	48.07	R.SSLGQSASETEEDTVSVSKK.E	Phospho (ST)	98.94	SSLGQSAS#ETEEDTVSVSKK	23.34						-----Y----------	-----Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
223	sp|O00499|BIN1_HUMAN	67	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
312	336	3	2590.2634	0.0093		1	35.73	R.VNHEPEPAGGATPGATLPKSPSQLR.K	Phospho (ST)	93.6	VNHEPEPAGGATPGATLPKS#PSQLR	21.8						----------N---	----------Y---
296	311	2	1657.7418	0.007		0	16.45	K.SPSPPDGSPAATPEIR.V	Phospho (ST)	48.16	SPSPPDGS#PAATPEIR	20.12						-------Y--------	-------Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
224	sp|Q9UKK3|PARP4_HUMAN	66	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1182	1193	2	1466.6016	0.005		0	23.29	R.DENESPFPDIPK.V	Phospho (ST)	82.04	DENES#PFPDIPK	1000						----N-------	----N-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
225	sp|Q96JM3|ZN828_HUMAN	66	6	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
421	440	2	2324.0454	0.0087		1	16.76	R.KPGPPLSPEIRSPAGSPELR.K	3 Phospho (ST)	33.84	KPGPPLS#PEIRS#PAGS#PELR	1000						------Y----Y---Y----	------Y----Y---Y----
457	470	2	1613.7422	0.0085		1	24.48	R.KTSPASLDFPESQK.S	Phospho (ST)	90.54	KTS#PASLDFPESQK	19.33						--Y----------	--Y----------
199	219	2	2313.1134	0.0076		0	31.01	K.LAPVPSPEPQKPAPVSPESVK.A	2 Phospho (ST)	88.4	LAPVPS#PEPQKPAPVS#PESVK	77.69	35.41					-----Y---------Y-----	-----Y---------Y-----
372	391	2	2276.9494	0.0103		1	17.81	K.SSSVSPSSWKSPPASPESWK.S	2 Phospho (ST)	73.64	SSSVSPSSWKS#PPAS#PESWK	26.21	53.2					----------Y---Y-----	----------Y---Y-----
400	410	2	1345.6106	0.0039		0	18.78	K.TAPTLSPEHWK.A	Phospho (ST)	47.75	TAPTLS#PEHWK	35.92						-----Y-----	-----Y-----
302	324	4	2568.2293	0.0101		0	17.6	R.RPAPAVSPGSWKPGPPGSPRPWK.S	2 Phospho (ST)	56.84	RPAPAVS#PGSWKPGPPGS#PRPWK	21.49	28.02					------Y----------Y-----	------Y----------Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
226	sp|Q53T59|H1BP3_HUMAN	66	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
188	208	2	2411.0194	0.0108		0	65.73	K.GEDAEESLEEEEALDPLGIMR.S	Phospho (ST)	137.7	GEDAEES#LEEEEALDPLGIMR	1000						------Y----------	------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
227	sp|P08621|RU17_HUMAN	66	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
311	346	3	3468.3622	0.0161		0	29.3	R.GGGGDMAEPSEAGDAPPDDGPPGELGPDGPDGPEEK.G	Oxidation (M); Phospho (ST)	39.53	GGGGDM!AEPS#EAGDAPPDDGPPGELGPDGPDGPEEK	1000						---------Y----------	---------Y----------
219	231	3	1599.727	0.0075		0	20.79	R.YDERPGPSPLPHR.D	Phospho (ST)	47.82	YDERPGPS#PLPHR	30.57						-------Y-----	-------Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
228	sp|Q96AT1|K1143_HUMAN	65	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
141	154	2	1691.6252	0.0053		0	37.31	K.NSSLLSFDNEDENE.-	Phospho (ST)	136.15	NSSLLS#FDNEDENE	53.53						-----Y--------	-----Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
229	sp|P02511|CRYAB_HUMAN	65	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
57	69	2	1591.645	0.0072		0	47	R.APSWFDTGLSEMR.L	Oxidation (M); Phospho (ST)	19.18	APS#WFDTGLSEMR	34.98						--Y----------	--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
230	sp|Q99613|EIF3C_HUMAN	65	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
34	47	2	1751.8044	0.0066		1	31.56	K.QPLLLSEDEEDTKR.V	Phospho (ST)	53.59	QPLLLS#EDEEDTKR	54.9						-----Y--------	-----Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
231	sp|P01130|LDLR_HUMAN	65	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
817	830	2	1744.7878	0.0057		0	64.89	K.NINSINFDNPVYQK.T	Phospho (Y)	172.42	NINSINFDNPVY#QK	144.55						----------N--	----------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
232	sp|P10412|H14_HUMAN	65	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
2	21	2	2024.9874	0.0055	1	43.33	M.SETAPAAPAAPAPAEKTPVK.K	Acetyl (Protein N-term); Phospho (ST)	54.2	SETAPAAPAAPAPAEKT#PVK	43.5						----------Y---	----------N---

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
233	sp|O14497|ARI1A_HUMAN	64	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
694	710	2	1739.7358	0.0078	0	46.23	R.GPSPSPVGSPASVAQSR.S	2 Phospho (ST)	83.47	GPS#PSPVGS#PASVAQSR	43.31	21.11					--Y-----Y--------	--Y-----Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
234	sp|Q9P2Q2|FRM4A_HUMAN	64	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
718	734	2	1947.8298	0.0047	0	36.89	K.LLGSENDTGSPDFYTPR.T	Phospho (ST)	138.48	LLGSENDTGS#PDFYTPR	24.75						---------N-------	---------N-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
235	sp|P26368|U2AF2_HUMAN	64	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
2	9	2	1165.402	0.0056	0	24.04	M.SDFDEFER.Q	Acetyl (Protein N-term); Phospho (ST)	35.55	S!#DFDEFER	1000						Y-------	Y-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
236	sp|Q9UIQ6|LCAP_HUMAN	64	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
57	75	2	2262.8214	0.0067	0	63.77	R.GLGEHEMEEDEEDYESSAK.L	Phospho (Y)	204.21	GLGEHEMEEDEEDY#ESSAK	64.79						----------N-----	----------Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
237	sp|Q4G0J3|LARP7_HUMAN	63	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
254	270	2	2006.7954	0.0084	0	37.17	R.SRPTSEGSDIESTEPQK.Q	2 Phospho (ST)	139.56	SRPT#S#EGSDIESTEPQK	29.98	33.17					---YY----------	---YY----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
238	sp|P35658|NU214_HUMAN	62	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
669	682	2	1441.7374	0.0044	0	17.63	R.ITPPAAKPGSPQAK.S	Phospho (ST)	43.74	ITPPAAKPGS#PQAK	36.29						---------Y----	---------Y----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
239	sp|Q5VZK9|LR16A_HUMAN	62	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1331	1343	2	1688.6882	0.0051	0	55.75	R.SWGQQAQEYQEQK.Q	Phospho (ST)	86.78	S#WGQQAQEYQEQK	78.66						Y----------	Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
240	sp|P38159|HNRPG_HUMAN	62	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
204	217	2	1694.7242	0.0054	1	37.78	R.DVYLSPRDDGYSTK.D	Phospho (ST)	74.31	DVYLS#PRDDGYSTK	52.75						----Y---------	----Y---------
348	355	2	965.4086	0.0045	0	23.47	R.GLPPSMER.G	Phospho (ST)	38.65	GLPPS#MER	1000						----Y---	----Y---

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
241	sp|Q53HL2|BOREA_HUMAN	62	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
211	225	2	1614.7372	0.0082	0	62.11	R.IYNISGNGSPLADSK.E	Phospho (ST)	173.28	IYNISGNGS#PLADSK	44.11						--------Y------	--------Y------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
242	sp|Q7L014|DDX46_HUMAN	62	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
797	824	3	3105.3142	0.0133	0	24.53	K.AALGLQDSDDEDAAVDIDEQIESMFNSK.K	Phospho (ST)	94.95	AALGLQDS#DDEDAAVDIDEQIESMFNSK	67.44						-------Y----------	-------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
243	sp|O75528|TADA3_HUMAN	62	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
130	144	2	1915.8302	0.0062	0	61.75	K.IQEYEFTDDPIDVPR.I	Phospho (Y)	175.9	IQEY#EFTDDPIDVPR	79.13							

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
244	sp|Q15459|SF3A1_HUMAN	62	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
317	338	3	2712.0238	0.0081	1	41.47	K.FGESEEVEMEVESDEEDDKQEK.A	Oxidation (M); Phospho (ST)	73.82	FGESEEVEMEVES#DEEDDKQEK	51.76						----------Y---------	----------Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
245	sp|Q9NRY4|GRLF1_HUMAN	62	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1173	1187	2	1658.7242	0.0053	0	35.68	R.TSFSVGSDDELGPIR.K	Phospho (ST)	78.05	TSFSVGS#DDELGPIR	49.62						------Y--------	------Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
246	sp|Q86UU1|PHLB1_HUMAN	61	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
428	436	2	1046.447	0.0037	0	41.68	R.TFSDGLATR.T	Phospho (ST)	64.09	TFS#DGLATR	24.75						--Y------	--Y------
1007	1020	2	1493.729	0.0051	0	35.08	K.SALLTQNGTGSLPR.N	Phospho (ST)	110.21	SALLTQNGTGS#LPR	24.24						----------N---	----------Y---

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
247	sp|P61247|RS3A_HUMAN	61	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
253	264	2	1369.549	0.0052	0	48.83	R.ADGYEPPVQESV.-	Phospho (Y)	91.83	ADGY#EPPVQESV	119.17						---Y--------	---N--------
250	264	2	1753.7618	0.0059	1	37.42	K.VERADGYEPPVQESV.-	Phospho (Y)	100.72	VERADGY#EPPVQESV	99.42						------Y--------	------N--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
248	sp|Q9BY44|EIF2A_HUMAN	61	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
503	520	2	1943.9036	0.0047	1	36.52	R.SDKSPDLAPTPAPQSTPR.N	Phospho (ST)	126.05	SDKS#PDLAPTPAPQSTPR	21.31						---Y----------	---Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?

<table>
<tr><td>249</td><td>sp|Q5VT52|RPRD2_HUMAN</td><td>60</td><td>2</td><td>Phosphoprotein</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Start</td><td>End</td><td>charge</td><td>Mr(expt)</td><td>Delta (Da)</td><td>MC</td><td>Ion score</td><td>Sequence</td><td>Modification</td><td>AScore</td><td>Ascore validated site(s) (*)</td><td>Ascore1</td><td>Ascore2</td><td>Ascore3</td><td>Ascore4</td><td>Ascore5</td><td>Ascore6</td><td>Annotated in Uniprot?</td><td>Annotated in Phosphosite.org?</td></tr>
<tr><td>609</td><td>623</td><td>2</td><td>1569.7484</td><td>0.0045</td><td>0</td><td>33.51</td><td>K.ASIGQSPGLPSTTFK.L</td><td>Phospho (ST)</td><td>109.86</td><td>ASIGQS#PGLPSTTFK</td><td>47.64</td><td></td><td></td><td></td><td></td><td></td><td>-----Y---------</td><td>-----Y---------</td></tr>
<tr><td>1097</td><td>1110</td><td>2</td><td>1681.791</td><td>0.0052</td><td>1</td><td>23.72</td><td>R.RMSGEPIQTVESIR.V</td><td>Phospho (ST)</td><td>70.54</td><td>RMS#GEPIQTVESIR</td><td>25.85</td><td></td><td></td><td></td><td></td><td></td><td>--Y-----------</td><td>--Y-----------</td></tr>
<tr><td>Index</td><td>AC</td><td>Mascot score</td><td>Nb distinct peptides</td><td>Is Uniprot phosphoprotein?</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>250</td><td>sp|Q05519|SFR11_HUMAN</td><td>60</td><td>1</td><td>Phosphoprotein</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Start</td><td>End</td><td>charge</td><td>Mr(expt)</td><td>Delta (Da)</td><td>MC</td><td>Ion score</td><td>Sequence</td><td>Modification</td><td>AScore</td><td>Ascore validated site(s) (*)</td><td>Ascore1</td><td>Ascore2</td><td>Ascore3</td><td>Ascore4</td><td>Ascore5</td><td>Ascore6</td><td>Annotated in Uniprot?</td><td>Annotated in Phosphosite.org?</td></tr>
<tr><td>198</td><td>211</td><td>2</td><td>1484.78</td><td>0.0048</td><td>0</td><td>56.64</td><td>K.LNHVAAGLVSPSLK.S</td><td>Phospho (ST)</td><td>131.16</td><td>LNHVAAGLVS#PSLK</td><td>48.87</td><td></td><td></td><td></td><td></td><td></td><td>---------Y----</td><td>---------Y----</td></tr>
<tr><td>Index</td><td>AC</td><td>Mascot score</td><td>Nb distinct peptides</td><td>Is Uniprot phosphoprotein?</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>251</td><td>sp|O95292|VAPB_HUMAN</td><td>60</td><td>1</td><td>Phosphoprotein</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
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<tr><td>156</td><td>168</td><td>3</td><td>1487.68</td><td>0.0044</td><td>1</td><td>19.38</td><td>K.SLSSSLDDTEVKK.V</td><td>Phospho (ST)</td><td>83.6</td><td>SLS#SSLDDTEVKK</td><td>37.41</td><td></td><td></td><td></td><td></td><td></td><td>--N----------</td><td>--Y----------</td></tr>
<tr><td>Index</td><td>AC</td><td>Mascot score</td><td>Nb distinct peptides</td><td>Is Uniprot phosphoprotein?</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>252</td><td>sp|Q86WB0|NIPA_HUMAN</td><td>60</td><td>3</td><td>Phosphoprotein</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Start</td><td>End</td><td>charge</td><td>Mr(expt)</td><td>Delta (Da)</td><td>MC</td><td>Ion score</td><td>Sequence</td><td>Modification</td><td>AScore</td><td>Ascore validated site(s) (*)</td><td>Ascore1</td><td>Ascore2</td><td>Ascore3</td><td>Ascore4</td><td>Ascore5</td><td>Ascore6</td><td>Annotated in Uniprot?</td><td>Annotated in Phosphosite.org?</td></tr>
<tr><td>381</td><td>398</td><td>2</td><td>1879.8424</td><td>0.0037</td><td>0</td><td>24.28</td><td>R.SMGTGDTPGLEVPSSPLR.K</td><td>Phospho (ST)</td><td>83.49</td><td>SMGTGDTPGLEVPSS#PLR</td><td>26.38</td><td></td><td></td><td></td><td></td><td></td><td>--------------Y---</td><td>--------------Y---</td></tr>
<tr><td>315</td><td>324</td><td>3</td><td>1242.6541</td><td>0.0055</td><td>1</td><td>16.82</td><td>R.LPLVPESPRR.M</td><td>Phospho (ST)</td><td>18.84</td><td>LPLVPES#PRR</td><td>1000</td><td></td><td></td><td></td><td></td><td></td><td>------Y---</td><td>------Y---</td></tr>
<tr><td>17</td><td>31</td><td>2</td><td>1704.805</td><td>0.0066</td><td>1</td><td>20.88</td><td>K.NWGAVVRSPEGTPQK.I</td><td>Phospho (ST)</td><td>49.86</td><td>NWGAVVRS#PEGTPQK</td><td>33.85</td><td></td><td></td><td></td><td></td><td></td><td>-------Y-------</td><td>-------Y-------</td></tr>
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<tr><td>253</td><td>sp|Q08945|SSRP1_HUMAN</td><td>59</td><td>1</td><td>Phosphoprotein</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
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<tr><td>432</td><td>455</td><td>3</td><td>2928.0808</td><td>0.0103</td><td>0</td><td>33.07</td><td>K.EGMNPSYDEYADSDEDQHDAYLER.M</td><td>Phospho (ST)</td><td>94.69</td><td>EGMNPSYDEYADS#DEDQHDAYLER</td><td>47.97</td><td></td><td></td><td></td><td></td><td></td><td>------------Y-----------</td><td>------------Y-----------</td></tr>
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<tr><td>254</td><td>sp|Q5TDH0|DDI2_HUMAN</td><td>59</td><td>1</td><td>Phosphoprotein</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Start</td><td>End</td><td>charge</td><td>Mr(expt)</td><td>Delta (Da)</td><td>MC</td><td>Ion score</td><td>Sequence</td><td>Modification</td><td>AScore</td><td>Ascore validated site(s) (*)</td><td>Ascore1</td><td>Ascore2</td><td>Ascore3</td><td>Ascore4</td><td>Ascore5</td><td>Ascore6</td><td>Annotated in Uniprot?</td><td>Annotated in Phosphosite.org?</td></tr>
<tr><td>192</td><td>205</td><td>2</td><td>1630.734</td><td>0.0061</td><td>0</td><td>45.13</td><td>R.LFSADPFDLEAQAK.I</td><td>Phospho (ST)</td><td>173.75</td><td>LFS#ADPFDLEAQAK</td><td>1000</td><td></td><td></td><td></td><td></td><td></td><td>--Y-----------</td><td>--Y-----------</td></tr>
<tr><td>Index</td><td>AC</td><td>Mascot score</td><td>Nb distinct peptides</td><td>Is Uniprot phosphoprotein?</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>255</td><td>sp|Q9BWT3|PAPOG_HUMAN</td><td>58</td><td>1</td><td>Phosphoprotein</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Start</td><td>End</td><td>charge</td><td>Mr(expt)</td><td>Delta (Da)</td><td>MC</td><td>Ion score</td><td>Sequence</td><td>Modification</td><td>AScore</td><td>Ascore validated site(s) (*)</td><td>Ascore1</td><td>Ascore2</td><td>Ascore3</td><td>Ascore4</td><td>Ascore5</td><td>Ascore6</td><td>Annotated in Uniprot?</td><td>Annotated in Phosphosite.org?</td></tr>
<tr><td>684</td><td>702</td><td>2</td><td>2024.9234</td><td>0.0109</td><td>0</td><td>58.4</td><td>K.SVDAIGGESMPIPTIDTSR.K</td><td>Phospho (ST)</td><td>123.51</td><td>S#VDAIGGESMPIPTIDTSR</td><td>71.86</td><td></td><td></td><td></td><td></td><td></td><td>Y------------------</td><td>Y------------------</td></tr>
<tr><td>Index</td><td>AC</td><td>Mascot score</td><td>Nb distinct peptides</td><td>Is Uniprot phosphoprotein?</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>256</td><td>sp|Q9P035|PTAD1_HUMAN</td><td>58</td><td>1</td><td>Phosphoprotein</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Start</td><td>End</td><td>charge</td><td>Mr(expt)</td><td>Delta (Da)</td><td>MC</td><td>Ion score</td><td>Sequence</td><td>Modification</td><td>AScore</td><td>Ascore validated site(s) (*)</td><td>Ascore1</td><td>Ascore2</td><td>Ascore3</td><td>Ascore4</td><td>Ascore5</td><td>Ascore6</td><td>Annotated in Uniprot?</td><td>Annotated in Phosphosite.org?</td></tr>
<tr><td>110</td><td>121</td><td>2</td><td>1588.6196</td><td>0.008</td><td>0</td><td>29.08</td><td>R.WLDESDAEMELR.A</td><td>Oxidation (M); Phospho (ST)</td><td>44.93</td><td>WLDES#DAEM!ELR</td><td>1000</td><td></td><td></td><td></td><td></td><td></td><td>----Y-------</td><td>----Y-------</td></tr>
<tr><td>Index</td><td>AC</td><td>Mascot score</td><td>Nb distinct peptides</td><td>Is Uniprot phosphoprotein?</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>257</td><td>sp|P53621|COPA_HUMAN</td><td>58</td><td>1</td><td>Phosphoprotein</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Start</td><td>End</td><td>charge</td><td>Mr(expt)</td><td>Delta (Da)</td><td>MC</td><td>Ion score</td><td>Sequence</td><td>Modification</td><td>AScore</td><td>Ascore validated site(s) (*)</td><td>Ascore1</td><td>Ascore2</td><td>Ascore3</td><td>Ascore4</td><td>Ascore5</td><td>Ascore6</td><td>Annotated in Uniprot?</td><td>Annotated in Phosphosite.org?</td></tr>
<tr><td>171</td><td>182</td><td>2</td><td>1322.5918</td><td>0.0051</td><td>0</td><td>34.56</td><td>K.NLSPGAVESDVR.G</td><td>Phospho (ST)</td><td>121.68</td><td>NLS#PGAVESDVR</td><td>95.84</td><td></td><td></td><td></td><td></td><td></td><td>--Y---------</td><td>--Y---------</td></tr>
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<tr><td>258</td><td>sp|Q96B97|SH3K1_HUMAN</td><td>58</td><td>1</td><td>Phosphoprotein</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Start</td><td>End</td><td>charge</td><td>Mr(expt)</td><td>Delta (Da)</td><td>MC</td><td>Ion score</td><td>Sequence</td><td>Modification</td><td>AScore</td><td>Ascore validated site(s) (*)</td><td>Ascore1</td><td>Ascore2</td><td>Ascore3</td><td>Ascore4</td><td>Ascore5</td><td>Ascore6</td><td>Annotated in Uniprot?</td><td>Annotated in Phosphosite.org?</td></tr>
<tr><td>230</td><td>242</td><td>2</td><td>1597.733</td><td>0.0054</td><td>0</td><td>53.94</td><td>R.SIEVENDFLPVEK.T</td><td>Phospho (ST)</td><td>161.55</td><td>S#IEVENDFLPVEK</td><td>1000</td><td></td><td></td><td></td><td></td><td></td><td>Y------------</td><td>Y------------</td></tr>
<tr><td>Index</td><td>AC</td><td>Mascot score</td><td>Nb distinct peptides</td><td>Is Uniprot phosphoprotein?</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>259</td><td>sp|Q9H8G2|CI082_HUMAN</td><td>58</td><td>1</td><td>Phosphoprotein</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Start</td><td>End</td><td>charge</td><td>Mr(expt)</td><td>Delta (Da)</td><td>MC</td><td>Ion score</td><td>Sequence</td><td>Modification</td><td>AScore</td><td>Ascore validated site(s) (*)</td><td>Ascore1</td><td>Ascore2</td><td>Ascore3</td><td>Ascore4</td><td>Ascore5</td><td>Ascore6</td><td>Annotated in Uniprot?</td><td>Annotated in Phosphosite.org?</td></tr>
<tr><td>301</td><td>317</td><td>2</td><td>1862.8686</td><td>0.0024</td><td>0</td><td>26.31</td><td>K.SVNEILGLAESSPNEPK.A</td><td>Phospho (ST)</td><td>92.19</td><td>SVNEILGLAESS#PNEPK</td><td>28.87</td><td></td><td></td><td></td><td></td><td></td><td>-----------Y-----</td><td>-----------Y-----</td></tr>
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<tr><td>260</td><td>sp|Q96S82|UBL7_HUMAN</td><td>57</td><td>1</td><td>Phosphoprotein</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
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<tr><td>219</td><td>241</td><td>3</td><td>2706.0679</td><td>0.0097</td><td>0</td><td>28.4</td><td>R.DMPGGFLFEGLSDDEDDFHPNTR.S</td><td>Oxidation (M); Phospho (ST)</td><td>44.85</td><td>DMPGGFLFEGLS#DDEDDFHPNTR</td><td>37.69</td><td></td><td></td><td></td><td></td><td></td><td>-----------Y-----------</td><td>-----------Y-----------</td></tr>
<tr><td>Index</td><td>AC</td><td>Mascot score</td><td>Nb distinct peptides</td><td>Is Uniprot phosphoprotein?</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>261</td><td>sp|Q9Y520|BA2L2_HUMAN</td><td>57</td><td>1</td><td>Phosphoprotein</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Start</td><td>End</td><td>charge</td><td>Mr(expt)</td><td>Delta (Da)</td><td>MC</td><td>Ion score</td><td>Sequence</td><td>Modification</td><td>AScore</td><td>Ascore validated site(s) (*)</td><td>Ascore1</td><td>Ascore2</td><td>Ascore3</td><td>Ascore4</td><td>Ascore5</td><td>Ascore6</td><td>Annotated in Uniprot?</td><td>Annotated in Phosphosite.org?</td></tr>
<tr><td>2101</td><td>2110</td><td>2</td><td>1190.563</td><td>0.0047</td><td>0</td><td>26.14</td><td>K.LPDLSPVENK.E</td><td>Phospho (ST)</td><td>76.03</td><td>LPDLS#PVENK</td><td>1000</td><td></td><td></td><td></td><td></td><td></td><td>----Y-----</td><td>----Y-----</td></tr>
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<tr><td>262</td><td>sp|Q86UP2|KTN1_HUMAN</td><td>56</td><td>1</td><td>Phosphoprotein</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Start</td><td>End</td><td>charge</td><td>Mr(expt)</td><td>Delta (Da)</td><td>MC</td><td>Ion score</td><td>Sequence</td><td>Modification</td><td>AScore</td><td>Ascore validated site(s) (*)</td><td>Ascore1</td><td>Ascore2</td><td>Ascore3</td><td>Ascore4</td><td>Ascore5</td><td>Ascore6</td><td>Annotated in Uniprot?</td><td>Annotated in Phosphosite.org?</td></tr>
<tr><td>66</td><td>82</td><td>2</td><td>1990.8338</td><td>0.0069</td><td>0</td><td>43.75</td><td>K.EIQNGNLHESDSESVPR.D</td><td>Deamidated (NQ); Phospho (ST)</td><td>68.29</td><td>EIQNGNLHES#DSESVPR</td><td>30.7</td><td></td><td></td><td></td><td></td><td></td><td>---------Y-------</td><td>---------Y-------</td></tr>
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<tr><td>263</td><td>sp|P04183|KITH_HUMAN</td><td>56</td><td>1</td><td>Phosphoprotein</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
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<tr><td>2</td><td>18</td><td>2</td><td>1948.9392</td><td>0.0063</td><td>1</td><td>43.06</td><td>M.SCINLPTVLPGSPSKTR.G</td><td>Acetyl (Protein N-term); Deamidated (NQ); Phospho (ST)</td><td>54.92</td><td>SCINLPTVLPGS#PSKTR</td><td>22.16</td><td></td><td></td><td></td><td></td><td></td><td>-----------Y-----</td><td>-----------Y-----</td></tr>
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<tr><td>264</td><td>sp|P46013|KI67_HUMAN</td><td>56</td><td>3</td><td>Phosphoprotein</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Start</td><td>End</td><td>charge</td><td>Mr(expt)</td><td>Delta (Da)</td><td>MC</td><td>Ion score</td><td>Sequence</td><td>Modification</td><td>AScore</td><td>Ascore validated site(s) (*)</td><td>Ascore1</td><td>Ascore2</td><td>Ascore3</td><td>Ascore4</td><td>Ascore5</td><td>Ascore6</td><td>Annotated in Uniprot?</td><td>Annotated in Phosphosite.org?</td></tr>
<tr><td>296</td><td>319</td><td>3</td><td>2472.1</td><td>0.0082</td><td>1</td><td>27.82</td><td>K.SGGSGHAVAEPASPEQELDQNKGK.G</td><td>Phospho (ST)</td><td>84.86</td><td>SGGSGHAVAEPAS#PEQELDQNKGK</td><td>36.18</td><td></td><td></td><td></td><td></td><td></td><td>------------Y-----------</td><td>------------Y-----------</td></tr>
<tr><td>2219</td><td>2240</td><td>3</td><td>2503.2382</td><td>0.0087</td><td>1</td><td>18.75</td><td>K.IACRSPQPDPVGTPTIFKPQSK.R</td><td>Phospho (ST)</td><td>75.04</td><td>IACRS#PQPDPVGTPTIFKPQSK</td><td>66.66</td><td></td><td></td><td></td><td></td><td></td><td>----Y-----------------</td><td>----Y-----------------</td></tr>
<tr><td>2101</td><td>2118</td><td>3</td><td>2053.8919</td><td>0.0069</td><td>1</td><td>28</td><td>K.IACKSPPPESMDTPTSTR.R</td><td>Phospho (ST)</td><td>88.25</td><td>IACKS#PPPESMDTPTSTR</td><td>53.97</td><td></td><td></td><td></td><td></td><td></td><td>----Y-------------</td><td>----Y-------------</td></tr>
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<tr><td>265</td><td>sp|Q8NCE2|MTMRE_HUMAN</td><td>55</td><td>1</td><td>Phosphoprotein</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Start</td><td>End</td><td>charge</td><td>Mr(expt)</td><td>Delta (Da)</td><td>MC</td><td>Ion score</td><td>Sequence</td><td>Modification</td><td>AScore</td><td>Ascore validated site(s) (*)</td><td>Ascore1</td><td>Ascore2</td><td>Ascore3</td><td>Ascore4</td><td>Ascore5</td><td>Ascore6</td><td>Annotated in Uniprot?</td><td>Annotated in Phosphosite.org?</td></tr>
</table>

620		638	2	1919.956		0.0054	0	55.46	R.AVAPSPSGAIGGLLEQFAR.G	Phospho (ST)		128.41	AVAPS#PSGAIGGLLEQFAR	24.75							----Y----------		----Y----------	

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																						
266	sp|P49327|FAS_HUMAN	55	1	Phosphoprotein																						
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?	
2194	2220	3	3062.4142	0.0126		1	43.51	K.ADEASELACPTPKEDGLAQQQTQLNLR.S	Phospho (ST)	120.39	ADEASELACPT#PKEDGLAQQQTQLNLR	29.6							----------Y----------		----------Y----------	

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																						
267	sp|P28066|PSA5_HUMAN	55	2	Phosphoprotein																						
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?	
21	32	2	1502.7472	0.0051		0	43.27	R.LFQVEYAIEAIK.L	Phospho (Y)	137.13	LFQVEY#AIEAIK	1000							-----N------		-----N------	
6	20	3	1792.7497	0.0079		1	16.02	R.SEYDRGVNTFSPEGR.L	Phospho (Y)	60.32	SEY#DRGVNTFSPEGR	24.76							--N----------		--N----------	

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																						
268	sp|Q8WVB6|CTF18_HUMAN	55	1	Phosphoprotein																						
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?	
862	885	3	2428.1629	0.0106		0	37.83	R.VENSPQVDGSPPGLEGLLGGIGEK.G	Phospho (ST)	149.87	VENSPQVDGS#PPGLEGLLGGIGEK	36.52							---------Y----------		---------N----------	

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																						
269	sp|Q13200|PSMD2_HUMAN	55	2	Phosphoprotein																						
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?	
7	31	3	2540.1994	0.0086		1	33.39	R.DKAPVQPQQSPAAAPGGTDEKPSGK.E	Phospho (ST)	81.06	DKAPVQPQQS#PAAAPGGTDEKPSGK	61.6							---------Y----------		---------Y----------	
9	31	3	2297.0737	0.0048		0	40.8	K.APVQPQQSPAAAPGGTDEKPSGK.E	Phospho (ST)	135.4	APVQPQQS#PAAAPGGTDEKPSGK	100.46							-------Y----------		-------Y----------	

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																						
270	sp|Q7Z460|CLAP1_HUMAN	55	1	Phosphoprotein																						
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?	
598	611	2	1483.6728	0.0061		1	29.28	R.SRSDIDVNAAASAK.S	Phospho (ST)	48.82	SRS#DIDVNAAASAK	33.68							--Y----------		--Y----------	

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																						
271	sp|P21127|CD11B_HUMAN	55	1	Phosphoprotein																						
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?	
274	287	2	1684.7256	0.0064		0	42.5	R.DLLSDLQDISDSER.K	Phospho (ST)	140.74	DLLSDLQDIS#DSER	48.87							---------Y----		---------Y----	

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																						
272	sp|A6NMY6|AXA2L_HUMAN	55	1	Phosphoprotein																						
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?	
11	28	2	1923.8668	0.0053		0	52.67	K.LSLEGDHSTPPSAYGSVK.A	Phospho (Y)	124.64	LSLEGDHSTPPSAY#GSVK	23.34							------------Y----		------------N----	

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																						
273	sp|P21333|FLNA_HUMAN	55	2	Phosphoprotein																						
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?	
2149	2165	3	1889.8876	0.0057		1	30.74	R.RAPSVANVGSHCDLSLK.I	Phospho (ST)	55.47	RAPS#VANVGSHCDLSLK	36.36							---Y----------		---Y----------	
1453	1464	2	1296.5416	0.006		0	24.05	K.CSGPGLSPGMVR.A	Phospho (ST)	69.72	CSGPGLS#PGMVR	60							------Y-----		------Y-----	

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																						
274	sp|Q99426|TBCB_HUMAN	54	2	Phosphoprotein																						
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?	
220	244	2	2809.2894	0.0119		0	38.45	K.YGAFVKPAVVTVGDFPEEDYGLDEI.-	Phospho (Y)	152.89	YGAFVKPAVVTVGDFPEEDY#GLDEI	102.68							------------------N-----		------------------Y-----	
95	103	2	1146.4636	0.0042		0	17.89	R.LGEYEDVSR.V	Phospho (Y)	99.9	LGEY#EDVSR	63.77							---Y-----		---Y-----	

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																						
275	sp|P56693|SOX10_HUMAN	54	2	Phosphoprotein																						
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?	
22	43	2	2034.8894	0.0064		0	43.07	R.CLSPGSAPSLGPDGGGGGSGLR.A	Phospho (ST)	76.16	CLS#PGSAPSLGPDGGGGGSGLR	44.73							--Y----------		--Y----------	
22	53	3	3008.3212	0.0111		1	28.85	R.CLSPGSAPSLGPDGGGGGSGLRASPGPGELGK.V	2 Phospho (ST)	64.5	CLS#PGSAPSLGPDGGGGGSGLRAS#PGPGELGK	26.79	58.67						--Y----------Y--------		--Y----------Y--------	

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																						
276	sp|Q06413|MEF2C_HUMAN	54	2	Phosphoprotein																						
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?	
221	234	2	1568.7058	0.0058		0	25.12	R.NSPGLLVSPGNLNK.N	2 Phospho (ST)	90.86	NS#PGLLVS#PGNLNK	1000							-N-----N------		-N-----N------	
240	251	2	1406.5894	0.0059		0	15.44	K.SPPPMNLGMNNR.K	Phospho (ST)	36.14	S#PPPMNLGMNNR	1000							N----------		N----------	

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																						
277	sp|Q15366|PCBP2_HUMAN	54	1	Phosphoprotein																						
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?	
246	276	4	3477.5585	0.0102		0	27.09	K.LHQLAMQQSHFPMTHGNTGFSGIESSSPEVK.G	Oxidation (M); Phospho (ST)	54.7	LHQLAMQQSHFPMTHGNTGFSGIESSS#PEVK	24.84							----------Y----		----------Y----	

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																						
278	sp|P47914|RL29_HUMAN	54	1	Phosphoprotein																						
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?	
135	149	2	1456.7118	0.0043		0	53.73	K.AQAAAPASVPAQAPK.R	Phospho (ST)	129.84	AQAAAPAS#VPAQAPK	1000							-------Y-------		-------Y-------	

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																						
279	sp|Q9H307|PININ_HUMAN	53	2	Phosphoprotein																						
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?	
374	397	3	2899.2586	0.0082		1	40.68	R.ESEKQQDSQPEEVMDVLEMVENVK.H	Phospho (ST)	76.02	ESEKQQDS#QPEEVMDVLEMVENVK	20.98							-------Y----------		-------N----------	
378	397	3	2426.0506	0.0123		0	36.3	K.QQDSQPEEVMDVLEMVENVK.H	Phospho (ST)	127.23	QQDS#QPEEVMDVLEMVENVK	1000							---Y----------		---N----------	

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																						
280	sp|Q5JTD0|TJAP1_HUMAN	53	1	Phosphoprotein																						
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?	

299		312	2	1621.733		0.0054	0	32.26	R.GSPEEELPLPAFEK.L	Phospho (ST)	85.49	GS#PEEELPLPAFEK	1000						-Y----------	-Y----------
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
281	sp|P05412|JUN_HUMAN		53	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
57		70	2	1550.7662		0.007	0	52.91	K.NSDLLTSPDVGLLK.L	Phospho (ST)	170.01	NSDLLTS#PDVGLLK	28.87						------Y-------	------Y-------					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
282	sp|Q93008|USP9X_HUMAN		52	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
2529		2545	2	1971.8174		0.0076	0	52.33	R.AQENYEGSEEVSPPQTK.D	Phospho (Y)	180.74	AQENY#EGSEEVSPPQTK	73.31						----Y----------	----Y----------					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
283	sp|P02786|TFR1_HUMAN		52	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
7		22	2	1824.8136		0.0053	0	52.22	R.SAFSNLFGGEPLSYTR.F	Phospho (Y)	116.39	SAFSNLFGGEPLSY#TR	32.4						----------Y--	----------Y--					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
284	sp|P53396|ACLY_HUMAN		52	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
470		483	2	1559.7216		0.0049	0	31.02	K.AKPAMPQDSVPSPR.S	Phospho (ST)	85.13	AKPAMPQDSVPS#PR	23.62						----------Y--	----------Y--					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
285	sp|O75643|U520_HUMAN		52	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
222		237	2	1845.6672		0.0061	0	52.1	R.EEASDDDMEGDEAVVR.C	Phospho (ST)	119.46	EEAS#DDDMEGDEAVVR	1000						---Y----------	---Y----------					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
286	sp|Q6XQN6|PNCB_HUMAN		52	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
525		538	2	1536.708		0.0073	0	40.23	R.LQALVNSLCAGQSP.-	Phospho (ST)	142.12	LQALVNSLCAGQS#P	93.74						----------Y--	----------N-					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
287	sp|Q9NQZ2|SAS10_HUMAN		52	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
354		375	2	2475.9474		0.0085	1	54.1	K.TSAAACAVTDLSDDSDFDEKAK.L	2 Phospho (ST)	133.82	TSAAACAVTDLS#DDS#DFDEKAK	79.13	79.31					----------Y--Y-------	----------Y--Y-------					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
288	sp|Q9NVU0|RPC5_HUMAN		52	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
497		529	4	3779.5505		0.0101	1	51.6	R.IKEEPVSEEGEEDEEQEAEEEPMDTSPSGLHSK.L	Phospho (ST)	91.45	IKEEPVS#EEGEEDEEQEAEEEPMDTSPSGLHSK	92.98						------Y------------------------	------Y------------------------					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
289	sp|Q09161|NCBP1_HUMAN		52	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
20		37	3	2168.9338		0.0041	1	36.62	R.KTSDANETEDHLESLICK.V	Phospho (ST)	107.9	KTS#DANETEDHLESLICK	19.84						-Y----------	-Y----------					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
290	sp|Q12874|SF3A3_HUMAN		52	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
471		490	2	2433.0074		0.0065	1	51.57	R.WQPDTEEEYEDSSGNVVNKK.T	Phospho (Y)	163.4	WQPDTEEEY#EDSSGNVVNKK	56.84						---------N----------	---------Y----------					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
291	sp|O43426|SYNJ1_HUMAN		51	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
820		836	2	1960.8368		0.0066	0	53.04	R.SAEDLDLLNASFQDESK.I	Phospho (ST)	160.3	SAEDLDLLNAS#FQDESK	80.68						----------Y------	----------Y------					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
292	sp|Q9UIG0|BAZ1B_HUMAN		51	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
1461		1477	2	1867.754		0.0068	0	51.05	R.LAEDEGDSEPEAVGQSR.G	Phospho (ST)	151.54	LAEDEGDS#EPEAVGQSR	119.6						-------Y---------	-------Y---------					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
293	sp|Q8IVM0|CCD50_HUMAN		51	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
260		290	4	3607.5897		0.011	0	50.97	K.NERPARPPPPIMTDGEDADYTHFTNQQSSTR.H	Phospho (Y)	99.94	NERPARPPPPIMTDGEDADY#THFTNQQSSTR	34.07						----------Y----------	----------Y----------					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
294	sp|Q9UKM9|RALY_HUMAN		51	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
134		141	2	943.4922		0.003	0	23.93	R.LSPVPVPR.A	Phospho (ST)	41.52	LS#PVPVPR	1000						-Y------	-Y------					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
295	sp|Q96I25|SPF45_HUMAN		51	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
150		165	3	2101.7938		0.0076	1	50.66	R.RPDPDSDEDEDYERER.R	Phospho (ST)	109.48	RPDPDS#DEDEDYERER	85.27						-----Y----------	-----Y----------					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
296	sp|Q8N0X7|SPG20_HUMAN		50	2	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
616		636	3	2469.1258		0.0085	0	38.05	K.TATQTGHTLLEDYQIVDNSQR.E	Phospho (Y)	133.88	TATQTGHTLLEDY#QIVDNSQR	57.66						----------N--------	----------Y--------					
615		636	3	2597.2219		0.0096	1	38.73	K.KTATQTGHTLLEDYQIVDNSQR.E	Phospho (Y)	97.67	KTATQTGHTLLEDY#QIVDNSQR	49.8						----------N--------	----------Y--------					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
297	sp|Q9NZT2|OGFR_HUMAN		50	2	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					

309		328	3	2203.9084		0.0065	1	49.53	R.KVEEEGSPGDPDHEASTQGR.T	Phospho (ST)		57.62	KVEEEGS#PGDPDHEASTQGR	49.17						------Y----------	------Y----------
361		380	3	2141.908		0.0065	0	14.54	R.SQGDEAGGHGEDRPEPLSPK.E	Phospho (ST)		69.46	SQGDEAGGHGEDRPEPLS#PK	82.46						----------Y--	----------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
298	sp|Q9UJU6|DBNL_HUMAN	49	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				
149	164	2	1798.833		0.0039	0	49.49	R.FQDVGPQAPVGSVYQK.T	Phospho (Y)	137.07	FQDVGPQAPVGSVY#QK	52.75						----------Y--	----------Y--				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
299	sp|O43815|STRN_HUMAN	49	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				
236	258	3	2654.0284		0.0103	1	49.43	K.FLESAAADFSDEDEDDDVDGREK.S	Phospho (ST)	146.73	FLESAAADFS#DEDEDDDVDGREK	66.99						---------Y----------	---------Y----------				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
300	sp|Q13895|BYST_HUMAN	49	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				
93	110	2	2215.8194		0.0054	0	49.39	R.MPQDGSDDEDEEWPTLEK.A	Oxidation (M); Phospho (ST)	63.59	MPQDGS#DDEDEEWPTLEK	44.19						-----Y----------	-----N----------				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
301	sp|Q6PL18|ATAD2_HUMAN	49	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				
317	332	3	1836.9103		0.0067	0	49.38	R.KPNIFYSGPASPARPR.Y	Phospho (ST)	64.66	KPNIFYSGPAS#PARPR	50.82						---------N-----	---------N-----				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
302	sp|O75607|NPM3_HUMAN	49	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				
2	17	2	1684.7866		0.0045	0	17.2	M.AAGTAAALAFLSQESR.T	Acetyl (Protein N-term); Phospho (ST)	33.25	AAGTAAALAFLS#QESR	28.16						----------N----	----------N----				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
303	sp|P11388|TOP2A_HUMAN	49	2	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				
1521	1531	2	1453.524		0.0067	0	14.92	K.YLEESDEDDLF.-	Phospho (ST)	52.51	YLEES#DEDDLF	52.37						----Y-------	----Y-------				
1374	1385	2	1355.5896		0.0039	0	49.27	K.SVVSDLEADDVK.G	Phospho (ST)	114.37	SVVS#DLEADDVK	27.06						---Y--------	---Y--------				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
304	sp|Q96EZ8|MCRS1_HUMAN	49	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				
275	292	2	2059.8714		0.0091	0	49.25	K.GDQVLNFSDAEDLIDDSK.L	Phospho (ST)	134.22	GDQVLNFS#DAEDLIDDSK	84.7						-------Y---------	-------Y---------				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
305	sp|Q9NWQ8|PAG1_HUMAN	49	3	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				
168	185	2	2212.8634		0.0093	0	26.91	K.DSSSQENMVEDCLYETVK.E	Phospho (Y)	109.66	DSSSQENMVEDCLY#ETVK	57.75						----------Y----	----------Y----				
414	427	2	1732.7014		0.0073	0	43.75	K.ENDYESISDLQQGR.D	Phospho (Y)	143.34	ENDY#ESISDLQQGR	30.7						---Y----------	---Y----------				
351	367	3	2039.8636		0.0089	1	33.83	R.SPSSCNDLYATVKDFEK.T	Phospho (Y)	106.4	SPSSCNDLY#ATVKDFEK	51.17						--------Y--------	--------Y--------				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
306	sp|P16885|PLCG2_HUMAN	49	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				
748	757	2	1260.5448		0.0061	0	48.88	R.DINSLYDVSR.M	Phospho (Y)	131.17	DINSLY#DVSR	40.04						-----Y----	-----Y----				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
307	sp|Q7KZF4|SND1_HUMAN	49	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				
900	910	2	1324.4656		0.0048	0	48.99	R.ADDADEFGYSR.-	Phospho (Y)	118.02	ADDADEFGY#SR	38.42						--------Y--	--------Y--				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
308	sp|Q9ULU4|PKCB1_HUMAN	49	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				
531	550	3	2302.1659		0.0089	1	48.8	K.ELSESVQQQSTPVPLISPKR.Q	Phospho (ST)	74.86	ELSESVQQQSTPVPLIS#PKR	107.06						----------Y---	----------Y---				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
309	sp|P11717|MPRI_HUMAN	49	2	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				
2398	2420	2	2576.1654		0.0124	0	43.34	K.ALSSLHGDDQDSEDEVLTIPEVK.V	Phospho (ST)	151.17	ALSSLHGDDQDS#EDEVLTIPEVK	78.89						----------Y----------	----------Y----------				
2477	2491	2	1833.7912		0.009	0	16.97	K.LVSFHDDSDEDLLHI.-	Phospho (ST)	98.56	LVSFHDDS#DEDLLHI	47.64						-------Y-------	-------Y-------				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
310	sp|Q86V81|THOC4_HUMAN	48	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				
2	14	2	1615.6946		0.0072	1	48.23	M.ADKMDMSLDDIIK.L	Acetyl (Protein N-term); Phospho (ST)	37.9	A!DKMDMS#LDDIIK	1000						------Y------	------N------				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
311	sp|P22059|OSBP1_HUMAN	48	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				
186	212	3	3187.2922		0.0133	1	48.12	K.MLAESDESGDEESVSQTDKTELQNTLR.T	Oxidation (M); 2 Phospho (ST)	84.32	MLAES#DES#GDEESVSQTDKTELQNTLR	38.63	34.6					----Y--Y----------	----Y--Y----------				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
312	sp|P78346|RPP30_HUMAN	48	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				
247	262	3	1864.8094		0.0068	0	47.91	K.KPRPSEGDEDCLPASK.K	Phospho (ST)	95.71	KPRPS#EGDEDCLPASK	75.54						----Y----------	----Y----------				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
313	sp|Q9UKE5|TNIK_HUMAN	48	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?				

638		652	2	1731.7528	0.0064	0	47.6	R.QNSDPTSENPPLPTR.I	Phospho (ST)	137.65	QNS#DPTSENPPLPTR	48.45							--Y----------	--Y----------
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
314	sp|Q5VTR2|BRE1A_HUMAN		47	2	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
125		142	2	2088.9434	0.007	1	40.55	R.KALVVPEPEPDSDSNQER.K	Phospho (ST)	93.12	KALVVPEPEPDSDS#NQER	24.75							----------Y----	----------Y----					
126		142	2	1960.8494	0.0079	0	35.91	K.ALVVPEPEPDSDSNQER.K	Phospho (ST)	105.83	ALVVPEPEPDSDS#NQER	33.7							----------Y----	----------Y----					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
315	sp|Q96QK1|VPS35_HUMAN		47	1	Not annotated																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
782		796	2	1711.7662	0.0069	0	47.4	R.ESPESEGPIYEGLIL.-	Phospho (Y)	119.44	ESPESEGPIY#EGLIL	75.77													
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
316	sp|O95997|PTTG1_HUMAN		47	2	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
158		168	2	1261.6518	0.0047	0	28.07	K.LFQLGPPSPVK.M	Phospho (ST)	86.84	LFQLGPPS#PVK	1000							-------Y---	-------Y---					
2		17	2	1883.8724	0.0059	1	48.81	M.ATLIYVDKENGEPGTR.V	Acetyl (Protein N-term); Phospho (Y)	70.87	ATLIY#VDKENGEPGTR	22.61							----N----------	----N----------					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
317	sp|P28482|MK01_HUMAN		47	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
173		191	3	2302.9381	0.0084	0	28.68	R.VADPDHDHTGFLTEYVATR.W	Phospho (ST); Phospho (Y)	121.31	VADPDHDHTGFLT#EY#VATR	47.47	38.19						----------Y-Y----	----------N-N----					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
318	sp|Q86UK7|ZN598_HUMAN		47	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
296		311	2	1901.7856	0.0064	1	47	R.RNEGVVGGEDYEEVDR.Y	Phospho (Y)	194.87	RNEGVVGGEDY#EEVDR	1000							----------Y-----	----------Y-----					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
319	sp|Q96LD4|TRI47_HUMAN		47	2	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
582		596	3	1676.812	0.0084	1	37.12	R.RGGIPASPIDPFQSR.L	Phospho (ST)	78.89	RGGIPAS#PIDPFQSR	99.68							------Y--------	------N--------					
583		596	2	1520.7078	0.0054	0	22.31	R.GGIPASPIDPFQSR.L	Phospho (ST)	69.69	GGIPAS#PIDPFQSR	66.68							-----Y--------	-----N--------					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
320	sp|O00151|PDLI1_HUMAN		47	2	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
139		166	3	3180.4492	0.0091	0	46.83	R.VITNQYNNPAGLYSSENISNFNNALESK.T	Phospho (Y)	133.7	VITNQYNNPAGLY#SSENISNFNNALESK	24.75							----------Y----------	----------N----------					
315		329	2	1740.8434	0.0059	0	15.76	R.VTPPEGYEVVTVFPK.-	Phospho (Y)	59.09	VTPPEGY#EVVTVFPK	34.49							------Y--------	------N--------					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
321	sp|Q8IWE2|NXP20_HUMAN		47	2	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
162		206	4	4562.9509	0.0161	0	46.69	R.IHGVNSGSSEGAQPNTENGVPEITDAATDQGPAESPPTSPSSASR.G	2 Phospho (ST)	86.92	IHGVNSGSSEGAQPNTENGVPEITDAATDQGPAES#PPTS#PSSASR	19.89	20.05						----------Y--Y-------	----------Y--Y-------					
259		267	2	1113.5286	0.0033	0	15.71	R.TVSLSQMLR.E	Phospho (ST)	44.11	TVS#LSQMLR	24.75							--N------	--N------					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
322	sp|O00267|SPT5H_HUMAN		46	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
653		668	2	1774.7824	0.0075	0	36.86	R.DVTNFTVGGFAPMSPR.I	Phospho (ST)	113.23	DVTNFTVGGFAPMS#PR	112.99							----------Y--	----------Y--					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
323	sp|Q8WX93|PALLD_HUMAN		46	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
1348		1359	2	1372.6354	0.0079	0	35.4	R.YAALSDQGLDIK.A	Phospho (Y)	148.18	Y#AALSDQGLDIK	93.87							N----------	N----------					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
324	sp|Q86YR5|GPSM1_HUMAN		46	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
467		481	2	1837.7546	0.0065	0	46.04	R.APSSDEECFFDLLTK.F	Phospho (ST)	115.85	APS#SDEECFFDLLTK	19.21							--Y----------	--Y----------					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
325	sp|Q15942|ZYX_HUMAN		46	2	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
344		354	2	1116.5626	0.0046	0	17.5	R.SPGAPGPLTLK.E	Phospho (ST)	40.89	S#PGAPGPLTLK	59.14							Y----------	Y----------					
254		272	2	1991.9208	0.005	1	21.14	R.GPPASSPAPAPKFSPVTPK.F	2 Phospho (ST)	58.87	GPPASSPAPAPKFS#PVT#PK	50.25	46.57						----------Y--Y--	----------Y--Y--					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
326	sp|Q5HYJ3|FA76B_HUMAN		46	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
189		202	2	1708.7752	0.0044	0	43.11	K.ISNLSPEEEQGLWK.Q	Phospho (ST)	113.58	ISNLS#PEEEQGLWK	64.56							----Y---------	----Y---------					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
327	sp|Q96GC9|TMM49_HUMAN		46	1	Not annotated																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
214		243	3	3538.4182	0.015	0	45.82	R.LSGAEPDDEEYQEFEEMLEHAESAQDFASR.A	Phospho (Y)	127.33	LSGAEPDDEEY#QEFEEMLEHAESAQDFASR	46.36													
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
328	sp|Q7Z434|MAVS_HUMAN		46	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
219		232	2	1520.746	0.0072	0	45.53	R.GPVSPSVSFQPLAR.S	Phospho (ST)	78.35	GPVS#PSVSFQPLAR	33.7							---Y----------	---Y----------					
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
329	sp|P12270|TPR_HUMAN		45	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?					
2146		2163	3	1930.9024	0.0085	0	31.73	R.TDGFAEAIHSPQVAGVPR.F	Phospho (ST)	94.94	TDGFAEAIHS#PQVAGVPR	57.9							---------Y--------	---------N--------					

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
330	sp|O43164|PJA2_HUMAN	45	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
59	73	2	1756.7516	0.0072	0	45.45	R.AGDDYEVLELDDVPK.E	Phospho (Y)	173.56	AGDDY#EVLELDDVPK	1000						----N----------	----Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
331	sp|Q9Y2Z0|SUGT1_HUMAN	45	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
312	326	2	1863.8458	0.0055	1	45.1	R.LFQQIYSDGSDEVKR.A	Phospho (Y)	157.2	LFQQIY#SDGSDEVKR	28.87						-----Y----------	-----Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
332	sp|Q66K14|TBC9B_HUMAN	45	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
749	768	2	2238.0794	0.0086	0	44.81	R.ALLSSSDDPPAEVDIFELLK.V	Phospho (ST)	113.55	ALLS#SSDDPPAEVDIFELLK	22.85						---N----------	---N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
333	sp|Q6DN90|IQEC1_HUMAN	45	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
511	524	2	1686.7048	0.0009	0	44.79	R.NSWDSPAFSNDVIR.K	Phospho (ST)	129.35	NS#WDSPAFSNDVIR	61.09						-Y----------	-Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
334	sp|Q96B36|AKTS1_HUMAN	45	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
183	194	2	1394.7034	0.0035	0	44.76	K.SLPVSVPVWGFK.E	Phospho (ST)	69.98	S#LPVSVPVWGFK	61.52						Y----------	Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
335	sp|Q8TCJ2|STT3B_HUMAN	45	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
13	30	2	1942.867	0.0063	0	44.6	K.SSLNSSPWSGLMALGNSR.H	Phospho (ST)	90.04	SSLNSSPWSGLMALGNS#R	74.42						----------Y-	----------Y-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
336	sp|Q8TC07|TBC15_HUMAN	44	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
673	687	2	1753.7416	0.0074	0	44.47	R.NDSPTQIPVSSDVCR.L	Phospho (ST)	148.68	NDS#PTQIPVSSDVCR	33.7						--Y----------	--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
337	sp|P11387|TOP1_HUMAN	44	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
2	17	2	1961.8014	0.011	0	25.9	M.SGDHLHNDSQIEADFR.L	Acetyl (Protein N-term); Phospho (ST)	42.96	SGDHLHNDS#QIEADFR	27.7						--------N-------	--------Y-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
338	sp|Q06124|PTN11_HUMAN	44	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
583	594	2	1515.6848	0.0056	0	44.21	R.VYENVGLMQQQK.S	Phospho (Y)	153.94	VY#ENVGLMQQQK	1000						-Y----------	-Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
339	sp|Q9Y6D5|BIG2_HUMAN	44	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
207	229	3	2604.304	0.0075	0	23.66	R.ELEKPIQSKPQSPVIQAAAVSPK.F	2 Phospho (ST)	78.33	ELEKPIQSKPQS#PVIQAAAVS#PK	27.79	88.52					----------Y--------Y--	----------Y--------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
340	sp|O43516|WIPF1_HUMAN	44	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
338	353	2	1688.8164	0.003	0	44.17	R.NLSLSSSTPPLPSPGR.S	Phospho (ST)	74.19	NLS#LSSSTPPLPSPGR	42.65						--Y----------	--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
341	sp|Q5VSL9|FA40A_HUMAN	44	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
333	349	2	1819.8418	0.0066	0	40.23	R.AASPPASASDLIEQQQK.R	Phospho (ST)	69.99	AAS#PPASASDLIEQQQK	41.19						--Y----------	--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
342	sp|Q96PK6|RBM14_HUMAN	44	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
204	212	2	1125.5052	0.0044	0	16.01	R.QPTPPFFGR.D	Phospho (ST)	62.56	QPT#PPFFGR	1000						--Y------	--Y------
616	625	2	1301.6166	0.0038	1	41.96	R.RLSESQLSFR.R	Phospho (ST)	42.67	RLS#ESQLSFR	30.7						--Y-------	--Y-------
579	585	2	905.4518	0.0035	1	20.33	R.TRLSPPR.A	Phospho (ST)	49.29	TRLS#PPR	27.69						---Y---	---Y---

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
343	sp|Q9Y2D5|AKAP2_HUMAN	43	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
141	160	2	2082.9554	0.0084	0	38.88	R.DALGDSLQVPVSPSSTTSSR.C	Phospho (ST)	107.87	DALGDSLQVPVS#PSSTTSSR	30.83						----------Y--------	----------N--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
344	sp|P25788|PSA3_HUMAN	43	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
242	255	2	1734.5876	0.0062	1	43.44	K.ESLKEEDESDDDNM.-	Phospho (ST)	115.36	ESLKEEDES#DDDNM	81.57						--------Y-----	--------N-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
345	sp|Q12792|TWF1_HUMAN	43	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
137	155	2	2154.0354	0.0109	0	43.43	K.YLLSQSSPAPLTAAEEELR.Q	Phospho (ST)	121.98	YLLSQSS#PAPLTAAEEELR	26.38						------Y----------	------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
346	sp|Q08AD1|CAMP2_HUMAN	43	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1311	1322	2	1373.5914	0.005	0	39.31	R.SESVEGFLSPSR.C	Phospho (ST)	108.79	SESVEGFLS#PSR	37.41						--------Y---	--------N---
462	477	3	1778.8252	0.0052	0	14.14	R.SISNEGLTLNNSHVSK.H	Phospho (ST)	31.97	SIS#NEGLTLNNSHVSK	21.21						--Y----------	--N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
347	sp|O14545|TRAD1_HUMAN	43	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
407	420	2	1675.7524	0.007	0	25.45	R.LDSQPQETSPELPR.R	Phospho (ST)	85.73	LDSQPQETS#PELPR	21.51						--------Y-----	--------Y-----
317	329	2	1365.6336	0.0047	0	37.51	R.ALPSLNTGSSSPR.G	Phospho (ST)	97.24	ALPSLNTGSSS#PR	26.38						----------Y--	----------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
348	sp|Q9Y2G3|AT11B_HUMAN	43	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1152	1164	2	1624.625	0.0055	0	42.95	R.SWSASDPFYTNDR.S	Phospho (ST)	101.18	SWS#ASDPFYTNDR	27.7						--Y----------	--N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
349	sp|P18858|DNLI1_HUMAN	43	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
63	79	2	1918.7534	0.0049	0	42.64	R.VLGSEGEEEDEALSPAK.G	2 Phospho (ST)	79.3	VLGS#EGEEEDEALS#PAK	1000						---Y---------Y---	---Y---------Y---

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
350	sp|Q01581|HMCS1_HUMAN	42	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
469	498	4	3259.5633	0.0123	0	41.53	R.RPTPNDDTLDEGVGLVHSNIATEHIPSPAK.K	Phospho (ST)	79.15	RPTPNDDTLDEGVGLVHSNIATEHIPS#PAK	33.79						----------Y---	----------Y---

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
351	sp|Q9HCH0|NCK5L_HUMAN	41	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
464	478	2	1596.771	0.0049	0	41.3	K.SPSPGGPQLSPQLPR.N	Phospho (ST)	77.25	SPSPGGPQLS#PQLPR	53.3						---------Y-----	---------Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
352	sp|Q9UHB6|LIMA1_HUMAN	41	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
350	366	3	1979.9518	0.0052	0	30.13	K.SEVQQPVHPKPLSPDSR.A	Phospho (ST)	86.25	SEVQQPVHPKPLS#PDSR	54.87						----------Y----	----------Y----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
353	sp|Q14814|MEF2D_HUMAN	41	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
119	129	2	1371.624	0.0057	1	37.01	R.RASEELDGLFR.R	Phospho (ST)	67.72	RAS#EELDGLFR	1000						--Y---------	--Y---------
178	188	2	1329.6866	0.0061	0	24.66	R.LLSPQQPALQR.N	Phospho (ST)	75.96	LLS#PQQPALQR	1000						--Y---------	--Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
354	sp|Q9NQ55|SSF1_HUMAN	41	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
356	369	2	1439.5984	0.0055	0	41.01	R.VGGSDEEASGIPSR.T	Phospho (ST)	96.01	VGGS#DEEASGIPSR	46.49						---Y----------	---Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
355	sp|Q9NZJ4|SACS_HUMAN	41	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1774	1783	2	1238.6098	0.0038	0	19.53	R.IADLQSPLFR.G	Phospho (ST)	88.15	IADLQS#PLFR	1000						-----N----	-----Y----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
356	sp|Q9NS69|TOM22_HUMAN	41	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
2	22	2	2083.9914	0.0088	0	40.93	M.AAAVAAAGAGEPQSPDELLPK.G	Acetyl (Protein N-term); Phospho (ST)	40.41	A!AAVAAAGAGEPQS#PDELLPK	1000						----------Y-------	----------N-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
357	sp|P35659|DEK_HUMAN	40	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
30	50	3	2721.928	0.0095	1	40.44	R.EESEEEEDEDDEEEEEEEKEK.S	Phospho (ST)	71.14	EES#EEEEDEDDEEEEEEEKEK	1000						--Y----------	--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
358	sp|Q92945|FUBP2_HUMAN	40	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
178	190	2	1434.6426	0.0035	0	15.08	K.VQISPDSGGLPER.S	Deamidated (NQ); Phospho (ST)	63.73	VQIS#PDSGGLPER	20.91						---Y---------	---Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
359	sp|O75122|CLAP2_HUMAN	40	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
591	607	2	1809.8472	0.0075	0	40.37	R.VLNTGSDVEEAVADALK.K	Phospho (ST)	151.33	VLNTGS#DVEEAVADALK	28.5						-----Y----------	-----Y----------
1018	1033	2	2002.8094	0.0109	0	25.15	R.DYNPYNYSDSISPFNK.S	Phospho (ST)	100.8	DYNPYNYSDSIS#PFNK	30.7						----------Y----	----------Y----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
360	sp|P47712|PA24A_HUMAN	40	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
726	736	2	1300.5532	0.005	0	18.53	R.CSVSLSNVEAR.R	Phospho (ST)	65.06	CS#VSLSNVEAR	30.83						-Y---------	-Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
361	sp|O95453|PARN_HUMAN	40	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
555	567	2	1457.6714	0.0051	1	24.16	R.NNSFTAPSTVGKR.N	Phospho (ST)	56.73	NNS#FTAPSTVGKR	37.41						--Y---------	--Y---------
555	566	2	1301.5698	0.0046	0	15.94	R.NNSFTAPSTVGK.R	Phospho (ST)	34.3	NNS#FTAPSTVGK	23.65						--Y---------	--Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
362	sp|O75030|MITF_HUMAN	40	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
401	420	3	2186.062	0.0065	0	39.85	R.AHGLSLIPSTGLCSPDLVNR.I	Phospho (ST)	124.36	AHGLSLIPSTGLCS#PDLVNR	93.16						----------Y------	----------Y------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
363	sp|O15014|ZN609_HUMAN	40	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1053	1061	2	1022.5096	0.0047	0	30.61	K.APSLTDLVK.S	Phospho (ST)	78.36	APS#LTDLVK	28.5						--Y------	--Y------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?

364	sp|Q6A1A2|PDPK2_HUMAN		40		1	Not annotated																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?		
212	230		2	2133.0114	0.0083		0	39.51	R.ANSFVGTAQYVSPELLTEK.S	Phospho (ST)	81.95	ANS#FVGTAQYVSPELLTEK	25.37										
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
365	sp|O43491|E41L2_HUMAN		39		2	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?		
762	786		3	3026.3482	0.0089		1	29.01	R.VTEGTIREEQEYEEEVEEEPRPAAK.V	Phospho (Y)	156.87	VTEGTIREEQEY#EEEVEEEPRPAAK	30.6						----------Y----------	----------Y----------		
617	625		2	1143.4996	0.0035		0	17.79	R.VEGDNIYVR.H	Phospho (Y)	80.46	VEGDNIY#VR	1000						------Y--	------Y--		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
366	sp|Q9H0C8|ILKAP_HUMAN		39		1	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?		
1	20		3	2320.0627	0.0068		1	29.03	-.MDLFGDLPEPERSPRPAAGK.E	Acetyl (Protein N-term); Oxidation (M); Phospho (ST)	30.57	M!!DLFGDLPEPERS#PRPAAGK	1000						----------Y-------	----------Y-------		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
367	sp|P26358|DNMT1_HUMAN		39		1	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?		
698	716		2	2223.8474	0.0072		0	37.14	K.EADDDEEVDDNIPEMPSPK.K	Phospho (ST)	136.77	EADDDEEVDDNIPEMPS#PK	1000						----------Y--	----------Y--		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
368	sp|O43865|SAHH2_HUMAN		39		1	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?		
21	36		3	1940.8543	0.0064		1	28.73	K.EIEDAEKYSFMATVTK.A	Phospho (Y)	91.9	EIEDAEKY#SFMATVTK	22.01						-------Y--------	-------Y--------		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
369	sp|Q13561|DCTN2_HUMAN		39		2	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?		
79	96		2	1997.8376	0.0047		0	30.9	R.TGYESGEYEMLGEGLGVK.E	Phospho (Y)	131.24	TGYESGEY#EMLGEGLGVK	34.46						-------Y----------	-------N----------		
6	14		2	1054.4892	0.0044		0	28.09	K.YADLPGIAR.N	Phospho (Y)	78.75	Y#ADLPGIAR	1000						N--------	N--------		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
370	sp|Q9UQC2|GAB2_HUMAN		39		1	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?		
532	547		2	1894.9516	0.0075		1	32.76	R.NNTVIDELPFKSPITK.S	Phospho (ST)	97.66	NNTVIDELPFKS#PITK	30.66						----------Y----	----------Y----		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
371	sp|Q2VIQ3|KIF4B_HUMAN		39		1	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?		
1034	1045		2	1546.671	0.0084		0	38.98	K.FLEQSMDIEDLK.Y	Phospho (ST)	96.23	FLEQS#MDIEDLK	1000						----Y-------	----Y-------		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
372	sp|Q9BXB4|OSB11_HUMAN		39		1	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?		
187	202		3	1867.8802	0.0071		0	38.93	R.RPSQNAISFFNVGHSK.L	Phospho (ST)	128.8	RPS#QNAISFFNVGHSK	56.62						--Y----------	--Y----------		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
373	sp|Q9UHD8|SEPT9_HUMAN		39		1	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?		
30	45		2	1896.8196	0.0054		0	38.53	R.SFEVEEVETPNSTPPR.R	Phospho (ST)	129.09	S#FEVEEVETPNSTPPR	71.28						Y----------	Y----------		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
374	sp|Q9UKJ3|GPTC8_HUMAN		38		2	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?		
730	745		3	1606.7566	0.0061		0	38.5	R.GPKPEPPGSGSPAPPR.R	Phospho (ST)	109.14	GPKPEPPGSGS#PAPPR	42.21						----------Y-----	----------N-----		
1105	1118		2	1592.7512	0.0066		0	17.87	R.KPSVSEEVQATPNK.A	Phospho (ST)	32.08	KPS#VSEEVQATPNK	21.3						--Y----------	--N----------		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
375	sp|Q13813|SPTA2_HUMAN		38		1	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?		
1153	1181		3	3345.4762	0.0158		0	38.3	K.VAEDLESEGLMAEEVQAVQQQEVYGMMPR.D	Phospho (Y)	112.34	VAEDLESEGLMAEEVQAVQQQEVY#GMMPR	90.11						----------Y-----	----------Y-----		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
376	sp|P31350|RIR2_HUMAN		38		1	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?		
6	23		3	2037.0982	0.007		0	25.46	R.VPLAPITDPQQLQLSPLK.G	Phospho (ST)	121.02	VPLAPITDPQQLQLS#PLK	149.98						----------Y---	----------Y---		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
377	sp|Q9Y6M1|IF2B2_HUMAN		38		1	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?		
152	168		2	1979.8928	0.0051		0	29.38	K.ISYIPDEEVSSPSPPQR.A	Phospho (ST)	110.31	ISYIPDEEVSS#PSPPQR	24.75						----------Y------	----------Y------		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
378	sp|P51149|RAB7A_HUMAN		38		1	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?		
70	79		2	1266.5858	0.006		0	38.08	R.FQSLGVAFYR.G	Phospho (ST)	101.04	FQS#LGVAFYR	91						--Y-------	--Y-------		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
379	sp|Q9ULX3|NOB1_HUMAN		38		1	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?		
198	215		2	1998.8274	0.0066		1	37.92	R.KDDSDDDGGGWITPSNIK.Q	Phospho (ST)	140.34	KDDS#DDDGGGWITPSNIK	117.16						---Y----------	---N----------		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
380	sp|Q99952|PTN18_HUMAN		38		1	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?		
308	321		2	1775.7668	0.0079		0	37.91	K.ENCAPLYDDALFLR.T	Phospho (Y)	85.76	ENCAPLY#DDALFLR	1000						------N-------	------N-------		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
381	sp|O00418|EF2K_HUMAN		38		1	Phosphoprotein																	

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
2	20	3	2194.9972	0.0076	1	26.24	M.ADEDLIFRLEGVDGGQSPR.A	Acetyl (Protein N-term); Phospho (ST)	18.88	A!DEDLIFRLEGVDGGQS#PR	1000						----------Y--	----------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
382	sp|Q13523|PRP4B_HUMAN	38	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
832	853	2	2516.1154	0.0111	0	37.83	K.LCDFGSASHVADNDITPYLVSR.F	Phospho (Y)	127.93	LCDFGSASHVADNDITPY#LVSR	27.73						----------Y----	----------Y----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
383	sp|Q9HCN4|GPN1_HUMAN	38	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
327	346	3	2355.8575	0.0075	0	16.21	R.GTLDEEDEEADSDTDDIDHR.V	Phospho (ST)	58.78	GTLDEEDEEADS#DTDDIDHR	20.12						----------Y--------	----------Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
384	sp|Q71RC2|LARP4_HUMAN	38	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
643	671	5	3238.5031	0.014	1	28.61	R.SNVVSPTKNEDNGAPENSVEKPHEKPEAR.A	Phospho (ST)	73.79	SNVVS#PTKNEDNGAPENSVEKPHEKPEAR	19.79						----Y----------	-----N----------
573	592	3	2175.0637	0.0064	0	27.64	K.DGLNQTTIPVSPPSTTKPSR.A	Phospho (ST)	65.29	DGLNQTTIPVS#PPSTTKPSR	20.81						----------Y----------	----------N---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
385	sp|O95239|KIF4A_HUMAN	38	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
799	806	2	1031.4728	0.004	0	22.56	R.TFSLTEVR.G	Phospho (ST)	54.77	TFS#LTEVR	21.3						--Y-----	--Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
386	sp|Q9H0D6|XRN2_HUMAN	38	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
495	510	2	1975.714	0.0056	1	37.57	R.KAEDSDSEPEPEDNVR.L	2 Phospho (ST)	120.1	KAEDS#DS#EPEPEDNVR	1000						----Y-Y---------	----Y-Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
387	sp|Q13242|SFRS9_HUMAN	38	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
210	221	2	1613.6148	0.0043	0	17.18	R.GSPHYFSPFRPY.-	2 Phospho (ST)	53.22	GS#PHYFS#PFRPY	24.76	24.75					-Y----Y-----	-Y----Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
388	sp|Q16555|DPYL2_HUMAN	38	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
497	511	2	1699.7582	0.0054	0	37.51	R.GLYDGPVCEVSVTPK.T	Phospho (ST)	76.84	GLYDGPVCEVSVT#PK	24.75						----------Y--	----------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
389	sp|Q2KHR2|RFX7_HUMAN	37	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1079	1093	2	1696.8258	0.0073	0	37.43	R.NLSGSTLYPVSNIPR.S	Phospho (ST)	124.97	NLS#GSTLYPVSNIPR	30.7						--Y----------	--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
390	sp|Q14135|VGLL4_HUMAN	37	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
138	157	3	2118.0166	0.0059	0	37.25	K.NSLDASRPAGLSPTLTPGER.Q	Phospho (ST)	99.61	NSLDASRPAGLS#PTLTPGER	25.78						----------Y--------	----------Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
391	sp|P08651|NFIC_HUMAN	37	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
312	327	2	1856.8066	0.0051	1	26.47	R.NWTEDMEGGISSPVKK.T	Phospho (ST)	120.54	NWTEDMEGGISS#PVKK	22.85						----------N-----	----------Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
392	sp|Q16204|CCDC6_HUMAN	37	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
235	246	2	1422.6002	0.0057	0	17.44	K.LDQPVSAPPSPR.D	2 Phospho (ST)	70.74	LDQPVS#APPS#PR	1000						-----Y---Y--	-----Y---Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
393	sp|Q8NDI1|EHBP1_HUMAN	37	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
164	179	2	1916.709	0.0083	0	36.69	K.ATDEDMQSLASLMSMK.Q	2 Phospho (ST)	106.57	ATDEDMQS#LAS#LMSMK	67.87	41.33					-------Y--Y-----	-------Y--Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
394	sp|P51116|FXR2_HUMAN	37	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
598	617	3	2295.9835	0.0061	1	24.24	R.TDGSISGDRQPVTVADYISR.A	2 Phospho (ST)	79.6	TDGS#IS#GDRQPVTVADYISR	20.91	23.84					----Y-Y----------	----Y-Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
395	sp|Q7Z5L2|GIDRP_HUMAN	37	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
213	222	2	1357.673	0.0048	0	36.62	K.VLEILYEFPR.V	Phospho (Y)	161.82	VLEILY#EFPR	1000							

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
396	sp|P04818|TYSY_HUMAN	37	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
127	140	2	1731.7356	0.0062	0	36.6	R.EEGDLGPVYGFQWR.H	Phospho (Y)	84.61	EEGDLGPVY#GFQWR	1000						--------N-----	--------N-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
397	sp|Q12996|CSTF3_HUMAN	37	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
686	709	4	2845.2665	0.0109	1	23.99	K.RPNEDSDEDEEKGAVVPPVHDIYR.A	Phospho (ST)	77.4	RPNEDS#DEDEEKGAVVPPVHDIYR	107.96						-----Y----------	-----Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
398	sp|P35269|T2FA_HUMAN	36	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
383	402	3	2077.8526	0.0059	0	34.48	R.GNSRPGTPSAEGGSTSSTLR.A	2 Phospho (ST)	75.86	GNS#RPGT#PSAEGGSTSSTLR	33.61	27.19					--Y---Y----------	--Y---Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
399	sp|P16402|H13_HUMAN	36	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
2	17	2	1713.8268	0.0043	0	24.16	M.SETAPLAPTIPAPAEK.T	Acetyl (Protein N-term); Phospho (ST)	39.36	S#ETAPLAPTIPAPAEK	19.33						--Y----------	--N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
400	sp|Q96G74|OTUD5_HUMAN	36	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
63	80	3	1824.9103	0.0067	0	26.07	R.ASPPPQGPLPGPPGALHR.W	Phospho (ST)	32.22	AS#PPPQGPLPGPPGALHR	1000						-Y----------	-Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
401	sp|Q9H788|SH24A_HUMAN	36	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
313	324	2	1398.6454	0.0063	0	35.96	R.TLSSSAQEDIIR.W	Phospho (ST)	89.58	TLS#SSAQEDIIR	20.35						--Y---------	--Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
402	sp|Q5JTV8|TOIP1_HUMAN	36	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
212	236	3	2835.1321	0.0077	0	27.94	K.VNFSEEGETEEDDQDSSHSSVTTVK.A	Phospho (ST)	44.98	VNFSEEGET#EEDDQDSSHSSVTTVK	20.27						---------Y----------	---------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
403	sp|O00161|SNP23_HUMAN	36	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
27	40	2	1506.7758	0.0064	0	35.82	R.ILGLAIESQDAGIK.T	Phospho (ST)	116.8	ILGLAIES#QDAGIK	1000						-------Y------	-------Y------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
404	sp|Q13206|DDX10_HUMAN	36	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
829	843	3	1706.6968	0.0071	0	35.76	R.SNSEVEDVGPTSHNR.K	Phospho (ST)	98.57	SNS#EVEDVGPTSHNR	20.91						--N----------	--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
405	sp|Q6ZU21|YB019_HUMAN	36	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
431	438	2	929.4298	0.0079	1	35.1	K.KVSSSTNK.N	Phospho (ST)	60.8	KVS#SSTNK	38.42							

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
406	sp|Q8WVT3|TTC15_HUMAN	36	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
182	194	2	1302.528	0.0039	0	35.62	K.SPSFGGASEASAR.T	Phospho (ST)	47.14	SPS#FGGASEASAR	27.7						--Y----------	--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
407	sp|P19174|PLCG1_HUMAN	35	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1253	1261	2	1308.5224	0.0048	0	30.18	R.YQQPFEDFR.I	Phospho (Y)	105.78	Y#QQPFEDFR	1000						Y--------	Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
408	sp|O43683|BUB1_HUMAN	35	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
596	613	3	1940.8768	0.0098	0	35.29	K.SPGDFTSAAQLASTPFHK.L	Phospho (ST)	58.19	S#PGDFTSAAQLASTPFHK	23.31						Y----------	Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
409	sp|P53367|ARFP1_HUMAN	35	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
359	373	2	1748.8092	0.007	1	35.26	K.LKTPGVDAPSWLEEQ.-	Phospho (ST)	142.29	LKT#PGVDAPSWLEEQ	93.67						--Y----------	--N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
410	sp|O75592|MYCB2_HUMAN	35	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
3465	3478	2	1512.687	0.0049	0	33.73	R.VNSGDTEVGSSLLR.H	Phospho (ST)	85.33	VNS#GDTEVGSSLLR	38.72						--Y----------	--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
411	sp|Q13573|SNW1_HUMAN	35	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
2	23	3	2537.2015	0.0077	0	22.35	M.ALTSFLPAPTQLSQDQLEAEEK.A	Acetyl (Protein N-term); Phospho (ST)	39.72	ALTSFLPAPTQLS#QDQLEAEEK	20.8						----------N---------	----------N---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
412	sp|Q6P5R6|RL22L_HUMAN	35	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
108	122	2	1899.6648	0.0077	0	35.12	R.YFQISQDEDESESED.-	Phospho (ST)	137.15	YFQISQDEDES#ESED	30.7						---------Y----	---------Y----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
413	sp|P29966|MARCS_HUMAN	35	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
166	173	2	992.4768	0.0036	1	27.82	K.LSGFSFKK.N	Phospho (ST)	57.05	LSGFS#FKK	35.82						----Y---	----Y---

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
414	sp|Q13595|TRA2A_HUMAN	35	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
200	232	4	2870.2549	0.0132	0	24.76	R.AHTPTPGIYMGRPTHSGGGGGGGGGGGGGGR.R	Phospho (ST)	73.22	AHT#PTPGIYMGRPTHSGGGGGGGGGGGGGR	25.37						--Y----------	--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
415	sp|Q02880|TOP2B_HUMAN	35	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1516	1532	2	1951.7896	0.0043	0	31.63	K.VVEAVNSDSDSEFGIPK.K	2 Phospho (ST)	172.07	VVEAVNS#DS#DSEFGIPK	48.99	24.84					------Y-Y--------	------Y-Y--------
1574	1599	3	3016.3492	0.0112	1	25.85	K.KTSFDQDSDVDIFPSDFPTEPPSLPR.T	Phospho (ST)	97.46	KTSFDQDS#DVDIFPSDFPTEPPSLPR	22.24						-------Y----------	-------Y----------
1515	1532	2	2079.8874	0.0072	1	18.52	K.KVVEAVNSDSDSEFGIPK.K	2 Phospho (ST)	95.81	KVVEAVNS#DS#DSEFGIPK	34.49	30.83					-------Y-Y--------	-------Y-Y--------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
416	sp|P30050|RL12_HUMAN	35	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
32	40	2	960.508	0.0035	0	34.63	K.IGPLGLSPK.K	Phospho (ST)	70.51	IGPLGLS#PK	1000						------Y--	------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
417	sp|Q9Y2X7|GIT1_HUMAN	34	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
359	372	2	1610.7612	0.006	0	28.2	K.SLSSPTDNLELSLR.S	Phospho (ST)	125.48	SLSSPT#DNLELSLR	24.24						---Y----------	---Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
418	sp|Q8IYB7|DI3L2_HUMAN	34	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
859	885	3	2963.2054	0.0112	1	34.45	K.RPGTQGHLGPEKEEEESDGEPEDSSTS.-	Phospho (ST)	88.18	RPGTQGHLGPEKEEEES#DGEPEDSSTS	49.9						----------Y----------	----------N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
419	sp|Q96PE2|ARHGH_HUMAN	34	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
418	429	2	1269.58	0.0046	0	34.36	R.SPSFGAGEGLLR.S	Phospho (ST)	60.85	SPS#FGAGEGLLR	33.68						--N---------	--N---------
733	741	2	1091.506	0.0048	0	20.68	R.SLSDPIPQR.H	Phospho (ST)	63.82	SLS#DPIPQR	21.3						--N------	--N------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
420	sp|P29320|EPHA3_HUMAN	34	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
930	945	2	1898.8064	0.0055	0	32.57	K.EIFTGVEYSSCDTIAK.I	Phospho (ST)	103.45	EIFTGVEY#SSCDTIAK	26.38						--------N-------	--------N-------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
421	sp|P27361|MK03_HUMAN	34	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
190	208	2	2330.9694	0.0084	0	37.76	R.IADPEHDHTGFLTEYVATR.W	Phospho (ST); Phospho (Y)	144.73	IADPEHDHTGFLT#EY#VATR	46.68	53.24					--------Y-----Y----	--------Y-----Y----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
422	sp|A2A3N6|PIPSL_HUMAN	34	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
285	298	2	1690.7152	0.0065	0	34.11	R.EPLSSETQYSVDTR.R	Phospho (Y)	80.16	EPLSSETQY#SVDTR	22.85							

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
423	sp|Q9P289|MST4_HUMAN	34	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
2	26	3	2813.323	0.0134	0	34.07	M.AHSPVAVQVPGMQNNIADPEELFTK.L	Acetyl (Protein N-term); Phospho (ST)	34.87	AHS#PVAVQVPGMQNNIADPEELFTK	44.1						--Y----------	--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
424	sp|Q86YP4|P66A_HUMAN	34	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
97	116	3	2429.0212	0.0146	0	33.97	R.RPPSPDVIVLSDNEQPSSPR.V	3 Phospho (ST)	126.64	RPPS#PDVIVLS#DNEQPSS#PR	131.08	73.89	22.85				---Y------Y------Y--	---Y------Y------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
425	sp|P16333|NCK1_HUMAN	34	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
104	114	2	1405.6404	0.0052	0	24.41	R.LYDLNMPAYVK.F	Phospho (Y)	92.5	LY#DLNMPAYVK	81.57						-Y---------	-Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
426	sp|P51608|MECP2_HUMAN	34	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
62	82	2	2008.8694	0.0068	0	32.1	K.AETSEGSGSAPAVPEASASPK.Q	Phospho (ST)	95.23	AETSEGSGSAPAVPEASAS#PK	52.75						----------Y--	----------Y--

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
427	sp|Q13404|UB2V1_HUMAN	34	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
136	147	2	1468.5754	0.0061	0	33.74	K.LPQPPEGQCYSN.-	Phospho (ST)	72.47	LPQPPEGQCYS#N	28.87						----------Y-	----------N-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
428	sp|O75448|MED24_HUMAN	34	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
860	877	2	2025.8934	0.0043	0	33.68	R.LLSSNEDDANILSSPTDR.S	Phospho (ST)	133.88	LLS#SNEDDANILSSPTDR	32.4						--Y----------	--Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
429	sp|O60271|JIP4_HUMAN	33	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
199	222	3	2664.3097	0.0132	0	33.41	K.ERPISLGIFPLPAGDGLLTPDAQK.G	2 Phospho (ST)	99.43	ERPIS#LGIFPLPAGDGLLT#PDAQK	1000						----Y----------Y-----	----Y----------Y-----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
430	sp|O14617|AP3D1_HUMAN	33	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
655	667	3	1617.6847	0.0063	0	33.28	K.HRPSEADEEELAR.R	Phospho (ST)	48.78	HRPS#EADEEELAR	1000						---Y---------	---Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
431	sp|Q9Y6E0|STK24_HUMAN	33	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
189	204	2	1915.9004	0.0061	0	33.21	R.NTFVGTPFWMAPEVIK.Q	Phospho (ST)	93.04	NT#FVGTPFWMAPEVIK	79.99						-Y----------	-Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
432	sp|Q9UJ70|NAGK_HUMAN	33	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
70	85	2	1640.7114	0.0071	0	33.05	R.SLGLSLSGGDQEDAGR.I	Phospho (ST)	94.94	SLGLSLS#GGDQEDAGR	24.84						------Y---------	------Y---------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
433	sp|Q6PD74|AAGAB_HUMAN	33	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
294	315	3	2639.0002	0.0078	1	33.02	K.AFWMAIGGDRDEIEGLSSDEEH.-	Oxidation (M); 2 Phospho (ST)	62.9	AFWM!AIGGDRDEIEGLS#S#DEEH	1000						----------YY----	----------YY----

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
434	sp|Q15022|SUZ12_HUMAN	33	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
538	555	2	2149.8574	0.0064	0	33.02	K.ASMSEFLESEDGEVEQQR.T	Phospho (ST)	118.08	ASMSEFLES#EDGEVEQQR	38.7						---N----------	---N----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
435	sp|Q29RF7|PDS5A_HUMAN	33	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
1299	1315	2	1634.7338	0.0037	0	32.7	R.AAVGQESPGGLEAGNAK.A	Phospho (ST)	97.73	AAVGQES#PGGLEAGNAK	1000						------Y----------	------Y----------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
436	sp|Q14005|IL16_HUMAN	33	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
584	590	2	942.4622	0.0047	0	32.7	K.SFEILVR.K	Phospho (ST)	57.29	S#FEILVR	1000						N------	N------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
437	sp|P27987|IP3KB_HUMAN	33	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
40	52	2	1432.6184	0.0032	0	32.67	R.AVLSPGSVFSPGR.G	2 Phospho (ST)	74.17	AVLS#PGSVFS#PGR	30.66	31.87					---Y-----Y---	---Y-----Y---

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
438	sp|Q14153|FA53B_HUMAN	32	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
165	173	2	1046.4472	0.0039	0	29.68	R.SSSFSLPSR.A	Phospho (ST)	75.73	SSS#FSLPSR	30.7						--Y------	--Y------

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
439	sp|Q8IY81|RRMJ3_HUMAN	32	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
683	691	2	1172.4906	0.0043	0	17.8	R.DLIDNSFNR.Y	Phospho (ST)	65.96	DLIDNS#FNR	1000						-----Y---	-----Y---

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
440	sp|O95297|MPZL1_HUMAN	31	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?
258	267	2	1217.5384	0.0055	0	22.59	K.SESVVYADIR.K	Phospho (Y)	132.14	SESVVY#ADIR	68.56						-----Y----	-----Y----

Supplementary Table S3: Phosphoproteins with the corresponding phosphopeptides and localized phosphosites from solprotSP (*S.pombe*) and from SKMel (human melanoma) samples
(*) Phosphorylated amino acid **X** is displayed as **X#**

***Human melanoma* - Glu-C digest of large tryptic peptides**

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
1	sp|Q04637|IF4G1_HUMAN	243	5	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1073	1096	4	2622.3013	0.0058	1	19.78	K.ITKPGSIDSNNQLFAPGGRLSWGK.G	Phospho (ST)	100.26	ITKPGSIDSNNQLFAPGGRLS#WGK	69.45						----------Y---	----------Y---	K.ITKPGSIDSNNQLFAPGGRLSWGKGSSGGSSGAKPSDAASEAARPATSTLNR.F
403	422	2	2067.9834	0.0069	0	23.87	E.LLNGAPSPPAVDLSPVSEPE.E	Phospho (ST)	83.32	LLNGAPS#PPAVDLSPVSEPE	48.76						------N----------	------N----------	R.LSPEPTPLAEPILEVEVTLSKPVPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDLEPEVESSPELAPPPACPSESPVPIAPTAQPEELLNGAPSPPAVDLSPVSEPEEQAK.E
380	401	3	2305.072	0.0018	1	15.65	E.LAPPPACPSESPVPIAPTAQPE.E	Phospho (ST)	82.81	LAPPPACPSES#PVPIAPTAQPE	19.55						----------N----------	----------N----------	R.LSPEPTPLAEPILEVEVTLSKPVPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDLEPEVESSPELAPPPACPSESPVPIAPTAQPEELLNGAPSPPAVDLSPVSEPEEQAK.E
307	326	2	2288.0994	0.0017	1	30.14	E.TGEPYRLSPEPTPLAEPILE.V	Phospho (ST)	129.42	TGEPYRLS#PEPTPLAEPILE	36.99						-------N----------	-------Y----------	R.ETGEPYRLSPEPTPLAEPILEVEVTLSKPVPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDLEPEVESSPELAPPPACPSESPVPIAPTAQPEELLNGAPSPPAVDLSPVSEPEEQAK.E
402	422	2	2197.0214	0.0023	1	57.99	E.ELLNGAPSPPAVDLSPVSEPE.E	Phospho (ST)	140.49	ELLNGAPS#PPAVDLSPVSEPE	63.13						-------N----------	-------N----------	R.LSPEPTPLAEPILEVEVTLSKPVPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDLEPEVESSPELAPPPACPSESPVPIAPTAQPEELLNGAPSPPAVDLSPVSEPEEQAK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
2	sp|Q13263|TIF1B_HUMAN	239	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
525	555	3	2780.3602	0.0034	1	47.37	R.GAAAAATGQPGTAPAGTPGAPPLAGMAIVKE.E	Phospho (ST)	187.02	GAAAAATGQPGTAPAGT#PGAPPLAGMAIVKE	57.66						----------Y----------	----------Y----------	R.GAAAAATGQPGTAPAGTPGAPPLAGMAIVKEEETEAAIGAPPTATEGPETKPVLMALAEGPGAEGPR.L
33	57	2	2083.8734	0.004	0	65.19	R.STAPSAAASASASAAASSPAGGGAE.A	Phospho (ST)	149.34	STAPSAAASASASAAASS#PAGGGAE	38.42						----------Y-------	----------Y-------	R.STAPSAAASASASAAASSPAGGGAEALELLEHCGVCR.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
3	sp|Q9H1E3|NUCKS_HUMAN	174	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
135	150	2	1997.6204	0.0042	1	63.74	E.DFLMEDDDDSDYGSSK.K	Phospho (ST); Phospho (Y)	159.2	DFLMEDDDS#DY#GSSK	66.6	28.5					---------Y-N----	---------Y-N----	K.DSGSDEDFLMEDDDDSDYGSSKK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
4	sp|Q00839|HNRPU_HUMAN	173	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
95	105	2	1214.4554	0.0028	0	35.78	E.GISALDGDQME.L	Phospho (ST)	97.81	GIS#ALDGDQME	1000						--N--------	--N--------	R.SGAGLEQEAAAGGDEEEEEEEEEEEEGISALDGDQMELGEENGAAGADSGPMEEEEAASEDENGDDQGFQEGEDELGDEEEGAGDENGHGEQQPQPPATQQQQPQQQR.G
47	69	3	2221.9453	0.003	0	53.64	E.AGGRPAMEPGNGSLDLGGDSAGR.S	Deamidated (NQ); Phospho (ST)	83.97	AGGRPAMEPGNGS#LDLGGDSAGR	36.71						----------Y----------	----------Y----------	R.LQAALDDEEAGGRPAMEPGNGSLDLGGDSAGRSGAGLEQEAAAGGDEEEEEEEEEEGISALDGDQMELGEENGAAGADSGPMEEEEAASEDENGDDQGFQEGEDELGDEEEGAGDENGHGEQQPQPPATQQQQPQQQR.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
5	sp|Q14566|MCM6_HUMAN	172	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
679	701	2	2262.9054	-0.0012	0	43.33	E.GAGGINGHADSPAPVNGINGYNE.D	3 Deamidated (NQ); Phospho (ST)	28.42	GAGGINGHADS#PAPVNGINGYNE	36.15						----------N----------	----------N----------	R.VETPDVNLDQEEEIQMEVDEGAGGINGHADSPAPVNGINGYNEDINQESAPK.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
6	sp|Q7Z6Z7|HUWE1_HUMAN	158	4	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
3906	3937	4	3652.6773	0.0116	1	14.15	E.SQLAHIKDEPPPLSPAPLTPATPSSLDPFFSR.E	3 Phospho (ST)	91.41	SQLAHIKDEPPPLS#PAPLT#PAT#PSSLDPFFSR	36.35	36.71	35.28				----------Y----Y--Y----------	----------Y----Y--Y----------	R.ESQLAHIKDEPPPLSPAPLTPATPSSLDPFFSRERPSSMHISSSLPPDTQK.F
1976	1992	2	2106.9174	0.0093	0	93.92	E.VGQLLQDMGDDVYQQYR.S	Phospho (Y)	204.22	VGQLLQDMGDDVY#QQYR	97.19						----------N----	----------N----	K.SDPKPGVMTQEVGQLLQDMGDDVYQQYRSLTR.Q
2470	2481	2	1456.6084	0.0027	0	28.62	E.DYPDMNASPLVR.F	Phospho (Y)	110.78	DY#PDMNASPLVR	108.47						-N----------	-N----------	R.EDSMNILDPEDEEEHTQEEDSSGSNEDEDDSQDEEEEEEEDEEDDQEDDEGEEGDEDDDDDGSEMELDEDYPDMNASPLVRFER.F
2825	2838	2	1547.761	0.0014	1	40.91	E.LSPAPTITSLSPER.A	Phospho (ST)	62.65	LS#PAPTITSLSPER	42.69						-N----------	-N----------	K.ETLGTLQSSQQQPTLPTPPALGEVPQELQSPAGEGGSSTQLLMPVEPEELGPTRPSGEAETTQMELSPAPTITSLSPERAEDSDALTAVSSQLEGSPMDTSSLASCTLEEAVGDTSAAGSSEQPR.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
7	sp|O15027|SC16A_HUMAN	150	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence

1736		1763	3	2857.4818		0.0079	0	47.79	E.QLDRPGLSQPGALGIANPLLAVPAPSPE.H	Phospho (ST)	128.84	QLDRPGLSQPGALGIANPLLAVPAPS#PE	129.93						----------N--	----------N--	K.EGAGVWHQDGALPQQCPGTPSSEMEQLDRPGLSQPGALGIANPLLAVPAPSPEHSSPSVR.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
8	sp|O75822|EIF3J_HUMAN	149	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
234	255	2	2524.9634	0.0017	1	83.54	K.ATMKDDLADYGGYDGGYVQDYE.D	Phospho (Y)	276.48	ATMKDDLADYGGYDGGYVQDY#E	96.04						----------Y-	----------N-	K.ATMKDDLADYGGYDGGYVQDYEDFM.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
9	sp|Q9UQ35|SRRM2_HUMAN	130	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1298	1313	2	1751.7052	0.0038	0	64.71	E.VPSMASSWGGPHFSPE.H	Phospho (ST)	150.41	VPSMASSWGGPHFS#PE	91.93						----------N--	----------N--	K.EMSTSNFESSPEVEERPAVSLTLDQSQSQASLEAVEVPSMASSWGGPHFSPEHK.E
304	325	2	2312.9474	0.004	1	32.65	R.GEGDAPFSEPGTTSTQRPSSPE.T	Phospho (ST)	110.98	GEGDAPFSEPGTTSTQRPSS#PE	20.35						----------Y---	----------Y---	R.GEGDAPFSEPGTTSTQRPSSPETATK.Q
1295	1313	2	2050.8554	0.0059	1	48.51	E.AVEVPSMASSWGGPHFSPE.H	Phospho (ST)	176.6	AVEVPSMASSWGGPHFS#PE	100.51						----------N--	----------N--	K.EMSTSNFESSPEVEERPAVSLTLDQSQSQASLEAVEVPSMASSWGGPHFSPEHK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
10	sp|P06748|NPM_HUMAN	128	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
69	80	2	1306.7292	0.0031	1	53.73	E.GSPIKVTLATLK.M	Phospho (ST)	46.7	GS#PIKVTLATLK	38.62						-Y----------	-Y----------	K.DELHIVEAEAMNYEGSPIKVTLATLKMSVQPTVSLGGFEITPPVVLR.L
132	141	2	1138.6012	0.0014	1	25.07	E.DVKLLSISGK.R	Phospho (ST)	50.27	DVKLLS#ISGK	22.01						-----Y----	-----Y----	K.CGSGPVHISGQHLVAVEEDAESEDEEEEDVKLLSISGKR.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
11	sp|P46821|MAP1B_HUMAN	122	7	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1728	1747	2	2074.9254	0.0046	0	45.05	E.ASPSTSSAHTPSQIASPLQE.D	Phospho (ST)	128.83	ASPSTSSAHTPSQIAS#PLQE	97.75						----------N----	----------N----	K.IPPMEEPSYTQDNDLSELISVSQVEASPSTSSAHTPSQIASPLQEDTLSDVAPPR.D
1687	1702	3	1874.743	0.0036	0	27.23	E.VDYSPSDMQDSSLSHK.I	Phospho (Y)	73.52	VDY#SPSDMQDSSLSHK	30.83						--N----------	--N----------	R.QSPDHPTVGAGVLHITENGPTEVDYSPSDMQDSSLSHKIPPMEEPSYTQDNDLSELISVSQVEASPSTSSAHTPSQIASPLQEDTLSDVAPPR.D
1811	1833	3	2488.0393	0.0027	0	22.11	K.TATCHSSSSPPIDAASAEPYGFR.A	Phospho (Y)	99.1	TATCHSSSSPPIDAASAEPY#GFR	50.41						----------Y---	----------Y---	K.TATCHSSSSPPIDAASAEPYGFRASVLFDTMQHHLALNR.D
1394	1407	2	1623.769	0.0016	1	19.32	K.VLSPLRSPPLIGSE.S	2 Phospho (ST)	84.46	VLS#PLRS#PPLIGSE	84.36	45.03					--Y---Y-------	--Y---Y-------	K.VLSPLRSPPLIGSESAYESFLSADDK.A
1682	1702	3	2373.9331	0.0023	1	33.27	E.NGPTEVDYSPSDMQDSSLSHK.I	Deamidated (NQ); Phospho (Y)	48.71	NGPTEVDY#SPSDMQDSSLSHK	28.5						-------N----------	-------N----------	R.QSPDHPTVGAGVLHITENGPTEVDYSPSDMQDSSLSHKIPPMEEPSYTQDNDLSELISVSQVEASPSTSSAHTPSQIASPLQEDTLSDVAPPR.D
1041	1051	2	1318.5538	0.0022	1	42.9	E.AEDYVMAVVDK.A	Phospho (Y)	113.62	AEDY#VMAVVDK	1000						---N-------	---N-------	K.MEAEDYVMAVVDKAAEAGGAEEQYGFLTTPTK.Q
1043	1051	2	1118.475	0.0031	0	28.33	E.DYVMAVVDK.A	Phospho (Y)	99.81	DY#VMAVVDK	1000						-N-------	-N-------	K.MEAEDYVMAVVDKAAEAGGAEEQYGFLTTPTK.Q

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
12	sp|P48681|NEST_HUMAN	119	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
462	478	2	1931.7724	0.0021	0	40.12	E.DHASLAPPLSPDHSSLE.A	2 Phospho (ST)	92.92	DHASLAPPLSPDHS#S#LE	40.34	37.11					----------NN--	----------YN--	R.QEASTGQSPEDHASLAPPLSPDHSSLEAK.D

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
13	sp|O75533|SF3B1_HUMAN	117	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
63	80	2	2066.8234	0.0029	1	75.68	E.LEDDDDDYSSSTSLLGQK.K	Phospho (Y)	195.89	LEDDDDDY#SSSTSLLGQK	21.51						-------N---------	-------N---------	R.FAGYVTSIAATELEDDDDDYSSSTSLLGQKKPGYHAPVALLNDIPQSTEQYDPFAEHRPPK.I

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
14	sp|Q14444|CAPR1_HUMAN	114	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
441	456	2	1828.771	0.0042	0	38.27	E.GYTASQPLYQPSHATE.Q	Phospho (Y)	118.8	GYTASQPLY#QPSHATE	55.1						--------N-------	--------Y-------	R.LAQPNQVPVQPEATQVPLVSSTSEGYTASQPLYQPSHATEQRPQK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
15	sp|Q96JM3|ZN828_HUMAN	113	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
167	189	3	2529.1843	0.0038	0	26	E.LQTPLPSPEPSKPASVSSPEPPK.S	2 Phospho (ST)	112.13	LQT#PLPS#PEPSKPASVSSPEPPK	98.83	41.91					--N---N----------	--N---N----------	K.LGSVLSPESPKPTPLTPLEPQKPGSVVSPELQTPLPSPEPSKPASVSSPEPPKSVPVCESQK.L
199	219	2	2313.1074	0.0016	1	40.62	K.LAPVPSPEPQKPAPVSPESVK.A	2 Phospho (ST)	120.36	LAPVPS#PEPQKPAPVS#PESVK	95.11	40.04					-----Y---------Y-----	-----Y---------Y-----	K.LAPVPSPEPQKPAPVSPESVKATLSNPKPQK.Q
302	324	4	2568.2253	0.0061	0	30.97	R.RPAPAVSPGSWKPGPPGSPRPWK.S	2 Phospho (ST)	75.31	RPAPAVS#PGSWKPGPPGS#PRPWK	21.49	32.49					-----Y---------Y-----	-----Y---------Y-----	R.RPAPAVSPGSWKPGPPGSPRPWKSNPSASSGPWKPAKPAPSVSPGPWKPIPSVSPGPWKPTPSVSSASWK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
16	sp|Q15365|PCBP1_HUMAN	103	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
216	237	3	2400.1771	0.0044	0	33.94	E.GPPLDAYSIQGQHTISPLDLAK.L	Phospho (Y)	116.39	GPPLDAY#SIQGQHTISPLDLAK	23.34						------N----------	------Y----------	R.CSDAAGYPHATHDLEGPPLDAYSIQGQHTISPLDLAKLNQVAR.Q
161	177	3	2038.9609	0.0028	1	26.83	K.QICLVMLETLSQSPQGR.V	Phospho (ST)	96.87	QICLVMLETLSQS#PQGR	28.28						----------Y----	----------Y----	K.QICLVMLETLSQSPQGRVMTIPYQPMPASSPVICAGGQDR.C

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
17	sp|Q70E73|RAPH1_HUMAN	102	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
880	899	3	2104.1128	0.0046	0	18.03	E.SQPLKPVPANVAPQSPPAVK.A	Phospho (ST)	68.22	SQPLKPVPANVAPQS#PPAVK	88.05						----------Y-----	----------N-----	K.QIASQFPPPPTPPAMESQPLKPVPANVAPQSPPAVKAKPK.W
1082	1100	2	2056.0694	0.0049	1	52.41	E.LPLPPIEIPAVFSGNTSPK.V	Phospho (ST)	137.25	LPLPPIEIPAVFSGNTS#PK	26.38						----------N--	----------N--	K.DSVVEFPSPPSDSDFPPPPPETELPLPPIEIPAVFSGNTSPKVAVVNPQPQQWSK.M

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
18	sp|Q96N67|DOCK7_HUMAN	102	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1267	1280	2	1704.6732	0.003	1	47.37	R.GRPICIATDDYESE.S	Phospho (Y)	154.81	GRPICIATDDY#ESE	30.7						----------N---	----------N---	R.GRPICIATDDYESESGSMISQTVAMAIAGTSVPQLTRPGSFLLTSTSGR.Q

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
19	sp|P37840|SYUA_HUMAN	98	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
132	140	2	1150.3878	0.0023	1	23.7	E.GYQDYEPEA.-	Phospho (Y)	96.34	GYQDY#EPEA	52.54						----N----	----Y----	K.NEEGAPQEGILEDMPVDPDNEAYEMPSEEGYQDYEPEA.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
20	sp|Q14247|SRC8_HUMAN	91	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
435	454	2	2233.9274	0.0036	1	70.29	R.GPVSGTEPEPVYSMEAADYR.E	Phospho (Y)	156.89	GPVSGTEPEPVY#SMEAADYR	32.4						----------Y--------	----------Y--------	R.GPVSGTEPEPVYSMEAADYREASSQQGLAYATEAVYESAEAPGHYPAEDSTYDEYENDLGITAVALYDYQAAGDDEISFDPDDIITNIEMIDDGWWR.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
21	sp|P49792|RBP2_HUMAN	90	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
2232	2255	3	2491.1635	0.0043	1	41.11	E.DALDDSVSSSSVHASPLASSPVRK.N	Phospho (ST)	110.68	DALDDSVSSSSVHASPLASS#PVRK	24.75						----------Y----	----------Y----	R.EDALDDSVSSSSVHASPLASSPVRKNLFR.F

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
22	sp|Q9Y520|BA2L2_HUMAN	89	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
331	346	2	1859.7234	0.0024	1	58.12	E.QLNFSDDDEQGSNSPK.E	Phospho (ST)	112.85	QLNFS#DDDEQGSNSPK	65.55						----N----------	----N----------	K.FDNLDAEADEGWAGAQMEVDYTEQLNFSDDDEQGSNSPKENNSEDQGSK.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
23	sp|Q92974|ARHG2_HUMAN	89	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
682	706	3	2516.1091	0.0023	1	22.01	R.EPALPLEPDSGGNTSPGVTANGEAR.T	Deamidated (NQ); Phospho (ST)	65.93	EPALPLEPDSGGNTS#PGVTANGEAR	22.13						----------Y----------	----------Y----------	R.EPALPLEPDSGGNTSPGVTANGEARTFNGSIELCR.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
24	sp|Q05655|KPCD_HUMAN	83	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
650	669	2	2267.0014	0.0045	0	58.67	K.NLIDSMDQSAFAGFSFVNPK.F	Phospho (ST)	179.77	NLIDSMDQSAFAGFS#FVNPK	126.46						----------Y-----	----------N-----	K.NLIDSMDQSAFAGFSFVNPKFEHLLED.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
25	sp|Q9H000|MKRN2_HUMAN	83	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
121	141	2	2309.9194	0.0013	1	39.73	R.KTQPSMVSNPGSCSDPQPSPE.M	Deamidated (NQ); Phospho (ST)	94.72	KTQPSMVSNPGSCSDPQPS#PE	24.41						----------Y--	----------N--	K.TQPSMVSNPGSCSDPQPSPEMKPHSYLDAIR.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
26	sp|P22626|ROA2_HUMAN	83	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
239	266	3	2574.0028	0.0041	0	45.06	R.GFGDGYNGYGGGPGGGNFGGSPGYGGGR.G	Phospho (ST)	104.38	GFGDGYNGYGGGPGGGNFGGS#PGYGGGR	38.19						----------Y-------	----------Y-------	R.GFGDGYNGYGGGPGGGNFGGSPGYGGGRGGYGGGGPGYGNQGGGYGGGYDNYGGGNYGSGNYNDFGNYNQQPSNYGPMK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
27	sp|Q92625|ANS1A_HUMAN	81	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
825	843	3	2257.114	-0.0004	1	27.24	R.IIASLADRPYEEPPQKPPR.F	Deamidated (NQ); Phospho (Y)	104.11	IIASLADRPY#EEPPQKPPR	30.39						---------N---------	---------N---------	R.IIASLADRPYEEPPQKPPRFSQLR.C

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
28	sp|Q86XP3|DDX42_HUMAN	81	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
100	117	2	2217.8194	0.0054	0	29.25	R.QQFHSKPVDSDSDDDPLE.A	2 Phospho (ST)	86.56	QQFHSKPVDS#DS#DDDPLE	57.41	63.13					---------Y-Y------	---------Y-Y------	R.QQFHSKPVDSDSDDDPLEAFMAEVEDQAAR.D

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
29	sp|P12270|TPR_HUMAN	79	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1883	1896	2	1662.6442	0.0032	0	39.02	E.TQVYNQDSQDSIGE.G	Phospho (ST)	99.39	TQVYNQDSQDS#IGE	46.32						----------N---	----------N---	K.SVTPVGTEEEVMAEESTDGEVETQVYNQDSQDSIGEGVTQGDYTPMEDSEETSQSLQIDLGPLQSDQQTTTSSQDGQGK.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
30	sp|Q02750|MP2K1_HUMAN	79	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
206	227	3	2453.0803	0.0046	0	49.01	K.LCDFGVSGQLIDSMANSFVGTR.S	Phospho (ST)	131.29	LCDFGVSGQLIDSMANS#FVGTR	31.81						----------Y-----	----------N-----	K.LCDFGVSGQLIDSMANSFVGTRSYMSPER.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
31	sp|P62826|RAN_HUMAN	79	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence

176		198	2	2509.1734		0.0061	1	48.34	E.FVAMPALAPPEVVMDPALAAQYE.H	Phospho (Y)	181.79	FVAMPALAPPEVVMDPALAAQY#E	1000						----------N-	----------N-	K.LIGDPNLEFVAMPALAPPEVVMDPALAAQYEHDLEVAQTTALPDEDDDL.-
187		198	2	1385.5982		0.0045	0	24.48	E.VVMDPALAAQYE.H	Phospho (Y)	94.17	VVMDPALAAQY#E	1000						----------N-	----------N-	K.LIGDPNLEFVAMPALAPPEVVMDPALAAQYEHDLEVAQTTALPDEDDDL.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
32	sp|Q15714|T22D1_HUMAN	79	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
31	56	2	2331.9974	0.0046	1	78.55	R.RGSGSGSASALNAAGTGVGSNATSSE.D	Phospho (ST)	220.08	RGS#GSGSASALNAAGTGVGSNATSSE	32.4						--N----------	--N----------	R.GSGSGSASALNAAGTGVGSNATSSEDFPPPSLLQPPPPAASSTSGPQPPPPQSLNLLSQAQLQAQPLAPGGTQMK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
33	sp|Q01804|OTUD4_HUMAN	78	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
566	580	2	1638.81	0.0082	0	51.1	E.HVSLSNPAPLLVSPE.V	Phospho (ST)	146.27	HVSLSNPAPLLVS#PE	162.16						----------N--	----------N--	K.LECPSPAEQKPAEHVSLSNPAPLLVSPEVHLTPAVPSLPATVPAWPSEPTTFGPTGVPAPIPVLSVTQTLTTGPDSAVSQAHLTPSPVPVSIQAVNQPLMPLPQTLSLYQDPLYPGFPCNEK.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
34	sp|Q9BZQ8|NIBAN_HUMAN	76	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
600	612	2	1348.6782	0.0031	1	23.17	R.RASAILPGVLGSE.T	Phospho (ST)	62.82	RAS#AILPGVLGSE	84.11						--Y----------	--Y----------	R.ASAILPGVLGSETLSNEVFQESEEEK.Q

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
35	sp|Q14157|UBP2L_HUMAN	74	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
439	459	2	2038.9994	0.0018	0	31.8	K.SPAVATSTAAPPPPSSPLPSK.S	Phospho (ST)	94.04	SPAVATSTAAPPPPSS#PLPSK	22.85						----------Y-----	----------Y-----	K.SPAVATSTAAPPPPSSPLPSKSTSAPQMSPGSSDNQSSSPQPAQQK.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
36	sp|Q15424|SAFB1_HUMAN	72	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
122	136	2	1811.7924	0.0025	0	37.85	E.NLQDIDIMDISVLDE.A	Phospho (ST)	132.17	NLQDIDIMDIS#VLDE	1000						----------N----	----------N----	R.KPEEEGVEDNGLEENSGDGQEDVETSLENLQDIDIMDISVLDEAEIDNGSVADCVEDDDADNLQESLSDSR.E
122	138	2	2011.8754	0.0058	1	25.05	E.NLQDIDIMDISVLDEAE.I	Phospho (ST)	118.08	NLQDIDIMDIS#VLDEAE	1000						----------N------	----------N------	R.KPEEEGVEDNGLEENSGDGQEDVETSLENLQDIDIMDISVLDEAEIDNGSVADCVEDDDADNLQESLSDSR.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
37	sp|Q8IYB3|SRRM1_HUMAN	71	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
763	788	4	2790.4125	0.0019	1	24.71	K.KPPAPPSPVQSQSPSTNWSPAVPVKK.A	Phospho (ST)	92.57	KPPAPPS#PVQSQSPSTNWSPAVPVKK	60.5						------Y----------	------Y----------	K.KPPAPPSPVQSQSPSTNWSPAVPVKKAK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
38	sp|P23588|IF4B_HUMAN	70	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
49	70	3	2595.1081	0.0053	1	39.85	E.GDVSTTWHSNDDDVYRAPPIDR.S	Phospho (Y)	116.79	GDVSTTWHSNDDDVY#RAPPIDR	66.23						----------N-------	----------N-------	K.TISLTDFLAEDGGTGGGSTYVSKPVSWADETDDLEGDVSTTWHSNDDDVYRAPPIDRSILPTAPR.A
24	43	2	2048.8414	0.005	0	39.27	E.DGGTGGGSTYVSKPVSWADE.T	Phospho (ST)	128.67	DGGTGGGSTYVSKPVS#WADE	63.77						----------N----	----------N----	K.TISLTDFLAEDGGTGGGSTYVSKPVSWADETDDLEGDVSTTWHSNDDDVYR.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
39	sp|Q2TAL8|QRIC1_HUMAN	69	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
336	353	3	1834.9024	0.0045	0	43.41	E.AYNAVHVSGSPTALAAVK.L	Phospho (ST)	66.5	AYNAVHVSGS#PTALAAVK	32.07						---------Y--------	---------Y--------	R.GDPQQQSITHIAIPQEAYNAVHVSGSPTALAAVKLEDDK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
40	sp|P98175|RBM10_HUMAN	69	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
539	559	2	2275.9834	0.0071	0	23.26	E.LQSPTHPSSALPPATSPTAQE.S	2 Phospho (ST)	91.62	LQS#PTHPSSALPPATS#PTAQE	22.01	24.44					--N----------N---	--N----------N---	K.SELQSPTHPSSALPPATSPTAQESYSQYPVPDVSTYQYDETSGYYYDPQTGLYYDPNSQYYYNAQSQQYLYWDGER.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
41	sp|O75970|MPDZ_HUMAN	68	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
903	911	2	1227.6044	0.0032	0	67.54	E.LYTQNLLQR.Q	Phospho (Y)	159	LY#TQNLLQR	38.42						-N-------	-N-------	K.DVIENSCDPVLDLHMSLEELYTQNLLQRQDENTPSVDISMGPASGFTINDYTPANAIEQQYECENTIVWTESHLPSEVISSAELPSVLPDSAGK.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
42	sp|O75410|TACC1_HUMAN	68	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
391	412	2	2394.0594	0.0065	0	62.65	E.SPSFNPFGSHSVLQNSPPLSSE.G	Phospho (ST)	108.99	SPSFNPFGSHSVLQNS#PPLSSE	58.55						----------Y------	----------N------	R.DGPLSQTSSKPDPSQWESPSFNPFGSHSVLQNSPPLSSEGSYHFDPDNFDESMDPFKPTTTLTSSDFCSPTGHVNEILESPK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
43	sp|O15061|SYNEM_HUMAN	68	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1152	1169	2	1710.7602	0.0028	0	25.27	E.VSAGGDLSQAASPTGASR.S	Phospho (ST)	77.94	VSAGGDLSQAAS#PTGASR	30.7						----------N------	----------N------	R.MSYEGPTAEVVEVSAGGDLSQAASPTGASRSVR.H
1082	1104	2	2259.0314	0.0033	1	25.91	E.VAGGASHSSGQRTPQGPVSATVE.V	Phospho (ST)	86.53	VAGGASHSSGQRT#PQGPVSATVE	25.78						----------N----------	----------N----------	R.ELVIPSGESEVAGGASHSSGQRTPQGPVSATVEVSSPTGFAQSQVLEDVSQAAR.H

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
44	sp|Q8N9T8|KRI1_HUMAN	67	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
273	291	2	2066.7914	0.0043	1	51.05	E.GVHGPPVQLAVDDSSDEGE.L	2 Phospho (ST)	183.71	GVHGPPVQLAVDDS#S#DEGE	1000						----------YY----	----------YY----	R.YEEEEEEEEDEEEMEEEEGVHGPPVQLAVDDSSDEGELFLK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
45	sp|O94916|NFAT5_HUMAN	65	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1498	1513	2	1808.833	0.0025	1	39.28	E.NSPLASSINTNQNIEK.I	Phospho (ST)	110.99	NS#PLASSINTNQNIEK	92.31								K.QPPPNMIFNPNQNPMANQEQQNQSIFHQQSNMAPMNQEQQPMQFQSQSTVSSLQNPGPTQSESSQTPLFHSSPQIQLVQGSPSSQEQQVTLFLSPASMSALQTSINQQDMQQSPLYSPQNNMPGIQGATSSPQPQATLFHNTAGGTMNQLQNSPGSSQQTSGMFLFGIQNNCSQLLTSGPATLPDQLMAISQPGQPQNEGQPPVTTLLSQQMPENSPLASSINTNQNIEKIDLLVSLQNQGNNLTGSF.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
46	sp|Q13283|G3BP1_HUMAN	65	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
165	185	2	2395.9434	0.0031	1	47.37	E.VVPDDSGTFYDQAVVSNDMEE.H	Phospho (ST)	158.93	VVPDDSGTFY#DQAVVSNDMEE	48.87						-------N----------	-------N----------	R.QQTPEVVPDDSGTFYDQAVVSNDMEEHLEEPVAEPEPDPEPEPEQEPVSEIQEEKPEPVLEETAPEDAQK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
47	sp|O75030|MITF_HUMAN	64	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
483	509	3	2873.3119	0.006	0	43.58	E.DILMDDTLSPVGVTDPLLSSVSPGASK.T	2 Phospho (ST)	237	DILMDDTLS#PVGVTDPLLSSVS#PGASK	24.15	23.62					------N----------------N-	------N----------------N-	K.LEDILMDDTLSPVGVTDPLLSSVSPGASKTSSR.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
48	sp|Q9UMY4|SNX12_HUMAN	62	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
12	31	2	2285.0294	0.0042	0	62.21	R.LNSKPQDLTDAYGPPSNFLE.I	Phospho (Y)	180.36	LNSKPQDLTDAY#GPPSNFLE	53.2						----------Y--------	----------Y--------	R.LNSKPQDLTDAYGPPSNFLEIDIFNPQTVGVGR.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
49	sp|Q13625|ASPP2_HUMAN	59	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
820	835	2	1797.6846	0.0042	0	42.35	E.NSDMPAPSPGLDYEPE.G	Phospho (Y)	99.23	NSDMPAPSPGLDY#EPE	29						----------N---	----------N---	K.EVVSLVPESLSPEDVGNASTENSDMPAPSPGLDYEPEGVPDNSPNLQNNPEEPNPEAPHVLDVYLEEYPPYPPPPYPSGEPEGPGEDSVSMRPPEITGQVSLPPGK.R
662	677	2	1782.7496	0.0035	0	30.78	E.NIYSNSQGKPGSPEPE.T	Phospho (ST)	103.86	NIYSNSQGKPGS#PEPE	44.15						----------N----	----------N----	R.GPHFSSVYGKPVIAAAQNQQQHPENIYSNSQGKPGSPEPETEPVSSVQENHENER.I

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
50	sp|Q9H1B7|EAP1_HUMAN	58	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
211	228	3	1881.8743	0.0049	1	28.91	E.LNRQSPNSSSAAASVASR.R	Phospho (ST)	63.4	LNRQS#PNSSSAAASVASR	37.87						----Y------------	----Y------------	R.LPNGLGGPNGFPKPTPEEGPPELNRQSPNSSSAAASVASRR.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
51	sp|Q12888|TP53B_HUMAN	57	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
287	298	2	1391.6352	0.0019	1	38.16	E.SGLQIQKSPEPE.V	Phospho (ST)	111.94	SGLQIQKS#PEPE	87.65						-------Y----	-------Y----	K.EQLSAQELMESGLQIQKSPEPEVLSTQEDLFDQSNK.T
884	897	2	1597.6588	-0.0007	0	25.55	K.LGKPSAHASQSFCE.S	Phospho (ST)	68.92	LGKPSAHASQS#FCE	21.3						----------N---	----------N---	K.LGKPSAHASQSFCESSSETPFHFTLPK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
52	sp|Q12830|BPTF_HUMAN	57	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
2394	2418	3	2719.2301	0.0062	0	30.89	E.AQPQTAQPSAQPQPQTQPQSPAQPE.V	Phospho (ST)	64.37	AQPQTAQPSAQPQPQTQPQS#PAQPE	35.45						----------N-----	----------N-----	K.TLPPAQSSSVGPAEAQPQTAQPSAQPQPQTQPQSPAQPEVQTQTTVSSHVPSEAQPTHAQSSKPQVAAQSQPQSNVQGQSPVR.V

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
53	sp|Q96D71|REPS1_HUMAN	57	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
207	228	2	2227.9214	0.0043	0	31.18	E.AQSGSSAGDAVWSGHSPPPPQE.N	Phospho (ST)	117.23	AQSGSSAGDAVWSGHS#PPPPQE	38.72						-------------N------	-------------N------	R.HPSGGNSERPLAGPGPFWSPFGEAQSGSSAGDAVWSGHSPPPPQENWVSFADTPPTSTLLTMHPASVQDQTTVR.T

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
54	sp|P05387|RLA2_HUMAN	57	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
3	21	2	1947.9376	0.0034	0	42.71	R.YVASYLLAALGGNSSPSAK.D	Phospho (ST)	156.06	YVASYLLAALGGNS#PSAK	26.38						-------------Y----	-------------Y----	R.YVASYLLAALGGNSSPSAKDIK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?

55	sp|P41743|KPCI_HUMAN		57		2	Phosphoprotein																			
Start	End		charge		Mr(expt)		Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
547		572	3		3076.3432		0.0092	0	45.13	E.FGLDNFDSQFTNEPVQLTPDDDDIVR.K	Phospho (ST)	168.97	FGLDNFDSQFTNEPVQLT#PDDDDIVR	155.6						----------Y--------	----------Y--------	K.QVVPPFKPNISGEFGLDNFDSQFTNEPVQLTPDDDDIVRK.I
547		573	3		3205.4392		0.0263	1	30.47	E.FGLDNFDSQFTNEPVQLTPDDDDIVRK.I	Deamidated (NQ); Phospho (ST)	51.28	FGLDNFDSQFTNEPVQLT#PDDDDIVRK	30.88						----------Y---------	----------Y---------	K.QVVPPFKPNISGEFGLDNFDSQFTNEPVQLTPDDDDIVRKIDQSEFEGFEYINPLLMSAEECV.-

Index	AC		Mascot score		Nb distinct peptides	Is Uniprot phosphoprotein?																			
56	sp|Q9NYJ8|TAB2_HUMAN		56		1	Phosphoprotein																			
Start	End		charge		Mr(expt)		Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
102		120	2		2037.8654		0.0014	0	56.17	R.TLTHSISDGQLQGGQSNSE.L	Phospho (ST)	121.29	TLTHSIS#DGQLQGGQSNSE	28.5						------N----------	------N----------	R.TLTHSISDGQLQGGQSNSELFQQEPQTAPAQVPQGFNVFGMSSSSGASNSAPHLGFHLGSK.G

Index	AC		Mascot score		Nb distinct peptides	Is Uniprot phosphoprotein?																			
57	sp|P04792|HSPB1_HUMAN		56		1	Phosphoprotein																			
Start	End		charge		Mr(expt)		Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
42		75	3		3703.8052		0.0075	1	55.65	E.WSQWLGGSSWPGYVRPLPPAAIESPAVAAPAYSR.A	Phospho (ST)	118.75	WSQWLGGSSWPGYVRPLPPAAIES#PAVAAPAYSR	72.17						----------Y----------	----------Y----------	R.LPEEWSQWLGGSSWPGYVRPLPPAAIESPAVAAPAYSRALSR.Q

Index	AC		Mascot score		Nb distinct peptides	Is Uniprot phosphoprotein?																			
58	sp|Q9NPI6|DCP1A_HUMAN		54		1	Phosphoprotein																			
Start	End		charge		Mr(expt)		Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
306		337	3		3477.7432		0.0082	1	45.26	K.HAPTYTIPLSPVLSPTLPAEAPTAQVPPSLPR.N	2 Phospho (ST)	130.88	HAPTYTIPLS#PVLS#PTLPAEAPTAQVPPSLPR	19.71	23.64					---------Y---Y----------	---------Y---Y----------	K.HAPTYTIPLSPVLSPTLPAEAPTAQVPPSLPRNSTMMQAVK.T

Index	AC		Mascot score		Nb distinct peptides	Is Uniprot phosphoprotein?																			
59	sp|Q9GZV5|WWTR1_HUMAN		54		1	Phosphoprotein																			
Start	End		charge		Mr(expt)		Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
342		356	2		1748.7698		0.0033	0	38.27	E.NAGQTPMNINPQQTR.F	Phospho (ST)	117.89	NAGQT#PMNINPQQTR	114.8						----N----------	----N----------	R.EQSTDSGLGLGCYSVPTTPEDFLSNVDEMDTGENAGQTPMNINPQQTRFPDFLDCLPGTNVDLGTLESEDLIPLFNDVESALNK.S

Index	AC		Mascot score		Nb distinct peptides	Is Uniprot phosphoprotein?																			
60	sp|O00257|CBX4_HUMAN		53		1	Phosphoprotein																			
Start	End		charge		Mr(expt)		Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
462		476	2		1804.891		0.0051	0	49.35	E.VILLDSDLDEPIDLR.C	Phospho (ST)	178.22	VILLDS#DLDEPIDLR	1000						-----N---------	-----N---------	R.SISTPTCLGGSPAAERPADLPPAAALPQPEVILLDSDLDEPIDLRCVK.T

Index	AC		Mascot score		Nb distinct peptides	Is Uniprot phosphoprotein?																			
61	sp|P52756|RBM5_HUMAN		52		1	Phosphoprotein																			
Start	End		charge		Mr(expt)		Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
430		453	3		2320.1011		0.0063	0	20.95	E.AQPSTSTSTQAPAASPTGVVPGTK.Y	Phospho (ST)	60.07	AQPSTSTSTQAPAAS#PTGVVPGTK	20.17						-------------N---------	-------------N---------	R.VSAFSVASTAIAAAQWSSTQSQSGEGGSVDYSYLQPGQDGYAQYAQYSQDYQQFYQQQAGGLESDASSASGTAVTTTSAAVVSQSPQLYNQTSNPPGSPTEEAQPSTSTSTQAPAASPTGVVPGTKYAVPDTSTYQYDESSGYYYDPTTGLYYDPNSQYYYNSLTQQYLYWDGEK.E

Index	AC		Mascot score		Nb distinct peptides	Is Uniprot phosphoprotein?																			
62	sp|Q14684|RRP1B_HUMAN		52		1	Phosphoprotein																			
Start	End		charge		Mr(expt)		Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
348		362	2		1712.7154		0.0013	1	52.27	E.DISADEDDQILSQGK.H	Phospho (ST)	131.46	DIS#ADEDDQILSQGK	128.61						--Y----------	--Y----------	K.FQDLSEGSSISQLSFAEDISADEDDQILSQGKHK.K

Index	AC		Mascot score		Nb distinct peptides	Is Uniprot phosphoprotein?																			
63	sp|Q66K74|MAP1S_HUMAN		52		2	Phosphoprotein																			
Start	End		charge		Mr(expt)		Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
626		642	3		1947.9256		0.0036	1	16.42	E.LPLAASSIPRPRTPSPE.S	2 Phospho (ST)	61.14	LPLAASSIPRPRT#PS#PE	22.48	30.71					----------Y-Y--	----------Y-Y--	K.ALELPLAASSIPRPRTPSPESHR.S
654		663	2		1107.534		0.0015	1	52.06	R.LSLSPLRGGE.A	Phospho (ST)	122.32	LSLS#PLRGGE	52.75						---Y------	---Y------	R.LSLSPLRGGEAGPDASPTVTTPTVTTPSLPAEVGSPHSTEVDESLSVSFEQVLPPSAPTSEAGLSLPLR.G

Index	AC		Mascot score		Nb distinct peptides	Is Uniprot phosphoprotein?																			
64	sp|Q8N122|RPTOR_HUMAN		52		1	Phosphoprotein																			
Start	End		charge		Mr(expt)		Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
868		894	3		2671.2262		0.0023	0	52	K.GVHIHQAGGSPPASSTSSSSLTNDVAK.Q	Phospho (ST)	108.14	GVHIHQAGGS#PPASSTSSSSLTNDVAK	54.26						---------Y----------	---------Y----------	K.GVHIHQAGGSPPASSTSSSSLTNDVAKQPVSR.D

Index	AC		Mascot score		Nb distinct peptides	Is Uniprot phosphoprotein?																			
65	sp|Q9Y5S1|TRPV2_HUMAN		52		1	Phosphoprotein																			
Start	End		charge		Mr(expt)		Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
754		764	2		1353.6356		0.0027	0	52	E.NYVPVQLLQSN.-	Phospho (Y)	128.14	NY#VPVQLLQSN	142.26						-N---------	-N---------	K.EDEDGASEENYVPVQLLQSN.-

Index	AC		Mascot score		Nb distinct peptides	Is Uniprot phosphoprotein?																			
66	sp|Q92797|SYMPK_HUMAN		52		1	Phosphoprotein																			
Start	End		charge		Mr(expt)		Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1159		1187	3		2792.3068		0.005	1	41.57	K.LKPGGVGAPSSSSPSPSPSARPGPPPPSEE.A	Phospho (ST)	101.45	LKPGGVGAPSSSSPSPS#PSARPGPPPSEE	22.47						----------Y----------	----------Y----------	K.LKPGGVGAPSSSSPSPSPSARPGPPPSEEAMDFR.E

Index	AC		Mascot score		Nb distinct peptides	Is Uniprot phosphoprotein?																			
67	sp|P15311|EZRI_HUMAN		50		1	Phosphoprotein																			
Start	End		charge		Mr(expt)		Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
463		487	3		2889.388		0.0067	0	25.8	E.LHLVMTAPPPPPPPVYEPVSYHVQE.S	Oxidation (M); Phospho (Y)	82.57	LHLVMTAPPPPPPVY#EPVSYHVQE	25.02						--------------N---------	--------------Y---------	K.EELHLVMTAPPPPPPPVYEPVSYHVQESLQDEGAEPTGYSAELSSEGIR.D

Index	AC		Mascot score		Nb distinct peptides	Is Uniprot phosphoprotein?																			
68	sp|Q8N0X7|SPG20_HUMAN		50		2	Phosphoprotein																			
Start	End		charge		Mr(expt)		Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence

616		636	3	2469.1231		0.0058	1	33.27	K.TATQTGHTLLEDYQIVDNSQR.E	Phospho (Y)	149.94	TATQTGHTLLEDY#QIVDNSQR	56.27						----------N--------	----------Y--------	K.TATQTGHTLLEDYQIVDNSQRENQEGAANVNVR.G
181		193	2	1451.5254		0.0012	0	38.84	E.GHYTVSYGTDSGE.F	Phospho (Y)	110.52	GHY#TVSYGTDSGE	19.33						--N---------	--N---------	K.LPEPQSFSSAPQHAEVNGNTSTPSAGAVAAPASLSLPSQSCPAEAPPAYTPQAAEGHYTVSYGTDSGEFSSVGEEFYR.N

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
69	sp|Q92538|GBF1_HUMAN	49	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
281	295	2	1469.6308	0.0022		0	33.22	E.AASAVVSPSTDSGLE.F	Phospho (ST)	102.69	AASAVVS#PSTDSGLE	21.99						----------N---	----------N---	K.VTPGSELPTPNGTTLSSNLTGGMPFIDVPTPISSASSEAASAVVSPSTDSGLEFSSQTTSK.E			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
70	sp|O75582|KS6A5_HUMAN	49	2	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
371	385	2	1875.8646	0.0033		0	30.06	K.LFQGYSFVAPSILFK.R	2 Phospho (ST)	129.05	LFQGYS#FVAPS#ILFK	24.44	88.21					-----Y----Y----	-----Y----Y----	K.LFQGYSFVAPSILFKR.N			
355	370	2	1800.7656	0.0015		1	39.53	E.MDPTYSPAALPQSSEK.L	Phospho (ST)	103.41	MDPTYS#PAALPQSSEK	28.87						-----Y----------	-----Y----------	R.DELDVSNFAEEFTEMDPTYSPAALPQSSEKLFQGYSFVAPSILFK.R			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
71	sp|Q9NVD7|PARVA_HUMAN	48	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
53	71	2	2146.0114	0.0057		1	48.25	E.GMNAINLPLSPIPFELDPE.D	Phospho (ST)	143.13	GMNAINLPLS#PIPFELDPE	1000						---------Y---------	---------Y---------	K.EVSELQEEGMNAINLPLSPIPFELDPEDTMLEENEVR.T			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
72	sp|Q14847|LASP1_HUMAN	47	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
158	197	4	4518.1949	0.0079		1	21.27	E.QQQPHHIPTSAPVYQQPQQQPVAQSYGGYKEPAAPVSIQR.S	Phospho (Y)	41.6	QQQPHHIPTSAPVY#QQPQQQPVAQSYGGYKEPAAPVSIQR	21.4						----------Y----------	----------Y----------	R.RPLEQQQPHHIPTSAPVYQQPQQQPVAQSYGGYKEPAAPVSIQRSAPGGGGK.R			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
73	sp|Q9NYV4|CDK12_HUMAN	46	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
664	689	3	2890.3492	0.0049		1	42.51	R.HLLTDLPLPPELPGGDLSPPDSPEPK.A	2 Phospho (ST)	165.36	HLLTDLPLPPELPGGDLS#PPDS#PEPK	184.73	178.16					----------Y---Y----	----------Y---Y----	R.HLLTDLPLPPELPGGDLSPPDSPEPKAITPPQQPYK.K			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
74	sp|O60343|TBCD4_HUMAN	46	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
802	813	2	1456.6382	0.0057		0	36.33	E.LLPLSPLSPTME.E	2 Phospho (ST)	123.73	LLPLS#PLS#PTME	48.83	24.75					----N--N----	----N--N----	R.NELLPLSPLSPTMEEEPLVVFLSGEDDPEK.I			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
75	sp|Q9Y2L9|LRCH1_HUMAN	46	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
531	550	2	2200.9974	0.0056		0	38.05	E.NSPAVSPTTNSTAPFGLKPR.S	2 Phospho (ST)	70.87	NS#PAVS#PTTNSTAPFGLKPR	37.28	24.75					-N---N----------	-Y---Y----------	R.ENSPAVSPTTNSTAPFGLKPRSVFLRPQR.N			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
76	sp|P46379|BAT3_HUMAN	45	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
88	118	3	2864.2885	0.0046		0	44.58	R.APPQTHLPSGASSGTGSASATHGGGSPPGTR.G	Phospho (ST)	35.27	APPQTHLPSGASSGTGSASATHGGGS#PPGTR	30.24						----------Y-----	----------Y-----	R.APPQTHLPSGASSGTGSASATHGGGSPPGTRGPGASVHDR.N			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
77	sp|P55072|TERA_HUMAN	45	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
773	806	3	3299.2822	0.0021		1	44.63	R.FPSGNQGGAGPSQGSGGGTGGSVYTEDNDDDLYG.-	Phospho (Y)	84.14	FPSGNQGGAGPSQGSGGGTGGSVYTEDNDDDLY#G	49.25						----------Y-	----------N-	R.FPSGNQGGAGPSQGSGGGTGGSVYTEDNDDDLYG.-			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
78	sp|O60271|JIP4_HUMAN	43	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
199	222	3	2664.3073	0.0108		1	25.5	K.ERPISLGIFPLPAGDGLLTPDAQK.G	2 Phospho (ST)	106.56	ERPIS#LGIFPLPAGDGLLT#PDAQK	1000						----Y----------Y-----	----Y----------Y-----	K.ERPISLGIFPLPAGDGLLTPDAQKGGETPGSEQWK.F			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
79	sp|P52943|CRIP2_HUMAN	43	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
66	83	2	1916.8962	0.0042		1	42.85	K.GVNIGGAGSYIYEKPLAE.G	Phospho (Y)	132.77	GVNIGGAGSYIY#EKPLAE	30.7						----------Y------	----------Y------	K.GVNIGGAGSYIYEKPLAEGPQVTGPIEVPAAR.A			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
80	sp|O00499|BIN1_HUMAN	42	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
312	336	4	2590.2569	0.0028		1	26.18	R.VNHEPEPAGGATPGATLPKSPSQLR.K	Phospho (ST)	77.34	VNHEPEPAGGATPGATLPKSPS#QLR	23.35						----------N---	----------Y---	R.VNHEPEPAGGATPGATLPKSPSQLRK.G			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
81	sp|P43355|MAGA1_HUMAN	42	1	Not annotated																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
46	72	3	2824.3141	0.0071		0	42.14	E.VPTAGSTDPPQSPQGASAFPTTINFTR.Q	Phospho (ST)	125.79	VPTAGSTDPPQS#PQGASAFPTTINFTR	22.83								R.SLHCKPEEALEAQQEALGLVCVQAATSSSSPLVLGTLEEVPTAGSTDPPQSPQGASAFPTTINFTRQR.Q			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
82	sp|P09497|CLCB_HUMAN	42	1	Not annotated																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			

80		95	2	1640.677	-0.0061	0	32.43	E.ANGPADGYAAIAQADR.L	Deamidated (NQ); Phospho (Y)	46.19	ANGPADGY#AAIAQADR	1000													- .MADDFGFFSSSESGAPEAAEEDPA AAFLAQQESEIAGIENDEGFGAPAGS HAAPAQPGPTSGAGSEDMGTTVNG DVFQEANGPADGYAAIAQADRLTQE PESIR.K
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
83	sp|Q96PK6|RBM14_HUMAN		41	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?		Extended tryptic sequence		
542		578	3	3773.6452	0.0035	1	41.35	R.GQPGNAYDGAGQPSAAYLSMSQ GAVANANSTPPPYER.T	Phospho (ST)	113.04	GQPGNAYDGAGQPSAAYLSMSQGA VANANST#PPPYER	21.75						----------Y------		----------Y------		R.GQPGNAYDGAGQPSAAYLSMSQ GAVANANSTPPPYERTR.L		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
84	sp|Q15417|CNN3_HUMAN		41	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?		Extended tryptic sequence		
312		329	2	2382.8994	0.004	1	40.86	E.YQDDYPRDYQYSDQGIDY.-	Phospho (Y)	127.54	YQDDYPRDY#QYSDQGIDY	30.7						--------N---------		--------N---------		K.YCAAPTEPVIHNGSQGTGTNGSEI SDSDYQAEYPDEYHGEYQDDYPRD YQYSDQGIDY.-		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
85	sp|O43294|TGFI1_HUMAN		40	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?		Extended tryptic sequence		
26		48	3	2591.0761	0.003	1	37.47	K.ERPAEPLTPPPSYGHQPQTGSGE. S	Phospho (ST); Phospho (Y)	119.79	ERPAEPLT#PPPSY#GHQPQTGSGE	50.76	22.01					-------Y----Y----------		--------N----N---------		K.ERPAEPLTPPPSYGHQPQTGSGE SSGASGDK.D		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
86	sp|Q9UK76|HN1_HUMAN		40	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?		Extended tryptic sequence		
121		141	3	2142.1294	0.0055	1	21.19	E.EKPVPAAPVPSPVAPAPVPSR.R	Phospho (ST)	73.94	EKPVPAAPVPS#PVAPAPVPSR	73.34						----------Y----------		----------Y----------		K.GEGDIHENVDTDLPGSLGQSEEK PVPAAPVPSPVAPAPVPSRR.N		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
87	sp|O00264|PGRC1_HUMAN		40	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?		Extended tryptic sequence		
45		67	3	2483.0998	0.0032	1	39.79	K.IVRGDQPAASGDSDDDEPPPLPR. L	Phospho (ST)	165.51	IVRGDQPAASGDS#DDDEPPPLPR	38.19						----------Y----------		----------N----------		K.IVRGDQPAASGDSDDDEPPPLPRL K.R		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
88	sp|Q14678|KANK1_HUMAN		40	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?		Extended tryptic sequence		
184		209	3	2600.176	0.0029	0	39.6	R.LASFGGMGTTSSLPSFVGSGNHN PAK.H	Phospho (ST)	49.05	LAS#FGGMGTTSSLPSFVGSGNHNP AK	60.87						--N----------		--N----------		R.LASFGGMGTTSSLPSFVGSGNHN PAKHQLQNGYQGNGDYGSYAPAAP TTSSMGSSIR.H		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
89	sp|Q9H0G5|CCD55_HUMAN		39	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?		Extended tryptic sequence		
15		38	3	2791.237	0.0032	1	39.24	K.KTQQLHPVLQKPSVFGNDSDDDD E.T	Phospho (ST)	102.74	KTQQLHPVLQKPSVFGNDS#DDDD E	36.44						----------Y-----		----------Y-----		K.TQQLHPVLQKPSVFGNDSDDDDE TSVSESLQR.E		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
90	sp|O95155|UBE4B_HUMAN		39	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?		Extended tryptic sequence		
17		35	2	2047.9634	0.0059	1	39.05	R.LAGGQTSQPTTPLTSPQRE.N	Phospho (ST)	128.19	LAGGQTSQPTTPLTS#PQRE	26.38						-------------Y----		-------------Y----		R.LAGGQTSQPTTPLTSPQRENPPG PPIAASAPGPSQSLGLNVHNMTPAT SPIGASGVAHR.S		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
91	sp|Q16630|CPSF6_HUMAN		38	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?		Extended tryptic sequence		
24		50	3	3012.2452	0.0041	1	38.04	E.YGGHDQIDLYDDVISPSANNGDAP EDR.D	Phospho (ST)	152.4	YGGHDQIDLYDDVIS#PSANNGDAPE DR	29.85						-------------N----------		-------------N----------		- .MADGVDHIDIYADVGEEFNQEAEYG GHDQIDLYDDVISPSANNGDAPEDR DYMDTLPPTVGDDVGK.G		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
92	sp|Q09666|AHNK_HUMAN		38	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?		Extended tryptic sequence		
5124		5132	2	1057.522	0.0012	0	15.8	E.LSLPAIHVE.G	Phospho (ST)	45.99	LS#LPAIHVE	1000						-N-------		-N-------		K.LEGELQAPDLELSLPAIHVEGLDIK. A		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
93	sp|Q9H467|CUED2_HUMAN		38	1	Not annotated																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?		Extended tryptic sequence		
95		118	3	2664.2914	0.0005	0	37.72	E.NLQPQSSGVQGQVPISPEPLQRP E.M	Phospho (ST)	128.78	NLQPQSSGVQGQVPIS#PEPLQRPE	108.23										K.ENLQPQSSGVQGQVPISPEPLQR PEMLK.E		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
94	sp|Q8TB72|PUM2_HUMAN		37	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?		Extended tryptic sequence		
388		407	3	2114.9539	0.0044	0	31.88	R.AGAGQRPLTPNQGQQGQQAE.S	Phospho (ST)	95.47	AGAGQRPLT#PNQGQQGQQAE	1000						--------N----------		--------Y----------		R.AGAGQRPLTPNQGQQGQQAESL AAAAAANPTLAFGQGLATGMPGYQV LAPTAYYDQTGALVVGPGAR.T		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
95	sp|P08621|RU17_HUMAN		37	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?		Extended tryptic sequence		
311		334	2	2260.8134	0.0031	1	37.23	R.GGGGDMAEPSEAGDAPPDDGPP GE.L	Phospho (ST)	123.47	GGGGDMAEPS#EAGDAPPDDGPPG E	1000						---------Y----------		---------Y----------		R.GGGGDMAEPSEAGDAPPDDGPP GELGPDGPDGPEEK.G		
Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																				
96	sp|Q9NQT8|KI13B_HUMAN		37	1	Phosphoprotein																				
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?		Annotated in Phosphosite.org?		Extended tryptic sequence		

1553		1563		2	1176.4732		0.0033	0	20.78	E.AQDGPPSPLSE.A	Phospho (ST)		69.89	AQDGPPS#PLSE	27.14						------N----	------N----	K.VPSPPPVIAVTAVTPAPEAQDGPPSPLSEASSGYFSHSVSTATLSDALGPGLDAAAPPGSMPTAPEAEPEAPISHPPPPTAVPAEEPPGPQQLVSPGR.E

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
97	sp|Q15366|PCBP2_HUMAN		36	1	Phosphoprotein																		
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
229		245	2	1985.9542		0.0043	0	36.29	E.AYTIQGQYAIPQPDLTK.L	Phospho (Y)		125.3	AYTIQGQY#AIPQPDLTK		42.62						-------Y---------	-------Y---------	R.YSTGSDSASFPHTTPSMCLNPDLEGPPLEAYTIQGQYAIPQPDLTKLHQLAMQQSHFPMTHGNTGFSGIESSSPEVK.G

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
98	sp|Q9NZZ3|CHMP5_HUMAN		36	1	Phosphoprotein																		
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
80		100	2	2522.1214		0.0066	1	36.23	R.DNLAQQSFNMEQANYTIQSLK.D	Phospho (Y)		129.94	DNLAQQSFNMEQANY#TIQSLK		32.4						-------------N------	-------------Y------	R.DNLAQQSFNMEQANYTIQSLKDTK.T

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
99	sp|Q9UER7|DAXX_HUMAN		36	1	Phosphoprotein																		
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
18		48	3	2995.3609		0.0035	1	35.76	E.AAAQPGPSHPLPNAASPGAEAPSSSEPHGAR.G	Phospho (ST)		130.44	AAAQPGPSHPLPNAAS#PGAEAPSSSEPHGAR		44.46						--------------N--------------	--------------N--------------	-.MATANSIIVLDDDDEDEAAAQPGPSHPLPNAASPGAEAPSSSEPHGARGSSSSGGK.K

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
100	sp|Q9H4A3|WNK1_HUMAN		36	1	Phosphoprotein																		
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
2001		2015	2	1644.67		0.0032	0	35.65	E.LSEPSHLNGPSSDPE.A	Phospho (ST)		83.1	LSEPSHLNGPS#DPE		24.44						----------Y---	----------Y---	K.EKPELSEPSHLNGPSSDPEAAFLSR.D

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
101	sp|Q9NQX3|GEPH_HUMAN		35	1	Phosphoprotein																		
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
183		203	3	2363.0881		0.0029	1	35.47	E.LEDLPSPPPPLSPPPTTSPHK.Q	2 Phospho (ST)		103.88	LEDLPS#PPPPLS#PPPTTSPHK		87.39	43.6					-----Y-----Y---------	-----Y-----Y---------	K.EVHDELEDLPSPPPPLSPPPTTSPHKQTEDK.G

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
102	sp|P15170|ERF3A_HUMAN		35	1	Not annotated																		
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
30		45	2	1603.6554		0.0039	1	35.28	E.AEPGGGSLGDGRPPEE.S	Phospho (ST)		62.27	AEPGGGS#LGDGRPPEE		1000								K.EEISEAEPGGGSLGDGRPPEESAHEMMEEEEEIPKPK.S

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
103	sp|Q96TA1|NIBL1_HUMAN		35	3	Phosphoprotein																		
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
624		639	2	1696.6312		0.0042	1	14.58	E.ASPESPPPASPDGVTE.I	2 Phospho (ST)		39.72	ASPES#PPPAS#PDGVTE		26.79	28.67					----Y----Y------	-----Y----Y------	K.QVVSVVQDEEVGLPFEASPESPPPASPDGVTEIR.G
673		692	2	2126.9834		0.0032	1	28.41	K.AAPEASSPPASPLQHLLPGK.A	2 Phospho (ST)		111.91	AAPEASS#PPAS#PLQHLLPGK		26.38	51					------Y---Y---------	------Y---Y---------	K.AAPEASSPPASPLQHLLPGKAVDLGPPKPSDQETGEQVSSPSSHPALHTTTEDSAGVQTEF.-
608		617	2	1210.5166		0.0048	1	16.68	K.QVVSVVQDEE.V	Phospho (ST)		64.45	QVVS#VVQDEE		1000						---Y------	----N------	K.QVVSVVQDEEVGLPFEASPESPPPASPDGVTEIR.G

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
104	sp|Q96ST3|SIN3A_HUMAN		34	1	Phosphoprotein																		
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
277		303	3	2887.4134		0.0017	0	34.06	R.SPPVQPHTPVTISLGTAPSLQNNQPVE.F	Phospho (ST)		107.27	S#PPVQPHTPVTISLGTAPSLQNNQPVE		48.96						Y----------	Y----------	R.SPPVQPHTPVTISLGTAPSLQNNQPVEFNHAINYVNK.I

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
105	sp|Q02952|AKA12_HUMAN		34	1	Phosphoprotein																		
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
723		745	2	2305.9354		0.0018	1	33.9	E.TGTDGILAGSQEHDPGQGSSSPE.Q	Phospho (ST)		65.08	TGTDGILAGS#QEHDPGQGSSSPE		29.68						---------Y----------	---------Y----------	K.ETGTDGILAGSQEHDPGQGSSSPEQAGSPTEGEGVSTWESFK.R

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
106	sp|O95159|ZFPL1_HUMAN		33	1	Not annotated																		
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
170		194	3	2605.2019		0.0057	0	26.18	E.VDSASAAPAFYSQAPRPPASPGRPE.Q	Phospho (ST)		57.97	VDSASAAPAFYSQAPRPPAS#PGRPE		22.47								R.AGLGLPLIDEVVSPEPEPLNTSDFSDWSSFNASSTPGPEEVDSASAAPAFYSQAPRPPASPGRPEQHTVIHMGNPEPLTHAPR.K

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
107	sp|O60493|SNX3_HUMAN		33	1	Phosphoprotein																		
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
11		30	2	2310.0974		0.0042	0	19.92	R.LITKPQNLNDAYGPPSNFLE.I	Phospho (Y)		82.46	LITKPQNLNDAY#GPPSNFLE		35.73						----------N--------	----------N--------	R.LITKPQNLNDAYGPPSNFLEIDVSNPQTVGVGR.G

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
108	sp|Q14839|CHD4_HUMAN		33	1	Phosphoprotein																		
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
359		374	2	1980.711		0.0026	1	38.35	E.VTAVDGYETDHQDYCE.V	Phospho (ST)		140.1	VTAVDGYET#DHQDYCE		38.66						--------N-------	--------N-------	K.GEEEVTAVDGYETDHQDYCEVCQQGGEIILCDTCPR.A

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
109	sp|Q13057|COASY_HUMAN		33	1	Phosphoprotein																		
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification		AScore	Ascore validated site(s) (*)		Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
161		189	4	3162.6329		0.0086	1	33.02	E.VPVEPLDVPLPSTIRPASPVAGSPKQPVR.G	2 Phospho (ST)		113.37	VPVEPLDVPLPSTIRPAS#PVAGS#PKQPVR		26.2	55.51					----------------Y----N------	----------------Y----N------	R.LASVLLYSDYGIGEVPVEPLDVPLPSTIRPASPVAGSPKQPVRGYYR.G

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
110	sp|Q9Y2H0|DLGP4_HUMAN		33	1	Phosphoprotein																		

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
761	773	2	1473.5686	0.0026	0	32.68	R.NLSYGDNSDPALE.A	Phospho (ST)	75.4	NLS#YGDNSDPALE	21.51						--N----------	--N----------	R.NLSYGDNSDPALEASSLPPPDPWLETSSSSPAEPAQPGACR.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
111	sp|Q92598|HS105_HUMAN	33	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
538	559	3	2361.0187	0.0065	0	32.66	E.AGTQPQVQTDAQQTSQSPPSPE.L	Phospho (ST)	66.12	AGTQPQVQTDAQQTSQSPPS#PE	38.62						----------Y--	----------Y--	K.NVQQDNSEAGTQPQVQTDAQQTSQSPPSPELTSEENK.I

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
112	sp|Q9C0C2|TB182_HUMAN	33	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1413	1429	2	1897.7118	0.0041	0	28.73	E.DYSSSSLEPHPADPGME.T	Phospho (Y)	121.93	DY#SSSSLEPHPADPGME	22.2						-N----------	-Y----------	R.ELGVGETSGPETQGEDYSSSSLEPHPADPGMETGEALSFGASPGR.C

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
113	sp|Q8WY36|BBX_HUMAN	33	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
224	238	2	1685.6614	0.001	1	32.64	E.VSSGTCRPDVSESPE.L	Phospho (ST)	76.64	VSSGTCRPDVSES#PE	42.65						----------N--	----------N--	K.TEEMPQLNFGMADPTQMGGLSMLLLAGEHALGTPEVSSGTCRPDVSESPELR.Q

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
114	sp|Q02880|TOP2B_HUMAN	32	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1574	1599	3	3016.3462	0.0082	1	34.37	K.KTSFDQDSDVDIFPSDFPTEPPSLPR.T	Phospho (ST)	176.73	KTSFDQDS#DVDIFPSDFPTEPPSLPR	23.52						-------Y----------	-------Y----------	K.TSFDQDSDVDIFPSDFPTEPPSLPRTGR.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
115	sp|P29590|PML_HUMAN	32	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
516	536	3	2334.9736	0.0048	1	22.96	K.AVSPPHLDGPPSPRSPVIGSE.V	3 Phospho (ST)	73.78	AVS#PPHLDGPPS#PRS#PVIGSE	94.94	41.96	37.73				--Y--------Y--Y------	--Y--------Y--Y------	K.AVSPPHLDGPPSPRSPVIGSEVFLPNSNHVASGAGEAEER.V

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
116	sp|P78362|SRPK2_HUMAN	32	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
370	382	2	1562.7428	0.0047	1	32.3	E.LANIDPTWIESPK.T	Phospho (ST)	92.79	LANIDPTWIES#PK	26.42						----------Y--	----------Y--	K.DEDDVDQELANIDPTWIESPKTNGHIENGPFSLEQQLDDEDDDEEDCPNPEEYNLDEPNAESDYTYSSSYEQFNGELPNGR.H

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
117	sp|Q15054|DPOD3_HUMAN	32	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
346	364	2	2158.9074	0.0045	1	31.48	E.AESPSPPPPPSPPLEPVPK.T	3 Phospho (ST)	78.98	AES#PS#PPPPPS#PPLEPVPK	1000						--N-N-----N--------	--N-N-----N--------	K.LPESDSSEDEVFPDSPGAYEAESPSPPPPPSPPLEPVPKTEPEPPSVK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
118	sp|Q13813|SPTA2_HUMAN	32	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1175	1181	2	932.3668	0.0019	0	31.82	E.VYGMMPR.D	Phospho (Y)	118.68	VY#GMMPR	1000						-Y-----	-Y-----	K.VAEDLESEGLMAEEVQAVQQQEVYGMMPRDETDSK.T

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
119	sp|Q53HL2|BOREA_HUMAN	31	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
211	226	2	1744.7572	0.0016	1	31.49	R.IYNISGNGSPLADSKE.I	Deamidated (NQ); Phospho (ST)	67.33	IYNISGNGS#PLADSKE	19.55						--------Y-------	--------Y-------	R.IYNISGNGSPLADSKEIFLTVPVGGGESLR.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
120	sp|P46060|RAGP1_HUMAN	31	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
353	363	2	1271.4832	0.0026	1	16.37	K.VLASLSDDEDE.E	Phospho (ST)	66.05	VLASLS#DDEDE	30.83						-----N-----	-----Y-----	K.VLASLSDDEDEEEEEEGEEEEEEAEEEEEEDEEEEEEEEEEEEEEPQQR.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
121	sp|P28482|MK01_HUMAN	31	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
173	191	3	2302.9333	0.0036	1	31.42	R.VADPDHDHTGFLTEYVATR.W	Phospho (ST); Phospho (Y)	128.83	VADPDHDHTGFLT#EY#VATR	29.09	28.35					----------Y-Y----	----------N-N----	R.VADPDHDHTGFLTEYVATRWYR.A

Supplementary Table S3: Phosphoproteins with the corresponding phosphopeptides and localized phosphosites from solprot*SRS.pombe*) and from SKMel (human melanoma) samples
(*) Phosphorylated amino acid**X** is displayed as **X#**

***Human melanoma* - Chymotrypsin digest of large tryptic peptides**

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
1	sp|Q13263|TIF1B_HUMAN	352	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
2	31	3	2508.0805	0.004	0	60.69	M.AASAAAASAAAASAASGSPGPGEGSAGGEK.R	Acetyl (Protein N-term); Phospho (ST)	96.25	AASAAAASAAAASAASGS#PGPGEGSAGGEK	24.05						----------Y----------	----------Y----------	-.MAASAAAASAAAASAASGSPGPGEGSAGGEKR.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
2	sp|P68363|TBA1B_HUMAN	278	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
423	451	3	3315.2722	0.0025	2	67.05	R.EDMAALEKDYEEVGVDSVEGEGEEEGEEY.-	Phospho (Y)	177.39	EDMAALEKDYEEVGVDSVEGEGEEEGEEY#	105.07						----------Y	----------Y	R.EDMAALEKDYEEVGVDSVEGEGEEEGEEY.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
3	sp|Q13838|UAP56_HUMAN	220	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
2	33	3	3471.4462	0.01	2	76.29	M.AENDVDNELLDYEDDEVETAAGGDGAEAPAKK.D	Acetyl (Protein N-term); Phospho (Y)	179.86	AENDVDNELLDY#EDDEVETAAGGDGAEAPAKK	89.73						----------N----------	----------Y----------	-.MAENDVDNELLDYEDDEVETAAGGDGAEAPAKKDVK.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
4	sp|O75643|U520_HUMAN	202	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
200	217	2	2138.7854	0.0013	1	70.11	Y.GVNVQFESDEEEGDEDVY.G	Phospho (ST)	173.82	GVNVQFES#DEEEGDEDVY	128.29						-------N----------	-------N----------	K.EIQNMDDNIDETYGVNVQFESDEEEGDEDVYGEVR.E
218	237	3	2302.8949	0.0052	1	36.52	Y.GEVREEASDDDMEGDEAVVR.C	Oxidation (M); Phospho (ST)	34.42	GEVREEAS#DDDMEGDEAVVR	1000						-------Y----------	-------Y----------	K.EIQNMDDNIDETYGVNVQFESDEEEGDEDVYGEVREEASDDDMEGDEAVVRCTLSANLVASGELMSSK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
5	sp|P49006|MRP_HUMAN	194	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
158	195	3	3704.5162	0.004	0	68.2	K.GAEASAASEEEAGPQATEPSTPSGPESGPTPASAEQNE.-	Phospho (ST)	185	GAEASAASEEEAGPQATEPST#PSGPESGPTPASAEQNE	30.83						----------Y----------	----------Y----------	K.GAEASAASEEEAGPQATEPSTPSGPESGPTPASAEQNE.-
11	35	4	2488.0885	0.0018	1	18.11	R.GDVTAEEAAGASPAKANGQENGHVK.S	Deamidated (NQ); Phospho (ST)	53.9	GDVTAEEAAGAS#PAKANGQENGHVK	49.69						----------Y----------	----------Y----------	R.GDVTAEEAAGASPAKANGQENGHVKSNGDLSPK.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
6	sp|Q7Z417|NUFP2_HUMAN	190	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
618	639	2	2427.1254	0.0048	1	67.4	K.DYEIESQNPLASPTNTLLGSAK.E	Phospho (ST)	191.28	DYEIESQNPLAS#PTNTLLGSAK	38.66						----------Y----------	----------Y----------	K.DYEIESQNPLASPTNTLLGSAKEQR.Y

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
7	sp|Q9Y3T9|NOC2L_HUMAN	182	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
111	138	4	3145.3065	0.0068	1	48.1	F.HSLPDVLEEASEEEDGAEEGEDGDRVPR.G	Phospho (ST)	139.99	HSLPDVLEEAS#EEEDGAEEGEDGDRVPR	69.38						----------Y----------	----------N----------	K.FLQENDQSLLNFSDSDSSEEEEGPFHSLPDVLEEASEEEDGAEEGEDGDRVPRGLK.G
666	684	2	2363.8374	0.0019	2	50.69	K.DLFDLNSSEEDDTEGFSER.G	2 Phospho (ST)	187.67	DLFDLNS#S#EEDDTEGFSER	68.94	72.25					------YY----------	------YY----------	K.DLFDLNSSEEDDTEGFSERGILRPLSTR.H

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
8	sp|Q14444|CAPR1_HUMAN	178	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
284	297	2	1750.6902	-0.0032	1	69.82	Y.TEQSEVESTEYVNR.Q	Deamidated (NQ); Phospho (Y)	158.95	TEQSEVESTEY#VNR	33.7						----------N---	----------N---	R.VFQSNYFDSTHNHQNGLCEEEEAASAPAVEDQVPEAEPEPAEEYTEQSEVESTEYVNRQFMAETQFTSGEK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
9	sp|Q15365|PCBP1_HUMAN	176	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
161	177	2	2039.9614	0.0194	0	24.19	K.QICLVMLETLSQSPQGR.V	Deamidated (NQ); Phospho (ST)	124.71	QICLVMLETLSQS#PQGR	43.03						----------Y----	----------Y----	K.QICLVMLETLSQSPQGRVMTIPYQPMPASSPVICAGGQDR.C

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
10	sp|Q92734|TFG_HUMAN	174	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
230	247	2	2097.8334	-0.0016	1	34.85	Y.TGAQTQAGQIEGQMYQQY.Q	Deamidated (NQ); Oxidation (M); Phospho (Y)	33.55	TGAQTQAGQIEGQMY#QQY	19.73						----------N---	----------N---	R.SGTPDSIASSSSAAHPPGVQPQQPPYTGAQTQAGQIEGQMYQQYQQQAGYGAQQPQAPPQQPQQYGIQYSASYSQQTGPQQPQQFQGYGQQPTSQAPAPAFSGQPQQLPAQPPQQYQASNYPAQTYTAQTSQPTNYTVAPASQPGMAPSQPGAYQPRPGFTSLPGSTMTPPPSGPNPYAR.N
330	357	3	2916.268	0.0043	1	37.67	Y.TAQTSQPTNYTVAPASQPGMAPSQPGAY.Q	Oxidation (M); Phospho (ST)	82.69	TAQTSQPTNYT#VAPASQPGMAPSQPGAY	33.7						----------N----------	----------N----------	R.SGTPDSIASSSSAAHPPGVQPQQPPYTGAQTQAGQIEGQMYQQYQQQAGYGAQQPQAPPQQPQQYGIQYSASYSQQTGPQQPQQFQGYGQQPTSQAPAPAFSGQPQQLPAQPPQQYQASNYPAQTYTAQTSQPTNYTVAPASQPGMAPSQPGAYQPRPGFTSLPGSTMTPPPSGPNPYAR.N

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
11	sp|P37840|SYUA_HUMAN	173	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
126	140	2	1852.6374	-0.0012	2	40.85	Y.EMPSEEGYQDYEPEA.-	Phospho (Y)	144.05	EMPSEEGYQDY#EPEA	29.64						----------N----	----------Y----	K.NEEGAPQEGILEDMPVDPDNEAYEMPSEEGYQDYEPEA.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
12	sp|P61978|HNRPK_HUMAN	169	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
340	357	2	2161.8154	0.0001	2	44.92	F.SADETWDSAIDTWSPSEW.Q	Phospho (ST)	173.15	SADETWDSAIDTWS#PSEW	24.84						----------N----	----------Y----	R.YDGMVGFSADETWDSAIDTWSPSEWQMAYEPQGGSGYDYSYAGGR.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
13	sp|Q00839|HNRPU_HUMAN	165	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
38	69	3	3222.3922	0.015	0	52.71	R.LQAALDDEEAGGRPAMEPGNGSLDLGGDSAGR.S	Deamidated (NQ); Oxidation (M); Phospho (ST)	65.26	LQAALDDEEAGGRPAMEPGNGS#LDLGGDSAGR	47.92						----------Y----------	----------Y----------	R.LQAALDDEEAGGRPAMEPGNGSLDLGGDSAGRSGAGLEQEAAAGGDEEEEEEEEEGISALDGIDQMELGEENGAAGAADSGPMEEEEAASEDENGDDQGFQEGEDELGDEEEGAGDENGHGEQQPQPPATQQQQPQQQR.G
269	293	3	2999.2462	0.0042	2	16.59	R.AKSPQPPVEEEDEHFDDTVVCLDTY.N	Phospho (ST)	78.66	AKS#PQPPVEEEDEHFDDTVVCLDTY	38.76						--Y----------	--Y----------	R.AKSPQPPVEEEDEHFDDTVVCLDTYNCDLHFK.I

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
14	sp|Q13283|G3BP1_HUMAN	162	4	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
142	173	3	3833.5312	0.007	1	24.85	F.VTEPQEESEEEVEEPEERQQTPEVVPDDSGTF.Y	2 Phospho (ST)	78.42	VTEPQEES#EEEVEEPEERQQT#PEVVPDDSGTF	22.24	48.25					-------Y----------N----------	-------Y----------N----------	R.YQDEVFGGFVTEPQEESEEEVEEPEERQQTPEVVPDDSGTFYDQAVVSNDMEEHLEEPVAEPEPDPEPEPEQEPVSEIQEEKPEPVLEETAPEDAQK.S
142	159	2	2252.8874	0.0029	0	30.18	F.VTEPQEESEEEVEEPEER.Q	Phospho (ST)	102.53	VTEPQEES#EEEVEEPEER	39.52						-------Y----------	-------Y----------	R.YQDEVFGGFVTEPQEESEEEVEEPEERQQTPEVVPDDSGTFYDQAVVSNDMEEHLEEPVAEPEPDPEPEPEQEPVSEIQEEKPEPVLEETAPEDAQK.S
230	247	2	1963.8928	0.0041	0	50.61	K.SSSPAPADIAQTVQEDLR.T	Phospho (ST)	113.67	SSS#PAPADIAQTVQEDLR	19.21						--Y----------	--Y----------	K.SSSPAPADIAQTVQEDLRTFSWASVTSK.N
139	159	3	2513.9992	0.0033	1	34.03	F.GGFVTEPQEESEEEVEEPEER.Q	Phospho (ST)	117.36	GGFVTEPQEES#EEEVEEPEER	36.36						----------Y----------	----------Y----------	R.YQDEVFGGFVTEPQEESEEEVEEPEERQQTPEVVPDDSGTFYDQAVVSNDMEEHLEEPVAEPEPDPEPEPEQEPVSEIQEEKPEPVLEETAPEDAQK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
15	sp|Q9H3N1|TMX1_HUMAN	158	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
234	254	2	2516.9854	0.0052	1	94.31	K.KVEEEQEADEEDVSEEEAESK.E	Phospho (ST)	166.27	KVEEEQEADEEDVS#EEEAESK	66.6						----------Y-------	----------Y-------	K.VEEEQEADEEDVSEEEAESKEGTNK.D
235	254	2	2388.8874	0.0021	0	73.93	K.VEEEQEADEEDVSEEEAESK.E	Phospho (ST)	181.82	VEEEQEADEEDVS#EEEAESK	75.46						----------Y-------	----------Y-------	K.VEEEQEADEEDVSEEEAESKEGTNK.D

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
16	sp|P48681|NEST_HUMAN	151	6	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1406	1436	3	3457.1902	0.0002	2	88.84	R.DGESDGFADEEESGEEGEEDQEEGREPGAGR.W	2 Phospho (ST)	148.48	DGES#DGFADEEES#GEEGEEDQEEGREPGAGR	1000						---Y--------Y----------	---Y--------Y----------	R.DGESDGFADEEESGEEGEEDQEEGREPGAGRWGPGSSVGSLQALSSSQR.G
768	789	3	2602.2751	0.0037	1	22.84	R.SLGEQDQMTLRPPEKVDLEPLK.S	Phospho (ST)	68.03	S#LGEQDQMTLRPPEKVDLEPLK	52.34						Y----------	Y----------	R.SLGEQDQMTLRPPEKVDLEPLKSLDQEIARPLENENQEFLK.S
673	694	3	2586.2368	0.0042	1	26.9	K.ENQEPLRSPEVGDEEALRPLTK.E	Phospho (ST)	82.5	ENQEPLRS#PEVGDEEALRPLTK	101.71						-------Y----------	-------Y----------	K.ENQEPLRSPEVGDEEALRPLTKENQEPLR.S
452	480	3	3065.3662	0.0047	0	42.02	R.QEASTGQSPEDHASLAPPLSPDHSSLEAK.D	Phospho (ST)	82.54	QEASTGQSPEDHASLAPPLS#PDHSSLEAK	25.88						----------Y----------	----------Y----------	R.QEASTGQSPEDHASLAPPLSPDHSSLEAKDGESGGSR.V
766	782	4	2120.0221	0.0024	2	27.76	R.RRSLGEQDQMTLRPPEK.V	Phospho (ST)	95.15	RRS#LGEQDQMTLRPPEK	91.84						--Y----------	--Y----------	R.RSLGEQDQMTLRPPEKVDLEPLK.S
916	933	3	2215.9666	0.0032	2	37.43	R.NLEEEENLGKGEYQESLR.S	Phospho (Y)	148.74	NLEEEENLGKGEY#QESLR	49.74						----------N-----	----------Y-----	R.NLEEEENLGKGEYQESLRSLEEEGQELPQSADVQR.W

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
17	sp|P33991|MCM4_HUMAN	150	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
38	69	3	3409.5442	0.0057	1	35.51	R.RGEDSTSTGELQPMPTSPGVDLQSPAAQDVLF.S	Phospho (ST)	107.39	RGEDSTSTGELQPMPTS#PGVDLQSPAAQDVLF	24.75						----------Y----------	----------Y----------	R.GEDSTSTGELQPMPTSPGVDLQSPAAQDVLFSSPPQMHSSAIPLDFDVSSPLTYGTPSSR.V
37	69	3	3645.6142	0.0082	2	79.58	R.RRGEDSTSTGELQPMPTSPGVDLQSPAAQDVLF.S	2 Phospho (ST)	93.67	RRGEDSTSTGELQPMPTS#PGVDLQS#PAAQDVLF	24.75	37.33					----------Y------N--------	----------Y------Y--------	R.RGEDSTSTGELQPMPTSPGVDLQSPAAQDVLFSSPPQMHSSAIPLDFDVSSPLTYGTPSSR.V

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
18	sp|P39687|AN32A_HUMAN	146	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
149	163	3	1761.6415	0.0048	2	17.68	R.DRDDKEAPDSDAEGY.V	Phospho (ST)	43.37	DRDDKEAPDS#DAEGY	55.58						---------Y-----	---------Y-----	K.LLPQLTYLDGYDRDDKEAPDSDAEGYVEGLDDEEEDEDEEEYDEDAQVVEDEEDEDEEEEGEEEDVSGEEEEDEEGYNDGEVDDEEDEEELGEEER.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
19	sp|P52701|MSH6_HUMAN	145	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
215	234	2	2413.0074	0.0017	1	63.84	Y.VTDKSEEDNEIESEEEVQPK.T	Phospho (ST)	157.26	VTDKSEEDNEIES#EEEVQPK	109.37						----------Y-------	----------Y-------	R.LELAVCDEPSEPEEEEEMEVGTTYVTDKSEEDNEIESEEEVQPKTQGSR.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
20	sp|Q9H1E3|NUCKS_HUMAN	141	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
105	125	2	2566.9154	0.0027	0	63.16	R.EMLMEDVGSEEEQEEEDEAPF.Q	Oxidation (M); Phospho (ST)	61.53	EMLMEDVGS#EEEQEEEDEAPF	1000						--------Y----------	--------Y----------	R.EMLMEDVGSEEEQEEEDEAPFQEK.D

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?

21	sp|Q9Y4E1|FA21C_HUMAN		139		3	Phosphoprotein																	
Start	End		charge	Mr(expt)		Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
536	557		2	2484.0214		-0.0003	2	107.9	K.GLFSDEEDSEDLFSSQSASNLK.G	Phospho (ST)	178.29	GLFS#DEEDSEDLFSSQSASNLK	60.34						---Y----------	---Y----------	K.GLFSDEEDSEDLFSSQSASNLKGASLLPGK.L
1146	1162		2	1877.7474		0.0044	0	28.99	K.SPMFPALGEASSDDDLF.Q	Phospho (ST)	91.07	SPMFPALGEASS#DDDLF	20.35						----------Y------	----------N------	K.SPMFPALGEASSDDDLFQSAKPKPAK.K
263	282		3	2455.0288		0.0013	1	44.56	F.ADSEKEEEDIEDIEENTRPK.R	Phospho (ST)	106.78	ADS#EKEEEDIEDIEENTRPK	128.89						--Y----------	--N----------	K.EEEESDEDFAHHSDNEQNQHTTQMSDEEEDDDGCDLFADSEKEEEDIEDIEENTRPKR.S

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
22	sp|P16401|H15_HUMAN		135		2	Phosphoprotein																	
Start	End		charge	Mr(expt)		Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
2	21		2	2102.9814		0.0042	1	15.16	M.SETAPAETATPAPVEKSPAK.K	Acetyl (Protein N-term); Phospho (ST)	23.12	SETAPAETATPAPVEKS#PAK	24.64						----------Y---	----------N---	-.MSETAPAETATPAPVEKSPAKK.K
2	22		3	2189.0632		0.0015	2	33.76	M.SETAPAETATPAPVEKSPAKK.K	Phospho (ST)	64.62	SETAPAETATPAPVEKS#PAKK	26.97						----------Y----	----------N----	-.MSETAPAETATPAPVEKSPAKKK.A

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
23	sp|Q9UNF0|PACN2_HUMAN		135		2	Phosphoprotein																	
Start	End		charge	Mr(expt)		Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
391	407		2	2081.7534		0.0007	1	26.64	K.TQSYPTDWSDDESNNPF.S	Phospho (ST)	100.09	TQSYPTDWS#DDESNNPF	24.15						--------N--------	--------N--------	K.TQSYPTDWSDDESNNPFSSTDANGDSNPFDDDATSGTEVR.V
362	381		3	2307.892		0.0016	2	30.96	Y.NPFEDEDDTGSTVSEKDDTK.A	Phospho (ST)	51.82	NPFEDEDDTGSTVS#EKDDTK	20.57						----------Y---------	----------Y---------	K.ATDGVTLTGINQTGDQSLPSKPSSTLNVPSNPAQSAQSQSSYNPFEDEDDTGSTVSEKDDTKAK.N

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
24	sp|P46937|YAP1_HUMAN		133		2	Phosphoprotein																	
Start	End		charge	Mr(expt)		Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
300	325		3	2835.2788		0.0042	0	41.37	R.SQLPTLEQDGGTQNPVSSPGMSQELR.T	Phospho (ST)	123.5	SQLPTLEQDGGTQNPVSS#PGMSQELR	23.34						----------Y--------	----------Y--------	R.SQLPTLEQDGGTQNPVSSPGMSQELRTMTTNSSDPFLNSGTYHSR.D
59	76		2	2029.8714		0.0011	1	66.44	R.GDSETDLEALFNAVMNPK.T	Phospho (ST)	165.79	GDS#ETDLEALFNAVMNPK	24.7						----N----------	----Y----------	R.GDSETDLEALFNAVMNPKTANVPQTVPMR.L

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
25	sp|Q03701|CEBPZ_HUMAN		131		3	Phosphoprotein																	
Start	End		charge	Mr(expt)		Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
830	851		2	2683.0154		0.0045	1	65.32	R.DADEESIEDVDDEEFEELIDTF.E	Phospho (ST)	202.61	DADEES#IEDVDDEEFEELIDTF	236.73						-----Y----------	-----Y----------	R.DADEESIEDVDDEEFEELIDTFEDNCFSSGK.D
17	40		2	2802.0214		-0.0086	0	26.7	W.RPEEAVEDPDEEDEDNTSEAENGF.S	Phospho (ST)	99.71	RPEEAVEDPDEEDEDNTS#EAENGF	19.21						----------Y------	----------Y------	K.RPWPREEAVEDPDEEDEDNTSEAENGFSLEEVLR.L
621	647		3	3278.2042		0.0011	2	49.4	R.SQLDDHPESDDEENFIDANDDEDMEKF.T	Phospho (ST)	138.03	SQLDDHPES#DDEENFIDANDDEDMEKF	20.65						--------Y----------	--------Y----------	R.SQLDDHPESDDEENFIDANDDEDMEKFTDADK.E

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
26	sp|P19338|NUCL_HUMAN		130		1	Phosphoprotein																	
Start	End		charge	Mr(expt)		Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
177	217		4	4605.4869		0.0007	0	37.8	K.AAAAAPASEDEDDEDDEDDEDDDDDEEDDSEEEAMETTPAK.G	2 Phospho (ST)	130.56	AAAAAPAS#EDEDDEDDEDDEDDDDEEDDS#EEEAMETTPAK	112.08	39.6					-------Y----------Y----------	-------Y----------Y----------	K.AAAAAPASEDEDDEDDEDDEDDDDEEDDSEEEAMETTPAKGK.K

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
27	sp|P05455|LA_HUMAN		128		2	Phosphoprotein																	
Start	End		charge	Mr(expt)		Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
364	384		4	2405.9465		0.0068	2	22.22	K.FASDDEHDEHDENGATGPVKR.A	Deamidated (NQ); Phospho (ST)	69.56	FAS#DDEHDEHDENGATGPVKR	83.38						---Y----------	---Y----------	K.FASDDEHDEHDENGATGPVKRAR.E
362	383		3	2477.9986		0.0013	2	47.18	K.TKFASDDEHDEHDENGATGPVK.R	Phospho (ST)	95.58	TKFAS#DDEHDEHDENGATGPVK	38.62						----Y----------	----Y----------	K.TKFASDDEHDEHDENGATGPVKR.A

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
28	sp|O15061|SYNEM_HUMAN		125		3	Phosphoprotein																	
Start	End		charge	Mr(expt)		Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
805	831		3	3119.2912		0.0031	2	49.27	R.TKQPQENTTHVEEVTEAGDSEGEQSYF.V	Phospho (ST)	133.26	TKQPQENTTHVEEVTEAGDS#EGEQSYF	35.99						----------N--------	----------N--------	R.TKQPQENTTHVEEVTEAGDSEGEQSYFVSTPDEHPGGHDR.D
1094	1111		2	1839.8292		0	0	37.97	R.TPQGPVSATVEVSSPTGF.A	Phospho (ST)	98.99	TPQGPVSATVEVSS#PTGF	24.75						----------N----	----------Y----	R.TPQGPVSATVEVSSPTGFAQSQVLEDVSQAAR.H
1042	1064		3	2299.0246		0.0016	1	39.37	R.QRSPAPGSPDEEGGAEAPAAGIR.F	Phospho (ST)	92.64	QRSPAPGS#PDEEGGAEAPAAGIR	26.51						-------Y----------	-------Y----------	R.QRSPAPGSPDEEGGAEAPAAGIRFR.R

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
29	sp|Q16630|CPSF6_HUMAN		121		3	Phosphoprotein																	
Start	End		charge	Mr(expt)		Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
25	52		3	3207.2392		0.0048	2	48.63	Y.GGHDQIDLYDDVISPSANNGDAPEDRDY.M	Phospho (ST); Phospho (Y)	151.51	GGHDQIDLY#DDVIS#PSANNGDAPEDRDY	101.69	34.98					--------N-----N----------	--------N----N----------	-.MADGVDHIDIYADVGEEFNQEAEYGGHDQIDLYDDVISPSANNGDAPEDRDYMDTLPPTVGDDVGK.G
34	52		2	2128.8294		0.0072	1	55.19	Y.DDVISPSANNGDAPEDRDY.M	Phospho (ST)	143.98	DDVIS#PSANNGDAPEDRDY	24.75						----N----------	----N----------	-.MADGVDHIDIYADVGEEFNQEAEYGGHDQIDLYDDVISPSANNGDAPEDRDYMDTLPPTVGDDVGK.G
25	50		3	2849.1832		0.0054	1	48.39	Y.GGHDQIDLYDDVISPSANNGDAPEDR.D	Phospho (ST)	143.81	GGHDQIDLYDDVIS#PSANNGDAPEDR	40.46						----------N----------	----------N----------	-.MADGVDHIDIYADVGEEFNQEAEYGGHDQIDLYDDVISPSANNGDAPEDRDYMDTLPPTVGDDVGK.G

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
30	sp|O75030|MITF_HUMAN		116		1	Phosphoprotein																	
Start	End		charge	Mr(expt)		Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
458	476		2	2057.9074		0.0019	1	76.1	F.NNNLGTGTEANQAYSVPTK.M	Phospho (Y)	146.93	NNNLGTGTEANQAY#SVPTK	26.38						----------N-----	----------N-----	K.QEPVLENCSQDLLQHHADLTCTTTLDLTDGTITFNNNLGTGTEANQAYSVPTKMGSK.L

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
31	sp|P55081|MFAP1_HUMAN		113		2	Phosphoprotein																	
Start	End		charge	Mr(expt)		Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence

258	280	3	2720.1043	0.0029	2	26.65	R.SLAALDALNTDDENDEEEYEAWK.V	Phospho (ST)	125.78	SLAALDALNT#DDENDEEEYEAWK	60.71						---------Y-------------	---------Y-------------	R.SLAALDALNTDDENDEEEYEAWKVR.E
107	126	2	2360.9474	0.0024	1	40.93	K.IVEPEVVGESDSEVEGDAWR.M	2 Phospho (ST)	151.79	IVEPEVVGES#DS#EVEGDAWR	1000						---------Y-Y--------	---------Y-Y--------	K.IVEPEVVGESDSEVEGDAWRMER.E
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
32	sp|O00410|IPO5_HUMAN	112	1	Phosphoprotein															
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
815	837	3	2927.08	0.0022	2	15.94	K.RQDEDYDEQVEESLQDEDDNDVY.I	Phospho (Y)	88.62	RQDEDY#DEQVEESLQDEDDNDVY	117.16						-----N-----------------	-----Y-----------------	R.QDEDYDEQVEESLQDEDDNDVYILTK.V
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
33	sp|Q9BQE3|TBA1C_HUMAN	112	1	Phosphoprotein															
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
423	449	3	3045.1162	0.0044	2	50.57	R.EDMAALEKDYEEVGADSADGEDEGEEY.-	Phospho (Y)	189.86	EDMAALEKDYEEVGADSADGEDEGEEY#	55.57						--------------------------N	--------------------------Y	R.EDMAALEKDYEEVGADSADGEDEGEEY.-
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
34	sp|Q15029|U5S1_HUMAN	112	2	Phosphoprotein															
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
13	28	2	1853.7196	-0.0008	0	55.98	Y.IGPELDSDEDDDELGR.E	Phospho (ST)	136.05	IGPELDS#DEDDDELGR	1000						------Y---------	------N---------	-.MDTDLYDEFGNYIGPELDSDEDDDELGRETK.D
13	31	2	2211.9074	0.0018	1	41.35	Y.IGPELDSDEDDDELGRETK.D	Phospho (ST)	107.38	IGPELDS#DEDDDELGRETK	94.38						------Y------------	------N------------	-.MDTDLYDEFGNYIGPELDSDEDDDELGRETKDLDEMDDDDDDDDVGDHDDDHPGMEVVLHEDK.K
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
35	sp|Q9UHR5|S30BP_HUMAN	107	1	Phosphoprotein															
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
15	38	3	2535.9448	0.0033	0	58.36	Y.AEDSEPESDGEAGIEAVGSAAEEK.G	2 Phospho (ST)	94.52	AEDS#EPES#DGEAGIEAVGSAAEEK	90.98	106.45					---Y---Y----------------	---Y---Y----------------	K.NVLSSLAVYAEDSEPESDGEAGIEAVGSAAEEKGGLVSDAYGEDDFSR.L
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
36	sp|O43670|ZN207_HUMAN	106	1	Not annotated															
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
108	127	2	2317.8074	0.0055	2	44.85	K.KQQDDSDEYDDDDSAASTSF.Q	Phospho (ST)	166.27	KQQDDS#DEYDDDDSAASTSF	41.33								K.QQDDSDEYDDDDSAASTSFQPQPVQPQQGYIPPMAQPGLPPVPGAPGMPPGIPPLMPGVPPLMPGMPPVMPGMPPGMMPMGGMMPPGPGIPPLMPGMPPGMPPPVPRPGIPPMTQAQAVSAPGILNRPPAPTATVPAPQPPVTKPLFPSAGQMGTPVTSSSTASSNSESLSASSK.A
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
37	sp|P13861|KAP2_HUMAN	106	2	Phosphoprotein															
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
71	93	3	2632.0522	0.0056	1	32.96	R.VADAKGDSESEEDEDLEVPVPSR.F	2 Phospho (ST)	84.95	VADAKGDS#ES#EEDEDLEVPVPSR	89.59	96.89					-------Y-Y-------------	-------N-N-------------	R.VADAKGDSESEEDEDLEVPVPSRFNR.R
97	117	2	2590.0194	0.0028	2	64.5	R.RVSVCAETYNPDEEEEDTDPR.V	Phospho (ST)	197.17	RVS#VCAETYNPDEEEEDTDPR	94.61						--Y------------------	--N------------------	R.VSVCAETYNPDEEEEDTDPRVIHPK.T
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
38	sp|Q02750|MP2K1_HUMAN	105	1	Phosphoprotein															
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
206	227	3	2453.0824	0.0067	2	17.65	K.LCDFGVSGQLIDSMANSFVGTR.S	Phospho (ST)	62.92	LCDFGVSGQLIDSMANS#FVGTR	38.19						----------------Y-----	----------------N-----	K.LCDFGVSGQLIDSMANSFVGTRSYMSPER.L
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
39	sp|Q8N9T8|KRI1_HUMAN	102	1	Phosphoprotein															
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
172	193	2	2318.9474	0.0047	1	101.75	R.AFVEDSEDEDGAGEGGSSLLQK.R	Phospho (ST)	200.57	AFVEDS#EDEDGAGEGGSSLLQK	160.39						-----Y----------------	-----Y----------------	R.AFVEDSEDEDGAGEGGSSLLQKR.A
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
40	sp|Q13765|NACA_HUMAN	99	1	Phosphoprotein															
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
145	179	4	3939.7333	0.0063	0	38.16	K.VQGEAVSNIQENTQTPTVQEESEEEEVDETGVEVK.D	Phospho (ST)	70.85	VQGEAVSNIQENTQTPTVQEES#EEEEVDETGVEVK	23.29						---------------------Y-------------	---------------------N-------------	K.VQGEAVSNIQENTQTPTVQEESEEEEVDETGVEVKDIELVMSQANVSR.A
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
41	sp|Q99426|TBCB_HUMAN	98	1	Phosphoprotein															
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
224	244	2	2371.0914	0.0042	1	73.31	F.VKPAVVTVGDFPEEDYGLDEI.-	Phospho (Y)	240.46	VKPAVVTVGDFPEEDY#GLDEI	189.55						---------------N-----	---------------Y-----	K.YGAFVKPAVVTVGDFPEEDYGLDEI.-
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
42	sp|Q9H6Y2|WDR55_HUMAN	98	2	Phosphoprotein															
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
4	27	3	2802.0298	0.0028	0	40.45	R.TCEERPAEDGSDEEDPDSMEAPTR.I	Phospho (ST)	111.87	TCEERPAEDGS#DEEDPDSMEAPTR	29.65						----------Y-------------	----------Y-------------	R.TCEERPAEDGSDEEDPDSMEAPTRIR.D
360	383	3	2706.0175	0.0051	2	38.15	F.AGLREEGEDSMAQEEKEETGDDSD.-	Phospho (ST)	138.03	AGLREEGEDSMAQEEKEETGDDS#D	72.65						----------------------Y-	----------------------Y-	K.TWSTDDFFAGLREEGEDSMAQEEKEETGDDSD.-
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
43	sp|Q12888|TP53B_HUMAN	98	1	Phosphoprotein															
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
349	371	3	2485.1425	0.0051	1	34.96	R.SLVQDSLSTNSSDLVAPSPDAFR.S	Phospho (ST)	134.75	SLVQDSLSTNSSDLVAPS#PDAFR	118.03						-----------------Y-----	-----------------Y-----	R.SLVQDSLSTNSSDLVAPSPDAFRSTPFIVPSSPTEQEGR.Q
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
44	sp|P06748|NPM_HUMAN	98	3	Phosphoprotein															
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence

104	134	3	3459.4432	0.0135	0	38.11	K.CGSGPVHISGQHLVAVEEDAESEDEEEEDVK.L	Phospho (ST)	111.79	CGSGPVHISGQHLVAVEEDAES#EDEEEEDVK	107.25						----------Y----------	----------Y----------	K.CGSGPVHISGQHLVAVEEDAESEDEEEEDVKLLSISGK.R
1	24	3	3028.2172	-0.0014	2	23.6	-.MEDSMDMDMSPLRPQNYLFGCELK.A	Acetyl (Protein N-term); Phospho (ST)	55.88	MEDS#MDMDMSPLRPQNYLFGCELK	31.11						---Y----------	---Y----------	-.MEDSMDMDMSPLRPQNYLFGCELKADK.D
1	17	2	2180.7974	0.0051	0	28.81	-.MEDSMDMDMSPLRPQNY.L	Acetyl (Protein N-term); Phospho (ST)	45.78	MEDSMDMDMS#PLRPQNY	22.06						---------Y-------	---------Y-------	-.MEDSMDMDMSPLRPQNYLFGCELK.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
45	sp|Q8IYB3|SRRM1_HUMAN	96	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
763	788	3	2790.4141	0.0035	2	21.44	K.KPPAPPSPVQSQSPSTNWSPAVPVKK.A	Phospho (ST)	70.83	KPPAPPS#PVQSQSPSTNWSPAVPVKK	20.98						------Y----------	------Y----------	K.KPPAPPSPVQSQSPSTNWSPAVPVKKAK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
46	sp|Q13428|TCOF_HUMAN	92	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1094	1120	3	2680.2613	0.002	0	41.68	R.TQPSSGVDSAVGTLPATSPQSTSVQAK.G	Phospho (ST)	117.8	TQPSSGVDSAVGTLPATS#PQSTSVQAK	45.71						----------Y----------	----------Y----------	R.TQPSSGVDSAVGTLPATSPQSTSVQAKGTNK.L
962	985	3	2410.141	0.0019	1	31.1	F.VDPNRSPAGPAATPAQAQAASTPR.K	Phospho (ST)	78.94	VDPNRS#PAGPAATPAQAQAASTPR	21.23						-----Y----------	-----Y----------	K.QDDSGSSSEESDSDGEAPAAVTSAQVIKPPLIFVDPNRSPAGPAATPAQAQAASTPRK.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
47	sp|P17096|HMGA1_HUMAN	90	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
31	55	4	2637.3485	0.007	2	42.23	R.KQPPVSPGTALVGSQKEPSEVPTPK.R	Phospho (ST)	65.21	KQPPVSPGTALVGS#QKEPSEVPTPK	35.83						----------Y----------	----------N----------	K.QPPVSPGTALVGSQKEPSEVPTPKRPR.G
89	107	2	2395.9234	0.0042	2	73.62	K.KLEKEEEEGISQESSEEEQ.-	2 Phospho (ST)	153.32	KLEKEEEEGISQES#S#EEEQ	65.16	58.55					----------YY----	----------YN----	K.LEKEEEEGISQESSEEEQ.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
48	sp|P22059|OSBP1_HUMAN	87	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
348	375	3	3274.3042	0.0046	2	50.07	K.GDMSDEDDENEFFDAPEIITMPENLGHK.R	Phospho (ST)	106.87	GDMS#DEDDENEFFDAPEIITMPENLGHK	119.09						---Y----------	---Y----------	K.GDMSDEDDENEFFDAPEIITMPENLGHKR.T

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
49	sp|Q05655|KPCD_HUMAN	86	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
661	669	2	1045.4636	0.0003	2	62.3	F.AGFSFVNPK.F	Phospho (ST)	101.36	AGFS#FVNPK	1000						---Y-----	---N-----	K.NLIDSMDQSAFAGFSFVNPKFEHLLED.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
50	sp|P55072|TERA_HUMAN	85	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
773	806	3	3299.2882	0.0081	2	22.37	R.FPSGNQGGAGPSQGSGGGTGGSVYTEDNDDDLYG.-	Phospho (Y)	54.13	FPSGNQGGAGPSQGSGGGTGGSVYTEDNDDDLY#G	29.06						----------Y-	----------N-	R.FPSGNQGGAGPSQGSGGGTGGSVYTEDNDDDLYG.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
51	sp|P35579|MYH9_HUMAN	85	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
10	16	2	977.4274	0.0015	2	40.1	Y.LYVDKNF.I	Phospho (Y)	111.67	LY#VDKNF	1000						-Y-----	-N-----	K.YLYVDKNFINNPLAQADWAAK.K
1937	1960	3	2381.9887	0.0027	2	43	R.KGAGDGSDEEVDGKADGAEAKPAE.-	Phospho (ST)	93.87	KGAGDGS#DEEVDGKADGAEAKPAE	1000						------Y----------	------N----------	K.GAGDGSDEEVDGKADGAEAKPAE.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
52	sp|Q13085|ACACA_HUMAN	85	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
19	38	2	2353.9974	0.0007	1	38.38	R.FIIGSVSEDNSEDEISNLVK.L	2 Phospho (ST)	107.37	FIIGS#VSEDNS#EDEISNLVK	28.5	53.45					----Y-----Y---------	----Y-----Y---------	R.FIIGSVSEDNSEDEISNLVKLDLLEEK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
53	sp|Q9H0G5|CCD55_HUMAN	85	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
30	47	2	2047.7534	0.0043	0	84.73	F.GNDSDDDDETSVSESLQR.E	Phospho (ST)	164.81	GNDS#DDDDETSVSESLQR	86.27						---Y----------	---Y----------	K.TQQLHPVLQKPSVFGNDSDDDDETSVSESLQREAAK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
54	sp|P18583|SON_HUMAN	84	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1678	1699	3	2460.2068	0.0031	1	29.63	K.DTEEPLPVKESDQTLAALLSPK.E	Phospho (ST)	84.24	DTEEPLPVKESDQTLAALLS#PK	94.57						----------Y--	----------Y--	K.DTEEPLPVKESDQTLAALLSPKESSGGEK.E
1544	1565	3	2424.0034	0.0059	0	38.75	K.EMEHNTVCAAGTSPVGEIGEEK.I	Phospho (ST)	168	EMEHNTVCAAGTS#PVGEIGEEK	40.71						----------Y---------	----------Y---------	K.EMEHNTVCAAGTSPVGEIGEEKILPTSETK.Q

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
55	sp|Q14157|UBP2L_HUMAN	83	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
439	459	2	2038.9974	-0.0002	0	28.62	K.SPAVATSTAAPPPPSSPLPSK.S	Phospho (ST)	123.54	SPAVATSTAAPPPPS#PLPSK	21.51						----------Y------	----------Y------	K.SPAVATSTAAPPPPSSPLPSKSTSAPQMSPGSSDNQSSSPQPAQQK.L
582	595	2	1684.7204	-0.0001	1	17.19	Y.TSQNNAQGPLYEQR.S	Phospho (Y)	61.24	TSQNNAQGPLY#EQR	42.8						----------N---	----------Y---	K.IPALAVEMPGSADISGLNLQFGALQFGSEPVLSDYESTPTTSASSSQAPSSLVTSTASESSSTSSNQSQESGYQSGPIQSTTYTSQNNAQGPLYEQRSTQTR.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
56	sp|Q16666|IF16_HUMAN	83	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
769	785	2	2040.8094	0.0031	2	34.83	K.DILNPDSSMETSPDFFF.-	Phospho (ST)	95.38	DILNPDSS#METSPDFFF	19.33						-------N---------	-------N---------	K.DILNPDSSMETSPDFFF.-
144	165	3	2267.9581	0.0029	0	28.78	K.VSEEQTQPPSPAGAGMSTAMGR.S	Phospho (ST)	76.24	VSEEQTQPPS#PAGAGMSTAMGR	30.65						----------Y----------	----------Y----------	K.VSEEQTQPPSPAGAGMSTAMGRSPSPK.T

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
57	sp|P62158|CALM_HUMAN	82	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence

128	149	2	2569.0434	0.0045	2	81.9	R.EADIDGDGQVNYEEFVQMMTAK.-	Phospho (Y)	177.51	EADIDGDGQVNY#EEFVQMMTAK	139.06						----------Y----------	----------N----------	R.EADIDGDGQVNYEEFVQMMTAK.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
58	sp|Q15424|SAFB1_HUMAN	81	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
307	348	3	4390.9222	0.0063	0	75.99	R.TDCEPVGLEPAVEQSSAASELAEASSEELAEAPTEAPSPEAR.D	Phospho (ST)	181.83	TDCEPVGLEPAVEQSSAASELAEASSEELAEAPTEAPS#PEAR	38.62						----------Y----	----------Y----	R.TDCEPVGLEPAVEQSSAASELAEASSEELAEAPTEAPSPEARDSK.E				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
59	sp|Q96RN5|MED15_HUMAN	81	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
481	496	3	1727.8255	0.0011	0	23.23	F.LPSPSPQPSQSPVTAR.T	Phospho (ST)	92.85	LPSPSPQPSQS#PVTAR	38.52						----------N-----	----------N-----	R.QPMAQVSQSSLPMLSSPSPGQQVQTPQSMPPPPQPSPQPGQPSSQPNSNVSSGPAPSPSSFLPSPSPQPSQSPVTARTPQNFSVPSPGPLNTPVNPSSVMSPAGSSQAEEQQYLDK.L				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
60	sp|Q15185|TEBP_HUMAN	80	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
107	120	2	1827.5828	0.001	2	32.74	W.KDWEDDSDEDMSNF.D	Oxidation (M); Phospho (ST)	56.29	KDWEDDS#DEDMSNF	37.11						------Y-------	------Y-------	K.DWEDDSDEDMSNFDR.F				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
61	sp|Q08J23|NSUN2_HUMAN	80	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
738	767	4	3173.2493	0.0058	0	32.96	R.AGEPNSPDAEEANSPDVTAGCDPAGVHPPR.-	2 Phospho (ST)	103.17	AGEPNS#PDAEEANS#PDVTAGCDPAGVHPPR	82.02	44.92					-----Y-------Y----------	-----N-------N----------	R.AGEPNSPDAEEANSPDVTAGCDPAGVHPPR.-				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
62	sp|Q9H1I8|ASCC2_HUMAN	79	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
621	639	2	2069.8214	0.004	0	79.04	Y.DGNQVGANDADSDDELISR.R	Phospho (ST)	187.04	DGNQVGANDADS#DDELISR	104.48						----------N-------	----------N-------	R.YEQYSVVVEEVPLQPGESLPYHSVVYYEDEYDDTYDGNQVGANDADSDDELISRRPFTIPQVLR.T				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
63	sp|Q92974|ARHG2_HUMAN	78	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
682	706	3	2515.1257	0.0029	0	25.99	R.EPALPLEPDSGGNTSPGVTANGEAR.T	Phospho (ST)	58.16	EPALPLEPDSGGNTS#PGVTANGEAR	48.87						----------Y----------	----------Y----------	R.EPALPLEPDSGGNTSPGVTANGEARTFNGSIELCR.A				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
64	sp|P11388|TOP2A_HUMAN	78	2	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
1097	1125	3	3322.3072	0.0026	2	43.64	K.VPDEEENEESDNEKETEKSDSVTDSGPTF.N	Phospho (ST)	105.72	VPDEEENEES#DNEKETEKSDSVTDSGPTF	51.96						---------Y----------	---------Y----------	K.VPDEEENEESDNEKETEKSDSVTDSGPTFNYLLDMPLWYLTK.E				
1092	1114	3	2813.1439	0.0039	2	42.87	K.EAQQKVPDEEENEESDNEKETEK.S	Phospho (ST)	112.68	EAQQKVPDEEENEES#DNEKETEK	64.3						--------------Y--------	--------------Y--------	K.EAQQKVPDEEENEESDNEKETEKSDSVTDSGPTFNYLLDMPLWYLTK.E				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
65	sp|Q9Y6D5|BIG2_HUMAN	77	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
207	229	3	2604.2989	0.0024	0	36.96	R.ELEKPIQSKPQSPVIQAAAVSPK.F	2 Phospho (ST)	93.22	ELEKPIQSKPQS#PVIQAAAVS#PK	39.27	108.36					----------Y--------Y--	----------Y--------Y--	R.ELEKPIQSKPQSPVIQAAAVSPKFVR.L				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
66	sp|P56693|SOX10_HUMAN	76	3	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
412	425	2	1523.6102	0.002	2	35.54	Y.YGHSGQASGLYSAF.S	Phospho (Y)	112.4	YGHSGQASGLY#SAF	24.44						----------N---	----------N---	K.TETAGPQGPPHYTDQPSTSQIAYTSLSLPHYGSAFPSISRPQFDYSDHQPSGPYYGHSGQASGLYSAFSYMGPSQRPLYTAISDPSPSGPQSHSPTHWEQPVYTTLSRP.-				
437	455	2	2067.8734	0.0047	0	38.7	Y.TAISDPSPSGPQSHSPTHW.E	Phospho (ST)	62.03	TAISDPSPSGPQSHS#PTHW	24.84						--------------N----	--------------N----	K.TETAGPQGPPHYTDQPSTSQIAYTSLSLPHYGSAFPSISRPQFDYSDHQPSGPYYGHSGQASGLYSAFSYMGPSQRPLYTAISDPSPSGPQSHSPTHWEQPVYTTLSRP.-				
334	353	3	2009.0632	0.0033	0	33.28	W.ISKPPGVALPTVSPPGVDAK.A	Phospho (ST)	81.94	ISKPPGVALPTVS#PPGVDAK	23.64						------------N-------	------------N-------	R.SMGEGGKPHIDFGNVDIGEISHEVMSNMETFDVAELDQYLPPNGHPGHVSSYSAAGYGLGSALAVASGHSAWISKPPGVALPTVSPPGVDAKAQVK.T				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
67	sp|Q13610|PWP1_HUMAN	76	2	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
41	67	3	2934.1354	0.0008	1	37.94	K.EKLQEEGGGSDEEETGSPSEDGMQSAR.T	Oxidation (M); Phospho (ST)	109.55	EKLQEEGGGS#DEEETGSPSEDGMQSAR	156.91						---------Y----------	---------Y----------	K.EKLQEEGGGSDEEETGSPSEDGMQSARTQARPR.E				
43	67	3	2661.0037	0.0016	0	32.87	K.LQEEGGGSDEEETGSPSEDGMQSAR.T	Phospho (ST)	154.61	LQEEGGGS#DEEETGSPSEDGMQSAR	32.25						-------Y----------	-------Y----------	K.LQEEGGGSDEEETGSPSEDGMQSARTQARPR.E				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
68	sp|Q13439|GOGA4_HUMAN	74	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
259	279	2	2324.9934	0.0037	1	71.38	F.TKEENPESDGEPVVEDGTSVK.T	Phospho (ST)	150.24	TKEENPES#DGEPVVEDGTSVK	78.33						-------Y----------	-------Y----------	R.NGPMNVDVLKPLPQLEPQAEVFTKEENPESDGEPVVEDGTSVKTLETLQQR.V				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
69	sp|O00148|DDX39_HUMAN	74	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
2	32	3	3632.5612	0.0045	2	63.53	M.AEQDVENDLLDYDEEEEPQAPQESTPAPPKK.D	Acetyl (Protein N-term); Phospho (Y)	76.22	AEQDVENDLLDY#DEEEEPQAPQESTPAPPKK	46.95						----------N----------	----------Y----------	-.MAEQDVENDLLDYDEEEEPQAPQESTPAPPKKDIK.G				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
70	sp|P63172|DYLT1_HUMAN	74	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1	22	2	2608.1334	0.0043		2	72.65	-.MEDYQAAEETAFVVDEVSNIVK.E	Acetyl (Protein N-term); Phospho (Y)	86.08	MEDY#QAAEETAFVVDEVSNIVK	60.66								- .MEDYQAAEETAFVVDEVSNIVKEA IESAIGGNAYQHSK.V

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
71	sp|Q14839|CHD4_HUMAN	74	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
422	451	3	3555.3742	0.0074		1	62.79	W.EAKEDNSEGEEILEEVGGDLEEEDDHHMEF.C	Oxidation (M); Phospho (ST)	16.39	EAKEDNS#EGEEILEEVGGDLEEEDDHHMEF	1000						------Y----------	------Y----------	K.EGIQWEAKEDNSEGEEILEEVG GDLEEEDDHHMEFCR.V

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
72	sp|Q8NAV1|PR38A_HUMAN	74	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
181	206	3	3229.1962	0.002		1	73.54	R.VSALEEDMDDVESSEEEEEEDEKLER.V	2 Phospho (ST)	148.5	VSALEEDMDDVES#S#EEEEEDEKLER	137.82	131.16					----------YY----------	----------YY----------	R.VSALEEDMDDVESSEEEEEDE KLERVPSPDHR.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
73	sp|Q7L014|DDX46_HUMAN	73	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
797	824	3	3105.3052	0.0043		1	49.54	K.AALGLQDSDDEDAAVDIDEQIESMFNSK.K	Phospho (ST)	168.96	AALGLQDS#DDEDAAVDIDEQIESMFNSK	147.4						-------Y----------	-------Y----------	K.AALGLQDSDDEDAAVDIDEQIES MFNSKK.R
797	821	3	2776.1338	0.0028		0	37.27	K.AALGLQDSDDEDAAVDIDEQIESMF.N	Phospho (ST)	128.83	AALGLQDS#DDEDAAVDIDEQIESMF	122.56						-------Y----------	-------Y----------	K.AALGLQDSDDEDAAVDIDEQIES MFNSK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
74	sp|Q99549|MPP8_HUMAN	73	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
44	63	2	2237.8574	0.0049		2	72.54	R.GAEAFGDSEEDGEDVFEVEK.I	Phospho (ST)	175.97	GAEAFGDS#EEDGEDVFEVEK	1000						-------Y----------	-------Y----------	R.GAEAFGDSEEDGEDVFEVEKILD MK.T

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
75	sp|Q01844|EWS_HUMAN	72	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
71	86	2	1728.7416	0.002		1	33.26	Y.GQPPTGYTTPTAPQAY.S	Phospho (ST)	116.02	GQPPTGYTT#PTAPQAY	21.3						--------N-------	--------Y-------	- .MASTDYSTYSQAAAQQGYSAYTA QPTQGYAQTTQAYGQQSYGTYGQ PTDVSYTQAQTTATYGQTAYATSY GQPPTGYTTPTAPQAYSQPVQGY GTGAYDTTTATVTTTQASYAAQSA YGTQPAYPAYGQQPAATAPTRPQ DGNKPTETSQPQSSTGGYNQPSL GYGQSNYSYPQVPGSYPMQPVTA PPSYPPTSYSSTQPTSYDQSSYSQ QNTYGQPSSYGQQSSYGQQSSY GQQPPTSYPPQTGSYSQAPSQ

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
76	sp|P42166|LAP2A_HUMAN	71	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
61	86	3	2729.1412	0.0041		2	46.37	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S	2 Phospho (ST)	147.7	GPPDFS#S#DEEREPTPVLGSGAAAAGR	49.76	53.38					-----YY----------	-----YN----------	K.GPPDFSSDEEREPTPVLGSGAA AAGRSR.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
77	sp|Q7Z739|YTHD3_HUMAN	71	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
107	124	2	1903.8666	0.0048		1	46.55	F.SQPGALGNTPPFLGQHGF.N	Phospho (ST)	79.32	SQPGALGNT#PPFLGQHGF	65.92								K.DAVNDDDFEPYLSSQTNQSNSY PPMSDPYMPSYYAPSIGFPYSLGE AAWSTAGDQPMPYLTTYGQMSNG EHHYIPDGVFSQPGALGNTPPFLG QHGFNFFPGNADFSTWGTSGSQG QSTQSSAYSSSYGYPPSSLGR.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
78	sp|P53396|ACLY_HUMAN	67	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
438	452	2	1537.7148	0.0011		0	62.03	F.LLNASGSTSTPAPSR.T	Phospho (ST)	157.42	LLNASGSTSTPAPS#R	86.22						----------N-	----------N-	K.TTGIPIIHVFGTETHMTAIVGMALG HRPIPNQPPTAAHTANFLLNASGST STPAPSRTASFSESR.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
79	sp|O94885|SASH1_HUMAN	66	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
88	108	3	2447.2072	0.0015		1	65.77	R.RVSQDLEVEKPDASPTSLQLR.S	Phospho (ST)	119.24	RVS#QDLEVEKPDASPTSLQLR	113.69						--Y----------	--Y----------	R.VSQDLEVEKPDASPTSLQLRSQI EESLGFCSAVSTPEVER.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
80	sp|Q99614|TTC1_HUMAN	65	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
83	102	2	2434.0334	0.0023		1	65.23	K.SNEDVNSSELDEEYLIELEK.N	Phospho (Y)	149.37	SNEDVNSSELDEEY#LIELEK	59.88						----------N------	----------Y------	K.SNEDVNSSELDEEYLIELEKNMS DEEK.Q

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
81	sp|P23588|IF4B_HUMAN	65	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
56	70	3	1848.7816	0.0024		2	20.14	W.HSNDDDVYRAPPIDR.S	Phospho (Y)	71.28	HSNDDDVY#RAPPIDR	41.38						-------N-------	-------N-------	K.TISLTDFLAEDGGTGGGSTYVSK PVSWADETDDLEGDVSTTWHSND DDVYRAPPIDRSILPTAPR.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
82	sp|Q9Y2X3|NOP58_HUMAN	63	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
495	517	3	2741.1577	0.0033		1	20.1	K.HIKEEPLSEEEPCTSTAIASPEK.K	2 Phospho (ST)	88.9	HIKEEPLS#EEEPCTSTAIAS#PEK	28.39	53.41					-------Y----------Y---	-------Y----------Y---	K.HIKEEPLSEEEPCTSTAIASPEKK .K

495	518	4	2869.2529	0.0036	2	35.5	K.HIKEEPLSEEEPCTSTAIASPEKK.K	2 Phospho (ST)	72.95	HIKEEPLS#EEEPCTSTAIAS#PEKK	23.01	19.84					-------Y----------Y----	-------Y----------Y----	K.HIKEEPLSEEEPCTSTAIASPEKKK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
83	sp|Q96JM3|ZN828_HUMAN	62	2 Phosphoprotein	

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
199	219	2	2313.1094	0.0036	0	42.99	K.LAPVPSPEPQKPAPVSPESVK.A	2 Phospho (ST)	79.23	LAPVPS#PEPQKPAPVS#PESVK	85.92	39.2					-----Y---------Y-----	-----Y---------Y-----	K.LAPVPSPEPQKPAPVSPESVKATLSNPKPQK.Q
302	324	4	2568.2229	0.0037	2	29.3	R.RPAPAVSPGSWKPGPPGSPRPWK.S	2 Phospho (ST)	101.12	RPAPAVS#PGSWKPGPPGS#PRPWK	55.58	40.31					------Y---------Y-----	------Y---------Y-----	R.RPAPAVSPGSWKPGPPGSPRPWKSNPSASSGPWKPAKPAPSVSPGPWKPIPSVSPGPWKPTPSVSSASWK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
84	sp|Q32MZ4|LRRF1_HUMAN	62	1 Phosphoprotein	

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
763	789	3	3003.3022	0.0026	2	61.53	K.ALDSNSLENDDLSAPGREPGHFNPESR.E	Phospho (ST)	101.86	ALDS#NSLENDDLSAPGREPGHFNPESR	24.75						---N----------	---N----------	K.ALDSNSLENDDLSAPGREPGHFNPESREDTR.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
85	sp|P12270|TPR_HUMAN	61	1 Phosphoprotein	

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
2210	2225	2	1705.8724	0.0032	0	29.33	R.SVPTTPLQVAAPVTVF.T	Phospho (ST)	105.91	SVPTT#PLQVAAPVTVF	24.44						----N----------	----N----------	R.SVPTTPLQVAAPVTVFTESTTSDASEHASQSVPMVTTSTGTLSTTNETATGDDGDEVFVEAESEGISSEAGLEIDSQQEEEPVQASDESDLPSTSQDPPSSSSVDTSSSQPKPFR.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
86	sp|Q16543|CDC37_HUMAN	61	1 Phosphoprotein	

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
8	29	2	2578.0414	0.003	0	61.2	W.DHIEVSDDEDETHPNIDTASLF.R	Phospho (ST)	91.26	DHIEVS#DDEDETHPNIDTASLF	54.9						-----Y----------	-----Y----------	-.MVDYSVWDHIEVSDDEDETHPNIDTASLFR.W

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
87	sp|Q7Z5K2|WAPL_HUMAN	61	1 Phosphoprotein	

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
64	87	2	2652.0654	0.0014	2	60.96	K.VEEESTGDPFGFDSDDESLPVSSK.N	Phospho (ST)	213.76	VEEESTGDPFGFDS#DDESLPVSSK	65.02						----------Y----------	----------Y----------	K.VEEESTGDPFGFDSDDESLPVSSKNLAQVK.C

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
88	sp|Q8WWM7|ATX2L_HUMAN	61	1 Phosphoprotein	

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
580	599	2	2168.9954	0.0042	1	50.17	K.EKEVDGLLTSEPMGSPVSSK.T	Phospho (ST)	110.46	EKEVDGLLTSEPMGS#PVSSK	38.7						----------Y-----	----------Y-----	K.EKEVDGLLTSEPMGSPVSSKTESVSDK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
89	sp|Q86W92|LIPB1_HUMAN	60	1 Phosphoprotein	

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
950	970	3	2621.0869	0.0029	2	60.18	R.LYEEDDLDRLEQMEDSEGTVR.Q	Phospho (Y)	173.44	LY#EEDDLDRLEQMEDSEGTVR	138.94						-N----------	-Y----------	R.LYEEDDLDRLEQMEDSEGTVRQIGAFSEGINNLTHMLK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
90	sp|Q9BTC0|DIDO1_HUMAN	59	1 Phosphoprotein	

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1454	1477	4	2613.2957	0.0045	1	24.16	R.RNSVERPAEPVAGAATPSLVEQQK.M	Phospho (ST)	70.9	RNS#VERPAEPVAGAATPSLVEQQK	25.31						--Y----------	--Y----------	R.NSVERPAEPVAGAATPSLVEQQKMLEELNK.Q

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
91	sp|P11717|MPRI_HUMAN	58	1 Phosphoprotein	

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
2398	2420	2	2576.1594	0.0064	0	49.53	K.ALSSLHGDDQDSEDEVLTIPEVK.V	Phospho (ST)	158.56	ALSSLHGDDQDS#EDEVLTIPEVK	77.16						----------Y----------	----------Y----------	K.ALSSLHGDDQDSEDEVLTIPEVKVHSGR.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
92	sp|Q12792|TWF1_HUMAN	58	1 Phosphoprotein	

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
137	155	2	2154.0314	0.0069	1	57.9	K.YLLSQSSPAPLTAAEEELR.Q	Phospho (ST)	132.67	YLLSQSS#PAPLTAAEEELR	28.87						------Y----------	------Y----------	K.YLLSQSSPAPLTAAEEELRQIK.I

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
93	sp|O95218|ZRAB2_HUMAN	58	3 Phosphoprotein	

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
115	127	2	1696.6156	0.0015	2	17.23	Y.IEREESDGEYDEF.G	Phospho (ST)	126.72	IEREES#DGEYDEF	55.22						-----Y-------	-----Y-------	R.ENVEYIEREESDGEYDEFGR.K
147	166	3	2418.8986	0.0027	1	32.2	K.EVEDKESEGEEEDEDEDLSK.Y	Phospho (ST)	119.92	EVEDKES#EGEEEDEDEDLSK	136.96						------Y----------	------Y----------	K.EVEDKESEGEEEDEDEDLSKYK.L
147	167	3	2581.9621	0.0029	2	19.62	K.EVEDKESEGEEEDEDEDLSKY.K	Phospho (ST)	70.97	EVEDKES#EGEEEDEDEDLSKY	87.84						------Y----------	------Y----------	K.EVEDKESEGEEEDEDEDLSKYK.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
94	sp|O60293|ZC3H1_HUMAN	57	1 Phosphoprotein	

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
510	523	2	1516.6468	0.0022	1	57.32	R.SLDKQPTDSGGGIY.Q	Phospho (ST)	158.74	S#LDKQPTDSGGGIY	94.11						N----------	N----------	R.SLDKQPTDSGGGIYQYDNYEEVAMDTDSETSSPAPSPVQPPFFSECSLGYFSPAPSLSLPPPPQVSSLPPLSQPYVEGLCVSLEPLPPLPPPLPPEDPEQPPKPPFADEEEEEEMLLR.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
95	sp|P36871|PGM1_HUMAN	57	1 Phosphoprotein	

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
108	130	3	2285.1235	0.0029	1	34.85	K.AIGGIILTASHNPGGPNGDFGIK.F	Phospho (ST)	141.71	AIGGIILTAS#HNPGGPNGDFGIK	24.15						---------Y----------	---------Y----------	K.AIGGIILTASHNPGGPNGDFGIKFNISNGGPAPEAITDK.I

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
96	sp|Q9BQG0|MBB1A_HUMAN	57	1 Phosphoprotein	

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1	25	3	2763.1771	0.0029	1	38.27	-.MESRDPAQPMSPGEATQSGARPADR.Y	Acetyl (Protein N-term); Phospho (ST)	71.78	MESRDPAQPMS#PGEATQSGARPADR	34.72						----------Y----------	----------Y----------	-.MESRDPAQPMSPGEATQSGARPADRYGLLK.H

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
97	sp|Q9UNF1|MAGD2_HUMAN	57	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
138	171	3	3657.5782	0.0078	0	60.74	K.AQETEAAPSQAPADEPEPESAAAQSQENQDTRPK.V	Phospho (ST)	156.32	AQETEAAPSQAPADEPEPESAAAQS#QENQDTRPK	21.36						----------Y----------	----------Y----------	K.AQETEAAPSQAPADEPEPESAAAQSQENQDTRPKVK.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
98	sp|Q8N122|RPTOR_HUMAN	56	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
868	894	3	2671.2259	0.002	0	55.92	K.GVHIHQAGGSPPASSTSSSSLTNDVAK.Q	Phospho (ST)	106.85	GVHIHQAGGS#PPASSTSSSSLTNDVAK	46.38						---------Y----------	---------Y----------	K.GVHIHQAGGSPPASSTSSSSLTNDVAKQPVSR.D

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
99	sp|P43307|SSRA_HUMAN	56	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
241	270	3	3470.5522	0.0038	2	42.66	K.VEMGTSSQNDVDMSWIPQETLNQINKASPR.R	Oxidation (M); Phospho (ST)	62.94	VEMGTSSQNDVDMSWIPQETLNQINKAS#PR	23.73						----------Y--	----------Y--	K.VEMGTSSQNDVDMSWIPQETLNQINKASPRR.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
100	sp|O60271|JIP4_HUMAN	56	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
920	944	2	2789.2014	0.0058	1	39.89	F.TDPLGVQIPEDLSPVYQSSNDSDAY.K	Phospho (ST)	164.98	TDPLGVQIPEDLSPVY#QSSNDSDAY	27.03						----------N---	----------N---	K.ASLCGSMTSNSSAETDSLLGGITVVGCSAEGVTGAATSPSTNGASPVMDKPPEMEAENSEVDENVPTAEEATEATEGNAGSAEDTVDISQTGVYTEHVFTDPLGVQIPEDLSPVYQSSNDSDAYK.D
199	222	3	2664.2998	0.0033	0	36.32	K.ERPISLGIFPLPAGDGLLTPDAQK.G	2 Phospho (ST)	100.85	ERPIS#LGIFPLPAGDGLLT#PDAQK	1000						----Y----------Y-----	----Y----------Y-----	K.ERPISLGIFPLPAGDGLLTPDAQKGGETPGSEQWK.F

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
101	sp|O00505|IMA3_HUMAN	55	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
50	67	2	2115.8554	0.0033	1	55.39	R.NVPQEESLEDSDVDADFK.A	Phospho (ST)	159.9	NVPQEESLEDS#DVDADFK	62.59						----------Y-------	----------Y-------	R.NVPQEESLEDSDVDADFKAQNVTLEAILQNATSDNPVVQLSAVQAAR.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
102	sp|P16070|CD44_HUMAN	55	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
695	715	4	2348.1229	0.0034	1	15.86	R.KPSGLNGEASKSQEMVHLVNK.E	Oxidation (M); Phospho (ST)	49.38	KPSGLNGEASKS#QEMVHLVNK	20.57						----------Y---------	----------Y---------	R.KPSGLNGEASKSQEMVHLVNKESSETPDQFMTADETR.N
682	705	3	2492.191	0.0002	1	27.06	K.LVINSGNGAVEDRKPSGLNGEASK.S	Deamidated (NQ); Phospho (ST)	24.87	LVINSGNGAVEDRKPS#GLNGEASK	22.53						---------------Y--------	---------------Y--------	K.LVINSGNGAVEDRKPSGLNGEASKSQEMVHLVNK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
103	sp|P27708|PYR1_HUMAN	54	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1855	1871	4	1952.9385	0.0028	2	50.2	R.IHRASDPGLPAEEPKEK.S	Phospho (ST)	99.8	IHRAS#DPGLPAEEPKEK	1000						----Y----------	----Y----------	R.IHRASDPGLPAEEPKEKSSR.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
104	sp|Q9NZM5|GSCR2_HUMAN	54	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
295	330	3	3848.5672	0.0006	0	54.26	F.QELCEGLLEESDGEGEPGQGEGPEAGDAEVCPTPAR.L	Phospho (ST)	149.84	QELCEGLLEES#DGEGEPGQGEGPEAGDAEVCPTPAR	112.35								R.QALPATEQAATQESTFQELCEGLLEESDGEGEPGQGEGPEAGDAEVCPTPARLATTEK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
105	sp|P35221|CTNA1_HUMAN	54	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
634	651	2	2237.8554	0.0029	2	51.23	R.TPEELDDSDFETEDFDVR.S	Phospho (ST)	150.2	TPEELDDS#DFETEDFDVR	44.37						-------Y----------	-------Y----------	R.TPEELDDSDFETEDFDVRSR.T

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
106	sp|Q9NYV4|CDK12_HUMAN	54	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
664	689	3	2890.3528	0.0085	0	39.15	R.HLLTDLPLPPELPGGDLSPPDSPEPK.A	2 Phospho (ST)	152.13	HLLTDLPLPPELPGGDLS#PPDS#PEPK	174.5	170.65					----------Y---Y----	----------Y---Y----	R.HLLTDLPLPPELPGGDLSPPDSPEPKAITPPQQPYK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
107	sp|Q9BVL2|NUPL1_HUMAN	54	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
530	553	2	2316.9954	0.0054	2	53.68	F.GFGTTNKPSGSLSAGFGSSSTSGF.N	Phospho (ST)	172.33	GFGTTNKPSGSLS#AGFGSSSTSGF	24.84								R.VTTGPTPFSTMPNAAAVAMAATLTQQQQPATGPQPSLGVSFGTPFGSGIGTGLQSSGLGSSNLGGFGTSSGFGCSTTGASTFGFGTTNKPSGSLSAGFGSSSTSGFNFSNPGITASAGLTFGVSNPASAGFGTGGQLLQLK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
108	sp|Q96TA1|NIBL1_HUMAN	54	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
623	641	3	2094.8572	0.0024	0	44.85	F.EASPESPPPASPDGVTEIR.G	2 Phospho (ST)	124.52	EASPES#PPPAS#PDGVTEIR	35.76	52.67					-----Y----Y--------	-----Y----Y--------	K.QVVSVVQDEEVGLPFEASPESPPPASPDGVTEIRGLLAQGLRPESPPPAGPLLNGAPAGESPQPK.A
642	672	3	3095.5852	0.0047	0	20.11	R.GLLAQGLRPESPPPAGPLLNGAPAGESPQPK.A	Phospho (ST)	97.84	GLLAQGLRPES#PPAGPLLNGAPAGESPQPK	99.74						----------Y----------	----------Y----------	R.GLLAQGLRPESPPPAGPLLNGAPAGESPQPKAAPEASSPPASPLQHLLPGK.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
109	sp|P54727|RD23B_HUMAN	53	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence

145	173	3	3024.3592	0.0031	0	33.53	K.QEKPAEKPAETPVATSPTATDST SGDSSR.S	Phospho (ST)	71.52	QEKPAEKPAET#PVATSPTATDST SGDSSR	30.65						----------Y----------	----------Y----------	K.QEKPAEKPAETPVATSPTATDST SGDSSRSNLFEDATSALVTGQSYE NMVTEIMSMGYER.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
110	sp|P49736|MCM2_HUMAN	53	2	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence		
134	150	3	2100.9019	0.0018	2	22.42	R.GLLYDSDEEDEERPARK.R	Phospho (ST)	86.77	GLLYDS#DEEDEERPARK	28.28						-----Y----------	-----Y----------	R.GLLYDSDEEDEERPARKR.R		
134	149	3	1972.8085	0.0034	1	29.14	R.GLLYDSDEEDEERPAR.K	Phospho (ST)	51.67	GLLYDS#DEEDEERPAR	20.17						-----Y----------	-----Y----------	R.GLLYDSDEEDEERPARK.R		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
111	sp|Q96DT7|ZBT10_HUMAN	53	1	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence		
539	556	2	2014.7814	-0.0012	0	53.11	W.VQDGSPEMAENESEGQTK.V	Phospho (ST)	110.04	VQDGS#PEMAENESEGQTK	105.86						----N----------	----N----------	K.IENDGCNVDEGQIENYQMNDSS WVQDGSPEMAENESEGQTKVFIW NNMGSQGIQETGK.T		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
112	sp|P40763|STAT3_HUMAN	53	2	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence		
710	729	2	2389.0574	0.0057	1	52.8	K.FICVTPTTCSNTIDLPMSPR.T	Phospho (ST)	192.45	FICVTPTTCSNTIDLPMS#PR	128.57						----------Y--	----------Y--	K.FICVTPTTCSNTIDLPMSPRTLDS LMQFGNNGEGAEPSAGGQFESLT FDMELTSECATSPM.-		
686	707	3	2581.0924	-0.002	2	19.7	K.YCRPESQEHPEADPGSAAPYLK. T	Phospho (Y)	89.36	YCRPESQEHPEADPGSAAPY#LK	24.81						----------Y--	----------Y--	K.YCRPESQEHPEADPGSAAPYLK TK.F		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
113	sp|Q15084|PDIA6_HUMAN	53	1	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence		
413	440	3	3165.3802	0.004	2	52.78	W.DGRDGELPVEDDIDLSDVELDDL GKDEL.-	Phospho (ST)	185.06	DGRDGELPVEDDIDLS#DVELDDLG KDEL	1000						----------Y----------	----------Y----------	R.EPWDGRDGELPVEDDIDLSDVE LDDLGKDEL.-		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
114	sp|Q9H6F5|CCD86_HUMAN	53	2	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence		
31	53	3	2634.202	0.0057	2	23.25	R.ALVEFESNPEETREPGSPPSVQ R.A	Phospho (ST)	91.22	ALVEFESNPEETREPGS#PPSVQR	19.94						----------Y------	----------Y------	R.ALVEFESNPEETREPGSPPSVQ RAGLGSPERPPK.T		
10	27	3	2020.0129	0.0026	1	33.87	R.RLGGLRPESPESLTSVSR.T	Phospho (ST)	64.73	RLGGLRPES#PESLTSVSR	46.11						--------Y---------	--------Y---------	R.LGGLRPESPESLTSVSRTR.R		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
115	sp|P41743|KPCI_HUMAN	52	1	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence		
557	572	2	1905.8364	0.0007	0	52.28	F.TNEPVQLTPDDDDIVR.K	Phospho (ST)	132.02	TNEPVQLT#PDDDDIVR	81.59						-------Y--------	-------Y--------	K.QVVPPFKPNISGEFGLDNFDSQF TNEPVQLTPDDDDIVRK.I		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
116	sp|Q8N201|INT1_HUMAN	52	1	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence		
914	937	3	2666.089	0.0021	1	51.79	F.LLHDAVDDAASGEEDDEGESKE QK.A	Phospho (ST)	82.48	LLHDAVDDAAS#GEEDDEGESKEQ K	29.71						----------N----------	----------N----------	R.QASSQSMPWLADLVQSSEGSLD VLPVQCLCEFLLHDAVDDAASGEE DDEGESKEQKAK.K		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
117	sp|Q15459|SF3A1_HUMAN	51	1	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence		
317	338	3	2696.0245	0.0037	2	51.4	K.FGESEEVEMEVESDEEDDKQEK .A	Phospho (ST)	164.8	FGESEEVEMEVES#DEEDDKQEK	86.9						----------Y---------	----------Y---------	K.FGESEEVEMEVESDEEDDKQEK AEEPPSQLDQDTQVQDMDEGSDD EEEGQK.V		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
118	sp|A6NER3|GG12J_HUMAN	51	1	Not annotated																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence		
33	50	2	2020.8274	0.0012	0	37.86	F.SDEVEPATPEEGEPATQR.Q	Phospho (ST)	117.47	SDEVEPAT#PEEGEPATQR	64.26								R.STYYWPRPRPYVQPPEMIGPMR PEQFSDEVEPATPEEGEPATQRQ DPAAAQEGEDEGASAGQGPKPEA DSQEQGHPQTGCECEDGPDGQE MDPPNPEEVK.T		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
119	sp|Q8NE71|ABCF1_HUMAN	51	2	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence		
223	250	3	3122.1532	0.0011	2	20.36	K.KAEQGSEEEGEGEEEEEEGGES KADDPY.A	Phospho (ST)	68.36	KAEQGS#EEEGEGEEEEEEGGES KADDPY	108.18						-----Y----------	-----Y----------	K.AEQGSEEEGEGEEEEEEGGESK ADDPYAHLSK.K		
133	158	3	3065.4262	0.0032	1	15.68	F.AALIQDQSEEEEEEEKHPPKPAK PEK.N	Phospho (ST)	74.44	AALIQDQS#EEEEEEEKHPPKPAK PEK	1000						--------Y----------	--------Y----------	K.GGNVFAALIQDQSEEEEEEEKHP PKPAKPEKNR.I		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
120	sp|O43768|ENSA_HUMAN	51	1	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence		
2	24	3	2812.1578	0.0018	2	50.87	M.SQKQEEENPAEETGEEKQDTQE K.E	Acetyl (Protein N-term); Phospho (ST)	49.79	S#QKQEEENPAEETGEEKQDTQE K	34.77						Y----------	N----------	- .MSQKQEEENPAEETGEEKQDTQE KEGILPER.A		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
121	sp|Q13625|ASPP2_HUMAN	51	1	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence		
774	791	2	1944.837	0.0017	0	50.85	K.SASVTASSESPVEIQNPY.L	Phospho (ST)	182.73	SASVTASSES#PVEIQNPY	30.7						--------N--------	--------N--------	K.SASVTASSESPVEIQNPYLHVEP EK.E		

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
122	sp|Q9Y3X0|CCDC9_HUMAN	51	2	Phosphoprotein																	
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence		
472	490	2	2058.9214	0.0027	0	34.93	F.SPEEPLLEPQAPGTPSSPF.S	Phospho (ST)	145.93	SPEEPLLEPQAPGTPSS#PF	22.85						----------N--	----------N--	K.ETPMQPPEIPAPAHRPPEDEGE ENEGEEDEEWEDISEDEEEEEIEV EEGDEEEPAQDHQAPEAAPTGIPC SEQAHGVPFSPEEPLLEPQAPGTP SSPFSPPSGHQPVSDWGEEVELN SPR.T		

491	512	3	2483.0797	0.0042	1	35.9	F.SPPSGHQPVSDWGEEVELNSPR.T	Phospho (ST)	95.95	SPPSGHQPVSDWGEEVELNS#PR	117.4						----------N--	----------N--	K.ETPMQPPEIPAPAHRPPEDEGEENEGEEDEEWEDISEDEEEEEIEVEEGDEEEPAQDHQAPEAAPTGIPCSEQAHGVPFSPEEPLLEPQAPGTPSSPFSPPSGHQPVSDWGEEVELNSPRTTHLAGALSPGEAWPFESV.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
123	sp|P35222|CTNB1_HUMAN	51	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
50	70	2	2550.0114	0.0003	2	50.79	K.GNPEEEDVDTSQVLYEWEQGF.S	Phospho (Y)	239.63	GNPEEEDVDTSQVLY#EWEQGF	72.42						----------N------	----------Y------	K.GNPEEEDVDTSQVLYEWEQGFSQSFTQEQVADIDGQYAMTR.A				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
124	sp|Q5F1R6|DJC21_HUMAN	50	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
357	379	3	2737.1086	0.0024	0	50.32	F.SRPQIDENPLDDNSEEEMEDAPK.Q	Phospho (ST)	233	SRPQIDENPLDDNS#EEEMEDAPK	176.73						----------Y---------	----------Y---------	K.QQLEEEEENFSRPQIDENPLDDNSEEEMEDAPKQK.L				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
125	sp|Q96JB2|COG3_HUMAN	50	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
661	679	2	2222.1014	0.0031	1	50.32	R.LNSNNALIEFLLEGTPEIR.E	Phospho (ST)	142.42	LNS#NNALIEFLLEGTPEIR	148.76						--Y----------	--Y----------	R.LNSNNALIEFLLEGTPEIREHYLDSK.K				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
126	sp|Q92785|REQU_HUMAN	50	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
157	178	2	2720.0834	0.0045	2	50.04	R.ILEPDDFLDDLDDEDYEEDTPK.R	Phospho (Y)	170.63	ILEPDDFLDDLDDEDY#EEDTPK	33.63						----------Y------	----------Y------	R.ILEPDDFLDDLDDEDYEEDTPKR.R				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
127	sp|P49750|YLPM1_HUMAN	50	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
491	506	3	1754.8006	0.0017	0	36.77	Y.HPPLQSAGPSEQVNSK.A	Phospho (ST)	106.42	HPPLQS#AGPSEQVNSK	62.73						-----N---------	-----N---------	K.HTQLQQILQQYQQIIQPPPHIQATTPPPGIPPPGVPQGIPPQLTAAPVPPASSSQSSQVPEKPRPALLPTPVSFGSAPPTTYHPPLQSAGPSEQVNSKAPLSK.S				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
128	sp|P27824|CALX_HUMAN	49	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
552	573	4	2541.0921	0.0053	2	33.29	K.QKSDAEEDGGTVSQEEEDRKPK.A	Phospho (ST)	24.19	QKS#DAEEDGGTVSQEEEDRKPK	25.78						--Y----------	--Y----------	K.QKSDAEEDGGTVSQEEEDRKPKAEEDEILNR.S				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
129	sp|Q1KMD3|HNRL2_HUMAN	49	2	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
161	187	3	2856.1099	0.0004	1	32.58	R.SGDETPGSEVPGDKAAEEQGDDQDSEK.S	Phospho (ST)	135.22	SGDET#PGSEVPGDKAAEEQGDDQDSEK	24.15						----Y----------	----Y----------	R.SGDETPGSEVPGDKAAEEQGDDQDSEKSKPAGSDGER.R				
152	174	3	2623.0555	-0.0004	2	36.48	K.REEDEPEERSGDETPGSEVPGDK.A	Phospho (ST)	70.95	REEDEPEERS#GDETPGSEVPGDK	45.02						---------Y----------	---------Y----------	R.EEDEPEERSGDETPGSEVPGDKAAEEQGDDQDSEK.S				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
130	sp|Q8NDC0|MISSL_HUMAN	49	2	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
226	245	3	2035.8652	0.004	1	20.35	F.QVPSGPSGAPPMPGGPHSYH.-	Phospho (Y)	42.42	QVPSGPSGAPPMPGGPHSY#H	19.84						----------N-	----------N-	K.TSAVSNTKPGQPPQGWPGSNPWNNPSAPSSVPSGLPPSATPSTVPFGPAPTGMYPSVPPTGPPPGPPAPFPPSGPSCPPPGGPYPAPTVPGPGPTGPYPTPNMPFPELPRPYGAPTDPAAAGPLGPWGSMSSGPWAPGMGGQYPTPNMPYPSPGPYPAPPPPQAPGAAPPVPWGTVPPGAWGPPAPYPATPGTSYPTPGLYPTPSNPFQVPSGPSGAPPMPGGPHSYH.- - .MSDEFSLADALPEHSPAKTSAVSNTKPGQPPQGWPGSNPWNNPSAPSSVPSGLPPSATPSTVPFGPAPTGMYPSVPPTGPPPGPPAPFPPSGPSCPPPGGPYPAPTVPGPGPTGPYPTPNMPFPELPRPYGAPTDPAAAGPLGPWGSMSSGPWAPGMGGQYPTPNMPYPSPGPYPAPPPPQAPGAAPPVPWGTVPPGAWGPPAPYPATPGTSYPTPGLYPTPSNPFQVPSGPSGAPPMPGGPHSYH.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
131	sp|Q6PD62|CTR9_HUMAN	49	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
914	933	2	2306.9134	0.003	2	49.24	K.GGEFDEFVNDDTDDDLPISK.K	Phospho (ST)	205	GGEFDEFVNDDT#DDDLPISK	90.91						----------Y--------	----------Y--------	K.GGEFDEFVNDDTDDDLPISKK.K				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
132	sp|P46821|MAP1B_HUMAN	48	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
1811	1833	3	2488.0408	0.0042	2	30.58	K.TATCHSSSSPPIDAASAEPYGFR.A	Phospho (Y)	104.94	TATCHSSSSPPIDAASAEPY#GFR	59.05						----------Y---	----------Y---	K.TATCHSSSSPPIDAASAEPYGFRASVLFDTMQHHLALNR.D				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
133	sp|O43290|SNUT1_HUMAN	48	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
446	467	3	2615.2162	0.0046	2	47.83	R.RVSEVEEEKEPVPQPLPSDDTR.V	Phospho (ST)	151.06	RVS#EVEEEKEPVPQPLPSDDTR	134.08						--Y------------------	--Y------------------	R.VSEVEEEKEPVPQPLPSDDTRVENMDISDEEEGGAPPPGSPQVLEEDEAELELQK.Q

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
134	sp|Q15003|CND2_HUMAN	48	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
562	579	2	2074.7754	0.004	0	47.8	F.CPGLQAADSDDEDLDDLF.V	Phospho (ST)	140.88	CPGLQAADS#DDEDLDDLF	1000						--------N---------	--------Y---------	R.VETEHYEEIEDYDYNNPNDTSNFCPGLQAADSDDEDLDDLFVGPVGNSDLSPYPCHPPK.T

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
135	sp|Q96JQ2|CLMN_HUMAN	48	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
880	903	3	2619.0883	0.0022	1	19.63	F.VAPGSVQSSDDLEEDSSDYSIPSR.T	Phospho (Y)	76.41	VAPGSVQSSDDLEEDSSDY#SIPSR	30.7						------------------N-----	------------------N-----	K.HVDHVESSLFVAPGSVQSSDDLEEDSSDYSIPSRTSHSDSSIYLR.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
136	sp|Q92625|ANS1A_HUMAN	48	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
825	843	3	2256.1339	0.0035	1	38.2	R.IIASLADRPYEEPPQKPPR.F	Phospho (Y)	146.53	IIASLADRPY#EEPPQKPPR	78.7						---------N---------	---------N---------	R.IIASLADRPYEEPPQKPPRFSQLR.C

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
137	sp|Q9C0D5|TANC1_HUMAN	48	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1455	1476	3	2593.0387	0.0046	0	34.18	F.HSEETEEEETSPQEESVSPTPR.S	Phospho (ST)	92.94	HSEETEEEETSPQEESVS#PTPR	37.81						-----------------N----	-----------------N----	K.QQGPLPAPLNDSENEEDTPTPGLSDHFHSEETEEEETSPQEESVSPTPRSQPSSSVPSSYIR.N

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
138	sp|O60841|IF2P_HUMAN	48	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
507	522	2	1845.7352	0.0013	1	47.51	W.EAMASDEETEKVEGNK.V	Phospho (ST)	63.74	EAMAS#DEETEKVEGNK	46.68						----N-----------	----N-----------	K.EETPPPVEPEEEEDTEDAGLDDWEAMASDEETEKVEGNKVHIEVK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
139	sp|P27816|MAP4_HUMAN	47	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
177	190	2	1582.6344	0.0035	0	20.82	Y.GMSPCNTAVVPQGW.S	Phospho (ST)	57.8	GMS#PCNTAVVPQGW	20.17						--N-----------	--N-----------	K.DSYGMSPCNTAVVPQGWSVEALNSPHSESFVSPEAVAEPPQPTAVPLELAK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
140	sp|Q9UKY7|CDV3_HUMAN	47	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
181	203	3	2599.2238	0.0031	2	33.6	R.KTPQGPPEIYSDTQFPSLQSTAK.H	Phospho (Y)	139.48	KTPQGPPEIY#SDTQFPSLQSTAK	26.53						---------Y-------------	---------Y-------------	K.TPQGPPEIYSDTQFPSLQSTAKHVESR.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
141	sp|Q09161|NCBP1_HUMAN	47	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
19	37	3	2325.0319	0.0011	2	35.86	R.RKTSDANETEDHLESLICK.V	Phospho (ST)	95.73	RKT#SDANETEDHLESLICK	28.95						--Y----------------	--Y----------------	R.KTSDANETEDHLESLICKVGEK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
142	sp|Q01831|XPC_HUMAN	46	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
869	898	3	3047.1712	0.0046	0	46.47	K.SEAAAPHTDAGGGLSSDEEEGTSSQAEAAR.I	2 Phospho (ST)	134.78	SEAAAPHTDAGGGLS#S#DEEEGTSSQAEAAR	21.48	27.93					--------------YY--------------	--------------YY--------------	K.SEAAAPHTDAGGGLSSDEEEGTSSQAEAARILAASWPQNR.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
143	sp|Q14247|SRC8_HUMAN	46	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
435	454	2	2233.9294	0.0056	2	46.41	R.GPVSGTEPEPVYSMEAADYR.E	Phospho (Y)	164.18	GPVSGTEPEPVY#SMEAADYR	28.87						-----------Y--------	-----------Y--------	R.GPVSGTEPEPVYSMEAADYREASSQQGLAYATEAVYESAEAPGHYPAEDSTYDEYENDLGITAVALYDYQAAGDDEISFDPDDIITNIEMIDDGWWR.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
144	sp|Q12800|TFCP2_HUMAN	46	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
286	301	2	1743.6898	0.0009	1	46.08	Y.VNNSPSPGFNSSHSSF.S	Phospho (ST)	103.34	VNNSPS#PGFNSSHSSF	42.65								K.YQPSYETTILTECSPWPEITYVNNSPSPGFNSSHSSFSLGEGNGSPNHQPEPPPPVTDNLLPTTTPQEAQQWLHR.N

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
145	sp|P10412|H14_HUMAN	46	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
2	21	2	2024.9834	0.0015	1	45.8	M.SETAPAAPAAPAPAEKTPVK.K	Acetyl (Protein N-term); Phospho (ST)	53.55	SETAPAAPAAPAPAEKT#PVK	59.72						----------------Y---	----------------N---	-.MSETAPAAPAAPAPAEKTPVKK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
146	sp|P49327|FAS_HUMAN	45	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
2194	2220	3	3062.4082	0.0066	1	45.36	K.ADEASELACPTPKEDGLAQQQTQLNLR.S	Phospho (ST)	134.48	ADEASELACPT#PKEDGLAQQQTQLNLR	29.69						----------Y----------------	----------Y----------------	K.ADEASELACPTPKEDGLAQQQTQLNLRSLLVNPEGPTLMR.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
147	sp|Q9BVJ6|UT14A_HUMAN	45	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
27	42	2	1951.7114	0.003	1	26.03	Y.LLSESEDEGDNDGERK.H	2 Phospho (ST)	59.04	LLS#ES#EDEGDNDGERK	1000						--Y-Y-----------	--Y-Y-----------	K.DYLLSESEDEGDNDGERKHQK.L
27	41	2	1823.6142	0.0007	0	38.7	Y.LLSESEDEGDNDGER.K	2 Phospho (ST)	106.6	LLS#ES#EDEGDNDGER	1000						--Y-Y----------	--Y-Y----------	K.DYLLSESEDEGDNDGERK.H

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
148	sp|Q9UKX7|NUP50_HUMAN	45	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
207	229	3	2477.0992	0.0033		2	45.09	R.NSESESNKVAAETQSPSLFGSTK.L	Phospho (ST)	159.13	NSESESNKVAAETQS#PSLFGSTK	20.17						----------Y--------	----------Y--------	R.NSESESNKVAAETQSPSLFGSTKLQQESTFLFHGNK.T

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
149	sp|Q9BUJ2|HNRL1_HUMAN	45	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
192	216	3	2874.1801	0.0044		2	33.77	R.GRSPQPPAEEDEDDFDDTLVAIDTY.N	Phospho (ST)	92.31	GRS#PQPPAEEDEDDFDDTLVAIDTY	41.97						--Y----------	--Y----------	R.GRSPQPPAEEDEDDFDDTLVAIDTYNCDLHFK.V

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
150	sp|O00264|PGRC1_HUMAN	44	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
45	67	3	2483.0989	0.0023		1	23.28	K.IVRGDQPAASGDSDDDEPPPLPR.L	Phospho (ST)	118.05	IVRGDQPAASGDS#DDDEPPPLPR	27.34						----------Y----------	----------N----------	K.IVRGDQPAASGDSDDDEPPPLPRLK.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
151	sp|P46087|NOP2_HUMAN	43	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
145	164	2	2318.8854	0.0026		0	38.37	Y.GADSNSEDEEEGEALLPIER.A	2 Phospho (ST)	148.13	GADS#NS#EDEEEGEALLPIER	1000						---N-Y----------	---N-N----------	K.RPAPGSDEEEEEEDSEEDGMVNHGDLWGSEDDADTVDDYGADSNSEDEEEGEALLPIERAAR.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
152	sp|P21333|FLNA_HUMAN	43	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1754	1763	2	1277.533	0.0001		1	24.74	R.SQQLAPQYTY.A	Phospho (Y)	65.96	SQQLAPQY#TY	38.42						-------N--	-------N--	R.SQQLAPQYTYAQGGQQTWAPERPLVGVNGLDVTSLRPFDLVIPFTIK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
153	sp|Q5TAQ9|DCAF8_HUMAN	42	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
95	115	3	2751.0319	0.0015		1	42.37	R.VHDRSEEEEEEEEEEEEEQPR.R	Phospho (ST)	161.31	VHDRS#EEEEEEEEEEEEQPR	1000						----Y----------	----Y----------	R.VHDRSEEEEEEEEEEEEQPRR.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
154	sp|O43318|M3K7_HUMAN	40	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
437	456	3	2266.1101	0.0034		2	40.23	R.RRSIQDLTVTGTEPGQVSSR.S	Phospho (ST)	80.85	RRS#IQDLTVTGTEPGQVSSR	25.57						--Y----------	--Y----------	R.RSIQDLTVTGTEPGQVSSRSSSPSVR.M

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
155	sp|Q9NQZ2|SAS10_HUMAN	40	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
147	170	3	3009.2992	0.0044		2	39.79	R.GRQSQQEAEEEEREEEEEAQIIQR.R	Phospho (ST)	56.29	GRQS#QQEAEEEEREEEEEAQIIQR	1000						---Y----------	---Y----------	R.GRQSQQEAEEEEREEEEEAQIIQRR.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
156	sp|Q6A1A2|PDPK2_HUMAN	39	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
212	230	2	2133.0034	0.0003		2	39.23	R.ANSFVGTAQYVSPELLTEK.S	Phospho (ST)	115.61	ANS#FVGTAQYVSPELLTEK	34.07								R.ANSFVGTAQYVSPELLTEKSACK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
157	sp|Q15366|PCBP2_HUMAN	39	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
231	245	2	1751.8504	0.0009		1	27.48	Y.TIQGQYAIPQPDLTK.L	Phospho (Y)	92.11	TIQGQY#AIPQPDLTK	37.38						-----Y---------	-----Y---------	R.YSTGSDSASFPHTTPSMCLNPDLEGPPLEAYTIQGQYAIPQPDLTKLHQLAMQQSHFPMTHGNTGFSGIESSSPEVK.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
158	sp|Q8WX92|NELFB_HUMAN	39	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
555	580	3	2641.3741	-0.0027		0	38.7	R.KPSPAQAAETPALELPLPSVPAPAPL.-	Phospho (ST)	136.73	KPS#PAQAAETPALELPLPSVPAPAPL	28.49						--Y----------	--Y----------	R.KPSPAQAAETPALELPLPSVPAPAPL.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
159	sp|P52943|CRIP2_HUMAN	39	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
76	97	3	2414.2261	0.0014		1	38.51	Y.IYEKPLAEGPQVTGPIEVPAAR.A	Phospho (Y)	158.42	IY#EKPLAEGPQVTGPIEVPAAR	118						-Y----------	-Y----------	K.GVNIGGAGSYIYEKPLAEGPQVTGPIEVPAARAEER.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
160	sp|O60763|USO1_HUMAN	38	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
927	962	4	4156.6949	0.0032		2	38.02	K.LKDLGHPVEEEDELESGDQEDEDDESEDPGKDLDHI.-	Phospho (ST)	101.45	LKDLGHPVEEEDELES#GDQEDEDDESEDPGKDLDHI	36.58						----------Y----------	----------Y----------	K.LKDLGHPVEEEDELESGDQEDEDDESEDPGKDLDHI.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
161	sp|Q01082|SPTB2_HUMAN	38	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
2109	2140	3	3565.5652	0.0058		2	37.69	K.VSEEAESQQQWDTSKGEQVSQNGLPAEQGSPR.M	Phospho (ST)	97.18	VSEEAESQQQWDTSKGEQVSQNGLPAEQGS#PR	36.08						----------Y--	----------Y--	K.VSEEAESQQQWDTSKGEQVSQNGLPAEQGSPRMAETVDTSEMVNGATEQR.T

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
162	sp|Q9P2N5|RBM27_HUMAN	38	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1042	1056	2	1920.644	0.0019		1	37.64	F.LPDDDDEDEDEYESR.S	Phospho (Y)	151.66	LPDDDDEDEDEY#ESR	37.45						----------N---	----------N---	K.EEETETSDLFLPDDDDEDEDEYESRSWR.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
163	sp|Q8NBN3|TM87A_HUMAN	37	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence

521	544	3	2663.2237	0.0022	0	37	W.VEENVPSSVTDVALPALLDSDEER.M	Phospho (ST)	170.79	VEENVPSSVTDVALPALLDS#DEER	171.56						-------------------Y----	-------------------Y----	K.WVEENVPSSVTDVALPALLDSDEERMITHFER.S
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
164	sp|Q68D10|SPT2_HUMAN	37	1	Phosphoprotein															
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
135	157	4	2900.1825	0.0035	2	26.9	Y.NHAESEQEYEEEQEPPKVESKPK.V	Phospho (ST); Phospho (Y)	66.4	NHAES#EQEY#EEEQEPPKVESKPK	63.99	59.09					----N---N--------------	----N---N--------------	R.GYEMEEENEFLEYNHAESEQEYEEEQEPPKVESKPKVPLK.S
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
165	sp|Q969T9|WBP2_HUMAN	36	1	Phosphoprotein															
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
136	145	2	1078.402	0.0012	1	24.39	R.GEVPSGAYGY.S	Phospho (Y)	110.62	GEVPSGAY#GY	48.87						-------N--	-------N--	R.GEVPSGAYGYSYMPSGAYVYPPPVANGMYPCPPGYPYPPPPPEFYPGPPMMDGAMGYVQPPPPPYPGPMEPPVSGPDVPSTPAAEAK.A
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
166	sp|Q5VT52|RPRD2_HUMAN	36	1	Phosphoprotein															
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1097	1114	3	2063.0266	0.0031	2	26.74	R.RMSGEPIQTVESIRVPGK.G	Phospho (ST)	70.26	RMS#GEPIQTVESIRVPGK	19.78						--Y---------------	--Y---------------	R.MSGEPIQTVESIRVPGKGNR.G
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
167	sp|P28482|MK01_HUMAN	36	1	Phosphoprotein															
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
173	191	3	2302.9333	0.0036	2	35.54	R.VADPDHDHTGFLTEYVATR.W	Phospho (ST); Phospho (Y)	105.7	VADPDHDHTGFLT#EY#VATR	47.47	48.83					------------Y-Y----	------------N-N----	R.VADPDHDHTGFLTEYVATRWYR.A
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
168	sp|P02794|FRIH_HUMAN	35	1	Phosphoprotein															
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
170	183	2	1656.6694	0.0026	2	35.21	Y.LFDKHTLGDSDNES.-	Phospho (ST)	69.78	LFDKHTLGDS#DNES	28.34						---------Y----	---------N----	K.MGAPESGLAEYLFDKHTLGDSDNES.-
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
169	sp|P35659|DEK_HUMAN	35	1	Phosphoprotein															
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
30	50	3	2721.9214	0.0029	1	35.1	R.EESEEEEDEDDEEEEEEEKEK.S	Phospho (ST)	62.35	EES#EEEEDEDDEEEEEEEKEK	1000						--Y-----------------	--Y-----------------	R.EESEEEEDEDDEEEEEEEKEKSLIVEGK.R
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
170	sp|Q9BZQ8|NIBAN_HUMAN	35	1	Phosphoprotein															
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
637	659	3	2412.1627	0.0053	0	20.54	K.GESLSLPGPSPPPDGTEQVIISR.V	Phospho (ST)	79.27	GESLSLPGPS#PPPDGTEQVIISR	25.22						--N-------------------	--N-------------------	K.GESLSLPGPSPPPDGTEQVIISRVDDPVVNPVATEDTAGLPGTCSSELEFGGTLEDEEPAQEEPEPITASGSLK.A
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
171	sp|Q8N0X7|SPG20_HUMAN	35	2	Phosphoprotein															
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
616	636	3	2469.1189	0.0016	1	34.85	K.TATQTGHTLLEDYQIVDNSQR.E	Phospho (Y)	145.44	TATQTGHTLLEDY#QIVDNSQR	50.73						------------N--------	------------Y--------	K.TATQTGHTLLEDYQIVDNSQRENQEGAANVNVR.G
615	636	3	2597.2156	0.0033	2	22.03	K.KTATQTGHTLLEDYQIVDNSQR.E	Phospho (Y)	104.76	KTATQTGHTLLEDY#QIVDNSQR	68.58						-------------N--------	-------------Y--------	K.TATQTGHTLLEDYQIVDNSQRENQEGAANVNVR.G
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
172	sp|Q14678|KANK1_HUMAN	35	1	Phosphoprotein															
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
184	209	3	2600.1766	0.0035	2	34.78	R.LASFGGMGTTSSLPSFVGSGNHNPAK.H	Phospho (ST)	108.83	LAS#FGGMGTTSSLPSFVGSGNHNPAK	43.85						--N----------------------	--N----------------------	R.LASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYGSYAPAAPTTSSMGSSIR.H
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?															
173	sp|Q8IVM0|CCD50_HUMAN	34	1	Phosphoprotein															
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
260	290	4	3607.5789	0.0002	2	34.3	K.NERPARPPPPIMTDGEDADYTHFTNQQSSTR.H	Phospho (Y)	106.15	NERPARPPPPIMTDGEDADY#THFTNQQSSTR	29.88						-------------------Y-----------	-------------------Y-----------	K.NERPARPPPPIMTDGEDADYTHFTNQQSSTRHFSK.S

Supplementary Table S3: Phosphoproteins with the corresponding phosphopeptides and localized phosphosites from solprot*SRS.pombe*) and from SKMel (human melanoma) samples
(*) Phosphorylated amino acid **X** is displayed as **X#**

***Human melanoma* - Asp-N digest of large tryptic peptides**

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
1	sp|P16989|DBPA_HUMAN	241	4	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
310	326	3	1934.8531	0.0047		1	29.65	E.DKENQQATSGPNQPSVR.R	Phospho (ST)	57.21	DKENQQATSGPNQPS#VR	89.07						----------N--	----------Y--	R.GPPRPRPAPAVGEAEDKENQQATSGPNQPSVRR.G
59	80	3	1924.8469	0.0054		1	59.44	G.DAAPAATGTAAAASLATAAGSE.D	Phospho (ST)	131.74	DAAPAATGTAAAASLATAAGS#E	107.16						----------Y-	----------Y-	K.SPVGSGAPQAAAPAPAAHVAGNPGGDAAPAATGTAAAASLATAAGSEDAEK.K
29	58	2	2696.2734	0.0027		1	35.44	Q.DPAPKSPVGSGAPQAAAPAPAAHVAGNPGG.D	Phospho (ST)	87.34	DPAPKS#PVGSGAPQAAAPAPAAHVAGNPGG	27.03						-----Y----------	-----Y----------	-.MSEAGEATTTTTTTLPQAPTEAAAAAPQDPAPKSPVGSGAPQAAAPAPAAHVAGNPGGDAAPAATGTAAAASLATAAGSEDAEK.K
34	58	2	2188.0114	0.0052		0	51.06	K.SPVGSGAPQAAAPAPAAHVAGNPGG.D	Phospho (ST)	134.63	S#PVGSGAPQAAAPAPAAHVAGNPGG	33.68						Y----------	Y----------	K.SPVGSGAPQAAAPAPAAHVAGNPGGDAAPAATGTAAAASLATAAGSEDAEK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
2	sp|Q8IWE2|NXP20_HUMAN	196	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
119	135	2	1767.708	0.0038		0	92.03	V.DSPPSGGGWAGWGSWGK.S	Phospho (ST)	125.55	DS#PPSGGGWAGWGSWGK	33.55						-N----------	-N----------	R.SEIPLQEQNYLAVDSPPSGGGWAGWGSWGKSLLSSASATVGHGLTAVK.E
190	206	2	1829.6916	0.0047		1	46.23	T.DQGPAESPPTSPSSASR.G	2 Phospho (ST)	98.64	DQGPAES#PPTS#PSSASR	26.79	20.35					------Y--Y-------	------Y--Y-------	R.IHGVNSGSSEGAQPNTENGVPEITDAATDQGPAESPPTSPSSASRGMLSAITNVVQNTGK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
3	sp|P55072|TERA_HUMAN	190	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
773	798	3	2391.9661	0.0055		1	23.26	R.FPSGNQGGAGPSQGSGGGTGGSVYTE.D	Phospho (Y)	62.78	FPSGNQGGAGPSQGSGGGTGGSVY#TE	38.42						----------N--	----------N--	R.FPSGNQGGAGPSQGSGGGTGGSVYTEDNDDDLYG.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
4	sp|Q13428|TCOF_HUMAN	134	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
967	985	2	1828.8522	0.0054		0	58.31	R.SPAGPAATPAQAQAASTPR.K	Phospho (ST)	65.84	S#PAGPAATPAQAQAASTPR	35.76						Y----------	Y----------	R.SPAGPAATPAQAQAASTPRK.A
963	985	3	2391.0394	0.0024		1	29.39	V.DPNRSPAGPAATPAQAQAASTPR.K	2 Phospho (ST)	82.09	DPNRS#PAGPAATPAQAQAAST#PR	54.53	24.44					----Y----------Y--	----Y----------Y--	K.QDDSGSSSSEESDSDGEAPAAVTSAQVIKPPLIFVDPNRSPAGPAATPAQAQAASTPRK.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
5	sp|P27361|MK03_HUMAN	130	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
196	208	2	1668.6634	0.0048		1	46.49	H.DHTGFLTEYVATR.W	Phospho (ST); Phospho (Y)	156.68	DHTGFLT#EY#VATR	78.39	58.33					------Y-Y----	------Y-Y----	R.IADPEHDHTGFLTEYVATRWYR.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
6	sp|Q15365|PCBP1_HUMAN	124	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
178	198	2	2283.0154	0.0015		0	60.65	R.VMTIPYQPMPASSPVICAGGQ.D	Phospho (ST)	186.56	VMTIPYQPMPASS#PVICAGGQ	32.4						----------Y--------	----------Y--------	R.VMTIPYQPMPASSPVICAGGQDR.C
220	233	2	1608.7232	0.0048		0	21.17	L.DAYSIQGQHTISPL.D	Phospho (Y)	45.04	DAY#SIQGQHTISPL	24.44						--N----------	--Y----------	R.CSDAAGYPHATHDLEGPPLDAYSIQGQHTISPLDLAK.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
7	sp|P43355|MAGA1_HUMAN	118	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
53	72	2	2211.0034	0.0037		0	60.78	T.DPPQSPQGASAFPTTINFTR.Q	Phospho (ST)	101.9	DPPQS#PQGASAFPTTINFTR	62.08								R.SLHCKPEEALEAQQEALGLVCVQAATSSSSPLVLGTLEEVPTAGSTDPPQSPQGASAFPTTINFTRQR.Q

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
8	sp|P22626|ROA2_HUMAN	110	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
242	266	2	2313.8774	0.0061		0	37.47	G.DGYNGYGGGPGGGNFGGSPGYGGGR.G	Deamidated (NQ); Phospho (ST)	54.9	DGYNGYGGGPGGGNFGGS#PGYGGGR	30.66						----------Y-------	----------Y-------	R.GFGDGYNGYGGGPGGGNFGGSPGYGGGRGGYGGGPGYGNQGGGYGGGYDNYGGGNYGSGNYNDFGNYNQQPSNYGPMK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
9	sp|O60711|LPXN_HUMAN	108	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
51	67	2	1953.915	0.0066		0	35.19	Q.DNTSPLPAQLVYTTNIQ.E	Phospho (ST)	135.09	DNTS#PLPAQLVYTTNIQ	20.35						---N----------	---N----------	K.ETNLDETSEILSIQDNTSPLPAQLVYTTNIQELNVYSEAQEPK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
10	sp|Q92598|HS105_HUMAN	105	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
547	562	2	1751.73	0.005		1	20.56	T.DAQQTSQSPPSPELTS.E	Phospho (ST)	79.13	DAQQTSQSPPS#PELTS	20.91						----------Y	----------N	K.NVQQDNSEAGTQPQVQTDAQQTSQSPPSPELTSEENK.I

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
11	sp|Q9H1B7|EAP1_HUMAN	103	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
704	719	2	1914.6796	0.0026		0	49.49	P.DSPMANSGPLCCTICH.E	Oxidation (M); Phospho (ST)	56.75	DS#PMANSGPLCCTICH	23.1						-N----------	-N----------	R.NGDLNLQVAPPPPSAHPGMDQVHPQNIPDSPMANSGPLCCTICHER.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
12	sp|Q04637|IF4G1_HUMAN	99	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence

1080	1096	2	1925.8828	0.0043	1	33.52	I.DSNNQLFAPGGRLSWGK.G	Phospho (ST)	83.11	DSNNQLFAPGGRLS#WGK	89.07							----------Y---	----------Y---	K.ITKPGSIDSNNQLFAPGGRLSWGKGSSGGSGAKPSDAASEAARPATSTLNR.F
401	413	2	1373.6148	0.0033	1	15.9	P.EELLNGAPSPPAV.D	Deamidated (NQ); Phospho (ST)	45.04	EELLNGAPS#PPAV	1000							--------N----	--------N----	R.LSPEPTPLAEPILEVEVTLSKPVPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDLEPEVESSPELAPPPACPSESPVPIAPTAQPEELLNGAPSPAVDLSPVSEPEEQAK.E
402	413	2	1244.5744	0.0055	0	23.93	E.ELLNGAPSPPAV.D	Deamidated (NQ); Phospho (ST)	42.08	ELLNGAPS#PPAV	1000							-------N----	-------N----	R.LSPEPTPLAEPILEVEVTLSKPVPESEFSSSPLQAPTPLASHTVEIHEPNGMVPSEDLEPEVESSPELAPPPACPSESPVPIAPTAQPEELLNGAPSPAVDLSPVSEPEEQAK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
13	sp|O60716|CTND1_HUMAN	98	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
166	180	2	1703.7544	0.0029	0	71.18	V.DASSVSNNYIQTLGR.D	Phospho (Y)	155.46	DASSVSNNY#IQTLGR	40.96						--------Y------	--------Y------	R.TVQPVAMGPDGLPVDASSVSNNYIQTLGRDFR.K
332	342	2	1470.599	0.0021	0	54.95	S.DQYYWAPLAQH.E	Phospho (Y)	143.87	DQY#YWAPLAQH	32.4						--Y--------	--Y--------	R.SYEDMIGEEVPSDQYYWAPLAQHER.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
14	sp|P48681|NEST_HUMAN	93	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
462	477	3	1722.7666	0.0052	1	35.65	E.DHASLAPPLSPDHSSL.E	Phospho (ST)	123.81	DHASLAPPLS#PDHSSL	19.59						----------N--	----------Y--	R.QEASTGQSPEDHASLAPPLSPDHSSLEAK.D
1240	1252	2	1469.5968	0.0032	1	38.85	A.EGSQEASWGVQGR.A	Phospho (ST)	95.09	EGS#QEASWGVQGR	44.28						--N----------	--N----------	R.GAEEAFPAETLGHTGSDAPSPWPLGSEEAEEDVPPVLVSPSPTYTPILEDAPGPQPQAEGSQEASWGVQGRAEALGK.V

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
15	sp|P50995|ANX11_HUMAN	87	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
40	51	2	1406.554	0.0037	0	63.49	L.DNVATYAGQFNQ.D	Phospho (Y)	144.95	DNVATY#AGQFNQ	38.42						-----N------	-----N------	-.MSYPGYPPPPGGYPPAAPGGGPWGGAAYPPPPSMPPIGLDNVATYAGQFNQDYLSGMAANMSGTFGGANMPNLYPGAPGAGYPPVPPGGFGQPPSAQQPVPPYGMYPPPGGNPPSR.M

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
16	sp|Q9UPT8|ZC3H4_HUMAN	82	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1094	1111	2	1751.7206	0.0038	1	31.23	R.AAKPGPAEAPSPTASPSG.D	2 Phospho (ST)	114.14	AAKPGPAEAPS#PTAS#PSG	24.75	19.84					----------Y---Y---	----------Y---Y---	R.AAKPGPAEAPSPTASPSGDASPATAPYDPR.V
563	573	2	1374.6224	0.0044	0	43.74	H.EPLSPQQLQQQ.D	Phospho (ST)	88.44	EPLS#PQQLQQQ	1000						---N-------	---N-------	K.QGINPLPKPPPGVGLLPTPPRPPGPQAPTSPNGRPMQGGPPPPPPPPPPPPGPPQMPMPVHEPLSPQQLQQQDMYNK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
17	sp|O60271|JIP4_HUMAN	76	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
850	868	2	1813.7484	0.0043	0	41.21	A.EGVTGAATSPSTNGASPVM.D	Deamidated (NQ); Phospho (ST)	48.72	EGVTGAATSPSTNGAS#PVM	23.64						----------N---	----------N---	K.ASLCGSMTSNSSAETDSLLGGITVVGCSAEGVTGAATSPSTNGASPVMDKPPEMEAENSEVDENVPTAEEATEATEGNAGSAEDTVDISQTGVYTEHVFTDPLGVQIPEDLSPVYQSSNDSDAYK.D

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
18	sp|Q16512|PKN1_HUMAN	75	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
108	127	2	2008.8354	0.0045	0	39.73	H.DGPQSPGAGGPTCSATNLSR.V	Phospho (ST)	68.09	DGPQS#PGAGGPTCSATNLSR	34.57						-----N----------	-----N----------	R.LDLLHQQLQELHAHVVLPDPAATHDGPQSPGAGGPTCSATNLSRVAGLEK.Q

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
19	sp|P31350|RIR2_HUMAN	74	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
13	23	2	1346.6512	0.003	0	49.96	T.DPQQLQLSPLK.G	Deamidated (NQ); Phospho (ST)	63.64	DPQQLQLS#PLK	1000						-------Y---	-------Y---	R.VPLAPITDPQQLQLSPLKGLSLVDK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
20	sp|Q14678|KANK1_HUMAN	71	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
221	240	2	2097.8774	0.006	0	36.33	G.DYGSYAPAAPTTSSMGSSIR.H	Phospho (Y)	130.85	DY#GSYAPAAPTTSSMGSSIR	30.53						-N----------	-N----------	K.HQLQNGYQGNGDYGSYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIR.E
957	970	2	1604.6224	0.0047	1	66.56	T.DDQIAAGLYACTNN.E	Phospho (Y)	182.24	DDQIAAGLY#ACTNN	79.13						--------N-----	--------N-----	K.CGGLQSGSPLSSQTSQPEQEVGTSEGKPISSLDAFPTQEGTLSPVNLTDDQIAAGLYACTNNESTLK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
21	sp|P51153|RAB13_HUMAN	69	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
31	43	2	1550.67	0.0047	0	43.77	E.DNFNNTYISTIGI.D	Phospho (Y)	92.31	DNFNNTY#ISTIGI	21.51						------N------	------Y------	R.FAEDNFNNTYISTIGIDFK.I

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
22	sp|Q92945|FUBP2_HUMAN	67	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
128	142	3	1679.8084	0.0051	0	31.67	G.DSISSQLGPIHPPPR.T	Phospho (ST)	56.34	DS#ISSQLGPIHPPPR	24.39						-N----------	-N----------	K.LASQGDSISSQLGPIHPPPRTSMTEEYR.V

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
23	sp|Q92974|ARHG2_HUMAN	67	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
149	160	2	1326.5642	0.0037		0	65.9	K.SVSTTNIAGHFN.D	Phospho (ST)	140.12	SVS#TTNIAGHFN	28.87						---Y---------	---Y---------	K.SVSTTNIAGHFNDESPLGLR.R			
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
24	sp|P49792|RBP2_HUMAN	66	2	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
1570	1585	2	1694.7954	0.0038		0	31.81	P.DKPSPSTSVPAPASFK.F	Phospho (ST)	70.04	DKPS#PSTSVPAPASFK	24.84						---Y----------	---Y----------	R.CVACQNPDKPSPSTSVPAPASFKFGTSETSK.A			
2731	2741	2	1363.5378	0.0036		0	39.86	K.LPPTFFCGVCS.D	Phospho (ST)	111.06	LPPTFFCGVCS#	159.45						----------Y	----------Y	K.LPPTFFCGVCSDTDEDNGNGEDFQSELQK.V			
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
25	sp|Q9GZV5|WWTR1_HUMAN	66	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
338	356	3	2150.9122	0.007		1	21.05	M.DTGENAGQTPMNINPQQTR.F	Phospho (ST)	116.33	DTGENAGQT#PMNINPQQTR	30.79						--------N----------	--------N----------	R.EQSTDSGLGLGCYSVPTTPEDFLSNVDEMDTGENAGQTPMNINPQQTRFPDFLDCLPGTNVDLGTLESEDLIPLFNDVESALNK.S			
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
26	sp|Q14C86|GAPD1_HUMAN	64	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
805	821	2	1883.809	0.004		1	21.47	M.DEITHGAHQLTSPPSQS.E	Phospho (ST)	65.81	DEITHGAHQLTS#PPSQS	26.38						----------N-----	----------N-----	K.DSVTSPDMDEITHGAHQLTSPPSQSESLLAMFDPLSSHEGASAVVRPK.V			
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
27	sp|Q9NRR5|UBQL4_HUMAN	64	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
103	129	2	2507.0734	0.0034		0	52.77	P.DPASAPSTTPASPATPAQPSTSGSASS.D	Phospho (ST)	144.57	DPASAPSTTPAS#PATPAQPSTSGSASS	53.6						----------N----------	----------Y----------	K.AQDPAAATASSPSTPDPASAPSTTPASPATPAQPSTSGSASSDAGSGSR.R			
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
28	sp|P04049|RAF1_HUMAN	62	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
23	40	2	2121.9234	0.0044		0	62.16	F.DGSSCISPTIVQQFGYQR.R	Phospho (ST)	173.51	DGSSCIS#PTIVQQFGYQR	51.64						------N----------	------Y----------	K.DAVFDGSSCISPTIVQQFGYQRR.A			
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
29	sp|Q9Y520|BA2L2_HUMAN	62	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
2189	2207	2	2089.9214	0.0009		0	62.11	T.DYTTPSSSLPNTVATNNTK.M	Phospho (Y)	191.02	DY#TTPSSSLPNTVATNNTK	19.21						-N----------	-Y----------	K.ESVTDYTTPSSSLPNTVATNNTKMEDTLVNNVPLPNTLPLPK.R			
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
30	sp|Q69YN4|VIR_HUMAN	61	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
137	156	3	2146.0552	0.0052		0	60.93	R.DSPPPPPPPPPPPQPQPSLK.R	Phospho (ST)	135.79	DS#PPPPPPPPPPQPQPSLK	156.11						-Y----------	-Y----------	R.DSPPPPPPPPPPQPQPSLKR.N			
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
31	sp|P35606|COPB2_HUMAN	60	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
854	872	3	1968.9718	0.0048		0	44.23	L.DGKPASPTPVIVASHTANK.E	Phospho (ST)	89.8	DGKPAS#PTPVIVASHTANK	26.42						-----Y----------	-----Y----------	R.STAQQELDGKPASPTPVIVASHTANKEEK.S			
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
32	sp|Q7Z4V5|HDGR2_HUMAN	60	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
122	137	2	1599.7362	0.0035		1	60.04	E.DRGVMAVTAVTATAAS.D	Phospho (ST)	157.75	DRGVMAVTAVTATAAS#	76.83						--------------N	--------------Y	K.GFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDDEDRGVMAVTAVTATAASDR.M			
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
33	sp|Q15398|DLGP5_HUMAN	60	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
805	820	2	1913.8014	0.0036		1	59.86	L.DSPGLNCSNPFTQLER.R	Phospho (ST)	93.93	DS#PGLNCSNPFTQLER	40.77						-Y----------	-Y----------	K.SLTTECHLLDSPGLNCSNPFTQLERR.H			
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
34	sp|P23588|IF4B_HUMAN	58	2	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
61	68	2	1009.4658	0.0025		1	17.79	D.DVYRAPPI.D	Phospho (Y)	62.74	DVY#RAPPI	1000						--N-----	--N-----	K.TISLTDFLAEDGGTGGGSTYVSKPVSWADETDDLEGDVSTTWHSNDDDVYRAPPIDR.S			
24	41	2	1804.7728	0.0059		0	35.12	E.DGGTGGGSTYVSKPVSWA.D	Phospho (Y)	112.81	DGGTGGGSTY#VSKPVSWA	20.35						---------N--------	---------Y--------	K.TISLTDFLAEDGGTGGGSTYVSKPVSWADETDDLEGDVSTTWHSNDDDVYR.A			
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
35	sp|Q96AC1|FERM2_HUMAN	58	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
197	209	2	1480.5348	0.0036		0	22.39	H.DGSPLSPTSAWFG.D	2 Phospho (ST)	100.5	DGS#PLS#PTSAWFG	70.2	24.24					--N--N-------	--N--N-------	K.TMTPTYDAHDGSPLSPTSAWFGDSALSEGNPGILAVSQPITSPEILAK.M			
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
36	sp|Q9BQG0|MBB1A_HUMAN	57	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
5	23	2	1962.8192	0.005		1	45.45	R.DPAQPMSPGEATQSGARPA.D	Oxidation (M); Phospho (ST)	93.42	DPAQPMS#PGEATQSGARPA	24.68						------Y----------	------Y----------	R.DPAQPMSPGEATQSGARPADR.Y			
Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
37	sp|Q9BTC0|DIDO1_HUMAN	57	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			

1250	1274	3	2617.2538	0.0056	1	24.76	A.DAAVSTTPPGSPPPPPPLPEPPVLK.V	2 Phospho (ST)	128.86	DAAVSTT#PPGS#PPPPPPLPEPPVLK	24.75	45.83					------Y---Y----------	------Y---Y----------	K.YPLCSADAAVSTTPPGSPPPPPPLPEPPVLKVLSSLKPAAPSPATAATTAAAASTAASSTASSASK.T

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
38	sp|Q00653|NFKB2_HUMAN	57	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
755	771	2	1745.7722	0.0044	0	17.88	M.EPPLTPPSPAGPGLSLG.D	2 Phospho (ST)	91.45	EPPLT#PPS#PAGPGLSLG	79.7	55.23					----N--N---------	----N--N---------	K.TLLLNAAQNTMEPPLPTPPSPAGPGLSLGDTALQNLEQLLDGPEAQGSWAELAER.L				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
39	sp|Q13200|PSMD2_HUMAN	55	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
7	24	2	1798.8286	0.0036	1	41.78	R.DKAPVQPQQSPAAAPGGT.D	Phospho (ST)	98.76	DKAPVQPQQS#PAAAPGGT	47.13						---------Y--------	---------Y--------	R.DKAPVQPQQSPAAAPGGTDEKPSGK.E				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
40	sp|Q96TA1|NIBL1_HUMAN	54	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
673	692	2	2126.9854	0.0052	1	33.86	K.AAPEASSPPASPLQHLLPGK.A	2 Phospho (ST)	107.31	AAPEASS#PPAS#PLQHLLPGK	21.51	63.94					------Y---Y---------	------Y---Y---------	K.AAPEASSPPASPLQHLLPGKAVDLGPPKPSDQETGEQVSSPSSHPALHTTTEDSAGVQTEF.-				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
41	sp|O75533|SF3B1_HUMAN	54	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
69	80	2	1364.5896	0.0036	0	49.36	D.DYSSSTSLLGQK.K	Phospho (Y)	109.3	DY#SSSTSLLGQK	38.42						-N---------	-N---------	R.FAGYVTSIAATELEDDDDDYSSSTSLLGQKKPGYHAPVALLNDIPQSTEQYDPFAEHRPPK.I				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
42	sp|O95104|SFR15_HUMAN	53	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
146	160	2	1657.7378	0.003	1	39	A.ENVTNNEGSPPPPVK.V	Phospho (ST)	123.32	ENVTNNEGS#PPPPVK	57.41						--------Y------	--------Y------	K.IEIIQPLLDMAAGTSNAAPVAENVTNNEGSPPPPVKVSSEPPTQATPNSVPAVPQLPSSDAFAAVAQLFQTTQGQQLQQILQTFQQPPKPQSPALDNAVMAQVQAITAQLK.T				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
43	sp|O95628|CNOT4_HUMAN	53	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
427	447	2	2266.0154	0.004	0	52.63	Q.DQPSLSPTSLQNSSSHTTTAK.G	Phospho (ST)	70.08	DQPSLS#PTSLQNSSSHTTTAK	21.3						-----Y----------	-----Y----------	K.ELSVQDQPSLSPTSLQNSSSHTTTAKGPGSGFLHPAAATNANSLNSTFSVLPQR.F				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
44	sp|Q6Y7W6|PERQ2_HUMAN	51	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
17	35	2	1938.9156	0.0052	0	28.8	R.ALSSGGSITSPPLSPALPK.Y	2 Phospho (ST)	95.72	ALSSGGSITS#PPLS#PALPK	32.4	53.16					---------Y---Y-----	---------Y---Y-----	R.ALSSGGSITSPPLSPALPKYK.L				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
45	sp|Q12888|TP53B_HUMAN	50	3	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
547	558	2	1396.5978	0.0033	1	31.36	E.DTEPMSPVLNSK.F	Phospho (ST)	108.45	DTEPMS#PVLNSK	78.86						-----Y------	-----Y------	R.IDEDGENTQIEDTEPMSPVLNSKFVPAENDSILMNPAQDGEVQLSQNDDK.T				
1060	1070	2	1235.5356	0.002	0	31.95	R.GNLLHFPSSQG.E	Phospho (ST)	94.83	GNLLHFPSS#QG	22.85						--------Y--	--------Y--	R.GNLLHFPSSQGEEEK.E				
162	173	2	1353.5294	0.004	0	27.03	E.DTASSQLGFGVL.E	2 Phospho (ST)	69.89	DTAS#S#QLGFGVL	21.24	27.99					-N--Y-------	-N--Y-------	K.EEDTSGNTTHSLGAEDTASSQLGFGVLELSQSQDVEENTVPYEVDK.E				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
46	sp|Q9H2D6|TARA_HUMAN	50	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
1944	1958	2	1782.8232	0.0043	1	49.98	L.DYVELSPLTQASPQR.A	Phospho (Y)	170.17	DY#VELSPLTQASPQR	97.75						-N----------	-Y----------	R.QALDYVELSPLTQASPQRAR.T				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
47	sp|O75030|MITF_HUMAN	48	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
452	476	3	2692.2064	0.0046	1	22.12	T.DGTITFNNNLGTGTEANQAYSVPTK.M	Phospho (Y)	96.97	DGTITFNNNLGTGTEANQAY#SVPTK	33.68						----------N-----	----------N-----	K.QEPVLENCSQDLLQHHADLTCTTTLDLTDGTITFNNNLGTGTEANQAYSVPTKMGSK.L				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
48	sp|Q15233|NONO_HUMAN	48	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
442	456	2	1535.7168	0.0035	0	48.07	M.EGIGAIGGTPPAFNR.A	Phospho (ST)	96.9	EGIGAIGGT#PPAFNR	1000						--------Y-------	--------Y-------	R.FGQAATMEGIGAIGGTPPAFNRAAPGAEFAPNK.R				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
49	sp|O95155|UBE4B_HUMAN	48	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
17	34	2	1919.9004	0.0015	0	25.6	R.LAGGQTSQPTTPLTSPQR.E	Deamidated (NQ); Phospho (ST)	87.63	LAGGQTSQPTTPLTS#PQR	22.85						-------------Y---	-------------Y---	R.LAGGQTSQPTTPLTSPQRENPPGPPIAASAPGPSQSLGLNVHNMTPATSPIGASGVAHR.S				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
50	sp|Q9UNF0|PACN2_HUMAN	47	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				
334	365	3	3471.5602	0.0135	1	29.39	G.DQSLPSKPSSTLNVPSNPAQSAQSQSSYNPFE.D	Phospho (Y)	98.64	DQSLPSKPSSTLNVPSNPAQSAQSQSSY#NPFE	23.24						--------------------------N----	--------------------------N----	K.ATDGVTLTGINQTGDQSLPSKPSSTLNVPSNPAQSAQSQSSYNPFEDEDDTGSTVSEK.D				

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
51	sp|P67809|YBOX1_HUMAN	47	1	Phosphoprotein																			
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence				

24		50		2	2264.9974		0.0064	0	46.15	A.DTKPGTTGSGAGSGGPGGLTSAAPAGG.D	Phospho (ST)	152.63	DTKPGTTGSGAGS#GGPGGLTSAAPAGG	22.24						----------N----------	----------N----------	-.MSSEAETQQPPAAPPAAPALSAADTKPGTTGSGAGSGGPGGLTSAAPAGGDK.K

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
52	sp|Q9UK76|HN1_HUMAN		47	1	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
121		141	3	2142.1279		0.004	0	46.92	E.EKPVPAAPVPSPVAPAPVPSR.R	Phospho (ST)	114.31	EKPVPAAPVPS#PVAPAPVPSR	113.99						----------Y----------	----------Y----------	K.GEGDIHENVDTDLPGSLGQSEEKPVPAAPVPSPVAPAPVPSRR.N

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
53	sp|Q9BZQ8|NIBAN_HUMAN		46	1	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
585		599	3	1617.7552		0.004	0	25.46	T.DLKPPTGSNQASPAR.R	Phospho (ST)	98.33	DLKPPTGSNQAS#PAR	90.35						----------Y---	----------Y---	K.HNLFEDNMALPSESVSSLTDLKPPTGSNQASPARR.A

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
54	sp|P43007|SATT_HUMAN		46	1	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
12		31	3	1758.7729		0.0042	0	22.38	L.DSAQAGPAAGPGAPGTAAGR.A	Phospho (ST)	62.03	DS#AQAGPAAGPGAPGTAAGR	78.3						-N----------	-N----------	K.SNETNGYLDSAQAGPAAGPGAPGTAAGRAR.R

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
55	sp|Q6UUV9|CRTC1_HUMAN		46	1	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
228		247	2	2115.9514		0.0041	1	30	A.DQENTTALIPATHNTGGSLP.D	Phospho (ST)	75.85	DQENTTALIPATHNTGGS#LP	20.11						----------N--	----------N--	K.SCEVPGINIFPSADQENTTALIPATHNTGGSLPDLTNIHFPSPLPTPLDPEEPTFPALSSSSSTGNLAANLTHLGIGGAGQGMSTPGSSPQHRPAGVSPLSLSTEAR.R

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
56	sp|P46821|MAP1B_HUMAN		45	2	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1611		1622	2	1478.5976		0.0042	1	18.09	K.EECPRPMSISPP.D	Phospho (ST)	58.88	EECPRPMSIS#PP	30.7						---------Y--	---------Y--	K.EECPRPMSISPPDFSPK.T
1440		1455	2	1850.7688		0.0043	1	22.22	P.DQVSPVSEMTSTSLYQ.D	Phospho (ST)	117.72	DQVS#PVSEMTSTSLYQ	43.47						---Y----------	---Y----------	K.QGSPDQVSPVSEMTSTSLYQDK.Q

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
57	sp|Q9Y478|AAKB1_HUMAN		44	1	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
175		189	2	1678.692		0.0045	1	44.29	S.DVSELSSSPPGPYHQ.E	Phospho (ST)	144.09	DVSELSSS#PPGPYHQ	22.85						-------Y-------	-------N-------	K.CSDVSELSSSPPGPYHQEPYVCKPEER.F

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
58	sp|Q9UNY4|TTF2_HUMAN		44	2	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
357		372	2	1865.828		0.0027	1	40.5	E.DDVVFVSSKPGSPLLF.D	2 Phospho (ST)	118.06	DDVVFVSS#KPGS#PLLF	28.87	52.52					-------N---N----	-------N---Y----	R.EAATSSDDEEEDDVVFVSSKPGSPLLFDSTLDLETK.E
358		372	2	1750.802		0.0036	0	23.48	D.DVVFVSSKPGSPLLF.D	2 Phospho (ST)	121.34	DVVFVSS#KPGS#PLLF	24.44	62.08					------N---N----	------N---Y----	R.EAATSSDDEEEDDVVFVSSKPGSPLLFDSTLDLETK.E

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
59	sp|Q8IYB3|SRRM1_HUMAN		44	1	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
763		788	4	2790.4193		0.0087	1	18.85	K.KPPAPPSPVQSQSPSTNWSPAVPVKK.A	Phospho (ST)	80.62	KPPAPPS#PVQSQSPSTNWSPAVPVKK	74.82						------Y----------	------Y----------	K.KPPAPPSPVQSQSPSTNWSPAVPVKKAK.S

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
60	sp|Q5UIP0|RIF1_HUMAN		44	1	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1766		1783	2	1955.8186		0.0037	1	28.58	A.DVQAPVSPSETSQANPYS.E	Phospho (ST)	146.79	DVQAPVS#PSETSQANPYS	22.01						------N----------	------N----------	K.ADVQAPVSPSETSQANPYSEGQFLDEHHSVNFHLGLK.E

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
61	sp|P36871|PGM1_HUMAN		43	1	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
108		125	2	1724.8276		0.003	0	33.76	K.AIGGIILTASHNPGGPNG.D	Phospho (ST)	102.8	AIGGIILTAS#HNPGGPNG	24.84						-------Y----------	-------Y----------	K.AIGGIILTASHNPGGPNGDFGIK.F

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
62	sp|P52594|AGFG1_HUMAN		43	1	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
325		333	2	1057.4878		0.0034	1	25.57	A.DKYAALANL.D	Phospho (Y)	53.41	DKY#AALANL	1000						--N------	--Y------	K.AGLQTADKYAALANLDNIFSAGQGGDQGSGFGTTGK.A

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
63	sp|O60239|3BP5_HUMAN		42	1	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
336		347	2	1364.6526		0.0037	0	41.77	P.DQFPAVVRPGSL.D	Phospho (ST)	106.6	DQFPAVVRPGS#L	1000						----------N-	----------N-	R.GCGVGAEGSSTSVEDLPGSKPEPDAISVASEAFEDDSCSNFVSEDDSETQSVSSFSSGPTSPSEMPDQFPAVVRPGSLDLPSPVSLSEFGMMFPVLGPR.S

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
64	sp|Q9BQS8|FYCO1_HUMAN		41	1	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
219		229	2	1278.552		0.0028	1	35.82	F.DLNSPLNNEAL.E	Phospho (ST)	96.27	DLNS#PLNNEAL	1000						----N-------	----N-------	R.SSSMSSLVSSYLQTQEMVSNFDLNSPLNNEALEGFDEMR.L

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																	
65	sp|Q14444|CAPR1_HUMAN		41	2	Phosphoprotein																	
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
322		350	3	3088.4902		0.0035	1	21.89	V.EVVNSLQQQPQAASPSVPEPHSLTPVAQA.D	Phospho (ST)	93.45	EVVNSLQQQPQAAS#PSVPEPHSLTPVAQA	24.15						----------N----------	----------Y----------	K.EQVDEWTVETVEVVNSLQQQPQAASPSVPEPHSLTPVAQADPLVR.R

564	577	2	1594.7066	0.0038	0	23.83	Q.EQLQTVVGTYHGSP.D	Phospho (ST)	65.5	EQLQTVVGTYHGS#P	32.07						----------N-	----------N-	K.QQNQYQASYNQSFSSQPHQVEQTELQQEQLQTVVGTYHGSPDQSHQVTGNHQQPPQQNTGFPR.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
66	sp|Q96PD2|DCBD2_HUMAN	41	1	Phosphoprotein																		
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
746	757	2	1485.641	0.0022	1	40.8	P.DELVYQVPQSTQ.E	Phospho (Y)	85.11	DELVY#QVPQSTQ	38.19						----Y-------	----Y-------	K.AGKPGLPAPDELVYQVPQSTQEVSGAGR.D			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
67	sp|Q8NC96|NECP1_HUMAN	40	1	Phosphoprotein																		
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
232	249	2	1815.8336	0.0045	0	40.47	L.DSPAPVTTPAPTPVSVSN.D	Phospho (ST)	114.2	DS#PAPVTTPAPTPVSVSN	46.2						-N----------	-N----------	K.SNHGGSDADILLDLDSPAPVTTPAPTPVSVSNDLWGDFSTASSSVPNQAPQPSNWVQF.-			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
68	sp|Q9Y450|HBS1L_HUMAN	40	1	Phosphoprotein																		
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
28	44	2	2152.8254	0.0041	1	39.98	E.DDYCISPSTAAQFIYSR.R	Phospho (ST); Phospho (Y)	142.42	DDY#CIS#PSTAAQFIYSR	81.69	35.82					--N--N----------	--N--N----------	R.GYNYDEDFEDDDLYGQSVEDDYCISPSTAAQFIYSRR.D			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
69	sp|Q96DH6|MSI2H_HUMAN	39	1	Phosphoprotein																		
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
262	283	2	2029.9054	0.0047	0	31.03	R.GSGSNPARPGGFPGANSPGPVA.D	Phospho (ST)	128.04	GSGSNPARPGGFPGANS#PGPVA	148.26						----------N-----	----------N-----	R.GSGSNPARPGGFPGANSPGPVADLYGPASQDSGVGNYISAASPQPGSGFGHGIAGPLIATAFTNGYH.-			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
70	sp|Q7Z6Z7|HUWE1_HUMAN	39	2	Phosphoprotein																		
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
3913	3931	2	2125.8734	0.0072	1	39.16	K.DEPPPLSPAPLTPATPSSL.D	3 Phospho (ST)	85.83	DEPPPLS#PAPLT#PAT#PSSL	110.27	63.94	21.3				------Y----Y--Y----	------Y----Y--Y----	K.DEPPPLSPAPLTPATPSSLDPFFSR.E			
2843	2852	2	1083.4868	0.0019	0	14.1	S.DALTAVSSQL.E	Phospho (ST)	52.03	DALTAVSS#QL	24.44						-------N--	-------N--	R.AEDSDALTAVSSQLEGSPMDTSSLASCTLEEAVGDTSAAGSSEQPR.A			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
71	sp|Q5SNT6|FA21B_HUMAN	39	1	Phosphoprotein																		
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
262	277	2	1595.6682	0.0025	0	38.92	E.DFSPFGSGGGLFSGGK.G	Phospho (ST)	76.61	DFS#PFGSGGGLFSGGK	40.34						--Y----------	--Y----------	K.LTDEDFSPFGSGGGLFSGGKGLFDDEDEESDLFTEAPQDR.Q			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
72	sp|Q2TAL8|QRIC1_HUMAN	38	1	Phosphoprotein																		
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
290	306	2	1757.755	0.0041	0	38.47	V.DSAHLYSATGTITSPTG.E	Phospho (ST)	133.36	DSAHLYSATGTITS#PTG	28.87						----------N---	----------N---	K.VDMPITVSYAISGQPVATVLAIPQGQQQSYVSLRPDLLTVDSAHLYSATGTITSPTGETWTIPVYSAQPR.G			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
73	sp|Q9Y4H2|IRS2_HUMAN	38	1	Phosphoprotein																		
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
584	595	2	1345.642	0.0029	0	38.2	R.QRPVPQPSSASL.D	Phospho (ST)	75.46	QRPVPQPSSAS#L	45.71						----------Y-	----------Y-	R.QRPVPQPSSASLDEYTLMR.A			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
74	sp|Q9NYZ3|GTSE1_HUMAN	38	1	Phosphoprotein																		
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
66	78	2	1577.6246	0.0042	1	38	S.ESPFAWSPLAGEK.F	2 Phospho (ST)	95.22	ES#PFAWS#PLAGEK	1000						-N----N------	-N----N------	R.CIAASLELNNPVPEQPPLPTSESPFAWSPLAGEKFVEVYK.E			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
75	sp|Q9NZN5|ARHGC_HUMAN	38	1	Phosphoprotein																		
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
1164	1177	2	1560.6852	0.0031	1	37.89	K.EEQHGISVTGLQSP.D	Phospho (ST)	113.62	EEQHGISVTGLQS#P	101.06						----------N-	----------N-	K.EEQHGISVTGLQSPDR.D			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
76	sp|Q8IZL8|PELP1_HUMAN	37	1	Phosphoprotein																		
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
1021	1035	2	1546.6954	0.0038	1	37.24	A.DTAPTLAPEALPSQG.E	Phospho (ST)	86.84	DTAPTLAPEALPS#QG	105.86						----------Y--	----------Y--	R.GADTAPTLAPEALPSQGEVER.E			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
77	sp|Q13085|ACACA_HUMAN	37	1	Phosphoprotein																		
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
1258	1275	2	2089.8134	0.0063	1	26.49	S.DSPPQSPTFPEAGHTSLY.D	2 Phospho (ST)	93.89	DS#PPQS#PTFPEAGHTSLY	54.87	24.75					-N---Y----------	-Y---Y----------	R.IFDEVMGCFSDSPPQSPTFPEAGHTSLYDEDK.V			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
78	sp|Q9H307|PININ_HUMAN	37	1	Phosphoprotein																		
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
441	452	2	1360.5708	0.0032	1	15.37	K.SLSPGKENVSAL.D	2 Phospho (ST)	56.57	SLS#PGKENVS#AL	24.21	72.91					--Y------Y--	--N------N--	K.SLSPGKENVSALDMEK.E			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																		
79	sp|Q9H8Y8|GORS2_HUMAN	36	1	Phosphoprotein																		
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence			
213	228	2	1782.8448	0.0056	0	36.44	K.ISLPGQMAGTPITPLK.D	2 Phospho (ST)	70.23	ISLPGQMAGT#PIT#PLK	61.72	87.99					---------Y--Y---	---------N--N---	K.ISLPGQMAGTPITPLKDGFTEVQLSSVNPPSLSPPGTTGIEQSLTGLSISSTPPAVSSVLSTGVPTVPLLPPQVNQSLTSVPPMNPATTLPGLMPLPAGLPNLPNLNLNLPAPHIMPGVGLPELVNPGLPPLPSMPPR.N			

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
80	sp|Q5VZ89|DEN4C_HUMAN	36	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1306	1318	2	1364.6034	0.0021	0	36.35	R.GSASFFLKPSTSG.D	Phospho (ST)	128.25	GSASFFLKPSTS#G	19.21						-----------Y-	-----------N-	R.GSASFFLKPSTSGDSLQSGSIPLANESLEHKPVSSLAEPDLINFMDFPK.H

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
81	sp|Q14847|LASP1_HUMAN	36	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
157	197	4	4647.2429	0.0133	1	36.11	L.EQQQPHHIPTSAPVYQQPQQQPVAQSYGGYKEPAAPVSIQR.S	Phospho (Y)	66.13	EQQQPHHIPTSAPVY#QQPQQQPVAQSYGGYKEPAAPVSIQR	19.36						-------------Y---------------------------	-------------Y-------------------------	R.RPLEQQQPHHIPTSAPVYQQPQQQPVAQSYGGYKEPAAPVSIQRSAPGGGK.R
157	187	3	3598.6762	0.0131	0	28.83	L.EQQQPHHIPTSAPVYQQPQQQPVAQSYGGYK.E	Phospho (Y)	94.38	EQQQPHHIPTSAPVY#QQPQQQPVAQSYGGYK	30.71						-------------Y----------------	-------------Y----------------	R.RPLEQQQPHHIPTSAPVYQQPQQQPVAQSYGGYKEPAAPVSIQR.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
82	sp|Q8IWU2|LMTK2_HUMAN	36	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
621	637	2	1966.8508	0.0046	1	36.02	G.DLHVTSGPESPFNNIFN.D	Phospho (ST)	124.54	DLHVTSGPES#PFNNIFN	72.42						---------N-------	---------N-------	K.DSSLPGDLHVTSGPESPFNNIFNDVDK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
83	sp|P50851|LRBA_HUMAN	35	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
5	15	2	1215.5312	0.0027	1	34.88	E.DNRVPSPPPTG.D	Phospho (ST)	78.6	DNRVPS#PPPTG	46.68						-----Y-----	-----Y-----	- .MASEDNRVPSPPPTGDDGGGGGR.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
84	sp|P42858|HD_HUMAN	35	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
589	601	2	1552.696	0.0038	0	33.91	T.DNQYLGLQIGQPQ.D	Phospho (Y)	130.53	DNQY#LGLQIGQPQ	1000						---N---------	---N---------	R.SQHTLQADSVDLASCDLTSSATDGDEEDILSHSSSQVSAVPSDPAMDLNDGTQASSPISDSSQTTTEGPDSAVTPSDSSEIVLDGTDNQYLGLQIGQPQDEDEEATGILPDEASEAFR.N

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
85	sp|P10644|KAP0_HUMAN	34	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
80	92	2	1467.7052	0.0042	1	14.87	E.DEISPPPPNPVVK.G	Phospho (ST)	77.24	DEIS#PPPPNPVVK	1000						---Y---------	---Y---------	R.EDEISPPPPNPVVKGR.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
86	sp|Q9Y6D5|BIG2_HUMAN	34	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
207	229	3	2604.3007	0.0042	1	34.22	R.ELEKPIQSKPQSPVIQAAAVSPK.F	2 Phospho (ST)	81.43	ELEKPIQSKPQS#PVIQAAAVS#PK	37.23	83.28					-----------Y--------Y--	-----------Y--------Y--	R.ELEKPIQSKPQSPVIQAAAVSPKFVR.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
87	sp|Q96B36|AKTS1_HUMAN	34	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
71	100	3	3123.5482	0.0062	0	34.16	R.AATAARPPAPPPAPQPPSPTPSPPRPTLAR.E	2 Phospho (ST)	96.37	AATAARPPAPPPAPQPPS#PTPS#PPRPTLAR	24.15	24.43					-----------------Y---Y--------	-----------------Y---Y--------	R.AATAARPPAPPPAPQPPSPTPSPPRPTLAREDNEEDEDEPTETETSGEQLGISDNGGLFVMDEDATLQDLPPFCESDPESTDDGSLSEETPAGPPTCSVPPASALPTQQYAK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
88	sp|Q14247|SRC8_HUMAN	34	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
399	412	2	1608.6498	0.0025	1	21.5	K.TQTPPVSPAPQPTE.E	2 Phospho (ST)	75.35	TQT#PPVS#PAPQPTE	19.84	44.74					Y-----Y-------	Y-----Y-------	K.TQTPPVSPAPQPTEER.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
89	sp|Q8TB72|PUM2_HUMAN	34	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
388	406	3	1985.9116	0.0047	0	30.99	R.AGAGQRPLTPNQGQQGQQA.E	Phospho (ST)	49.55	AGAGQRPLT#PNQGQQGQQA	1000						--------N----------	--------Y----------	R.AGAGQRPLTPNQGQQGQQAESLAAAAAANPTLAFGQGLATGMPGYQVLAPTAYYDQTGALVVGPGAR.T

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
90	sp|Q13263|TIF1B_HUMAN	34	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
33	59	3	2267.9977	0.007	1	32.64	R.STAPSAAASASASAAASSPAGGGAEAL.E	Phospho (ST)	102.49	STAPSAAASASASAAASS#PAGGGAEAL	37.41						-----------------Y---------	-----------------Y---------	R.STAPSAAASASASAAASSPAGGGAEALELLEHCGVCR.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
91	sp|Q53ET0|CRTC2_HUMAN	34	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
257	276	2	2053.9594	0.0051	0	33.52	P.DQPANVPVLPPAMNTGGSLP.D	Phospho (ST)	85.27	DQPANVPVLPPAMNTGGS#LP	27.03						-----------------N--	-----------------N--	R.SCEVPGINIFPSPDQPANVPVLPPAMNTGGSLPDLTNLHFPPPLPTPLDPEETAYPSLSGGNSTSNLTHTMTHLGISR.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
92	sp|Q3YEC7|PARF_HUMAN	34	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
449	465	2	1778.8402	0.005	1	27.54	E.DQPRGSPPLPAGPVPSQ.D	Phospho (ST)	82.29	DQPRGS#PPLPAGPVPSQ	79.25						-----Y-----------	-----N-----------	K.AAQQDSDSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITLSSEEEAEVAAPTK.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
93	sp|P17544|ATF7_HUMAN	33	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence

312	333	3	2225.017	0.0056	0	33.23	P.DAPSPAQPQVSPAQPTPSTGGR.R	Phospho (ST)	98.93	DAPSPAQPQVS#PAQPTPSTGGR	56.84						----------N----------	----------N----------	K.ATLTHQVSSINGGCGMVVGTASTMVTARPEQSQILIQHPDAPSPAQPQVSPAQPTPSTGGRR.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
94	sp|Q16254|E2F4_HUMAN	33	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
238	256	2	2038.8814	0.0053	0	15.16	Q.EASRPNSPQLTPTAVPGSA.E	2 Phospho (ST)	52.81	EAS#RPNS#PQLTPTAVPGSA	33.63	28.28							K.EAWSSPPVAVPVPPPEDLLQSPSAVSTPPPLPKPALAQSQEASRPNSPQLTPTAVPGSAEVQGMAGPAAEITVSGGPGTDSK.D

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
95	sp|Q9GZR7|DDX24_HUMAN	33	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
55	71	2	2039.9074	0.0068	1	33.04	T.DYQLVSPAKNPSSLFSK.E	Phospho (ST); Phospho (Y)	128.75	DY#QLVS#PAKNPSSLFSK	125.85	54.9					-N---N----------	-N---N----------	K.IDPNMFADGQMDDLVCFEELTDYQLVSPAKNPSSLFSKEAPK.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
96	sp|O43432|IF4G3_HUMAN	33	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
225	236	2	1466.698	0.0045	1	32.63	P.DPVLKSPSPVLR.L	2 Phospho (ST)	78.43	DPVLKS#PS#PVLR	1000						-----Y-Y----	-----Y-Y----	K.QEEKPKPDPVLKSPSPVLRLVLSGEK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
97	sp|Q99618|CDCA3_HUMAN	32	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
123	133	2	1250.5842	0.0047	1	32.32	L.DLPLGTQLSVE.E	Phospho (ST)	96.14	DLPLGTQLS#VE	41.33						--------N--	--------N--	K.SNLPPEPVLPPEAPLSSELDLPLGTQLSVEEQMPPWNQTEFPSK.Q

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
98	sp|Q02750|MP2K1_HUMAN	32	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
217	227	2	1263.4976	0.0021	0	32.16	I.DSMANSFVGTR.S	Phospho (ST)	64.31	DSMANS#FVGTR	31.27						-----Y-----	-----N-----	K.LCDFGVSGQLIDSMANSFVGTRSYMSPER.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
99	sp|O75820|ZN189_HUMAN	32	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
438	452	2	1948.801	-0.0032	1	31.67	F.DPNCSLVIQQEVYPK.E	Phospho (ST); Phospho (Y)	73.6	DPNCS#LVIQQEVY#PK	1000								K.ESFDPNCSLVIQQEVYPKEK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
100	sp|Q9BRL6|SFR2B_HUMAN	31	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	
19	27	2	1145.4782	0.0028	1	31.02	V.DNLTYRTSP.D	Phospho (ST)	116.52	DNLTYRTS#P	24.44						-------N-	-------N-	K.VDNLTYRTSPDSLR.R

Supplementary Table S3: Phosphoproteins with the corresponding phosphopeptides and localized phosphosites from solprotSP (*S.pombe*) and from SKMel (human melanoma) samples
(*) Phosphorylated amino acid **X** is displayed as **X#**

***Human melanoma* - Formic acid digest of large tryptic peptides**

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
1	sp|P19338|NUCL_HUMAN	453	4	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
205	217	2	1532.5592	0.0003	1	19.08	D.DSEEEAMETTPAK.G	Oxidation (M); Phospho (ST)	17.09	DS#EEEAMETTPAK	19.88						-Y----------	-Y----------	K.AAAAAPASEDEDDDEDDEDDDDDDEEDDSEEEAMETTPAKGK.K
206	217	2	1417.5328	0.0009	0	20.07	D.SEEEAMETTPAK.G	Oxidation (M); Phospho (ST)	20.62	S#EEEAMETTPAK	19.88						Y----------	Y----------	K.AAAAAPASEDEDDDEDDEDDDDDDEEDDSEEEAMETTPAKGK.K
41	52	2	1460.6176	-0.0024	1	21.72	D.SSGEEVVIPQKK.G	Deamidated (NQ); 2 Phospho (ST)	23.87	S#S#GEEVVIPQKK	1000						YY----------	YY----------	K.EVEEDSEDEEMSEDEEDDSSGEEVVIPQKKGK.K
41	51	2	1332.5268	0.0017	0	15.41	D.SSGEEVVIPQK.K	Deamidated (NQ); 2 Phospho (ST)	31.74	S#S#GEEVVIPQK	1000						YY---------	YY---------	K.EVEEDSEDEEMSEDEEDDSSGEEVVIPQKK.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
2	sp|P61978|HNRPK_HUMAN	422	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
104	139	4	4133.9949	0.0041	1	35.77	K.IIPTLEEGLQLPSPTATSQLPLESDAVECLNYQHYK.G	Phospho (ST)	81.72	IIPTLEEGLQLPS#PTATSQLPLESDAVECLNYQHYK	28.35						----------Y----------	----------Y----------	K.IIPTLEEGLQLPSPTATSQLPLESDAVECLNYQHYKGSDFDCELR.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
3	sp|Q13428|TCOF_HUMAN	287	5	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
620	637	2	1863.882	0.002	0	35.5	D.SEEAPAAMTAAQAKPALK.I	Phospho (ST)	87.84	S#EEAPAAMTAAQAKPALK	53.03						Y----------	N----------	K.AEKPMDNSESSEESSDSADSEEAPAAMTAAQAKPALKIPQTK.A
1243	1259	3	1847.8999	0.0034	1	27.84	D.GKQEAKPQQAAGMLSPK.T	Phospho (ST)	65.47	GKQEAKPQQAAGMLS#PK	1000						----------Y--	----------Y--	K.DDPDGKQEAKPQQAAGMLSPKTGGK.E
964	985	3	2197.0267	-0.001	1	55.62	D.PNRSPAGPAATPAQAQAASTPR.K	Deamidated (NQ); Phospho (ST)	43.54	PNRS#PAGPAATPAQAQAASTPR	28.1						---Y----------	---Y----------	K.QDDSGSSSSEESDSDGEAPAAVTSAQVIKPPLIFVDPNRSPAGPAATPAQAQAASTPRK.A
1367	1387	2	2071.9314	0.0004	1	51.76	K.LGAGEGGEASVSPEKTSTTSK.G	Phospho (ST)	87.14	LGAGEGGEASVS#PEKTSTTSK	22.01						----------Y---------	----------Y---------	K.LGAGEGGEASVSPEKTSTTSKGK.A
668	692	3	2363.0794	0.0039	1	32.78	R.KAGTATSPAGSSPAVAGGTQRPAED.S	Phospho (ST)	88.28	KAGTATSPAGSS#PAVAGGTQRPAED	28.5						----------Y----------	----------N----------	K.AGTATSPAGSSPAVAGGTQRPAEDSSSSEESDSEEEK.T

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
4	sp|P48681|NEST_HUMAN	275	4	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
344	373	3	3134.7382	0.0098	0	27.46	R.LGSLLPVLVSPTSLPSPLPATLETPVPAFLK.N	Phospho (ST)	126.27	LGSLLPVLVSPTS#LPSPLPATLETPVPAFLK	20.57						----------N----------	----------Y----------	R.LGSLLPVLVSPTSLPSPLPATLETPVPAFLKNQEFLQAR.T
1575	1588	3	1613.7115	0.0028	1	37.42	D.RGSPFQEEEGSALK.T	Phospho (ST)	117.52	RGS#PFQEEEGSALK	116.23						--N----------	--Y----------	R.GSPFQEEEGSALKTSWAGAPVHLGQGQFLK.F
1334	1361	3	3064.2832	-0.0024	1	40.12	D.PAVLASEGLEAPPSEKEEGEEGEEECGR.D	Phospho (ST)	87.68	PAVLASEGLEAPPS#EKEEGEEGEECGR	38.77						----------Y----------	----------Y----------	K.EGWDPAVLASEGLEAPPSEKEEGEEGEEECGRDSDLSEEFEDLGTEAPFLPGVPGEVAEPLGQVPQLLLDPAAWDR.D
916	933	3	2215.9636	0.0002	1	23.31	R.NLEEEENLGKGEYQESLR.S	Phospho (Y)	90.15	NLEEEENLGKGEY#QESLR	34.22						----------N-----	----------Y-----	R.NLEEEENLGKGEYQESLRSLEEEGQELPQSADVQR.W

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
5	sp|P22626|ROA2_HUMAN	272	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
243	266	2	2197.8614	0.0011	0	35.77	D.GYNGYGGGPGGGNFGGSPGYGGGR.G	Phospho (ST)	55.81	GYNGYGGGPGGGNFGGS#PGYGGGR	20.91						----------Y-------	----------Y-------	R.GFGDGYNGYGGGPGGGNFGGSPGYGGGRGGYGGGGPGYGNQGGGYGGGYDNYGGGNYGSGNYNDFGNYNQQPSNYGPMK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
6	sp|Q00839|HNRPU_HUMAN	250	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
118	134	2	1874.606	0.0024	1	15.68	D.SGPMEEEEAASEDENGD.D	Phospho (ST)	64.85	SGPMEEEEAAS#EDENGD	44.1						----------N------	----------N------	R.SGAGLEQEAAAGGDEEEEEEEEEEGEGISALDGDQMELGEENGAAGAADSGPMEEEEAASEDENGDDQGFQEGEDELGDEEEGAGDENGHGEQQPQPPATQQQQPQQQR.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
7	sp|P49006|MRP_HUMAN	249	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
158	195	3	3704.5162	0.004	0	70.14	K.GAEASAASEEEAGPQATEPSTPSGPESGPTPASAEQNE.-	Phospho (ST)	160.78	GAEASAASEEEAGPQATEPST#PSGPESGPTPASAEQNE	30.83						----------Y----------	----------Y----------	K.GAEASAASEEEAGPQATEPSTPSGPESGPTPASAEQNE.-
116	144	3	3077.1922	-0.0007	1	62.71	D.SSASSPTEEEQEQGEIGACSDEGTAQEGK.A	Phospho (ST)	249.76	SSASS#PTEEEQEQGEIGACSDEGTAQEGK	24.75						----Y----------	----Y----------	K.EGGGDSSASSPTEEEQEQGEIGACSDEGTAQEGKAAATPESQEPQAK.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
8	sp|Q13765|NACA_HUMAN	211	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
145	179	3	3939.7312	0.0042	1	63.61	K.VQGEAVSNIQENTQTPTVQEESEEEVDETGVEVK.D	Phospho (ST)	159.33	VQGEAVSNIQENTQTPTVQEES#EEEVDETGVEVK	28.83						----------Y----------	----------N----------	K.VQGEAVSNIQENTQTPTVQEESEEEVDETGVEVKDIELVMSQANVSR.A
145	172	3	3198.3532	0.0283	0	22.49	K.VQGEAVSNIQENTQTPTVQEESEEEVD.E	Deamidated (NQ); Phospho (ST)	73.94	VQGEAVSNIQENTQTPTVQEES#EEEVD	19.61						----------Y------	----------N------	K.VQGEAVSNIQENTQTPTVQEESEEEVDETGVEVK.D

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
9	sp|Q15365|PCBP1_HUMAN	177	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
221	237	3	1920.9367	0.0021	1	18.39	D.AYSIQGQHTISPLDLAK.L	Phospho (Y)	54.53	AY#SIQGQHTISPLDLAK	33.68						-N----------	-Y----------	R.CSDAAGYPHATHDLEGPPLDAYSIQGQHTISPLDLAKLNQVAR.Q
178	199	2	2399.0274	0.0026	0	38.05	R.VMTIPYQPMPASSPVICAGGQD.R	Deamidated (NQ); Phospho (ST)	128.41	VMTIPYQPMPASS#PVICAGGQD	22.85						----------Y---------	----------Y---------	R.VMTIPYQPMPASSPVICAGGQDR.C

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?

10	sp|Q9NQC3|RTN4_HUMAN		163		2	Phosphoprotein																			
Start	End		charge	Mr(expt)		Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
92		109	2	1964.9028		-0.0005	1	50.51	R.GPLPAAPPVAPERQPSWD.P	Deamidated (NQ); Phospho (ST)	143.3	GPLPAAPPVAPERQPS#WD	1000						----------Y--	----------Y--	R.GPLPAAPPVAPERQPSWDPSPVSSTVPAPSPLSAAAVSPSK.L
15		24	2	1203.5804		0.0003	0	17.24	D.SPPRPQPAFK.Y	Phospho (ST)	28.93	S#PPRPQPAFK	1000						Y---------	Y---------	-
																									.MEDLDQSPLVSSSDSPPRPQPAFKYQFVR.E

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
11	sp|Q7Z417|NUFP2_HUMAN		160	1	Phosphoprotein																			
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
618		639	2	2428.1034	-0.0012		1	83.51	K.DYEIESQNPLASPTNTLLGSAK.E	Deamidated (NQ); Phospho (ST)	120.36	DYEIESQNPLAS#PTNTLLGSAK	26.53						----------Y----------	----------Y----------	K.DYEIESQNPLASPTNTLLGSAKEQR.Y

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
12	sp|P16401|H15_HUMAN		133	1	Phosphoprotein																			
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
2		21	2	2102.9794	0.0022		1	43.86	M.SETAPAETATPAPVEKSPAK.K	Acetyl (Protein N-term); Phospho (ST)	48.26	SETAPAETATPAPVEKS#PAK	26.52						---------------Y---	---------------N---	-.MSETAPAETATPAPVEKSPAKK.K

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
13	sp|Q9BTC0|DIDO1_HUMAN		116	1	Phosphoprotein																			
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1454		1477	3	2614.2763	0.0011		1	52.63	R.RNSVERPAEPVAGAATPSLVEQQK.M	Deamidated (NQ); Phospho (ST)	54.97	RNS#VERPAEPVAGAATPSLVEQQK	59.05						--Y----------	--Y----------	R.NSVERPAEPVAGAATPSLVEQQKMLEELNK.Q

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
14	sp|P16989|DBPA_HUMAN		112	2	Phosphoprotein																			
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
30		59	3	2696.2711	0.0003		1	29.1	D.PAPKSPVGSGAPQAAAPAPAAHVAGNPGGD.A	Phospho (ST)	95.5	PAPKSPVGS#GAPQAAAPAPAAHVAGNPGGD	19						----Y----------	----Y----------	-
60		81	2	1924.8442	0.0028		0	42.04	D.AAPAATGTAAAASLATAAGSED.A	Phospho (ST)	123.79	AAPAATGTAAAASLATAAGS#ED	63.77						----------Y--	----------Y--	.MSEAGEATTTTTTTLPQAPTEAAAAAPQDPAPKSPVGSGAPQAAAPAPAAHVAGNPGGDAAPAATGTAAAASLATAAGSEDAEK.K K.SPVGSGAPQAAAPAPAAHVAGNPGGDAAPAATGTAAAASLATAAGSEDAEK.K

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
15	sp|P56693|SOX10_HUMAN		102	3	Phosphoprotein																			
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
2		21	2	2400.9614	0.0004		1	38.14	M.AEEQDLSEVELSPVGSEEPR.C	Acetyl (Protein N-term); 2 Phospho (ST)	68.09	AEEQDLS#EVELS#PVGSEEPR	65.95	39.8					------N----N--------	------N----N--------	- .MAEEQDLSEVELSPVGSEEPRCLSPGSAPSLGPDGGGGGSGLR.A
7		21	2	1866.7114	0.0024		0	25.82	D.LSEVELSPVGSEEPR.C	3 Phospho (ST)	84.3	LS#EVELS#PVGS#EEPR	1000						-N----N---N----	-N----N---N----	- .MAEEQDLSEVELSPVGSEEPRCLSPGSAPSLGPDGGGGGSGLR.A
35		53	3	1689.7843	0.0007		1	38.55	D.GGGGGSGLRASPGPGELGK.V	Phospho (ST)	75.12	GGGGGSGLRAS#PGPGELGK	49.98						----------Y---------	----------Y---------	R.CLSPGSAPSLGPDGGGGGSGLRASPGPGELGKVK.K

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
16	sp|P43355|MAGA1_HUMAN		98	1	Not annotated																			
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
54		72	2	2096.9554	-0.0014		0	53.62	D.PPQSPQGASAFPTTINFTR.Q	Deamidated (NQ); Phospho (ST)	72.97	PPQS#PQGASAFPTTINFTR	31.67								R.SLHCKPEEALEAQQEALGLVCVQAATSSSSPLVLGTLEEVPTAGSTDPPQSPQGASAFPTTINFTRQR.Q

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
17	sp|P29590|PML_HUMAN		94	2	Phosphoprotein																			
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
524		555	4	3403.5289	0.0054		1	40.78	D.GPPSPRSPVIGSEVFLPNSNHVASGAGEAEER.V	2 Phospho (ST)	104.77	GPPS#PRS#PVIGSEVFLPNSNHVASGAGEAEER	52.39	56.4					---Y--Y----------	---Y--Y----------	K.AVSPPHLDGPPSPRSPVIGSEVFLPNSNHVASGAGEAEERVVVISSSEDSDAENSSSR.E
1		14	2	1700.7354	0.0013		1	16.15	-.MEPAPARSPRPQQD.P	Acetyl (Protein N-term); Phospho (ST)	11.68	MEPAPARS#PRPQQD	1000						-------Y------	-------Y------	- .MEPAPARSPRPQQDPARPQEPTMPPPETPSEGR.Q

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
18	sp|Q16666|IF16_HUMAN		92	1	Phosphoprotein																			
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
144		165	2	2268.9434	0.0043		0	63.46	K.VSEEQTQPPSPAGAGMSTAMGR.S	Deamidated (NQ); Phospho (ST)	78.46	VSEEQTQPPS#PAGAGMSTAMGR	24.43						---------Y----------	---------Y----------	K.VSEEQTQPPSPAGAGMSTAMGRSPSPK.T

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
19	sp|Q86XP3|DDX42_HUMAN		91	1	Phosphoprotein																			
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
83		99	2	1938.8722	-0.0002		1	25.09	D.SSNVDLPYIPAENSPTR.Q	Phospho (ST)	75.61	SSNVDLPYIPAENS#PTR	23.34						------------Y---	------------Y---	R.ANFDEENAYFEDEEEDSSNVDLPYIPAENSPTRQQFHSKPVDSDSDDDPLEAFMAEVEDQAAR.D

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
20	sp|Q96JM3|ZN828_HUMAN		89	2	Phosphoprotein																			
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
280		301	3	2525.2054	0.0062		0	33.36	R.KPSPSESPEPWKPFPAVSPEPR.R	Phospho (ST)	74.52	KPSPS#ESPEPWKPFPAVSPEPR	21.31						--Y----------	--Y----------	R.KPSPSESPEPWKPFPAVSPEPRRPAPAVSPGSWKPGPPGSPRPWK.S
199		219	2	2314.0914	0.0016		0	54.01	K.LAPVPSPEPQKPAPVSPESVK.A	Deamidated (NQ); 2 Phospho (ST)	108.74	LAPVPS#PEPQKPAPVS#PESVK	116.26	46.32					-----Y---------Y-----	-----Y---------Y-----	K.LAPVPSPEPQKPAPVSPESVKATLSNPKPQK.Q

Index	AC		Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																			
21	sp|O15541|R113A_HUMAN		87	1	Phosphoprotein																			
Start	End		charge	Mr(expt)	Delta (Da)		MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
83		101	2	2325.9194	0.0016		0	78.19	D.LSSEEEEENEPESLGVVYK.S	2 Phospho (ST)	153.66	LS#S#EEEEENEPESLGVVYK	143.06	143.06					-YY----------	-YY----------	K.AAYGDLSSEEEEENEPESLGVVYKSTR.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
22	sp|Q14839|CHD4_HUMAN	80	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
39	50	2	1453.5862	0.0001	1	61.34	D.PEEDLSETETPK.L	Phospho (ST)	122.62	PEEDLS#ETETPK	24.75						-----N------	-----N------	- .MASGLGSPSPCSAGSEEEDMDALL NNSLPPPHPENEEDPEEDLSETETP KLK.K
527	541	3	1753.8529	0.0017	0	22.03	D.PNTPSPKPLEGRPER.Q	Phospho (ST)	63.08	PNTPS#PKPLEGRPER	24.15						----Y----------	----Y----------	K.WGQPPSPTPVPRPPDADPNTPSP KPLEGRPERQFFVK.W

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
23	sp|Q16512|PKN1_HUMAN	72	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
109	127	2	1894.7832	-0.0048	0	26.22	D.GPQSPGAGGPTCSATNLSR.V	Deamidated (NQ); Phospho (ST)	47.72	GPQS#PGAGGPTCSATNLSR	48.76						---N----------	---N----------	R.LDLLHQQLQELHAHVVLPDPAATH DGPQSPGAGGPTCSATNLSRVAGL EK.Q

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
24	sp|Q12888|TP53B_HUMAN	68	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1107	1127	2	2281.9874	0.0027	1	68.38	K.MVIQGPSSPQGEAMVTDVLED.Q	Phospho (ST)	177.64	MVIQGPSS#PQGEAMVTDVLED	26.38						-------Y----------	-------Y----------	K.MVIQGPSSPQGEAMVTDVLEDQK. E
460	473	2	1654.7142	0.0015	0	15.07	D.IFIPSPSLEEQSND.G	Phospho (ST)	75.66	IFIPSPS#LEEQSND	30.7						------N-------	------N-------	K.LQSGEPVELENPPLLPESTVSPQA STPISQSTPVFPPGSLPIPSQPQFSH DIFIPSPSLEEQSNDGK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
25	sp|Q08211|DHX9_HUMAN	66	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
72	93	2	2389.1474	0.002	1	40.36	R.INEIKSEEVPAFGVASPPPLTD.T	Phospho (ST)	129.78	INEIKSEEVPAFGVAS#PPPLTD	48.99						---------------Y------	---------------Y------	R.INEIKSEEVPAFGVASPPPLTDTPD TTANAEGDLPTTMGGPLPPHLALK.A
77	93	2	1791.8016	0.0048	0	16.86	K.SEEVPAFGVASPPPLTD.T	Phospho (ST)	109.09	SEEVPAFGVAS#PPPLTD	57.41						----------Y------	----------Y------	K.SEEVPAFGVASPPPLTDTPDTTAN AEGDLPTTMGGPLPPHLALK.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
26	sp|Q13066|GAGE2_HUMAN	64	3	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
16	49	3	3921.7132	0.0018	1	24.19	R.YVEPPEMIGPMRPEQFSDEVEPAT PEEGEPATQR.Q	Phospho (ST)	99.78	YVEPPEMIGPMRPEQFSDEVEPAT# PEEGEPATQR	39.77						----------Y----------	----------Y----------	R.YVEPPEMIGPMRPEQFSDEVEPAT PEEGEPATQRQDPAAAQEGEDEGA SAGQGPKPEAHSQEQGHPQTGCEC EDGPDGQEMDPPNPEEVK.T
34	49	3	1818.7699	0.0026	0	25.78	D.EVEPATPEEGEPATQR.Q	Phospho (ST)	101.14	EVEPAT#PEEGEPATQR	102.06						-----Y----------	-----Y----------	R.YVEPPEMIGPMRPEQFSDEVEPAT PEEGEPATQRQDPAAAQEGEDEGA SAGQGPKPEAHSQEQGHPQTGCEC EDGPDGQEMDPPNPEEVK.T
98	112	3	1758.7744	0.0031	1	15.17	D.PPNPEEVKTPEEGEK.Q	Phospho (ST)	72.08	PPNPEEVKT#PEEGEK	1000						--------N------	--------N------	R.QDPAAAQEGEDEGASAGQGPKPE AHSQEQGHPQTGCECEDGPDGQE MDPPNPEEVKTPEEGEKQSQC.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
27	sp|Q71U36|TBA1A_HUMAN	63	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
439	451	2	1521.5042	0.0011	0	46.36	D.SVEGEGEEEGEEY.-	Phospho (Y)	161.65	SVEGEGEEEGEEY#	183.16						----------N	----------Y	K.DYEEVGVDSVEGEGEEEGEEY.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
28	sp|P06748|NPM_HUMAN	63	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
9	24	3	2031.9346	0.0034	0	18.23	D.MSPLRPQNYLFGCELK.A	Phospho (ST)	69.42	MS#PLRPQNYLFGCELK	48.77						-Y----------	-Y----------	- .MEDSMDMDMSPLRPQNYLFGCEL KADK.D
104	127	3	2602.0576	0.0045	1	20.17	K.CGSGPVHISGQHLVAVEEDAESED .E	Deamidated (NQ); Phospho (ST)	12.22	CGSGPVHISGQHLVAVEEDAES#ED	24.31						----------Y--	----------Y--	K.CGSGPVHISGQHLVAVEEDAESED EEEEDVK.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
29	sp|Q13283|G3BP1_HUMAN	62	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
136	159	3	2889.1792	0.0039	0	31.22	D.EVFGGFVTEPQEESEEEVEEPEE R.Q	Phospho (ST)	107.07	EVFGGFVTEPQEES#EEEVEEPEER	21.4						----------Y----------	----------Y----------	R.YQDEVFGGFVTEPQEESEEEVEE PEERQQTPEVVPDDSGTFYDQAVVS NDMEEHLEEPVAEPEPDPEPEPEQE PVSEIQEEKPEPVLEETAPEDAQK.S
133	159	3	3295.3252	0.001	1	28.61	R.YQDEVFGGFVTEPQEESEEEVEE PEER.Q	Phospho (ST)	96.86	YQDEVFGGFVTEPQEES#EEEVEEP EER	37.31						----------Y----------	----------Y----------	R.YQDEVFGGFVTEPQEESEEEVEE PEERQQTPEVVPDDSGTFYDQAVVS NDMEEHLEEPVAEPEPDPEPEPEQE PVSEIQEEKPEPVLEETAPEDAQK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
30	sp|Q12792|TWF1_HUMAN	62	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
137	155	2	2154.0254	0.0009	0	61.88	K.YLLSQSSPAPLTAAEEELR.Q	Phospho (ST)	131.75	YLLSQSS#PAPLTAAEEELR	21.51						------Y----------	------Y----------	K.YLLSQSSPAPLTAAEEELRQIK.I

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
31	sp|Q9C0C2|TB182_HUMAN	61	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1503	1512	2	1245.52	0.0021	0	38.66	D.SPPSWRPQPD.G	Phospho (ST)	58.1	S#PPSWRPQPD	28.52						N---------	N---------	R.DSPPSWRPQPDGEASQTEDVDG TWGSSAAR.W

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
32	sp|P36871|PGM1_HUMAN	60	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence

108		130	3	2285.1226	0.002	1	23.6	K.AIGGIILTASHNPGGPNGDFGIK.F	Phospho (ST)	104.34	AIGGIILTAS#HNPGGPNGDFGIK	24.15						---------Y----------	---------Y----------	K.AIGGIILTASHNPGGPNGDFGIKFNISNGGPAPEAITDK.I
108		126	2	1840.832	-0.0036	0	45.3	K.AIGGIILTASHNPGGPNGD.F	Deamidated (NQ); Phospho (ST)	76.51	AIGGIILTAS#HNPGGPNGD	37.41						-------Y----------	-------Y----------	K.AIGGIILTASHNPGGPNGDFGIK.F

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																
33	sp|P39687|AN32A_HUMAN	59	1	Phosphoprotein																
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
158	168	2	1233.4452	0.0014	1	38.95	D.SDAEGYVEGLD.D	Phospho (ST)	100.98	S#DAEGYVEGLD	37.38						Y----------	Y----------	K.EAPDSDAEGYVEGLDDEEEDEDEEEYDEDAQVVEDEEDEDEEEEGEEEDVSGEEEEDEEGYNDGEVDDEEDEEELGEEER.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																
34	sp|Q92974|ARHG2_HUMAN	57	1	Phosphoprotein																
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
682	706	3	2515.1254	0.0026	1	16.68	R.EPALPLEPDSGGNTSPGVTANGEAR.T	Phospho (ST)	34.29	EPALPLEPDSGGNTS#PGVTANGEAR	36.83						----------Y----------	----------Y----------	R.EPALPLEPDSGGNTSPGVTANGEARTFNGSIELCR.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																
35	sp|Q9H6F5|CCD86_HUMAN	56	2	Phosphoprotein																
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
31	53	3	2634.2008	0.0045	1	16.76	R.ALVEFESNPEETREPGSPPSVQR.A	Phospho (ST)	99.5	ALVEFESNPEETREPGS#PPSVQR	24.66						----------Y------	----------Y------	R.ALVEFESNPEETREPGSPPSVQRAGLGSPERPPK.T
11	27	3	1863.9109	0.0017	0	37.74	R.LGGLRPESPESLTSVSR.T	Phospho (ST)	100.22	LGGLRPES#PESLTSVSR	34.22						-------Y---------	-------Y---------	R.LGGLRPESPESLTSVSRTR.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																
36	sp|P49023|PAXI_HUMAN	56	1	Phosphoprotein																
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
126	147	2	2357.0454	-0.0003	1	55.63	K.SAEPSPTVMSTSLGSNLSELDR.L	Phospho (ST)	178.33	SAEPSPTVMSTS#LGSNLSELDR	19.33						----------Y----------	----------N----------	K.SAEPSPTVMSTSLGSNLSELDRLLLELNAVQHNPPGFPADEANSSPPLPGALSPLYGVPETNSPLGGK.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																
37	sp|Q14247|SRC8_HUMAN	55	1	Phosphoprotein																
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
435	454	2	2233.9234	-0.0004	1	55.46	R.GPVSGTEPEPVYSMEAADYR.E	Phospho (Y)	128.47	GPVSGTEPEPVY#SMEAADYR	26.38						----------Y---------	----------Y---------	R.GPVSGTEPEPVYSMEAADYREASSQQGLAYATEAVYESAEAPGHYPAEDSTYDEYENDLGITAVALYDYQAAGDDEISFDPDDIITNIEMIDDGWWR.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																
38	sp|Q9BUR4|WAP53_HUMAN	54	2	Phosphoprotein																
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
20	34	3	1697.6791	0.0005	0	22.85	D.PAPAHPSPHASPMNK.N	2 Phospho (ST)	94.36	PAPAHPS#PHAS#PMNK	1000						------Y---Y----	------Y---Y----	K.TLETQPLAPDCCPSDQDPAPAHPSPHASPMNKNADSELMPPPPER.G
72	92	3	2389.0546	0.0054	0	21.36	D.PVSLSTPLETEFGSPSELSPR.I	2 Phospho (ST)	139.65	PVSLSTPLETEFGS#PSELS#PR	46.68	45.11					----------N--Y--	----------Y--Y--	R.EGDPVSLSTPLETEFGSPSELSPRIEEQELSENTSLPAEEANGSLSEEEANGPELGSGK.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																
39	sp|Q05655|KPCD_HUMAN	52	1	Phosphoprotein																
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
654	669	2	1811.76	0.0011	1	29.11	D.SMDQSAFAGFSFVNPK.F	Phospho (ST)	131.96	SMDQSAFAGFS#FVNPK	106.34						----------Y-----	----------N-----	K.NLIDSMDQSAFAGFSFVNPKFEHLLED.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																
40	sp|P40763|STAT3_HUMAN	51	1	Phosphoprotein																
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
710	729	2	2389.0574	0.0057	1	44.95	K.FICVTPTTCSNTIDLPMSPR.T	Phospho (ST)	164.03	FICVTPTTCSNTIDLPMS#PR	109.23						----------Y--	----------Y--	K.FICVTPTTCSNTIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESLTFDMELTSECATSPM.-

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																
41	sp|Q96GQ7|DDX27_HUMAN	51	1	Phosphoprotein																
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
56	69	2	1565.6622	0.0012	1	50.88	D.SGDEEEEGPIVLGR.R	Phospho (ST)	140.68	S#GDEEEEGPIVLGR	1000						Y----------	N----------	R.AGPQAVLASGSGFCDNMLADLGLIGTIGEDDEVPVEPESDSGDEEEEGPIVLGRR.Q

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																
42	sp|Q9Y2X3|NOP58_HUMAN	51	1	Phosphoprotein																
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
495	517	3	2741.1556	0.0012	1	40.78	K.HIKEEPLSEEEPCTSTAIASPEK.K	2 Phospho (ST)	98.55	HIKEEPLS#EEEPCTSTAIAS#PEK	61.54	38.37					-------Y----------Y---	-------Y----------Y---	K.HIKEEPLSEEEPCTSTAIASPEKK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																
43	sp|P51610|HCFC1_HUMAN	51	1	Phosphoprotein																
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1483	1511	3	3003.5002	0.0047	0	21.61	R.AVTTVTQSTPVPGPSVPPPEELQVSPGPGR.Q	Phospho (ST)	78.75	AVTTVTQSTPVPGPSVPPPEELQVS#PGPR	68.38						----------Y----	----------Y----	R.AVTTVTQSTPVPGPSVPPPEELQVSPGPRQQLPPR.Q

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																
44	sp|Q8WWM7|ATX2L_HUMAN	50	1	Phosphoprotein																
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
585	599	2	1568.7166	0.0009	0	20.55	D.GLLTSEPMGSPVSSK.T	Phospho (ST)	70.81	GLLTSEPMGS#PVSSK	22.87						---------Y-----	---------Y-----	K.EVDGLLTSEPMGSPVSSKTESVSDK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?																
45	sp|O15061|SYNEM_HUMAN	50	2	Phosphoprotein																
Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
1094	1125	3	3322.5712	-0.0007	1	39.83	R.TPQGPVSATVEVSSPTGFAQSQVLEDVSQAAR.H	Phospho (ST)	117.67	TPQGPVSATVEVSS#PTGFAQSQVLEDVSQAAR	22.81						----------N----------	----------N----------	R.TPQGPVSATVEVSSPTGFAQSQVLEDVSQAARHIK.L
701	710	2	1187.548	0.0006	1	28.43	D.EAGLDYLLSK.D	Phospho (Y)	57.58	EAGLDY#LLSK	34.46						-----N----	-----N----	K.LTEDVDVSDEAGLDYLLSKDIK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
46	sp|P13693|TCTP_HUMAN	50	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
46	85	4	4191.9349	0.0041	1	19.16	D.SLIGGNASAEGPEGEGTESTVITGVDIVMNHHLQETSFTK.E	Phospho (ST)	45.03	S#LIGGNASAEGPEGEGTESTVITGVDIVMNHHLQETSFTK	30.16						Y----------	Y----------	R.TEGNIDDSLIGGNASAEGPEGEGTESTVITGVDIVMNHHLQETSFTKEAYK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
47	sp|P10412|H14_HUMAN	49	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
2	21	2	2024.9834	0.0015	1	49.46	M.SETAPAAPAAPAPAEKTPVK.K	Acetyl (Protein N-term); Phospho (ST)	45.29	SETAPAAPAAPAPAEKT#PVK	64.25						----------Y---	----------N---	-.MSETAPAAPAAPAPAEKTPVKK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
48	sp|O75030|MITF_HUMAN	48	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
401	420	3	2186.0587	0.0032	1	40.72	R.AHGLSLIPSTGLCSPDLVNR.I	Phospho (ST)	106.94	AHGLSLIPSTGLCS#PDLVNR	82.44						----------Y------	----------Y------	R.AHGLSLIPSTGLCSPDLVNRIIK.Q

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
49	sp|Q5T4S7|UBR4_HUMAN	48	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
2951	2969	2	2025.7574	0.0026	1	28.93	D.GSEGEGEGETEGDVHTSNR.L	Phospho (ST)	56.59	GS#EGEGEGETEGDVHTSNR	32.44						-N----------	-N----------	R.SSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDGSEGEGEGETEGDVHTSNRLHMVR.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
50	sp|P05387|RLA2_HUMAN	47	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
3	21	2	1947.9364	0.0022	0	47.2	R.YVASYLLAALGGNSSPSAK.D	Phospho (ST)	143.08	YVASYLLAALGGNSS#PSAK	28.87						----------Y----	----------Y----	R.YVASYLLAALGGNSSPSAKDIK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
51	sp|Q8IYB3|SRRM1_HUMAN	46	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
763	788	4	2790.4085	-0.0021	1	30.75	K.KPPAPPSPVQSQSPSTNWSPAVPVKK.A	Phospho (ST)	84.83	KPPAPPS#PVQSQSPSTNWSPAVPVKK	74.82						------Y----------	------Y----------	K.KPPAPPSPVQSQSPSTNWSPAVPVKKAK.S
247	263	3	1976.9887	0.0027	1	28.17	K.VPKPEPIPEPKEPSPEK.N	Phospho (ST)	96.91	VPKPEPIPEPKEPS#PEK	1000						----------Y---	----------Y---	K.VPKPEPIPEPKEPSPEKNSK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
52	sp|Q15459|SF3A1_HUMAN	46	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
317	330	2	1710.588	0.0025	0	45.5	K.FGESEEVEMEVESD.E	Oxidation (M); Phospho (ST)	69.45	FGESEEVEMEVES#D	102.68						----------Y-	----------Y-	K.FGESEEVEMEVESDEEDDK.Q

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
53	sp|O14979|HNRDL_HUMAN	44	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
123	137	2	1826.7074	0.0005	0	44.43	D.MNEYSNIEEFAEGSK.I	Phospho (Y)	149.86	MNEY#SNIEEFAEGSK	32.4						---N----------	---Y----------	R.QHPPADSSVTMEDMNEYSNIEEFAEGSKINASK.N

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
54	sp|Q8N5F7|NKAP_HUMAN	43	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
137	151	2	1631.7966	0.0006	0	42.72	R.IGELGAPEVWGLSPK.N	Phospho (ST)	95.88	IGELGAPEVWGLS#PK	1000						----------Y--	----------Y--	R.IGELGAPEVWGLSPKNPEPDSDEHTPVEDEEPK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
55	sp|Q92625|ANS1A_HUMAN	43	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
832	843	3	1573.7284	-0.0006	0	37.46	D.RPYEEPPQKPPR.F	Deamidated (NQ); Phospho (Y)	49.99	RPY#EEPPQKPPR	1000						--N---------	--N---------	R.IIASLADRPYEEPPQKPPRRFSQLRC
825	843	3	2256.133	0.0026	1	36.94	R.IIASLADRPYEEPPQKPPR.F	Phospho (Y)	138.42	IIASLADRPY#EEPPQKPPR	64.11						---------N---------	---------N---------	R.IIASLADRPYEEPPQKPPRRFSQLRC

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
56	sp|Q9BZQ8|NIBAN_HUMAN	42	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
693	710	2	1990.8796	0.0025	0	42.41	D.EEPAQEEPEPITASGSLK.A	Phospho (ST)	74.61	EEPAQEEPEPITASGS#LK	21.3						----------N--	----------N--	R.VDDPVVNPVATEDTAGLPGTCSSELEFGGTLEDEEPAQEEPEPITASGSLKALR.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
57	sp|Q15233|NONO_HUMAN	41	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
435	456	3	2242.0243	0.0001	0	41.41	R.FGQAATMEGIGAIGGTPPAFNR.A	Phospho (ST)	114.9	FGQAATMEGIGAIGGT#PPAFNR	130.74						----------Y------	----------Y------	R.FGQAATMEGIGAIGGTPPAFNRAAPGAEFAPNK.R

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
58	sp|P20810|ICAL_HUMAN	40	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
234	249	2	1648.6814	0.001	1	40.19	D.ALSSDFTCGSPTAAGK.K	Phospho (ST)	115.27	ALSSDFTCGS#PTAAGK	20.11						---------Y------	---------Y------	K.EGITGPPADSSKPIGPDDAIDALSSDFTCGSPTAAGKK.T

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
59	sp|O75607|NPM3_HUMAN	40	2	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
158	172	2	1807.7956	0.0006	1	32.74	D.SDEEEVELCPILPAK.K	Phospho (ST)	132.61	S#DEEEVELCPILPAK	1000						Y----------	Y----------	R.HQIVTMSNDVSEEESEEEEEDSDEEEVELCPILPAKK.Q
2	17	2	1684.7832	0.0011	0	28.85	M.AAGTAAALAFLSQESR.T	Acetyl (Protein N-term); Phospho (ST)	43.16	AAGTAAALAFLS#QESR	26.66						----------N----	----------N----	-.MAAGTAAALAFLSQESRTR.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
60	sp|Q14678|KANK1_HUMAN	40	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
184	209	3	2600.1736	0.0005	0	40.06	R.LASFGGMGTTSSLPSFVGSGNHNPAK.H	Phospho (ST)	53.8	LAS#FGGMGTTSSLPSFVGSGNHNPAK	44.18						--N----------	--N----------	R.LASFGGMGTTSSLPSFVGSGNHNPAKHQLQNGYQGNGDYGSYAPAAPTTSSMGSSIR.H

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
61	sp|Q8NE71|ABCF1_HUMAN	39	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
223	245	3	2560.9465	0.0015	1	39.24	K.KAEQGSEEEGEGEEEEEEGGESK.A	Phospho (ST)	151.22	KAEQGS#EEEGEGEEEEEEGGESK	156.45						-----Y----------	-----Y----------	K.AEQGSEEEGEGEEEEEEGGESKADDPYAHLSK.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
62	sp|Q9BUA3|CK084_HUMAN	38	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
251	263	2	1454.6466	0.0024	0	38.47	D.SPTETFAAPAEVR.H	Phospho (ST)	110.63	S#PTETFAAPAEVR	22.85						--Y----------	--Y----------	K.NLDPDPEPPSPDSPTETFAAPAEVRHFTDGSFPAGFVLQLFSHTQLR.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
63	sp|Q9UK76|HN1_HUMAN	38	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
112	141	3	3010.5562	0.0033	0	38.3	D.LPGSLGQSEEKPVPAAPVPSPVAPAPVPSR.R	Phospho (ST)	131.7	LPGSLGQSEEKPVPAAPVPS#PVAPAPVPSR	46.41						----------Y----------	----------Y----------	K.GEGDIHENVDTDLPGSLGQSEEKPVPAAPVPSPVAPAPVPSRR.N

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
64	sp|P55081|MFAP1_HUMAN	38	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
106	117	2	1379.6244	0.0023	1	37.84	R.KIVEPEVVGESD.S	Phospho (ST)	73.21	KIVEPEVVGES#D	1000						----------Y-	----------Y-	K.IVEPEVVGESDSEVEGDAWR.M

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
65	sp|P35611|ADDA_HUMAN	36	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
634	647	2	1551.7232	0.0011	1	35.78	D.AATFKPTLPDLSPD.E	Phospho (ST)	117.19	AATFKPTLPDLS#PD	63.94						----------N--	----------N--	K.LEEDLVPEPTTGDDSDAATFKPTLPDLSPDEPSEALGFPMLEK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
66	sp|P27361|MK03_HUMAN	36	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
193	208	3	2031.8143	0.0014	1	35.57	D.PEHDHTGFLTEYVATR.W	Phospho (ST); Phospho (Y)	119.51	PEHDHTGFLT#EY#VATR	35.13	35.76					---------Y-Y----	---------Y-Y----	R.IADPEHDHTGFLTEYVATRWYR.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
67	sp|Q5R372|RBG1L_HUMAN	35	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
107	133	3	2934.3703	0.0055	1	35.43	D.PSNTEISTPRPSSPGGLPEEDSVLFNK.L	Phospho (ST)	129.6	PSNTEISTPRPS#SPGGLPEEDSVLFNK	22.01						----------Y----------	----------N----------	K.RPSSLLVDCQSSSEISDHSFGDIPASQTNKPSLQLILDPSNTEISTPRPSSPGGLPEEDSVLFNKLTYLGCMK.V

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
68	sp|Q92945|FUBP2_HUMAN	35	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
129	142	3	1564.7752	-0.0011	0	35.18	D.SISSQLGPIHPPPR.T	Phospho (ST)	76.16	S#ISSQLGPIHPPPR	22.61						N----------	N----------	K.LASQGDSISSQLGPIHPPPRTSMTEEYR.V

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
69	sp|O00499|BIN1_HUMAN	35	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
312	336	4	2590.2581	0.004	1	25.39	R.VNHEPEPAGGATPGATLPKSPSQLR.K	Phospho (ST)	74.01	VNHEPEPAGGATPGATLPKSPS#QLR	19.55						----------N---	----------Y---	R.VNHEPEPAGGATPGATLPKSPSQLRK.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
70	sp|Q99733|NP1L4_HUMAN	35	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
119	136	3	2167.8253	0.0034	1	34.94	D.AESEWHSENEEEEKLAGD.M	Phospho (ST)	140.58	AESEWHS#ENEEEEKLAGD	24.76						------Y----------	------Y----------	R.EFITGDVEPTDAESEWHSENEEEEKLAGDMK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
71	sp|P06400|RB_HUMAN	34	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
37	46	2	1161.5444	0.0014	1	34.44	D.SGPEDLPLVR.L	Phospho (ST)	83.19	S#GPEDLPLVR	1000						Y---------	Y---------	K.TAATAAAAAAEPPAPPPPPPPEEDPEQDSGPEDLPLVRLEFEETEEPDFTALCQK.L

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
72	sp|O95373|IPO7_HUMAN	34	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
912	921	2	1242.5892	-0.0004	0	34.43	D.GQEYLEILAK.Q	Phospho (Y)	100.79	GQEY#LEILAK	1000						---N------	---Y------	R.AYACHAEHENDSDDDDEAEDDDETEELGSDEDDIDEDGQEYLEILAKQAGEDGDDEDWEEDDAEETALEGYSTIIDDEDNPVDEYQIFK.A

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
73	sp|Q6P2E9|EDC4_HUMAN	34	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
644	658	2	1743.8816	0.0009	0	14.34	D.PSLTRPPEELTLSPK.L	Phospho (ST)	45.05	PSLTRPPEELTLS#PK	21.3						----------N--	----------N--	K.LMTPDAFMTPSASLQQITASPSSSSSGSSSSSSSSSSSLTAVSAMSSTSAVDPSLTRPPEELTLSPKLQLDGSLTMSSSGSLQASPR.G

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
74	sp|Q13085|ACACA_HUMAN	34	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
28	38	2	1326.574	0.0036	1	33.59	D.NSEDEISNLVK.L	Phospho (ST)	62.06	NS#EDEISNLVK	49.62						-Y---------	-Y---------	R.FIIGSVSEDNSEDEISNLVKLDLLEEK.E

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
75	sp|P57729|RAB38_HUMAN	33	1	Not annotated

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
184	201	3	2119.0294	0.0022	1	33.18	D.LMESIEPDVVKPHLTSTK.V	Oxidation (M); Phospho (ST)	67.95	LMES#IEPDVVKPHLTSTK	85.09								K.HILANECDLMESIEPDVVKPHLTSTKVASCSGCAK.S

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
76	sp|O43159|RRP8_HUMAN	33	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
46	63	2	1974.8802	0.0045	0	33.05	R.ALEAASLSQHPPSLCISD.S	Phospho (ST)	148.07	ALEAASLSQHPPSLCIS#D	67.66						----------Y-	----------Y-	R.ALEAASLSQHPPSLCISDSEEEEEER.K

Index	AC	Mascot score	Nb distinct peptides	Is Uniprot phosphoprotein?
77	sp|Q99613|EIF3C_HUMAN	31	1	Phosphoprotein

Start	End	charge	Mr(expt)	Delta (Da)	MC	Ion score	Sequence	Modification	AScore	Ascore validated site(s) (*)	Ascore1	Ascore2	Ascore3	Ascore4	Ascore5	Ascore6	Annotated in Uniprot?	Annotated in Phosphosite.org?	Extended tryptic sequence
242	255	2	1613.6938	0.0005	1	31.1	D.SEEEEGKQTALASR.F	Phospho (ST)	63.82	S#EEEEGKQTALASR	38.54						N----------	N----------	K.MDDEDEDSEDSEDDEDWDTGSTSSDSDSEEEEGKQTALASRFLK.K