

Table 2: Peptidomic analysis of HF3-treated skin by LC-MS/MS:

MATRIX Mas

User :
 Email :
 Search title :
 MS data file :
 Database :
 Timestamp : 18 May 2009 at 18:16:08 GMT
 Protein hits :
[IPI00845802](#) Tax_Id=10090 Gene_Symbol=Hba-a1;Hba-a2 hemoglobin alpha, adult chain 2
[IPI00869381](#) Tax_Id=10090 Gene_Symbol=Apoa2 apolipoprotein A-II
[IPI00885793](#) Tax_Id=10090 Gene_Symbol=Fga fibrinogen, alpha polypeptide isoform 1
[IPI00553333](#) Tax_Id=10090 Gene_Symbol=Hbb-b1 Hemoglobin subunit beta-1
[IPI00316491](#) Tax_Id=10090 Gene_Symbol=Hbb-b2 Hemoglobin subunit beta-2
[IPI00170288](#) Tax_Id=10090 Gene_Symbol=Flg similar to filaggrin
[IPI00831055](#) Tax_Id=10090 Gene_Symbol=Hbb-b1 Beta-globin
[IPI00654081](#) Tax_Id=10090 Gene_Symbol=Fl3a1 Putative uncharacterized protein
[IPI00406870](#) Tax_Id=10090 Gene_Symbol=Flg2 Filaggrin-2
[IPI00124742](#) Tax_Id=10090 Gene_Symbol=Eif4h Isoform Long of Eukaryotic translation initiation factor 4H
[IPI00458924](#) Tax_Id=10090 Gene_Symbol=Calr 57-KD Calcium-binding protein (Fragment)
[IPI00121319](#) Tax_Id=10090 Gene_Symbol=Crip2 Cysteine-rich protein 2

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
 Individual ions scores > 52 indicate identity or extensive homology ($p < 0.05$).
 Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Error: try setting browser cache to automatic.

Peptide Summary Report

Format As [Help](#)

Significance threshold p< Max. number of hits

Standard scoring ☐ MudPIT scoring ☒ Ions score or expect cut-off Show sub-sets

Show pop-ups ☒ Suppress pop-ups ☐ Sort unassigned Require bold red ☐

Select All Select None Search Selected ☐ Error tolerant Archive Report

1. [IPI00845802](#) Mass: 15103 Score: 882 Queries matched: 166 emPAI: 67515.04
 Tax_Id=10090 Gene_Symbol=Hba-a1;Hba-a2 hemoglobin alpha, adult chain 2
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta Miss	Score	Expect	Rank	Peptide
6	623.2996	622.2923	622.2962	-0.0039	0	4	4.6e+003	F.ASFPTT.K
27	381.1796	760.3447	760.3544	-0.0098	0	20	1.2e+002	Y.FPHFDV.S
28	381.1805	760.3465	760.3544	-0.0080	0	(20)	1.3e+002	Y.FPHFDV.S
☒ 35	423.7214	845.4282	845.4396	-0.0114	0	33	7.5	L.RVDPVNF.K
37	424.7019	847.3893	847.3865	0.0029	0	23	58	Y.FPHFDV.S
☒ 38	426.7242	851.4338	851.4389	-0.0051	0	53	0.049	F.ASFPTTKT.Y
☒ 39	426.7243	851.4341	851.4389	-0.0048	0	(38)	1.9	F.ASFPTTKT.Y
☒ 41	432.7427	863.4709	863.4752	-0.0043	0	33	5.1	H.ASLDKFLA.S
☒ 43	438.7146	875.4147	875.4171	-0.0024	0	49	0.17	Y.GAEALERM.F
44	438.7156	875.4167	875.4171	-0.0004	0	(35)	4.2	Y.GAEALERM.F
☒ 47	446.7586	891.5027	891.5066	-0.0038	0	27	19	S.LDKFLASV.S
51	460.7488	919.4831	919.4875	-0.0044	0	12	7.2e+002	L.SDLHAHL.R
☒ 52	461.2569	920.4992	920.5179	-0.0186	0	45	0.33	A.SVSTVLTSG.Y
☒ 52	475.7379	949.4612	949.4617	-0.0005	0	41	0.9	L.SALSDLHAH.K
63	476.2578	950.5010	950.5073	-0.0063	0	22	74	H.ASLDKFLAS.V
64	477.2460	952.4774	952.4879	-0.0105	0	16	2.4e+002	A.AWGKIGGHGA.E
☒ 65	477.7314	953.4482	953.4607	-0.0125	0	57	0.02	H.PADFTPAVH.A
☒ 68	483.7386	965.4626	965.4640	-0.0014	0	24	44	A.EALERMFA.S
☒ 72	490.2738	978.5331	978.5386	-0.0055	0	(38)	1.6	A.SLDKFLASV.S
☒ 73	490.2739	978.5332	978.5386	-0.0053	0	51	0.087	A.SLDKFLASV.S
☒ 78	494.7448	987.4751	987.4774	-0.0023	0	20	1.2e+002	W.GKIGGHGA.EY.G
☒ 79	499.2749	996.5353	996.5492	-0.0138	0	54	0.04	S.VSTVLTISKY.R
☒ 83	508.2554	1014.4962	1014.5022	-0.0060	0	48	0.19	F.ASFPTTKTY.F
☒ 85	512.2473	1022.4801	1022.4855	-0.0054	0	62	0.007	Y.GAEALERMFA.S
87	513.2411	1024.4677	1024.4655	0.0023	0	18	1.7e+002	K.TYFPHFDV.S
☒ 88	513.2541	1024.4937	1024.4978	-0.0041	0	64	0.0041	H.PADFTPAVHA.S
☒ 89	513.2563	1024.4981	1024.4978	0.0003	0	(40)	1.2	H.PADFTPAVHA.S
☒ 94	519.2542	1036.4939	1036.5011	-0.0072	0	29	13	G.AEALERMFA.S
☒ 99	524.7623	1047.5100	1047.5196	-0.0096	0	29	16	L.SGEDKSNKA.A
☒ 100	525.7919	1049.5692	1049.5757	-0.0065	0	57	0.023	H.ASLDKFLASV.S
☒ 107	534.2634	1066.5123	1066.5043	0.0080	0	45	0.37	A.DALANAAGHLD.D

✓	109	542.7935	1083.5724	1083.5812	-0.0087	0	62	0.007	1	A.SVSTVLTSKY.R
	111	544.3129	1086.6112	1086.6186	-0.0074	0	28	17	2	L.RVDPVNFKL.L
✓	113	546.2689	1090.5232	1090.5196	0.0036	0	20	1.3e+002	1	H.HPADFTPAVH.A
	114	546.2699	1090.5253	1090.5196	0.0057	0	(16)	3.2e+002	2	H.HPADFTPAVH.A
✓	117	547.7629	1093.5112	1093.5226	-0.0114	0	(29)	15	1	Y.GAEALERMFA.S
	118	547.7685	1093.5224	1093.5226	-0.0002	0	48	0.18	1	Y.GAEALERMFA.S
✓	127	556.7518	1111.4890	1111.4975	-0.0085	0	24	37	1	K.TYFFPHFDVS.H
✓	130	560.2797	1118.5448	1118.5567	-0.0119	0	35	3.8	1	L.SGEDKSNIAA.W
✓	136	566.2600	1130.5055	1130.4992	0.0063	0	66	0.0028	1	I.GGHGAETGAEL.E
✓	141	569.7802	1137.5457	1137.5414	0.0043	0	67	0.0023	1	V.ADALANAAGHLD.D
	144	380.2260	1137.6563	1137.6618	-0.0055	0	13	3.4e+002	2	G.SAQVKGHGKKV.A
✓	157	581.3026	1160.5907	1160.6037	-0.0130	0	27	26	1	V.LSGEDKSNIAA.A
✓	158	581.3039	1160.5933	1160.6037	-0.0104	0	(20)	1.2e+002	1	V.LSGEDKSNIAA.A
✓	160	581.7825	1161.5503	1161.5567	-0.0064	0	38	1.8	1	H.HPADFTPAVHA.S
✓	161	581.7942	1161.5739	1161.5706	0.0033	0	25	40	1	F.ASFPTTKTYF.P
✓	164	583.2966	1164.5786	1164.5775	0.0011	0	29	14	1	A.GHLDLPGALSA.L
✓	167	584.3092	1166.6038	1166.6183	-0.0145	0	71	0.0008	1	A.SLDKFLASVST.V
✓	169	585.3053	1168.5961	1168.6241	-0.0280	0	30	11	1	V.DPVNFKLLSH.C
	173	589.7817	1177.5488	1177.5516	-0.0029	0	14	4.7e+002	2	A.SHHPADFTPAV.H
✓	178	591.2875	1180.5605	1180.5546	0.0058	0	48	0.18	1	Y.GAEALERMFA.S
	183	397.8834	1190.6282	1190.6407	-0.0125	0	37	2.5	1	L.SALSDLHAHL.R
✓	188	600.7895	1199.5645	1199.5645	0.0001	0	42	0.61	1	A.EALERMFAF.P
	189	600.8514	1199.6883	1199.7026	-0.0144	0	29	9.7	9	L.RVDPVNFKLL.S
✓	195	410.1977	1227.5714	1227.5785	-0.0072	0	26	28	1	S.SHHPADFTPAVH.A
	197	411.5507	1231.6303	1231.6408	-0.0105	0	14	5.1e+002	8	V.LSGEDKSNIAA.W
✓	198	618.8131	1235.6117	1235.6146	-0.0029	0	54	0.046	1	A.AGHLDLPGALSA.L
✓	200	619.8331	1237.6516	1237.6554	-0.0038	0	32	5.8	1	H.ASLDKFLASVST.V
	201	620.8062	1239.5979	1239.5924	0.0055	0	18	1.7e+002	2	T.KTYFFPHFDVS.H
✓	203	622.8024	1243.5902	1243.5833	0.0069	0	43	0.61	1	K.IGGHGAETGAEL.E
✓	205	623.2961	1244.5776	1244.5786	-0.0009	0	39	1.3	1	W.KIGGGHGAETGAEL.E
✓	207	625.3046	1248.5947	1248.5887	0.0060	0	15	3.5e+002	1	L.ASHHPADFTPAV.H
✓	211	627.2998	1252.5851	1252.5684	0.0168	0	41	0.84	1	V.ADALANAAGHLD.L
	215	630.3180	1258.6215	1258.6234	-0.0019	0	12	7.4e+002	8	F.ASFPTTKTYF.P
✓	220	420.8867	1259.6382	1259.6721	-0.0339	0	(34)	4.6	1	M.VLSGEDKSNIAA.A
✓	221	630.8306	1259.6467	1259.6721	-0.0254	0	56	0.03	1	M.VLSGEDKSNIAA.A
✓	222	420.8916	1259.6531	1259.6721	-0.0190	0	(28)	18	1	M.VLSGEDKSNIAA.A
✓	229	633.8442	1265.6738	1265.6867	-0.0129	0	58	0.017	1	A.SLDKFLASVSTV.L
✓	230	634.8516	1267.6886	1267.7024	-0.0138	0	72	0.00063	1	F.LASVSTVLTSKY.R
	240	639.8334	1277.6522	1277.6616	-0.0093	0	23	53	2	A.GHLDLPGALSA.L
✓	251	434.2370	1299.6893	1299.7048	-0.0155	0	22	77	1	S.DLHAHLKLRVDP.V
	253	653.3247	1304.6349	1304.6360	-0.0012	0	6	3.1e+003	5	L.SGEDKSNIAA.W
✓	266	439.2036	1314.5891	1314.6106	-0.0215	0	42	0.56	1	A.SHHPADFTPAVH.A
✓	267	439.2053	1314.5941	1314.6106	-0.0164	0	(40)	0.84	1	A.SHHPADFTPAVH.A
✓	268	439.2072	1314.5999	1314.6106	-0.0106	0	(39)	1.2	1	A.SHHPADFTPAVH.A
✓	269	658.3104	1314.6063	1314.6106	-0.0042	0	(29)	12	1	A.SHHPADFTPAVH.A
✓	275	664.8165	1327.6184	1327.6230	-0.0046	0	69	0.0011	1	Y.GAEALERMFAF.P
✓	279	444.5688	1330.6845	1330.7092	-0.0247	0	24	44	1	M.VLSGEDKSNIAA.W
✓	280	444.5696	1330.6870	1330.7092	-0.0222	0	(15)	3.7e+002	1	M.VLSGEDKSNIAA.W
✓	281	333.9354	1331.7127	1331.7422	-0.0296	0	46	0.28	1	S.HGSAQVKGHGKKV.A
✓	282	333.9357	1331.7137	1331.7422	-0.0286	0	(14)	4.3e+002	1	S.HGSAQVKGHGKKV.A
✓	283	333.9360	1331.7149	1331.7422	-0.0274	0	(20)	1e+002	1	S.HGSAQVKGHGKKV.A
✓	284	333.9362	1331.7155	1331.7422	-0.0267	0	(15)	3.5e+002	1	S.HGSAQVKGHGKKV.A
✓	285	333.9366	1331.7175	1331.7422	-0.0248	0	(23)	61	1	S.HGSAQVKGHGKKV.A
✓	286	333.9370	1331.7188	1331.7422	-0.0234	0	(22)	76	1	S.HGSAQVKGHGKKV.A
✓	287	333.9371	1331.7193	1331.7422	-0.0230	0	(14)	3.9e+002	1	S.HGSAQVKGHGKKV.A
✓	288	333.9373	1331.7203	1331.7422	-0.0219	0	(14)	4.5e+002	1	S.HGSAQVKGHGKKV.A
✓	293	669.3663	1336.7180	1336.7238	-0.0058	0	33	4.4	1	H.ASLDKFLASVSTV.L
✓	296	675.3524	1348.6903	1348.6987	-0.0084	0	31	9.1	1	A.AGHLDLPGALSA.L
✓	308	690.3802	1378.7459	1378.7708	-0.0249	0	(24)	35	1	A.SLDKFLASVSTVL.T
✓	309	690.3876	1378.7606	1378.7708	-0.0101	0	43	0.48	1	A.SLDKFLASVSTVL.T
✓	310	690.3908	1378.7671	1378.7708	-0.0037	0	(29)	9.2	1	A.SLDKFLASVSTVL.T
✓	314	462.8833	1385.6282	1385.6477	-0.0195	0	41	0.74	1	A.SHHPADFTPAVHA.S
✓	315	462.8836	1385.6291	1385.6477	-0.0186	0	(57)	0.019	1	L.ASHHPADFTPAVH.A
✓	316	462.8847	1385.6322	1385.6477	-0.0154	0	59	0.012	1	L.ASHHPADFTPAVH.A
✓	317	693.8234	1385.6322	1385.6285	0.0037	0	61	0.0081	1	A.EYGAEALERMFA.S
✓	318	462.8849	1385.6330	1385.6477	-0.0147	0	(30)	9.5	1	A.SHHPADFTPAVHA.S
✓	319	693.8251	1385.6356	1385.6477	-0.0121	0	(38)	1.7	1	A.SHHPADFTPAVHA.S
✓	320	693.8283	1385.6419	1385.6477	-0.0057	0	(24)	44	1	L.ASHHPADFTPAVH.A
	331	355.6945	1418.7488	1418.7742	-0.0255	0	(6)	2.7e+003	2	V.SHGSAQVKGHGKKV.A
✓	334	355.6955	1418.7528	1418.7742	-0.0214	0	7	2.4e+003	1	V.SHGSAQVKGHGKKV.A
	338	710.8695	1419.7245	1419.7358	-0.0113	0	24	50	4	N.AAGHLDLPGALSA.L
✓	342	475.5933	1423.7582	1423.7936	-0.0354	0	53	0.05	1	L.RVDPVNFKLLSH.C
✓	343	475.5975	1423.7707	1423.7936	-0.0229	0	(40)	0.97	1	L.RVDPVNFKLLSH.C
✓	344	712.8950	1423.7754	1423.7936	-0.0181	0	(21)	69	1	L.RVDPVNFKLLSH.C
✓	347	716.3327	1430.6509	1430.6579	-0.0070	0	31	7.2	1	A.WKIGGGHGAETGAEL.E
✓	356	725.9085	1449.8024	1449.8079	-0.0055	0	40	0.82	1	H.ASLDKFLASVSTVL.T
✓	358	484.9039	1451.6899	1451.7085	-0.0186	0	32	6.3	1	F.PTKTYFFPHFDV.S
✓	360	486.5627	1456.6664	1456.6848	-0.0183	0	(30)	9.9	1	L.ASHHPADFTPAVHA.S
✓	361	486.5635	1456.6686	1456.6848	-0.0162	0	62	0.0059	1	L.ASHHPADFTPAVHA.S
✓	362	729.3433	1456.6720	1456.6848	-0.0128	0	(31)	7.4	1	L.ASHHPADFTPAVHA.S
✓	375	740.9113	1479.8081	1479.8185	-0.0104	0	74	0.00037	1	A.SLDKFLASVSTVL.T
✓	377	497.5862	1489.7369	1489.7525	-0.0156	0	16	2.7e+002	1	L.SGEDKSNIAA.W
	381	750.3642	1498.7138	1498.7126	0.0012	0	17	2.1e+002	9	A.EALERMFAFPTT.K

✓	384	751.8510	1501.6873	1501.6950	-0.0076	0	42	0.56	1	A.AWGKIGGHGAEGYGA.E.A
✓	386	501.5728	1501.6966	1501.6950	0.0017	0	(24)	39	3	A.AWGKIGGHGAEGYGA.E.A
✓	390	506.5970	1516.7693	1516.7885	-0.0193	0	(23)	64	2	M.VLSGEDKSNIAKAAW.G
✓	391	759.3954	1516.7763	1516.7885	-0.0122	0	26	32	1	M.VLSGEDKSNIAKAAW.G
✓	394	380.4534	1517.7845	1517.8063	-0.0218	0	(11)	8.6e+002	1	S.HGSAQVKGHGKKVAD.A
✓	395	380.4534	1517.7846	1517.8063	-0.0217	0	(20)	1.2e+002	1	S.HGSAQVKGHGKKVAD.A
✓	396	380.4539	1517.7867	1517.8063	-0.0196	0	(8)	1.9e+003	1	S.HGSAQVKGHGKKVAD.A
✓	397	380.4543	1517.7882	1517.8063	-0.0181	0	23	56	1	S.HGSAQVKGHGKKVAD.A
✓	398	380.4544	1517.7887	1517.8063	-0.0176	0	(8)	1.7e+003	1	S.HGSAQVKGHGKKVAD.A
✓	409	513.9136	1538.7190	1538.7406	-0.0216	0	(16)	2.3e+002	4	F.PTTKTYFFPHFDVS.H
✓	410	770.3720	1538.7294	1538.7406	-0.0111	0	38	1.5	1	F.PTTKTYFFPHFDVS.H
✓	426	784.4233	1566.8320	1566.8505	-0.0184	0	93	4.8e-006	1	A.SLDKFLASVSTVLT.S.K
✓	427	784.4255	1566.8365	1566.8505	-0.0140	0	(47)	0.19	1	A.SLDKFLASVSTVLT.S.K
✓	428	524.2595	1569.7568	1569.7688	-0.0121	0	40	1.1	1	T.LASHHPADFTPAVHA.S
✓	430	525.6051	1573.7935	1573.8100	-0.0165	0	34	5.1	1	M.VLSGEDKSNIAKAAW.K
✓	444	402.2115	1604.8168	1604.8383	-0.0215	0	1	8.5e+003	5	V.SHGSAQVKGHGKKVAD.A
✓	450	539.2601	1614.7584	1614.7790	-0.0207	0	28	16	1	A.WGKIGGHGAEGYGA.E.A
✓	457	810.8715	1619.7284	1619.7290	-0.0006	0	37	1.8	1	A.EYGAEALRMFASF.P
✓	463	819.9461	1637.8777	1637.8876	-0.0099	0	57	0.018	1	H.ASLDKFLASVSTVLT.S.K
✓	469	553.5934	1657.7583	1657.7777	-0.0194	0	35	2.5	1	F.ASPFTTKTYFFPHFDV.S
✓	473	557.9397	1670.7974	1670.8165	-0.0192	0	52	0.059	1	V.TLASHHPADFTPAVHA.S
✓	486	562.9399	1685.7979	1685.8161	-0.0183	0	33	4.7	1	A.AWGKIGGHGAEGYGA.E.A
✓	491	564.5936	1690.7589	1690.7740	-0.0152	0	16	2.1e+002	2	K.TYFFPHFDVSHGSAQV.K
✓	498	565.9817	1694.9234	1694.9454	-0.0221	0	(90)	7.9e-006	1	A.SLDKFLASVSTVLT.S.K
✓	499	848.4721	1694.9296	1694.9454	-0.0158	0	95	2.5e-006	1	A.SLDKFLASVSTVLT.S.K
✓	500	426.4746	1701.8693	1701.9050	-0.0357	0	(22)	67	1	M.VLSGEDKSNIAKAAW.G
✓	501	568.3000	1701.8782	1701.9050	-0.0268	0	56	0.028	1	M.VLSGEDKSNIAKAAW.G
✓	511	576.9624	1727.8654	1727.8552	0.0101	0	36	3	1	A.EALRMFASFPTTKT.Y
✓	510	583.3062	1746.8969	1746.9165	-0.0197	0	15	3.4e+002	9	L.SDLHAHLRVDVNF.K
✓	516	586.6187	1756.8342	1756.8461	-0.0119	0	32	6.5	1	F.ASPFTTKTYFFPHFDV.S
✓	517	879.4285	1756.8425	1756.8461	-0.0036	0	(17)	2.2e+002	1	F.ASPFTTKTYFFPHFDV.S
✓	524	589.6638	1765.9696	1765.9826	-0.0129	0	48	0.12	1	H.ASLDKFLASVSTVLT.S.K
✓	561	615.6272	1843.8598	1843.8781	-0.0183	0	21	83	1	F.ASPFTTKTYFFPHFDVS.H
✓	562	922.9406	1843.8667	1843.8781	-0.0115	0	(17)	1.8e+002	1	F.ASPFTTKTYFFPHFDVS.H
✓	568	620.3366	1857.9879	1858.0088	-0.0208	0	(63)	0.0046	1	A.SLDKFLASVSTVLT.S.K
✓	569	620.3380	1857.9921	1858.0088	-0.0167	0	(27)	18	1	A.SLDKFLASVSTVLT.S.K
✓	570	930.0040	1857.9933	1858.0088	-0.0154	0	76	0.00025	1	A.SLDKFLASVSTVLT.S.K
✓	571	931.9622	1861.9098	1861.9170	-0.0072	0	28	16	1	V.ADALANAAGHLDLPGALSA.L
✓	577	626.9589	1877.8549	1877.8730	-0.0181	0	46	0.2	1	K.IGGHGAEGYGAELRMFASF.P
✓	594	644.0164	1929.0275	1929.0459	-0.0184	0	48	0.15	1	H.ASLDKFLASVSTVLT.S.K
✓	596	646.9905	1937.9495	1937.9595	-0.0100	0	33	5.1	1	A.GHLDLPGALSA.SDLHAH.K
✓	657	705.0005	2111.9796	2111.9735	0.0062	0	49	0.11	1	K.IGGHGAEGYGAELRMFASF.P
✓	662	530.5040	2117.9869	2118.0171	-0.0302	0	5	2.8e+003	3	F.PTTKTYFFPHFDVSHGSAQV.K
✓	711	774.3725	2320.0957	2320.1058	-0.0102	0	12	6.3e+002	3	A.AWGKIGGHGAEGYGAELRMFASF.P
✓	730	605.3021	2417.1792	2417.2128	-0.0336	0	18	1.6e+002	1	L.ASHHPADFTPAVHASLDKFLASV.S
✓	748	622.5623	2486.2201	2486.2554	-0.0352	0	11	8.5e+002	1	M.VLSGEDKSNIAKAAWKGIGGHGAEGY.G
✓	766	652.3241	2605.2672	2605.2925	-0.0253	0	22	56	1	L.ASHHPADFTPAVHASLDKFLASVST.V
✓	870	734.6217	2934.4575	2934.4876	-0.0301	0	6	2.4e+003	1	A.SHHHPADFTPAVHASLDKFLASVSTVLT.S.K
✓	896	765.1253	3056.4721	3056.5203	-0.0482	0	9	1.1e+003	1	M.VLSGEDKSNIAKAAWKGIGGHGAEGYGA.E.A
✓	897	1019.8382	3056.4928	3056.5203	-0.0275	0	(2)	5.6e+003	4	M.VLSGEDKSNIAKAAWKGIGGHGAEGYGA.E.A
✓	988	836.9128	3343.6223	3343.6619	-0.0396	0	17	1.8e+002	1	M.VLSGEDKSNIAKAAWKGIGGHGAEGYGAELRM.F
✓	1049	891.4395	3561.7287	3561.7674	-0.0387	0	16	2.2e+002	1	M.VLSGEDKSNIAKAAWKGIGGHGAEGYGAELRMFASF.P

2. [IP100869381](#) Mass: 11302 Score: 353 Queries matched: 28 emPAI: 67.95

Tax Id: 10090 Gene_Symbol: Apoa2 apolipoprotein A-II

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
✓ 95	520.2707	1038.5269	1038.5345	-0.0077	0	33	4.9	1	M.NLLEKPPAA.A.K
✓ 122	551.3023	1100.5900	1100.6190	-0.0289	0	23	54	1	L.TPLVRSAGTSL.V
✓ 170	585.7922	1169.5698	1169.5750	-0.0052	0	(44)	0.44	1	L.MNLEKPPAA.A.K
✓ 171	585.7953	1169.5759	1169.5750	0.0009	0	(35)	3.3	1	L.MNLEKPPAA.A.K
✓ 180	593.7891	1185.5637	1185.5699	-0.0062	0	44	0.4	1	L.MNLEKPPAA.A.K + Oxidation (M)
✓ 243	642.3331	1282.6516	1282.6591	-0.0075	0	63	0.0054	1	S.LMNLEKPPAA.A.K
✓ 303	685.8518	1369.6890	1369.6911	-0.0021	0	56	0.027	1	S.SLMNLEKPPAA.A.K
✓ 364	729.3606	1456.7067	1456.7231	-0.0164	0	78	0.00018	1	F.SSLMNLEKPPAA.A.K
✓ 365	731.3978	1460.7810	1460.7987	-0.0178	0	22	60	1	L.TPLVRSAGTSLVNF.F
✓ 421	782.8412	1563.6679	1563.6585	0.0094	0	15	1.8e+002	2	Y.FQSMTDYGDLMKE.A.K
✓ 443	802.8929	1603.7713	1603.7915	-0.0202	0	77	0.00023	1	F.FSSLMNLEKPPAA.A.K
✓ 452	539.5760	1615.7062	1615.7222	-0.0159	0	50	0.074	1	F.QSMTDYGDLMKEA.K
✓ 453	808.8686	1615.7226	1615.7222	0.0005	0	(24)	31	1	F.QSMTDYGDLMKEA.K
✓ 518	588.5993	1762.7760	1762.7906	-0.0146	0	(40)	0.62	1	Y.FQSMTDYGDLMKEA.K
✓ 520	882.4070	1762.7994	1762.7906	0.0089	0	49	0.11	1	Y.FQSMTDYGDLMKEA.K
✓ 572	933.4497	1864.8848	1864.9029	-0.0181	0	113	5.5e-008	1	V.NFFSSLMNLEKPPAA.A.K
✓ 573	933.4569	1864.8992	1864.9029	-0.0037	0	(26)	25	1	V.NFFSSLMNLEKPPAA.A.K
✓ 578	941.4579	1880.9013	1880.8978	0.0035	0	(30)	11	1	V.NFFSSLMNLEKPPAA.A.K + Oxidation (M)
✓ 659	530.2802	2117.0917	2117.1269	-0.0352	0	14	4.7e+002	9	A.KAYFEKTHEQLTPLVRS.A.G
✓ 671	1083.0549	2164.0952	2164.0874	0.0078	0	47	0.22	1	T.SLVNFFSSLMNLEKPPAA.A.K
✓ 677	546.0468	2180.1581	2180.0823	0.0757	0	(14)	3.6e+002	6	T.SLVNFFSSLMNLEKPPAA.A.K + Oxidation (M)
✓ 707	768.3473	2302.0202	2302.0286	-0.0084	0	37	1.1	1	L.FTQYFQSMTDYGDLMKEA.K
✓ 712	775.0578	2322.1517	2322.1566	-0.0049	0	(29)	12	1	A.GTSLVNFFSSLMNLEKPPAA.A.K
✓ 713	1162.0848	2322.1550	2322.1566	-0.0015	0	80	0.0001	1	A.GTSLVNFFSSLMNLEKPPAA.A.K

☒	745	1241.1173	2480.2200	2480.2257	-0.0056	0	67	0.002	1	R.SAGTSLVNFSSLMNLEKPAPAA.K
☒	746	827.7491	2480.2255	2480.2257	-0.0002	0	(30)		11	R.SAGTSLVNFSSLMNLEKPAPAA.K
☒	749	833.0752	2496.2039	2496.2206	-0.0168	0	(49)	0.12	1	R.SAGTSLVNFSSLMNLEKPAPAA.K + Oxidation (M)
☒	901	773.3997	3089.5698	3089.6145	-0.0447	0	29		14	A.KTSEIQSQAKAYFEKTHEQLTPLVRS.A

3. [IPI00885793](#) Mass: 87375 Score: 317 Queries matched: 16 emPAI: 0.34

Tax_Id=10090 Gene_Symbol=Fga Fibrinogen, alpha polypeptide isoform 1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☒ 340	712.8331	1423.6516	1423.6467	0.0049	0	80	9.8e-005	1	D.TEDKGEFLSEGGGV.R
☒ 374	493.9038	1478.6894	1478.7001	-0.0107	0	35	3.1	1	T.EDKGEFLSEGGGV.R
☒ 408	770.3525	1538.6905	1538.6737	0.0169	0	47	0.15	1	T.DTEDKGEFLSEGGGV.R
☒ 424	783.8339	1565.6533	1565.7369	-0.0836	0	14	2.1e+002	2	I.QQRMDGSLNPNRT.W
☒ 435	527.5853	1579.7342	1579.7478	-0.0136	0	43	0.52	1	D.TEDKGEFLSEGGGV.R
☒ 436	790.8759	1579.7373	1579.7478	-0.0105	0	(42)	0.58	1	D.TEDKGEFLSEGGGV.R
☒ 464	820.8588	1639.7031	1639.7213	-0.0182	0	(58)	0.0094	1	T.TDTEKGEFLSEGGGV.R
☒ 465	820.8661	1639.7176	1639.7213	-0.0038	0	65	0.002	1	T.TDTEKGEFLSEGGGV.R
☒ 495	565.9280	1694.7622	1694.7748	-0.0126	0	(39)	0.97	1	T.DTEDKGEFLSEGGGV.R
☒ 496	848.3888	1694.7630	1694.7748	-0.0117	0	78	0.00011	1	T.DTEDKGEFLSEGGGV.R
☒ 497	565.9287	1694.7642	1694.7748	-0.0106	0	(40)	0.86	1	T.DTEDKGEFLSEGGGV.R
☒ 498	898.9007	1795.7868	1795.8224	-0.0356	0	(57)	0.014	1	T.TDTEKGEFLSEGGGV.R
☒ 543	599.6040	1795.7902	1795.8224	-0.0322	0	(60)	0.007	1	T.TDTEKGEFLSEGGGV.R
☒ 544	599.6083	1795.8032	1795.8224	-0.0192	0	(71)	0.00064	1	T.TDTEKGEFLSEGGGV.R
☒ 545	898.9106	1795.8067	1795.8224	-0.0157	0	87	1.5e-005	1	T.TDTEKGEFLSEGGGV.R
☒ 546	898.9127	1795.8109	1795.8224	-0.0115	0	(54)	0.031	1	T.TDTEKGEFLSEGGGV.R

4. [IPI00553333](#) Mass: 15830 Score: 298 Queries matched: 39 emPAI: 31.16

Tax_Id=10090 Gene_Symbol=Hbb-b1 Hemoglobin subunit beta-1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☒ 74	492.2417	982.4688	982.4720	-0.0031	0	50	0.11	1	N.DGLNHLDSL.K
☒ 75	492.2574	982.5003	982.5083	-0.0081	0	31	8.7	1	M.VHLTDAEKA.A
☒ 76	492.7905	983.5665	983.5764	-0.0099	0	46	0.21	1	V.GGEALGRLLV.V
☒ 80	503.2550	1004.4955	1004.4927	0.0028	0	(27)		28	L.GKDFTPAQA.A
☒ 81	503.2560	1004.4975	1004.4927	0.0048	0	28		19	L.GKDFTPAQA.A
☒ 112	545.8097	1089.6049	1089.6183	-0.0134	0	73	0.00053	1	A.AFQKVVAGVAT.A
☒ 119	549.2707	1096.5269	1096.5149	0.0120	0	24		38	F.NDGLNHLDSL.K
☒ 129	557.3088	1112.6031	1112.6190	-0.0159	0	25		32	D.EVGGEALGRLLV.V
☒ 152	577.3036	1152.5926	1152.6139	-0.0213	0	28		18	M.VHLTDAEKA.V.S
☒ 159	581.3239	1160.6333	1160.6554	-0.0221	0	38		1.8	Q.AAFQKVVAGVAT.A
☒ 191	606.8505	1211.6865	1211.6874	-0.0009	0	50	0.081	1	D.EVGGEALGRLLV.V
☒ 199	413.5540	1237.6403	1237.6567	-0.0165	0	48	0.19	1	V.AGVATALAKTH.-
☒ 236	638.3022	1274.5899	1274.5720	0.0179	0	14	4.8e+002	6	V.YPWTQRYFD.S
☒ 271	658.3428	1314.6711	1314.6779	-0.0069	0	26		32	N.SDEVGGEALGRLLV.V
☒ 276	665.3219	1328.6292	1328.6361	-0.0069	0	60	0.01	1	V.ITAFNDGLNHL.D.S
☒ 306	687.8241	1373.6336	1373.6404	-0.0068	0	22		57	V.VYPWTQRYFD.S
☒ 307	460.2291	1377.6655	1377.6790	-0.0135	0	25		35	L.GHHLGKDFTPAAQ.A
☒ 328	707.8728	1413.7311	1413.7464	-0.0152	0	26		26	N.SDEVGGEALGRLLV.V
☒ 329	708.8424	1415.6703	1415.6681	0.0022	0	54	0.041	1	I.TAFNDGLNHLDSL.K
☒ 355	725.3596	1448.7046	1448.7161	-0.0115	0	28		17	L.GHHLGKDFTPAAQ.A
☒ 372	737.3656	1472.7166	1472.7089	0.0077	0	16	3.1e+002	3	L.VVYPWTQRYFD.S
☒ 402	764.8909	1527.7673	1527.7893	-0.0220	0	25		40	V.NSDEVGGEALGRLLV.V
☒ 403	765.3827	1528.7509	1528.7522	-0.0012	0	37		2.4	V.ITAFNDGLNHLDSL.K
☒ 413	516.9306	1547.7700	1547.7977	-0.0277	0	55	0.034	1	F.GDLSSASAIMGNKAKV.A
☒ 441	801.3931	1600.7716	1600.7845	-0.0129	0	41	0.84	1	F.NDGLNHLDSLKGTF.A.S
☒ 442	534.5982	1600.7727	1600.7845	-0.0118	0	(31)		8.1	F.NDGLNHLDSLKGTF.A.S
☒ 446	804.8816	1607.7487	1607.7409	0.0078	0	32		6.3	V.VYPWTQRYFDSF.G
☒ 482	559.9617	1676.8634	1676.8886	-0.0252	0	50		0.1	L.GKDFTPAQAQAFQKVV.A
☒ 511	583.6177	1747.8313	1747.8530	-0.0217	0	27		23	A.FNDGLNHLDSLKGTF.A.S
☒ 512	583.6432	1747.9079	1747.9257	-0.0178	0	52	0.075	1	L.GKDFTPAQAQAFQKVV.A
☒ 514	586.3031	1755.8874	1755.8937	-0.0063	0	51	0.081	1	F.GDLSSASAIMGNKAKV.A
☒ 592	640.9824	1919.9255	1919.9377	-0.0123	0	52	0.065	1	I.TAFNDGLNHLDSLKGTF.A.S
☒ 629	678.6781	2033.0126	2033.0218	-0.0092	0	43	0.54	1	V.ITAFNDGLNHLDSLKGTF.A.S
☒ 639	693.0337	2076.0792	2076.1004	-0.0212	0	(26)		27	L.GKDFTPAQAQAFQKVVAGVAT.A
☒ 640	1039.0529	2076.0912	2076.1004	-0.0092	0	45	0.35	1	L.GKDFTPAQAQAFQKVVAGVAT.A
☒ 667	716.7148	2147.1226	2147.1375	-0.0149	0	24		40	L.GKDFTPAQAQAFQKVVAGVAT.A
☒ 688	754.3945	2260.1618	2260.1852	-0.0234	0	9	1.3e+003	10	K.KVITAFNDGLNHLDSLKGTF.A.S
☒ 689	754.4088	2260.2046	2260.2216	-0.0170	0	58	0.016	1	L.GKDFTPAQAQAFQKVVAGVAT.A
☒ 752	841.1087	2520.3041	2520.3238	-0.0196	0	78	0.00017	1	L.GHHLGKDFTPAAQAQAFQKVVAGVAT.A

5. [IPI00316491](#) Mass: 15868 Score: 230 Queries matched: 28 emPAI: 9.11

Tax_Id=10090 Gene_Symbol=Hbb-b2 Hemoglobin subunit beta-2

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☒ 76	492.7905	983.5665	983.5764	-0.0099	0	46	0.21	1	V.GGEALGRLLV.V
☒ 80	503.2550	1004.4955	1004.4927	0.0028	0	(27)		28	L.GKDFTPAQA.A
☒ 81	503.2560	1004.4975	1004.4927	0.0048	0	28		19	L.GKDFTPAQA.A
☒ 112	545.8097	1089.6049	1089.6183	-0.0134	0	73	0.00053	1	A.AFQKVVAGVAT.A

129	557.3088	1112.6031	1112.6190	-0.0159	0	25	32	1	D.EVGGEALGRLL.V
159	581.3239	1160.6333	1160.6554	-0.0221	0	38	1.8	1	Q.AAFQKVVAGVAT.A
191	606.8505	1211.6865	1211.6874	-0.0009	0	50	0.081	1	D.EVGGEALGRLL.V
194	614.3078	1226.6010	1226.6143	-0.0133	0	44	0.47	1	A.KVNPDEVGGEAL.G
199	413.5540	1237.6403	1237.6567	-0.0165	0	48	0.19	1	V.AGVATALAHKYH.-
236	638.3022	1274.5899	1274.5720	0.0179	0	14	4.8e+002	6	V.YFWTQRYFD.S
291	667.8353	1333.6561	1333.6878	-0.0316	0	34	4.9	1	V.ITAFNEGLKNLD.N
306	687.8241	1373.6336	1373.6404	-0.0068	0	22	57	1	V.VYFWTQRYFD.S
307	460.2291	1377.6655	1377.6790	-0.0135	0	25	35	1	L.GHHLGKDFTPAAQ.A
353	720.3740	1438.7334	1438.7416	-0.0081	0	11	8.5e+002	7	V.NPDEVGGEALGRLL.V
355	725.3596	1448.7046	1448.7161	-0.0115	0	28	17	1	L.GHHLGKDFTPAAQ.A
372	737.3656	1472.7166	1472.7089	0.0077	0	16	3.1e+002	3	L.VYFWTQRYFD.S
446	804.8816	1607.7487	1607.7409	0.0078	0	32	6.3	1	V.VYFWTQRYFDSF.G
482	559.9617	1676.8634	1676.8886	-0.0252	0	50	0.1	1	L.GKDFTPAAQAAPQKVV.A
512	583.6432	1747.9079	1747.9257	-0.0178	0	52	0.075	1	L.GKDFTPAAQAAPQKVV.A
522	589.3261	1764.9564	1764.9734	-0.0169	0	63	0.004	1	A.KVNPDEVGGEALGRLL.V
534	594.3030	1779.8873	1779.9155	-0.0283	0	14	4.5e+002	1	A.FNEGLKNLDNLKGTFA.S
601	651.6653	1951.9741	1952.0003	-0.0262	0	25	35	1	I.TAFNEGLKNLDNLKGTFA.S
637	689.3634	2065.0684	2065.0844	-0.0160	0	41	0.83	1	V.ITAFNEGLKNLDNLKGTFA.S
639	693.0337	2076.0792	2076.1004	-0.0212	0	(26)	27	1	L.GKDFTPAAQAAPQKVVAGVAT.A
640	1039.0529	2076.0912	2076.1004	-0.0092	0	45	0.35	1	L.GKDFTPAAQAAPQKVVAGVAT.A
667	716.7148	2147.1226	2147.1375	-0.0149	0	24	40	1	L.GKDFTPAAQAAPQKVVAGVAT.A
689	754.4088	2260.2046	2260.2216	-0.0170	0	58	0.016	1	L.GKDFTPAAQAAPQKVVAGVAT.A
752	841.1087	2520.3041	2520.3238	-0.0196	0	78	0.00017	1	L.GHHLGKDFTPAAQAAPQKVVAGVAT.A

Proteins matching the same set of peptides:
IPI00918032 Mass: 15838 Score: 230 Queries matched: 28
Tax_Id=10090 Gene_Symbol=Hbb-b1 Beta-globin
IPI00918757 Mass: 15856 Score: 230 Queries matched: 28
Tax_Id=10090 Gene_Symbol=Hbb-b1 Beta-globin

6. **IPI00170288** Mass: 10202660 Score: 208 Queries matched: 23 emPAI: 0.00
Tax_Id=10090 Gene_Symbol=Flg similar to filaggrin
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
184	399.2118	1194.6135	1194.6106	0.0030	0	1	8.3e+003	4	S.QVHSGVQVEGR.R
242	428.2174	1281.6303	1281.6426	-0.0123	0	28	17	1	D.SQVHSGVQVEGR.R
429	524.5814	1570.7225	1570.7336	-0.0111	0	38	1.4	1	Q.SSDSQVHSGVQVEGR.R
487	563.6053	1687.7941	1687.7986	-0.0045	0	21	75	2	G.SQGGQAGRVGSSADRQG.R
509	582.6125	1744.8157	1744.8201	-0.0044	0	38	1.5	1	A.GSQGQAGRVGSSADRQG.R
538	596.2777	1785.9114	1785.9242	-0.0128	0	57	0.017	1	P.SQSSDSQVHSGVQVEGR.R
541	897.8754	1793.7362	1793.7453	-0.0091	0	20	33	1	R.RGVSSQASDSSEGHDF.S
552	606.2874	1815.8404	1815.8572	-0.0168	0	58	0.014	1	R.AGSQGGQAGRVGSSADRQG.R
553	606.2906	1815.8499	1815.8572	-0.0073	0	(28)	14	1	R.AGSQGGQAGRVGSSADRQG.R
591	960.9490	1919.8834	1919.8933	-0.0099	0	55	0.028	1	R.RAGSSSGSGVQASAGGLAASRR.S
602	491.2319	1960.8985	1960.9212	-0.0227	0	16	1.9e+002	1	F.SEGQAVGAHRQSGAGQRHE.Q
603	657.6384	1969.8933	1969.9090	-0.0157	0	37	1.6	1	P.SPSQSSDSQVHSGVQVEGR.R
614	669.3226	2004.9460	2004.9573	-0.0113	0	33	4.6	1	A.GSSSGSGVQASAGGLAASRR.S
616	502.7323	2006.9003	2006.9267	-0.0264	0	8	1.1e+003	1	G.SNQGHSSSRHQADSPRVA.R
617	502.7328	2006.9023	2006.9267	-0.0244	0	(7)	1.6e+003	1	G.SNQGHSSSRHQADSPRVA.R
629	678.6781	2033.0126	2033.0066	0.0060	0	13	4.9e+002	8	P.LTAPAAQCTGTDPSGPAPASV.T
638	692.9985	2075.9736	2075.9944	-0.0209	0	53	0.05	1	R.AGSSSGSGVQASAGGLAASRR.S
650	523.2455	2088.9528	2088.9798	-0.0270	0	10	8e+002	1	F.SEGQAVGAHRQSGAGQRHE.Q
701	764.6966	2291.0680	2291.0850	-0.0170	0	90	7.8e-006	1	R.AGSSSGSGVQASAGGLAASRRSGA.R
773	877.7089	2630.1048	2630.1229	-0.0181	0	29	2.6	1	R.RGVSSQASDSSEGHDFSEGGQAVGAH.R
786	680.8222	2719.2596	2719.3022	-0.0427	0	8	1.1e+003	1	R.DRPRQPSPSQSSDSQVHSGVQVEGR.R
953	822.1743	3284.6683	3284.5954	0.0728	0	40	1.1	1	R.RAGSSSGSGVQASAGGLAASRRSGARQQPSPS.Q
1027	873.3721	3489.4594	3489.5222	-0.0628	0	2	7e+002	4	Q.AELTGLSEPARQMSGGPPEASMAPDSTQYTTMS.K + 2 Oxidation (M)

7. **IPI00831055** Mass: 15711 Score: 177 Queries matched: 29 emPAI: 11.47
Tax_Id=10090 Gene_Symbol=Hbb-b1 Beta-globin
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
74	492.2417	982.4688	982.4720	-0.0031	0	50	0.11	1	N.DGLNHLDSL.K
75	492.2574	982.5003	982.5083	-0.0081	0	31	8.7	1	M.VHLTDAEKA.A
76	492.7905	983.5665	983.5764	-0.0099	0	46	0.21	1	V.GGEALGRLL.V
80	503.2550	1004.4955	1004.4927	0.0028	0	(27)	28	1	L.GKDFTPAAQ.A
81	503.2560	1004.4975	1004.4927	0.0048	0	28	19	1	L.GKDFTPAAQ.A
119	549.2707	1096.5269	1096.5149	0.0120	0	24	38	1	F.NDGLNHLDSL.K
129	557.3088	1112.6031	1112.6190	-0.0159	0	25	32	1	D.EVGGEALGRLL.V
152	577.3036	1152.5926	1152.6139	-0.0213	0	28	18	1	M.VHLTDAEKA.V
191	606.8505	1211.6865	1211.6874	-0.0009	0	50	0.081	1	D.EVGGEALGRLL.V
236	638.3022	1274.5899	1274.5720	0.0179	0	14	4.8e+002	6	V.YFWTQRYFD.S
276	665.3219	1328.6292	1328.6361	-0.0069	0	60	0.01	1	V.ITAFNDGLNHLDSL.S
306	687.8241	1373.6336	1373.6404	-0.0068	0	22	57	1	V.VYFWTQRYFD.S
307	460.2291	1377.6655	1377.6790	-0.0135	0	25	35	1	L.GHHLGKDFTPAAQ.A
329	708.8424	1415.6703	1415.6681	0.0022	0	54	0.041	1	I.TAFNDGLNHLDSL.K
355	725.3596	1448.7046	1448.7161	-0.0115	0	28	17	1	L.GHHLGKDFTPAAQ.A
372	737.3656	1472.7166	1472.7089	0.0077	0	16	3.1e+002	3	L.VYFWTQRYFD.S
403	765.3827	1528.7509	1528.7522	-0.0012	0	37	2.4	1	V.ITAFNDGLNHLDSL.K
413	516.9306	1547.7700	1547.7977	-0.0277	0	55	0.034	1	F.GDLSSASAIMGNKAVK.A
441	801.3931	1600.7716	1600.7845	-0.0129	0	41	0.84	1	F.NDGLNHLDSLKGTFA.S
442	534.5982	1600.7727	1600.7845	-0.0118	0	(31)	8.1	1	F.NDGLNHLDSLKGTFA.S
446	804.8816	1607.7487	1607.7409	0.0078	0	32	6.3	1	V.VYFWTQRYFDSF.G

	482	559.9617	1676.8634	1676.8886	-0.0252	0	50	0.1	1	L.GKDFTPAAQAAPQKV.V.A
	511	583.6177	1747.8313	1747.8530	-0.0217	0	27	23	1	A.FNDGLNHLDSLKGTF.A.S
	512	583.6432	1747.9079	1747.9257	-0.0178	0	52	0.075	1	L.GKDFTPAAQAAPQKV.V.A
	514	586.3031	1755.8874	1755.8937	-0.0063	0	51	0.081	1	F.GDLSSASAIMGNKVKAR.G
	592	640.9824	1919.9255	1919.9377	-0.0123	0	52	0.065	1	I.TAFNDGLNHLDSLKGTF.A.S
	629	678.6781	2033.0126	2033.0218	-0.0092	0	43	0.54	1	V.ITAFNDGLNHLDSLKGTF.A.S
	688	754.3945	2260.1618	2260.1852	-0.0234	0	9	1.3e+003	10	K.KVITAFNDGLNHLDSLKGTF.A.S
☒	880	757.1508	3024.5741	3024.5880	-0.0139	0	17	1.9e+002	1	L.TDARKAAVSGLWGKVNADVEVGALGRLLV.V

8. [IP100654081](#) Mass: 29116 Score: 120 Queries matched: 3 emPAI: 0.11
Tax_Id=10090 Gene_Symbol=Pl3a1 Putative uncharacterized protein
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta Miss Score	Expect Rank	Peptide
☒ 794	929.4747	2785.4024	2785.4358	-0.0334	0 93	5.2e-006 1 R.RAVPPNNSNAEVDLPTEELQGLVPR.G
☒ 795	929.4780	2785.4121	2785.4358	-0.0237	0 (53)	0.053 1 R.RAVPPNNSNAEVDLPTEELQGLVPR.G
☒ 796	929.4804	2785.4192	2785.4358	-0.0166	0 (41)	0.76 1 R.RAVPPNNSNAEVDLPTEELQGLVPR.G

Proteins matching the same set of peptides:
[IP100402967](#) Mass: 83155 Score: 120 Queries matched: 3
Tax_Id=10090 Gene_Symbol=Pl3a1 Coagulation factor XIII A chain

9. [IP100406870](#) Mass: 251223 Score: 98 Queries matched: 7 emPAI: 0.05
Tax_Id=10090 Gene_Symbol=Plg2 Filaggrin-2
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta Miss Score	Expect Rank	Peptide
519	588.6042	1762.7909	1762.8084	-0.0175	0 18	1.1e+002 3 K.MKSGSAYLDSNTPLYT.Y + Oxidation (M)
☒ 584	637.3067	1908.8983	1908.9151	-0.0168	0 54	0.036 1 S.RQFQAGQGQPSQSGSGRSP.R
595	644.2927	1929.8564	1929.8705	-0.0140	0 15	2.3e+002 4 R.SPVPHPESSEGEHESVVPQ.R
☒ 645	522.4916	2085.9374	2085.9716	-0.0342	0 (26)	17 1 R.RSPVHPESSEGEHESVVPQ.R
☒ 647	696.3256	2085.9550	2085.9716	-0.0166	0 57	0.016 1 R.RSPVHPESSEGEHESVVPQ.R
☒ 687	560.7727	2239.0615	2239.0802	-0.0187	0 21	68 1 D.SSRQFQAGQGQPSQSGSGRSP.R
☒ 804	706.3302	2821.2917	2821.3452	-0.0534	0 45	0.22 1 V.RPEVPTQDSRQFQAGQGQPSQSGSGR.S

10. [IP100124742](#) Mass: 27324 Score: 69 Queries matched: 4 emPAI: 0.41
Tax_Id=10090 Gene_Symbol=Rif4h Isoform Long of Eukaryotic translation initiation factor 4H
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta Miss Score	Expect Rank	Peptide
☒ 467	414.2091	1652.8075	1652.8342	-0.0268	0 10	9.9e+002 1 F.REPTREERAQRPR.L
☒ 871	979.1749	2934.5029	2934.5312	-0.0283	0 53	0.054 1 R.TVATPLNQVANPNSAIFGGARPREVVQ.K
☒ 1029	863.1866	3448.7175	3448.7699	-0.0524	0 (26)	25 1 R.TVATPLNQVANPNSAIFGGARPREVVQKEQE.-
☒ 1030	1150.5840	3448.7302	3448.7699	-0.0397	0 42	0.58 1 R.TVATPLNQVANPNSAIFGGARPREVVQKEQE.-

Proteins matching the same set of peptides:
[IP100222560](#) Mass: 25171 Score: 69 Queries matched: 4
Tax_Id=10090 Gene_Symbol=Rif4h Isoform Short of Eukaryotic translation initiation factor 4H

11. [IP100458924](#) Mass: 19948 Score: 55 Queries matched: 2 emPAI: 0.17
Tax_Id=10090 Gene_Symbol=Calr 57-KD Calcium-binding protein (Fragment)
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta Miss Score	Expect Rank	Peptide
☒ 556	611.6025	1831.7857	1831.7959	-0.0102	0 55	0.015 1 E.KEDEERESPGQAKDEL.S
557	916.9043	1831.7941	1831.7959	-0.0018	0 (6)	1.4e+003 2 E.KEDEERESPGQAKDEL.S

Proteins matching the same set of peptides:
[IP100123639](#) Mass: 47965 Score: 55 Queries matched: 2
Tax_Id=10090 Gene_Symbol=Calr Calreticulin

12. [IP100121318](#) Mass: 22712 Score: 54 Queries matched: 4 emPAI: 0.31
Tax_Id=10090 Gene_Symbol=Crip2 Cysteine-rich protein 2
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta Miss Score	Expect Rank	Peptide
☒ 110	543.2660	1084.5174	1084.5037	0.0137	0 58	0.017 1 Y.DKDPPEGTVPQ.-
☒ 206	624.7900	1247.5654	1247.5670	-0.0016	0 24	36 1 I.YDKDPPEGTVPQ.-
☒ 298	681.3297	1360.6449	1360.6511	-0.0061	0 40	1.1 1 Y.IYDKDPPEGTVPQ.-
☒ 656	527.4944	2105.9485	2105.9809	-0.0323	0 4	2.6e+003 1 E.FCLKRCRCNKTLTTPGHAR.H

Peptide matches not assigned to protein hits: (no details means no match)

Query	Observed	Mr(expt)	Mr(calc)	Delta Miss Score	Expect Rank	Peptide
☒ 797	933.4349	2797.2830	2797.2824	0.0006	0 47	0.12 1 NSKQQLSARELDAQLDAYNARMDS
☒ 84	511.2656	1020.5167	1020.5466	-0.0299	0 46	0.28 1 MAAPIKFPF
☒ 367	735.3625	1468.7104	1468.6962	0.0142	0 46	0.25 1 QSVLCFWSKW
☒ 422	783.3569	1564.6992	1564.7984	-0.0993	0 44	0.35 1 KDLLVTGAYEITDQ
☒ 193	608.3097	1214.6048	1214.6084	-0.0036	0 42	0.81 1 FGVPRLPDEN
☒ 300	682.3630	1362.7114	1362.7659	-0.0545	0 41	0.85 1 ASYLRLWALSIA
☒ 153	579.3052	1156.5959	1156.5976	-0.0017	0 41	0.96 1 GDVDVSLPKVE
☒ 249	646.8524	1291.6901	1291.6595	0.0307	0 40	0.98 1 MAPDRVVAISSP

✓	189	600.8514	1199.6883	1199.6662	0.0220	0	40	0.83	1	KFPSEFNRL
✓	484	561.5848	1681.7326	1681.7379	-0.0054	0	40	0.63	1	QGGNMDKFGQGAHHA
✓	44	438.7156	875.4167	875.4600	-0.0433	0	40	1.3	1	KEALESLS
✓	684	741.7491	2222.2253	2222.2457	-0.0204	0	40	0.68	1	GGIGTVVGRVETGVLKPGMVVT
✓	675	724.3714	2170.0924	2170.0940	-0.0016	0	40	1.1	1	AMSLSDALKGVTDNVVDTVVH
✓	368	735.3702	1468.7259	1468.7198	0.0061	0	39	1.4	1	AHEDPVEKVEIEGF
✓	274	443.2615	1326.7628	1326.7871	-0.0243	0	38	1.1	1	QTVAVGVKAVDK
✓	66	478.2538	1431.7394	1431.7028	0.0367	0	37	5.9	1	ISMMAATSTALATAH + Oxidation (M)
✓	549	602.2987	1803.8744	1803.8963	-0.0219	0	37	2.3	1	KTVETRDGQVINETSQ
✓	213	629.3237	1256.6327	1256.6361	-0.0033	0	36	2.7	1	DNQLQEGKNVI
✓	202	622.3399	1242.6652	1242.7547	-0.0895	0	36	2.6	1	KEVAVKIIDET
✓	685	742.3819	2224.1240	2224.1335	-0.0095	0	36	2.6	1	SSLNLRETNLSESLPLVDTHS
✓	116	546.7865	1091.5585	1091.5135	0.0450	0	35	3.5	1	DSPALFSGDAL
✓	262	657.3198	1312.6250	1312.6200	0.0050	0	35	3.1	1	PRLPDEMSQW
✓	407	768.9177	1535.8209	1535.8460	-0.0251	0	35	3	1	NLPPLPPPPPRGGDL
✓	86	512.7335	1023.4525	1023.4444	0.0081	0	35	2.9	1	QGGNMDKFP
✓	447	804.9260	1607.8375	1607.7791	0.0584	0	34	3.9	1	KNLFGGGGSEKKKE
✓	162	582.3002	1162.5858	1162.6380	-0.0522	0	34	4.7	1	MAAVLTTLERT
✓	323	700.3390	1398.6634	1398.6602	0.0032	0	34	4.1	1	GVNDNPGHYIMTV
✓	31	514.8146	1027.6147	1027.6100	0.0047	0	34	3.2	1	MVGNLGIIVL
✓	67	480.2668	958.5190	958.5335	-0.0145	0	33	5.7	1	IEDLTQL
✓	258	436.5759	1306.7060	1306.7244	-0.0185	0	32	5.8	1	KEAPAPPEAKAKA
✓	208	625.8159	1249.6172	1249.6667	-0.0495	0	32	7.3	1	QGAVPPSGVPALGA
✓	678	729.3611	2185.0615	2185.0692	-0.0077	0	32	6.6	1	GNLPYDVTEDSIKDFFRGL
✓	627	677.6896	2030.0468	2030.0644	-0.0176	0	32	7.4	1	LIKTVETRDGQVINETSQ
✓	304	687.3284	1372.6423	1372.6730	-0.0307	0	32	7.4	1	LMAPKDQICPEI + Oxidation (M)
✓	21	353.7068	705.3991	705.4061	-0.0070	0	32	8.6	1	KDFIIA
✓	270	658.3218	1971.9435	1971.8844	0.0591	0	31	22	1	ASESSSGVGNADQPLPPC
✓	21	397.2250	792.4354	792.4051	0.0303	0	31	7.8	1	TAA ML LLAS + Oxidation (M)
✓	416	520.2524	1557.7354	1557.7059	0.0295	0	31	8	1	FLNENSGAPVAGES
✓	663	707.7083	2120.1029	2120.1212	-0.0183	0	31	8.7	1	AVDTSSIEITTKDLKEKKEV
✓	412	514.2791	1539.8156	1539.8256	-0.0100	0	31	9	1	AGEKAPDTKEKKPAA
✓	26	424.6883	847.3621	847.4109	-0.0489	0	30	11	1	KPSSP TVS + Oxidation (M)
✓	555	610.6060	1828.7961	1828.8064	-0.0102	0	30	5.5	1	QGGNMDKFGQGAHHAF
✓	264	657.3201	1312.6257	1312.7238	-0.0981	0	30	10	1	KETLIIPEKN
✓	387	753.8768	1505.7391	1505.7766	-0.0375	0	30	12	1	EPATPOLYVPALGA
✓	664	708.0678	2121.1816	2121.1980	-0.0164	0	30	6.3	1	GGIGTVVGRVETGVLKPGMVV
✓	13	331.6470	661.2795	661.2748	0.0047	0	30	14	1	FSFDF
✓	124	554.7838	1107.5530	1107.5560	-0.0030	0	30	13	1	KSSSFNPAALS
✓	492	565.5918	1693.7536	1693.7981	-0.0445	0	30	8.3	1	TAAGTYTLEAVVH MSQ + Oxidation (M)
✓	111	544.3129	1086.6112	1086.6186	-0.0074	0	29	13	1	AKNVNENFLK
✓	190	603.2954	1204.5762	1204.5758	0.0004	0	29	16	1	QSVKKTCPHAD
✓	209	625.8213	1249.6281	1249.6233	0.0048	0	29	16	1	QLILGCCMVALS
✓	338	710.8695	1419.7245	1419.6711	0.0534	0	29	16	1	SMALARSQCRNSP
✓	166	583.2987	1164.5829	1164.5332	0.0497	0	28	16	1	VEDSEEMKA
✓	272	661.3364	1320.6583	1320.6673	-0.0091	0	28	17	1	EAKENFNKALTG
✓	462	818.8766	1635.7387	1635.7641	-0.0254	0	28	12	1	QDLTRAHVDSFNVA
✓	466	412.2324	1644.9005	1644.8696	0.0310	0	28	13	1	KPQERILHRDAGP
✓	108	534.7763	1067.5381	1067.5400	-0.0018	0	28	16	1	GVPRLPDEN
✓	37	424.7019	847.3893	847.4110	-0.0216	0	28	21	1	VSVNVFMS + Oxidation (M)
✓	218	630.7839	1259.5533	1259.5236	0.0297	0	28	14	1	EMATKMDMLE
✓	174	590.3015	1178.5884	1178.5931	-0.0047	0	28	20	1	GKAVNYADAALS
✓	137	566.2709	1130.5273	1130.5244	0.0029	0	27	21	1	PGFKGEGPEVD
✓	505	859.9352	1717.8558	1717.8635	-0.0077	0	27	21	1	NVAABEQKAAPSPAPARPA
✓	405	766.9061	1531.7976	1531.8358	-0.0382	0	27	23	1	QTVKTFQNKPAAI
✓	135	564.8016	1127.5887	1127.6087	-0.0201	0	27	25	1	VFERDPPRL
✓	237	426.5648	1276.6726	1276.6888	-0.0162	0	27	25	1	KDPNAPKRPSSA
✓	101	525.7938	1049.5730	1049.4852	0.0878	0	26	23	1	DLKMNTAAD
✓	125	556.3075	1110.6004	1110.6285	-0.0281	0	26	23	1	GPPVSELITKA
✓	297	678.3429	1354.6713	1354.7456	-0.0743	0	26	27	1	QDAKILKIGAGAGL
✓	665	713.3715	2137.0927	2137.1015	-0.0088	0	26	26	1	SLNLRETNLSESLPLVDTHS
✓	386	501.5728	1501.6966	1501.6936	0.0030	0	26	25	1	EKFAGGDYTTTIEA
✓	859	729.3773	2913.4799	2913.5139	-0.0339	0	26	26	1	RLCVILEPQMELMSRHKTYNLSPR
✓	1035	867.6594	3466.6086	3466.6448	-0.0362	0	26	16	1	SRPLNAVSQDGKETKAGEAPTENPAPATEQSSAE
✓	62	476.2578	950.5010	950.5073	-0.0063	0	26	29	1	KDIFLASAS
✓	390	506.5970	1516.7693	1516.8461	-0.0768	0	26	31	1	DPSSSKTKQVISKI
✓	510	583.3062	1746.8969	1746.8042	0.0926	0	26	29	1	AFSHKSMRDRHVM + 2 Oxidation (M)
✓	346	713.3511	1424.6876	1424.6896	-0.0020	0	26	28	1	QDEITQLSHLGGG
✓	690	755.7389	2264.1949	2264.2124	-0.0175	0	26	25	1	VAPLGAEQLQESARQKLQELQG
✓	14	331.6485	661.2824	661.2530	0.0294	0	26	36	1	MPHDF + Oxidation (M)
✓	540	895.4756	1788.9367	1788.8750	0.0617	0	26	30	1	QPLSAMVSMVTKDNPGV + Oxidation (M)
✓	702	765.0984	2292.2735	2292.2195	0.0540	0	25	17	1	LAPRQTTSMPPKLKTPHSRM + Oxidation (M)
✓	370	368.7142	1470.8277	1470.8558	-0.0281	0	25	23	1	SAKPAPPEPEPEPK
✓	277	665.3549	1328.6952	1328.7565	-0.0613	0	25	33	1	QAPLGQHQLPIK
✓	311	692.8693	1383.7241	1383.7299	-0.0058	0	25	34	1	GWPGYVRPLPAAT
✓	126	556.3180	1110.6215	1110.6550	-0.0335	0	25	27	1	PARVPPPPPIA
✓	528	592.2679	1773.7818	1773.7899	-0.0081	0	25	22	1	PSWEPFRDNYPAHS
✓	672	722.7189	2165.1348	2165.1038	0.0311	0	25	32	1	APILNVSPGNLSLAPQMEIEG + Oxidation (M)
✓	104	531.2710	1060.5274	1060.5037	0.0238	0	25	42	1	QTLSDKSGPE
✓	574	938.4663	1874.9180	1874.9302	-0.0121	0	25	38	1	TNGKEPELEPIPIYEF
✓	28	381.1805	760.3465	760.3796	-0.0331	0	25	47	1	PSYFVV

738	821.0984	2460.2733	2460.1804	0.0928	0	24	37	1	YLLGSDYTBGIPVTCVTAMEIL + Oxidation (M)
265	657.3501	1312.6857	1312.7755	-0.0898	0	24	41	1	KIQLGPGIGFDII
131	560.2803	1118.5460	1118.5641	-0.0181	0	24	48	1	KEMELLAAGAA + Oxidation (M)
348	717.8794	1433.7442	1433.7626	-0.0184	0	24	43	1	REEPIAHKAISSP
163	583.2943	1746.8611	1746.9087	-0.0476	0	24	1.3e+002	1	NIQSSIPASKHMPIPQ
425	783.8505	1565.6865	1565.7573	-0.0708	0	24	29	1	QGGDTAAEKLEKVV
240	639.8334	1277.6522	1277.6140	0.0382	0	24	47	1	DSSSPVGVVLGVD
438	531.2754	1590.8045	1590.8505	-0.0460	0	24	46	1	DLPATPVAPARPTTVL
521	588.6181	1762.8324	1762.8485	-0.0162	0	24	44	1	NNTAADKQPYEKKAA
154	579.8363	1157.6581	1157.6880	-0.0300	0	24	40	1	QITQEKKEK
204	415.8637	1244.5694	1244.5166	0.0528	0	23	46	1	MAPGPPDGLNAPC + Oxidation (M)
487	563.6053	1687.7941	1687.8464	-0.0523	0	23	47	1	KSKGAHTTMADALNR + Oxidation (M)
262	656.3264	1310.6381	1310.6978	-0.0597	0	23	51	1	SKFNTLLDMLL
214	629.3247	1884.9521	1884.9680	-0.0159	0	23	1.6e+002	1	EDLEKILEQITSAPGGSV
27	381.1796	760.3447	760.4120	-0.0673	0	23	67	1	FEVDGKV
239	639.3481	1276.6817	1276.5857	0.0960	0	23	54	1	QDAMLVDIEDL + Oxidation (M)
175	590.3032	1178.5918	1178.6183	-0.0265	0	23	58	1	ISFQITEALGT
455	810.4171	1618.8197	1618.8249	-0.0052	0	23	58	1	FDMAALRNHNAIRD
382	750.3754	2997.4724	2997.5274	-0.0550	0	23	1.6e+002	1	KPMIDMLVFFVIMLVVLSFGVARQ + 4 Oxidation (M)
128	556.7599	1111.5052	1111.5042	0.0010	0	23	50	1	KPMQNPDTL + Oxidation (M)
246	644.3625	1286.7104	1286.7156	-0.0052	0	23	53	1	KPELLDMLVT + Oxidation (M)
196	616.8184	1231.6223	1231.6660	-0.0437	0	23	67	1	SISEVTLLGNV
352	720.3574	1438.7003	1438.6212	0.0791	0	23	59	1	EKEVDGNDIYGN
658	530.2802	2117.0917	2117.0364	0.0553	0	23	59	1	AGMVLGPGPPGPGYFGKQFNG + Oxidation (M)
519	588.6042	1762.7909	1762.8493	-0.0584	0	23	44	1	NRQNVSSQFSRSRT + Oxidation (M)
432	788.3808	1574.7470	1574.7788	-0.0318	0	22	62	1	ADVQKITELNETSQ
417	520.2971	1557.8695	1557.9090	-0.0395	0	22	49	1	KATTPAKKVVSQT
718	783.4018	2347.1835	2347.1954	-0.0119	0	22	65	1	PSPTASSREKSWTRKQML + Oxidation (M)
23	518.2904	1034.5663	1034.5185	0.0477	0	22	1.6e+002	1	KPTASQWFA
60	474.2853	946.5560	946.5892	-0.0331	0	22	57	1	PVVIPLFL
64	477.2460	952.4774	952.5342	-0.0568	0	22	68	1	ASVVIQVHT
862	729.3876	2913.5215	2913.5139	0.0076	0	22	62	1	RLCVILEPMQELMSRHKTYNLSR
241	427.2543	1278.7412	1278.7192	0.0220	0	22	42	1	RLCAFILMVLVV + Oxidation (M)
539	596.2801	1785.8185	1785.8567	-0.0382	0	22	57	1	MAASSKFPPIITHDDVS + Oxidation (M)
376	744.8489	1487.6833	1487.7191	-0.0358	0	22	67	1	QVLFCRLTDEQH
1077	927.8962	3707.5555	3707.6488	-0.0934	0	21	7.9	1	THPQTEGDSWMDLHPGTSMWDLPHQTQALTSFGH
254	822.1763	3284.6761	3284.6209	0.0552	0	21	74	1	KEDLQVMEKQNMIPNIVLGPHEDEVP
492	565.5967	1693.7682	1693.7869	-0.0187	0	21	63	1	EMELYELAQAGAID
142	569.7806	1137.5467	1137.6030	-0.0563	0	21	82	1	KETLPTQAPGP
575	938.9692	1875.9238	1875.9221	0.0017	0	21	85	1	RTLASASRPSTEGAMADR
669	719.3329	2154.9767	2154.9971	-0.0203	0	21	58	1	TAGYPEVNIQNFTTSWRDG
861	972.1806	2913.5200	2913.4843	0.0357	0	21	77	1	VTMSQVTLILLGVVYMGFGGAMART + Oxidation (M)
244	642.7883	1283.5621	1283.5605	0.0016	0	21	65	1	PEDAMGTHPK + Oxidation (M)
61	475.2434	948.4722	948.4110	0.0612	0	21	1.1e+002	1	MSEILPDE + Oxidation (M)
895	765.1169	3056.4387	3056.4379	0.0008	0	21	67	1	RMRNDRGNVLPFNPDSLTGNGFTMAL + Oxidation (M)
87	513.2411	1024.4677	1024.4392	0.0285	0	21	85	1	GQVTFMFM + 2 Oxidation (M)
28	763.4177	762.4104	762.4640	-0.0536	0	21	1.1e+002	1	KGVILFS
46	446.7560	891.4975	891.4848	0.0128	0	21	95	1	GLSSILPM + Oxidation (M)
225	632.3278	2525.2819	2525.3197	-0.0378	0	21	2.9e+002	1	KKQNDLQKREGEVEDSKPNVG
325	707.3179	1412.6213	1412.6619	-0.0406	0	21	67	1	SRKAYCRWDQ
798	934.1275	2799.3607	2799.3228	0.0379	0	21	87	1	GPQGHITVGESKYNHWFGLALLHSF
385	501.5710	1501.6912	1501.7426	-0.0514	0	20	85	1	KKNWNQIHFSN
1016	856.9833	3423.9039	3423.9336	-0.0296	0	20	36	1	IYVLPARGLNWILHPLPPRYQADVFKIQI
231	423.8919	1268.6538	1268.6911	-0.0373	0	20	99	1	KQMDALNPKPK
197	411.5507	1231.6303	1231.6269	0.0034	0	20	1.1e+002	1	LSRDGNTSGRGL
165	583.2972	1164.5799	1164.5332	0.0467	0	20	1.1e+002	1	VEDSEEMCKA
48	446.8964	1337.6673	1337.6723	-0.0050	0	20	1e+002	1	QSYMPGVLLVAM
642	694.6787	2081.0144	2080.9953	0.0191	0	20	1e+002	1	DHDIYDIPDPGVLIENE
709	770.4025	2308.1856	2308.2031	-0.0176	0	20	1e+002	1	LKVTKQHNDECKHLLSLMG + Oxidation (M)
82	506.2346	1010.4547	1010.5073	-0.0526	0	20	95	1	GQVTFIYS
139	568.9741	1703.9004	1703.9134	-0.0131	0	20	1.1e+002	1	LDVLEKPPINPFFFE
381	750.3642	1498.7138	1498.7093	0.0045	0	20	1.1e+002	1	QFGSSGNALTFPT
201	620.8062	1239.5979	1239.6282	-0.0303	0	20	1.1e+002	1	KQENLPHVGS + Oxidation (M)
372	737.3656	1472.7166	1472.6857	0.0308	0	20	1.2e+002	1	VVYESVGGAMFDLA + Oxidation (M)
341	475.5851	1423.7334	1423.7572	-0.0238	0	20	1.1e+002	1	FKPDNAPKRPPSA
261	655.8767	1309.7389	1309.6990	0.0399	0	20	79	1	SIETLERHVVQ
654	701.3269	2100.9590	2101.0410	-0.0820	0	20	81	1	MSTYPMIICWISRLKDI + 2 Oxidation (M)
26	520.2873	1557.8400	1557.8250	0.0150	0	20	3e+002	1	ESTVKLTAAEGVNL
716	585.2980	2337.1630	2337.1754	-0.0124	0	20	1.2e+002	1	KGPKVDIDVDVDVHGPDNHL
185	599.2808	1196.5470	1196.6230	-0.0760	0	19	1.1e+002	1	WGVASIGTFPI
1041	873.4261	3489.6752	3489.7232	-0.0481	0	19	98	1	SLRQGGTLTGKFMSTSSIPGCLLGVALEGDTSPHG + Oxidation (M)
236	638.3022	1274.5899	1274.6659	-0.0760	0	19	1.2e+002	1	FLWDIREVPT
56	465.2528	928.4911	928.4436	0.0474	0	19	1.4e+002	1	QCMGAIHLS + Oxidation (M)
105	532.2454	1593.7144	1593.7855	-0.0710	0	19	3e+002	1	KDVTTVGVMAANNAK
50	307.4989	919.4749	919.4134	0.0615	0	19	1.5e+002	1	SLDISADAE
224	631.7876	1261.5606	1261.5649	-0.0043	0	19	1.1e+002	1	CDKAFSQYSTL
494	847.8941	1693.7737	1693.8424	-0.0687	0	19	1e+002	1	QLLDDYKEGNHII
785	679.8317	2715.2978	2715.2998	-0.0020	0	19	1.1e+002	1	SDMGLSFSSLPMTLKIFFFNAMAI + 3 Oxidation (M)
630	682.6717	2044.9933	2045.0139	-0.0206	0	19	1.3e+002	1	DKDEIRIPDVEPAAPLAM + Oxidation (M)
295	674.8424	1347.6702	1347.7261	-0.0558	0	19	1.4e+002	1	WLAVLPTMPAAL + Oxidation (M)
181	594.8130	1187.6115	1187.5458	0.0657	0	19	1.5e+002	1	LAENEQVAM

454	810.4152	1618.8158	1618.8177	-0.0019	0	16	2.8e+002	1	NSSTIAALLCALYPHF
781	673.0550	2688.1907	2688.2351	-0.0444	0	16	1.2e+002	1	LQQTQERPCNTSPGHVSTTPG
581	634.3164	1899.9273	1899.8450	0.0823	0	16	2.7e+002	1	LSTCCLLTAVEMSNTPSM
683	556.5339	2222.1065	2222.0500	0.0565	0	16	2.8e+002	1	LRIIDGSGYLCEMEFVAHF + Oxidation (M)
872	744.3791	2973.4874	2973.4728	0.0146	0	16	2.7e+002	1	QKSLYRDVMLENYSHLSVGLCIYQ + Oxidation (M)
173	589.7817	1177.5488	1177.4921	0.0567	0	16	2.9e+002	1	QSSCSSEPSPLG
212	419.2235	1254.6486	1254.5954	0.0531	0	16	2.9e+002	1	MLYKFPAPGP + Oxidation (M)
691	567.2944	2265.1484	2265.0848	0.0636	0	16	2.9e+002	1	LSDTQCSRLSRWPPVSEFS
210	625.8320	1249.6494	1249.6125	0.0369	0	16	3.1e+002	1	KNKEQMPQTF
349	479.2730	1434.7973	1434.8558	-0.0586	0	16	2.3e+002	1	KVAPAPAVVKKQEA
1	604.2955	603.2882	603.3050	-0.0168	0	16	4.3e+002	1	KMNVP + Oxidation (M)
235	637.3317	1272.6488	1272.6384	0.0104	0	16	9.2e+002	1	QPENSMKLTPL + Oxidation (M)
628	1017.5088	2033.0030	2032.9378	0.0653	0	16	3e+002	1	QRYQDLQLDYSLTDEF
177	590.7773	1179.5401	1179.5740	-0.0339	0	16	2.9e+002	1	LVMCKESQR
550	903.4485	1804.8824	1804.9683	-0.0859	0	16	3.1e+002	1	VTGTVLAVLSAKDDGRF
692	758.4142	2272.2207	2272.1959	0.0248	0	16	2.4e+002	1	BETAPLWVRGLMWSAIEKL
252	652.8053	1303.5959	1303.5721	0.0239	0	15	3e+002	1	QPDWIFPESG
582	635.3449	1903.0128	1902.9884	0.0244	0	15	2.8e+002	1	KDAAQAGARSQYGRSRSP
700	763.3854	2287.1343	2287.2028	-0.0685	0	15	3.1e+002	1	LLSDLTNCTVKLCGNPTLRL
472	834.9116	1667.8086	1667.7315	0.0771	0	15	3.1e+002	1	PSYSPTSPSYPTSPN
327	707.3644	1412.7143	1412.7664	-0.0520	0	15	9.8e+002	1	SQVLLAPYHSVIS
560	615.2874	1842.8404	1842.7988	0.0416	0	15	2.5e+002	1	QCAQYAADREBEKM + Oxidation (M)
115	546.3093	2181.2080	2181.1755	0.0325	0	15	7.5e+002	1	KDVEPLAQLKMDYSLVG
132	373.8783	1118.6131	1118.6196	-0.0065	0	15	3.3e+002	1	KDPNAPKRFP
721	790.0472	2367.1199	2367.2198	-0.0999	0	15	2.8e+002	1	PHLAPLPHSYFLSLAFFCTR
729	603.6191	2410.4472	2410.3518	0.0954	0	15	39	1	KTLMRSRRTKKFISAINLAGA + Oxidation (M)
353	720.3740	1438.7334	1438.8296	-0.0962	0	15	3.4e+002	1	KSNVAYRIKLF
1165	1078.3020	4309.1789	4309.1799	-0.0010	0	15	3.1e+002	1	AEDDDYESEPDQNRVVGPRKGLGPASAVKLAANRTTAGAR
1051	899.7040	3594.7870	3594.8392	-0.0522	0	15	3.2e+002	1	DIDENELKEFFMSPGNVVELRINTKGVGKLP
724	802.4040	2404.1901	2404.2308	-0.0408	0	15	3.4e+002	1	APAVANTPTSPAPAVSMSPFVAGVLS + Oxidation (M)
156	387.8695	1160.5866	1160.6077	-0.0212	0	15	4e+002	1	LSFVPSQSQP
566	924.9413	1847.8681	1847.9273	-0.0592	0	15	3.2e+002	1	KKEMKEELIEGVRMA
215	779.1713	3112.6561	3112.6049	0.0512	0	15	2.6e+002	1	QMLFSNPLDQPVNVCVLLVEGSGLLRGL
502	568.3019	1701.0840	1701.8145	0.0695	0	15	3.6e+002	1	GSVGMAGSPQPPQPPP
708	578.0213	2308.0559	2308.0866	-0.0306	0	15	2.4e+002	1	RNDELPLRERQTVENMQ + Oxidation (M)
555	701.3760	2101.1062	2101.0368	0.0695	0	15	3.2e+002	1	PTSEQAGPPELPPPPFAEPF
337	710.8647	1419.7149	1419.7358	-0.0208	0	15	7.3e+002	1	DALAVTRYVLQDG
526	591.9484	1772.8233	1772.7483	0.0751	0	15	3e+002	1	SNSGGKTDGSIINNTS + Oxidation (M)
625	676.3559	2026.0457	2026.0418	0.0039	0	15	3.5e+002	1	GAPVTHNGCLLREAEHP
90	514.2716	1026.5287	1026.5498	-0.0211	0	15	3.6e+002	1	FIHNSLTV
881	758.6370	3030.5189	3030.6033	-0.0844	0	15	3.5e+002	1	KGVPLDGRPMIDQLVTSQIDPQRRPAQ + Oxidation (M)
1072	927.9450	3707.7508	3707.6714	0.0793	0	15	2.5e+002	1	MTMETIMKCAFYSQGSVQLEENSKYKAVED + 3 Oxidation (M)
595	644.2927	1929.8564	1929.8125	0.0440	0	15	2.2e+002	1	QDPFMKALSMFSDDFG + Oxidation (M)
792	694.8582	2775.4037	2775.4205	-0.0168	0	15	3.5e+002	1	NVMSDRKFKEKVRNNALHFLTTS
1192	1200.6204	4798.4525	4798.5299	-0.0774	0	15	3.2e+002	1	CLLFVLTLGNSIVIATIKLEPSLHQPMPYFPLCMLANNIDILL + 3 Oxidation (M)
440	800.3656	1598.7166	1598.7172	-0.0007	0	15	2.7e+002	1	ASNGDTPTHEDLTKN
522	882.4298	1762.8450	1762.8308	0.0142	0	15	3.6e+002	1	TWELSGGNDPMSEKR + Oxidation (M)
1220	1315.8950	5259.5509	5259.5465	0.0044	0	15	2.7e+002	1	QNSMFLGRSRRTKSDLSLKMYYQEIQWYEHAREBQEQKL + 2 Oxidation (M)
301	341.9381	1363.7233	1363.6593	0.0641	0	15	3.6e+002	1	KGGGGHANRPDAG
461	818.8734	1635.7322	1635.8079	-0.0757	0	15	2.7e+002	1	QPIDPFPFVCHLNS
948	813.1075	3248.4011	3248.4440	-0.0430	0	15	80	1	AEAPTGRVARDEDDVDTKKQKTEED
561	923.3905	1844.7664	1844.8042	-0.0377	0	15	1.3e+002	1	DNRKVMQMQMSQFF + 2 Oxidation (M)
424	783.8339	1565.6533	1565.7151	-0.0618	0	15	1.7e+002	1	VGSEFFYHLFDGQA
790	920.1547	2757.4422	2757.3453	0.0970	0	15	3.3e+002	1	DSLLEIMTKDGGDMPAPLEVSTVPAVG + Oxidation (M)
831	714.3241	2853.2672	2853.3277	-0.0605	0	15	1.5e+002	1	VMPCLQSDTDMALKAMSLSLHCTM + Oxidation (M)
215	630.3180	1258.6215	1258.6414	-0.0199	0	15	4.2e+002	1	CAINKVLMDVP
1229	1480.2361	5916.9153	5916.8690	0.0463	0	14	3.2e+002	1	DMDMIRDCAEKVASHWQQLMKMEDLKLNVASVAFYKTSBQVCSVLESLE
714	582.3063	2325.1961	2325.1708	0.0252	0	14	3.7e+002	1	TMCTSLLLVYSSLSGSKERFP + Oxidation (M)
437	792.3493	1582.6840	1582.6716	0.0125	0	14	2.3e+002	1	QADGVSCKRTDCVD
459	545.2831	1632.8276	1632.8294	-0.0018	0	14	4.2e+002	1	NEGILLAERGFGAMV
787	682.3615	2725.4170	2725.3403	0.0767	0	14	3.6e+002	1	VTGVLMGRRWVCTGATKLEH + 2 Oxidation (M)
322	699.3421	1396.6696	1396.6623	0.0073	0	14	3.9e+002	1	HSEVHLVYEPTS
138	567.3056	1132.5966	1132.4996	0.0969	0	14	4.5e+002	1	QEQIEDRDT
1034	864.9267	3455.6777	3455.6554	0.0223	0	14	3.4e+002	1	KASEIADKIYNLYNGYTSKGQQTAYNTLM
644	695.3460	2083.0161	2083.0334	-0.0173	0	14	3.9e+002	1	AHEDPVKEVIEGFSRGLSN
70	487.2589	972.5032	972.4923	0.0109	0	14	4.9e+002	1	RSFGCGLQR
947	812.1903	3244.7322	3244.6696	0.0626	0	14	2.9e+002	1	KTVLTDASHTKCLCDRLSTFAILAQQPRE
719	591.2767	2361.0779	2361.1205	-0.0427	0	14	2.7e+002	1	RMESEATPLPVSCQWTRQGL + Oxidation (M)
155	386.8939	1157.6599	1157.5789	0.0810	0	14	3.5e+002	1	PAGAGSRSSSPGK
837	714.3387	2853.3258	2853.3277	-0.0019	0	14	2.8e+002	1	VMPCLQSDTDMALKAMSLSLHCTM + Oxidation (M)
819	947.7438	2840.2096	2840.2811	-0.0715	0	14	93	1	SPDSGPAQPSIEGAIMDTWAISSSPQ + Oxidation (M)
963	824.9240	3295.6669	3295.5673	0.0995	0	14	3.9e+002	1	PRDAADLFTDLNAPQKIDAIYFETSKY
470	829.8968	1657.7791	1657.7981	-0.0190	0	14	3.9e+002	1	GSQDTSQCKKLSPPPL
471	834.4416	1666.8686	1666.8865	-0.0179	0	14	4e+002	1	NLPLPPPPPPRGGLM
742	618.8548	2471.3902	2471.3604	0.0298	0	14	1.9e+002	1	KICTVPNSSQLMKVTVAPVN
620	1008.0022	2013.9898	2013.9023	0.0875	0	14	4.2e+002	1	TDELLADCSQPLCDIHEI
1228	1451.4961	5801.9553	5801.8756	0.0797	0	14	3.7e+002	1	EQPAGEARSAAATMASEAGAPRIMITHIVNQNFKSYAGEKVLGPFHKKRFSCTII
144	380.2260	1137.6563	1137.6506	0.0057	0	14	2.7e+002	1	SARASQLLFVA
876	826.9117	3303.6178	3303.6928	-0.0750	0	14	3.8e+002	1	VRQVETACAPMRLLAYPRSGDERDEKTV + Oxidation (M)
419	781.4363	2341.2870	2341.1921	0.0949	0	14	8.4e+002	1	DGNGPVRSQTCIRIKVLDAND
121	550.2842	1098.5539	1098.5669	-0.0130	0	14	4.6e+002	1	TPLELRQN

✓	623	506.7513	2022.9763	2022.9422	0.0341	0	14	4.2e+002	1	GLTADTYIDLADEEGLWA
✓	674	543.2944	2169.1487	2169.2157	-0.0670	0	14	3.9e+002	1	FLAEGTAIKDLKNPDRVLIG
✓	133	562.2932	1693.8578	1693.8865	-0.0287	0	14	1.3e+003	1	KQEAIPEDIQGGCKI
✓	57	466.9308	1397.7705	1397.7377	0.0327	0	14	4.1e+002	1	PGPIVLTVAKCWD
✓	934	783.8749	3131.4704	3131.4872	-0.0168	0	14	3.1e+002	1	QETAPPGPGVSRGDSPIIEKMKRRTCALC + Oxidation (M)
✓	839	714.3528	2853.3821	2853.4079	-0.0258	0	14	4e+002	1	TLQHDNIVITHYKMIHQDLQL + Oxidation (M)
✓	965	826.4485	3301.7647	3301.7277	0.0370	0	14	3.1e+002	1	QMPQPPLQPLAQVPPQMPQMPVVPITPLT + 2 Oxidation (M)
✓	313	693.3958	2769.5541	2769.5575	-0.0033	0	14	7.8e+002	1	SNKLLTFFLTMRASVNLNLSLRGP
✓	145	381.2067	1140.5983	1140.6543	-0.0560	0	14	4.5e+002	1	TRVLLLEGLF
✓	612	995.5113	1989.0080	1989.0643	-0.0562	0	14	4.7e+002	1	QELLSNGELNHLPLKER
✓	1121	988.5344	3950.1086	3950.1182	-0.0096	0	14	3e+002	1	KKNMVVSPGDSIFVILHQVWKHPVHQDFLGF
✓	699	572.7898	2287.1301	2287.1603	-0.0303	0	14	4.6e+002	1	RKEERQAHLTNQYIQMA + Oxidation (M)
✓	740	616.8109	2463.2145	2463.3117	-0.0971	0	14	4.5e+002	1	AAILGLVAMASDVEGLYAAVKALVC + Oxidation (M)
✓	182	397.2136	1188.6190	1188.6139	0.0051	0	14	5.2e+002	1	SPPSLPAGAGAAP
✓	710	772.3519	2314.0339	2314.1189	-0.0851	0	14	2.6e+002	1	TIQGSDAAHENGLEQLTFDRLL
✓	1142	1027.0670	4104.2389	4104.2591	-0.0202	0	14	2.1e+002	1	LAIHMYLESTRIPRLLLPQDPQKRAIVRMISDLIA + Oxidation (M)
✓	168	585.2873	1168.5600	1168.5724	-0.0124	0	14	4.6e+002	1	QTVTEENKQPP
✓	776	663.3291	2649.2871	2649.2201	0.0670	0	14	4.3e+002	1	QHRADNSAHSGLLSPSCSSTNAIPA
✓	515	586.6154	1756.8245	1756.8424	-0.0179	0	14	4.2e+002	1	LIALSLPLACMCCTLP
✓	636	517.2507	2064.9738	2065.0276	-0.0538	0	14	4.1e+002	1	QGLSHRQNRFRFDGQPI + Oxidation (M)
✓	611	995.5103	1989.0060	1988.9634	0.0426	0	13	5e+002	1	APLRPGMPPTMDPFKEK + 3 Oxidation (M)
✓	918	779.1747	3112.6698	3112.5723	0.0974	0	13	3.4e+002	1	PSVITLPSRKRTKEQAHSRSHYLSGMSA + Oxidation (M)
✓	565	616.9605	1847.8596	1847.8836	-0.0239	0	13	4.3e+002	1	RHFEELETIMDEK + Oxidation (M)
✓	725	609.8013	2435.1763	2435.1890	-0.0127	0	13	4.6e+002	1	GSVLEDTWKKEGKTDMEEIIQ
✓	485	562.9373	1685.7901	1685.8808	-0.0907	0	13	4.6e+002	1	KKRASQAASSSRPSE
✓	20	343.6619	685.3091	685.3105	-0.0014	0	13	4.4e+002	1	CPGPLAE
✓	580	474.4952	1893.9515	1894.0411	-0.0896	0	13	5.3e+002	1	QKKAESPTETIIQAIIP
✓	213	630.8261	1259.6376	1259.5881	0.0494	0	13	5.9e+002	1	EDQGLGETTPLT
✓	71	489.2504	1952.9724	1953.0281	-0.0557	0	13	1.7e+003	1	LMSTLNNINIFLVSDFL
✓	321	465.2365	1392.6878	1392.7548	-0.0670	0	13	5.8e+002	1	KRSFGGVCVVTLQ
✓	404	511.2658	1530.7756	1530.7348	0.0409	0	13	5.9e+002	1	IEQNRKIPMEEE + Oxidation (M)
✓	294	670.0992	2007.2759	2007.1894	0.0865	0	13	5.5e+002	1	KHLSVNLKPFINKKE
✓	172	392.1903	1173.5490	1173.5666	-0.0176	0	13	5.7e+002	1	EVPIPRDGEY
✓	22	400.2215	798.4284	798.3508	0.0776	0	13	5.1e+002	1	QPPGNGAS
✓	621	506.4968	2021.9579	2022.0455	-0.0877	0	13	4.9e+002	1	KSSINDAARFKVADAMKV
✓	750	626.8106	2503.2135	2503.2776	-0.0642	0	13	5.1e+002	1	SLSLIDFCQSTVVIPKIMMSFL + 2 Oxidation (M)
✓	823	713.3467	2849.3576	2849.4494	-0.0918	0	13	4.5e+002	1	IPTLVIMBQFATANQRTKSERTHY + Oxidation (M)
✓	260	437.5587	1309.6544	1309.6738	-0.0195	0	13	5.6e+002	1	KDRETSKSRGF
✓	782	676.0835	2700.3047	2700.3839	-0.0792	0	13	5e+002	1	QGLKAAMLGQEDFPQGRPLRLAAAC + Oxidation (M)
✓	1168	1091.5455	4362.1533	4362.0686	0.0846	0	13	4.9e+002	1	SEYPVILSFENHCKSKYQYKMSKYCEDLPGLLLKQ + Oxidation (M)
✓	1201	1223.8308	4891.2941	4891.3354	-0.0414	0	13	2.9e+002	1	EVTRECPRIYGEIMDTATQHFAVVGDSVSETQHVLSKDDFLKL + Oxidation (M)
✓	724	609.3027	2433.1818	2433.2360	-0.0542	0	13	5.3e+002	1	QEAFAQSRRNLSDDLVAADS
✓	905	779.1599	3112.6104	3112.5360	0.0744	0	13	5.1e+002	1	EALSTATHVQSLQGLQKKNVERKMSQL + Oxidation (M)
✓	769	655.0656	2616.2333	2616.2312	0.0021	0	13	4.5e+002	1	TCNNVSAGLSAQLGQEPILFCSLHD
✓	910	779.1694	3112.6443	3112.6089	0.0354	0	13	4.6e+002	1	QMLQMLLESSRKLPLPSKYVTGVPH + Oxidation (M)
✓	906	779.1636	3112.6253	3112.6222	0.0032	0	13	5e+002	1	CRLVHFEPHPRSRSSQKKAIVRTK + Oxidation (M)
✓	69	484.2454	1449.7144	1449.6864	0.0281	0	13	1.8e+003	1	GAGFTFHAMLCLO
✓	366	489.5729	1465.6970	1465.6979	-0.0009	0	13	5.8e+002	1	KMGSDKPKIMINE + Oxidation (M)
✓	558	613.3131	1836.9176	1836.9525	-0.0348	0	13	5.9e+002	1	SFALFMVINIIFYTA + Oxidation (M)
✓	1127	991.5292	3962.0875	3961.9982	0.0893	0	13	4.5e+002	1	GASLFFPLNKELEKDLIDRHGEVTPEDVLSAAMP + Oxidation (M)
✓	843	714.3668	2853.4379	2853.3875	0.0504	0	13	5.9e+002	1	QMLGGPGGYPFERDDHROGRQVISTM + Oxidation (M)
✓	711	774.3725	2320.0957	2320.0788	0.0169	0	12	5.1e+002	1	QASGVLLCCDRVDNATRVQD
✓	590	638.0079	1911.0019	1910.9408	0.0611	0	12	5.8e+002	1	QTSDVSGYICLVKNAYTN
✓	273	443.2592	1326.7557	1326.7143	0.0414	0	12	4.5e+002	1	BANGITIKLQSP
✓	525	591.3214	1770.9423	1770.9305	0.0118	0	12	5.8e+002	1	YQLLAHPNFTERTIP
✓	589	638.0066	1910.9980	1910.9780	0.0200	0	12	6e+002	1	LRQVAAAVMIVASLCFQVV + Oxidation (M)
✓	873	997.4704	2989.3893	2989.4381	-0.0488	0	12	4.2e+002	1	SPSGLMKKSISLEAVSGAGCEMLPCPIPS + Oxidation (M)
✓	1175	1120.3620	4477.4189	4477.3470	0.0719	0	12	3.3e+002	1	AESVPMIAVIGVAVGAVAPLVLMATIVAFCCARSQSTGGRPGI + 2 Oxidation (M)
✓	624	675.3415	2023.0027	2022.9746	0.0282	0	12	6.6e+002	1	ENPSLSVYPSNSVTSVSI
✓	1056	901.4910	3601.9350	3601.8942	0.0408	0	12	4.1e+002	1	KCPKVKDGRSLPSVMYIGHFLPKYPFKDKVTG
✓	751	629.8193	2515.2480	2515.2781	-0.0301	0	12	6.5e+002	1	QPSSSITRDQKFMALFYAVIT + Oxidation (M)
✓	847	714.3724	2853.4604	2853.4901	-0.0297	0	12	6.3e+002	1	RCTMDPVKMTVTPPTTRRYRHR
✓	875	752.3813	3005.4962	3005.5105	-0.0143	0	12	6.3e+002	1	KTHYFLVVICFLFSQMPGUGILTS + 2 Oxidation (M)
✓	788	686.8374	2743.3207	2743.3866	-0.0659	0	12	5.8e+002	1	KSSHISYKGCMTQVFFLIWVLGAE
✓	732	606.8171	2423.2391	2423.2267	0.0125	0	12	6.5e+002	1	PYSECQNAQIYRKVTSGIKFA
✓	508	865.4304	1728.8463	1728.8505	-0.0042	0	12	6.9e+002	1	QDASFCKLIHEGATPI
✓	878	755.1058	3016.3942	3016.4149	-0.0208	0	12	4.2e+002	1	SDFPDLDLVIGANDTVNSAAQEDPNSI
✓	1045	883.1761	3528.6754	3528.7381	-0.0627	0	12	5e+002	1	SKNSQMIFTFQNGCVATLRTSGTSPKIKYY + Oxidation (M)
✓	350	480.5689	1438.6850	1438.7276	-0.0426	0	12	6.6e+002	1	KKEARKKHQER
✓	1170	1098.8186	4391.2453	4391.2206	0.0247	0	12	6.2e+002	1	ESFLVLINDLLASGDIPDLFSDDEMDKIISGIRNEVRGLG + Oxidation (M)
✓	433	526.2700	1575.7883	1575.7966	-0.0083	0	12	7.4e+002	1	QELLAALQFCAGEAL
✓	653	699.9691	2096.8855	2096.9718	-0.0863	0	12	2.3e+002	1	NAGGKMKMKLENQSSLLS + 2 Oxidation (M)
✓	147	382.1854	1143.5344	1143.5271	0.0073	0	12	7.1e+002	1	VFPMTYSGNL + Oxidation (M)
✓	176	394.1759	1179.5059	1179.5078	-0.0019	0	12	5.3e+002	1	SLDSSNVTPNP + Oxidation (M)
✓	1060	901.5061	3601.9953	3601.8966	0.0987	0	12	2.6e+002	1	QMQQISAAASVWGNLAGNLGPPQYLALYLQLL
✓	1180	1137.6625	4546.6209	4546.5302	0.0907	0	12	55	1	DVALDTLAVQLLEPKELSPGNTVQVYAYKLGSALAGGGLLVLFPT
✓	956	822.1812	3284.6955	3284.6893	0.0063	0	12	6.4e+002	1	QLSINDLMTCTTVPKMATNPLSGGKLISLG + Oxidation (M)
✓	253	653.2247	1304.6249	1304.6758	-0.0409	0	12	8e+002	1	RSIGLKLAMAD + Oxidation (M)
✓	1080	927.9534	3707.7847	3707.8547	-0.0700	0	12	5.8e+002	1	KERIGYMKHFEVLKSLGQPPQELLKELMMA + 3 Oxidation (M)
✓	1052	901.4640	3601.8269	3601.8464	-0.0194	0	12	6.8e+002	1	QBGKVTFLCQATAQPPVTGYRWAKGGSFVLGAR
✓	586	478.2360	1908.9151	1908.8386	0.0765	0	12	6.8e+002	1	GYSEKCVNNYFGIGLD

✓	1093	951.9570	3803.7990	3803.7997	-0.0008	0	12	4.9e+002	1	EMRDTNESTNRVLYPSIFSPCLIGLATWQV + 2 Oxidation (M)
✓	192	607.3114	1212.6082	1212.5663	0.0420	0	12	2.2e+003	1	SPSYIGLSFQD
✓	1186	1184.3713	4733.4561	4733.5487	-0.0926	0	12	6e+002	1	CLFLVLGLFLYSAWKLHLLQWEDSKYDRGLGFLKLDLSDL
✓	900	1025.4839	3073.4299	3073.4525	-0.0226	0	12	4.7e+002	1	ALPSSCAPAGTQCLISGWGNTLNLTVSEPD
✓	535	594.6099	1780.8079	1780.8665	-0.0586	0	12	5.5e+002	1	TQELLMAREEKNPHL
✓	33	406.2291	810.4437	810.4599	-0.0162	0	12	6e+002	1	KEKAPPAA
✓	557	916.9043	1831.7941	1831.8424	-0.0483	0	12	3.9e+002	1	MEVHEESRQPTFRH
✓	179	394.8656	1181.5750	1181.5387	0.0364	0	12	7.4e+002	1	QICTPTFSAGSA
✓	649	523.2409	2088.9345	2088.8585	0.0760	0	12	4.6e+002	1	GMPGASAGANNMNTAAGVTAMGT + 3 Oxidation (M)
✓	431	525.9195	1574.7368	1574.7255	0.0113	0	11	7.3e+002	1	LKQREISCHPSCIAM + Oxidation (M)
✓	1132	993.0906	3968.3332	3968.2534	0.0797	0	11	39	1	KEGQTIKLSIGNITAKKGGASKPRASGTGGLGLLPPPPGGK
✓	1050	892.2550	3564.9907	3564.9926	-0.0019	0	11	2.5e+002	1	QEITDLKQFVLVSQPKRRRGPQGLTGPAPMLIP + Oxidation (M)
✓	1162	1076.8256	4303.2733	4303.2142	0.0591	0	11	5.5e+002	1	QHPNVLCQLGVCEVETLFFLLIMEFCQGLDLKRYLRAQ + Oxidation (M)
✓	1218	1315.8839	5259.5065	5259.4475	0.0590	0	11	4.9e+002	1	GGMTGFHMQTEDRTMKSVNDQPSGNLPLFKPDDIQYFDKLLVDVDE + 2 Oxidation (M)
✓	393	506.9347	1517.7822	1517.8426	-0.0604	0	11	8.3e+002	1	KNPQTNLHILIAN
✓	1085	1248.3583	3742.0531	3742.0055	0.0476	0	11	3.4e+002	1	ADLLSAKDEEITKTFFEVNILGHFWIIKALLPSM
✓	1007	856.9563	3423.7962	3423.8112	-0.0150	0	11	6.4e+002	1	TGLRGLLFPASQIIPPTARETWLALLTIMDHT + Oxidation (M)
✓	821	949.1547	2844.4424	2844.5028	-0.0604	0	11	7.7e+002	1	GDAAKNQVAMNPTNTIPDAKRLIGRK + Oxidation (M)
✓	609	658.6503	1972.9290	1972.9677	-0.0387	0	11	7e+002	1	VMIQKSDAKWSEVSH
✓	1091	946.2171	3780.8392	3780.9293	-0.0901	0	11	6.8e+002	1	ASIRELAWNELERLGFISQVFTVPLINGMDSE
✓	833	714.3302	2853.2916	2853.3499	-0.0584	0	11	4.2e+002	1	KMLAGFIGSEENHGQLISFEACMTQL
✓	682	551.5764	2202.2767	2202.2062	0.0705	0	11	2.5e+002	1	SKKGPKAHFFSPQKRLQAP
✓	688	754.3945	2260.1618	2260.2487	-0.0869	0	11	7.9e+002	1	GAVPRSHHPPSPQKIMREPL
✓	917	779.1735	3112.6647	3112.6089	0.0558	0	11	5.8e+002	1	QMLQMLLESSLRKYLPELKYVGYTVFH + Oxidation (M)
✓	641	694.3509	2080.0309	2080.0953	-0.0643	0	11	8.3e+002	1	QPLQVLTNLNLEDEYRLH
✓	1187	1184.3739	4733.4665	4733.5487	-0.0822	0	11	6.7e+002	1	CLFLVLGLFLYSAWKLHLLQWEDSKYDRGLGFLKLDLSDL
✓	597	647.9671	1940.8795	1940.9666	-0.0872	0	11	5.9e+002	1	VLVPHPEVYVNGESQGT
✓	1174	1109.3692	4433.4477	4433.3713	0.0764	0	11	2.7e+002	1	KTVKGLDGGKHHRYVFTSSPQAREATLASSSEAGGR LTC
✓	1043	874.9381	3495.7233	3495.7959	-0.0726	0	11	7.9e+002	1	ITLQNDTGSRYKRIPLSEILCLPAPKAP
✓	1195	1217.6204	4866.4525	4866.3625	0.0900	0	11	7.9e+002	1	QPDGAGGGGSSPSPAPATSPVFPSPSPVPTPASPGPATLDFTSQFGAALVGAA
✓	1217	1276.1376	5100.5213	5100.4569	0.0644	0	11	7.5e+002	1	DEAAADSRRTYSLADYKSTFRVKSYSLSLWVSDFEYLYKQEN
✓	758	850.3989	2548.1748	2548.1621	0.0127	0	11	5.9e+002	1	DVVVADCESSPSFRFTYFVSLAF
✓	1167	1091.5099	4362.0105	4361.9257	0.0848	0	11	3.8e+002	1	CPSSPSCSVTASTENLVDPDYWDGNSRDLGDFFEVESEL
✓	302	455.5855	1363.7346	1363.7864	-0.0517	0	11	8.1e+002	1	LLPLFLKDAITH
✓	911	779.1689	3112.6466	3112.5762	0.0704	0	11	6.9e+002	1	QNPQTQNMAGQDKELPAGGKAVNTAPVG
✓	930	779.2041	3112.7871	3112.7760	0.0111	0	11	1.8e+002	1	KPFLSEDTRRKIVVLGNSWKEGLKL
✓	1095	952.0012	3803.9757	3803.9273	0.0484	0	11	7.5e+002	1	TNPNYGATGQCELPENLKINFSVAMMVDPDRII + Oxidation (M)
✓	679	732.0578	2193.1516	2193.1688	-0.0171	0	11	8.1e+002	1	GVSKYSIQNLSREARLKN
✓	599	650.3456	1948.0148	1948.0265	-0.0117	0	11	8.8e+002	1	LETQGINLEGTALTRYQ
✓	779	666.8326	2663.3014	2663.3510	-0.0496	0	11	9.5e+002	1	TADVVMMLDATKGDDVQSRLEKE + Oxidation (M)
✓	379	499.9151	1496.7233	1496.7695	-0.0462	0	11	9.1e+002	1	REGENRAGASPALAV
✓	703	574.5516	2294.1772	2294.1762	0.0010	0	11	8.8e+002	1	PSNMSKYQSNPFVNLISKL + Oxidation (M)
✓	631	683.3162	2046.9267	2047.0044	-0.0777	0	11	6.2e+002	1	EHMISPIAVQDPDATAAAAAA + Oxidation (M)
✓	850	717.6082	2866.4037	2866.4465	-0.0428	0	11	8.6e+002	1	QFMKNLKEEVTCPCLNLQVVKPVA + 2 Oxidation (M)
✓	1115	977.0173	3904.0401	3904.0252	0.0149	0	11	7.5e+002	1	KEITITKANGETSVGTVRIWNETVNLTLMLGSSAP + Oxidation (M)
✓	564	462.7174	1846.8404	1846.8809	-0.0405	0	11	7.1e+002	1	YQQSLQELAIQQQQQQ
✓	480	558.9576	1673.8511	1673.7977	0.0533	0	11	9.9e+002	1	QEVTRMLCKKHON + Oxidation (M)
✓	855	967.1457	2898.4152	2898.4110	0.0043	0	11	8.6e+002	1	AGEYIPTVFUNYSANVMVDGKPVNLG + Oxidation (M)
✓	829	714.3210	2853.2551	2853.3499	-0.0949	0	11	3.4e+002	1	KMLAGFIGSEENHGQLISFEACMTQL
✓	920	779.1755	3112.6730	3112.7471	-0.0741	0	10	6.6e+002	1	ALALFQNSLVIVVYTRSKAMRTVTNIFI + Oxidation (M)
✓	1015	856.9833	3423.9039	3423.8840	0.0200	0	10	3.6e+002	1	QDKMTSLFTYLIVPLNPLIYSLRNKDKV + Oxidation (M)
✓	1189	1184.4138	4733.6261	4733.6153	0.0108	0	10	2.5e+002	1	RITTEKMLQKEVEKLFNFTFLRLKLNLTNKKLVEIES + Oxidation (M)
✓	598	486.2514	1940.9765	1940.9599	0.0166	0	10	1e+003	1	EKANSVIIMQRTQRCNS
✓	643	695.0365	2082.0876	2082.0013	0.0863	0	10	9.3e+002	1	QILHIIYPPSSQLGEMSL + Oxidation (M)
✓	931	1038.8536	3113.5390	3113.5047	0.0343	0	10	9.4e+002	1	KGGTTSKGDANQEMNSLAYSNLGVKDRK + Oxidation (M)
✓	97	523.2621	1044.5097	1044.5240	-0.0143	0	10	1.2e+003	1	QGVPLFSYQY
✓	1004	856.9156	3423.6331	3423.7020	-0.0689	0	10	7.8e+002	1	QKRNMGELEMLVLESTAKENRRMRLLQ + 3 Oxidation (M)
✓	969	826.4567	3301.7976	3301.7758	0.0218	0	10	5.6e+002	1	RTSVRGQFQFSRLLCVVHQIPGLDVLGY
✓	335	355.6975	1418.7611	1418.7406	0.0205	0	10	9.8e+002	1	QPVYATIGSGIVNT
✓	1070	915.6986	3658.7652	3658.8182	-0.0530	0	10	8.3e+002	1	AGNEEFDQAIRAVPDGHTFKGFPFHFVYRNA
✓	123	367.8886	1100.6440	1100.6342	0.0098	0	10	8.1e+002	1	QVSYLKVHK
✓	944	804.4083	3213.6040	3213.5686	0.0355	0	10	9.8e+002	1	LATEVDMCFNYAKKNVQNNLSDLIV
✓	1191	1200.6043	4798.3881	4798.3912	-0.0031	0	10	9.2e+002	1	LFTDLNQAATASKLLWSSRGAKLSPPAAEQPEEMYNQNALSSQ + Oxidation (M)
✓	458	815.9045	1629.7944	1629.8587	-0.0643	0	10	1.1e+003	1	SVGGVGRSHKPTAPSP
✓	715	585.2880	2337.1230	2337.1708	-0.0479	0	10	9.3e+002	1	ADEMGLGKTLQITSLGYMKH + 2 Oxidation (M)
✓	957	823.1811	3288.6953	3288.7903	-0.0949	0	10	9.3e+002	1	KDTGLNLPVGGGLQETSTARTVKTQAVSRV
✓	909	779.1677	3112.6418	3112.5723	0.0694	0	10	8.4e+002	1	PSVITLPSRRKRTQAEHSSHYSLGMSA + Oxidation (M)
✓	150	384.8596	1151.5569	1151.6451	-0.0883	0	10	1.1e+003	1	KVPAHFVALNG
✓	646	696.3220	2085.9441	2085.9877	-0.0436	0	10	6.9e+002	1	PKLEGMAFHCHKDPVPQ + Oxidation (M)
✓	753	631.3305	2521.2927	2521.2529	0.0398	0	10	1e+003	1	QVARLMEMGFSGDAELASRN
✓	727	602.8042	2407.1877	2407.1988	-0.0111	0	10	1e+003	1	THRQLTSVMELRSLQTMF + Oxidation (M)
✓	1119	987.2004	3944.7726	3944.8066	-0.0341	0	10	3.4e+002	1	TVDATSQIHCIEDFHRKFPAPRCVCGGAIMPEPGQE + Oxidation (M)
✓	867	732.8647	2927.4299	2927.4846	-0.0548	0	10	9.8e+002	1	MIPPTSKTFLVNNLASGTMYDLCLVLA + Oxidation (M)
✓	914	779.1709	3112.6544	3112.5964	0.0580	0	10	8e+002	1	RPDCVPLFGGGRKLFWSAVPLCPGHALAG
✓	811	708.6066	2830.3974	2830.4270	-0.0297	0	10	1e+003	1	KSSLGPGVGLDKMLVDDIGDVTITNDGAT
✓	255	436.5386	1306.5940	1306.5825	0.0115	0	10	9.9e+002	1	DMDHVIIVIIY + 2 Oxidation (M)
✓	941	795.9076	3179.6015	3179.6720	-0.0705	0	10	1e+003	1	SGVIOBALANRNLKQDIARQKSSLEATH
✓	1092	951.2565	3800.9967	3800.9449	0.0518	0	10	8.4e+002	1	ALVSSLANEHQICLLQWAAQKKDSLQCLCLMTI + Oxidation (M)
✓	913	779.1702	3112.6516	3112.5974	0.0542	0	10	8.3e+002	1	TVATQTGASVTSSTRGTSPTRGTAPGARSSPPR
✓	92	517.2741	1032.5336	1032.5274	0.0062	0	10	1.3e+003	1	VDIRVDGLM + Oxidation (M)
✓	1032	863.4360	3449.7147	3449.7323	-0.0176	0	10	1e+003	1	PAMGVGILSSAPPEAQGNATPMVIKADSTPVRA + Oxidation (M)

✓	974	826.4731	3301.8631	3301.8288	0.0344	0	10	3.1e+002	1	KAEVMADTAVLASGNVSLVSSKVI GRMCKII
✓	588	637.6207	1909.8403	1909.7822	0.0581	0	10	6.3e+002	1	IDVSAADSGQMBQHEYM
✓	985	829.9305	3315.6929	3315.7140	-0.0211	0	10	1e+003	1	QWGGLLREALTDADDGLQPPVLDLVKVA
✓	1172	1101.5621	4402.2193	4402.3042	-0.0849	0	10	1e+003	1	NEPSIRMFQKLHFKQVAMSNVQEVTLRLAVSEPERK + Oxidation (M)
✓	1097	952.0287	3804.0856	3804.0389	0.0467	0	10	4.8e+002	1	QMLKKREBQGRLLPPGAGLEPKSAQDKALLQWVE + Oxidation (M)
✓	705	767.7606	2300.2599	2300.2124	0.0475	0	10	7.6e+002	1	TEVTPAYQGRDSEKATQVPKP
✓	143	380.2244	1137.4513	1137.6506	0.0007	0	10	7.7e+002	1	SAKTKPHIKE
✓	526	446.2346	1780.9091	1780.8414	0.0678	0	10	1.1e+003	1	EDNLTSLGAMNPAGRSV
✓	1224	1386.4241	5541.6673	5541.6452	0.0221	0	10	7.8e+002	1	QHLSTSLMQLLDSELKQISMGAQQPNLDVQICELFASSEPVPGQGD + 2
✓	942	801.6221	3202.4592	3202.4807	-0.0215	0	10	5.8e+002	1	KEDAKVKLCKMFCGDSFDSLQDLVHMI + Oxidation (M)
✓	1212	1251.3182	5001.2437	5001.2954	-0.0517	0	10	2.6e+002	1	MLTDPDLQFERFMSKRSPASPYGETDGEVAMVTSRQKVEEES + Oxidation (M)
✓	106	534.2606	1066.5067	1066.5369	-0.0302	0	10	1.2e+003	1	AIALLMPTFG + Oxidation (M)
✓	400	506.9380	1517.7921	1517.6933	0.0989	0	10	1.2e+003	1	SERTNIEFWVCAN
✓	662	530.5040	2117.9869	2117.9506	0.0363	0	10	9.4e+002	1	MSLSLSFGSGLMIVVGFACM + 2 Oxidation (M)
✓	58	473.7689	1891.0465	1891.0163	0.0302	0	10	2.1e+003	1	QAEVKRLKEQLSQFTS
✓	866	732.8646	2927.4293	2927.4957	-0.0663	0	10	1.1e+003	1	SPLPPVPVPPPPPLSPPPYPAPKQESF
✓	1117	987.1991	3944.7673	3944.8174	-0.0500	0	10	3.6e+002	1	AGHYMLQGASSMLPMALAPQHEHRLDMCCAPGGK + 2 Oxidation (M)
✓	755	636.3680	2541.4429	2541.3587	0.0842	0	10	4.4e+002	1	PTTQTLMLPSGLTSLGSLVVVIC
✓	414	776.4324	1550.8502	1550.7684	0.0818	0	10	9.4e+002	1	QMLLDSLEKQISM + Oxidation (M)
✓	1124	1000.7012	3998.7757	3998.8460	-0.0703	0	10	3.1e+002	1	LETCSQLSAGSHRSHLPSHESAGRECRTPPPGGTSGGGAQS
✓	1012	856.9772	3423.8796	3423.9336	-0.0540	0	9	5.7e+002	1	IVLFGARLNLWHLNPLPPRYQADVKFIQI
✓	807	708.3541	2829.3873	2829.4120	-0.0247	0	9	1.2e+003	1	DMNETHPLSQLHSGPGLLQWGLQTL + Oxidation (M)
✓	554	455.2606	1817.0133	1816.9373	0.0760	0	9	8.3e+002	1	DGFQKPPHFKSNFR
✓	1040	873.4040	3489.5870	3489.5765	0.0105	0	9	5.6e+002	1	HQNNHVGKSYACTDCGGEVFCYKSHLTLHQ
✓	768	872.4381	2614.2926	2614.2270	0.0656	0	9	1.2e+003	1	LVPCLAQFSVAMADDMMKPLNY + Oxidation (M)
✓	841	714.3591	2853.4073	2853.3776	0.0296	0	9	1.2e+003	1	PSSQPSVVGAGFPMDLGELVGMTPETIQ + Oxidation (M)
✓	661	706.9763	2117.9071	2117.8671	0.0400	0	9	4.8e+002	1	QNDVQDQGYPMFDCVVTG + Oxidation (M)
✓	824	714.3370	2853.3190	2853.3500	-0.0310	0	9	8.1e+002	1	KMIVMASHMQEVEGVDGTFNVLVFPAG + Oxidation (M)
✓	728	804.0362	2409.0868	2409.0803	0.0065	0	9	7.2e+002	1	KNPPQMDDLWLWVEFCGAGSV + Oxidation (M)
✓	233	635.3407	1268.6669	1268.6547	0.0122	0	9	1.2e+003	1	DQPMKPLDRAV
✓	902	779.1352	3112.5117	3112.6049	-0.0933	0	9	1.1e+003	1	QMLFSNFLDQPVNCCVLLVEGSGLLRGSL
✓	666	536.7785	2143.0848	2143.0505	0.0343	0	9	1.3e+003	1	BTGGKSAAGAVEGRATSPVA
✓	587	637.3131	1908.9174	1909.0057	-0.0884	0	9	1.2e+003	1	HSYLERLLNVEVFQNV
✓	652	524.5106	2094.0133	2094.0382	-0.0249	0	9	1.2e+003	1	HKEVALDAPSPDRTPFVSF
✓	1163	1076.8310	4303.2949	4303.2724	0.0225	0	9	8e+002	1	LFPNWDVITLMLRGLGKHAMLSSGLWGGGLMVLLAATLIS + 2 Oxidation
✓	632	684.3671	2050.0795	2050.0483	0.0311	0	9	1.2e+003	1	SQRGSATYLVVPGNPKFY
✓	605	657.9966	1970.9679	1970.9958	-0.0279	0	9	1.3e+003	1	MMAPTELELQHALQIGPT
✓	876	754.1762	3012.6755	3012.6178	0.0577	0	9	5.5e+002	1	LEVVAITPVARYPPIVASMTADSKAQRQ + Oxidation (M)
✓	721	606.7908	2423.1340	2423.2294	-0.0954	0	9	1e+003	1	EVDLSNIFLEGIAILNIPSYG + Oxidation (M)
✓	991	843.4175	3369.6411	3369.7187	-0.0776	0	9	1.2e+003	1	KPGKVGPELCTTWRVVLSSGGIGEGHRQRA
✓	1176	1120.3755	4477.4729	4477.3946	0.0783	0	9	4.1e+002	1	MLMMAVQSVLQKLQQRRTRELVSQGMPPLESAPAFH + Oxidation (M)
✓	1221	1343.0816	5368.2973	5368.3403	-0.0430	0	9	93	1	FEYLMRLEKESYFESHNGKDPNALVDEDAVCCICNDGECQNSNVL
✓	1055	901.4838	3601.9062	3601.9298	-0.0237	0	9	9.9e+002	1	KQLRMETDKKEVKELCAPSRQLWKFIPQMTL + Oxidation (M)
✓	805	943.8015	2828.3825	2828.4066	-0.0241	0	9	1.3e+003	1	SSSRFGQGGPDGNHQAAPKGVWVRK
✓	949	1083.8141	3248.4205	3248.4440	-0.0236	0	9	3.7e+002	1	AEAPTGRKVAEDDDDDVTKKQTERED
✓	916	779.1728	3112.6621	3112.6563	0.0058	0	9	1e+003	1	NLPPFLLRQNMMAASNIGISHSRLQTQI + Oxidation (M)
✓	523	593.2799	1776.8178	1776.8988	-0.0810	0	9	1.2e+003	1	QRMNLISGSLFFW
✓	994	845.6829	3378.7023	3378.6635	0.0388	0	9	1.3e+003	1	DVLGSMQVMNKRTRIMEQGAHPINAFVT
✓	1169	1091.5490	4362.1669	4362.1396	0.0273	0	9	1.3e+003	1	ESPLVQVMDNRGLVSLCCCKLIQWAMSYTHRKL + Oxidation (M)
✓	686	744.6734	2230.9984	2231.0706	-0.0722	0	9	8.1e+002	1	KEPLRLALEENSQEFQD
✓	1054	901.4804	3601.8923	3601.8484	0.0439	0	9	1.1e+003	1	GKAFSLPEVKASMKVQAPQVSSPTASMSLINPNAT + Oxidation (M)
✓	908	779.1659	3112.6344	3112.6730	-0.0386	0	9	1.2e+003	1	TVSLEBQPLKPLVMWTTITLNLATSLALQ + Oxidation (M)
✓	1210	1244.3364	4973.3165	4973.3330	-0.0165	0	9	6.6e+002	1	KEPABADINELCRDMFSMATYLTGELTATSEDYKLENNMKL + 3 Oxidation (M)
✓	1140	1010.6844	4038.7085	4038.7488	-0.0403	0	9	1.4e+002	1	PSVNMMSGTGDGTFSCPTSLNSMQISGMSPLQYIMP + Oxidation (M)
✓	676	546.0427	2180.1415	2180.2101	-0.0686	0	9	1.3e+003	1	KMMKTSQPKYLIYPLVP + Oxidation (M)
✓	1235	1526.4746	6101.8693	6101.8610	0.0083	0	9	6.5e+002	1	LKFDYTIYFCHSCQNYLPSVEFVSPTSHRVYCRHCINLENLTQRRESF
✓	1181	1139.7054	4554.7925	4554.8496	-0.0571	0	9	29	1	QNGAPRPGPGPDSDSDSDEEGEREEDQRNQREDEGN
✓	892	764.2018	3052.7779	3052.7518	0.0262	0	9	2.1e+002	1	KLSGSKLMIRHILQKLQPHQPSCLGL
✓	1200	1223.7924	4891.1405	4891.1696	-0.0291	0	9	2e+002	1	NIASQADVQRFMMASMEPLWEPMEHQGESNTFFSPDSNSLKL + Oxidation (M)
✓	287	654.3112	1306.6078	1306.7067	-0.0990	0	9	1.5e+003	1	KPDTRFQMKIV + Oxidation (M)
✓	1025	857.0066	3423.9973	3423.9248	0.0724	0	9	1.6e+002	1	KMLAKALRVNTRLSVINDRNNTSALGLD
✓	1183	1160.9471	4639.7593	4639.8448	-0.0855	0	9	35	1	REGEGEREDEDEGELEKKKGDIETEEEEEEEGEGEDER
✓	1208	1239.1293	4952.4881	4952.5365	-0.0484	0	9	1.3e+003	1	ARLEINVLRKIKKEDKENKFLCVLMSDWFNPHGHMCIAPEL
✓	1227	1399.3629	5593.4225	5593.4975	-0.0750	0	9	1.2e+002	1	SRLPVFQFDNQGYFNSCTMKSCCFAGDRDQYILSGSDDFNLYMKIPA + Oxidation (M)
✓	292	668.0973	2668.3601	2668.3725	-0.0124	0	9	1.5e+003	1	DRYIAICKPLHYLTIMSLRMC + Oxidation (M)
✓	903	779.1471	3112.5593	3112.5047	0.0546	0	9	1.5e+003	1	KMLVDMGPKNKSIPFWGCAVQFFISCT + Oxidation (M)
✓	434	526.2744	1575.8015	1575.7021	0.0994	0	9	1.6e+003	1	ISFMHMGPPNSTTS + 2 Oxidation (M)
✓	1193	1207.6183	4826.4441	4826.5124	-0.0683	0	9	1.4e+003	1	DLGETQSRITVTTRVTATVDVTGREGVKDIDITSPEFMKI + Oxidation (M)
✓	613	501.4866	2001.9175	2001.9069	0.0106	0	9	1.1e+003	1	THETAIVYRSPFEGFDPE
✓	937	789.9797	3155.8897	3155.7985	0.0912	0	9	82	1	SEVLFIVLGATSITTFILIVVSSYLILIT
✓	1216	1276.1251	5100.4713	5100.5297	-0.0584	0	9	1.1e+003	1	HEMPEIYLKLQVGSNSAVLEYCGRSLQARHLDRSPGVWRPE + Oxidation (M)
✓	479	558.9545	1673.8417	1673.8373	0.0044	0	8	1.6e+003	1	VNLQQQLFQKEQEN
✓	1021	856.9926	3423.9411	3423.9486	-0.0075	0	8	3.6e+002	1	EKKTLNSLLRMAIQKALATQLELELD + Oxidation (M)
✓	607	493.9904	1971.9325	1971.8810	0.0515	0	8	1.4e+003	1	QPPFAPGFSTMAASGEGGASTE
✓	1088	939.2477	3752.9615	3752.9739	-0.0124	0	8	1.3e+003	1	GLLMRLKQKYQKAARKTGSSEHAVALCSMVPSLA + Oxidation (M)
✓	234	635.8026	1269.5907	1269.6313	-0.0407	0	8	2.5e+003	1	AAAGGEGVRGVETP
✓	1123	991.4738	3961.8659	3961.9111	-0.0452	0	8	9.8e+002	1	QGECAVATVMCEKTKNNGEFSVAYEGKNKVLLETD + Oxidation (M)
✓	1011	856.9766	3423.8773	3423.8112	0.0661	0	8	7.5e+002	1	TGLRGFLLPASQIIPTAETETWALLTIMDHT + Oxidation (M)
✓	863	730.6446	2918.5494	2918.5324	0.0170	0	8	1.2e+003	1	TVYQKTIQKKTIACIESHQFPQT
✓	849	953.2171	2856.6294	2856.5684	0.0611	0	8	4.4e+002	1	KKDQVQAMHKVPVSDLPNLLFLDHALK
✓	970	826.4568	3301.7981	3301.8697	-0.0715	0	8	8.7e+002	1	KKMEGGARKLVRIALDSQVPPPIGLGLT

1160	1073.2701	4289.0513	4289.1062	-0.0550	0	8	1.1e+003	1	TKESACVKDYDLERGDEKPEDEPLHLDLENVPQSLPW
789	689.5490	2754.1690	2754.1169	0.0501	0	8	3.5e+002	1	AGVNRQFAISEATLMAWSMDGEDM + 3 Oxidation (M)
868	976.8279	2927.4619	2927.3887	0.0731	0	8	1.6e+003	1	VITHMQRVAVVPGSSMLASTPEFY
418	779.9556	1557.8967	1557.8337	0.0630	0	8	9.7e+002	1	AGFLMALGALNGHLTK + Oxidation (M)
415	518.9525	1553.8356	1553.7872	0.0484	0	8	1.4e+003	1	QGFSKSDKKGPKTM + Oxidation (M)
933	783.0743	3128.2682	3128.1827	0.0855	0	8	1.3e+002	1	QHGGTCRGVGGYVCECPAGYAGDSCEDNI + Oxidation (M)
993	844.6992	3374.7676	3374.6996	0.0680	0	8	1.3e+003	1	KQMLVSMRAQSSPGLHMRKSVSIAVSTGASL + Oxidation (M)
371	491.2835	1470.8286	1470.8116	0.0170	0	8	1.2e+003	1	KSKLSLYKKTMS + Oxidation (M)
1024	856.9995	3423.9689	3424.0181	-0.0492	0	8	2.7e+002	1	NINSTGLSTQGLLIFAELISAVKRTLARLLVI
747	621.0666	2480.2374	2480.2983	-0.0609	0	8	1.6e+003	1	QSPGGLVSLLSNPSGTTKHTGRLS
1019	856.9865	3423.9169	3423.9250	-0.0081	0	8	5.3e+002	1	LVRELAWBGLKRLGMSIRLFAFLPVQGLMD
1207	1239.1243	4952.4681	4952.5415	-0.0734	0	8	1.5e+003	1	QBAEDASEKMSKDKVTKQLVQYIYKTSYDPDVLVMSKARN + 2 Oxidation (M)
802	705.7939	2819.1464	2819.2113	-0.0649	0	8	1.8e+002	1	QDDMAEKSGSETPDGFLSPGMDDISP + Oxidation (M)
1071	915.9889	3659.9264	3659.8587	0.0676	0	8	1.3e+003	1	LMRALQECNSTIFVKLIPMLPMIQNTKHL + 2 Oxidation (M)
1164	1076.8423	4303.3401	4303.3588	-0.0187	0	8	7.7e+002	1	YVLGYKQTKLMIRQGHAKLVILANSFCALRKSEIEYY + Oxidation (M)
1135	1005.7327	4018.9017	4018.9742	-0.0725	0	8	1.1e+003	1	SPAAPRPQPLMAQMATTAAGVAVGSVGHGLHAITGGPSSGG + 2 Oxidation (M)
1143	1035.4540	4137.7869	4137.8844	-0.0975	0	8	2.5e+002	1	DSNSGLDGTQCFRFRQSSGGRVSLHCLLDEPKD
1203	1223.8553	4891.3921	4891.4902	-0.0981	0	8	1.4e+003	1	NGNSDPRPGHIGIAVPDVTYACKRFEELGVFKVKKPDDGKMKGL + Oxidation (M)
1013	856.9778	3423.8822	3423.8238	0.0584	0	8	7.9e+002	1	ALNLSHALLMIAHTFQNVFIIESLHRGPPG
894	1018.7605	3053.2597	3053.3374	-0.0777	0	8	1.9e+002	1	GAQAWTPPAGSGDDALPEDAEAKGEAEVE
938	714.3407	2853.3336	2853.2619	0.0717	0	8	1.2e+003	1	TIASDCQDMAKELVPGNSSSSCLAQP + Oxidation (M)
354	481.9228	1442.7466	1442.6567	0.0899	0	8	1.8e+003	1	QKMTSLSSCMAQL + Oxidation (M)
879	1006.4756	3016.4050	3016.3955	0.0095	0	8	1.2e+003	1	EGKVQCHEVTEGFEKMPAAMPGLKLG
604	657.9964	1970.9672	1970.9628	0.0045	0	8	1.7e+003	1	KSGIILFMRGVNMFSTQ + 3 Oxidation (M)
1219	1315.8870	5259.5189	5259.5385	-0.0196	0	8	1.2e+003	1	PYTDVPSLSTSNKNIEVEPTVSQVQEGRGHNSYQNPYDLPKNSH
912	779.1700	3112.6508	3112.6300	0.0208	0	8	1.4e+003	1	LSLMEDKNLLMLKKKADKSTAFAPR
874	749.1148	2992.4302	2992.4083	0.0218	0	8	1.5e+003	1	EMKPEASGIGQKQKHDESVTEIESE + Oxidation (M)
840	714.3541	2853.3873	2853.3838	0.0034	0	8	1.6e+003	1	MRSCEHLIMVWINAFVMLTTQL + 2 Oxidation (M)
825	714.3071	2853.1992	2853.1139	0.0853	0	8	3.2e+002	1	DCIPVAMRCDGTFECEDHSDELNCP
964	824.9459	3295.7544	3295.6933	0.0611	0	8	1.3e+003	1	LATVLLTLRAWRKICPTGPCCTPAPHYAP
1048	891.3671	3561.4393	3561.5303	-0.0910	0	8	92	1	QNMPLNAPAGMGPVPMPTGNSGNEQPTQMTTNGPV + 4 Oxidation (M)
783	676.3319	2701.2985	2701.2217	0.0768	0	8	1.6e+003	1	KTRQTDPSIMNTNKEENLYDPR
693	569.3075	2273.2011	2273.1763	0.0248	0	8	1.6e+003	1	AQAAATEKELHQLKRAYAS
1230	1480.2426	5916.9413	5917.0117	-0.0705	0	8	1.6e+003	1	LGHNGAGKTTLSILSGLFPSSSGSASILGHVDVQTNMAAIRPHLGICPQYVNLFI
1022	856.9961	3423.9553	3423.9242	0.0311	0	8	3.7e+002	1	KEDWGSKEQLILPKTITAEVHPVPLRPKPS
120	549.7695	1097.5245	1097.4989	0.0256	0	8	1.8e+003	1	EEPPGGERVE
388	503.2432	1506.7079	1506.6443	0.0636	0	8	1.8e+003	1	KNQMDTLTMDAAH + 2 Oxidation (M)
791	692.8667	2767.4378	2767.3597	0.0781	0	8	1.7e+003	1	GBGVQNAKKGVGGAQNGQKKGEANQN
924	779.1826	3112.7015	3112.7217	-0.0202	0	8	1e+003	1	QKKLIDKIHTKTESKVRGRDRDL
919	779.1749	3112.6705	3112.6201	0.0504	0	8	1.3e+003	1	KMLKEMFFIEAGEIHTENRVIPHPAP + Oxidation (M)
926	779.1847	3112.7097	3112.6201	0.0896	0	8	9.5e+002	1	KMLKEMFFIEAGEIHTENRVIPHPAP + Oxidation (M)
1204	1223.8586	4891.4053	4891.4376	-0.0323	0	8	1.6e+003	1	ALVLVFNVYGGGKYWKHSHWGLTVADLVFPWFVFMST + 2 Oxidation (M)
1234	1519.4615	6073.8169	6073.7719	0.0450	0	8	6.7e+002	1	GPSSEAAQBGDAQYFYSQSVGVRLDKQSTVPPANDAWGDPVGTGTRCASGPQCH
483	839.4724	1676.9302	1676.9574	-0.0271	0	7	1.4e+003	1	QAVNIISQKQVAHLT
1039	873.3834	3489.5047	3489.5765	-0.0718	0	7	3.6e+002	1	RQRNVGKSTACTDCGEVYFCKSHLTLHQ
619	671.3290	2010.9652	2010.9243	0.0409	0	7	1.8e+003	1	KQGETTGHGSGSAGEASLQAP
704	576.0671	2300.2394	2300.2349	0.0045	0	7	1.5e+003	1	BETGKPREKARLVFQNSQK
987	836.6590	3342.6069	3342.6502	-0.0433	0	7	1.6e+003	1	KALPSPMKYMNWRALNHEAAQAQARANAA + Oxidation (M)
784	677.3607	2705.4139	2705.3960	0.0179	0	7	1.7e+003	1	RTVYYPQVHLGTISGAGVRPSTVT + Oxidation (M)
312	346.9561	1383.7953	1383.7874	0.0079	0	7	1.3e+003	1	AGGSVGGLLPLHPH
1061	901.5228	3602.0621	3602.0307	0.0314	0	7	3.3e+002	1	KISESAKQELIDFKTRVAAFRKNLVELAEL
698	763.3255	2286.9546	2287.0256	-0.0710	0	7	5e+002	1	QBEIDCVIGRHSPCMQDR + Oxidation (M)
1126	991.5217	3962.0575	3962.0677	-0.0101	0	7	1.7e+003	1	QBAPLVNILYSSSQNLNLSQGDPIQDQFLPKTLL
1211	1246.6058	4982.3941	4982.4398	-0.0457	0	7	1.4e+003	1	GABRGNLNGETIKSGTCLIFKGBGLRMLISRDLCNTMYVQFSL + 2 Oxidation (M)
929	779.1963	3112.7560	3112.7259	0.0301	0	7	6.3e+002	1	LAPKTLQPFPAIPQYSRNKWLMIQI
1100	952.0458	3804.1543	3804.1096	0.0446	0	7	4.1e+002	1	KMIASQMKELQRIKQSHWILRALDTIKAE
1084	936.2110	3740.8149	3740.7558	0.0591	0	7	1.7e+003	1	KDELLAERANVMQQLNPNYIVRMIGICEAESWM + 2 Oxidation (M)
1098	952.0317	3804.0979	3804.0028	0.0951	0	7	7.9e+002	1	AGPFENAKLPVIRVFKLMGYSVMSVCSVPVSVLG + 2 Oxidation (M)
836	714.3380	2853.3229	2853.2730	0.0500	0	7	1.4e+003	1	VEGSAHDFISGPPQGYDTEVGETGNQL
1094	951.9950	3803.9507	3803.9120	0.0387	0	7	1.9e+003	1	QABEITKMRNDPERQVREIAKYDKMKM + 2 Oxidation (M)
1018	856.9856	3423.9133	3423.8204	0.0929	0	7	7.1e+002	1	AGMLSMILRVFRDNRHTDTRPQKEAG
1161	1076.7944	4303.1485	4303.2174	-0.0689	0	7	1.9e+003	1	GTYNQNMIVDYKAPLNGSPSGSRVLTILEQIPGMVVV
778	666.8176	2663.2415	2663.1989	0.0426	0	7	1.5e+003	1	KHNMCQDTEEEKIRVDIMENQI + 2 Oxidation (M)
828	714.3185	2853.2449	2853.2646	-0.0197	0	7	6.8e+002	1	PPCSDLLMESYHEDIEDFKTLQI + Oxidation (M)
49	451.2527	900.4909	900.4301	0.0608	0	7	2.5e+003	1	PGGEAESVR
1096	952.0152	3804.0316	3803.9628	0.0688	0	7	1.4e+003	1	ENNHLDVAVKLIKAGAQVDPKDAEGSTCLHLAAKKG
1158	1070.9901	4279.9313	4279.9101	0.0212	0	7	6.8e+002	1	GEWGKPNQNHSSSDISGKGTGWSASASQSTPALQPGSEHM + Oxidation (M)
737	612.2531	2444.9834	2445.0689	-0.0854	0	7	2.7e+002	1	YQWSEAAAMERARQVSTKDC
1118	987.2002	3944.7717	3944.8585	-0.0868	0	7	7e+002	1	LCVYPSGMPALRHPANPCVFSLLMGLISNGYFSGVPM + 3 Oxidation (M)
1001	854.7332	3414.9038	3414.9126	-0.0088	0	7	7.6e+002	1	KPSVPSLLEKDVVLSDSFGTSIVFPQKKRLT
1114	974.1938	3892.7460	3892.8360	-0.0899	0	7	7e+002	1	GAPLSGSDYNNRLTIANTPVSADAGYECAMLES + Oxidation (M)
997	846.3290	3381.2868	3381.3620	-0.0752	0	7	42	1	ESVEAQVDSASAEATAPMDVDHEECGAEGSSV + Oxidation (M)
1214	1256.4396	5021.7253	5021.6623	0.0630	0	7	8.9e+002	1	KPLKCTVFPKAQVEDAFRYMAQKHIGKVLVQVREEPVLPGA + Oxidation (M)
899	506.9373	1517.7900	1517.8388	-0.0488	0	7	2.3e+003	1	FIQCKALKENINLN
1020	856.9871	3423.9193	3424.0088	-0.0895	0	7	6.9e+002	1	AKRKSKNIRKQRMKILPNVLEAREPGS
943	804.1189	3212.4464	3212.3966	0.0498	0	7	9.3e+002	1	QNPGRFGYHETQDATVERAASNSMSASHD
962	824.8920	3295.5387	3295.5159	0.0229	0	7	1.4e+003	1	KSKGPIDFETKRTYTNIEAKDGGQMASEC + 2 Oxidation (M)
955	822.1770	3284.6788	3284.6209	0.0579	0	7	2.1e+003	1	KEDLQVMKQNMNIPNIVLGPPEHDEVP
478	419.4670	1673.8387	1673.9101	-0.0714	0	7	2.4e+003	1	PQQKIQIVPQPPSSQ
401	506.9408	1517.8005	1517.7198	0.0808	0	7	2.3e+003	1	CKYDQGRVWLHN
1047	889.6963	3554.7562	3554.8167	-0.0605	0	7	2.1e+003	1	VHLPSCVTFSNFPVKKSTLSRVQTMDFSPR

✓	762	861.4353	2581.2842	2581.3249	-0.0407	0	5	3.2e+003	1	ASGIFVQSSEALQVVANVIHANGDR
✓	1232	1495.0924	5976.3405	5976.3851	-0.0446	0	5	4.4e+002	1	IPSGGPDATGHGLRFRSGAIRRRKLARERALLPGGGAAAAAARQGLLPTFTV
✓	1202	1223.8334	4891.3045	4891.3256	-0.0211	0	5	1.8e+003	1	QMRGSPFVPSGPPFEDGLRWTPKSPLDPSGLLSCTLPNGPGLSGP + 2 Oxidation
✓	1188	1184.4020	4733.5789	4733.5589	0.0200	0	5	1.3e+003	1	QPKFLGIREQVTVGLMIFILMGLSVFMTSVLKFIPMPVLYG + 4 Oxidation
✓	927	779.1851	3112.7113	3112.7879	-0.0766	0	5	1.6e+003	1	KMQQLNALHQVILQKRLLEDRLQ
✓	972	826.4633	3301.8239	3301.7751	0.0488	0	5	1.4e+003	1	GFTVTVKGVASLEAIPFVVAPHSTFFDGLA
✓	1083	932.0647	3724.2297	3724.3048	-0.0751	0	5	97	1	RDDDDDDDDDDDEAEDRGAWCSTYAFDGSQP
✓	1145	1042.9505	4167.7729	4167.7942	-0.0213	0	5	3.3e+002	1	SWFGSMFNPISLSEFELICSYIFMPPSPFMDGVWDQ + 2 Oxidation (M)
✓	45	445.1409	888.2672	888.3544	-0.0872	0	5	3.8e+002	1	VMITPGCC + Oxidation (M)
✓	1036	873.3374	3489.3206	3489.4073	-0.0867	0	5	47	1	SCEDNIDECAQPCQNGSGCIDLVARYLCSCPP
✓	1190	1185.1788	4736.6861	4736.5945	0.0916	0	5	4.1e+002	1	NERLLTARQALLQKARQSPPTLPFVGGGCPAPALTEMLLK + Oxidation
✓	651	523.2456	2088.9533	2088.8985	0.0548	0	5	2.4e+003	1	DHEAPPGHEAGSSSQLLDLA
✓	1127	1008.4926	4029.9413	4029.8780	0.0633	0	5	2.6e+003	1	RPISSEBQVQSYMHEHCNNSTHRRILIMFMDIC + Oxidation (M)
✓	793	926.4554	2776.3443	2776.2747	0.0695	0	5	3e+003	1	AALVTSIHETNSNQDTSATSGNSIQS
✓	887	762.9754	3047.8725	3047.8420	0.0305	0	5	78	1	KKKGRGKRVGLKFRFGGSKRKKGSSS
✓	1113	967.1544	3864.5884	3864.6274	-0.0390	0	5	2.1e+002	1	DENDSIIIESDELDENMLKLELNSDMVEP + 2 Oxidation (M)
✓	1206	1236.8060	4943.1949	4943.2709	-0.0760	0	5	6.3e+002	1	QHCNLLCLFENYQMKYFFPHGLSWPQLSYIAEDEDKIVGY + Oxidation
✓	1000	852.0975	3404.3609	3404.4396	-0.0787	0	5	1.6e+002	1	DFHEEVTPKSVSTPSVDLSQDGDQEGMDTTQ + 2 Oxidation (M)
✓	392	506.9324	1517.7755	1517.7766	-0.0011	0	5	3.7e+003	1	YTPYISSVFKVN
✓	1076	923.8043	3691.1883	3691.0944	0.0938	0	5	1.7e+002	1	CLVARPPSQKVRPPFPADSVTRRVTTNVRGVL
✓	858	727.9403	2907.7322	2907.6561	0.0761	0	5	3e+002	1	AVLLFYPIIGLIGATHRFQKHLSPVV + Oxidation (M)
✓	986	835.0010	3335.9747	3335.8969	0.0779	0	5	2.5e+002	1	GAPDKRLKAEPAAPFVTPAAPALPVVKEIPAA
✓	1157	1070.9739	4279.8665	4279.9606	-0.0941	0	5	5.7e+002	1	ITDSAGHILYAKEDATKGFATTTEDYDMFEVCPESKG + Oxidation (M)
✓	928	779.1917	3112.7376	3112.6539	0.0837	0	5	1.4e+003	1	RGLACDFRGLVAYSAGCVVFLNPKKH
✓	339	356.1768	1420.6781	1420.7344	-0.0563	0	5	3.6e+003	1	QDGSSTKLIMV + Oxidation (M)
✓	475	419.4646	1673.8293	1673.8446	-0.0154	0	5	3.8e+003	1	LALAAAAHKLQCMY + Oxidation (M)
✓	1205	1232.5594	4926.2085	4926.1550	0.0535	0	5	8.1e+002	1	KEAFYKFEQSRASECECPGNMTHSRASCQMDDVIDDIISLES
✓	289	839.5659	3354.2344	3354.3035	-0.0691	0	5	36	1	QFELTEDECDSEKTSKSGSVEEDTSCSD
✓	1082	1241.0506	3720.1300	3720.0318	0.0982	0	5	5.5e+002	1	QITGSFVTAGVITKLPLPANSKIVANVPATQGM + 2 Oxidation (M)
✓	1105	952.0834	3804.3043	3804.2216	0.0827	0	5	65	1	SVDAVTLIFVLVAHPKMKRLVLLNVKVLKPGR
✓	695	569.3352	2273.3116	2273.2420	0.0697	0	5	1.2e+003	1	AAFQATLKSGSLPTVTWLEDN
✓	1067	911.3432	3641.3435	3641.2487	0.0947	0	5	30	1	TVVTAIVAGVALVLKLLNEKLHRLPLPIGEL
✓	743	620.8145	2479.2288	2479.2965	-0.0677	0	5	3.6e+003	1	LGVTTCASNNRLGTAVSRGARLSV
✓	1042	1164.4711	3490.3915	3490.4567	-0.0653	0	5	1.5e+002	1	RDNYSVLCCLKGTTPNCEINLDDCANPCDSDG
✓	832	714.3266	2853.2774	2853.2765	0.0009	0	5	1.7e+003	1	QMLLYSQVEGDYSCEEDLFLVF
✓	1075	923.7944	3691.1487	3691.0494	0.0993	0	4	3.6e+002	1	EALYVLLCDQVLGLRPLAAPERLSQALAVVS
✓	1184	1168.8232	4671.2637	4671.2955	-0.0318	0	4	3.1e+003	1	QGPLPGVQGPFGKGTQGEPPPGTGABGQPQEGPTQGLGTQGLPGQSP
✓	1149	1056.8047	4223.1897	4223.1792	0.0105	0	4	3.4e+003	1	DKDLHSVYGGSVHRAEMTDLISLMCLVKKKKILIPGIN
✓	448	806.0050	1609.9954	1609.9416	0.0538	0	4	7.2e+002	1	WIKPAKSRGRDI
✓	680	549.5335	2194.1049	2194.1845	-0.0795	0	4	4e+003	1	ALALDKVELANQQLLQEQE
✓	1133	1000.6797	3998.6897	3998.6884	0.0013	0	4	3.9e+002	1	SLYLVCXKSTXDSALTGRADGPLNTMSKYGFLOCXI + Oxidation (M)
✓	489	423.4665	1689.8371	1689.7749	0.0622	0	4	4.3e+003	1	TCQSPCLNGKCKIRPN
✓	800	704.0527	2812.1819	2812.1567	0.0252	0	4	7.5e+002	1	CSDCYDNANIYSTREYCPYTYI
✓	939	791.3777	3161.4818	3161.4701	0.0117	0	4	2.8e+003	1	HERWKEMVKKCKGALSCVNVHCDS + Oxidation (M)
✓	877	754.6237	3014.4655	3014.5389	-0.0734	0	4	3.7e+003	1	KQCANLQAIADAEQGEKALKDLARGLK + Oxidation (M)
✓	760	643.6342	2570.5079	2570.4328	0.0751	0	4	7.6e+002	1	LNLKLMCWELVPTLDDKVVSV + Oxidation (M)
✓	503	568.9699	1703.8878	1703.8770	0.0108	0	4	4.2e+003	1	KKYSIEEFTQKL
✓	726	803.2871	2406.8396	2406.9283	-0.0888	0	4	42	1	RNDTASNAEMSFTDVTME + Oxidation (M)
✓	1009	956.9607	3423.8137	3423.7570	0.0566	0	4	3.2e+003	1	QMSDLEMAHGLFPALFKEAIDGRYIKLIK + 2 Oxidation (M)
✓	975	826.4736	3301.8654	3301.7822	0.0832	0	4	1.2e+003	1	KQENVYLQYQRLNLQKPLSLKQEE
✓	246	808.7558	3230.9941	3230.9026	0.0915	0	4	64	1	RISMKLPRIPLRQKLKVVVAHDDL + Oxidation (M)
✓	808	708.5499	2830.1704	2830.2637	-0.0932	0	4	6e+002	1	CNLSLGEDCNVKSVEKENIATGYS
✓	971	826.4594	3301.8087	3301.7578	0.0509	0	4	2.2e+003	1	GAARWAEVAFARFARLGEQGRVVLITSGGT + Oxidation (M)
✓	897	1019.8382	3056.4928	3056.5019	-0.0091	0	4	4e+003	1	LVSITHFVLTYTEHTPLSDYFVFPED
✓	980	827.7084	3306.8047	3306.7744	0.0303	0	4	2.3e+003	1	KDKREKISPTDSLAKDLIVSALMLIQY + Oxidation (M)
✓	983	827.7288	3306.8863	3306.9099	-0.0236	0	4	9.4e+002	1	KPSKPERKVTESSEALKAEKKRLIKDVG
✓	925	779.1840	3112.7071	3112.7581	-0.0511	0	4	2.3e+003	1	TAILKKGLGARRAVSVPHDAPASTSRPQKT
✓	968	826.4542	3301.7879	3301.7459	0.0420	0	4	2.6e+003	1	QEISGYLSWLQKQPDGTVKRLIYAATSLH
✓	950	813.1608	3248.6139	3248.6620	-0.0482	0	4	4.3e+003	1	PVKKATVLYQGMKRVKIQEFKNGMMD + Oxidation (M)
✓	759	643.5069	2569.9987	2569.9859	0.0128	0	4	2.8e+002	1	SSNDPQDDHMCFFVPMNMDL + Oxidation (M)
✓	1063	907.6281	3626.4832	3626.5824	-0.0993	0	4	2.8e+002	1	NYSQDKCAGPNGANGDTVNATLMQPGINGPMGTNF + Oxidation (M)
✓	932	781.5875	3122.3210	3122.4181	-0.0971	0	4	7.6e+002	1	ESMPTQIISCGELPTPPSGHRIGTMSVY + 2 Oxidation (M)
✓	1144	1037.1844	4144.7085	4144.7897	-0.0812	0	4	2.5e+002	1	RCLLPSMNSCFLEVSVCFCVNMCMGSGIFPNFYVY + 2 Oxidation (M)
✓	1182	1141.7637	4563.0257	4563.0426	-0.0169	0	4	9.9e+002	1	QPLYDCPMGLVCTNYHILQEHVDLHLESSFQQQMDRV + Oxidation (M)
✓	806	708.2501	2828.9713	2829.0451	-0.0738	0	4	22	1	SFNCIDEPSRCYFHDGDMCEFE
✓	799	704.0527	2812.1818	2812.1567	0.0251	0	4	8.7e+002	1	CSDCYDNANIYSTREYCPYTYI
✓	1005	856.9296	3423.6894	3423.7003	-0.0108	0	4	4.3e+003	1	KRHSQGFVLQDYFVLTAANCTGSSMNVILGA
✓	1023	856.9979	3423.9627	3423.9711	-0.0084	0	4	8.3e+002	1	LEKDLRTQVELMRKQKERRKQLKLLQ + Oxidation (M)
✓	1002	854.7502	3414.9718	3414.9126	0.0591	0	4	6.7e+002	1	KPSFVSLLEKDVVLSDFSFTSIVFPQKRLT
✓	1166	1088.9253	4351.6721	4351.7322	-0.0601	0	4	79	1	AGRVQPTLPFEGASAPPEGMSDSDIECDTENESQEHNTSM + Oxidation
✓	322	473.9244	1418.7514	1418.7882	-0.0367	0	4	4.8e+003	1	VISAKVFDVDRATN
✓	635	517.2442	2064.9478	2065.0415	-0.0937	0	4	3.5e+003	1	EIMEAVSPGVIIQRWANH + Oxidation (M)
✓	1146	1043.6972	4170.7597	4170.8399	-0.0802	0	4	4.1e+002	1	GAEEGAEPQAQEEEEEEEAEPQPEBAQIAGLVYKK
✓	945	808.4677	3229.8417	3229.7528	0.0889	0	3	1.1e+003	1	LRDLIEMSIGITGLAYTLVSVCVLLRY + 2 Oxidation (M)
✓	1006	856.9551	3423.7911	3423.8298	-0.0387	0	3	4.1e+003	1	KMKLPKNTQTLTSGYKAPMDLSFIKLTPSQ
✓	1179	1137.6598	4546.6101	4546.5136	0.0965	0	3	4.4e+002	1	ELSFVAGAPRANHGAUVILRKDSASRLIPEVVLSSGERLTSGF
✓	772	877.2905	2628.8496	2628.7522	0.0974	0	3	14	1	KFMQVIFKLAKLKKKKKKKK
✓	818	709.6978	2834.7621	2834.6835	0.0786	0	3	1e+002	1	FLRQVAFGLGFIPICVLLLLLIM
✓	826	714.3111	2853.2151	2853.2765	-0.0614	0	3	1.1e+003	1	QMLLYSQVEGDYSCEEDLFLVF
✓	899	769.3637	3073.4257	3073.4307	-0.0050	0	3	3.3e+003	1	DSGGREHVEAIVSMTAVAWYINDMKR + Oxidation (M)
✓	810	708.5734	2830.2644	2830.2836	-0.0193	0	3	2.3e+003	1	AVMEERECTVERRAHITYSEFMQ + Oxidation (M)

✓	1086	936.5222	3742.0599	3742.0604	-0.0005	0	3	2.1e+003	1	HARFVGTDPASDEVVLMKILQVLRLTLTLPVGT + Oxidation (M)
✓	1116	987.1545	3944.5889	3944.6611	-0.0722	0	3	2e+002	1	WEERRPMTTARGWHSMLCSLGDSTYISGGSDHME + 3 Oxidation (M)
✓	1130	993.0469	3968.1584	3968.1631	-0.0047	0	3	2.6e+003	1	QKLVTLFYSVGTPLNFMITYSLRNKMKNALQKI + 2 Oxidation (M)
✓	383	501.2648	1500.7725	1500.7433	0.0292	0	3	5.7e+003	1	FENAHVRVRSADT
✓	1148	1046.6933	4182.7441	4182.6540	0.0901	0	3	3.5e+002	1	QNTPTSYSKCSCKPGYQGEGRQCEMDECDNTLNGGCVH + Oxidation (M)
✓	1209	1244.2929	4973.1425	4973.1671	-0.0246	0	3	5.1e+002	1	WMRQEETPEQDSNLKDQTNQVDGSQLPVNMOPHMSVMQPP + 4 Oxidation (M)
✓	733	811.5970	2431.7691	2431.8412	-0.0722	0	3	9.8	1	SSSSSSSSSSSTTTDESSSSSDEEA
✓	1069	912.5905	3646.3327	3646.4278	-0.0951	0	3	38	1	CEDVDCKQGNPCPQLCVNTKGGFECFCYDGY
✓	1152	1067.5484	4266.1645	4266.1269	0.0376	0	3	5e+003	1	SDFDPKLESTLLSQLPAYKHHMFMLTLPVTDSTID + Oxidation (M)
✓	532	444.9232	1775.6639	1775.7205	-0.0566	0	3	5.3e+002	1	CDLPETCSGSKFICPD
✓	610	498.2081	1988.8033	1988.8431	-0.0398	0	3	1.1e+003	1	IRVLCDDYSHCPTTTY
✓	4	307.0772	612.1398	612.1883	-0.0485	0	3	5.5e+002	1	DMNS + Oxidation (M)
✓	827	714.3159	2853.2344	2853.2765	-0.0421	0	3	1.6e+003	1	QMLLYSQVEGDSYSPCEDLFLVF
✓	840	795.7449	3178.9505	3178.8701	0.0803	0	3	1.1e+002	1	KITFLMILINGPSKLVLHKMVVNILKNS + Oxidation (M)
✓	1087	936.5518	3742.1783	3742.1158	0.0624	0	3	4.9e+002	1	AKFSKQHVPEEHKDKKDFVDRVKRLLKAGV
✓	813	709.5548	2834.1902	2834.1611	0.0291	0	3	1e+003	1	MMSTPLLGATASGGMSMPQMAPPTSGDM + 5 Oxidation (M)
✓	1199	1223.7567	4890.9977	4891.0874	-0.0897	0	3	1.8e+002	1	GDLSLMAPMGDSLMAFMGDSLMLALMGDSLMLALMGDSLMLAL + 6 Oxidation (M)
✓	1044	878.1860	3508.7150	3508.6476	0.0674	0	3	5.2e+003	1	KLQAFDWSSEKNYFHYNQSPPPSYNIKN
✓	148	573.2517	1144.4889	1144.5811	-0.0923	0	3	4.2e+003	1	NMKRQGWLP + Oxidation (M)
✓	1053	901.4769	3601.8783	3601.8484	0.0299	0	3	4.9e+003	1	GKAFSLPEVKASMKVQAPQVSSPTASMSILNPNAT + Oxidation (M)
✓	1074	922.0685	3684.2449	3684.1640	0.0809	0	3	91	1	VCVAASRVYKSKRNILGAGILFVAAGLSNIGVIV
✓	531	444.9095	1775.6089	1775.6107	-0.0018	0	3	1.6e+002	1	QDDADQDMQAGMASQ + 2 Oxidation (M)
✓	780	669.6701	2674.6513	2674.5933	0.0580	0	3	1.9e+002	1	SMSLAPRCILLFPLLLPLLLPL
✓	1196	1220.9582	4879.8037	4879.7544	0.0493	0	3	4.4e+002	1	IRRLREIRVKSAAKEEQTKSGKSEKKKPEKEKYDMKI
✓	1037	873.3721	3489.4594	3489.4919	-0.0325	0	3	6.2e+002	1	QDSPTSCKFRPQSGSACSLPCCCGRDSPEHSL
✓	1226	1394.0645	5572.2289	5572.2335	-0.0046	0	3	2.9e+002	1	NSQKITLAKPAQOTLTGLVSALTGLVNSLVPVNAKGPVKGSVATLKLGVSTP
✓	184	399.2118	1194.6135	1194.7084	-0.0949	0	3	6.1e+003	1	RLAPAVSPEKK
✓	824	714.2939	2853.1463	2853.1263	0.0200	0	3	4.9e+002	1	TSDDIDCYMIAEMTTGGNEGSGAQPSTS + Oxidation (M)
✓	814	709.5774	2834.2806	2834.3738	-0.0932	0	2	3.1e+003	1	QSPFGSALADFWMPVDLYIGGEHAV
✓	952	814.3416	3253.3373	3253.3950	-0.0577	0	2	5.6e+002	1	KNVRENGYCEKMYNSCAPACPVTCQHP
✓	1107	952.0871	3804.3195	3804.2203	0.0992	0	2	87	1	VTKAPVSVCVESVAPQPLPAPVGLTVTKVVPVTALPKL
✓	5	307.0778	612.1411	612.1883	-0.0473	0	2	6.5e+002	1	DMNS + Oxidation (M)
✓	1141	1011.1701	4040.6513	4040.7463	-0.0950	0	2	3.1e+002	1	PDEILVYVMEGGSHLEPRGAAGADPTTPQDPKDCSC + Oxidation (M)
✓	1028	857.0169	3424.0387	3424.0957	-0.0570	0	2	3.4e+002	1	KRFQALKNLGLLPLLVMLICYAGIIRI + Oxidation (M)
✓	1215	1260.2887	5037.1257	5037.2049	-0.0792	0	2	3.7e+002	1	EDKDMTQTLPSLEDMAMYISQEMDHDQPSKRLSRVYVQD + 4 Oxidation (M)
✓	936	789.9719	3155.8587	3155.7662	0.0925	0	2	6.3e+002	1	AKNSKTLSSGSASVVVKLSAAAVAMVIVPVPT + Oxidation (M)
✓	1089	1253.1878	3756.5416	3756.6413	-0.0997	0	2	4e+002	1	KPCDAKVINSCCMLHMLNGCHPWTQYFRG
✓	1090	943.0637	3768.2256	3768.2440	-0.0184	0	2	3.3e+002	1	TPMLNPLIYTLRNEKVKGAFKRLVTRILSRK
✓	579	630.9414	1889.8023	1889.8942	-0.0919	0	2	2.8e+003	1	SREGGGEVGDNCVWLLLS
✓	966	826.4526	3301.7813	3301.7578	0.0234	0	2	4.2e+003	1	GAARWAEVMAFPAARLGEQGRRVVLITSGGT + Oxidation (M)
✓	1065	911.3138	3641.2261	3641.1396	0.0865	0	2	94	1	VTEFVDLGNISALRTFRVLRAKLTITVPLGLKT
✓	967	826.4541	3301.7873	3301.8373	-0.0499	0	2	4.1e+003	1	IQKKAIRKQKRLNSCKVCQTAGVAARM + Oxidation (M)
✓	815	709.5861	2834.3155	2834.2970	0.0185	0	2	4.8e+003	1	QVASQASRGVEPNVAYGYVYMPSGAVY + Oxidation (M)
✓	890	762.9795	3047.8890	3047.8420	0.0469	0	2	1.2e+002	1	KKKGRGKRVAGLKFPGGSIKRRKGGSS
✓	134	564.1396	1126.2647	1126.3575	-0.0927	0	2	27	1	DVDDDDDDGF
✓	1198	1223.7391	4890.9273	4891.0226	-0.0953	0	2	1.7e+002	1	MQNSHMEERYNSDNGSTGNSSEVAVVHEPDPSTEIMNVTEMQ + 2 Oxidation (M)
✓	1038	873.3738	3489.4660	3489.5591	-0.0931	0	2	8.1e+002	1	QSAGSQGRGGGSGNFMGRGNFGGGGNFGRGNFGG
✓	1155	1070.9407	4279.7337	4279.7374	-0.0037	0	2	2.5e+002	1	QMLATSSMDSQMLASGAMDSQMLASGTMDAQMLASGTMDAQ + 5 Oxidation (M)
✓	1138	1008.6253	4030.4721	4030.5178	-0.0457	0	2	81	1	SLHNSSSGSETYCMFQNGNDLPSDPDQYDYDQDDYE + Oxidation (M)
✓	474	418.9740	1671.8668	1671.8468	0.0200	0	2	7.4e+003	1	PGQIQVGIQYGEDAV
✓	559	921.8064	1841.5982	1841.6801	-0.0819	0	2	80	1	ECQDNNGGQCQICVNM + Oxidation (M)
✓	959	823.2071	3288.7992	3288.7394	0.0597	0	2	3.7e+003	1	QPPYIGIFIQNKTEGINITIVDREVTFF
✓	1231	1495.0821	5976.2993	5976.3167	-0.0174	0	2	1.6e+003	1	GAAILGLVMAASDVEGLYAANKVLCVVSNNPLASKEMERIKGYQLLMLLKK
✓	978	827.6278	3306.4821	3306.5501	-0.0680	0	2	2.9e+003	1	QPSBAQSPASHPVASNQSKPEPAASAAVAHEQP
✓	1109	952.1053	3804.3922	3804.3485	0.0437	0	2	61	1	LSLILVLISLLLTVALLSHRRTLQKKIWPGPS
✓	507	432.4794	1725.8886	1725.8475	0.0411	0	1	7.8e+003	1	KPAPAGKQDSTWTWGP
✓	336	473.9303	1418.7690	1418.7895	-0.0204	0	1	7.1e+003	1	LKANVQEHPR
✓	851	719.7970	2875.1589	2875.1479	0.0110	0	1	6.6e+002	1	QPGCENDAIQDPDADMLDYLMMGQIS + 2 Oxidation (M)
✓	530	444.9081	1775.6031	1775.6107	-0.0075	0	1	1.8e+002	1	QDDADQDMQAGMASQ + 2 Oxidation (M)
✓	1103	952.0564	3804.1963	3804.1198	0.0766	0	1	9.1e+002	1	KMFAPMLSPBQTSIFRQRLIYSLLGKIPKE
✓	1108	952.0993	3804.3683	3804.3660	0.0023	0	1	66	1	QEDGDADPEPENYNDDDDDEEEETNMIPGS
✓	537	446.2500	1780.9707	1780.9166	0.0541	0	1	6.3e+003	1	QDDTASTSKTSKKKKE
✓	460	409.2199	1632.8505	1632.8691	-0.0187	0	1	8.4e+003	1	VSSLMKATVLMRQPG + Oxidation (M)
✓	761	643.9118	2571.6181	2571.5410	0.0771	0	1	1.4e+002	1	ALRVLSQFERMKVVLRLIKTT
✓	996	846.3147	3381.2295	3381.2191	0.0104	0	1	65	1	CDEEDEDEGEAADMEYERSGLLETDEAT
✓	706	576.2085	2300.8049	2300.8838	-0.0789	0	1	1.2e+002	1	SEDSSQFWDNSACVDPSCFI
✓	809	708.5715	2830.2567	2830.3454	-0.0887	0	1	3.5e+003	1	VDFCYSVCTPKMLMGFVSEKSIIS
✓	1129	992.9874	3967.9203	3968.0151	-0.0947	0	1	6.9e+003	1	FTGIETFMVLVAMAFDRYIAICNPLRYNTILTNR
✓	764	650.6238	2598.4661	2598.4857	-0.0196	0	1	3.4e+003	1	ATKRPSAGKFKSTVAPLETLDRL
✓	290	444.9179	1331.7318	1331.7482	-0.0165	0	1	8e+003	1	KGILPVKMKSE + Oxidation (M)
✓	767	653.4683	2609.8441	2609.8383	0.0058	0	1	21	1	CGECDTLMGEGCGLTMGEGCGLTM + 3 Oxidation (M)
✓	771	657.9261	2627.6753	2627.5962	0.0791	0	1	73	1	QTSKSKKKNKAPLSFKVGVGVKIVR
✓	1003	1141.1312	3420.3718	3420.4665	-0.0948	0	1	4.5e+002	1	ALAPTEGPFPMQAVGQPPSGNFCEMPCNGADCR + 2 Oxidation (M)
✓	445	402.2122	1604.8196	1604.8198	-0.0003	0	1	9.5e+003	1	KGKFPQTATENAEI
✓	822	713.2899	2849.1303	2849.2174	-0.0871	0	1	5.9e+002	1	APAPEAEVQASGGSVHGEPPCCSGPSWN
✓	1110	952.1156	3804.4332	3804.5187	-0.0856	0	1	1.1e+002	1	QMPGPNHMPMGPGPSQLSMNTNSMNMPSNNGSMG + 4 Oxidation (M)
✓	984	828.5695	3310.2489	3310.3444	-0.0955	0	1	1.5e+002	1	QNKHEFTQYSDHFSGMHNNYACSH
✓	992	844.6416	3374.5373	3374.6010	-0.0637	0	1	4.6e+003	1	PFFMIDENNVDGEALSSDIKLKEKHM + Oxidation (M)
✓	608	658.3235	1971.9487	1971.9712	-0.0225	0	0	9.3e+003	1	PASMLPFPWSRWR + Oxidation (M)
✓	289	444.9178	1331.7315	1331.6429	0.0885	0	0	9.1e+003	1	NDEAVADTSRRV
✓	977	827.6132	3306.4239	3306.5198	-0.0959	0	0	2e+003	1	DEEDPGSGCHDIYKNTSAPLTVLDATSDKTK

✓	548	601.9331	1802.7775	1802.7959	-0.0184	0	0	5e+003	1	EGLEARDWAQGVVEASGG
✓	1154	1070.9268	4279.6781	4279.6853	-0.0072	0	0	1.9e+002	1	MMSAYERSMSPNADRSMMMSGADRSMMSSYSAADRS + Oxidation (M)
✓	935	785.5106	3138.0133	3137.9267	0.0866	0	0	35	1	QLIKSQKFLNKLVLVETEKELRK
✓	2	306.0860	610.1574	610.2091	-0.0517	0	0	2.1e+003	1	ANEMM + Oxidation (M)
✓	333	355.6953	1418.7521	1418.6902	0.0618	0	0	1.1e+004	1	GAVDRPRDPENPP
✓	889	762.9777	3047.8915	3047.8263	0.0552	0	0	2.1e+002	1	KSLKPAPHLFAQLSKVLKLSKVQEVIF
✓	856	1453.9710	2905.9274	2905.8282	0.0993	0	0	18	1	GALITLLMLILLVRLPFIKDKERK
✓	7	654.0780	653.0707							
✓	8	654.0842	653.0770							
✓	9	659.7789	658.7716							
✓	10	659.7882	658.7809							
✓	11	659.7924	658.7851							
✓	12	659.7983	658.7910							
✓	15	669.0941	668.0868							
✓	16	669.0952	668.0880							
✓	17	669.1011	668.0938							
✓	18	339.0643	676.1140							
✓	19	339.0652	676.1159							
✓	22	708.9096	707.9024							
✓	23	362.5218	723.0291							
✓	25	741.0508	740.0435							
✓	30	778.1499	777.1426							
✓	42	873.8118	872.8045							
✓	53	462.1028	922.1909							
✓	54	462.1059	922.1973							
✓	102	353.1205	1056.3397							
✓	226	633.1821	1264.3497							
✓	227	633.1834	1264.3523							
✓	228	633.1841	1264.3536							
✓	254	654.0782	1306.1419							
✓	468	414.2300	1652.8910							
✓	476	419.4655	1673.8329							
✓	481	419.7198	1674.8499							
✓	513	439.8538	1755.3862							
✓	529	444.9013	1775.5760							
✓	583	637.1408	1908.4005							
✓	583	643.4941	1927.4605							
✓	634	688.9903	2063.9490							
✓	658	705.8524	2114.5353							
✓	673	542.4147	2165.6296							
✓	717	586.4410	2341.7349							
✓	723	593.6884	2370.7245							
✓	725	803.2198	2406.6377							
✓	741	617.6926	2466.7412							
✓	756	636.9288	2543.6861							
✓	763	648.1990	2588.7668							
✓	765	650.6674	2598.6403							
✓	774	659.2265	2632.8771							
✓	775	882.5451	2644.6134							
✓	801	705.7748	2819.0702							
✓	803	705.7992	2819.1679							
✓	817	709.6814	2834.6966							
✓	852	720.0166	2876.0372							
✓	853	720.9895	2879.9289							
✓	864	731.2527	2920.9817							
✓	869	733.0130	2928.0229							
✓	882	762.9553	3047.7923							
✓	883	762.9612	3047.8155							
✓	884	762.9630	3047.8229							
✓	885	762.9712	3047.8558							
✓	886	762.9749	3047.8704							
✓	888	762.9773	3047.8799							
✓	893	1018.6611	3052.9615							
✓	898	768.7560	3070.9949							
✓	951	814.3416	3253.3371							
✓	990	840.5526	3358.1012							
✓	995	846.3068	3381.1982							
✓	998	849.0673	3392.2400							
✓	999	849.0711	3392.2555							
✓	1026	857.0072	3423.9998							
✓	1066	911.3343	3641.3082							
✓	1073	916.8740	3663.4667							
✓	1099	952.0421	3804.1393							
✓	1101	952.0471	3804.1594							
✓	1106	952.0861	3804.3155							
✓	1111	952.1200	3804.4508							
✓	1120	987.6162	3946.4356							
✓	1128	992.9802	3967.8915							
✓	1147	1046.6663	4182.6361							
✓	1151	1062.6650	4246.6309							
✓	1153	1070.8971	4279.5593							

☒ [1178](#) 1131.4464 4521.7565
☒ [1197](#) 1223.7304 4890.8925

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : None
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 0.1 Da
Fragment Mass Tolerance: ± 0.1 Da
Max Missed Cleavages : 0
Instrument type : ESI-QUAD-TOF
Number of queries : 1236

Mascot: <http://www.matrixscience.com/>