

Supporting Information

Annotated MS/MS spectra of single peptide per protein

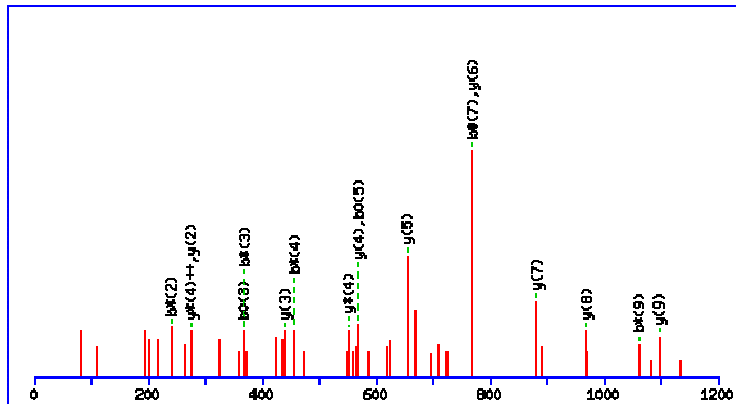
Peptide Number: 143

MS/MS Fragmentation of **QEQSIISEYEK**Found in **IPI00465161** in **IPI_human**, Tax_Id=9606 Gene_Symbol=RPAIN Isoform 1 of RPA-interacting protein

Match to Query 23770: 1352.635288 from(677.324920,2+) index(22712)

Title: Elution from: 54.2333333333333 to 54.2333333333333 period: 0 cycle: 2011 experiment: 10 polarity:+

Data file 120129ry_604A1-46_1_2.mgf



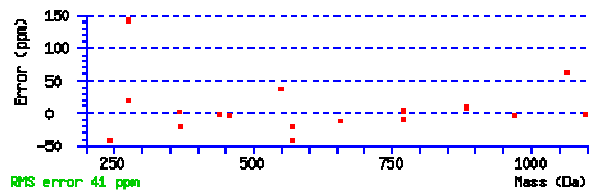
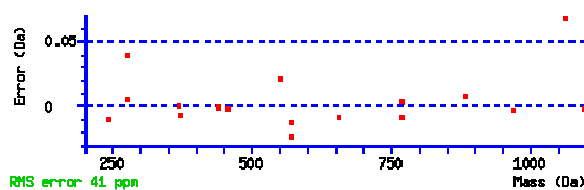
Monoisotopic mass of neutral peptide Mr(calc): 1352.6459

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 38 Expect: 0.0077

Matches : 18/116 fragment ions using 29 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.0659	65.0366	112.0393	56.5233			Q							11
2	258.1084	129.5579	241.0819	121.0446	240.0979	120.5526	E	1225.5947	613.3010	1208.5681	604.7877	1207.5841	604.2957	10
3	386.1670	193.5872	369.1405	185.0739	368.1565	184.5819	Q	1096.5521	548.7797	1079.5255	540.2664	1078.5415	539.7744	9
4	473.1991	237.1032	456.1725	228.5899	455.1885	228.0979	S	968.4935	484.7504	951.4670	476.2371	950.4829	475.7451	8
5	586.2831	293.6452	569.2566	285.1319	568.2726	284.6399	I	881.4615	441.2344	864.4349	432.7211	863.4509	432.2291	7
6	699.3672	350.1872	682.3406	341.6740	681.3566	341.1819	I	768.3774	384.6923	751.3509	376.1791	750.3668	375.6871	6
7	786.3992	393.7032	769.3727	385.1900	768.3886	384.6980	S	655.2933	328.1503	638.2668	319.6370	637.2828	319.1450	5
8	915.4418	458.2245	898.4153	449.7113	897.4312	449.2193	E	568.2613	284.6343	551.2348	276.1210	550.2508	275.6290	4
9	1078.5051	539.7562	1061.4786	531.2429	1060.4946	530.7509	Y	439.2187	220.1130	422.1922	211.5997	421.2082	211.1077	3
10	1207.5477	604.2775	1190.5212	595.7642	1189.5372	595.2722	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
11							K	147.1128	74.0600	130.0863	65.5468			1



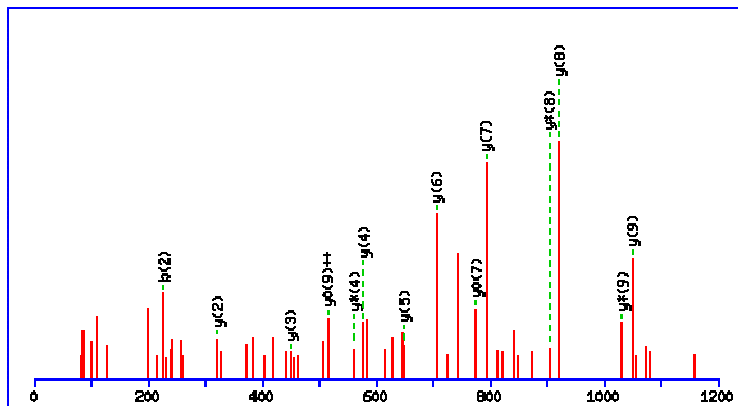
Peptide Number: 363

MS/MS Fragmentation of **LLQQSGAQQFR**Found in **IPI00926933** in **IPI_human**, Tax_Id=9606 Gene_Symbol=FYTTD1 14 kDa protein

Match to Query 19488: 1274.650708 from(638.332630,2+) index(28484)

Title: Elution from: 106.933333333333 to 106.933333333333 period: 0 cycle: 7406 experiment: 9 polarity:+

Data file 120208ry_Tig120slc-P8_3_1.mgf



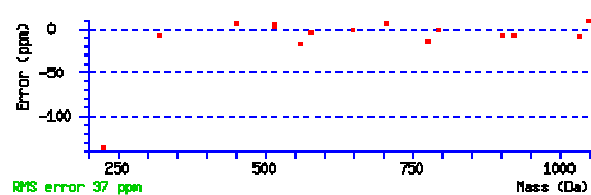
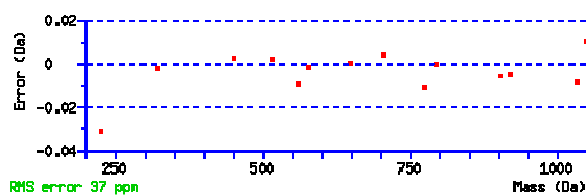
Monoisotopic mass of neutral peptide Mr(calc): 1274.6731

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 39 Expect: 0.0099

Matches : 14/96 fragment ions using 38 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							11
2	227.1754	114.0913					L	1162.5963	581.8018	1145.5698	573.2885	1144.5858	572.7965	10
3	355.2340	178.1206	338.2074	169.6074			Q	1049.5123	525.2598	1032.4857	516.7465	1031.5017	516.2545	9
4	483.2926	242.1499	466.2660	233.6366			Q	921.4537	461.2305	904.4272	452.7172	903.4431	452.2252	8
5	570.3246	285.6659	553.2980	277.1527	552.3140	276.6606	S	793.3951	397.2012	776.3686	388.6879	775.3846	388.1959	7
6	627.3461	314.1767	610.3195	305.6634	609.3355	305.1714	G	706.3631	353.6852	689.3366	345.1719			6
7	698.3832	349.6952	681.3566	341.1819	680.3726	340.6899	A	649.3416	325.1745	632.3151	316.6612			5
8	826.4417	413.7245	809.4152	405.2112	808.4312	404.7192	Q	578.3045	289.6559	561.2780	281.1426			4
9	954.5003	477.7538	937.4738	469.2405	936.4898	468.7485	Q	450.2459	225.6266	433.2194	217.1133			3
10	1101.5687	551.2880	1084.5422	542.7747	1083.5582	542.2827	F	322.1874	161.5973	305.1608	153.0840			2
11							R	175.1190	88.0631	158.0924	79.5498			1



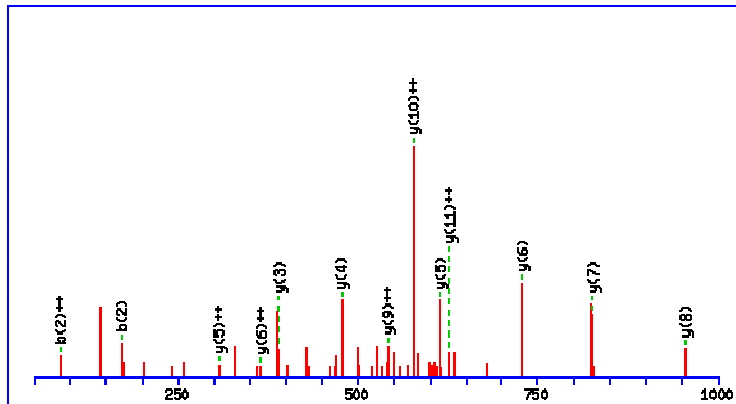
Peptide Number: 509

MS/MS Fragmentation of **AVAEQVLHSQSR**Found in **IPI00399254** in **IPI_human**, Tax_Id=9606 Gene_Symbol=OTUD4 Isoform 1 of OTU domain-containing protein 4

Match to Query 21597: 1323.689472 from(442.237100,3+) index(19170)

Title: Elution from: 84.0333333333333 to 84.0333333333333 period: 0 cycle: 7967 experiment: 4 polarity:+

Data file 120210ry_32R1-32_2_1.mgf



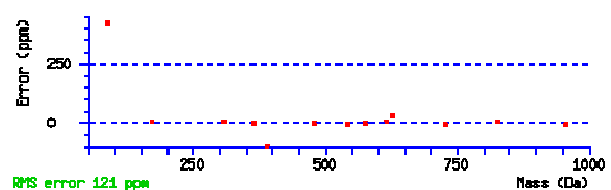
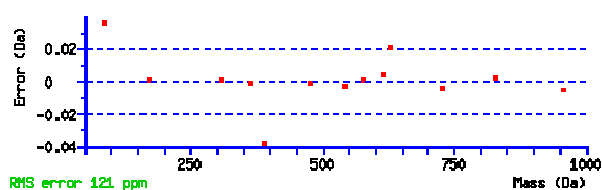
Monoisotopic mass of neutral peptide Mr(calc): 1323.6895

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 39 Expect: 0.0082

Matches : 13/116 fragment ions using 28 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							12
2	171.1128	86.0600					V	1253.6597	627.3335	1236.6331	618.8202	1235.6491	618.3282	11
3	242.1499	121.5786					A	1154.5913	577.7993	1137.5647	569.2860	1136.5807	568.7940	10
4	371.1925	186.0999			353.1819	177.0946	E	1083.5541	542.2807	1066.5276	533.7674	1065.5436	533.2754	9
5	499.2511	250.1292	482.2245	241.6159	481.2405	241.1239	Q	954.5116	477.7594	937.4850	469.2461	936.5010	468.7541	8
6	598.3195	299.6634	581.2930	291.1501	580.3089	290.6581	V	826.4530	413.7301	809.4264	405.2169	808.4424	404.7248	7
7	711.4036	356.2054	694.3770	347.6921	693.3930	347.2001	L	727.3846	364.1959	710.3580	355.6826	709.3740	355.1906	6
8	848.4625	424.7349	831.4359	416.2216	830.4519	415.7296	H	614.3005	307.6539	597.2739	299.1406	596.2899	298.6486	5
9	935.4945	468.2509	918.4680	459.7376	917.4839	459.2456	S	477.2416	239.1244	460.2150	230.6112	459.2310	230.1191	4
10	1063.5531	532.2802	1046.5265	523.7669	1045.5425	523.2749	Q	390.2096	195.6084	373.1830	187.0951	372.1990	186.6031	3
11	1150.5851	575.7962	1133.5586	567.2829	1132.5745	566.7909	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
12							R	175.1190	88.0631	158.0924	79.5498			1



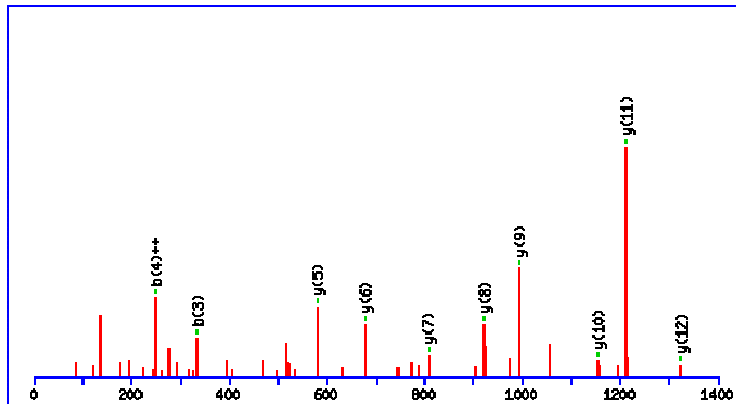
Peptide Number: 835

MS/MS Fragmentation of **YLGYANEVGGEAFR**Found in **IPI00456009** in **IPI_human**, Tax_Id=9606 Gene_Symbol=MTFP1 Isoform 2 of Mitochondrial fission process protein 1

Match to Query 10333: 1487.704548 from(744.859550,2+) index(1120)

Title: Elution from: 2.68333333333333 to 2.68333333333333 period: 0 cycle: 101 experiment: 9 polarity: +

Data file 120214ry_414C2-43_4_3.mgf



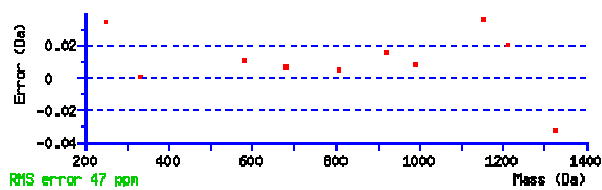
Monoisotopic mass of neutral peptide Mr(calc): 1487.7045

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

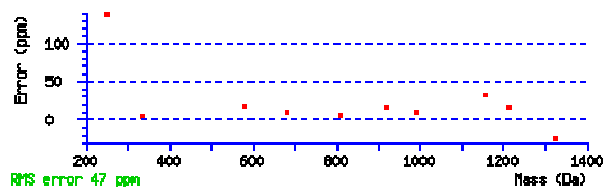
Ions Score: 70 Expect: 4.7e-006

Matches : 10/116 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389					Y							13
2	277.1547	139.0810					L	1325.6484	663.3279	1308.6219	654.8146	1307.6379	654.3226	12
3	334.1761	167.5917					G	1212.5644	606.7858	1195.5378	598.2726	1194.5538	597.7805	11
4	497.2395	249.1234					Y	1155.5429	578.2751	1138.5164	569.7618	1137.5323	569.2698	10
5	568.2766	284.6419					A	992.4796	496.7434	975.4530	488.2302	974.4690	487.7381	9
6	682.3195	341.6634	665.2930	333.1501			N	921.4425	461.2249	904.4159	452.7116	903.4319	452.2196	8
7	811.3621	406.1847	794.3355	397.6714	793.3515	397.1794	E	807.3995	404.2034	790.3730	395.6901	789.3890	395.1981	7
8	910.4305	455.7189	893.4040	447.2056	892.4199	446.7136	V	678.3570	339.6821	661.3304	331.1688	660.3464	330.6768	6
9	967.4520	484.2296	950.4254	475.7164	949.4414	475.2243	G	579.2885	290.1479	562.2620	281.6346	561.2780	281.1426	5
10	1096.4946	548.7509	1079.4680	540.2376	1078.4840	539.7456	E	522.2671	261.6372	505.2405	253.1239	504.2565	252.6319	4
11	1167.5317	584.2695	1150.5051	575.7562	1149.5211	575.2642	A	393.2245	197.1159	376.1979	188.6026			3
12	1314.6001	657.8037	1297.5735	649.2904	1296.5895	648.7984	F	322.1874	161.5973	305.1608	153.0840			2
13							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 47 ppm



RMS error 47 ppm

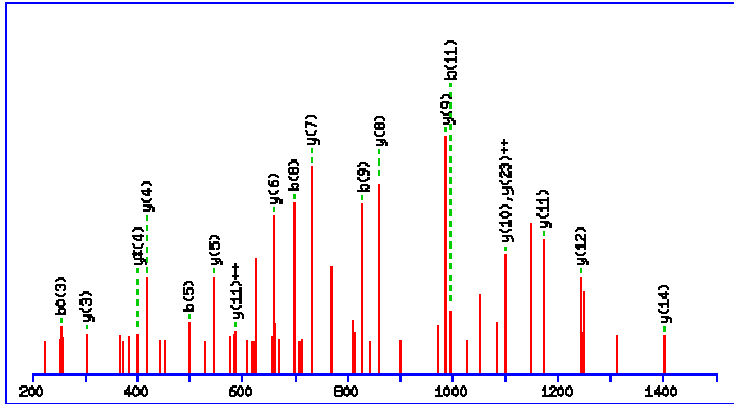
Peptide Number: 992

MS/MS Fragmentation of **PSSLLGAAMPASTSAAALQEALENAGR**Found in **IPI00026625** in **IPI_human**, Tax_Id=9606 Gene_Symbol=NUP155 Isoform 1 of Nuclear pore complex protein Nup155

Match to Query 27203: 2583.301122 from(862.107650,3+) index(6606)

Title: Elution from: 17.6 to 17.6 period: 0 cycle: 669 experiment: 7 polarity: +

Data file 120210ry_32R1-32_2_4.mgf



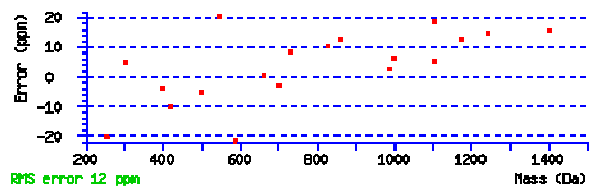
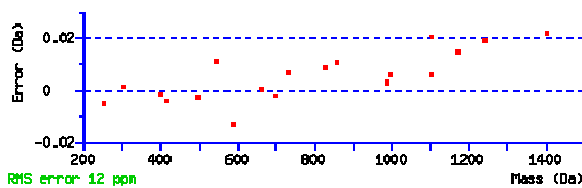
Monoisotopic mass of neutral peptide Mr(calc): 2583.2962

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 84 Expect: 2.5e-007

Matches : 19/266 fragment ions using 23 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	98.0600	49.5337					P							27
2	185.0921	93.0497			167.0815	84.0444	S	2487.2508	1244.1290	2470.2242	1235.6158	2469.2402	1235.1237	26
3	272.1241	136.5657			254.1135	127.5604	S	2400.2188	1200.6130	2383.1922	1192.0997	2382.2082	1191.6077	25
4	385.2082	193.1077			367.1976	184.1024	L	2313.1867	1157.0970	2296.1602	1148.5837	2295.1762	1148.0917	24
5	498.2922	249.6497			480.2817	240.6445	L	2200.1027	1100.5550	2183.0761	1092.0417	2182.0921	1091.5497	23
6	555.3137	278.1605			537.3031	269.1552	G	2087.0186	1044.0129	2069.9920	1035.4997	2069.0080	1035.0077	22
7	626.3508	313.6790			608.3402	304.6738	A	2029.9971	1015.5022	2012.9706	1006.9889	2011.9866	1006.4969	21
8	697.3879	349.1976			679.3774	340.1923	A	1958.9600	979.9836	1941.9335	971.4704	1940.9495	970.9784	20
9	828.4284	414.7178			810.4178	405.7126	M	1887.9229	944.4651	1870.8964	935.9518	1869.9123	935.4598	19
10	925.4812	463.2442			907.4706	454.2389	P	1756.8824	878.9448	1739.8559	870.4316	1738.8719	869.9396	18
11	996.5183	498.7628			978.5077	489.7575	A	1659.8297	830.4185	1642.8031	821.9052	1641.8191	821.4132	17
12	1083.5503	542.2788			1065.5397	533.2735	S	1588.7925	794.8999	1571.7660	786.3866	1570.7820	785.8946	16
13	1184.5980	592.8026			1166.5874	583.7973	T	1501.7605	751.3839	1484.7340	742.8706	1483.7499	742.3786	15
14	1271.6300	636.3186			1253.6194	627.3134	S	1400.7128	700.8601	1383.6863	692.3468	1382.7023	691.8548	14
15	1342.6671	671.8372			1324.6566	662.8319	A	1313.6808	657.3440	1296.6543	648.8308	1295.6702	648.3388	13
16	1413.7042	707.3558			1395.6937	698.3505	A	1242.6437	621.8255	1225.6171	613.3122	1224.6331	612.8202	12
17	1484.7414	742.8743			1466.7308	733.8690	A	1171.6066	586.3069	1154.5800	577.7937	1153.5960	577.3016	11
18	1597.8254	799.4163			1579.8149	790.4111	L	1100.5695	550.7884	1083.5429	542.2751	1082.5589	541.7831	10
19	1725.8840	863.4456	1708.8574	854.9324	1707.8734	854.4404	Q	987.4854	494.2463	970.4589	485.7331	969.4748	485.2411	9
20	1854.9266	927.9669	1837.9000	919.4537	1836.9160	918.9617	E	859.4268	430.2170	842.4003	421.7038	841.4163	421.2118	8
21	1925.9637	963.4855	1908.9372	954.9722	1907.9531	954.4802	A	730.3842	365.6958	713.3577	357.1825	712.3737	356.6905	7
22	2039.0478	1020.0275	2022.0212	1011.5142	2021.0372	1011.0222	L	659.3471	330.1772	642.3206	321.6639	641.3365	321.1719	6
23	2168.0904	1084.5488	2151.0638	1076.0355	2150.0798	1075.5435	E	546.2631	273.6352	529.2365	265.1219	528.2525	264.6299	5
24	2282.1333	1141.5703	2265.1067	1133.0570	2264.1227	1132.5650	N	417.2205	209.1139	400.1939	200.6006			4
25	2353.1704	1177.0888	2336.1439	1168.5756	2335.1598	1168.0836	A	303.1775	152.0924	286.1510	143.5791			3
26	2410.1919	1205.5996	2393.1653	1197.0863	2392.1813	1196.5943	G		232.1404	116.5738	215.1139	108.0606		2
27							R	175.1190	88.0631	158.0924	79.5498			1



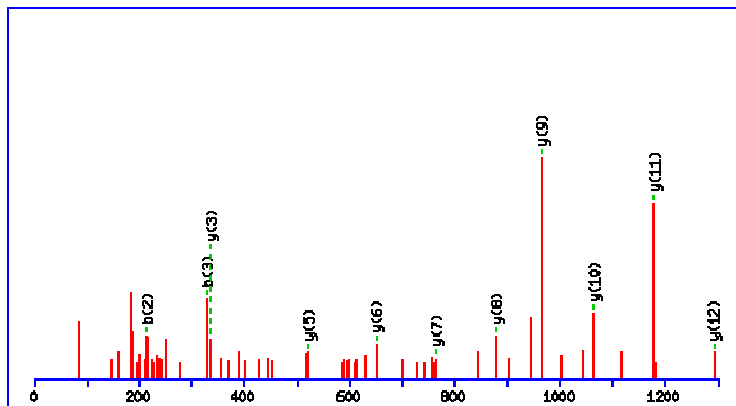
Peptide Number: 1025

MS/MS Fragmentation of **VLDVSDLESVTSK**Found in **IPI00171057** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SSH3 Isoform 2 of Protein phosphatase Slingshot homolog 3

Match to Query 7798: 1390.719568 from(696.367060,2+) index(2117)

Title: Elution from: 5.1 to 5.1 period: 0 cycle: 194 experiment: 7 polarity: +

Data file 120208ry_Tig120slc-P8_2_3.mgf



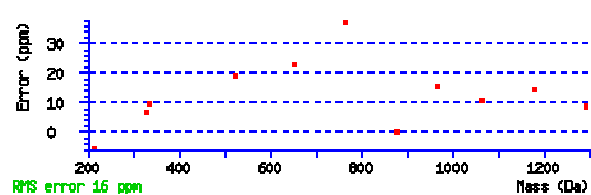
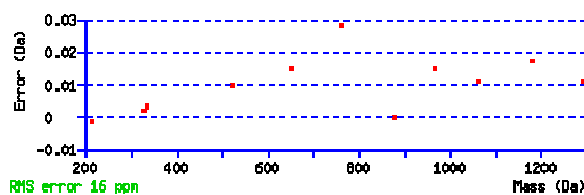
Monoisotopic mass of neutral peptide Mr(calc): 1390.7191

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 60 Expect: 7.9e-005

Matches : 11/114 fragment ions using 23 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415			V							13
2	213.1598	107.0835			L	1292.6580	646.8326	1275.6315	638.3194	1274.6474	637.8274	12
3	328.1867	164.5970	310.1761	155.5917	D	1179.5739	590.2906	1162.5474	581.7773	1161.5634	581.2853	11
4	427.2551	214.1312	409.2445	205.1259	V	1064.5470	532.7771	1047.5204	524.2639	1046.5364	523.7719	10
5	514.2871	257.6472	496.2766	248.6419	S	965.4786	483.2429	948.4520	474.7297	947.4680	474.2376	9
6	629.3141	315.1607	611.3035	306.1554	D	878.4466	439.7269	861.4200	431.2136	860.4360	430.7216	8
7	742.3981	371.7027	724.3876	362.6974	L	763.4196	382.2134	746.3931	373.7002	745.4090	373.2082	7
8	871.4407	436.2240	853.4302	427.2187	E	650.3355	325.6714	633.3090	317.1581	632.3250	316.6661	6
9	958.4728	479.7400	940.4622	470.7347	S	521.2930	261.1501	504.2664	252.6368	503.2824	252.1448	5
10	1057.5412	529.2742	1039.5306	520.2689	V	434.2609	217.6341	417.2344	209.1208	416.2504	208.6288	4
11	1158.5889	579.7981	1140.5783	570.7928	T	335.1925	168.0999	318.1660	159.5866	317.1819	159.0946	3
12	1245.6209	623.3141	1227.6103	614.3088	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
13					K	147.1128	74.0600	130.0863	65.5468			1



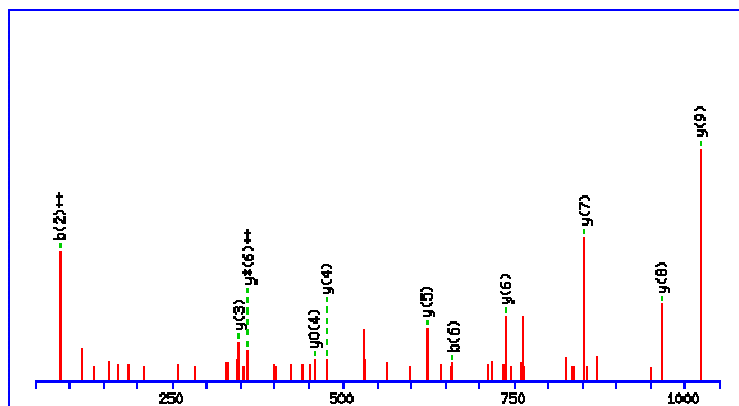
Peptide Number: 1243

MS/MS Fragmentation of **LGLDDFESLK**Found in **IPI01015336** in **IPI_human**, Tax_Id=9606 Gene_Symbol=STK38L Protein

Match to Query 2794: 1135.576628 from(568.795590,2+) index(16451)

Title: Elution from: 39.45 to 39.45 period: 0 cycle: 1483 experiment: 5 polarity: +

Data file 120214ry_32R1-32_4_3.mgf



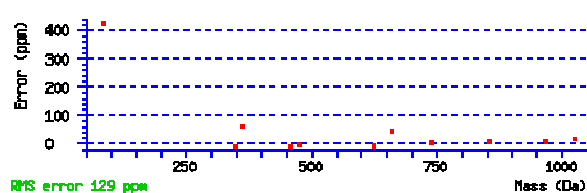
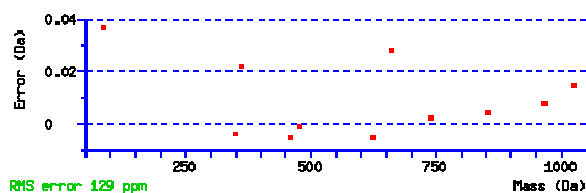
Monoisotopic mass of neutral peptide Mr(calc): 1135.5761

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 50 Expect: 0.00076

Matches : 11/80 fragment ions using 19 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							10
2	171.1128	86.0600			G	1023.4993	512.2533	1006.4728	503.7400	1005.4888	503.2480	9
3	284.1969	142.6021			L	966.4779	483.7426	949.4513	475.2293	948.4673	474.7373	8
4	399.2238	200.1155	381.2132	191.1103	D	853.3938	427.2005	836.3672	418.6873	835.3832	418.1953	7
5	514.2508	257.6290	496.2402	248.6237	D	738.3668	369.6871	721.3403	361.1738	720.3563	360.6818	6
6	661.3192	331.1632	643.3086	322.1579	F	623.3399	312.1736	606.3134	303.6603	605.3293	303.1683	5
7	790.3618	395.6845	772.3512	386.6792	E	476.2715	238.6394	459.2449	230.1261	458.2609	229.6341	4
8	877.3938	439.2005	859.3832	430.1952	S	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
9	990.4779	495.7426	972.4673	486.7373	L	260.1969	130.6021	243.1703	122.0888			2
10					K	147.1128	74.0600	130.0863	65.5468			1



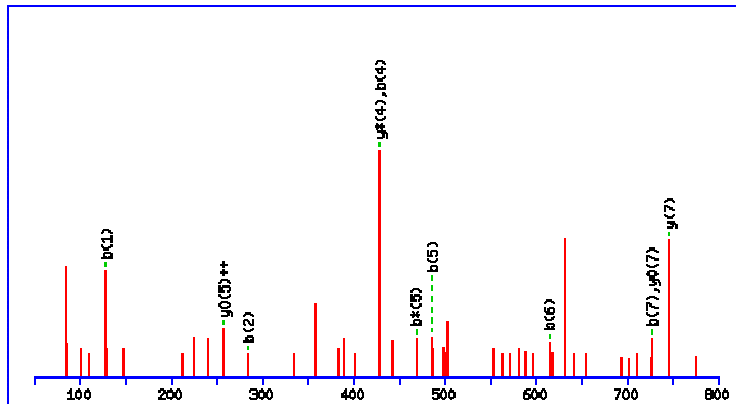
Peptide Number: 1664

MS/MS Fragmentation of **QRGSSELK**Found in **IPI00795475** in **IPI_human**, Tax_Id=9606 Gene_Symbol=BORA FLJ22624 protein, isoform CRA_a

Match to Query 6370: 873.475748 from(437.745150,2+) index(6074)

Title: Elution from: 61.6833333333333 to 61.6833333333333 period: 0 cycle: 6957 experiment: 8 polarity:+

Data file 120118ry_201B7-32_3_1.mgf



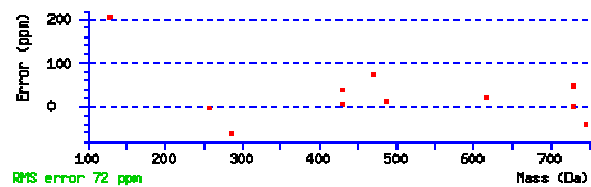
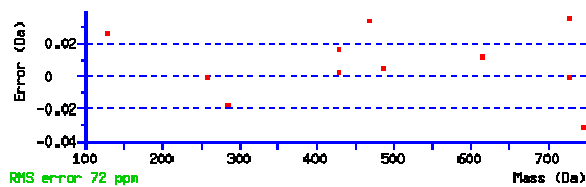
Monoisotopic mass of neutral peptide Mr(calcd): 873.4668

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 48 Expect: 0.0015

Matches : 11/74 fragment ions using 14 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	129.0659	65.0366	112.0393	56.5233			Q							8
2	285.1670	143.0871	268.1404	134.5738			R	746.4155	373.7114	729.3890	365.1981	728.4050	364.7061	7
3	342.1884	171.5979	325.1619	163.0846			G	590.3144	295.6608	573.2879	287.1476	572.3039	286.6556	6
4	429.2205	215.1139	412.1939	206.6006	411.2099	206.1086	S	533.2930	267.1501	516.2664	258.6368	515.2824	258.1448	5
5	486.2419	243.6246	469.2154	235.1113	468.2314	234.6193	G	446.2609	223.6341	429.2344	215.1208	428.2504	214.6288	4
6	615.2845	308.1459	598.2580	299.6326	597.2739	299.1406	E	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
7	728.3686	364.6879	711.3420	356.1747	710.3580	355.6826	L	260.1969	130.6021	243.1703	122.0888			2
8							K	147.1128	74.0600	130.0863	65.5468			1



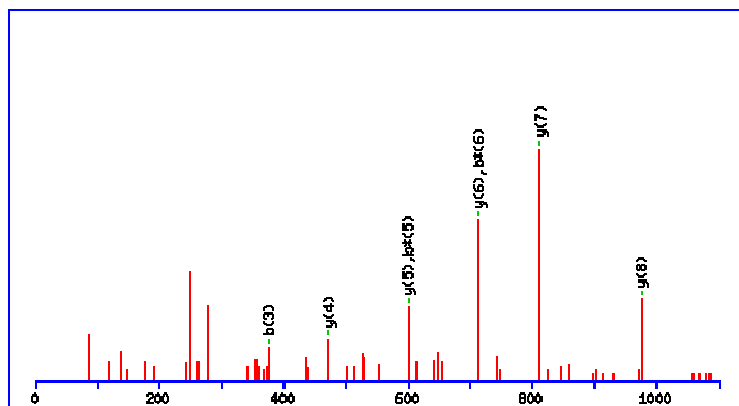
Peptide Number: 1967

MS/MS Fragmentation of **IYVLQLLAR**Found in **IPI00002946** in **IPI_human**, Tax_Id=9606 Gene_Symbol=GJC1 Gap junction gamma-1 protein

Match to Query 2038: 1087.676868 from(544.845710,2+) index(37106)

Title: Elution from: 98.1 to 98.1 period: 0 cycle: 3747 experiment: 1 polarity: +

Data file 120214ry_aHDF1419-P10_4_3.mgf



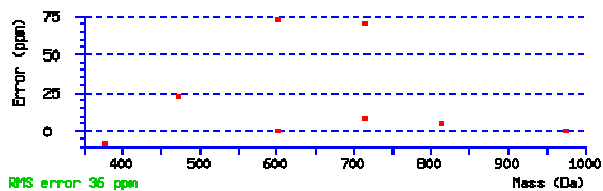
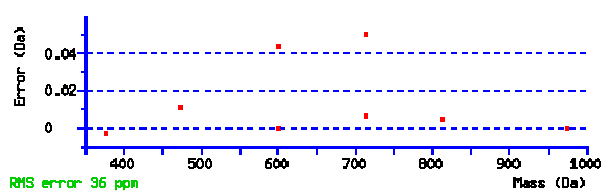
Monoisotopic mass of neutral peptide Mr(calc): 1087.6753

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 32 Expect: 0.0057

Matches : 8/56 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	#
1	114.0913	57.5493			I					9
2	277.1547	139.0810			Y	975.5986	488.3029	958.5720	479.7897	8
3	376.2231	188.6152			V	812.5353	406.7713	795.5087	398.2580	7
4	489.3071	245.1572			L	713.4668	357.2371	696.4403	348.7238	6
5	617.3657	309.1865	600.3392	300.6732	Q	600.3828	300.6950	583.3562	292.1817	5
6	730.4498	365.7285	713.4232	357.2153	L	472.3242	236.6657	455.2976	228.1525	4
7	843.5339	422.2706	826.5073	413.7573	L	359.2401	180.1237	342.2136	171.6104	3
8	914.5710	457.7891	897.5444	449.2758	A	246.1561	123.5817	229.1295	115.0684	2
9					R	175.1190	88.0631	158.0924	79.5498	1



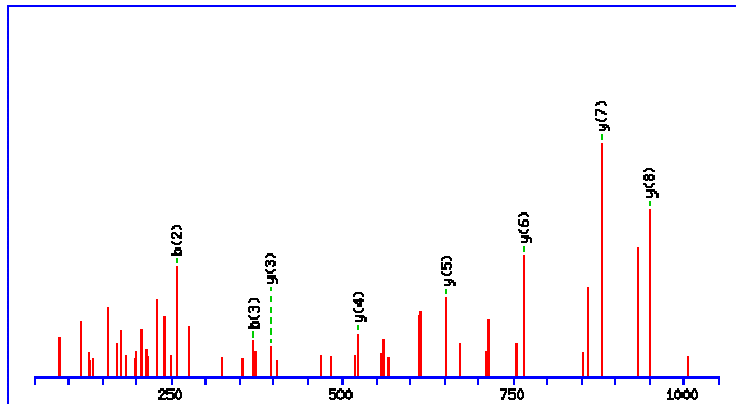
Peptide Number: 1994

MS/MS Fragmentation of **WAIEEFTK**Found in **IPI00007979** in **IPI_human**, Tax_Id=9606 Gene_Symbol=MT-ND2 NADH-ubiquinone oxidoreductase chain 2

Match to Query 2460: 1135.587188 from(568.800870,2+) index(27743)

Title: Elution from: 66.4833333333333 to 66.4833333333333 period: 0 cycle: 2517 experiment: 1 polarity: +

Data file 120212ry_aHDF1388-P9_2_3.mgf



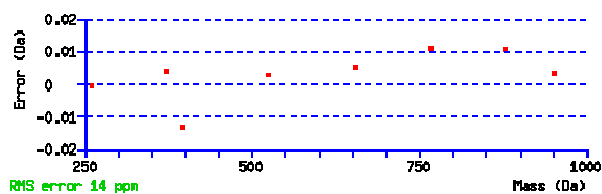
Monoisotopic mass of neutral peptide Mr(calc): 1135.5913

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

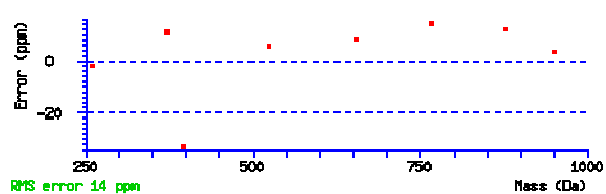
Ions Score: 51 Expect: 0.00064

Matches : 8/70 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	187.0866	94.0469			W							9
2	258.1237	129.5655			A	950.5193	475.7633	933.4928	467.2500	932.5088	466.7580	8
3	371.2078	186.1075			I	879.4822	440.2447	862.4557	431.7315	861.4716	431.2395	7
4	484.2918	242.6496			I	766.3981	383.7027	749.3716	375.1894	748.3876	374.6974	6
5	613.3344	307.1709	595.3239	298.1656	E	653.3141	327.1607	636.2875	318.6474	635.3035	318.1554	5
6	742.3770	371.6921	724.3665	362.6869	E	524.2715	262.6394	507.2449	254.1261	506.2609	253.6341	4
7	889.4454	445.2264	871.4349	436.2211	F	395.2289	198.1181	378.2023	189.6048	377.2183	189.1128	3
8	990.4931	495.7502	972.4825	486.7449	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
9					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 14 ppm



RMS error 14 ppm

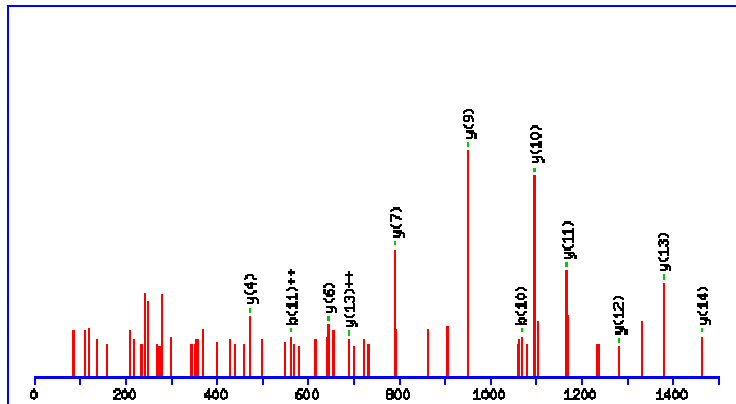
Peptide Number: 2200

MS/MS Fragmentation of **SCSPLAFSAFGDLTIK**Found in **IPI00744702** in **IPI_human**, Tax_Id=9606 Gene_Symbol=FAM125A Isoform 1 of Multivesicular body subunit 12A

Match to Query 17217: 1712.848268 from(857.431410,2+) index(43259)

Title: Elution from: 107.2 to 107.2 period: 0 cycle: 4054 experiment: 8 polarity:+

Data file 120206ry_aHDF1419-P10_2_3.mgf



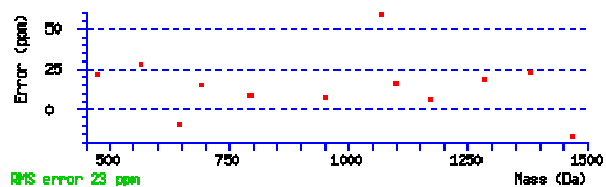
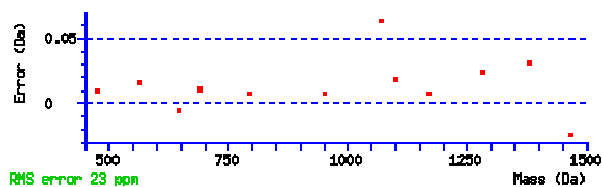
Monoisotopic mass of neutral peptide Mr(calc): 1712.8444

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 49 Expect: 0.00076

Matches : 12/146 fragment ions using 27 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233	70.0287	35.5180	S							16
2	248.0700	124.5386	230.0594	115.5333	C	1626.8196	813.9134	1609.7931	805.4002	1608.8090	804.9082	15
3	335.1020	168.0546	317.0914	159.0493	S	1466.7890	733.8981	1449.7624	725.3848	1448.7784	724.8928	14
4	432.1547	216.5810	414.1442	207.5757	P	1379.7569	690.3821	1362.7304	681.8688	1361.7464	681.3768	13
5	545.2388	273.1230	527.2282	264.1178	L	1282.7042	641.8557	1265.6776	633.3424	1264.6936	632.8504	12
6	616.2759	308.6416	598.2654	299.6363	A	1169.6201	585.3137	1152.5936	576.8004	1151.6095	576.3084	11
7	763.3443	382.1758	745.3338	373.1705	F	1098.5830	549.7951	1081.5564	541.2819	1080.5724	540.7898	10
8	850.3764	425.6918	832.3658	416.6865	S	951.5146	476.2609	934.4880	467.7477	933.5040	467.2556	9
9	921.4135	461.2104	903.4029	452.2051	A	864.4825	432.7449	847.4560	424.2316	846.4720	423.7396	8
10	1068.4819	534.7446	1050.4713	525.7393	F	793.4454	397.2264	776.4189	388.7131	775.4349	388.2211	7
11	1125.5034	563.2553	1107.4928	554.2500	G	646.3770	323.6921	629.3505	315.1789	628.3665	314.6869	6
12	1240.5303	620.7688	1222.5197	611.7635	D	589.3556	295.1814	572.3290	286.6681	571.3450	286.1761	5
13	1353.6144	677.3108	1335.6038	668.3055	L	474.3286	237.6679	457.3021	229.1547	456.3180	228.6627	4
14	1454.6620	727.8347	1436.6515	718.8294	T	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
15	1567.7461	784.3767	1549.7355	775.3714	I	260.1969	130.6021	243.1703	122.0888			2
16					K	147.1128	74.0600	130.0863	65.5468			1



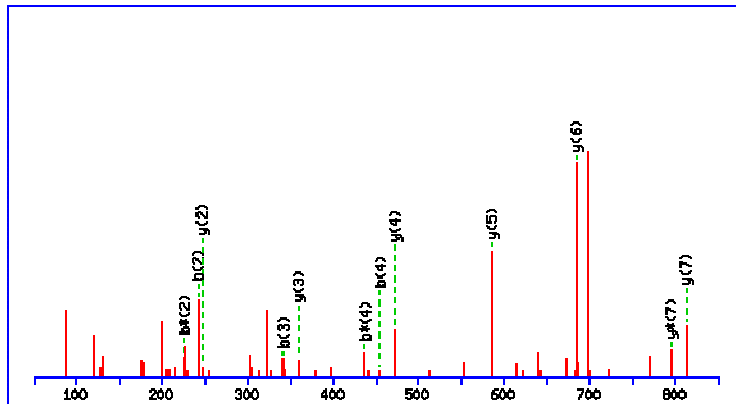
Peptide Number: 2212

MS/MS Fragmentation of **LQVMIQV**Found in **IPI00292033** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CCL25 Isoform 2 of C-C motif chemokine 25

Match to Query 318: 924.615568 from(463.315060,2+) index(901)

Title: Elution from: 2.26666666666667 to 2.26666666666667 period: 0 cycle: 87 experiment: 2 polarity: +

Data file 120208ry_Tig120slc-P8_1_3.mgf



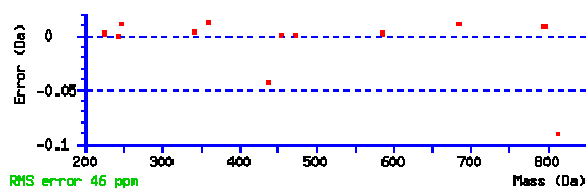
Monoisotopic mass of neutral peptide Mr(calcd): 924.6008

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

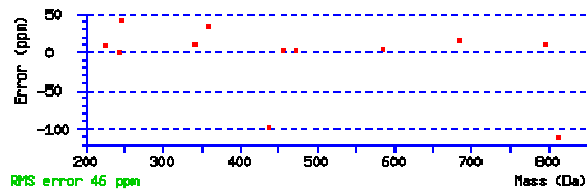
Ions Score: 27 Expect: 0.0076

Matches : 12/52 fragment ions using 34 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	#
1	114.0913	57.5493			L					8
2	242.1499	121.5786	225.1234	113.0653	Q	812.5240	406.7656	795.4975	398.2524	7
3	341.2183	171.1128	324.1918	162.5995	V	684.4654	342.7364	667.4389	334.2231	6
4	454.3024	227.6548	437.2758	219.1416	I	585.3970	293.2022	568.3705	284.6889	5
5	567.3865	284.1969	550.3599	275.6836	I	472.3130	236.6601	455.2864	228.1468	4
6	680.4705	340.7389	663.4440	332.2256	I	359.2289	180.1181	342.2023	171.6048	3
7	808.5291	404.7682	791.5026	396.2549	Q	246.1448	123.5761	229.1183	115.0628	2
8					V	118.0863	59.5468			1



RMS error 46 ppm



RMS error 46 ppm

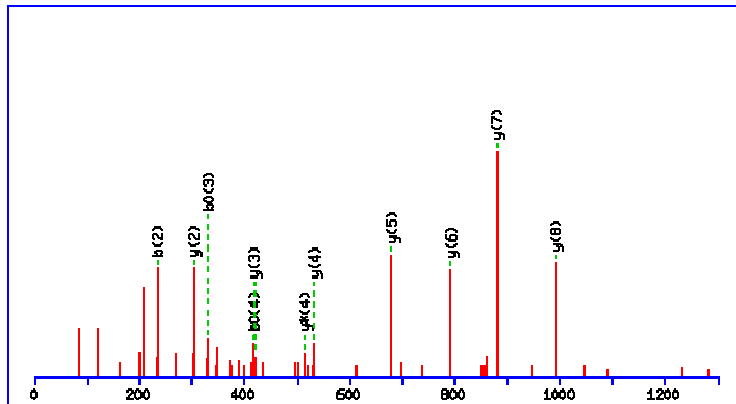
Peptide Number: 2390

MS/MS Fragmentation of **SFLSLFLDER**Found in **IPI00007165** in **IPI_human**, Tax_Id=9606 Gene_Symbol=DOLK Dolichol kinase

Match to Query 462: 1225.637128 from(613.825840,2+) index(15481)

Title: Elution from: 41.05 to 41.05 period: 0 cycle: 1561 experiment: 3 polarity:+

Data file 120206ry_aHDF1419-P10_2_4.mgf



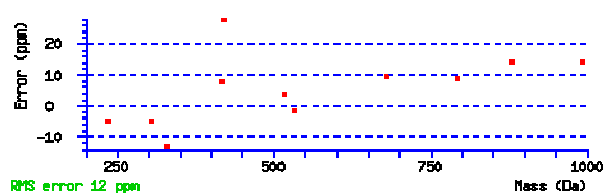
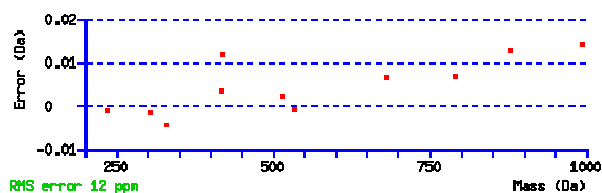
Monoisotopic mass of neutral peptide Mr(calc): 1225.6343

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 47 Expect: 0.0012

Matches : 11/88 fragment ions using 20 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233	70.0287	35.5180	S							10
2	235.1077	118.0575	217.0972	109.0522	F	1139.6095	570.3084	1122.5830	561.7951	1121.5990	561.3031	9
3	348.1918	174.5995	330.1812	165.5942	L	992.5411	496.7742	975.5146	488.2609	974.5306	487.7689	8
4	435.2238	218.1155	417.2132	209.1103	S	879.4571	440.2322	862.4305	431.7189	861.4465	431.2269	7
5	548.3079	274.6576	530.2973	265.6523	L	792.4250	396.7162	775.3985	388.2029	774.4145	387.7109	6
6	695.3763	348.1918	677.3657	339.1865	F	679.3410	340.1741	662.3144	331.6608	661.3304	331.1688	5
7	808.4604	404.7338	790.4498	395.7285	L	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
8	923.4873	462.2473	905.4767	453.2420	D	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	3
9	1052.5299	526.7686	1034.5193	517.7633	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
10					R	175.1190	88.0631	158.0924	79.5498			1

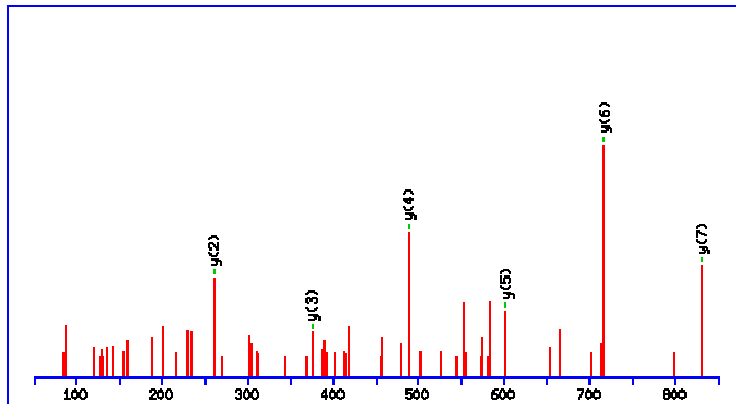


Peptide Number: 3003MS/MS Fragmentation of **ADDILDLK**Found in **IPI00149849** in **IPI_human**, Tax_Id=9606 Gene_Symbol=COG4 conserved oligomeric Golgi complex subunit 4 isoform 1

Match to Query 3611: 901.469148 from(451.741850,2+) index(26474)

Title: Elution from: 64.5166666666667 to 64.5166666666667 period: 0 cycle: 2445 experiment: 3 polarity:+

Data file 120214ry_414C2-43_4_2.mgf



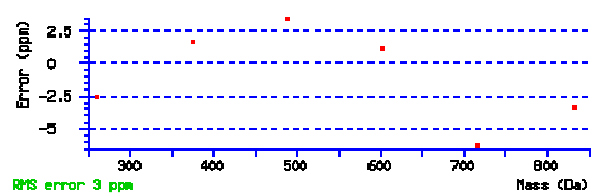
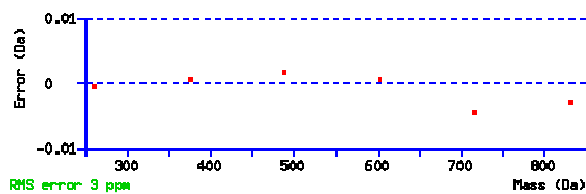
Monoisotopic mass of neutral peptide Mr(calc): 901.4756

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 53 Expect: 0.00047

Matches : 6/64 fragment ions using 8 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258			A							8
2	187.0713	94.0393	169.0608	85.0340	D	831.4458	416.2266	814.4193	407.7133	813.4353	407.2213	7
3	302.0983	151.5528	284.0877	142.5475	D	716.4189	358.7131	699.3923	350.1998	698.4083	349.7078	6
4	415.1823	208.0948	397.1718	199.0895	I	601.3919	301.1996	584.3654	292.6863	583.3814	292.1943	5
5	528.2664	264.6368	510.2558	255.6316	L	488.3079	244.6576	471.2813	236.1443	470.2973	235.6523	4
6	643.2933	322.1503	625.2828	313.1450	D	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
7	756.3774	378.6923	738.3668	369.6871	L	260.1969	130.6021	243.1703	122.0888			2
8					K	147.1128	74.0600	130.0863	65.5468			1

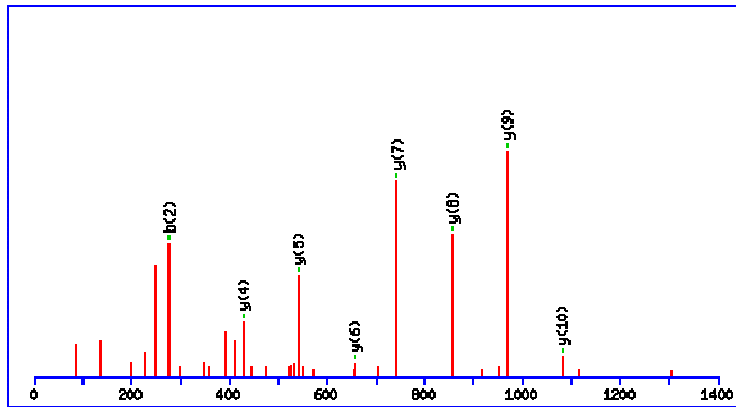


Peptide Number: 3087MS/MS Fragmentation of **YLLLSDLPGVR**Found in **IPI00017816** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ATP5S Isoform 1 of ATP synthase subunit s, mitochondrial

Match to Query 7523: 1244.702228 from(623.358390,2+) index(32006)

Title: Elution from: 80 to 80 period: 0 cycle: 2977 experiment: 4 polarity:+

Data file 120126ry_585A1-55_2_3.mgf



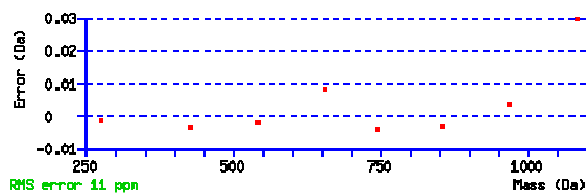
Monoisotopic mass of neutral peptide Mr(calc): 1244.7129

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

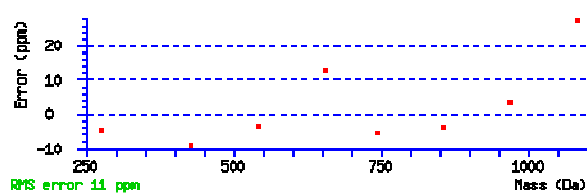
Ions Score: 60 Expect: 5e-005

Matches : 8/82 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389			Y							11
2	277.1547	139.0810			L	1082.6568	541.8320	1065.6303	533.3188	1064.6463	532.8268	10
3	390.2387	195.6230			L	969.5728	485.2900	952.5462	476.7767	951.5622	476.2847	9
4	503.3228	252.1650			L	856.4887	428.7480	839.4621	420.2347	838.4781	419.7427	8
5	590.3548	295.6811	572.3443	286.6758	S	743.4046	372.2060	726.3781	363.6927	725.3941	363.2007	7
6	705.3818	353.1945	687.3712	344.1892	D	656.3726	328.6899	639.3461	320.1767	638.3620	319.6847	6
7	818.4658	409.7366	800.4553	400.7313	L	541.3457	271.1765	524.3191	262.6632			5
8	915.5186	458.2629	897.5080	449.2577	P	428.2616	214.6344	411.2350	206.1212			4
9	972.5401	486.7737	954.5295	477.7684	G	331.2088	166.1081	314.1823	157.5948			3
10	1071.6085	536.3079	1053.5979	527.3026	V	274.1874	137.5973	257.1608	129.0840			2
11					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 11 ppm



RMS error 11 ppm

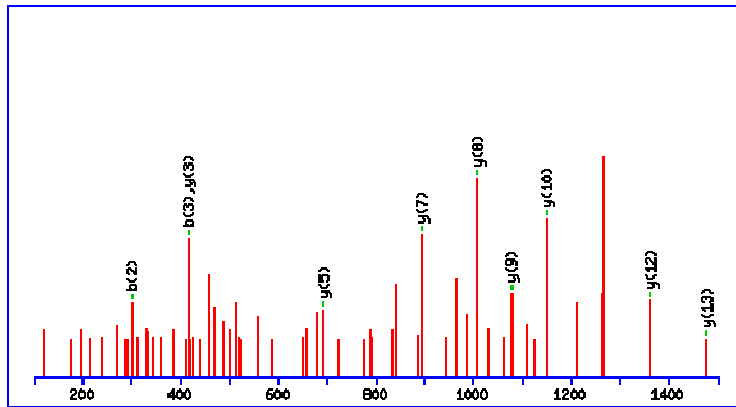
Peptide Number: 3191

MS/MS Fragmentation of **NWDVNAALSDFEQLR**Found in **IPI00024658** in **IPI_human**, Tax_Id=9606 Gene_Symbol=OTUD7B OTU domain-containing protein 7B

Match to Query 8901: 1776.841088 from(889.427820,2+) index(11264)

Title: Elution from: 29.1166666666667 to 29.1166666666667 period: 0 cycle: 1103 experiment: 8 polarity: +

Data file 120210ry_32R1-32_2_4.mgf



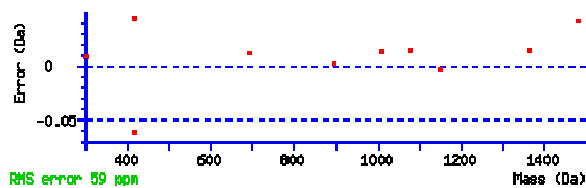
Monoisotopic mass of neutral peptide Mr(calc): 1776.8431

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

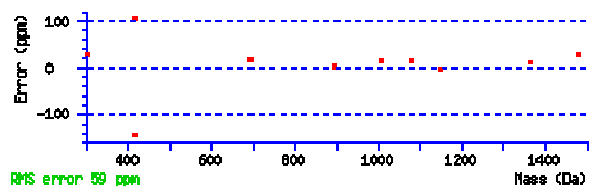
Ions Score: 55 Expect: 0.00017

Matches : 10/158 fragment ions using 14 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							15
2	301.1295	151.0684	284.1030	142.5551			W	1663.8075	832.4074	1646.7809	823.8941	1645.7969	823.4021	14
3	416.1565	208.5819	399.1299	200.0686	398.1459	199.5766	D	1477.7281	739.3677	1460.7016	730.8544	1459.7176	730.3624	13
4	515.2249	258.1161	498.1983	249.6028	497.2143	249.1108	V	1362.7012	681.8542	1345.6747	673.3410	1344.6906	672.8490	12
5	629.2678	315.1375	612.2413	306.6243	611.2572	306.1323	N	1263.6328	632.3200	1246.6062	623.8068	1245.6222	623.3148	11
6	700.3049	350.6561	683.2784	342.1428	682.2943	341.6508	A	1149.5899	575.2986	1132.5633	566.7853	1131.5793	566.2933	10
7	771.3420	386.1747	754.3155	377.6614	753.3315	377.1694	A	1078.5528	539.7800	1061.5262	531.2667	1060.5422	530.7747	9
8	884.4261	442.7167	867.3995	434.2034	866.4155	433.7114	L	1007.5156	504.2615	990.4891	495.7482	989.5051	495.2562	8
9	971.4581	486.2327	954.4316	477.7194	953.4476	477.2274	S	894.4316	447.7194	877.4050	439.2061	876.4210	438.7141	7
10	1086.4851	543.7462	1069.4585	535.2329	1068.4745	534.7409	D	807.3995	404.2034	790.3730	395.6901	789.3890	395.1981	6
11	1233.5535	617.2804	1216.5269	608.7671	1215.5429	608.2751	F	692.3726	346.6899	675.3461	338.1767	674.3620	337.6847	5
12	1362.5961	681.8017	1345.5695	673.2884	1344.5855	672.7964	E	545.3042	273.1557	528.2776	264.6425	527.2936	264.1504	4
13	1490.6546	745.8310	1473.6281	737.3177	1472.6441	736.8257	Q	416.2616	208.6344	399.2350	200.1212			3
14	1603.7387	802.3730	1586.7122	793.8597	1585.7281	793.3677	L	288.2030	144.6051	271.1765	136.0919			2
15							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 59 ppm



RMS error 59 ppm

Peptide Number: 3500

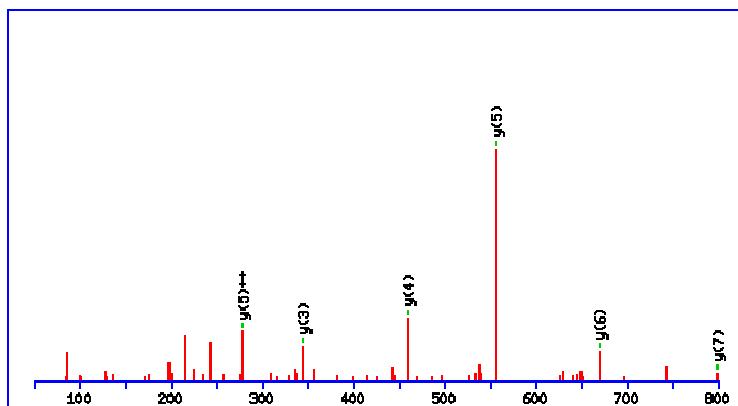
MS/MS Fragmentation of IELPDLGR

Found in **IPI00788666** in **IPI_human**, Tax_Id=9606 Gene_Symbol=LOXHD1 lipoygenase homology domain-containing protein 1 isoform 1

Match to Query 4582: 911.504628 from(456.759590,2+) index(18208)

Title: Elution from: 44.6 to 44.6 period: 0 cycle: 1684 experiment: 3 polarity: +

Data file 120210ry_32R1-32_2_2.mgf



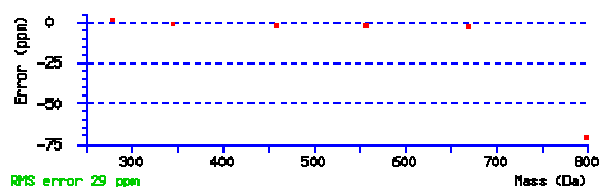
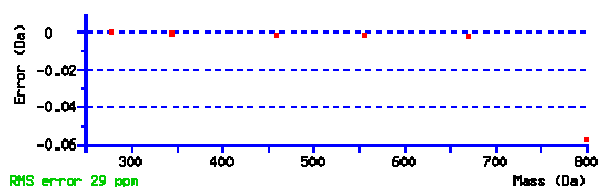
Monoisotopic mass of neutral peptide Mr(calc): 911.5076

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 43 Expect: 0.0021

Matches : 6/62 fragment ions using 8 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			I							8
2	243.1339	122.0706	225.1234	113.0653	E	799.4308	400.2191	782.4043	391.7058	781.4203	391.2138	7
3	356.2180	178.6126	338.2074	169.6074	L	670.3883	335.6978	653.3617	327.1845	652.3777	326.6925	6
4	453.2708	227.1390	435.2602	218.1337	P	557.3042	279.1557	540.2776	270.6425	539.2936	270.1504	5
5	568.2977	284.6525	550.2871	275.6472	D	460.2514	230.6293	443.2249	222.1161	442.2409	221.6241	4
6	681.3818	341.1945	663.3712	332.1892	L	345.2245	173.1159	328.1979	164.6026			3
7	738.4032	369.7053	720.3927	360.7000	G	232.1404	116.5738	215.1139	108.0606			2
8					R	175.1190	88.0631	158.0924	79.5498			1



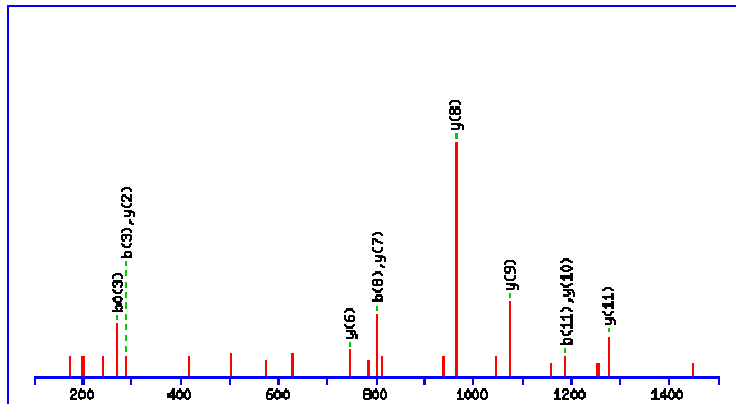
Peptide Number: 3617

MS/MS Fragmentation of **SLSLICGALSWLR**Found in **IPI00332293** in **IPI_human**, Tax_Id=9606 Gene_Symbol=DDX11 Isoform 4 of Probable ATP-dependent RNA helicase DDX11

Match to Query 3004: 1474.773288 from(738.393920,2+) index(25812)

Title: Elution from: 67.4333333333333 to 67.4333333333333 period: 0 cycle: 2559 experiment: 6 polarity:+

Data file 120210ry_32R1-32_3_4.mgf



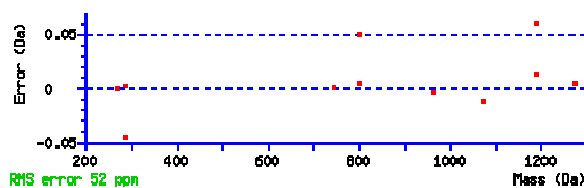
Monoisotopic mass of neutral peptide Mr(calc): 1474.7966

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

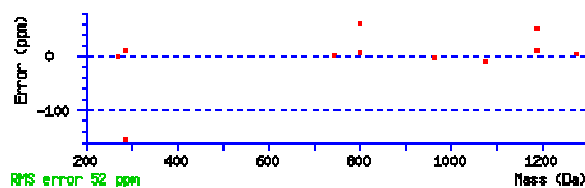
Ions Score: 52 Expect: 0.00055

Matches : 11/114 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233	70.0287	35.5180	S							13
2	201.1234	101.0653	183.1128	92.0600	L	1388.7719	694.8896	1371.7453	686.3763	1370.7613	685.8843	12
3	288.1554	144.5813	270.1448	135.5761	S	1275.6878	638.3475	1258.6613	629.8343	1257.6772	629.3423	11
4	401.2395	201.1234	383.2289	192.1181	L	1188.6558	594.8315	1171.6292	586.3183	1170.6452	585.8262	10
5	514.3235	257.6654	496.3130	248.6601	I	1075.5717	538.2895	1058.5452	529.7762	1057.5611	529.2842	9
6	674.3542	337.6807	656.3436	328.6754	C	962.4876	481.7475	945.4611	473.2342	944.4771	472.7422	8
7	731.3756	366.1915	713.3651	357.1862	G	802.4570	401.7321	785.4304	393.2189	784.4464	392.7269	7
8	802.4128	401.7100	784.4022	392.7047	A	745.4355	373.2214	728.4090	364.7081	727.4250	364.2161	6
9	915.4968	458.2520	897.4863	449.2468	L	674.3984	337.7028	657.3719	329.1896	656.3879	328.6976	5
10	1002.5288	501.7681	984.5183	492.7628	S	561.3144	281.1608	544.2878	272.6475	543.3038	272.1555	4
11	1188.6082	594.8077	1170.5976	585.8024	W	474.2823	237.6448	457.2558	229.1315			3
12	1301.6922	651.3497	1283.6817	642.3445	L	288.2030	144.6051	271.1765	136.0919			2
13					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 52 ppm



RMS error 52 ppm

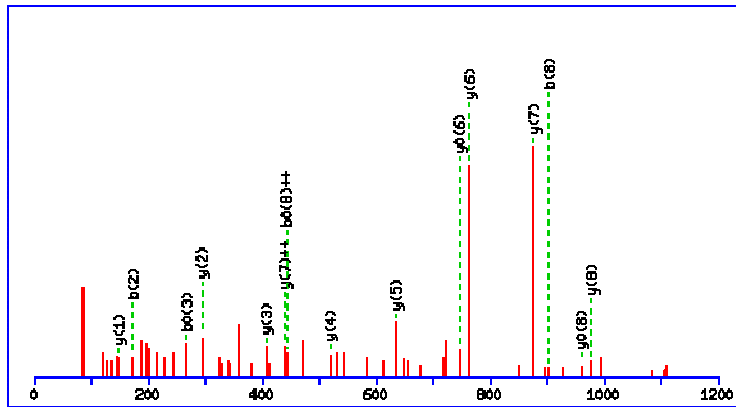
Peptide Number: 4040

MS/MS Fragmentation of **ATIEDILFK**Found in **IPI00964639** in **IPI_human**, Tax_Id=9606 Gene_Symbol=GTF2H2;GTF2H2C;GTF2H2D Uncharacterized protein

Match to Query 1822: 1048.583748 from(525.299150,2+) index(31770)

Title: Elution from: 79.8833333333333 to 79.8833333333333 period: 0 cycle: 3014 experiment: 1 polarity:+

Data file 120210ry_32R1-32_2_3.mgf



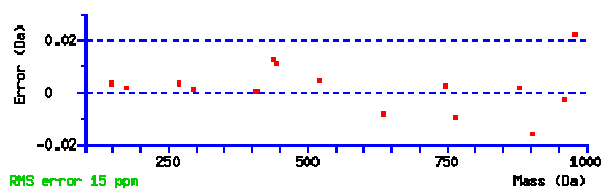
Monoisotopic mass of neutral peptide Mr(calc): 1048.5804

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

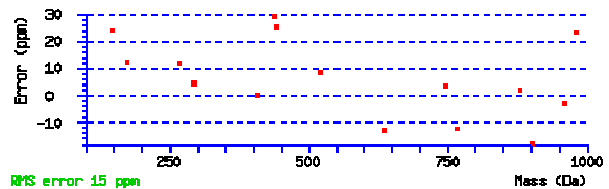
Ions Score: 40 Expect: 0.0059

Matches : 15/70 fragment ions using 42 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258			A							9
2	173.0921	87.0497	155.0815	78.0444	T	978.5506	489.7790	961.5241	481.2657	960.5401	480.7737	8
3	286.1761	143.5917	268.1656	134.5864	I	877.5029	439.2551	860.4764	430.7418	859.4924	430.2498	7
4	415.2187	208.1130	397.2082	199.1077	E	764.4189	382.7131	747.3923	374.1998	746.4083	373.7078	6
5	530.2457	265.6265	512.2351	256.6212	D	635.3763	318.1918	618.3497	309.6785	617.3657	309.1865	5
6	643.3297	322.1685	625.3192	313.1632	I	520.3493	260.6783	503.3228	252.1650			4
7	756.4138	378.7105	738.4032	369.7053	L	407.2653	204.1363	390.2387	195.6230			3
8	903.4822	452.2447	885.4716	443.2395	F	294.1812	147.5942	277.1547	139.0810			2
9					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 15 ppm



RMS error 15 ppm

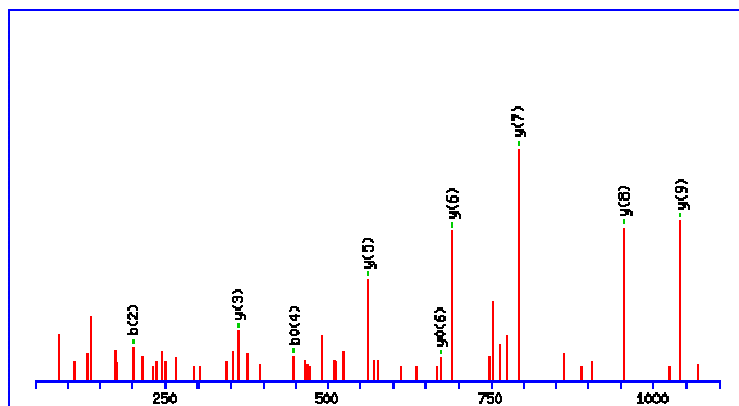
Peptide Number: 4049

MS/MS Fragmentation of **LSYTEAEGER**Found in **IPI00384529** in **IPI_human**, Tax_Id=9606 Gene_Symbol=COBL Isoform 1 of Protein cordon-bleu

Match to Query 16394: 1153.524688 from(577.769620,2+) index(24566)

Title: Elution from: 101.25 to 101.25 period: 0 cycle: 9129 experiment: 7 polarity:+

Data file 120210ry_32R1-32_3_1.mgf



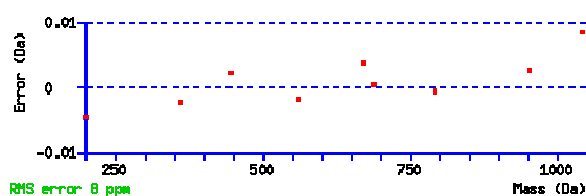
Monoisotopic mass of neutral peptide Mr(calc): 1153.5251

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

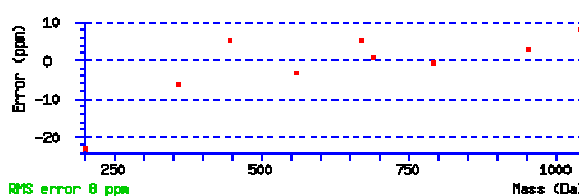
Ions Score: 57 Expect: 7.5e-005

Matches : 9/86 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							10
2	201.1234	101.0653	183.1128	92.0600	S	1041.4483	521.2278	1024.4218	512.7145	1023.4378	512.2225	9
3	364.1867	182.5970	346.1761	173.5917	Y	954.4163	477.7118	937.3898	469.1985	936.4058	468.7065	8
4	465.2344	233.1208	447.2238	224.1155	T	791.3530	396.1801	774.3264	387.6669	773.3424	387.1748	7
5	594.2770	297.6421	576.2664	288.6368	E	690.3053	345.6563	673.2788	337.1430	672.2947	336.6510	6
6	665.3141	333.1607	647.3035	324.1554	A	561.2627	281.1350	544.2362	272.6217	543.2522	272.1297	5
7	794.3567	397.6820	776.3461	388.6767	E	490.2256	245.6164	473.1991	237.1032	472.2150	236.6112	4
8	851.3781	426.1927	833.3676	417.1874	G	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	3
9	980.4207	490.7140	962.4102	481.7087	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
10					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 8 ppm



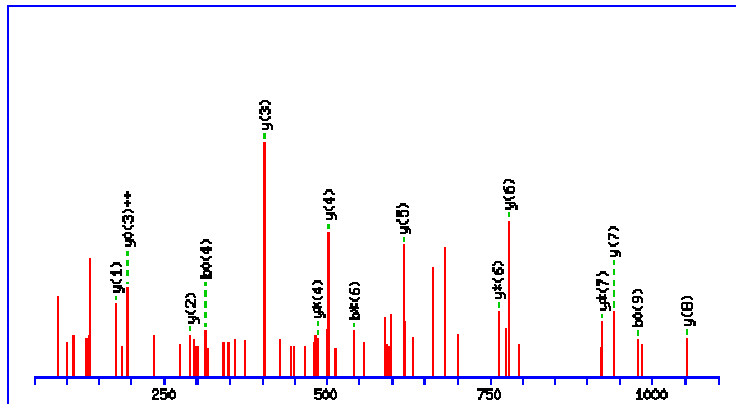
RMS error 8 ppm

Peptide Number: 4352MS/MS Fragmentation of **GATTNICYNVLDLR**Found in **IPI00413730** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ACSS2 Acetyl-coenzyme A synthetase, cytoplasmic

Match to Query 27081: 1495.700022 from(499.573950,3+) index(32252)

Title: Elution from: 76.8 to 76.8 period: 0 cycle: 2909 experiment: 3 polarity: +

Data file 120208ry_Tig120slc-P8_2_2.mgf



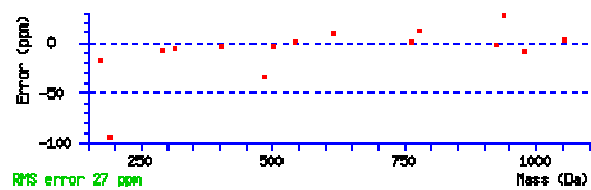
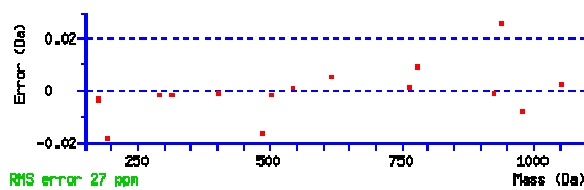
Monoisotopic mass of neutral peptide Mr(calc): 1495.7089

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 45 Expect: 0.0016

Matches : 15/130 fragment ions using 26 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							13
2	129.0659	65.0366					A	1439.6947	720.3510	1422.6682	711.8377	1421.6842	711.3457	12
3	230.1135	115.5604			212.1030	106.5551	T	1368.6576	684.8325	1351.6311	676.3192	1350.6471	675.8272	11
4	331.1612	166.0842			313.1506	157.0790	T	1267.6099	634.3086	1250.5834	625.7953	1249.5994	625.3033	10
5	445.2041	223.1057	428.1776	214.5924	427.1936	214.1004	N	1166.5623	583.7848	1149.5357	575.2715	1148.5517	574.7795	9
6	558.2882	279.6477	541.2617	271.1345	540.2776	270.6425	I	1052.5193	526.7633	1035.4928	518.2500	1034.5088	517.7580	8
7	718.3189	359.6631	701.2923	351.1498	700.3083	350.6578	C	939.4353	470.2213	922.4087	461.7080	921.4247	461.2160	7
8	881.3822	441.1947	864.3556	432.6815	863.3716	432.1894	Y	779.4046	390.2060	762.3781	381.6927	761.3941	381.2007	6
9	995.4251	498.2162	978.3986	489.7029	977.4145	489.2109	N	616.3413	308.6743	599.3148	300.1610	598.3307	299.6690	5
10	1094.4935	547.7504	1077.4670	539.2371	1076.4830	538.7451	V	502.2984	251.6528	485.2718	243.1395	484.2878	242.6475	4
11	1207.5776	604.2924	1190.5510	595.7792	1189.5670	595.2871	L	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
12	1322.6045	661.8059	1305.5780	653.2926	1304.5940	652.8006	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
13							R	175.1190	88.0631	158.0924	79.5498			1



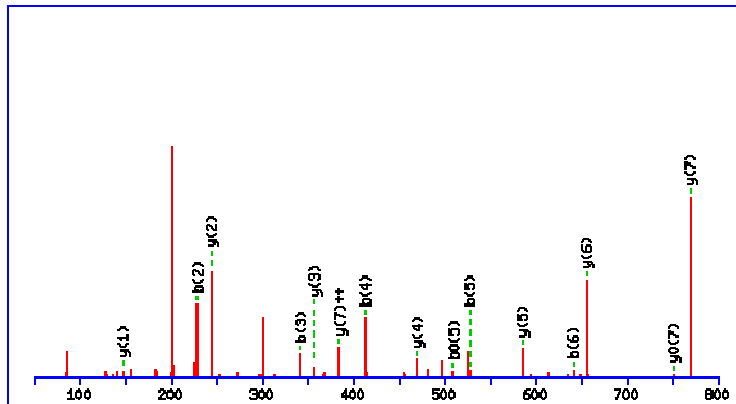
Peptide Number: 5114

MS/MS Fragmentation of **DILADLIPK**Found in **IPI00025366** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CS Citrate synthase, mitochondrial

Match to Query 787: 996.587588 from(499.301070,2+) index(33632)

Title: Elution from: 93.9666666666667 to 93.9666666666667 period: 0 cycle: 3612 experiment: 1 polarity: +

Data file 120208ry_Tig120slc-P8_1_3.mgf



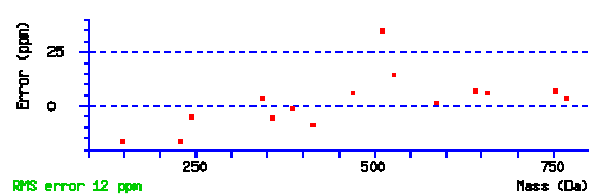
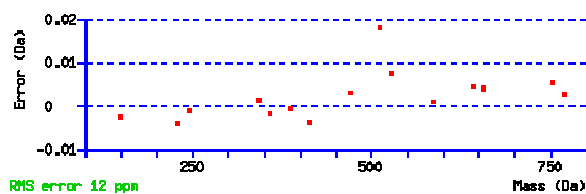
Monoisotopic mass of neutral peptide Mr(calcd): 996.5855

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 52 Expect: 0.00015

Matches : 15/72 fragment ions using 27 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	98.0237	49.5155	D							9
2	229.1183	115.0628	211.1077	106.0575	I	882.5659	441.7866	865.5393	433.2733	864.5553	432.7813	8
3	342.2023	171.6048	324.1918	162.5995	L	769.4818	385.2445	752.4553	376.7313	751.4713	376.2393	7
4	413.2395	207.1234	395.2289	198.1181	A	656.3978	328.7025	639.3712	320.1892	638.3872	319.6972	6
5	528.2664	264.6368	510.2558	255.6316	D	585.3606	293.1840	568.3341	284.6707	567.3501	284.1787	5
6	641.3505	321.1789	623.3399	312.1736	L	470.3337	235.6705	453.3071	227.1572			4
7	754.4345	377.7209	736.4240	368.7156	I	357.2496	179.1285	340.2231	170.6152			3
8	851.4873	426.2473	833.4767	417.2420	P	244.1656	122.5864	227.1390	114.0731			2
9					K	147.1128	74.0600	130.0863	65.5468			1

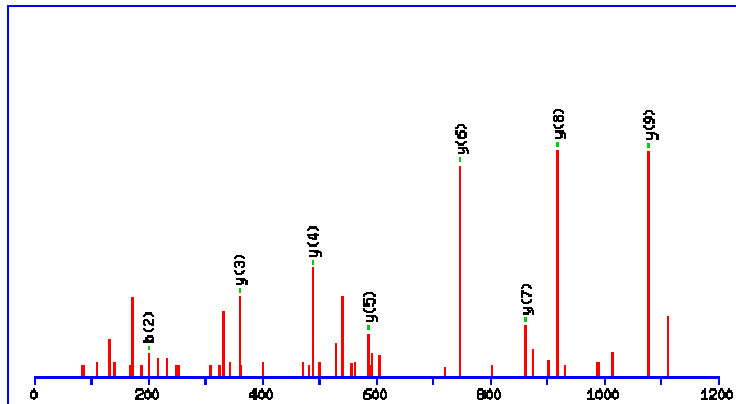


Peptide Number: 5266MS/MS Fragmentation of **SICGDCVQGQR**Found in **IPI00400935** in **IPI_human**, Tax_Id=9606 Gene_Symbol=COL16A1 Isoform 1 of Collagen alpha-1(XVI) chain

Match to Query 19500: 1278.540388 from(640.277470,2+) index(14392)

Title: Elution from: 68.85 to 68.85 period: 0 cycle: 6396 experiment: 10 polarity:+

Data file 120208ry_Tig120slc-P8_1_1.mgf



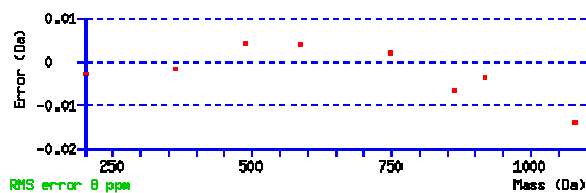
Monoisotopic mass of neutral peptide Mr(calc): 1278.5445

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

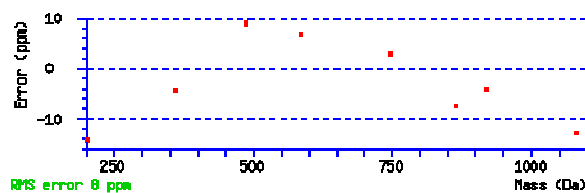
Ions Score: 60 Expect: 1.2e-005

Matches : 8/94 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{++*}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{++*}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							11
2	201.1234	101.0653			183.1128	92.0600	I	1192.5198	596.7635	1175.4932	588.2502	1174.5092	587.7582	10
3	361.1540	181.0806			343.1435	172.0754	C	1079.4357	540.2215	1062.4091	531.7082	1061.4251	531.2162	9
4	418.1755	209.5914			400.1649	200.5861	G	919.4050	460.2062	902.3785	451.6929	901.3945	451.2009	8
5	533.2024	267.1049			515.1919	258.0996	D	862.3836	431.6954	845.3570	423.1822	844.3730	422.6901	7
6	693.2331	347.1202			675.2225	338.1149	C	747.3566	374.1820	730.3301	365.6687			6
7	792.3015	396.6544			774.2909	387.6491	V	587.3260	294.1666	570.2994	285.6534			5
8	920.3601	460.6837	903.3335	452.1704	902.3495	451.6784	Q	488.2576	244.6324	471.2310	236.1191			4
9	977.3815	489.1944	960.3550	480.6811	959.3710	480.1891	G	360.1990	180.6031	343.1724	172.0899			3
10	1105.4401	553.2237	1088.4136	544.7104	1087.4295	544.2184	Q	303.1775	152.0924	286.1510	143.5791			2
11							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 8 ppm



RMS error 8 ppm

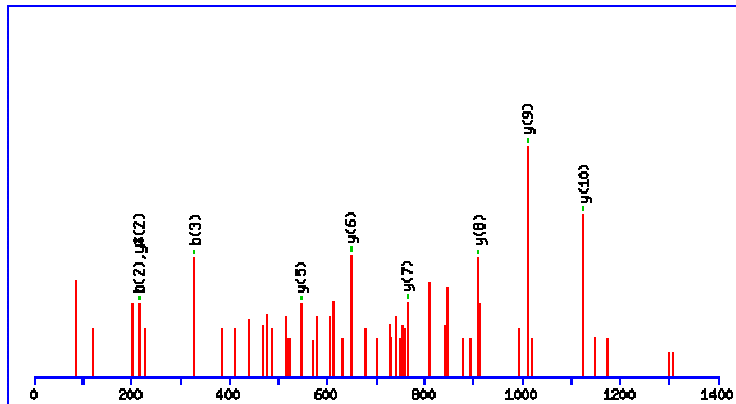
Peptide Number: 5539

MS/MS Fragmentation of **VDLITFDTPFAGR**Found in **IPI00218413** in **IPI_human**, Tax_Id=9606 Gene_Symbol=BTD Biotinidase

Match to Query 14901: 1450.737828 from(726.376190,2+) index(36277)

Title: Elution from: 91.1333333333333 to 91.1333333333333 period: 0 cycle: 3397 experiment: 9 polarity:+

Data file 120126ry_585A1-55_2_3.mgf



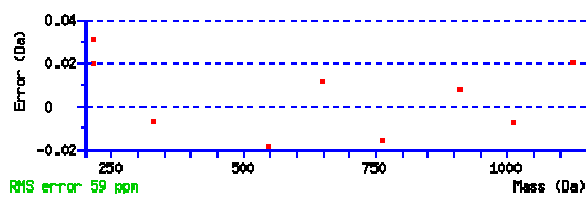
Monoisotopic mass of neutral peptide Mr(calc): 1450.7457

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

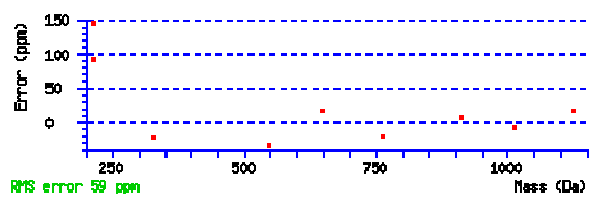
Ions Score: 40 Expect: 0.0065

Matches : 9/108 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415			V							13
2	215.1026	108.0550	197.0921	99.0497	D	1352.6845	676.8459	1335.6579	668.3326	1334.6739	667.8406	12
3	328.1867	164.5970	310.1761	155.5917	L	1237.6576	619.3324	1220.6310	610.8191	1219.6470	610.3271	11
4	441.2708	221.1390	423.2602	212.1337	I	1124.5735	562.7904	1107.5469	554.2771	1106.5629	553.7851	10
5	542.3184	271.6629	524.3079	262.6576	T	1011.4894	506.2483	994.4629	497.7351	993.4789	497.2431	9
6	689.3869	345.1971	671.3763	336.1918	F	910.4417	455.7245	893.4152	447.2112	892.4312	446.7192	8
7	804.4138	402.7105	786.4032	393.7053	D	763.3733	382.1903	746.3468	373.6770	745.3628	373.1850	7
8	905.4615	453.2344	887.4509	444.2291	T	648.3464	324.6768	631.3198	316.1636	630.3358	315.6715	6
9	1002.5142	501.7608	984.5037	492.7555	P	547.2987	274.1530	530.2722	265.6397			5
10	1149.5827	575.2950	1131.5721	566.2897	F	450.2459	225.6266	433.2194	217.1133			4
11	1220.6198	610.8135	1202.6092	601.8082	A	303.1775	152.0924	286.1510	143.5791			3
12	1277.6412	639.3243	1259.6307	630.3190	G	232.1404	116.5738	215.1139	108.0606			2
13					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 59 ppm



RMS error 59 ppm

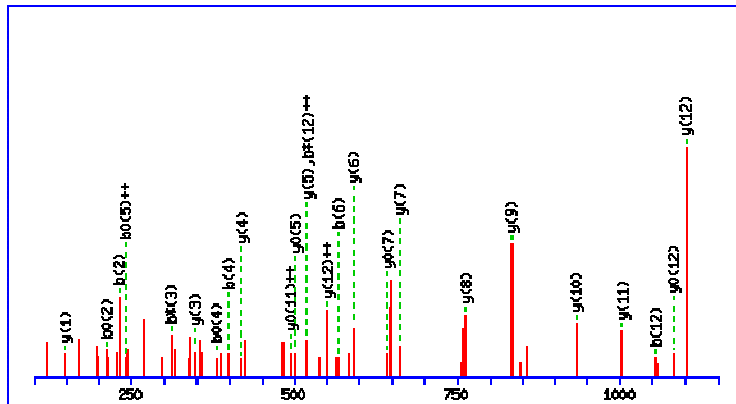
Peptide Number: 5643

MS/MS Fragmentation of **TQPAVATAATAAEK**Found in **IPI00645192** in **IPI_human**, Tax_Id=9606 Gene_Symbol=MECP2 Mutant methyl CpG binding protein 2 variant 1

Match to Query 21623: 1328.687048 from(665.350800,2+) index(21012)

Title: Elution from: 85.5666666666667 to 85.5666666666667 period: 0 cycle: 7450 experiment: 8 polarity: +

Data file 120208ry_Tig120slc-P8_2_1.mgf



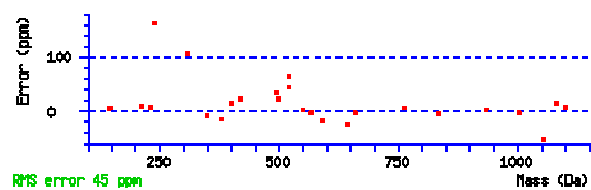
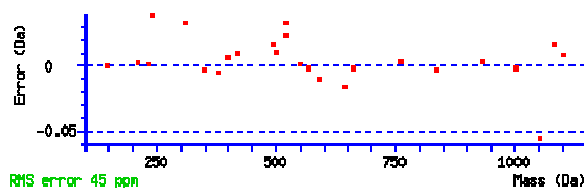
Monoisotopic mass of neutral peptide Mr(calc): 1328.6936

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 64 Expect: 2.9e-005

Matches : 25/152 fragment ions using 55 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							14
2	230.1135	115.5604	213.0870	107.0471	212.1030	106.5551	Q	1228.6532	614.8302	1211.6266	606.3170	1210.6426	605.8250	13
3	327.1663	164.0868	310.1397	155.5735	309.1557	155.0815	P	1100.5946	550.8009	1083.5681	542.2877	1082.5841	541.7957	12
4	398.2034	199.6053	381.1769	191.0921	380.1928	190.6001	A	1003.5419	502.2746	986.5153	493.7613	985.5313	493.2693	11
5	497.2718	249.1396	480.2453	240.6263	479.2613	240.1343	V	932.5047	466.7560	915.4782	458.2427	914.4942	457.7507	10
6	568.3089	284.6581	551.2824	276.1448	550.2984	275.6528	A	833.4363	417.2218	816.4098	408.7085	815.4258	408.2165	9
7	669.3566	335.1819	652.3301	326.6687	651.3461	326.1767	T	762.3992	381.7032	745.3727	373.1900	744.3886	372.6980	8
8	740.3937	370.7005	723.3672	362.1872	722.3832	361.6952	A	661.3515	331.1794	644.3250	322.6661	643.3410	322.1741	7
9	811.4308	406.2191	794.4043	397.7058	793.4203	397.2138	A	590.3144	295.6608	573.2879	287.1476	572.3039	286.6556	6
10	912.4785	456.7429	895.4520	448.2296	894.4680	447.7376	T	519.2773	260.1423	502.2508	251.6290	501.2667	251.1370	5
11	983.5156	492.2615	966.4891	483.7482	965.5051	483.2562	A	418.2296	209.6185	401.2031	201.1052	400.2191	200.6132	4
12	1054.5528	527.7800	1037.5262	519.2667	1036.5422	518.7747	A	347.1925	174.0999	330.1660	165.5866	329.1819	165.0946	3
13	1183.5953	592.3013	1166.5688	583.7880	1165.5848	583.2960	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
14							K	147.1128	74.0600	130.0863	65.5468			1



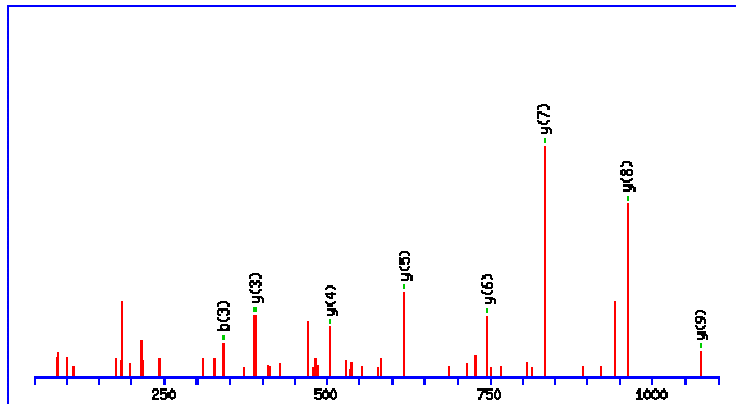
Peptide Number: 5949

MS/MS Fragmentation of **VLQSQDLTLR**Found in **IPI00152001** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TRIM3 Isoform Alpha of Tripartite motif-containing protein 3

Match to Query 12858: 1171.653648 from(586.834100,2+) index(14202)

Title: Elution from: 33.7666666666667 to 33.7666666666667 period: 0 cycle: 1280 experiment: 7 polarity:+

Data file 120208ry_Tig120slc-P8_2_2.mgf



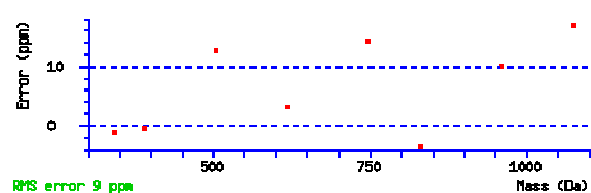
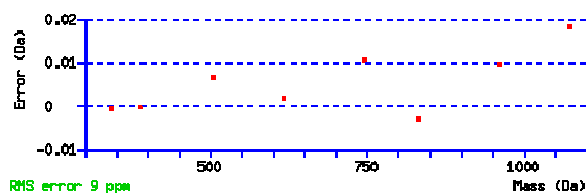
Monoisotopic mass of neutral peptide Mr(calc): 1171.6561

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 65 Expect: 2.4e-005

Matches : 8/94 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							10
2	213.1598	107.0835					L	1073.5949	537.3011	1056.5684	528.7878	1055.5844	528.2958	9
3	341.2183	171.1128	324.1918	162.5995			Q	960.5109	480.7591	943.4843	472.2458	942.5003	471.7538	8
4	428.2504	214.6288	411.2238	206.1155	410.2398	205.6235	S	832.4523	416.7298	815.4258	408.2165	814.4417	407.7245	7
5	556.3089	278.6581	539.2824	270.1448	538.2984	269.6528	Q	745.4203	373.2138	728.3937	364.7005	727.4097	364.2085	6
6	669.3930	335.2001	652.3665	326.6869	651.3824	326.1949	L	617.3617	309.1845	600.3352	300.6712	599.3511	300.1792	5
7	784.4199	392.7136	767.3934	384.2003	766.4094	383.7083	D	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	4
8	885.4676	443.2375	868.4411	434.7242	867.4571	434.2322	T	389.2507	195.1290	372.2241	186.6157	371.2401	186.1237	3
9	998.5517	499.7795	981.5251	491.2662	980.5411	490.7742	L	288.2030	144.6051	271.1765	136.0919			2
10							R	175.1190	88.0631	158.0924	79.5498			1



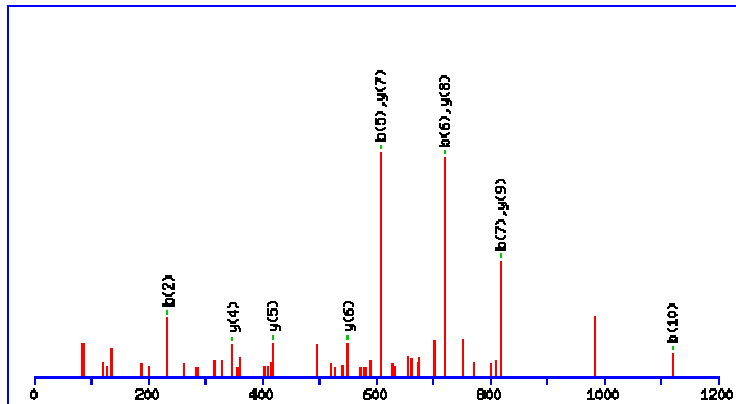
Peptide Number: 6077

MS/MS Fragmentation of **HPVCLLVLMAGSGK**Found in **IPI00027035** in **IPI_human**, Tax_Id=9606 Gene_Symbol=GPN1 GPN-loop GTPase 1 isoform a

Match to Query 13572: 1537.802682 from(513.608170,3+) index(7847)

Title: Elution from: 19.35 to 19.35 period: 0 cycle: 729 experiment: 5 polarity:+

Data file 120210ry_32R1-32_2_3.mgf



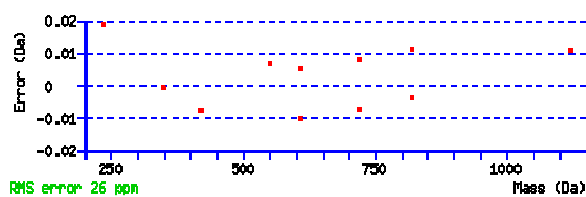
Monoisotopic mass of neutral peptide Mr(calc): 1537.8109

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

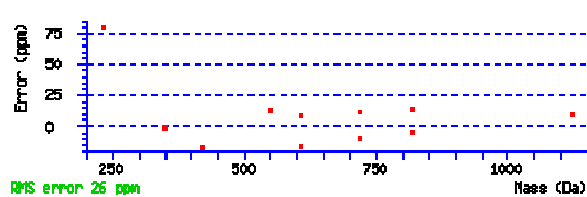
Ions Score: 52 Expect: 0.00046

Matches : 11/112 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	138.0662	69.5367			H							15
2	235.1190	118.0631			P	1401.7593	701.3833	1384.7327	692.8700	1383.7487	692.3780	14
3	334.1874	167.5973			V	1304.7065	652.8569	1287.6799	644.3436	1286.6959	643.8516	13
4	494.2180	247.6126			C	1205.6381	603.3227	1188.6115	594.8094	1187.6275	594.3174	12
5	607.3021	304.1547			L	1045.6074	523.3074	1028.5809	514.7941	1027.5969	514.3021	11
6	720.3861	360.6967			L	932.5234	466.7653	915.4968	458.2520	914.5128	457.7600	10
7	819.4546	410.2309			V	819.4393	410.2233	802.4128	401.7100	801.4287	401.2180	9
8	932.5386	466.7729			L	720.3709	360.6891	703.3443	352.1758	702.3603	351.6838	8
9	989.5601	495.2837			G	607.2868	304.1470	590.2603	295.6338	589.2763	295.1418	7
10	1120.6006	560.8039			M	550.2654	275.6363	533.2388	267.1230	532.2548	266.6310	6
11	1191.6377	596.3225			A	419.2249	210.1161	402.1983	201.6028	401.2143	201.1108	5
12	1248.6591	624.8332			G	348.1878	174.5975	331.1612	166.0842	330.1772	165.5922	4
13	1335.6912	668.3492	1317.6806	659.3439	S	291.1663	146.0868	274.1397	137.5735	273.1557	137.0815	3
14	1392.7126	696.8600	1374.7021	687.8547	G	204.1343	102.5708	187.1077	94.0575			2
15					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 26 ppm



RMS error 26 ppm

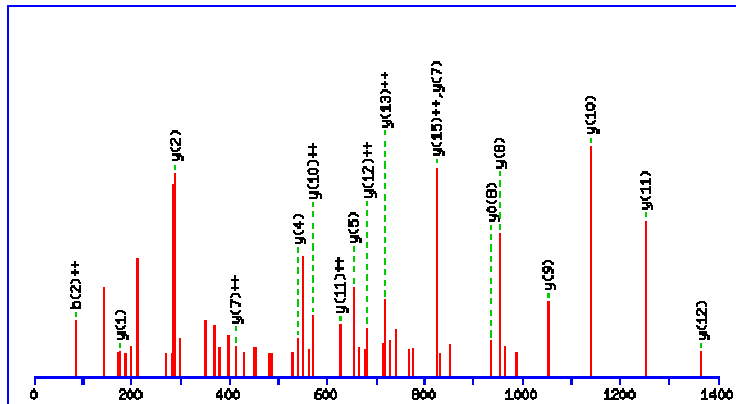
Peptide Number: 6417

MS/MS Fragmentation of **GIPNAISVEGINHDIR**Found in **IPI00643389** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CPXM2 Uncharacterized protein

Match to Query 20634: 1816.977462 from(606.666430,3+) index(12850)

Title: Elution from: 31.7166666666667 to 31.7166666666667 period: 0 cycle: 1201 experiment: 3 polarity: +

Data file 120206ry_aHDF1419-P10_2_3.mgf



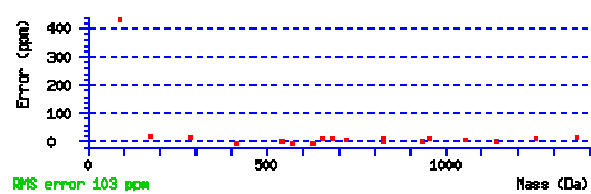
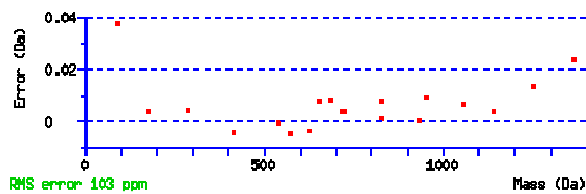
Monoisotopic mass of neutral peptide Mr(calc): 1816.9795

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 60 Expect: 4.8e-005

Matches : 18/168 fragment ions using 32 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							17
2	171.1128	86.0600					I	1760.9654	880.9863	1743.9388	872.4730	1742.9548	871.9810	16
3	268.1656	134.5864					P	1647.8813	824.4443	1630.8547	815.9310	1629.8707	815.4390	15
4	382.2085	191.6079	365.1819	183.0946			N	1550.8285	775.9179	1533.8020	767.4046	1532.8180	766.9126	14
5	453.2456	227.1264	436.2191	218.6132			A	1436.7856	718.8964	1419.7591	710.3832	1418.7750	709.8912	13
6	566.3297	283.6685	549.3031	275.1552			I	1365.7485	683.3779	1348.7219	674.8646	1347.7379	674.3726	12
7	679.4137	340.2105	662.3872	331.6972			I	1252.6644	626.8359	1235.6379	618.3226	1234.6539	617.8306	11
8	766.4458	383.7265	749.4192	375.2132	748.4352	374.7212	S	1139.5804	570.2938	1122.5538	561.7805	1121.5698	561.2885	10
9	865.5142	433.2607	848.4876	424.7475	847.5036	424.2554	V	1052.5483	526.7778	1035.5218	518.2645	1034.5378	517.7725	9
10	994.5568	497.7820	977.5302	489.2687	976.5462	488.7767	E	953.4799	477.2436	936.4534	468.7303	935.4694	468.2383	8
11	1051.5782	526.2928	1034.5517	517.7795	1033.5677	517.2875	G	824.4373	412.7223	807.4108	404.2090	806.4268	403.7170	7
12	1164.6623	582.8348	1147.6358	574.3215	1146.6517	573.8295	I	767.4159	384.2116	750.3893	375.6983	749.4053	375.2063	6
13	1278.7052	639.8563	1261.6787	631.3430	1260.6947	630.8510	N	654.3318	327.6695	637.3052	319.1563	636.3212	318.6643	5
14	1415.7641	708.3857	1398.7376	699.8724	1397.7536	699.3804	H	540.2889	270.6481	523.2623	262.1348	522.2783	261.6428	4
15	1530.7911	765.8992	1513.7645	757.3859	1512.7805	756.8939	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
16	1643.8751	822.4412	1626.8486	813.9279	1625.8646	813.4359	I	288.2030	144.6051	271.1765	136.0919			2
17							R	175.1190	88.0631	158.0924	79.5498			1



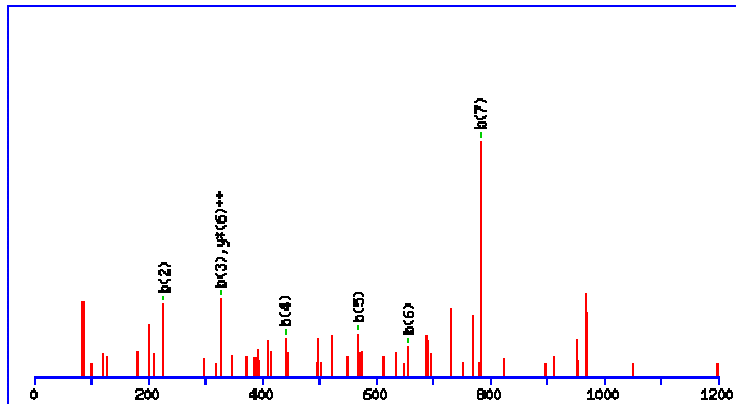
Peptide Number: 6523

MS/MS Fragmentation of **KVVIKSEAASPALPVITK**Found in **IPI00019155** in **IPI_human**, Tax_Id=9606 Gene_Symbol=FOXC2 Forkhead box protein C2

Match to Query 8566: 1850.114292 from(617.712040,3+) index(5466)

Title: Elution from: 16.0833333333333 to 16.0833333333333 period: 0 cycle: 624 experiment: 2 polarity: +

Data file 120210ry_585A1-55_3_4.mgf



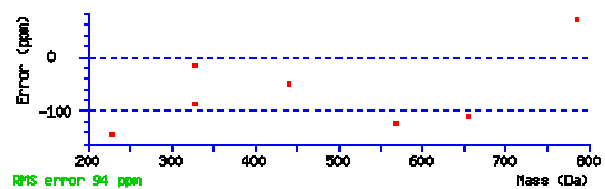
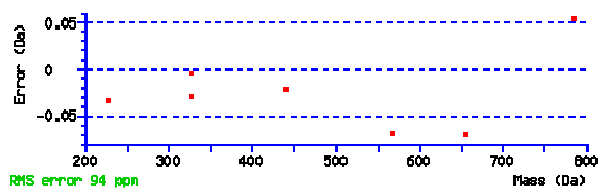
Monoisotopic mass of neutral peptide Mr(calc): 1850.1241

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 33 Expect: 0.0018

Matches : 7/192 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.1022	65.0548	112.0757	56.5415			K							18
2	228.1707	114.5890	211.1441	106.0757			V	1723.0364	862.0218	1706.0098	853.5086	1705.0258	853.0166	17
3	327.2391	164.1232	310.2125	155.6099			V	1623.9680	812.4876	1606.9414	803.9744	1605.9574	803.4823	16
4	440.3231	220.6652	423.2966	212.1519			I	1524.8996	762.9534	1507.8730	754.4401	1506.8890	753.9481	15
5	568.4181	284.7127	551.3915	276.1994			K	1411.8155	706.4114	1394.7890	697.8981	1393.8049	697.4061	14
6	655.4501	328.2287	638.4236	319.7154	637.4396	319.2234	S	1283.7205	642.3639	1266.6940	633.8506	1265.7100	633.3586	13
7	784.4927	392.7500	767.4662	384.2367	766.4822	383.7447	E	1196.6885	598.8479	1179.6620	590.3346	1178.6780	589.8426	12
8	855.5298	428.2686	838.5033	419.7553	837.5193	419.2633	A	1067.6459	534.3266	1050.6194	525.8133	1049.6354	525.3213	11
9	926.5669	463.7871	909.5404	455.2738	908.5564	454.7818	A	996.6088	498.8080	979.5823	490.2948	978.5982	489.8028	10
10	1013.5990	507.3031	996.5724	498.7898	995.5884	498.2978	S	925.5717	463.2895	908.5451	454.7762	907.5611	454.2842	9
11	1110.6517	555.8295	1093.6252	547.3162	1092.6412	546.8242	P	838.5397	419.7735	821.5131	411.2602	820.5291	410.7682	8
12	1181.6888	591.3481	1164.6623	582.8348	1163.6783	582.3428	A	741.4869	371.2471	724.4604	362.7338	723.4763	362.2418	7
13	1294.7729	647.8901	1277.7464	639.3768	1276.7623	638.8848	L	670.4498	335.7285	653.4232	327.2153	652.4392	326.7233	6
14	1391.8257	696.4165	1374.7991	687.9032	1373.8151	687.4112	P	557.3657	279.1865	540.3392	270.6732	539.3552	270.1812	5
15	1490.8941	745.9507	1473.8675	737.4374	1472.8835	736.9454	V	460.3130	230.6601	443.2864	222.1468	442.3024	221.6548	4
16	1603.9782	802.4927	1586.9516	793.9794	1585.9676	793.4874	I	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
17	1705.0258	853.0166	1687.9993	844.5033	1687.0153	844.0113	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
18							K	147.1128	74.0600	130.0863	65.5468			1



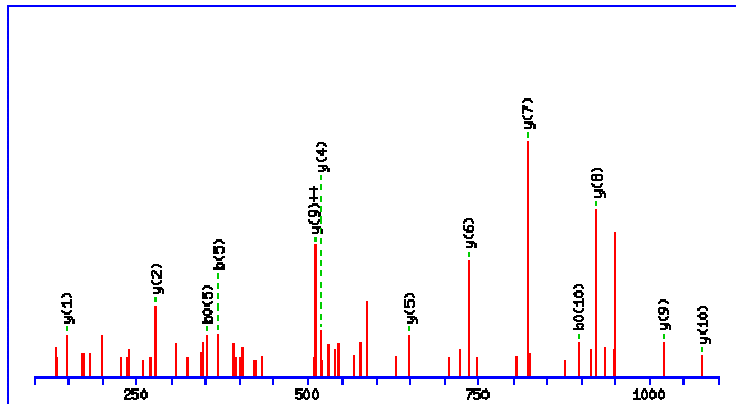
Peptide Number: 6802

MS/MS Fragmentation of **GGGPTSSEQIMK**Found in **IPI00071059** in **IPI_human**, Tax_Id=9606 Gene_Symbol=BAX Isoform Epsilon of Apoptosis regulator BAX

Match to Query 17641: 1190.564508 from(596.289530,2+) index(17859)

Title: Elution from: 80.9333333333333 to 80.9333333333333 period: 0 cycle: 7848 experiment: 9 polarity:+

Data file 120210ry_32R1-32_2_1.mgf



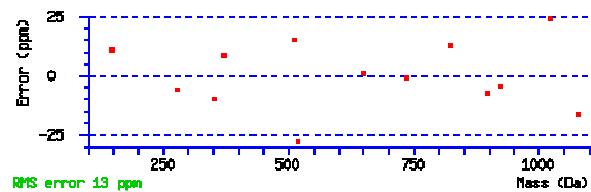
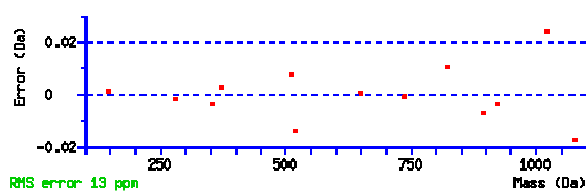
Monoisotopic mass of neutral peptide Mr(calc): 1190.5601

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 84 Expect: 1.9e-007

Matches : 13/100 fragment ions using 19 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							12
2	115.0502	58.0287					G	1134.5460	567.7766	1117.5194	559.2633	1116.5354	558.7713	11
3	172.0717	86.5395					G	1077.5245	539.2659	1060.4979	530.7526	1059.5139	530.2606	10
4	269.1244	135.0659					P	1020.5030	510.7551	1003.4765	502.2419	1002.4925	501.7499	9
5	370.1721	185.5897			352.1615	176.5844	T	923.4503	462.2288	906.4237	453.7155	905.4397	453.2235	8
6	457.2041	229.1057			439.1936	220.1004	S	822.4026	411.7049	805.3760	403.1917	804.3920	402.6996	7
7	544.2362	272.6217			526.2256	263.6164	S	735.3706	368.1889	718.3440	359.6756	717.3600	359.1836	6
8	673.2788	337.1430			655.2682	328.1377	E	648.3385	324.6729	631.3120	316.1596	630.3280	315.6676	5
9	801.3373	401.1723	784.3108	392.6590	783.3268	392.1670	Q	519.2959	260.1516	502.2694	251.6383			4
10	914.4214	457.7143	897.3949	449.2011	896.4108	448.7091	I	391.2374	196.1223	374.2108	187.6090			3
11	1045.4619	523.2346	1028.4353	514.7213	1027.4513	514.2293	M	278.1533	139.5803	261.1267	131.0670			2
12							K	147.1128	74.0600	130.0863	65.5468			1



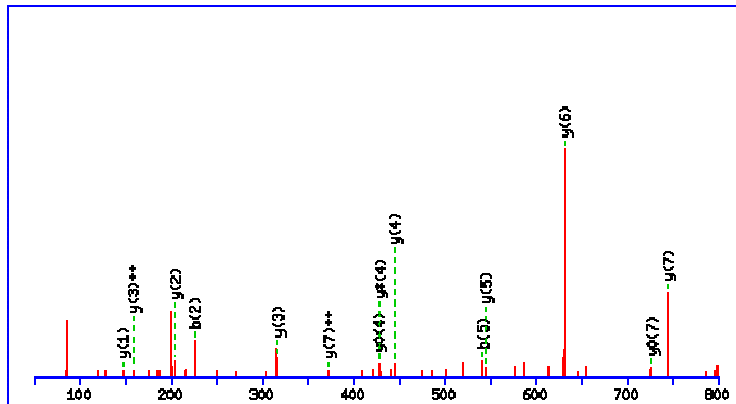
Peptide Number: 7268

MS/MS Fragmentation of **ILSVELGK**Found in **IPI00784651** in **IPI_human**, Tax_Id=9606 Gene_Symbol=FADS1 fatty acid desaturase 1

Match to Query 2243: 857.522088 from(429.768320,2+) index(14073)

Title: Elution from: 35.9833333333333 to 35.9833333333333 period: 0 cycle: 1372 experiment: 3 polarity:+

Data file 120206ry_aHDF1419-P10_3_2.mgf



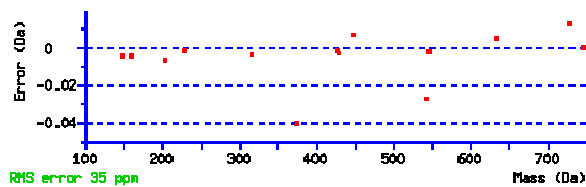
Monoisotopic mass of neutral peptide Mr(calcd): 857.5222

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

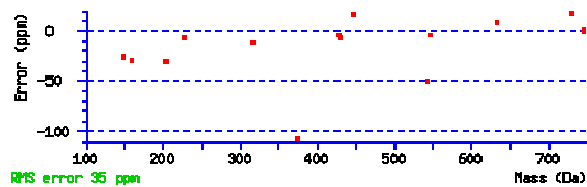
Ions Score: 44 Expect: 0.0027

Matches : 14/60 fragment ions using 35 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			I							8
2	227.1754	114.0913			L	745.4454	373.2264	728.4189	364.7131	727.4349	364.2211	7
3	314.2074	157.6074	296.1969	148.6021	S	632.3614	316.6843	615.3348	308.1710	614.3508	307.6790	6
4	413.2758	207.1416	395.2653	198.1363	V	545.3293	273.1683	528.3028	264.6550	527.3188	264.1630	5
5	542.3184	271.6629	524.3079	262.6576	E	446.2609	223.6341	429.2344	215.1208	428.2504	214.6288	4
6	655.4025	328.2049	637.3919	319.1996	L	317.2183	159.1128	300.1918	150.5995			3
7	712.4240	356.7156	694.4134	347.7103	G	204.1343	102.5708	187.1077	94.0575			2
8					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 35 ppm



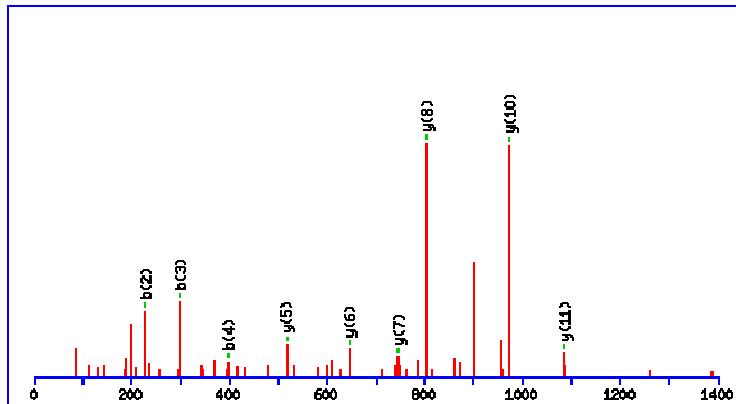
RMS error 35 ppm

Peptide Number: 7654MS/MS Fragmentation of **ILAVGTQTGALR**Found in **IPI00645854** in **IPI_human**, Tax_Id=9606 Gene_Symbol=STXBP5 Isoform 2 of Syntaxin-binding protein 5

Match to Query 14046: 1198.695148 from(600.354850,2+) index(12078)

Title: Elution from: 28.7 to 28.7 period: 0 cycle: 1087 experiment: 7 polarity: +

Data file 120208ry_Tig120slc-P8_2_2.mgf



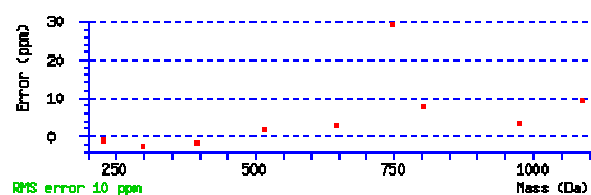
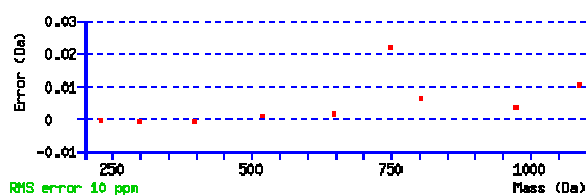
Monoisotopic mass of neutral peptide Mr(calc): 1198.7034

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 56 Expect: 0.00013

Matches : 9/102 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							12
2	227.1754	114.0913					L	1086.6266	543.8169	1069.6000	535.3037	1068.6160	534.8116	11
3	298.2125	149.6099					A	973.5425	487.2749	956.5160	478.7616	955.5320	478.2696	10
4	397.2809	199.1441					V	902.5054	451.7563	885.4789	443.2431	884.4948	442.7511	9
5	454.3024	227.6548					G	803.4370	402.2221	786.4104	393.7089	785.4264	393.2169	8
6	555.3501	278.1787			537.3395	269.1734	T	746.4155	373.7114	729.3890	365.1981	728.4050	364.7061	7
7	683.4087	342.2080	666.3821	333.6947	665.3981	333.2027	Q	645.3679	323.1876	628.3413	314.6743	627.3573	314.1823	6
8	784.4563	392.7318	767.4298	384.2185	766.4458	383.7265	T	517.3093	259.1583	500.2827	250.6450	499.2987	250.1530	5
9	841.4778	421.2425	824.4512	412.7293	823.4672	412.2373	G	416.2616	208.6344	399.2350	200.1212			4
10	912.5149	456.7611	895.4884	448.2478	894.5043	447.7558	A	359.2401	180.1237	342.2136	171.6104			3
11	1025.5990	513.3031	1008.5724	504.7899	1007.5884	504.2978	L	288.2030	144.6051	271.1765	136.0919			2
12							R	175.1190	88.0631	158.0924	79.5498			1



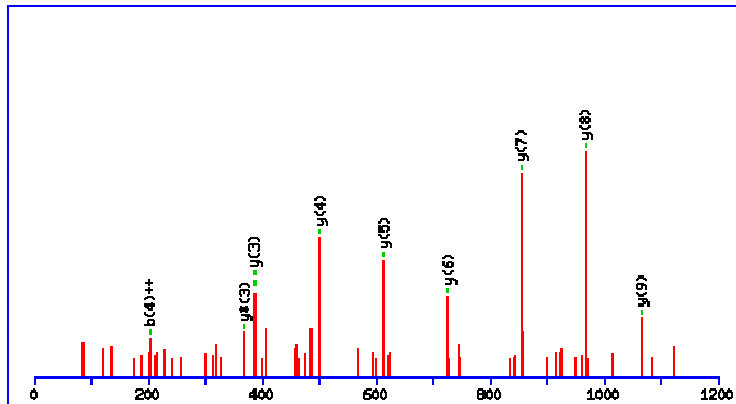
Peptide Number: 7809

MS/MS Fragmentation of **SDDSVIQLLNPNR**Found in **IPI01011813** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CADM1 Protein

Match to Query 10123: 1469.759468 from(735.887010,2+) index(14812)

Title: Elution from: 36 to 36 period: 0 cycle: 1354 experiment: 6 polarity: +

Data file 120212ry_414C2-43_3.mgf



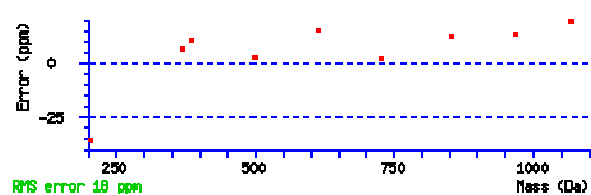
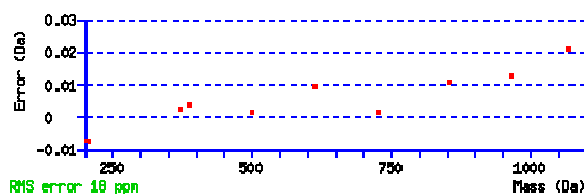
Monoisotopic mass of neutral peptide Mr(calc): 1469.7474

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 60 Expect: 6.8e-005

Matches : 10/114 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							13
2	203.0662	102.0368			185.0557	93.0315	D	1383.7227	692.3650	1366.6961	683.8517	1365.7121	683.3597	12
3	318.0932	159.5502			300.0826	150.5450	D	1268.6957	634.8515	1251.6692	626.3382	1250.6852	625.8462	11
4	405.1252	203.0662			387.1147	194.0610	S	1153.6688	577.3380	1136.6422	568.8248	1135.6582	568.3327	10
5	504.1936	252.6005			486.1831	243.5952	V	1066.6368	533.8220	1049.6102	525.3087			9
6	617.2777	309.1425			599.2671	300.1372	I	967.5683	484.2878	950.5418	475.7745			8
7	745.3363	373.1718	728.3097	364.6585	727.3257	364.1665	Q	854.4843	427.7458	837.4577	419.2325			7
8	858.4203	429.7138	841.3938	421.2005	840.4098	420.7085	L	726.4257	363.7165	709.3991	355.2032			6
9	971.5044	486.2558	954.4779	477.7426	953.4938	477.2506	L	613.3416	307.1745	596.3151	298.6612			5
10	1085.5473	543.2773	1068.5208	534.7640	1067.5368	534.2720	N	500.2576	250.6324	483.2310	242.1191			4
11	1182.6001	591.8037	1165.5735	583.2904	1164.5895	582.7984	P	386.2146	193.6110	369.1881	185.0977			3
12	1296.6430	648.8251	1279.6165	640.3119	1278.6325	639.8199	N	289.1619	145.0846	272.1353	136.5713			2
13							R	175.1190	88.0631	158.0924	79.5498			1



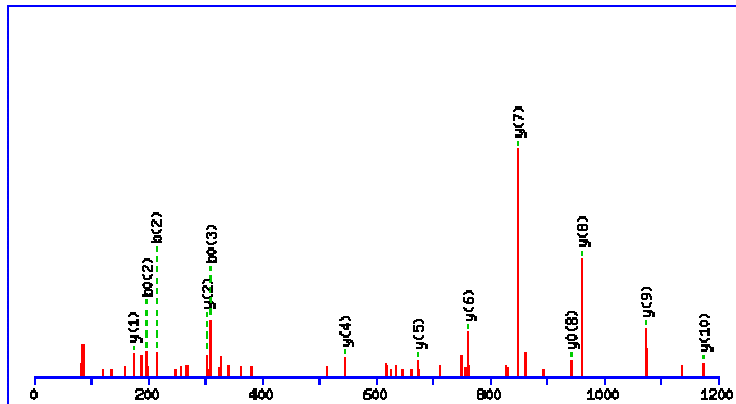
Peptide Number: 7927

MS/MS Fragmentation of **LTLSSLEQQR**Found in **IPI00604494** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CCDC92 Coiled-coil domain-containing protein 92

Match to Query 18301: 1287.700788 from(644.857670,2+) index(44300)

Title: Elution from: 106.733333333333 to 106.733333333333 period: 0 cycle: 4056 experiment: 6 polarity: +

Data file 120212ry_aHDF1388-P9_2_2.mgf



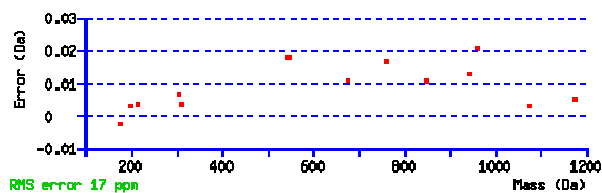
Monoisotopic mass of neutral peptide Mr(calc): 1287.7034

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

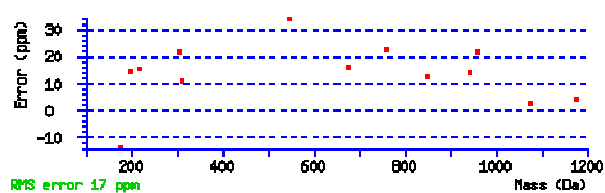
Ions Score: 75 Expect: 2e-006

Matches : 13/96 fragment ions using 20 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							11
2	215.1390	108.0731			197.1285	99.0679	T	1175.6266	588.3170	1158.6001	579.8037	1157.6161	579.3117	10
3	328.2231	164.6152			310.2125	155.6099	L	1074.5790	537.7931	1057.5524	529.2798	1056.5684	528.7878	9
4	441.3071	221.1572			423.2966	212.1519	L	961.4949	481.2511	944.4684	472.7378	943.4843	472.2458	8
5	528.3392	264.6732			510.3286	255.6679	S	848.4108	424.7091	831.3843	416.1958	830.4003	415.7038	7
6	615.3712	308.1892			597.3606	299.1840	S	761.3788	381.1930	744.3523	372.6798	743.3682	372.1878	6
7	744.4138	372.7105			726.4032	363.7053	E	674.3468	337.6770	657.3202	329.1638	656.3362	328.6717	5
8	857.4979	429.2526			839.4873	420.2473	L	545.3042	273.1557	528.2776	264.6425	527.2936	264.1504	4
9	986.5405	493.7739			968.5299	484.7686	E	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	3
10	1114.5990	557.8032	1097.5725	549.2899	1096.5885	548.7979	Q	303.1775	152.0924	286.1510	143.5791			2
11							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 17 ppm



RMS error 17 ppm

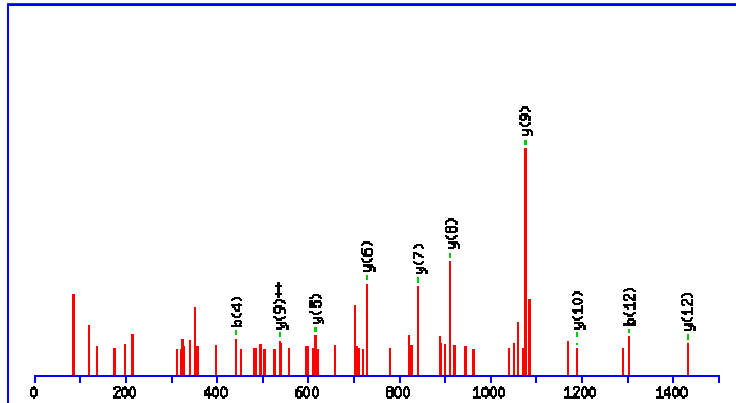
Peptide Number: 8126

MS/MS Fragmentation of **IIDTPGLLKPEQVSALFGNIENIYALNSQLLR**Found in **IPI00291711** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PLEKHG3 Isoform 1 of Pleckstrin homology domain-containing family G member 3

Match to Query 7249: 3538.946096 from(885.743800,4+) index(4976)

Title: Elution from: 23.6666666666667 to 23.6666666666667 period: 0 cycle: 927 experiment: 3 polarity:+

Data file 120210ry_32R1-32_2_5.mgf



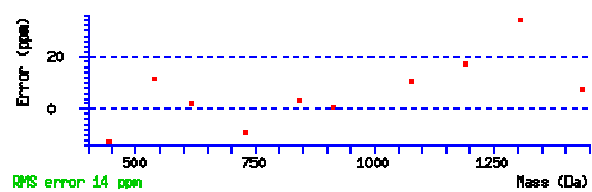
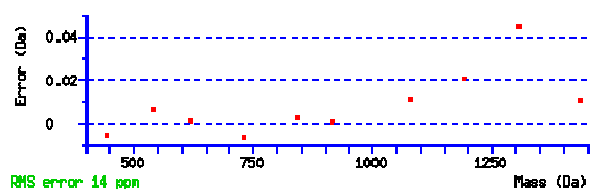
Monoisotopic mass of neutral peptide Mr(calc): 3538.9399

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 40 Expect: 0.0016

Matches : 10/344 fragment ions using 14 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							32
2	227.1754	114.0913					I	3426.8631	1713.9352	3409.8366	1705.4219	3408.8526	1704.9299	31
3	342.2023	171.6048			324.1918	162.5995	D	3313.7791	1657.3932	3296.7525	1648.8799	3295.7685	1648.3879	30
4	443.2500	222.1287			425.2395	213.1234	T	3198.7521	1599.8797	3181.7256	1591.3664	3180.7416	1590.8744	29
5	540.3028	270.6550			522.2922	261.6498	P	3097.7044	1549.3559	3080.6779	1540.8426	3079.6939	1540.3506	28
6	597.3243	299.1658			579.3137	290.1605	G	3000.6517	1500.8295	2983.6251	1492.3162	2982.6411	1491.8242	27
7	710.4083	355.7078			692.3978	346.7025	L	2943.6302	1472.3187	2926.6037	1463.8055	2925.6197	1463.3135	26
8	823.4924	412.2498			805.4818	403.2445	L	2830.5462	1415.7767	2813.5196	1407.2634	2812.5356	1406.7714	25
9	951.5873	476.2973	934.5608	467.7840	933.5768	467.2920	K	2717.4621	1359.2347	2700.4355	1350.7214	2699.4515	1350.2294	24
10	1048.6401	524.8237	1031.6136	516.3104	1030.6295	515.8184	P	2589.3671	1295.1872	2572.3406	1286.6739	2571.3566	1286.1819	23
11	1177.6827	589.3450	1160.6562	580.8317	1159.6721	580.3397	E	2492.3144	1246.6608	2475.2878	1238.1475	2474.3038	1237.6555	22
12	1305.7413	653.3743	1288.7147	644.8610	1287.7307	644.3690	Q	2363.2718	1182.1395	2346.2452	1173.6262	2345.2612	1173.1342	21
13	1404.8097	702.9085	1387.7831	694.3952	1386.7991	693.9032	V	2235.2132	1118.1102	2218.1866	1109.5970	2217.2026	1109.1050	20
14	1491.8417	746.4245	1474.8152	737.9112	1473.8312	737.4192	S	2136.1448	1068.5760	2119.1182	1060.0628	2118.1342	1059.5707	19
15	1562.8788	781.9431	1545.8523	773.4298	1544.8683	772.9378	A	2049.1128	1025.0600	2032.0862	1016.5467	2031.1022	1016.0547	18
16	1675.9629	838.4851	1658.9364	829.9718	1657.9523	829.4798	L	1978.0756	989.5415	1961.0491	981.0282	1960.0651	980.5362	17
17	1823.0313	912.0193	1806.0048	903.5060	1805.0207	903.0140	F	1864.9916	932.9994	1847.9650	924.4862	1846.9810	923.9941	16
18	1880.0528	940.5300	1863.0262	932.0168	1862.0422	931.5247	G	1717.9232	859.4652	1700.8966	850.9519	1699.9126	850.4599	15
19	1994.0957	997.5515	1977.0692	989.0382	1976.0851	988.5462	N	1660.9017	830.9545	1643.8751	822.4412	1642.8911	821.9492	14
20	2107.1798	1054.0935	2090.1532	1045.5802	2089.1692	1045.0882	I	1546.8588	773.9330	1529.8322	765.4197	1528.8482	764.9277	13
21	2236.2224	1118.6148	2219.1958	1110.1015	2218.2118	1109.6095	E	1433.7747	717.3910	1416.7482	708.8777	1415.7641	708.3857	12
22	2350.2653	1175.6363	2333.2387	1167.1230	2332.2547	1166.6310	N	1304.7321	652.8697	1287.7056	644.3564	1286.7215	643.8644	11
23	2463.3494	1232.1783	2446.3228	1223.6650	2445.3388	1223.1730	I	1190.6892	595.8482	1173.6626	587.3350	1172.6786	586.8429	10
24	2626.4127	1313.7100	2609.3861	1305.1967	2608.4021	1304.7047	Y	1077.6051	539.3062	1060.5786	530.7929	1059.5946	530.3009	9
25	2697.4498	1349.2285	2680.4232	1340.7153	2679.4392	1340.2233	A	914.5418	457.7745	897.5152	449.2613	896.5312	448.7693	8
26	2810.5339	1405.7706	2793.5073	1397.2573	2792.5233	1396.7653	L	843.5047	422.2560	826.4781	413.7427	825.4941	413.2507	7
27	2924.5768	1462.7920	2907.5502	1454.2788	2906.5662	1453.7867	N	730.4206	365.7139	713.3941	357.2007	712.4100	356.7087	6
28	3011.6088	1506.3080	2994.5823	1497.7948	2993.5983	1497.3028	S	616.3777	308.6925	599.3511	300.1792	598.3671	299.6872	5
29	3139.6674	1570.3373	3122.6408	1561.8241	3121.6568	1561.3321	Q	529.3457	265.1765	512.3191	256.6632			4
30	3252.7515	1626.8794	3235.7249	1618.3661	3234.7409	1617.8741	L	401.2871	201.1472	384.2605	192.6339			3
31	3365.8355	1683.4214	3348.8090	1674.9081	3347.8250	1674.4161	L	288.2030	144.6051	271.1765	136.0919			2
32							R	175.1190	88.0631	158.0924	79.5498			1



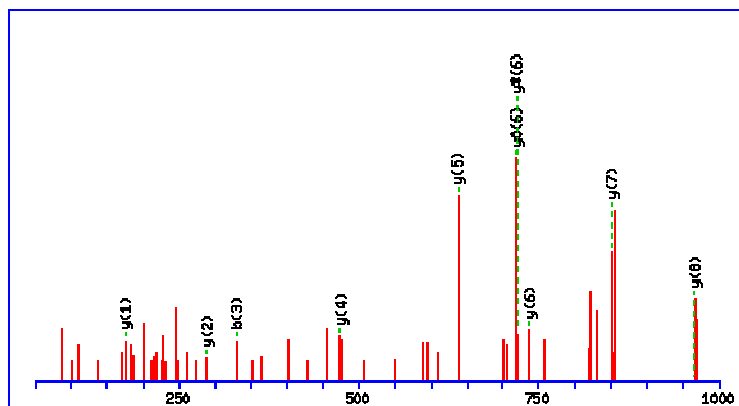
Peptide Number: 8373

MS/MS Fragmentation of **VDDVYSVL**RFound in **IPI00926023** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CTDSP1 Protein

Match to Query 8650: 1064.550928 from(533.282740,2+) index(29284)

Title: Elution from: 75.8 to 75.8 period: 0 cycle: 2892 experiment: 5 polarity: +

Data file 120206ry_aHDF1419-P10_2_2.mgf



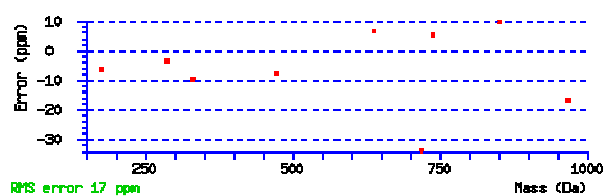
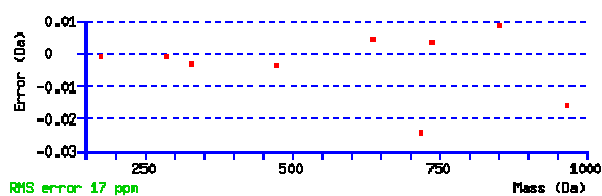
Monoisotopic mass of neutral peptide Mr(calc): 1064.5502

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 39 Expect: 0.008

Matches : 10/72 fragment ions using 25 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415			V							9
2	215.1026	108.0550	197.0921	99.0497	D	966.4891	483.7482	949.4625	475.2349	948.4785	474.7429	8
3	330.1296	165.5684	312.1190	156.5631	D	851.4621	426.2347	834.4356	417.7214	833.4516	417.2294	7
4	429.1980	215.1026	411.1874	206.0974	V	736.4352	368.7212	719.4087	360.2080	718.4246	359.7160	6
5	592.2613	296.6343	574.2508	287.6290	Y	637.3668	319.1870	620.3402	310.6738	619.3562	310.1817	5
6	679.2933	340.1503	661.2828	331.1450	S	474.3035	237.6554	457.2769	229.1421	456.2929	228.6501	4
7	778.3618	389.6845	760.3512	380.6792	V	387.2714	194.1394	370.2449	185.6261			3
8	891.4458	446.2266	873.4353	437.2213	L	288.2030	144.6051	271.1765	136.0919			2
9					R	175.1190	88.0631	158.0924	79.5498			1



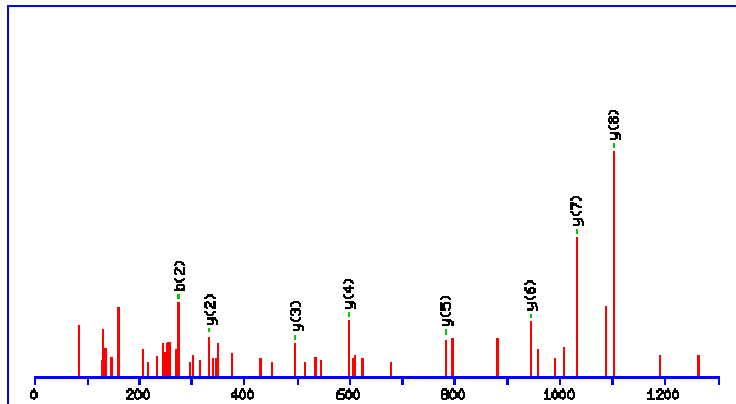
Peptide Number: 8411

MS/MS Fragmentation of **LCASCWTYWK**Found in **IPI00012773** in **IPI_human**, Tax_Id=9606 Gene_Symbol=MTA1 Isoform Long of Metastasis-associated protein MTA1

Match to Query 8605: 1373.585748 from(687.800150,2+) index(9779)

Title: Elution from: 24.1166666666667 to 24.1166666666667 period: 0 cycle: 907 experiment: 6 polarity: +

Data file 120210ry_32R1-32_2_3.mgf



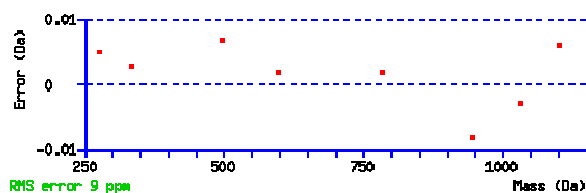
Monoisotopic mass of neutral peptide Mr(calc): 1373.5897

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

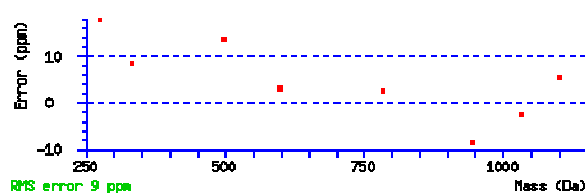
Ions Score: 53 Expect: 6.8e-005

Matches : 8/78 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							10
2	274.1220	137.5646			C	1261.5129	631.2601	1244.4863	622.7468	1243.5023	622.2548	9
3	345.1591	173.0832			A	1101.4822	551.2448	1084.4557	542.7315	1083.4717	542.2395	8
4	432.1911	216.5992	414.1806	207.5939	S	1030.4451	515.7262	1013.4186	507.2129	1012.4346	506.7209	7
5	592.2218	296.6145	574.2112	287.6092	C	943.4131	472.2102	926.3865	463.6969	925.4025	463.2049	6
6	778.3011	389.6542	760.2905	380.6489	W	783.3824	392.1949	766.3559	383.6816	765.3719	383.1896	5
7	879.3488	440.1780	861.3382	431.1727	T	597.3031	299.1552	580.2766	290.6419	579.2926	290.1499	4
8	1042.4121	521.7097	1024.4015	512.7044	Y	496.2554	248.6314	479.2289	240.1181			3
9	1228.4914	614.7493	1210.4808	605.7441	W	333.1921	167.0997	316.1656	158.5864			2
10					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 9 ppm



RMS error 9 ppm

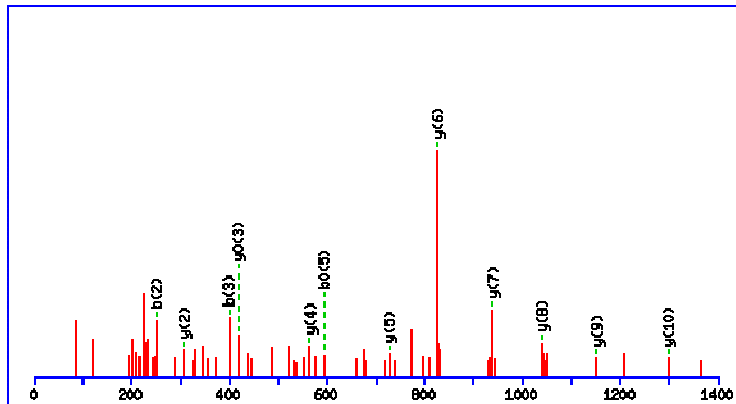
Peptide Number: 8477

MS/MS Fragmentation of **SYFLTIPYEECK**Found in **IPI00178946** in **IPI_human**, Tax_Id=9606 Gene_Symbol=C9orf95 Isoform 1 of Nicotinamide riboside kinase 1

Match to Query 11665: 1548.737408 from(775.375980,2+) index(18086)

Title: Elution from: 45.9833333333333 to 45.9833333333333 period: 0 cycle: 1749 experiment: 9 polarity:+

Data file 120206ry_aHDF1419-P10_3.mgf



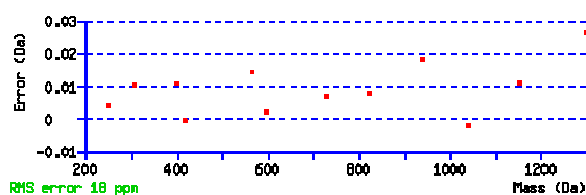
Monoisotopic mass of neutral peptide Mr(calc): 1548.7170

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

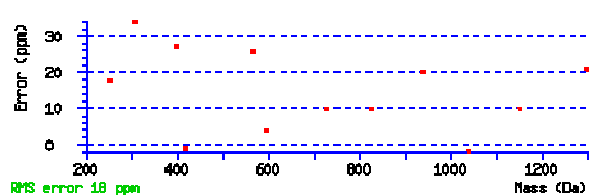
Ions Score: 47 Expect: 0.001

Matches : 12/106 fragment ions using 24 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233	70.0287	35.5180	S							12
2	251.1026	126.0550	233.0921	117.0497	Y	1462.6923	731.8498	1445.6657	723.3365	1444.6817	722.8445	11
3	398.1710	199.5892	380.1605	190.5839	F	1299.6290	650.3181	1282.6024	641.8048	1281.6184	641.3128	10
4	511.2551	256.1312	493.2445	247.1259	L	1152.5605	576.7839	1135.5340	568.2706	1134.5500	567.7786	9
5	612.3028	306.6550	594.2922	297.6498	T	1039.4765	520.2419	1022.4499	511.7286	1021.4659	511.2366	8
6	725.3869	363.1971	707.3763	354.1918	I	938.4288	469.7180	921.4022	461.2048	920.4182	460.7128	7
7	822.4396	411.7234	804.4291	402.7182	P	825.3447	413.1760	808.3182	404.6627	807.3342	404.1707	6
8	985.5029	493.2551	967.4924	484.2498	Y	728.2920	364.6496	711.2654	356.1363	710.2814	355.6443	5
9	1114.5455	557.7764	1096.5350	548.7711	E	565.2286	283.1180	548.2021	274.6047	547.2181	274.1127	4
10	1243.5881	622.2977	1225.5776	613.2924	E	436.1860	218.5967	419.1595	210.0834	418.1755	209.5914	3
11	1403.6188	702.3130	1385.6082	693.3077	C	307.1435	154.0754	290.1169	145.5621			2
12					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 18 ppm



RMS error 18 ppm

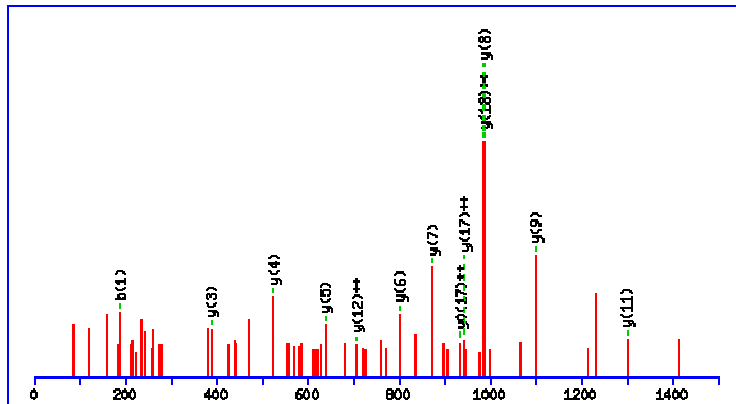
Peptide Number: 9143

MS/MS Fragmentation of **WSAGTLENSILNAYLHTIR**Found in **IPI00024727** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PLD2 Isoform PLD2A of Phospholipase D2

Match to Query 17039: 2158.146762 from(720.389530,3+) index(24163)

Title: Elution from: 60.65 to 60.65 period: 0 cycle: 2293 experiment: 1 polarity: +

Data file 120212ry_414C2-43_3_4.mgf



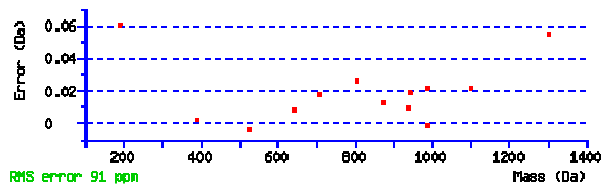
Monoisotopic mass of neutral peptide Mr(calc): 2158.1171

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

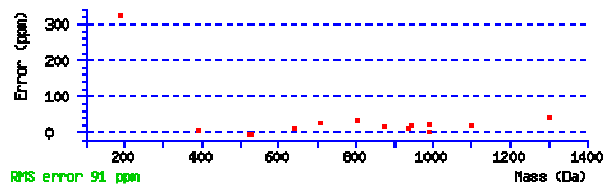
Ions Score: 40 Expect: 0.0054

Matches : 13/196 fragment ions using 26 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	187.0866	94.0469					W							19
2	274.1186	137.5629			256.1081	128.5577	S	1973.0451	987.0262	1956.0185	978.5129	1955.0345	978.0209	18
3	345.1557	173.0815			327.1452	164.0762	A	1886.0130	943.5102	1868.9865	934.9969	1868.0025	934.5049	17
4	402.1772	201.5922			384.1666	192.5870	G	1814.9759	907.9916	1797.9494	899.4783	1796.9654	898.9863	16
5	503.2249	252.1161			485.2143	243.1108	T	1757.9545	879.4809	1740.9279	870.9676	1739.9439	870.4756	15
6	616.3089	308.6581			598.2984	299.6528	L	1656.9068	828.9570	1639.8802	820.4438	1638.8962	819.9517	14
7	745.3515	373.1794			727.3410	364.1741	E	1543.8227	772.4150	1526.7962	763.9017	1525.8122	763.4097	13
8	859.3945	430.2009	842.3679	421.6876	841.3839	421.1956	N	1414.7801	707.8937	1397.7536	699.3804	1396.7696	698.8884	12
9	946.4265	473.7169	929.3999	465.2036	928.4159	464.7116	S	1300.7372	650.8722	1283.7106	642.3590	1282.7266	641.8670	11
10	1059.5106	530.2589	1042.4840	521.7456	1041.5000	521.2536	I	1213.7052	607.3562	1196.6786	598.8429	1195.6946	598.3509	10
11	1172.5946	586.8009	1155.5681	578.2877	1154.5840	577.7957	L	1100.6211	550.8142	1083.5946	542.3009	1082.6105	541.8089	9
12	1286.6375	643.8224	1269.6110	635.3091	1268.6270	634.8171	N	987.5370	494.2722	970.5105	485.7589	969.5265	485.2669	8
13	1357.6747	679.3410	1340.6481	670.8277	1339.6641	670.3357	A	873.4941	437.2507	856.4676	428.7374	855.4835	428.2454	7
14	1520.7380	760.8726	1503.7114	752.3594	1502.7274	751.8673	Y	802.4570	401.7321	785.4305	393.2189	784.4464	392.7269	6
15	1633.8220	817.4147	1616.7955	808.9014	1615.8115	808.4094	L	639.3937	320.2005	622.3671	311.6872	621.3831	311.1952	5
16	1770.8810	885.9441	1753.8544	877.4308	1752.8704	876.9388	H	526.3096	263.6584	509.2831	255.1452	508.2990	254.6532	4
17	1871.9286	936.4680	1854.9021	927.9547	1853.9181	927.4627	T	389.2507	195.1290	372.2241	186.6157	371.2401	186.1237	3
18	1985.0127	993.0100	1967.9862	984.4967	1967.0021	984.0047	I	288.2030	144.6051	271.1765	136.0919			2
19							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 91 ppm



RMS error 91 ppm

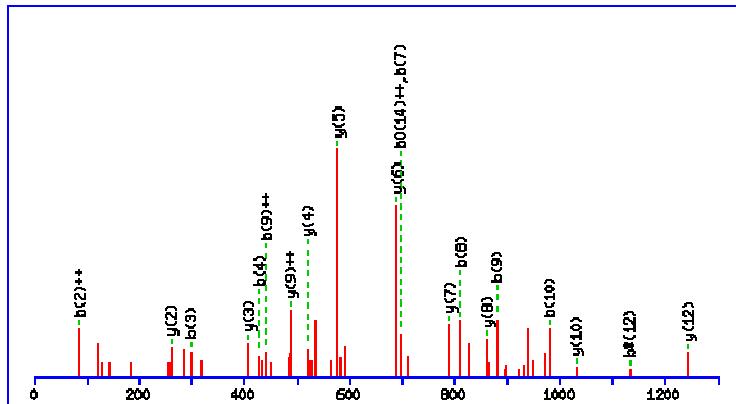
Peptide Number: 9332

MS/MS Fragmentation of **AVQQPDGLAVLGIFLK**Found in **IPI00218414** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CA2 Carbonic anhydrase 2

Match to Query 7186: 1667.952852 from(556.991560,3+) index(24692)

Title: Elution from: 62.5333333333333 to 62.5333333333333 period: 0 cycle: 2340 experiment: 1 polarity: +

Data file 120118ry_201B7-32_3_4.mgf



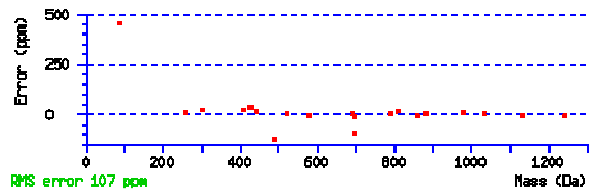
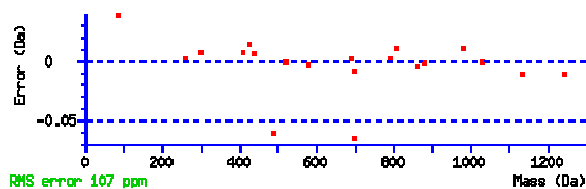
Monoisotopic mass of neutral peptide Mr(calc): 1667.9610

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 57 Expect: 5.2e-005

Matches : 20/146 fragment ions using 32 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							16
2	171.1128	86.0600					V	1597.9312	799.4692	1580.9047	790.9560	1579.9206	790.4640	15
3	299.1714	150.0893	282.1448	141.5761			Q	1498.8628	749.9350	1481.8362	741.4218	1480.8522	740.9298	14
4	427.2300	214.1186	410.2034	205.6053			Q	1370.8042	685.9057	1353.7777	677.3925	1352.7936	676.9005	13
5	524.2827	262.6450	507.2562	254.1317			P	1242.7456	621.8765	1225.7191	613.3632	1224.7351	612.8712	12
6	639.3097	320.1585	622.2831	311.6452	621.2991	311.1532	D	1145.6929	573.3501	1128.6663	564.8368	1127.6823	564.3448	11
7	696.3311	348.6692	679.3046	340.1559	678.3206	339.6639	G	1030.6659	515.8366	1013.6394	507.3233			10
8	809.4152	405.2112	792.3886	396.6980	791.4046	396.2060	L	973.6445	487.3259	956.6179	478.8126			9
9	880.4523	440.7298	863.4258	432.2165	862.4417	431.7245	A	860.5604	430.7838	843.5339	422.2706			8
10	979.5207	490.2640	962.4942	481.7507	961.5102	481.2587	V	789.5233	395.2653	772.4967	386.7520			7
11	1092.6048	546.8060	1075.5782	538.2928	1074.5942	537.8007	L	690.4549	345.7311	673.4283	337.2178			6
12	1149.6263	575.3168	1132.5997	566.8035	1131.6157	566.3115	G	577.3708	289.1890	560.3443	280.6758			5
13	1262.7103	631.8588	1245.6838	623.3455	1244.6997	622.8535	I	520.3493	260.6783	503.3228	252.1650			4
14	1409.7787	705.3930	1392.7522	696.8797	1391.7682	696.3877	F	407.2653	204.1363	390.2387	195.6230			3
15	1522.8628	761.9350	1505.8362	753.4218	1504.8522	752.9298	L	260.1969	130.6021	243.1703	122.0888			2
16							K	147.1128	74.0600	130.0863	65.5468			1

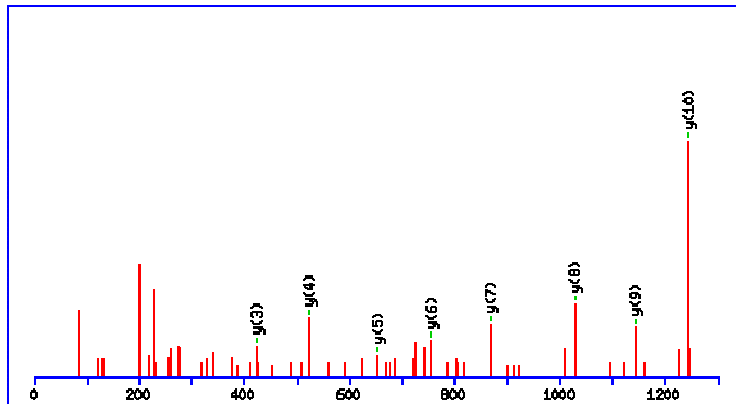


Peptide Number: 9342MS/MS Fragmentation of **LLTDCNTETFQK**Found in **IPI00656021** in **IPI_human**, Tax_Id=9606 Gene_Symbol=VPS53 vacuolar protein sorting-associated protein 53 homolog isoform 1

Match to Query 26051: 1468.682588 from(735.348570,2+) index(8279)

Title: Elution from: 19.7166666666667 to 19.7166666666667 period: 0 cycle: 747 experiment: 9 polarity: +

Data file 120208ry_Tig120slc-P8_2_2.mgf



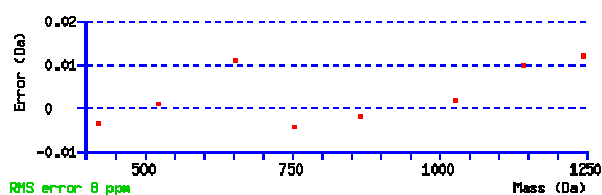
Monoisotopic mass of neutral peptide Mr(calc): 1468.6868

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

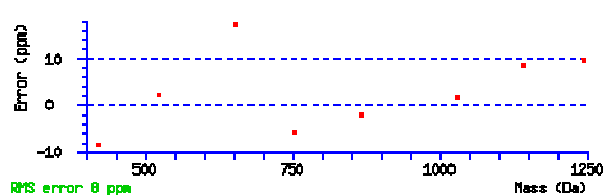
Ions Score: 63 Expect: 2.2e-005

Matches : 8/112 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							12
2	227.1754	114.0913					L	1356.6100	678.8086	1339.5835	670.2954	1338.5994	669.8034	11
3	328.2231	164.6152			310.2125	155.6099	T	1243.5259	622.2666	1226.4994	613.7533	1225.5154	613.2613	10
4	443.2500	222.1287			425.2395	213.1234	D	1142.4783	571.7428	1125.4517	563.2295	1124.4677	562.7375	9
5	603.2807	302.1440			585.2701	293.1387	C	1027.4513	514.2293	1010.4248	505.7160	1009.4408	505.2240	8
6	717.3236	359.1654	700.2971	350.6522	699.3130	350.1602	N	867.4207	434.2140	850.3941	425.7007	849.4101	425.2087	7
7	818.3713	409.6893	801.3447	401.1760	800.3607	400.6840	T	753.3777	377.1925	736.3512	368.6792	735.3672	368.1872	6
8	947.4139	474.2106	930.3873	465.6973	929.4033	465.2053	E	652.3301	326.6687	635.3035	318.1554	634.3195	317.6634	5
9	1048.4616	524.7344	1031.4350	516.2211	1030.4510	515.7291	T	523.2875	262.1474	506.2609	253.6341	505.2769	253.1421	4
10	1195.5300	598.2686	1178.5034	589.7553	1177.5194	589.2633	F	422.2398	211.6235	405.2132	203.1103			3
11	1323.5885	662.2979	1306.5620	653.7846	1305.5780	653.2926	Q	275.1714	138.0893	258.1448	129.5761			2
12							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 8 ppm



RMS error 8 ppm

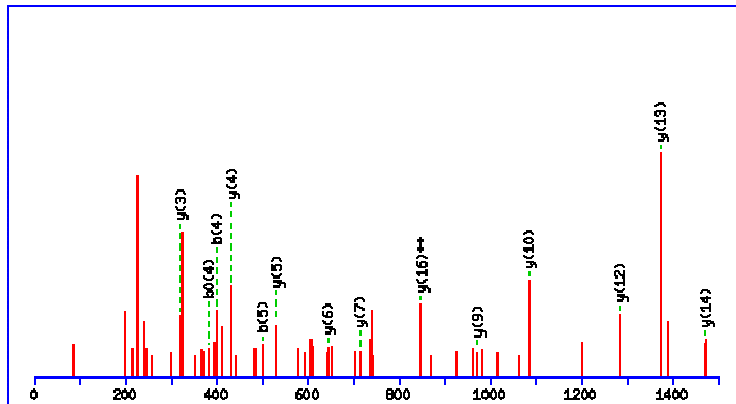
Peptide Number: 9933

MS/MS Fragmentation of **SSPEVSSINQEALVLTAK**Found in **IPI00010158** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CHRA1 Chromatin accessibility complex protein 1

Match to Query 24505: 1871.985368 from(936.999960,2+) index(2936)

Title: Elution from: 7.1 to 7.1 period: 0 cycle: 266 experiment: 9 polarity: +

Data file 120214ry_32R1-32_4_3.mgf



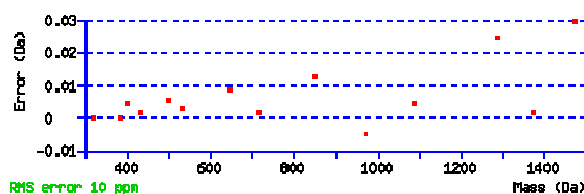
Monoisotopic mass of neutral peptide Mr(calc): 1871.9840

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

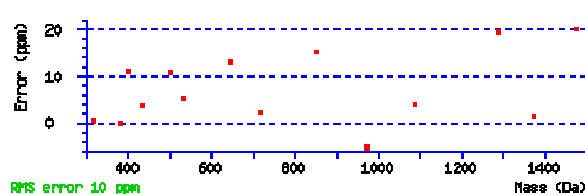
Ions Score: 39 Expect: 0.0085

Matches : 14/184 fragment ions using 42 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							18
2	175.0713	88.0393			157.0608	79.0340	S	1785.9593	893.4833	1768.9327	884.9700	1767.9487	884.4780	17
3	272.1241	136.5657			254.1135	127.5604	P	1698.9272	849.9673	1681.9007	841.4540	1680.9167	840.9620	16
4	401.1667	201.0870			383.1561	192.0817	E	1601.8745	801.4409	1584.8479	792.9276	1583.8639	792.4356	15
5	500.2351	250.6212			482.2245	241.6159	V	1472.8319	736.9196	1455.8053	728.4063	1454.8213	727.9143	14
6	587.2671	294.1372			569.2566	285.1319	S	1373.7635	687.3854	1356.7369	678.8721	1355.7529	678.3801	13
7	674.2992	337.6532			656.2886	328.6479	S	1286.7314	643.8694	1269.7049	635.3561	1268.7209	634.8641	12
8	787.3832	394.1952			769.3727	385.1900	I	1199.6994	600.3533	1182.6729	591.8401	1181.6889	591.3481	11
9	901.4262	451.2167	884.3996	442.7034	883.4156	442.2114	N	1086.6154	543.8113	1069.5888	535.2980	1068.6048	534.8060	10
10	1029.4847	515.2460	1012.4582	506.7327	1011.4742	506.2407	Q	972.5724	486.7899	955.5459	478.2766	954.5619	477.7846	9
11	1158.5273	579.7673	1141.5008	571.2540	1140.5168	570.7620	E	844.5138	422.7606	827.4873	414.2473	826.5033	413.7553	8
12	1229.5644	615.2859	1212.5379	606.7726	1211.5539	606.2806	A	715.4713	358.2393	698.4447	349.7260	697.4607	349.2340	7
13	1342.6485	671.8279	1325.6220	663.3146	1324.6379	662.8226	L	644.4341	322.7207	627.4076	314.2074	626.4236	313.7154	6
14	1441.7169	721.3621	1424.6904	712.8488	1423.7063	712.3568	V	531.3501	266.1787	514.3235	257.6654	513.3395	257.1734	5
15	1554.8010	777.9041	1537.7744	769.3909	1536.7904	768.8988	L	432.2817	216.6445	415.2551	208.1312	414.2711	207.6392	4
16	1655.8487	828.4280	1638.8221	819.9147	1637.8381	819.4227	T	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	3
17	1726.8858	863.9465	1709.8592	855.4332	1708.8752	854.9412	A	218.1499	109.5786	201.1234	101.0653			2
18							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 10 ppm



RMS error 10 ppm

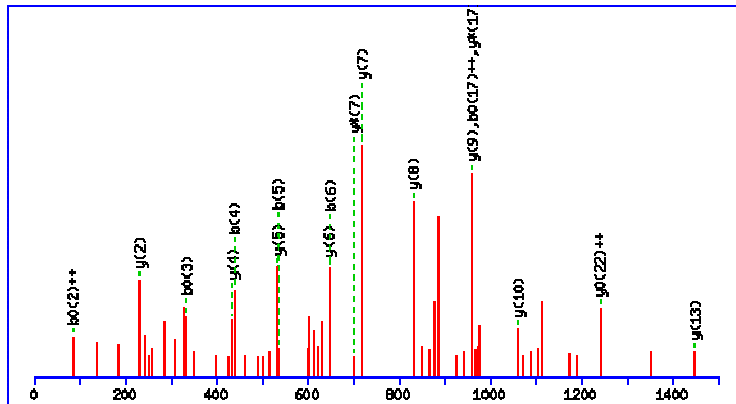
Peptide Number: 10023

MS/MS Fragmentation of **STYSPLPDDYNCNVELALTSDDR**Found in **IPI00022320** in **IPI_human**, Tax_Id=9606 Gene_Symbol=MRPL42 39S ribosomal protein L42, mitochondrial

Match to Query 39033: 2586.151422 from(863.057750,3+) index(25405)

Title: Elution from: 63.5333333333333 to 63.5333333333333 period: 0 cycle: 2393 experiment: 8 polarity: +

Data file 120210ry_32R1-32_2_3.mgf



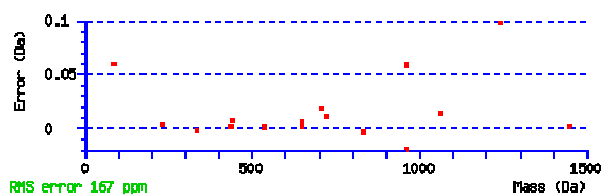
Monoisotopic mass of neutral peptide Mr(calc): 2586.1544

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

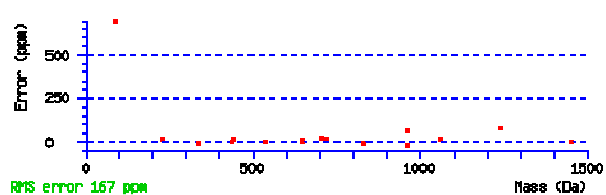
Ions Score: 53 Expect: 0.00011

Matches : 18/240 fragment ions using 26 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							23
2	189.0870	95.0471			171.0764	86.0418	T	2500.1297	1250.5685	2483.1031	1242.0552	2482.1191	1241.5632	22
3	352.1503	176.5788			334.1397	167.5735	Y	2399.0820	1200.0446	2382.0554	1191.5314	2381.0714	1191.0393	21
4	439.1823	220.0948			421.1718	211.0895	S	2236.0187	1118.5130	2218.9921	1109.9997	2218.0081	1109.5077	20
5	536.2351	268.6212			518.2245	259.6159	P	2148.9866	1074.9970	2131.9601	1066.4837	2130.9761	1065.9917	19
6	649.3192	325.1632			631.3086	316.1579	L	2051.9339	1026.4706	2034.9073	1017.9573	2033.9233	1017.4653	18
7	746.3719	373.6896			728.3614	364.6843	P	1938.8498	969.9285	1921.8232	961.4153	1920.8392	960.9233	17
8	861.3989	431.2031			843.3883	422.1978	D	1841.7970	921.4022	1824.7705	912.8889	1823.7865	912.3969	16
9	976.4258	488.7165			958.4153	479.7113	D	1726.7701	863.8887	1709.7435	855.3754	1708.7595	854.8834	15
10	1139.4891	570.2482			1121.4786	561.2429	Y	1611.7431	806.3752	1594.7166	797.8619	1593.7326	797.3699	14
11	1253.5321	627.2697	1236.5055	618.7564	1235.5215	618.2644	N	1448.6798	724.8435	1431.6533	716.3303	1430.6693	715.8383	13
12	1413.5627	707.2850	1396.5362	698.7717	1395.5522	698.2797	C	1334.6369	667.8221	1317.6103	659.3088	1316.6263	658.8168	12
13	1527.6057	764.3065	1510.5791	755.7932	1509.5951	755.3012	N	1174.6062	587.8068	1157.5797	579.2935	1156.5957	578.8015	11
14	1626.6741	813.8407	1609.6475	805.3274	1608.6635	804.8354	V	1060.5633	530.7853	1043.5368	522.2720	1042.5527	521.7800	10
15	1755.7167	878.3620	1738.6901	869.8487	1737.7061	869.3567	E	961.4949	481.2511	944.4684	472.7378	943.4843	472.2458	9
16	1868.8007	934.9040	1851.7742	926.3907	1850.7902	925.8987	L	832.4523	416.7298	815.4258	408.2165	814.4417	407.7245	8
17	1939.8378	970.4226	1922.8113	961.9093	1921.8273	961.4173	A	719.3682	360.1878	702.3417	351.6745	701.3577	351.1825	7
18	2052.9219	1026.9646	2035.8954	1018.4513	2034.9113	1017.9593	L	648.3311	324.6692	631.3046	316.1559	630.3206	315.6639	6
19	2153.9696	1077.4884	2136.9430	1068.9752	2135.9590	1068.4831	T	535.2471	268.1272	518.2205	259.6139	517.2365	259.1219	5
20	2241.0016	1121.0044	2223.9751	1112.4912	2222.9910	1111.9992	S	434.1994	217.6033	417.1728	209.0901	416.1888	208.5980	4
21	2356.0285	1178.5179	2339.0020	1170.0046	2338.0180	1169.5126	D	347.1674	174.0873	330.1408	165.5740	329.1568	165.0820	3
22	2413.0500	1207.0286	2396.0235	1198.5154	2395.0394	1198.0234	G	232.1404	116.5738	215.1139	108.0606			2
23							R	175.1190	88.0631	158.0924	79.5498			1



RMS error: 167 ppm



RMS error: 167 ppm

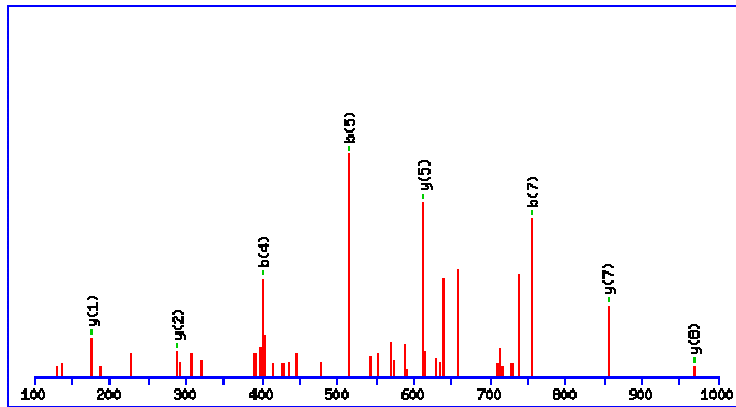
Peptide Number: 10139

MS/MS Fragmentation of **VTTVIQNPMPIR**Found in **IPI01013876** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CD22 CD22 protein

Match to Query 11665: 1367.751522 from(456.924450,3+) index(22421)

Title: Elution from: 54.1333333333333 to 54.1333333333333 period: 0 cycle: 2009 experiment: 2 polarity:+

Data file 120126ry_585A1-55_1_3.mgf



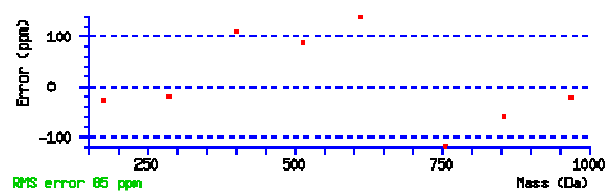
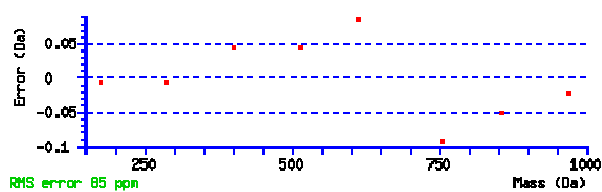
Monoisotopic mass of neutral peptide Mr(calc): 1367.7595

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 42 Expect: 0.0027

Matches : 8/102 fragment ions using 9 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							12
2	201.1234	101.0653			183.1128	92.0600	T	1269.6984	635.3528	1252.6718	626.8395	1251.6878	626.3475	11
3	302.1710	151.5892			284.1605	142.5839	T	1168.6507	584.8290	1151.6241	576.3157	1150.6401	575.8237	10
4	401.2395	201.1234			383.2289	192.1181	V	1067.6030	534.3051	1050.5765	525.7919			9
5	514.3235	257.6654			496.3130	248.6601	I	968.5346	484.7709	951.5080	476.2577			8
6	642.3821	321.6947	625.3556	313.1814	624.3715	312.6894	Q	855.4505	428.2289	838.4240	419.7156			7
7	756.4250	378.7162	739.3985	370.2029	738.4145	369.7109	N	727.3920	364.1996	710.3654	355.6863			6
8	853.4778	427.2425	836.4512	418.7293	835.4672	418.2373	P	613.3490	307.1782	596.3225	298.6649			5
9	984.5183	492.7628	967.4917	484.2495	966.5077	483.7575	M	516.2963	258.6518	499.2697	250.1385			4
10	1081.5710	541.2892	1064.5445	532.7759	1063.5605	532.2839	P	385.2558	193.1315	368.2292	184.6183			3
11	1194.6551	597.8312	1177.6286	589.3179	1176.6445	588.8259	I	288.2030	144.6051	271.1765	136.0919			2
12							R	175.1190	88.0631	158.0924	79.5498			1



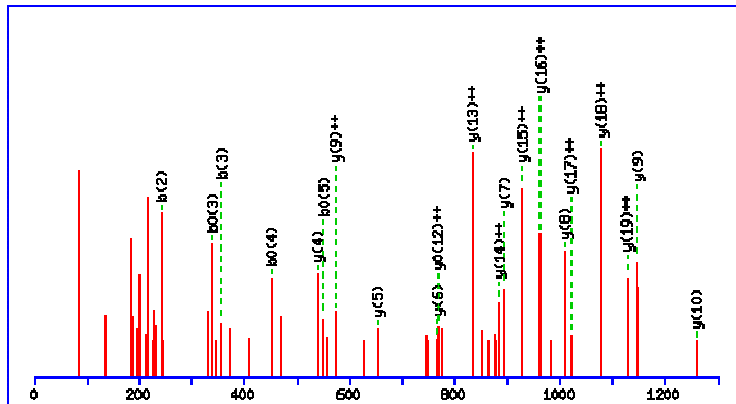
Peptide Number: 10177

MS/MS Fragmentation of **EILVDDASVDEYLHDKLDEYVK**Found in **IPI00004670** in **IPI_human**, Tax_Id=9606 Gene_Symbol=GALNT3 Isoform 1 of Polypeptide N-acetylgalactosaminyltransferase 3

Match to Query 24876: 2720.351576 from(681.095170,4+) index(3197)

Title: Elution from: 10.3333333333333 to 10.3333333333333 period: 0 cycle: 406 experiment: 4 polarity:+

Data file 120210ry_585A1-55_3_4.mgf



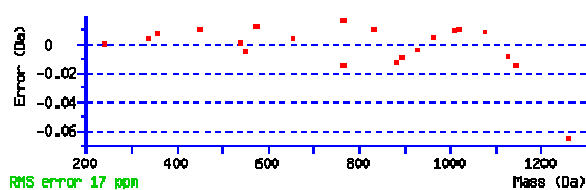
Monoisotopic mass of neutral peptide Mr(calc): 2720.3432

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

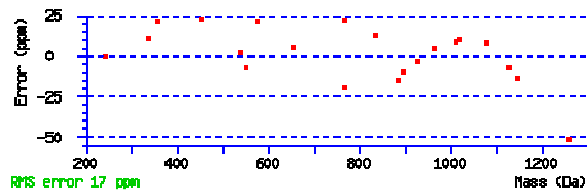
Ions Score: 50 Expect: 0.00057

Matches : 21/226 fragment ions using 41 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							23
2	243.1339	122.0706			225.1234	113.0653	I	2592.3079	1296.6576	2575.2814	1288.1443	2574.2974	1287.6523	22
3	356.2180	178.6126			338.2074	169.6074	I	2479.2239	1240.1156	2462.1973	1231.6023	2461.2133	1231.1103	21
4	469.3021	235.1547			451.2915	226.1494	L	2366.1398	1183.5735	2349.1133	1175.0603	2348.1292	1174.5683	20
5	568.3705	284.6889			550.3599	275.6836	V	2253.0557	1127.0315	2236.0292	1118.5182	2235.0452	1118.0262	19
6	683.3974	342.2023			665.3869	333.1971	D	2153.9873	1077.4973	2136.9608	1068.9840	2135.9768	1068.4920	18
7	798.4244	399.7158			780.4138	390.7105	D	2038.9604	1019.9838	2021.9338	1011.4706	2020.9498	1010.9786	17
8	869.4615	435.2344			851.4509	426.2291	A	1923.9335	962.4704	1906.9069	953.9571	1905.9229	953.4651	16
9	956.4935	478.7504			938.4829	469.7451	S	1852.8963	926.9518	1835.8698	918.4385	1834.8858	917.9465	15
10	1055.5619	528.2846			1037.5514	519.2793	V	1765.8643	883.4358	1748.8378	874.9225	1747.8537	874.4305	14
11	1170.5889	585.7981			1152.5783	576.7928	D	1666.7959	833.9016	1649.7693	825.3883	1648.7853	824.8963	13
12	1299.6315	650.3194			1281.6209	641.3141	E	1551.7690	776.3881	1534.7424	767.8748	1533.7584	767.3828	12
13	1462.6948	731.8510			1444.6842	722.8457	Y	1422.7264	711.8668	1405.6998	703.3535	1404.7158	702.8615	11
14	1575.7788	788.3931			1557.7683	779.3878	L	1259.6630	630.3352	1242.6365	621.8219	1241.6525	621.3299	10
15	1712.8378	856.9225			1694.8272	847.9172	H	1146.5790	573.7931	1129.5524	565.2798	1128.5684	564.7878	9
16	1827.8647	914.4360			1809.8541	905.4307	D	1009.5201	505.2637	992.4935	496.7504	991.5095	496.2584	8
17	1955.9597	978.4835	1938.9331	969.9702	1937.9491	969.4782	K	894.4931	447.7502	877.4666	439.2369	876.4825	438.7449	7
18	2069.0437	1035.0255	2052.0172	1026.5122	2051.0332	1026.0202	L	766.3981	383.7027	749.3716	375.1894	748.3876	374.6974	6
19	2184.0707	1092.5390	2167.0441	1084.0257	2166.0601	1083.5337	D	653.3141	327.1607	636.2875	318.6474	635.3035	318.1554	5
20	2313.1133	1157.0603	2296.0867	1148.5470	2295.1027	1148.0550	E	538.2871	269.6472	521.2606	261.1339	520.2766	260.6419	4
21	2476.1766	1238.5919	2459.1500	1230.0787	2458.1660	1229.5867	Y	409.2445	205.1259	392.2180	196.6126			3
22	2575.2450	1288.1261	2558.2185	1279.6129	2557.2344	1279.1209	V	246.1812	123.5942	229.1547	115.0810			2
23							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 17 ppm



RMS error 17 ppm

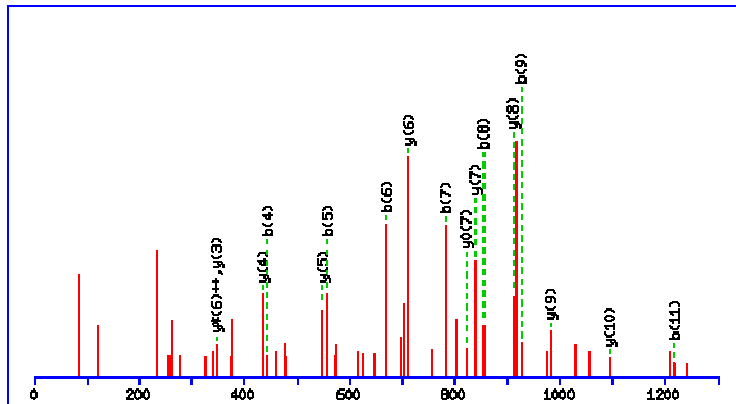
Peptide Number: 10263

MS/MS Fragmentation of **KAEIDILAAEYISTVK**Found in **IPI00513864** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ING5 Isoform 2 of Inhibitor of growth protein 5

Match to Query 18538: 1762.973532 from(588.665120,3+) index(31775)

Title: Elution from: 82 to 82 period: 0 cycle: 3104 experiment: 2 polarity:+

Data file 120210ry_585A1-55_3_3.mgf



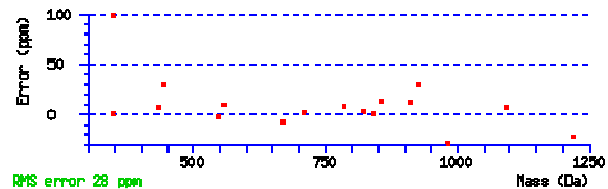
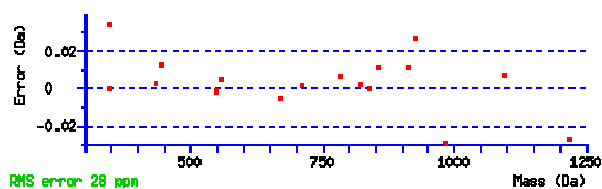
Monoisotopic mass of neutral peptide Mr(calc): 1762.9716

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 38 Expect: 0.0072

Matches : 17/172 fragment ions using 41 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	129.1022	65.0548	112.0757	56.5415			K							16
2	200.1394	100.5733	183.1128	92.0600			A	1635.8840	818.4456	1618.8574	809.9324	1617.8734	809.4403	15
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	E	1564.8469	782.9271	1547.8203	774.4138	1546.8363	773.9218	14
4	442.2660	221.6366	425.2395	213.1234	424.2554	212.6314	I	1435.8043	718.4058	1418.7777	709.8925	1417.7937	709.4005	13
5	557.2930	279.1501	540.2664	270.6368	539.2824	270.1448	D	1322.7202	661.8637	1305.6937	653.3505	1304.7096	652.8585	12
6	670.3770	335.6921	653.3505	327.1789	652.3665	326.6869	I	1207.6933	604.3503	1190.6667	595.8370	1189.6827	595.3450	11
7	783.4611	392.2342	766.4345	383.7209	765.4505	383.2289	L	1094.6092	547.8082	1077.5827	539.2950	1076.5986	538.8030	10
8	854.4982	427.7527	837.4716	419.2395	836.4876	418.7475	A	981.5251	491.2662	964.4986	482.7529	963.5146	482.2609	9
9	925.5353	463.2713	908.5088	454.7580	907.5247	454.2660	A	910.4880	455.7477	893.4615	447.2344	892.4775	446.7424	8
10	1054.5779	527.7926	1037.5514	519.2793	1036.5673	518.7873	E	839.4509	420.2291	822.4244	411.7158	821.4403	411.2238	7
11	1217.6412	609.3243	1200.6147	600.8110	1199.6307	600.3190	Y	710.4083	355.7078	693.3818	347.1945	692.3978	346.7025	6
12	1330.7253	665.8663	1313.6987	657.3530	1312.7147	656.8610	I	547.3450	274.1761	530.3184	265.6629	529.3344	265.1709	5
13	1417.7573	709.3823	1400.7308	700.8690	1399.7468	700.3770	S	434.2609	217.6341	417.2344	209.1208	416.2504	208.6288	4
14	1518.8050	759.9061	1501.7785	751.3929	1500.7944	750.9009	T	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
15	1617.8734	809.4403	1600.8469	800.9271	1599.8629	800.4351	V	246.1812	123.5942	229.1547	115.0810			2
16							K	147.1128	74.0600	130.0863	65.5468			1



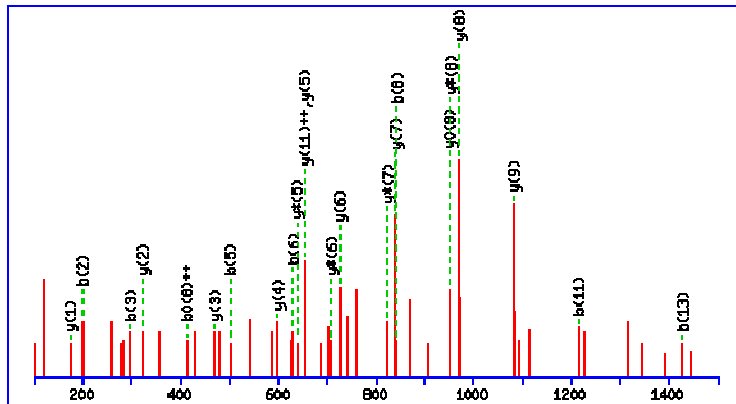
Peptide Number: 10579

MS/MS Fragmentation of **AQPFQQLTDEQVIENAGEFFR**Found in **IPI00965006** in **IPI_human**, Tax_Id=9606 Gene_Symbol=DDR1 epithelial discoidin domain-containing receptor 1 isoform 6 precursor

Match to Query 18729: 2395.158762 from(799.393530,3+) index(9058)

Title: Elution from: 25.0166666666667 to 25.0166666666667 period: 0 cycle: 961 experiment: 10 polarity:+

Data file 120210ry_585A1-55_3_4.mgf



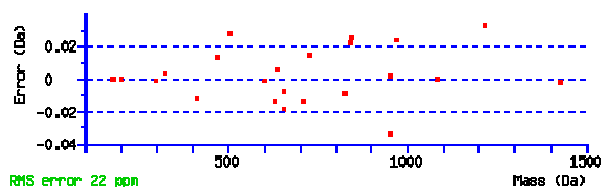
Monoisotopic mass of neutral peptide Mr(calc): 2395.1444

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

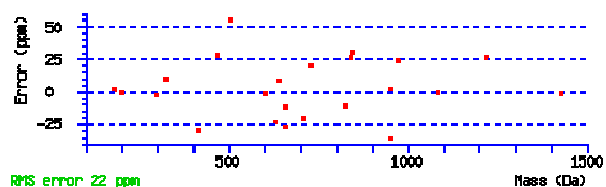
Ions Score: 52 Expect: 0.00037

Matches : 23/218 fragment ions using 50 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							21
2	200.1030	100.5551	183.0764	92.0418			Q	2325.1146	1163.0609	2308.0881	1154.5477	2307.1040	1154.0557	20
3	297.1557	149.0815	280.1292	140.5682			P	2197.0560	1099.0317	2180.0295	1090.5184	2179.0455	1090.0264	19
4	444.2241	222.6157	427.1976	214.1024			F	2100.0033	1050.5053	2082.9767	1041.9920	2081.9927	1041.5000	18
5	501.2456	251.1264	484.2191	242.6132			G	1952.9348	976.9711	1935.9083	968.4578	1934.9243	967.9658	17
6	629.3042	315.1557	612.2776	306.6425			Q	1895.9134	948.4603	1878.8868	939.9471	1877.9028	939.4550	16
7	742.3883	371.6978	725.3617	363.1845			L	1767.8548	884.4310	1750.8283	875.9178	1749.8442	875.4258	15
8	843.4359	422.2216	826.4094	413.7083	825.4254	413.2163	T	1654.7707	827.8890	1637.7442	819.3757	1636.7602	818.8837	14
9	958.4629	479.7351	941.4363	471.2218	940.4523	470.7298	D	1553.7231	777.3652	1536.6965	768.8519	1535.7125	768.3599	13
10	1087.5055	544.2564	1070.4789	535.7431	1069.4949	535.2511	E	1438.6961	719.8517	1421.6696	711.3384	1420.6856	710.8464	12
11	1215.5640	608.2857	1198.5375	599.7724	1197.5535	599.2804	Q	1309.6535	655.3304	1292.6270	646.8171	1291.6430	646.3251	11
12	1314.6325	657.8199	1297.6059	649.3066	1296.6219	648.8146	V	1181.5949	591.3011	1164.5684	582.7878	1163.5844	582.2958	10
13	1427.7165	714.3619	1410.6900	705.8486	1409.7060	705.3566	I	1082.5265	541.7669	1065.5000	533.2536	1064.5160	532.7616	9
14	1556.7591	778.8832	1539.7326	770.3699	1538.7486	769.8779	E	969.4425	485.2249	952.4159	476.7116	951.4319	476.2196	8
15	1670.8020	835.9047	1653.7755	827.3914	1652.7915	826.8994	N	840.3999	420.7036	823.3733	412.1903	822.3893	411.6983	7
16	1741.8392	871.4232	1724.8126	862.9099	1723.8286	862.4179	A	726.3570	363.6821	709.3304	355.1688	708.3464	354.6768	6
17	1798.8606	899.9339	1781.8341	891.4207	1780.8501	890.9287	G	655.3198	328.1636	638.2933	319.6503	637.3093	319.1583	5
18	1927.9032	964.4552	1910.8767	955.9420	1909.8926	955.4500	E	598.2984	299.6528	581.2718	291.1395	580.2878	290.6475	4
19	2074.9716	1037.9895	2057.9451	1029.4762	2056.9611	1028.9842	F	469.2558	235.1315	452.2292	226.6183			3
20	2222.0400	1111.5237	2205.0135	1103.0104	2204.0295	1102.5184	F	322.1874	161.5973	305.1608	153.0840			2
21							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 22 ppm



RMS error 22 ppm

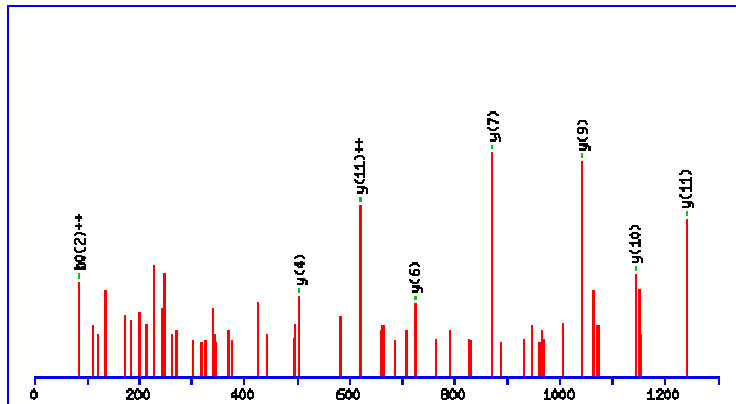
Peptide Number: 10633

MS/MS Fragmentation of **STPTGLFGYWGNK**Found in **IPI00374574** in **IPI_human**, Tax_Id=9606 Gene_Symbol=INPP5K Isoform 1 of Inositol polyphosphate 5-phosphatase K

Match to Query 8867: 1426.687068 from(714.350810,2+) index(19379)

Title: Elution from: 51.5 to 51.5 period: 0 cycle: 1970 experiment: 8 polarity: +

Data file 120214ry_aHDF1419-P10_4_3.mgf



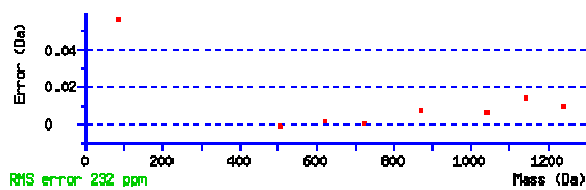
Monoisotopic mass of neutral peptide Mr(calc): 1426.6881

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

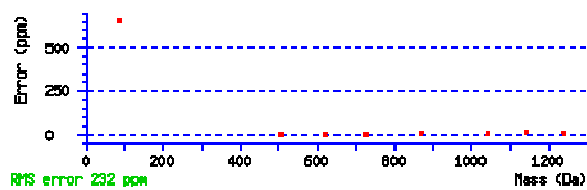
Ions Score: 38 Expect: 0.0075

Matches : 8/104 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							13
2	189.0870	95.0471			171.0764	86.0418	T	1340.6634	670.8353	1323.6368	662.3220	1322.6528	661.8300	12
3	286.1397	143.5735			268.1292	134.5682	P	1239.6157	620.3115	1222.5891	611.7982	1221.6051	611.3062	11
4	387.1874	194.0974			369.1769	185.0921	T	1142.5629	571.7851	1125.5364	563.2718	1124.5524	562.7798	10
5	444.2089	222.6081			426.1983	213.6028	G	1041.5152	521.2613	1024.4887	512.7480			9
6	557.2930	279.1501			539.2824	270.1448	L	984.4938	492.7505	967.4672	484.2373			8
7	704.3614	352.6843			686.3508	343.6790	F	871.4097	436.2085	854.3832	427.6952			7
8	761.3828	381.1951			743.3723	372.1898	G	724.3413	362.6743	707.3148	354.1610			6
9	924.4462	462.7267			906.4356	453.7214	Y	667.3198	334.1636	650.2933	325.6503			5
10	1110.5255	555.7664			1092.5149	546.7611	W	504.2565	252.6319	487.2300	244.1186			4
11	1167.5469	584.2771			1149.5364	575.2718	G	318.1772	159.5922	301.1506	151.0790			3
12	1281.5899	641.2986	1264.5633	632.7853	1263.5793	632.2933	N	261.1557	131.0815	244.1292	122.5682			2
13							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 232 ppm



RMS error 232 ppm

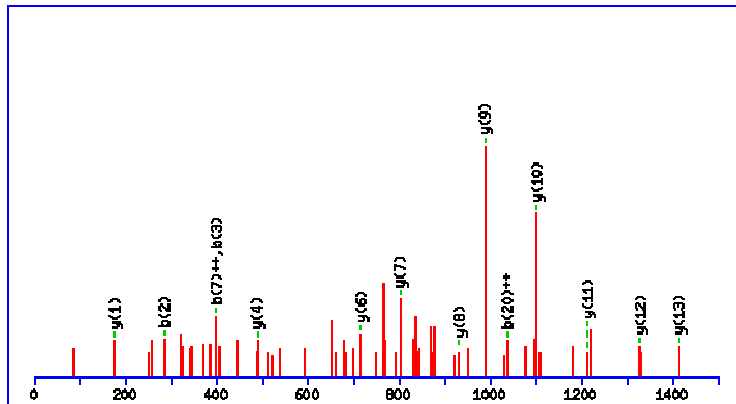
Peptide Number: 10798

MS/MS Fragmentation of **WVISLTPLSQPGPSSNIIGQSVEEAIR**Found in **IPI00012429** in **IPI_human**, Tax_Id=9606 Gene_Symbol=C9orf5 Uncharacterised protein family UPF0118 protein

Match to Query 32821: 2877.530232 from(960.184020,3+) index(20552)

Title: Elution from: 54.15 to 54.15 period: 0 cycle: 2065 experiment: 9 polarity:+

Data file 120210ry_32R1-32_2_4.mgf



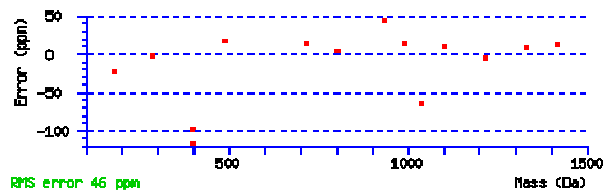
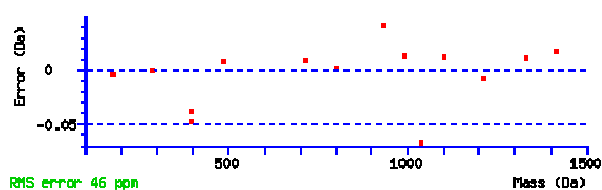
Monoisotopic mass of neutral peptide Mr(calc): 2877.5236

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 49 Expect: 0.0004

Matches : 14/282 fragment ions using 27 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	187.0866	94.0469					W							27
2	286.1550	143.5811					V	2692.4516	1346.7294	2675.4250	1338.2162	2674.4410	1337.7241	26
3	399.2391	200.1232					I	2593.3832	1297.1952	2576.3566	1288.6819	2575.3726	1288.1899	25
4	486.2711	243.6392			468.2605	234.6339	S	2480.2991	1240.6532	2463.2726	1232.1399	2462.2885	1231.6479	24
5	599.3552	300.1812			581.3446	291.1759	L	2393.2671	1197.1372	2376.2405	1188.6239	2375.2565	1188.1319	23
6	700.4028	350.7051			682.3923	341.6998	T	2280.1830	1140.5951	2263.1565	1132.0819	2262.1725	1131.5899	22
7	797.4556	399.2314			779.4450	390.2262	P	2179.1353	1090.0713	2162.1088	1081.5580	2161.1248	1081.0660	21
8	910.5397	455.7735			892.5291	446.7682	L	2082.0826	1041.5449	2065.0560	1033.0316	2064.0720	1032.5396	20
9	997.5717	499.2895			979.5611	490.2842	S	1968.9985	985.0029	1951.9720	976.4896	1950.9879	975.9976	19
10	1125.6303	563.3188	1108.6037	554.8055	1107.6197	554.3135	Q	1881.9665	941.4869	1864.9399	932.9736	1863.9559	932.4816	18
11	1222.6830	611.8452	1205.6565	603.3319	1204.6725	602.8399	P	1753.9079	877.4576	1736.8814	868.9443	1735.8973	868.4523	17
12	1279.7045	640.3559	1262.6780	631.8426	1261.6939	631.3506	G	1656.8551	828.9312	1639.8286	820.4179	1638.8446	819.9259	16
13	1376.7573	688.8823	1359.7307	680.3690	1358.7467	679.8770	P	1599.8337	800.4205	1582.8071	791.9072	1581.8231	791.4152	15
14	1463.7893	732.3983	1446.7627	723.8850	1445.7787	723.3930	S	1502.7809	751.8941	1485.7544	743.3808	1484.7703	742.8888	14
15	1550.8213	775.9143	1533.7948	767.4010	1532.8108	766.9090	S	1415.7489	708.3781	1398.7223	699.8648	1397.7383	699.3728	13
16	1664.8642	832.9358	1647.8377	824.4225	1646.8537	823.9305	N	1328.7169	664.8621	1311.6903	656.3488	1310.7063	655.8568	12
17	1777.9483	889.4778	1760.9218	880.9645	1759.9377	880.4725	I	1214.6739	607.8406	1197.6474	599.3273	1196.6634	598.8353	11
18	1891.0324	946.0198	1874.0058	937.5066	1873.0218	937.0145	I	1101.5899	551.2986	1084.5633	542.7853	1083.5793	542.2933	10
19	1948.0538	974.5306	1931.0273	966.0173	1930.0433	965.5253	G	988.5058	494.7565	971.4793	486.2433	970.4952	485.7513	9
20	2076.1124	1038.5598	2059.0859	1030.0466	2058.1019	1029.5546	Q	931.4843	466.2458	914.4578	457.7325	913.4738	457.2405	8
21	2163.1444	1082.0759	2146.1179	1073.5626	2145.1339	1073.0706	S	803.4258	402.2165	786.3992	393.7032	785.4152	393.2112	7
22	2262.2129	1131.6101	2245.1863	1123.0968	2244.2023	1122.6048	V	716.3937	358.7005	699.3672	350.1872	698.3832	349.6952	6
23	2391.2555	1196.1314	2374.2289	1187.6181	2373.2449	1187.1261	E	617.3253	309.1663	600.2988	300.6530	599.3148	300.1610	5
24	2520.2980	1260.6527	2503.2715	1252.1394	2502.2875	1251.6474	E	488.2827	244.6450	471.2562	236.1317	470.2722	235.6397	4
25	2591.3352	1296.1712	2574.3086	1287.6579	2573.3246	1287.1659	A	359.2401	180.1237	342.2136	171.6104			3
26	2704.4192	1352.7132	2687.3927	1344.2000	2686.4087	1343.7080	I	288.2030	144.6051	271.1765	136.0919			2
27							R	175.1190	88.0631	158.0924	79.5498			1

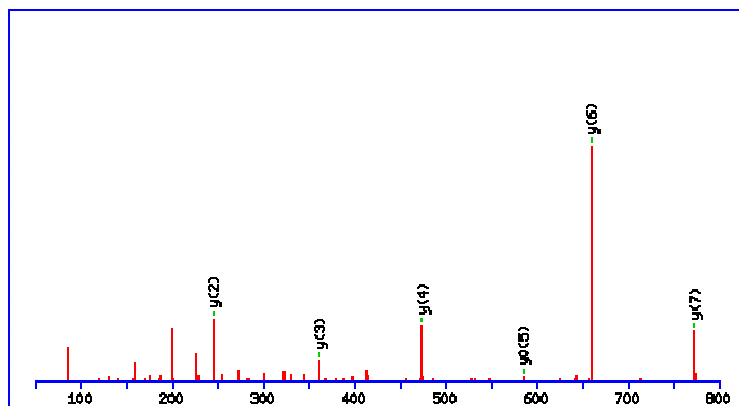


Peptide Number: 10945MS/MS Fragmentation of **LLGELDVK**Found in **IPI00968126** in **IPI_human**, Tax_Id=9606 Gene_Symbol=-- Uncharacterized protein

Match to Query 188: 885.511748 from(443.763150,2+) index(13)

Title: Elution from: 0.0333333333333333 to 0.0333333333333333 period: 0 cycle: 1 experiment: 4 polarity:+

Data file 120206ry_aHDF1419-P10_2_3.mgf



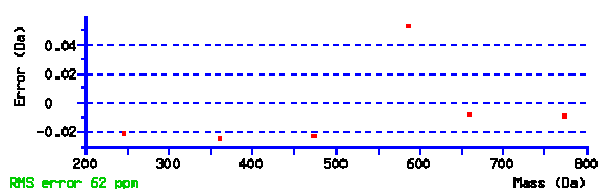
Monoisotopic mass of neutral peptide Mr(calcd): 885.5171

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

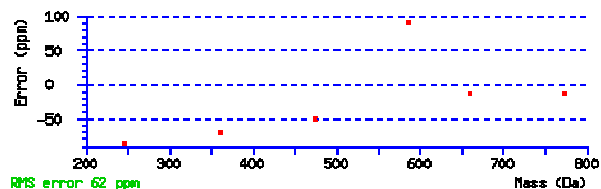
Ions Score: 49 Expect: 0.001

Matches : 6/60 fragment ions using 7 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							8
2	227.1754	114.0913			L	773.4403	387.2238	756.4138	378.7105	755.4298	378.2185	7
3	284.1969	142.6021			G	660.3563	330.6818	643.3297	322.1685	642.3457	321.6765	6
4	413.2395	207.1234	395.2289	198.1181	E	603.3348	302.1710	586.3083	293.6578	585.3243	293.1658	5
5	526.3235	263.6654	508.3130	254.6601	L	474.2922	237.6498	457.2657	229.1365	456.2817	228.6445	4
6	641.3505	321.1789	623.3399	312.1736	D	361.2082	181.1077	344.1816	172.5944	343.1976	172.1024	3
7	740.4189	370.7131	722.4083	361.7078	V	246.1812	123.5942	229.1547	115.0810			2
8					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 62 ppm



RMS error 62 ppm

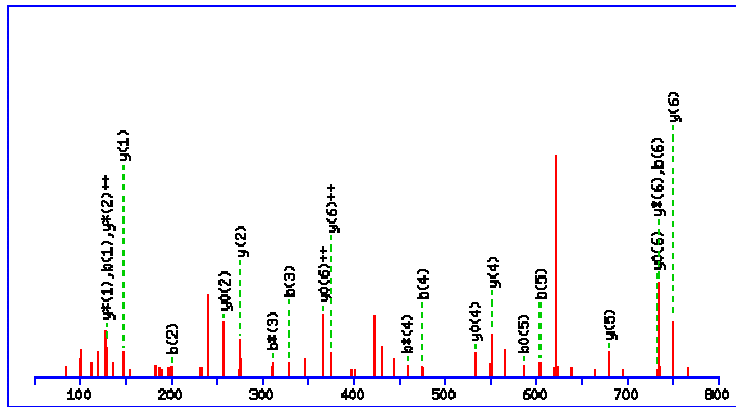
Peptide Number: 11055

MS/MS Fragmentation of **EAKMEEK**Found in **IPI00166468** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TAPT1 cDNA FLJ52307

Match to Query 6750: 879.394248 from(440.704400,2+) index(20354)

Title: Elution from: 91.25 to 91.25 period: 0 cycle: 8751 experiment: 4 polarity: +

Data file 120210ry_32R1-32_3_1.mgf



Monoisotopic mass of neutral peptide Mr(calc): 879.4007

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

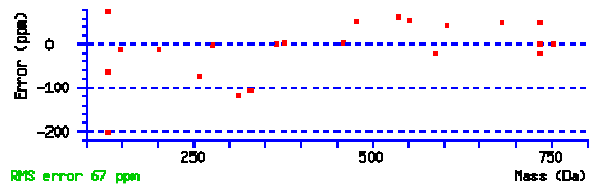
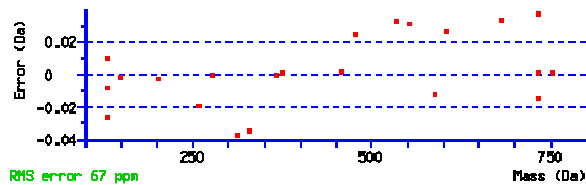
Variable modifications:

M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

Ions Score: 40 Expect: 0.0034

Matches : 22/102 fragment ions using 34 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							7
2	201.0870	101.0471			183.0764	92.0418	A	751.3655	376.1864	734.3389	367.6731	733.3549	367.1811	6
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	K	680.3284	340.6678	663.3018	332.1545	662.3178	331.6625	5
4	476.2173	238.6123	459.1908	230.0990	458.2068	229.6070	M	552.2334	276.6203	535.2068	268.1071	534.2228	267.6151	4
5	605.2599	303.1336	588.2334	294.6203	587.2494	294.1283	E	405.1980	203.1026	388.1714	194.5894	387.1874	194.0974	3
6	734.3025	367.6549	717.2760	359.1416	716.2920	358.6496	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
7							K	147.1128	74.0600	130.0863	65.5468			1



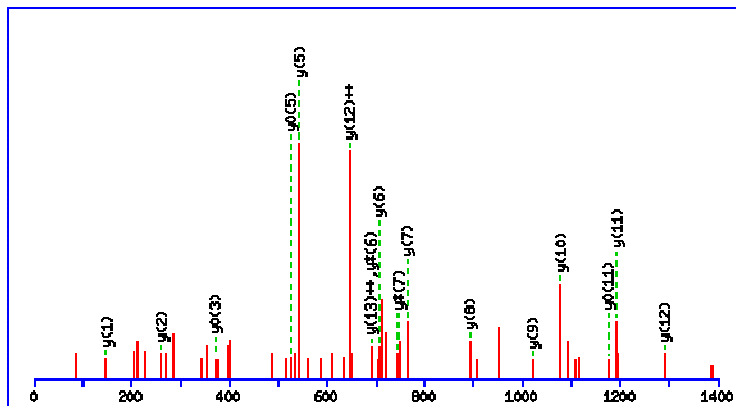
Peptide Number: 11485

MS/MS Fragmentation of **ISPDGEEGYPGELK**Found in **IPI00060200** in **IPI_human**, Tax_Id=9606 Gene_Symbol=GALM Aldose 1-epimerase

Match to Query 25248: 1489.697588 from(745.856070,2+) index(14019)

Title: Elution from: 36.4 to 36.4 period: 0 cycle: 1394 experiment: 10 polarity:+

Data file 120208ry_Tig120slc-P8_1_2.mgf



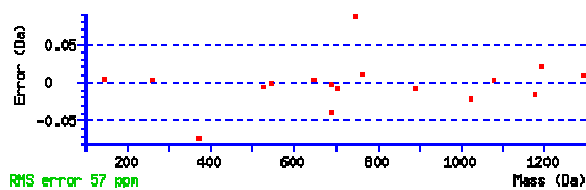
Monoisotopic mass of neutral peptide Mr(calc): 1489.6936

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

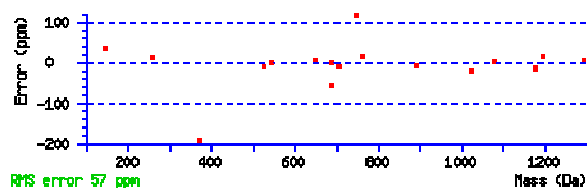
Ions Score: 45 Expect: 0.0014

Matches : 17/124 fragment ions using 50 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			I							14
2	201.1234	101.0653	183.1128	92.0600	S	1377.6169	689.3121	1360.5903	680.7988	1359.6063	680.3068	13
3	298.1761	149.5917	280.1656	140.5864	P	1290.5848	645.7961	1273.5583	637.2828	1272.5743	636.7908	12
4	413.2031	207.1052	395.1925	198.0999	D	1193.5321	597.2697	1176.5055	588.7564	1175.5215	588.2644	11
5	470.2245	235.6159	452.2140	226.6106	G	1078.5051	539.7562	1061.4786	531.2429	1060.4946	530.7509	10
6	599.2671	300.1372	581.2566	291.1319	E	1021.4837	511.2455	1004.4571	502.7322	1003.4731	502.2402	9
7	728.3097	364.6585	710.2992	355.6532	E	892.4411	446.7242	875.4145	438.2109	874.4305	437.7189	8
8	785.3312	393.1692	767.3206	384.1640	G	763.3985	382.2029	746.3719	373.6896	745.3879	373.1976	7
9	948.3945	474.7009	930.3840	465.6956	Y	706.3770	353.6921	689.3505	345.1789	688.3665	344.6869	6
10	1045.4473	523.2273	1027.4367	514.2220	P	543.3137	272.1605	526.2871	263.6472	525.3031	263.1552	5
11	1102.4687	551.7380	1084.4582	542.7327	G	446.2609	223.6341	429.2344	215.1208	428.2504	214.6288	4
12	1231.5113	616.2593	1213.5008	607.2540	E	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
13	1344.5954	672.8013	1326.5848	663.7961	L	260.1969	130.6021	243.1703	122.0888			2
14					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 57 ppm



RMS error 57 ppm

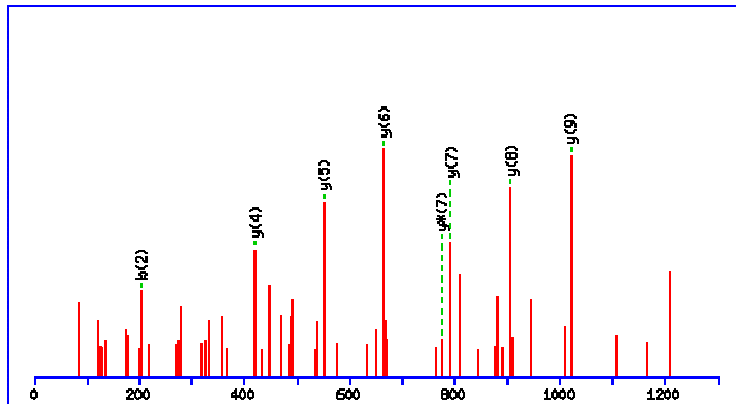
Peptide Number: 11934

MS/MS Fragmentation of **AMLDQLMGTSR**Found in **IPI01012991** in **IPI_human**, Tax_Id=9606 Gene_Symbol=LUC7L2 Isoform 1 of Putative RNA-binding protein Luc7-like 2

Match to Query 4274: 1221.582548 from(611.798550,2+) index(379)

Title: Elution from: 0.933333333333333 to 0.933333333333333 period: 0 cycle: 35 experiment: 6 polarity:+

Data file 120214ry_32R1-32_4_3.mgf



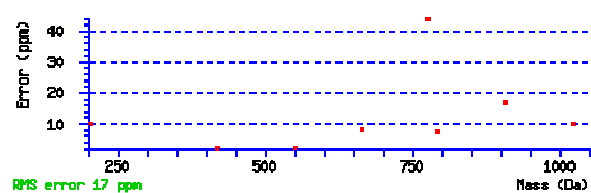
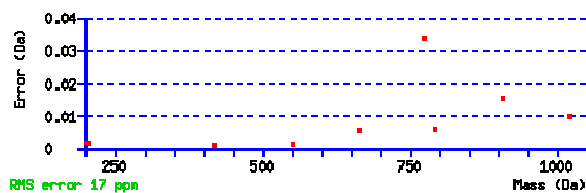
Monoisotopic mass of neutral peptide Mr(calc): 1221.5846

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 43 Expect: 0.0029

Matches : 8/104 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							11
2	203.0849	102.0461					M	1151.5547	576.2810	1134.5282	567.7677	1133.5442	567.2757	10
3	316.1689	158.5881					L	1020.5143	510.7608	1003.4877	502.2475	1002.5037	501.7555	9
4	431.1959	216.1016			413.1853	207.0963	D	907.4302	454.2187	890.4036	445.7055	889.4196	445.2135	8
5	559.2545	280.1309	542.2279	271.6176	541.2439	271.1256	Q	792.4033	396.7053	775.3767	388.1920	774.3927	387.7000	7
6	672.3385	336.6729	655.3120	328.1596	654.3280	327.6676	L	664.3447	332.6760	647.3181	324.1627	646.3341	323.6707	6
7	803.3790	402.1931	786.3525	393.6799	785.3684	393.1879	M	551.2606	276.1339	534.2341	267.6207	533.2500	267.1287	5
8	860.4005	430.7039	843.3739	422.1906	842.3899	421.6986	G	420.2201	210.6137	403.1936	202.1004	402.2096	201.6084	4
9	961.4482	481.2277	944.4216	472.7144	943.4376	472.2224	T	363.1987	182.1030	346.1721	173.5897	345.1881	173.0977	3
10	1048.4802	524.7437	1031.4536	516.2305	1030.4696	515.7384	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
11							R	175.1190	88.0631	158.0924	79.5498			1

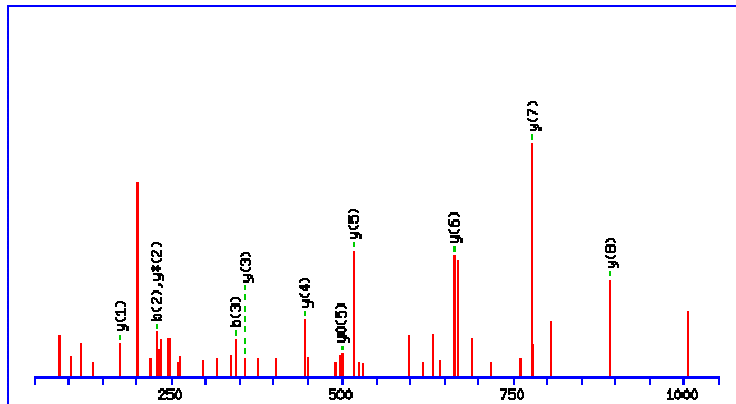


Peptide Number: 12201MS/MS Fragmentation of **DLDFA~~S~~SLAR**Found in **IPI01010332** in **IPI_human**, Tax_Id=9606 Gene_Symbol=DDX55 Uncharacterized protein

Match to Query 1057: 1006.508488 from(504.261520,2+) index(5537)

Title: Elution from: 13.3166666666667 to 13.3166666666667 period: 0 cycle: 501 experiment: 1 polarity: +

Data file 120214ry_32R1-32_4_3.mgf



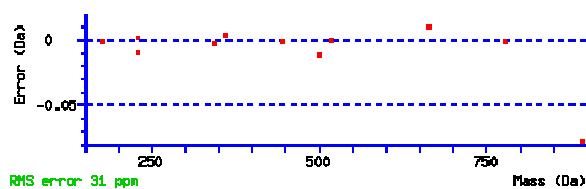
Monoisotopic mass of neutral peptide Mr(calc): 1006.5083

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

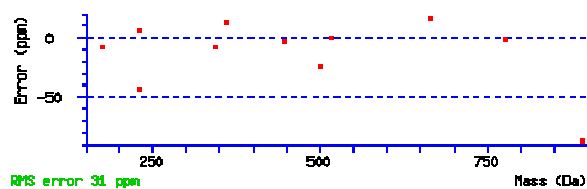
Ions Score: 41 Expect: 0.0063

Matches : 11/74 fragment ions using 24 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	98.0237	49.5155	D							9
2	229.1183	115.0628	211.1077	106.0575	L	892.4887	446.7480	875.4621	438.2347	874.4781	437.7427	8
3	344.1452	172.5763	326.1347	163.5710	D	779.4046	390.2060	762.3781	381.6927	761.3941	381.2007	7
4	491.2136	246.1105	473.2031	237.1052	F	664.3777	332.6925	647.3511	324.1792	646.3671	323.6872	6
5	562.2508	281.6290	544.2402	272.6237	A	517.3093	259.1583	500.2827	250.6450	499.2987	250.1530	5
6	649.2828	325.1450	631.2722	316.1397	S	446.2722	223.6397	429.2456	215.1264	428.2616	214.6344	4
7	762.3668	381.6871	744.3563	372.6818	L	359.2401	180.1237	342.2136	171.6104			3
8	833.4040	417.2056	815.3934	408.2003	A	246.1561	123.5817	229.1295	115.0684			2
9					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 31 ppm



RMS error 31 ppm

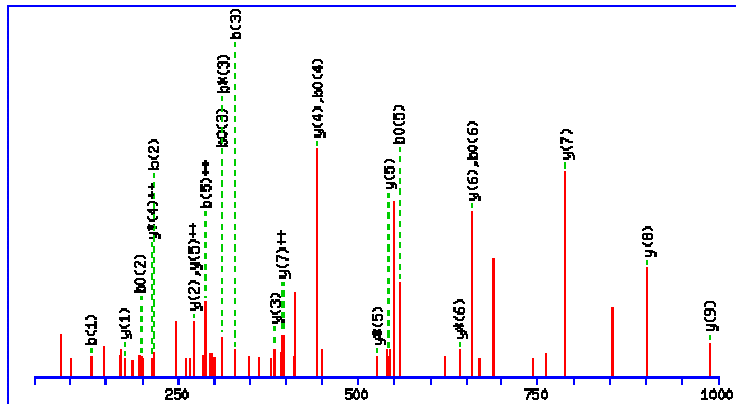
Peptide Number: 12295

MS/MS Fragmentation of **KSLMDTGLPR**Found in **IPI00977396** in **IPI_human**, Tax_Id=9606 Gene_Symbol=RANBP17 Protein

Match to Query 13832: 1116.608328 from(559.311440,2+) index(15937)

Title: Elution from: 37.9 to 37.9 period: 0 cycle: 1410 experiment: 9 polarity: +

Data file 120124ry_414C2-43_1_2.mgf



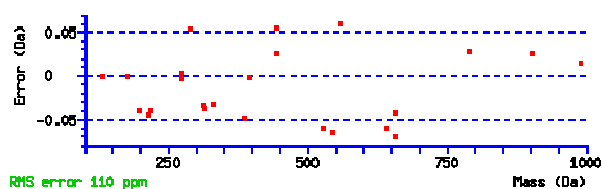
Monoisotopic mass of neutral peptide Mr(calc): 1116.5961

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

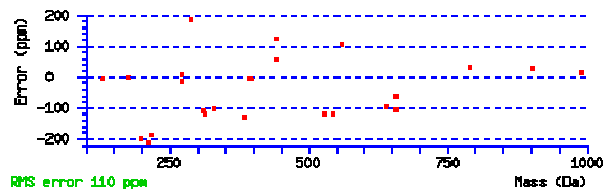
Ions Score: 60 Expect: 8.3e-005

Matches : 24/98 fragment ions using 45 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.1022	65.0548	112.0757	56.5415			K							10
2	216.1343	108.5708	199.1077	100.0575	198.1237	99.5655	S	989.5084	495.2579	972.4819	486.7446	971.4979	486.2526	9
3	329.2183	165.1128	312.1918	156.5995	311.2078	156.1075	L	902.4764	451.7418	885.4499	443.2286	884.4659	442.7366	8
4	460.2588	230.6330	443.2323	222.1198	442.2483	221.6278	M	789.3924	395.1998	772.3658	386.6865	771.3818	386.1945	7
5	575.2858	288.1465	558.2592	279.6332	557.2752	279.1412	D	658.3519	329.6796	641.3253	321.1663	640.3413	320.6743	6
6	676.3334	338.6704	659.3069	330.1571	658.3229	329.6651	T	543.3249	272.1661	526.2984	263.6528	525.3144	263.1608	5
7	733.3549	367.1811	716.3284	358.6678	715.3443	358.1758	G	442.2772	221.6423	425.2507	213.1290			4
8	846.4390	423.7231	829.4124	415.2098	828.4284	414.7178	L	385.2558	193.1315	368.2292	184.6183			3
9	943.4917	472.2495	926.4652	463.7362	925.4812	463.2442	P	272.1717	136.5895	255.1452	128.0762			2
10							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 110 ppm



RMS error 110 ppm

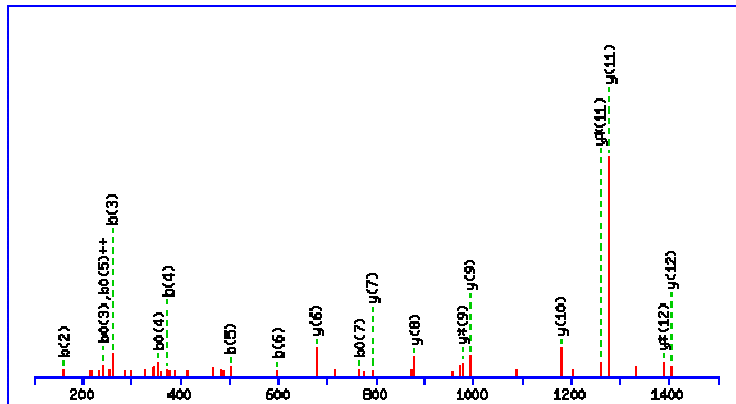
Peptide Number: 12950

MS/MS Fragmentation of **TGTLQPWNSDSTLNSR**Found in **IPI00152946** in **IPI_human**, Tax_Id=9606 Gene_Symbol=RACGAP1 Rac GTPase-activating protein 1

Match to Query 37530: 1775.832748 from(888.923650,2+) index(28920)

Title: Elution from: 70.2833333333333 to 70.2833333333333 period: 0 cycle: 2662 experiment: 10 polarity:+

Data file 120210ry_32R1-32_3_2.mgf



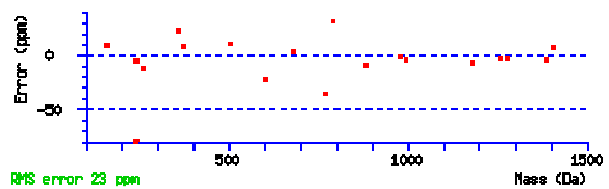
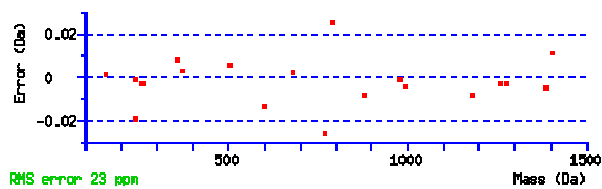
Monoisotopic mass of neutral peptide Mr(calc): 1775.8438

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 54 Expect: 0.00019

Matches : 19/170 fragment ions using 24 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							16
2	159.0764	80.0418			141.0659	71.0366	G	1675.8034	838.4054	1658.7769	829.8921	1657.7929	829.4001	15
3	260.1241	130.5657			242.1135	121.5604	T	1618.7820	809.8946	1601.7554	801.3814	1600.7714	800.8893	14
4	373.2082	187.1077			355.1976	178.1024	L	1517.7343	759.3708	1500.7077	750.8575	1499.7237	750.3655	13
5	501.2667	251.1370	484.2402	242.6237	483.2562	242.1317	Q	1404.6502	702.8288	1387.6237	694.3155	1386.6397	693.8235	12
6	598.3195	299.6634	581.2930	291.1501	580.3089	290.6581	P	1276.5917	638.7995	1259.5651	630.2862	1258.5811	629.7942	11
7	784.3988	392.7030	767.3723	384.1898	766.3883	383.6978	W	1179.5389	590.2731	1162.5123	581.7598	1161.5283	581.2678	10
8	898.4417	449.7245	881.4152	441.2112	880.4312	440.7192	N	993.4596	497.2334	976.4330	488.7202	975.4490	488.2281	9
9	985.4738	493.2405	968.4472	484.7272	967.4632	484.2352	S	879.4166	440.2120	862.3901	431.6987	861.4061	431.2067	8
10	1100.5007	550.7540	1083.4742	542.2407	1082.4901	541.7487	D	792.3846	396.6959	775.3581	388.1827	774.3741	387.6907	7
11	1187.5327	594.2700	1170.5062	585.7567	1169.5222	585.2647	S	677.3577	339.1825	660.3311	330.6692	659.3471	330.1772	6
12	1288.5804	644.7938	1271.5539	636.2806	1270.5699	635.7886	T	590.3257	295.6665	573.2991	287.1532	572.3151	286.6612	5
13	1401.6645	701.3359	1384.6379	692.8226	1383.6539	692.3306	L	489.2780	245.1426	472.2514	236.6293	471.2674	236.1373	4
14	1515.7074	758.3573	1498.6809	749.8441	1497.6968	749.3521	N	376.1939	188.6006	359.1674	180.0873	358.1833	179.5953	3
15	1602.7394	801.8734	1585.7129	793.3601	1584.7289	792.8681	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
16							R	175.1190	88.0631	158.0924	79.5498			1

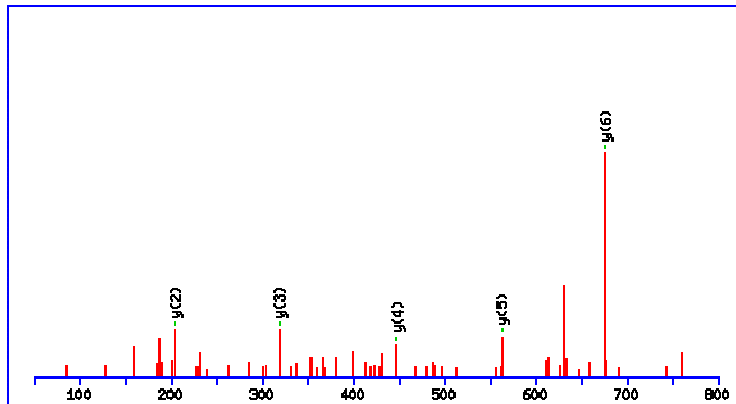


Peptide Number: 13057MS/MS Fragmentation of **WLDEDGK**Found in **IPI00878518** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SGSM3 Small G protein signaling modulator 3

Match to Query 2707: 861.386328 from(431.700440,2+) index(3103)

Title: Elution from: 7.43333333333333 to 7.43333333333333 period: 0 cycle: 277 experiment: 3 polarity: +

Data file 120129ry_604A1-46_2_2.mgf



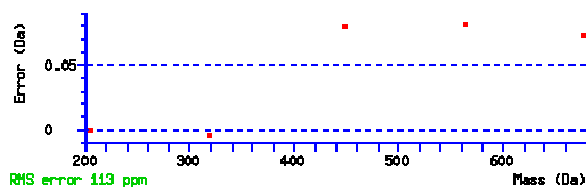
Monoisotopic mass of neutral peptide Mr(calc): 861.3868

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

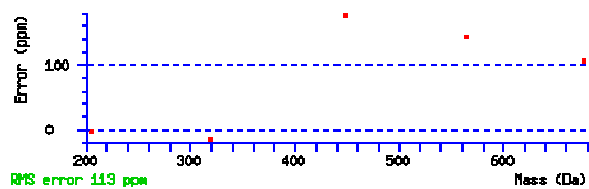
Ions Score: 42 Expect: 0.0019

Matches : 5/52 fragment ions using 7 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	187.0866	94.0469			W							7
2	300.1707	150.5890			L	676.3148	338.6610	659.2883	330.1478	658.3042	329.6558	6
3	415.1976	208.1024	397.1870	199.0972	D	563.2307	282.1190	546.2042	273.6057	545.2202	273.1137	5
4	544.2402	272.6237	526.2296	263.6185	E	448.2038	224.6055	431.1773	216.0923	430.1932	215.6003	4
5	659.2671	330.1372	641.2566	321.1319	D	319.1612	160.0842	302.1347	151.5710	301.1506	151.0790	3
6	716.2886	358.6479	698.2780	349.6427	G	204.1343	102.5708	187.1077	94.0575			2
7					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 113 ppm



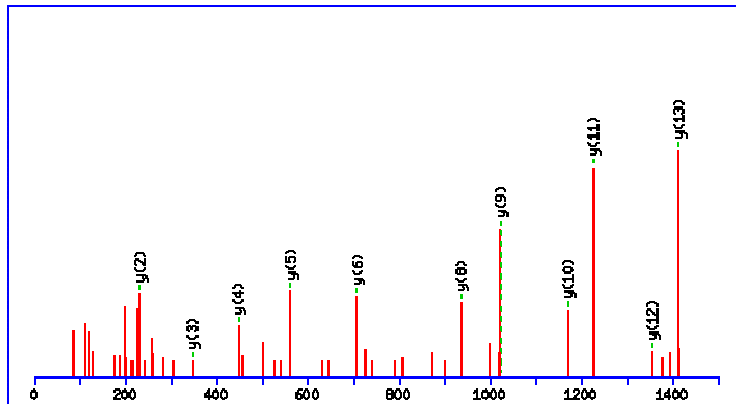
RMS error 113 ppm

Peptide Number: 13088MS/MS Fragmentation of **LLGEGFSDLFLTDGR**Found in **IPI00030618** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PCDH18 Isoform 1 of Protocadherin-18

Match to Query 5836: 1638.834468 from(820.424510,2+) index(1742)

Title: Elution from: 4.36666666666667 to 4.36666666666667 period: 0 cycle: 167 experiment: 8 polarity: +

Data file 120208ry_Tig120slc-P8_2_4.mgf



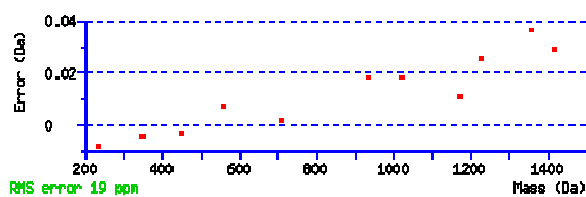
Monoisotopic mass of neutral peptide Mr(calc): 1638.8253

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

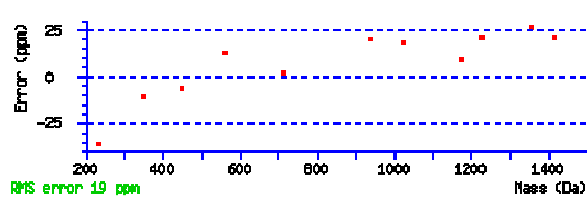
Ions Score: 107 Expect: 1.3e-009

Matches : 11/130 fragment ions using 14 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							15
2	227.1754	114.0913			L	1526.7486	763.8779	1509.7220	755.3646	1508.7380	754.8726	14
3	284.1969	142.6021			G	1413.6645	707.3359	1396.6379	698.8226	1395.6539	698.3306	13
4	413.2395	207.1234	395.2289	198.1181	E	1356.6430	678.8251	1339.6165	670.3119	1338.6325	669.8199	12
5	470.2609	235.6341	452.2504	226.6288	G	1227.6004	614.3039	1210.5739	605.7906	1209.5899	605.2986	11
6	617.3293	309.1683	599.3188	300.1630	F	1170.5790	585.7931	1153.5524	577.2798	1152.5684	576.7878	10
7	704.3614	352.6843	686.3508	343.6790	S	1023.5106	512.2589	1006.4840	503.7456	1005.5000	503.2536	9
8	819.3883	410.1978	801.3777	401.1925	D	936.4785	468.7429	919.4520	460.2296	918.4680	459.7376	8
9	932.4724	466.7398	914.4618	457.7345	L	821.4516	411.2294	804.4250	402.7162	803.4410	402.2241	7
10	1079.5408	540.2740	1061.5302	531.2687	F	708.3675	354.6874	691.3410	346.1741	690.3570	345.6821	6
11	1192.6249	596.8161	1174.6143	587.8108	L	561.2991	281.1532	544.2726	272.6399	543.2885	272.1479	5
12	1293.6725	647.3399	1275.6620	638.3346	T	448.2150	224.6112	431.1885	216.0979	430.2045	215.6059	4
13	1408.6995	704.8534	1390.6889	695.8481	D	347.1674	174.0873	330.1408	165.5740	329.1568	165.0820	3
14	1465.7209	733.3641	1447.7104	724.3588	G	232.1404	116.5738	215.1139	108.0606			2
15					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 19 ppm



RMS error 19 ppm

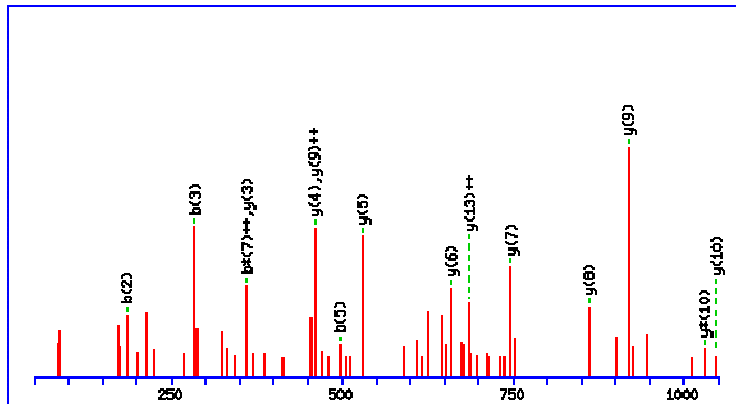
Peptide Number: 13141

MS/MS Fragmentation of **NAVDPDQGDSEAVSVR**Found in **IPI00032010** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PKIG cAMP-dependent protein kinase inhibitor gamma

Match to Query 30588: 1655.820342 from(552.947390,3+) index(18852)

Title: Elution from: 47.6166666666667 to 47.6166666666667 period: 0 cycle: 1811 experiment: 9 polarity:+

Data file 120206ry_aHDF1419-P10_3_2.mgf



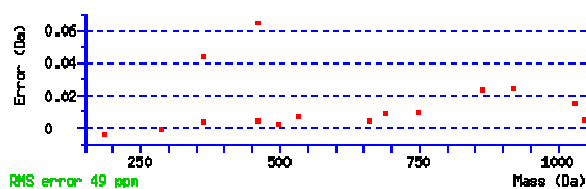
Monoisotopic mass of neutral peptide Mr(calc): 1655.8115

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

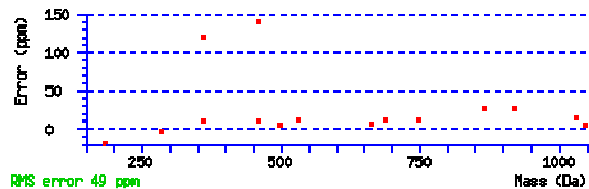
Ions Score: 58 Expect: 9.9e-005

Matches : 15/168 fragment ions using 19 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							16
2	186.0873	93.5473	169.0608	85.0340			A	1542.7758	771.8916	1525.7493	763.3783	1524.7653	762.8863	15
3	285.1557	143.0815	268.1292	134.5682			V	1471.7387	736.3730	1454.7122	727.8597	1453.7281	727.3677	14
4	382.2085	191.6079	365.1819	183.0946			P	1372.6703	686.8388	1355.6438	678.3255	1354.6597	677.8335	13
5	497.2354	249.1214	480.2089	240.6081	479.2249	240.1161	D	1275.6175	638.3124	1258.5910	629.7991	1257.6070	629.3071	12
6	610.3195	305.6634	593.2930	297.1501	592.3089	296.6581	I	1160.5906	580.7989	1143.5640	572.2857	1142.5800	571.7937	11
7	738.3781	369.6927	721.3515	361.1794	720.3675	360.6874	Q	1047.5065	524.2569	1030.4800	515.7436	1029.4960	515.2516	10
8	795.3995	398.2034	778.3730	389.6901	777.3890	389.1981	G	919.4480	460.2276	902.4214	451.7143	901.4374	451.2223	9
9	910.4265	455.7169	893.3999	447.2036	892.4159	446.7116	D	862.4265	431.7169	845.3999	423.2036	844.4159	422.7116	8
10	997.4585	499.2329	980.4320	490.7196	979.4479	490.2276	S	747.3995	374.2034	730.3730	365.6901	729.3890	365.1981	7
11	1126.5011	563.7542	1109.4746	555.2409	1108.4905	554.7489	E	660.3675	330.6874	643.3410	322.1741	642.3570	321.6821	6
12	1197.5382	599.2727	1180.5117	590.7595	1179.5277	590.2675	A	531.3249	266.1661	514.2984	257.6528	513.3144	257.1608	5
13	1296.6066	648.8070	1279.5801	640.2937	1278.5961	639.8017	V	460.2878	230.6475	443.2613	222.1343	442.2772	221.6423	4
14	1383.6387	692.3230	1366.6121	683.8097	1365.6281	683.3177	S	361.2194	181.1133	344.1928	172.6001	343.2088	172.1081	3
15	1482.7071	741.8572	1465.6805	733.3439	1464.6965	732.8519	V	274.1874	137.5973	257.1608	129.0840			2
16							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 49 ppm



RMS error 49 ppm

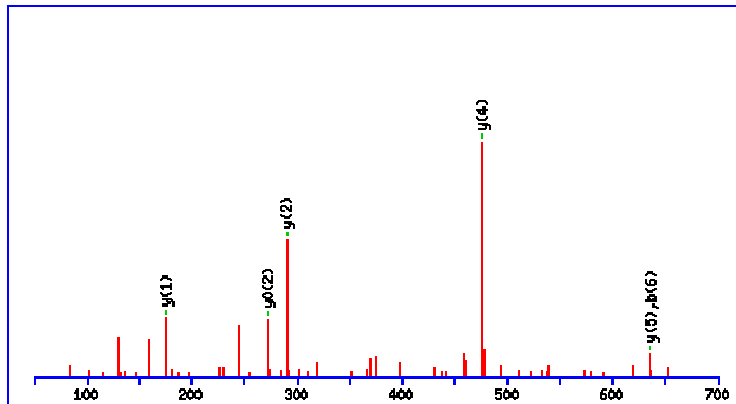
Peptide Number: 13304

MS/MS Fragmentation of **RMSSGTEECGEDR**Found in **IPI00031422** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SCN5A Isoform 4 of Sodium channel protein type 5 subunit alpha

Match to Query 24868: 1528.583776 from(383.153220,4+) index(13209)

Title: Elution from: 75.45 to 75.45 period: 0 cycle: 7007 experiment: 4 polarity: +

Data file 120201ry_aHDF1388-P9_1_1.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1528.5882

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

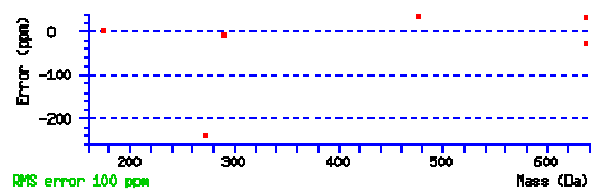
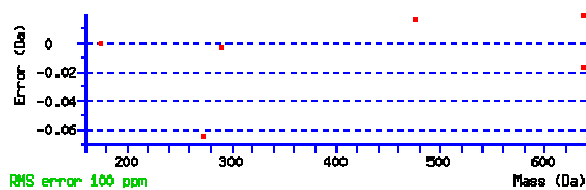
Variable modifications:

M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

Ions Score: 31 Expect: 0.0021

Matches : 6/208 fragment ions using 6 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	157.1084	79.0578	140.0818	70.5446			R							13
2	304.1438	152.5755	287.1172	144.0623			M	1373.4944	687.2508	1356.4678	678.7376	1355.4838	678.2455	12
3	391.1758	196.0915	374.1493	187.5783	373.1653	187.0863	S	1226.4590	613.7331	1209.4324	605.2199	1208.4484	604.7278	11
4	478.2078	239.6076	461.1813	231.0943	460.1973	230.6023	S	1139.4270	570.2171	1122.4004	561.7038	1121.4164	561.2118	10
5	535.2293	268.1183	518.2028	259.6050	517.2187	259.1130	G	1052.3949	526.7011	1035.3684	518.1878	1034.3844	517.6958	9
6	636.2770	318.6421	619.2504	310.1289	618.2664	309.6368	T	995.3735	498.1904	978.3469	489.6771	977.3629	489.1851	8
7	765.3196	383.1634	748.2930	374.6502	747.3090	374.1581	E	894.3258	447.6665	877.2992	439.1533	876.3152	438.6612	7
8	894.3622	447.6847	877.3356	439.1714	876.3516	438.6794	E	765.2832	383.1452	748.2566	374.6320	747.2726	374.1400	6
9	1054.3928	527.7000	1037.3663	519.1868	1036.3823	518.6948	C	636.2406	318.6239	619.2141	310.1107	618.2300	309.6187	5
10	1111.4143	556.2108	1094.3877	547.6975	1093.4037	547.2055	G	476.2100	238.6086	459.1834	230.0953	458.1994	229.6033	4
11	1240.4569	620.7321	1223.4303	612.2188	1222.4463	611.7268	E	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	3
12	1355.4838	678.2455	1338.4573	669.7323	1337.4733	669.2403	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
13							R	175.1190	88.0631	158.0924	79.5498			1



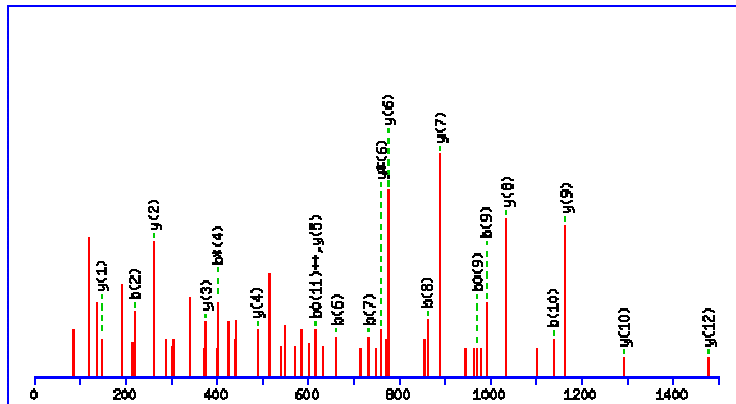
Peptide Number: 13909

MS/MS Fragmentation of **GYAQQDAQEFLCELLDK**Found in **IPI00030306** in **IPI_human**, Tax_Id=9606 Gene_Symbol=USP44 Ubiquitin carboxyl-terminal hydrolase 44

Match to Query 14440: 2026.933722 from(676.651850,3+) index(19358)

Title: Elution from: 51.2333333333333 to 51.2333333333333 period: 0 cycle: 1958 experiment: 5 polarity:+

Data file 120210ry_32R1-32_2_4.mgf



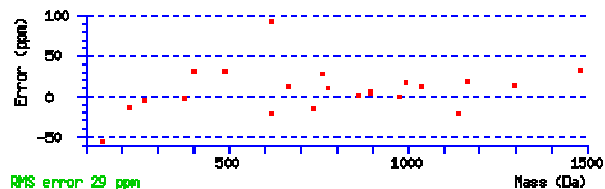
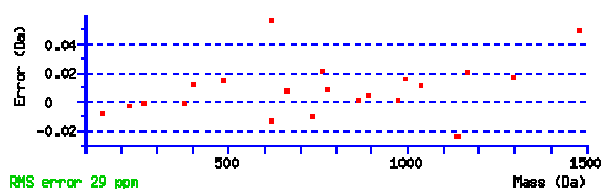
Monoisotopic mass of neutral peptide Mr(calc): 2026.9306

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 62 Expect: 2.3e-005

Matches : 21/174 fragment ions using 41 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							17
2	221.0921	111.0497					Y	1970.9164	985.9618	1953.8899	977.4486	1952.9059	976.9566	16
3	292.1292	146.5682					A	1807.8531	904.4302	1790.8265	895.9169	1789.8425	895.4249	15
4	420.1878	210.5975	403.1612	202.0842			Q	1736.8160	868.9116	1719.7894	860.3984	1718.8054	859.9063	14
5	548.2463	274.6268	531.2198	266.1135			Q	1608.7574	804.8823	1591.7309	796.3691	1590.7468	795.8771	13
6	663.2733	332.1403	646.2467	323.6270	645.2627	323.1350	D	1480.6988	740.8530	1463.6723	732.3398	1462.6883	731.8478	12
7	734.3104	367.6588	717.2838	359.1456	716.2998	358.6536	A	1365.6719	683.3396	1348.6453	674.8263	1347.6613	674.3343	11
8	862.3690	431.6881	845.3424	423.1749	844.3584	422.6828	Q	1294.6348	647.8210	1277.6082	639.3077	1276.6242	638.8157	10
9	991.4116	496.2094	974.3850	487.6961	973.4010	487.2041	E	1166.5762	583.7917	1149.5496	575.2785	1148.5656	574.7864	9
10	1138.4800	569.7436	1121.4534	561.2304	1120.4694	560.7383	F	1037.5336	519.2704	1020.5070	510.7572	1019.5230	510.2652	8
11	1251.5640	626.2857	1234.5375	617.7724	1233.5535	617.2804	L	890.4652	445.7362	873.4386	437.2230	872.4546	436.7309	7
12	1411.5947	706.3010	1394.5681	697.7877	1393.5841	697.2957	C	777.3811	389.1942	760.3546	380.6809	759.3706	380.1889	6
13	1540.6373	770.8223	1523.6107	762.3090	1522.6267	761.8170	E	617.3505	309.1789	600.3239	300.6656	599.3399	300.1736	5
14	1653.7214	827.3643	1636.6948	818.8510	1635.7108	818.3590	L	488.3079	244.6576	471.2813	236.1443	470.2973	235.6523	4
15	1766.8054	883.9063	1749.7789	875.3931	1748.7948	874.9011	L	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
16	1881.8324	941.4198	1864.8058	932.9065	1863.8218	932.4145	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
17							K	147.1128	74.0600	130.0863	65.5468			1

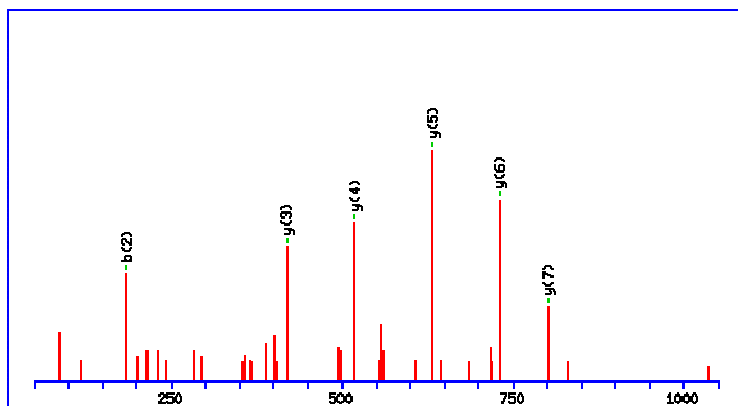


Peptide Number: 13974MS/MS Fragmentation of **LAVLPFPR**Found in **IPI00002792** in **IPI_human**, Tax_Id=9606 Gene_Symbol=B4GALT7 Beta-1,4-galactosyltransferase 7

Match to Query 886: 913.567868 from(457.791210,2+) index(9259)

Title: Elution from: 22.8833333333333 to 22.8833333333333 period: 0 cycle: 851 experiment: 2 polarity: +

Data file 120126ry_585A1-55_2_3.mgf



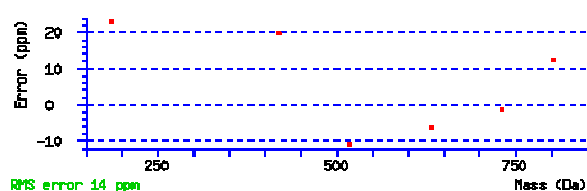
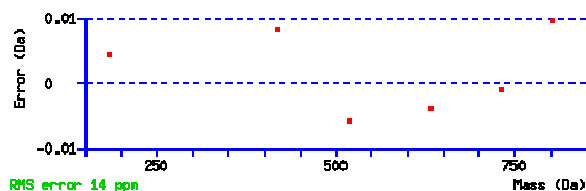
Monoisotopic mass of neutral peptide Mr(calc): 913.5749

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 43 Expect: 0.0021

Matches : 6/42 fragment ions using 8 most intense peaks ([help](#))

#	b	b ⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	#
1	114.0913	57.5493	L					8
2	185.1285	93.0679	A	801.4981	401.2527	784.4716	392.7394	7
3	284.1969	142.6021	V	730.4610	365.7341	713.4345	357.2209	6
4	397.2809	199.1441	L	631.3926	316.1999	614.3661	307.6867	5
5	496.3493	248.6783	V	518.3085	259.6579	501.2820	251.1446	4
6	593.4021	297.2047	P	419.2401	210.1237	402.2136	201.6104	3
7	740.4705	370.7389	F	322.1874	161.5973	305.1608	153.0840	2
8			R	175.1190	88.0631	158.0924	79.5498	1



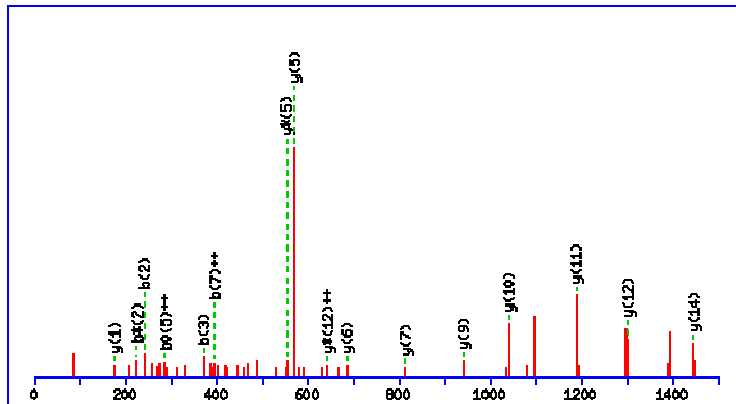
Peptide Number: 14597

MS/MS Fragmentation of **LQEYGSIFTGAQDPGLQR**Found in **IPI01012444** in **IPI_human**, Tax_Id=9606 Gene_Symbol=WASH3P;WASH1 Putative uncharacterized protein DKFZp686C24272

Match to Query 27654: 1978.993488 from(990.504020,2+) index(3330)

Title: Elution from: 7.98333333333333 to 7.98333333333333 period: 0 cycle: 300 experiment: 8 polarity: +

Data file 120214ry_32R1-32_4_3.mgf



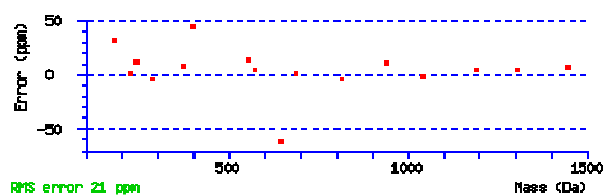
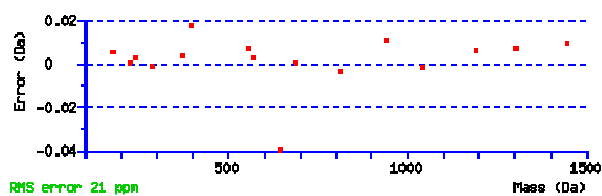
Monoisotopic mass of neutral peptide Mr(calc): 1978.9749

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 66 Expect: 1.9e-005

Matches : 16/188 fragment ions using 23 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							18
2	242.1499	121.5786	225.1234	113.0653			Q	1866.8981	933.9527	1849.8715	925.4394	1848.8875	924.9474	17
3	371.1925	186.0999	354.1660	177.5866	353.1819	177.0946	E	1738.8395	869.9234	1721.8129	861.4101	1720.8289	860.9181	16
4	534.2558	267.6316	517.2293	259.1183	516.2453	258.6263	Y	1609.7969	805.4021	1592.7704	796.8888	1591.7863	796.3968	15
5	591.2773	296.1423	574.2508	287.6290	573.2667	287.1370	G	1446.7336	723.8704	1429.7070	715.3571	1428.7230	714.8651	14
6	678.3093	339.6583	661.2828	331.1450	660.2988	330.6530	S	1389.7121	695.3597	1372.6856	686.8464	1371.7015	686.3544	13
7	791.3934	396.2003	774.3668	387.6871	773.3828	387.1951	I	1302.6801	651.8437	1285.6535	643.3304	1284.6695	642.8384	12
8	938.4618	469.7345	921.4353	461.2213	920.4512	460.7293	F	1189.5960	595.3016	1172.5695	586.7884	1171.5854	586.2964	11
9	1039.5095	520.2584	1022.4829	511.7451	1021.4989	511.2531	T	1042.5276	521.7674	1025.5011	513.2542	1024.5170	512.7622	10
10	1096.5310	548.7691	1079.5044	540.2558	1078.5204	539.7638	G	941.4799	471.2436	924.4534	462.7303	923.4694	462.2383	9
11	1167.5681	584.2877	1150.5415	575.7744	1149.5575	575.2824	A	884.4585	442.7329	867.4319	434.2196	866.4479	433.7276	8
12	1295.6266	648.3170	1278.6001	639.8037	1277.6161	639.3117	Q	813.4213	407.2143	796.3948	398.7010	795.4108	398.2090	7
13	1410.6536	705.8304	1393.6270	697.3172	1392.6430	696.8251	D	685.3628	343.1850	668.3362	334.6717	667.3522	334.1797	6
14	1507.7064	754.3568	1490.6798	745.8435	1489.6958	745.3515	P	570.3358	285.6715	553.3093	277.1583			5
15	1564.7278	782.8675	1547.7013	774.3543	1546.7173	773.8623	G	473.2831	237.1452	456.2565	228.6319			4
16	1677.8119	839.4096	1660.7853	830.8963	1659.8013	830.4043	L	416.2616	208.6344	399.2350	200.1212			3
17	1805.8705	903.4389	1788.8439	894.9256	1787.8599	894.4336	Q	303.1775	152.0924	286.1510	143.5791			2
18							R	175.1190	88.0631	158.0924	79.5498			1

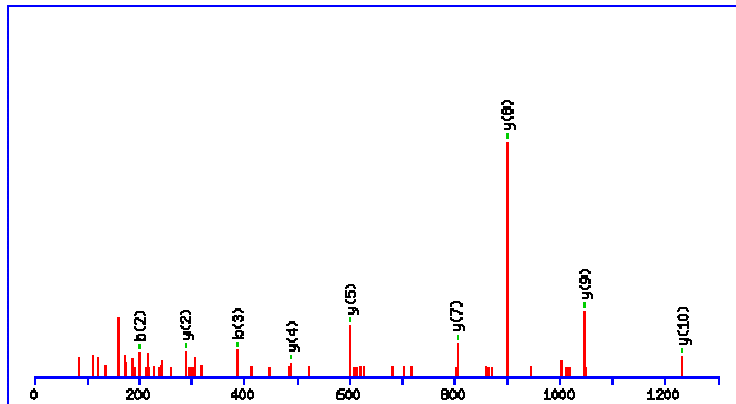


Peptide Number: 14789MS/MS Fragmentation of **SLWFPSDLAELR**Found in **IPI00441956** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TMEM41A 10 kDa protein

Match to Query 2036: 1432.746028 from(717.380290,2+) index(478)

Title: Elution from: 1.2 to 1.2 period: 0 cycle: 45 experiment: 6 polarity:+

Data file 120208ry_Tig120slc-P8_1_4.mgf



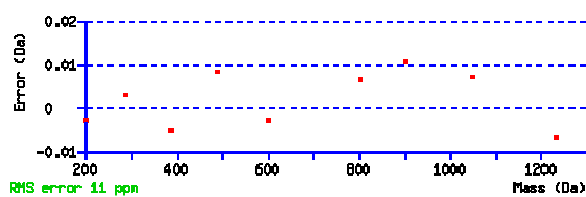
Monoisotopic mass of neutral peptide Mr(calc): 1432.7350

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

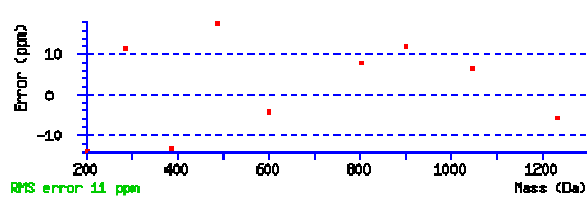
Ions Score: 62 Expect: 5e-005

Matches : 9/106 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233	70.0287	35.5180	S							12
2	201.1234	101.0653	183.1128	92.0600	L	1346.7103	673.8588	1329.6838	665.3455	1328.6997	664.8535	11
3	387.2027	194.1050	369.1921	185.0997	W	1233.6262	617.3168	1216.5997	608.8035	1215.6157	608.3115	10
4	534.2711	267.6392	516.2605	258.6339	F	1047.5469	524.2771	1030.5204	515.7638	1029.5364	515.2718	9
5	631.3239	316.1656	613.3133	307.1603	P	900.4785	450.7429	883.4520	442.2296	882.4680	441.7376	8
6	718.3559	359.6816	700.3453	350.6763	S	803.4258	402.2165	786.3992	393.7032	785.4152	393.2112	7
7	833.3828	417.1951	815.3723	408.1898	D	716.3937	358.7005	699.3672	350.1872	698.3832	349.6952	6
8	946.4669	473.7371	928.4563	464.7318	L	601.3668	301.1870	584.3402	292.6738	583.3562	292.1817	5
9	1017.5040	509.2556	999.4934	500.2504	A	488.2827	244.6450	471.2562	236.1317	470.2722	235.6397	4
10	1146.5466	573.7769	1128.5360	564.7717	E	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
11	1259.6307	630.3190	1241.6201	621.3137	L	288.2030	144.6051	271.1765	136.0919			2
12					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 11 ppm



RMS error 11 ppm

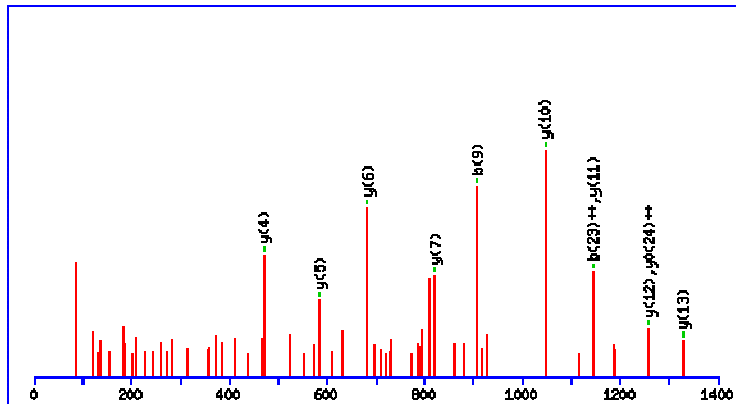
Peptide Number: 14821

MS/MS Fragmentation of **GPAPDPCLVPLALEALVGAVHVLHASR**Found in **IPI00180515** in **IPI_human**, Tax_Id=9606 Gene_Symbol=NBEAL2 Uncharacterized protein

Match to Query 4847: 2758.498256 from(690.631840,4+) index(6301)

Title: Elution from: 33.3 to 33.3 period: 0 cycle: 1298 experiment: 2 polarity: +

Data file 120210ry_32R1-32_2_5.mgf



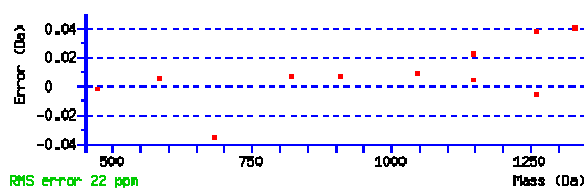
Monoisotopic mass of neutral peptide Mr(calc): 2758.4952

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

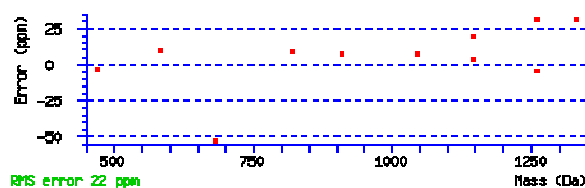
Ions Score: 52 Expect: 0.00018

Matches : 11/250 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180			G							27
2	155.0815	78.0444			P	2702.4811	1351.7442	2685.4545	1343.2309	2684.4705	1342.7389	26
3	226.1186	113.5629			A	2605.4283	1303.2178	2588.4017	1294.7045	2587.4177	1294.2125	25
4	323.1714	162.0893			P	2534.3912	1267.6992	2517.3646	1259.1860	2516.3806	1258.6939	24
5	438.1983	219.6028	420.1878	210.5975	D	2437.3384	1219.1728	2420.3119	1210.6596	2419.3278	1210.1676	23
6	535.2511	268.1292	517.2405	259.1239	P	2322.3115	1161.6594	2305.2849	1153.1461	2304.3009	1152.6541	22
7	695.2817	348.1445	677.2712	339.1392	C	2225.2587	1113.1330	2208.2322	1104.6197	2207.2481	1104.1277	21
8	808.3658	404.6865	790.3552	395.6813	L	2065.2281	1033.1177	2048.2015	1024.6044	2047.2175	1024.1124	20
9	907.4342	454.2207	889.4237	445.2155	V	1952.1440	976.5756	1935.1174	968.0624	1934.1334	967.5704	19
10	1004.4870	502.7471	986.4764	493.7418	P	1853.0756	927.0414	1836.0490	918.5282	1835.0650	918.0361	18
11	1117.5710	559.2892	1099.5605	550.2839	L	1756.0228	878.5150	1738.9963	870.0018	1738.0123	869.5098	17
12	1188.6082	594.8077	1170.5976	585.8024	A	1642.9388	821.9730	1625.9122	813.4597	1624.9282	812.9677	16
13	1301.6922	651.3497	1283.6817	642.3445	L	1571.9016	786.4545	1554.8751	777.9412	1553.8911	777.4492	15
14	1430.7348	715.8710	1412.7243	706.8658	E	1458.8176	729.9124	1441.7910	721.3992	1440.8070	720.9071	14
15	1501.7719	751.3896	1483.7614	742.3843	A	1329.7750	665.3911	1312.7484	656.8779	1311.7644	656.3858	13
16	1614.8560	807.9316	1596.8454	798.9264	L	1258.7379	629.8726	1241.7113	621.3593	1240.7273	620.8673	12
17	1713.9244	857.4658	1695.9138	848.4606	V	1145.6538	573.3305	1128.6273	564.8173	1127.6432	564.3253	11
18	1770.9459	885.9766	1752.9353	876.9713	G	1046.5854	523.7963	1029.5588	515.2831	1028.5748	514.7910	10
19	1841.9830	921.4951	1823.9724	912.4898	A	989.5639	495.2856	972.5374	486.7723	971.5534	486.2803	9
20	1941.0514	971.0293	1923.0408	962.0241	V	918.5268	459.7670	901.5003	451.2538	900.5162	450.7618	8
21	2078.1103	1039.5588	2060.0997	1030.5535	H	819.4584	410.2328	802.4318	401.7196	801.4478	401.2276	7
22	2177.1787	1089.0930	2159.1682	1080.0877	V	682.3995	341.7034	665.3729	333.1901	664.3889	332.6981	6
23	2290.2628	1145.6350	2272.2522	1136.6297	L	583.3311	292.1692	566.3045	283.6559	565.3205	283.1639	5
24	2427.3217	1214.1645	2409.3111	1205.1592	H	470.2470	235.6271	453.2205	227.1139	452.2364	226.6219	4
25	2498.3588	1249.6830	2480.3483	1240.6778	A	333.1881	167.0977	316.1615	158.5844	315.1775	158.0924	3
26	2585.3908	1293.1991	2567.3803	1284.1938	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
27					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 22 ppm



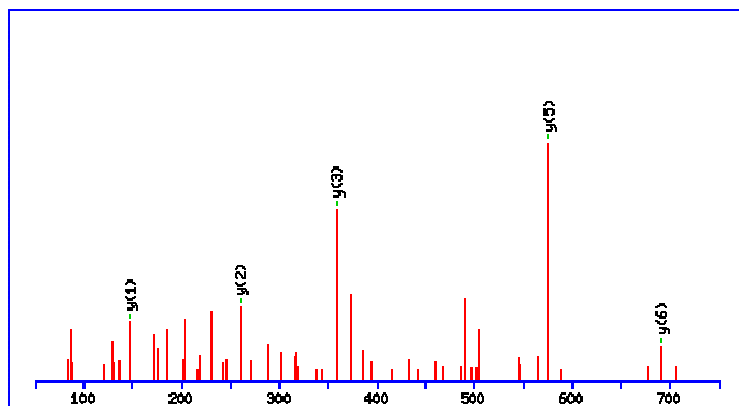
RMS error 22 ppm

Peptide Number: 14984**MS/MS Fragmentation of DDDTVLK**Found in **IPI00871500** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TBC1D3P2 HCG95695, isoform CRA_c

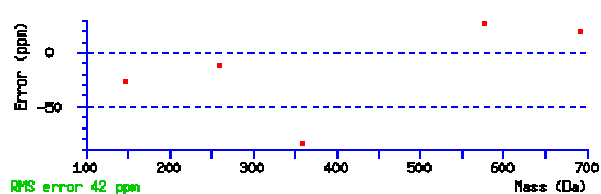
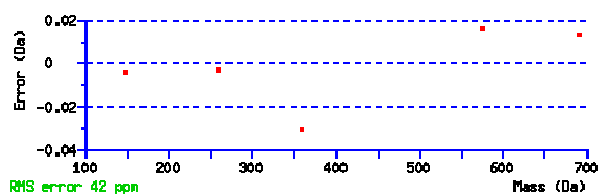
Match to Query 1418: 804.398128 from(403.206340,2+) index(4546)

Title: Elution from: 10.7333333333333 to 10.7333333333333 period: 0 cycle: 398 experiment: 2 polarity: +

Data file 120129ry_604A1-46_1_2.mgf

**Monoisotopic mass of neutral peptide Mr(calc):** 804.3865**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 42 **Expect:** 0.0037**Matches :** 5/54 fragment ions using 7 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	98.0237	49.5155	D							7
2	231.0612	116.0342	213.0506	107.0289	D	690.3668	345.6871	673.3403	337.1738	672.3563	336.6818	6
3	346.0881	173.5477	328.0775	164.5424	D	575.3399	288.1736	558.3134	279.6603	557.3293	279.1683	5
4	447.1358	224.0715	429.1252	215.0662	T	460.3130	230.6601	443.2864	222.1468	442.3024	221.6548	4
5	546.2042	273.6057	528.1936	264.6005	V	359.2653	180.1363	342.2387	171.6230			3
6	659.2883	330.1478	641.2777	321.1425	L	260.1969	130.6021	243.1703	122.0888			2
7					K	147.1128	74.0600	130.0863	65.5468			1



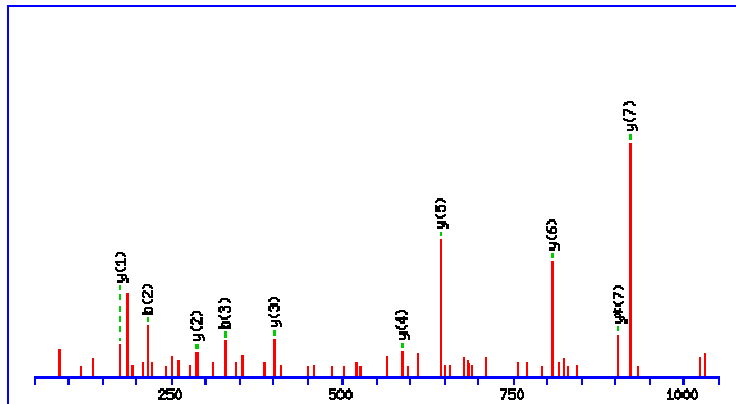
Peptide Number: 14989

MS/MS Fragmentation of **DVNYGWIR**Found in **IPI00935962** in **IPI_human**, Tax_Id=9606 Gene_Symbol=MT-CYB Cytochrome b

Match to Query 2276: 1134.581408 from(568.297980,2+) index(14593)

Title: Elution from: 37.7333333333333 to 37.7333333333333 period: 0 cycle: 1443 experiment: 3 polarity:+

Data file 120208ry_Tig120slc-P8_3_3.mgf



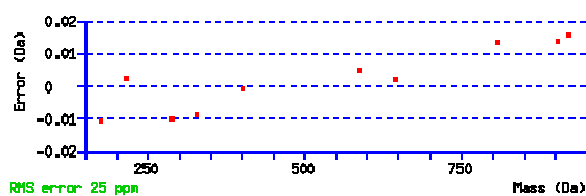
Monoisotopic mass of neutral peptide Mr(calc): 1134.5822

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

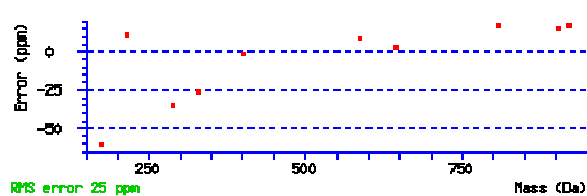
Ions Score: 46 Expect: 0.0021

Matches : 10/76 fragment ions using 20 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D					9
2	215.1026	108.0550			197.0921	99.0497	V	1020.5625	510.7849	1003.5360	502.2716	8
3	329.1456	165.0764	312.1190	156.5631	311.1350	156.0711	N	921.4941	461.2507	904.4676	452.7374	7
4	492.2089	246.6081	475.1823	238.0948	474.1983	237.6028	Y	807.4512	404.2292	790.4246	395.7160	6
5	549.2304	275.1188	532.2038	266.6055	531.2198	266.1135	G	644.3879	322.6976	627.3613	314.1843	5
6	735.3097	368.1585	718.2831	359.6452	717.2991	359.1532	W	587.3664	294.1868	570.3398	285.6736	4
7	848.3937	424.7005	831.3672	416.1872	830.3832	415.6952	I	401.2871	201.1472	384.2605	192.6339	3
8	961.4778	481.2425	944.4512	472.7293	943.4672	472.2373	I	288.2030	144.6051	271.1765	136.0919	2
9							R	175.1190	88.0631	158.0924	79.5498	1



RMS error 25 ppm



RMS error 25 ppm

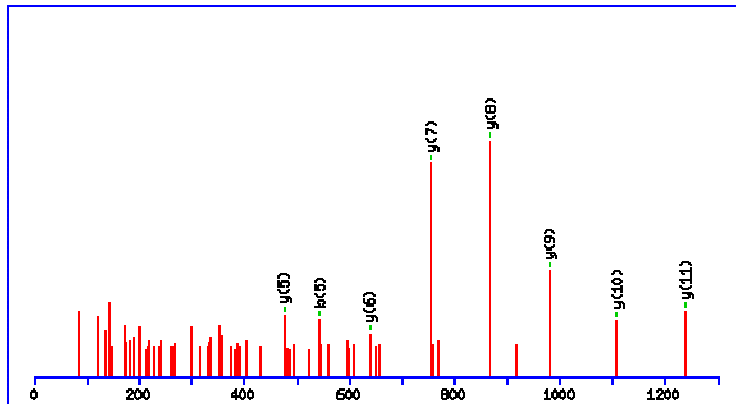
Peptide Number: 15048

MS/MS Fragmentation of **GLEELIDYTGGLK**Found in **IPI00009707** in **IPI_human**, Tax_Id=9606 Gene_Symbol=RMND5A Isoform 1 of Protein RMD5 homolog A

Match to Query 9420: 1406.716048 from(704.365300,2+) index(36817)

Title: Elution from: 89.4833333333333 to 89.4833333333333 period: 0 cycle: 3314 experiment: 5 polarity:+

Data file 120118ry_201B7-32_1_3.mgf



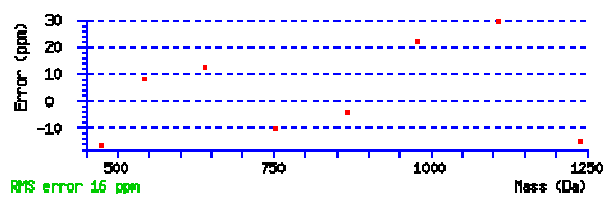
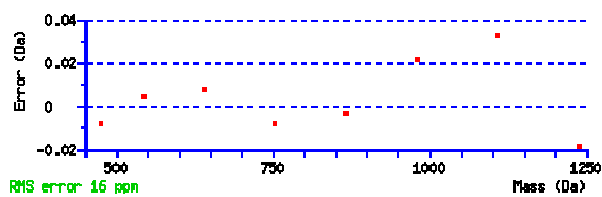
Monoisotopic mass of neutral peptide Mr(calc): 1406.7293

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 56 Expect: 0.00017

Matches : 8/108 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180			Q							13
2	171.1128	86.0600			L	1350.7151	675.8612	1333.6886	667.3479	1332.7046	666.8559	12
3	300.1554	150.5813	282.1448	141.5761	E	1237.6311	619.3192	1220.6045	610.8059	1219.6205	610.3139	11
4	429.1980	215.1026	411.1874	206.0974	E	1108.5885	554.7979	1091.5619	546.2846	1090.5779	545.7926	10
5	542.2821	271.6447	524.2715	262.6394	L	979.5459	490.2766	962.5193	481.7633	961.5353	481.2713	9
6	655.3661	328.1867	637.3556	319.1814	I	866.4618	433.7345	849.4353	425.2213	848.4512	424.7293	8
7	770.3931	385.7002	752.3825	376.6949	D	753.3777	377.1925	736.3512	368.6792	735.3672	368.1872	7
8	933.4564	467.2318	915.4458	458.2266	Y	638.3508	319.6790	621.3243	311.1658	620.3402	310.6738	6
9	1034.5041	517.7557	1016.4935	508.7504	T	475.2875	238.1474	458.2609	229.6341	457.2769	229.1421	5
10	1091.5255	546.2664	1073.5150	537.2611	Q	374.2398	187.6235	357.2132	179.1103			4
11	1148.5470	574.7771	1130.5364	565.7719	Q	317.2183	159.1128	300.1918	150.5995			3
12	1261.6311	631.3192	1243.6205	622.3139	L	260.1969	130.6021	243.1703	122.0888			2
13					K	147.1128	74.0600	130.0863	65.5468			1



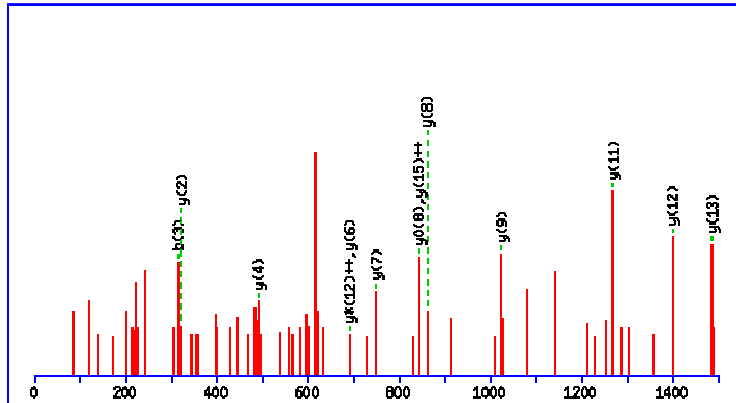
Peptide Number: 15113

MS/MS Fragmentation of **SLNEASMDEYLGSLGLFR**Found in **IPI00967654** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ALG13 Isoform 4 of UDP-N-acetylglucosamine transferase subunit ALG13 homolog

Match to Query 14691: 2000.975348 from(1001.494950,2+) index(16396)

Title: Elution from: 39.4166666666667 to 39.4166666666667 period: 0 cycle: 1483 experiment: 9 polarity: +

Data file 120214ry_32R1-32_4_4.mgf



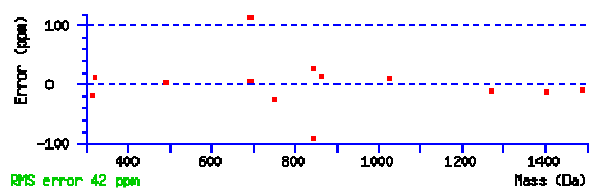
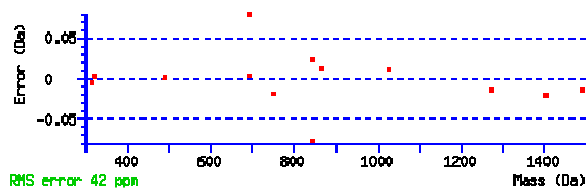
Monoisotopic mass of neutral peptide Mr(calc): 2000.9513

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 41 Expect: 0.0048

Matches : 13/190 fragment ions using 28 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							18
2	201.1234	101.0653			183.1128	92.0600	L	1914.9266	957.9669	1897.9000	949.4537	1896.9160	948.9617	17
3	315.1663	158.0868	298.1397	149.5735	297.1557	149.0815	N	1801.8425	901.4249	1784.8160	892.9116	1783.8320	892.4196	16
4	444.2089	222.6081	427.1823	214.0948	426.1983	213.6028	E	1687.7996	844.4034	1670.7730	835.8902	1669.7890	835.3982	15
5	515.2460	258.1266	498.2195	249.6134	497.2354	249.1214	A	1558.7570	779.8821	1541.7305	771.3689	1540.7464	770.8769	14
6	602.2780	301.6427	585.2515	293.1294	584.2675	292.6374	S	1487.7199	744.3636	1470.6933	735.8503	1469.7093	735.3583	13
7	733.3185	367.1629	716.2920	358.6496	715.3080	358.1576	M	1400.6879	700.8476	1383.6613	692.3343	1382.6773	691.8423	12
8	848.3455	424.6764	831.3189	416.1631	830.3349	415.6711	D	1269.6474	635.3273	1252.6208	626.8141	1251.6368	626.3220	11
9	977.3881	489.1977	960.3615	480.6844	959.3775	480.1924	E	1154.6204	577.8139	1137.5939	569.3006	1136.6099	568.8086	10
10	1140.4514	570.7293	1123.4248	562.2161	1122.4408	561.7240	Y	1025.5778	513.2926	1008.5513	504.7793	1007.5673	504.2873	9
11	1253.5354	627.2714	1236.5089	618.7581	1235.5249	618.2661	L	862.5145	431.7609	845.4880	423.2476	844.5039	422.7556	8
12	1310.5569	655.7821	1293.5304	647.2688	1292.5463	646.7768	G	749.4304	375.2189	732.4039	366.7056	731.4199	366.2136	7
13	1397.5889	699.2981	1380.5624	690.7848	1379.5784	690.2928	S	692.4090	346.7081	675.3824	338.1949	674.3984	337.7028	6
14	1510.6730	755.8401	1493.6465	747.3269	1492.6624	746.8349	L	605.3770	303.1921	588.3504	294.6788			5
15	1567.6945	784.3509	1550.6679	775.8376	1549.6839	775.3456	G	492.2929	246.6501	475.2663	238.1368			4
16	1680.7785	840.8929	1663.7520	832.3796	1662.7680	831.8876	L	435.2714	218.1394	418.2449	209.6261			3
17	1827.8469	914.4271	1810.8204	905.9138	1809.8364	905.4218	F	322.1874	161.5973	305.1608	153.0840			2
18							R	175.1190	88.0631	158.0924	79.5498			1



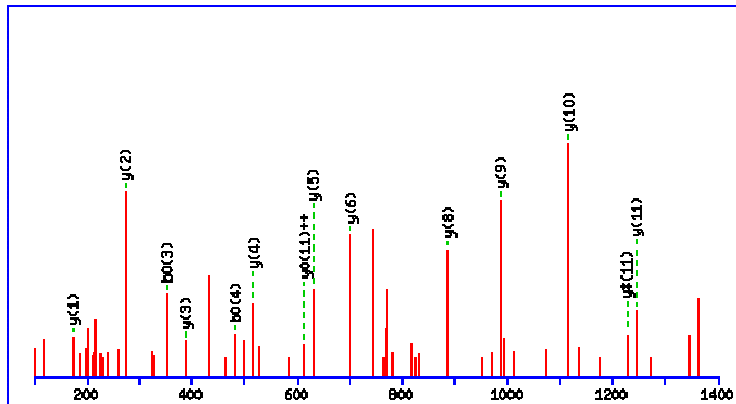
Peptide Number: 15567

MS/MS Fragmentation of **ELQETNAALQDVR**Found in **IPI00028030** in **IPI_human**, Tax_Id=9606 Gene_Symbol=COMP Cartilage oligomeric matrix protein

Match to Query 26679: 1485.740408 from(743.877480,2+) index(11852)

Title: Elution from: 28.1666666666667 to 28.1666666666667 period: 0 cycle: 1066 experiment: 9 polarity: +

Data file 120208ry_Tig120slc-P8_2_2.mgf



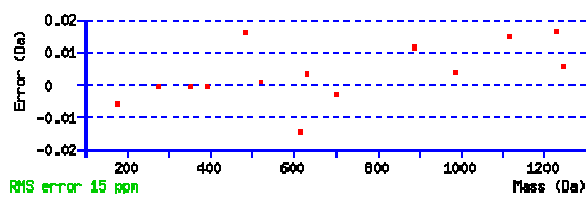
Monoisotopic mass of neutral peptide Mr(calc): 1485.7423

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

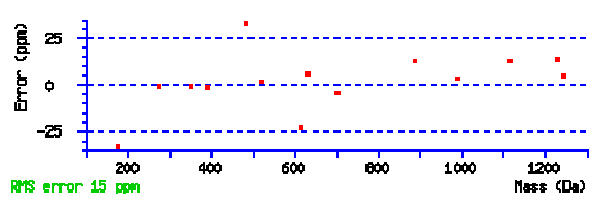
Ions Score: 66 Expect: 2e-005

Matches : 14/136 fragment ions using 26 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							13
2	243.1339	122.0706			225.1234	113.0653	L	1357.7070	679.3571	1340.6805	670.8439	1339.6965	670.3519	12
3	371.1925	186.0999	354.1660	177.5866	353.1819	177.0946	Q	1244.6230	622.8151	1227.5964	614.3018	1226.6124	613.8098	11
4	500.2351	250.6212	483.2086	242.1079	482.2245	241.6159	E	1116.5644	558.7858	1099.5378	550.2726	1098.5538	549.7805	10
5	601.2828	301.1450	584.2562	292.6318	583.2722	292.1397	T	987.5218	494.2645	970.4952	485.7513	969.5112	485.2592	9
6	715.3257	358.1665	698.2992	349.6532	697.3151	349.1612	N	886.4741	443.7407	869.4476	435.2274	868.4635	434.7354	8
7	786.3628	393.6851	769.3363	385.1718	768.3523	384.6798	A	772.4312	386.7192	755.4046	378.2060	754.4206	377.7139	7
8	857.3999	429.2036	840.3734	420.6903	839.3894	420.1983	A	701.3941	351.2007	684.3675	342.6874	683.3835	342.1954	6
9	970.4840	485.7456	953.4575	477.2324	952.4734	476.7404	L	630.3570	315.6821	613.3304	307.1688	612.3464	306.6768	5
10	1098.5426	549.7749	1081.5160	541.2617	1080.5320	540.7696	Q	517.2729	259.1401	500.2463	250.6268	499.2623	250.1348	4
11	1213.5695	607.2884	1196.5430	598.7751	1195.5590	598.2831	D	389.2143	195.1108	372.1878	186.5975	371.2037	186.1055	3
12	1312.6379	656.8226	1295.6114	648.3093	1294.6274	647.8173	V	274.1874	137.5973	257.1608	129.0840			2
13							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 15 ppm



RMS error 15 ppm

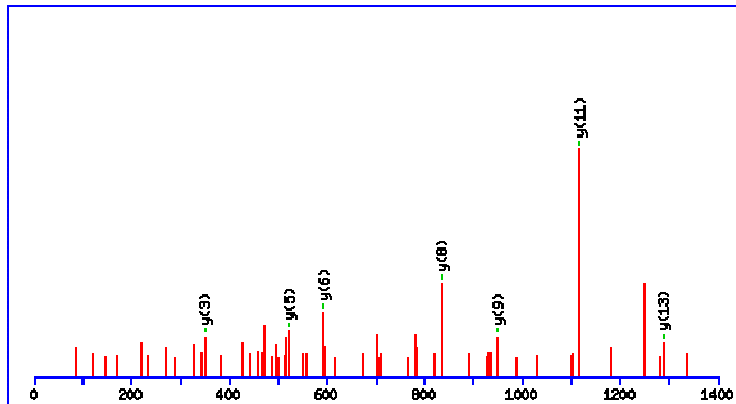
Peptide Number: 15661

MS/MS Fragmentation of **GTEFAESADAALQGDPALQDAGDSSR**Found in **IPI00026299** in **IPI_human**, Tax_Id=9606 Gene_Symbol=GYPC Isoform Glycophorin-C of Glycophorin-C

Match to Query 33265: 2578.151982 from(860.391270,3+) index(3961)

Title: Elution from: 10.4 to 10.4 period: 0 cycle: 402 experiment: 9 polarity: +

Data file 120208ry_Tig120slc-P8_1_3.mgf



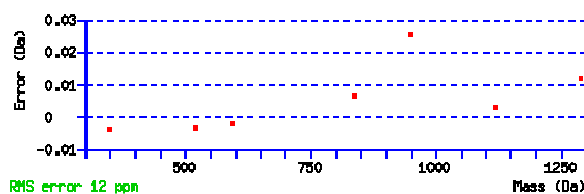
Monoisotopic mass of neutral peptide Mr(calc): 2578.1419

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

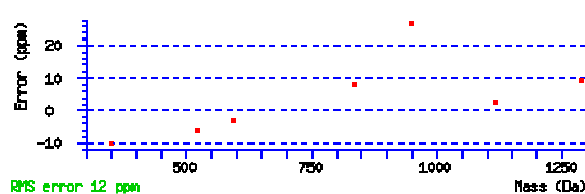
Ions Score: 36 Expect: 0.0069

Matches : 7/272 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							26
2	159.0764	80.0418			141.0659	71.0366	T	2522.1277	1261.5675	2505.1012	1253.0542	2504.1172	1252.5622	25
3	288.1190	144.5631			270.1084	135.5579	E	2421.0801	1211.0437	2404.0535	1202.5304	2403.0695	1202.0384	24
4	435.1874	218.0974			417.1769	209.0921	F	2292.0375	1146.5224	2275.0109	1138.0091	2274.0269	1137.5171	23
5	506.2245	253.6159			488.2140	244.6106	A	2144.9691	1072.9882	2127.9425	1064.4749	2126.9585	1063.9829	22
6	635.2671	318.1372			617.2566	309.1319	E	2073.9319	1037.4696	2056.9054	1028.9563	2055.9214	1028.4643	21
7	722.2992	361.6532			704.2886	352.6479	S	1944.8894	972.9483	1927.8628	964.4350	1926.8788	963.9430	20
8	793.3363	397.1718			775.3257	388.1665	A	1857.8573	929.4323	1840.8308	920.9190	1839.8468	920.4270	19
9	908.3632	454.6852			890.3527	445.6800	D	1786.8202	893.9137	1769.7937	885.4005	1768.8096	884.9085	18
10	979.4003	490.2038			961.3898	481.1985	A	1671.7933	836.4003	1654.7667	827.8870	1653.7827	827.3950	17
11	1050.4374	525.7224			1032.4269	516.7171	A	1600.7562	800.8817	1583.7296	792.3684	1582.7456	791.8764	16
12	1163.5215	582.2644			1145.5109	573.2591	L	1529.7190	765.3632	1512.6925	756.8499	1511.7085	756.3579	15
13	1291.5801	646.2937	1274.5535	637.7804	1273.5695	637.2884	Q	1416.6350	708.8211	1399.6084	700.3079	1398.6244	699.8158	14
14	1348.6016	674.8044	1331.5750	666.2911	1330.5910	665.7991	G	1288.5764	644.7918	1271.5498	636.2786	1270.5658	635.7866	13
15	1463.6285	732.3179	1446.6019	723.8046	1445.6179	723.3126	D	1231.5549	616.2811	1214.5284	607.7678	1213.5444	607.2758	12
16	1560.6813	780.8443	1543.6547	772.3310	1542.6707	771.8390	P	1116.5280	558.7676	1099.5014	550.2544	1098.5174	549.7624	11
17	1631.7184	816.3628	1614.6918	807.8496	1613.7078	807.3575	A	1019.4752	510.2413	1002.4487	501.7280	1001.4647	501.2360	10
18	1744.8024	872.9049	1727.7759	864.3916	1726.7919	863.8996	L	948.4381	474.7227	931.4116	466.2094	930.4275	465.7174	9
19	1872.8610	936.9341	1855.8345	928.4209	1854.8504	927.9289	Q	835.3540	418.1807	818.3275	409.6674	817.3435	409.1754	8
20	1987.8880	994.4476	1970.8614	985.9343	1969.8774	985.4423	D	707.2955	354.1514	690.2689	345.6381	689.2849	345.1461	7
21	2058.9251	1029.9662	2041.8985	1021.4529	2040.9145	1020.9609	A	592.2685	296.6379	575.2420	288.1246	574.2580	287.6326	6
22	2115.9465	1058.4769	2098.9200	1049.9636	2097.9360	1049.4716	G	521.2314	261.1193	504.2049	252.6061	503.2208	252.1141	5
23	2230.9735	1115.9904	2213.9469	1107.4771	2212.9629	1106.9851	D	464.2100	232.6086	447.1834	224.0953	446.1994	223.6033	4
24	2318.0055	1159.5064	2300.9790	1150.9931	2299.9949	1150.5011	S	349.1830	175.0951	332.1565	166.5819	331.1724	166.0899	3
25	2405.0375	1203.0224	2388.0110	1194.5091	2387.0270	1194.0171	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
26							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 12 ppm



RMS error 12 ppm

Peptide Number: 15840

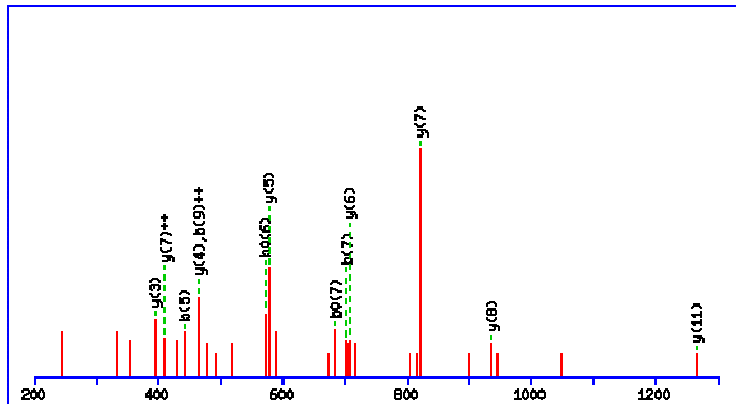
MS/MS Fragmentation of **ASVLAFLINELACSK**

Found in **IPI00061354** in **IPI_human**, Tax_Id=9606 Gene_Symbol=BAZ2B Isoform 2 of Bromodomain adjacent to zinc finger domain protein 2B

Match to Query 7685: 1634.851002 from(545.957610,3+) index(39492)

Title: Elution from: 112.366666666667 to 112.366666666667 period: 0 cycle: 4210 experiment: 1 polarity: +

Data file 120126ry_585A1-55_2_4.mgf



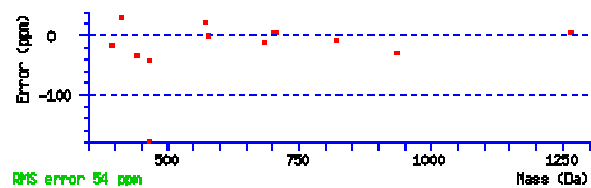
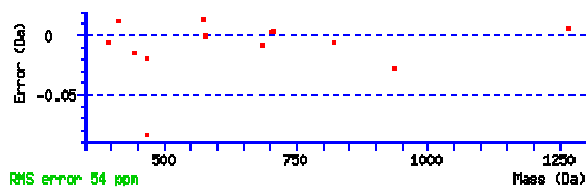
Monoisotopic mass of neutral peptide Mr(calc): 1634.8701

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 42 Expect: 0.0052

Matches : 13/148 fragment ions using 22 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							15
2	159.0764	80.0418			141.0659	71.0366	S	1564.8403	782.9238	1547.8138	774.4105	1546.8298	773.9185	14
3	258.1448	129.5761			240.1343	120.5708	V	1477.8083	739.4078	1460.7818	730.8945	1459.7977	730.4025	13
4	371.2289	186.1181			353.2183	177.1128	L	1378.7399	689.8736	1361.7134	681.3603	1360.7293	680.8683	12
5	442.2660	221.6366			424.2554	212.6314	A	1265.6558	633.3316	1248.6293	624.8183	1247.6453	624.3263	11
6	589.3344	295.1709			571.3239	286.1656	F	1194.6187	597.8130	1177.5922	589.2997	1176.6082	588.8077	10
7	702.4185	351.7129			684.4079	342.7076	L	1047.5503	524.2788	1030.5238	515.7655	1029.5397	515.2735	9
8	815.5026	408.2549			797.4920	399.2496	I	934.4662	467.7368	917.4397	459.2235	916.4557	458.7315	8
9	929.5455	465.2764	912.5189	456.7631	911.5349	456.2711	N	821.3822	411.1947	804.3556	402.6815	803.3716	402.1894	7
10	1058.5881	529.7977	1041.5615	521.2844	1040.5775	520.7924	E	707.3393	354.1733	690.3127	345.6600	689.3287	345.1680	6
11	1171.6721	586.3397	1154.6456	577.8264	1153.6616	577.3344	L	578.2967	289.6520	561.2701	281.1387	560.2861	280.6467	5
12	1242.7092	621.8583	1225.6827	613.3450	1224.6987	612.8530	A	465.2126	233.1099	448.1860	224.5967	447.2020	224.1047	4
13	1402.7399	701.8736	1385.7134	693.3603	1384.7293	692.8683	C	394.1755	197.5914	377.1489	189.0781	376.1649	188.5861	3
14	1489.7719	745.3896	1472.7454	736.8763	1471.7614	736.3843	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
15							K	147.1128	74.0600	130.0863	65.5468			1



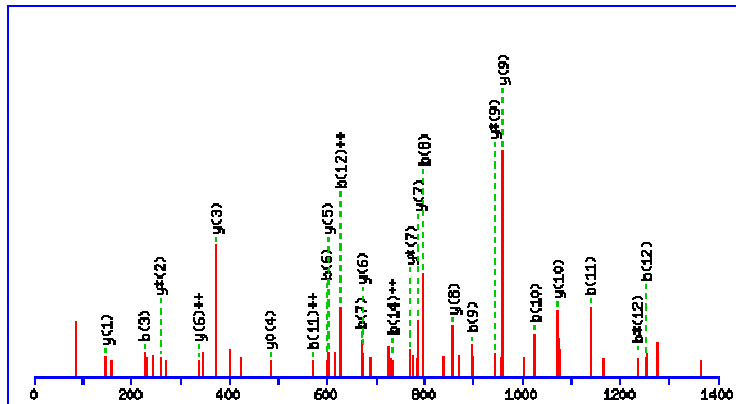
Peptide Number: 16191

MS/MS Fragmentation of **APGDDEEAQVENLITANATEPQK**Found in **IPI00004367** in **IPI_human**, Tax_Id=9606 Gene_Symbol=FXYP6 FXYP domain-containing ion transport regulator 6

Match to Query 34314: 2324.144982 from(775.722270,3+) index(16297)

Title: Elution from: 39.7 to 39.7 period: 0 cycle: 1495 experiment: 9 polarity: +

Data file 120212ry_414C2-43_3_3.mgf



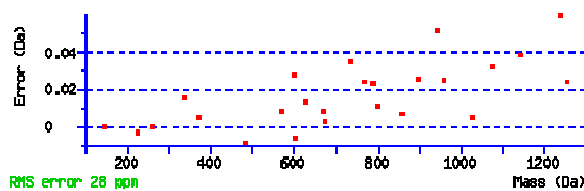
Monoisotopic mass of neutral peptide Mr(calc): 2324.1132

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

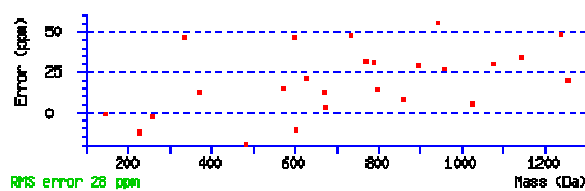
Ions Score: 51 Expect: 0.00053

Matches : 25/226 fragment ions using 55 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							22
2	169.0972	85.0522					P	2254.0834	1127.5453	2237.0568	1119.0320	2236.0728	1118.5400	21
3	226.1186	113.5629					G	2157.0306	1079.0189	2140.0040	1070.5057	2139.0200	1070.0137	20
4	341.1456	171.0764			323.1350	162.0711	D	2100.0091	1050.5082	2082.9826	1041.9949	2081.9986	1041.5029	19
5	470.1882	235.5977			452.1776	226.5924	E	1984.9822	992.9947	1967.9556	984.4815	1966.9716	983.9895	18
6	599.2307	300.1190			581.2202	291.1137	E	1855.9396	928.4734	1838.9131	919.9602	1837.9290	919.4682	17
7	670.2679	335.6376			652.2573	326.6323	A	1726.8970	863.9521	1709.8705	855.4389	1708.8864	854.9469	16
8	798.3264	399.6669	781.2999	391.1536	780.3159	390.6616	Q	1655.8599	828.4336	1638.8333	819.9203	1637.8493	819.4283	15
9	897.3949	449.2011	880.3683	440.6878	879.3843	440.1958	V	1527.8013	764.4043	1510.7748	755.8910	1509.7907	755.3990	14
10	1026.4374	513.7224	1009.4109	505.2091	1008.4269	504.7171	E	1428.7329	714.8701	1411.7064	706.3568	1410.7223	705.8648	13
11	1140.4804	570.7438	1123.4538	562.2306	1122.4698	561.7385	N	1299.6903	650.3488	1282.6638	641.8355	1281.6797	641.3435	12
12	1253.5644	627.2859	1236.5379	618.7726	1235.5539	618.2806	L	1185.6474	593.3273	1168.6208	584.8141	1167.6368	584.3220	11
13	1366.6485	683.8279	1349.6220	675.3146	1348.6379	674.8226	I	1072.5633	536.7853	1055.5368	528.2720	1054.5528	527.7800	10
14	1467.6962	734.3517	1450.6696	725.8385	1449.6856	725.3464	T	959.4793	480.2433	942.4527	471.7300	941.4687	471.2380	9
15	1538.7333	769.8703	1521.7067	761.3570	1520.7227	760.8650	A	858.4316	429.7194	841.4050	421.2062	840.4210	420.7141	8
16	1652.7762	826.8917	1635.7497	818.3785	1634.7657	817.8865	N	787.3945	394.2009	770.3679	385.6876	769.3839	385.1956	7
17	1723.8133	862.4103	1706.7868	853.8970	1705.8028	853.4050	A	673.3515	337.1794	656.3250	328.6661	655.3410	328.1741	6
18	1824.8610	912.9341	1807.8345	904.4209	1806.8504	903.9289	T	602.3144	301.6608	585.2879	293.1476	584.3039	292.6556	5
19	1953.9036	977.4554	1936.8771	968.9422	1935.8930	968.4502	E	501.2667	251.1370	484.2402	242.6237	483.2562	242.1317	4
20	2050.9564	1025.9818	2033.9298	1017.4685	2032.9458	1016.9765	P	372.2241	186.6157	355.1976	178.1024			3
21	2179.0149	1090.0111	2161.9884	1081.4978	2161.0044	1081.0058	Q	275.1714	138.0893	258.1448	129.5761			2
22							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 28 ppm



RMS error 28 ppm

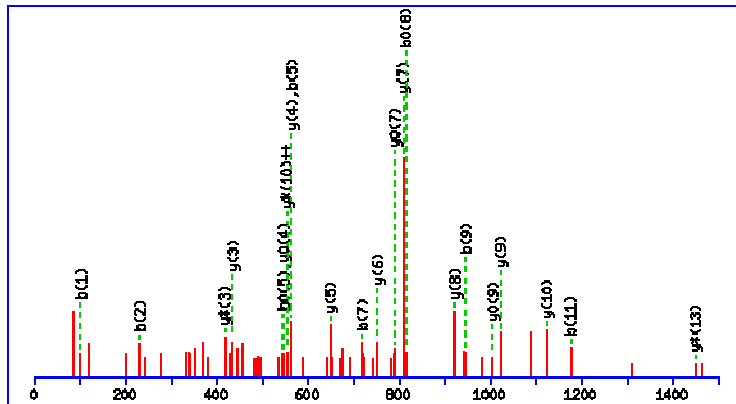
Peptide Number: 16987

MS/MS Fragmentation of **TEGYIGVLIDDLTTLGTSEPYR**Found in **IPI00032630** in **IPI_human**, Tax_Id=9606 Gene_Symbol=MT01 Isoform 3 of Protein MT01 homolog, mitochondrial

Match to Query 6086: 2412.199032 from(805.073620,3+) index(8114)

Title: Elution from: 22.65 to 22.65 period: 0 cycle: 858 experiment: 2 polarity:+

Data file 120214ry_32R1-32_4_5.mgf



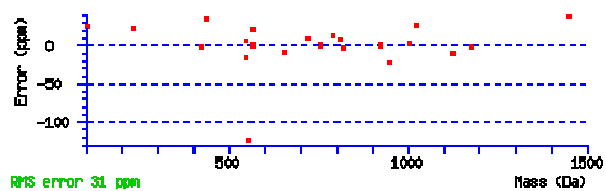
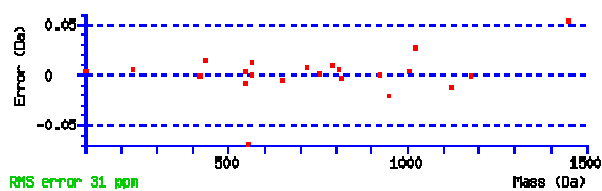
Monoisotopic mass of neutral peptide Mr(calc): 2412.2060

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 53 Expect: 0.00029

Matches : 22/204 fragment ions using 35 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311	84.0444	42.5258	T							22
2	231.0975	116.0524	213.0870	107.0471	E	2312.1656	1156.5865	2295.1391	1148.0732	2294.1551	1147.5812	21
3	288.1190	144.5631	270.1084	135.5579	G	2183.1230	1092.0652	2166.0965	1083.5519	2165.1125	1083.0599	20
4	451.1823	226.0948	433.1718	217.0895	Y	2126.1016	1063.5544	2109.0750	1055.0412	2108.0910	1054.5491	19
5	564.2664	282.6368	546.2558	273.6316	I	1963.0383	982.0228	1946.0117	973.5095	1945.0277	973.0175	18
6	621.2879	311.1476	603.2773	302.1423	G	1849.9542	925.4807	1832.9276	916.9675	1831.9436	916.4754	17
7	720.3563	360.6818	702.3457	351.6765	V	1792.9327	896.9700	1775.9062	888.4567	1774.9222	887.9647	16
8	833.4403	417.2238	815.4298	408.2185	L	1693.8643	847.4358	1676.8378	838.9225	1675.8537	838.4305	15
9	946.5244	473.7658	928.5138	464.7606	I	1580.7802	790.8938	1563.7537	782.3805	1562.7697	781.8885	14
10	1061.5514	531.2793	1043.5408	522.2740	D	1467.6962	734.3517	1450.6696	725.8385	1449.6856	725.3464	13
11	1176.5783	588.7928	1158.5677	579.7875	D	1352.6692	676.8383	1335.6427	668.3250	1334.6587	667.8330	12
12	1289.6624	645.3348	1271.6518	636.3295	L	1237.6423	619.3248	1220.6157	610.8115	1219.6317	610.3195	11
13	1390.7100	695.8587	1372.6995	686.8534	T	1124.5582	562.7828	1107.5317	554.2695	1106.5477	553.7775	10
14	1491.7577	746.3825	1473.7472	737.3772	T	1023.5106	512.2589	1006.4840	503.7456	1005.5000	503.2536	9
15	1604.8418	802.9245	1586.8312	793.9192	L	922.4629	461.7351	905.4363	453.2218	904.4523	452.7298	8
16	1661.8632	831.4353	1643.8527	822.4300	G	809.3788	405.1930	792.3523	396.6798	791.3682	396.1878	7
17	1762.9109	881.9591	1744.9004	872.9538	T	752.3573	376.6823	735.3308	368.1690	734.3468	367.6770	6
18	1849.9430	925.4751	1831.9324	916.4698	S	651.3097	326.1585	634.2831	317.6452	633.2991	317.1532	5
19	1978.9855	989.9964	1960.9750	980.9911	E	564.2776	282.6425	547.2511	274.1292	546.2671	273.6372	4
20	2076.0383	1038.5228	2058.0277	1029.5175	P	435.2350	218.1212	418.2085	209.6079			3
21	2239.1016	1120.0545	2221.0911	1111.0492	Y	338.1823	169.5948	321.1557	161.0815			2
22					R	175.1190	88.0631	158.0924	79.5498			1



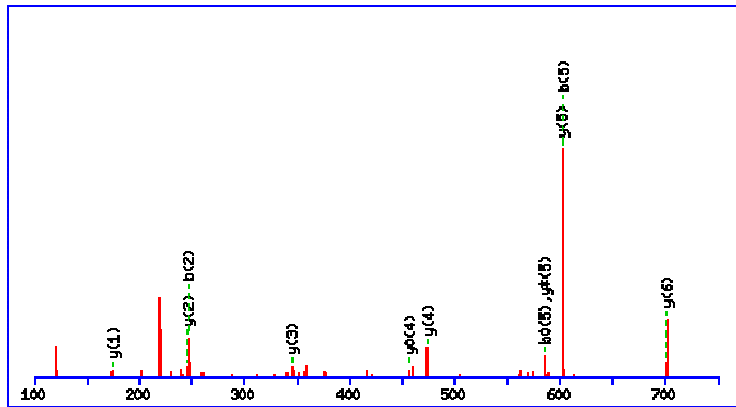
Peptide Number: 16991

MS/MS Fragmentation of **MVKEVAR**Found in **IPI01010843** in **IPI_human**, Tax_Id=9606 Gene_Symbol=AMPD3 AMP deaminase 3 isoform 1A

Match to Query 5191: 847.455588 from(424.735070,2+) index(19119)

Title: Elution from: 80.2333333333333 to 80.2333333333333 period: 0 cycle: 6829 experiment: 5 polarity:+

Data file 120208ry_Tig120slc-P8_1_1.mgf



Monoisotopic mass of neutral peptide Mr(calc): 847.4586

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

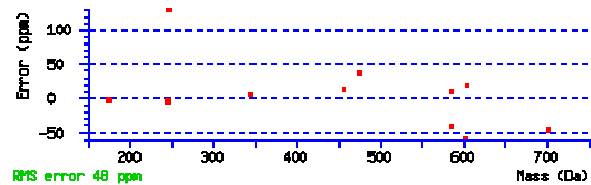
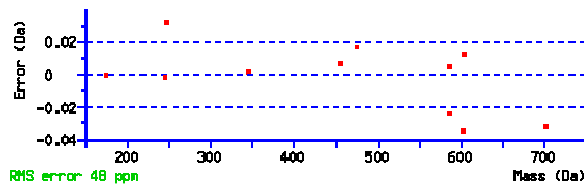
Variable modifications:

M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

Ions Score: 40 Expect: 0.0075

Matches : 11/82 fragment ions using 22 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	148.0427	74.5250					M							7
2	247.1111	124.0592					V	701.4305	351.2189	684.4039	342.7056	683.4199	342.2136	6
3	375.2061	188.1067	358.1795	179.5934			K	602.3620	301.6847	585.3355	293.1714	584.3515	292.6794	5
4	504.2486	252.6280	487.2221	244.1147	486.2381	243.6227	E	474.2671	237.6372	457.2405	229.1239	456.2565	228.6319	4
5	603.3171	302.1622	586.2905	293.6489	585.3065	293.1569	V	345.2245	173.1159	328.1979	164.6026			3
6	674.3542	337.6807	657.3276	329.1675	656.3436	328.6754	A	246.1561	123.5817	229.1295	115.0684			2
7							R	175.1190	88.0631	158.0924	79.5498			1



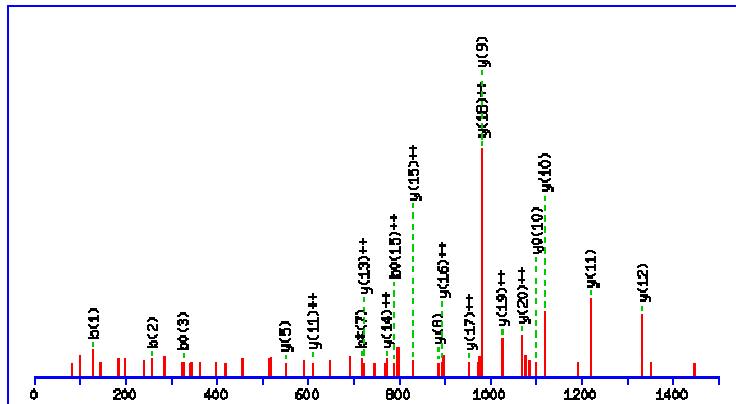
Peptide Number: 17509

MS/MS Fragmentation of **QESSGDMDVLLTHPSFTSESTK**Found in **IPI00979489** in **IPI_human**, Tax_Id=9606 Gene_Symbol=POLB Protein

Match to Query 36053: 2395.059012 from(799.360280,3+) index(4238)

Title: Elution from: 10.5333333333333 to 10.5333333333333 period: 0 cycle: 398 experiment: 6 polarity: +

Data file 120210ry_32R1-32_3_3.mgf



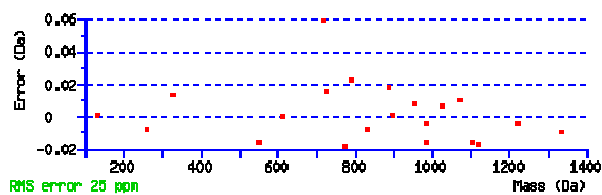
Monoisotopic mass of neutral peptide Mr(calc): 2395.0849

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

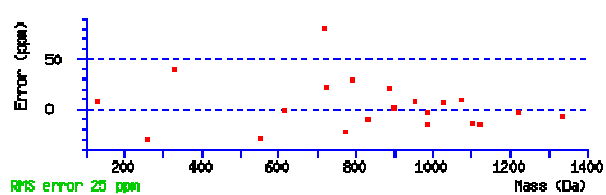
Ions Score: 43 Expect: 0.0011

Matches : 21/248 fragment ions using 53 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.0659	65.0366	112.0393	56.5233			Q							22
2	258.1084	129.5579	241.0819	121.0446	240.0979	120.5526	E	2268.0336	1134.5205	2251.0071	1126.0072	2250.0231	1125.5152	21
3	345.1405	173.0739	328.1139	164.5606	327.1299	164.0686	S	2138.9910	1069.9992	2121.9645	1061.4859	2120.9805	1060.9939	20
4	432.1725	216.5899	415.1460	208.0766	414.1619	207.5846	S	2051.9590	1026.4831	2034.9325	1017.9699	2033.9484	1017.4779	19
5	489.1940	245.1006	472.1674	236.5873	471.1834	236.0953	G	1964.9270	982.9671	1947.9004	974.4539	1946.9164	973.9618	18
6	604.2209	302.6141	587.1944	294.1008	586.2103	293.6088	D	1907.9055	954.4564	1890.8790	945.9431	1889.8950	945.4511	17
7	735.2614	368.1343	718.2348	359.6211	717.2508	359.1291	M	1792.8786	896.9429	1775.8520	888.4297	1774.8680	887.9376	16
8	850.2883	425.6478	833.2618	417.1345	832.2778	416.6425	D	1661.8381	831.4227	1644.8115	822.9094	1643.8275	822.4174	15
9	949.3568	475.1820	932.3302	466.6687	931.3462	466.1767	V	1546.8111	773.9092	1529.7846	765.3959	1528.8006	764.9039	14
10	1062.4408	531.7240	1045.4143	523.2108	1044.4303	522.7188	L	1447.7427	724.3750	1430.7162	715.8617	1429.7322	715.3697	13
11	1175.5249	588.2661	1158.4983	579.7528	1157.5143	579.2608	L	1334.6587	667.8330	1317.6321	659.3197	1316.6481	658.8277	12
12	1276.5726	638.7899	1259.5460	630.2766	1258.5620	629.7846	T	1221.5746	611.2909	1204.5481	602.7777	1203.5640	602.2857	11
13	1413.6315	707.3194	1396.6049	698.8061	1395.6209	698.3141	H	1120.5269	560.7671	1103.5004	552.2538	1102.5164	551.7618	10
14	1510.6842	755.8458	1493.6577	747.3325	1492.6737	746.8405	P	983.4680	492.2376	966.4415	483.7244	965.4575	483.2324	9
15	1597.7163	799.3618	1580.6897	790.8485	1579.7057	790.3565	S	886.4153	443.7113	869.3887	435.1980	868.4047	434.7060	8
16	1744.7847	872.8960	1727.7581	864.3827	1726.7741	863.8907	F	799.3832	400.1953	782.3567	391.6820	781.3727	391.1900	7
17	1845.8324	923.4198	1828.8058	914.9065	1827.8218	914.4145	T	652.3148	326.6610	635.2883	318.1478	634.3042	317.6558	6
18	1932.8644	966.9358	1915.8378	958.4226	1914.8538	957.9305	S	551.2671	276.1372	534.2406	267.6239	533.2566	267.1319	5
19	2061.9070	1031.4571	2044.8804	1022.9439	2043.8964	1022.4518	E	464.2351	232.6212	447.2086	224.1079	446.2245	223.6159	4
20	2148.9390	1074.9731	2131.9125	1066.4599	2130.9284	1065.9679	S	335.1925	168.0999	318.1660	159.5866	317.1819	159.0946	3
21	2249.9867	1125.4970	2232.9601	1116.9837	2231.9761	1116.4917	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
22							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 25 ppm



RMS error 25 ppm

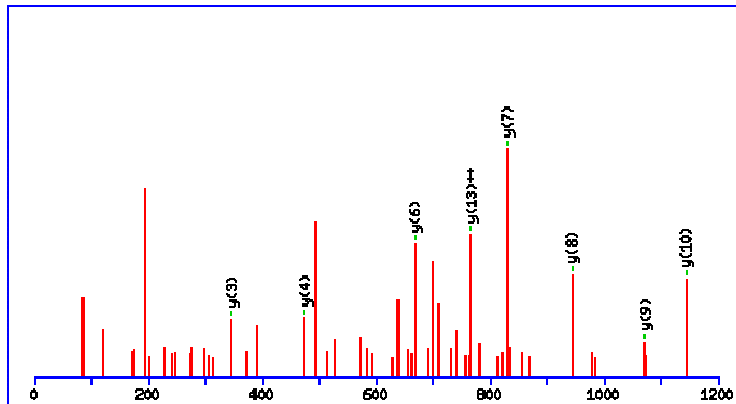
Peptide Number: 18722

MS/MS Fragmentation of **GSLDCLAQIYGHEGLR**Found in **IPI00184708** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SLC25A29 Mitochondrial carnitine/acylcarnitine carrier protein CACL

Match to Query 19410: 1787.865402 from(596.962410,3+) index(12052)

Title: Elution from: 30.3166666666667 to 30.3166666666667 period: 0 cycle: 1140 experiment: 6 polarity: +

Data file 120210ry_585A1-55_3_3.mgf



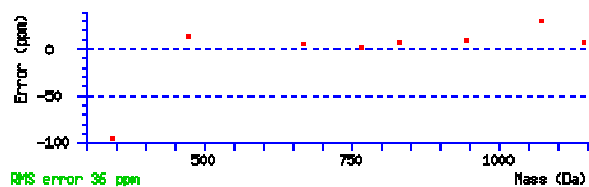
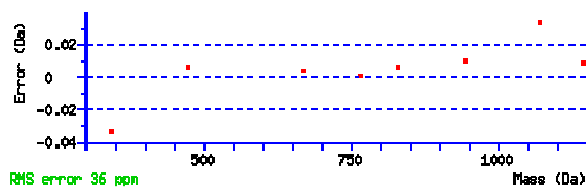
Monoisotopic mass of neutral peptide Mr(calc): 1787.8625

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 51 Expect: 0.00041

Matches : 8/158 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							16
2	145.0608	73.0340			127.0502	64.0287	S	1731.8483	866.4278	1714.8217	857.9145	1713.8377	857.4225	15
3	258.1448	129.5761			240.1343	120.5708	L	1644.8163	822.9118	1627.7897	814.3985	1626.8057	813.9065	14
4	373.1718	187.0895			355.1612	178.0842	D	1531.7322	766.3697	1514.7056	757.8565	1513.7216	757.3645	13
5	533.2024	267.1049			515.1919	258.0996	C	1416.7052	708.8563	1399.6787	700.3430	1398.6947	699.8510	12
6	646.2865	323.6469			628.2759	314.6416	L	1256.6746	628.8409	1239.6480	620.3277	1238.6640	619.8357	11
7	717.3236	359.1654			699.3130	350.1602	A	1143.5905	572.2989	1126.5640	563.7856	1125.5800	563.2936	10
8	845.3822	423.1947	828.3556	414.6815	827.3716	414.1894	Q	1072.5534	536.7803	1055.5269	528.2671	1054.5429	527.7751	9
9	958.4662	479.7368	941.4397	471.2235	940.4557	470.7315	I	944.4948	472.7511	927.4683	464.2378	926.4843	463.7458	8
10	1121.5296	561.2684	1104.5030	552.7552	1103.5190	552.2631	Y	831.4108	416.2090	814.3842	407.6958	813.4002	407.2037	7
11	1178.5510	589.7792	1161.5245	581.2659	1160.5405	580.7739	G	668.3474	334.6774	651.3209	326.1641	650.3369	325.6721	6
12	1315.6099	658.3086	1298.5834	649.7953	1297.5994	649.3033	H	611.3260	306.1666	594.2994	297.6534	593.3154	297.1613	5
13	1444.6525	722.8299	1427.6260	714.3166	1426.6420	713.8246	E	474.2671	237.6372	457.2405	229.1239	456.2565	228.6319	4
14	1501.6740	751.3406	1484.6475	742.8274	1483.6634	742.3354	G	345.2245	173.1159	328.1979	164.6026			3
15	1614.7581	807.8827	1597.7315	799.3694	1596.7475	798.8774	L	288.2030	144.6051	271.1765	136.0919			2
16							R	175.1190	88.0631	158.0924	79.5498			1



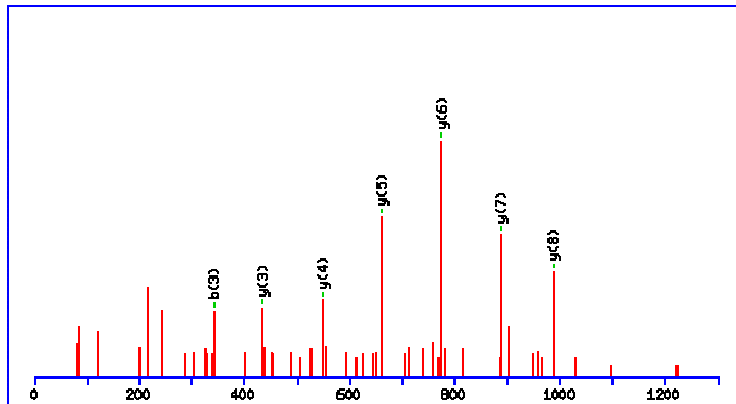
Peptide Number: 18790**MS/MS Fragmentation of ELVLLLEER**

Found in **IPI00657798** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CCDC85C Coiled-coil domain-containing protein 85C

Match to Query 6858: 1227.665188 from(614.839870,2+) index(16060)

Title: Elution from: 38.5166666666667 to 38.5166666666667 period: 0 cycle: 1429 experiment: 4 polarity:+

Data file 120126ry_585A1-55_1_3.mgf



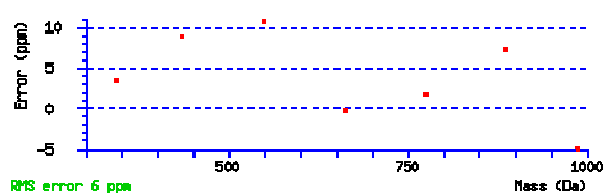
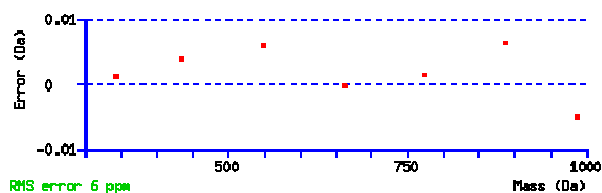
Monoisotopic mass of neutral peptide Mr(calc): 1227.6710

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 41 **Expect:** 0.0065

Matches : 7/88 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286	112.0393	56.5233	E							10
2	243.1339	122.0706	225.1234	113.0653	L	1099.6358	550.3215	1082.6092	541.8082	1081.6252	541.3162	9
3	342.2023	171.6048	324.1918	162.5995	V	986.5517	493.7795	969.5251	485.2662	968.5411	484.7742	8
4	455.2864	228.1468	437.2758	219.1416	L	887.4833	444.2453	870.4567	435.7320	869.4727	435.2400	7
5	568.3705	284.6889	550.3599	275.6836	L	774.3992	387.7032	757.3727	379.1900	756.3886	378.6980	6
6	681.4545	341.2309	663.4440	332.2256	L	661.3151	331.1612	644.2886	322.6479	643.3046	322.1559	5
7	796.4815	398.7444	778.4709	389.7391	D	548.2311	274.6192	531.2045	266.1059	530.2205	265.6139	4
8	925.5241	463.2657	907.5135	454.2604	E	433.2041	217.1057	416.1776	208.5924	415.1936	208.1004	3
9	1054.5667	527.7870	1036.5561	518.7817	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
10					R	175.1190	88.0631	158.0924	79.5498			1



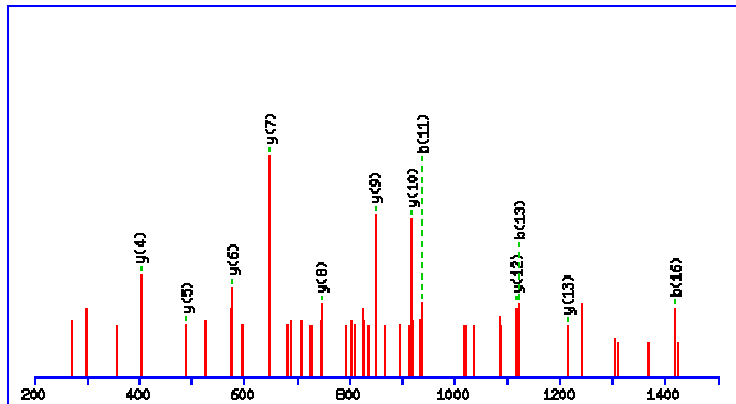
Peptide Number: 18846

MS/MS Fragmentation of **LSTGPALVAAGLAPAEVVAATVASSGVVK**Found in **IPI00163729** in **IPI_human**, Tax_Id=9606 Gene_Symbol=MKL1 MKL1 protein

Match to Query 30270: 2633.493282 from(878.838370,3+) index(49176)

Title: Elution from: 119.966666666667 to 119.966666666667 period: 0 cycle: 4507 experiment: 9 polarity:+

Data file 120214ry_32R1-32_4_4.mgf



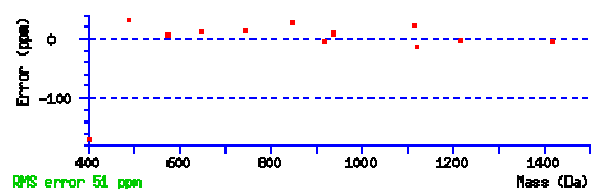
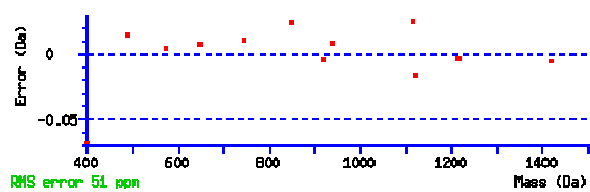
Monoisotopic mass of neutral peptide Mr(calc): 2633.5004

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 45 Expect: 0.00033

Matches : 12/270 fragment ions using 23 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							29
2	201.1234	101.0653	183.1128	92.0600	S	2521.4236	1261.2154	2504.3970	1252.7022	2503.4130	1252.2101	28
3	302.1710	151.5892	284.1605	142.5839	T	2434.3916	1217.6994	2417.3650	1209.1861	2416.3810	1208.6941	27
4	359.1925	180.0999	341.1819	171.0946	G	2333.3439	1167.1756	2316.3173	1158.6623	2315.3333	1158.1703	26
5	456.2453	228.6263	438.2347	219.6210	P	2276.3224	1138.6648	2259.2959	1130.1516	2258.3118	1129.6596	25
6	527.2824	264.1448	509.2718	255.1395	A	2179.2696	1090.1385	2162.2431	1081.6252	2161.2591	1081.1332	24
7	640.3665	320.6869	622.3559	311.6816	L	2108.2325	1054.6199	2091.2060	1046.1066	2090.2220	1045.6146	23
8	739.4349	370.2211	721.4243	361.2158	V	1995.1485	998.0779	1978.1219	989.5646	1977.1379	989.0726	22
9	810.4720	405.7396	792.4614	396.7343	A	1896.0801	948.5437	1879.0535	940.0304	1878.0695	939.5384	21
10	881.5091	441.2582	863.4985	432.2529	A	1825.0429	913.0251	1808.0164	904.5118	1807.0324	904.0198	20
11	938.5306	469.7689	920.5200	460.7636	G	1754.0058	877.5066	1736.9793	868.9933	1735.9953	868.5013	19
12	1051.6146	526.3109	1033.6041	517.3057	L	1696.9844	848.9958	1679.9578	840.4825	1678.9738	839.9905	18
13	1122.6517	561.8295	1104.6412	552.8242	A	1583.9003	792.4538	1566.8738	783.9405	1565.8897	783.4485	17
14	1219.7045	610.3559	1201.6939	601.3506	P	1512.8632	756.9352	1495.8366	748.4220	1494.8526	747.9299	16
15	1290.7416	645.8744	1272.7310	636.8692	A	1415.8104	708.4088	1398.7839	699.8956	1397.7999	699.4036	15
16	1419.7842	710.3957	1401.7736	701.3905	E	1344.7733	672.8903	1327.7468	664.3770	1326.7627	663.8850	14
17	1518.8526	759.9299	1500.8421	750.9247	V	1215.7307	608.3690	1198.7042	599.8557	1197.7202	599.3637	13
18	1617.9210	809.4642	1599.9105	800.4589	V	1116.6623	558.8348	1099.6358	550.3215	1098.6517	549.8295	12
19	1716.9895	858.9984	1698.9789	849.9931	V	1017.5939	509.3006	1000.5673	500.7873	999.5833	500.2953	11
20	1788.0266	894.5169	1770.0160	885.5116	A	918.5255	459.7664	901.4989	451.2531	900.5149	450.7611	10
21	1889.0742	945.0408	1871.0637	936.0355	T	847.4884	424.2478	830.4618	415.7345	829.4778	415.2425	9
22	1988.1427	994.5750	1970.1321	985.5697	V	746.4407	373.7240	729.4141	365.2107	728.4301	364.7187	8
23	2059.1798	1030.0935	2041.1692	1021.0882	A	647.3723	324.1898	630.3457	315.6765	629.3617	315.1845	7
24	2146.2118	1073.6095	2128.2012	1064.6043	S	576.3352	288.6712	559.3086	280.1579	558.3246	279.6659	6
25	2233.2438	1117.1256	2215.2333	1108.1203	S	489.3031	245.1552	472.2766	236.6419	471.2926	236.1499	5
26	2290.2653	1145.6363	2272.2547	1136.6310	G	402.2711	201.6392	385.2445	193.1259			4
27	2389.3337	1195.1705	2371.3231	1186.1652	V	345.2496	173.1285	328.2231	164.6152			3
28	2488.4021	1244.7047	2470.3916	1235.6994	V	246.1812	123.5942	229.1547	115.0810			2
29					K	147.1128	74.0600	130.0863	65.5468			1

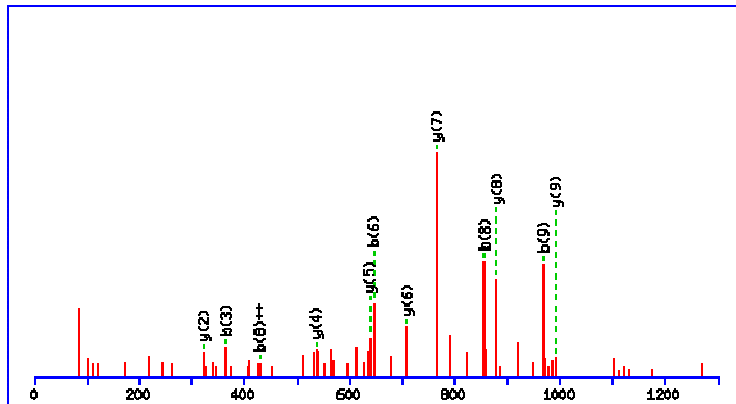


Peptide Number: 18900MS/MS Fragmentation of **LLHPALPLLGLTFR**Found in **IPI00060523** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TLCD1 TLC domain-containing protein 1

Match to Query 8506: 1845.127392 from(616.049740,3+) index(17200)

Title: Elution from: 48.4833333333333 to 48.4833333333333 period: 0 cycle: 1874 experiment: 1 polarity: +

Data file 120210ry_585A1-55_3_4.mgf



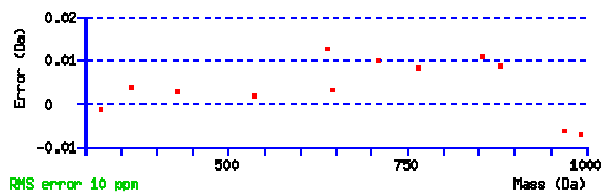
Monoisotopic mass of neutral peptide Mr(calc): 1845.1240

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

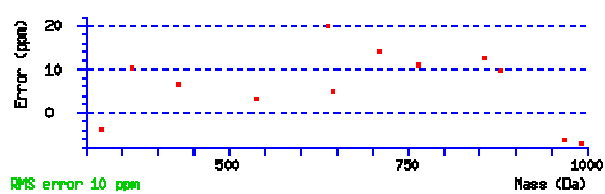
Ions Score: 40 Expect: 0.00018

Matches : 12/132 fragment ions using 22 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							17
2	227.1754	114.0913			L	1733.0472	867.0273	1716.0207	858.5140	1715.0367	858.0220	16
3	364.2343	182.6208			H	1619.9632	810.4852	1602.9366	801.9720	1601.9526	801.4799	15
4	461.2871	231.1472			P	1482.9043	741.9558	1465.8777	733.4425	1464.8937	732.9505	14
5	532.3242	266.6657			A	1385.8515	693.4294	1368.8250	684.9161	1367.8409	684.4241	13
6	645.4083	323.2078			L	1314.8144	657.9108	1297.7878	649.3976	1296.8038	648.9055	12
7	742.4610	371.7341			P	1201.7303	601.3688	1184.7038	592.8555	1183.7198	592.3635	11
8	855.5451	428.2762			L	1104.6776	552.8424	1087.6510	544.3291	1086.6670	543.8371	10
9	968.6292	484.8182			L	991.5935	496.3004	974.5669	487.7871	973.5829	487.2951	9
10	1081.7132	541.3602			L	878.5094	439.7584	861.4829	431.2451	860.4989	430.7531	8
11	1138.7347	569.8710			G	765.4254	383.2163	748.3988	374.7030	747.4148	374.2110	7
12	1209.7718	605.3895			A	708.4039	354.7056	691.3774	346.1923	690.3933	345.7003	6
13	1310.8195	655.9134	1292.8089	646.9081	T	637.3668	319.1870	620.3402	310.6738	619.3562	310.1817	5
14	1423.9035	712.4554	1405.8930	703.4501	L	536.3191	268.6632	519.2926	260.1499	518.3085	259.6579	4
15	1524.9512	762.9792	1506.9406	753.9740	T	423.2350	212.1212	406.2085	203.6079	405.2245	203.1159	3
16	1672.0196	836.5135	1654.0091	827.5082	F	322.1874	161.5973	305.1608	153.0840			2
17					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 10 ppm



RMS error 10 ppm

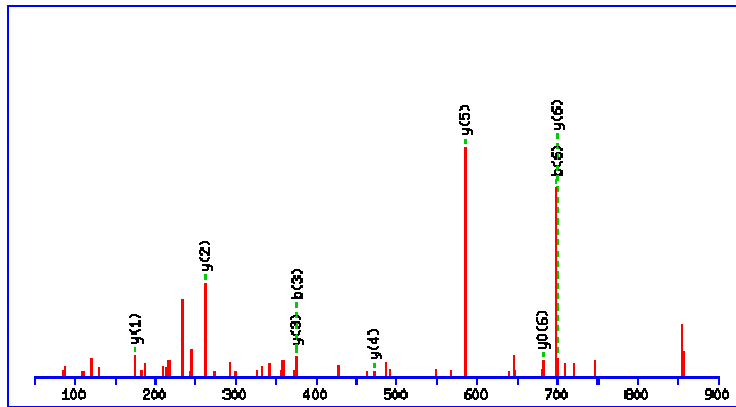
Peptide Number: 19092**MS/MS Fragmentation of YPDLPISR**

Found in **IPI00384419** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TDRD9 Isoform 1 of Putative ATP-dependent RNA helicase TDRD9

Match to Query 5145: 959.515048 from(480.764800,2+) index(13097)

Title: Elution from: 35.2666666666667 to 35.2666666666667 period: 0 cycle: 1347 experiment: 1 polarity: +

Data file 120212ry_aHDF1388-P9_3_2.mgf



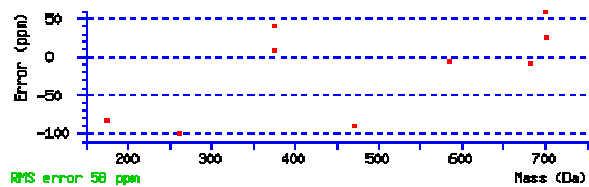
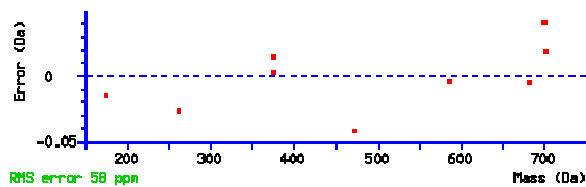
Monoisotopic mass of neutral peptide Mr(calc): 959.5076

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 43 **Expect:** 0.0046

Matches : 9/64 fragment ions using 16 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389			Y							8
2	261.1234	131.0653			P	797.4516	399.2294	780.4250	390.7162	779.4410	390.2241	7
3	376.1503	188.5788	358.1397	179.5735	D	700.3988	350.7030	683.3723	342.1898	682.3883	341.6978	6
4	489.2344	245.1208	471.2238	236.1155	L	585.3719	293.1896	568.3453	284.6763	567.3613	284.1843	5
5	586.2871	293.6472	568.2766	284.6419	P	472.2878	236.6475	455.2613	228.1343	454.2772	227.6423	4
6	699.3712	350.1892	681.3606	341.1840	I	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
7	786.4032	393.7053	768.3927	384.7000	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
8					R	175.1190	88.0631	158.0924	79.5498			1



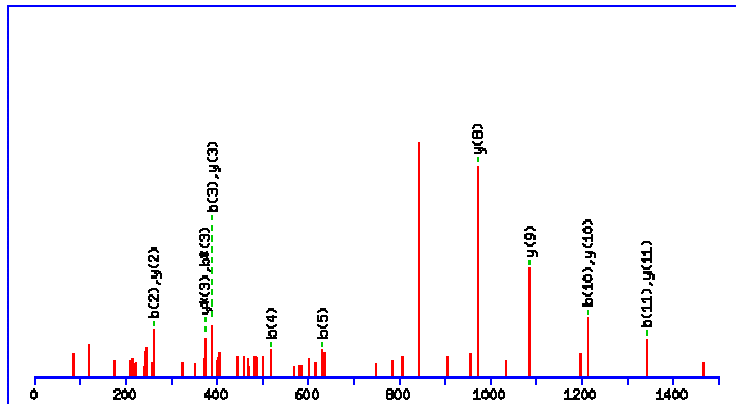
Peptide Number: 19179

MS/MS Fragmentation of **NFEKIRNSLLES**RFound in **IPI00398940** in **IPI_human**, Tax_Id=9606 Gene_Symbol=IQSEC3 Isoform 2 of IQ motif and SEC7 domain-containing protein 3

Match to Query 6023: 1604.836828 from(803.425690,2+) index(28)

Title: Elution from: 0.0666666666666667 to 0.0666666666666667 period: 0 cycle: 2 experiment: 9 polarity: +

Data file 120118ry_201B7-32_3_4.mgf



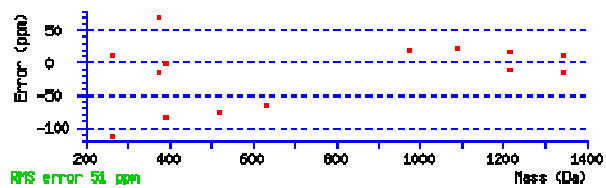
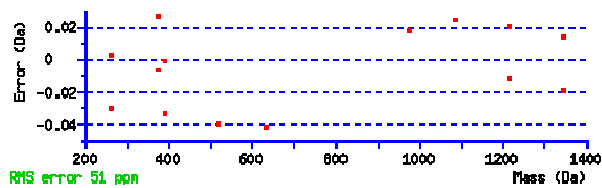
Monoisotopic mass of neutral peptide Mr(calc): 1604.8634

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 45 Expect: 0.0024

Matches : 14/138 fragment ions using 14 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							13
2	262.1186	131.5629	245.0921	123.0497			F	1491.8278	746.4175	1474.8013	737.9043	1473.8172	737.4123	12
3	391.1612	196.0842	374.1347	187.5710	373.1506	187.0790	E	1344.7594	672.8833	1327.7328	664.3701	1326.7488	663.8780	11
4	519.2562	260.1317	502.2296	251.6185	501.2456	251.1264	K	1215.7168	608.3620	1198.6902	599.8488	1197.7062	599.3568	10
5	632.3402	316.6738	615.3137	308.1605	614.3297	307.6685	I	1087.6218	544.3146	1070.5953	535.8013	1069.6113	535.3093	9
6	788.4413	394.7243	771.4148	386.2110	770.4308	385.7190	R	974.5378	487.7725	957.5112	479.2592	956.5272	478.7672	8
7	902.4843	451.7458	885.4577	443.2325	884.4737	442.7405	N	818.4367	409.7220	801.4101	401.2087	800.4261	400.7167	7
8	989.5163	495.2618	972.4898	486.7485	971.5057	486.2565	S	704.3937	352.7005	687.3672	344.1872	686.3832	343.6952	6
9	1102.6004	551.8038	1085.5738	543.2905	1084.5898	542.7985	L	617.3617	309.1845	600.3352	300.6712	599.3511	300.1792	5
10	1215.6844	608.3459	1198.6579	599.8326	1197.6739	599.3406	L	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	4
11	1344.7270	672.8672	1327.7005	664.3539	1326.7165	663.8619	E	391.1936	196.1004	374.1670	187.5872	373.1830	187.0951	3
12	1431.7591	716.3832	1414.7325	707.8699	1413.7485	707.3779	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
13							R	175.1190	88.0631	158.0924	79.5498			1



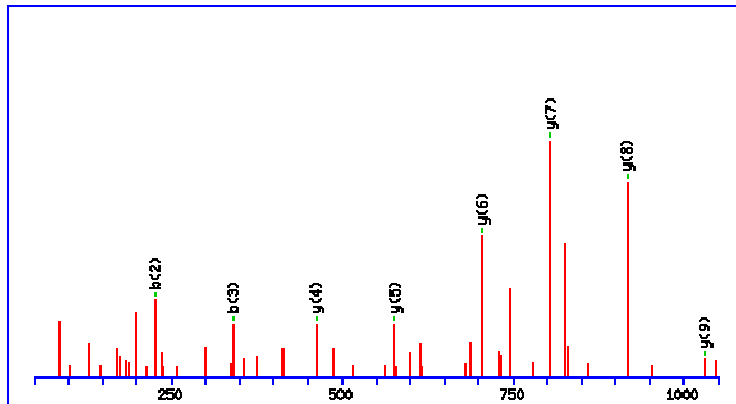
Peptide Number: 19315

MS/MS Fragmentation of **LLIVQDASER**Found in **IPI00759702** in **IPI_human**, Tax_Id=9606 Gene_Symbol=STARD3NL Isoform 2 of MLN64 N-terminal domain homolog

Match to Query 12869: 1142.618468 from(572.316510,2+) index(15455)

Title: Elution from: 37.1333333333333 to 37.1333333333333 period: 0 cycle: 1413 experiment: 4 polarity:+

Data file 120201ry_aHDF1388-P9_1_2.mgf



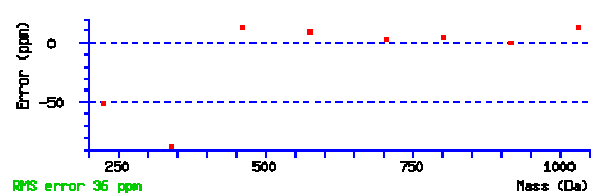
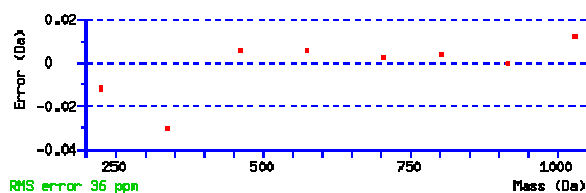
Monoisotopic mass of neutral peptide Mr(calc): 1142.6295

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 52 Expect: 0.00055

Matches : 8/88 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							10
2	227.1754	114.0913					L	1030.5528	515.7800	1013.5262	507.2667	1012.5422	506.7747	9
3	340.2595	170.6334					I	917.4687	459.2380	900.4421	450.7247	899.4581	450.2327	8
4	439.3279	220.1676					V	804.3846	402.6959	787.3581	394.1827	786.3741	393.6907	7
5	567.3865	284.1969	550.3599	275.6836			Q	705.3162	353.1617	688.2897	344.6485	687.3056	344.1565	6
6	682.4134	341.7103	665.3869	333.1971	664.4028	332.7051	D	577.2576	289.1325	560.2311	280.6192	559.2471	280.1272	5
7	753.4505	377.2289	736.4240	368.7156	735.4400	368.2236	A	462.2307	231.6190	445.2041	223.1057	444.2201	222.6137	4
8	840.4825	420.7449	823.4560	412.2316	822.4720	411.7396	S	391.1936	196.1004	374.1670	187.5871	373.1830	187.0951	3
9	969.5251	485.2662	952.4986	476.7529	951.5146	476.2609	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
10							R	175.1190	88.0631	158.0924	79.5498			1



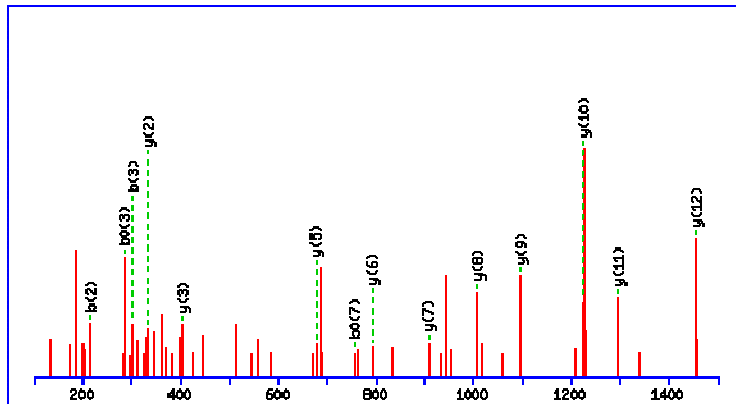
Peptide Number: 19563

MS/MS Fragmentation of **TISLCAESTDDCLAWK**Found in **IPI00031228** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PLEKHB2 Isoform 2 of Pleckstrin homology domain-containing family B member 2

Match to Query 22413: 1868.831488 from(935.423020,2+) index(5420)

Title: Elution from: 12.8166666666667 to 12.8166666666667 period: 0 cycle: 486 experiment: 9 polarity: +

Data file 120212ry_aHDF1388-P9_2_3.mgf



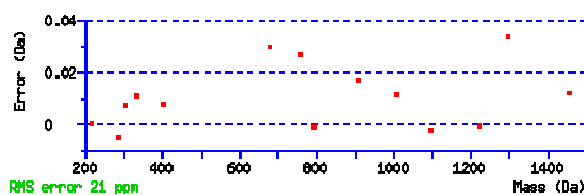
Monoisotopic mass of neutral peptide Mr(calc): 1868.8284

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

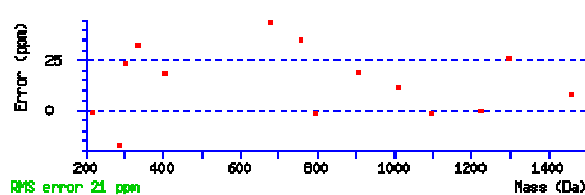
Ions Score: 50 Expect: 0.00018

Matches : 14/140 fragment ions using 35 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311	84.0444	42.5258	T							16
2	215.1390	108.0731	197.1285	99.0679	I	1768.7880	884.8977	1751.7615	876.3844	1750.7775	875.8924	15
3	302.1710	151.5892	284.1605	142.5839	S	1655.7040	828.3556	1638.6774	819.8424	1637.6934	819.3503	14
4	415.2551	208.1312	397.2445	199.1259	L	1568.6720	784.8396	1551.6454	776.3263	1550.6614	775.8343	13
5	575.2858	288.1465	557.2752	279.1412	C	1455.5879	728.2976	1438.5613	719.7843	1437.5773	719.2923	12
6	646.3229	323.6651	628.3123	314.6598	A	1295.5572	648.2823	1278.5307	639.7690	1277.5467	639.2770	11
7	775.3655	388.1864	757.3549	379.1811	E	1224.5201	612.7637	1207.4936	604.2504	1206.5096	603.7584	10
8	862.3975	431.7024	844.3869	422.6971	S	1095.4775	548.2424	1078.4510	539.7291	1077.4670	539.2371	9
9	963.4452	482.2262	945.4346	473.2209	T	1008.4455	504.7264	991.4190	496.2131	990.4349	495.7211	8
10	1078.4721	539.7397	1060.4616	530.7344	D	907.3978	454.2026	890.3713	445.6893	889.3873	445.1973	7
11	1193.4991	597.2532	1175.4885	588.2479	D	792.3709	396.6891	775.3443	388.1758	774.3603	387.6838	6
12	1353.5297	677.2685	1335.5191	668.2632	C	677.3439	339.1756	660.3174	330.6623			5
13	1466.6138	733.8105	1448.6032	724.8052	L	517.3133	259.1603	500.2867	250.6470			4
14	1537.6509	769.3291	1519.6403	760.3238	A	404.2292	202.6183	387.2027	194.1050			3
15	1723.7302	862.3687	1705.7196	853.3635	W	333.1921	167.0997	316.1656	158.5864			2
16					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 21 ppm



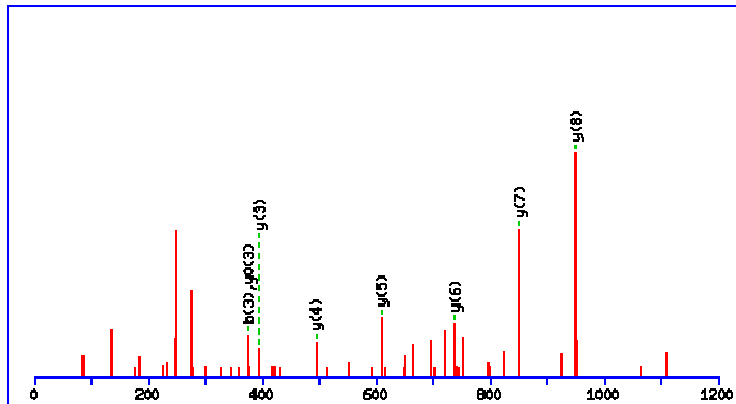
RMS error 21 ppm

Peptide Number: 19803MS/MS Fragmentation of **YIVLQDTCSK**Found in **IPI00739099** in **IPI_human**, Tax_Id=9606 Gene_Symbol=COL5A2 Collagen alpha-2(V) chain

Match to Query 14873: 1225.595208 from(613.804880,2+) index(9251)

Title: Elution from: 23.8666666666667 to 23.8666666666667 period: 0 cycle: 914 experiment: 6 polarity: +

Data file 120208ry_Tig120slc-P8_1_2.mgf



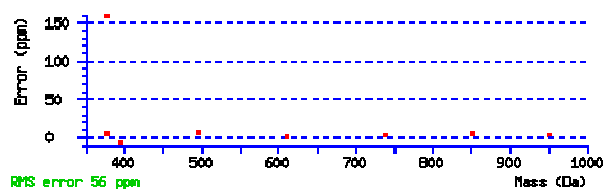
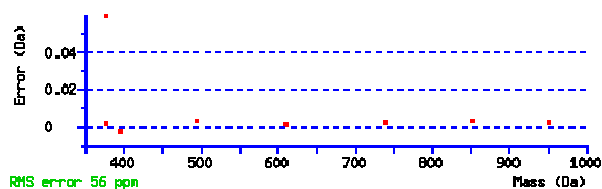
Monoisotopic mass of neutral peptide Mr(calc): 1225.6013

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 43 Expect: 0.0026

Matches : 8/88 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389					Y							10
2	277.1547	139.0810					I	1063.5452	532.2762	1046.5187	523.7630	1045.5347	523.2710	9
3	376.2231	188.6152					V	950.4612	475.7342	933.4346	467.2209	932.4506	466.7289	8
4	489.3071	245.1572					L	851.3927	426.2000	834.3662	417.6867	833.3822	417.1947	7
5	617.3657	309.1865	600.3392	300.6732			Q	738.3087	369.6580	721.2821	361.1447	720.2981	360.6527	6
6	732.3927	366.7000	715.3661	358.1867	714.3821	357.6947	D	610.2501	305.6287	593.2236	297.1154	592.2395	296.6234	5
7	833.4403	417.2238	816.4138	408.7105	815.4298	408.2185	T	495.2232	248.1152	478.1966	239.6019	477.2126	239.1099	4
8	993.4710	497.2391	976.4444	488.7259	975.4604	488.2339	C	394.1755	197.5914	377.1489	189.0781	376.1649	188.5861	3
9	1080.5030	540.7552	1063.4765	532.2419	1062.4925	531.7499	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
10							K	147.1128	74.0600	130.0863	65.5468			1



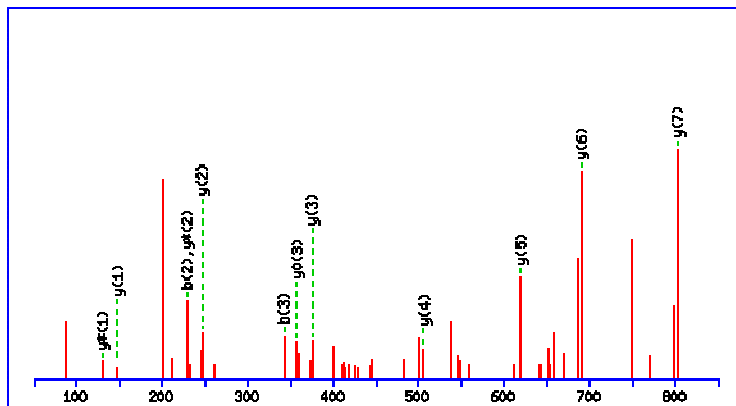
Peptide Number: 19835

MS/MS Fragmentation of **DILALMEVK**Found in **IPI00061523** in **IPI_human**, Tax_Id=9606 Gene_Symbol=THAP11 THAP domain-containing protein 11

Match to Query 1603: 1030.571328 from(516.292940,2+) index(35778)

Title: Elution from: 90.2833333333333 to 90.2833333333333 period: 0 cycle: 3412 experiment: 1 polarity: +

Data file 120210ry_32R1-32_2_3.mgf



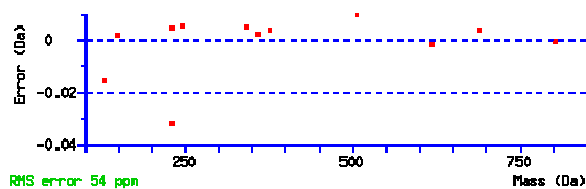
Monoisotopic mass of neutral peptide Mr(calc): 1030.5732

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

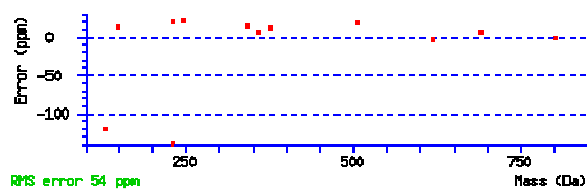
Ions Score: 44 Expect: 0.0032

Matches : 12/76 fragment ions using 23 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	98.0237	49.5155	D							9
2	229.1183	115.0628	211.1077	106.0575	I	916.5536	458.7804	899.5271	450.2672	898.5430	449.7752	8
3	342.2023	171.6048	324.1918	162.5995	L	803.4695	402.2384	786.4430	393.7251	785.4590	393.2331	7
4	413.2395	207.1234	395.2289	198.1181	A	690.3855	345.6964	673.3589	337.1831	672.3749	336.6911	6
5	526.3235	263.6654	508.3130	254.6601	L	619.3484	310.1778	602.3218	301.6645	601.3378	301.1725	5
6	657.3640	329.1856	639.3534	320.1804	M	506.2643	253.6358	489.2377	245.1225	488.2537	244.6305	4
7	786.4066	393.7069	768.3960	384.7017	E	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
8	885.4750	443.2411	867.4645	434.2359	V	246.1812	123.5942	229.1547	115.0810			2
9					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 54 ppm



RMS error 54 ppm

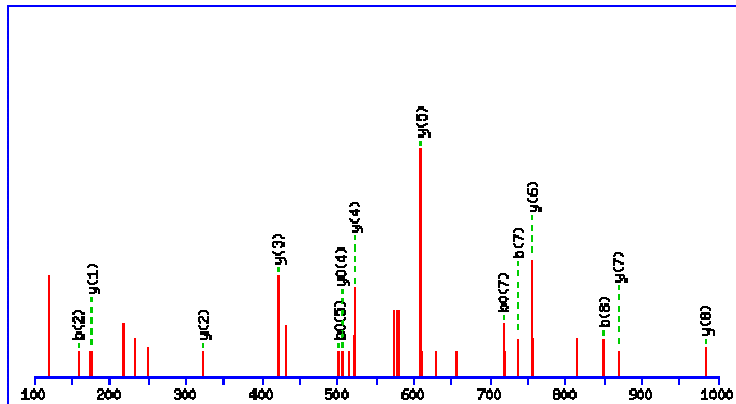
Peptide Number: 20391

MS/MS Fragmentation of **ASTFLTDLFSTVFR**Found in **IPI00004527** in **IPI_human**, Tax_Id=9606 Gene_Symbol=KIAA0355 Uncharacterized protein KIAA0355

Match to Query 968: 1603.816362 from(535.612730,3+) index(4901)

Title: Elution from: 23.0333333333333 to 23.0333333333333 period: 0 cycle: 894 experiment: 2 polarity: +

Data file 120214ry_414C2-43_4_5.mgf



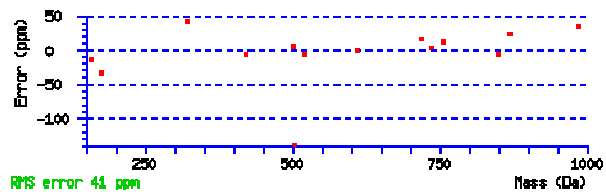
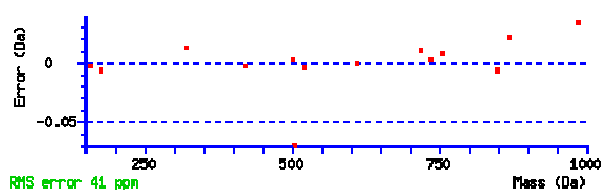
Monoisotopic mass of neutral peptide Mr(calcd): 1603.8246

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 51 Expect: 0.00068

Matches : 14/122 fragment ions using 25 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258			A							14
2	159.0764	80.0418	141.0659	71.0366	S	1533.7948	767.4010	1516.7682	758.8877	1515.7842	758.3957	13
3	260.1241	130.5657	242.1135	121.5604	T	1446.7627	723.8850	1429.7362	715.3717	1428.7522	714.8797	12
4	407.1925	204.0999	389.1819	195.0946	F	1345.7151	673.3612	1328.6885	664.8479	1327.7045	664.3559	11
5	520.2766	260.6419	502.2660	251.6366	L	1198.6467	599.8270	1181.6201	591.3137	1180.6361	590.8217	10
6	621.3243	311.1658	603.3137	302.1605	T	1085.5626	543.2849	1068.5360	534.7717	1067.5520	534.2796	9
7	736.3512	368.6792	718.3406	359.6740	D	984.5149	492.7611	967.4884	484.2478	966.5043	483.7558	8
8	849.4353	425.2213	831.4247	416.2160	L	869.4880	435.2476	852.4614	426.7343	851.4774	426.2423	7
9	996.5037	498.7555	978.4931	489.7502	F	756.4039	378.7056	739.3774	370.1923	738.3933	369.7003	6
10	1083.5357	542.2715	1065.5251	533.2662	S	609.3355	305.1714	592.3089	296.6581	591.3249	296.1661	5
11	1184.5834	592.7953	1166.5728	583.7900	T	522.3035	261.6554	505.2769	253.1421	504.2929	252.6501	4
12	1283.6518	642.3295	1265.6412	633.3243	V	421.2558	211.1315	404.2292	202.6183			3
13	1430.7202	715.8637	1412.7096	706.8585	F	322.1874	161.5973	305.1608	153.0840			2
14					R	175.1190	88.0631	158.0924	79.5498			1



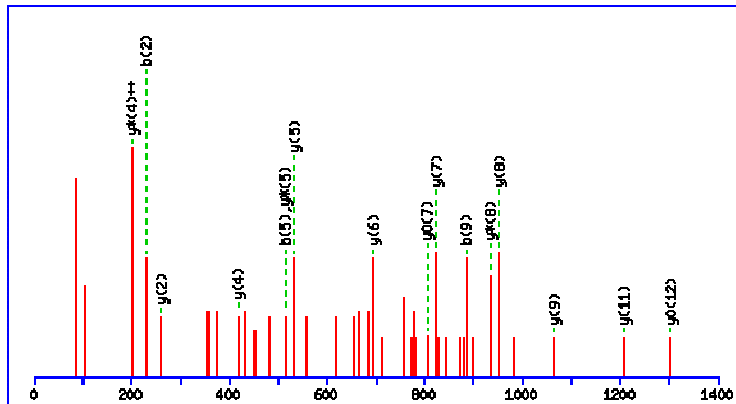
Peptide Number: 20443

MS/MS Fragmentation of **DLEGVISGLQEYLGTIK**Found in **IPI00376383** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CNTRL Isoform 2 of Centriolin

Match to Query 1495: 1833.971772 from(612.331200,3+) index(4141)

Title: Elution from: 18.75 to 18.75 period: 0 cycle: 732 experiment: 1 polarity: +

Data file 120210ry_32R1-32_2_5.mgf



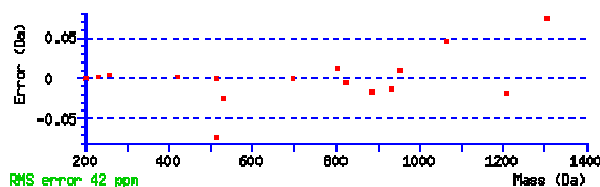
Monoisotopic mass of neutral peptide Mr(calc): 1833.9724

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

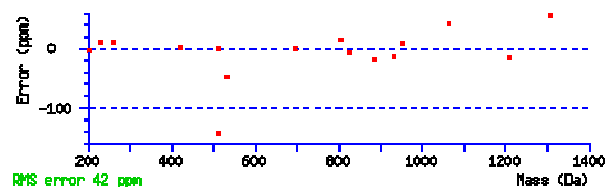
Ions Score: 43 Expect: 0.0028

Matches : 16/170 fragment ions using 29 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							17
2	229.1183	115.0628			211.1077	106.0575	L	1719.9527	860.4800	1702.9262	851.9667	1701.9422	851.4747	16
3	358.1609	179.5841			340.1503	170.5788	E	1606.8687	803.9380	1589.8421	795.4247	1588.8581	794.9327	15
4	415.1823	208.0948			397.1718	199.0895	G	1477.8261	739.4167	1460.7995	730.9034	1459.8155	730.4114	14
5	514.2508	257.6290			496.2402	248.6237	V	1420.8046	710.9059	1403.7781	702.3927	1402.7940	701.9007	13
6	627.3348	314.1710			609.3243	305.1658	I	1321.7362	661.3717	1304.7096	652.8585	1303.7256	652.3665	12
7	714.3668	357.6871			696.3563	348.6818	S	1208.6521	604.8297	1191.6256	596.3164	1190.6416	595.8244	11
8	771.3883	386.1978			753.3777	377.1925	G	1121.6201	561.3137	1104.5936	552.8004	1103.6095	552.3084	10
9	884.4724	442.7398			866.4618	433.7345	L	1064.5986	532.8030	1047.5721	524.2897	1046.5881	523.7977	9
10	1012.5310	506.7691	995.5044	498.2558	994.5204	497.7638	Q	951.5146	476.2609	934.4880	467.7477	933.5040	467.2556	8
11	1141.5735	571.2904	1124.5470	562.7771	1123.5630	562.2851	E	823.4560	412.2316	806.4294	403.7184	805.4454	403.2264	7
12	1304.6369	652.8221	1287.6103	644.3088	1286.6263	643.8168	Y	694.4134	347.7103	677.3869	339.1971	676.4028	338.7051	6
13	1417.7209	709.3641	1400.6944	700.8508	1399.7104	700.3588	L	531.3501	266.1787	514.3235	257.6654	513.3395	257.1734	5
14	1474.7424	737.8748	1457.7159	729.3616	1456.7318	728.8696	G	418.2660	209.6366	401.2395	201.1234	400.2554	200.6314	4
15	1575.7901	788.3987	1558.7635	779.8854	1557.7795	779.3934	T	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
16	1688.8741	844.9407	1671.8476	836.4274	1670.8636	835.9354	I	260.1969	130.6021	243.1703	122.0888			2
17							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 42 ppm



RMS error 42 ppm

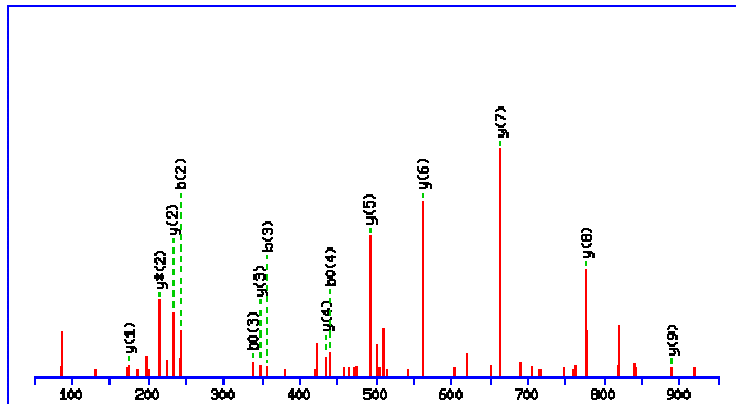
Peptide Number: 20639**MS/MS Fragmentation of ELLTAGSDGR**

Found in **IPI00166861** in **IPI_human**, Tax_Id=9606 Gene_Symbol=C12orf45 Conserved hypothetical protein

Match to Query 11857: 1017.505928 from(509.760240,2+) index(19146)

Title: Elution from: 87.7833333333333 to 87.7833333333333 period: 0 cycle: 8615 experiment: 3 polarity:+

Data file 120210ry_32R1-32_3_1.mgf



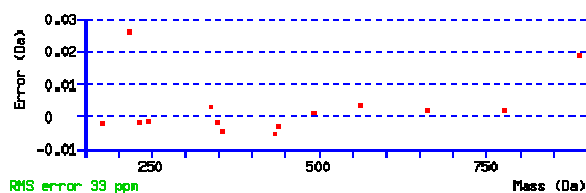
Monoisotopic mass of neutral peptide Mr(calcd): 1017.5091

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

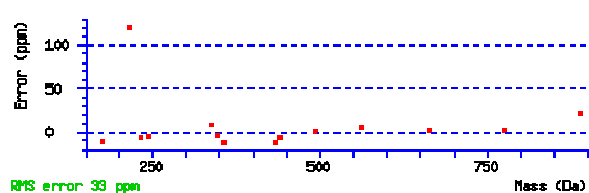
Ions Score: 72 **Expect:** 4.4e-006

Matches : 14/86 fragment ions using 26 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286	112.0393	56.5233	E							10
2	243.1339	122.0706	225.1234	113.0653	L	889.4738	445.2405	872.4472	436.7272	871.4632	436.2352	9
3	356.2180	178.6126	338.2074	169.6074	L	776.3897	388.6985	759.3632	380.1852	758.3791	379.6932	8
4	457.2657	229.1365	439.2551	220.1312	T	663.3056	332.1565	646.2791	323.6432	645.2951	323.1512	7
5	528.3028	264.6550	510.2922	255.6498	A	562.2580	281.6326	545.2314	273.1193	544.2474	272.6273	6
6	585.3243	293.1658	567.3137	284.1605	G	491.2209	246.1141	474.1943	237.6008	473.2103	237.1088	5
7	672.3563	336.6818	654.3457	327.6765	S	434.1994	217.6033	417.1728	209.0901	416.1888	208.5980	4
8	787.3832	394.1953	769.3727	385.1900	D	347.1674	174.0873	330.1408	165.5740	329.1568	165.0820	3
9	844.4047	422.7060	826.3941	413.7007	G	232.1404	116.5738	215.1139	108.0606			2
10					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 33 ppm



RMS error 33 ppm

Peptide Number: 20858

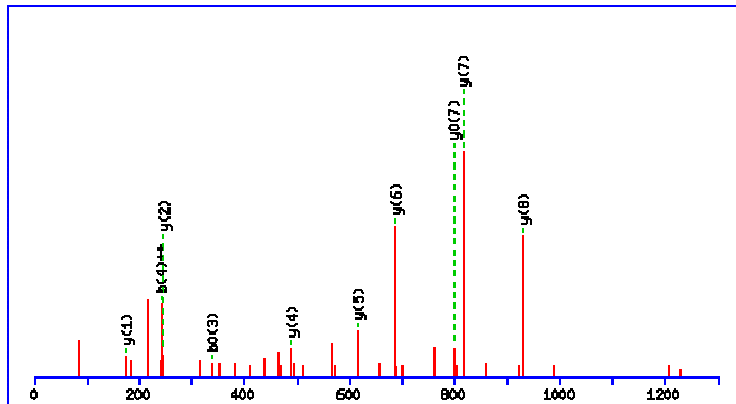
MS/MS Fragmentation of **ELIEAQELAR**

Found in **IPI00794566** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SLMAP Isoform 2 of Sarcolemmal membrane-associated protein

Match to Query 21217: 1170.621908 from(586.318230,2+) index(29183)

Title: Elution from: 68.8166666666667 to 68.8166666666667 period: 0 cycle: 2578 experiment: 6 polarity: +

Data file 120126ry_585A1-55_1_2.mgf



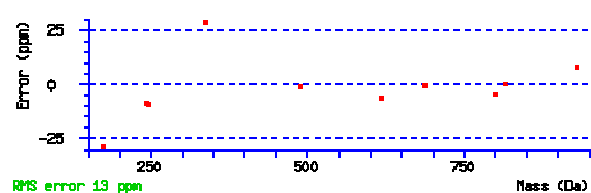
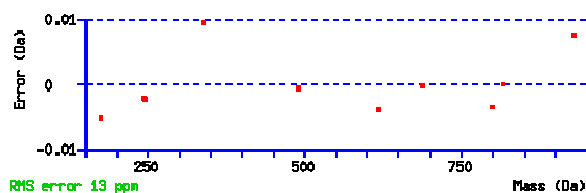
Monoisotopic mass of neutral peptide Mr(calc): 1170.6244

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 40 Expect: 0.007

Matches : 11/92 fragment ions using 26 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							10
2	243.1339	122.0706			225.1234	113.0653	L	1042.5891	521.7982	1025.5626	513.2849	1024.5786	512.7929	9
3	356.2180	178.6126			338.2074	169.6074	I	929.5051	465.2562	912.4785	456.7429	911.4945	456.2509	8
4	485.2606	243.1339			467.2500	234.1287	E	816.4210	408.7141	799.3945	400.2009	798.4104	399.7089	7
5	556.2977	278.6525			538.2871	269.6472	A	687.3784	344.1928	670.3519	335.6796	669.3679	335.1876	6
6	684.3563	342.6818	667.3297	334.1685	666.3457	333.6765	Q	616.3413	308.6743	599.3148	300.1610	598.3307	299.6690	5
7	813.3989	407.2031	796.3723	398.6898	795.3883	398.1978	E	488.2827	244.6450	471.2562	236.1317	470.2722	235.6397	4
8	926.4829	463.7451	909.4564	455.2318	908.4724	454.7398	L	359.2401	180.1237	342.2136	171.6104			3
9	997.5201	499.2637	980.4935	490.7504	979.5095	490.2584	A	246.1561	123.5817	229.1295	115.0684			2
10							R	175.1190	88.0631	158.0924	79.5498			1



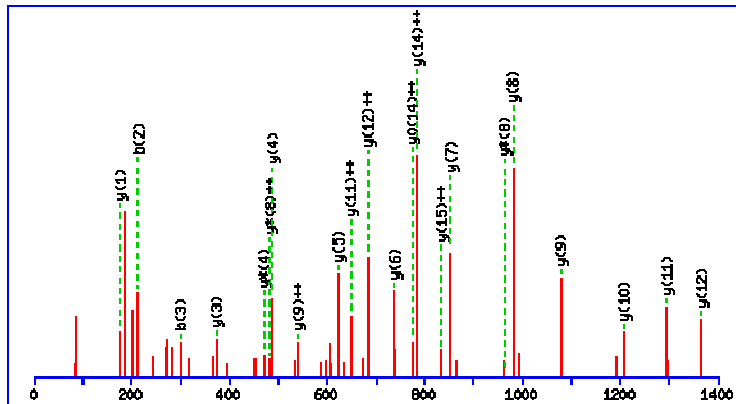
Peptide Number: 20883

MS/MS Fragmentation of **LVSLASEVQDLHLAQR**Found in **IPI00170436** in **IPI_human**, Tax_Id=9606 Gene_Symbol=MBOAT7 Uncharacterized protein

Match to Query 17077: 1777.969962 from(593.663930,3+) index(16188)

Title: Elution from: 44.5333333333333 to 44.5333333333333 period: 0 cycle: 1719 experiment: 6 polarity: +

Data file 120208ry_Tig120slc-P8_1.3.mgf



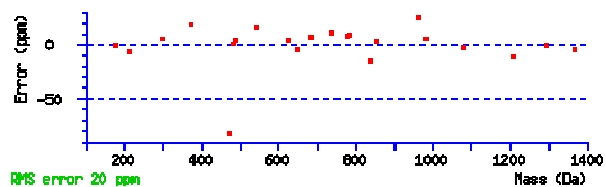
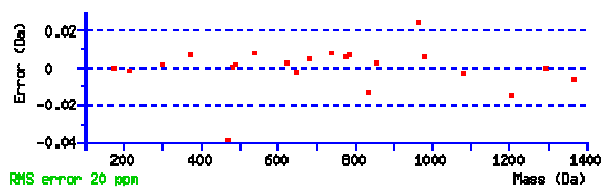
Monoisotopic mass of neutral peptide Mr(calc): 1777.9686

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 84 Expect: 1.7e-007

Matches : 22/148 fragment ions using 33 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							16
2	213.1598	107.0835					V	1665.8919	833.4496	1648.8653	824.9363	1647.8813	824.4443	15
3	300.1918	150.5995			282.1812	141.5942	S	1566.8234	783.9154	1549.7969	775.4021	1548.8129	774.9101	14
4	413.2758	207.1416			395.2653	198.1363	L	1479.7914	740.3993	1462.7649	731.8861	1461.7809	731.3941	13
5	484.3130	242.6601			466.3024	233.6548	A	1366.7074	683.8573	1349.6808	675.3440	1348.6968	674.8520	12
6	571.3450	286.1761			553.3344	277.1708	S	1295.6702	648.3388	1278.6437	639.8255	1277.6597	639.3335	11
7	700.3876	350.6974			682.3770	341.6921	E	1208.6382	604.8227	1191.6117	596.3095	1190.6276	595.8175	10
8	799.4560	400.2316			781.4454	391.2264	V	1079.5956	540.3014	1062.5691	531.7882	1061.5851	531.2962	9
9	927.5146	464.2609	910.4880	455.7477	909.5040	455.2556	Q	980.5272	490.7672	963.5007	482.2540	962.5166	481.7620	8
10	1042.5415	521.7744	1025.5150	513.2611	1024.5310	512.7691	D	852.4686	426.7380	835.4421	418.2247	834.4581	417.7327	7
11	1155.6256	578.3164	1138.5990	569.8032	1137.6150	569.3111	L	737.4417	369.2245	720.4151	360.7112			6
12	1292.6845	646.8459	1275.6579	638.3326	1274.6739	637.8406	H	624.3576	312.6824	607.3311	304.1692			5
13	1405.7686	703.3879	1388.7420	694.8746	1387.7580	694.3826	L	487.2987	244.1530	470.2722	235.6397			4
14	1476.8057	738.9065	1459.7791	730.3932	1458.7951	729.9012	A	374.2146	187.6110	357.1881	179.0977			3
15	1604.8642	802.9358	1587.8377	794.4225	1586.8537	793.9305	Q	303.1775	152.0924	286.1510	143.5791			2
16							R	175.1190	88.0631	158.0924	79.5498			1



Peptide Number: 21014

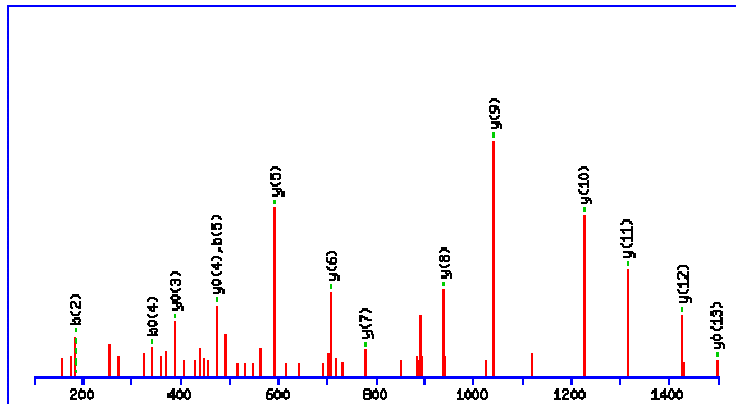
MS/MS Fragmentation of SPSSDSWTCADTSTER

Found in **IPI00175169** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ARFGAP1 Isoform 1 of ADP-ribosylation factor GTPase-activating protein 1

Match to Query 34033: 1785.710228 from(893.862390,2+) index(4016)

Title: Elution from: 10.5333333333333 to 10.5333333333333 period: 0 cycle: 405 experiment: 10 polarity: +

Data file 120208ry_Tig120slc-P8_1_2.mgf



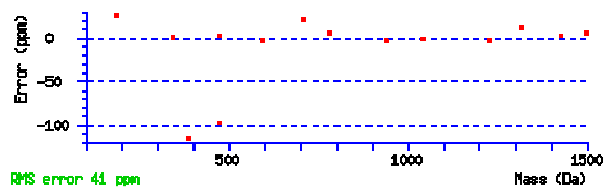
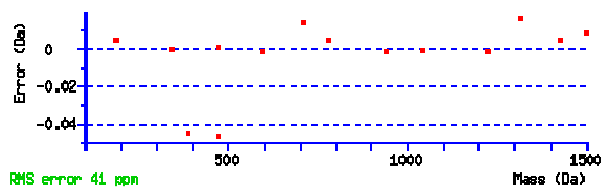
Monoisotopic mass of neutral peptide Mr(calc): 1785.7112

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 75 Expect: 1.2e-007

Matches : 14/148 fragment ions using 14 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233	70.0287	35.5180	S							16
2	185.0921	93.0497	167.0815	84.0444	P	1699.6864	850.3468	1682.6599	841.8336	1681.6759	841.3416	15
3	272.1241	136.5657	254.1135	127.5604	S	1602.6337	801.8205	1585.6071	793.3072	1584.6231	792.8152	14
4	359.1561	180.0817	341.1456	171.0764	S	1515.6016	758.3045	1498.5751	749.7912	1497.5911	749.2992	13
5	474.1831	237.5952	456.1725	228.5899	D	1428.5696	714.7884	1411.5431	706.2752	1410.5590	705.7832	12
6	561.2151	281.1112	543.2045	272.1059	S	1313.5427	657.2750	1296.5161	648.7617	1295.5321	648.2697	11
7	747.2944	374.1508	729.2838	365.1456	W	1226.5106	613.7590	1209.4841	605.2457	1208.5001	604.7537	10
8	848.3421	424.6747	830.3315	415.6694	T	1040.4313	520.7193	1023.4048	512.2060	1022.4208	511.7140	9
9	1008.3727	504.6900	990.3622	495.6847	C	939.3836	470.1955	922.3571	461.6822	921.3731	461.1902	8
10	1079.4099	540.2086	1061.3993	531.2033	A	779.3530	390.1801	762.3264	381.6669	761.3424	381.1748	7
11	1194.4368	597.7220	1176.4262	588.7168	D	708.3159	354.6616	691.2893	346.1483	690.3053	345.6563	6
12	1295.4845	648.2459	1277.4739	639.2406	T	593.2889	297.1481	576.2624	288.6348	575.2784	288.1428	5
13	1382.5165	691.7619	1364.5059	682.7566	S	492.2413	246.6243	475.2147	238.1110	474.2307	237.6190	4
14	1483.5642	742.2857	1465.5536	733.2804	T	405.2092	203.1083	388.1827	194.5950	387.1987	194.1030	3
15	1612.6068	806.8070	1594.5962	797.8017	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
16					R	175.1190	88.0631	158.0924	79.5498			1



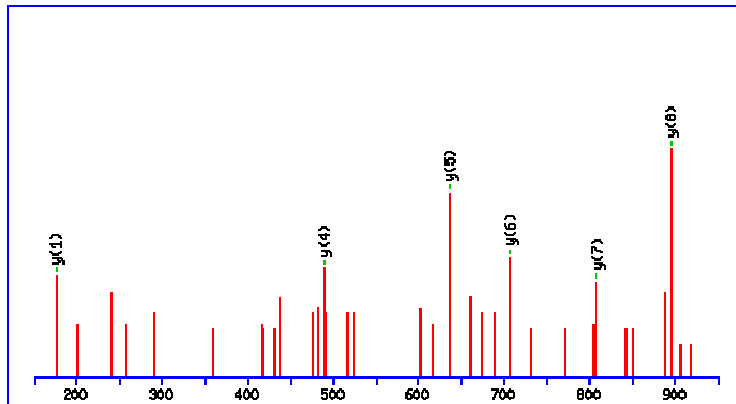
Peptide Number: 21445

MS/MS Fragmentation of **VASTAFAENR**Found in **IPI00304379** in **IPI_human**, Tax_Id=9606 Gene_Symbol=USP1 Ubiquitin carboxyl-terminal hydrolase 1

Match to Query 13845: 1064.51548 from(533.265050,2+) index(12636)

Title: Elution from: 77.05 to 77.05 period: 0 cycle: 7523 experiment: 7 polarity: +

Data file 120118ry_201B7-32_3_1.mgf



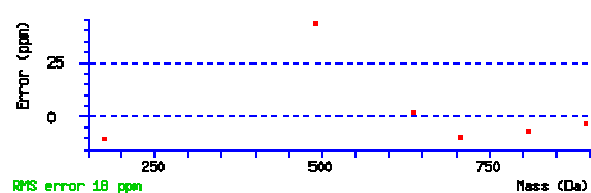
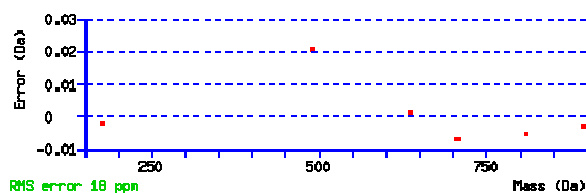
Monoisotopic mass of neutral peptide Mr(calc): 1064.5251

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 51 Expect: 0.00042

Matches : 6/84 fragment ions using 8 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							10
2	171.1128	86.0600					A	966.4639	483.7356	949.4374	475.2223	948.4534	474.7303	9
3	258.1448	129.5761			240.1343	120.5708	S	895.4268	448.2170	878.4003	439.7038	877.4163	439.2118	8
4	359.1925	180.0999			341.1819	171.0946	T	808.3948	404.7010	791.3682	396.1878	790.3842	395.6958	7
5	430.2296	215.6185			412.2191	206.6132	A	707.3471	354.1772	690.3206	345.6639	689.3365	345.1719	6
6	577.2980	289.1527			559.2875	280.1474	F	636.3100	318.6586	619.2835	310.1454	618.2994	309.6534	5
7	648.3352	324.6712			630.3246	315.6659	A	489.2416	245.1244	472.2150	236.6112	471.2310	236.1191	4
8	777.3777	389.1925			759.3672	380.1872	E	418.2045	209.6059	401.1779	201.0926	400.1939	200.6006	3
9	891.4207	446.2140	874.3941	437.7007	873.4101	437.2087	N	289.1619	145.0846	272.1353	136.5713			2
10							R	175.1190	88.0631	158.0924	79.5498			1



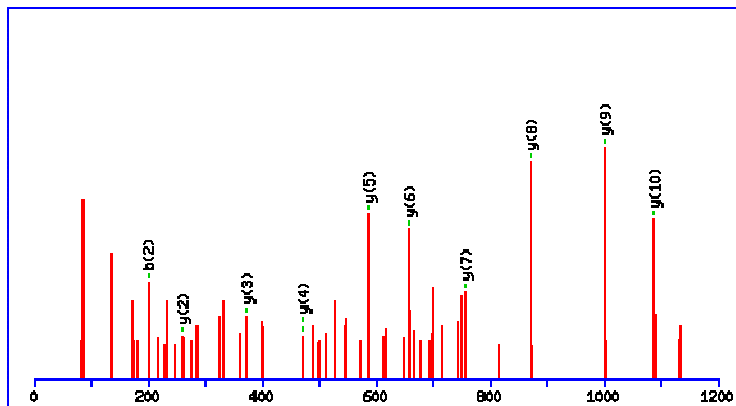
Peptide Number: 21475

MS/MS Fragmentation of **LSEDVADVLLK**Found in **IPI00030618** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PCDH18 Isoform 1 of Protocadherin-18

Match to Query 3179: 1200.658808 from(601.336680,2+) index(7181)

Title: Elution from: 18.7166666666667 to 18.7166666666667 period: 0 cycle: 718 experiment: 6 polarity: +

Data file 120208ry_Tig120slc-P8_1_3.mgf



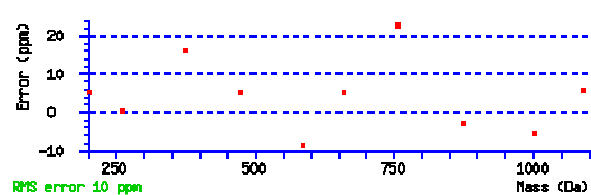
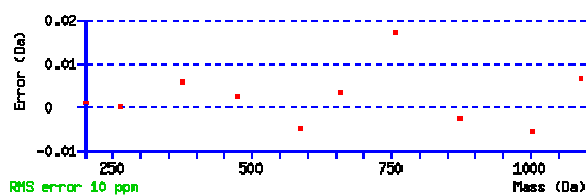
Monoisotopic mass of neutral peptide Mr(calc): 1200.6602

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 51 Expect: 0.00061

Matches : 10/90 fragment ions using 29 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							11
2	201.1234	101.0653	183.1128	92.0600	S	1088.5834	544.7953	1071.5568	536.2821	1070.5728	535.7900	10
3	330.1660	165.5866	312.1554	156.5813	E	1001.5514	501.2793	984.5248	492.7660	983.5408	492.2740	9
4	445.1929	223.1001	427.1823	214.0948	D	872.5088	436.7580	855.4822	428.2447	854.4982	427.7527	8
5	544.2613	272.6343	526.2508	263.6290	V	757.4818	379.2445	740.4553	370.7313	739.4713	370.2393	7
6	615.2984	308.1529	597.2879	299.1476	A	658.4134	329.7103	641.3869	321.1971	640.4028	320.7051	6
7	730.3254	365.6663	712.3148	356.6610	D	587.3763	294.1918	570.3497	285.6785	569.3657	285.1865	5
8	829.3938	415.2005	811.3832	406.1952	V	472.3493	236.6783	455.3228	228.1650			4
9	942.4779	471.7426	924.4673	462.7373	L	373.2809	187.1441	356.2544	178.6308			3
10	1055.5619	528.2846	1037.5514	519.2793	L	260.1969	130.6021	243.1703	122.0888			2
11					K	147.1128	74.0600	130.0863	65.5468			1



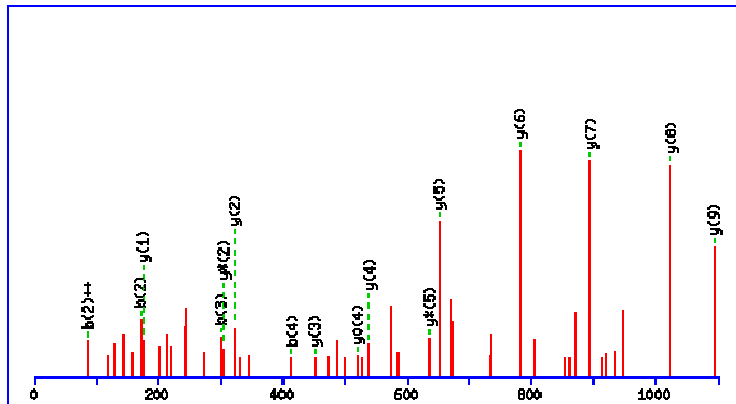
Peptide Number: 21485

MS/MS Fragmentation of **VAELENSEFR**Found in **IPI00017529** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CD58 Isoform 1 of Lymphocyte function-associated antigen 3

Match to Query 13755: 1192.566288 from(597.290420,2+) index(6281)

Title: Elution from: 16.55 to 16.55 period: 0 cycle: 633 experiment: 8 polarity: +

Data file 120210ry_585A1-55_3_2.mgf



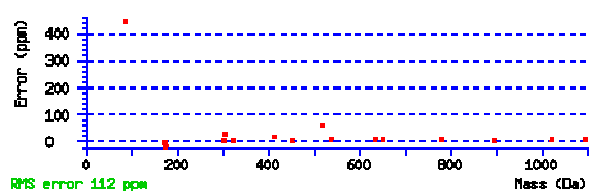
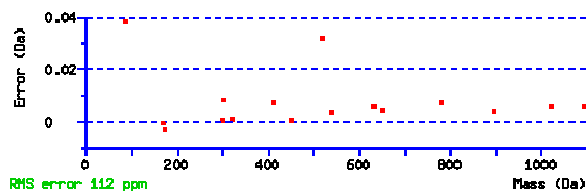
Monoisotopic mass of neutral peptide Mr(calc): 1192.5724

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 56 Expect: 0.00014

Matches : 16/90 fragment ions using 36 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							10
2	171.1128	86.0600					A	1094.5113	547.7593	1077.4847	539.2460	1076.5007	538.7540	9
3	300.1554	150.5813			282.1448	141.5761	E	1023.4742	512.2407	1006.4476	503.7274	1005.4636	503.2354	8
4	413.2395	207.1234			395.2289	198.1181	L	894.4316	447.7194	877.4050	439.2061	876.4210	438.7141	7
5	542.2821	271.6447			524.2715	262.6394	E	781.3475	391.1774	764.3210	382.6641	763.3369	382.1721	6
6	656.3250	328.6661	639.2984	320.1529	638.3144	319.6608	N	652.3049	326.6561	635.2784	318.1428	634.2943	317.6508	5
7	743.3570	372.1821	726.3305	363.6689	725.3464	363.1769	S	538.2620	269.6346	521.2354	261.1214	520.2514	260.6293	4
8	872.3996	436.7034	855.3731	428.1902	854.3890	427.6982	E	451.2300	226.1186	434.2034	217.6053	433.2194	217.1133	3
9	1019.4680	510.2376	1002.4415	501.7244	1001.4575	501.2324	F	322.1874	161.5973	305.1608	153.0840			2
10							R	175.1190	88.0631	158.0924	79.5498			1



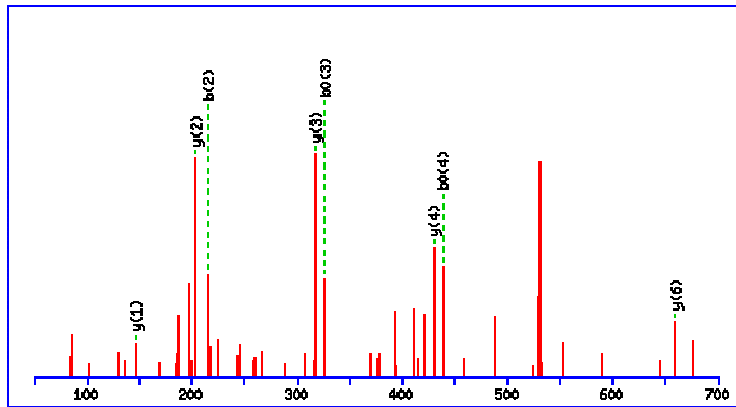
Peptide Number: 21882

MS/MS Fragmentation of **ITEILGK**Found in **IPI00892629** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SLC22A4 Protein

Match to Query 840: 772.466288 from(387.240420,2+) index(22545)

Title: Elution from: 53.8666666666667 to 53.8666666666667 period: 0 cycle: 1998 experiment: 1 polarity: +

Data file 120129ry_604A1-46_1_2.mgf



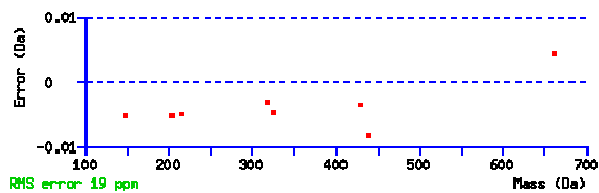
Monoisotopic mass of neutral peptide Mr(calc): 772.4694

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

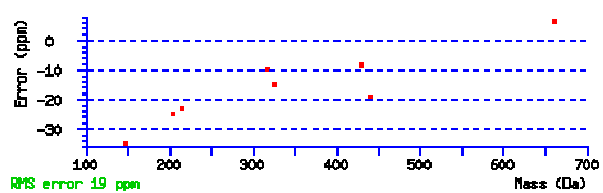
Ions Score: 41 Expect: 0.0072

Matches : 8/50 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			I							7
2	215.1390	108.0731	197.1285	99.0679	T	660.3927	330.7000	643.3661	322.1867	642.3821	321.6947	6
3	344.1816	172.5944	326.1710	163.5892	E	559.3450	280.1761	542.3184	271.6629	541.3344	271.1709	5
4	457.2657	229.1365	439.2551	220.1312	I	430.3024	215.6548	413.2758	207.1416			4
5	570.3497	285.6785	552.3392	276.6732	L	317.2183	159.1128	300.1918	150.5995			3
6	627.3712	314.1892	609.3606	305.1840	G	204.1343	102.5708	187.1077	94.0575			2
7					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 19 ppm



RMS error 19 ppm

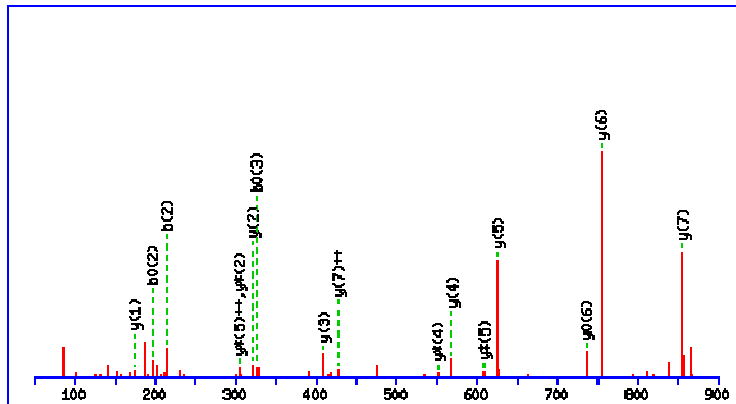
Peptide Number: 21917

MS/MS Fragmentation of **LTEGCSFR**Found in **IPI00847956** in **IPI_human**, Tax_Id=9606 Gene_Symbol=- Similar to 40S ribosomal protein S27

Match to Query 9242: 968.437588 from(485.226070,2+) index(22943)

Title: Elution from: 90.85 to 90.85 period: 0 cycle: 7244 experiment: 7 polarity:+

Data file 120208ry_Tig120slc-P8_1_1.mgf



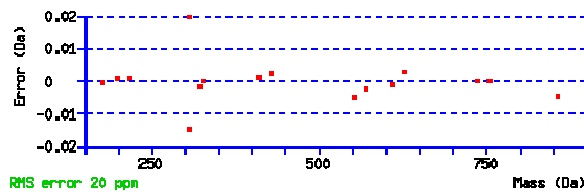
Monoisotopic mass of neutral peptide Mr(calc): 968.4386

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

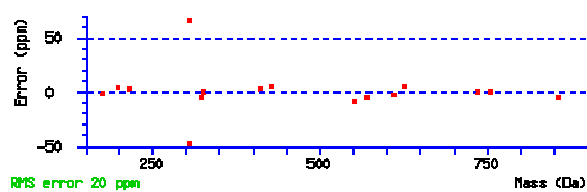
Ions Score: 58 Expect: 4.7e-005

Matches : 16/64 fragment ions using 24 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							8
2	215.1390	108.0731	197.1285	99.0679	T	856.3618	428.6845	839.3352	420.1713	838.3512	419.6792	7
3	344.1816	172.5944	326.1710	163.5892	E	755.3141	378.1607	738.2876	369.6474	737.3035	369.1554	6
4	401.2031	201.1052	383.1925	192.0999	G	626.2715	313.6394	609.2450	305.1261	608.2609	304.6341	5
5	561.2337	281.1205	543.2232	272.1152	C	569.2500	285.1287	552.2235	276.6154	551.2395	276.1234	4
6	648.2658	324.6365	630.2552	315.6312	S	409.2194	205.1133	392.1928	196.6001	391.2088	196.1081	3
7	795.3342	398.1707	777.3236	389.1654	F	322.1874	161.5973	305.1608	153.0840			2
8					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 20 ppm



RMS error 20 ppm

Mass (Da)

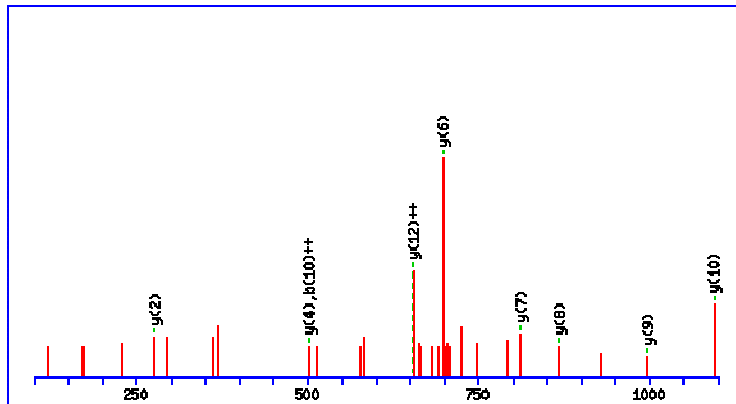
Peptide Number: 22536

MS/MS Fragmentation of **VVPTLPEGLPVLEK**Found in **IPI00785015** in **IPI_human**, Tax_Id=9606 Gene_Symbol=UBN2 Isoform 1 of Ubinuclein-2

Match to Query 20612: 1602.961782 from(535.327870,3+) index(42323)

Title: Elution from: 102.5 to 102.5 period: 0 cycle: 3813 experiment: 3 polarity:+

Data file 120126ry_585A1-55_1_3.mgf



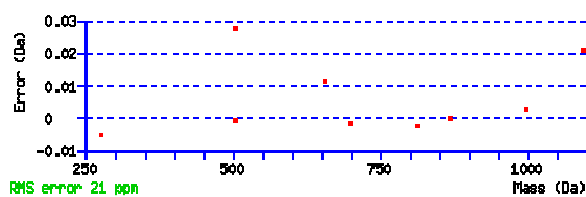
Monoisotopic mass of neutral peptide Mr(calc): 1602.9596

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

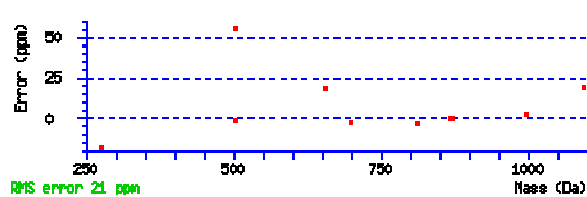
Ions Score: 38 Expect: 0.0018

Matches : 9/132 fragment ions using 18 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415			V							15
2	199.1441	100.0757			V	1504.8985	752.9529	1487.8720	744.4396	1486.8879	743.9476	14
3	296.1969	148.6021			P	1405.8301	703.4187	1388.8035	694.9054	1387.8195	694.4134	13
4	397.2445	199.1259	379.2340	190.1206	T	1308.7773	654.8923	1291.7508	646.3790	1290.7668	645.8870	12
5	510.3286	255.6679	492.3180	246.6627	L	1207.7297	604.3685	1190.7031	595.8552	1189.7191	595.3632	11
6	607.3814	304.1943	589.3708	295.1890	P	1094.6456	547.8264	1077.6190	539.3132	1076.6350	538.8211	10
7	736.4240	368.7156	718.4134	359.7103	E	997.5928	499.3001	980.5663	490.7868	979.5823	490.2948	9
8	793.4454	397.2264	775.4349	388.2211	G	868.5502	434.7788	851.5237	426.2655	850.5397	425.7735	8
9	906.5295	453.7684	888.5189	444.7631	L	811.5288	406.2680	794.5022	397.7547	793.5182	397.2627	7
10	1003.5823	502.2948	985.5717	493.2895	P	698.4447	349.7260	681.4182	341.2127	680.4341	340.7207	6
11	1102.6507	551.8290	1084.6401	542.8237	V	601.3919	301.1996	584.3654	292.6863	583.3814	292.1943	5
12	1215.7347	608.3710	1197.7242	599.3657	L	502.3235	251.6654	485.2970	243.1521	484.3130	242.6601	4
13	1328.8188	664.9130	1310.8082	655.9078	L	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
14	1457.8614	729.4343	1439.8508	720.4291	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
15					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 21 ppm



RMS error 21 ppm

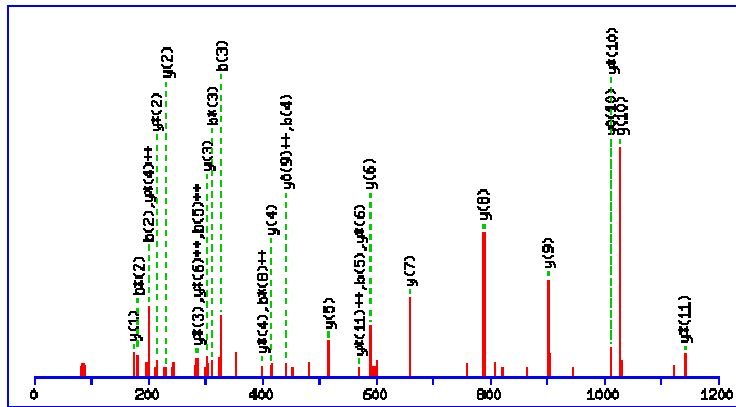
Peptide Number: 22778

MS/MS Fragmentation of **AQEIEAATLAGR**Found in **IPI00374721** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SMTN Isoform B3 of Smoothelin

Match to Query 14994: 1228.634768 from(615.324660,2+) index(9876)

Title: Elution from: 25.8166666666667 to 25.8166666666667 period: 0 cycle: 992 experiment: 9 polarity:+

Data file 120208ry_Tig120slc-P8_1_2.mgf



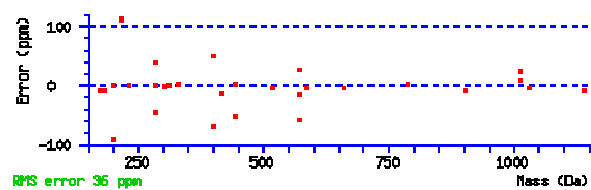
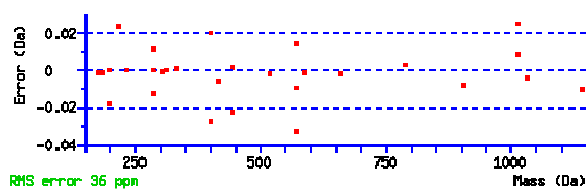
Monoisotopic mass of neutral peptide Mr(calc): 1228.6411

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 63 Expect: 3.2e-005

Matches : 29/118 fragment ions using 50 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ^{++*}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{++*}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							12
2	200.1030	100.5551	183.0764	92.0418			Q	1158.6113	579.8093	1141.5848	571.2960	1140.6008	570.8040	11
3	329.1456	165.0764	312.1190	156.5631	311.1350	156.0711	E	1030.5528	515.7800	1013.5262	507.2667	1012.5422	506.7747	10
4	442.2296	221.6185	425.2031	213.1052	424.2191	212.6132	I	901.5102	451.2587	884.4836	442.7454	883.4996	442.2534	9
5	571.2722	286.1397	554.2457	277.6265	553.2617	277.1345	E	788.4261	394.7167	771.3995	386.2034	770.4155	385.7114	8
6	642.3093	321.6583	625.2828	313.1450	624.2988	312.6530	A	659.3835	330.1954	642.3570	321.6821	641.3729	321.1901	7
7	713.3464	357.1769	696.3199	348.6636	695.3359	348.1716	A	588.3464	294.6768	571.3198	286.1636	570.3358	285.6715	6
8	814.3941	407.7007	797.3676	399.1874	796.3836	398.6954	T	517.3093	259.1583	500.2827	250.6450	499.2987	250.1530	5
9	927.4782	464.2427	910.4516	455.7295	909.4676	455.2375	L	416.2616	208.6344	399.2350	200.1212			4
10	998.5153	499.7613	981.4888	491.2480	980.5047	490.7560	A	303.1775	152.0924	286.1510	143.5791			3
11	1055.5368	528.2720	1038.5102	519.7587	1037.5262	519.2667	G	232.1404	116.5738	215.1139	108.0606			2
12							R	175.1190	88.0631	158.0924	79.5498			1



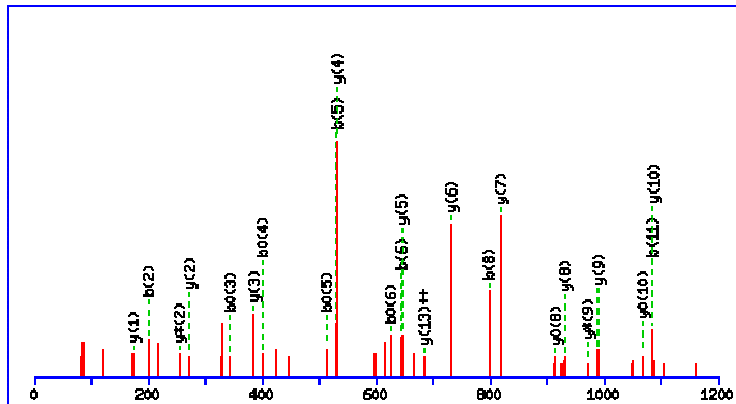
Peptide Number: 23190

MS/MS Fragmentation of **SLCGIIPGLSSIFLPR**Found in **IPI00102329** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SLC30A6 Isoform 1 of Zinc transporter 6

Match to Query 7734: 1728.962622 from(577.328150,3+) index(27073)

Title: Elution from: 70.15 to 70.15 period: 0 cycle: 2663 experiment: 1 polarity: +

Data file 120208ry_Tig120slc-P8_2_4.mgf



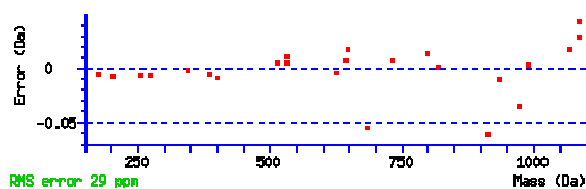
Monoisotopic mass of neutral peptide Mr(calc): 1728.9597

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

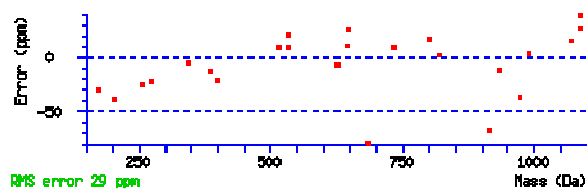
Ions Score: 68 Expect: 5.5e-006

Matches : 24/140 fragment ions using 38 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233	70.0287	35.5180	S							16
2	201.1234	101.0653	183.1128	92.0600	L	1642.9349	821.9711	1625.9084	813.4578	1624.9243	812.9658	15
3	361.1540	181.0806	343.1435	172.0754	C	1529.8508	765.4291	1512.8243	756.9158	1511.8403	756.4238	14
4	418.1755	209.5914	400.1649	200.5861	G	1369.8202	685.4137	1352.7936	676.9005	1351.8096	676.4085	13
5	531.2595	266.1334	513.2490	257.1281	I	1312.7987	656.9030	1295.7722	648.3897	1294.7882	647.8977	12
6	644.3436	322.6754	626.3330	313.6702	I	1199.7147	600.3610	1182.6881	591.8477	1181.7041	591.3557	11
7	741.3964	371.2018	723.3858	362.1965	P	1086.6306	543.8189	1069.6041	535.3057	1068.6200	534.8137	10
8	798.4178	399.7126	780.4073	390.7073	G	989.5778	495.2926	972.5513	486.7793	971.5673	486.2873	9
9	911.5019	456.2546	893.4913	447.2493	L	932.5564	466.7818	915.5298	458.2686	914.5458	457.7765	8
10	998.5339	499.7706	980.5234	490.7653	S	819.4723	410.2398	802.4458	401.7265	801.4617	401.2345	7
11	1085.5660	543.2866	1067.5554	534.2813	S	732.4403	366.7238	715.4137	358.2105	714.4297	357.7185	6
12	1198.6500	599.8286	1180.6395	590.8234	I	645.4083	323.2078	628.3817	314.6945			5
13	1345.7184	673.3629	1327.7079	664.3576	F	532.3242	266.6657	515.2976	258.1525			4
14	1458.8025	729.9049	1440.7919	720.8996	L	385.2558	193.1315	368.2292	184.6183			3
15	1555.8553	778.4313	1537.8447	769.4260	P	272.1717	136.5895	255.1452	128.0762			2
16					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 29 ppm



RMS error 29 ppm

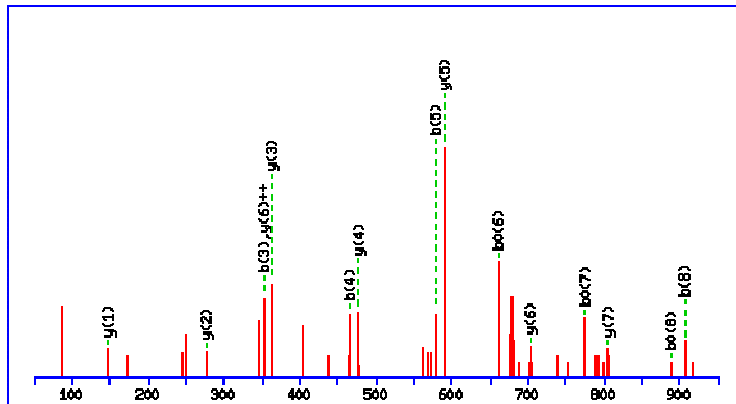
Peptide Number: 23691

MS/MS Fragmentation of **TLHLLTLNLSEK**Found in **IPI00006098** in **IPI_human**, Tax_Id=9606 Gene_Symbol=FEZ2 Isoform 1 of Fasciculation and elongation protein zeta-2

Match to Query 6675: 1380.797412 from(461.273080,3+) index(8545)

Title: Elution from: 22.4166666666667 to 22.4166666666667 period: 0 cycle: 861 experiment: 1 polarity: +

Data file 120208ry_Tig120slc-P8_1_3.mgf



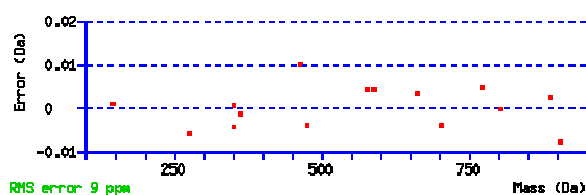
Monoisotopic mass of neutral peptide Mr(calc): 1380.7976

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

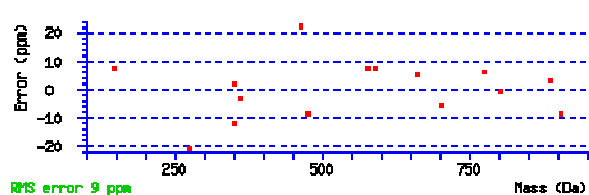
Ions Score: 58 Expect: 4.3e-005

Matches : 15/116 fragment ions using 18 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							12
2	215.1390	108.0731			197.1285	99.0679	L	1280.7573	640.8823	1263.7307	632.3690	1262.7467	631.8770	11
3	352.1979	176.6026			334.1874	167.5973	H	1167.6732	584.3402	1150.6467	575.8270	1149.6626	575.3350	10
4	465.2820	233.1446			447.2714	224.1394	L	1030.6143	515.8108	1013.5877	507.2975	1012.6037	506.8055	9
5	578.3661	289.6867			560.3555	280.6814	L	917.5302	459.2687	900.5037	450.7555	899.5197	450.2635	8
6	679.4137	340.2105			661.4032	331.2052	T	804.4462	402.7267	787.4196	394.2134	786.4356	393.7214	7
7	792.4978	396.7525			774.4872	387.7473	L	703.3985	352.2029	686.3719	343.6896	685.3879	343.1976	6
8	906.5407	453.7740	889.5142	445.2607	888.5302	444.7687	N	590.3144	295.6608	573.2879	287.1476	572.3039	286.6556	5
9	1019.6248	510.3160	1002.5982	501.8028	1001.6142	501.3108	L	476.2715	238.6394	459.2449	230.1261	458.2609	229.6341	4
10	1106.6568	553.8320	1089.6303	545.3188	1088.6463	544.8268	S	363.1874	182.0974	346.1609	173.5841	345.1769	173.0921	3
11	1235.6994	618.3533	1218.6729	609.8401	1217.6888	609.3481	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
12							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 9 ppm



RMS error 9 ppm

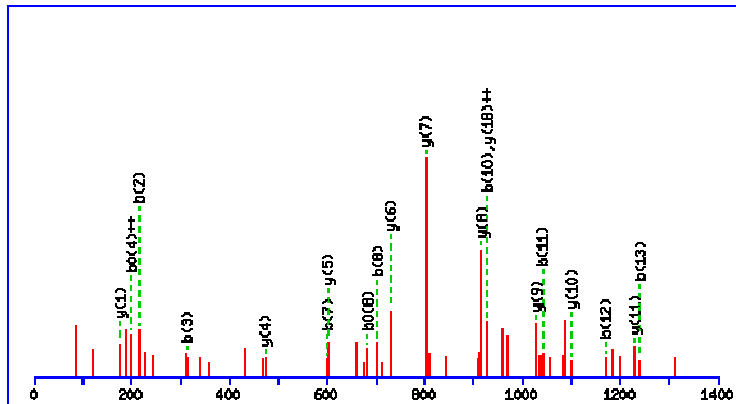
Peptide Number: 24036

MS/MS Fragmentation of **TLVTGGATPELEALJAEENALR**Found in **IPI00164387** in **IPI_human**, Tax_Id=9606 Gene_Symbol=KCNMA1 Isoform 5 of Calcium-activated potassium channel subunit alpha-1

Match to Query 19861: 2267.206542 from(756.742790,3+) index(2366)

Title: Elution from: 7.63333333333333 to 7.63333333333333 period: 0 cycle: 296 experiment: 3 polarity: +

Data file 120206ry_aHDF1419-P10_2_4.mgf



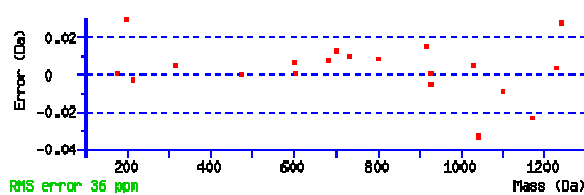
Monoisotopic mass of neutral peptide Mr(calcd): 2267.2009

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

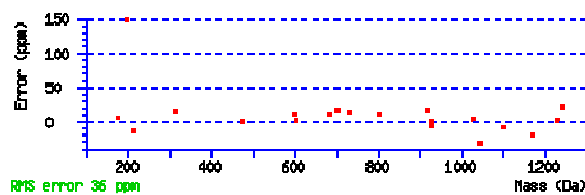
Ions Score: 52 Expect: 0.00033

Matches : 20/208 fragment ions using 44 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							22
2	215.1390	108.0731			197.1285	99.0679	L	2167.1605	1084.0839	2150.1339	1075.5706	2149.1499	1075.0786	21
3	314.2074	157.6074			296.1969	148.6021	V	2054.0764	1027.5419	2037.0499	1019.0286	2036.0659	1018.5366	20
4	415.2551	208.1312			397.2445	199.1259	T	1955.0080	978.0076	1937.9815	969.4944	1936.9974	969.0024	19
5	472.2766	236.6419			454.2660	227.6366	G	1853.9603	927.4838	1836.9338	918.9705	1835.9498	918.4785	18
6	529.2980	265.1527			511.2875	256.1474	G	1796.9389	898.9731	1779.9123	890.4598	1778.9283	889.9678	17
7	600.3352	300.6712			582.3246	291.6659	A	1739.9174	870.4623	1722.8909	861.9491	1721.9068	861.4571	16
8	701.3828	351.1951			683.3723	342.1898	T	1668.8803	834.9438	1651.8537	826.4305	1650.8697	825.9385	15
9	798.4356	399.7214			780.4250	390.7162	P	1567.8326	784.4199	1550.8061	775.9067	1549.8220	775.4147	14
10	927.4782	464.2427			909.4676	455.2375	E	1470.7798	735.8936	1453.7533	727.3803	1452.7693	726.8883	13
11	1040.5623	520.7848			1022.5517	511.7795	L	1341.7373	671.3723	1324.7107	662.8590	1323.7267	662.3670	12
12	1169.6048	585.3061			1151.5943	576.3008	E	1228.6532	614.8302	1211.6266	606.3170	1210.6426	605.8250	11
13	1240.6420	620.8246			1222.6314	611.8193	A	1099.6106	550.3089	1082.5840	541.7957	1081.6000	541.3037	10
14	1353.7260	677.3667			1335.7155	668.3614	L	1028.5735	514.7904	1011.5469	506.2771	1010.5629	505.7851	9
15	1466.8101	733.9087			1448.7995	724.9034	I	915.4894	458.2483	898.4629	449.7351	897.4789	449.2431	8
16	1537.8472	769.4272			1519.8366	760.4220	A	802.4054	401.7063	785.3788	393.1930	784.3948	392.7010	7
17	1666.8898	833.9485			1648.8792	824.9433	E	731.3682	366.1878	714.3417	357.6745	713.3577	357.1825	6
18	1795.9324	898.4698			1777.9218	889.4645	E	602.3257	301.6665	585.2991	293.1532	584.3151	292.6612	5
19	1909.9753	955.4913	1892.9488	946.9780	1891.9648	946.4860	N	473.2831	237.1452	456.2565	228.6319			4
20	1981.0124	991.0099	1963.9859	982.4966	1963.0019	982.0046	A	359.2401	180.1237	342.2136	171.6104			3
21	2094.0965	1047.5519	2077.0699	1039.0386	2076.0859	1038.5466	L	288.2030	144.6051	271.1765	136.0919			2
22							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 36 ppm



RMS error 36 ppm

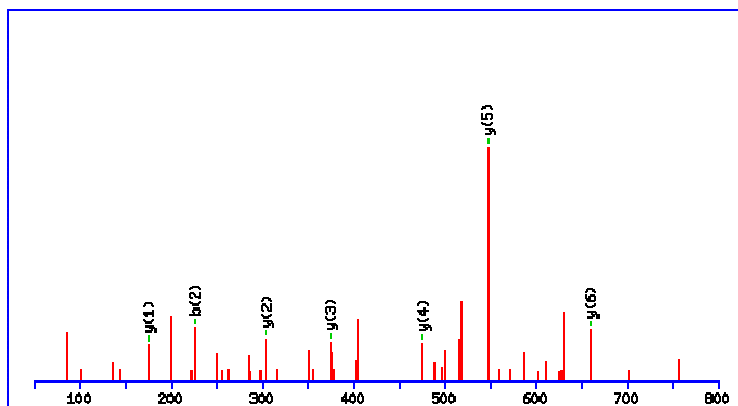
Peptide Number: 24046**MS/MS Fragmentation of LLATAER**

Found in **IPI00172576** in **IPI_human**, Tax_Id=9606 Gene_Symbol=NOXO1 Isoform 1 of NADPH oxidase organizer 1

Match to Query 3117: 772.444088 from(387.229320,2+) index(17591)

Title: Elution from: 85.7833333333333 to 85.7833333333333 period: 0 cycle: 8289 experiment: 3 polarity:+

Data file 120214ry_aHDF1419-P10_4_1.mgf



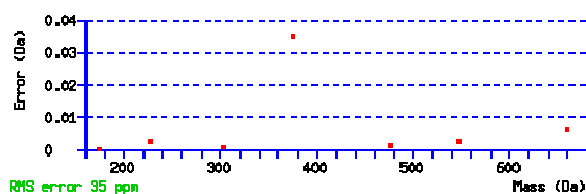
Monoisotopic mass of neutral peptide Mr(calc): 772.4443

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

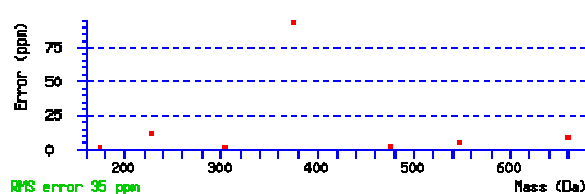
Ions Score: 45 **Expect:** 0.0034

Matches : 7/52 fragment ions using 14 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							7
2	227.1754	114.0913			L	660.3675	330.6874	643.3410	322.1741	642.3570	321.6821	6
3	298.2125	149.6099			A	547.2835	274.1454	530.2569	265.6321	529.2729	265.1401	5
4	399.2602	200.1337	381.2496	191.1285	T	476.2463	238.6268	459.2198	230.1135	458.2358	229.6215	4
5	470.2973	235.6523	452.2867	226.6470	A	375.1987	188.1030	358.1721	179.5897	357.1881	179.0977	3
6	599.3399	300.1736	581.3293	291.1683	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
7					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 35 ppm



RMS error 35 ppm

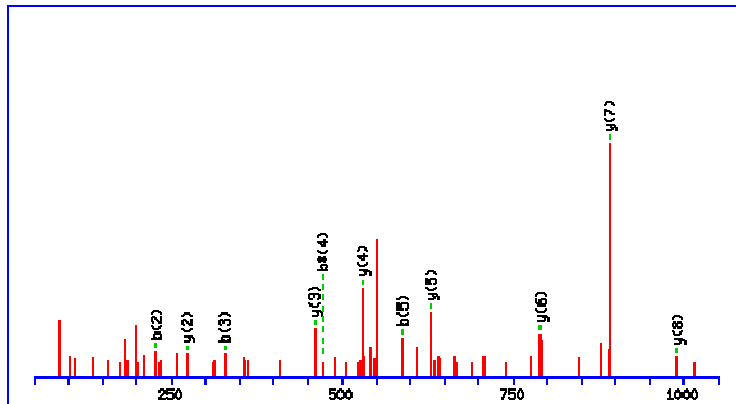
Peptide Number: 24070

MS/MS Fragmentation of **QVTCVAWVR**Found in **IPI00014298** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PWP1 Periodic tryptophan protein 1 homolog

Match to Query 13860: 1117.568148 from(559.791350,2+) index(24086)

Title: Elution from: 57.45 to 57.45 period: 0 cycle: 2136 experiment: 8 polarity:+

Data file 120124ry_414C2-43_1_2.mgf



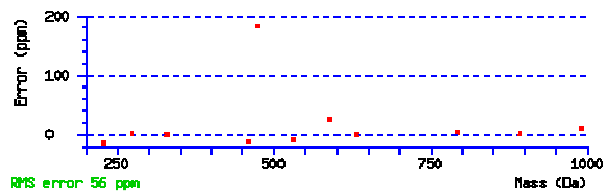
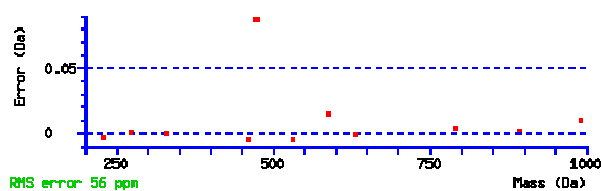
Monoisotopic mass of neutral peptide Mr(calc): 1117.5703

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 40 Expect: 0.0082

Matches : 11/80 fragment ions using 28 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.0659	65.0366	112.0393	56.5233			Q							9
2	228.1343	114.5708	211.1077	106.0575			V	990.5189	495.7631	973.4924	487.2498	972.5084	486.7578	8
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	T	891.4505	446.2289	874.4240	437.7156	873.4400	437.2236	7
4	489.2126	245.1099	472.1860	236.5967	471.2020	236.1047	C	790.4029	395.7051	773.3763	387.1918			6
5	588.2810	294.6441	571.2545	286.1309	570.2704	285.6389	V	630.3722	315.6897	613.3457	307.1765			5
6	659.3181	330.1627	642.2916	321.6494	641.3076	321.1574	A	531.3038	266.1555	514.2772	257.6423			4
7	845.3974	423.2024	828.3709	414.6891	827.3869	414.1971	W	460.2667	230.6370	443.2401	222.1237			3
8	944.4659	472.7366	927.4393	464.2233	926.4553	463.7313	V	274.1874	137.5973	257.1608	129.0840			2
9							R	175.1190	88.0631	158.0924	79.5498			1

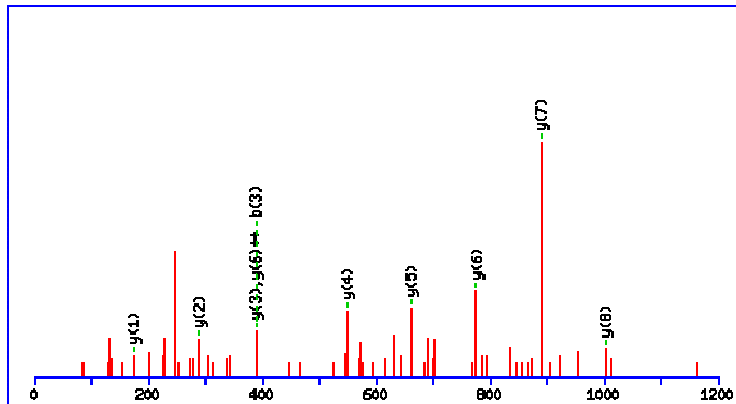


Peptide Number: 24819MS/MS Fragmentation of **CLDNLCVNR**Found in **IPI00296936** in **IPI_human**, Tax_Id=9606 Gene_Symbol=GLIPR1 Glioma pathogenesis-related protein 1

Match to Query 11642: 1162.534088 from(582.274320,2+) index(2085)

Title: Elution from: 4.91666666666667 to 4.91666666666667 period: 0 cycle: 185 experiment: 8 polarity: +

Data file 120206ry_aHDF1419-P10_3_2.mgf



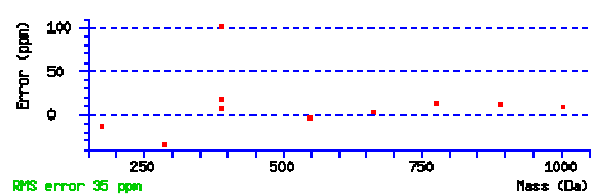
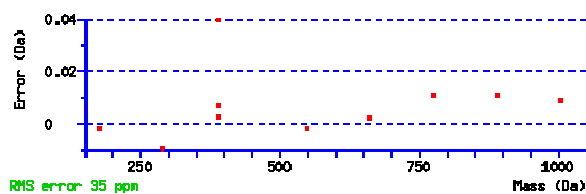
Monoisotopic mass of neutral peptide Mr(calc): 1162.5223

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 56 Expect: 0.00011

Matches : 10/74 fragment ions using 20 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	161.0379	81.0226					C							9
2	274.1220	137.5646					L	1003.4989	502.2531	986.4724	493.7398	985.4884	493.2478	8
3	389.1489	195.0781			371.1384	186.0728	D	890.4149	445.7111	873.3883	437.1978	872.4043	436.7058	7
4	503.1919	252.0996	486.1653	243.5863	485.1813	243.0943	N	775.3879	388.1976	758.3614	379.6843			6
5	616.2759	308.6416	599.2494	300.1283	598.2654	299.6363	L	661.3450	331.1761	644.3185	322.6629			5
6	776.3066	388.6569	759.2800	380.1436	758.2960	379.6516	C	548.2609	274.6341	531.2344	266.1208			4
7	875.3750	438.1911	858.3484	429.6779	857.3644	429.1858	V	388.2303	194.6188	371.2037	186.1055			3
8	989.4179	495.2126	972.3914	486.6993	971.4073	486.2073	N	289.1619	145.0846	272.1353	136.5713			2
9							R	175.1190	88.0631	158.0924	79.5498			1



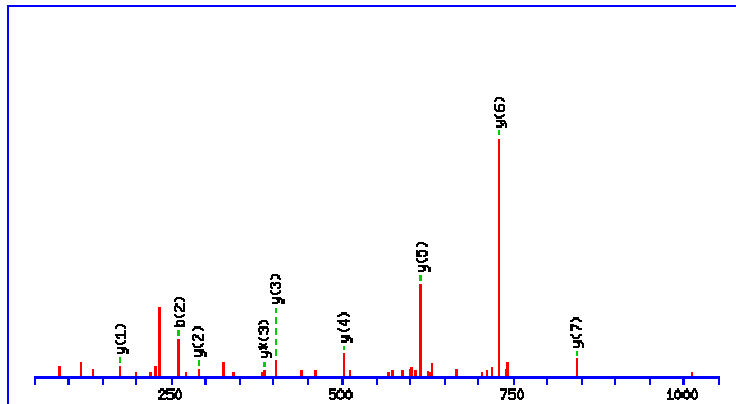
Peptide Number: 24868

MS/MS Fragmentation of **FLLNVLDR**Found in **IPI00550117** in **IPI_human**, Tax_Id=9606 Gene_Symbol=LHX1 LIM/homeobox protein Lhx1

Match to Query 784: 988.564268 from(495.289410,2+) index(14585)

Title: Elution from: 36.2833333333333 to 36.2833333333333 period: 0 cycle: 1371 experiment: 2 polarity:+

Data file 120214ry_414C2-43_4_3.mgf



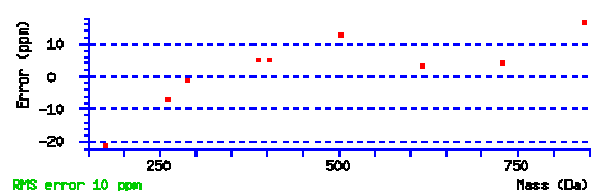
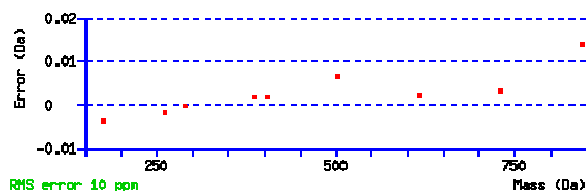
Monoisotopic mass of neutral peptide Mr(calc): 988.5706

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 45 Expect: 0.0015

Matches : 9/64 fragment ions using 22 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415					F							8
2	261.1598	131.0835					L	842.5094	421.7584	825.4829	413.2451	824.4989	412.7531	7
3	374.2438	187.6255					L	729.4254	365.2163	712.3988	356.7030	711.4148	356.2110	6
4	488.2867	244.6470	471.2602	236.1337			N	616.3413	308.6743	599.3148	300.1610	598.3307	299.6690	5
5	587.3552	294.1812	570.3286	285.6679			V	502.2984	251.6528	485.2718	243.1396	484.2878	242.6475	4
6	700.4392	350.7232	683.4127	342.2100			L	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
7	815.4662	408.2367	798.4396	399.7234	797.4556	399.2314	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
8							R	175.1190	88.0631	158.0924	79.5498			1



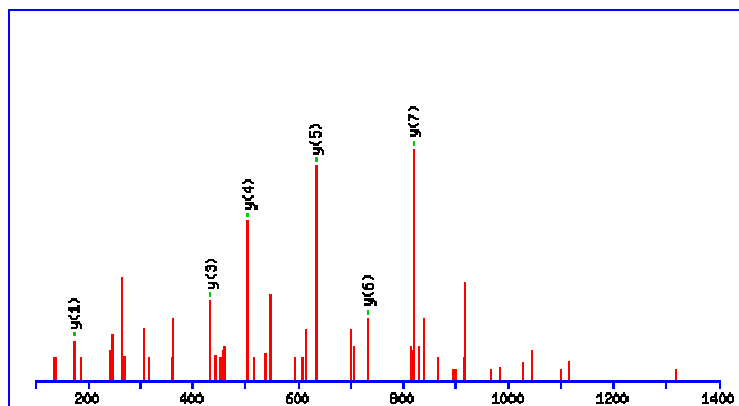
Peptide Number: 25086**MS/MS Fragmentation of EYSVEAEER**

Found in **IPI00216737** in **IPI_human**, Tax_Id=9606 Gene_Symbol=MINA Isoform 1 of MYC-induced nuclear antigen

Match to Query 14205: 1110.485068 from(556.249810,2+) index(16818)

Title: Elution from: 80.65 to 80.65 period: 0 cycle: 8429 experiment: 8 polarity:+

Data file 120210ry_585A1-55_3_1.mgf



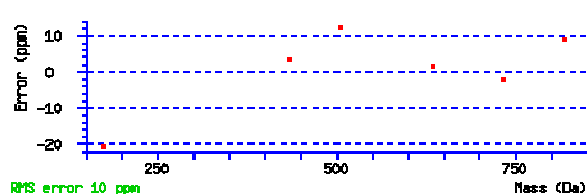
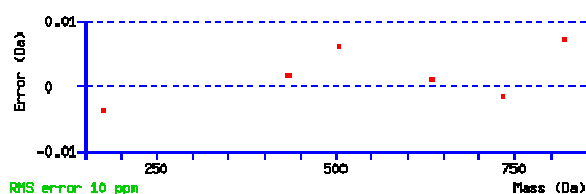
Monoisotopic mass of neutral peptide Mr(calcd): 1110.4829

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 43 **Expect:** 0.001

Matches : 6/78 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286	112.0393	56.5233	E							9
2	293.1132	147.0602	275.1026	138.0550	Y	982.4476	491.7274	965.4211	483.2142	964.4371	482.7222	8
3	380.1452	190.5763	362.1347	181.5710	S	819.3843	410.1958	802.3577	401.6825	801.3737	401.1905	7
4	479.2136	240.1105	461.2031	231.1052	V	732.3523	366.6798	715.3257	358.1665	714.3417	357.6745	6
5	608.2562	304.6318	590.2457	295.6265	E	633.2838	317.1456	616.2573	308.6323	615.2733	308.1403	5
6	679.2933	340.1503	661.2828	331.1450	A	504.2413	252.6243	487.2147	244.1110	486.2307	243.6190	4
7	808.3359	404.6716	790.3254	395.6663	E	433.2041	217.1057	416.1776	208.5924	415.1936	208.1004	3
8	937.3785	469.1929	919.3680	460.1876	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
9					R	175.1190	88.0631	158.0924	79.5498			1



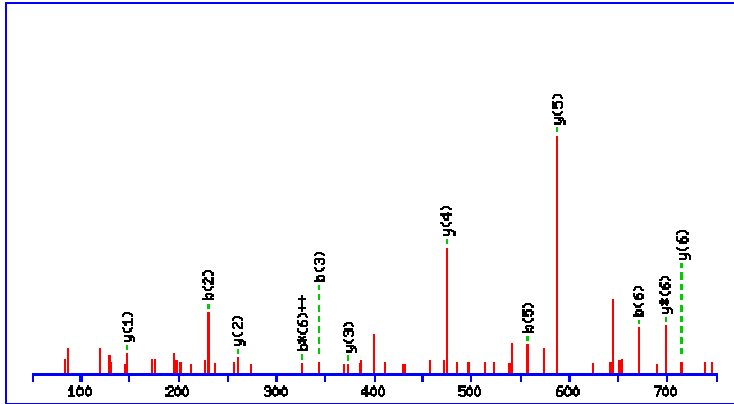
Peptide Number: 25194

MS/MS Fragmentation of **TQLTLIK**Found in **IPI00646366** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CNTRL Uncharacterized protein

Match to Query 4025: 815.503888 from(408.759220,2+) index(30252)

Title: Elution from: 114.333333333333 to 114.333333333333 period: 0 cycle: 7482 experiment: 2 polarity: +

Data file 120129ry_604A1-46_1_1.mgf



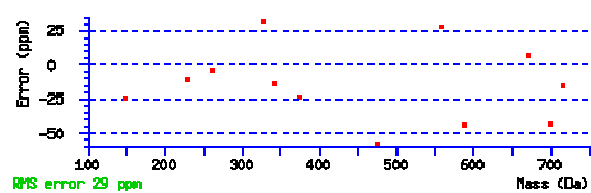
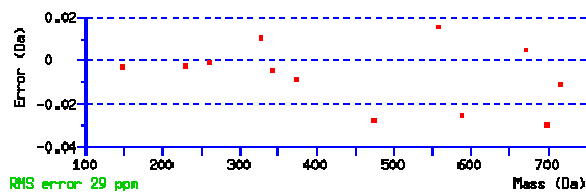
Monoisotopic mass of neutral peptide Mr(calc): 815.5116

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 46 Expect: 0.0006

Matches : 12/64 fragment ions using 21 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							7
2	230.1135	115.5604	213.0870	107.0471	212.1030	106.5551	Q	715.4713	358.2393	698.4447	349.7260	697.4607	349.2340	6
3	343.1976	172.1024	326.1710	163.5892	325.1870	163.0972	L	587.4127	294.2100	570.3861	285.6967	569.4021	285.2047	5
4	444.2453	222.6263	427.2187	214.1130	426.2347	213.6210	T	474.3286	237.6679	457.3021	229.1547	456.3180	228.6627	4
5	557.3293	279.1683	540.3028	270.6550	539.3188	270.1630	L	373.2809	187.1441	356.2544	178.6308			3
6	670.4134	335.7103	653.3869	327.1971	652.4028	326.7051	I	260.1969	130.6021	243.1703	122.0888			2
7							K	147.1128	74.0600	130.0863	65.5468			1



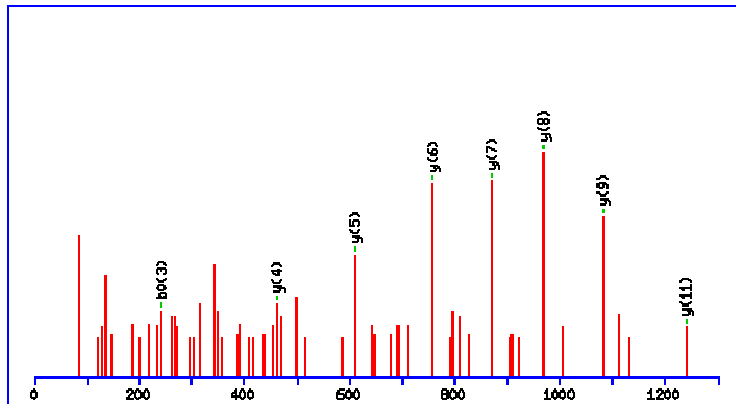
Peptide Number: 25529

MS/MS Fragmentation of **GNSDGLVLFSSDLK**Found in **IPI00217049** in **IPI_human**, Tax_Id=9606 Gene_Symbol=OAS2 Isoform p71 of 2'-5'-oligoadenylate synthase 2

Match to Query 5245: 1611.804568 from(806.909560,2+) index(9735)

Title: Elution from: 26.2833333333333 to 26.2833333333333 period: 0 cycle: 999 experiment: 6 polarity: +

Data file 120212ry_aHDF1388-P9_3_4.mgf



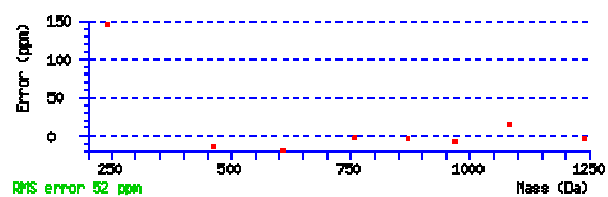
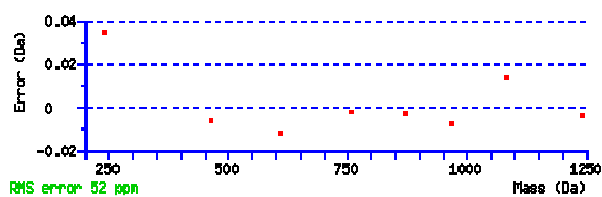
Monoisotopic mass of neutral peptide Mr(calc): 1611.8145

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 46 Expect: 0.0018

Matches : 8/158 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							15
2	172.0717	86.5395	155.0451	78.0262			N	1555.8003	778.4038	1538.7737	769.8905	1537.7897	769.3985	14
3	259.1037	130.0555	242.0771	121.5422	241.0931	121.0502	S	1441.7573	721.3823	1424.7308	712.8690	1423.7468	712.3770	13
4	374.1306	187.5690	357.1041	179.0557	356.1201	178.5637	D	1354.7253	677.8663	1337.6987	669.3530	1336.7147	668.8610	12
5	431.1521	216.0797	414.1256	207.5664	413.1415	207.0744	G	1239.6984	620.3528	1222.6718	611.8395	1221.6878	611.3475	11
6	532.1998	266.6035	515.1732	258.0903	514.1892	257.5982	T	1182.6769	591.8421	1165.6503	583.3288	1164.6663	582.8368	10
7	645.2838	323.1456	628.2573	314.6323	627.2733	314.1403	L	1081.6292	541.3182	1064.6027	532.8050	1063.6186	532.3130	9
8	744.3523	372.6798	727.3257	364.1665	726.3417	363.6745	V	968.5451	484.7762	951.5186	476.2629	950.5346	475.7709	8
9	857.4363	429.2218	840.4098	420.7085	839.4258	420.2165	L	869.4767	435.2420	852.4502	426.7287	851.4662	426.2367	7
10	1004.5047	502.7560	987.4782	494.2427	986.4942	493.7507	F	756.3927	378.7000	739.3661	370.1867	738.3821	369.6947	6
11	1151.5732	576.2902	1134.5466	567.7769	1133.5626	567.2849	F	609.3243	305.1658	592.2977	296.6525	591.3137	296.1605	5
12	1238.6052	619.8062	1221.5786	611.2930	1220.5946	610.8009	S	462.2558	231.6316	445.2293	223.1183	444.2453	222.6263	4
13	1353.6321	677.3197	1336.6056	668.8064	1335.6216	668.3144	D	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
14	1466.7162	733.8617	1449.6896	725.3485	1448.7056	724.8564	L	260.1969	130.6021	243.1703	122.0888			2
15							K	147.1128	74.0600	130.0863	65.5468			1



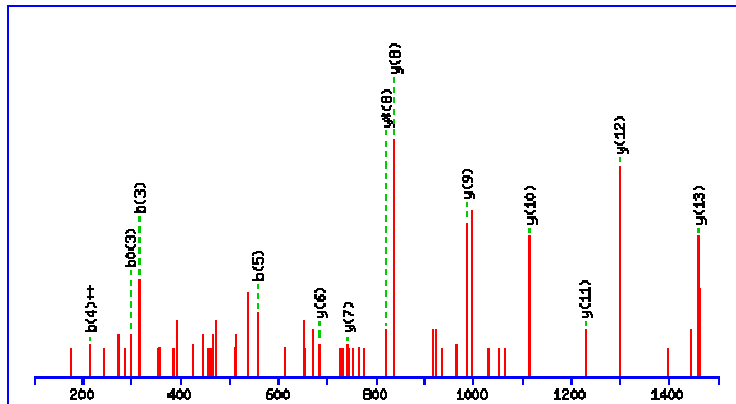
Peptide Number: 25638

MS/MS Fragmentation of **ISDLEICAEFPGSSATYR**Found in **IPI00376351** in **IPI_human**, Tax_Id=9606 Gene_Symbol=METTL2A Isoform 1 of Methyltransferase-like protein 2A

Match to Query 31072: 2129.957648 from(1065.986100,2+) index(14275)

Title: Elution from: 35.4333333333333 to 35.4333333333333 period: 0 cycle: 1334 experiment: 10 polarity:+

Data file 120210ry_32R1-32_2_3.mgf



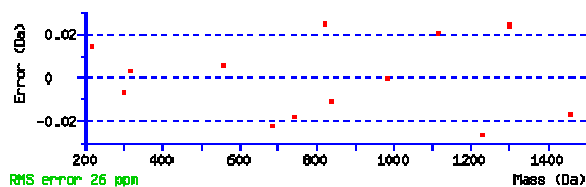
Monoisotopic mass of neutral peptide Mr(calcd): 2129.9575

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

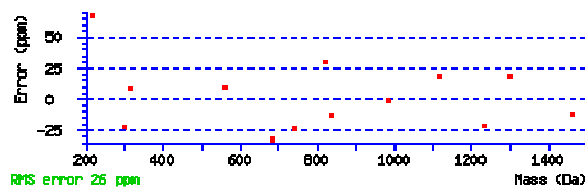
Ions Score: 45 Expect: 0.00083

Matches : 13/174 fragment ions using 23 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			I							19
2	201.1234	101.0653	183.1128	92.0600	S	2017.8808	1009.4440	2000.8542	1000.9307	1999.8702	1000.4387	18
3	316.1503	158.5788	298.1397	149.5735	D	1930.8487	965.9280	1913.8222	957.4147	1912.8382	956.9227	17
4	429.2344	215.1208	411.2238	206.1155	L	1815.8218	908.4145	1798.7952	899.9013	1797.8112	899.4093	16
5	558.2770	279.6421	540.2664	270.6368	E	1702.7377	851.8725	1685.7112	843.3592	1684.7272	842.8672	15
6	671.3610	336.1842	653.3505	327.1789	I	1573.6951	787.3512	1556.6686	778.8379	1555.6846	778.3459	14
7	831.3917	416.1995	813.3811	407.1942	C	1460.6111	730.8092	1443.5845	722.2959	1442.6005	721.8039	13
8	902.4288	451.7180	884.4182	442.7128	A	1300.5804	650.7938	1283.5539	642.2806	1282.5699	641.7886	12
9	1017.4557	509.2315	999.4452	500.2262	D	1229.5433	615.2753	1212.5168	606.7620	1211.5327	606.2700	11
10	1146.4983	573.7528	1128.4878	564.7475	E	1114.5164	557.7618	1097.4898	549.2485	1096.5058	548.7565	10
11	1293.5667	647.2870	1275.5562	638.2817	F	985.4738	493.2405	968.4472	484.7272	967.4632	484.2352	9
12	1390.6195	695.8134	1372.6089	686.8081	P	838.4054	419.7063	821.3788	411.1930	820.3948	410.7010	8
13	1447.6410	724.3241	1429.6304	715.3188	G	741.3526	371.1799	724.3260	362.6667	723.3420	362.1747	7
14	1534.6730	767.8401	1516.6624	758.8349	S	684.3311	342.6692	667.3046	334.1559	666.3206	333.6639	6
15	1621.7050	811.3562	1603.6945	802.3509	S	597.2991	299.1532	580.2726	290.6399	579.2885	290.1479	5
16	1692.7421	846.8747	1674.7316	837.8694	A	510.2671	255.6372	493.2405	247.1239	492.2565	246.6319	4
17	1793.7898	897.3985	1775.7793	888.3933	T	439.2300	220.1186	422.2034	211.6053	421.2194	211.1133	3
18	1956.8532	978.9302	1938.8426	969.9249	Y	338.1823	169.5948	321.1557	161.0815			2
19					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 26 ppm



RMS error 26 ppm

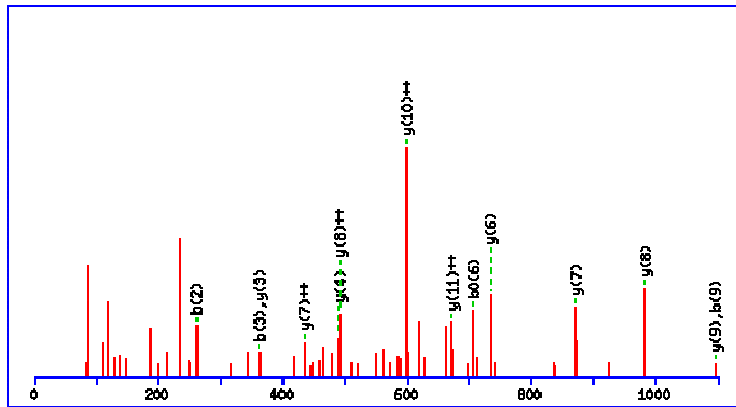
Peptide Number: 25795

MS/MS Fragmentation of **LFTILHLEESQK**Found in **IPI00178611** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CCDC109B Coiled-coil domain-containing protein 109B

Match to Query 9355: 1456.792482 from(486.604770,3+) index(5607)

Title: Elution from: 13.2833333333333 to 13.2833333333333 period: 0 cycle: 504 experiment: 2 polarity: +

Data file 120212ry_aHDF1388-P9_2_3.mgf



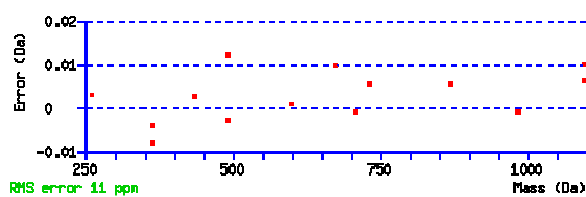
Monoisotopic mass of neutral peptide Mr(calc): 1456.7926

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

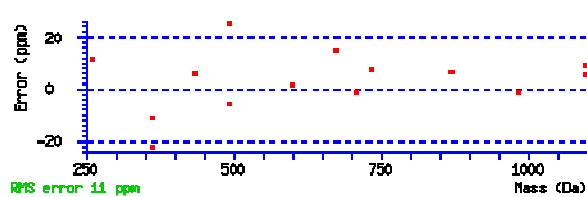
Ions Score: 40 Expect: 0.007

Matches : 14/104 fragment ions using 19 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							12
2	261.1598	131.0835					F	1344.7158	672.8615	1327.6892	664.3483	1326.7052	663.8563	11
3	362.2074	181.6074			344.1969	172.6021	T	1197.6474	599.3273	1180.6208	590.8141	1179.6368	590.3220	10
4	475.2915	238.1494			457.2809	229.1441	I	1096.5997	548.8035	1079.5732	540.2902	1078.5891	539.7982	9
5	588.3756	294.6914			570.3650	285.6861	L	983.5156	492.2615	966.4891	483.7482	965.5051	483.2562	8
6	725.4345	363.2209			707.4239	354.2156	H	870.4316	435.7194	853.4050	427.2061	852.4210	426.7141	7
7	838.5185	419.7629			820.5080	410.7576	L	733.3727	367.1900	716.3461	358.6767	715.3621	358.1847	6
8	967.5611	484.2842			949.5506	475.2789	E	620.2886	310.6479	603.2620	302.1347	602.2780	301.6427	5
9	1096.6037	548.8055			1078.5932	539.8002	E	491.2460	246.1266	474.2195	237.6134	473.2354	237.1214	4
10	1183.6358	592.3215			1165.6252	583.3162	S	362.2034	181.6053	345.1769	173.0921	344.1928	172.6001	3
11	1311.6943	656.3508	1294.6678	647.8375	1293.6838	647.3455	Q	275.1714	138.0893	258.1448	129.5761			2
12							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 11.11 ppm



RMS error 11.11 ppm

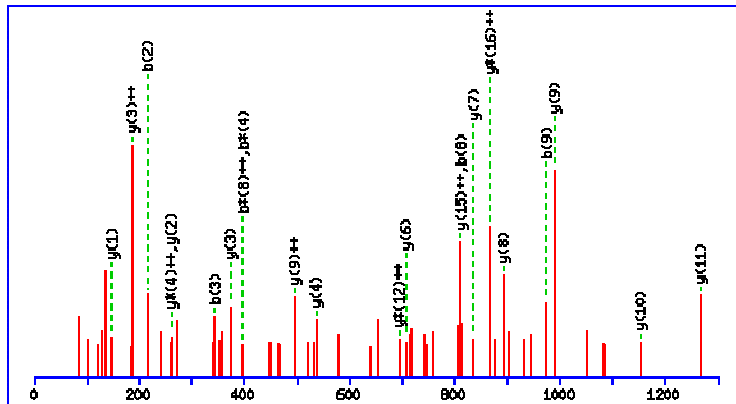
Peptide Number: 25975

MS/MS Fragmentation of **DVQAGSHDYPGEGIYLLK**Found in **IPI00292812** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TMED8 Protein TMED8

Match to Query 25555: 1960.962942 from(654.661590,3+) index(1866)

Title: Elution from: 4.6 to 4.6 period: 0 cycle: 171 experiment: 6 polarity: +

Data file 120212ry_414C2-43_3_3.mgf



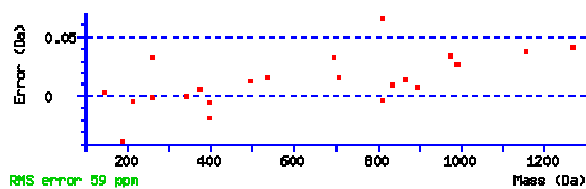
Monoisotopic mass of neutral peptide Mr(calc): 1960.9530

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

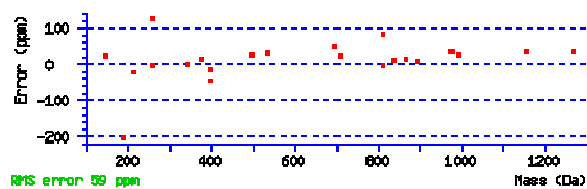
Ions Score: 42 Expect: 0.0045

Matches : 22/188 fragment ions using 52 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							18
2	215.1026	108.0550			197.0921	99.0497	V	1846.9334	923.9703	1829.9068	915.4571	1828.9228	914.9651	17
3	343.1612	172.0842	326.1347	163.5710	325.1506	163.0790	Q	1747.8650	874.4361	1730.8384	865.9229	1729.8544	865.4308	16
4	414.1983	207.6028	397.1718	199.0895	396.1878	198.5975	A	1619.8064	810.4068	1602.7799	801.8936	1601.7958	801.4016	15
5	471.2198	236.1135	454.1932	227.6003	453.2092	227.1083	G	1548.7693	774.8883	1531.7427	766.3750	1530.7587	765.8830	14
6	558.2518	279.6295	541.2253	271.1163	540.2413	270.6243	S	1491.7478	746.3775	1474.7213	737.8643	1473.7373	737.3723	13
7	695.3107	348.1590	678.2842	339.6457	677.3002	339.1537	H	1404.7158	702.8615	1387.6892	694.3483	1386.7052	693.8563	12
8	810.3377	405.6725	793.3111	397.1592	792.3271	396.6672	D	1267.6569	634.3321	1250.6303	625.8188	1249.6463	625.3268	11
9	973.4010	487.2041	956.3745	478.6909	955.3904	478.1989	Y	1152.6299	576.8186	1135.6034	568.3053	1134.6194	567.8133	10
10	1070.4538	535.7305	1053.4272	527.2172	1052.4432	526.7252	P	989.5666	495.2869	972.5401	486.7737	971.5560	486.2817	9
11	1127.4752	564.2413	1110.4487	555.7280	1109.4647	555.2360	G	892.5138	446.7606	875.4873	438.2473	874.5033	437.7553	8
12	1256.5178	628.7625	1239.4913	620.2493	1238.5073	619.7573	E	835.4924	418.2498	818.4658	409.7366	817.4818	409.2445	7
13	1313.5393	657.2733	1296.5127	648.7600	1295.5287	648.2680	G	706.4498	353.7285	689.4232	345.2153			6
14	1426.6233	713.8153	1409.5968	705.3020	1408.6128	704.8100	I	649.4283	325.2178	632.4018	316.7045			5
15	1589.6867	795.3470	1572.6601	786.8337	1571.6761	786.3417	Y	536.3443	268.6758	519.3177	260.1625			4
16	1702.7707	851.8890	1685.7442	843.3757	1684.7602	842.8837	L	373.2809	187.1441	356.2544	178.6308			3
17	1815.8548	908.4310	1798.8283	899.9178	1797.8442	899.4258	L	260.1969	130.6021	243.1703	122.0888			2
18							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 59 ppm



RMS error 59 ppm

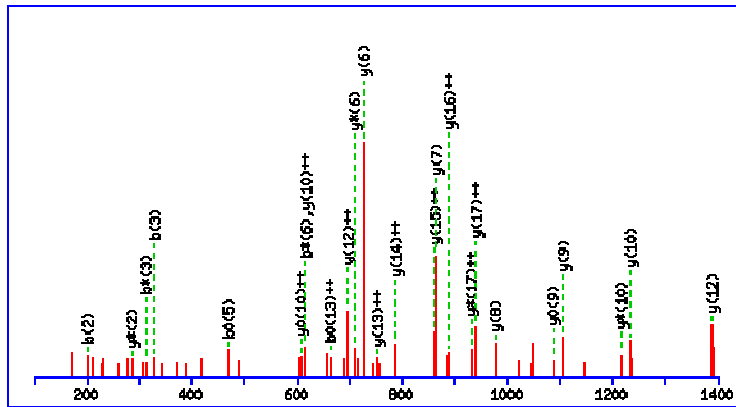
Peptide Number: 26040

MS/MS Fragmentation of **SLQTGFAGVQQLHPTLIQR**Found in **IPI00306057** in **IPI_human**, Tax_Id=9606 Gene_Symbol=RBM38 Isoform 1 of RNA-binding protein 38

Match to Query 32801: 2206.203012 from(736.408280,3+) index(23702)

Title: Elution from: 59.2833333333333 to 59.2833333333333 period: 0 cycle: 2234 experiment: 5 polarity:+

Data file 120210ry_32R1-32_2_3.mgf



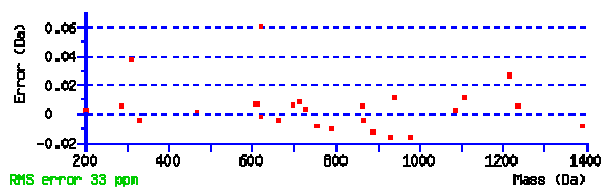
Monoisotopic mass of neutral peptide Mr(calcd): 2206.2222

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

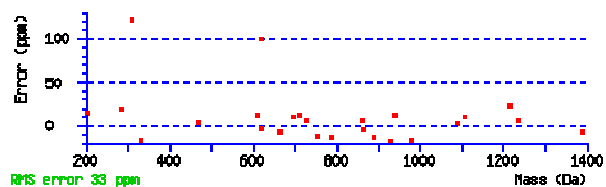
Ions Score: 45 Expect: 0.0011

Matches : 25/216 fragment ions using 41 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							20
2	201.1234	101.0653			183.1128	92.0600	L	2120.1975	1060.6024	2103.1709	1052.0891	2102.1869	1051.5971	19
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	Q	2007.1134	1004.0604	1990.0869	995.5471	1989.1029	995.0551	18
4	430.2296	215.6185	413.2031	207.1052	412.2191	206.6132	T	1879.0548	940.0311	1862.0283	931.5178	1861.0443	931.0258	17
5	487.2511	244.1292	470.2245	235.6159	469.2405	235.1239	G	1778.0072	889.5072	1760.9806	880.9939	1759.9966	880.5019	16
6	634.3195	317.6634	617.2930	309.1501	616.3089	308.6581	F	1720.9857	860.9965	1703.9592	852.4832	1702.9751	851.9912	15
7	705.3566	353.1819	688.3301	344.6687	687.3461	344.1767	A	1573.9173	787.4623	1556.8907	778.9490	1555.9067	778.4570	14
8	818.4407	409.7240	801.4141	401.2107	800.4301	400.7187	I	1502.8802	751.9437	1485.8536	743.4305	1484.8696	742.9384	13
9	875.4621	438.2347	858.4356	429.7214	857.4516	429.2294	G	1389.7961	695.4017	1372.7696	686.8884	1371.7855	686.3964	12
10	974.5306	487.7689	957.5040	479.2556	956.5200	478.7636	V	1332.7746	666.8910	1315.7481	658.3777	1314.7641	657.8857	11
11	1102.5891	551.7982	1085.5626	543.2849	1084.5786	542.7929	Q	1233.7062	617.3568	1216.6797	608.8435	1215.6957	608.3515	10
12	1230.6477	615.8275	1213.6212	607.3142	1212.6372	606.8222	Q	1105.6477	553.3275	1088.6211	544.8142	1087.6371	544.3222	9
13	1343.7318	672.3695	1326.7052	663.8563	1325.7212	663.3642	L	977.5891	489.2982	960.5625	480.7849	959.5785	480.2929	8
14	1480.7907	740.8990	1463.7641	732.3857	1462.7801	731.8937	H	864.5050	432.7561	847.4785	424.2429	846.4944	423.7509	7
15	1577.8435	789.4254	1560.8169	780.9121	1559.8329	780.4201	P	727.4461	364.2267	710.4196	355.7134	709.4355	355.2214	6
16	1678.8911	839.9492	1661.8646	831.4359	1660.8806	830.9439	T	630.3933	315.7003	613.3668	307.1870	612.3828	306.6950	5
17	1791.9752	896.4912	1774.9486	887.9780	1773.9646	887.4860	L	529.3457	265.1765	512.3191	256.6632			4
18	1905.0593	953.0333	1888.0327	944.5200	1887.0487	944.0280	I	416.2616	208.6344	399.2350	200.1212			3
19	2033.1178	1017.0626	2016.0913	1008.5493	2015.1073	1008.0573	Q	303.1775	152.0924	286.1510	143.5791			2
20							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 33 ppm



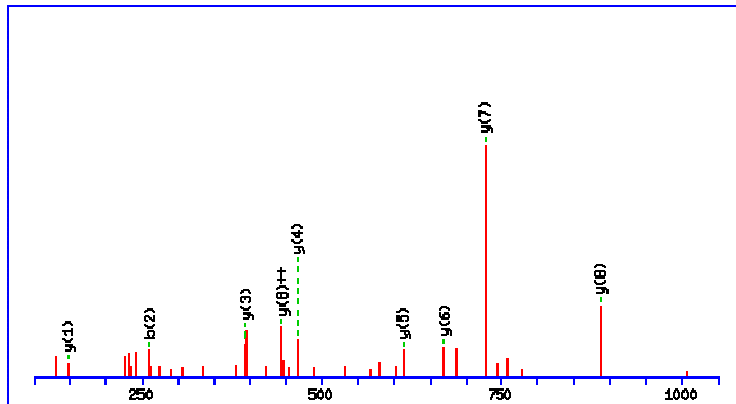
RMS error 33 ppm

Peptide Number: 26532MS/MS Fragmentation of **VCGGFACSK**Found in **IPI00030418** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TSPAN31 Tetraspanin-31

Match to Query 10636: 984.415288 from(493.214920,2+) index(10881)

Title: Elution from: 64.15 to 64.15 period: 0 cycle: 7211 experiment: 6 polarity: +

Data file 120210ry_32R1-32_2_1.mgf



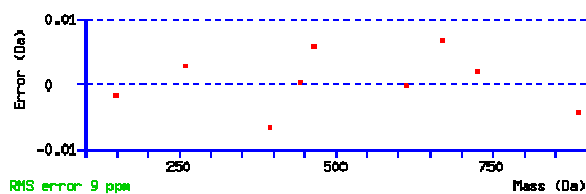
Monoisotopic mass of neutral peptide Mr(calc): 984.4157

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

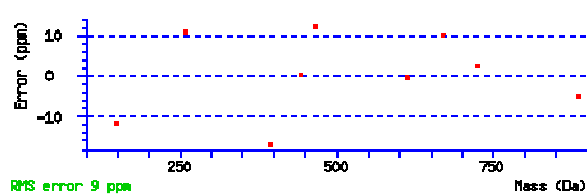
Ions Score: 45 Expect: 0.00037

Matches : 9/64 fragment ions using 22 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415			V							9
2	260.1063	130.5568			C	886.3546	443.6809	869.3280	435.1677	868.3440	434.6756	8
3	317.1278	159.0675			G	726.3239	363.6656	709.2974	355.1523	708.3134	354.6603	7
4	374.1493	187.5783			G	669.3025	335.1549	652.2759	326.6416	651.2919	326.1496	6
5	521.2177	261.1125			F	612.2810	306.6441	595.2545	298.1309	594.2704	297.6389	5
6	592.2548	296.6310			A	465.2126	233.1099	448.1860	224.5967	447.2020	224.1047	4
7	752.2854	376.6464			C	394.1755	197.5914	377.1489	189.0781	376.1649	188.5861	3
8	839.3175	420.1624	821.3069	411.1571	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
9					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 9 ppm



RMS error 9 ppm

Mass (Da)

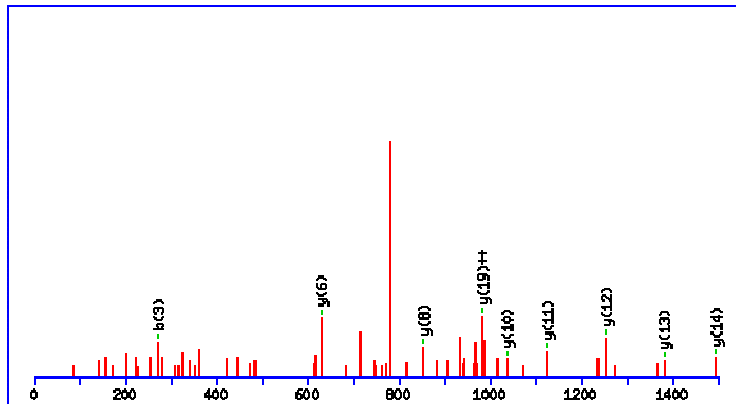
Peptide Number: 26618

MS/MS Fragmentation of **EAAVSASDILQESAIHSPGTVKEK**Found in **IPI00795249** in **IPI_human**, Tax_Id=9606 Gene_Symbol=C12orf43 Uncharacterized protein C12orf43

Match to Query 44929: 2338.177572 from(780.399800,3+) index(47895)

Title: Elution from: 116.283333333333 to 116.283333333333 period: 0 cycle: 4390 experiment: 9 polarity:+

Data file 120212ry_414C2-43_3_2.mgf



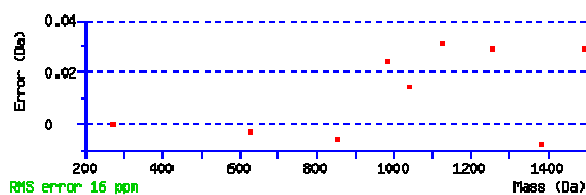
Monoisotopic mass of neutral peptide Mr(calc): 2338.1652

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

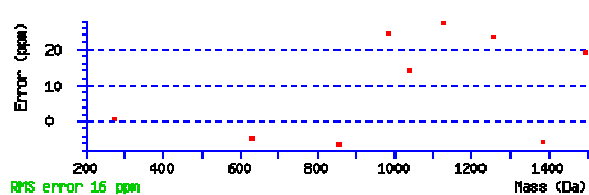
Ions Score: 43 Expect: 0.0036

Matches : 9/242 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							23
2	201.0870	101.0471			183.0764	92.0418	A	2210.1299	1105.5686	2193.1034	1097.0553	2192.1194	1096.5633	22
3	272.1241	136.5657			254.1135	127.5604	A	2139.0928	1070.0500	2122.0663	1061.5368	2121.0822	1061.0448	21
4	371.1925	186.0999			353.1819	177.0946	V	2068.0557	1034.5315	2051.0291	1026.0182	2050.0451	1025.5262	20
5	458.2245	229.6159			440.2140	220.6106	S	1968.9873	984.9973	1951.9607	976.4840	1950.9767	975.9920	19
6	529.2617	265.1345			511.2511	256.1292	A	1881.9552	941.4813	1864.9287	932.9680	1863.9447	932.4760	18
7	616.2937	308.6505			598.2831	299.6452	S	1810.9181	905.9627	1793.8916	897.4494	1792.9076	896.9574	17
8	731.3206	366.1640			713.3101	357.1587	D	1723.8861	862.4467	1706.8596	853.9334	1705.8755	853.4414	16
9	844.4047	422.7060			826.3941	413.7007	I	1608.8592	804.9332	1591.8326	796.4199	1590.8486	795.9279	15
10	957.4888	479.2480			939.4782	470.2427	L	1495.7751	748.3912	1478.7486	739.8779	1477.7645	739.3859	14
11	1085.5473	543.2773	1068.5208	534.7640	1067.5368	534.2720	Q	1382.6910	691.8492	1365.6645	683.3359	1364.6805	682.8439	13
12	1214.5899	607.7986	1197.5634	599.2853	1196.5794	598.7933	E	1254.6325	627.8199	1237.6059	619.3066	1236.6219	618.8146	12
13	1301.6220	651.3146	1284.5954	642.8013	1283.6114	642.3093	S	1125.5899	563.2986	1108.5633	554.7853	1107.5793	554.2933	11
14	1372.6591	686.8332	1355.6325	678.3199	1354.6485	677.8279	A	1038.5578	519.7826	1021.5313	511.2693	1020.5473	510.7773	10
15	1485.7431	743.3752	1468.7166	734.8619	1467.7326	734.3699	I	967.5207	484.2640	950.4942	475.7507	949.5102	475.2587	9
16	1622.8020	811.9047	1605.7755	803.3914	1604.7915	802.8994	H	854.4367	427.7220	837.4101	419.2087	836.4261	418.7167	8
17	1709.8341	855.4207	1692.8075	846.9074	1691.8235	846.4154	S	717.3777	359.1925	700.3512	350.6792	699.3672	350.1872	7
18	1806.8868	903.9471	1789.8603	895.4338	1788.8763	894.9418	P	630.3457	315.6765	613.3192	307.1632	612.3352	306.6712	6
19	1863.9083	932.4578	1846.8817	923.9445	1845.8977	923.4525	G	533.2930	267.1501	516.2664	258.6368	515.2824	258.1448	5
20	1964.9560	982.9816	1947.9294	974.4684	1946.9454	973.9763	T	476.2715	238.6394	459.2449	230.1261	458.2609	229.6341	4
21	2064.0244	1032.5158	2046.9978	1024.0026	2046.0138	1023.5106	V	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
22	2193.0670	1097.0371	2176.0404	1088.5239	2175.0564	1088.0318	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
23							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 16 ppm



RMS error 16 ppm

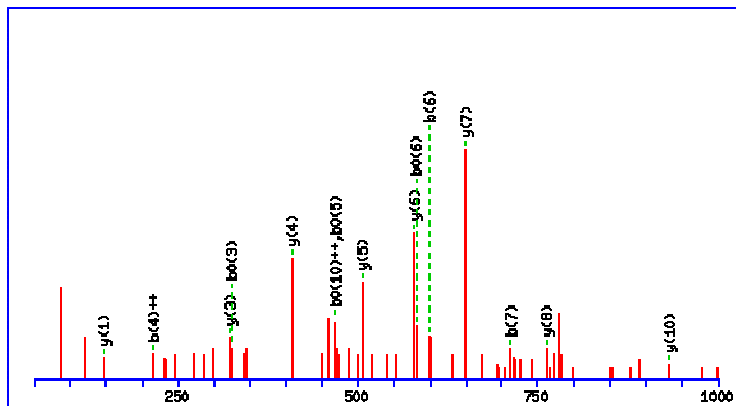
Peptide Number: 26808

MS/MS Fragmentation of **EIVSGLLAIVSSSK**Found in **IPI00400812** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SSFA2 Isoform 1 of Sperm-specific antigen 2

Match to Query 7255: 1359.747822 from(454.256550,3+) index(26337)

Title: Elution from: 70.0666666666667 to 70.0666666666667 period: 0 cycle: 2677 experiment: 1 polarity:+

Data file 120214ry_aHDF1419-P10_4_3.mgf



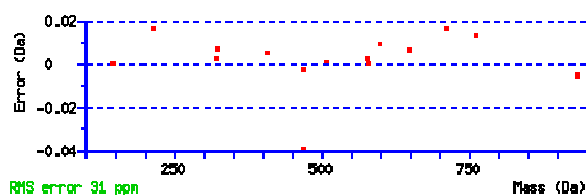
Monoisotopic mass of neutral peptide Mr(calc): 1359.7609

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

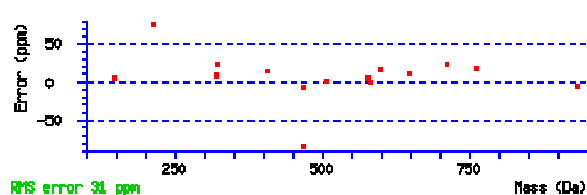
Ions Score: 47 Expect: 0.0014

Matches : 15/128 fragment ions using 28 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286	112.0393	56.5233	E							14
2	243.1339	122.0706	225.1234	113.0653	I	1231.7256	616.3665	1214.6991	607.8532	1213.7151	607.3612	13
3	342.2023	171.6048	324.1918	162.5995	V	1118.6416	559.8244	1101.6150	551.3111	1100.6310	550.8191	12
4	429.2344	215.1208	411.2238	206.1155	S	1019.5732	510.2902	1002.5466	501.7769	1001.5626	501.2849	11
5	486.2558	243.6316	468.2453	234.6263	G	932.5411	466.7742	915.5146	458.2609	914.5306	457.7689	10
6	599.3399	300.1736	581.3293	291.1683	L	875.5197	438.2635	858.4931	429.7502	857.5091	429.2582	9
7	712.4240	356.7156	694.4134	347.7103	L	762.4356	381.7214	745.4090	373.2082	744.4250	372.7162	8
8	783.4611	392.2342	765.4505	383.2289	A	649.3515	325.1794	632.3250	316.6661	631.3410	316.1741	7
9	854.4982	427.7527	836.4876	418.7475	A	578.3144	289.6608	561.2879	281.1476	560.3039	280.6556	6
10	953.5666	477.2869	935.5560	468.2817	V	507.2773	254.1423	490.2508	245.6290	489.2667	245.1370	5
11	1040.5986	520.8030	1022.5881	511.7977	S	408.2089	204.6081	391.1823	196.0948	390.1983	195.6028	4
12	1127.6307	564.3190	1109.6201	555.3137	S	321.1769	161.0921	304.1503	152.5788	303.1663	152.0868	3
13	1214.6627	607.8350	1196.6521	598.8297	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
14					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 31 ppm



RMS error 31 ppm

Mass (Da)

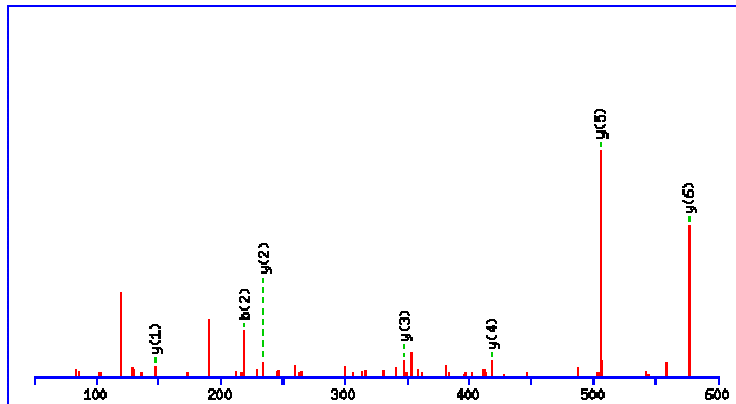
Peptide Number: 26835**MS/MS Fragmentation of FASALSK**

Found in **IPI00004511** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PFKFB3 Isoform 1 of 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3

Match to Query 3050: 722.395668 from(362.205110,2+) index(13144)

Title: Elution from: 80.2833333333333 to 80.2833333333333 period: 0 cycle: 6681 experiment: 4 polarity:+

Data file 120126ry_585A1-55_1_1.mgf



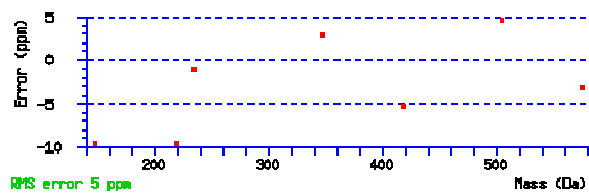
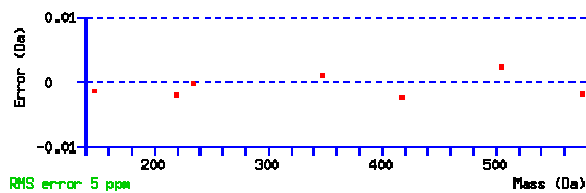
Monoisotopic mass of neutral peptide Mr(calcd): 722.3963

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 48 **Expect:** 0.00067

Matches : 7/54 fragment ions using 15 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415			F							7
2	219.1128	110.0600			A	576.3352	288.6712	559.3086	280.1579	558.3246	279.6659	6
3	306.1448	153.5761	288.1343	144.5708	S	505.2980	253.1527	488.2715	244.6394	487.2875	244.1474	5
4	377.1819	189.0946	359.1714	180.0893	A	418.2660	209.6366	401.2395	201.1234	400.2554	200.6314	4
5	490.2660	245.6366	472.2554	236.6314	L	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
6	577.2980	289.1527	559.2875	280.1474	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
7					K	147.1128	74.0600	130.0863	65.5468			1



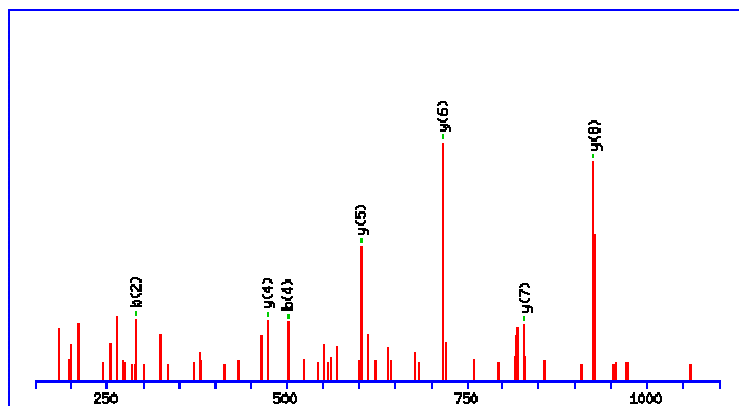
Peptide Number: 26839

MS/MS Fragmentation of **CEPIIMTVPR**Found in **IPI00867509** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CORO1C Coronin-1C_i3 protein

Match to Query 14585: 1214.616848 from(608.315700,2+) index(31792)

Title: Elution from: 83.4166666666667 to 83.4166666666667 period: 0 cycle: 3194 experiment: 9 polarity:+

Data file 120214ry_aHDF1419-P10_4_2.mgf



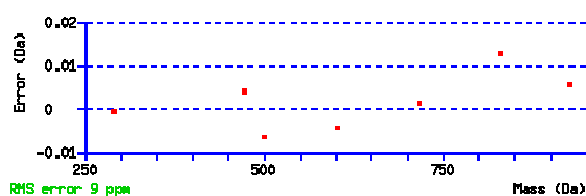
Monoisotopic mass of neutral peptide Mr(calc): 1214.6151

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

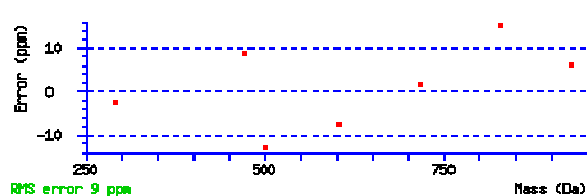
Ions Score: 39 Expect: 0.0089

Matches : 7/82 fragment ions using 9 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	161.0379	81.0226			C							10
2	290.0805	145.5439	272.0700	136.5386	E	1055.5918	528.2995	1038.5652	519.7863	1037.5812	519.2942	9
3	387.1333	194.0703	369.1227	185.0650	P	926.5492	463.7782	909.5226	455.2650	908.5386	454.7729	8
4	500.2173	250.6123	482.2068	241.6070	I	829.4964	415.2518	812.4699	406.7386	811.4859	406.2466	7
5	613.3014	307.1543	595.2908	298.1491	I	716.4124	358.7098	699.3858	350.1965	698.4018	349.7045	6
6	744.3419	372.6746	726.3313	363.6693	M	603.3283	302.1678	586.3017	293.6545	585.3177	293.1625	5
7	845.3896	423.1984	827.3790	414.1931	T	472.2878	236.6475	455.2613	228.1343	454.2772	227.6423	4
8	944.4580	472.7326	926.4474	463.7273	V	371.2401	186.1237	354.2136	177.6104			3
9	1041.5108	521.2590	1023.5002	512.2537	P	272.1717	136.5895	255.1452	128.0762			2
10					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 9 ppm



RMS error 9 ppm

Peptide Number: 27062

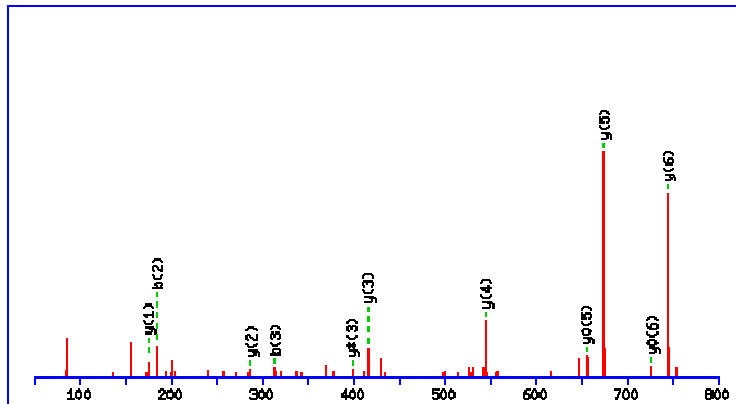
MS/MS Fragmentation of **LAEEQLR**

Found in **IPI00478834** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ARGLU1 Isoform 1 of Arginine and glutamate-rich protein 1

Match to Query 5802: 857.461128 from(429.737840,2+) index(15297)

Title: Elution from: 80.3666666666667 to 80.3666666666667 period: 0 cycle: 6684 experiment: 5 polarity:+

Data file 120124ry_414C2-43_1_1.mgf



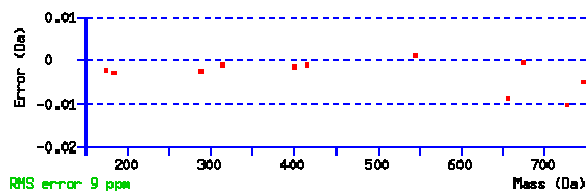
Monoisotopic mass of neutral peptide Mr(calc): 857.4606

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

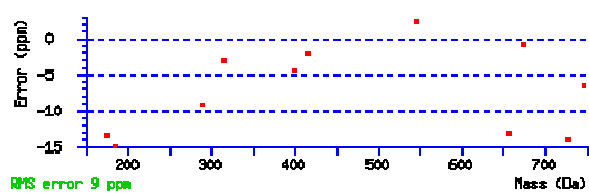
Ions Score: 42 Expect: 0.0041

Matches : 11/54 fragment ions using 21 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							7
2	185.1285	93.0679					A	745.3839	373.1956	728.3573	364.6823	727.3733	364.1903	6
3	314.1710	157.5892			296.1605	148.5839	E	674.3468	337.6770	657.3202	329.1638	656.3362	328.6717	5
4	443.2136	222.1105			425.2031	213.1052	E	545.3042	273.1557	528.2776	264.6425	527.2936	264.1504	4
5	571.2722	286.1397	554.2457	277.6265	553.2617	277.1345	Q	416.2616	208.6344	399.2350	200.1212			3
6	684.3563	342.6818	667.3297	334.1685	666.3457	333.6765	L	288.2030	144.6051	271.1765	136.0919			2
7							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 9 ppm



RMS error 9 ppm

Peptide Number: 27159

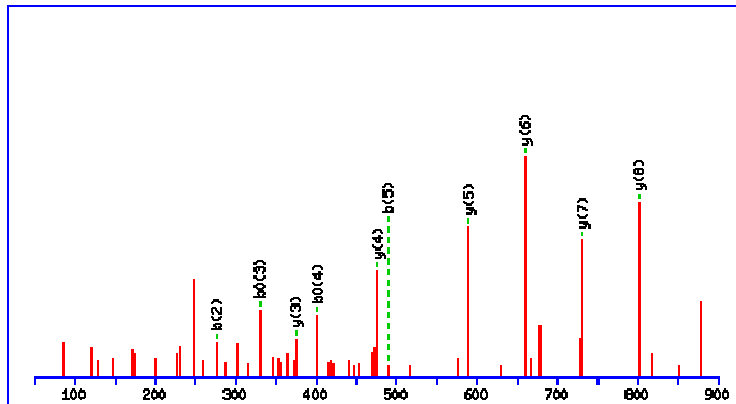
MS/MS Fragmentation of **EFAAALTAER**

Found in **IPI00171252** in **IPI_human**, Tax_Id=9606 Gene_Symbol=EZH2 Isoform 3 of Histone-lysine N-methyltransferase EZH2

Match to Query 9502: 1077.548548 from(539.781550,2+) index(13026)

Title: Elution from: 31.5833333333333 to 31.5833333333333 period: 0 cycle: 1192 experiment: 8 polarity: +

Data file 120212ry_414C2-43_3_2.mgf



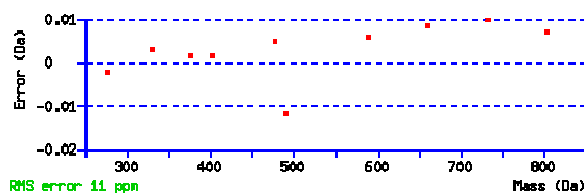
Monoisotopic mass of neutral peptide Mr(calc): 1077.5454

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

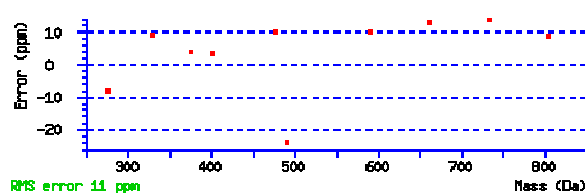
Ions Score: 44 Expect: 0.0032

Matches : 10/88 fragment ions using 16 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286	112.0393	56.5233	E							10
2	277.1183	139.0628	259.1077	130.0575	F	949.5102	475.2587	932.4836	466.7454	931.4996	466.2534	9
3	348.1554	174.5813	330.1448	165.5761	A	802.4417	401.7245	785.4152	393.2112	784.4312	392.7192	8
4	419.1925	210.0999	401.1819	201.0946	A	731.4046	366.2060	714.3781	357.6927	713.3941	357.2007	7
5	490.2296	245.6185	472.2191	236.6132	A	660.3675	330.6874	643.3410	322.1741	642.3570	321.6821	6
6	603.3137	302.1605	585.3031	293.1552	L	589.3304	295.1688	572.3039	286.6556	571.3198	286.1636	5
7	704.3614	352.6843	686.3508	343.6790	T	476.2463	238.6268	459.2198	230.1135	458.2358	229.6215	4
8	775.3985	388.2029	757.3879	379.1976	A	375.1987	188.1030	358.1721	179.5897	357.1881	179.0977	3
9	904.4411	452.7242	886.4305	443.7189	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
10					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 11 ppm



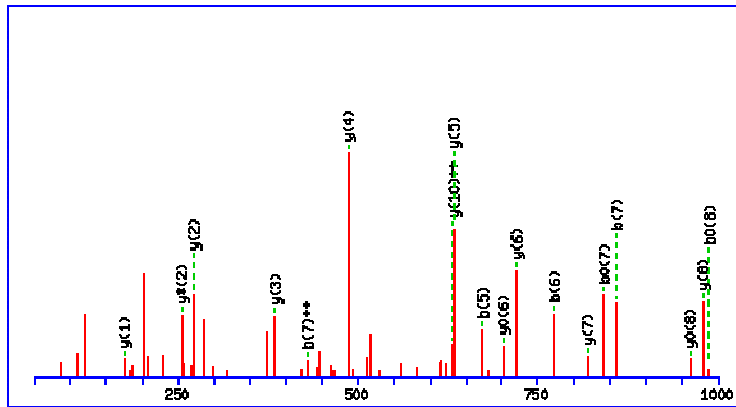
RMS error 11 ppm

Peptide Number: 27234**MS/MS Fragmentation of DLFHCVSFTLPR**Found in **IPI00025426** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PZP Isoform 1 of Pregnancy zone protein

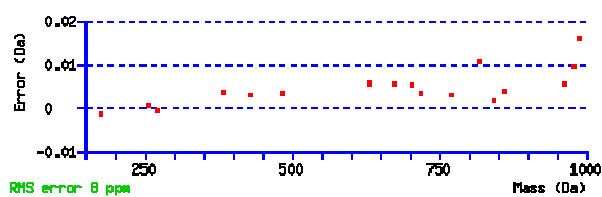
Match to Query 9237: 1490.736972 from(497.919600,3+) index(25628)

Title: Elution from: 71.2333333333333 to 71.2333333333333 period: 0 cycle: 2740 experiment: 2 polarity:+

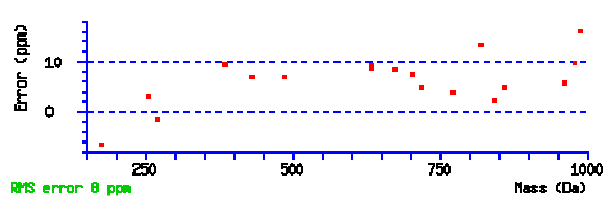
Data file 120208ry_Tig120slc-P8_1_3.mgf

**Monoisotopic mass of neutral peptide Mr(calc):** 1490.7340**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 58 **Expect:** 0.00013**Matches :** 18/104 fragment ions using 27 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	98.0237	49.5155	D							12
2	229.1183	115.0628	211.1077	106.0575	L	1376.7144	688.8608	1359.6878	680.3475	1358.7038	679.8555	11
3	376.1867	188.5970	358.1761	179.5917	F	1263.6303	632.3188	1246.6037	623.8055	1245.6197	623.3135	10
4	513.2456	257.1264	495.2350	248.1212	H	1116.5619	558.7846	1099.5353	550.2713	1098.5513	549.7793	9
5	673.2763	337.1418	655.2657	328.1365	C	979.5030	490.2551	962.4764	481.7418	961.4924	481.2498	8
6	772.3447	386.6760	754.3341	377.6707	V	819.4723	410.2398	802.4458	401.7265	801.4617	401.2345	7
7	859.3767	430.1920	841.3661	421.1867	S	720.4039	360.7056	703.3774	352.1923	702.3933	351.7003	6
8	1006.4451	503.7262	988.4345	494.7209	F	633.3719	317.1896	616.3453	308.6763	615.3613	308.1843	5
9	1107.4928	554.2500	1089.4822	545.2448	T	486.3035	243.6554	469.2769	235.1421	468.2929	234.6501	4
10	1220.5769	610.7921	1202.5663	601.7868	L	385.2558	193.1315	368.2292	184.6183			3
11	1317.6296	659.3184	1299.6191	650.3132	P	272.1717	136.5895	255.1452	128.0762			2
12					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 8 ppm



RMS error 8 ppm

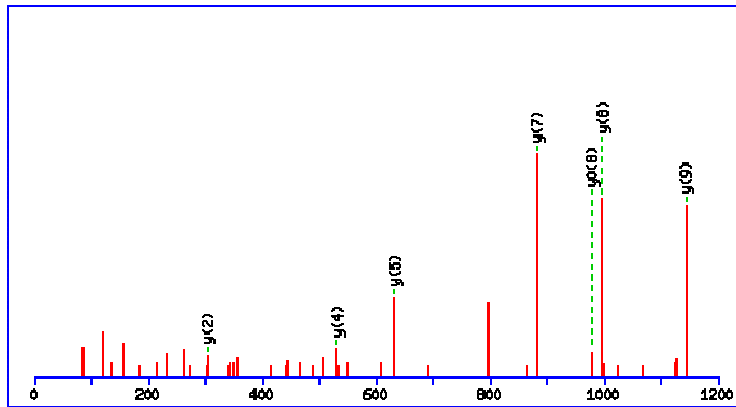
Peptide Number: 27316

MS/MS Fragmentation of **ALFDSYTNLER**Found in **IPI00299588** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ABI2 Uncharacterized protein

Match to Query 7359: 1327.637208 from(664.825880,2+) index(3452)

Title: Elution from: 8.43333333333333 to 8.43333333333333 period: 0 cycle: 317 experiment: 4 polarity: +

Data file 120210ry_32R1-32_2_3.mgf



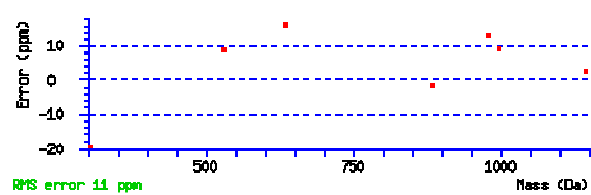
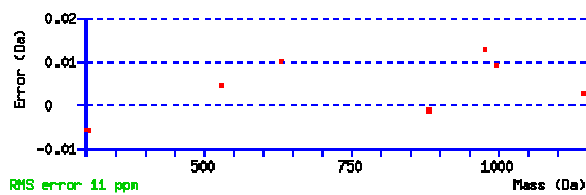
Monoisotopic mass of neutral peptide Mr(calc): 1327.6408

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 44 Expect: 0.0017

Matches : 7/98 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							11
2	185.1285	93.0679					L	1257.6110	629.3091	1240.5844	620.7959	1239.6004	620.3039	10
3	332.1969	166.6021					F	1144.5269	572.7671	1127.5004	564.2538	1126.5164	563.7618	9
4	447.2238	224.1155			429.2132	215.1103	D	997.4585	499.2329	980.4320	490.7196	979.4479	490.2276	8
5	534.2558	267.6316			516.2453	258.6263	S	882.4316	441.7194	865.4050	433.2061	864.4210	432.7141	7
6	697.3192	349.1632			679.3086	340.1579	Y	795.3995	398.2034	778.3730	389.6901	777.3890	389.1981	6
7	798.3668	399.6871			780.3563	390.6818	T	632.3362	316.6717	615.3097	308.1585	614.3256	307.6665	5
8	912.4098	456.7085	895.3832	448.1953	894.3992	447.7032	N	531.2885	266.1479	514.2620	257.6346	513.2780	257.1426	4
9	1025.4938	513.2506	1008.4673	504.7373	1007.4833	504.2453	L	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
10	1154.5364	577.7719	1137.5099	569.2586	1136.5259	568.7666	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
11							R	175.1190	88.0631	158.0924	79.5498			1



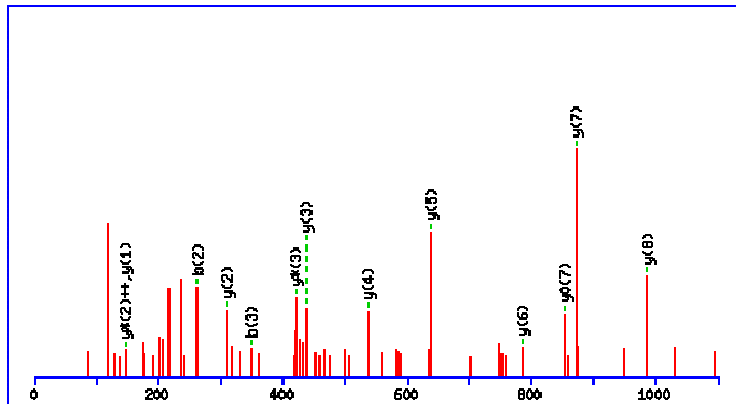
Peptide Number: 27464

MS/MS Fragmentation of **FDSFTVQYK**Found in **IPI00025276** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TNXB Isoform XB of Tenascin-X

Match to Query 11371: 1133.536828 from(567.775690,2+) index(27191)

Title: Elution from: 65.5333333333333 to 65.5333333333333 period: 0 cycle: 2487 experiment: 5 polarity:+

Data file 120212ry_aHDF1388-P9_2_2.mgf



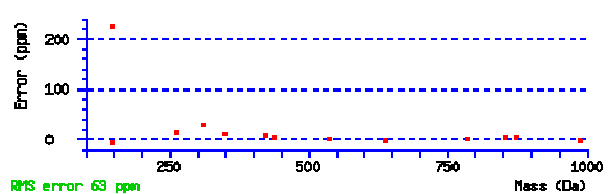
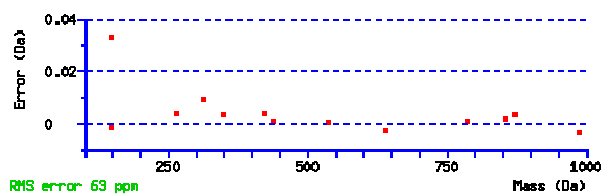
Monoisotopic mass of neutral peptide Mr(calc): 1133.5393

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 46 Expect: 0.0013

Matches : 13/74 fragment ions using 29 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415					F							9
2	263.1026	132.0550			245.0921	123.0497	D	987.4782	494.2427	970.4516	485.7295	969.4676	485.2375	8
3	350.1347	175.5710			332.1241	166.5657	S	872.4512	436.7293	855.4247	428.2160	854.4407	427.7240	7
4	497.2031	249.1052			479.1925	240.0999	F	785.4192	393.2132	768.3927	384.7000	767.4087	384.2080	6
5	598.2508	299.6290			580.2402	290.6237	T	638.3508	319.6790	621.3243	311.1658	620.3402	310.6738	5
6	697.3192	349.1632			679.3086	340.1579	V	537.3031	269.1552	520.2766	260.6419			4
7	825.3777	413.1925	808.3512	404.6792	807.3672	404.1872	Q	438.2347	219.6210	421.2082	211.1077			3
8	988.4411	494.7242	971.4145	486.2109	970.4305	485.7189	Y	310.1761	155.5917	293.1496	147.0784			2
9							K	147.1128	74.0600	130.0863	65.5468			1



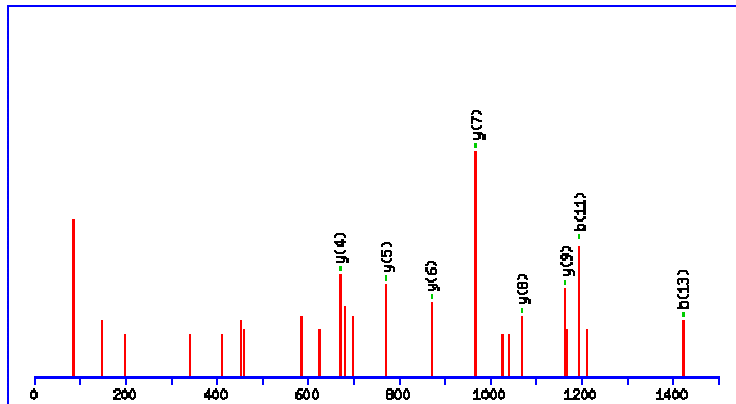
Peptide Number: 27729

MS/MS Fragmentation of **LFNSPLKPLADLPVVVTFWYR**Found in **IPI00026791** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CDK8 Isoform 1 of Cyclin-dependent kinase 8

Match to Query 26216: 2589.395022 from(864.138950,3+) index(34887)

Title: Elution from: 92.3166666666667 to 92.3166666666667 period: 0 cycle: 3516 experiment: 7 polarity: +

Data file 120210ry_32R1-32_3_4.mgf



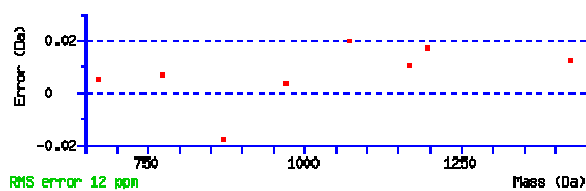
Monoisotopic mass of neutral peptide Mr(calc): 2589.3995

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

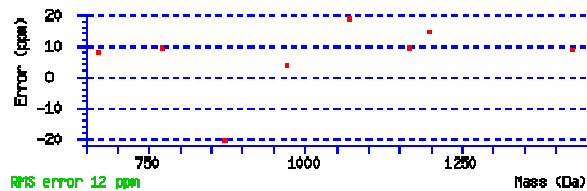
Ions Score: 36 Expect: 0.0083

Matches : 8/234 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							22
2	261.1598	131.0835					F	2477.3227	1239.1650	2460.2962	1230.6517	2459.3122	1230.1597	21
3	375.2027	188.1050	358.1761	179.5917			N	2330.2543	1165.6308	2313.2278	1157.1175	2312.2438	1156.6255	20
4	462.2347	231.6210	445.2082	223.1077	444.2241	222.6157	S	2216.2114	1108.6093	2199.1849	1100.0961	2198.2008	1099.6041	19
5	559.2875	280.1474	542.2609	271.6341	541.2769	271.1421	P	2129.1794	1065.0933	2112.1528	1056.5801	2111.1688	1056.0880	18
6	672.3715	336.6894	655.3450	328.1761	654.3610	327.6841	L	2032.1266	1016.5669	2015.1001	1008.0537	2014.1160	1007.5617	17
7	800.4665	400.7369	783.4400	392.2236	782.4559	391.7316	K	1919.0425	960.0249	1902.0160	951.5116	1901.0320	951.0196	16
8	897.5193	449.2633	880.4927	440.7500	879.5087	440.2580	P	1790.9476	895.9774	1773.9210	887.4642	1772.9370	886.9721	15
9	1010.6033	505.8053	993.5768	497.2920	992.5928	496.8000	L	1693.8948	847.4510	1676.8683	838.9378	1675.8843	838.4458	14
10	1081.6404	541.3239	1064.6139	532.8106	1063.6299	532.3186	A	1580.8108	790.9090	1563.7842	782.3957	1562.8002	781.9037	13
11	1196.6674	598.8373	1179.6408	590.3241	1178.6568	589.8320	D	1509.7736	755.3905	1492.7471	746.8772	1491.7631	746.3852	12
12	1309.7514	655.3794	1292.7249	646.8661	1291.7409	646.3741	L	1394.7467	697.8770	1377.7202	689.3637	1376.7361	688.8717	11
13	1424.7784	712.8928	1407.7518	704.3796	1406.7678	703.8876	D	1281.6626	641.3350	1264.6361	632.8217	1263.6521	632.3297	10
14	1521.8312	761.4192	1504.8046	752.9059	1503.8206	752.4139	P	1166.6357	583.8215	1149.6091	575.3082	1148.6251	574.8162	9
15	1620.8996	810.9534	1603.8730	802.4401	1602.8890	801.9481	V	1069.5829	535.2951	1052.5564	526.7818	1051.5724	526.2898	8
16	1719.9680	860.4876	1702.9414	851.9744	1701.9574	851.4823	V	970.5145	485.7609	953.4880	477.2476	952.5040	476.7556	7
17	1819.0364	910.0218	1802.0098	901.5086	1801.0258	901.0166	V	871.4461	436.2267	854.4196	427.7134	853.4355	427.2214	6
18	1920.0841	960.5457	1903.0575	952.0324	1902.0735	951.5404	T	772.3777	386.6925	755.3511	378.1792	754.3671	377.6872	5
19	2067.1525	1034.0799	2050.1259	1025.5666	2049.1419	1025.0746	F	671.3300	336.1686	654.3035	327.6554			4
20	2253.2318	1127.1195	2236.2053	1118.6063	2235.2212	1118.1143	W	524.2616	262.6344	507.2350	254.1212			3
21	2416.2951	1208.6512	2399.2686	1200.1379	2398.2846	1199.6459	Y	338.1823	169.5948	321.1557	161.0815			2
22							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 12 ppm



RMS error 12 ppm

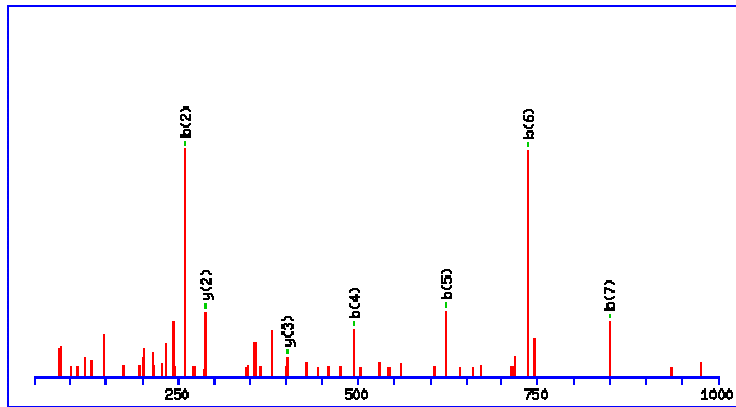
Mass (Da)

Peptide Number: 27780MS/MS Fragmentation of **KMSFEILR**Found in **IPI00397474** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ESPL1 Isoform 1 of Separin

Match to Query 1117: 1022.541208 from(512.277880,2+) index(11164)

Title: Elution from: 26.7333333333333 to 26.7333333333333 period: 0 cycle: 1012 experiment: 2 polarity: +

Data file 120208ry_Tig120slc-P8_2_3.mgf



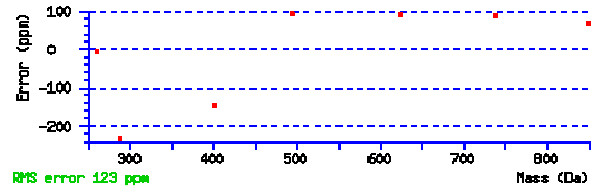
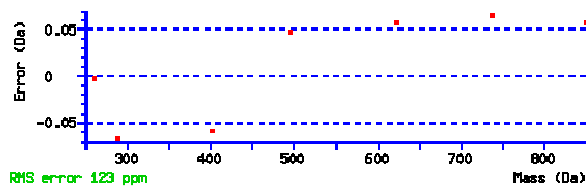
Monoisotopic mass of neutral peptide Mr(calc): 1022.5583

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 42 Expect: 0.0043

Matches : 7/74 fragment ions using 9 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.1022	65.0548	112.0757	56.5415			K							8
2	260.1427	130.5750	243.1162	122.0617			M	895.4706	448.2389	878.4441	439.7257	877.4600	439.2337	7
3	347.1748	174.0910	330.1482	165.5777	329.1642	165.0857	S	764.4301	382.7187	747.4036	374.2054	746.4196	373.7134	6
4	494.2432	247.6252	477.2166	239.1119	476.2326	238.6199	F	677.3981	339.2027	660.3715	330.6894	659.3875	330.1974	5
5	623.2858	312.1465	606.2592	303.6332	605.2752	303.1412	E	530.3297	265.6685	513.3031	257.1552	512.3191	256.6632	4
6	736.3698	368.6885	719.3433	360.1753	718.3593	359.6833	I	401.2871	201.1472	384.2605	192.6339			3
7	849.4539	425.2306	832.4273	416.7173	831.4433	416.2253	L	288.2030	144.6051	271.1765	136.0919			2
8							R	175.1190	88.0631	158.0924	79.5498			1



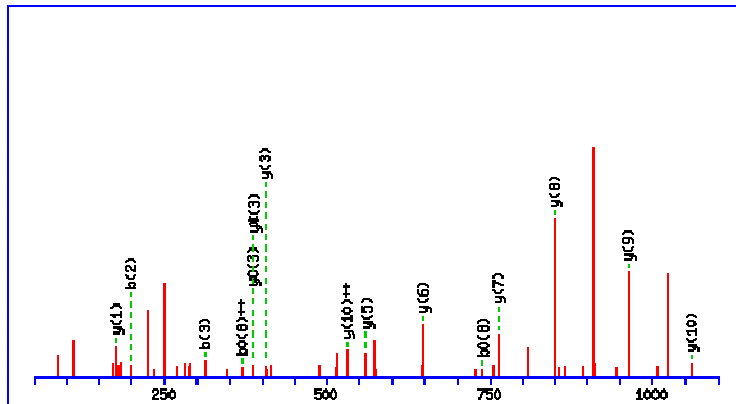
Peptide Number: 27830

MS/MS Fragmentation of **TPLSDSGVTQR**Found in **IPI00015809** in **IPI_human**, Tax_Id=9606 Gene_Symbol=OSGEP Probable tRNA threonylcarbamoyladenosine biosynthesis protein OSGEP

Match to Query 16584: 1159.569208 from(580.791880,2+) index(18485)

Title: Elution from: 86.2 to 86.2 period: 0 cycle: 8555 experiment: 8 polarity: +

Data file 120210ry_32R1-32_3_1.mgf



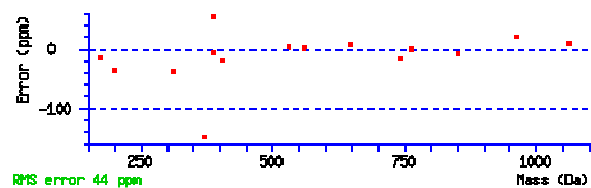
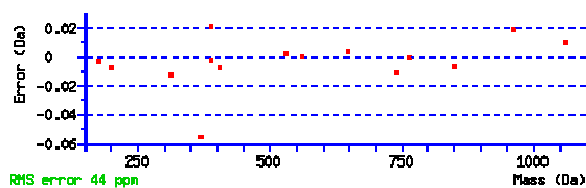
Monoisotopic mass of neutral peptide Mr(calc): 1159.5833

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 43 Expect: 0.0036

Matches : 15/98 fragment ions using 37 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							11
2	199.1077	100.0575			181.0972	91.0522	P	1059.5429	530.2751	1042.5164	521.7618	1041.5323	521.2698	10
3	312.1918	156.5995			294.1812	147.5942	L	962.4902	481.7487	945.4636	473.2354	944.4796	472.7434	9
4	399.2238	200.1155			381.2132	191.1103	S	849.4061	425.2067	832.3795	416.6934	831.3955	416.2014	8
5	514.2508	257.6290			496.2402	248.6237	D	762.3741	381.6907	745.3475	373.1774	744.3635	372.6854	7
6	601.2828	301.1450			583.2722	292.1397	S	647.3471	324.1772	630.3206	315.6639	629.3366	315.1719	6
7	658.3042	329.6558			640.2937	320.6505	G	560.3151	280.6612	543.2885	272.1479	542.3045	271.6559	5
8	757.3727	379.1900			739.3621	370.1847	V	503.2936	252.1504	486.2671	243.6372	485.2831	243.1452	4
9	858.4203	429.7138			840.4098	420.7085	T	404.2252	202.6162	387.1987	194.1030	386.2146	193.6110	3
10	986.4789	493.7431	969.4524	485.2298	968.4684	484.7378	Q	303.1775	152.0924	286.1510	143.5791			2
11							R	175.1190	88.0631	158.0924	79.5498			1



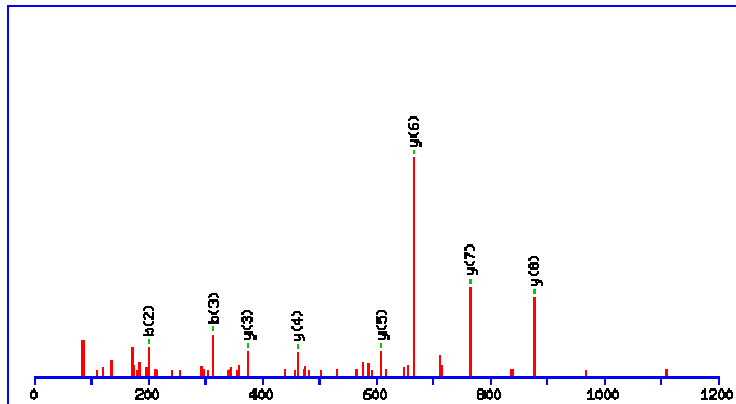
Peptide Number: 28172

MS/MS Fragmentation of **SLLVGFSLSR**Found in **IPI00299425** in **IPI_human**, Tax_Id=9606 Gene_Symbol=GPR108 Protein GPR108

Match to Query 1626: 1077.613048 from(539.813800,2+) index(16719)

Title: Elution from: 39.95 to 39.95 period: 0 cycle: 1514 experiment: 1 polarity: +

Data file 120212ry_aHDF1388-P9_2_3.mgf



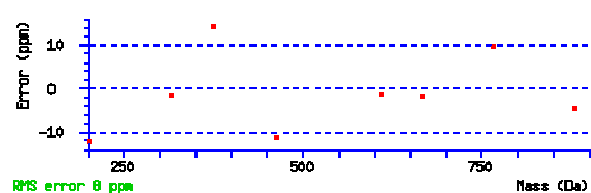
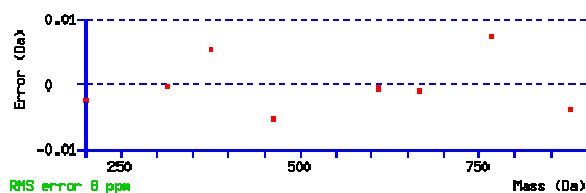
Monoisotopic mass of neutral peptide Mr(calc): 1077.6182

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 38 Expect: 0.0072

Matches : 8/88 fragment ions using 17 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233	70.0287	35.5180	S							10
2	201.1234	101.0653	183.1128	92.0600	L	991.5935	496.3004	974.5669	487.7871	973.5829	487.2951	9
3	314.2074	157.6074	296.1969	148.6021	L	878.5094	439.7584	861.4829	431.2451	860.4989	430.7531	8
4	413.2758	207.1416	395.2653	198.1363	V	765.4254	383.2163	748.3988	374.7030	747.4148	374.2110	7
5	470.2973	235.6523	452.2867	226.6470	G	666.3570	333.6821	649.3304	325.1688	648.3464	324.6768	6
6	617.3657	309.1865	599.3552	300.1812	F	609.3355	305.1714	592.3089	296.6581	591.3249	296.1661	5
7	704.3978	352.7025	686.3872	343.6972	S	462.2671	231.6372	445.2405	223.1239	444.2565	222.6319	4
8	817.4818	409.2445	799.4713	400.2393	L	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
9	904.5138	452.7606	886.5033	443.7553	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
10					R	175.1190	88.0631	158.0924	79.5498			1

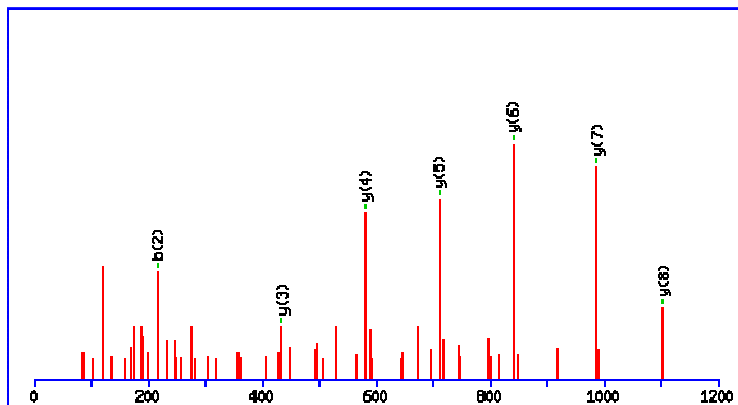


Peptide Number: 28467MS/MS Fragmentation of **TDFEFFLR**Found in **IPI01009633** in **IPI_human**, Tax_Id=9606 Gene_Symbol=UQCC cDNA FLJ55209, highly similar to Basic FGF-repressed Zic-binding protein

Match to Query 4023: 1202.554208 from(602.284380,2+) index(41219)

Title: Elution from: 100.116666666667 to 100.116666666667 period: 0 cycle: 3705 experiment: 3 polarity:+

Data file 120118ry_201B7-32_1_3.mgf

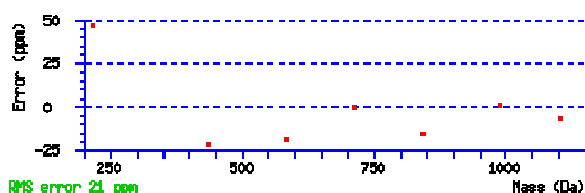
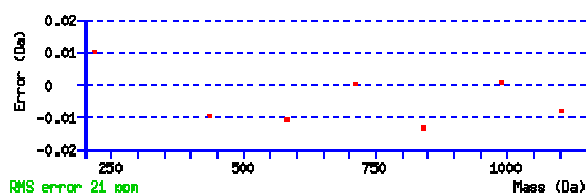
Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1202.5608

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 45 Expect: 0.0012

Matches : 7/72 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311	84.0444	42.5258	T							9
2	217.0819	109.0446	199.0713	100.0393	D	1102.5204	551.7638	1085.4938	543.2506	1084.5098	542.7585	8
3	364.1503	182.5788	346.1397	173.5735	F	987.4934	494.2504	970.4669	485.7371	969.4829	485.2451	7
4	493.1929	247.1001	475.1823	238.0948	E	840.4250	420.7162	823.3985	412.2029	822.4145	411.7109	6
5	622.2355	311.6214	604.2249	302.6161	E	711.3824	356.1949	694.3559	347.6816	693.3719	347.1896	5
6	769.3039	385.1556	751.2933	376.1503	F	582.3398	291.6736	565.3133	283.1603			4
7	916.3723	458.6898	898.3618	449.6845	F	435.2714	218.1394	418.2449	209.6261			3
8	1029.4564	515.2318	1011.4458	506.2266	L	288.2030	144.6051	271.1765	136.0919			2
9					R	175.1190	88.0631	158.0924	79.5498			1

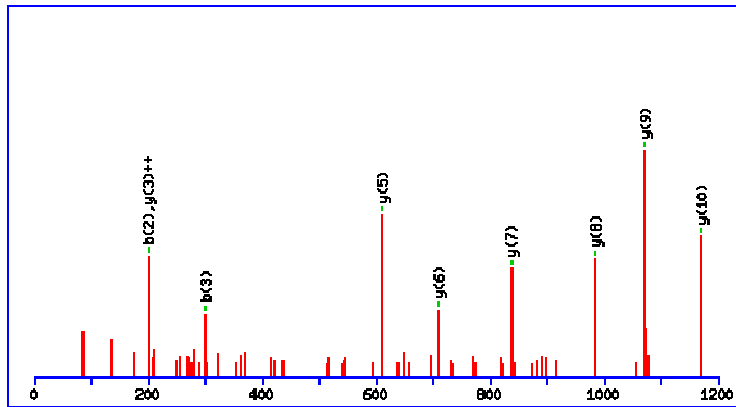


Peptide Number: 28584MS/MS Fragmentation of **EAVVSFQVPLLR**Found in **IPI00473077** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SIDT2 Isoform 1 of SID1 transmembrane family member 2

Match to Query 8702: 1469.865988 from(735.940270,2+) index(40209)

Title: Elution from: 111.733333333333 to 111.733333333333 period: 0 cycle: 4286 experiment: 8 polarity:+

Data file 120208ry_Tig120slc-P8_1_3.mgf



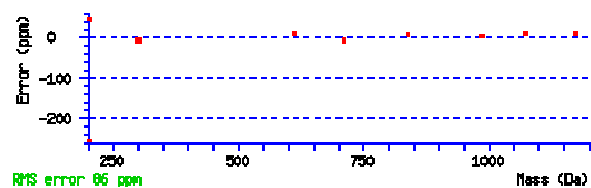
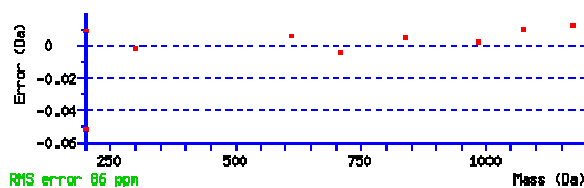
Monoisotopic mass of neutral peptide Mr(calc): 1469.8606

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 46 Expect: 0.00066

Matches : 9/116 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							13
2	201.0870	101.0471			183.0764	92.0418	A	1341.8253	671.4163	1324.7987	662.9030	1323.8147	662.4110	12
3	300.1554	150.5813			282.1448	141.5761	V	1270.7882	635.8977	1253.7616	627.3844	1252.7776	626.8924	11
4	399.2238	200.1155			381.2132	191.1103	V	1171.7198	586.3635	1154.6932	577.8502	1153.7092	577.3582	10
5	486.2558	243.6316			468.2453	234.6263	S	1072.6513	536.8293	1055.6248	528.3160	1054.6408	527.8240	9
6	633.3243	317.1658			615.3137	308.1605	F	985.6193	493.3133	968.5928	484.8000			8
7	761.3828	381.1951	744.3563	372.6818	743.3723	372.1898	Q	838.5509	419.7791	821.5244	411.2658			7
8	860.4512	430.7293	843.4247	422.2160	842.4407	421.7240	V	710.4923	355.7498	693.4658	347.2365			6
9	957.5040	479.2556	940.4775	470.7424	939.4934	470.2504	P	611.4239	306.2156	594.3974	297.7023			5
10	1070.5881	535.7977	1053.5615	527.2844	1052.5775	526.7924	L	514.3711	257.6892	497.3446	249.1759			4
11	1183.6721	592.3397	1166.6456	583.8264	1165.6616	583.3344	I	401.2871	201.1472	384.2605	192.6339			3
12	1296.7562	648.8817	1279.7297	640.3685	1278.7456	639.8765	L	288.2030	144.6051	271.1765	136.0919			2
13							R	175.1190	88.0631	158.0924	79.5498			1



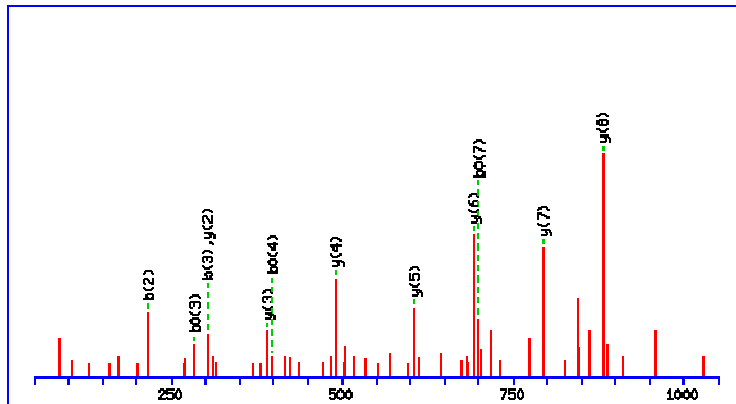
Peptide Number: 28700

MS/MS Fragmentation of **SQSLTNSLSTSDTSQR**Found in **IPI00298984** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SYN3 Synapsin-3

Match to Query 28518: 1710.802092 from(571.274640,3+) index(32443)

Title: Elution from: 116.116666666667 to 116.116666666667 period: 0 cycle: 9186 experiment: 7 polarity:+

Data file 120210ry_32R1-32_2_1.mgf



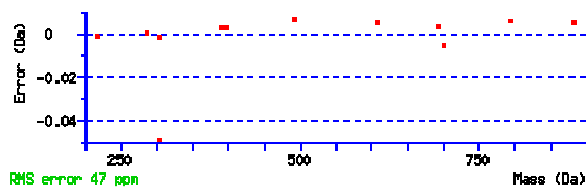
Monoisotopic mass of neutral peptide Mr(calc): 1710.8020

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

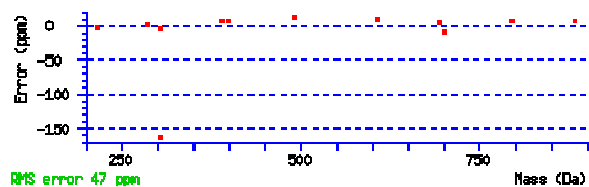
Ions Score: 43 Expect: 0.0023

Matches : 12/174 fragment ions using 19 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							16
2	216.0979	108.5526	199.0713	100.0393	198.0873	99.5473	Q	1624.7773	812.8923	1607.7507	804.3790	1606.7667	803.8870	15
3	303.1299	152.0686	286.1034	143.5553	285.1193	143.0633	S	1496.7187	748.8630	1479.6922	740.3497	1478.7081	739.8577	14
4	416.2140	208.6106	399.1874	200.0974	398.2034	199.6053	L	1409.6867	705.3470	1392.6601	696.8337	1391.6761	696.3417	13
5	517.2617	259.1345	500.2351	250.6212	499.2511	250.1292	T	1296.6026	648.8049	1279.5761	640.2917	1278.5920	639.7997	12
6	631.3046	316.1559	614.2780	307.6427	613.2940	307.1506	N	1195.5549	598.2811	1178.5284	589.7678	1177.5444	589.2758	11
7	718.3366	359.6719	701.3101	351.1587	700.3260	350.6667	S	1081.5120	541.2596	1064.4855	532.7464	1063.5014	532.2544	10
8	831.4207	416.2140	814.3941	407.7007	813.4101	407.2087	L	994.4800	497.7436	977.4534	489.2304	976.4694	488.7383	9
9	918.4527	459.7300	901.4262	451.2167	900.4421	450.7247	S	881.3959	441.2016	864.3694	432.6883	863.3854	432.1963	8
10	1019.5004	510.2538	1002.4738	501.7406	1001.4898	501.2485	T	794.3639	397.6856	777.3373	389.1723	776.3533	388.6803	7
11	1106.5324	553.7698	1089.5059	545.2566	1088.5218	544.7646	S	693.3162	347.1617	676.2897	338.6485	675.3056	338.1565	6
12	1221.5594	611.2833	1204.5328	602.7700	1203.5488	602.2780	D	606.2842	303.6457	589.2576	295.1325	588.2736	294.6404	5
13	1322.6070	661.8072	1305.5805	653.2939	1304.5965	652.8019	T	491.2572	246.1323	474.2307	237.6190	473.2467	237.1270	4
14	1409.6391	705.3232	1392.6125	696.8099	1391.6285	696.3179	S	390.2096	195.6084	373.1830	187.0951	372.1990	186.6031	3
15	1537.6976	769.3525	1520.6711	760.8392	1519.6871	760.3472	Q	303.1775	152.0924	286.1510	143.5791			2
16							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 47 ppm



RMS error 47 ppm

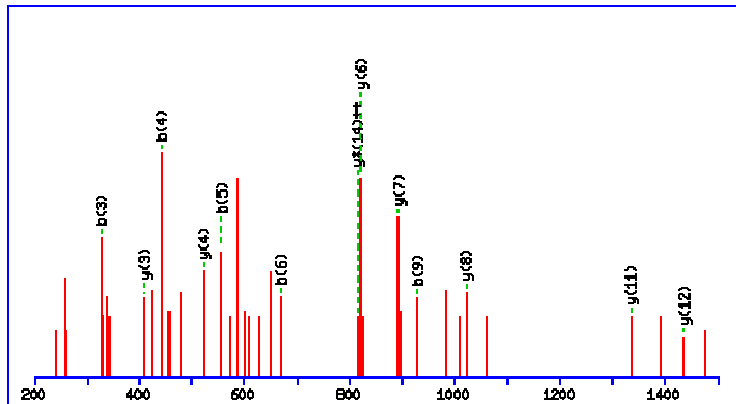
Peptide Number: 28941

MS/MS Fragmentation of **LLTDIISDGVPCSQNPTEAIEAWINFNK**Found in **IPI00334927** in **IPI_human**, Tax_Id=9606 Gene_Symbol=KBTD4 Kelch repeat and BTB domain-containing protein 4

Match to Query 37126: 3144.597252 from(1049.206360,3+) index(38623)

Title: Elution from: 97.55 to 97.55 period: 0 cycle: 3688 experiment: 8 polarity: +

Data file 120212ry_414C2-43_3_4.mgf



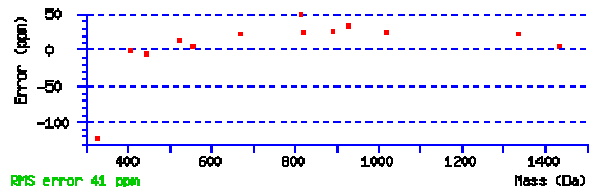
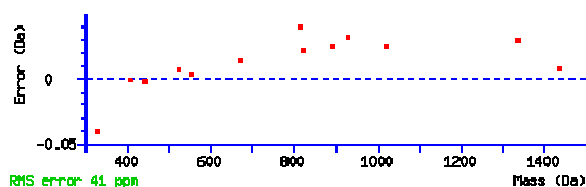
Monoisotopic mass of neutral peptide Mr(calc): 3144.5437

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 47 Expect: 0.0011

Matches : 13/280 fragment ions using 21 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							28
2	227.1754	114.0913					L	3032.4670	1516.7371	3015.4404	1508.2239	3014.4564	1507.7318	27
3	328.2231	164.6152			310.2125	155.6099	T	2919.3829	1460.1951	2902.3564	1451.6818	2901.3724	1451.1898	26
4	443.2500	222.1287			425.2395	213.1234	D	2818.3352	1409.6713	2801.3087	1401.1580	2800.3247	1400.6660	25
5	556.3341	278.6707			538.3235	269.6654	I	2703.3083	1352.1578	2686.2817	1343.6445	2685.2977	1343.1525	24
6	669.4182	335.2127			651.4076	326.2074	I	2590.2242	1295.6158	2573.1977	1287.1025	2572.2137	1286.6105	23
7	756.4502	378.7287			738.4396	369.7234	S	2477.1402	1239.0737	2460.1136	1230.5604	2459.1296	1230.0684	22
8	871.4771	436.2422			853.4666	427.2369	D	2390.1081	1195.5577	2373.0816	1187.0444	2372.0976	1186.5524	21
9	928.4986	464.7529			910.4880	455.7477	G	2275.0812	1138.0442	2258.0546	1129.5310	2257.0706	1129.0390	20
10	1027.5670	514.2871			1009.5564	505.2819	V	2218.0597	1109.5335	2201.0332	1101.0202	2200.0492	1100.5282	19
11	1124.6198	562.8135			1106.6092	553.8082	P	2118.9913	1059.9993	2101.9648	1051.4860	2100.9808	1050.9940	18
12	1284.6504	642.8288			1266.6399	633.8236	C	2021.9386	1011.4729	2004.9120	1002.9596	2003.9280	1002.4676	17
13	1371.6824	686.3449			1353.6719	677.3396	S	1861.9079	931.4576	1844.8814	922.9443	1843.8973	922.4523	16
14	1499.7410	750.3741	1482.7145	741.8609	1481.7305	741.3689	Q	1774.8759	887.9416	1757.8493	879.4283	1756.8653	878.9363	15
15	1613.7839	807.3956	1596.7574	798.8823	1595.7734	798.3903	N	1646.8173	823.9123	1629.7907	815.3990	1628.8067	814.9070	14
16	1710.8367	855.9220	1693.8102	847.4087	1692.8261	846.9167	P	1532.7744	766.8908	1515.7478	758.3775	1514.7638	757.8855	13
17	1811.8844	906.4458	1794.8578	897.9326	1793.8738	897.4406	T	1435.7216	718.3644	1418.6951	709.8512	1417.7110	709.3592	12
18	1940.9270	970.9671	1923.9004	962.4539	1922.9164	961.9618	E	1334.6739	667.8406	1317.6474	659.3273	1316.6634	658.8353	11
19	2011.9641	1006.4857	1994.9376	997.9724	1993.9535	997.4804	A	1205.6313	603.3193	1188.6048	594.8060	1187.6208	594.3140	10
20	2125.0482	1063.0277	2108.0216	1054.5144	2107.0376	1054.0224	I	1134.5942	567.8007	1117.5677	559.2875	1116.5837	558.7955	9
21	2254.0908	1127.5490	2237.0642	1119.0357	2236.0802	1118.5437	E	1021.5102	511.2587	1004.4836	502.7454	1003.4996	502.2534	8
22	2325.1279	1163.0676	2308.1013	1154.5543	2307.1173	1154.0623	A	892.4676	446.7374	875.4410	438.2241			7
23	2511.2072	1256.1072	2494.1806	1247.5940	2493.1966	1247.1019	W	821.4304	411.2189	804.4039	402.7056			6
24	2624.2912	1312.6493	2607.2647	1304.1360	2606.2807	1303.6440	I	635.3511	318.1792	618.3246	309.6659			5
25	2738.3342	1369.6707	2721.3076	1361.1575	2720.3236	1360.6654	N	522.2671	261.6372	505.2405	253.1239			4
26	2885.4026	1443.2049	2868.3760	1434.6917	2867.3920	1434.1996	F	408.2241	204.6157	391.1976	196.1024			3
27	2999.4455	1500.2264	2982.4190	1491.7131	2981.4350	1491.2211	N	261.1557	131.0815	244.1292	122.5682			2
28							K	147.1128	74.0600	130.0863	65.5468			1



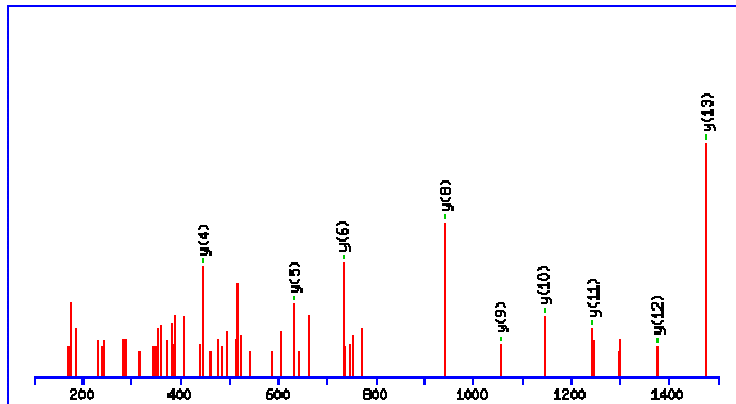
Peptide Number: 29017

MS/MS Fragmentation of **TEQGPTGVTMTSNPITWGQIK**Found in **IPI00549942** in **IPI_human**, Tax_Id=9606 Gene_Symbol=cDNA FLJ30306 fis, clone BRACE2003319

Match to Query 33629: 2245.087028 from(1123.550790,2+) index(18661)

Title: Elution from: 46.5666666666667 to 46.5666666666667 period: 0 cycle: 1753 experiment: 10 polarity:+

Data file 120210ry_32R1-32_2_3.mgf



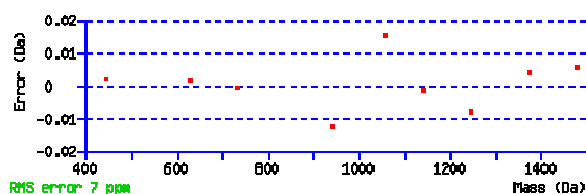
Monoisotopic mass of neutral peptide Mr(calc): 2245.1049

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

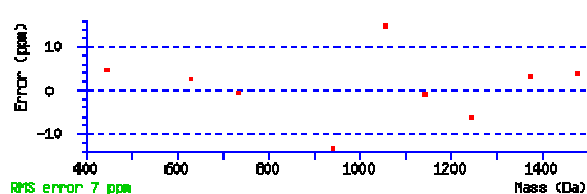
Ions Score: 66 Expect: 1.5e-005

Matches : 9/226 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							21
2	231.0975	116.0524			213.0870	107.0471	E	2145.0645	1073.0359	2128.0379	1064.5226	2127.0539	1064.0306	20
3	359.1561	180.0817	342.1296	171.5684	341.1456	171.0764	Q	2016.0219	1008.5146	1998.9953	1000.0013	1998.0113	999.5093	19
4	416.1776	208.5924	399.1510	200.0792	398.1670	199.5872	G	1887.9633	944.4853	1870.9368	935.9720	1869.9527	935.4800	18
5	513.2304	257.1188	496.2038	248.6055	495.2198	248.1135	P	1830.9418	915.9746	1813.9153	907.4613	1812.9313	906.9693	17
6	614.2780	307.6427	597.2515	299.1294	596.2675	298.6374	T	1733.8891	867.4482	1716.8625	858.9349	1715.8785	858.4429	16
7	671.2995	336.1534	654.2729	327.6401	653.2889	327.1481	G	1632.8414	816.9243	1615.8149	808.4111	1614.8308	807.9191	15
8	770.3679	385.6876	753.3414	377.1743	752.3573	376.6823	V	1575.8199	788.4136	1558.7934	779.9003	1557.8094	779.4083	14
9	871.4156	436.2114	854.3890	427.6982	853.4050	427.2062	T	1476.7515	738.8794	1459.7250	730.3661	1458.7410	729.8741	13
10	1002.4561	501.7317	985.4295	493.2184	984.4455	492.7264	M	1375.7038	688.3556	1358.6773	679.8423	1357.6933	679.3503	12
11	1103.5038	552.2555	1086.4772	543.7422	1085.4932	543.2502	T	1244.6634	622.8353	1227.6368	614.3220	1226.6528	613.8300	11
12	1190.5358	595.7715	1173.5092	587.2583	1172.5252	586.7662	S	1143.6157	572.3115	1126.5891	563.7982	1125.6051	563.3062	10
13	1304.5787	652.7930	1287.5522	644.2797	1286.5681	643.7877	N	1056.5837	528.7955	1039.5571	520.2822	1038.5731	519.7902	9
14	1401.6315	701.3194	1384.6049	692.8061	1383.6209	692.3141	P	942.5407	471.7740	925.5142	463.2607	924.5302	462.7687	8
15	1514.7155	757.8614	1497.6890	749.3481	1496.7050	748.8561	I	845.4880	423.2476	828.4614	414.7343	827.4774	414.2423	7
16	1615.7632	808.3852	1598.7367	799.8720	1597.7527	799.3800	T	732.4039	366.7056	715.3774	358.1923	714.3933	357.7003	6
17	1801.8425	901.4249	1784.8160	892.9116	1783.8320	892.4196	W	631.3562	316.1817	614.3297	307.6685			5
18	1858.8640	929.9356	1841.8374	921.4224	1840.8534	920.9304	G	445.2769	223.1421	428.2504	214.6288			4
19	1986.9226	993.9649	1969.8960	985.4516	1968.9120	984.9596	Q	388.2554	194.6314	371.2289	186.1181			3
20	2100.0066	1050.5070	2082.9801	1041.9937	2081.9961	1041.5017	I	260.1969	130.6021	243.1703	122.0888			2
21							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 7 ppm



RMS error 7 ppm

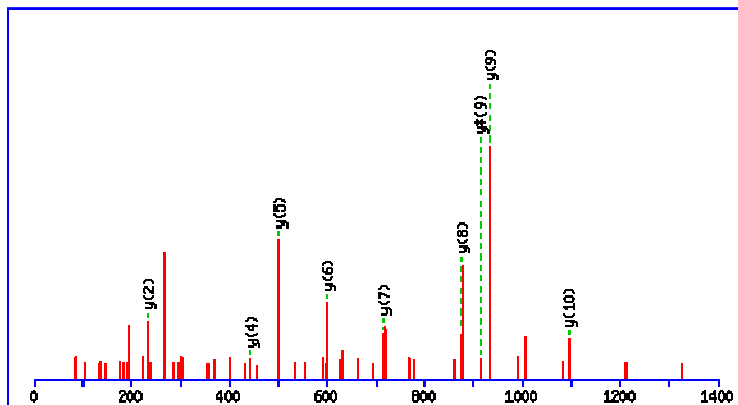
Peptide Number: 29198

MS/MS Fragmentation of **MYGCDVGPDGR**Found in **IP100651697** in **IP1_human**, Tax_Id=9606 Gene_Symbol=HLA-B;HLA-C;HLA-A;MICA;LOC441528 HLA class I histocompatibility antigen, Cw-3 alpha chain

Match to Query 18491: 1225.478308 from(613.746430,2+) index(27887)

Title: Elution from: 101.366666666667 to 101.366666666667 period: 0 cycle: 8047 experiment: 8 polarity:+

Data file 120208ry_Tig120slc-P8_2_1.mgf



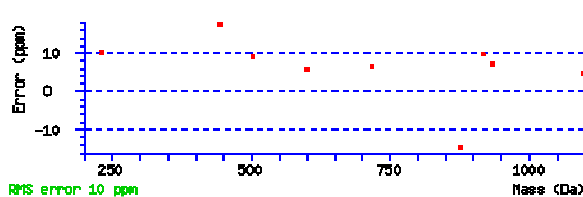
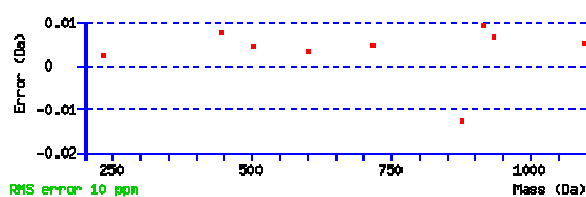
Monoisotopic mass of neutral peptide Mr(calc): 1225.4856

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 35 Expect: 0.0014

Matches : 9/88 fragment ions using 31 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	132.0478	66.5275			M							11
2	295.1111	148.0592			Y	1095.4524	548.2298	1078.4258	539.7166	1077.4418	539.2245	10
3	352.1326	176.5699			G	932.3891	466.6982	915.3625	458.1849	914.3785	457.6929	9
4	512.1632	256.5852			C	875.3676	438.1874	858.3410	429.6742	857.3570	429.1822	8
5	627.1901	314.0987	609.1796	305.0934	D	715.3369	358.1721	698.3104	349.6588	697.3264	349.1668	7
6	726.2586	363.6329	708.2480	354.6276	V	600.3100	300.6586	583.2835	292.1454	582.2994	291.6534	6
7	783.2800	392.1437	765.2695	383.1384	G	501.2416	251.1244	484.2150	242.6112	483.2310	242.1191	5
8	880.3328	440.6700	862.3222	431.6647	P	444.2201	222.6137	427.1936	214.1004	426.2096	213.6084	4
9	995.3597	498.1835	977.3492	489.1782	D	347.1674	174.0873	330.1408	165.5740	329.1568	165.0820	3
10	1052.3812	526.6942	1034.3706	517.6890	G	232.1404	116.5738	215.1139	108.0606			2
11					R	175.1190	88.0631	158.0924	79.5498			1



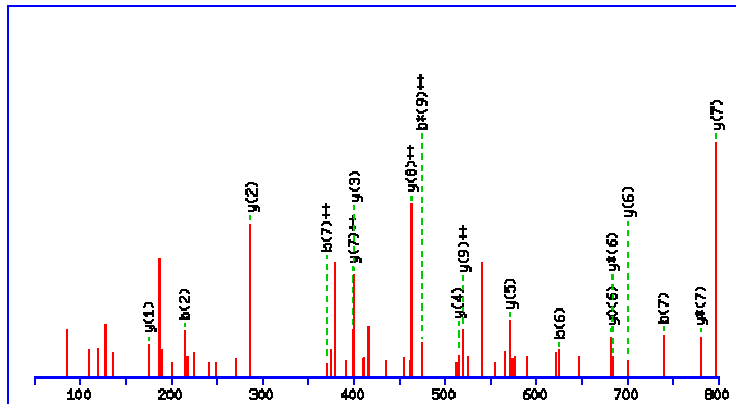
Peptide Number: 29257

MS/MS Fragmentation of **TLKPEGNLR**Found in **IPI00024567** in **IPI_human**, Tax_Id=9606 Gene_Symbol=GLTSCR2 Glioma tumor suppressor candidate region gene 2 protein

Match to Query 15151: 1139.667402 from(380.896410,3+) index(26205)

Title: Elution from: 105.083333333333 to 105.083333333333 period: 0 cycle: 9363 experiment: 3 polarity: +

Data file 120210ry_585A1-55_3_1.mgf



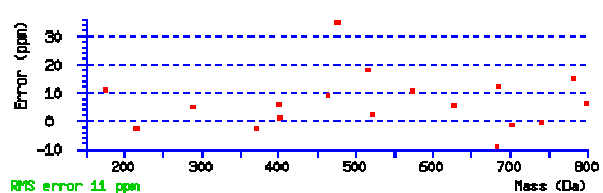
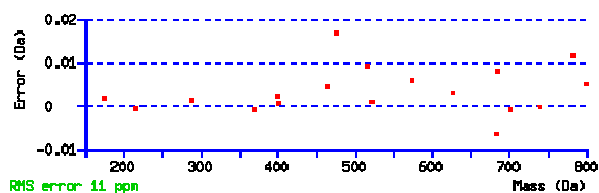
Monoisotopic mass of neutral peptide Mr(calc): 1139.6662

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 41 Expect: 0.0021

Matches : 18/94 fragment ions using 33 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							10
2	215.1390	108.0731			197.1285	99.0679	L	1039.6259	520.3166	1022.5993	511.8033	1021.6153	511.3113	9
3	343.2340	172.1206	326.2074	163.6074	325.2234	163.1153	K	926.5418	463.7745	909.5152	455.2613	908.5312	454.7693	8
4	440.2867	220.6470	423.2602	212.1337	422.2762	211.6417	P	798.4468	399.7271	781.4203	391.2138	780.4363	390.7218	7
5	569.3293	285.1683	552.3028	276.6550	551.3188	276.1630	E	701.3941	351.2007	684.3675	342.6874	683.3835	342.1954	6
6	626.3508	313.6790	609.3243	305.1658	608.3402	304.6738	G	572.3515	286.6794	555.3249	278.1661			5
7	740.3937	370.7005	723.3672	362.1872	722.3832	361.6952	N	515.3300	258.1686	498.3035	249.6554			4
8	853.4778	427.2425	836.4512	418.7293	835.4672	418.2373	I	401.2871	201.1472	384.2605	192.6339			3
9	966.5619	483.7846	949.5353	475.2713	948.5513	474.7793	L	288.2030	144.6051	271.1765	136.0919			2
10							R	175.1190	88.0631	158.0924	79.5498			1



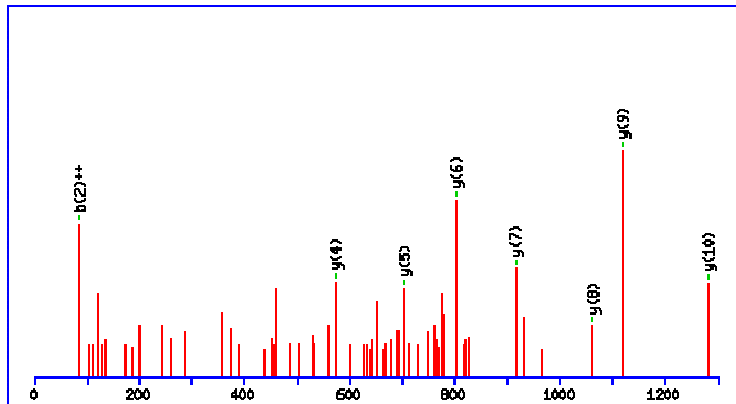
Peptide Number: 29912

MS/MS Fragmentation of **IGDVYGFLEHYVR**Found in **IPI00642186** in **IPI_human**, Tax_Id=9606 Gene_Symbol=IFT140 Intraflagellar transport protein 140 homolog

Match to Query 17832: 1665.864372 from(556.295400,3+) index(40761)

Title: Elution from: 102.766666666667 to 102.766666666667 period: 0 cycle: 3882 experiment: 2 polarity: +

Data file 120210ry_32R1-32_2_3.mgf



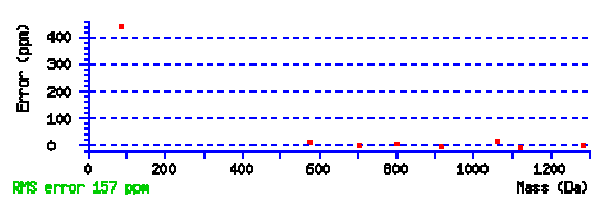
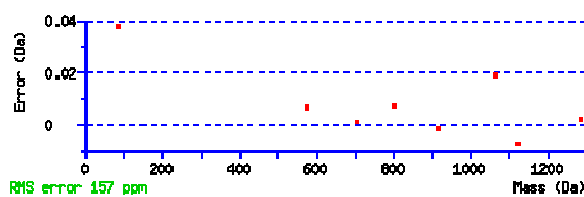
Monoisotopic mass of neutral peptide Mr(calc): 1665.8515

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 49 Expect: 0.00081

Matches : 8/118 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			I							14
2	171.1128	86.0600			G	1553.7747	777.3910	1536.7482	768.8777	1535.7641	768.3857	13
3	286.1397	143.5735	268.1292	134.5682	D	1496.7532	748.8803	1479.7267	740.3670	1478.7427	739.8750	12
4	385.2082	193.1077	367.1976	184.1024	V	1381.7263	691.3668	1364.6998	682.8535	1363.7157	682.3615	11
5	548.2715	274.6394	530.2609	265.6341	Y	1282.6579	641.8326	1265.6313	633.3193	1264.6473	632.8273	10
6	605.2930	303.1501	587.2824	294.1448	G	1119.5946	560.3009	1102.5680	551.7876	1101.5840	551.2956	9
7	752.3614	376.6843	734.3508	367.6790	F	1062.5731	531.7902	1045.5465	523.2769	1044.5625	522.7849	8
8	865.4454	433.2264	847.4349	424.2211	L	915.5047	458.2560	898.4781	449.7427	897.4941	449.2507	7
9	964.5138	482.7606	946.5033	473.7553	V	802.4206	401.7139	785.3941	393.2007	784.4100	392.7087	6
10	1093.5564	547.2819	1075.5459	538.2766	E	703.3522	352.1797	686.3257	343.6665	685.3416	343.1745	5
11	1230.6154	615.8113	1212.6048	606.8060	H	574.3096	287.6584	557.2831	279.1452			4
12	1393.6787	697.3430	1375.6681	688.3377	Y	437.2507	219.1290	420.2241	210.6157			3
13	1492.7471	746.8772	1474.7365	737.8719	V	274.1874	137.5973	257.1608	129.0840			2
14					R	175.1190	88.0631	158.0924	79.5498			1



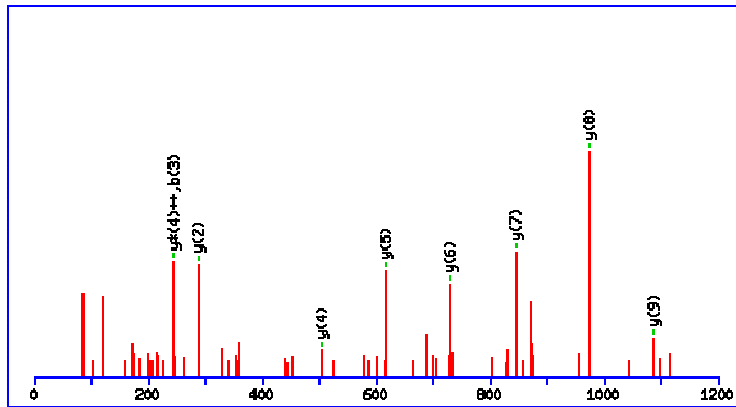
Peptide Number: 29942

MS/MS Fragmentation of **DGAIEDITDLR**Found in **IPI00044748** in **IPI_human**, Tax_Id=9606 Gene_Symbol=FMNL2 Similar to FMNL2

Match to Query 6216: 1329.679328 from(665.846940,2+) index(46106)

Title: Elution from: 115.166666666667 to 115.166666666667 period: 0 cycle: 4342 experiment: 5 polarity:+

Data file 120214ry_414C2-43_4_3.mgf



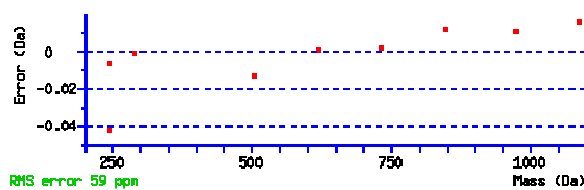
Monoisotopic mass of neutral peptide Mr(calc): 1329.6776

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

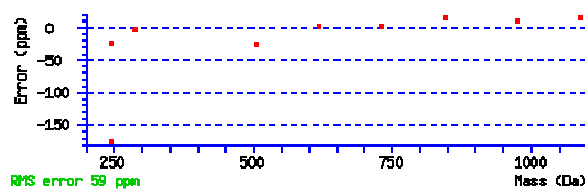
Ions Score: 59 Expect: 0.0001

Matches : 9/106 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	98.0237	49.5155	D							12
2	173.0557	87.0315	155.0451	78.0262	G	1215.6579	608.3326	1198.6314	599.8193	1197.6474	599.3273	11
3	244.0928	122.5500	226.0822	113.5448	A	1158.6365	579.8219	1141.6099	571.3086	1140.6259	570.8166	10
4	357.1769	179.0921	339.1663	170.0868	I	1087.5994	544.3033	1070.5728	535.7900	1069.5888	535.2980	9
5	486.2195	243.6134	468.2089	234.6081	E	974.5153	487.7613	957.4888	479.2480	956.5047	478.7560	8
6	601.2464	301.1268	583.2358	292.1216	D	845.4727	423.2400	828.4462	414.7267	827.4621	414.2347	7
7	714.3305	357.6689	696.3199	348.6636	I	730.4458	365.7265	713.4192	357.2132	712.4352	356.7212	6
8	827.4145	414.2109	809.4040	405.2056	I	617.3617	309.1845	600.3352	300.6712	599.3511	300.1792	5
9	928.4622	464.7347	910.4516	455.7295	T	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	4
10	1043.4891	522.2482	1025.4786	513.2429	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
11	1156.5732	578.7902	1138.5626	569.7850	L	288.2030	144.6051	271.1765	136.0919			2
12					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 59 ppm



RMS error 59 ppm

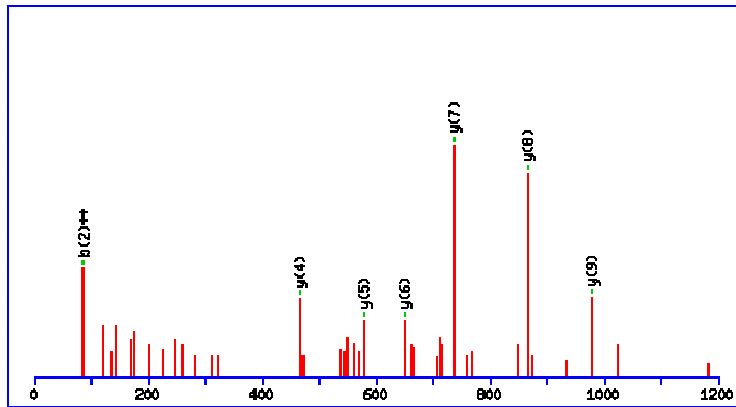
Peptide Number: 30189

MS/MS Fragmentation of **GLIESALSFGR**Found in **IPI00465048** in **IPI_human**, Tax_Id=9606 Gene_Symbol=RUFY2 Isoform 2 of RUN and FYVE domain-containing protein 2

Match to Query 2427: 1148.621268 from(575.317910,2+) index(23043)

Title: Elution from: 63.8166666666667 to 63.8166666666667 period: 0 cycle: 2455 experiment: 2 polarity:+

Data file 120208ry_Tig120slc-P8_1_3.mgf



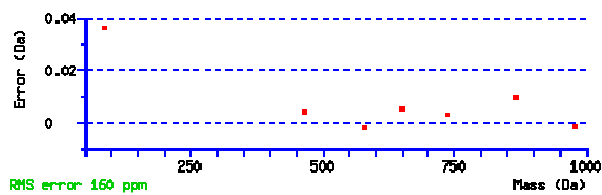
Monoisotopic mass of neutral peptide Mr(calc): 1148.6190

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

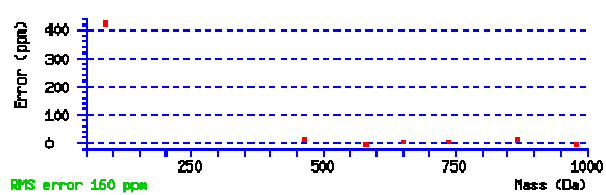
Ions Score: 48 Expect: 0.0011

Matches : 7/88 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180			G							11
2	171.1128	86.0600			L	1092.6048	546.8060	1075.5782	538.2928	1074.5942	537.8007	10
3	284.1969	142.6021			I	979.5207	490.2640	962.4942	481.7507	961.5102	481.2587	9
4	413.2395	207.1234	395.2289	198.1181	E	866.4367	433.7220	849.4101	425.2087	848.4261	424.7167	8
5	500.2715	250.6394	482.2609	241.6341	S	737.3941	369.2007	720.3675	360.6874	719.3835	360.1954	7
6	571.3086	286.1579	553.2980	277.1527	A	650.3620	325.6847	633.3355	317.1714	632.3515	316.6794	6
7	684.3927	342.7000	666.3821	333.6947	L	579.3249	290.1661	562.2984	281.6528	561.3144	281.1608	5
8	771.4247	386.2160	753.4141	377.2107	S	466.2409	233.6241	449.2143	225.1108	448.2303	224.6188	4
9	918.4931	459.7502	900.4825	450.7449	F	379.2088	190.1081	362.1823	181.5948			3
10	975.5146	488.2609	957.5040	479.2556	G	232.1404	116.5738	215.1139	108.0606			2
11					R	175.1190	88.0631	158.0924	79.5498			1



RMS error: 160 ppm



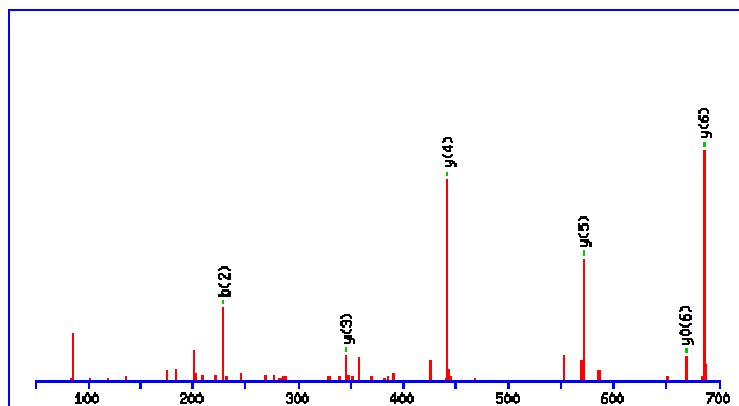
RMS error: 160 ppm

Peptide Number: 30251**MS/MS Fragmentation of LDEPLGR**Found in **IPI00376874** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CCDC33 Uncharacterized protein

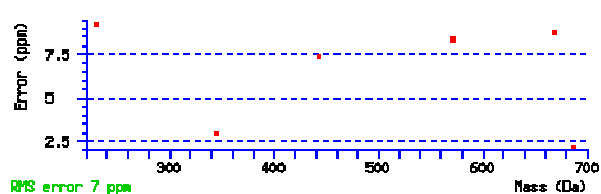
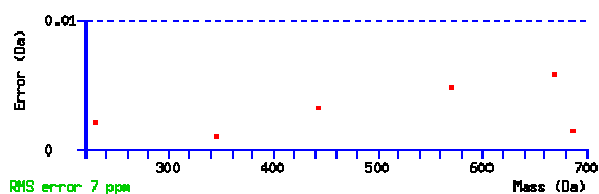
Match to Query 3797: 798.429908 from(400.222230,2+) index(18194)

Title: Elution from: 85.55 to 85.55 period: 0 cycle: 8277 experiment: 1 polarity: +

Data file 120212ry_aHDF1388-P9_2_1.mgf

**Monoisotopic mass of neutral peptide Mr(calc):** 798.4236**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 37 **Expect:** 0.0072**Matches :** 6/50 fragment ions using 7 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							7
2	229.1183	115.0628	211.1077	106.0575	D	686.3468	343.6770	669.3202	335.1638	668.3362	334.6717	6
3	358.1609	179.5841	340.1503	170.5788	E	571.3198	286.1636	554.2933	277.6503	553.3093	277.1583	5
4	455.2136	228.1105	437.2031	219.1052	P	442.2772	221.6423	425.2507	213.1290			4
5	568.2977	284.6525	550.2871	275.6472	L	345.2245	173.1159	328.1979	164.6026			3
6	625.3192	313.1632	607.3086	304.1579	G	232.1404	116.5738	215.1139	108.0606			2
7					R	175.1190	88.0631	158.0924	79.5498			1



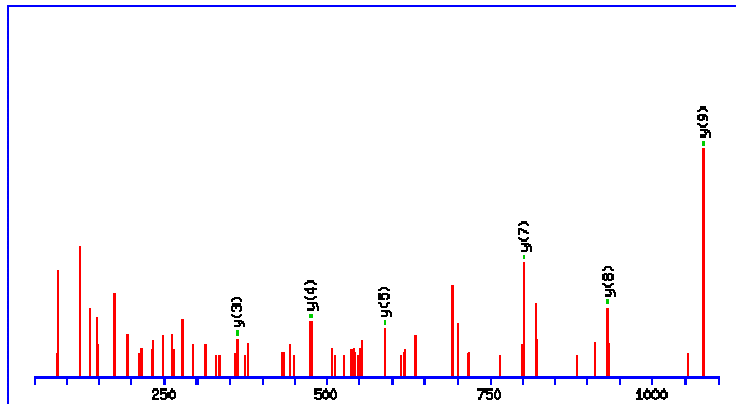
Peptide Number: 30352

MS/MS Fragmentation of **TAFETILLTK**Found in **IPI00167638** in **IPI_human**, Tax_Id=9606 Gene_Symbol=GTPBP10 Isoform 1 of GTP-binding protein 10

Match to Query 7638: 1248.725108 from(625.369830,2+) index(39069)

Title: Elution from: 98.2333333333333 to 98.2333333333333 period: 0 cycle: 3665 experiment: 3 polarity:+

Data file 120126ry_585A1-55_2_3.mgf



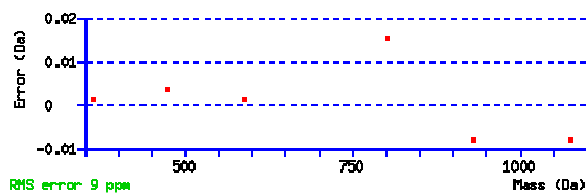
Monoisotopic mass of neutral peptide Mr(calc): 1248.7329

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

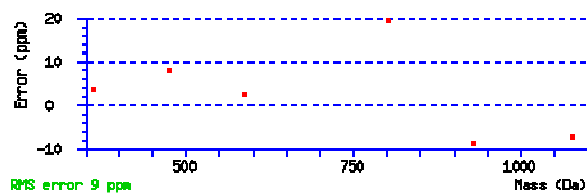
Ions Score: 40 Expect: 0.0025

Matches : 6/98 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311	84.0444	42.5258	T							11
2	173.0921	87.0497	155.0815	78.0444	A	1148.6925	574.8499	1131.6660	566.3366	1130.6820	565.8446	10
3	320.1605	160.5839	302.1499	151.5786	F	1077.6554	539.3314	1060.6289	530.8181	1059.6449	530.3261	9
4	449.2031	225.1052	431.1925	216.0999	E	930.5870	465.7971	913.5605	457.2839	912.5764	456.7919	8
5	550.2508	275.6290	532.2402	266.6237	T	801.5444	401.2758	784.5179	392.7626	783.5339	392.2706	7
6	663.3348	332.1710	645.3243	323.1658	I	700.4967	350.7520	683.4702	342.2387	682.4862	341.7467	6
7	776.4189	388.7131	758.4083	379.7078	I	587.4127	294.2100	570.3861	285.6967	569.4021	285.2047	5
8	889.5029	445.2551	871.4924	436.2498	L	474.3286	237.6679	457.3021	229.1547	456.3180	228.6627	4
9	1002.5870	501.7971	984.5764	492.7919	L	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
10	1103.6347	552.3210	1085.6241	543.3157	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
11					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 9 ppm



RMS error 9 ppm

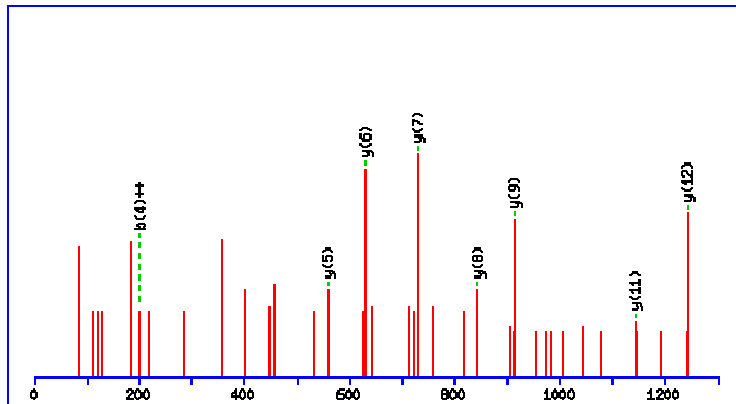
Peptide Number: 30809

MS/MS Fragmentation of **LVTSPNFVVTQALVALLADK**Found in **IPI00022479** in **IPI_human**, Tax_Id=9606 Gene_Symbol=HERC1 Uncharacterized protein

Match to Query 4164: 2098.197972 from(700.406600,3+) index(3301)

Title: Elution from: 8.9 to 8.9 period: 0 cycle: 342 experiment: 5 polarity: +

Data file 120214ry_32R1-32_4_5.mgf



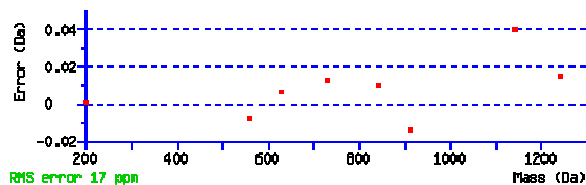
Monoisotopic mass of neutral peptide Mr(calc): 2098.2038

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

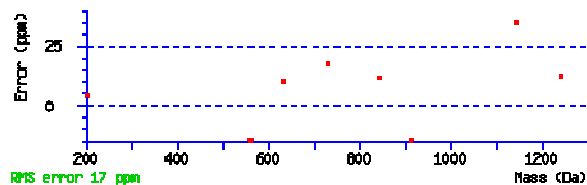
Ions Score: 46 Expect: 0.00047

Matches : 8/212 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							20
2	213.1598	107.0835					V	1986.1270	993.5671	1969.1005	985.0539	1968.1164	984.5619	19
3	314.2074	157.6074			296.1969	148.6021	T	1887.0586	944.0329	1870.0320	935.5197	1869.0480	935.0277	18
4	401.2395	201.1234			383.2289	192.1181	S	1786.0109	893.5091	1768.9844	884.9958	1768.0003	884.5038	17
5	498.2922	249.6498			480.2817	240.6445	P	1698.9789	849.9931	1681.9523	841.4798	1680.9683	840.9878	16
6	612.3352	306.6712	595.3086	298.1579	594.3246	297.6659	N	1601.9261	801.4667	1584.8996	792.9534	1583.9156	792.4614	15
7	759.4036	380.2054	742.3770	371.6921	741.3930	371.2001	F	1487.8832	744.4452	1470.8566	735.9320	1469.8726	735.4400	14
8	858.4720	429.7396	841.4454	421.2264	840.4614	420.7343	V	1340.8148	670.9110	1323.7882	662.3978	1322.8042	661.9057	13
9	957.5404	479.2738	940.5138	470.7606	939.5298	470.2686	V	1241.7464	621.3768	1224.7198	612.8635	1223.7358	612.3715	12
10	1058.5881	529.7977	1041.5615	521.2844	1040.5775	520.7924	T	1142.6780	571.8426	1125.6514	563.3293	1124.6674	562.8373	11
11	1186.6467	593.8270	1169.6201	585.3137	1168.6361	584.8217	Q	1041.6303	521.3188	1024.6037	512.8055	1023.6197	512.3135	10
12	1257.6838	629.3455	1240.6572	620.8322	1239.6732	620.3402	A	913.5717	457.2895	896.5451	448.7762	895.5611	448.2842	9
13	1370.7678	685.8876	1353.7413	677.3743	1352.7573	676.8823	L	842.5346	421.7709	825.5080	413.2577	824.5240	412.7656	8
14	1469.8362	735.4218	1452.8097	726.9085	1451.8257	726.4165	V	729.4505	365.2289	712.4240	356.7156	711.4400	356.2236	7
15	1540.8734	770.9403	1523.8468	762.4270	1522.8628	761.9350	A	630.3821	315.6947	613.3556	307.1814	612.3715	306.6894	6
16	1653.9574	827.4823	1636.9309	818.9691	1635.9469	818.4771	L	559.3450	280.1761	542.3184	271.6629	541.3344	271.1708	5
17	1767.0415	884.0244	1750.0149	875.5111	1749.0309	875.0191	L	446.2609	223.6341	429.2344	215.1208	428.2504	214.6288	4
18	1838.0786	919.5429	1821.0520	911.0297	1820.0680	910.5377	A	333.1769	167.0921	316.1503	158.5788	315.1663	158.0868	3
19	1953.1055	977.0564	1936.0790	968.5431	1935.0950	968.0511	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
20							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 17 ppm



RMS error 17 ppm

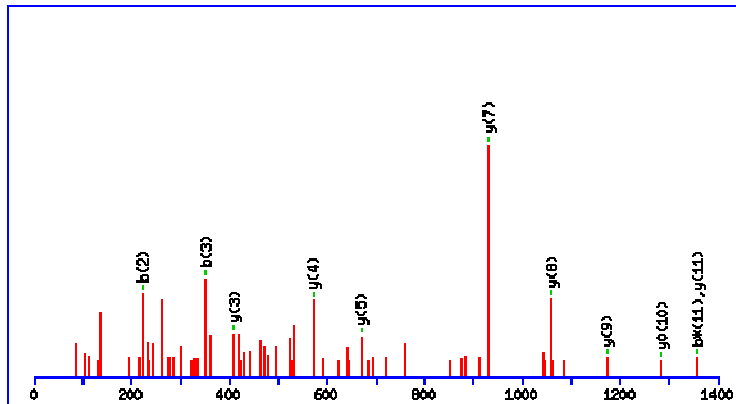
Peptide Number: 31128

MS/MS Fragmentation of **YGELEPYVYFNK**Found in **IPI00043564** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SFXN2 Sideroflexin-2

Match to Query 11280: 1520.727348 from(761.370950,2+) index(11648)

Title: Elution from: 28.8333333333333 to 28.8333333333333 period: 0 cycle: 1087 experiment: 7 polarity: +

Data file 120214ry_414C2-43_4_3.mgf



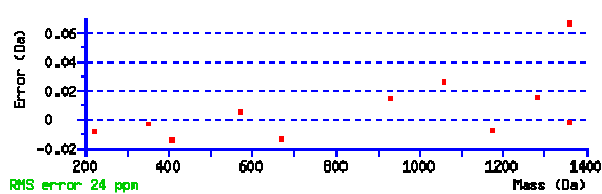
Monoisotopic mass of neutral peptide Mr(calc): 1520.7187

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

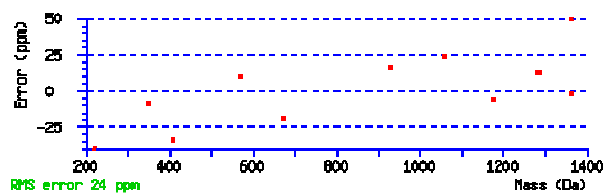
Ions Score: 56 Expect: 0.00015

Matches : 11/94 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389					Y							12
2	221.0921	111.0497					G	1358.6627	679.8350	1341.6361	671.3217	1340.6521	670.8297	11
3	350.1347	175.5710			332.1241	166.5657	E	1301.6412	651.3243	1284.6147	642.8110	1283.6307	642.3190	10
4	463.2187	232.1130			445.2082	223.1077	L	1172.5986	586.8030	1155.5721	578.2897	1154.5881	577.7977	9
5	592.2613	296.6343			574.2508	287.6290	E	1059.5146	530.2609	1042.4880	521.7477	1041.5040	521.2556	8
6	689.3141	345.1607			671.3035	336.1554	P	930.4720	465.7396	913.4454	457.2264			7
7	852.3774	426.6923			834.3668	417.6871	Y	833.4192	417.2132	816.3927	408.7000			6
8	951.4458	476.2266			933.4353	467.2213	V	670.3559	335.6816	653.3293	327.1683			5
9	1114.5092	557.7582			1096.4986	548.7529	Y	571.2875	286.1474	554.2609	277.6341			4
10	1261.5776	631.2924			1243.5670	622.2871	F	408.2241	204.6157	391.1976	196.1024			3
11	1375.6205	688.3139	1358.5939	679.8006	1357.6099	679.3086	N	261.1557	131.0815	244.1292	122.5682			2
12							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 24 ppm



RMS error 24 ppm

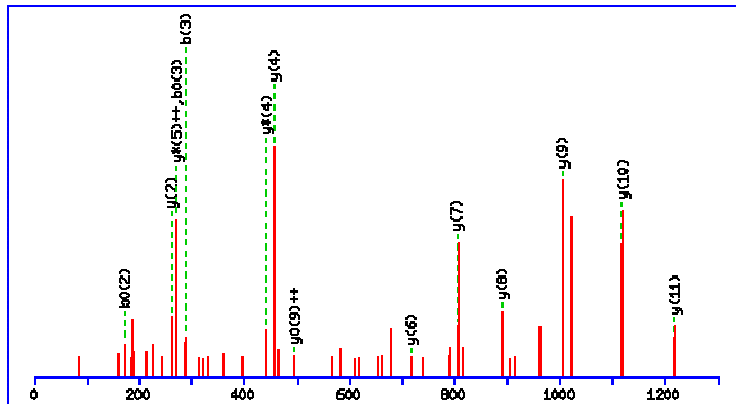
Peptide Number: 31525

MS/MS Fragmentation of **STVIDSSCPVNK**Found in **IPI00658045** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SLC2A13 Proton myo-inositol cotransporter

Match to Query 23499: 1404.689548 from(703.352050,2+) index(1128)

Title: Elution from: 2.96666666666667 to 2.96666666666667 period: 0 cycle: 114 experiment: 5 polarity: +

Data file 120212ry_aHDF1388-P9_2_2.mgf



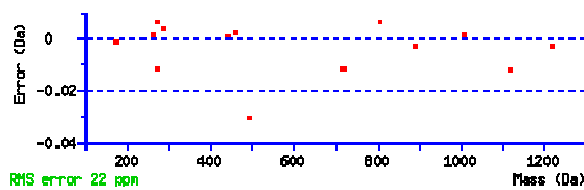
Monoisotopic mass of neutral peptide Mr(calc): 1404.6919

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

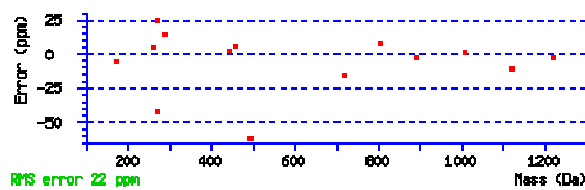
Ions Score: 52 Expect: 0.0004

Matches : 14/110 fragment ions using 24 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							13
2	189.0870	95.0471			171.0764	86.0418	T	1318.6671	659.8372	1301.6406	651.3239	1300.6566	650.8319	12
3	288.1554	144.5813			270.1448	135.5761	V	1217.6194	609.3134	1200.5929	600.8001	1199.6089	600.3081	11
4	401.2395	201.1234			383.2289	192.1181	I	1118.5510	559.7792	1101.5245	551.2659	1100.5405	550.7739	10
5	516.2664	258.6368			498.2558	249.6316	D	1005.4670	503.2371	988.4404	494.7238	987.4564	494.2318	9
6	603.2984	302.1529			585.2879	293.1476	S	890.4400	445.7237	873.4135	437.2104	872.4295	436.7184	8
7	690.3305	345.6689			672.3199	336.6636	S	803.4080	402.2076	786.3815	393.6944	785.3974	393.2024	7
8	850.3611	425.6842			832.3505	416.6789	C	716.3760	358.6916	699.3494	350.1783			6
9	949.4295	475.2184			931.4190	466.2131	V	556.3453	278.6763	539.3188	270.1630			5
10	1046.4823	523.7448			1028.4717	514.7395	P	457.2769	229.1421	440.2504	220.6288			4
11	1145.5507	573.2790			1127.5401	564.2737	V	360.2241	180.6157	343.1976	172.1024			3
12	1259.5936	630.3005	1242.5671	621.7872	1241.5831	621.2952	N	261.1557	131.0815	244.1292	122.5682			2
13							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 22 ppm



RMS error 22 ppm

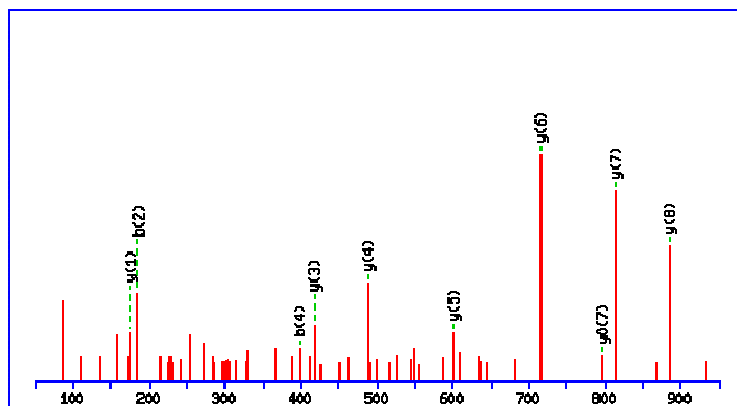
Peptide Number: 31527

MS/MS Fragmentation of **IAVNIALER**Found in **IPI00010200** in **IPI_human**, Tax_Id=9606 Gene_Symbol=YTHDC2 Probable ATP-dependent RNA helicase YTHDC2

Match to Query 6583: 997.588948 from(499.801750,2+) index(23975)

Title: Elution from: 58.3 to 58.3 period: 0 cycle: 2207 experiment: 3 polarity:+

Data file 120214ry_414C2-43_4_2.mgf



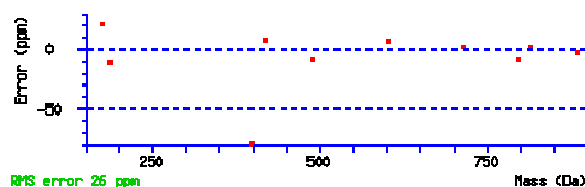
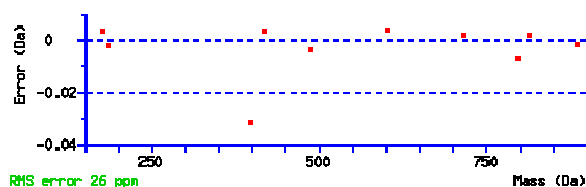
Monoisotopic mass of neutral peptide Mr(calc): 997.5920

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 45 Expect: 0.001

Matches : 10/74 fragment ions using 23 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							9
2	185.1285	93.0679					A	885.5152	443.2613	868.4887	434.7480	867.5047	434.2560	8
3	284.1969	142.6021					V	814.4781	407.7427	797.4516	399.2294	796.4676	398.7374	7
4	398.2398	199.6235	381.2132	191.1103			N	715.4097	358.2085	698.3832	349.6952	697.3991	349.2032	6
5	511.3239	256.1656	494.2973	247.6523			I	601.3668	301.1870	584.3402	292.6738	583.3562	292.1817	5
6	582.3610	291.6841	565.3344	283.1709			A	488.2827	244.6450	471.2562	236.1317	470.2722	235.6397	4
7	695.4450	348.2262	678.4185	339.7129			L	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
8	824.4876	412.7475	807.4611	404.2342	806.4771	403.7422	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
9							R	175.1190	88.0631	158.0924	79.5498			1

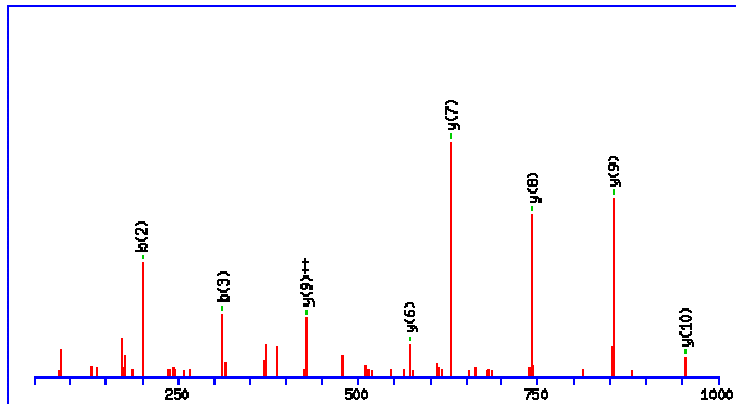


Peptide Number: 31579MS/MS Fragmentation of **VVLLGDPGVGK**Found in **IPI00289912** in **IPI_human**, Tax_Id=9606 Gene_Symbol=REM1 GTP-binding protein REM 1

Match to Query 12816: 1052.639408 from(527.326980,2+) index(17665)

Title: Elution from: 82.7166666666667 to 82.7166666666667 period: 0 cycle: 8138 experiment: 3 polarity:+

Data file 120212ry_414C2-43_3_1.mgf



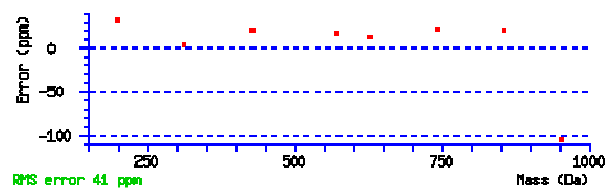
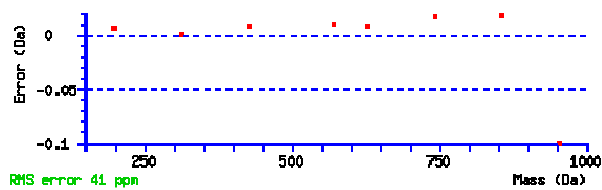
Monoisotopic mass of neutral peptide Mr(calc): 1052.6230

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 45 Expect: 0.0005

Matches : 8/80 fragment ions using 9 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415			V							11
2	199.1441	100.0757			V	954.5619	477.7846	937.5353	469.2713	936.5513	468.7793	10
3	312.2282	156.6177			L	855.4934	428.2504	838.4669	419.7371	837.4829	419.2451	9
4	425.3122	213.1598			L	742.4094	371.7083	725.3828	363.1951	724.3988	362.7030	8
5	482.3337	241.6705			G	629.3253	315.1663	612.2988	306.6530	611.3148	306.1610	7
6	597.3606	299.1840	579.3501	290.1787	D	572.3039	286.6556	555.2773	278.1423	554.2933	277.6503	6
7	694.4134	347.7103	676.4028	338.7051	P	457.2769	229.1421	440.2504	220.6288			5
8	751.4349	376.2211	733.4243	367.2158	G	360.2241	180.6157	343.1976	172.1024			4
9	850.5033	425.7553	832.4927	416.7500	V	303.2027	152.1050	286.1761	143.5917			3
10	907.5247	454.2660	889.5142	445.2607	G	204.1343	102.5708	187.1077	94.0575			2
11					K	147.1128	74.0600	130.0863	65.5468			1



Peptide Number: 31790

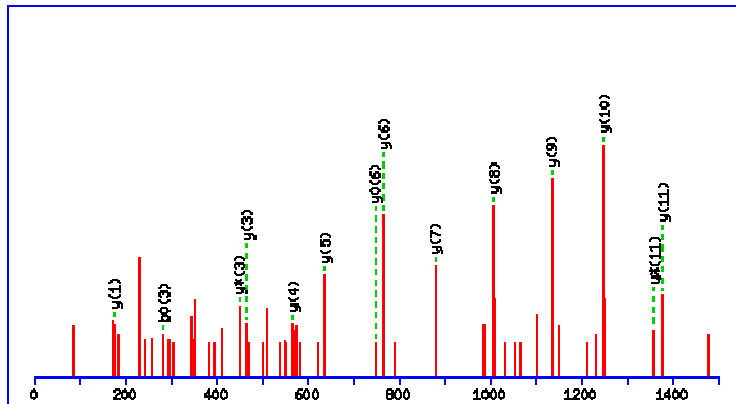
MS/MS Fragmentation of **SLTELQLEAVYER**

Found in **IPI00149849** in **IPI_human**, Tax_Id=9606 Gene_Symbol=COG4 conserved oligomeric Golgi complex subunit 4 isoform 1

Match to Query 18292: 1678.846988 from(840.430770,2+) index(37034)

Title: Elution from: 93.3833333333333 to 93.3833333333333 period: 0 cycle: 3528 experiment: 7 polarity:+

Data file 120210ry_32R1-32_2_3.mgf



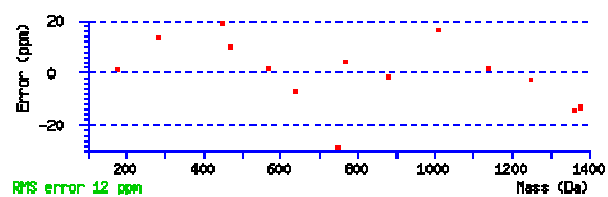
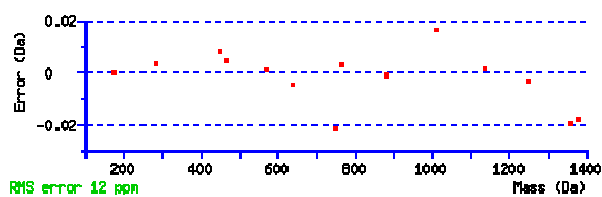
Monoisotopic mass of neutral peptide Mr(calc): 1678.8413

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 66 Expect: 2e-005

Matches : 14/144 fragment ions using 25 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							14
2	201.1234	101.0653			183.1128	92.0600	L	1592.8166	796.9120	1575.7901	788.3987	1574.8061	787.9067	13
3	302.1710	151.5892			284.1605	142.5839	T	1479.7326	740.3699	1462.7060	731.8566	1461.7220	731.3646	12
4	431.2136	216.1105			413.2031	207.1052	E	1378.6849	689.8461	1361.6583	681.3328	1360.6743	680.8408	11
5	544.2977	272.6525			526.2871	263.6472	L	1249.6423	625.3248	1232.6157	616.8115	1231.6317	616.3195	10
6	672.3563	336.6818	655.3297	328.1685	654.3457	327.6765	Q	1136.5582	568.7828	1119.5317	560.2695	1118.5477	559.7775	9
7	801.3989	401.2031	784.3723	392.6898	783.3883	392.1978	E	1008.4997	504.7535	991.4731	496.2402	990.4891	495.7482	8
8	914.4829	457.7451	897.4564	449.2318	896.4724	448.7398	L	879.4571	440.2322	862.4305	431.7189	861.4465	431.2269	7
9	1043.5255	522.2664	1026.4990	513.7531	1025.5150	513.2611	E	766.3730	383.6901	749.3464	375.1769	748.3624	374.6849	6
10	1114.5626	557.7850	1097.5361	549.2717	1096.5521	548.7797	A	637.3304	319.1688	620.3039	310.6556	619.3198	310.1636	5
11	1213.6311	607.3192	1196.6045	598.8059	1195.6205	598.3139	V	566.2933	283.6503	549.2667	275.1370	548.2827	274.6450	4
12	1376.6944	688.8508	1359.6678	680.3376	1358.6838	679.8456	Y	467.2249	234.1161	450.1983	225.6028	449.2143	225.1108	3
13	1505.7370	753.3721	1488.7104	744.8589	1487.7264	744.3668	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
14							R	175.1190	88.0631	158.0924	79.5498			1



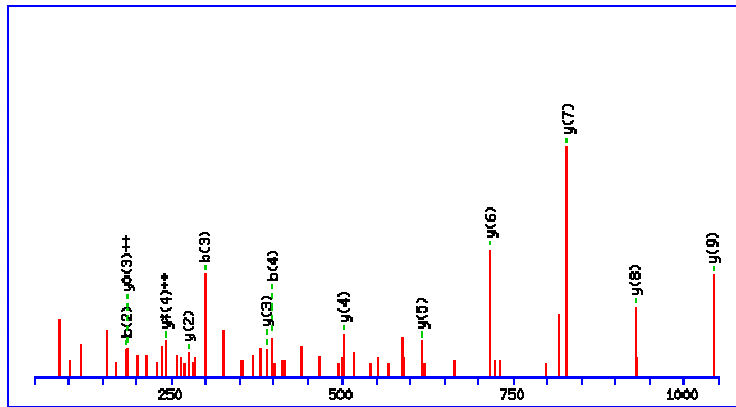
Peptide Number: 31904

MS/MS Fragmentation of **ALNVIVDLLEK**Found in **IPI00002311** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SCRN3 SCR3 protein

Match to Query 499: 1225.718568 from(613.866560,2+) index(1256)

Title: Elution from: 3.01666666666667 to 3.01666666666667 period: 0 cycle: 114 experiment: 4 polarity: +

Data file 120212ry_aHDF1388-P9_3_4.mgf



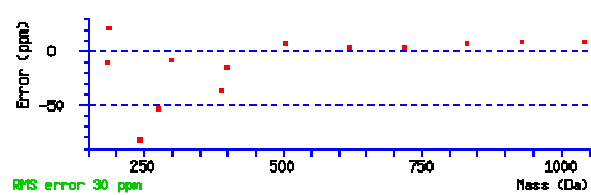
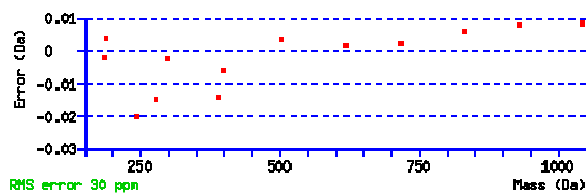
Monoisotopic mass of neutral peptide Mr(calc): 1225.7282

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 41 Expect: 0.002

Matches : 13/102 fragment ions using 34 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							11
2	185.1285	93.0679					L	1155.6984	578.3528	1138.6718	569.8395	1137.6878	569.3475	10
3	299.1714	150.0893	282.1448	141.5761			N	1042.6143	521.8108	1025.5877	513.2975	1024.6037	512.8055	9
4	398.2398	199.6235	381.2132	191.1103			V	928.5714	464.7893	911.5448	456.2760	910.5608	455.7840	8
5	511.3239	256.1656	494.2973	247.6523			I	829.5029	415.2551	812.4764	406.7418	811.4924	406.2498	7
6	610.3923	305.6998	593.3657	297.1865			V	716.4189	358.7131	699.3923	350.1998	698.4083	349.7078	6
7	725.4192	363.2132	708.3927	354.7000	707.4087	354.2080	D	617.3505	309.1789	600.3239	300.6656	599.3399	300.1736	5
8	838.5033	419.7553	821.4767	411.2420	820.4927	410.7500	L	502.3235	251.6654	485.2970	243.1521	484.3130	242.6601	4
9	951.5873	476.2973	934.5608	467.7840	933.5768	467.2920	L	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
10	1080.6299	540.8186	1063.6034	532.3053	1062.6194	531.8133	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
11							K	147.1128	74.0600	130.0863	65.5468			1



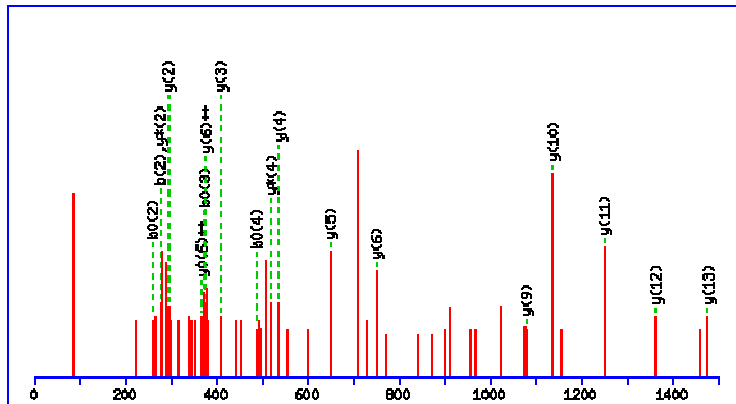
Peptide Number: 31926

MS/MS Fragmentation of **EFLDLLGDTITLQDFK**Found in **IPI00401939** in **IPI_human**, Tax_Id=9606 Gene_Symbol=RAP1GAP2 Isoform 3 of Rap1 GTPase-activating protein 2

Match to Query 11406: 1866.940308 from(934.477430,2+) index(29575)

Title: Elution from: 72.9166666666667 to 72.9166666666667 period: 0 cycle: 2746 experiment: 7 polarity:+

Data file 120214ry_32R1-32_4_4.mgf



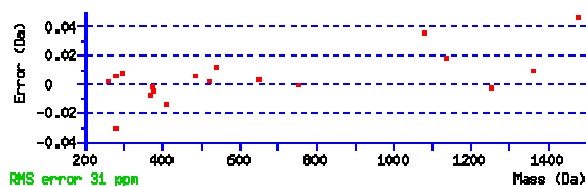
Monoisotopic mass of neutral peptide Mr(calc): 1866.9615

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

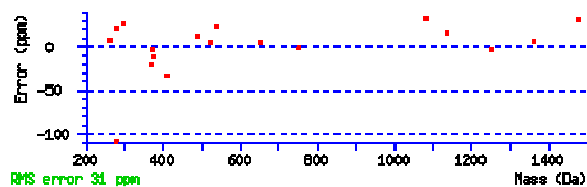
Ions Score: 40 Expect: 0.0062

Matches : 18/152 fragment ions using 43 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							16
2	277.1183	139.0628			259.1077	130.0575	F	1738.9262	869.9667	1721.8996	861.4535	1720.9156	860.9614	15
3	390.2023	195.6048			372.1918	186.5995	L	1591.8578	796.4325	1574.8312	787.9192	1573.8472	787.4272	14
4	505.2293	253.1183			487.2187	244.1130	D	1478.7737	739.8905	1461.7472	731.3772	1460.7631	730.8852	13
5	618.3134	309.6603			600.3028	300.6550	L	1363.7468	682.3770	1346.7202	673.8637	1345.7362	673.3717	12
6	731.3974	366.2023			713.3869	357.1971	L	1250.6627	625.8350	1233.6361	617.3217	1232.6521	616.8297	11
7	788.4189	394.7131			770.4083	385.7078	G	1137.5786	569.2930	1120.5521	560.7797	1119.5681	560.2877	10
8	903.4458	452.2266			885.4353	443.2213	D	1080.5572	540.7822	1063.5306	532.2689	1062.5466	531.7769	9
9	1004.4935	502.7504			986.4829	493.7451	T	965.5302	483.2688	948.5037	474.7555	947.5197	474.2635	8
10	1117.5776	559.2924			1099.5670	550.2871	I	864.4825	432.7449	847.4560	424.2316	846.4720	423.7396	7
11	1218.6252	609.8163			1200.6147	600.8110	T	751.3985	376.2029	734.3719	367.6896	733.3879	367.1976	6
12	1331.7093	666.3583			1313.6987	657.3530	L	650.3508	325.6790	633.3243	317.1658	632.3402	316.6738	5
13	1459.7679	730.3876	1442.7413	721.8743	1441.7573	721.3823	Q	537.2667	269.1370	520.2402	260.6237	519.2562	260.1317	4
14	1574.7948	787.9011	1557.7683	779.3878	1556.7843	778.8958	D	409.2082	205.1077	392.1816	196.5944	391.1976	196.1024	3
15	1721.8632	861.4353	1704.8367	852.9220	1703.8527	852.4300	F	294.1812	147.5942	277.1547	139.0810			2
16							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 31 ppm



RMS error 31 ppm

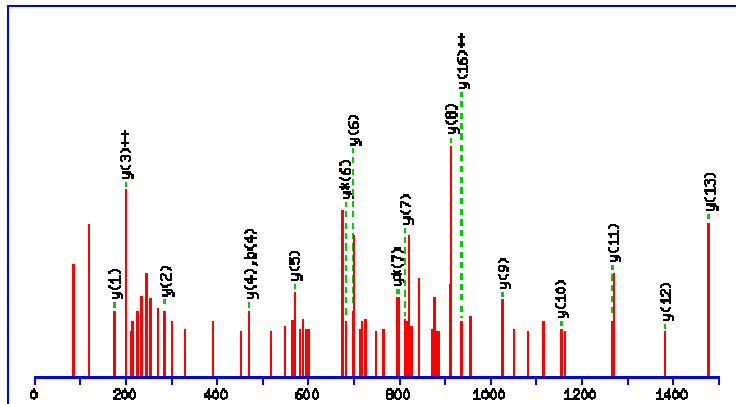
Peptide Number: 32050

MS/MS Fragmentation of **NIPFFPDQLQTDQVALLR**Found in **IPI00028611** in **IPI_human**, Tax_Id=9606 Gene_Symbol=NR2F2 COUP transcription factor 2

Match to Query 15702: 2099.140662 from(700.720830,3+) index(28475)

Title: Elution from: 74.0666666666667 to 74.0666666666667 period: 0 cycle: 2812 experiment: 3 polarity:+

Data file 120208ry_Tig120slc-P8_2_4.mgf



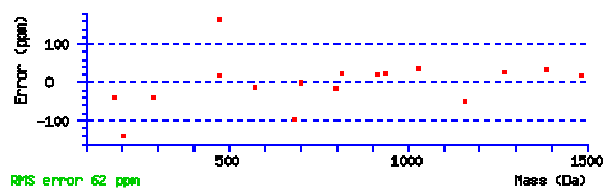
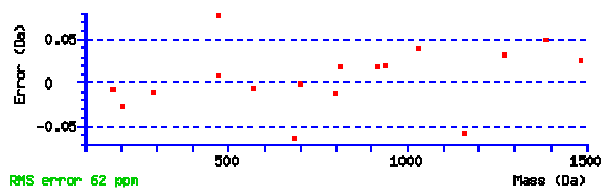
Monoisotopic mass of neutral peptide Mr(calc): 2099.1415

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 55 Expect: 0.00014

Matches : 17/180 fragment ions using 48 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							18
2	228.1343	114.5708	211.1077	106.0575			I	1986.1059	993.5566	1969.0793	985.0433	1968.0953	984.5513	17
3	325.1870	163.0972	308.1605	154.5839			P	1873.0218	937.0145	1855.9953	928.5013	1855.0112	928.0093	16
4	472.2554	236.6314	455.2289	228.1181			F	1775.9690	888.4882	1758.9425	879.9749	1757.9585	879.4829	15
5	619.3239	310.1656	602.2973	301.6523			F	1628.9006	814.9540	1611.8741	806.4407	1610.8901	805.9487	14
6	716.3766	358.6919	699.3501	350.1787			P	1481.8322	741.4197	1464.8057	732.9065	1463.8217	732.4145	13
7	831.4036	416.2054	814.3770	407.6921	813.3930	407.2001	D	1384.7795	692.8934	1367.7529	684.3801	1366.7689	683.8881	12
8	944.4876	472.7475	927.4611	464.2342	926.4771	463.7422	L	1269.7525	635.3799	1252.7260	626.8666	1251.7419	626.3746	11
9	1072.5462	536.7767	1055.5197	528.2635	1054.5356	527.7715	Q	1156.6684	578.8379	1139.6419	570.3246	1138.6579	569.8326	10
10	1185.6303	593.3188	1168.6037	584.8055	1167.6197	584.3135	I	1028.6099	514.8086	1011.5833	506.2953	1010.5993	505.8033	9
11	1286.6780	643.8426	1269.6514	635.3293	1268.6674	634.8373	T	915.5258	458.2665	898.4993	449.7533	897.5152	449.2613	8
12	1401.7049	701.3561	1384.6783	692.8428	1383.6943	692.3508	D	814.4781	407.7427	797.4516	399.2294	796.4676	398.7374	7
13	1529.7635	765.3854	1512.7369	756.8721	1511.7529	756.3801	Q	699.4512	350.2292	682.4246	341.7160			6
14	1628.8319	814.9196	1611.8053	806.4063	1610.8213	805.9143	V	571.3926	286.1999	554.3661	277.6867			5
15	1699.8690	850.4381	1682.8425	841.9249	1681.8584	841.4329	A	472.3242	236.6657	455.2976	228.1525			4
16	1812.9531	906.9802	1795.9265	898.4669	1794.9425	897.9749	L	401.2871	201.1472	384.2605	192.6339			3
17	1926.0371	963.5222	1909.0106	955.0089	1908.0266	954.5169	L	288.2030	144.6051	271.1765	136.0919			2
18							R	175.1190	88.0631	158.0924	79.5498			1

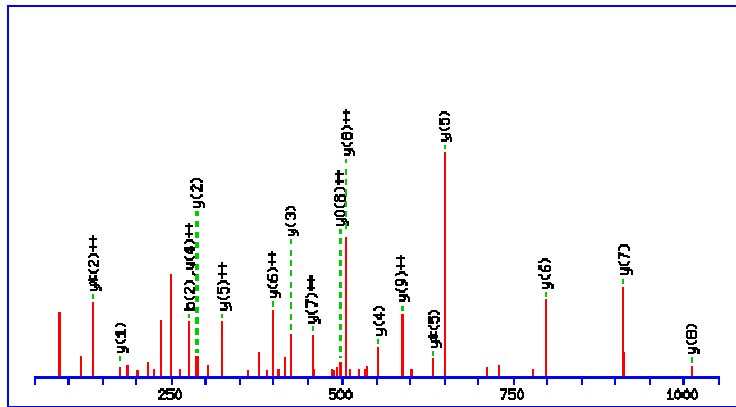


Peptide Number: 32416MS/MS Fragmentation of **LYVDFPQHRLR**Found in **IPI00030782** in **IPI_human**, Tax_Id=9606 Gene_Symbol=STAT6 Isoform 1 of Signal transducer and activator of transcription 6

Match to Query 18208: 1286.675592 from(429.899140,3+) index(42207)

Title: Elution from: 100.3 to 100.3 period: 0 cycle: 3805 experiment: 2 polarity: +

Data file 120208ry_Tig120slc-P8_2_2.mgf



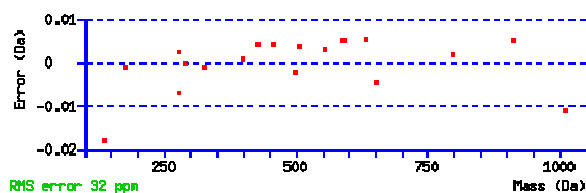
Monoisotopic mass of neutral peptide Mr(calc): 1286.6772

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

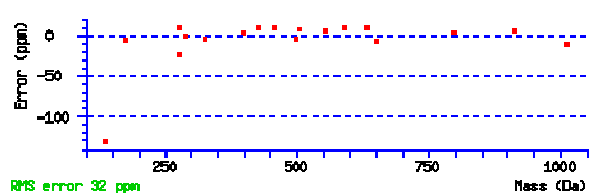
Ions Score: 53 Expect: 0.00036

Matches : 18/78 fragment ions using 31 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							10
2	277.1547	139.0810					Y	1174.6004	587.8038	1157.5738	579.2905	1156.5898	578.7985	9
3	376.2231	188.6152					V	1011.5370	506.2722	994.5105	497.7589	993.5265	497.2669	8
4	491.2500	246.1287			473.2395	237.1234	D	912.4686	456.7380	895.4421	448.2247	894.4581	447.7327	7
5	638.3184	319.6629			620.3079	310.6576	F	797.4417	399.2245	780.4151	390.7112			6
6	735.3712	368.1892			717.3606	359.1840	P	650.3733	325.6903	633.3467	317.1770			5
7	863.4298	432.2185	846.4032	423.7053	845.4192	423.2132	Q	553.3205	277.1639	536.2940	268.6506			4
8	1000.4887	500.7480	983.4621	492.2347	982.4781	491.7427	H	425.2619	213.1346	408.2354	204.6213			3
9	1113.5728	557.2900	1096.5462	548.7767	1095.5622	548.2847	L	288.2030	144.6051	271.1765	136.0919			2
10							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 32 ppm



RMS error 32 ppm

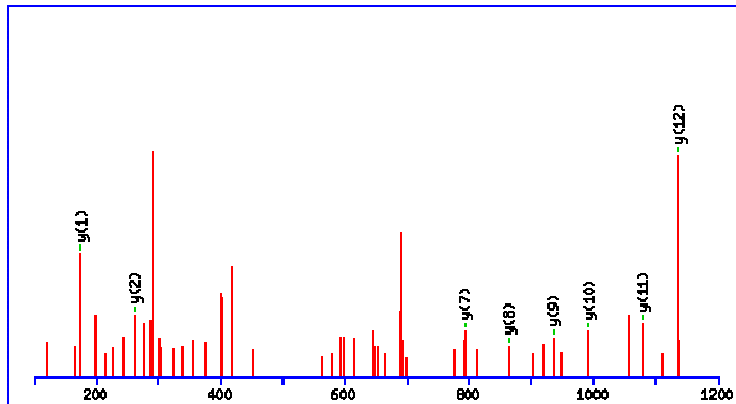
Peptide Number: 32610

MS/MS Fragmentation of **FQGSGAATETAESR**Found in **IPI00179016** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SETD1A Histone-lysine N-methyltransferase SETD1A

Match to Query 22922: 1410.655288 from(706.334920,2+) index(10388)

Title: Elution from: 65.85 to 65.85 period: 0 cycle: 7637 experiment: 10 polarity: +

Data file 120214ry_414C2-43_4_1.mgf



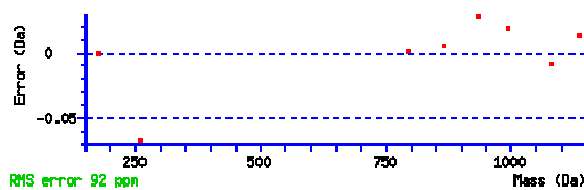
Monoisotopic mass of neutral peptide Mr(calc): 1410.6375

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

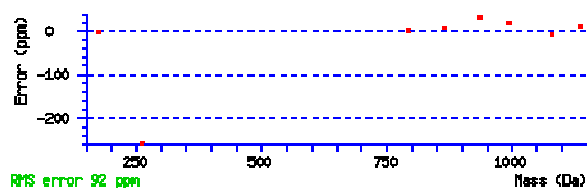
Ions Score: 40 Expect: 0.0032

Matches : 8/146 fragment ions using 21 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415					F							14
2	276.1343	138.5708	259.1077	130.0575			Q	1264.5764	632.7918	1247.5499	624.2786	1246.5658	623.7866	13
3	333.1557	167.0815	316.1292	158.5682			G	1136.5178	568.7625	1119.4913	560.2493	1118.5073	559.7573	12
4	420.1878	210.5975	403.1612	202.0842	402.1772	201.5922	S	1079.4964	540.2518	1062.4698	531.7385	1061.4858	531.2465	11
5	477.2092	239.1082	460.1827	230.5950	459.1987	230.1030	G	992.4643	496.7358	975.4378	488.2225	974.4538	487.7305	10
6	548.2463	274.6268	531.2198	266.1135	530.2358	265.6215	A	935.4429	468.2251	918.4163	459.7118	917.4323	459.2198	9
7	619.2835	310.1454	602.2569	301.6321	601.2729	301.1401	A	864.4058	432.7065	847.3792	424.1932	846.3952	423.7012	8
8	720.3311	360.6692	703.3046	352.1559	702.3206	351.6639	T	793.3686	397.1880	776.3421	388.6747	775.3581	388.1827	7
9	849.3737	425.1905	832.3472	416.6772	831.3632	416.1852	E	692.3210	346.6641	675.2944	338.1508	674.3104	337.6588	6
10	950.4214	475.7143	933.3949	467.2011	932.4108	466.7091	T	563.2784	282.1428	546.2518	273.6295	545.2678	273.1375	5
11	1021.4585	511.2329	1004.4320	502.7196	1003.4480	502.2276	A	462.2307	231.6190	445.2041	223.1057	444.2201	222.6137	4
12	1150.5011	575.7542	1133.4746	567.2409	1132.4905	566.7489	E	391.1936	196.1004	374.1670	187.5871	373.1830	187.0951	3
13	1237.5331	619.2702	1220.5066	610.7569	1219.5226	610.2649	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
14							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 92 ppm



RMS error 92 ppm

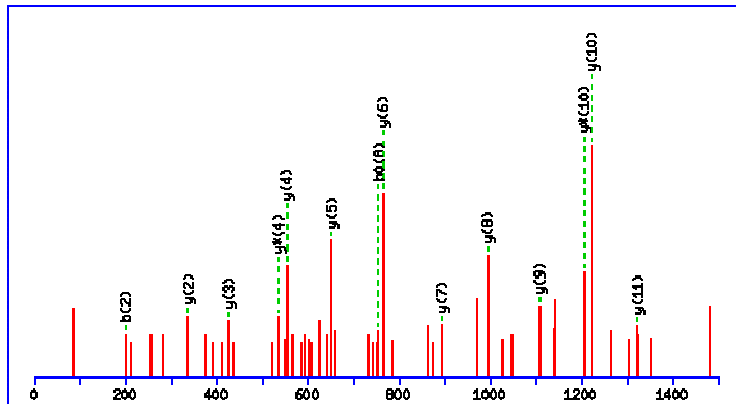
Peptide Number: 32722

MS/MS Fragmentation of **LSGLTSTLPDVTLSHLFSQEELVNNTLVQSYR**Found in **IPI00008269** in **IPI_human**, Tax_Id=9606 Gene_Symbol=NDRG4 Isoform 5 of Protein NDRG4

Match to Query 40455: 3689.860376 from(923.472370,4+) index(30801)

Title: Elution from: 81.7666666666667 to 81.7666666666667 period: 0 cycle: 3116 experiment: 6 polarity:+

Data file 120210ry_32R1-32_3_4.mgf



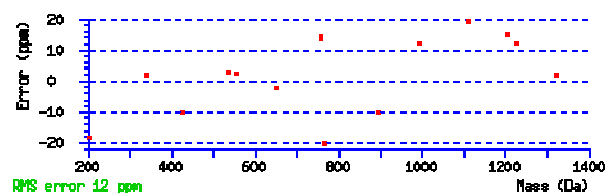
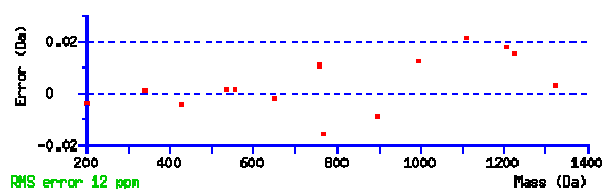
Monoisotopic mass of neutral peptide Mr(calc): 3689.8788

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 48 Expect: 0.00067

Matches : 14/342 fragment ions using 27 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							33
2	201.1234	101.0653			183.1128	92.0600	S	3577.8020	1789.4047	3560.7755	1780.8914	3559.7915	1780.3994	32
3	258.1448	129.5761			240.1343	120.5708	G	3490.7700	1745.8886	3473.7435	1737.3754	3472.7595	1736.8834	31
4	371.2289	186.1181			353.2183	177.1128	L	3433.7486	1717.3779	3416.7220	1708.8646	3415.7380	1708.3726	30
5	472.2766	236.6419			454.2660	227.6366	T	3320.6645	1660.8359	3303.6379	1652.3226	3302.6539	1651.8306	29
6	559.3086	280.1579			541.2980	271.1527	S	3219.6168	1610.3120	3202.5903	1601.7988	3201.6062	1601.3068	28
7	660.3563	330.6818			642.3457	321.6765	T	3132.5848	1566.7960	3115.5582	1558.2828	3114.5742	1557.7907	27
8	773.4403	387.2238			755.4298	378.2185	L	3031.5371	1516.2722	3014.5106	1507.7589	3013.5265	1507.2669	26
9	870.4931	435.7502			852.4825	426.7449	P	2918.4530	1459.7302	2901.4265	1451.2169	2900.4425	1450.7249	25
10	985.5201	493.2637			967.5095	484.2584	D	2821.4003	1411.2038	2804.3737	1402.6905	2803.3897	1402.1985	24
11	1086.5677	543.7875			1068.5572	534.7822	T	2706.3733	1353.6903	2689.3468	1345.1770	2688.3628	1344.6850	23
12	1185.6361	593.3217			1167.6256	584.3164	V	2605.3257	1303.1665	2588.2991	1294.6532	2587.3151	1294.1612	22
13	1298.7202	649.8637			1280.7096	640.8585	L	2506.2572	1253.6323	2489.2307	1245.1190	2488.2467	1244.6270	21
14	1385.7522	693.3798			1367.7417	684.3745	S	2393.1732	1197.0902	2376.1466	1188.5770	2375.1626	1188.0849	20
15	1522.8112	761.9092			1504.8006	752.9039	H	2306.1412	1153.5742	2289.1146	1145.0609	2288.1306	1144.5689	19
16	1635.8952	818.4512			1617.8846	809.4460	L	2169.0822	1085.0448	2152.0557	1076.5315	2151.0717	1076.0395	18
17	1782.9636	891.9855			1764.9531	882.9802	F	2055.9982	1028.5027	2038.9716	1019.9895	2037.9876	1019.4974	17
18	1869.9957	935.5015			1851.9851	926.4962	S	1908.9298	954.9685	1891.9032	946.4552	1890.9192	945.9632	16
19	1998.0542	999.5308	1981.0277	991.0175	1980.0437	990.5255	Q	1821.8977	911.4525	1804.8712	902.9392	1803.8872	902.4472	15
20	2127.0968	1064.0521	2110.0703	1055.5388	2109.0863	1055.0468	E	1693.8392	847.4232	1676.8126	838.9099	1675.8286	838.4179	14
21	2256.1394	1128.5733	2239.1129	1120.0601	2238.1289	1119.5681	E	1564.7966	782.9019	1547.7700	774.3886	1546.7860	773.8966	13
22	2369.2235	1185.1154	2352.1969	1176.6021	2351.2129	1176.1101	L	1435.7540	718.3806	1418.7274	709.8673	1417.7434	709.3753	12
23	2468.2919	1234.6496	2451.2653	1226.1363	2450.2813	1225.6443	V	1322.6699	661.8386	1305.6434	653.3253	1304.6593	652.8333	11
24	2582.3348	1291.6711	2565.3083	1283.1578	2564.3243	1282.6658	N	1223.6015	612.3044	1206.5749	603.7911	1205.5909	603.2991	10
25	2696.3778	1348.6925	2679.3512	1340.1792	2678.3672	1339.6872	N	1109.5586	555.2829	1092.5320	546.7696	1091.5480	546.2776	9
26	2797.4254	1399.2164	2780.3989	1390.7031	2779.4149	1390.2111	T	995.5156	498.2615	978.4891	489.7482	977.5051	489.2562	8
27	2926.4680	1463.7376	2909.4415	1455.2244	2908.4575	1454.7324	E	894.4680	447.7376	877.4414	439.2243	876.4574	438.7323	7
28	3039.5521	1520.2797	3022.5255	1511.7664	3021.5415	1511.2744	L	765.4254	383.2163	748.3988	374.7030	747.4148	374.2110	6
29	3138.6205	1569.8139	3121.5940	1561.3006	3120.6099	1560.8086	V	652.3413	326.6743	635.3148	318.1610	634.3307	317.6690	5
30	3266.6791	1633.8432	3249.6525	1625.3299	3248.6685	1624.8379	Q	553.2729	277.1401	536.2463	268.6268	535.2623	268.1348	4
31	3353.7111	1677.3592	3336.6846	1668.8459	3335.7005	1668.3539	S	425.2143	213.1108	408.1878	204.5975	407.2037	204.1055	3
32	3516.7744	1758.8909	3499.7479	1750.3776	3498.7639	1749.8856	Y	338.1823	169.5948	321.1557	161.0815			2
33							R	175.1190	88.0631	158.0924	79.5498			1

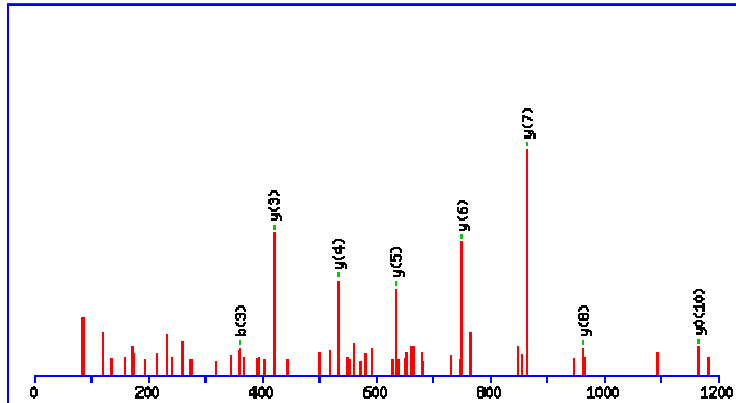


Peptide Number: 32747MS/MS Fragmentation of **FITVGYVDDTLFVR**Found in **IPI00472416** in **IPI_human**, Tax_Id=9606 Gene_Symbol=HLA-B;HLA-C;HLA-A;MICA;LOC441528 HLA class I histocompatibility antigen, B-45 alpha chain

Match to Query 15349: 1643.854332 from(548.958720,3+) index(44499)

Title: Elution from: 106.75 to 106.75 period: 0 cycle: 4032 experiment: 2 polarity: +

Data file 120208ry_Tig120slc-P8_2_3.mgf



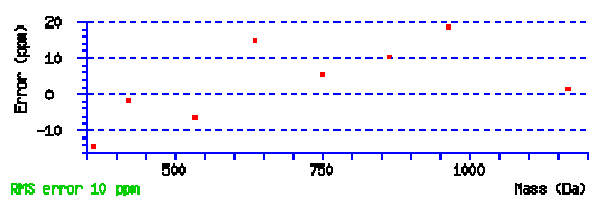
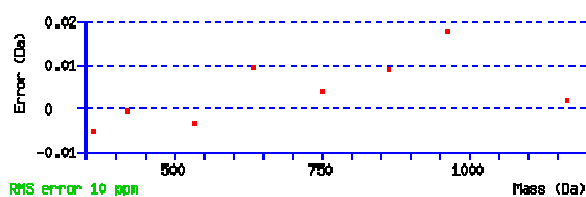
Monoisotopic mass of neutral peptide Mr(calc): 1643.8559

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 47 Expect: 0.0014

Matches : 8/118 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415			F							14
2	261.1598	131.0835			I	1497.7948	749.4010	1480.7682	740.8877	1479.7842	740.3957	13
3	362.2074	181.6074	344.1969	172.6021	T	1384.7107	692.8590	1367.6842	684.3457	1366.7001	683.8537	12
4	461.2758	231.1416	443.2653	222.1363	V	1283.6630	642.3352	1266.6365	633.8219	1265.6525	633.3299	11
5	518.2973	259.6523	500.2867	250.6470	G	1184.5946	592.8009	1167.5681	584.2877	1166.5841	583.7957	10
6	681.3606	341.1840	663.3501	332.1787	Y	1127.5732	564.2902	1110.5466	555.7769	1109.5626	555.2849	9
7	780.4291	390.7182	762.4185	381.7129	V	964.5098	482.7585	947.4833	474.2453	946.4993	473.7533	8
8	895.4560	448.2316	877.4454	439.2264	D	865.4414	433.2243	848.4149	424.7111	847.4308	424.2191	7
9	1010.4829	505.7451	992.4724	496.7398	D	750.4145	375.7109	733.3879	367.1976	732.4039	366.7056	6
10	1111.5306	556.2689	1093.5201	547.2637	T	635.3875	318.1974	618.3610	309.6841	617.3770	309.1921	5
11	1224.6147	612.8110	1206.6041	603.8057	L	534.3398	267.6736	517.3133	259.1603			4
12	1371.6831	686.3452	1353.6725	677.3399	F	421.2558	211.1315	404.2292	202.6183			3
13	1470.7515	735.8794	1452.7409	726.8741	V	274.1874	137.5973	257.1608	129.0840			2
14					R	175.1190	88.0631	158.0924	79.5498			1

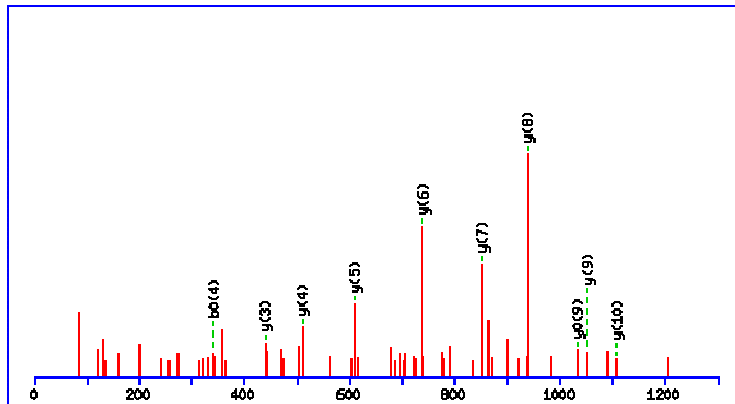


Peptide Number: 32928MS/MS Fragmentation of **TGLSLEVATYR**Found in **IPI00299301** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SYNM Isoform 1 of Synemin

Match to Query 13906: 1208.629568 from(605.322060,2+) index(35379)

Title: Elution from: 92.05 to 92.05 period: 0 cycle: 3509 experiment: 4 polarity: +

Data file 120212ry_aHDF1388-P9_3_2.mgf



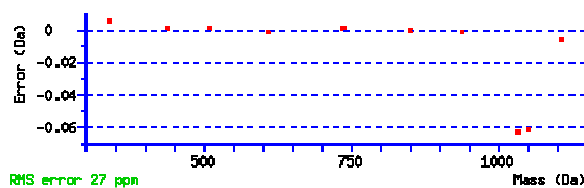
Monoisotopic mass of neutral peptide Mr(calc): 1208.6401

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

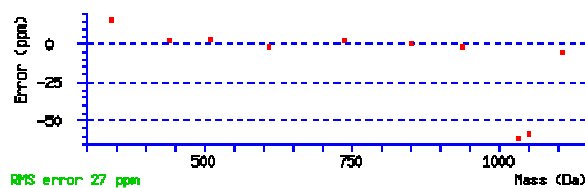
Ions Score: 48 Expect: 0.00099

Matches : 10/96 fragment ions using 23 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311	84.0444	42.5258	T							11
2	159.0764	80.0418	141.0659	71.0366	G	1108.5997	554.8035	1091.5732	546.2902	1090.5891	545.7982	10
3	272.1605	136.5839	254.1499	127.5786	L	1051.5782	526.2928	1034.5517	517.7795	1033.5677	517.2875	9
4	359.1925	180.0999	341.1819	171.0946	S	938.4942	469.7507	921.4676	461.2375	920.4836	460.7454	8
5	472.2766	236.6419	454.2660	227.6366	L	851.4621	426.2347	834.4356	417.7214	833.4516	417.2294	7
6	601.3192	301.1632	583.3086	292.1579	E	738.3781	369.6927	721.3515	361.1794	720.3675	360.6874	6
7	700.3876	350.6974	682.3770	341.6921	V	609.3355	305.1714	592.3089	296.6581	591.3249	296.1661	5
8	771.4247	386.2160	753.4141	377.2107	A	510.2671	255.6372	493.2405	247.1239	492.2565	246.6319	4
9	872.4724	436.7398	854.4618	427.7345	T	439.2300	220.1186	422.2034	211.6053	421.2194	211.1133	3
10	1035.5357	518.2715	1017.5251	509.2662	Y	338.1823	169.5948	321.1557	161.0815			2
11					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 27 ppm



RMS error 27 ppm

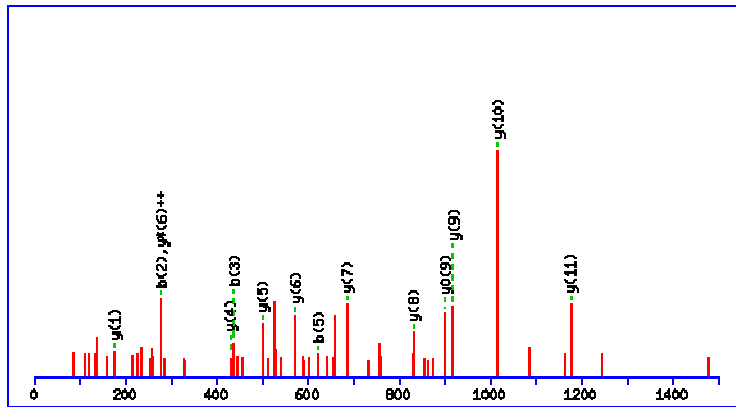
Peptide Number: 33200

MS/MS Fragmentation of **YNCPSFLAAALAR**Found in **IPI00103630** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PPM1E Isoform 2 of Protein phosphatase 1E

Match to Query 10364: 1452.712408 from(727.363480,2+) index(21837)

Title: Elution from: 52.3 to 52.3 period: 0 cycle: 1965 experiment: 5 polarity: +

Data file 120214ry_32R1-32_4_3.mgf



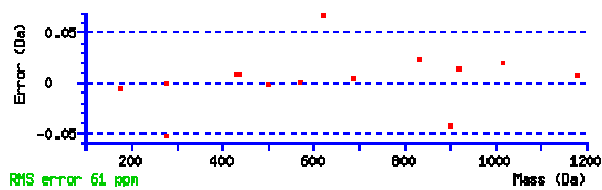
Monoisotopic mass of neutral peptide Mr(calc): 1452.7183

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

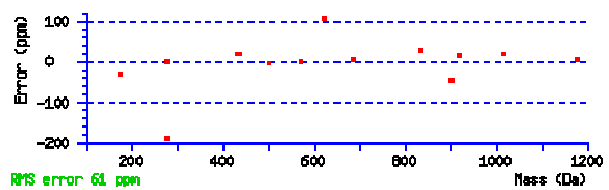
Ions Score: 42 Expect: 0.0038

Matches : 14/118 fragment ions using 38 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389					Y							13
2	278.1135	139.5604	261.0870	131.0471			N	1290.6623	645.8348	1273.6358	637.3215	1272.6518	636.8295	12
3	438.1442	219.5757	421.1176	211.0625			C	1176.6194	588.8133	1159.5928	580.3001	1158.6088	579.8081	11
4	535.1969	268.1021	518.1704	259.5888			P	1016.5887	508.7980	999.5622	500.2847	998.5782	499.7927	10
5	622.2290	311.6181	605.2024	303.1049	604.2184	302.6128	S	919.5360	460.2716	902.5094	451.7584	901.5254	451.2663	9
6	769.2974	385.1523	752.2708	376.6391	751.2868	376.1470	F	832.5039	416.7556	815.4774	408.2423			8
7	882.3815	441.6944	865.3549	433.1811	864.3709	432.6891	L	685.4355	343.2214	668.4090	334.7081			7
8	953.4186	477.2129	936.3920	468.6996	935.4080	468.2076	A	572.3515	286.6794	555.3249	278.1661			6
9	1024.4557	512.7315	1007.4291	504.2182	1006.4451	503.7262	A	501.3144	251.1608	484.2878	242.6475			5
10	1095.4928	548.2500	1078.4662	539.7368	1077.4822	539.2448	A	430.2772	215.6423	413.2507	207.1290			4
11	1208.5769	604.7921	1191.5503	596.2788	1190.5663	595.7868	L	359.2401	180.1237	342.2136	171.6104			3
12	1279.6140	640.3106	1262.5874	631.7973	1261.6034	631.3053	A	246.1561	123.5817	229.1295	115.0684			2
13							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 61 ppm



RMS error 61 ppm

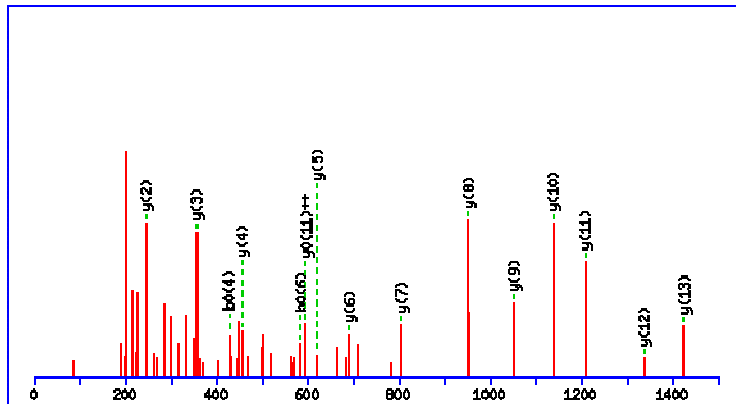
Peptide Number: 33208

MS/MS Fragmentation of **DISEASVFDAYVLPK**Found in **IPI00655650** in **IPI_human**, Tax_Id=9606 Gene_Symbol=RPS26 40S ribosomal protein S26

Match to Query 13756: 1652.839008 from(827.426780,2+) index(32439)

Title: Elution from: 90.6666666666667 to 90.6666666666667 period: 0 cycle: 3485 experiment: 7 polarity: +

Data file 120208ry_Tig120slc-P8_1.3.mgf



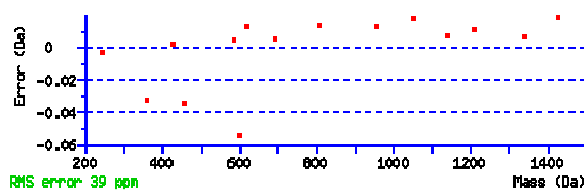
Monoisotopic mass of neutral peptide Mr(calc): 1652.8297

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

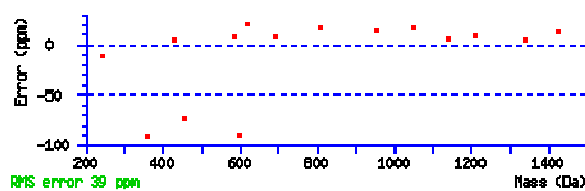
Ions Score: 88 Expect: 1.1e-007

Matches : 15/128 fragment ions using 27 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	98.0237	49.5155	D							15
2	229.1183	115.0628	211.1077	106.0575	I	1538.8101	769.9087	1521.7835	761.3954	1520.7995	760.9034	14
3	316.1503	158.5788	298.1397	149.5735	S	1425.7260	713.3666	1408.6995	704.8534	1407.7155	704.3614	13
4	445.1929	223.1001	427.1823	214.0948	E	1338.6940	669.8506	1321.6674	661.3374	1320.6834	660.8454	12
5	516.2300	258.6186	498.2195	249.6134	A	1209.6514	605.3293	1192.6249	596.8161	1191.6408	596.3241	11
6	603.2620	302.1347	585.2515	293.1294	S	1138.6143	569.8108	1121.5877	561.2975	1120.6037	560.8055	10
7	702.3305	351.6689	684.3199	342.6636	V	1051.5823	526.2948	1034.5557	517.7815	1033.5717	517.2895	9
8	849.3989	425.2031	831.3883	416.1978	F	952.5138	476.7606	935.4873	468.2473	934.5033	467.7553	8
9	964.4258	482.7165	946.4153	473.7113	D	805.4454	403.2264	788.4189	394.7131	787.4349	394.2211	7
10	1035.4629	518.2351	1017.4524	509.2298	A	690.4185	345.7129	673.3919	337.1996			6
11	1198.5263	599.7668	1180.5157	590.7615	Y	619.3814	310.1943	602.3548	301.6811			5
12	1297.5947	649.3010	1279.5841	640.2957	V	456.3180	228.6627	439.2915	220.1494			4
13	1410.6787	705.8430	1392.6682	696.8377	L	357.2496	179.1285	340.2231	170.6152			3
14	1507.7315	754.3694	1489.7209	745.3641	P	244.1656	122.5864	227.1390	114.0731			2
15					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 39 ppm



RMS error 39 ppm

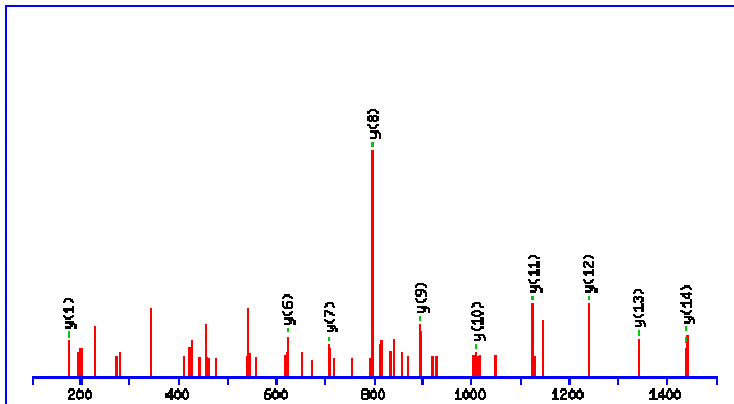
Peptide Number: 33266

MS/MS Fragmentation of **TNPEDIYPSNPTDDDVSSGSSSER**Found in **IPI00984539** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CD44 Uncharacterized protein

Match to Query 43811: 2568.105492 from(857.042440,3+) index(14603)

Title: Elution from: 37.3666666666667 to 37.3666666666667 period: 0 cycle: 1425 experiment: 10 polarity:+

Data file 120206ry_aHDF1419-P10_3_2.mgf



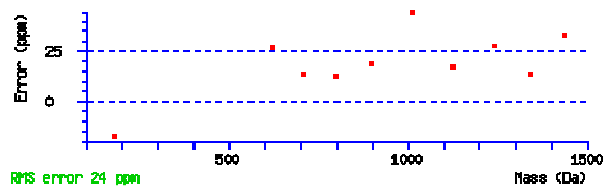
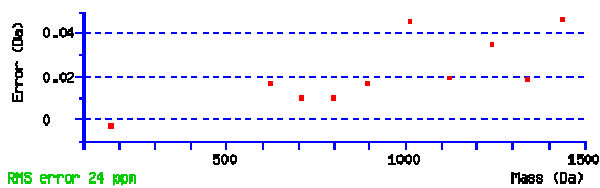
Monoisotopic mass of neutral peptide Mr(calc): 2568.0736

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 47 Expect: 0.00032

Matches : 10/272 fragment ions using 25 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							24
2	216.0979	108.5526	199.0713	100.0393	198.0873	99.5473	N	2468.0332	1234.5202	2451.0066	1226.0070	2450.0226	1225.5149	23
3	313.1506	157.0790	296.1241	148.5657	295.1401	148.0737	P	2353.9902	1177.4988	2336.9637	1168.9855	2335.9797	1168.4935	22
4	442.1932	221.6003	425.1667	213.0870	424.1827	212.5950	E	2256.9375	1128.9724	2239.9109	1120.4591	2238.9269	1119.9671	21
5	557.2202	279.1137	540.1936	270.6005	539.2096	270.1084	D	2127.8949	1064.4511	2110.8683	1055.9378	2109.8843	1055.4458	20
6	670.3042	335.6558	653.2777	327.1425	652.2937	326.6505	I	2012.8679	1006.9376	1995.8414	998.4243	1994.8574	997.9323	19
7	833.3676	417.1874	816.3410	408.6742	815.3570	408.1821	Y	1899.7839	950.3956	1882.7573	941.8823	1881.7733	941.3903	18
8	930.4203	465.7138	913.3938	457.2005	912.4098	456.7085	P	1736.7206	868.8639	1719.6940	860.3506	1718.7100	859.8586	17
9	1017.4524	509.2298	1000.4258	500.7165	999.4418	500.2245	S	1639.6678	820.3375	1622.6412	811.8243	1621.6572	811.3323	16
10	1131.4953	566.2513	1114.4687	557.7380	1113.4847	557.2460	N	1552.6358	776.8215	1535.6092	768.3082	1534.6252	767.8162	15
11	1228.5481	614.7777	1211.5215	606.2644	1210.5375	605.7724	P	1438.5928	719.8001	1421.5663	711.2868	1420.5823	710.7948	14
12	1329.5957	665.3015	1312.5692	656.7882	1311.5852	656.2962	T	1341.5401	671.2737	1324.5135	662.7604	1323.5295	662.2684	13
13	1444.6227	722.8150	1427.5961	714.3017	1426.6121	713.8097	D	1240.4924	620.7498	1223.4658	612.2366	1222.4818	611.7446	12
14	1559.6496	780.3284	1542.6231	771.8152	1541.6391	771.3232	D	1125.4654	563.2364	1108.4389	554.7231	1107.4549	554.2311	11
15	1674.6766	837.8419	1657.6500	829.3286	1656.6660	828.8366	D	1010.4385	505.7229	993.4120	497.2096	992.4279	496.7176	10
16	1773.7450	887.3761	1756.7184	878.8629	1755.7344	878.3708	V	895.4116	448.2094	878.3850	439.6961	877.4010	439.2041	9
17	1860.7770	930.8921	1843.7505	922.3789	1842.7664	921.8869	S	796.3431	398.6752	779.3166	390.1619	778.3326	389.6699	8
18	1947.8090	974.4082	1930.7825	965.8949	1929.7985	965.4029	S	709.3111	355.1592	692.2846	346.6459	691.3006	346.1539	7
19	2004.8305	1002.9189	1987.8040	994.4056	1986.8199	993.9136	G	622.2791	311.6432	605.2525	303.1299	604.2685	302.6379	6
20	2091.8625	1046.4349	2074.8360	1037.9216	2073.8520	1037.4296	S	565.2576	283.1325	548.2311	274.6192	547.2471	274.1272	5
21	2178.8946	1089.9509	2161.8680	1081.4376	2160.8840	1080.9456	S	478.2256	239.6164	461.1991	231.1032	460.2150	230.6112	4
22	2265.9266	1133.4669	2248.9000	1124.9537	2247.9160	1124.4616	S	391.1936	196.1004	374.1670	187.5872	373.1830	187.0951	3
23	2394.9692	1197.9882	2377.9426	1189.4750	2376.9586	1188.9829	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
24							R	175.1190	88.0631	158.0924	79.5498			1



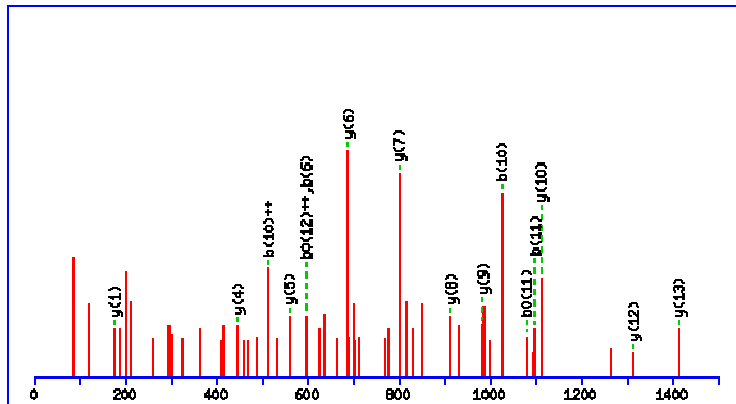
Peptide Number: 33421

MS/MS Fragmentation of **TLVGLLTSNQALLQLEAAR**Found in **IPI00644486** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TMCO6 Isoform 1 of Transmembrane and coiled-coil domain-containing protein 6

Match to Query 14933: 2010.116412 from(671.046080,3+) index(11555)

Title: Elution from: 28.65 to 28.65 period: 0 cycle: 1069 experiment: 3 polarity:+

Data file 120118ry_201B7-32_2_4.mgf



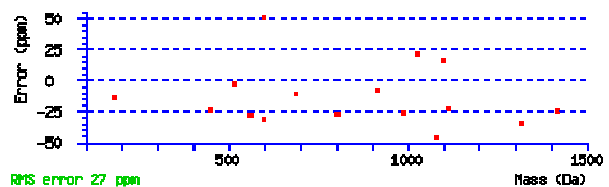
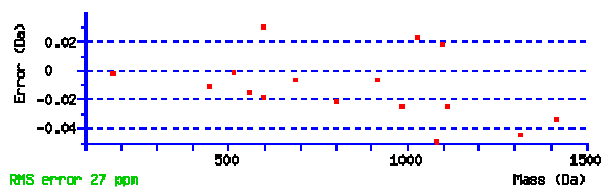
Monoisotopic mass of neutral peptide Mr(calc): 2010.1473

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 47 Expect: 0.0007

Matches : 16/194 fragment ions using 36 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							19
2	215.1390	108.0731			197.1285	99.0679	L	1910.1069	955.5571	1893.0804	947.0438	1892.0964	946.5518	18
3	314.2074	157.6074			296.1969	148.6021	V	1797.0229	899.0151	1779.9963	890.5018	1779.0123	890.0098	17
4	371.2289	186.1181			353.2183	177.1128	G	1697.9545	849.4809	1680.9279	840.9676	1679.9439	840.4756	16
5	484.3130	242.6601			466.3024	233.6548	L	1640.9330	820.9701	1623.9064	812.4569	1622.9224	811.9649	15
6	597.3970	299.2022			579.3865	290.1969	L	1527.8489	764.4281	1510.8224	755.9148	1509.8384	755.4228	14
7	698.4447	349.7260			680.4341	340.7207	T	1414.7649	707.8861	1397.7383	699.3728	1396.7543	698.8808	13
8	785.4767	393.2420			767.4662	384.2367	S	1313.7172	657.3622	1296.6906	648.8490	1295.7066	648.3570	12
9	899.5197	450.2635	882.4931	441.7502	881.5091	441.2582	N	1226.6852	613.8462	1209.6586	605.3329	1208.6746	604.8409	11
10	1027.5782	514.2928	1010.5517	505.7795	1009.5677	505.2875	Q	1112.6422	556.8248	1095.6157	548.3115	1094.6317	547.8195	10
11	1098.6154	549.8113	1081.5888	541.2980	1080.6048	540.8060	A	984.5837	492.7955	967.5571	484.2822	966.5731	483.7902	9
12	1211.6994	606.3533	1194.6729	597.8401	1193.6888	597.3481	L	913.5465	457.2769	896.5200	448.7636	895.5360	448.2716	8
13	1324.7835	662.8954	1307.7569	654.3821	1306.7729	653.8901	L	800.4625	400.7349	783.4359	392.2216	782.4519	391.7296	7
14	1452.8421	726.9247	1435.8155	718.4114	1434.8315	717.9194	Q	687.3784	344.1928	670.3519	335.6796	669.3678	335.1876	6
15	1565.9261	783.4667	1548.8996	774.9534	1547.9156	774.4614	L	559.3198	280.1636	542.2933	271.6503	541.3093	271.1583	5
16	1694.9687	847.9880	1677.9422	839.4747	1676.9581	838.9827	E	446.2358	223.6215	429.2092	215.1082	428.2252	214.6162	4
17	1766.0058	883.5066	1748.9793	874.9933	1747.9953	874.5013	A	317.1932	159.1002	300.1666	150.5870			3
18	1837.0429	919.0251	1820.0164	910.5118	1819.0324	910.0198	A	246.1561	123.5817	229.1295	115.0684			2
19							R	175.1190	88.0631	158.0924	79.5498			1

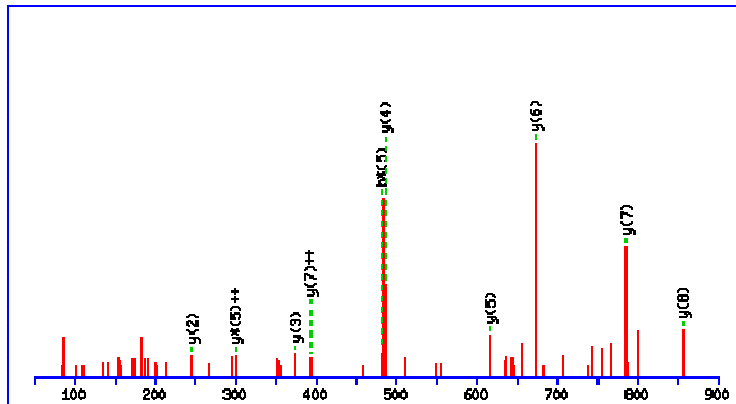


Peptide Number: 34348**MS/MS Fragmentation of QALGELQAR**Found in **IPI00220299** in **IPI_human**, Tax_Id=9606 Gene_Symbol=FLAD1 Isoform 1 of FAD synthase

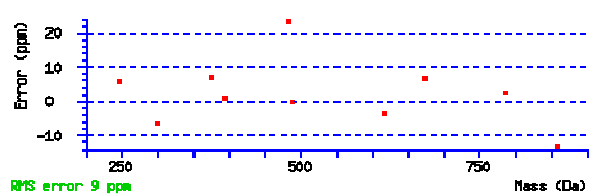
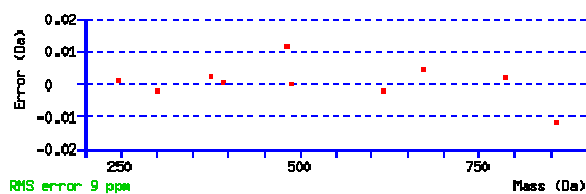
Match to Query 9998: 984.518868 from(493.266710,2+) index(23781)

Title: Elution from: 97.7333333333333 to 97.7333333333333 period: 0 cycle: 8849 experiment: 7 polarity:+

Data file 120214ry_414C2-43_4_1.mgf

**Monoisotopic mass of neutral peptide Mr(calcd):** 984.5352**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 58 **Expect:** 7.6e-005**Matches :** 10/80 fragment ions using 16 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.0659	65.0366	112.0393	56.5233			Q							9
2	200.1030	100.5551	183.0764	92.0418			A	857.4839	429.2456	840.4574	420.7323	839.4734	420.2403	8
3	313.1870	157.0972	296.1605	148.5839			L	786.4468	393.7271	769.4203	385.2138	768.4363	384.7218	7
4	370.2085	185.6079	353.1819	177.0946			G	673.3628	337.1850	656.3362	328.6717	655.3522	328.1797	6
5	499.2511	250.1292	482.2245	241.6159	481.2405	241.1239	E	616.3413	308.6743	599.3148	300.1610	598.3307	299.6690	5
6	612.3352	306.6712	595.3086	298.1579	594.3246	297.6659	L	487.2987	244.1530	470.2722	235.6397			4
7	740.3937	370.7005	723.3672	362.1872	722.3832	361.6952	Q	374.2146	187.6110	357.1881	179.0977			3
8	811.4308	406.2191	794.4043	397.7058	793.4203	397.2138	A	246.1561	123.5817	229.1295	115.0684			2
9							R	175.1190	88.0631	158.0924	79.5498			1



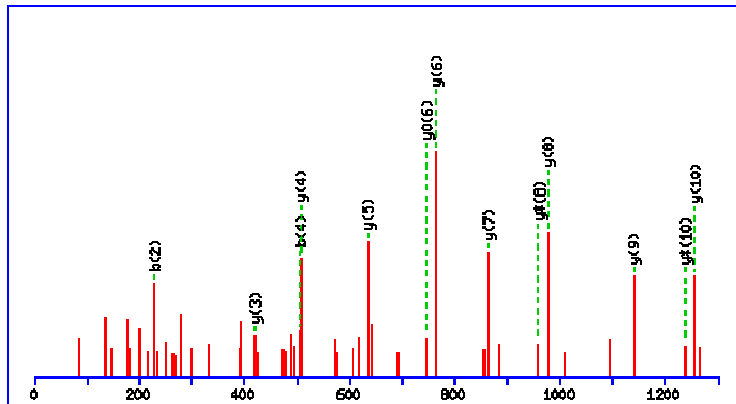
Peptide Number: 34524

MS/MS Fragmentation of **IDYNVEQSCIK**Found in **IPI00746941** in **IPI_human**, Tax_Id=9606 Gene_Symbol=STX16-NPEPL1;STX16 Uncharacterized protein

Match to Query 21597: 1367.641128 from(684.827840,2+) index(9890)

Title: Elution from: 25.4 to 25.4 period: 0 cycle: 965 experiment: 8 polarity: +

Data file 120210ry_585A1-55_3_2.mgf



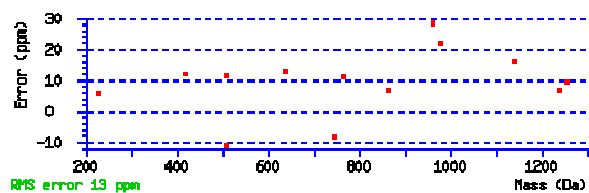
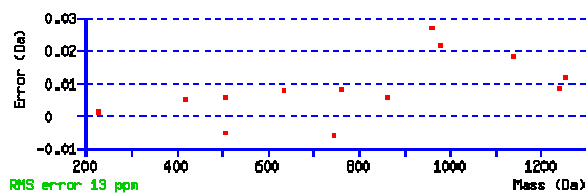
Monoisotopic mass of neutral peptide Mr(calc): 1367.6391

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 54 Expect: 0.00016

Matches : 13/106 fragment ions using 23 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							11
2	229.1183	115.0628			211.1077	106.0575	D	1255.5623	628.2848	1238.5358	619.7715	1237.5518	619.2795	10
3	392.1816	196.5944			374.1710	187.5892	Y	1140.5354	570.7713	1123.5088	562.2581	1122.5248	561.7660	9
4	506.2245	253.6159	489.1980	245.1026	488.2140	244.6106	N	977.4721	489.2397	960.4455	480.7264	959.4615	480.2344	8
5	605.2930	303.1501	588.2664	294.6368	587.2824	294.1448	V	863.4291	432.2182	846.4026	423.7049	845.4186	423.2129	7
6	734.3355	367.6714	717.3090	359.1581	716.3250	358.6661	E	764.3607	382.6840	747.3342	374.1707	746.3502	373.6787	6
7	862.3941	431.7007	845.3676	423.1874	844.3836	422.6954	Q	635.3181	318.1627	618.2916	309.6494	617.3076	309.1574	5
8	949.4262	475.2167	932.3996	466.7034	931.4156	466.2114	S	507.2595	254.1334	490.2330	245.6201	489.2490	245.1281	4
9	1109.4568	555.2320	1092.4303	546.7188	1091.4462	546.2268	C	420.2275	210.6174	403.2010	202.1041			3
10	1222.5409	611.7741	1205.5143	603.2608	1204.5303	602.7688	I	260.1969	130.6021	243.1703	122.0888			2
11							K	147.1128	74.0600	130.0863	65.5468			1

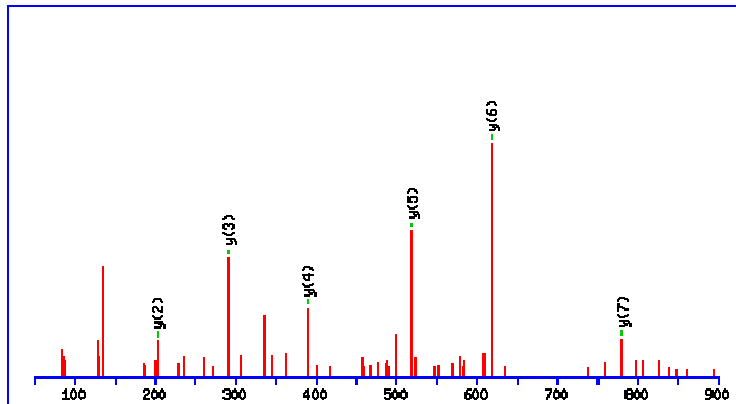


Peptide Number: 34544MS/MS Fragmentation of **DGYVEVSGK**Found in **IP100007264** in **IP1_human**, Tax_Id=9606 Gene_Symbol=HSPB8 Heat shock protein beta-8

Match to Query 8637: 952.448768 from(477.231660,2+) index(21275)

Title: Elution from: 86.2166666666667 to 86.2166666666667 period: 0 cycle: 7062 experiment: 8 polarity:+

Data file 120208ry_Tig120slc-P8_1_1.mgf



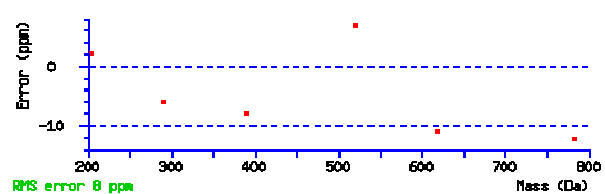
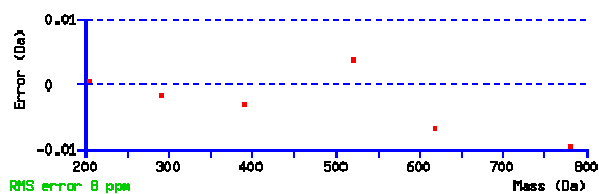
Monoisotopic mass of neutral peptide Mr(calc): 952.4502

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 51 Expect: 0.00034

Matches : 6/76 fragment ions using 9 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	98.0237	49.5155	D							9
2	173.0557	87.0315	155.0451	78.0262	G	838.4305	419.7189	821.4040	411.2056	820.4199	410.7136	8
3	336.1190	168.5631	318.1084	159.5579	Y	781.4090	391.2082	764.3825	382.6949	763.3985	382.2029	7
4	435.1874	218.0974	417.1769	209.0921	V	618.3457	309.6765	601.3192	301.1632	600.3352	300.6712	6
5	564.2300	282.6186	546.2195	273.6134	E	519.2773	260.1423	502.2508	251.6290	501.2667	251.1370	5
6	663.2984	332.1529	645.2879	323.1476	V	390.2347	195.6210	373.2082	187.1077	372.2241	186.6157	4
7	750.3305	375.6689	732.3199	366.6636	S	291.1663	146.0868	274.1397	137.5735	273.1557	137.0815	3
8	807.3519	404.1796	789.3414	395.1743	G	204.1343	102.5708	187.1077	94.0575			2
9					K	147.1128	74.0600	130.0863	65.5468			1



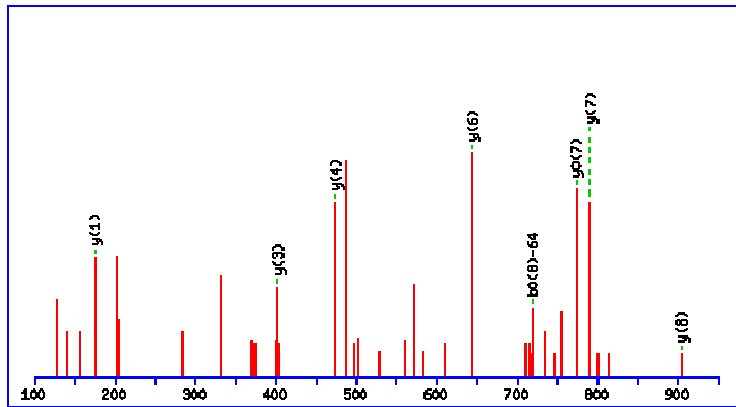
Peptide Number: 34582**MS/MS Fragmentation of ANMLGADLR**

Found in **IPI00940499** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PDE4A Isoform 7 of cAMP-specific 3',5'-cyclic phosphodiesterase 4A

Match to Query 12383: 975.478028 from(488.746290,2+) index(6083)

Title: Elution from: 64.6833333333333 to 64.6833333333333 period: 0 cycle: 6095 experiment: 8 polarity:+

Data file 120126ry_585A1-55_1_1.mgf



Monoisotopic mass of neutral peptide Mr(calc): 975.4807

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

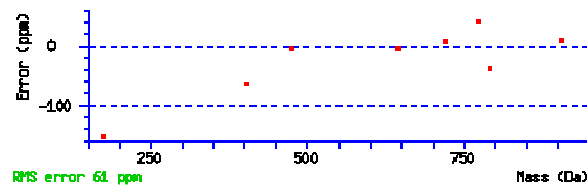
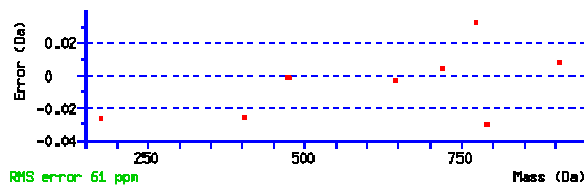
Variable modifications:

M3 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

Ions Score: 41 **Expect:** 0.0056

Matches : 8/118 fragment ions using 14 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							9
2	186.0873	93.5473	169.0608	85.0340			N	905.4509	453.2291	888.4244	444.7158	887.4404	444.2238	8
3	333.1227	167.0650	316.0962	158.5517			M	791.4080	396.2076	774.3815	387.6944	773.3974	387.2024	7
4	446.2068	223.6070	429.1802	215.0938			L	644.3726	322.6899	627.3461	314.1767	626.3620	313.6847	6
5	503.2282	252.1178	486.2017	243.6045			G	531.2885	266.1479	514.2620	257.6346	513.2780	257.1426	5
6	574.2654	287.6363	557.2388	279.1230			A	474.2671	237.6372	457.2405	229.1239	456.2565	228.6319	4
7	689.2923	345.1498	672.2658	336.6365	671.2817	336.1445	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
8	802.3764	401.6918	785.3498	393.1785	784.3658	392.6865	L	288.2030	144.6051	271.1765	136.0919			2
9							R	175.1190	88.0631	158.0924	79.5498			1



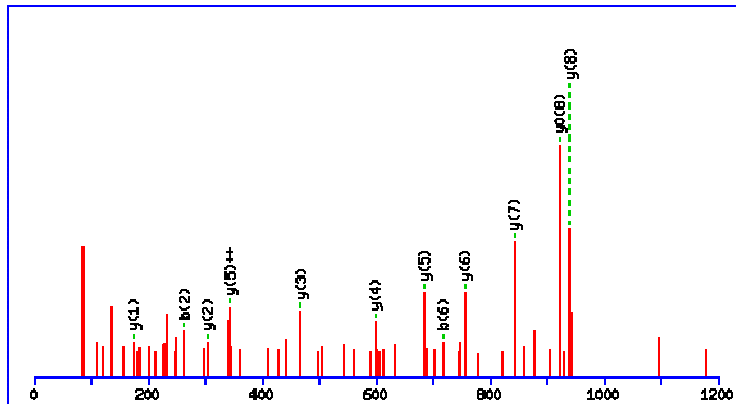
Peptide Number: 34587

MS/MS Fragmentation of **VYLDNLPSASMYER**Found in **IP100149650** in **IP1_human**, Tax_Id=9606 Gene_Symbol=PPWD1 Peptidylprolyl isomerase domain and WD repeat-containing protein 1

Match to Query 17515: 1656.788622 from(553.270150,3+) index(4979)

Title: Elution from: 12.2 to 12.2 period: 0 cycle: 457 experiment: 5 polarity: +

Data file 120210ry_32R1-32_2_3.mgf



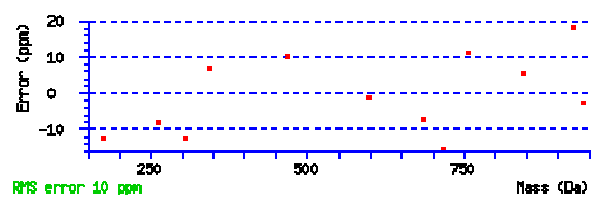
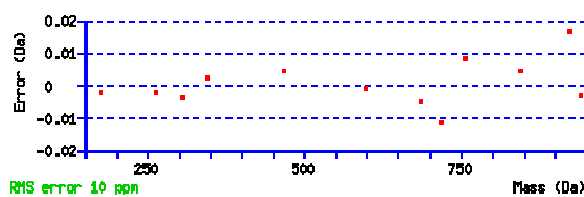
Monoisotopic mass of neutral peptide Mr(calc): 1656.7817

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 39 Expect: 0.0064

Matches : 12/140 fragment ions using 29 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							14
2	263.1390	132.0731					Y	1558.7206	779.8639	1541.6941	771.3507	1540.7101	770.8587	13
3	376.2231	188.6152					L	1395.6573	698.3323	1378.6307	689.8190	1377.6467	689.3270	12
4	491.2500	246.1287			473.2395	237.1234	D	1282.5732	641.7903	1265.5467	633.2770	1264.5627	632.7850	11
5	605.2930	303.1501	588.2664	294.6368	587.2824	294.1448	N	1167.5463	584.2768	1150.5197	575.7635	1149.5357	575.2715	10
6	718.3770	359.6921	701.3505	351.1789	700.3665	350.6869	L	1053.5034	527.2553	1036.4768	518.7420	1035.4928	518.2500	9
7	815.4298	408.2185	798.4032	399.7053	797.4192	399.2132	P	940.4193	470.7133	923.3927	462.2000	922.4087	461.7080	8
8	902.4618	451.7345	885.4353	443.2213	884.4512	442.7293	S	843.3665	422.1869	826.3400	413.6736	825.3560	413.1816	7
9	973.4989	487.2531	956.4724	478.7398	955.4884	478.2478	A	756.3345	378.6709	739.3080	370.1576	738.3239	369.6656	6
10	1060.5310	530.7691	1043.5044	522.2558	1042.5204	521.7638	S	685.2974	343.1523	668.2708	334.6391	667.2868	334.1470	5
11	1191.5714	596.2894	1174.5449	587.7761	1173.5609	587.2841	M	598.2654	299.6363	581.2388	291.1230	580.2548	290.6310	4
12	1354.6348	677.8210	1337.6082	669.3077	1336.6242	668.8157	Y	467.2249	234.1161	450.1983	225.6028	449.2143	225.1108	3
13	1483.6774	742.3423	1466.6508	733.8290	1465.6668	733.3370	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
14							R	175.1190	88.0631	158.0924	79.5498			1



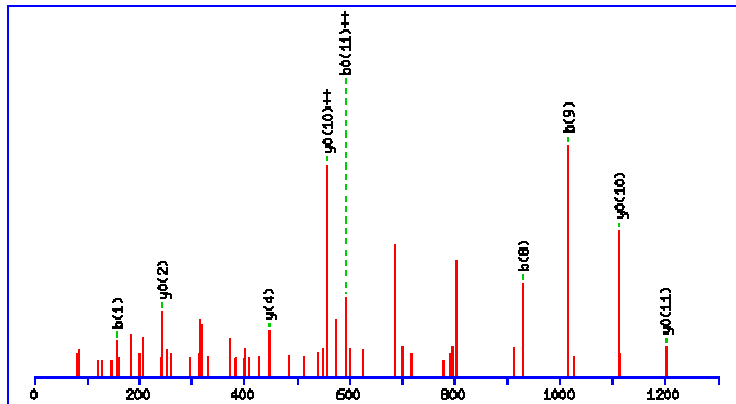
Peptide Number: 35418

MS/MS Fragmentation of **RSRMDLPGSPSR**Found in **IPI00064158** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TTBK1 Isoform 1 of Tau-tubulin kinase 1

Match to Query 7565: 1373.702888 from(687.858720,2+) index(12297)

Title: Elution from: 31.4 to 31.4 period: 0 cycle: 1195 experiment: 5 polarity: +

Data file 120214ry_aHDF1419-P10_4_3.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1373.6834

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

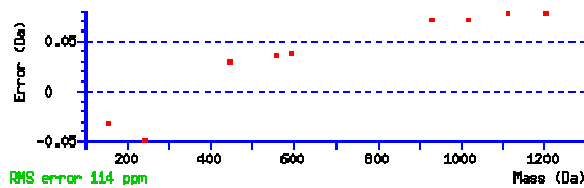
Variable modifications:

M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

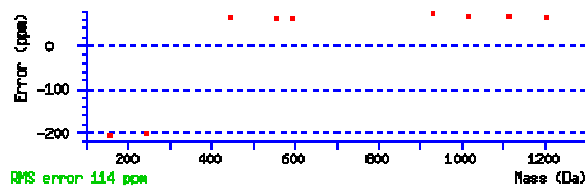
Ions Score: 46 Expect: 0.0019

Matches : 13/194 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	157.1084	79.0578	140.0818	70.5446			R							12
2	244.1404	122.5738	227.1139	114.0606	226.1298	113.5686	S	1218.5895	609.7984	1201.5630	601.2851	1200.5790	600.7931	11
3	400.2415	200.6244	383.2150	192.1111	382.2310	191.6191	R	1131.5575	566.2824	1114.5310	557.7691	1113.5470	557.2771	10
4	547.2769	274.1421	530.2504	265.6288	529.2664	265.1368	M	975.4564	488.2318	958.4299	479.7186	957.4458	479.2266	9
5	662.3039	331.6556	645.2773	323.1423	644.2933	322.6503	D	828.4210	414.7141	811.3945	406.2009	810.4104	405.7089	8
6	775.3879	388.1976	758.3614	379.6843	757.3774	379.1923	L	713.3941	357.2007	696.3675	348.6874	695.3835	348.1954	7
7	872.4407	436.7240	855.4141	428.2107	854.4301	427.7187	P	600.3100	300.6586	583.2835	292.1454	582.2994	291.6534	6
8	929.4622	465.2347	912.4356	456.7214	911.4516	456.2294	G	503.2572	252.1323	486.2307	243.6190	485.2467	243.1270	5
9	1016.4942	508.7507	999.4676	500.2375	998.4836	499.7455	S	446.2358	223.6215	429.2092	215.1082	428.2252	214.6162	4
10	1113.5470	557.2771	1096.5204	548.7638	1095.5364	548.2718	P	359.2037	180.1055	342.1772	171.5922	341.1932	171.1002	3
11	1200.5790	600.7931	1183.5524	592.2799	1182.5684	591.7878	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
12							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 114 ppm



RMS error 114 ppm

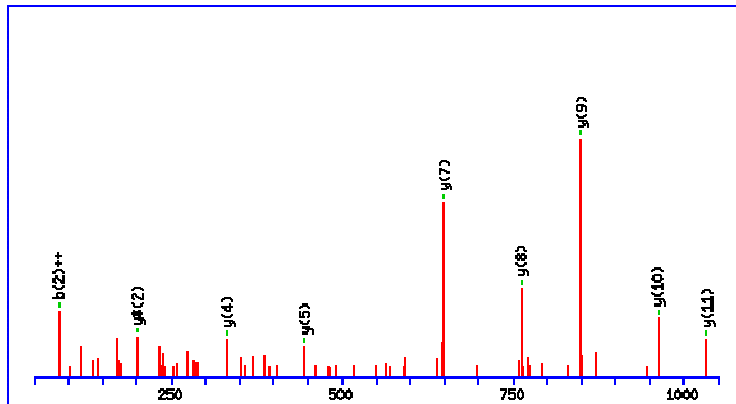
Peptide Number: 36063**MS/MS Fragmentation of VAISLGFLGGAK**

Found in **IPI00306748** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ABCB7 Isoform 1 of ATP-binding cassette sub-family B member 7, mitochondrial

Match to Query 3404: 1131.659308 from(566.836930,2+) index(23053)

Title: Elution from: 56.45 to 56.45 period: 0 cycle: 2089 experiment: 2 polarity: +

Data file 120124ry_414C2-43_1_3.mgf



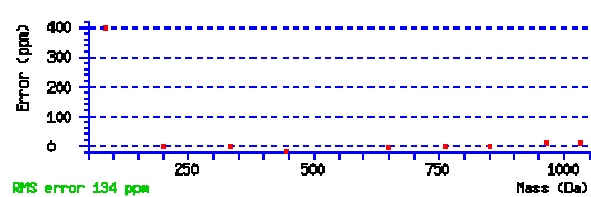
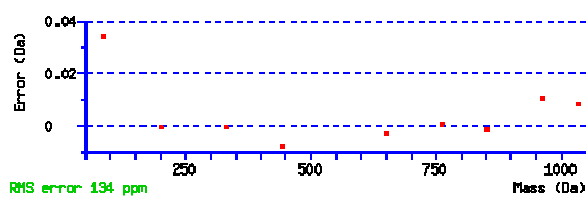
Monoisotopic mass of neutral peptide Mr(calc): 1131.6652

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 68 **Expect:** 5.2e-006

Matches : 9/88 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415			V							12
2	171.1128	86.0600			A	1033.6041	517.3057	1016.5775	508.7924	1015.5935	508.3004	11
3	284.1969	142.6021			I	962.5669	481.7871	945.5404	473.2738	944.5564	472.7818	10
4	371.2289	186.1181	353.2183	177.1128	S	849.4829	425.2451	832.4563	416.7318	831.4723	416.2398	9
5	484.3130	242.6601	466.3024	233.6548	L	762.4509	381.7291	745.4243	373.2158			8
6	541.3344	271.1709	523.3239	262.1656	G	649.3668	325.1870	632.3402	316.6738			7
7	688.4028	344.7051	670.3923	335.6998	F	592.3453	296.6763	575.3188	288.1630			6
8	801.4869	401.2471	783.4763	392.2418	L	445.2769	223.1421	428.2504	214.6288			5
9	858.5084	429.7578	840.4978	420.7525	G	332.1928	166.6001	315.1663	158.0868			4
10	915.5298	458.2686	897.5193	449.2633	G	275.1714	138.0893	258.1448	129.5761			3
11	986.5669	493.7871	968.5564	484.7818	A	218.1499	109.5786	201.1234	101.0653			2
12					K	147.1128	74.0600	130.0863	65.5468			1

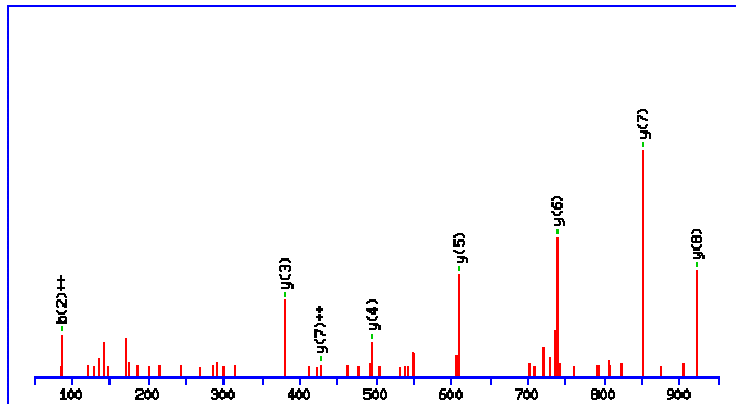


Peptide Number: 36246MS/MS Fragmentation of **VALEDDGFR**Found in **IPI00100930** in **IPI_human**, Tax_Id=9606 Gene_Symbol=C12orf43 cDNA FLJ58610

Match to Query 7350: 1020.488488 from(511.251520,2+) index(10290)

Title: Elution from: 26.3666666666667 to 26.3666666666667 period: 0 cycle: 1002 experiment: 5 polarity:+

Data file 120210ry_585A1-55_3_2.mgf



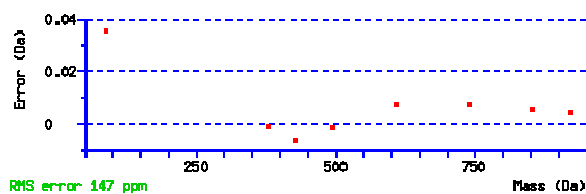
Monoisotopic mass of neutral peptide Mr(calc): 1020.4876

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

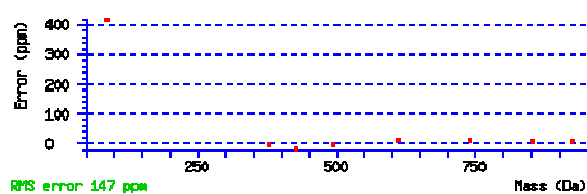
Ions Score: 58 Expect: 8.1e-005

Matches : 8/68 fragment ions using 9 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415			V							9
2	171.1128	86.0600			A	922.4265	461.7169	905.3999	453.2036	904.4159	452.7116	8
3	284.1969	142.6021			L	851.3894	426.1983	834.3628	417.6850	833.3788	417.1930	7
4	413.2395	207.1234	395.2289	198.1181	E	738.3053	369.6563	721.2788	361.1430	720.2947	360.6510	6
5	528.2664	264.6368	510.2558	255.6316	D	609.2627	305.1350	592.2362	296.6217	591.2522	296.1297	5
6	643.2933	322.1503	625.2828	313.1450	D	494.2358	247.6215	477.2092	239.1082	476.2252	238.6162	4
7	700.3148	350.6610	682.3042	341.6558	G	379.2088	190.1081	362.1823	181.5948			3
8	847.3832	424.1953	829.3727	415.1900	F	322.1874	161.5973	305.1608	153.0840			2
9					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 147 ppm



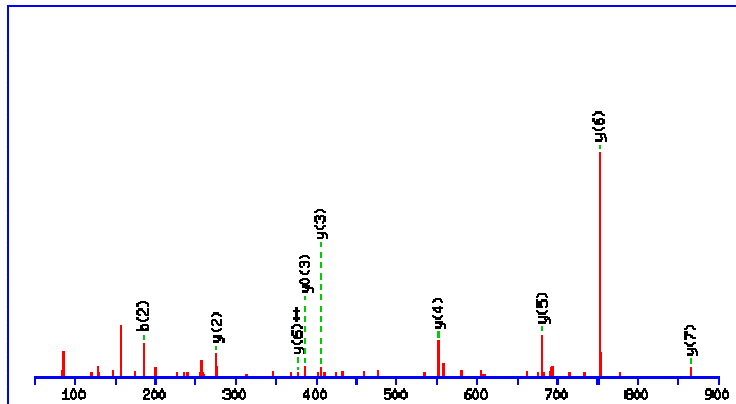
RMS error 147 ppm

Peptide Number: 36548MS/MS Fragmentation of **ALAEFE EK**Found in **IPI00167696** in **IPI_human**, Tax_Id=9606 Gene_Symbol=FAM133A Protein FAM133A

Match to Query 8302: 935.465648 from(468.740100,2+) index(29846)

Title: Elution from: 113.816666666667 to 113.816666666667 period: 0 cycle: 9695 experiment: 6 polarity: +

Data file 120210ry_585A1-55_3_1.mgf



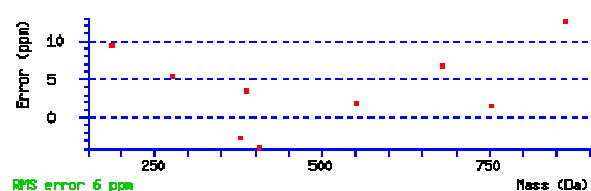
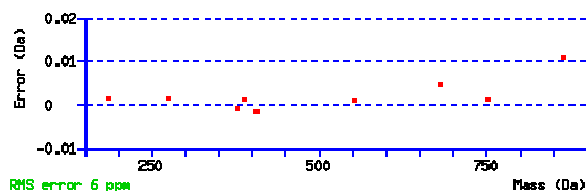
Monoisotopic mass of neutral peptide Mr(calc): 935.4600

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 46 Expect: 0.0014

Matches : 9/62 fragment ions using 15 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258			A							8
2	185.1285	93.0679			L	865.4302	433.2187	848.4036	424.7055	847.4196	424.2134	7
3	256.1656	128.5864			A	752.3461	376.6767	735.3196	368.1634	734.3355	367.6714	6
4	385.2082	193.1077	367.1976	184.1024	E	681.3090	341.1581	664.2824	332.6449	663.2984	332.1529	5
5	532.2766	266.6419	514.2660	257.6366	F	552.2664	276.6368	535.2399	268.1236	534.2558	267.6316	4
6	661.3192	331.1632	643.3086	322.1579	E	405.1980	203.1026	388.1714	194.5894	387.1874	194.0974	3
7	790.3618	395.6845	772.3512	386.6792	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
8					K	147.1128	74.0600	130.0863	65.5468			1



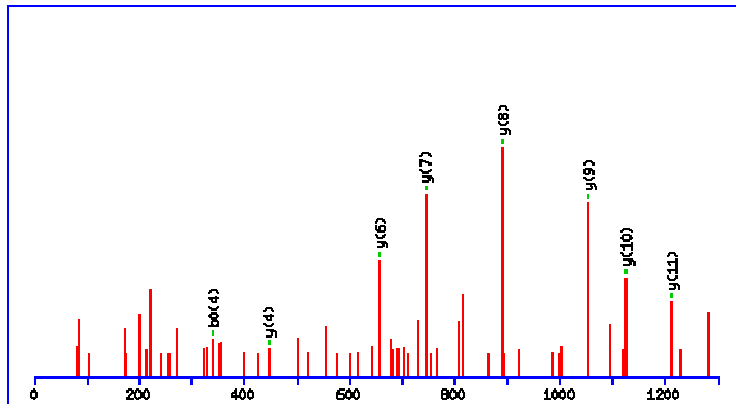
Peptide Number: 36720

MS/MS Fragmentation of **SIASAYFSPLTGNR**Found in **IPI00016542** in **IPI_human**, Tax_Id=9606 Gene_Symbol=WDR76 WD repeat-containing protein 76

Match to Query 11273: 1482.730008 from(742.372280,2+) index(9205)

Title: Elution from: 22.8666666666667 to 22.8666666666667 period: 0 cycle: 858 experiment: 9 polarity:+

Data file 120210ry_32R1-32_3.mgf



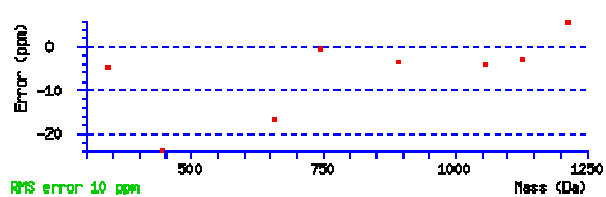
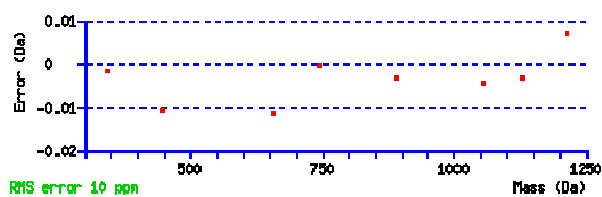
Monoisotopic mass of neutral peptide Mr(calc): 1482.7467

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 48 Expect: 0.00075

Matches : 8/126 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							14
2	201.1234	101.0653			183.1128	92.0600	I	1396.7219	698.8646	1379.6954	690.3513	1378.7114	689.8593	13
3	272.1605	136.5839			254.1499	127.5786	A	1283.6379	642.3226	1266.6113	633.8093	1265.6273	633.3173	12
4	359.1925	180.0999			341.1819	171.0946	S	1212.6008	606.8040	1195.5742	598.2907	1194.5902	597.7987	11
5	430.2296	215.6184			412.2191	206.6132	A	1125.5687	563.2880	1108.5422	554.7747	1107.5582	554.2827	10
6	593.2930	297.1501			575.2824	288.1448	Y	1054.5316	527.7694	1037.5051	519.2562	1036.5211	518.7642	9
7	740.3614	370.6843			722.3508	361.6790	F	891.4683	446.2378	874.4417	437.7245	873.4577	437.2325	8
8	827.3934	414.2003			809.3828	405.1951	S	744.3999	372.7036	727.3733	364.1903	726.3893	363.6983	7
9	924.4462	462.7267			906.4356	453.7214	P	657.3678	329.1876	640.3413	320.6743	639.3573	320.1823	6
10	1037.5302	519.2687			1019.5197	510.2635	L	560.3151	280.6612	543.2885	272.1479	542.3045	271.6559	5
11	1138.5779	569.7926			1120.5673	560.7873	T	447.2310	224.1191	430.2045	215.6059	429.2205	215.1139	4
12	1195.5994	598.3033			1177.5888	589.2980	G	346.1833	173.5953	329.1568	165.0820			3
13	1309.6423	655.3248	1292.6157	646.8115	1291.6317	646.3195	N	289.1619	145.0846	272.1353	136.5713			2
14							R	175.1190	88.0631	158.0924	79.5498			1



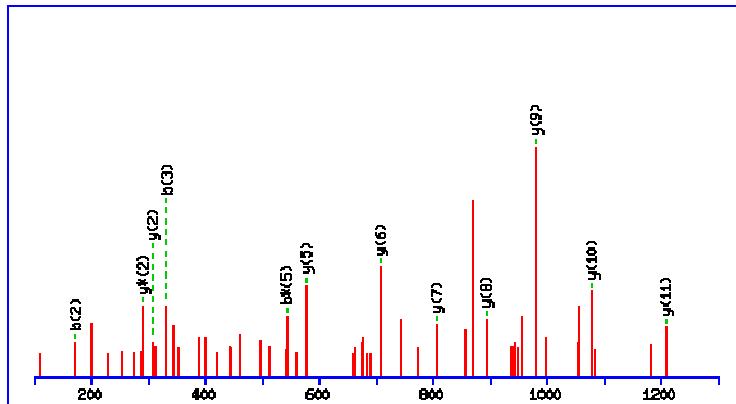
Peptide Number: 36848

MS/MS Fragmentation of **GNCEVSSVEGTLCK**Found in **IPI00789398** in **IPI_human**, Tax_Id=9606 Gene_Symbol=LY75 Isoform 3 of Lymphocyte antigen 75

Match to Query 28764: 1538.681368 from(770.347960,2+) index(15234)

Title: Elution from: 36.2166666666667 to 36.2166666666667 period: 0 cycle: 1374 experiment: 10 polarity: +

Data file 120208ry_Tig120slc-P8_2_2.mgf



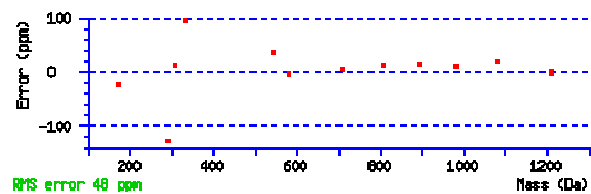
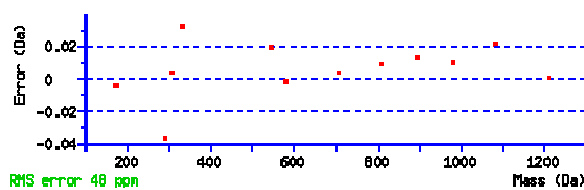
Monoisotopic mass of neutral peptide Mr(calc): 1538.6705

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 51 Expect: 0.0002

Matches : 12/142 fragment ions using 22 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							14
2	172.0717	86.5395	155.0451	78.0262			N	1482.6563	741.8318	1465.6298	733.3185	1464.6457	732.8265	13
3	332.1023	166.5548	315.0758	158.0415			C	1368.6134	684.8103	1351.5868	676.2971	1350.6028	675.8050	12
4	461.1449	231.0761	444.1184	222.5628	443.1343	222.0708	E	1208.5827	604.7950	1191.5562	596.2817	1190.5722	595.7897	11
5	560.2133	280.6103	543.1868	272.0970	542.2028	271.6050	V	1079.5401	540.2737	1062.5136	531.7604	1061.5296	531.2684	10
6	647.2454	324.1263	630.2188	315.6130	629.2348	315.1210	S	980.4717	490.7395	963.4452	482.2262	962.4612	481.7342	9
7	734.2774	367.6423	717.2508	359.1291	716.2668	358.6370	S	893.4397	447.2235	876.4131	438.7102	875.4291	438.2182	8
8	833.3458	417.1765	816.3192	408.6633	815.3352	408.1713	V	806.4077	403.7075	789.3811	395.1942	788.3971	394.7022	7
9	962.3884	481.6978	945.3618	473.1846	944.3778	472.6925	E	707.3393	354.1733	690.3127	345.6600	689.3287	345.1680	6
10	1019.4099	510.2086	1002.3833	501.6953	1001.3993	501.2033	G	578.2967	289.6520	561.2701	281.1387	560.2861	280.6467	5
11	1120.4575	560.7324	1103.4310	552.2191	1102.4470	551.7271	T	521.2752	261.1412	504.2486	252.6280	503.2646	252.1360	4
12	1233.5416	617.2744	1216.5150	608.7612	1215.5310	608.2692	L	420.2275	210.6174	403.2010	202.1041			3
13	1393.5722	697.2898	1376.5457	688.7765	1375.5617	688.2845	C	307.1435	154.0754	290.1169	145.5621			2
14							K	147.1128	74.0600	130.0863	65.5468			1



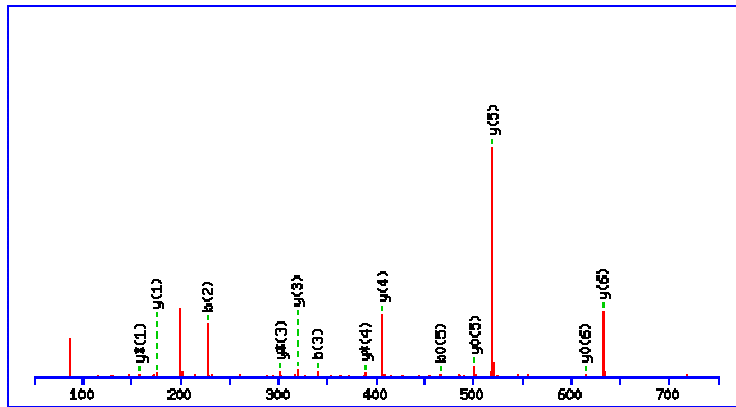
Peptide Number: 36878**MS/MS Fragmentation of ILISGSR**

Found in **IPI00480208** in **IPI_human**, Tax_Id=9606 Gene_Symbol=WDR64 Isoform 1 of WD repeat-containing protein 64

Match to Query 2622: 744.450528 from(373.232540,2+) index(17114)

Title: Elution from: 81.1833333333333 to 81.1833333333333 period: 0 cycle: 8079 experiment: 5 polarity:+

Data file 120212ry_414C2-43_3_1.mgf



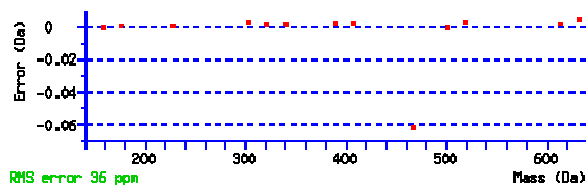
Monoisotopic mass of neutral peptide Mr(calc): 744.4494

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

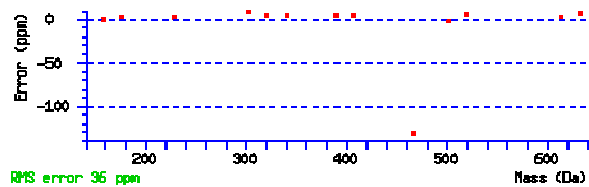
Ions Score: 40 **Expect:** 0.0083

Matches : 13/52 fragment ions using 19 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			I							7
2	227.1754	114.0913			L	632.3726	316.6899	615.3461	308.1767	614.3620	307.6847	6
3	340.2595	170.6334			I	519.2885	260.1479	502.2620	251.6346	501.2780	251.1426	5
4	427.2915	214.1494	409.2809	205.1441	S	406.2045	203.6059	389.1779	195.0926	388.1939	194.6006	4
5	484.3130	242.6601	466.3024	233.6548	G	319.1724	160.0899	302.1459	151.5766	301.1619	151.0846	3
6	571.3450	286.1761	553.3344	277.1708	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
7					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 36 ppm



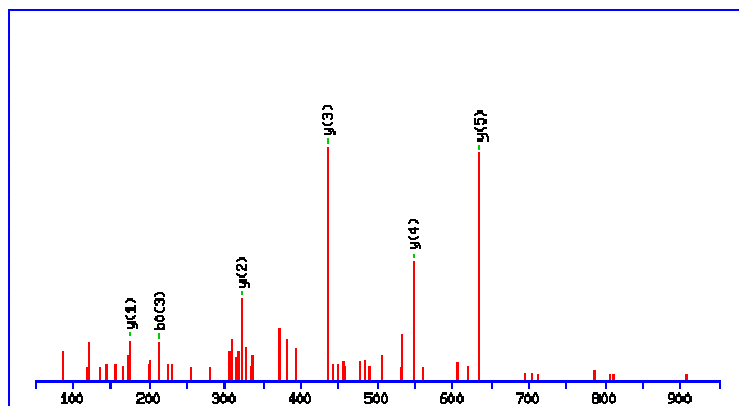
RMS error 36 ppm

Peptide Number: 36907**MS/MS Fragmentation of SGSLLFR**Found in IPI00550463 in IPI_human, Tax_Id=9606 Gene_Symbol=BEND7 Isoform 1 of BEN domain-containing protein 7

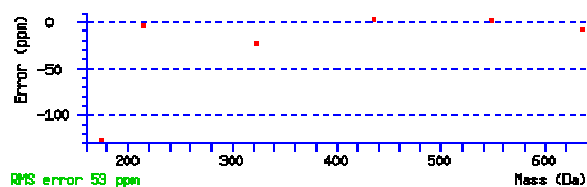
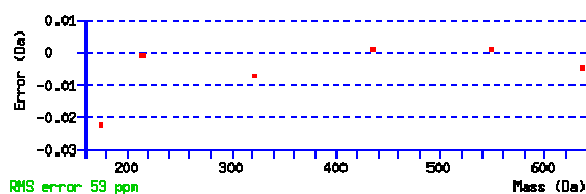
Match to Query 941: 778.418228 from(390.216390,2+) index(18478)

Title: Elution from: 44.3833333333333 to 44.3833333333333 period: 0 cycle: 1645 experiment: 1 polarity: +

Data file 120129ry_604A1-46_1_2.mgf

**Monoisotopic mass of neutral peptide Mr(calc):** 778.4337**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 43 **Expect:** 0.0029**Matches :** 6/52 fragment ions using 7 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233	70.0287	35.5180	S							7
2	145.0608	73.0340	127.0502	64.0287	G	692.4090	346.7081	675.3824	338.1949	674.3984	337.7028	6
3	232.0928	116.5500	214.0822	107.5448	S	635.3875	318.1974	618.3610	309.6841	617.3770	309.1921	5
4	345.1769	173.0921	327.1663	164.0868	L	548.3555	274.6814	531.3289	266.1681			4
5	458.2609	229.6341	440.2504	220.6288	L	435.2714	218.1394	418.2449	209.6261			3
6	605.3293	303.1683	587.3188	294.1630	F	322.1874	161.5973	305.1608	153.0840			2
7					R	175.1190	88.0631	158.0924	79.5498			1

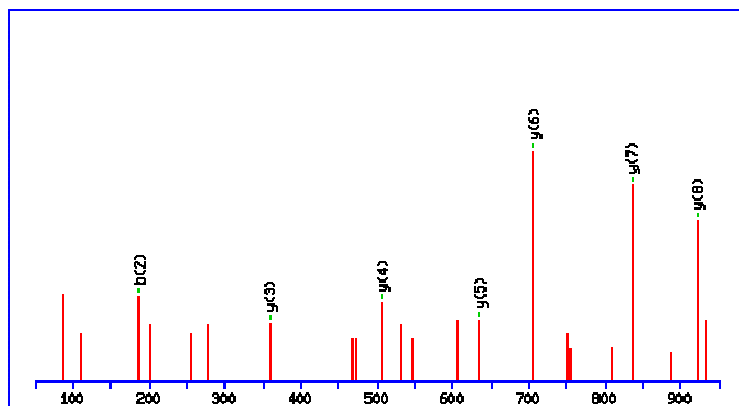


Peptide Number: 36909MS/MS Fragmentation of **VSEAEFLAR**Found in **IPI00376346** in **IPI_human**, Tax_Id=9606 Gene_Symbol=MTERFD2 mTERF domain-containing protein 2

Match to Query 13229: 1020.519768 from(511.267160,2+) index(25628)

Title: Elution from: 60.4 to 60.4 period: 0 cycle: 2264 experiment: 7 polarity:+

Data file 120126ry_585A1-55_1_2.mgf



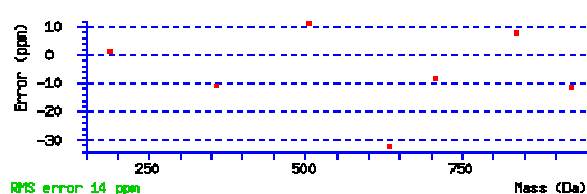
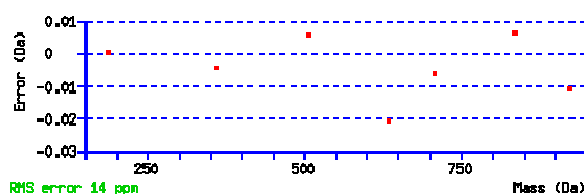
Monoisotopic mass of neutral peptide Mr(calc): 1020.5240

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 54 Expect: 0.00033

Matches : 7/70 fragment ions using 9 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415			V							9
2	187.1077	94.0575	169.0972	85.0522	S	922.4629	461.7351	905.4363	453.2218	904.4523	452.7298	8
3	316.1503	158.5788	298.1397	149.5735	E	835.4308	418.2191	818.4043	409.7058	817.4203	409.2138	7
4	387.1874	194.0974	369.1769	185.0921	A	706.3883	353.6978	689.3617	345.1845	688.3777	344.6925	6
5	516.2300	258.6186	498.2195	249.6134	E	635.3511	318.1792	618.3246	309.6659	617.3406	309.1739	5
6	663.2984	332.1529	645.2879	323.1476	F	506.3085	253.6579	489.2820	245.1446			4
7	776.3825	388.6949	758.3719	379.6896	L	359.2401	180.1237	342.2136	171.6104			3
8	847.4196	424.2134	829.4090	415.2082	A	246.1561	123.5817	229.1295	115.0684			2
9					R	175.1190	88.0631	158.0924	79.5498			1



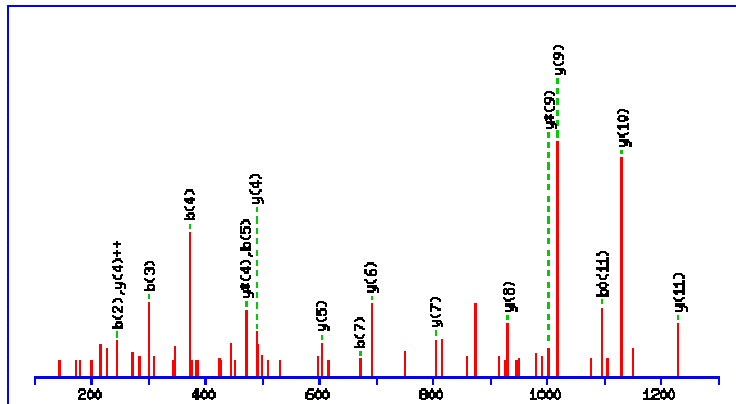
Peptide Number: 37270

MS/MS Fragmentation of **DEGAVISQISDISNR**Found in **IPI00982286** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TACC1 Uncharacterized protein

Match to Query 13863: 1602.791208 from(802.402880,2+) index(5278)

Title: Elution from: 13 to 13 period: 0 cycle: 495 experiment: 8 polarity: +

Data file 120206ry_aHDF1419-P10_2_3.mgf



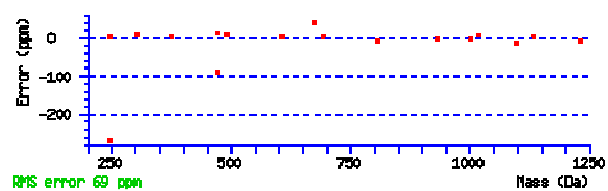
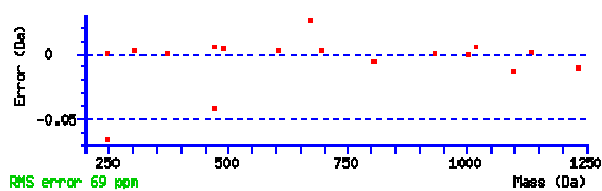
Monoisotopic mass of neutral peptide Mr(calc): 1602.7849

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 59 Expect: 7.3e-005

Matches : 17/150 fragment ions using 22 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							15
2	245.0788	123.0420			227.0662	114.0368	E	1488.7653	744.8863	1471.7387	736.3730	1470.7547	735.8810	14
3	302.0983	151.5528			284.0877	142.5475	G	1359.7227	680.3650	1342.6961	671.8517	1341.7121	671.3597	13
4	373.1354	187.0713			355.1248	178.0661	A	1302.7012	651.8542	1285.6747	643.3410	1284.6906	642.8490	12
5	472.2038	236.6055			454.1932	227.6003	V	1231.6641	616.3357	1214.6375	607.8224	1213.6535	607.3304	11
6	585.2879	293.1476			567.2773	284.1423	I	1132.5957	566.8015	1115.5691	558.2882	1114.5851	557.7962	10
7	672.3199	336.6636			654.3093	327.6583	S	1019.5116	510.2594	1002.4851	501.7462	1001.5010	501.2542	9
8	800.3785	400.6929	783.3519	392.1796	782.3679	391.6876	Q	932.4796	466.7434	915.4530	458.2302	914.4690	457.7381	8
9	913.4625	457.2349	896.4360	448.7216	895.4520	448.2296	I	804.4210	402.7141	787.3945	394.2009	786.4104	393.7089	7
10	1000.4946	500.7509	983.4680	492.2376	982.4840	491.7456	S	691.3369	346.1721	674.3104	337.6588	673.3264	337.1668	6
11	1115.5215	558.2644	1098.4950	549.7511	1097.5109	549.2591	D	604.3049	302.6561	587.2784	294.1428	586.2943	293.6508	5
12	1228.6056	614.8064	1211.5790	606.2931	1210.5950	605.8011	I	489.2780	245.1426	472.2514	236.6293	471.2674	236.1373	4
13	1315.6376	658.3224	1298.6111	649.8092	1297.6270	649.3172	S	376.1939	188.6006	359.1674	180.0873	358.1833	179.5953	3
14	1429.6805	715.3439	1412.6540	706.8306	1411.6700	706.3386	N	289.1619	145.0846	272.1353	136.5713			2
15							R	175.1190	88.0631	158.0924	79.5498			1



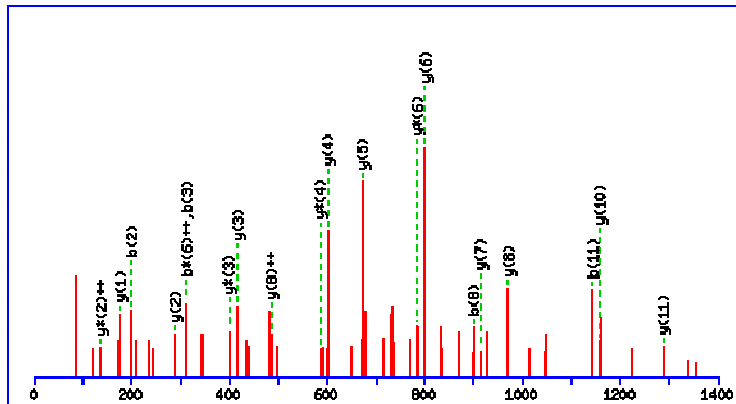
Peptide Number: 37367

MS/MS Fragmentation of **VVLLSQEMDAGLQAWQLR**Found in **IPI00328616** in **IPI_human**, Tax_Id=9606 Gene_Symbol=MRPL52 39S ribosomal protein L52, mitochondrial

Match to Query 17685: 2056.052742 from(686.358190,3+) index(6367)

Title: Elution from: 17.0833333333333 to 17.0833333333333 period: 0 cycle: 642 experiment: 6 polarity: +

Data file 120126ry_585A1-55_2_4.mgf



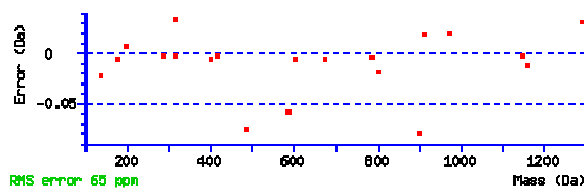
Monoisotopic mass of neutral peptide Mr(calc): 2056.0775

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

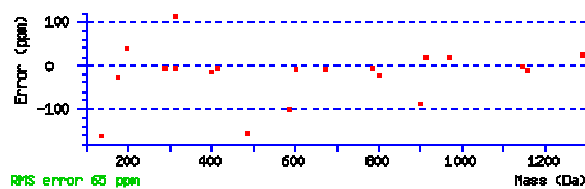
Ions Score: 44 Expect: 0.0024

Matches : 20/168 fragment ions using 46 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							18
2	199.1441	100.0757					V	1958.0164	979.5118	1940.9899	970.9986	1940.0058	970.5066	17
3	312.2282	156.6177					L	1858.9480	929.9776	1841.9214	921.4644	1840.9374	920.9724	16
4	425.3122	213.1598					L	1745.8639	873.4356	1728.8374	864.9223	1727.8534	864.4303	15
5	512.3443	256.6758			494.3337	247.6705	S	1632.7799	816.8936	1615.7533	808.3803	1614.7693	807.8883	14
6	640.4028	320.7051	623.3763	312.1918	622.3923	311.6998	Q	1545.7478	773.3776	1528.7213	764.8643	1527.7373	764.3723	13
7	769.4454	385.2264	752.4189	376.7131	751.4349	376.2211	E	1417.6893	709.3483	1400.6627	700.8350	1399.6787	700.3430	12
8	900.4859	450.7466	883.4594	442.2333	882.4754	441.7413	M	1288.6467	644.8270	1271.6201	636.3137	1270.6361	635.8217	11
9	1015.5129	508.2601	998.4863	499.7468	997.5023	499.2548	D	1157.6062	579.3067	1140.5796	570.7935	1139.5956	570.3014	10
10	1086.5500	543.7786	1069.5234	535.2654	1068.5394	534.7733	A	1042.5792	521.7933	1025.5527	513.2800			9
11	1143.5714	572.2894	1126.5449	563.7761	1125.5609	563.2841	G	971.5421	486.2747	954.5156	477.7614			8
12	1256.6555	628.8314	1239.6290	620.3181	1238.6449	619.8261	L	914.5207	457.7640	897.4941	449.2507			7
13	1384.7141	692.8607	1367.6875	684.3474	1366.7035	683.8554	Q	801.4366	401.2219	784.4101	392.7087			6
14	1455.7512	728.3792	1438.7246	719.8660	1437.7406	719.3740	A	673.3780	337.1926	656.3515	328.6794			5
15	1641.8305	821.4189	1624.8040	812.9056	1623.8199	812.4136	W	602.3409	301.6741	585.3144	293.1608			4
16	1769.8891	885.4482	1752.8625	876.9349	1751.8785	876.4429	Q	416.2616	208.6344	399.2350	200.1212			3
17	1882.9731	941.9902	1865.9466	933.4769	1864.9626	932.9849	R	288.2030	144.6051	271.1765	136.0919			2
18							L	175.1190	88.0631	158.0924	79.5498			1



RMS error 65 ppm



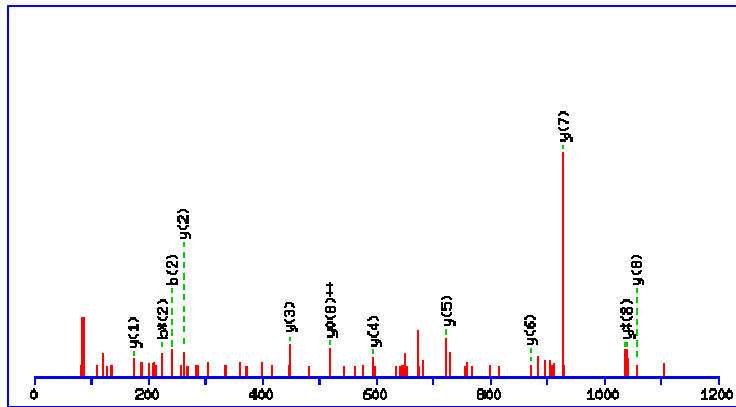
RMS error 65 ppm

Peptide Number: 37377MS/MS Fragmentation of **LQGFEFWSR**Found in **IPI00335251** in **IPI_human**, Tax_Id=9606 Gene_Symbol=DUS1L tRNA-dihydrouridine synthase 1-like

Match to Query 3042: 1168.571488 from(585.293020,2+) index(21244)

Title: Elution from: 51.7833333333333 to 51.7833333333333 period: 0 cycle: 1947 experiment: 6 polarity:+

Data file 120212ry_414C2-43_3.mgf



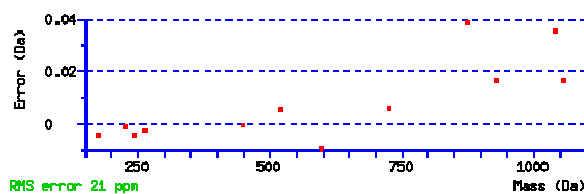
Monoisotopic mass of neutral peptide Mr(calcd): 1168.5665

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

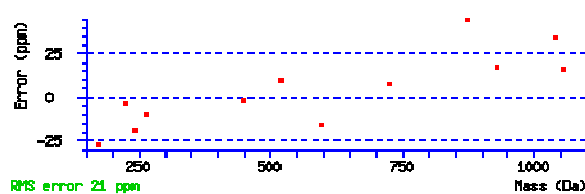
Ions Score: 42 Expect: 0.0036

Matches : 12/84 fragment ions using 31 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							9
2	242.1499	121.5786	225.1234	113.0653			Q	1056.4898	528.7485	1039.4632	520.2352	1038.4792	519.7432	8
3	299.1714	150.0893	282.1448	141.5761			G	928.4312	464.7192	911.4046	456.2060	910.4206	455.7139	7
4	446.2398	223.6235	429.2132	215.1103			F	871.4097	436.2085	854.3832	427.6952	853.3991	427.2032	6
5	575.2824	288.1448	558.2558	279.6316	557.2718	279.1396	E	724.3413	362.6743	707.3148	354.1610	706.3307	353.6690	5
6	722.3508	361.6790	705.3243	353.1658	704.3402	352.6738	F	595.2987	298.1530	578.2722	289.6397	577.2881	289.1477	4
7	908.4301	454.7187	891.4036	446.2054	890.4196	445.7134	W	448.2303	224.6188	431.2037	216.1055	430.2197	215.6135	3
8	995.4621	498.2347	978.4356	489.7214	977.4516	489.2294	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
9							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 21 ppm



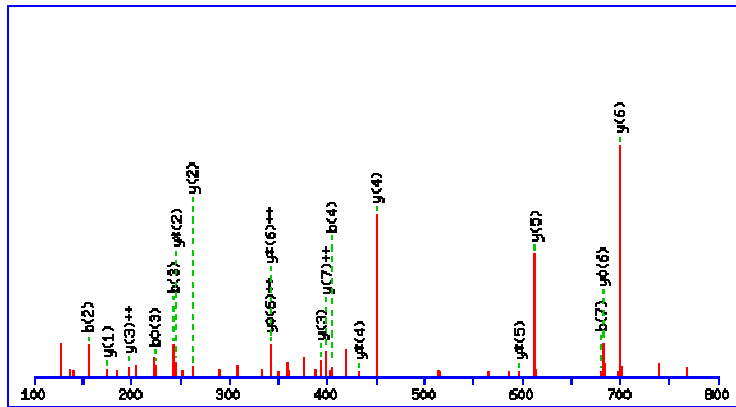
RMS error 21 ppm

Peptide Number: 37456**MS/MS Fragmentation of GPSYGMSR**Found in **IPI00216138** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TAGLN Transgelin

Match to Query 5779: 853.377148 from(427.695850,2+) index(9162)

Title: Elution from: 62.2166666666667 to 62.2166666666667 period: 0 cycle: 7731 experiment: 6 polarity: +

Data file 120206ry_aHDF1419-P10_3_1.mgf



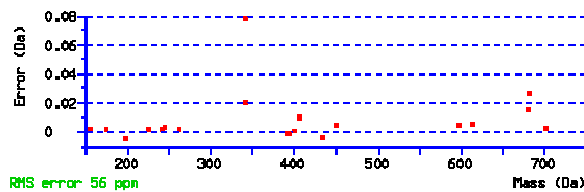
Monoisotopic mass of neutral peptide Mr(calcd): 853.3752

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

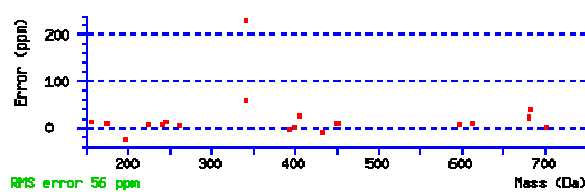
Ions Score: 37 Expect: 0.0049

Matches : 19/64 fragment ions using 40 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180			G							8
2	155.0815	78.0444			P	797.3611	399.1842	780.3345	390.6709	779.3505	390.1789	7
3	242.1135	121.5604	224.1030	112.5551	S	700.3083	350.6578	683.2817	342.1445	682.2977	341.6525	6
4	405.1769	203.0921	387.1663	194.0868	Y	613.2763	307.1418	596.2497	298.6285	595.2657	298.1365	5
5	462.1983	231.6028	444.1878	222.5975	G	450.2129	225.6101	433.1864	217.0968	432.2024	216.6048	4
6	593.2388	297.1230	575.2282	288.1178	M	393.1915	197.0994	376.1649	188.5861	375.1809	188.0941	3
7	680.2708	340.6391	662.2603	331.6338	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
8					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 56 ppm



RMS error 56 ppm

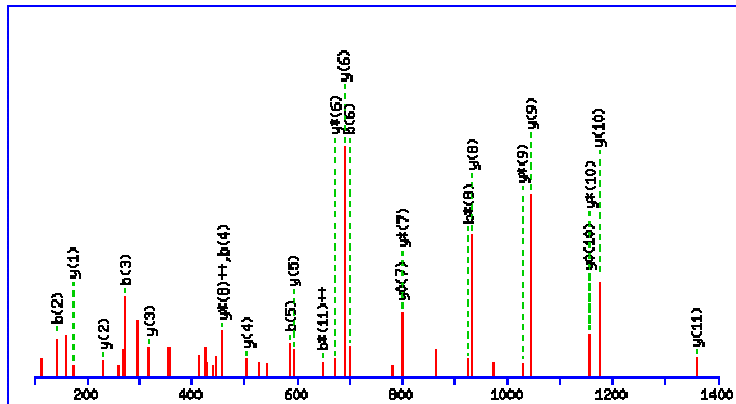
Peptide Number: 37514

MS/MS Fragmentation of **AAEWQLDQPSWSGR**Found in **IP100018188** in **IP1_human**, Tax_Id=9606 Gene_Symbol=NECAP2 Isoform 1 of Adaptin ear-binding coat-associated protein 2

Match to Query 14946: 1629.760308 from(815.887430,2+) index(600)

Title: Elution from: 1.45 to 1.45 period: 0 cycle: 55 experiment: 9 polarity:+

Data file 120208ry_Tig120slc-P8_2_3.mgf



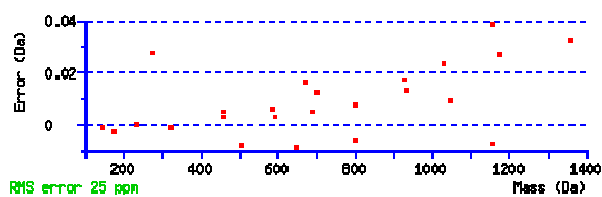
Monoisotopic mass of neutral peptide Mr(calc): 1629.7536

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

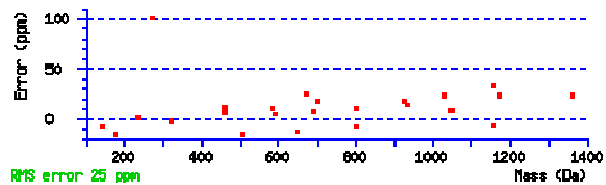
Ions Score: 70 Expect: 3.5e-006

Matches : 24/140 fragment ions using 38 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							14
2	143.0815	72.0444					A	1559.7237	780.3655	1542.6972	771.8522	1541.7132	771.3602	13
3	272.1241	136.5657			254.1135	127.5604	E	1488.6866	744.8469	1471.6601	736.3337	1470.6761	735.8417	12
4	458.2034	229.6053			440.1928	220.6001	W	1359.6440	680.3257	1342.6175	671.8124	1341.6335	671.3204	11
5	586.2620	293.6346	569.2354	285.1214	568.2514	284.6293	Q	1173.5647	587.2860	1156.5382	578.7727	1155.5541	578.2807	10
6	699.3461	350.1767	682.3195	341.6634	681.3355	341.1714	L	1045.5061	523.2567	1028.4796	514.7434	1027.4956	514.2514	9
7	814.3730	407.6901	797.3464	399.1769	796.3624	398.6849	D	932.4221	466.7147	915.3955	458.2014	914.4115	457.7094	8
8	942.4316	471.7194	925.4050	463.2062	924.4210	462.7141	Q	817.3951	409.2012	800.3686	400.6879	799.3846	400.1959	7
9	1039.4843	520.2458	1022.4578	511.7325	1021.4738	511.2405	P	689.3365	345.1719	672.3100	336.6586	671.3260	336.1666	6
10	1126.5164	563.7618	1109.4898	555.2485	1108.5058	554.7565	S	592.2838	296.6455	575.2572	288.1323	574.2732	287.6402	5
11	1312.5957	656.8015	1295.5691	648.2882	1294.5851	647.7962	W	505.2518	253.1295	488.2252	244.6162	487.2412	244.1242	4
12	1399.6277	700.3175	1382.6012	691.8042	1381.6171	691.3122	S	319.1724	160.0899	302.1459	151.5766	301.1619	151.0846	3
13	1456.6492	728.8282	1439.6226	720.3149	1438.6386	719.8229	G	232.1404	116.5738	215.1139	108.0606			2
14							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 25 ppm



RMS error 25 ppm

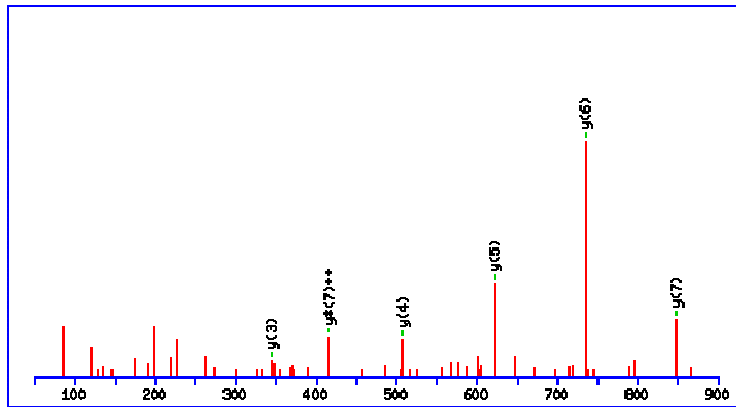
Peptide Number: 38006**MS/MS Fragmentation of LLLNYAVR**

Found in **IPI00024381** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CLP1 Isoform 1 of Polyribonucleotide 5'-hydroxyl-kinase Clp1

Match to Query 5516: 960.577988 from(481.296270,2+) index(32696)

Title: Elution from: 78.6666666666667 to 78.6666666666667 period: 0 cycle: 2969 experiment: 6 polarity:+

Data file 120212ry_414C2-43_3_2.mgf



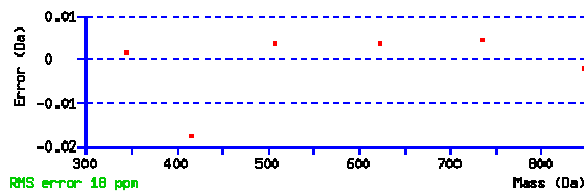
Monoisotopic mass of neutral peptide Mr(calc): 960.5756

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

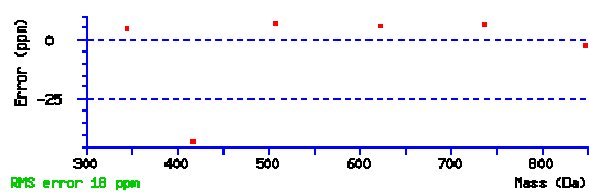
Ions Score: 42 **Expect:** 0.0018

Matches : 6/50 fragment ions using 8 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	#
1	114.0913	57.5493			L					8
2	227.1754	114.0913			L	848.4989	424.7531	831.4723	416.2398	7
3	340.2595	170.6334			L	735.4148	368.2110	718.3883	359.6978	6
4	454.3024	227.6548	437.2758	219.1416	N	622.3307	311.6690	605.3042	303.1557	5
5	617.3657	309.1865	600.3392	300.6732	Y	508.2878	254.6475	491.2613	246.1343	4
6	688.4028	344.7051	671.3763	336.1918	A	345.2245	173.1159	328.1979	164.6026	3
7	787.4713	394.2393	770.4447	385.7260	V		274.1874	137.5973	257.1608	2
8					R	175.1190	88.0631	158.0924	79.5498	1



RMS error 18 ppm



RMS error 18 ppm

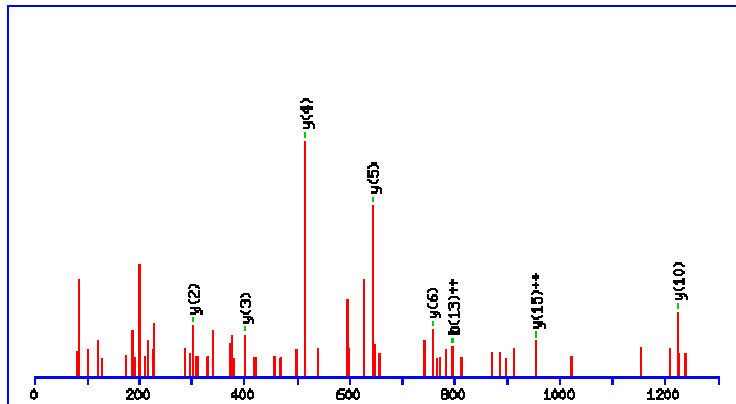
Peptide Number: 38082

MS/MS Fragmentation of **LTINQQWKPIEELQNVQR**Found in **IPI00031772** in **IPI_human**, Tax_Id=9606 Gene_Symbol=C15orf48 Normal mucosa of esophagus-specific gene 1 protein

Match to Query 32834: 2349.307736 from(588.334210,4+) index(23504)

Title: Elution from: 60.1666666666667 to 60.1666666666667 period: 0 cycle: 2288 experiment: 3 polarity: +

Data file 120206ry_aHDF1419-P10_3_3.mgf



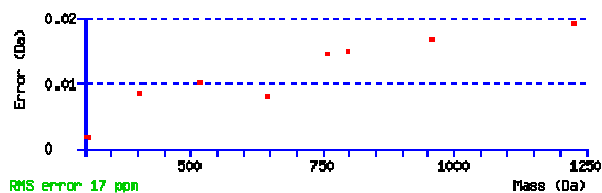
Monoisotopic mass of neutral peptide Mr(calc): 2349.2804

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

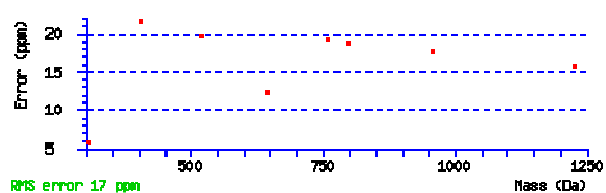
Ions Score: 35 Expect: 0.0085

Matches : 8/192 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							19
2	227.1754	114.0913					I	2237.2037	1119.1055	2220.1771	1110.5922	2219.1931	1110.1002	18
3	328.2231	164.6152			310.2125	155.6099	T	2124.1196	1062.5635	2107.0931	1054.0502	2106.1091	1053.5582	17
4	441.3071	221.1572			423.2966	212.1519	I	2023.0719	1012.0396	2006.0454	1003.5263	2005.0614	1003.0343	16
5	555.3501	278.1787	538.3235	269.6654	537.3395	269.1734	N	1909.9879	955.4976	1892.9613	946.9843	1891.9773	946.4923	15
6	683.4087	342.2080	666.3821	333.6947	665.3981	333.2027	Q	1795.9450	898.4761	1778.9184	889.9628	1777.9344	889.4708	14
7	811.4672	406.2373	794.4407	397.7240	793.4567	397.2320	Q	1667.8864	834.4468	1650.8598	825.9336	1649.8758	825.4415	13
8	997.5465	499.2769	980.5200	490.7636	979.5360	490.2716	W	1539.8278	770.4175	1522.8013	761.9043	1521.8172	761.4123	12
9	1125.6415	563.3244	1108.6150	554.8111	1107.6309	554.3191	K	1353.7485	677.3779	1336.7219	668.8646	1335.7379	668.3726	11
10	1222.6943	611.8508	1205.6677	603.3375	1204.6837	602.8455	P	1225.6535	613.3304	1208.6270	604.8171	1207.6430	604.3251	10
11	1335.7783	668.3928	1318.7518	659.8795	1317.7678	659.3875	I	1128.6008	564.8040	1111.5742	556.2907	1110.5902	555.7987	9
12	1464.8209	732.9141	1447.7944	724.4008	1446.8104	723.9088	E	1015.5167	508.2620	998.4901	499.7487	997.5061	499.2567	8
13	1593.8635	797.4354	1576.8370	788.9221	1575.8530	788.4301	E	886.4741	443.7407	869.4476	435.2274	868.4635	434.7354	7
14	1706.9476	853.9774	1689.9210	845.4642	1688.9370	844.9721	L	757.4315	379.2194	740.4050	370.7061			6
15	1835.0062	918.0067	1817.9796	909.4934	1816.9956	909.0014	Q	644.3474	322.6774	627.3209	314.1641			5
16	1949.0491	975.0282	1932.0225	966.5149	1931.0385	966.0229	N	516.2889	258.6481	499.2623	250.1348			4
17	2048.1175	1024.5624	2031.0910	1016.0491	2030.1069	1015.5571	V	402.2459	201.6266	385.2194	193.1133			3
18	2176.1761	1088.5917	2159.1495	1080.0784	2158.1655	1079.5864	Q	303.1775	152.0924	286.1510	143.5791			2
19							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 17 ppm



RMS error 17 ppm

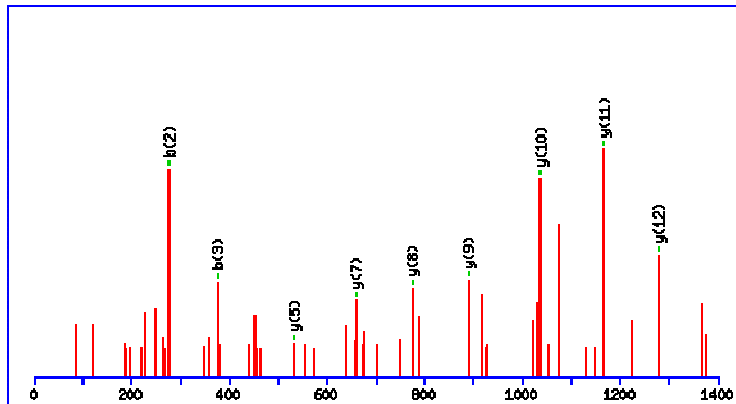
Peptide Number: 38108

MS/MS Fragmentation of **FEVIEFDDGAGSVLR**Found in **IPI00107831** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PTPRF Isoform 1 of Receptor-type tyrosine-protein phosphatase F

Match to Query 16763: 1652.802328 from(827.408440,2+) index(26478)

Title: Elution from: 65.8 to 65.8 period: 0 cycle: 2479 experiment: 6 polarity: +

Data file 120210ry_32R1-32_3_3.mgf



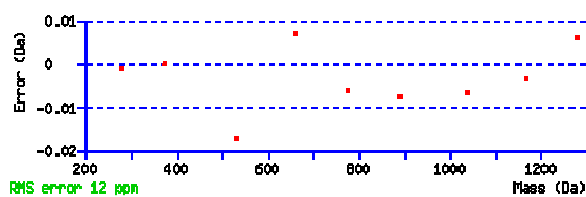
Monoisotopic mass of neutral peptide Mr(calc): 1652.8046

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

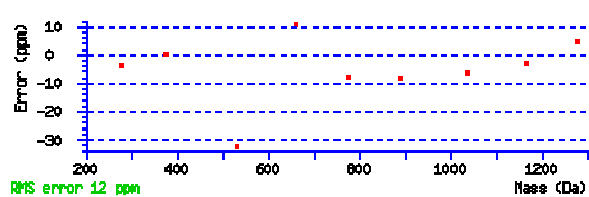
Ions Score: 51 Expect: 0.00046

Matches : 9/132 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415			F							15
2	277.1183	139.0628	259.1077	130.0575	E	1506.7435	753.8754	1489.7169	745.3621	1488.7329	744.8701	14
3	376.1867	188.5970	358.1761	179.5917	V	1377.7009	689.3541	1360.6743	680.8408	1359.6903	680.3488	13
4	489.2708	245.1390	471.2602	236.1337	I	1278.6325	639.8199	1261.6059	631.3066	1260.6219	630.8146	12
5	618.3134	309.6603	600.3028	300.6550	E	1165.5484	583.2778	1148.5218	574.7646	1147.5378	574.2726	11
6	765.3818	383.1945	747.3712	374.1892	F	1036.5058	518.7565	1019.4793	510.2433	1018.4952	509.7513	10
7	880.4087	440.7080	862.3981	431.7027	D	889.4374	445.2223	872.4108	436.7091	871.4268	436.2170	9
8	995.4357	498.2215	977.4251	489.2162	D	774.4104	387.7089	757.3839	379.1956	756.3999	378.7036	8
9	1052.4571	526.7322	1034.4466	517.7269	G	659.3835	330.1954	642.3570	321.6821	641.3729	321.1901	7
10	1123.4942	562.2508	1105.4837	553.2455	A	602.3620	301.6847	585.3355	293.1714	584.3515	292.6794	6
11	1180.5157	590.7615	1162.5051	581.7562	G	531.3249	266.1661	514.2984	257.6528	513.3144	257.1608	5
12	1267.5477	634.2775	1249.5372	625.2722	S	474.3035	237.6554	457.2769	229.1421	456.2929	228.6501	4
13	1366.6161	683.8117	1348.6056	674.8064	V	387.2714	194.1394	370.2449	185.6261			3
14	1479.7002	740.3537	1461.6896	731.3485	L	288.2030	144.6051	271.1765	136.0919			2
15					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 12 ppm



RMS error 12 ppm

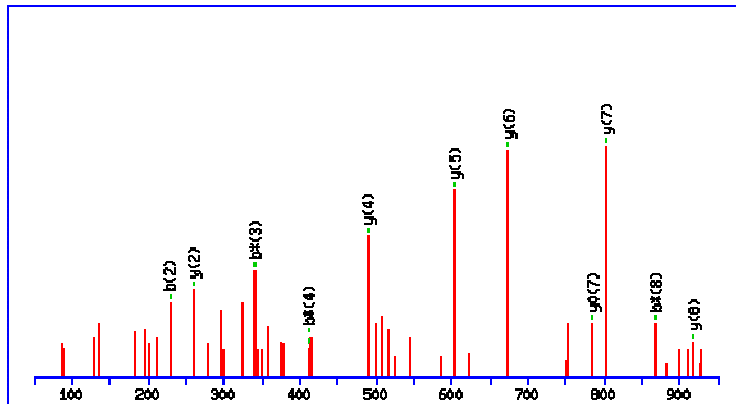
Peptide Number: 38122

MS/MS Fragmentation of **NNEALDDLK**Found in **IPI00028369** in **IPI_human**, Tax_Id=9606 Gene_Symbol=KIAA1715 Isoform 1 of Protein lunapark

Match to Query 7570: 1030.492988 from(516.253770,2+) index(579)

Title: Elution from: 1.41666666666667 to 1.41666666666667 period: 0 cycle: 55 experiment: 8 polarity: +

Data file 120208ry_Tig120slc-P8_1_2.mgf



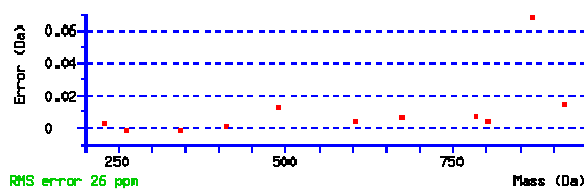
Monoisotopic mass of neutral peptide Mr(calc): 1030.4931

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

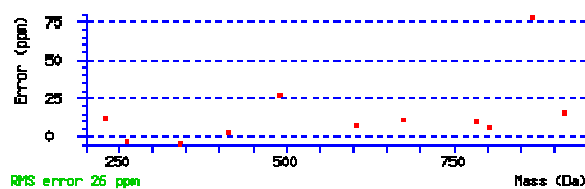
Ions Score: 45 Expect: 0.0014

Matches : 11/88 fragment ions using 18 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							9
2	229.0931	115.0502	212.0666	106.5369			N	917.4575	459.2324	900.4309	450.7191	899.4469	450.2271	8
3	358.1357	179.5715	341.1092	171.0582	340.1252	170.5662	E	803.4145	402.2109	786.3880	393.6976	785.4040	393.2056	7
4	429.1728	215.0901	412.1463	206.5768	411.1623	206.0848	A	674.3719	337.6896	657.3454	329.1763	656.3614	328.6843	6
5	542.2569	271.6321	525.2304	263.1188	524.2463	262.6268	L	603.3348	302.1710	586.3083	293.6578	585.3243	293.1658	5
6	657.2838	329.1456	640.2573	320.6323	639.2733	320.1403	D	490.2508	245.6290	473.2242	237.1157	472.2402	236.6237	4
7	772.3108	386.6590	755.2842	378.1458	754.3002	377.6537	D	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
8	885.3949	443.2011	868.3683	434.6878	867.3843	434.1958	L	260.1969	130.6021	243.1703	122.0888			2
9							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 26 ppm



RMS error 26 ppm

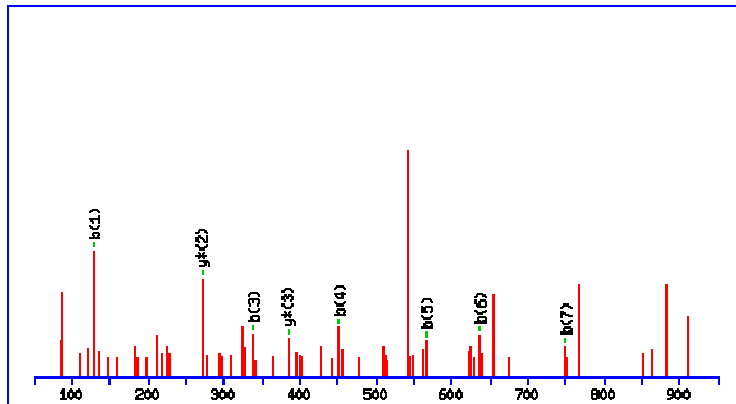
Peptide Number: 38229**MS/MS Fragmentation of KIPLNALIR**

Found in **IPI00472977** in **IPI_human**, Tax_Id=9606 Gene_Symbol=USP37 Isoform 1 of Ubiquitin carboxyl-terminal hydrolase 37

Match to Query 1193: 1036.666548 from(519.340550,2+) index(7149)

Title: Elution from: 17.0333333333333 to 17.0333333333333 period: 0 cycle: 644 experiment: 3 polarity:+

Data file 120212ry_aHDF1388-P9_2_3.mgf



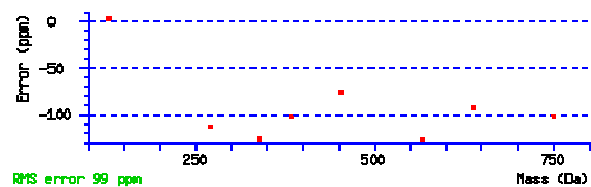
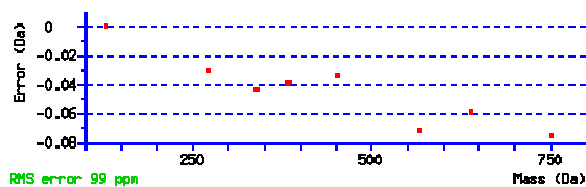
Monoisotopic mass of neutral peptide Mr(calcd): 1036.6757

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 27 **Expect:** 0.0089

Matches : 8/64 fragment ions using 17 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	Seq.	y	y ⁺⁺	y*	y ^{*++}	#
1	129.1022	65.0548	112.0757	56.5415	K					9
2	242.1863	121.5968	225.1598	113.0835	I	909.5880	455.2976	892.5615	446.7844	8
3	339.2391	170.1232	322.2125	161.6099	P	796.5039	398.7556	779.4774	390.2423	7
4	452.3231	226.6652	435.2966	218.1519	L	699.4512	350.2292	682.4246	341.7160	6
5	566.3661	283.6867	549.3395	275.1734	N	586.3671	293.6872	569.3406	285.1739	5
6	637.4032	319.2052	620.3766	310.6919	A	472.3242	236.6657	455.2976	228.1525	4
7	750.4872	375.7473	733.4607	367.2340	L	401.2871	201.1472	384.2605	192.6339	3
8	863.5713	432.2893	846.5448	423.7760	I	288.2030	144.6051	271.1765	136.0919	2
9					R	175.1190	88.0631	158.0924	79.5498	1



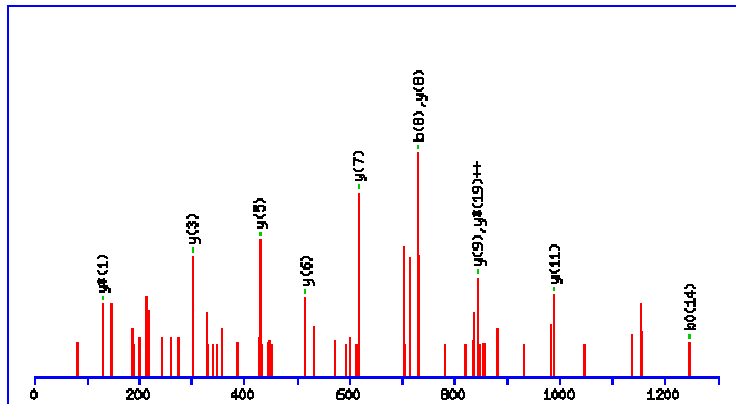
Peptide Number: 38339

MS/MS Fragmentation of **SEGEGEAASADDGSLNTSGAGPK**Found in **IPI00101987** in **IPI_human**, Tax_Id=9606 Gene_Symbol=BABAM1 Isoform 1 of BRISC and BRCA1-A complex member 1

Match to Query 31248: 2105.897892 from(702.973240,3+) index(28959)

Title: Elution from: 105.583333333333 to 105.583333333333 period: 0 cycle: 7806 experiment: 9 polarity:+

Data file 120208ry_Tig120slc-P8_1_1.mgf



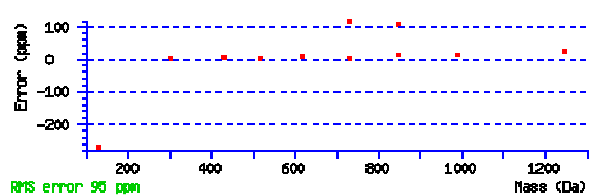
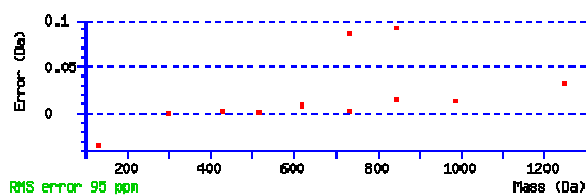
Monoisotopic mass of neutral peptide Mr(calc): 2105.8985

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 47 Expect: 0.00028

Matches : 11/224 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							23
2	217.0819	109.0446			199.0713	100.0393	E	2019.8738	1010.4405	2002.8472	1001.9272	2001.8632	1001.4352	22
3	274.1034	137.5553			256.0928	128.5500	G	1890.8312	945.9192	1873.8046	937.4059	1872.8206	936.9139	21
4	403.1460	202.0766			385.1354	193.0713	E	1833.8097	917.4085	1816.7832	908.8952	1815.7991	908.4032	20
5	460.1674	230.5873			442.1569	221.5821	G	1704.7671	852.8872	1687.7406	844.3739	1686.7565	843.8819	19
6	589.2100	295.1086			571.1994	286.1034	E	1647.7456	824.3765	1630.7191	815.8632	1629.7351	815.3712	18
7	660.2471	330.6272			642.2366	321.6219	A	1518.7031	759.8552	1501.6765	751.3419	1500.6925	750.8499	17
8	731.2842	366.1458			713.2737	357.1405	A	1447.6659	724.3366	1430.6394	715.8233	1429.6554	715.3313	16
9	818.3163	409.6618			800.3057	400.6565	S	1376.6288	688.8181	1359.6023	680.3048	1358.6183	679.8128	15
10	889.3534	445.1803			871.3428	436.1750	A	1289.5968	645.3020	1272.5703	636.7888	1271.5862	636.2968	14
11	1004.3803	502.6938			986.3698	493.6885	D	1218.5597	609.7835	1201.5331	601.2702	1200.5491	600.7782	13
12	1119.4073	560.2073			1101.3967	551.2020	D	1103.5327	552.2700	1086.5062	543.7567	1085.5222	543.2647	12
13	1176.4287	588.7180			1158.4182	579.7127	G	988.5058	494.7565	971.4793	486.2433	970.4952	485.7513	11
14	1263.4608	632.2340			1245.4502	623.2287	S	931.4843	466.2458	914.4578	457.7325	913.4738	457.2405	10
15	1376.5448	688.7760			1358.5343	679.7708	L	844.4523	422.7298	827.4258	414.2165	826.4417	413.7245	9
16	1490.5877	745.7975	1473.5612	737.2842	1472.5772	736.7922	N	731.3682	366.1878	714.3417	357.6745	713.3577	357.1825	8
17	1591.6354	796.3214	1574.6089	787.8081	1573.6249	787.3161	T	617.3253	309.1663	600.2988	300.6530	599.3148	300.1610	7
18	1678.6675	839.8374	1661.6409	831.3241	1660.6569	830.8321	S	516.2776	258.6425	499.2511	250.1292	498.2671	249.6372	6
19	1735.6889	868.3481	1718.6624	859.8348	1717.6784	859.3428	G	429.2456	215.1264	412.2191	206.6132			5
20	1806.7260	903.8667	1789.6995	895.3534	1788.7155	894.8614	A	372.2241	186.6157	355.1976	178.1024			4
21	1863.7475	932.3774	1846.7209	923.8641	1845.7369	923.3721	G	301.1870	151.0972	284.1605	142.5839			3
22	1960.8003	980.9038	1943.7737	972.3905	1942.7897	971.8985	P	244.1656	122.5864	227.1390	114.0731			2
23							K	147.1128	74.0600	130.0863	65.5468			1



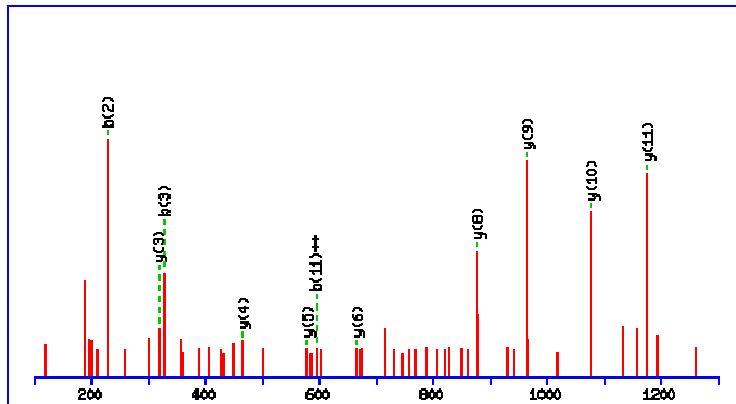
Peptide Number: 38342

MS/MS Fragmentation of **TQVLSPDSLFTAK**Found in **IPI00398718** in **IPI_human**, Tax_Id=9606 Gene_Symbol=MLLT4 Isoform 2 of Afadin

Match to Query 8149: 1405.745068 from(703.879810,2+) index(6164)

Title: Elution from: 15.15 to 15.15 period: 0 cycle: 572 experiment: 9 polarity: +

Data file 120214ry_414C2-43_4_3.mgf



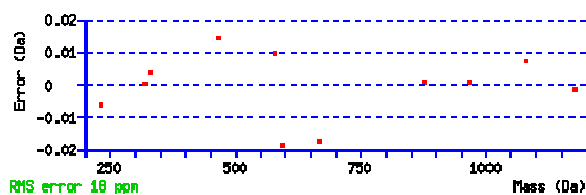
Monoisotopic mass of neutral peptide Mr(calc): 1405.7453

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

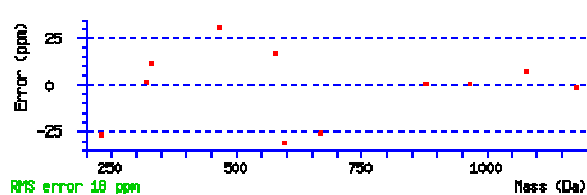
Ions Score: 49 Expect: 0.0008

Matches : 11/138 fragment ions using 23 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							13
2	230.1135	115.5604	213.0870	107.0471	212.1030	106.5551	Q	1305.7049	653.3561	1288.6783	644.8428	1287.6943	644.3508	12
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	V	1177.6463	589.3268	1160.6198	580.8135	1159.6358	580.3215	11
4	442.2660	221.6366	425.2395	213.1234	424.2554	212.6314	L	1078.5779	539.7926	1061.5514	531.2793	1060.5673	530.7873	10
5	529.2980	265.1527	512.2715	256.6394	511.2875	256.1474	S	965.4938	483.2506	948.4673	474.7373	947.4833	474.2453	9
6	626.3508	313.6790	609.3243	305.1658	608.3402	304.6738	P	878.4618	439.7345	861.4353	431.2213	860.4512	430.7293	8
7	741.3777	371.1925	724.3512	362.6792	723.3672	362.1872	D	781.4090	391.2082	764.3825	382.6949	763.3985	382.2029	7
8	828.4098	414.7085	811.3832	406.1953	810.3992	405.7032	S	666.3821	333.6947	649.3556	325.1814	648.3715	324.6894	6
9	941.4938	471.2506	924.4673	462.7373	923.4833	462.2453	L	579.3501	290.1787	562.3235	281.6654	561.3395	281.1734	5
10	1088.5623	544.7848	1071.5357	536.2715	1070.5517	535.7795	F	466.2660	233.6366	449.2395	225.1234	448.2554	224.6314	4
11	1189.6099	595.3086	1172.5834	586.7953	1171.5994	586.3033	T	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	3
12	1260.6470	630.8272	1243.6205	622.3139	1242.6365	621.8219	A	218.1499	109.5786	201.1234	101.0653			2
13							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 18 ppm



RMS error 18 ppm

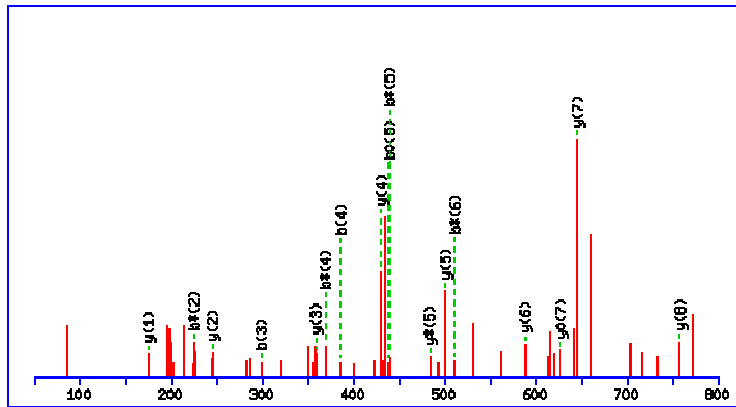
Peptide Number: 38388**MS/MS Fragmentation of QLGSAAALAR**

Found in **IPI00297322** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ARFGAP2 ADP-ribosylation factor GTPase-activating protein 2

Match to Query 5920: 885.493508 from(443.754030,2+) index(20361)

Title: Elution from: 85.2833333333333 to 85.2833333333333 period: 0 cycle: 8059 experiment: 4 polarity: +

Data file 120206ry_aHDF1419-P10_2_1.mgf



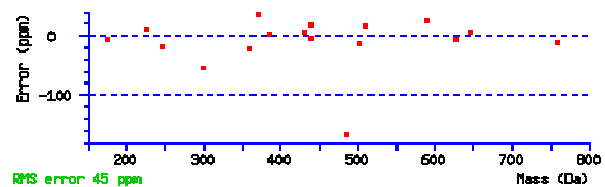
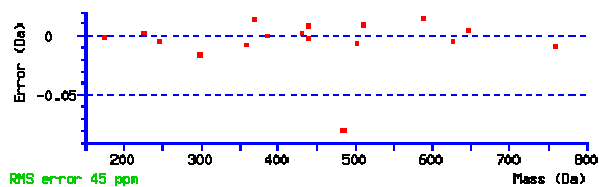
Monoisotopic mass of neutral peptide Mr(calcd): 885.5032

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 44 **Expect:** 0.003

Matches : 17/80 fragment ions using 50 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	129.0659	65.0366	112.0393	56.5233			Q							9
2	242.1499	121.5786	225.1234	113.0653			L	758.4519	379.7296	741.4254	371.2163	740.4413	370.7243	8
3	299.1714	150.0893	282.1448	141.5761			G	645.3679	323.1876	628.3413	314.6743	627.3573	314.1823	7
4	386.2034	193.6053	369.1769	185.0921	368.1928	184.6001	S	588.3464	294.6768	571.3198	286.1636	570.3358	285.6715	6
5	457.2405	229.1239	440.2140	220.6106	439.2300	220.1186	A	501.3144	251.1608	484.2878	242.6475			5
6	528.2776	264.6425	511.2511	256.1292	510.2671	255.6372	A	430.2772	215.6423	413.2507	207.1290			4
7	641.3617	321.1845	624.3352	312.6712	623.3511	312.1792	L	359.2401	180.1237	342.2136	171.6104			3
8	712.3988	356.7030	695.3723	348.1898	694.3883	347.6978	A	246.1561	123.5817	229.1295	115.0684			2
9							R	175.1190	88.0631	158.0924	79.5498			1

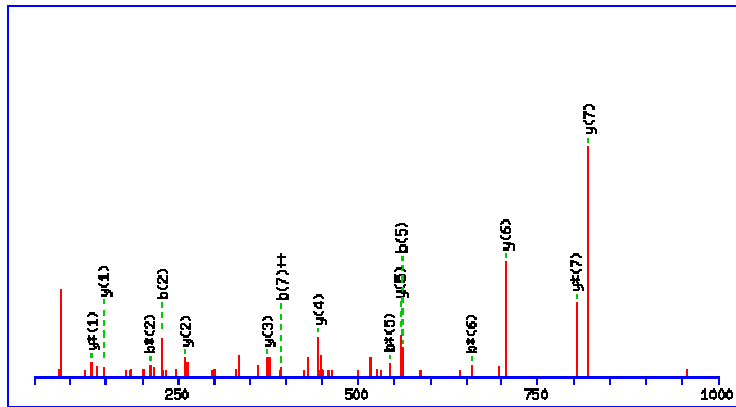


Peptide Number: 38550**MS/MS Fragmentation of INFDALLK**Found in **IPI00022748** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TMBIM6 Bax inhibitor 1

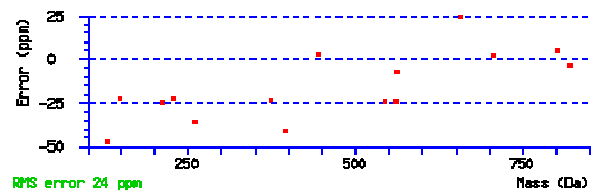
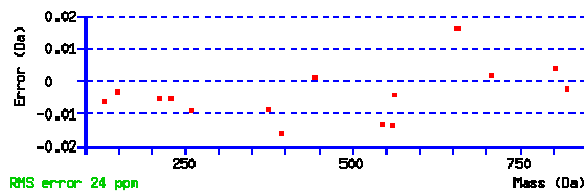
Match to Query 496: 932.522848 from(467.268700,2+) index(16244)

Title: Elution from: 39.4833333333333 to 39.4833333333333 period: 0 cycle: 1458 experiment: 1 polarity:+

Data file 120118ry_201B7-32_1_3.mgf

**Monoisotopic mass of neutral peptide Mr(calc):** 932.5331**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 42 **Expect:** 0.0045**Matches :** 15/68 fragment ions using 33 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							8
2	228.1343	114.5708	211.1077	106.0575			N	820.4563	410.7318	803.4298	402.2185	802.4458	401.7265	7
3	375.2027	188.1050	358.1761	179.5917			F	706.4134	353.7103	689.3869	345.1971	688.4028	344.7051	6
4	490.2296	245.6185	473.2031	237.1052	472.2191	236.6132	D	559.3450	280.1761	542.3184	271.6629	541.3344	271.1709	5
5	561.2667	281.1370	544.2402	272.6237	543.2562	272.1317	A	444.3180	222.6627	427.2915	214.1494			4
6	674.3508	337.6790	657.3243	329.1658	656.3402	328.6738	L	373.2809	187.1441	356.2544	178.6308			3
7	787.4349	394.2211	770.4083	385.7078	769.4243	385.2158	L	260.1969	130.6021	243.1703	122.0888			2
8							K	147.1128	74.0600	130.0863	65.5468			1

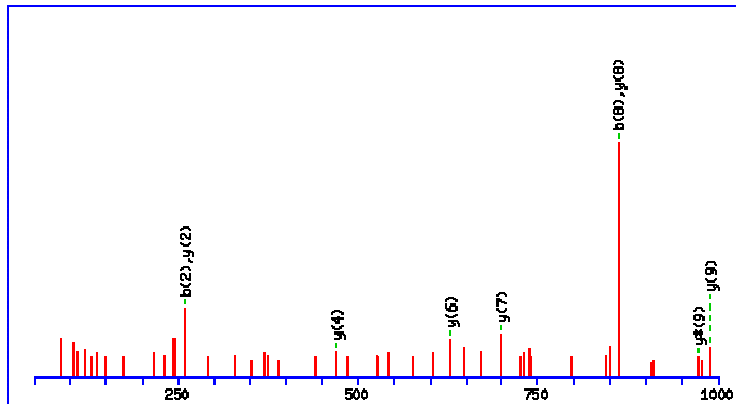


Peptide Number: 38965MS/MS Fragmentation of **MQYATGPLLK**Found in **IPI00008351** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SELT Selenoprotein T

Match to Query 10079: 1120.596228 from(561.305390,2+) index(20266)

Title: Elution from: 51.0833333333333 to 51.0833333333333 period: 0 cycle: 1942 experiment: 4 polarity: +

Data file 120206ry_aHDF1419-P10_3_2.mgf



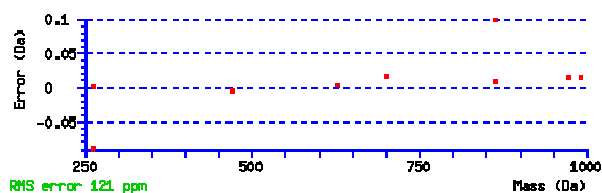
Monoisotopic mass of neutral peptide Mr(calc): 1120.5950

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

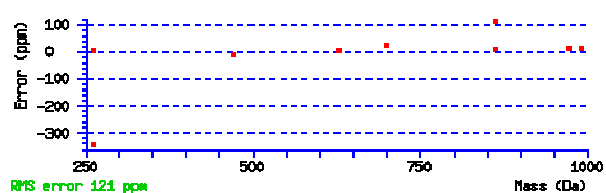
Ions Score: 47 Expect: 0.0013

Matches : 9/88 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	132.0478	66.5275					M							10
2	260.1063	130.5568	243.0798	122.0435			Q	990.5619	495.7846	973.5353	487.2713	972.5513	486.7793	9
3	423.1697	212.0885	406.1431	203.5752			Y	862.5033	431.7553	845.4767	423.2420	844.4927	422.7500	8
4	494.2068	247.6070	477.1802	239.0938			A	699.4400	350.2236	682.4134	341.7103	681.4294	341.2183	7
5	595.2545	298.1309	578.2279	289.6176	577.2439	289.1256	T	628.4028	314.7051	611.3763	306.1918	610.3923	305.6998	6
6	652.2759	326.6416	635.2494	318.1283	634.2654	317.6363	G	527.3552	264.1812	510.3286	255.6679			5
7	749.3287	375.1680	732.3021	366.6547	731.3181	366.1627	P	470.3337	235.6705	453.3071	227.1572			4
8	862.4128	431.7100	845.3862	423.1967	844.4022	422.7047	L	373.2809	187.1441	356.2544	178.6308			3
9	975.4968	488.2520	958.4703	479.7388	957.4863	479.2468	L	260.1969	130.6021	243.1703	122.0888			2
10							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 121 ppm



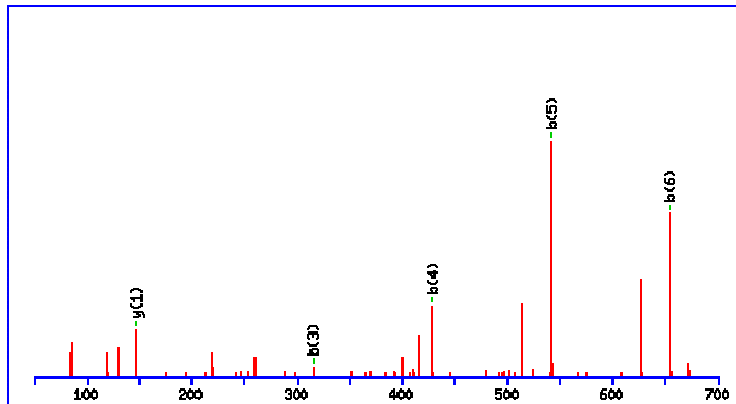
RMS error 121 ppm

Peptide Number: 39053MS/MS Fragmentation of **NSLLLIK**Found in **IPI00744077** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CAPRIN2 caprin-2 isoform 4

Match to Query 3840: 799.531028 from(400.772790,2+) index(14330)

Title: Elution from: 76.15 to 76.15 period: 0 cycle: 7917 experiment: 2 polarity:+

Data file 120212ry_aHDF1388-P9_2_1.mgf



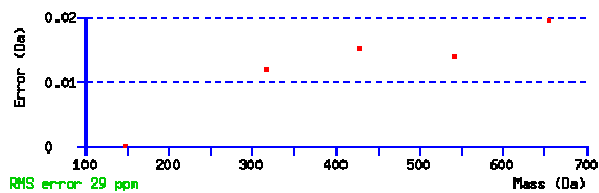
Monoisotopic mass of neutral peptide Mr(calc): 799.5167

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

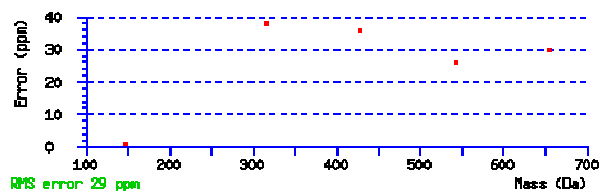
Ions Score: 35 Expect: 0.0065

Matches : 5/60 fragment ions using 6 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							7
2	202.0822	101.5448	185.0557	93.0315	184.0717	92.5395	S	686.4811	343.7442	669.4545	335.2309	668.4705	334.7389	6
3	315.1663	158.0868	298.1397	149.5735	297.1557	149.0815	L	599.4491	300.2282	582.4225	291.7149			5
4	428.2504	214.6288	411.2238	206.1155	410.2398	205.6235	L	486.3650	243.6861	469.3384	235.1729			4
5	541.3344	271.1708	524.3079	262.6576	523.3239	262.1656	L	373.2809	187.1441	356.2544	178.6308			3
6	654.4185	327.7129	637.3919	319.1996	636.4079	318.7076	I	260.1969	130.6021	243.1703	122.0888			2
7							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 29 ppm



RMS error 29 ppm

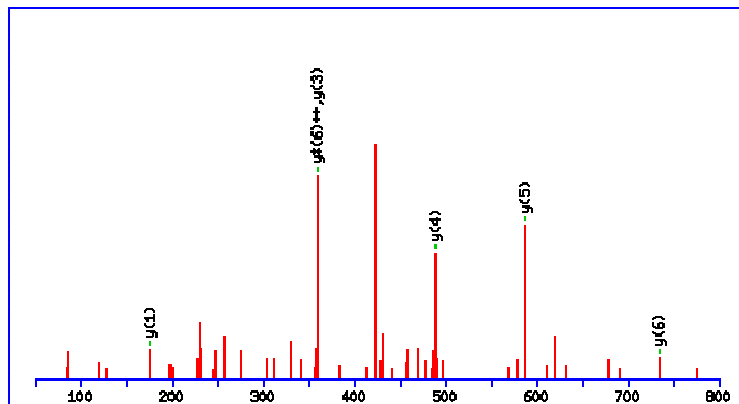
Peptide Number: 39539**MS/MS Fragmentation of EFVEALR**

Found in **IPI00005577** in **IPI_human**, Tax_Id=9606 Gene_Symbol=IFIH1 Isoform 1 of Interferon-induced helicase C domain-containing protein 1

Match to Query 5656: 862.439308 from(432.226930,2+) index(12861)

Title: Elution from: 73.1166666666667 to 73.1166666666667 period: 0 cycle: 7799 experiment: 7 polarity:+

Data file 120214ry_aHDF1419-P10_4_1.mgf



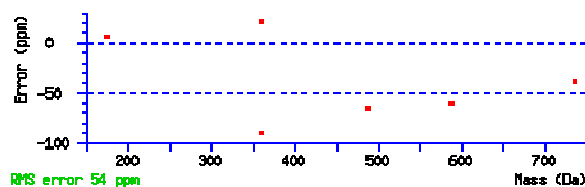
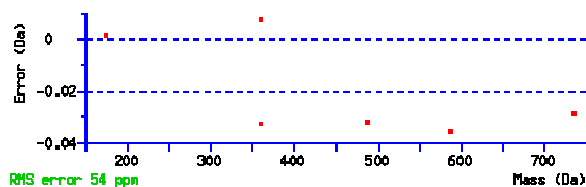
Monoisotopic mass of neutral peptide Mr(calc): 862.4548

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 42 **Expect:** 0.0048

Matches : 6/54 fragment ions using 7 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286	112.0393	56.5233	E							7
2	277.1183	139.0628	259.1077	130.0575	F	734.4196	367.7134	717.3930	359.2001	716.4090	358.7081	6
3	376.1867	188.5970	358.1761	179.5917	V	587.3511	294.1792	570.3246	285.6659	569.3406	285.1739	5
4	505.2293	253.1183	487.2187	244.1130	E	488.2827	244.6450	471.2562	236.1317	470.2722	235.6397	4
5	576.2664	288.6368	558.2558	279.6316	A	359.2401	180.1237	342.2136	171.6104			3
6	689.3505	345.1789	671.3399	336.1736	L	288.2030	144.6051	271.1765	136.0919			2
7					R	175.1190	88.0631	158.0924	79.5498			1



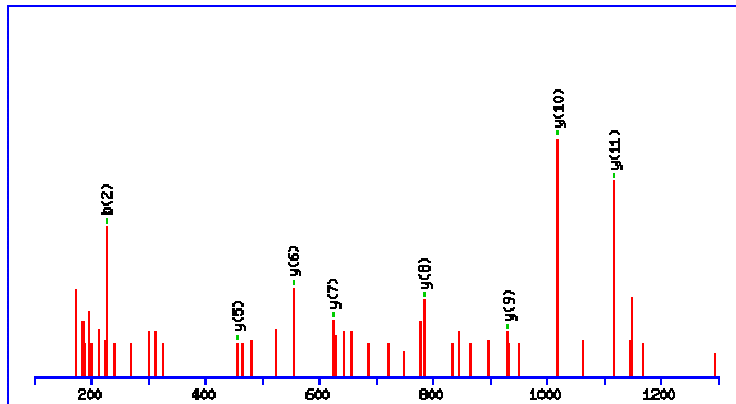
Peptide Number: 39566

MS/MS Fragmentation of **VQVSFCAPGAPGR**Found in **IPI00397768** in **IPI_human**, Tax_Id=9606 Gene_Symbol=RAVER2 Isoform 2 of Ribonucleoprotein PTB-binding 2

Match to Query 22951: 1344.648128 from(673.331340,2+) index(21679)

Title: Elution from: 52.6333333333333 to 52.6333333333333 period: 0 cycle: 1990 experiment: 9 polarity:+

Data file 120210ry_32R1-32_3_2.mgf



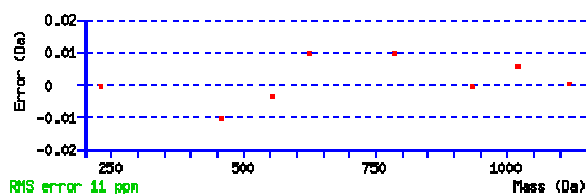
Monoisotopic mass of neutral peptide Mr(calc): 1344.6609

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

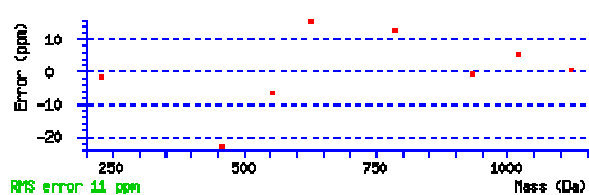
Ions Score: 57 Expect: 0.00012

Matches : 8/118 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							13
2	228.1343	114.5708	211.1077	106.0575			Q	1246.5997	623.8035	1229.5732	615.2902	1228.5892	614.7982	12
3	327.2027	164.1050	310.1761	155.5917			V	1118.5411	559.7742	1101.5146	551.2609	1100.5306	550.7689	11
4	414.2347	207.6210	397.2082	199.1077	396.2241	198.6157	S	1019.4727	510.2400	1002.4462	501.7267	1001.4622	501.2347	10
5	561.3031	281.1552	544.2766	272.6419	543.2926	272.1499	F	932.4407	466.7240	915.4141	458.2107			9
6	721.3338	361.1705	704.3072	352.6573	703.3232	352.1652	C	785.3723	393.1898	768.3457	384.6765			8
7	792.3709	396.6891	775.3443	388.1758	774.3603	387.6838	A	625.3416	313.1745	608.3151	304.6612			7
8	889.4237	445.2155	872.3971	436.7022	871.4131	436.2102	P	554.3045	277.6559	537.2780	269.1426			6
9	946.4451	473.7262	929.4186	465.2129	928.4346	464.7209	G	457.2518	229.1295	440.2252	220.6162			5
10	1017.4822	509.2448	1000.4557	500.7315	999.4717	500.2395	A	400.2303	200.6188	383.2037	192.1055			4
11	1114.5350	557.7711	1097.5084	549.2579	1096.5244	548.7659	P	329.1932	165.1002	312.1666	156.5870			3
12	1171.5565	586.2819	1154.5299	577.7686	1153.5459	577.2766	G	232.1404	116.5738	215.1139	108.0606			2
13							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 11 ppm



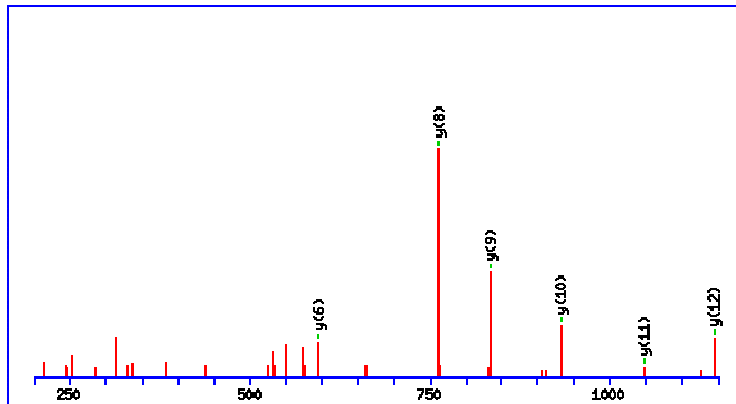
RMS error 11 ppm

Peptide Number: 39662MS/MS Fragmentation of **AAAPDVAPAPGPAPR**Found in **IPI00153005** in **IPI_human**, Tax_Id=9606 Gene_Symbol=HVCN1 Isoform 1 of Voltage-gated hydrogen channel 1

Match to Query 22132: 1356.711308 from(679.362930,2+) index(21007)

Title: Elution from: 90.8166666666667 to 90.8166666666667 period: 0 cycle: 8447 experiment: 10 polarity: +

Data file 120212ry_414C2-43_3_1.mgf



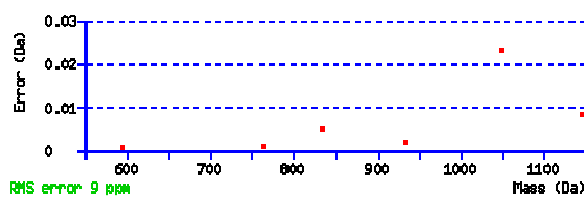
Monoisotopic mass of neutral peptide Mr(calc): 1356.7150

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

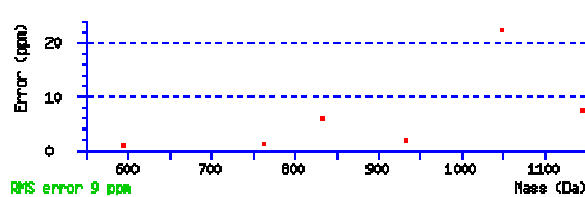
Ions Score: 41 Expect: 0.0063

Matches : 6/112 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258			A							15
2	143.0815	72.0444			A	1286.6852	643.8462	1269.6586	635.3329	1268.6746	634.8409	14
3	214.1186	107.5629			A	1215.6480	608.3277	1198.6215	599.8144	1197.6375	599.3224	13
4	311.1714	156.0893			P	1144.6109	572.8091	1127.5844	564.2958	1126.6004	563.8038	12
5	426.1983	213.6028	408.1878	204.5975	D	1047.5582	524.2827	1030.5316	515.7694	1029.5476	515.2774	11
6	525.2667	263.1370	507.2562	254.1317	V	932.5312	466.7693	915.5047	458.2560			10
7	596.3039	298.6556	578.2933	289.6503	A	833.4628	417.2350	816.4363	408.7218			9
8	693.3566	347.1819	675.3461	338.1767	P	762.4257	381.7165	745.3992	373.2032			8
9	764.3937	382.7005	746.3832	373.6952	A	665.3729	333.1901	648.3464	324.6768			7
10	861.4465	431.2269	843.4359	422.2216	P	594.3358	297.6715	577.3093	289.1583			6
11	918.4680	459.7376	900.4574	450.7323	G	497.2831	249.1452	480.2565	240.6319			5
12	1015.5207	508.2640	997.5102	499.2587	P	440.2616	220.6344	423.2350	212.1212			4
13	1086.5578	543.7826	1068.5473	534.7773	A	343.2088	172.1081	326.1823	163.5948			3
14	1183.6106	592.3089	1165.6000	583.3037	P	272.1717	136.5895	255.1452	128.0762			2
15					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 9 ppm



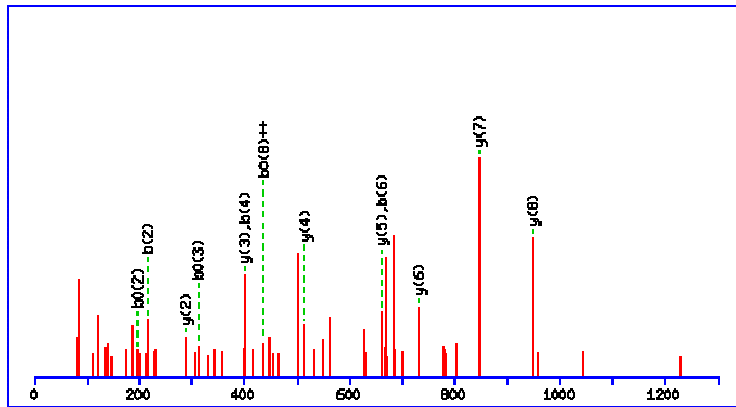
RMS error 9 ppm

Peptide Number: 39918MS/MS Fragmentation of **LTDAFLLLR**Found in **IPI00023149** in **IPI_human**, Tax_Id=9606 Gene_Symbol=STX16-NPEPL1;STX16 Isoform B of Syntaxin-16

Match to Query 1687: 1060.623928 from(531.319240,2+) index(27130)

Title: Elution from: 65.1666666666667 to 65.1666666666667 period: 0 cycle: 2451 experiment: 1 polarity: +

Data file 120214ry_32R1-32_4_3.mgf



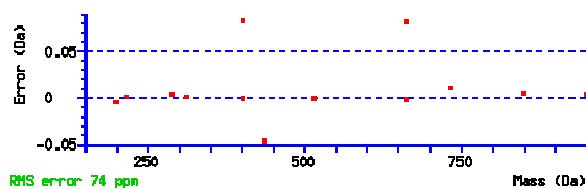
Monoisotopic mass of neutral peptide Mr(calc): 1060.6281

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

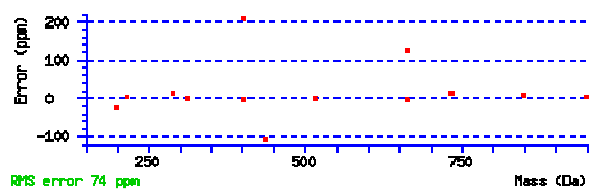
Ions Score: 40 Expect: 0.004

Matches : 13/66 fragment ions using 27 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							9
2	215.1390	108.0731	197.1285	99.0679	T	948.5513	474.7793	931.5247	466.2660	930.5407	465.7740	8
3	330.1660	165.5866	312.1554	156.5813	D	847.5036	424.2554	830.4771	415.7422	829.4930	415.2502	7
4	401.2031	201.1052	383.1925	192.0999	A	732.4767	366.7420	715.4501	358.2287			6
5	548.2715	274.6394	530.2609	265.6341	F	661.4396	331.2234	644.4130	322.7101			5
6	661.3556	331.1814	643.3450	322.1761	L	514.3711	257.6892	497.3446	249.1759			4
7	774.4396	387.7234	756.4291	378.7182	L	401.2871	201.1472	384.2605	192.6339			3
8	887.5237	444.2655	869.5131	435.2602	L	288.2030	144.6051	271.1765	136.0919			2
9					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 74 ppm



RMS error 74 ppm

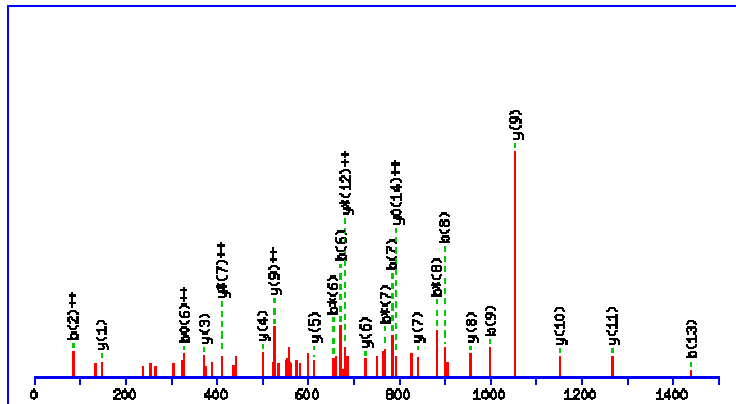
Peptide Number: 39955

MS/MS Fragmentation of **AVCDNLLNVPDDILQLLK**Found in **IPI00007131** in **IPI_human**, Tax_Id=9606 Gene_Symbol=DPEP3 dipeptidase 3 isoform a

Match to Query 1674: 2052.066132 from(685.029320,3+) index(1786)

Title: Elution from: 17.2333333333333 to 17.2333333333333 period: 0 cycle: 731 experiment: 1 polarity: +

Data file 120126ry_585A1-55_2_5.mgf



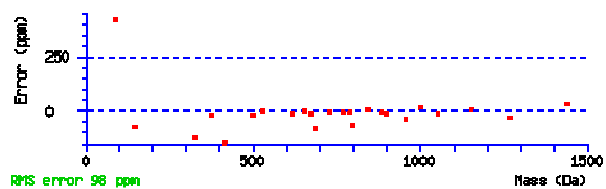
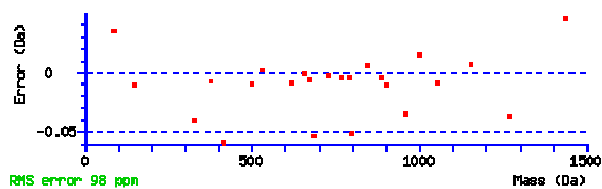
Monoisotopic mass of neutral peptide Mr(calc): 2052.0925

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 48 Expect: 0.00088

Matches : 24/178 fragment ions using 49 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							18
2	171.1128	86.0600					V	1982.0627	991.5350	1965.0361	983.0217	1964.0521	982.5297	17
3	331.1435	166.0754					C	1882.9943	942.0008	1865.9677	933.4875	1864.9837	932.9955	16
4	446.1704	223.5888			428.1598	214.5836	D	1722.9636	861.9855	1705.9371	853.4722	1704.9531	852.9802	15
5	560.2133	280.6103	543.1868	272.0970	542.2028	271.6050	N	1607.9367	804.4720	1590.9101	795.9587	1589.9261	795.4667	14
6	673.2974	337.1523	656.2708	328.6391	655.2868	328.1470	L	1493.8938	747.4505	1476.8672	738.9372	1475.8832	738.4452	13
7	786.3815	393.6944	769.3549	385.1811	768.3709	384.6891	L	1380.8097	690.9085	1363.7831	682.3952	1362.7991	681.9032	12
8	900.4244	450.7158	883.3978	442.2026	882.4138	441.7105	N	1267.7256	634.3665	1250.6991	625.8532	1249.7151	625.3612	11
9	999.4928	500.2500	982.4662	491.7368	981.4822	491.2448	V	1153.6827	577.3450	1136.6562	568.8317	1135.6721	568.3397	10
10	1096.5456	548.7764	1079.5190	540.2631	1078.5350	539.7711	P	1054.6143	527.8108	1037.5877	519.2975	1036.6037	518.8055	9
11	1211.5725	606.2899	1194.5460	597.7766	1193.5619	597.2846	D	957.5615	479.2844	940.5350	470.7711	939.5510	470.2791	8
12	1326.5994	663.8034	1309.5729	655.2901	1308.5889	654.7981	D	842.5346	421.7709	825.5080	413.2577	824.5240	412.7656	7
13	1439.6835	720.3454	1422.6570	711.8321	1421.6729	711.3401	I	727.5076	364.2575	710.4811	355.7442			6
14	1552.7676	776.8874	1535.7410	768.3741	1534.7570	767.8821	L	614.4236	307.7154	597.3970	299.2022			5
15	1680.8261	840.9167	1663.7996	832.4034	1662.8156	831.9114	Q	501.3395	251.1734	484.3130	242.6601			4
16	1793.9102	897.4587	1776.8837	888.9455	1775.8996	888.4535	L	373.2809	187.1441	356.2544	178.6308			3
17	1906.9943	954.0008	1889.9677	945.4875	1888.9837	944.9955	L	260.1969	130.6021	243.1703	122.0888			2
18							K	147.1128	74.0600	130.0863	65.5468			1



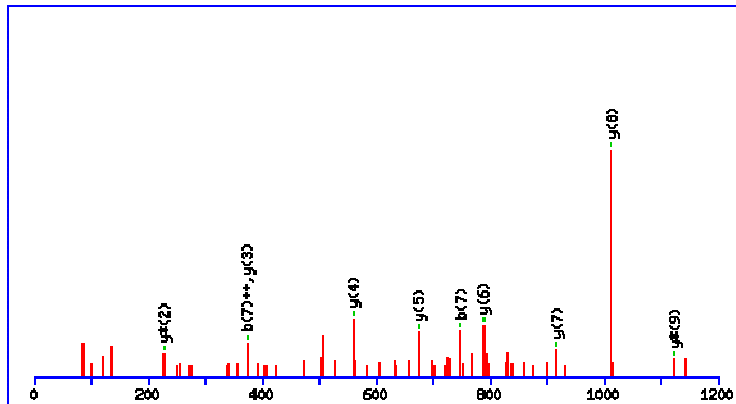
Peptide Number: 39970

MS/MS Fragmentation of **LAALTNYLQPQLDWQAR**Found in **IPI00384646** in **IPI_human**, Tax_Id=9606 Gene_Symbol=C22orf25 Isoform 3 of Uncharacterized protein C22orf25

Match to Query 25811: 2000.046642 from(667.689490,3+) index(38212)

Title: Elution from: 91.6 to 91.6 period: 0 cycle: 3465 experiment: 4 polarity:+

Data file 120208ry_Tig120slc-P8_2_3.mgf



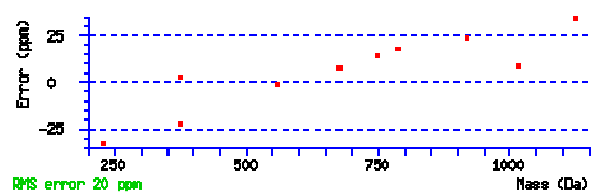
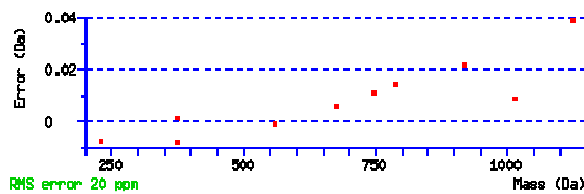
Monoisotopic mass of neutral peptide Mr(calc): 2000.0479

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 44 Expect: 0.0026

Matches : 10/166 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							17
2	185.1285	93.0679					A	1887.9712	944.4892	1870.9446	935.9760	1869.9606	935.4839	16
3	256.1656	128.5864					A	1816.9341	908.9707	1799.9075	900.4574	1798.9235	899.9654	15
4	369.2496	185.1285					L	1745.8969	873.4521	1728.8704	864.9388	1727.8864	864.4468	14
5	470.2973	235.6523			452.2867	226.6470	T	1632.8129	816.9101	1615.7863	808.3968	1614.8023	807.9048	13
6	584.3402	292.6738	567.3137	284.1605	566.3297	283.6685	N	1531.7652	766.3862	1514.7387	757.8730	1513.7546	757.3810	12
7	747.4036	374.2054	730.3770	365.6921	729.3930	365.2001	Y	1417.7223	709.3648	1400.6957	700.8515	1399.7117	700.3595	11
8	860.4876	430.7475	843.4611	422.2342	842.4771	421.7422	L	1254.6589	627.8331	1237.6324	619.3198	1236.6484	618.8278	10
9	988.5462	494.7767	971.5197	486.2635	970.5356	485.7715	Q	1141.5749	571.2911	1124.5483	562.7778	1123.5643	562.2858	9
10	1085.5990	543.3031	1068.5724	534.7899	1067.5884	534.2978	P	1013.5163	507.2618	996.4898	498.7485	995.5057	498.2565	8
11	1213.6576	607.3324	1196.6310	598.8191	1195.6470	598.3271	Q	916.4635	458.7354	899.4370	450.2221	898.4530	449.7301	7
12	1326.7416	663.8744	1309.7151	655.3612	1308.7310	654.8692	L	788.4050	394.7061	771.3784	386.1928	770.3944	385.7008	6
13	1441.7686	721.3879	1424.7420	712.8746	1423.7580	712.3826	D	675.3209	338.1641	658.2944	329.6508	657.3103	329.1588	5
14	1627.8479	814.4276	1610.8213	805.9143	1609.8373	805.4223	W	560.2940	280.6506	543.2674	272.1373			4
15	1755.9064	878.4569	1738.8799	869.9436	1737.8959	869.4516	Q	374.2146	187.6110	357.1881	179.0977			3
16	1826.9436	913.9754	1809.9170	905.4621	1808.9330	904.9701	A	246.1561	123.5817	229.1295	115.0684			2
17							R	175.1190	88.0631	158.0924	79.5498			1



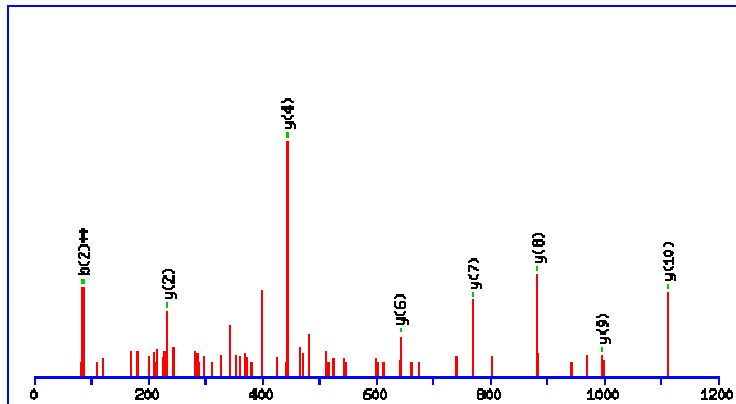
Peptide Number: 40187

MS/MS Fragmentation of **LGLDILEVVPISK**Found in **IPI00410110** in **IPI_human**, Tax_Id=9606 Gene_Symbol=DHX40 Isoform 1 of Probable ATP-dependent RNA helicase DHX40

Match to Query 1910: 1394.853108 from(698.433830,2+) index(366)

Title: Elution from: 1.48333333333333 to 1.48333333333333 period: 0 cycle: 63 experiment: 5 polarity:+

Data file 120212ry_414C2-43_3_4.mgf



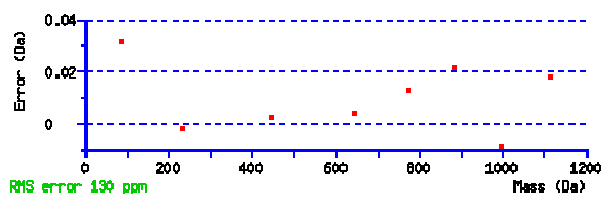
Monoisotopic mass of neutral peptide Mr(calc): 1394.8385

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

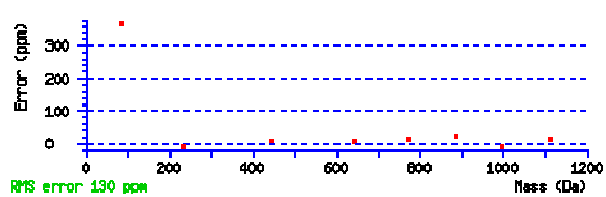
Ions Score: 57 Expect: 1.5e-005

Matches : 8/112 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							13
2	171.1128	86.0600			G	1282.7617	641.8845	1265.7351	633.3712	1264.7511	632.8792	12
3	284.1969	142.6021			L	1225.7402	613.3737	1208.7137	604.8605	1207.7297	604.3685	11
4	399.2238	200.1155	381.2132	191.1103	D	1112.6562	556.8317	1095.6296	548.3184	1094.6456	547.8264	10
5	512.3079	256.6576	494.2973	247.6523	I	997.6292	499.3182	980.6027	490.8050	979.6186	490.3130	9
6	625.3919	313.1996	607.3814	304.1943	L	884.5451	442.7762	867.5186	434.2629	866.5346	433.7709	8
7	754.4345	377.7209	736.4240	368.7156	E	771.4611	386.2342	754.4345	377.7209	753.4505	377.2289	7
8	853.5029	427.2551	835.4924	418.2498	V	642.4185	321.7129	625.3919	313.1996	624.4079	312.7076	6
9	952.5714	476.7893	934.5608	467.7840	V	543.3501	272.1787	526.3235	263.6654	525.3395	263.1734	5
10	1049.6241	525.3157	1031.6136	516.3104	P	444.2817	222.6445	427.2551	214.1312	426.2711	213.6392	4
11	1162.7082	581.8577	1144.6976	572.8524	I	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
12	1249.7402	625.3737	1231.7297	616.3685	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
13					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 139 ppm



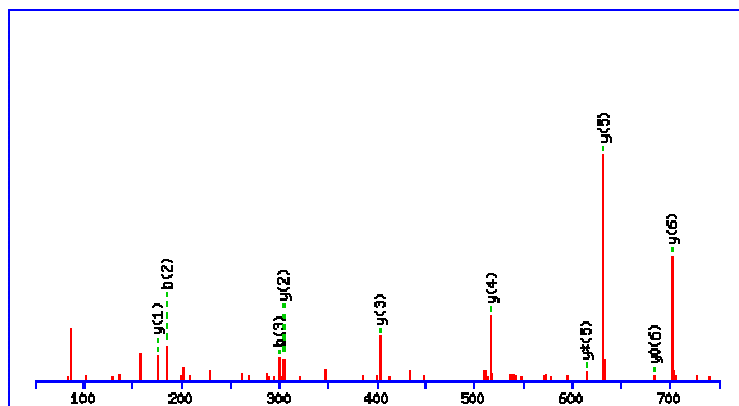
RMS error 139 ppm

Peptide Number: 40388MS/MS Fragmentation of **LADLVER**Found in **IPI01011938** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ALDH1A2 Uncharacterized protein

Match to Query 4401: 814.455568 from(408.235060,2+) index(28884)

Title: Elution from: 103.6 to 103.6 period: 0 cycle: 8132 experiment: 1 polarity: +

Data file 120208ry_Tig120slc-P8_2_1.mgf



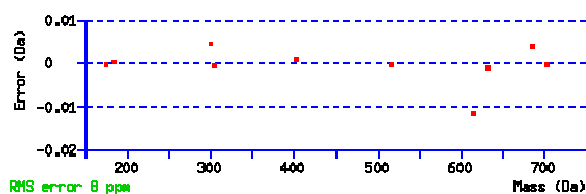
Monoisotopic mass of neutral peptide Mr(calc): 814.4548

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

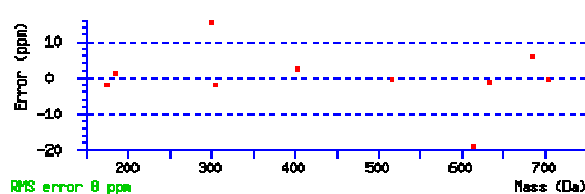
Ions Score: 43 Expect: 0.0051

Matches : 10/54 fragment ions using 21 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							7
2	185.1285	93.0679			A	702.3781	351.6927	685.3515	343.1794	684.3675	342.6874	6
3	300.1554	150.5813	282.1448	141.5761	D	631.3410	316.1741	614.3144	307.6608	613.3304	307.1688	5
4	413.2395	207.1234	395.2289	198.1181	L	516.3140	258.6606	499.2875	250.1474	498.3035	249.6554	4
5	512.3079	256.6576	494.2973	247.6523	V	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
6	641.3505	321.1789	623.3399	312.1736	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
7					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 8 ppm



RMS error 8 ppm

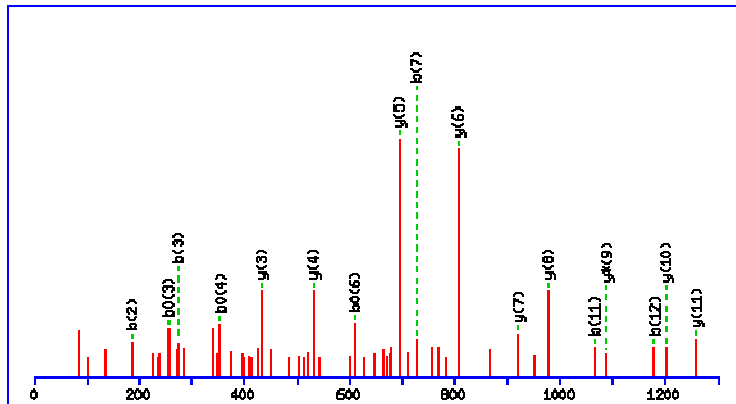
Peptide Number: 40419

MS/MS Fragmentation of **GQSVQQVGPQGLLYVQQR**Found in **IPI00470626** in **IPI_human**, Tax_Id=9606 Gene_Symbol=NTAN1 Protein N-terminal asparagine amidohydrolase

Match to Query 38014: 1984.067622 from(662.363150,3+) index(40998)

Title: Elution from: 105.6 to 105.6 period: 0 cycle: 4030 experiment: 5 polarity:+

Data file 120206ry_aHDF1419-P10_3_2.mgf



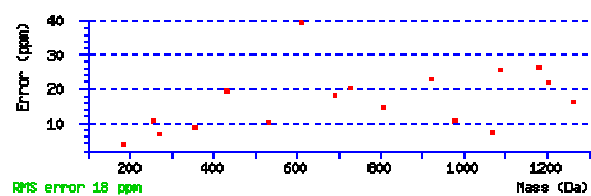
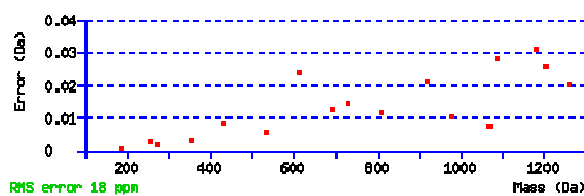
Monoisotopic mass of neutral peptide Mr(calc): 1984.0490

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 56 Expect: 0.00012

Matches : 17/168 fragment ions using 24 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					Q							18
2	186.0873	93.5473	169.0608	85.0340			Q	1928.0348	964.5211	1911.0083	956.0078	1910.0243	955.5158	17
3	273.1193	137.0633	256.0928	128.5500	255.1088	128.0580	S	1799.9763	900.4918	1782.9497	891.9785	1781.9657	891.4865	16
4	372.1878	186.5975	355.1612	178.0842	354.1772	177.5922	V	1712.9442	856.9758	1695.9177	848.4625			15
5	500.2463	250.6268	483.2198	242.1135	482.2358	241.6215	Q	1613.8758	807.4415	1596.8493	798.9283			14
6	628.3049	314.6561	611.2784	306.1428	610.2944	305.6508	Q	1485.8172	743.4123	1468.7907	734.8990			13
7	727.3733	364.1903	710.3468	355.6770	709.3628	355.1850	V	1357.7587	679.3830	1340.7321	670.8697			12
8	784.3948	392.7010	767.3682	384.1878	766.3842	383.6958	G	1258.6902	629.8488	1241.6637	621.3355			11
9	881.4476	441.2274	864.4210	432.7141	863.4370	432.2221	P	1201.6688	601.3380	1184.6422	592.8248			10
10	1009.5061	505.2567	992.4796	496.7434	991.4956	496.2514	Q	1104.6160	552.8116	1087.5895	544.2984			9
11	1066.5276	533.7674	1049.5011	525.2542	1048.5170	524.7622	G	976.5574	488.7824	959.5309	480.2691			8
12	1179.6117	590.3095	1162.5851	581.7962	1161.6011	581.3042	L	919.5360	460.2716	902.5094	451.7584			7
13	1292.6957	646.8515	1275.6692	638.3382	1274.6852	637.8462	L	806.4519	403.7296	789.4254	395.2163			6
14	1455.7591	728.3832	1438.7325	719.8699	1437.7485	719.3779	Y	693.3679	347.1876	676.3413	338.6743			5
15	1554.8275	777.9174	1537.8009	769.4041	1536.8169	768.9121	V	530.3045	265.6559	513.2780	257.1426			4
16	1682.8860	841.9467	1665.8595	833.4334	1664.8755	832.9414	Q	431.2361	216.1217	414.2096	207.6084			3
17	1810.9446	905.9760	1793.9181	897.4627	1792.9341	896.9707	Q	303.1775	152.0924	286.1510	143.5791			2
18							R	175.1190	88.0631	158.0924	79.5498			1



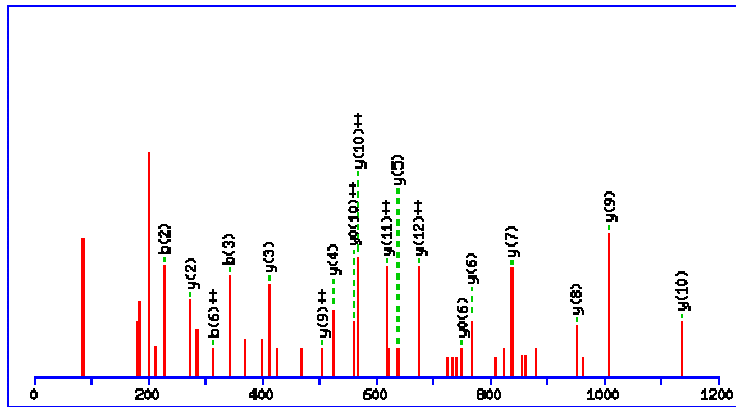
Peptide Number: 40670

MS/MS Fragmentation of **DLLVEGLAEILHQQ**Found in **IPI00294653** in **IPI_human**, Tax_Id=9606 Gene_Symbol=DOPEY2 Isoform 1 of Protein dopey-2

Match to Query 4638: 1576.872222 from(526.631350,3+) index(17617)

Title: Elution from: 48.0333333333333 to 48.0333333333333 period: 0 cycle: 1837 experiment: 1 polarity: +

Data file 120212ry_aHDF1388-P9_3_4.mgf



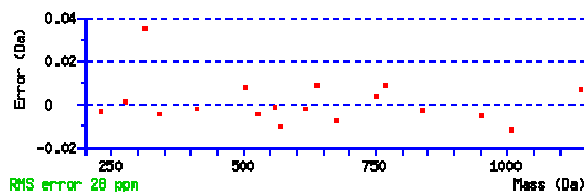
Monoisotopic mass of neutral peptide Mr(calcd): 1576.8824

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

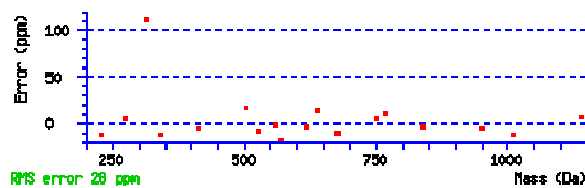
Ions Score: 50 Expect: 0.00039

Matches : 18/122 fragment ions using 36 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							14
2	229.1183	115.0628			211.1077	106.0575	L	1462.8628	731.9350	1445.8362	723.4218	1444.8522	722.9298	13
3	342.2023	171.6048			324.1918	162.5995	L	1349.7787	675.3930	1332.7522	666.8797	1331.7682	666.3877	12
4	441.2708	221.1390			423.2602	212.1337	V	1236.6947	618.8510	1219.6681	610.3377	1218.6841	609.8457	11
5	570.3134	285.6603			552.3028	276.6550	E	1137.6263	569.3168	1120.5997	560.8035	1119.6157	560.3115	10
6	627.3348	314.1710			609.3243	305.1658	G	1008.5837	504.7955	991.5571	496.2822	990.5731	495.7902	9
7	740.4189	370.7131			722.4083	361.7078	L	951.5622	476.2847	934.5356	467.7715	933.5516	467.2795	8
8	811.4560	406.2316			793.4454	397.2264	A	838.4781	419.7427	821.4516	411.2294	820.4676	410.7374	7
9	940.4986	470.7529			922.4880	461.7477	E	767.4410	384.2241	750.4145	375.7109	749.4304	375.2189	6
10	1053.5827	527.2950			1035.5721	518.2897	I	638.3984	319.7028	621.3719	311.1896			5
11	1166.6667	583.8370			1148.6562	574.8317	L	525.3144	263.1608	508.2878	254.6475			4
12	1303.7256	652.3665			1285.7151	643.3612	H	412.2303	206.6188	395.2037	198.1055			3
13	1431.7842	716.3957	1414.7577	707.8825	1413.7736	707.3905	Q	275.1714	138.0893	258.1448	129.5761			2
14							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 28 ppm



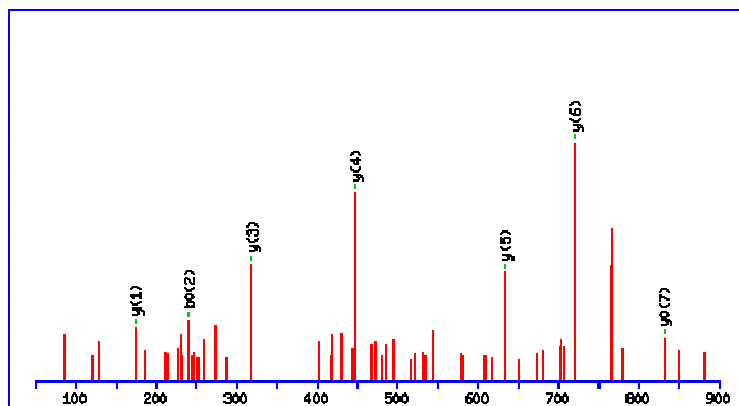
RMS error 28 ppm

Peptide Number: 40782MS/MS Fragmentation of **EESWESGR**Found in **IPI00071318** in **IPI_human**, Tax_Id=9606 Gene_Symbol=LUC7L Isoform 1 of Putative RNA-binding protein Luc7-like 1

Match to Query 11064: 978.401308 from(490.207930,2+) index(14842)

Title: Elution from: 80.0166666666667 to 80.0166666666667 period: 0 cycle: 7376 experiment: 6 polarity:+

Data file 120118ry_201B7-32_2_1.mgf



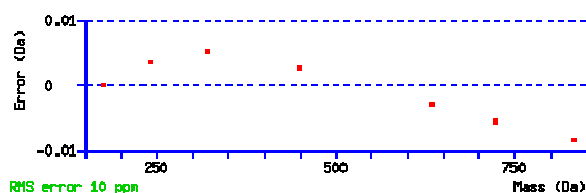
Monoisotopic mass of neutral peptide Mr(calc): 978.4043

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

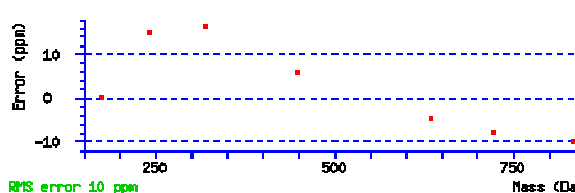
Ions Score: 41 Expect: 0.00095

Matches : 7/66 fragment ions using 8 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286	112.0393	56.5233	E							8
2	259.0925	130.0499	241.0819	121.0446	E	850.3690	425.6881	833.3424	417.1748	832.3584	416.6828	7
3	346.1245	173.5659	328.1139	164.5606	S	721.3264	361.1668	704.2998	352.6536	703.3158	352.1615	6
4	532.2038	266.6055	514.1932	257.6003	W	634.2944	317.6508	617.2678	309.1375	616.2838	308.6455	5
5	661.2464	331.1268	643.2358	322.1216	E	448.2150	224.6112	431.1885	216.0979	430.2045	215.6059	4
6	748.2784	374.6429	730.2679	365.6376	S	319.1724	160.0899	302.1459	151.5766	301.1619	151.0846	3
7	805.2999	403.1536	787.2893	394.1483	G	232.1404	116.5738	215.1139	108.0606			2
8					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 10 ppm



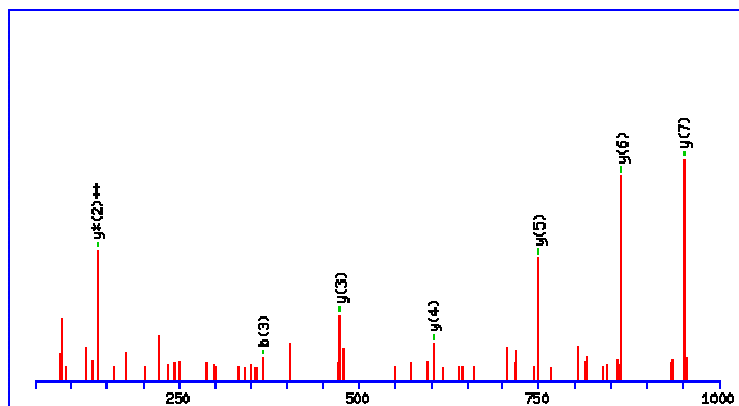
RMS error 10 ppm

Peptide Number: 41134MS/MS Fragmentation of **YSDFEWLR**Found in **IPI00552276** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SNX3 Isoform 4 of Sorting nexin-3

Match to Query 2557: 1114.502968 from(558.258760,2+) index(14615)

Title: Elution from: 35.5666666666667 to 35.5666666666667 period: 0 cycle: 1313 experiment: 2 polarity: +

Data file 120118ry_201B7-32_1_3.mgf



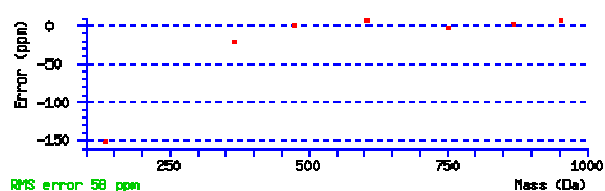
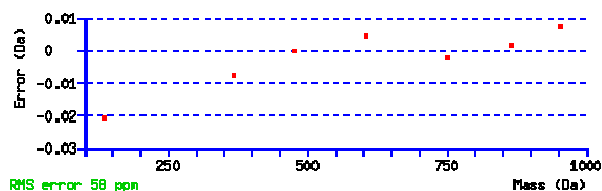
Monoisotopic mass of neutral peptide Mr(calc): 1114.5083

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 40 Expect: 0.0023

Matches : 7/62 fragment ions using 9 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389			Y							8
2	251.1026	126.0550	233.0921	117.0497	S	952.4523	476.7298	935.4258	468.2165	934.4417	467.7245	7
3	366.1296	183.5684	348.1190	174.5631	D	865.4203	433.2138	848.3937	424.7005	847.4097	424.2085	6
4	513.1980	257.1026	495.1874	248.0974	F	750.3933	375.7003	733.3668	367.1870	732.3828	366.6950	5
5	642.2406	321.6239	624.2300	312.6186	E	603.3249	302.1661	586.2984	293.6528	585.3144	293.1608	4
6	828.3199	414.6636	810.3093	405.6583	W	474.2823	237.6448	457.2558	229.1315			3
7	941.4040	471.2056	923.3934	462.2003	L	288.2030	144.6051	271.1765	136.0919			2
8					R	175.1190	88.0631	158.0924	79.5498			1



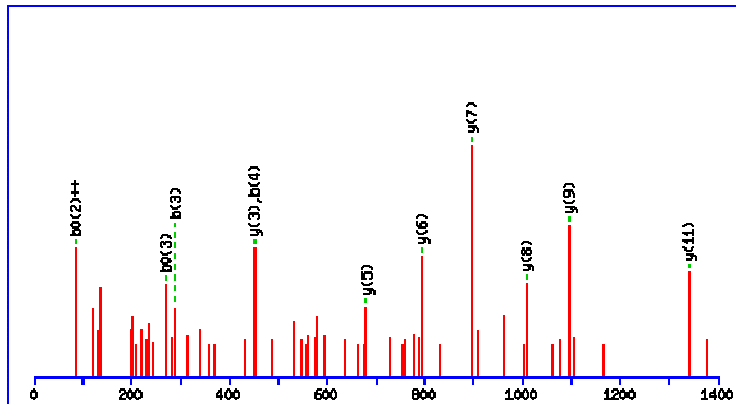
Peptide Number: 41235

MS/MS Fragmentation of **STVYVSNLPFSLTNNDLYR**Found in **IPI00154614** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ZCRB1 Zinc finger CCHC-type and RNA-binding motif-containing protein 1

Match to Query 33895: 2202.077712 from(735.033180,3+) index(40286)

Title: Elution from: 97.7666666666667 to 97.7666666666667 period: 0 cycle: 3619 experiment: 6 polarity: +

Data file 120118ry_201B7-32_1_3.mgf



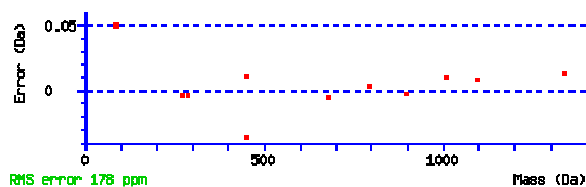
Monoisotopic mass of neutral peptide Mr(calcd): 2202.0957

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

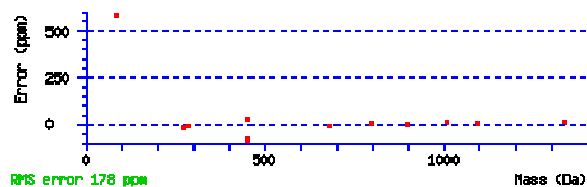
Ions Score: 54 Expect: 0.00028

Matches : 11/198 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							19
2	189.0870	95.0471			171.0764	86.0418	T	2116.0709	1058.5391	2099.0444	1050.0258	2098.0604	1049.5338	18
3	288.1554	144.5813			270.1448	135.5761	V	2015.0233	1008.0153	1997.9967	999.5020	1997.0127	999.0100	17
4	451.2187	226.1130			433.2082	217.1077	Y	1915.9549	958.4811	1898.9283	949.9678	1897.9443	949.4758	16
5	550.2871	275.6472			532.2766	266.6419	V	1752.8915	876.9494	1735.8650	868.4361	1734.8810	867.9441	15
6	637.3192	319.1632			619.3086	310.1579	S	1653.8231	827.4152	1636.7966	818.9019	1635.8125	818.4099	14
7	751.3621	376.1847	734.3355	367.6714	733.3515	367.1794	N	1566.7911	783.8992	1549.7645	775.3859	1548.7805	774.8939	13
8	864.4462	432.2267	847.4196	424.2134	846.4356	423.7214	L	1452.7482	726.8777	1435.7216	718.3644	1434.7376	717.8724	12
9	961.4989	481.2531	944.4724	472.7398	943.4884	472.2478	P	1339.6641	670.3357	1322.6375	661.8224	1321.6535	661.3304	11
10	1108.5673	554.7873	1091.5408	546.2740	1090.5568	545.7820	F	1242.6113	621.8093	1225.5848	613.2960	1224.6008	612.8040	10
11	1195.5994	598.3033	1178.5728	589.7900	1177.5888	589.2980	S	1095.5429	548.2751	1078.5164	539.7618	1077.5323	539.2698	9
12	1308.6834	654.8454	1291.6569	646.3321	1290.6729	645.8401	L	1008.5109	504.7591	991.4843	496.2458	990.5003	495.7538	8
13	1409.7311	705.3692	1392.7046	696.8559	1391.7205	696.3639	T	895.4268	448.2170	878.4003	439.7038	877.4163	439.2118	7
14	1523.7740	762.3907	1506.7475	753.8774	1505.7635	753.3854	N	794.3791	397.6932	777.3526	389.1799	776.3686	388.6879	6
15	1637.8170	819.4121	1620.7904	810.8988	1619.8064	810.4068	N	680.3362	340.6717	663.3097	332.1585	662.3257	331.6665	5
16	1752.8439	876.9256	1735.8174	868.4123	1734.8333	867.9203	D	566.2933	283.6503	549.2667	275.1370	548.2827	274.6450	4
17	1865.9280	933.4676	1848.9014	924.9543	1847.9174	924.4623	L	451.2663	226.1368	434.2398	217.6235			3
18	2028.9913	1014.9993	2011.9647	1006.4860	2010.9807	1005.9940	Y	338.1823	169.5948	321.1557	161.0815			2
19							R	175.1190	88.0631	158.0924	79.5498			1



RMS error: 178 ppm



RMS error: 178 ppm

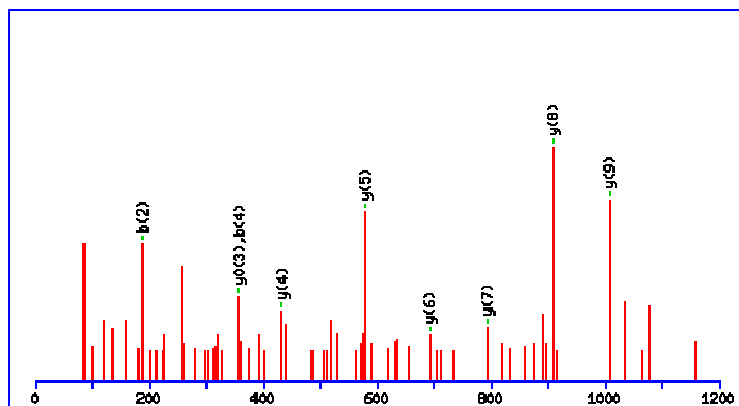
Peptide Number: 41734

MS/MS Fragmentation of **DAAVDTLFGDLK**Found in **IPI00011237** in **IPI_human**, Tax_Id=9606 Gene_Symbol=NARF Uncharacterized protein

Match to Query 6114: 1263.624288 from(632.819420,2+) index(29441)

Title: Elution from: 72.55 to 72.55 period: 0 cycle: 2667 experiment: 6 polarity: +

Data file 120118ry_201B7-32_3_3.mgf



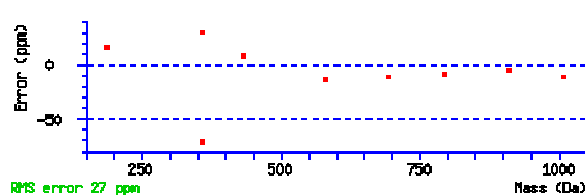
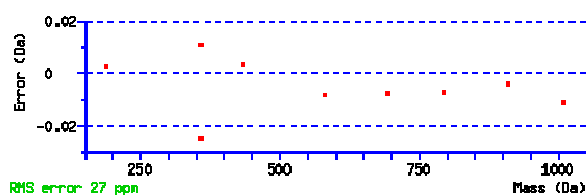
Monoisotopic mass of neutral peptide Mr(calc): 1263.6347

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 46 Expect: 0.0019

Matches : 9/106 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	98.0237	49.5155	D							12
2	187.0713	94.0393	169.0608	85.0340	A	1149.6150	575.3111	1132.5885	566.7979	1131.6045	566.3059	11
3	258.1084	129.5579	240.0979	120.5526	A	1078.5779	539.7926	1061.5514	531.2793	1060.5673	530.7873	10
4	357.1769	179.0921	339.1663	170.0868	V	1007.5408	504.2740	990.5142	495.7608	989.5302	495.2688	9
5	472.2038	236.6055	454.1932	227.6003	D	908.4724	454.7398	891.4458	446.2266	890.4618	445.7345	8
6	573.2515	287.1294	555.2409	278.1241	T	793.4454	397.2264	776.4189	388.7131	775.4349	388.2211	7
7	686.3355	343.6714	668.3250	334.6661	L	692.3978	346.7025	675.3712	338.1892	674.3872	337.6972	6
8	833.4040	417.2056	815.3934	408.2003	F	579.3137	290.1605	562.2871	281.6472	561.3031	281.1552	5
9	890.4254	445.7164	872.4149	436.7111	G	432.2453	216.6263	415.2187	208.1130	414.2347	207.6210	4
10	1005.4524	503.2298	987.4418	494.2245	D	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
11	1118.5364	559.7719	1100.5259	550.7666	L	260.1969	130.6021	243.1703	122.0888			2
12					K	147.1128	74.0600	130.0863	65.5468			1



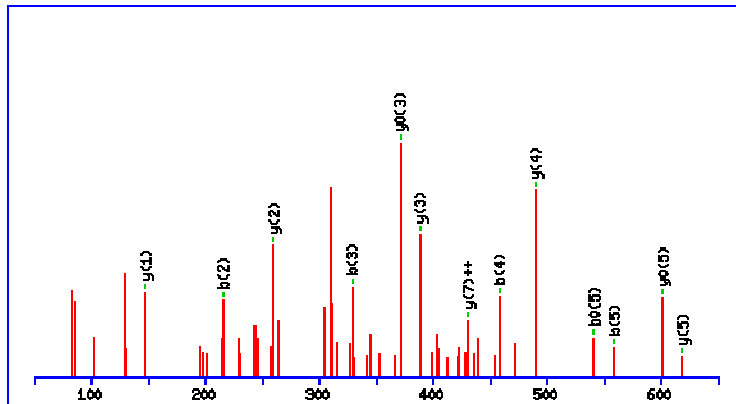
Peptide Number: 42080

MS/MS Fragmentation of **SKIETEIK**Found in **IPI00395627** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CACYBP Isoform 1 of Calcyclin-binding protein

Match to Query 9221: 946.532112 from(316.517980,3+) index(8959)

Title: Elution from: 59.2 to 59.2 period: 0 cycle: 7023 experiment: 1 polarity: +

Data file 120210ry_32R1-32_2_1.mgf



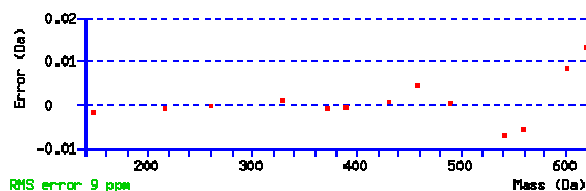
Monoisotopic mass of neutral peptide Mr(calc): 946.5335

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

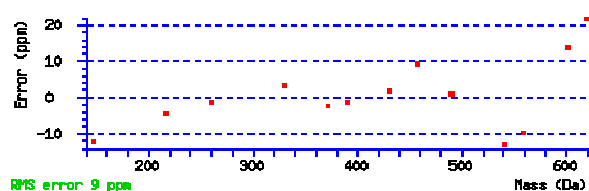
Ions Score: 41 Expect: 0.0046

Matches : 13/78 fragment ions using 17 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							8
2	216.1343	108.5708	199.1077	100.0575	198.1237	99.5655	K	860.5088	430.7580	843.4822	422.2447	842.4982	421.7527	7
3	329.2183	165.1128	312.1918	156.5995	311.2078	156.1075	I	732.4138	366.7105	715.3872	358.1973	714.4032	357.7053	6
4	458.2609	229.6341	441.2344	221.1208	440.2504	220.6288	E	619.3297	310.1685	602.3032	301.6552	601.3192	301.1632	5
5	559.3086	280.1579	542.2821	271.6447	541.2980	271.1527	T	490.2871	245.6472	473.2606	237.1339	472.2766	236.6419	4
6	688.3512	344.6792	671.3246	336.1660	670.3406	335.6740	E	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
7	801.4353	401.2213	784.4087	392.7080	783.4247	392.2160	I	260.1969	130.6021	243.1703	122.0888			2
8							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 9 ppm



RMS error 9 ppm

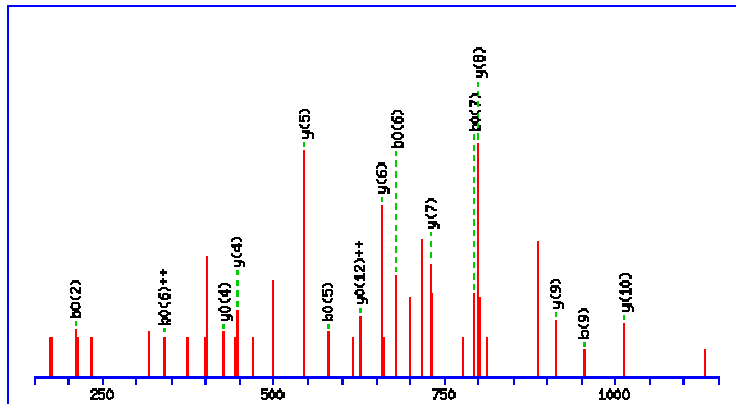
Peptide Number: 42126

MS/MS Fragmentation of **EVIQQTAAIVDAIK**Found in **IPI00914930** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ANKRD11 Ankyrin repeat domain-containing protein 11

Match to Query 4613: 1610.940642 from(537.987490,3+) index(35231)

Title: Elution from: 104.4 to 104.4 period: 0 cycle: 4004 experiment: 1 polarity: +

Data file 120210ry_585A1-55_3_4.mgf



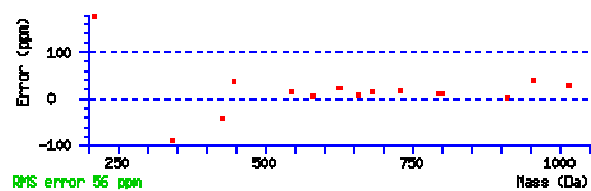
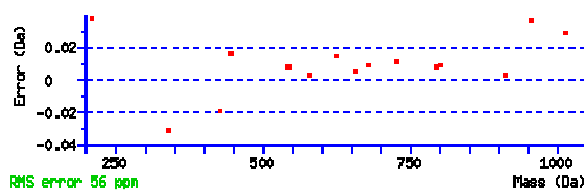
Monoisotopic mass of neutral peptide Mr(calc): 1610.9243

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 44 Expect: 0.00086

Matches : 15/156 fragment ions using 24 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							15
2	229.1183	115.0628			211.1077	106.0575	V	1482.8890	741.9481	1465.8625	733.4349	1464.8784	732.9429	14
3	342.2023	171.6048			324.1918	162.5995	I	1383.8206	692.4139	1366.7940	683.9007	1365.8100	683.4087	13
4	470.2609	235.6341	453.2344	227.1208	452.2504	226.6288	Q	1270.7365	635.8719	1253.7100	627.3586	1252.7260	626.8666	12
5	598.3195	299.6634	581.2930	291.1501	580.3089	290.6581	Q	1142.6780	571.8426	1125.6514	563.3293	1124.6674	562.8373	11
6	699.3672	350.1872	682.3406	341.6740	681.3566	341.1819	T	1014.6194	507.8133	997.5928	499.3001	996.6088	498.8080	10
7	812.4512	406.7293	795.4247	398.2160	794.4407	397.7240	L	913.5717	457.2895	896.5451	448.7762	895.5611	448.2842	9
8	883.4884	442.2478	866.4618	433.7345	865.4778	433.2425	A	800.4876	400.7475	783.4611	392.2342	782.4771	391.7422	8
9	954.5255	477.7664	937.4989	469.2531	936.5149	468.7611	A	729.4505	365.2289	712.4240	356.7156	711.4400	356.2236	7
10	1067.6095	534.3084	1050.5830	525.7951	1049.5990	525.3031	I	658.4134	329.7103	641.3869	321.1971	640.4028	320.7051	6
11	1166.6780	583.8426	1149.6514	575.3293	1148.6674	574.8373	V	545.3293	273.1683	528.3028	264.6550	527.3188	264.1630	5
12	1281.7049	641.3561	1264.6783	632.8428	1263.6943	632.3508	D	446.2609	223.6341	429.2344	215.1208	428.2504	214.6288	4
13	1352.7420	676.8746	1335.7155	668.3614	1334.7314	667.8694	A	331.2340	166.1206	314.2074	157.6074			3
14	1465.8261	733.4167	1448.7995	724.9034	1447.8155	724.4114	I	260.1969	130.6021	243.1703	122.0888			2
15							K	147.1128	74.0600	130.0863	65.5468			1

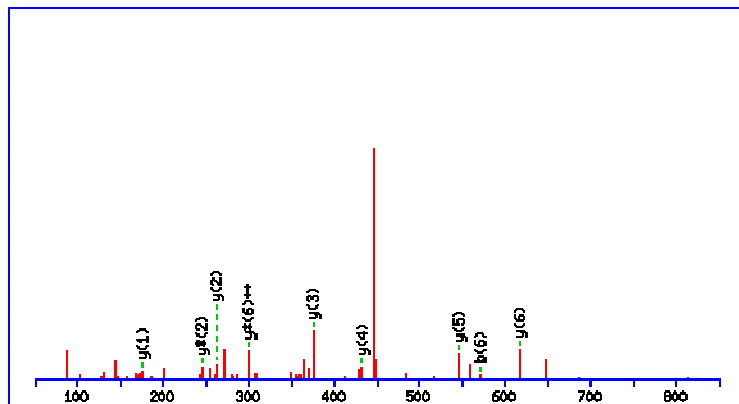


Peptide Number: 42153MS/MS Fragmentation of **EAIGLSR**Found in **IPI00384734** in **IPI_human**, Tax_Id=9606 Gene_Symbol=BTN3A2 Butyrophilin

Match to Query 1017: 744.412628 from(373.213590,2+) index(3062)

Title: Elution from: 6.88333333333333 to 6.88333333333333 period: 0 cycle: 258 experiment: 2 polarity: +

Data file 120126ry_585A1-55_2_2.mgf



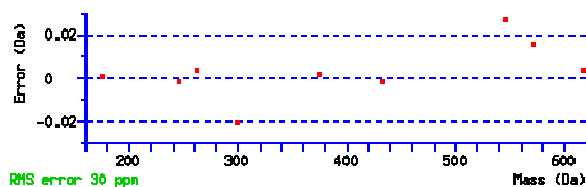
Monoisotopic mass of neutral peptide Mr(calcd): 744.4130

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

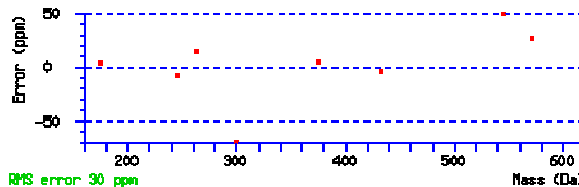
Ions Score: 43 Expect: 0.0076

Matches : 9/58 fragment ions using 19 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286	112.0393	56.5233	E							7
2	201.0870	101.0471	183.0764	92.0418	A	616.3777	308.6925	599.3511	300.1792	598.3671	299.6872	6
3	314.1710	157.5892	296.1605	148.5839	I	545.3406	273.1739	528.3140	264.6606	527.3300	264.1686	5
4	371.1925	186.0999	353.1819	177.0946	G	432.2565	216.6319	415.2300	208.1186	414.2459	207.6266	4
5	484.2766	242.6419	466.2660	233.6366	L	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
6	571.3086	286.1579	553.2980	277.1527	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
7					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 30 ppm



RMS error 30 ppm

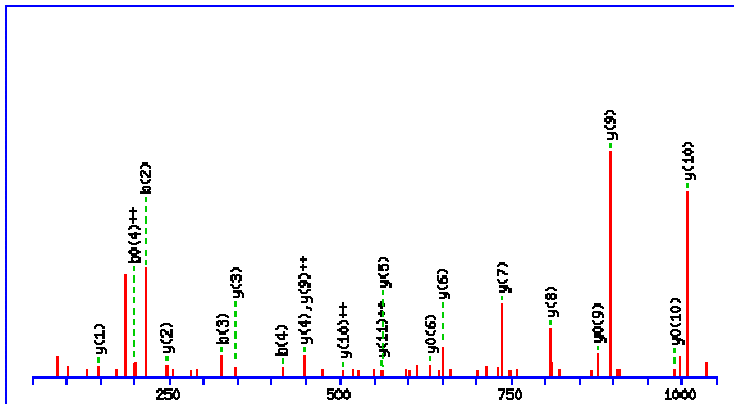
Peptide Number: 42191

MS/MS Fragmentation of **TLISASSDTTVK**Found in **IPI00658210** in **IPI_human**, Tax_Id=9606 Gene_Symbol=WDR48 Isoform 1 of WD repeat-containing protein 48

Match to Query 18283: 1221.643108 from(611.828830,2+) index(25733)

Title: Elution from: 101.95 to 101.95 period: 0 cycle: 8865 experiment: 9 polarity:+

Data file 120212ry_414C2-43_3_1.mgf



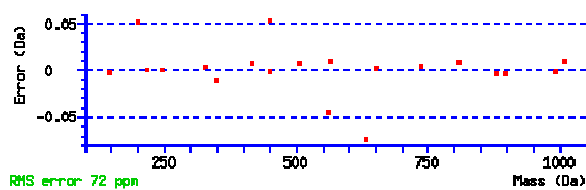
Monoisotopic mass of neutral peptide Mr(calc): 1221.6452

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

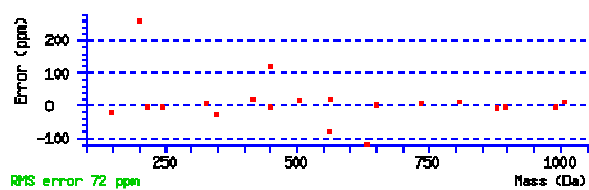
Ions Score: 62 Expect: 4.3e-005

Matches : 20/106 fragment ions using 47 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311	84.0444	42.5258	T							12
2	215.1390	108.0731	197.1285	99.0679	L	1121.6048	561.3061	1104.5783	552.7928	1103.5943	552.3008	11
3	328.2231	164.6152	310.2125	155.6099	I	1008.5208	504.7640	991.4942	496.2508	990.5102	495.7587	10
4	415.2551	208.1312	397.2445	199.1259	S	895.4367	448.2220	878.4102	439.7087	877.4262	439.2167	9
5	486.2922	243.6498	468.2817	234.6445	A	808.4047	404.7060	791.3781	396.1927	790.3941	395.7007	8
6	573.3243	287.1658	555.3137	278.1605	S	737.3676	369.1874	720.3410	360.6742	719.3570	360.1821	7
7	660.3563	330.6818	642.3457	321.6765	S	650.3355	325.6714	633.3090	317.1581	632.3250	316.6661	6
8	775.3832	388.1952	757.3727	379.1900	D	563.3035	282.1554	546.2770	273.6421	545.2930	273.1501	5
9	876.4309	438.7191	858.4203	429.7138	T	448.2766	224.6419	431.2500	216.1287	430.2660	215.6366	4
10	977.4786	489.2429	959.4680	480.2376	T	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
11	1076.5470	538.7771	1058.5364	529.7719	V	246.1812	123.5942	229.1547	115.0810			2
12					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 72 ppm



RMS error 72 ppm

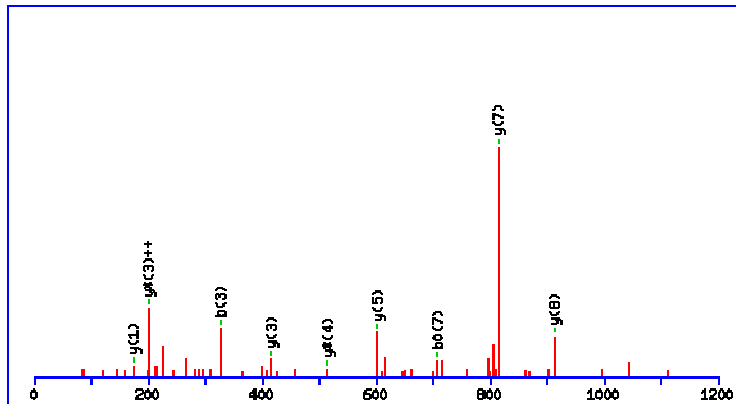
Peptide Number: 42339

MS/MS Fragmentation of **NLVPDADIQR**Found in **IPI00219655** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PHYH Phytanoyl-CoA dioxygenase, peroxisomal precursor

Match to Query 13132: 1139.588348 from(570.801450,2+) index(13379)

Title: Elution from: 32.75 to 32.75 period: 0 cycle: 1235 experiment: 7 polarity:+

Data file 120210ry_32R1-32_2_2.mgf



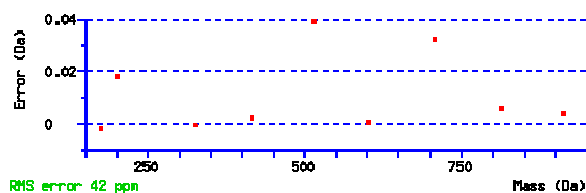
Monoisotopic mass of neutral peptide Mr(calc): 1139.5935

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

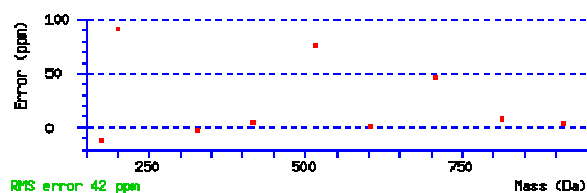
Ions Score: 41 Expect: 0.0045

Matches : 9/94 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							10
2	228.1343	114.5708	211.1077	106.0575			L	1026.5578	513.7826	1009.5313	505.2693	1008.5473	504.7773	9
3	327.2027	164.1050	310.1761	155.5917			V	913.4738	457.2405	896.4472	448.7272	895.4632	448.2352	8
4	424.2554	212.6314	407.2289	204.1181			P	814.4054	407.7063	797.3788	399.1930	796.3948	398.7010	7
5	539.2824	270.1448	522.2558	261.6316	521.2718	261.1395	D	717.3526	359.1799	700.3260	350.6667	699.3420	350.1747	6
6	610.3195	305.6634	593.2930	297.1501	592.3089	296.6581	A	602.3257	301.6665	585.2991	293.1532	584.3151	292.6612	5
7	725.3464	363.1769	708.3199	354.6636	707.3359	354.1716	D	531.2885	266.1479	514.2620	257.6346	513.2780	257.1426	4
8	838.4305	419.7189	821.4040	411.2056	820.4199	410.7136	I	416.2616	208.6344	399.2350	200.1212			3
9	966.4891	483.7482	949.4625	475.2349	948.4785	474.7429	Q	303.1775	152.0924	286.1510	143.5791			2
10							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 42 ppm



RMS error 42 ppm

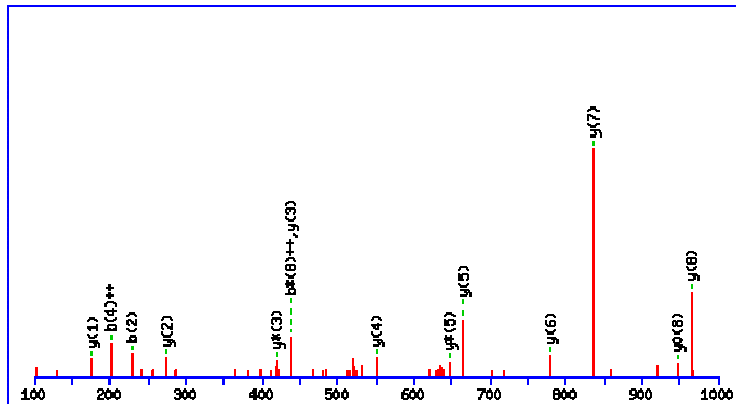
Peptide Number: 42589

MS/MS Fragmentation of **VEGDNIYVR**Found in **IPI00015973** in **IPI_human**, Tax_Id=9606 Gene_Symbol=EPB41L2 Band 4.1-like protein 2

Match to Query 12918: 1063.532608 from(532.773580,2+) index(29216)

Title: Elution from: 104.3 to 104.3 period: 0 cycle: 8159 experiment: 7 polarity: +

Data file 120208ry_Tig120slc-P8_2_1.mgf



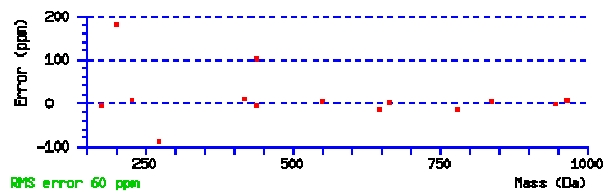
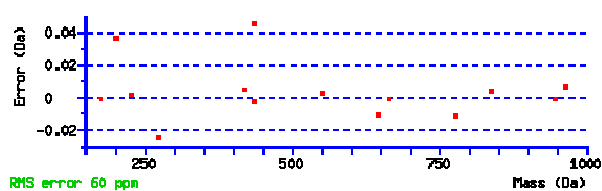
Monoisotopic mass of neutral peptide Mr(calc): 1063.5298

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 74 Expect: 2.9e-006

Matches : 14/76 fragment ions using 18 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							9
2	229.1183	115.0628			211.1077	106.0575	E	965.4687	483.2380	948.4421	474.7247	947.4581	474.2327	8
3	286.1397	143.5735			268.1292	134.5682	G	836.4261	418.7167	819.3995	410.2034	818.4155	409.7114	7
4	401.1667	201.0870			383.1561	192.0817	D	779.4046	390.2060	762.3781	381.6927	761.3941	381.2007	6
5	515.2096	258.1084	498.1831	249.5952	497.1991	249.1032	N	664.3777	332.6925	647.3511	324.1792			5
6	628.2937	314.6505	611.2671	306.1372	610.2831	305.6452	I	550.3348	275.6710	533.3082	267.1577			4
7	791.3570	396.1821	774.3305	387.6689	773.3464	387.1769	Y	437.2507	219.1290	420.2241	210.6157			3
8	890.4254	445.7164	873.3989	437.2031	872.4149	436.7111	V	274.1874	137.5973	257.1608	129.0840			2
9							R	175.1190	88.0631	158.0924	79.5498			1

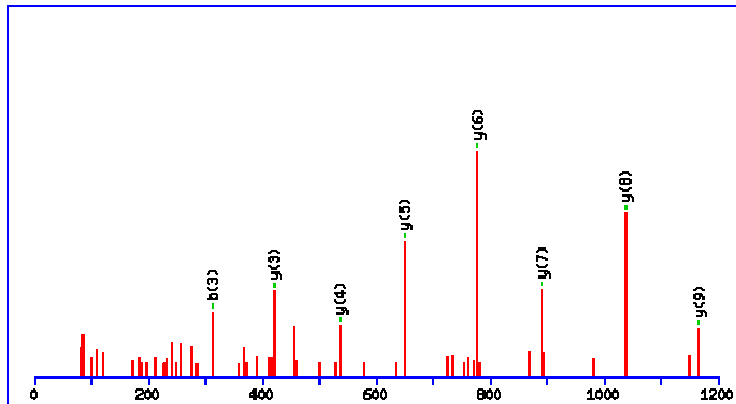


Peptide Number: 42663MS/MS Fragmentation of **ALQLFLQIDSCR**Found in **IPI00300601** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ENOSF1 Isoform 1 of Mitochondrial enolase superfamily member 1

Match to Query 6715: 1349.676708 from(675.845630,2+) index(6481)

Title: Elution from: 15.4666666666667 to 15.4666666666667 period: 0 cycle: 585 experiment: 6 polarity: +

Data file 120212ry_aHDF1388-P9_2_3.mgf



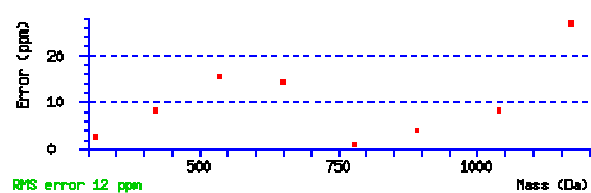
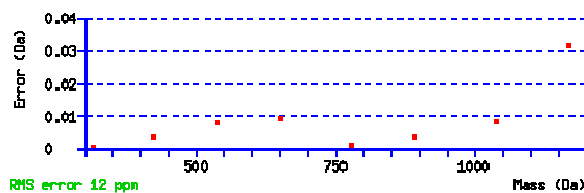
Monoisotopic mass of neutral peptide Mr(calc): 1349.6762

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 58 Expect: 0.00014

Matches : 8/98 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							11
2	185.1285	93.0679					L	1279.6463	640.3268	1262.6198	631.8135	1261.6358	631.3215	10
3	313.1870	157.0972	296.1605	148.5839			Q	1166.5623	583.7848	1149.5357	575.2715	1148.5517	574.7795	9
4	460.2554	230.6314	443.2289	222.1181			F	1038.5037	519.7555	1021.4771	511.2422	1020.4931	510.7502	8
5	573.3395	287.1734	556.3130	278.6601			L	891.4353	446.2213	874.4087	437.7080	873.4247	437.2160	7
6	701.3981	351.2027	684.3715	342.6894			Q	778.3512	389.6792	761.3247	381.1660	760.3406	380.6740	6
7	814.4822	407.7447	797.4556	399.2314			I	650.2926	325.6500	633.2661	317.1367	632.2821	316.6447	5
8	929.5091	465.2582	912.4825	456.7449	911.4985	456.2529	D	537.2086	269.1079	520.1820	260.5946	519.1980	260.1026	4
9	1016.5411	508.7742	999.5146	500.2609	998.5306	499.7689	S	422.1816	211.5945	405.1551	203.0812	404.1711	202.5892	3
10	1176.5718	588.7895	1159.5452	580.2762	1158.5612	579.7842	C	335.1496	168.0784	318.1231	159.5652			2
11							R	175.1190	88.0631	158.0924	79.5498			1



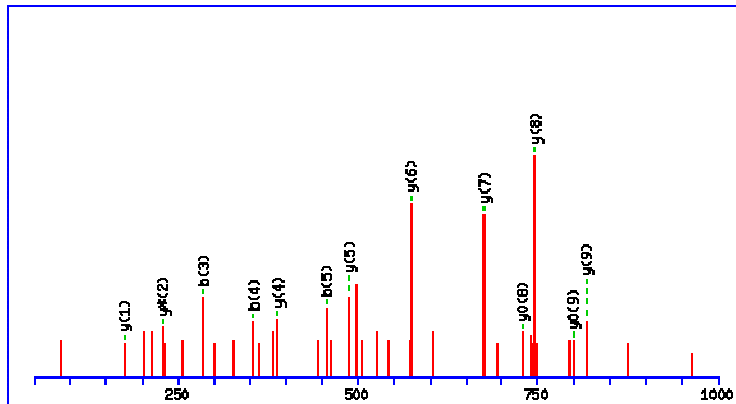
Peptide Number: 42787**MS/MS Fragmentation of DPAATSVAAAR**

Found in **IPI00013002** in **IPI_human**, Tax_Id=9606 Gene_Symbol=UBE2C Ubiquitin-conjugating enzyme E2 C

Match to Query 12495: 1028.519808 from(515.267180,2+) index(6734)

Title: Elution from: 63.3666666666667 to 63.3666666666667 period: 0 cycle: 7020 experiment: 3 polarity: +

Data file 120118ry_201B7-32_3_1.mgf



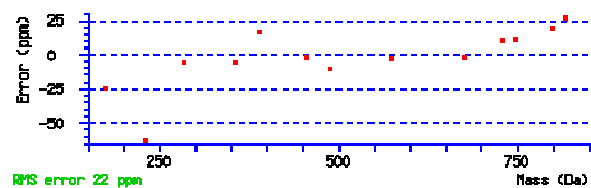
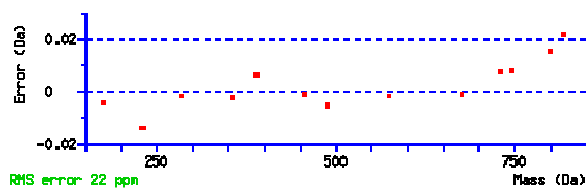
Monoisotopic mass of neutral peptide Mr(calcd): 1028.5251

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 48 **Expect:** 0.00085

Matches: 13/90 fragment ions using 24 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	98.0237	49.5155	D							11
2	213.0870	107.0471	195.0764	98.0418	P	914.5054	457.7563	897.4789	449.2431	896.4948	448.7511	10
3	284.1241	142.5657	266.1135	133.5604	A	817.4526	409.2300	800.4261	400.7167	799.4421	400.2247	9
4	355.1612	178.0842	337.1506	169.0790	A	746.4155	373.7114	729.3890	365.1981	728.4050	364.7061	8
5	456.2089	228.6081	438.1983	219.6028	T	675.3784	338.1928	658.3519	329.6796	657.3678	329.1876	7
6	543.2409	272.1241	525.2304	263.1188	S	574.3307	287.6690	557.3042	279.1557	556.3202	278.6637	6
7	642.3093	321.6583	624.2988	312.6530	V	487.2987	244.1530	470.2722	235.6397			5
8	713.3464	357.1769	695.3359	348.1716	A	388.2303	194.6188	371.2037	186.1055			4
9	784.3836	392.6954	766.3730	383.6901	A	317.1932	159.1002	300.1666	150.5870			3
10	855.4207	428.2140	837.4101	419.2087	A	246.1561	123.5817	229.1295	115.0684			2
11					R	175.1190	88.0631	158.0924	79.5498			1

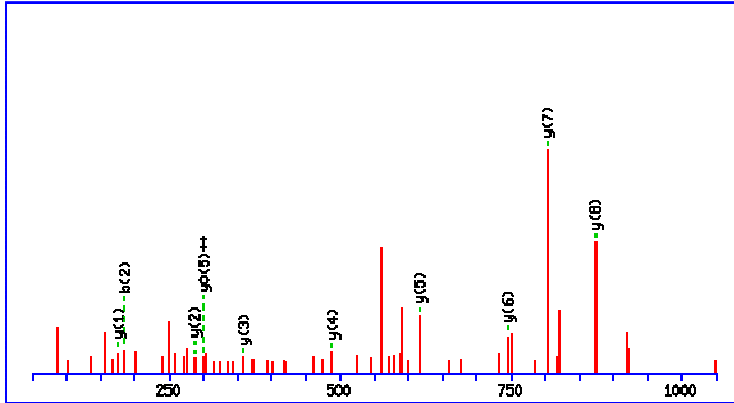


Peptide Number: 43915MS/MS Fragmentation of **LAGEEEALR**Found in **IPI00783058** in **IPI_human**, Tax_Id=9606 Gene_Symbol=RBCK1 Isoform 1 of RanBP-type and C3HC4-type zinc finger-containing protein 1

Match to Query 9762: 986.503428 from(494.258990,2+) index(18760)

Title: Elution from: 88.6333333333333 to 88.6333333333333 period: 0 cycle: 8397 experiment: 7 polarity: +

Data file 120214ry_aHDF1419-P10_4_1.mgf

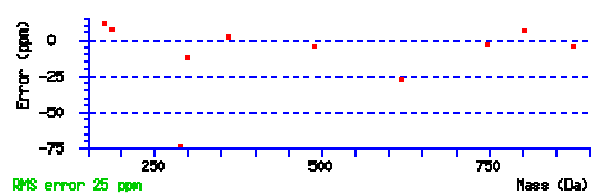
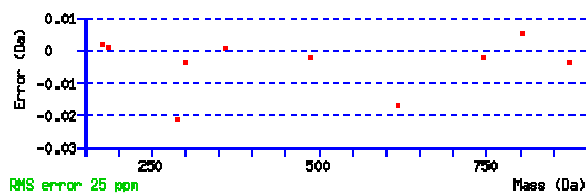
Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 986.5032

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 39 Expect: 0.0081

Matches : 10/68 fragment ions using 34 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							9
2	185.1285	93.0679			A	874.4265	437.7169	857.3999	429.2036	856.4159	428.7116	8
3	242.1499	121.5786			G	803.3894	402.1983	786.3628	393.6851	785.3788	393.1930	7
4	371.1925	186.0999	353.1819	177.0946	E	746.3679	373.6876	729.3414	365.1743	728.3573	364.6823	6
5	500.2351	250.6212	482.2245	241.6159	E	617.3253	309.1663	600.2988	300.6530	599.3148	300.1610	5
6	629.2777	315.1425	611.2671	306.1372	E	488.2827	244.6450	471.2562	236.1317	470.2722	235.6397	4
7	700.3148	350.6610	682.3042	341.6558	A	359.2401	180.1237	342.2136	171.6104			3
8	813.3989	407.2031	795.3883	398.1978	L	288.2030	144.6051	271.1765	136.0919			2
9					R	175.1190	88.0631	158.0924	79.5498			1



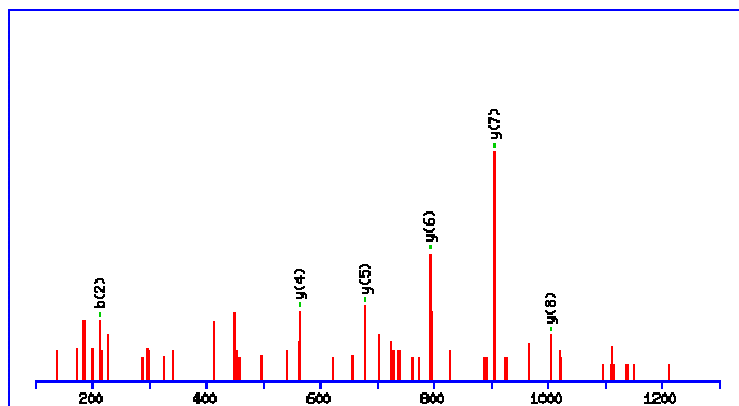
Peptide Number: 44007

MS/MS Fragmentation of **LVLIDYIIR**Found in **IPI00291068** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PI4K2B Phosphatidylinositol 4-kinase type 2-beta

Match to Query 715: 1116.685508 from(559.350030,2+) index(1990)

Title: Elution from: 4.88333333333333 to 4.88333333333333 period: 0 cycle: 181 experiment: 2 polarity: +

Data file 120126ry_585A1-55_2_4.mgf



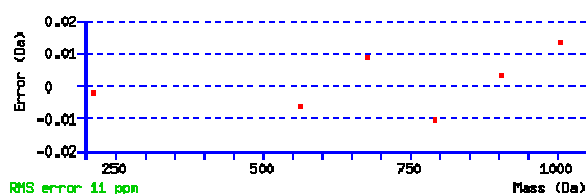
Monoisotopic mass of neutral peptide Mr(calc): 1116.6907

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

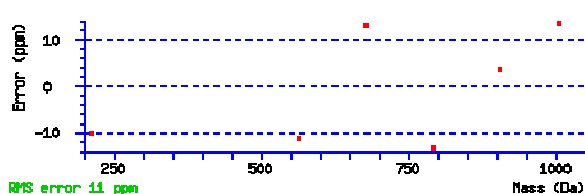
Ions Score: 32 Expect: 0.01

Matches : 6/64 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							9
2	213.1598	107.0835			V	1004.6139	502.8106	987.5873	494.2973	986.6033	493.8053	8
3	326.2438	163.6255			I	905.5455	453.2764	888.5189	444.7631	887.5349	444.2711	7
4	439.3279	220.1676			L	792.4614	396.7343	775.4349	388.2211	774.4509	387.7291	6
5	554.3548	277.6811	536.3443	268.6758	D	679.3774	340.1923	662.3508	331.6790	661.3668	331.1870	5
6	717.4182	359.2127	699.4076	350.2074	Y	564.3504	282.6788	547.3239	274.1656			4
7	830.5022	415.7547	812.4917	406.7495	I	401.2871	201.1472	384.2605	192.6339			3
8	943.5863	472.2968	925.5757	463.2915	I	288.2030	144.6051	271.1765	136.0919			2
9					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 11 ppm



RMS error 11 ppm

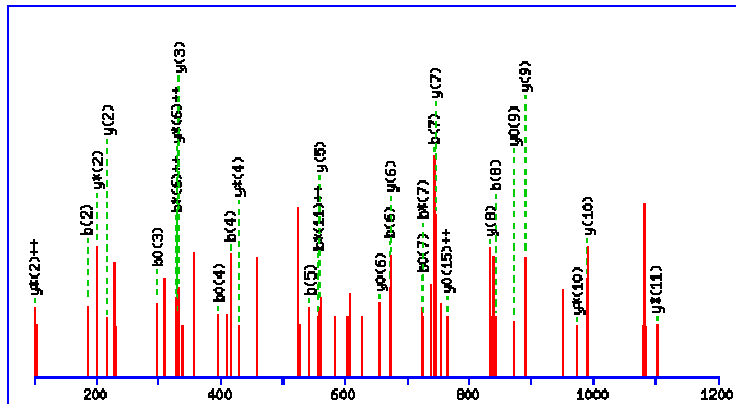
Peptide Number: 44077

MS/MS Fragmentation of **SPMVEQAVQTGSADNLNAK**Found in **IPI00032635** in **IPI_human**, Tax_Id=9606 Gene_Symbol=LSM14B Isoform 1 of Protein LSM14 homolog B

Match to Query 41016: 1958.929782 from(653.983870,3+) index(18797)

Title: Elution from: 45.7333333333333 to 45.7333333333333 period: 0 cycle: 1731 experiment: 8 polarity:+

Data file 120210ry_32R1-32_3_2.mgf



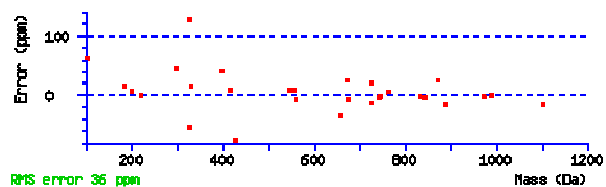
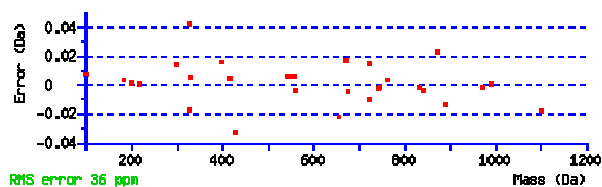
Monoisotopic mass of neutral peptide Mr(calcd): 1958.9367

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 47 Expect: 0.00098

Matches : 29/196 fragment ions using 61 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							19
2	185.0921	93.0497			167.0815	84.0444	P	1872.9120	936.9596	1855.8855	928.4464	1854.9014	927.9544	18
3	316.1326	158.5699			298.1220	149.5646	M	1775.8592	888.4333	1758.8327	879.9200	1757.8487	879.4280	17
4	415.2010	208.1041			397.1904	199.0988	V	1644.8188	822.9130	1627.7922	814.3997	1626.8082	813.9077	16
5	544.2436	272.6254			526.2330	263.6201	E	1545.7503	773.3788	1528.7238	764.8655	1527.7398	764.3735	15
6	672.3021	336.6547	655.2756	328.1414	654.2916	327.6494	Q	1416.7077	708.8575	1399.6812	700.3442	1398.6972	699.8522	14
7	743.3393	372.1733	726.3127	363.6600	725.3287	363.1680	A	1288.6492	644.8282	1271.6226	636.3149	1270.6386	635.8229	13
8	842.4077	421.7075	825.3811	413.1942	824.3971	412.7022	V	1217.6121	609.3097	1200.5855	600.7964	1199.6015	600.3044	12
9	970.4662	485.7368	953.4397	477.2235	952.4557	476.7315	Q	1118.5436	559.7755	1101.5171	551.2622	1100.5331	550.7702	11
10	1071.5139	536.2606	1054.4874	527.7473	1053.5034	527.2553	T	990.4851	495.7462	973.4585	487.2329	972.4745	486.7409	10
11	1128.5354	564.7713	1111.5088	556.2581	1110.5248	555.7660	G	889.4374	445.2223	872.4108	436.7091	871.4268	436.2170	9
12	1215.5674	608.2873	1198.5409	599.7741	1197.5568	599.2821	S	832.4159	416.7116	815.3894	408.1983	814.4054	407.7063	8
13	1286.6045	643.8059	1269.5780	635.2926	1268.5940	634.8006	A	745.3839	373.1956	728.3573	364.6823	727.3733	364.1903	7
14	1401.6315	701.3194	1384.6049	692.8061	1383.6209	692.3141	D	674.3468	337.6770	657.3202	329.1638	656.3362	328.6717	6
15	1515.6744	758.3408	1498.6479	749.8276	1497.6638	749.3356	N	559.3198	280.1636	542.2933	271.6503			5
16	1628.7585	814.8829	1611.7319	806.3696	1610.7479	805.8776	L	445.2769	223.1421	428.2504	214.6288			4
17	1742.8014	871.9043	1725.7748	863.3911	1724.7908	862.8991	N	332.1928	166.6001	315.1663	158.0868			3
18	1813.8385	907.4229	1796.8120	898.9096	1795.8279	898.4176	A	218.1499	109.5786	201.1234	101.0653			2
19							K	147.1128	74.0600	130.0863	65.5468			1



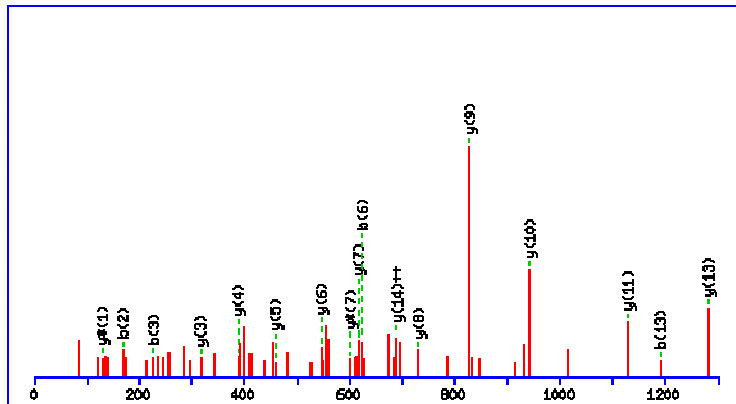
Peptide Number: 44106

MS/MS Fragmentation of **APGPWDPLASAAGLK**Found in **IPI00927277** in **IPI_human**, Tax_Id=9606 Gene_Symbol=DNAJB6 cDNA FLJ60022, highly similar to DnaJ homolog subfamily B member 6

Match to Query 11755: 1449.759408 from(725.886980,2+) index(26201)

Title: Elution from: 64.1666666666667 to 64.1666666666667 period: 0 cycle: 2373 experiment: 4 polarity: +

Data file 120124ry_414C2-43_1_3.mgf



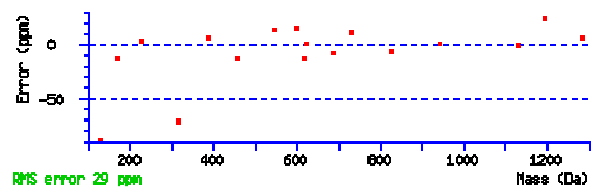
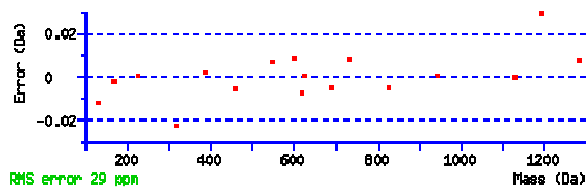
Monoisotopic mass of neutral peptide Mr(calc): 1449.7616

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 39 Expect: 0.0088

Matches : 17/120 fragment ions using 55 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258			A							15
2	169.0972	85.0522			P	1379.7318	690.3695	1362.7052	681.8563	1361.7212	681.3642	14
3	226.1186	113.5629			G	1282.6790	641.8431	1265.6525	633.3299	1264.6684	632.8379	13
4	323.1714	162.0893			P	1225.6575	613.3324	1208.6310	604.8191	1207.6470	604.3271	12
5	509.2507	255.1290			W	1128.6048	564.8060	1111.5782	556.2928	1110.5942	555.8007	11
6	624.2776	312.6425	606.2671	303.6372	D	942.5255	471.7664	925.4989	463.2531	924.5149	462.7611	10
7	721.3304	361.1688	703.3198	352.1636	P	827.4985	414.2529	810.4720	405.7396	809.4880	405.2476	9
8	834.4145	417.7109	816.4039	408.7056	L	730.4458	365.7265	713.4192	357.2132	712.4352	356.7212	8
9	905.4516	453.2294	887.4410	444.2241	A	617.3617	309.1845	600.3352	300.6712	599.3511	300.1792	7
10	992.4836	496.7454	974.4730	487.7402	S	546.3246	273.6659	529.2980	265.1527	528.3140	264.6606	6
11	1063.5207	532.2640	1045.5102	523.2587	A	459.2926	230.1499	442.2660	221.6366			5
12	1134.5578	567.7826	1116.5473	558.7773	A	388.2554	194.6314	371.2289	186.1181			4
13	1191.5793	596.2933	1173.5687	587.2880	G	317.2183	159.1128	300.1918	150.5995			3
14	1304.6634	652.8353	1286.6528	643.8300	L	260.1969	130.6021	243.1703	122.0888			2
15					K	147.1128	74.0600	130.0863	65.5468			1



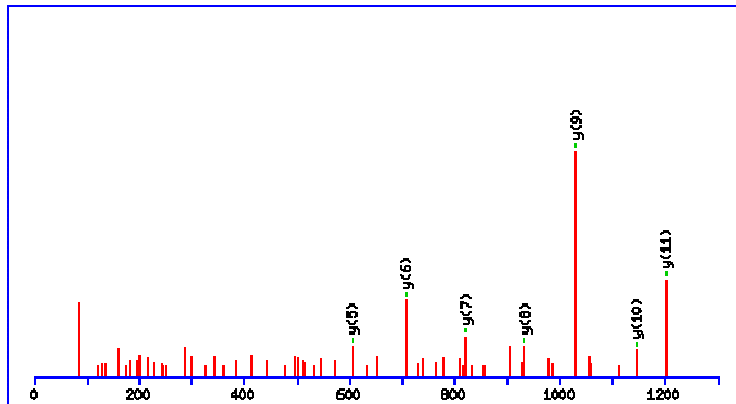
Peptide Number: 44139

MS/MS Fragmentation of **GVIGDPLLTIFVAR**Found in **IPI00007576** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SNRNP35 Isoform 1 of U11/U12 small nuclear ribonucleoprotein 35 kDa protein

Match to Query 2727: 1469.864688 from(735.939620,2+) index(19655)

Title: Elution from: 50.65 to 50.65 period: 0 cycle: 1926 experiment: 4 polarity: +

Data file 120214ry_414C2-43_4_4.mgf



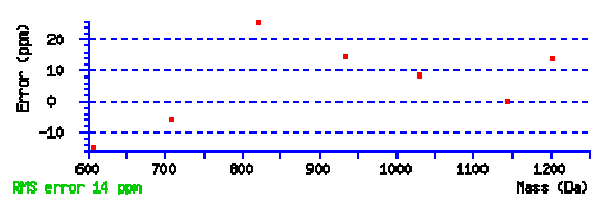
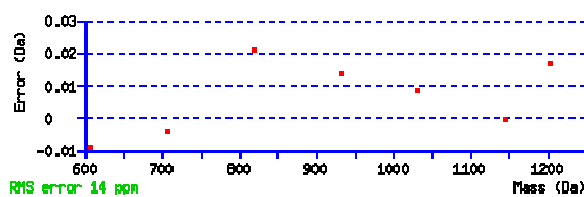
Monoisotopic mass of neutral peptide Mr(calc): 1469.8606

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 48 Expect: 0.00037

Matches : 7/112 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180			G							14
2	157.0972	79.0522			V	1413.8464	707.4268	1396.8199	698.9136	1395.8358	698.4216	13
3	270.1812	135.5942			I	1314.7780	657.8926	1297.7515	649.3794	1296.7674	648.8874	12
4	327.2027	164.1050			G	1201.6939	601.3506	1184.6674	592.8373	1183.6834	592.3453	11
5	442.2296	221.6185	424.2191	212.6132	D	1144.6725	572.8399	1127.6459	564.3266	1126.6619	563.8346	10
6	539.2824	270.1448	521.2718	261.1396	P	1029.6455	515.3264	1012.6190	506.8131	1011.6350	506.3211	9
7	652.3665	326.6869	634.3559	317.6816	L	932.5928	466.8000	915.5662	458.2867	914.5822	457.7947	8
8	765.4505	383.2289	747.4400	374.2236	L	819.5087	410.2580	802.4822	401.7447	801.4981	401.2527	7
9	866.4982	433.7527	848.4876	424.7475	T	706.4246	353.7160	689.3981	345.2027	688.4141	344.7107	6
10	979.5823	490.2948	961.5717	481.2895	L	605.3770	303.1921	588.3504	294.6788			5
11	1126.6507	563.8290	1108.6401	554.8237	F	492.2929	246.6501	475.2663	238.1368			4
12	1225.7191	613.3632	1207.7085	604.3579	V	345.2245	173.1159	328.1979	164.6026			3
13	1296.7562	648.8817	1278.7456	639.8765	A	246.1561	123.5817	229.1295	115.0684			2
14					R	175.1190	88.0631	158.0924	79.5498			1



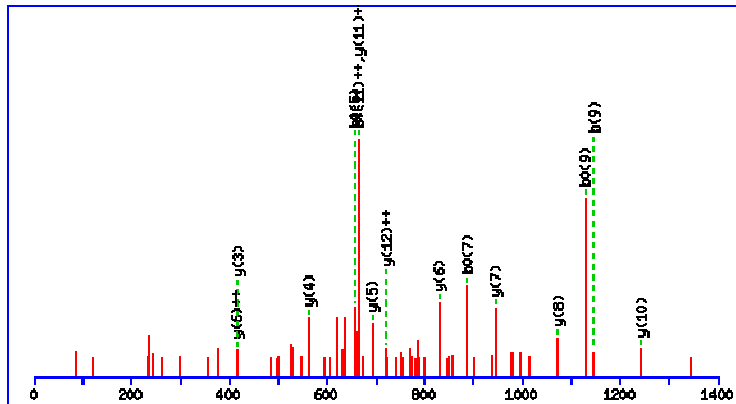
Peptide Number: 44171

MS/MS Fragmentation of **ETFCHLDQDISGLQDHEFQIR**Found in **IPI00025646** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ACTR8 Isoform 1 of Actin-related protein 8

Match to Query 37222: 2587.181456 from(647.802640,4+) index(17854)

Title: Elution from: 45.4666666666667 to 45.4666666666667 period: 0 cycle: 1716 experiment: 6 polarity: +

Data file 120210ry_585A1-55_3_3.mgf



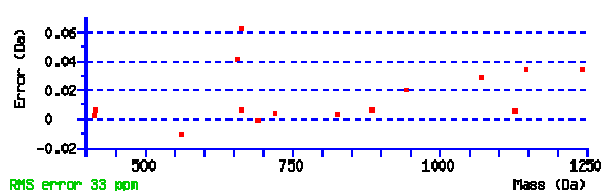
Monoisotopic mass of neutral peptide Mr(calc): 2587.1762

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

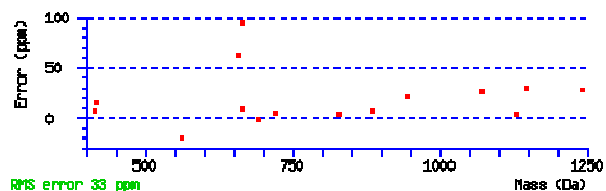
Ions Score: 35 Expect: 0.01

Matches : 15/218 fragment ions using 24 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							21
2	231.0975	116.0524			213.0870	107.0471	T	2459.1408	1230.0741	2442.1143	1221.5608	2441.1303	1221.0688	20
3	378.1660	189.5866			360.1554	180.5813	F	2358.0932	1179.5502	2341.0666	1171.0369	2340.0826	1170.5449	19
4	538.1966	269.6019			520.1860	260.5967	C	2211.0247	1106.0160	2193.9982	1097.5027	2193.0142	1097.0107	18
5	675.2555	338.1314			657.2450	329.1261	H	2050.9941	1026.0007	2033.9675	1017.4874	2032.9835	1016.9954	17
6	788.3396	394.6734			770.3290	385.6681	L	1913.9352	957.4712	1896.9086	948.9580	1895.9246	948.4659	16
7	903.3665	452.1869			885.3560	443.1816	D	1800.8511	900.9292	1783.8246	892.4159	1782.8406	891.9239	15
8	1031.4251	516.2162	1014.3986	507.7029	1013.4145	507.2109	Q	1685.8242	843.4157	1668.7976	834.9025	1667.8136	834.4104	14
9	1146.4521	573.7297	1129.4255	565.2164	1128.4415	564.7244	D	1557.7656	779.3864	1540.7390	770.8732	1539.7550	770.3812	13
10	1259.5361	630.2717	1242.5096	621.7584	1241.5256	621.2664	I	1442.7387	721.8730	1425.7121	713.3597	1424.7281	712.8677	12
11	1346.5681	673.7877	1329.5416	665.2744	1328.5576	664.7824	S	1329.6546	665.3309	1312.6280	656.8177	1311.6440	656.3257	11
12	1403.5896	702.2984	1386.5631	693.7852	1385.5790	693.2932	G	1242.6226	621.8149	1225.5960	613.3016	1224.6120	612.8096	10
13	1516.6737	758.8405	1499.6471	750.3272	1498.6631	749.8352	L	1185.6011	593.3042	1168.5745	584.7909	1167.5905	584.2989	9
14	1644.7322	822.8698	1627.7057	814.3565	1626.7217	813.8645	Q	1072.5170	536.7622	1055.4905	528.2489	1054.5065	527.7569	8
15	1759.7592	880.3832	1742.7326	871.8700	1741.7486	871.3780	D	944.4585	472.7329	927.4319	464.2196	926.4479	463.7276	7
16	1896.8181	948.9127	1879.7916	940.3994	1878.8075	939.9074	H	829.4315	415.2194	812.4050	406.7061	811.4209	406.2141	6
17	2025.8607	1013.4340	2008.8341	1004.9207	2007.8501	1004.4287	E	692.3726	346.6899	675.3461	338.1767	674.3620	337.6847	5
18	2172.9291	1086.9682	2155.9026	1078.4549	2154.9185	1077.9629	F	563.3300	282.1686	546.3035	273.6554			4
19	2300.9877	1150.9975	2283.9611	1142.4842	2282.9771	1141.9922	Q	416.2616	208.6344	399.2350	200.1212			3
20	2414.0718	1207.5395	2397.0452	1199.0262	2396.0612	1198.5342	I	288.2030	144.6051	271.1765	136.0919			2
21							R	175.1190	88.0631	158.0924	79.5498			1



RMS error: 33 ppm



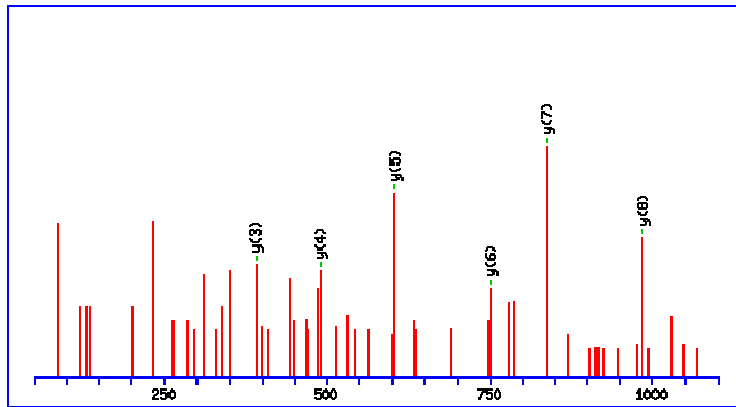
RMS error: 33 ppm

Peptide Number: 44205MS/MS Fragmentation of **IFSFNVWGK**Found in **IPI00514611** in **IPI_human**, Tax_Id=9606 Gene_Symbol=BCAP29 B-cell receptor-associated protein 29 isoform a

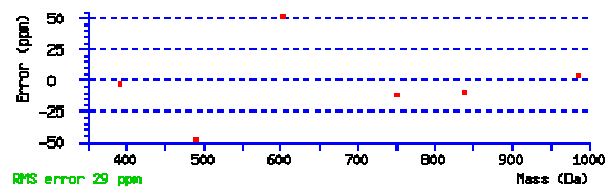
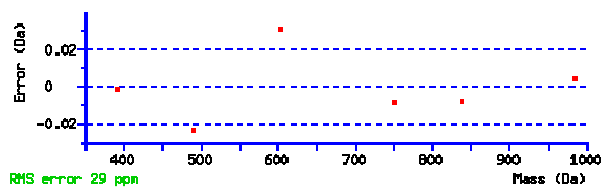
Match to Query 3898: 1096.567728 from(549.291140,2+) index(30154)

Title: Elution from: 72.7833333333333 to 72.7833333333333 period: 0 cycle: 2703 experiment: 2 polarity:+

Data file 120126ry_585A1-55_1_3.mgf

**Monoisotopic mass of neutral peptide Mr(calc):** 1096.5706**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 43 **Expect:** 0.0026**Matches :** 6/72 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							9
2	261.1598	131.0835					F	984.4938	492.7505	967.4672	484.2373	966.4832	483.7452	8
3	348.1918	174.5995			330.1812	165.5942	S	837.4254	419.2163	820.3988	410.7030	819.4148	410.2110	7
4	495.2602	248.1337			477.2496	239.1285	F	750.3933	375.7003	733.3668	367.1870			6
5	609.3031	305.1552	592.2766	296.6419	591.2926	296.1499	N	603.3249	302.1661	586.2984	293.6528			5
6	708.3715	354.6894	691.3450	346.1761	690.3610	345.6841	V	489.2820	245.1446	472.2554	236.6314			4
7	894.4508	447.7291	877.4243	439.2158	876.4403	438.7238	W	390.2136	195.6104	373.1870	187.0972			3
8	951.4723	476.2398	934.4458	467.7265	933.4617	467.2345	G	204.1343	102.5708	187.1077	94.0575			2
9							K	147.1128	74.0600	130.0863	65.5468			1

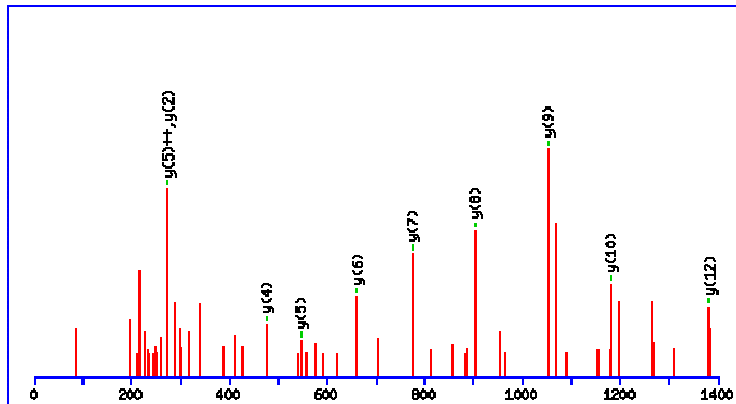


Peptide Number: 44385MS/MS Fragmentation of **ELDSEFEDLASDVR**Found in **IPI00168698** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PDZD8 PDZ domain-containing protein 8

Match to Query 15947: 1623.730368 from(812.872460,2+) index(24252)

Title: Elution from: 58.1666666666667 to 58.1666666666667 period: 0 cycle: 2185 experiment: 8 polarity: +

Data file 120214ry_32R1-32_4_3.mgf



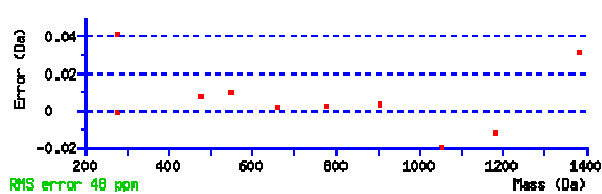
Monoisotopic mass of neutral peptide Mr(calc): 1623.7264

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

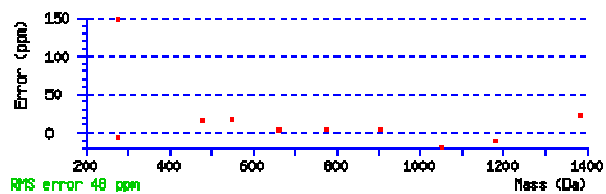
Ions Score: 74 Expect: 1.3e-006

Matches : 10/126 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286	112.0393	56.5233	E							14
2	243.1339	122.0706	225.1234	113.0653	L	1495.6911	748.3492	1478.6645	739.8359	1477.6805	739.3439	13
3	358.1609	179.5841	340.1503	170.5788	D	1382.6070	691.8072	1365.5805	683.2939	1364.5965	682.8019	12
4	445.1929	223.1001	427.1823	214.0948	S	1267.5801	634.2937	1250.5535	625.7804	1249.5695	625.2884	11
5	574.2355	287.6214	556.2249	278.6161	E	1180.5481	590.7777	1163.5215	582.2644	1162.5375	581.7724	10
6	721.3039	361.1556	703.2933	352.1503	F	1051.5055	526.2564	1034.4789	517.7431	1033.4949	517.2511	9
7	850.3465	425.6769	832.3359	416.6716	E	904.4371	452.7222	887.4105	444.2089	886.4265	443.7169	8
8	965.3734	483.1904	947.3629	474.1851	D	775.3945	388.2009	758.3679	379.6876	757.3839	379.1956	7
9	1078.4575	539.7324	1060.4469	530.7271	L	660.3675	330.6874	643.3410	322.1741	642.3570	321.6821	6
10	1149.4946	575.2510	1131.4841	566.2457	A	547.2835	274.1454	530.2569	265.6321	529.2729	265.1401	5
11	1236.5267	618.7670	1218.5161	609.7617	S	476.2463	238.6268	459.2198	230.1135	458.2358	229.6215	4
12	1351.5536	676.2804	1333.5430	667.2752	D	389.2143	195.1108	372.1878	186.5975	371.2037	186.1055	3
13	1450.6220	725.8146	1432.6114	716.8094	V	274.1874	137.5973	257.1608	129.0840			2
14					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 48 ppm



RMS error 48 ppm

Peptide Number: 44418

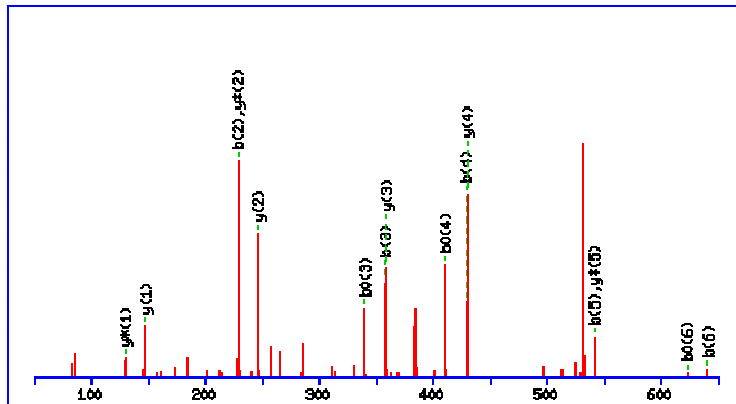
MS/MS Fragmentation of **DLEALVK**

Found in **IPI00969184** in **IPI_human**, Tax_Id=9606 Gene_Symbol=WDR65 Isoform 1 of WD repeat-containing protein 65

Match to Query 18: 786.434908 from(394.224730,2+) index(3327)

Title: Elution from: 8.81666666666667 to 8.81666666666667 period: 0 cycle: 343 experiment: 1 polarity: +

Data file 120208ry_Tig120slc-P8_1_3.mgf



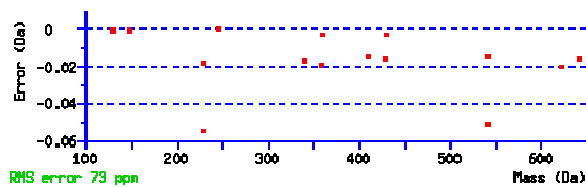
Monoisotopic mass of neutral peptide Mr(calc): 786.4487

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

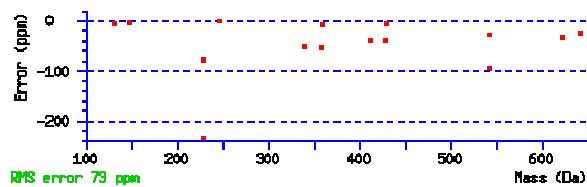
Ions Score: 42 Expect: 0.0066

Matches : 15/52 fragment ions using 17 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	98.0237	49.5155	D							7
2	229.1183	115.0628	211.1077	106.0575	L	672.4291	336.7182	655.4025	328.2049	654.4185	327.7129	6
3	358.1609	179.5841	340.1503	170.5788	E	559.3450	280.1761	542.3184	271.6629	541.3344	271.1709	5
4	429.1980	215.1026	411.1874	206.0974	A	430.3024	215.6548	413.2758	207.1416			4
5	542.2821	271.6447	524.2715	262.6394	L	359.2653	180.1363	342.2387	171.6230			3
6	641.3505	321.1789	623.3399	312.1736	V	246.1812	123.5942	229.1547	115.0810			2
7					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 73 ppm



RMS error 73 ppm

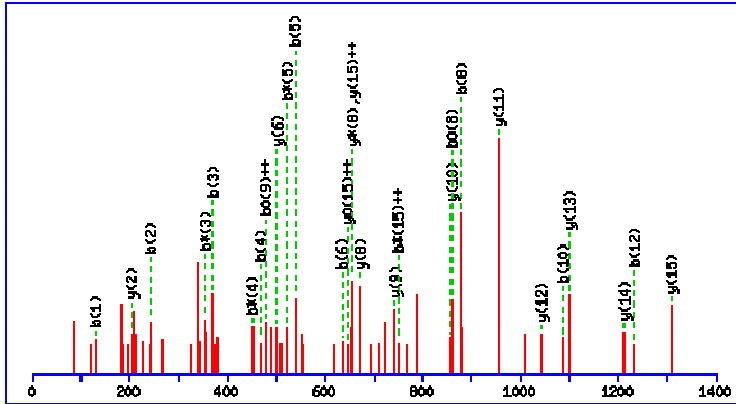
Peptide Number: 44569

MS/MS Fragmentation of **QLQPAPLEPLGSPDAGLGAAVGK**Found in **IPI00029403** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SNX4 Sorting nexin-4

Match to Query 27081: 2185.180452 from(729.400760,3+) index(9506)

Title: Elution from: 24.9666666666667 to 24.9666666666667 period: 0 cycle: 957 experiment: 10 polarity: +

Data file 120208ry_Tig120slc-P8_1_3.mgf



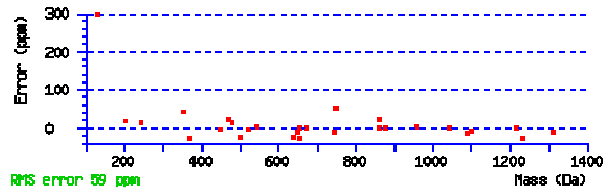
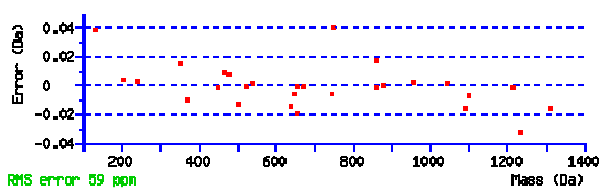
Monoisotopic mass of neutral peptide Mr(calc): 2185.1743

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 72 Expect: 2.7e-006

Matches : 28/232 fragment ions using 48 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.0659	65.0366	112.0393	56.5233			Q							23
2	242.1499	121.5786	225.1234	113.0653			L	2058.1230	1029.5651	2041.0964	1021.0519	2040.1124	1020.5598	22
3	370.2085	185.6079	353.1819	177.0946			Q	1945.0389	973.0231	1928.0124	964.5098	1927.0284	964.0178	21
4	467.2613	234.1343	450.2347	225.6210			P	1816.9803	908.9938	1799.9538	900.4805	1798.9698	899.9885	20
5	538.2984	269.6528	521.2718	261.1396			A	1719.9276	860.4674	1702.9010	851.9542	1701.9170	851.4621	19
6	635.3511	318.1792	618.3246	309.6659			P	1648.8905	824.9489	1631.8639	816.4356	1630.8799	815.9436	18
7	748.4352	374.7212	731.4087	366.2080			L	1551.8377	776.4225	1534.8112	767.9092	1533.8271	767.4172	17
8	877.4778	439.2425	860.4512	430.7293	859.4672	430.2373	E	1438.7536	719.8805	1421.7271	711.3672	1420.7431	710.8752	16
9	974.5306	487.7689	957.5040	479.2556	956.5200	478.7636	P	1309.7110	655.3592	1292.6845	646.8459	1291.7005	646.3539	15
10	1087.6146	544.3109	1070.5881	535.7977	1069.6041	535.3057	L	1212.6583	606.8328	1195.6317	598.3195	1194.6477	597.8275	14
11	1144.6361	572.8217	1127.6095	564.3084	1126.6255	563.8164	G	1099.5742	550.2907	1082.5477	541.7775	1081.5636	541.2855	13
12	1231.6681	616.3377	1214.6416	607.8244	1213.6576	607.3324	S	1042.5528	521.7800	1025.5262	513.2667	1024.5422	512.7747	12
13	1328.7209	664.8641	1311.6943	656.3508	1310.7103	655.8588	P	955.5207	478.2640	938.4942	469.7507	937.5102	469.2587	11
14	1443.7478	722.3775	1426.7213	713.8643	1425.7373	713.3723	D	858.4680	429.7376	841.4414	421.2243	840.4574	420.7323	10
15	1514.7849	757.8961	1497.7584	749.3828	1496.7744	748.8908	A	743.4410	372.2241	726.4145	363.7109			9
16	1571.8064	786.4068	1554.7799	777.8936	1553.7958	777.4016	G	672.4039	336.7056	655.3774	328.1923			8
17	1684.8905	842.9489	1667.8639	834.4356	1666.8799	833.9436	L	615.3824	308.1949	598.3559	299.6816			7
18	1741.9119	871.4596	1724.8854	862.9463	1723.9014	862.4543	G	502.2984	251.6528	485.2718	243.1396			6
19	1812.9490	906.9782	1795.9225	898.4649	1794.9385	897.9729	A	445.2769	223.1421	428.2504	214.6288			5
20	1883.9862	942.4967	1866.9596	933.9834	1865.9756	933.4914	A	374.2398	187.6235	357.2132	179.1103			4
21	1983.0546	992.0309	1966.0280	983.5176	1965.0440	983.0256	V	303.2027	152.1050	286.1761	143.5917			3
22	2040.0760	1020.5417	2023.0495	1012.0284	2022.0655	1011.5364	G	204.1343	102.5708	187.1077	94.0575			2
23							K	147.1128	74.0600	130.0863	65.5468			1



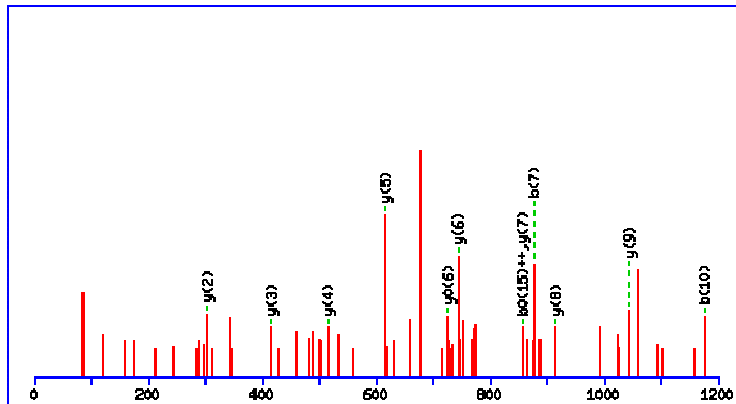
Peptide Number: 45212

MS/MS Fragmentation of **VLDEEEYIEGLQTVIQR**Found in **IPI00165171** in **IPI_human**, Tax_Id=9606 Gene_Symbol=DGCR14 Protein DGCR14

Match to Query 28246: 2033.020422 from(678.680750,3+) index(42343)

Title: Elution from: 105.666666666667 to 105.666666666667 period: 0 cycle: 3984 experiment: 3 polarity:+

Data file 120210ry_32R1-32_3_3.mgf



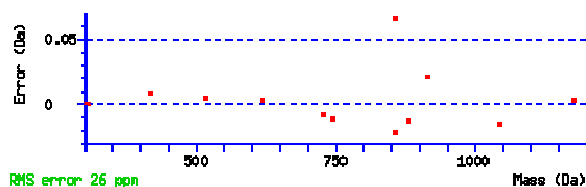
Monoisotopic mass of neutral peptide Mr(calc): 2033.0317

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

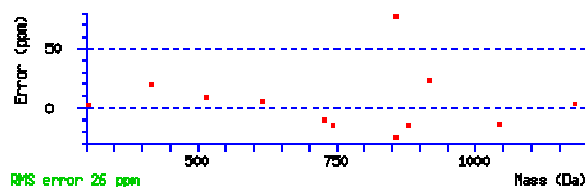
Ions Score: 42 Expect: 0.005

Matches : 12/158 fragment ions using 22 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							17
2	213.1598	107.0835					L	1934.9706	967.9889	1917.9440	959.4756	1916.9600	958.9836	16
3	328.1867	164.5970			310.1761	155.5917	D	1821.8865	911.4469	1804.8600	902.9336	1803.8759	902.4416	15
4	457.2293	229.1183			439.2187	220.1130	E	1706.8596	853.9334	1689.8330	845.4201	1688.8490	844.9281	14
5	586.2719	293.6396			568.2613	284.6343	E	1577.8170	789.4121	1560.7904	780.8988	1559.8064	780.4068	13
6	715.3145	358.1609			697.3039	349.1556	E	1448.7744	724.8908	1431.7478	716.3775	1430.7638	715.8855	12
7	878.3778	439.6925			860.3672	430.6873	Y	1319.7318	660.3695	1302.7052	651.8563	1301.7212	651.3642	11
8	991.4619	496.2346			973.4513	487.2293	I	1156.6684	578.8379	1139.6419	570.3246	1138.6579	569.8326	10
9	1120.5045	560.7559			1102.4939	551.7506	E	1043.5844	522.2958	1026.5578	513.7826	1025.5738	513.2905	9
10	1177.5259	589.2666			1159.5154	580.2613	Q	914.5418	457.7745	897.5152	449.2613	896.5312	448.7693	8
11	1290.6100	645.8086			1272.5994	636.8034	L	857.5203	429.2638	840.4938	420.7505	839.5098	420.2585	7
12	1418.6686	709.8379	1401.6420	701.3246	1400.6580	700.8326	Q	744.4363	372.7218	727.4097	364.2085	726.4257	363.7165	6
13	1519.7162	760.3618	1502.6897	751.8485	1501.7057	751.3565	T	616.3777	308.6925	599.3511	300.1792	598.3671	299.6872	5
14	1618.7847	809.8960	1601.7581	801.3827	1600.7741	800.8907	V	515.3300	258.1686	498.3035	249.6554			4
15	1731.8687	866.4380	1714.8422	857.9247	1713.8582	857.4327	I	416.2616	208.6344	399.2350	200.1212			3
16	1859.9273	930.4673	1842.9008	921.9540	1841.9167	921.4620	Q	303.1775	152.0924	286.1510	143.5791			2
17							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 26 ppm



RMS error 26 ppm

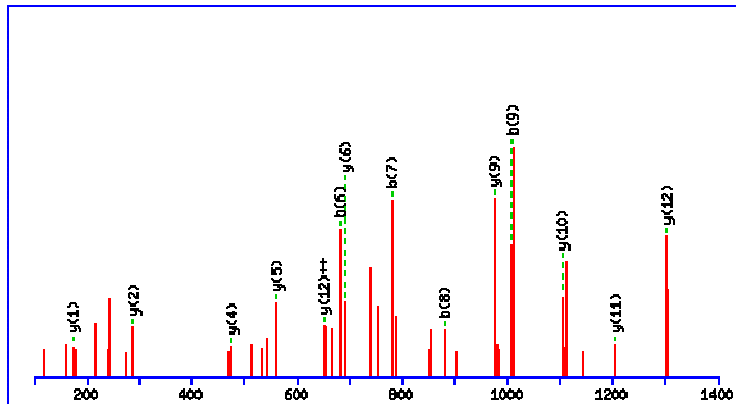
Peptide Number: 45291

MS/MS Fragmentation of **DRLPSIVVEPTTEGEVESGELR**Found in **IPI00333338** in **IPI_human**, Tax_Id=9606 Gene_Symbol=LBH Protein LBH

Match to Query 33167: 2310.181212 from(771.067680,3+) index(4873)

Title: Elution from: 11.7166666666667 to 11.7166666666667 period: 0 cycle: 446 experiment: 9 polarity: +

Data file 120208ry_Tig120slc-P8_2_3.mgf



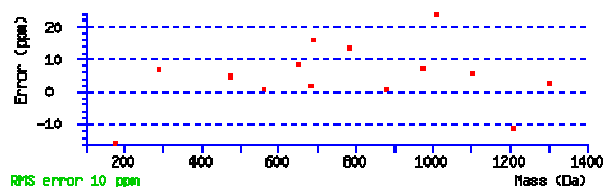
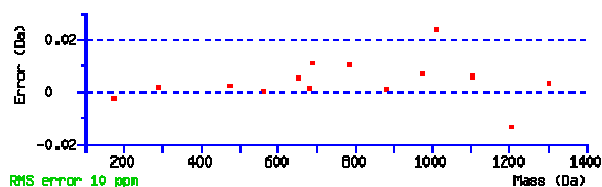
Monoisotopic mass of neutral peptide Mr(calc): 2310.1703

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 41 Expect: 0.0048

Matches : 14/234 fragment ions using 31 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							21
2	272.1353	136.5713	255.1088	128.0580	254.1248	127.5660	R	2196.1507	1098.5790	2179.1241	1090.0657	2178.1401	1089.5737	20
3	385.2194	193.1133	368.1928	184.6001	367.2088	184.1081	L	2040.0495	1020.5284	2023.0230	1012.0151	2022.0390	1011.5231	19
4	482.2722	241.6397	465.2456	233.1264	464.2616	232.6344	P	1926.9655	963.9864	1909.9389	955.4731	1908.9549	954.9811	18
5	569.3042	285.1557	552.2776	276.6425	551.2936	276.1504	S	1829.9127	915.4600	1812.8862	906.9467	1811.9021	906.4547	17
6	682.3883	341.6978	665.3617	333.1845	664.3777	332.6925	I	1742.8807	871.9440	1725.8541	863.4307	1724.8701	862.9387	16
7	781.4567	391.2320	764.4301	382.7187	763.4461	382.2267	V	1629.7966	815.4019	1612.7701	806.8887	1611.7861	806.3967	15
8	880.5251	440.7662	863.4985	432.2529	862.5145	431.7609	V	1530.7282	765.8677	1513.7017	757.3545	1512.7176	756.8625	14
9	1009.5677	505.2875	992.5411	496.7742	991.5571	496.2822	E	1431.6598	716.3335	1414.6332	707.8203	1413.6492	707.3283	13
10	1106.6204	553.8139	1089.5939	545.3006	1088.6099	544.8086	P	1302.6172	651.8122	1285.5907	643.2990	1284.6066	642.8070	12
11	1207.6681	604.3377	1190.6416	595.8244	1189.6575	595.3324	T	1205.5644	603.2859	1188.5379	594.7726	1187.5539	594.2806	11
12	1336.7107	668.8590	1319.6842	660.3457	1318.7001	659.8537	E	1104.5168	552.7620	1087.4902	544.2487	1086.5062	543.7567	10
13	1393.7322	697.3697	1376.7056	688.8564	1375.7216	688.3644	G	975.4742	488.2407	958.4476	479.7274	957.4636	479.2354	9
14	1522.7748	761.8910	1505.7482	753.3777	1504.7642	752.8857	E	918.4527	459.7300	901.4262	451.2167	900.4421	450.7247	8
15	1621.8432	811.4252	1604.8166	802.9120	1603.8326	802.4199	V	789.4101	395.2087	772.3836	386.6954	771.3995	386.2034	7
16	1750.8858	875.9465	1733.8592	867.4332	1732.8752	866.9412	E	690.3417	345.6745	673.3151	337.1612	672.3311	336.6692	6
17	1837.9178	919.4625	1820.8913	910.9493	1819.9072	910.4573	S	561.2991	281.1532	544.2726	272.6399	543.2885	272.1479	5
18	1894.9393	947.9733	1877.9127	939.4600	1876.9287	938.9680	G	474.2671	237.6372	457.2405	229.1239	456.2565	228.6319	4
19	2023.9819	1012.4946	2006.9553	1003.9813	2005.9713	1003.4893	E	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
20	2137.0659	1069.0366	2120.0394	1060.5233	2119.0554	1060.0313	L	288.2030	144.6051	271.1765	136.0919			2
21							R	175.1190	88.0631	158.0924	79.5498			1



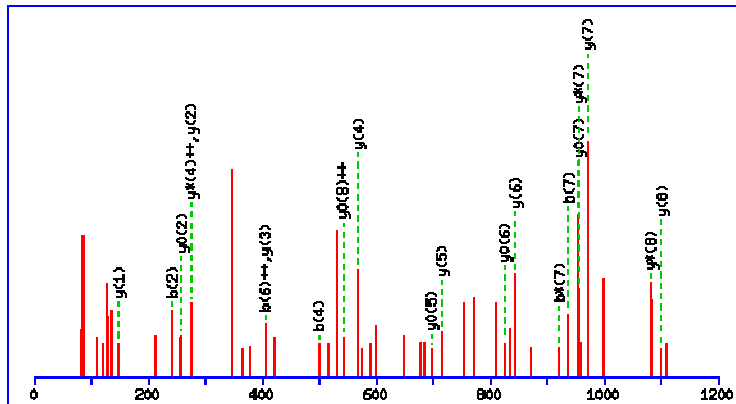
Peptide Number: 45294

MS/MS Fragmentation of **LQQEFYEEK**Found in **IPI00160290** in **IPI_human**, Tax_Id=9606 Gene_Symbol=BCL9 B-cell CLL/lymphoma 9 protein

Match to Query 17964: 1212.580588 from(607.297570,2+) index(33405)

Title: Elution from: 119.783333333333 to 119.783333333333 period: 0 cycle: 9538 experiment: 10 polarity:+

Data file 120212ry_414C2-43_3_1.mgf



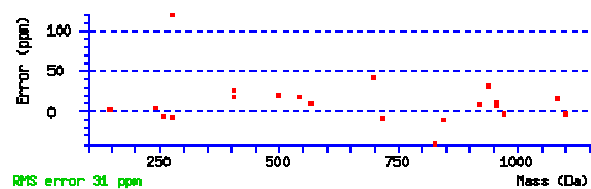
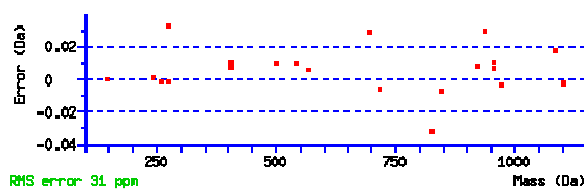
Monoisotopic mass of neutral peptide Mr(calc): 1212.5662

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 37 Expect: 0.0084

Matches : 21/86 fragment ions using 53 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							9
2	242.1499	121.5786	225.1234	113.0653			Q	1100.4895	550.7484	1083.4629	542.2351	1082.4789	541.7431	8
3	370.2085	185.6079	353.1819	177.0946			Q	972.4309	486.7191	955.4044	478.2058	954.4203	477.7138	7
4	499.2511	250.1292	482.2245	241.6159	481.2405	241.1239	E	844.3723	422.6898	827.3458	414.1765	826.3618	413.6845	6
5	646.3195	323.6634	629.2930	315.1501	628.3089	314.6581	F	715.3297	358.1685	698.3032	349.6552	697.3192	349.1632	5
6	809.3828	405.1951	792.3563	396.6818	791.3723	396.1898	Y	568.2613	284.6343	551.2348	276.1210	550.2508	275.6290	4
7	938.4254	469.7164	921.3989	461.2031	920.4149	460.7111	E	405.1980	203.1026	388.1714	194.5894	387.1874	194.0974	3
8	1067.4680	534.2376	1050.4415	525.7244	1049.4575	525.2324	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
9							K	147.1128	74.0600	130.0863	65.5468			1



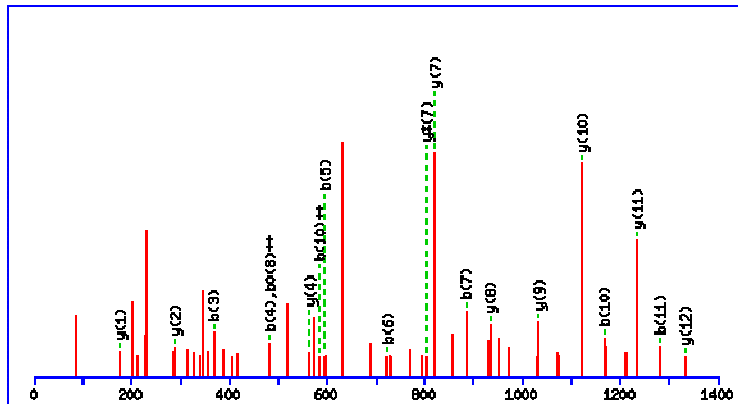
Peptide Number: 45310

MS/MS Fragmentation of **ACHILECPEGLAQDVISTIGQAFELR**Found in **IPI00021326** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SHC1 Isoform 6 of SHC-transforming protein 1

Match to Query 7240: 2926.473732 from(976.498520,3+) index(10660)

Title: Elution from: 40.9166666666667 to 40.9166666666667 period: 0 cycle: 1551 experiment: 8 polarity: +

Data file 120212ry_414C2-43_3_5.mgf



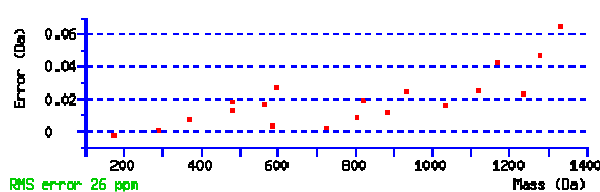
Monoisotopic mass of neutral peptide Mr(calc): 2926.4317

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

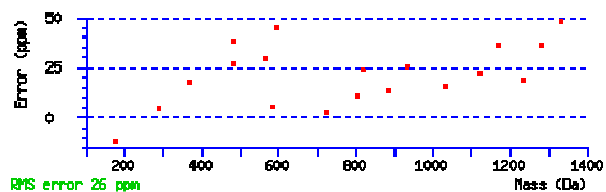
Ions Score: 40 Expect: 0.0057

Matches : 19/262 fragment ions using 51 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							26
2	232.0750	116.5412					C	2856.4019	1428.7046	2839.3753	1420.1913	2838.3913	1419.6993	25
3	369.1340	185.0706					H	2696.3712	1348.6893	2679.3447	1340.1760	2678.3607	1339.6840	24
4	482.2180	241.6126					I	2559.3123	1280.1598	2542.2858	1271.6465	2541.3018	1271.1545	23
5	595.3021	298.1547					L	2446.2283	1223.6178	2429.2017	1215.1045	2428.2177	1214.6125	22
6	724.3447	362.6760			706.3341	353.6707	E	2333.1442	1167.0757	2316.1176	1158.5625	2315.1336	1158.0705	21
7	884.3753	442.6913			866.3648	433.6860	C	2204.1016	1102.5544	2187.0750	1094.0412	2186.0910	1093.5492	20
8	981.4281	491.2177			963.4175	482.2124	P	2044.0709	1022.5391	2027.0444	1014.0258	2026.0604	1013.5338	19
9	1110.4707	555.7390			1092.4601	546.7337	E	1947.0182	974.0127	1929.9916	965.4995	1929.0076	965.0074	18
10	1167.4921	584.2497			1149.4816	575.2444	G	1817.9756	909.4914	1800.9490	900.9782	1799.9650	900.4862	17
11	1280.5762	640.7917			1262.5656	631.7865	L	1760.9541	880.9807	1743.9276	872.4674	1742.9436	871.9754	16
12	1351.6133	676.3103			1333.6028	667.3050	A	1647.8701	824.4387	1630.8435	815.9254	1629.8595	815.4334	15
13	1479.6719	740.3396	1462.6453	731.8263	1461.6613	731.3343	Q	1576.8329	788.9201	1559.8064	780.4068	1558.8224	779.9148	14
14	1594.6988	797.8531	1577.6723	789.3398	1576.6883	788.8478	D	1448.7744	724.8908	1431.7478	716.3775	1430.7638	715.8855	13
15	1693.7673	847.3873	1676.7407	838.8740	1675.7567	838.3820	V	1333.7474	667.3774	1316.7209	658.8641	1315.7369	658.3721	12
16	1806.8513	903.9293	1789.8248	895.4160	1788.8408	894.9240	I	1234.6790	617.8431	1217.6525	609.3299	1216.6684	608.8379	11
17	1893.8833	947.4453	1876.8568	938.9320	1875.8728	938.4400	S	1121.5950	561.3011	1104.5684	552.7878	1103.5844	552.2958	10
18	1994.9310	997.9692	1977.9045	989.4559	1976.9205	988.9639	T	1034.5629	517.7851	1017.5364	509.2718	1016.5524	508.7798	9
19	2108.0151	1054.5112	2090.9885	1045.9979	2090.0045	1045.5059	I	933.5152	467.2613	916.4887	458.7480	915.5047	458.2560	8
20	2165.0366	1083.0219	2148.0100	1074.5086	2147.0260	1074.0166	G	820.4312	410.7192	803.4046	402.2060	802.4206	401.7139	7
21	2293.0951	1147.0512	2276.0686	1138.5379	2275.0846	1138.0459	Q	763.4097	382.2085	746.3832	373.6952	745.3992	373.2032	6
22	2364.1322	1182.5698	2347.1057	1174.0565	2346.1217	1173.5645	A	635.3511	318.1792	618.3246	309.6659	617.3406	309.1739	5
23	2511.2007	1256.1040	2494.1741	1247.5907	2493.1901	1247.0987	F	564.3140	282.6606	547.2875	274.1474	546.3035	273.6554	4
24	2640.2433	1320.6253	2623.2167	1312.1120	2622.2327	1311.6200	E	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
25	2753.3273	1377.1673	2736.3008	1368.6540	2735.3168	1368.1620	L	288.2030	144.6051	271.1765	136.0919			2
26							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 26 ppm



RMS error 26 ppm

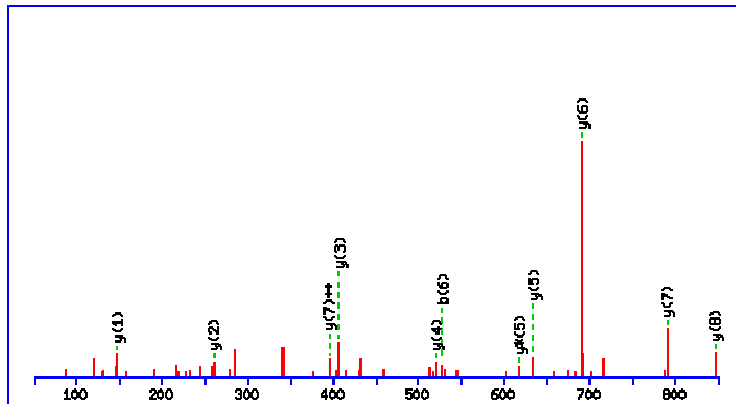
Peptide Number: 45760

MS/MS Fragmentation of **SGVGNIFIK**Found in **IPI00008524** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PABPC1 Isoform 1 of Polyadenylate-binding protein 1

Match to Query 4607: 933.532428 from(467.773490,2+) index(27768)

Title: Elution from: 71.8333333333333 to 71.8333333333333 period: 0 cycle: 2748 experiment: 1 polarity:+

Data file 120208ry_Tig120slc-P8_1_2.mgf



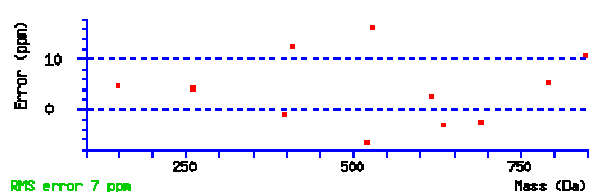
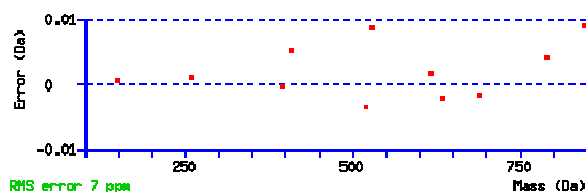
Monoisotopic mass of neutral peptide Mr(calc): 933.5284

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 76 Expect: 1.3e-006

Matches : 11/72 fragment ions using 16 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	#
1	88.0393	44.5233			70.0287	35.5180	S					9
2	145.0608	73.0340			127.0502	64.0287	G	847.5036	424.2554	830.4771	415.7422	8
3	244.1292	122.5682			226.1186	113.5629	V	790.4822	395.7447	773.4556	387.2314	7
4	301.1506	151.0790			283.1401	142.0737	G	691.4137	346.2105	674.3872	337.6972	6
5	415.1936	208.1004	398.1670	199.5872	397.1830	199.0951	N	634.3923	317.6998	617.3657	309.1865	5
6	528.2776	264.6425	511.2511	256.1292	510.2671	255.6372	I	520.3493	260.6783	503.3228	252.1650	4
7	675.3461	338.1767	658.3195	329.6634	657.3355	329.1714	F	407.2653	204.1363	390.2387	195.6230	3
8	788.4301	394.7187	771.4036	386.2054	770.4195	385.7134	I	260.1969	130.6021	243.1703	122.0888	2
9							K	147.1128	74.0600	130.0863	65.5468	1



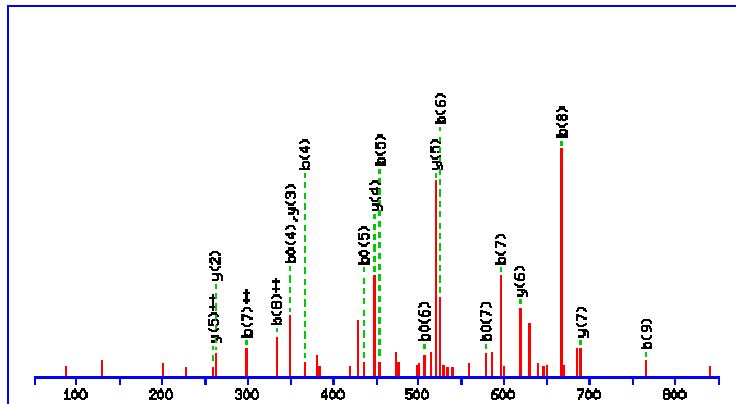
Peptide Number: 45993

MS/MS Fragmentation of **HSAASAAAVVSSR**Found in **IPI00333770** in **IPI_human**, Tax_Id=9606 Gene_Symbol=DOCK10 Isoform 1 of Dedicator of cytokinesis protein 10

Match to Query 18643: 1283.657892 from(428.893240,3+) index(12008)

Title: Elution from: 71.0666666666667 to 71.0666666666667 period: 0 cycle: 7721 experiment: 5 polarity:+

Data file 120214ry_aHDF1419-P10_4_1.mgf



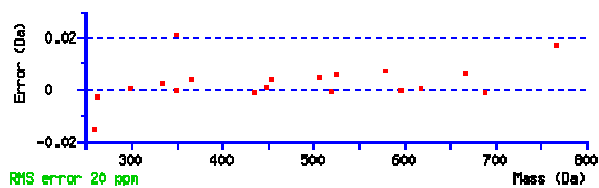
Monoisotopic mass of neutral peptide Mr(calc): 1283.6582

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

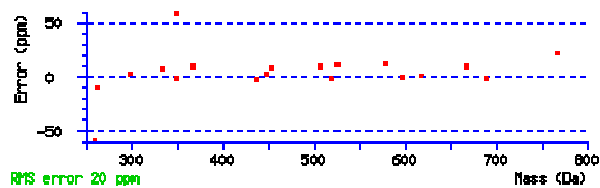
Ions Score: 41 Expect: 0.0051

Matches : 19/126 fragment ions using 33 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	138.0662	69.5367			H							14
2	225.0982	113.0527	207.0877	104.0475	S	1147.6066	574.3069	1130.5800	565.7937	1129.5960	565.3016	13
3	296.1353	148.5713	278.1248	139.5660	A	1060.5745	530.7909	1043.5480	522.2776	1042.5640	521.7856	12
4	367.1724	184.0899	349.1619	175.0846	A	989.5374	495.2724	972.5109	486.7591	971.5269	486.2671	11
5	454.2045	227.6059	436.1939	218.6006	S	918.5003	459.7538	901.4738	451.2405	900.4898	450.7485	10
6	525.2416	263.1244	507.2310	254.1191	A	831.4683	416.2378	814.4417	407.7245	813.4577	407.2325	9
7	596.2787	298.6430	578.2681	289.6377	A	760.4312	380.7192	743.4046	372.2060	742.4206	371.7139	8
8	667.3158	334.1615	649.3052	325.1563	A	689.3941	345.2007	672.3675	336.6874	671.3835	336.1954	7
9	766.3842	383.6958	748.3737	374.6905	V	618.3569	309.6821	601.3304	301.1688	600.3464	300.6768	6
10	837.4213	419.2143	819.4108	410.2090	A	519.2885	260.1479	502.2620	251.6346	501.2780	251.1426	5
11	936.4898	468.7485	918.4792	459.7432	V	448.2514	224.6293	431.2249	216.1161	430.2409	215.6241	4
12	1023.5218	512.2645	1005.5112	503.2592	S	349.1830	175.0951	332.1565	166.5819	331.1724	166.0899	3
13	1110.5538	555.7805	1092.5432	546.7753	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
14					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 20 ppm



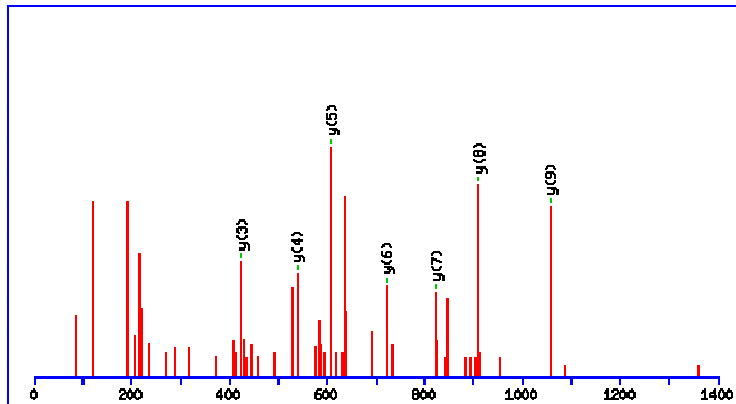
RMS error 20 ppm

Peptide Number: 46180MS/MS Fragmentation of **AFSQFSTLALHLR**Found in **IPI00014305** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ZNF146 Zinc finger protein OZF

Match to Query 11510: 1489.795422 from(497.605750,3+) index(17707)

Title: Elution from: 43.8 to 43.8 period: 0 cycle: 1649 experiment: 1 polarity: +

Data file 120210ry_32R1-32_3_3.mgf



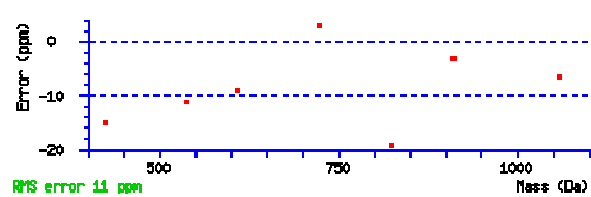
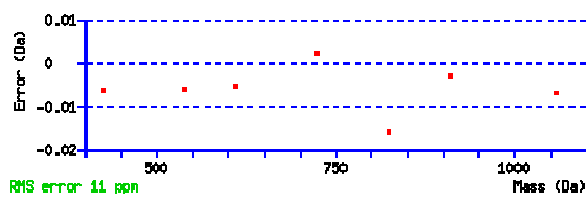
Monoisotopic mass of neutral peptide Mr(calc): 1489.8041

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 48 Expect: 0.001

Matches : 7/122 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							13
2	219.1128	110.0600					F	1419.7743	710.3908	1402.7478	701.8775	1401.7637	701.3855	12
3	306.1448	153.5761			288.1343	144.5708	S	1272.7059	636.8566	1255.6793	628.3433	1254.6953	627.8513	11
4	434.2034	217.6053	417.1769	209.0921	416.1928	208.6001	Q	1185.6739	593.3406	1168.6473	584.8273	1167.6633	584.3353	10
5	581.2718	291.1396	564.2453	282.6263	563.2613	282.1343	F	1057.6153	529.3113	1040.5887	520.7980	1039.6047	520.3060	9
6	668.3039	334.6556	651.2773	326.1423	650.2933	325.6503	S	910.5469	455.7771	893.5203	447.2638	892.5363	446.7718	8
7	769.3515	385.1794	752.3250	376.6661	751.3410	376.1741	T	823.5148	412.2611	806.4883	403.7478	805.5043	403.2558	7
8	882.4356	441.7214	865.4090	433.2082	864.4250	432.7162	L	722.4672	361.7372	705.4406	353.2239			6
9	953.4727	477.2400	936.4462	468.7267	935.4621	468.2347	A	609.3831	305.1952	592.3566	296.6819			5
10	1066.5568	533.7820	1049.5302	525.2688	1048.5462	524.7767	L	538.3460	269.6766	521.3194	261.1634			4
11	1203.6157	602.3115	1186.5891	593.7982	1185.6051	593.3062	H	425.2619	213.1346	408.2354	204.6213			3
12	1316.6997	658.8535	1299.6732	650.3402	1298.6892	649.8482	L	288.2030	144.6051	271.1765	136.0919			2
13							R	175.1190	88.0631	158.0924	79.5498			1

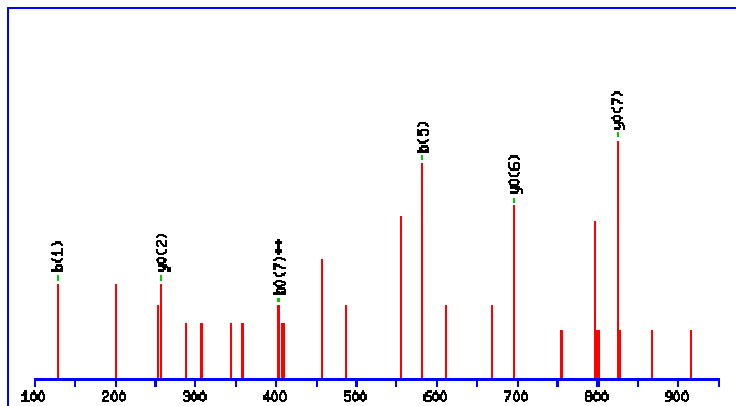


Peptide Number: 46340MS/MS Fragmentation of **KEEPVLEK**Found in **IPI00760877** in **IPI_human**, Tax_Id=9606 Gene_Symbol=BDP1 Isoform 1 of Transcription factor TFIIIB component B" homolog

Match to Query 10738: 970.516768 from(486.265660,2+) index(1618)

Title: Elution from: 49.5333333333333 to 49.5333333333333 period: 0 cycle: 6253 experiment: 7 polarity:+

Data file 120118ry_201B7-32_2_1.mgf



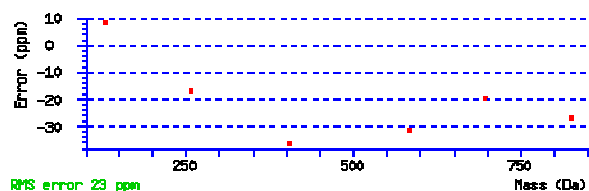
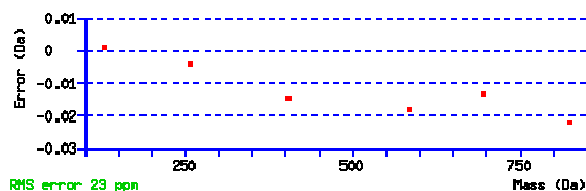
Monoisotopic mass of neutral peptide Mr(calcd): 970.5335

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 42 Expect: 0.0038

Matches : 9/80 fragment ions using 8 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.1022	65.0548	112.0757	56.5415			K							8
2	258.1448	129.5761	241.1183	121.0628	240.1343	120.5708	E	843.4458	422.2266	826.4193	413.7133	825.4353	413.2213	7
3	387.1874	194.0974	370.1609	185.5841	369.1769	185.0921	E	714.4032	357.7053	697.3767	349.1920	696.3927	348.7000	6
4	484.2402	242.6237	467.2136	234.1105	466.2296	233.6185	P	585.3606	293.1840	568.3341	284.6707	567.3501	284.1787	5
5	583.3086	292.1579	566.2821	283.6447	565.2980	283.1527	V	488.3079	244.6576	471.2813	236.1443	470.2973	235.6523	4
6	696.3927	348.7000	679.3661	340.1867	678.3821	339.6947	L	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
7	825.4353	413.2213	808.4087	404.7080	807.4247	404.2160	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
8							K	147.1128	74.0600	130.0863	65.5468			1



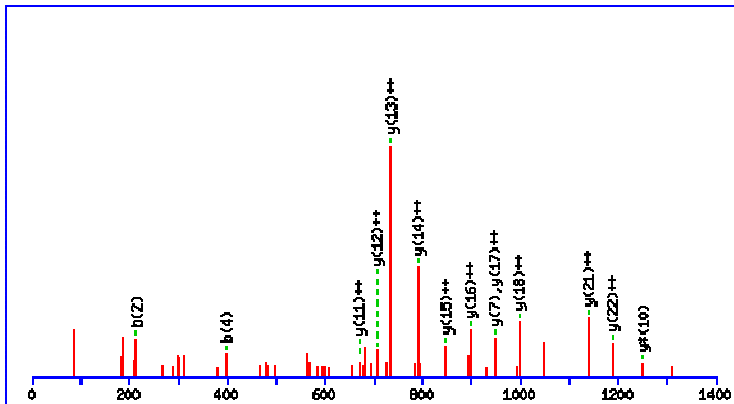
Peptide Number: 46479

MS/MS Fragmentation of **IVSPIVSVVVVTLTGAAASYFKLNRR**Found in **IPI00026514** in **IPI_human**, Tax_Id=9606 Gene_Symbol=XG Isoform 3 of Glycoprotein Xg

Match to Query 11025: 2885.693536 from(722.430660,4+) index(16684)

Title: Elution from: 41.4166666666667 to 41.4166666666667 period: 0 cycle: 1556 experiment: 5 polarity:+

Data file 120212ry_aHDF1388-P9_2_5.mgf



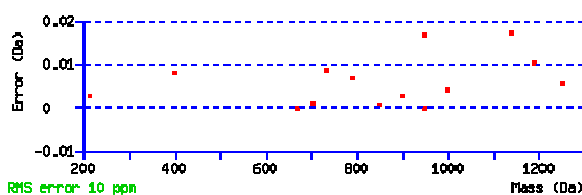
Monoisotopic mass of neutral peptide Mr(calc): 2885.6855

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

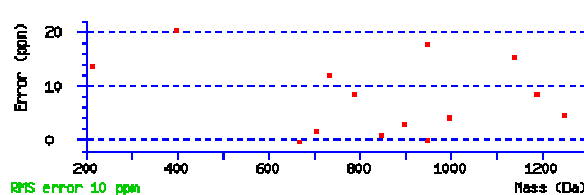
Ions Score: 56 Expect: 7.3e-006

Matches : 14/250 fragment ions using 24 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							27
2	213.1598	107.0835					V	2773.6087	1387.3080	2756.5821	1378.7947	2755.5981	1378.3027	26
3	300.1918	150.5995			282.1812	141.5942	S	2674.5403	1337.7738	2657.5137	1329.2605	2656.5297	1328.7685	25
4	397.2445	199.1259			379.2340	190.1206	P	2587.5083	1294.2578	2570.4817	1285.7445	2569.4977	1285.2525	24
5	510.3286	255.6679			492.3180	246.6627	I	2490.4555	1245.7314	2473.4289	1237.2181	2472.4449	1236.7261	23
6	609.3970	305.2022			591.3865	296.1969	V	2377.3714	1189.1894	2360.3449	1180.6761	2359.3609	1180.1841	22
7	696.4291	348.7182			678.4185	339.7129	S	2278.3030	1139.6551	2261.2765	1131.1419	2260.2924	1130.6499	21
8	795.4975	398.2524			777.4869	389.2471	V	2191.2710	1096.1391	2174.2444	1087.6259	2173.2604	1087.1338	20
9	894.5659	447.7866			876.5553	438.7813	V	2092.2026	1046.6049	2075.1760	1038.0916	2074.1920	1037.5996	19
10	993.6343	497.3208			975.6237	488.3155	V	1993.1342	997.0707	1976.1076	988.5574	1975.1236	988.0654	18
11	1092.7027	546.8550			1074.6921	537.8497	V	1894.0657	947.5365	1877.0392	939.0232	1876.0552	938.5312	17
12	1193.7504	597.3788			1175.7398	588.3735	T	1794.9973	898.0023	1777.9708	889.4890	1776.9868	888.9970	16
13	1306.8345	653.9209			1288.8239	644.9156	L	1693.9496	847.4785	1676.9231	838.9652	1675.9391	838.4732	15
14	1419.9185	710.4629			1401.9079	701.4576	L	1580.8656	790.9364	1563.8390	782.4232	1562.8550	781.9311	14
15	1476.9400	738.9736			1458.9294	729.9683	G	1467.7815	734.3944	1450.7550	725.8811	1449.7710	725.3891	13
16	1547.9771	774.4922			1529.9665	765.4869	A	1410.7601	705.8837	1393.7335	697.3704	1392.7495	696.8784	12
17	1619.0142	810.0107			1601.0036	801.0055	A	1339.7229	670.3651	1322.6964	661.8518	1321.7124	661.3598	11
18	1690.0513	845.5293			1672.0408	836.5240	A	1268.6858	634.8466	1251.6593	626.3333	1250.6753	625.8413	10
19	1777.0833	889.0453			1759.0728	880.0400	S	1197.6487	599.3280	1180.6222	590.8147	1179.6382	590.3227	9
20	1940.1467	970.5770			1922.1361	961.5717	Y	1110.6167	555.8120	1093.5901	547.2987			8
21	2087.2151	1044.1112			2069.2045	1035.1059	F	947.5534	474.2803	930.5268	465.7670			7
22	2215.3101	1108.1587	2198.2835	1099.6454	2197.2995	1099.1534	K	800.4849	400.7461	783.4584	392.2328			6
23	2328.3941	1164.7007	2311.3676	1156.1874	2310.3836	1155.6954	L	672.3900	336.6986	655.3634	328.1854			5
24	2442.4370	1221.7222	2425.4105	1213.2089	2424.4265	1212.7169	N	559.3059	280.1566	542.2794	271.6433			4
25	2556.4800	1278.7436	2539.4534	1270.2303	2538.4694	1269.7383	N	445.2630	223.1351	428.2364	214.6219			3
26	2712.5811	1356.7942	2695.5545	1348.2809	2694.5705	1347.7889	R	331.2201	166.1137	314.1935	157.6004			2
27							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 10 ppm



RMS error 10 ppm

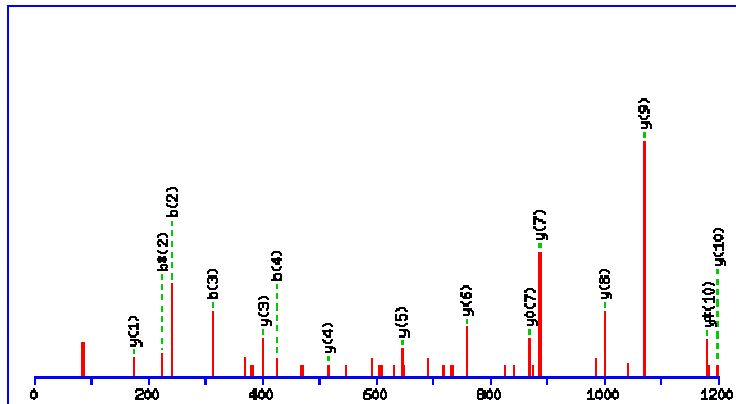
Peptide Number: 46992

MS/MS Fragmentation of **IQAIELEDLLR**Found in **IPI00010790** in **IPI_human**, Tax_Id=9606 Gene_Symbol=BGN Biglycan

Match to Query 5227: 1311.744308 from(656.879430,2+) index(35121)

Title: Elution from: 97.9166666666667 to 97.9166666666667 period: 0 cycle: 3761 experiment: 4 polarity:+

Data file 120208ry_Tig120slc-P8_1_3.mgf



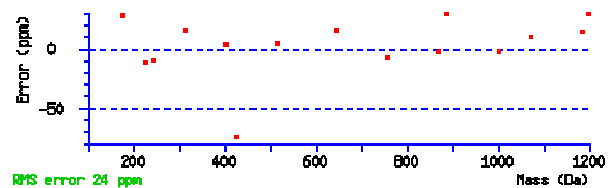
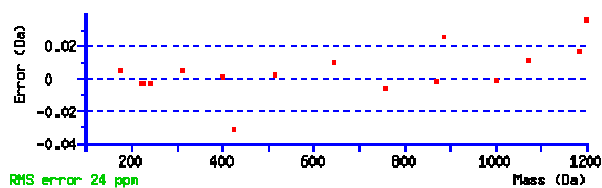
Monoisotopic mass of neutral peptide Mr(calc): 1311.7398

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 77 Expect: 8.6e-007

Matches : 15/104 fragment ions using 22 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							11
2	242.1499	121.5786	225.1234	113.0653			Q	1199.6630	600.3352	1182.6365	591.8219	1181.6525	591.3299	10
3	313.1870	157.0972	296.1605	148.5839			A	1071.6045	536.3059	1054.5779	527.7926	1053.5939	527.3006	9
4	426.2711	213.6392	409.2445	205.1259			I	1000.5673	500.7873	983.5408	492.2740	982.5568	491.7820	8
5	555.3137	278.1605	538.2871	269.6472	537.3031	269.1552	E	887.4833	444.2453	870.4567	435.7320	869.4727	435.2400	7
6	668.3978	334.7025	651.3712	326.1892	650.3872	325.6972	L	758.4407	379.7240	741.4141	371.2107	740.4301	370.7187	6
7	797.4403	399.2238	780.4138	390.7105	779.4298	390.2185	E	645.3566	323.1819	628.3301	314.6687	627.3461	314.1767	5
8	912.4673	456.7373	895.4407	448.2240	894.4567	447.7320	D	516.3140	258.6606	499.2875	250.1474	498.3035	249.6554	4
9	1025.5514	513.2793	1008.5248	504.7660	1007.5408	504.2740	L	401.2871	201.1472	384.2605	192.6339			3
10	1138.6354	569.8213	1121.6089	561.3081	1120.6249	560.8161	L	288.2030	144.6051	271.1765	136.0919			2
11							R	175.1190	88.0631	158.0924	79.5498			1



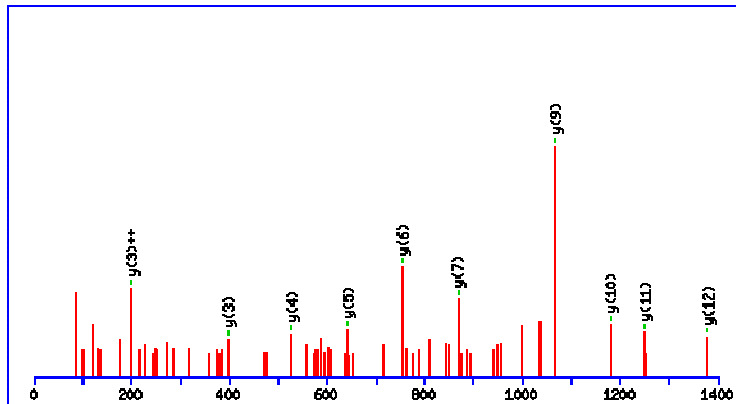
Peptide Number: 47141

MS/MS Fragmentation of **LLQSADEEAIAELLDEHLK**Found in **IPI00026157** in **IPI_human**, Tax_Id=9606 Gene_Symbol=MTRF1 Peptide chain release factor 1, mitochondrial

Match to Query 13629: 2136.100092 from(713.040640,3+) index(3237)

Title: Elution from: 10.4333333333333 to 10.4333333333333 period: 0 cycle: 410 experiment: 4 polarity: +

Data file 120210ry_585A1-55_3_4.mgf



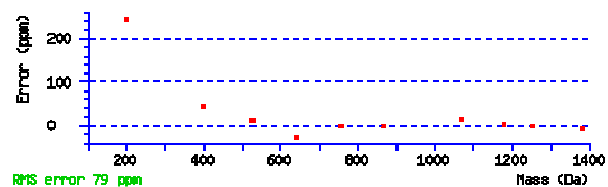
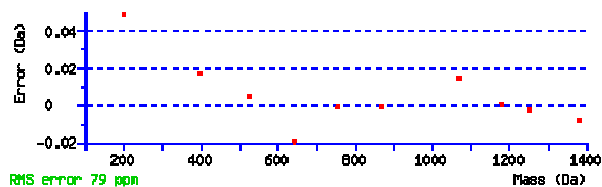
Monoisotopic mass of neutral peptide Mr(calc): 2136.0950

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 71 Expect: 4.1e-006

Matches : 10/200 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							19
2	227.1754	114.0913					L	2024.0182	1012.5128	2006.9917	1003.9995	2006.0077	1003.5075	18
3	355.2340	178.1206	338.2074	169.6074			Q	1910.9342	955.9707	1893.9076	947.4575	1892.9236	946.9654	17
4	442.2660	221.6366	425.2395	213.1234	424.2554	212.6314	S	1782.8756	891.9414	1765.8491	883.4282	1764.8650	882.9362	16
5	513.3031	257.1552	496.2766	248.6419	495.2926	248.1499	A	1695.8436	848.4254	1678.8170	839.9121	1677.8330	839.4201	15
6	628.3301	314.6687	611.3035	306.1554	610.3195	305.6634	D	1624.8065	812.9069	1607.7799	804.3936	1606.7959	803.9016	14
7	757.3727	379.1900	740.3461	370.6767	739.3621	370.1847	E	1509.7795	755.3934	1492.7530	746.8801	1491.7689	746.3881	13
8	886.4153	443.7113	869.3887	435.1980	868.4047	434.7060	E	1380.7369	690.8721	1363.7104	682.3588	1362.7264	681.8668	12
9	957.4524	479.2298	940.4258	470.7165	939.4418	470.2245	A	1251.6943	626.3508	1234.6678	617.8375	1233.6838	617.3455	11
10	1070.5364	535.7719	1053.5099	527.2586	1052.5259	526.7666	I	1180.6572	590.8322	1163.6307	582.3190	1162.6466	581.8270	10
11	1141.5735	571.2904	1124.5470	562.7771	1123.5630	562.2851	A	1067.5732	534.2902	1050.5466	525.7769	1049.5626	525.2849	9
12	1270.6161	635.8117	1253.5896	627.2984	1252.6056	626.8064	E	996.5360	498.7717	979.5095	490.2584	978.5255	489.7664	8
13	1383.7002	692.3537	1366.6737	683.8405	1365.6896	683.3485	L	867.4934	434.2504	850.4669	425.7371	849.4829	425.2451	7
14	1496.7843	748.8958	1479.7577	740.3825	1478.7737	739.8905	L	754.4094	377.7083	737.3828	369.1951	736.3988	368.7030	6
15	1611.8112	806.4092	1594.7847	797.8960	1593.8006	797.4040	D	641.3253	321.1663	624.2988	312.6530	623.3148	312.1610	5
16	1740.8538	870.9305	1723.8273	862.4173	1722.8432	861.9253	E	526.2984	263.6528	509.2718	255.1396	508.2878	254.6475	4
17	1877.9127	939.4600	1860.8862	930.9467	1859.9021	930.4547	H	397.2558	199.1315	380.2292	190.6183			3
18	1990.9968	996.0020	1973.9702	987.4888	1972.9862	986.9967	L	260.1969	130.6021	243.1703	122.0888			2
19							K	147.1128	74.0600	130.0863	65.5468			1



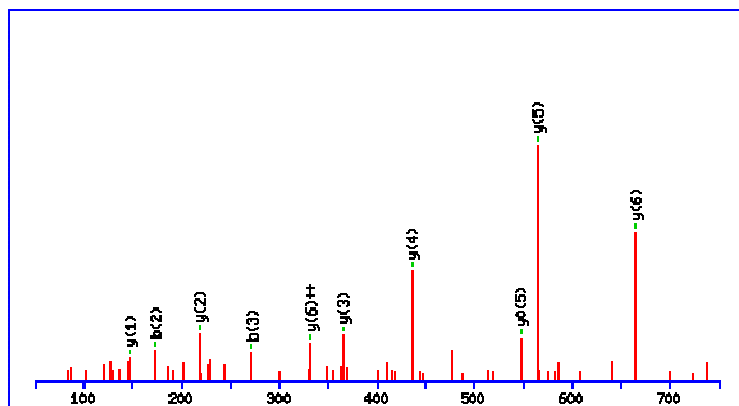
Peptide Number: 47597

MS/MS Fragmentation of **GDVEAFAK**Found in **IPI00033030** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ADRM1 Proteasomal ubiquitin receptor ADRM1

Match to Query 4975: 835.406348 from(418.710450,2+) index(19959)

Title: Elution from: 85.5833333333333 to 85.5833333333333 period: 0 cycle: 6590 experiment: 6 polarity:+

Data file 120208ry_Tig120slc-P8_3_1.mgf



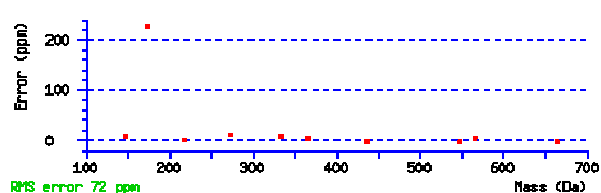
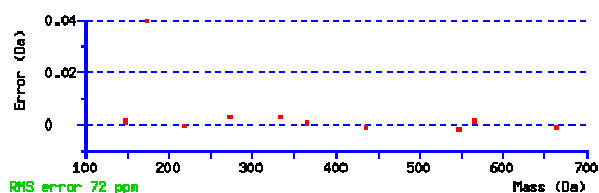
Monoisotopic mass of neutral peptide Mr(calc): 835.4076

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 53 Expect: 0.00029

Matches : 10/60 fragment ions using 14 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180			Q							8
2	173.0557	87.0315	155.0451	78.0262	D	779.3934	390.2003	762.3668	381.6871	761.3828	381.1951	7
3	272.1241	136.5657	254.1135	127.5604	V	664.3665	332.6869	647.3399	324.1736	646.3559	323.6816	6
4	401.1667	201.0870	383.1561	192.0817	E	565.2980	283.1527	548.2715	274.6394	547.2875	274.1474	5
5	472.2038	236.6055	454.1932	227.6003	A	436.2554	218.6314	419.2289	210.1181			4
6	619.2722	310.1397	601.2617	301.1345	F	365.2183	183.1128	348.1918	174.5995			3
7	690.3093	345.6583	672.2988	336.6530	A	218.1499	109.5786	201.1234	101.0653			2
8					K	147.1128	74.0600	130.0863	65.5468			1

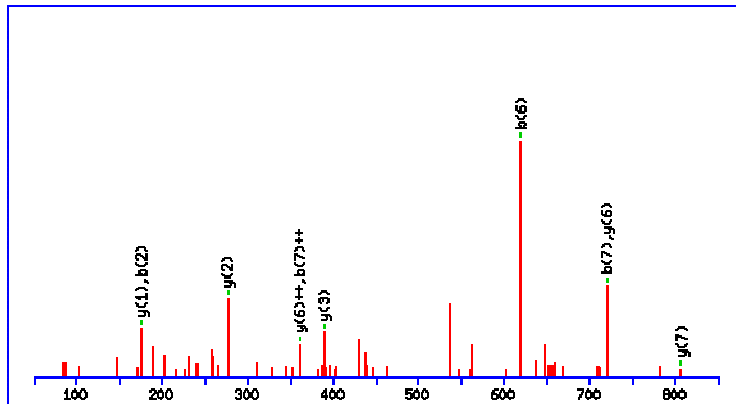


Peptide Number: 48198MS/MS Fragmentation of **SSPHPLTR**Found in **IPI00748501** in **IPI_human**, Tax_Id=9606 Gene_Symbol= CDNA: FLJ21777 fis, clone HEP00173

Match to Query 8428: 893.459728 from(447.737140,2+) index(12428)

Title: Elution from: 71.1666666666667 to 71.1666666666667 period: 0 cycle: 6777 experiment: 3 polarity: +

Data file 120212ry_aHDF1388-P9_3_1.mgf



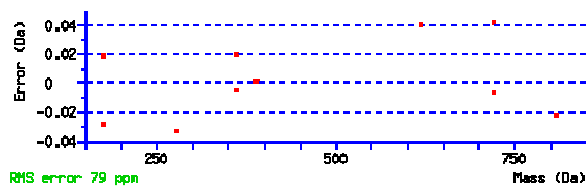
Monoisotopic mass of neutral peptide Mr(calc): 893.4719

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

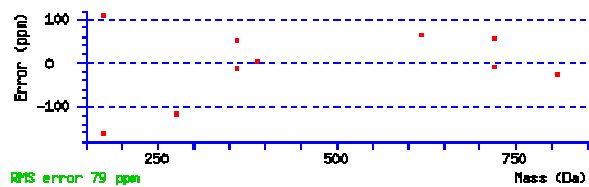
Ions Score: 46 Expect: 0.0016

Matches : 10/68 fragment ions using 8 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233	70.0287	35.5180	S							8
2	175.0713	88.0393	157.0608	79.0340	S	807.4472	404.2272	790.4206	395.7139	789.4366	395.2219	7
3	272.1241	136.5657	254.1135	127.5604	P	720.4151	360.7112	703.3886	352.1979	702.4046	351.7059	6
4	409.1830	205.0951	391.1724	196.0899	H	623.3624	312.1848	606.3358	303.6715	605.3518	303.1795	5
5	506.2358	253.6215	488.2252	244.6162	P	486.3035	243.6554	469.2769	235.1421	468.2929	234.6501	4
6	619.3198	310.1636	601.3093	301.1583	L	389.2507	195.1290	372.2241	186.6157	371.2401	186.1237	3
7	720.3675	360.6874	702.3569	351.6821	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
8					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 79 ppm



RMS error 79 ppm

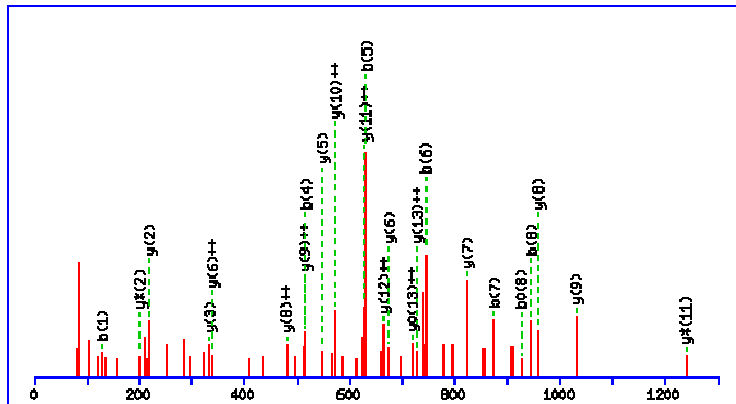
Peptide Number: 48227

MS/MS Fragmentation of **KEEEDLEALIAHFQTLDAK**Found in **IPI00152182** in **IPI_human**, Tax_Id=9606 Gene_Symbol=KLHDC4 Isoform 1 of Kelch domain-containing protein 4

Match to Query 17987: 2199.122136 from(550.787810,4+) index(574)

Title: Elution from: 1.96666666666667 to 1.96666666666667 period: 0 cycle: 81 experiment: 1 polarity: +

Data file 120212ry_414C2-43_3_4.mgf



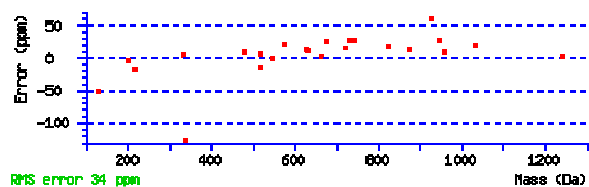
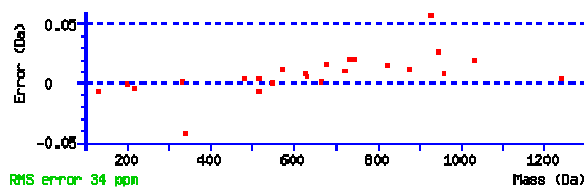
Monoisotopic mass of neutral peptide Mr(calc): 2199.1059

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 45 Expect: 0.0021

Matches : 24/210 fragment ions using 48 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.1022	65.0548	112.0757	56.5415			K							19
2	258.1448	129.5761	241.1183	121.0628	240.1343	120.5708	E	2072.0182	1036.5128	2054.9917	1027.9995	2054.0077	1027.5075	18
3	387.1874	194.0974	370.1609	185.5841	369.1769	185.0921	E	1942.9756	971.9915	1925.9491	963.4782	1924.9651	962.9862	17
4	516.2300	258.6186	499.2035	250.1054	498.2195	249.6134	E	1813.9331	907.4702	1796.9065	898.9569	1795.9225	898.4649	16
5	631.2570	316.1321	614.2304	307.6188	613.2464	307.1268	D	1684.8905	842.9489	1667.8639	834.4356	1666.8799	833.9436	15
6	744.3410	372.6742	727.3145	364.1609	726.3305	363.6689	L	1569.8635	785.4354	1552.8370	776.9221	1551.8530	776.4301	14
7	873.3836	437.1954	856.3571	428.6822	855.3731	428.1902	E	1456.7795	728.8934	1439.7529	720.3801	1438.7689	719.8881	13
8	944.4207	472.7140	927.3942	464.2007	926.4102	463.7087	A	1327.7369	664.3721	1310.7103	655.8588	1309.7263	655.3668	12
9	1057.5048	529.2560	1040.4782	520.7428	1039.4942	520.2508	L	1256.6997	628.8535	1239.6732	620.3402	1238.6892	619.8482	11
10	1170.5889	585.7981	1153.5623	577.2848	1152.5783	576.7928	I	1143.6157	572.3115	1126.5891	563.7982	1125.6051	563.3062	10
11	1241.6260	621.3166	1224.5994	612.8034	1223.6154	612.3113	A	1030.5316	515.7694	1013.5051	507.2562	1012.5211	506.7642	9
12	1378.6849	689.8461	1361.6583	681.3328	1360.6743	680.8408	H	959.4945	480.2509	942.4680	471.7376	941.4839	471.2456	8
13	1525.7533	763.3803	1508.7268	754.8670	1507.7427	754.3750	F	822.4356	411.7214	805.4090	403.2082	804.4250	402.7162	7
14	1653.8119	827.4096	1636.7853	818.8963	1635.8013	818.4043	Q	675.3672	338.1872	658.3406	329.6740	657.3566	329.1819	6
15	1754.8596	877.9334	1737.8330	869.4201	1736.8490	868.9281	T	547.3086	274.1579	530.2821	265.6447	529.2980	265.1527	5
16	1867.9436	934.4754	1850.9171	925.9622	1849.9331	925.4702	L	446.2609	223.6341	429.2344	215.1208	428.2504	214.6288	4
17	1982.9706	991.9889	1965.9440	983.4756	1964.9600	982.9836	D	333.1769	167.0921	316.1503	158.5788	315.1663	158.0868	3
18	2054.0077	1027.5075	2036.9811	1018.9942	2035.9971	1018.5022	A	218.1499	109.5786	201.1234	101.0653			2
19							K	147.1128	74.0600	130.0863	65.5468			1

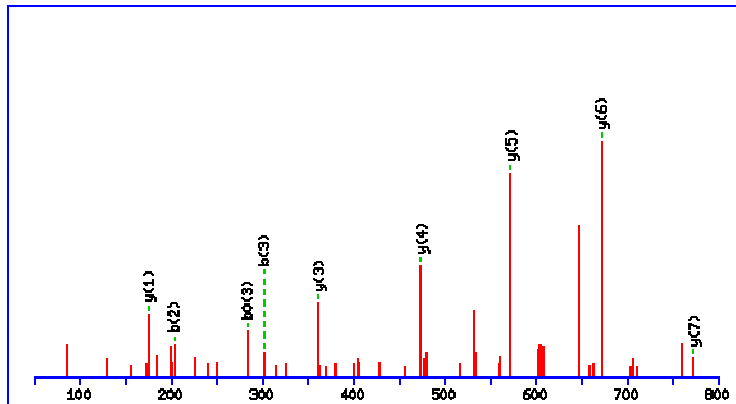


Peptide Number: 48256MS/MS Fragmentation of **TTVVLGER**Found in **IPI00964406** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ANK2 115 kDa protein

Match to Query 6100: 873.490228 from(437.752390,2+) index(17737)

Title: Elution from: 84.5333333333333 to 84.5333333333333 period: 0 cycle: 8238 experiment: 5 polarity:+

Data file 120212ry_aHDF1388-P9_2_1.mgf



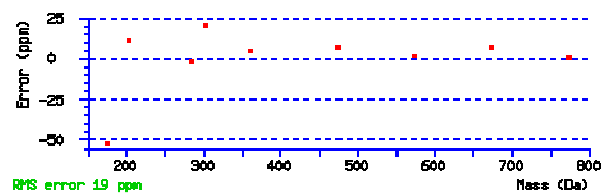
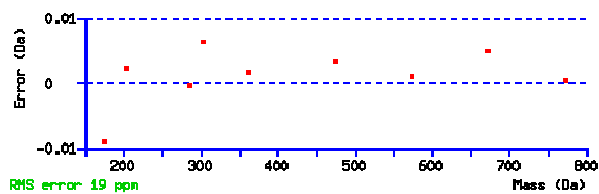
Monoisotopic mass of neutral peptide Mr(calc): 873.4920

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 50 Expect: 0.001

Matches : 9/68 fragment ions using 14 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311	84.0444	42.5258	T							8
2	203.1026	102.0550	185.0921	93.0497	T	773.4516	387.2294	756.4250	378.7162	755.4410	378.2241	7
3	302.1710	151.5892	284.1605	142.5839	V	672.4039	336.7056	655.3774	328.1923	654.3933	327.7003	6
4	401.2395	201.1234	383.2289	192.1181	V	573.3355	287.1714	556.3089	278.6581	555.3249	278.1661	5
5	514.3235	257.6654	496.3130	248.6601	L	474.2671	237.6372	457.2405	229.1239	456.2565	228.6319	4
6	571.3450	286.1761	553.3344	277.1709	G	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	3
7	700.3876	350.6974	682.3770	341.6921	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
8					R	175.1190	88.0631	158.0924	79.5498			1



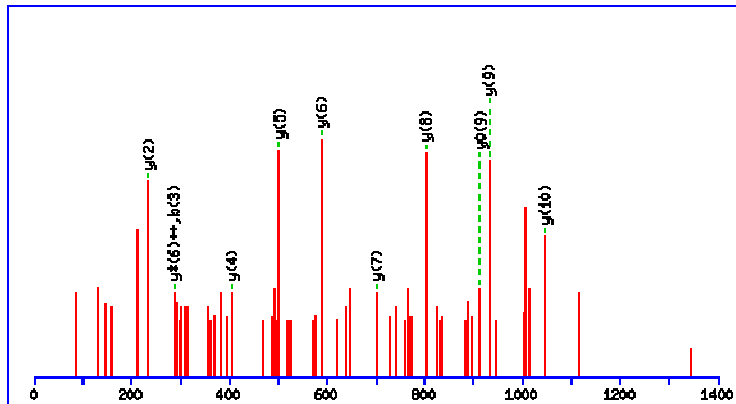
Peptide Number: 48767

MS/MS Fragmentation of **GVEIETISPGDGR**Found in **IPI00073704** in **IPI_human**, Tax_Id=9606 Gene_Symbol=FKBP1B Isoform 2 of Peptidyl-prolyl cis-trans isomerase FKBP1B

Match to Query 24849: 1328.637248 from(665.325900,2+) index(15198)

Title: Elution from: 36.1 to 36.1 period: 0 cycle: 1331 experiment: 9 polarity: +

Data file 120118ry_201B7-32_2_2.mgf



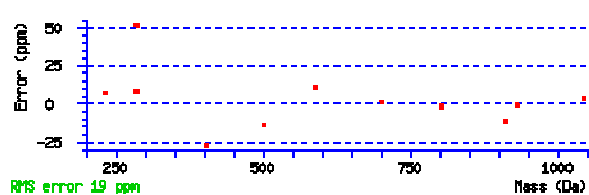
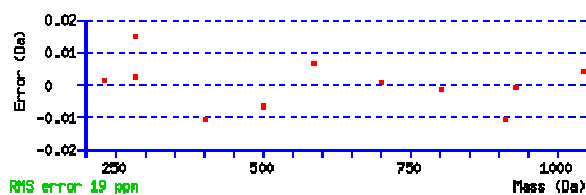
Monoisotopic mass of neutral peptide Mr(calc): 1328.6572

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 52 Expect: 0.00034

Matches : 11/112 fragment ions using 21 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180			G							13
2	157.0972	79.0522			V	1272.6430	636.8251	1255.6165	628.3119	1254.6325	627.8199	12
3	286.1397	143.5735	268.1292	134.5682	E	1173.5746	587.2909	1156.5481	578.7777	1155.5640	578.2857	11
4	399.2238	200.1155	381.2132	191.1103	I	1044.5320	522.7696	1027.5055	514.2564	1026.5215	513.7644	10
5	528.2664	264.6368	510.2558	255.6316	E	931.4480	466.2276	914.4214	457.7143	913.4374	457.2223	9
6	629.3141	315.1607	611.3035	306.1554	T	802.4054	401.7063	785.3788	393.1930	784.3948	392.7010	8
7	742.3981	371.7027	724.3876	362.6974	I	701.3577	351.1825	684.3311	342.6692	683.3471	342.1772	7
8	829.4302	415.2187	811.4196	406.2134	S	588.2736	294.6404	571.2471	286.1272	570.2631	285.6352	6
9	926.4829	463.7451	908.4724	454.7398	P	501.2416	251.1244	484.2150	242.6112	483.2310	242.1191	5
10	983.5044	492.2558	965.4938	483.2506	G	404.1888	202.5980	387.1623	194.0848	386.1783	193.5928	4
11	1098.5313	549.7693	1080.5208	540.7640	D	347.1674	174.0873	330.1408	165.5740	329.1568	165.0820	3
12	1155.5528	578.2800	1137.5422	569.2748	G	232.1404	116.5738	215.1139	108.0606			2
13					R	175.1190	88.0631	158.0924	79.5498			1



Peptide Number: 48770

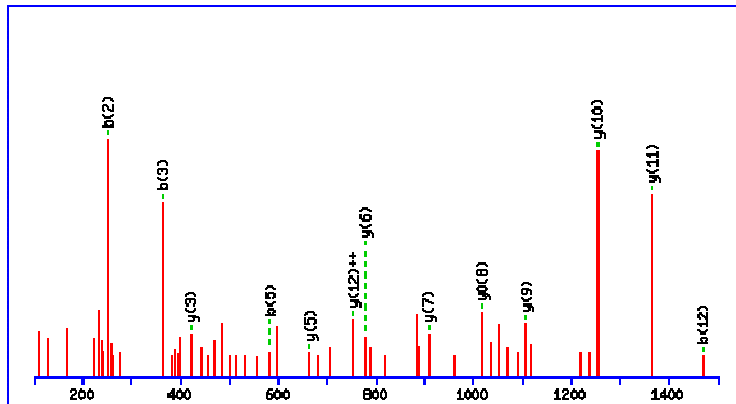
MS/MS Fragmentation of **IHIFAQQNDQFQK**

Found in **IPI00909025** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ELP2 cDNA FLJ58621, highly similar to Stat3-interacting protein

Match to Query 33770: 1615.810428 from(808.912490,2+) index(16604)

Title: Elution from: 39.1166666666667 to 39.1166666666667 period: 0 cycle: 1477 experiment: 10 polarity:+

Data file 120214ry_32R1-32_4_2.mgf



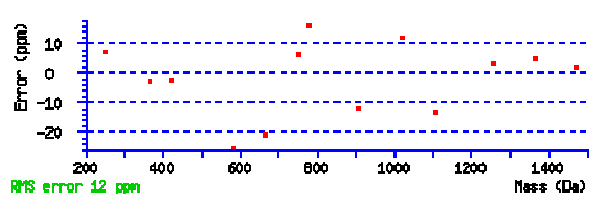
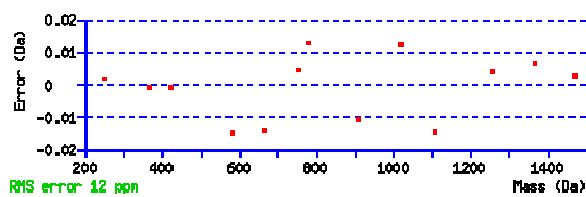
Monoisotopic mass of neutral peptide Mr(calc): 1615.8107

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 39 Expect: 0.0094

Matches : 13/110 fragment ions using 25 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							13
2	251.1503	126.0788					H	1503.7339	752.3706	1486.7074	743.8573	1485.7233	743.3653	12
3	364.2343	182.6208					I	1366.6750	683.8411	1349.6484	675.3279	1348.6644	674.8359	11
4	511.3027	256.1550					F	1253.5909	627.2991	1236.5644	618.7858	1235.5804	618.2938	10
5	582.3398	291.6736					A	1106.5225	553.7649	1089.4960	545.2516	1088.5119	544.7596	9
6	710.3984	355.7028	693.3719	347.1896			Q	1035.4854	518.2463	1018.4589	509.7331	1017.4748	509.2411	8
7	838.4570	419.7321	821.4305	411.2189			Q	907.4268	454.2170	890.4003	445.7038	889.4163	445.2118	7
8	952.4999	476.7536	935.4734	468.2403			N	779.3682	390.1878	762.3417	381.6745	761.3577	381.1825	6
9	1067.5269	534.2671	1050.5003	525.7538	1049.5163	525.2618	D	665.3253	333.1663	648.2988	324.6530	647.3148	324.1610	5
10	1195.5854	598.2964	1178.5589	589.7831	1177.5749	589.2911	Q	550.2984	275.6528	533.2718	267.1396			4
11	1342.6539	671.8306	1325.6273	663.3173	1324.6433	662.8253	F	422.2398	211.6235	405.2132	203.1103			3
12	1470.7124	735.8599	1453.6859	727.3466	1452.7019	726.8546	Q	275.1714	138.0893	258.1448	129.5761			2
13							K	147.1128	74.0600	130.0863	65.5468			1



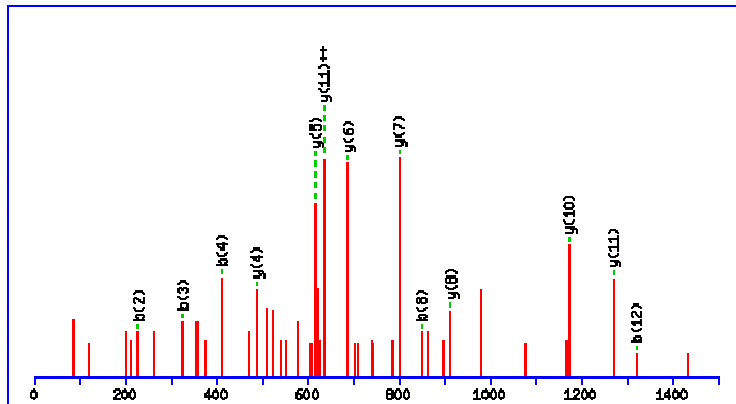
Peptide Number: 48891

MS/MS Fragmentation of **DLPSLDPLPPYILAEQLR**Found in **IPI00455719** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CTU2 Isoform 1 of Cytoplasmic tRNA 2-thiolation protein 2

Match to Query 17291: 2120.115012 from(707.712280,3+) index(18524)

Title: Elution from: 46.2166666666667 to 46.2166666666667 period: 0 cycle: 1726 experiment: 4 polarity:+

Data file 120118ry_201B7-32_2_4.mgf



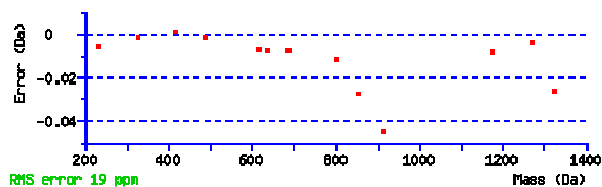
Monoisotopic mass of neutral peptide Mr(calc): 2120.1517

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

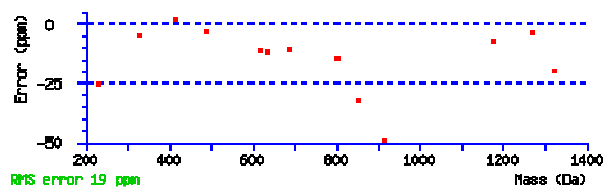
Ions Score: 40 Expect: 0.0051

Matches : 13/176 fragment ions using 25 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							19
2	229.1183	115.0628			211.1077	106.0575	L	2006.1321	1003.5697	1989.1055	995.0564	1988.1215	994.5644	18
3	326.1710	163.5892			308.1605	154.5839	P	1893.0480	947.0277	1876.0215	938.5144	1875.0375	938.0224	17
4	413.2031	207.1052			395.1925	198.0999	S	1795.9953	898.5013	1778.9687	889.9880	1777.9847	889.4960	16
5	526.2871	263.6472			508.2766	254.6419	L	1708.9632	854.9853	1691.9367	846.4720	1690.9527	845.9800	15
6	641.3141	321.1607			623.3035	312.1554	D	1595.8792	798.4432	1578.8526	789.9299	1577.8686	789.4379	14
7	738.3668	369.6871			720.3563	360.6818	P	1480.8522	740.9298	1463.8257	732.4165	1462.8417	731.9245	13
8	851.4509	426.2291			833.4403	417.2238	L	1383.7995	692.4034	1366.7729	683.8901	1365.7889	683.3981	12
9	948.5037	474.7555			930.4931	465.7502	P	1270.7154	635.8613	1253.6889	627.3481	1252.7048	626.8561	11
10	1045.5564	523.2819			1027.5459	514.2766	P	1173.6626	587.3350	1156.6361	578.8217	1155.6521	578.3297	10
11	1208.6198	604.8135			1190.6092	595.8082	Y	1076.6099	538.8086	1059.5833	530.2953	1058.5993	529.8033	9
12	1321.7038	661.3556			1303.6933	652.3503	I	913.5465	457.2769	896.5200	448.7636	895.5360	448.2716	8
13	1434.7879	717.8976			1416.7773	708.8923	L	800.4625	400.7349	783.4359	392.2216	782.4519	391.7296	7
14	1505.8250	753.4161			1487.8144	744.4109	A	687.3784	344.1928	670.3519	335.6796	669.3679	335.1876	6
15	1634.8676	817.9374			1616.8570	808.9322	E	616.3413	308.6743	599.3148	300.1610	598.3307	299.6690	5
16	1705.9047	853.4560			1687.8942	844.4507	A	487.2987	244.1530	470.2722	235.6397			4
17	1833.9633	917.4853	1816.9367	908.9720	1815.9527	908.4800	Q	416.2616	208.6344	399.2350	200.1212			3
18	1947.0474	974.0273	1930.0208	965.5140	1929.0368	965.0220	L	288.2030	144.6051	271.1765	136.0919			2
19							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 19 ppm



RMS error 19 ppm

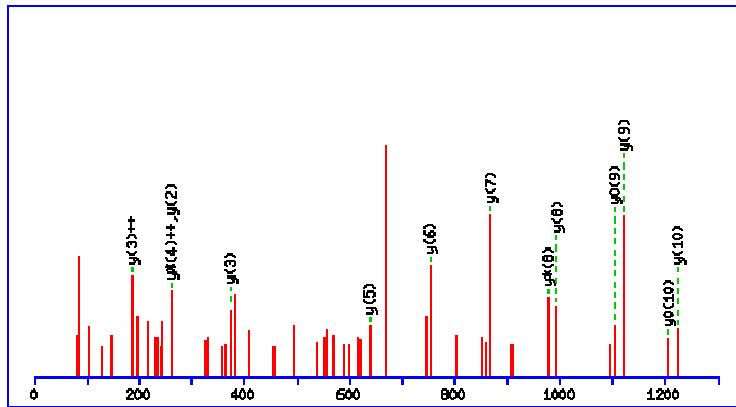
Peptide Number: 49131

MS/MS Fragmentation of **LTEQLDITYLK**Found in **IPI00156791** in **IPI_human**, Tax_Id=9606 Gene_Symbol=KLHL22 Kelch-like protein 22

Match to Query 6464: 1335.726868 from(668.870710,2+) index(2703)

Title: Elution from: 6.45 to 6.45 period: 0 cycle: 245 experiment: 5 polarity: +

Data file 120208ry_Tig120slc-P8_2_3.mgf



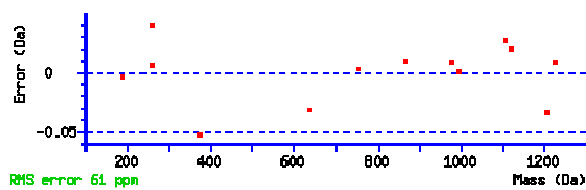
Monoisotopic mass of neutral peptide Mr(calc): 1335.7286

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

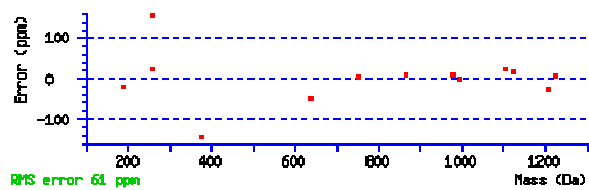
Ions Score: 51 Expect: 0.00049

Matches : 13/104 fragment ions using 23 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							11
2	215.1390	108.0731			197.1285	99.0679	T	1223.6518	612.3295	1206.6252	603.8163	1205.6412	603.3243	10
3	344.1816	172.5944			326.1710	163.5892	E	1122.6041	561.8057	1105.5776	553.2924	1104.5936	552.8004	9
4	472.2402	236.6237	455.2136	228.1105	454.2296	227.6185	Q	993.5615	497.2844	976.5350	488.7711	975.5510	488.2791	8
5	585.3243	293.1658	568.2977	284.6525	567.3137	284.1605	L	865.5029	433.2551	848.4764	424.7418	847.4924	424.2498	7
6	700.3512	350.6792	683.3246	342.1660	682.3406	341.6740	D	752.4189	376.7131	735.3923	368.1998	734.4083	367.7078	6
7	801.3989	401.2031	784.3723	392.6898	783.3883	392.1978	T	637.3919	319.1996	620.3654	310.6863	619.3814	310.1943	5
8	964.4622	482.7347	947.4357	474.2215	946.4516	473.7295	Y	536.3443	268.6758	519.3177	260.1625			4
9	1077.5463	539.2768	1060.5197	530.7635	1059.5357	530.2715	I	373.2809	187.1441	356.2544	178.6308			3
10	1190.6303	595.8188	1173.6038	587.3055	1172.6198	586.8135	L	260.1969	130.6021	243.1703	122.0888			2
11							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 61 ppm



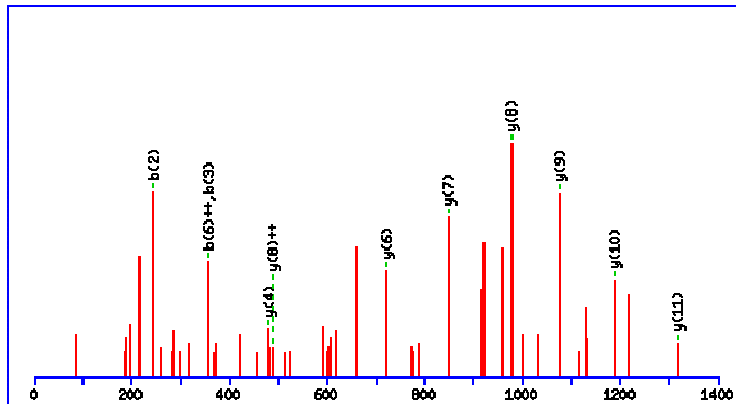
RMS error 61 ppm

Peptide Number: 49146MS/MS Fragmentation of **LELVQQLGSCR**Found in **IPI00550013** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ZFAND3 AN1-type zinc finger protein 3

Match to Query 25228: 1430.733028 from(716.373790,2+) index(28652)

Title: Elution from: 68.8666666666667 to 68.8666666666667 period: 0 cycle: 2602 experiment: 7 polarity: +

Data file 120212ry_414C2-43_3_2.mgf



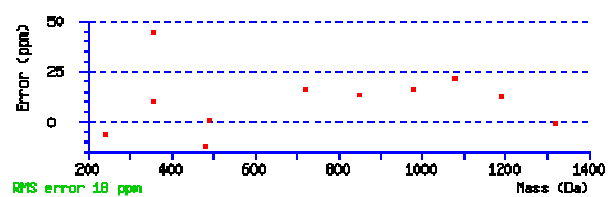
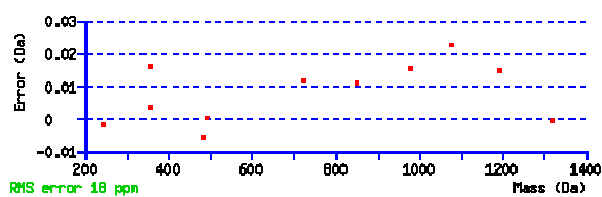
Monoisotopic mass of neutral peptide Mr(calc): 1430.7188

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 58 Expect: 0.00015

Matches : 11/118 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							12
2	243.1339	122.0706			225.1234	113.0653	E	1318.6420	659.8246	1301.6154	651.3114	1300.6314	650.8193	11
3	356.2180	178.6126			338.2074	169.6074	L	1189.5994	595.3033	1172.5728	586.7901	1171.5888	586.2980	10
4	455.2864	228.1468			437.2758	219.1416	V	1076.5153	538.7613	1059.4888	530.2480	1058.5048	529.7560	9
5	583.3450	292.1761	566.3184	283.6629	565.3344	283.1709	Q	977.4469	489.2271	960.4204	480.7138	959.4363	480.2218	8
6	711.4036	356.2054	694.3770	347.6921	693.3930	347.2001	Q	849.3883	425.1978	832.3618	416.6845	831.3778	416.1925	7
7	840.4462	420.7267	823.4196	412.2134	822.4356	411.7214	E	721.3298	361.1685	704.3032	352.6552	703.3192	352.1632	6
8	953.5302	477.2688	936.5037	468.7555	935.5197	468.2635	L	592.2872	296.6472	575.2606	288.1339	574.2766	287.6419	5
9	1010.5517	505.7795	993.5251	497.2662	992.5411	496.7742	G	479.2031	240.1052	462.1765	231.5919	461.1925	231.0999	4
10	1097.5837	549.2955	1080.5572	540.7822	1079.5732	540.2902	S	422.1816	211.5945	405.1551	203.0812	404.1711	202.5892	3
11	1257.6144	629.3108	1240.5878	620.7975	1239.6038	620.3055	C	335.1496	168.0784	318.1231	159.5652			2
12							R	175.1190	88.0631	158.0924	79.5498			1



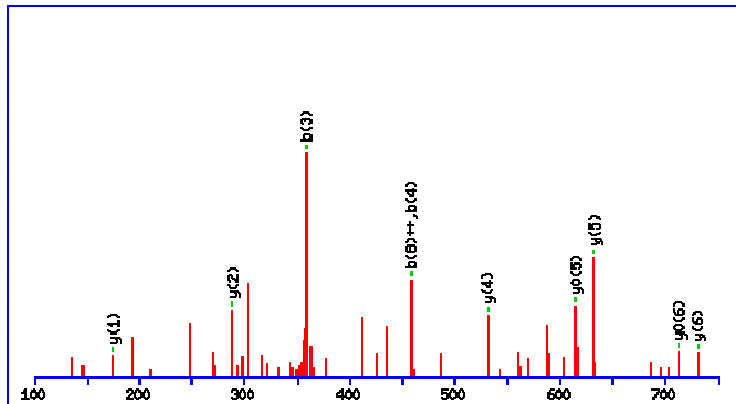
Peptide Number: 49162

MS/MS Fragmentation of **TQEVTSRIR**Found in **IPI00218845** in **IPI_human**, Tax_Id=9606 Gene_Symbol=NOS3 Nitric oxide synthase, endothelial

Match to Query 14332: 1088.605092 from(363.875640,3+) index(23046)

Title: Elution from: 97.55 to 97.55 period: 0 cycle: 8988 experiment: 1 polarity: +

Data file 120210ry_32R1-32_3_1.mgf



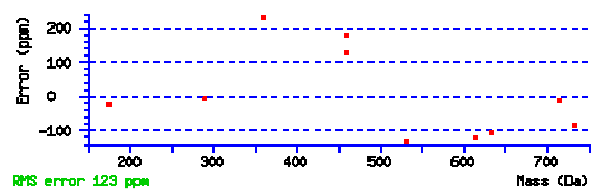
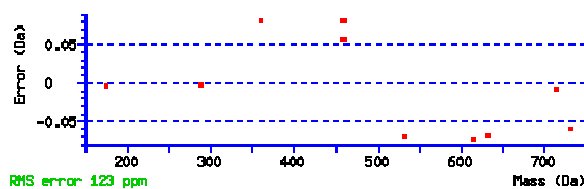
Monoisotopic mass of neutral peptide Mr(calc): 1088.5938

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 39 Expect: 0.0087

Matches : 10/88 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							9
2	230.1135	115.5604	213.0870	107.0471	212.1030	106.5551	Q	988.5534	494.7803	971.5269	486.2671	970.5429	485.7751	8
3	359.1561	180.0817	342.1296	171.5684	341.1456	171.0764	E	860.4948	430.7511	843.4683	422.2378	842.4843	421.7458	7
4	458.2245	229.6159	441.1980	221.1026	440.2140	220.6106	V	731.4522	366.2298	714.4257	357.7165	713.4417	357.2245	6
5	559.2722	280.1397	542.2457	271.6265	541.2617	271.1345	T	632.3838	316.6956	615.3573	308.1823	614.3733	307.6903	5
6	646.3042	323.6558	629.2777	315.1425	628.2937	314.6505	S	531.3362	266.1717	514.3096	257.6584	513.3256	257.1664	4
7	802.4054	401.7063	785.3788	393.1930	784.3948	392.7010	R	444.3041	222.6557	427.2776	214.1424			3
8	915.4894	458.2483	898.4629	449.7351	897.4789	449.2431	I	288.2030	144.6051	271.1765	136.0919			2
9							R	175.1190	88.0631	158.0924	79.5498			1



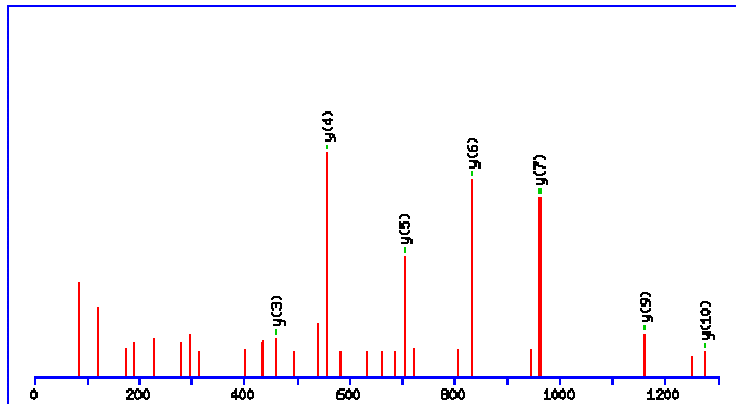
Peptide Number: 49875

MS/MS Fragmentation of **AFDTFLDSLQEFPWVR**Found in **IPI00020364** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CRADD Death domain-containing protein CRADD

Match to Query 12633: 1969.972332 from(657.664720,3+) index(41439)

Title: Elution from: 104.75 to 104.75 period: 0 cycle: 3956 experiment: 2 polarity: +

Data file 120208ry_Tig120slc-P8_2_4.mgf



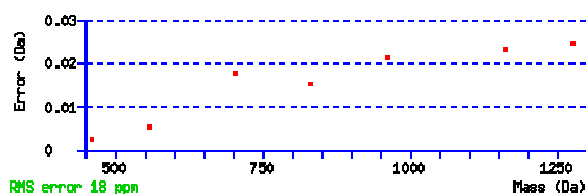
Monoisotopic mass of neutral peptide Mr(calc): 1969.9574

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

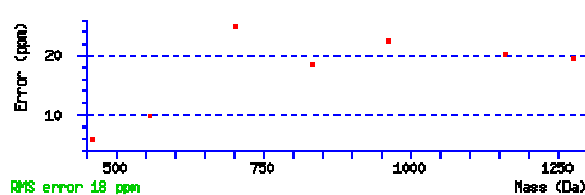
Ions Score: 49 Expect: 0.00086

Matches : 7/148 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							16
2	219.1128	110.0600					F	1899.9276	950.4674	1882.9010	941.9542	1881.9170	941.4621	15
3	334.1397	167.5735			316.1292	158.5682	D	1752.8592	876.9332	1735.8326	868.4199	1734.8486	867.9279	14
4	435.1874	218.0974			417.1769	209.0921	T	1637.8322	819.4197	1620.8057	810.9065	1619.8217	810.4145	13
5	582.2558	291.6316			564.2453	282.6263	F	1536.7845	768.8959	1519.7580	760.3826	1518.7740	759.8906	12
6	695.3399	348.1736			677.3293	339.1683	L	1389.7161	695.3617	1372.6896	686.8484	1371.7056	686.3564	11
7	810.3668	405.6871			792.3563	396.6818	D	1276.6321	638.8197	1259.6055	630.3064	1258.6215	629.8144	10
8	897.3989	449.2031			879.3883	440.1978	S	1161.6051	581.3062	1144.5786	572.7929	1143.5946	572.3009	9
9	1010.4829	505.7451			992.4724	496.7398	L	1074.5731	537.7902	1057.5465	529.2769	1056.5625	528.7849	8
10	1138.5415	569.7744	1121.5150	561.2611	1120.5310	560.7691	Q	961.4890	481.2482	944.4625	472.7349	943.4785	472.2429	7
11	1267.5841	634.2957	1250.5576	625.7824	1249.5735	625.2904	E	833.4305	417.2189	816.4039	408.7056	815.4199	408.2136	6
12	1414.6525	707.8299	1397.6260	699.3166	1396.6420	698.8246	F	704.3879	352.6976	687.3613	344.1843			5
13	1511.7053	756.3563	1494.6787	747.8430	1493.6947	747.3510	P	557.3194	279.1634	540.2929	270.6501			4
14	1697.7846	849.3959	1680.7581	840.8827	1679.7740	840.3907	W	460.2667	230.6370	443.2401	222.1237			3
15	1796.8530	898.9301	1779.8265	890.4169	1778.8425	889.9249	V	274.1874	137.5973	257.1608	129.0840			2
16							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 18 ppm



RMS error 18 ppm

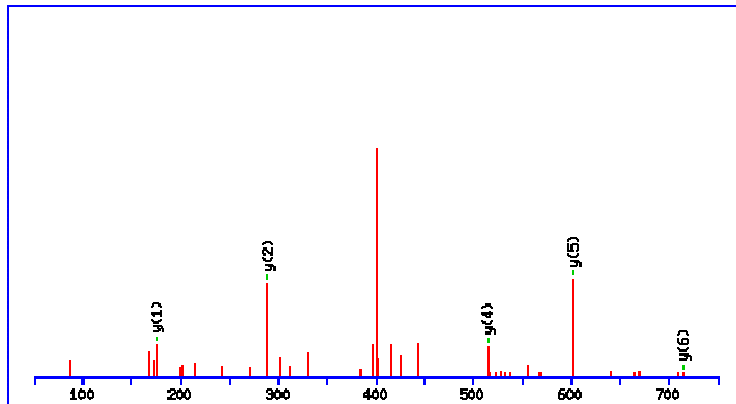
Peptide Number: 50319**MS/MS Fragmentation of EISPEIR**

Found in **IPI00217691** in **IPI_human**, Tax_Id=9606 Gene_Symbol=C17orf57;ITGB3 Isoform 1 of EF-hand domain-containing protein C17orf57

Match to Query 197: 842.461508 from(422.238030,2+) index(24020)

Title: Elution from: 59.8333333333333 to 59.8333333333333 period: 0 cycle: 2223 experiment: 1 polarity:+

Data file 120126ry_585A1-55_2_3.mgf



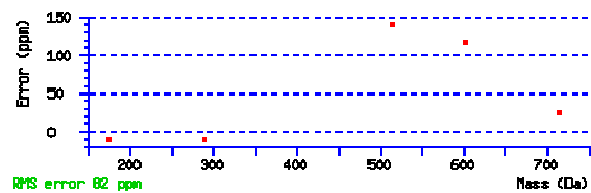
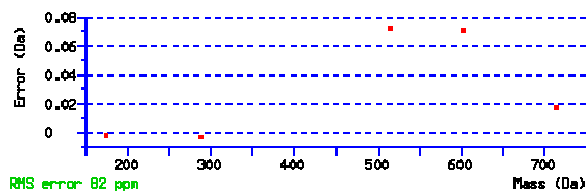
Monoisotopic mass of neutral peptide Mr(calcd): 842.4498

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 42 **Expect:** 0.0043

Matches : 5/56 fragment ions using 7 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286	112.0393	56.5233	E							7
2	243.1339	122.0706	225.1234	113.0653	I	714.4145	357.7109	697.3879	349.1976	696.4039	348.7056	6
3	330.1660	165.5866	312.1554	156.5813	S	601.3304	301.1688	584.3039	292.6556	583.3198	292.1636	5
4	427.2187	214.1130	409.2082	205.1077	P	514.2984	257.6528	497.2718	249.1396	496.2878	248.6475	4
5	556.2613	278.6343	538.2508	269.6290	E	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
6	669.3454	335.1763	651.3348	326.1710	I	288.2030	144.6051	271.1765	136.0919			2
7					R	175.1190	88.0631	158.0924	79.5498			1



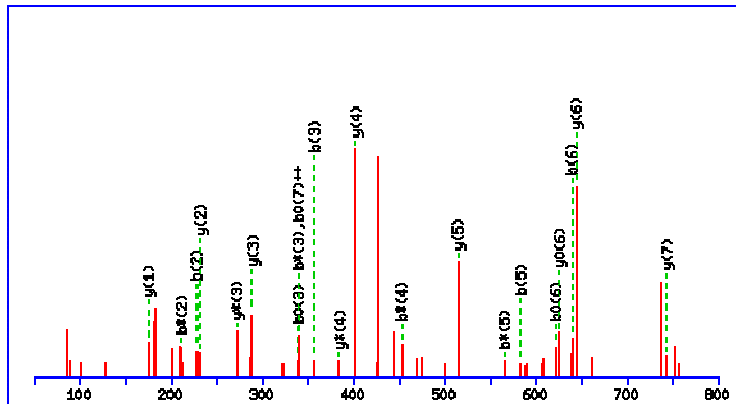
Peptide Number: 50742

MS/MS Fragmentation of **QVEILGGR**Found in **IPI00217802** in **IPI_human**, Tax_Id=9606 Gene_Symbol=FAM186B Protein FAM186B

Match to Query 6263: 870.487788 from(436.251170,2+) index(24901)

Title: Elution from: 105.4 to 105.4 period: 0 cycle: 8571 experiment: 3 polarity: +

Data file 120118ry_201B7-32_3_1.mgf



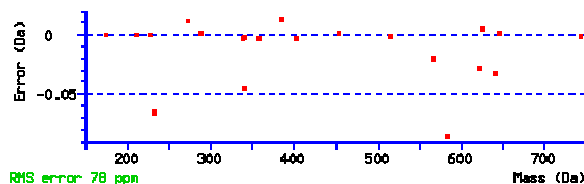
Monoisotopic mass of neutral peptide Mr(calcd): 870.4923

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

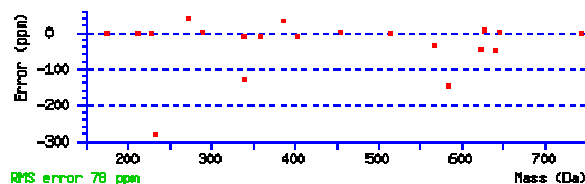
Ions Score: 51 Expect: 0.00044

Matches : 21/70 fragment ions using 38 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.0659	65.0366	112.0393	56.5233			Q							8
2	228.1343	114.5708	211.1077	106.0575			V	743.4410	372.2241	726.4145	363.7109	725.4305	363.2189	7
3	357.1769	179.0921	340.1503	170.5788	339.1663	170.0868	E	644.3726	322.6899	627.3461	314.1767	626.3620	313.6847	6
4	470.2609	235.6341	453.2344	227.1208	452.2504	226.6288	I	515.3300	258.1686	498.3035	249.6554			5
5	583.3450	292.1761	566.3184	283.6629	565.3344	283.1709	L	402.2459	201.6266	385.2194	193.1133			4
6	640.3665	320.6869	623.3399	312.1736	622.3559	311.6816	G	289.1619	145.0846	272.1353	136.5713			3
7	697.3879	349.1976	680.3614	340.6843	679.3774	340.1923	G	232.1404	116.5738	215.1139	108.0606			2
8							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 78 ppm



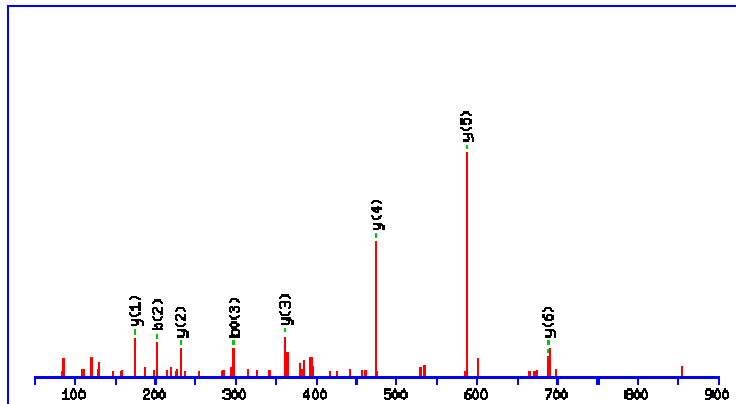
RMS error 78 ppm

Peptide Number: 50758MS/MS Fragmentation of **TTIIIEGR**Found in **IPI00018691** in **IPI_human**, Tax_Id=9606 Gene_Symbol=MRPS18A Isoform 1 of 28S ribosomal protein S18a, mitochondrial

Match to Query 3583: 788.438868 from(395.226710,2+) index(11141)

Title: Elution from: 67.0833333333333 to 67.0833333333333 period: 0 cycle: 7909 experiment: 2 polarity: +

Data file 120210ry_585A1-55_3_1.mgf



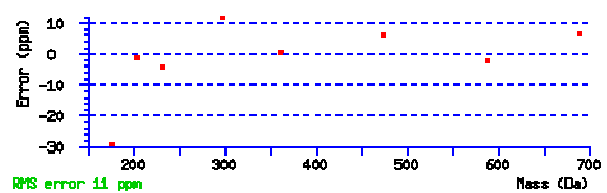
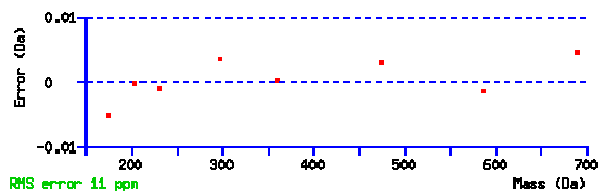
Monoisotopic mass of neutral peptide Mr(calcd): 788.4392

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 47 Expect: 0.0015

Matches : 8/56 fragment ions using 14 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311	84.0444	42.5258	T							7
2	203.1026	102.0550	185.0921	93.0497	T	688.3988	344.7030	671.3723	336.1898	670.3883	335.6978	6
3	316.1867	158.5970	298.1761	149.5917	I	587.3511	294.1792	570.3246	285.6659	569.3406	285.1739	5
4	429.2708	215.1390	411.2602	206.1337	I	474.2671	237.6372	457.2405	229.1239	456.2565	228.6319	4
5	558.3134	279.6603	540.3028	270.6550	E	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	3
6	615.3348	308.1710	597.3243	299.1658	G	232.1404	116.5738	215.1139	108.0606			2
7					R	175.1190	88.0631	158.0924	79.5498			1

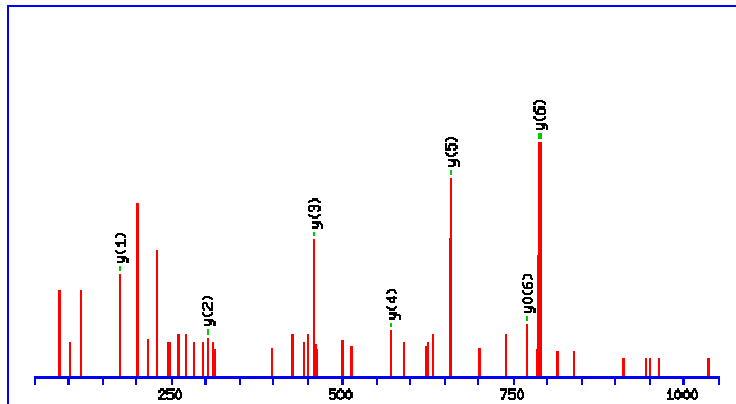


Peptide Number: 50791MS/MS Fragmentation of **QVESNRQR**Found in **IPI00030282** in **IPI_human**, Tax_Id=9606 Gene_Symbol=BFSP1 Isoform 1 of Filensin

Match to Query 2467: 1015.501548 from(508.758050,2+) index(3753)

Title: Elution from: 9.16666666666667 to 9.16666666666667 period: 0 cycle: 342 experiment: 4 polarity: +

Data file 120126ry_585A1-55_2_3.mgf



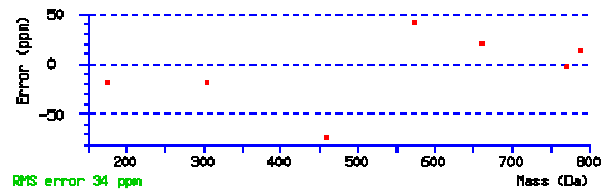
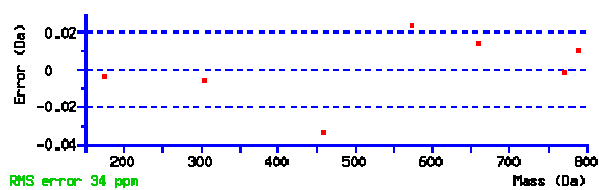
Monoisotopic mass of neutral peptide Mr(calc): 1015.5159

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 51 Expect: 0.00044

Matches : 7/72 fragment ions using 9 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.0659	65.0366	112.0393	56.5233			Q							8
2	228.1343	114.5708	211.1077	106.0575			V	888.4646	444.7359	871.4381	436.2227	870.4540	435.7307	7
3	357.1769	179.0921	340.1503	170.5788	339.1663	170.0868	E	789.3962	395.2017	772.3696	386.6885	771.3856	386.1965	6
4	444.2089	222.6081	427.1823	214.0948	426.1983	213.6028	S	660.3536	330.6804	643.3270	322.1672	642.3430	321.6752	5
5	558.2518	279.6295	541.2253	271.1163	540.2413	270.6243	N	573.3216	287.1644	556.2950	278.6511			4
6	714.3529	357.6801	697.3264	349.1668	696.3424	348.6748	R	459.2786	230.1430	442.2521	221.6297			3
7	842.4115	421.7094	825.3850	413.1961	824.4009	412.7041	Q	303.1775	152.0924	286.1510	143.5791			2
8							R	175.1190	88.0631	158.0924	79.5498			1



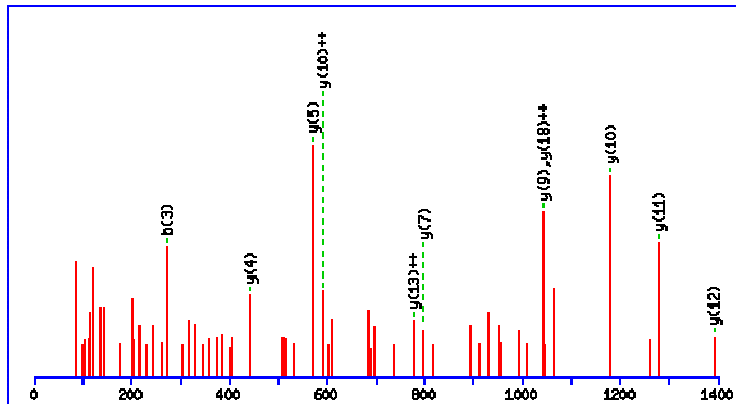
Peptide Number: 50896

MS/MS Fragmentation of **AAELFGLTAEVYLVHDELDKPLGR**Found in **IPI00048572** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PTRH1 Similar to Tetratricopeptide repeat protein 16

Match to Query 31423: 2784.444816 from(697.118480,4+) index(15936)

Title: Elution from: 40.4833333333333 to 40.4833333333333 period: 0 cycle: 1536 experiment: 2 polarity: +

Data file 120212ry_aHDF1388-P9_2_4.mgf



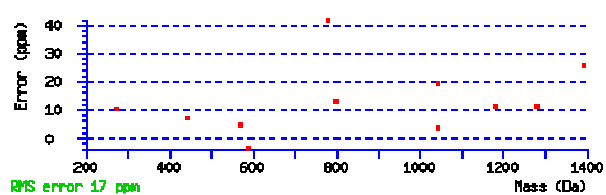
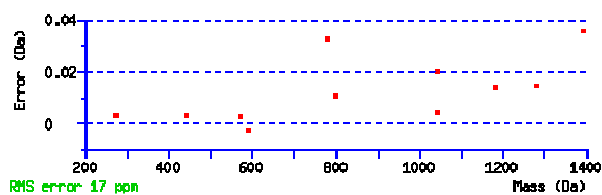
Monoisotopic mass of neutral peptide Mr(calc): 2784.4334

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 46 Expect: 0.0011

Matches : 11/234 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							25
2	143.0815	72.0444					A	2714.4036	1357.7054	2697.3770	1349.1922	2696.3930	1348.7001	24
3	272.1241	136.5657			254.1135	127.5604	E	2643.3665	1322.1869	2626.3399	1313.6736	2625.3559	1313.1816	23
4	385.2082	193.1077			367.1976	184.1024	L	2514.3239	1257.6656	2497.2973	1249.1523	2496.3133	1248.6603	22
5	532.2766	266.6419			514.2660	257.6366	F	2401.2398	1201.1235	2384.2133	1192.6103	2383.2292	1192.1183	21
6	589.2980	295.1527			571.2875	286.1474	G	2254.1714	1127.5893	2237.1448	1119.0761	2236.1608	1118.5841	20
7	702.3821	351.6947			684.3715	342.6894	L	2197.1499	1099.0786	2180.1234	1090.5653	2179.1394	1090.0733	19
8	803.4298	402.2185			785.4192	393.2132	T	2084.0659	1042.5366	2067.0393	1034.0233	2066.0553	1033.5313	18
9	874.4669	437.7371			856.4563	428.7318	A	1983.0182	992.0127	1965.9916	983.4995	1965.0076	983.0074	17
10	1003.5095	502.2584			985.4989	493.2531	E	1911.9811	956.4942	1894.9545	947.9809	1893.9705	947.4889	16
11	1132.5521	566.7797			1114.5415	557.7744	E	1782.9385	891.9729	1765.9119	883.4596	1764.9279	882.9676	15
12	1231.6205	616.3139			1213.6099	607.3086	V	1653.8959	827.4516	1636.8693	818.9383	1635.8853	818.4463	14
13	1394.6838	697.8456			1376.6733	688.8403	Y	1554.8275	777.9174	1537.8009	769.4041	1536.8169	768.9121	13
14	1507.7679	754.3876			1489.7573	745.3823	L	1391.7641	696.3857	1374.7376	687.8724	1373.7536	687.3804	12
15	1606.8363	803.9218			1588.8257	794.9165	V	1278.6801	639.8437	1261.6535	631.3304	1260.6695	630.8384	11
16	1743.8952	872.4512			1725.8847	863.4460	H	1179.6117	590.3095	1162.5851	581.7962	1161.6011	581.3042	10
17	1858.9222	929.9647			1840.9116	920.9594	D	1042.5528	521.7800	1025.5262	513.2667	1024.5422	512.7747	9
18	1987.9648	994.4860			1969.9542	985.4807	E	927.5258	464.2665	910.4993	455.7533	909.5152	455.2613	8
19	2101.0488	1051.0280			2083.0383	1042.0228	L	798.4832	399.7452	781.4567	391.2320	780.4726	390.7400	7
20	2216.0758	1108.5415			2198.0652	1099.5362	D	685.3991	343.2032	668.3726	334.6899	667.3886	334.1979	6
21	2344.1707	1172.5890	2327.1442	1164.0757	2326.1602	1163.5837	K	570.3722	285.6897	553.3457	277.1765			5
22	2441.2235	1221.1154	2424.1969	1212.6021	2423.2129	1212.1101	P	442.2772	221.6423	425.2507	213.1290			4
23	2554.3075	1277.6574	2537.2810	1269.1441	2536.2970	1268.6521	L	345.2245	173.1159	328.1979	164.6026			3
24	2611.3290	1306.1681	2594.3025	1297.6549	2593.3184	1297.1629	G	232.1404	116.5738	215.1139	108.0606			2
25							R	175.1190	88.0631	158.0924	79.5498			1



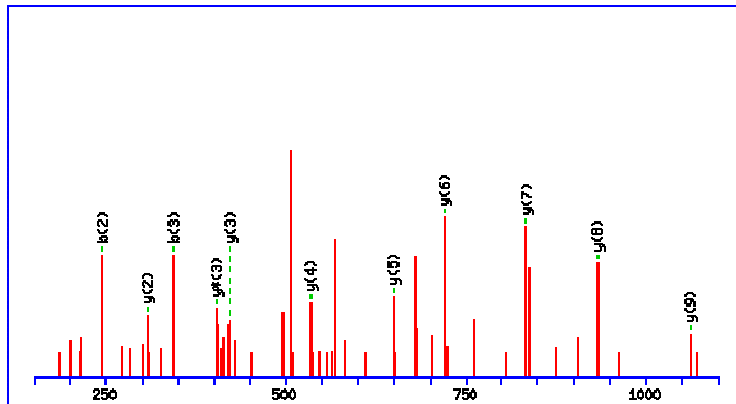
Peptide Number: 51013

MS/MS Fragmentation of **NEVIADINCK**Found in **IPI00075080** in **IPI_human**, Tax_Id=9606 Gene_Symbol=OSBPL1A Isoform B of Oxysterol-binding protein-related protein 1

Match to Query 14786: 1174.584508 from(588.299530,2+) index(2215)

Title: Elution from: 5.23333333333333 to 5.23333333333333 period: 0 cycle: 196 experiment: 10 polarity: +

Data file 120210ry_32R1-32_3_2.mgf



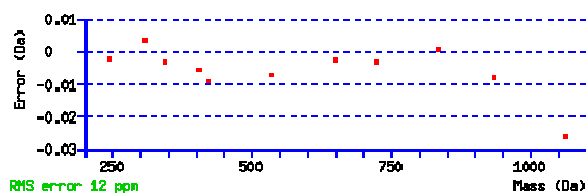
Monoisotopic mass of neutral peptide Mr(calc): 1174.5652

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

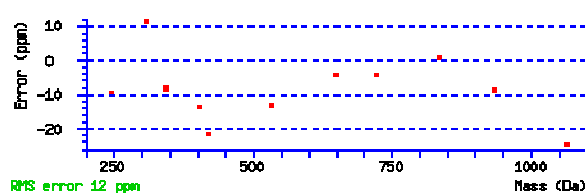
Ions Score: 48 Expect: 0.0011

Matches : 11/98 fragment ions using 26 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							10
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	E	1061.5296	531.2684	1044.5030	522.7551	1043.5190	522.2631	9
3	343.1612	172.0842	326.1347	163.5710	325.1506	163.0790	V	932.4870	466.7471	915.4604	458.2339	914.4764	457.7418	8
4	456.2453	228.6263	439.2187	220.1130	438.2347	219.6210	I	833.4186	417.2129	816.3920	408.6996	815.4080	408.2076	7
5	527.2824	264.1448	510.2558	255.6316	509.2718	255.1395	A	720.3345	360.6709	703.3080	352.1576	702.3239	351.6656	6
6	642.3093	321.6583	625.2828	313.1450	624.2988	312.6530	D	649.2974	325.1523	632.2708	316.6391	631.2868	316.1470	5
7	755.3934	378.2003	738.3668	369.6871	737.3828	369.1951	I	534.2704	267.6389	517.2439	259.1256			4
8	869.4363	435.2218	852.4098	426.7085	851.4258	426.2165	N	421.1864	211.0968	404.1598	202.5836			3
9	1029.4670	515.2371	1012.4404	506.7238	1011.4564	506.2318	C	307.1435	154.0754	290.1169	145.5621			2
10							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 12 ppm



RMS error 12 ppm

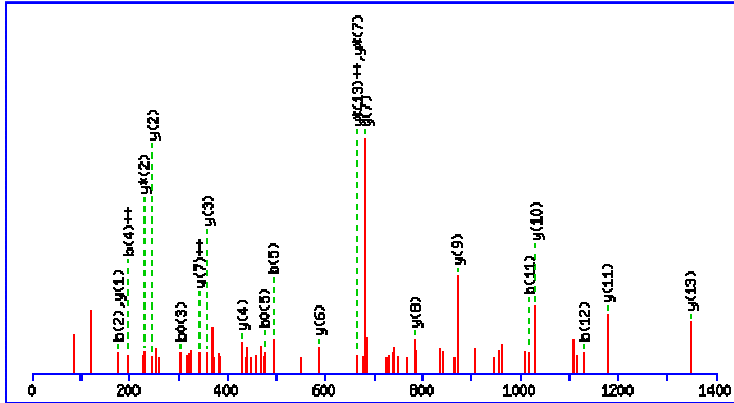
Peptide Number: 51085

MS/MS Fragmentation of **SSFATPGVNVGLFCSTPGVALAR**Found in **IPI00256376** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ECHDC3 Isoform 1 of Enoyl-CoA hydratase domain-containing protein 3, mitochondrial

Match to Query 40114: 2307.154842 from(770.058890,3+) index(35681)

Title: Elution from: 89.7 to 89.7 period: 0 cycle: 3344 experiment: 9 polarity:+

Data file 120126ry_585A1-55_2_3.mgf



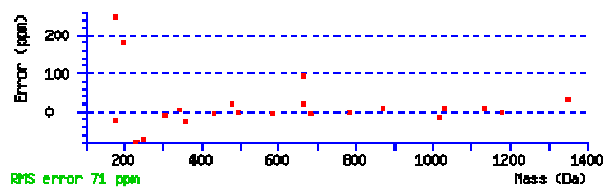
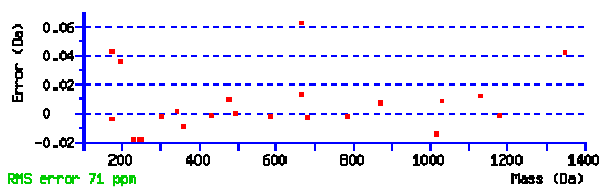
Monoisotopic mass of neutral peptide Mr(calc): 2307.1682

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 47 Expect: 0.0013

Matches : 23/234 fragment ions using 48 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							23
2	175.0713	88.0393			157.0608	79.0340	S	2221.1434	1111.0753	2204.1169	1102.5621	2203.1328	1102.0701	22
3	322.1397	161.5735			304.1292	152.5682	F	2134.1114	1067.5593	2117.0848	1059.0461	2116.1008	1058.5540	21
4	393.1769	197.0921			375.1663	188.0868	A	1987.0430	994.0251	1970.0164	985.5118	1969.0324	985.0198	20
5	494.2245	247.6159			476.2140	238.6106	T	1916.0058	958.5066	1898.9793	949.9933	1897.9953	949.5013	19
6	591.2773	296.1423			573.2667	287.1370	P	1814.9582	907.9827	1797.9316	899.4694	1796.9476	898.9774	18
7	648.2988	324.6530			630.2882	315.6477	G	1717.9054	859.4563	1700.8789	850.9431	1699.8948	850.4511	17
8	747.3672	374.1872			729.3566	365.1819	V	1660.8839	830.9456	1643.8574	822.4323	1642.8734	821.9403	16
9	861.4101	431.2087	844.3836	422.6954	843.3995	422.2034	N	1561.8155	781.4114	1544.7890	772.8981	1543.8050	772.4061	15
10	960.4785	480.7429	943.4520	472.2296	942.4680	471.7376	V	1447.7726	724.3899	1430.7460	715.8767	1429.7620	715.3847	14
11	1017.5000	509.2536	1000.4734	500.7404	999.4894	500.2483	G	1348.7042	674.8557	1331.6776	666.3425	1330.6936	665.8504	13
12	1130.5840	565.7957	1113.5575	557.2824	1112.5735	556.7904	L	1291.6827	646.3450	1274.6562	637.8317	1273.6722	637.3397	12
13	1277.6525	639.3299	1260.6259	630.8166	1259.6419	630.3246	F	1178.5987	589.8030	1161.5721	581.2897	1160.5881	580.7977	11
14	1437.6831	719.3452	1420.6566	710.8319	1419.6725	710.3399	C	1031.5302	516.2688	1014.5037	507.7555	1013.5197	507.2635	10
15	1524.7151	762.8612	1507.6886	754.3479	1506.7046	753.8559	S	871.4996	436.2534	854.4730	427.7402	853.4890	427.2482	9
16	1625.7628	813.3850	1608.7363	804.8718	1607.7523	804.3798	T	784.4676	392.7374	767.4410	384.2241	766.4570	383.7321	8
17	1722.8156	861.9114	1705.7890	853.3982	1704.8050	852.9061	P	683.4199	342.2136	666.3933	333.7003			7
18	1779.8370	890.4222	1762.8105	881.9089	1761.8265	881.4169	G	586.3671	293.6872	569.3406	285.1739			6
19	1878.9055	939.9564	1861.8789	931.4431	1860.8949	930.9511	V	529.3457	265.1765	512.3191	256.6632			5
20	1949.9426	975.4749	1932.9160	966.9617	1931.9320	966.4696	A	430.2772	215.6423	413.2507	207.1290			4
21	2063.0266	1032.0170	2046.0001	1023.5037	2045.0161	1023.0117	L	359.2401	180.1237	342.2136	171.6104			3
22	2134.0638	1067.5355	2117.0372	1059.0222	2116.0532	1058.5302	A	246.1561	123.5817	229.1295	115.0684			2
23							R	175.1190	88.0631	158.0924	79.5498			1

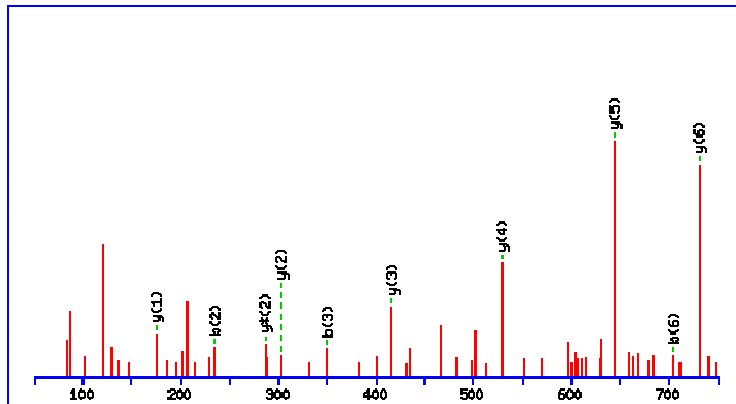


Peptide Number: 51213MS/MS Fragmentation of **FSDLLQR**Found in **IPI00164768** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CREBZF CREB/ATF bZIP transcription factor

Match to Query 3336: 877.460248 from(439.737400,2+) index(10334)

Title: Elution from: 24.9833333333333 to 24.9833333333333 period: 0 cycle: 951 experiment: 3 polarity: +

Data file 120201ry_aHDF1388-P9_1_2.mgf



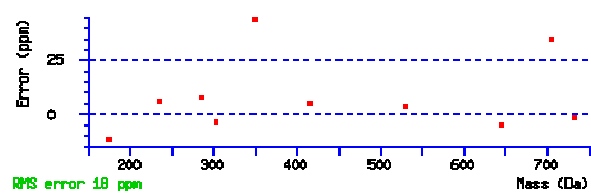
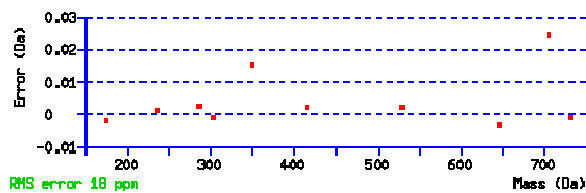
Monoisotopic mass of neutral peptide Mr(calc): 877.4658

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 39 Expect: 0.0093

Matches : 10/52 fragment ions using 21 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415					F							7
2	235.1077	118.0575			217.0972	109.0522	S	731.4046	366.2060	714.3781	357.6927	713.3941	357.2007	6
3	350.1347	175.5710			332.1241	166.5657	D	644.3726	322.6899	627.3461	314.1767	626.3620	313.6847	5
4	463.2187	232.1130			445.2082	223.1077	L	529.3457	265.1765	512.3191	256.6632			4
5	576.3028	288.6550			558.2922	279.6498	L	416.2616	208.6344	399.2350	200.1212			3
6	704.3614	352.6843	687.3348	344.1710	686.3508	343.6790	Q	303.1775	152.0924	286.1510	143.5791			2
7							R	175.1190	88.0631	158.0924	79.5498			1



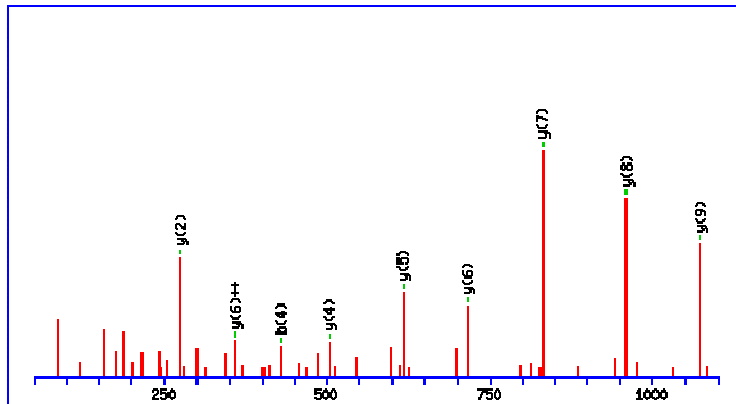
Peptide Number: 51392

MS/MS Fragmentation of **SVIEDVINDVR**Found in **IPI00004350** in **IPI_human**, Tax_Id=9606 Gene_Symbol=GTF2A1 Isoform 42 kDa of Transcription initiation factor IIA subunit 1

Match to Query 4118: 1257.660828 from(629.837690,2+) index(25096)

Title: Elution from: 69.6166666666667 to 69.6166666666667 period: 0 cycle: 2677 experiment: 5 polarity:+

Data file 120208ry_Tig120slc-P8_1_3.mgf



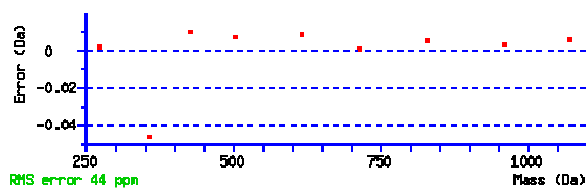
Monoisotopic mass of neutral peptide Mr(calc): 1257.6565

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

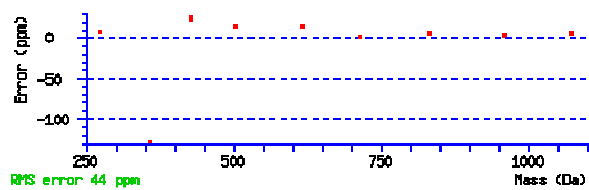
Ions Score: 69 Expect: 1e-005

Matches : 9/102 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							11
2	187.1077	94.0575			169.0972	85.0522	V	1171.6317	586.3195	1154.6052	577.8062	1153.6212	577.3142	10
3	300.1918	150.5995			282.1812	141.5942	I	1072.5633	536.7853	1055.5368	528.2720	1054.5527	527.7800	9
4	429.2344	215.1208			411.2238	206.1155	E	959.4792	480.2433	942.4527	471.7300	941.4687	471.2380	8
5	544.2613	272.6343			526.2508	263.6290	D	830.4367	415.7220	813.4101	407.2087	812.4261	406.7167	7
6	643.3297	322.1685			625.3192	313.1632	V	715.4097	358.2085	698.3832	349.6952	697.3991	349.2032	6
7	756.4138	378.7105			738.4032	369.7053	I	616.3413	308.6743	599.3148	300.1610	598.3307	299.6690	5
8	870.4567	435.7320	853.4302	427.2187	852.4462	426.7267	N	503.2572	252.1323	486.2307	243.6190	485.2467	243.1270	4
9	985.4837	493.2455	968.4571	484.7322	967.4731	484.2402	D	389.2143	195.1108	372.1878	186.5975	371.2037	186.1055	3
10	1084.5521	542.7797	1067.5255	534.2664	1066.5415	533.7744	V	274.1874	137.5973	257.1608	129.0840			2
11							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 44 ppm



RMS error 44 ppm

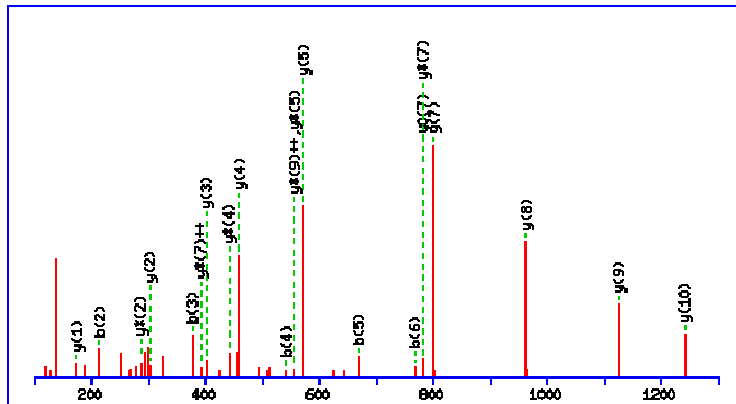
Peptide Number: 51491

MS/MS Fragmentation of **VDYYEVLGVQR**Found in **IPI00024523** in **IPI_human**, Tax_Id=9606 Gene_Symbol=DNAJB6 Isoform A of DnaJ homolog subfamily B member 6

Match to Query 7697: 1339.674348 from(670.844450,2+) index(6324)

Title: Elution from: 15.6 to 15.6 period: 0 cycle: 588 experiment: 6 polarity: +

Data file 120210ry_32R1-32_2_3.mgf



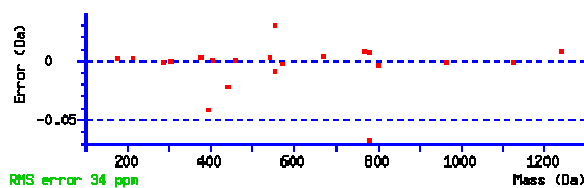
Monoisotopic mass of neutral peptide Mr(calcd): 1339.6772

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

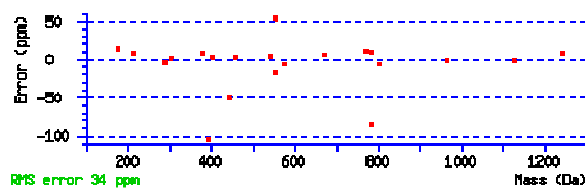
Ions Score: 62 Expect: 3.5e-005

Matches : 21/88 fragment ions using 35 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							11
2	215.1026	108.0550			197.0921	99.0497	D	1241.6161	621.3117	1224.5895	612.7984	1223.6055	612.3064	10
3	378.1660	189.5866			360.1554	180.5813	Y	1126.5891	563.7982	1109.5626	555.2849	1108.5786	554.7929	9
4	541.2293	271.1183			523.2187	262.1130	Y	963.5258	482.2665	946.4993	473.7533	945.5152	473.2613	8
5	670.2719	335.6396			652.2613	326.6343	E	800.4625	400.7349	783.4359	392.2216	782.4519	391.7296	7
6	769.3403	385.1738			751.3297	376.1685	V	671.4199	336.2136	654.3933	327.7003			6
7	882.4244	441.7158			864.4138	432.7105	L	572.3515	286.6794	555.3249	278.1661			5
8	939.4458	470.2266			921.4353	461.2213	G	459.2674	230.1373	442.2409	221.6241			4
9	1038.5142	519.7608			1020.5037	510.7555	V	402.2459	201.6266	385.2194	193.1133			3
10	1166.5728	583.7900	1149.5463	575.2768	1148.5623	574.7848	Q	303.1775	152.0924	286.1510	143.5791			2
11							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 34 ppm



RMS error 34 ppm

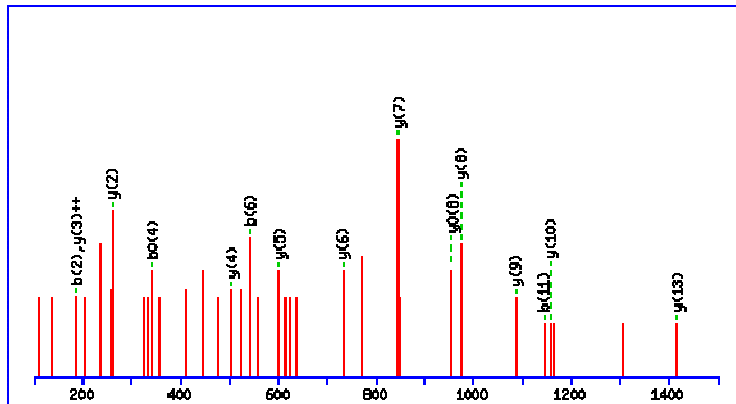
Peptide Number: 51506

MS/MS Fragmentation of **VSGDALQLMVELLK**Found in **IPI00795646** in **IPI_human**, Tax_Id=9606 Gene_Symbol=STRA13 Isoform 1 of Centromere protein X

Match to Query 4164: 1514.810928 from(758.412740,2+) index(32136)

Title: Elution from: 79.3166666666667 to 79.3166666666667 period: 0 cycle: 2955 experiment: 4 polarity: +

Data file 120118ry_201B7-32_2_4.mgf



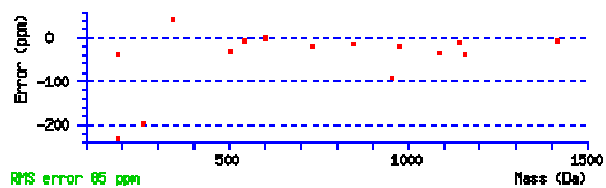
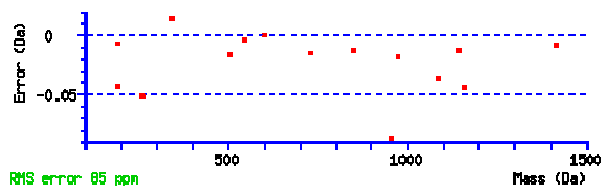
Monoisotopic mass of neutral peptide Mr(calcd): 1514.8378

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 52 Expect: 0.0004

Matches : 15/136 fragment ions using 31 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							14
2	187.1077	94.0575			169.0972	85.0522	S	1416.7767	708.8920	1399.7501	700.3787	1398.7661	699.8867	13
3	244.1292	122.5682			226.1186	113.5629	G	1329.7447	665.3760	1312.7181	656.8627	1311.7341	656.3707	12
4	359.1561	180.0817			341.1456	171.0764	D	1272.7232	636.8652	1255.6966	628.3520	1254.7126	627.8599	11
5	430.1932	215.6003			412.1827	206.5950	A	1157.6962	579.3518	1140.6697	570.8385	1139.6857	570.3465	10
6	543.2773	272.1423			525.2667	263.1370	L	1086.6591	543.8332	1069.6326	535.3199	1068.6486	534.8279	9
7	671.3359	336.1716	654.3093	327.6583	653.3253	327.1663	Q	973.5751	487.2912	956.5485	478.7779	955.5645	478.2859	8
8	784.4199	392.7136	767.3934	384.2003	766.4094	383.7083	L	845.5165	423.2619	828.4899	414.7486	827.5059	414.2566	7
9	915.4604	458.2339	898.4339	449.7206	897.4499	449.2286	M	732.4324	366.7198	715.4059	358.2066	714.4219	357.7146	6
10	1014.5288	507.7681	997.5023	499.2548	996.5183	498.7628	V	601.3919	301.1996	584.3654	292.6863	583.3814	292.1943	5
11	1143.5714	572.2894	1126.5449	563.7761	1125.5609	563.2841	E	502.3235	251.6654	485.2970	243.1521	484.3130	242.6601	4
12	1256.6555	628.8314	1239.6290	620.3181	1238.6449	619.8261	L	373.2809	187.1441	356.2544	178.6308			3
13	1369.7396	685.3734	1352.7130	676.8601	1351.7290	676.3681	L	260.1969	130.6021	243.1703	122.0888			2
14							K	147.1128	74.0600	130.0863	65.5468			1



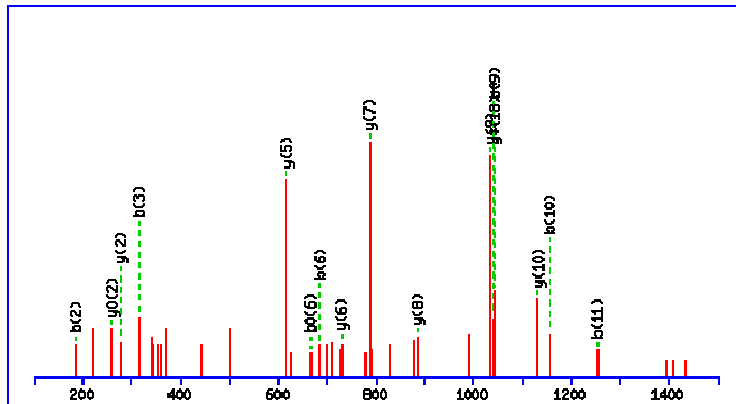
Peptide Number: 51620

MS/MS Fragmentation of **LAELPCLDLVFVGNPLEEK**Found in **IP101024781** in **IPI_human**, Tax_Id=9606 Gene_Symbol=DNAL1 12 kDa protein

Match to Query 19568: 2284.149552 from(762.390460,3+) index(26630)

Title: Elution from: 70.4666666666667 to 70.4666666666667 period: 0 cycle: 2682 experiment: 5 polarity: +

Data file 120210ry_32R1-32_3_4.mgf



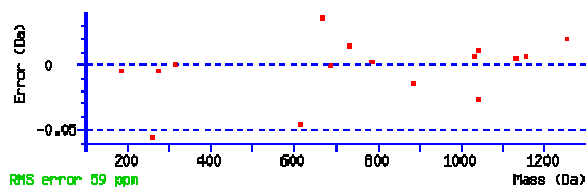
Monoisotopic mass of neutral peptide Mr(calc): 2284.1661

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

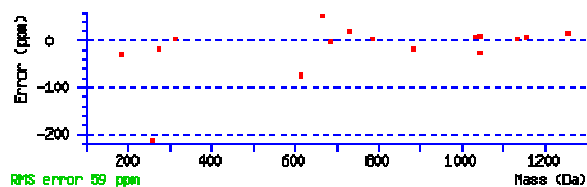
Ions Score: 39 Expect: 0.0087

Matches : 16/194 fragment ions using 35 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							20
2	185.1285	93.0679					A	2172.0893	1086.5483	2155.0627	1078.0350	2154.0787	1077.5430	19
3	314.1710	157.5892			296.1605	148.5839	E	2101.0522	1051.0297	2084.0256	1042.5165	2083.0416	1042.0244	18
4	427.2551	214.1312			409.2445	205.1259	L	1972.0096	986.5084	1954.9830	977.9952	1953.9990	977.5032	17
5	524.3079	262.6576			506.2973	253.6523	P	1858.9255	929.9664	1841.8990	921.4531	1840.9150	920.9611	16
6	684.3385	342.6729			666.3280	333.6676	C	1761.8728	881.4400	1744.8462	872.9267	1743.8622	872.4347	15
7	797.4226	399.2149			779.4120	390.2096	L	1601.8421	801.4247	1584.8156	792.9114	1583.8316	792.4194	14
8	926.4652	463.7362			908.4546	454.7309	E	1488.7581	744.8827	1471.7315	736.3694	1470.7475	735.8774	13
9	1041.4921	521.2497			1023.4816	512.2444	D	1359.7155	680.3614	1342.6889	671.8481	1341.7049	671.3561	12
10	1154.5762	577.7917			1136.5656	568.7864	L	1244.6885	622.8479	1227.6620	614.3346	1226.6780	613.8426	11
11	1253.6446	627.3259			1235.6340	618.3207	V	1131.6045	566.3059	1114.5779	557.7926	1113.5939	557.3006	10
12	1400.7130	700.8601			1382.7025	691.8549	F	1032.5360	516.7717	1015.5095	508.2584	1014.5255	507.7664	9
13	1499.7814	750.3944			1481.7709	741.3891	V	885.4676	443.2374	868.4411	434.7242	867.4571	434.2322	8
14	1556.8029	778.9051			1538.7923	769.8998	G	786.3992	393.7032	769.3727	385.1900	768.3886	384.6980	7
15	1670.8458	835.9265	1653.8193	827.4133	1652.8353	826.9213	N	729.3777	365.1925	712.3512	356.6792	711.3672	356.1872	6
16	1767.8986	884.4529	1750.8720	875.9397	1749.8880	875.4476	P	615.3348	308.1710	598.3083	299.6578	597.3243	299.1658	5
17	1880.9826	940.9950	1863.9561	932.4817	1862.9721	931.9897	L	518.2821	259.6447	501.2555	251.1314	500.2715	250.6394	4
18	2010.0252	1005.5163	1992.9987	997.0030	1992.0147	996.5110	E	405.1980	203.1026	388.1714	194.5894	387.1874	194.0974	3
19	2139.0678	1070.0376	2122.0413	1061.5243	2121.0573	1061.0323	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
20							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 59 ppm



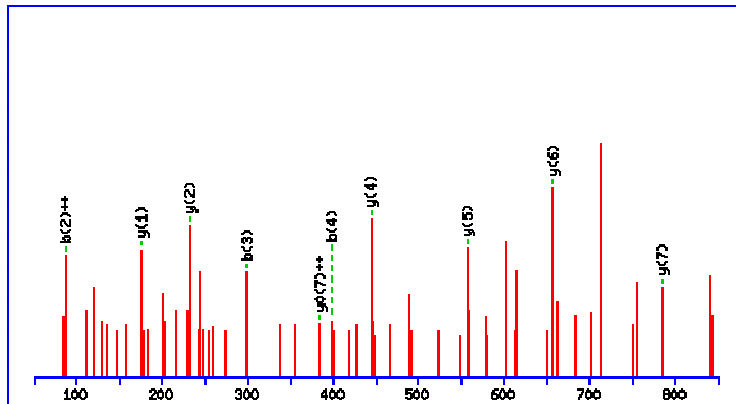
RMS error 59 ppm

Peptide Number: 51868MS/MS Fragmentation of **GIQVLPDGR**Found in **IPI00005011** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CNOT2 Isoform 1 of CCR4-NOT transcription complex subunit 2

Match to Query 5783: 953.514348 from(477.764450,2+) index(10251)

Title: Elution from: 24.8 to 24.8 period: 0 cycle: 944 experiment: 4 polarity: +

Data file 120201ry_aHDF1388-P9_1_2.mgf



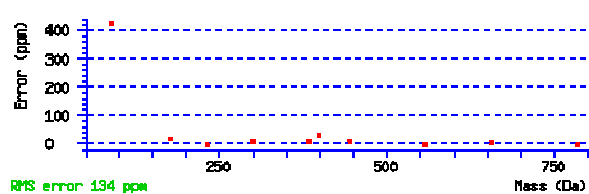
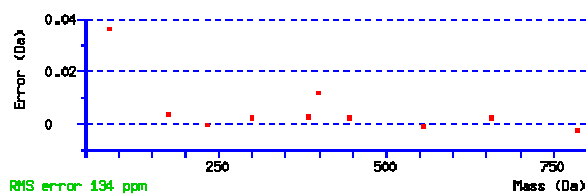
Monoisotopic mass of neutral peptide Mr(calc): 953.5294

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 43 Expect: 0.002

Matches : 10/76 fragment ions using 16 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					Q							9
2	171.1128	86.0600					I	897.5152	449.2613	880.4887	440.7480	879.5047	440.2560	8
3	299.1714	150.0893	282.1448	141.5761			Q	784.4312	392.7192	767.4046	384.2060	766.4206	383.7139	7
4	398.2398	199.6235	381.2132	191.1103			V	656.3726	328.6899	639.3461	320.1767	638.3620	319.6847	6
5	511.3239	256.1656	494.2973	247.6523			L	557.3042	279.1557	540.2776	270.6425	539.2936	270.1504	5
6	608.3766	304.6920	591.3501	296.1787			P	444.2201	222.6137	427.1936	214.1004	426.2096	213.6084	4
7	723.4036	362.2054	706.3770	353.6921	705.3930	353.2001	D	347.1674	174.0873	330.1408	165.5740	329.1568	165.0820	3
8	780.4250	390.7162	763.3985	382.2029	762.4145	381.7109	G	232.1404	116.5738	215.1139	108.0606			2
9							R	175.1190	88.0631	158.0924	79.5498			1



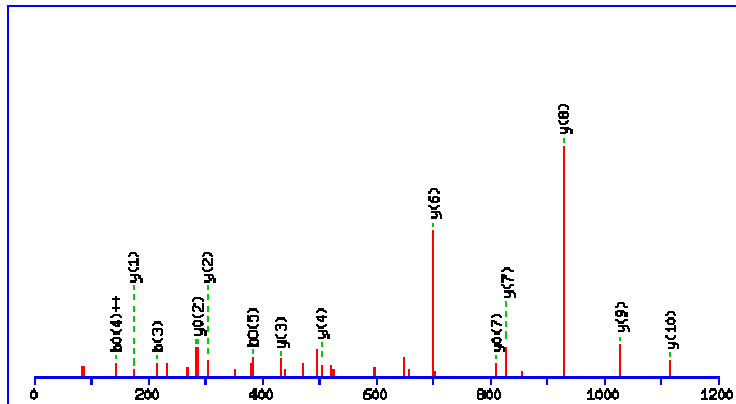
Peptide Number: 52252

MS/MS Fragmentation of **SGASVTEPVAEER**Found in **IPI00006073** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TNFRSF8 Isoform Long of Tumor necrosis factor receptor superfamily member 8

Match to Query 20641: 1330.647908 from(666.331230,2+) index(15943)

Title: Elution from: 78.6166666666667 to 78.6166666666667 period: 0 cycle: 8351 experiment: 9 polarity:+

Data file 120210ry_585A1-55_3_1.mgf



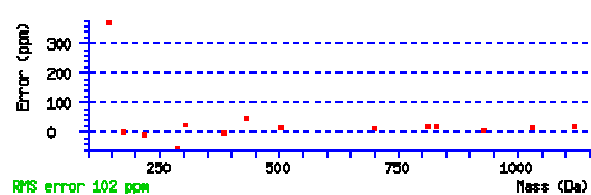
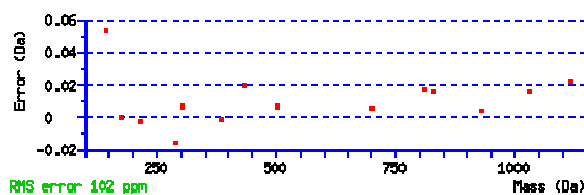
Monoisotopic mass of neutral peptide Mr(calc): 1330.6365

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 67 Expect: 1.1e-005

Matches : 14/118 fragment ions using 27 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233	70.0287	35.5180	S							13
2	145.0608	73.0340	127.0502	64.0287	G	1244.6117	622.8095	1227.5852	614.2962	1226.6012	613.8042	12
3	216.0979	108.5526	198.0873	99.5473	A	1187.5903	594.2988	1170.5637	585.7855	1169.5797	585.2935	11
4	303.1299	152.0686	285.1193	143.0633	S	1116.5531	558.7802	1099.5266	550.2669	1098.5426	549.7749	10
5	402.1983	201.6028	384.1878	192.5975	V	1029.5211	515.2642	1012.4946	506.7509	1011.5106	506.2589	9
6	503.2460	252.1266	485.2354	243.1214	T	930.4527	465.7300	913.4262	457.2167	912.4421	456.7247	8
7	632.2886	316.6479	614.2780	307.6427	E	829.4050	415.2061	812.3785	406.6929	811.3945	406.2009	7
8	729.3414	365.1743	711.3308	356.1690	P	700.3624	350.6849	683.3359	342.1716	682.3519	341.6796	6
9	828.4098	414.7085	810.3992	405.7032	V	603.3097	302.1585	586.2831	293.6452	585.2991	293.1532	5
10	899.4469	450.2271	881.4363	441.2218	A	504.2413	252.6243	487.2147	244.1110	486.2307	243.6190	4
11	1028.4895	514.7484	1010.4789	505.7431	E	433.2041	217.1057	416.1776	208.5924	415.1936	208.1004	3
12	1157.5321	579.2697	1139.5215	570.2644	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
13					R	175.1190	88.0631	158.0924	79.5498			1



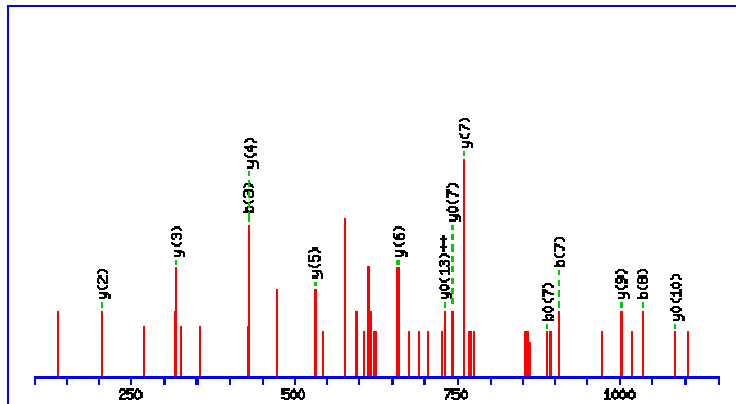
Peptide Number: 52358

MS/MS Fragmentation of **EHYDFLTEVLTNGK**Found in **IPI00002856** in **IPI_human**, Tax_Id=9606 Gene_Symbol=STEAP4 Uncharacterized protein

Match to Query 8838: 1906.961772 from(636.661200,3+) index(26576)

Title: Elution from: 84.3 to 84.3 period: 0 cycle: 3321 experiment: 3 polarity: +

Data file 120208ry_Tig120slc-P8_1_4.mgf



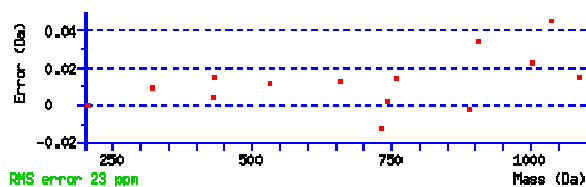
Monoisotopic mass of neutral peptide Mr(calc): 1906.9312

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

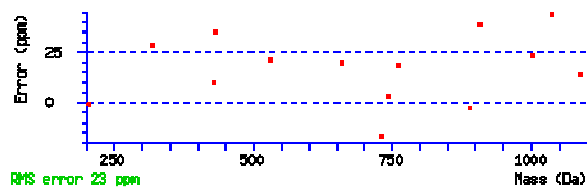
Ions Score: 46 Expect: 0.0019

Matches : 14/144 fragment ions using 20 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							16
2	267.1088	134.0580			249.0982	125.0527	H	1778.8959	889.9516	1761.8694	881.4383	1760.8854	880.9463	15
3	430.1721	215.5897			412.1615	206.5844	Y	1641.8370	821.4222	1624.8105	812.9089	1623.8265	812.4169	14
4	545.1991	273.1032			527.1885	264.0979	D	1478.7737	739.8905	1461.7472	731.3772	1460.7631	730.8852	13
5	692.2675	346.6374			674.2569	337.6321	F	1363.7468	682.3770	1346.7202	673.8637	1345.7362	673.3717	12
6	805.3515	403.1794			787.3410	394.1741	L	1216.6783	608.8428	1199.6518	600.3295	1198.6678	599.8375	11
7	906.3992	453.7032			888.3886	444.6980	T	1103.5943	552.3008	1086.5677	543.7875	1085.5837	543.2955	10
8	1035.4418	518.2245			1017.4312	509.2193	E	1002.5466	501.7769	985.5201	493.2637	984.5360	492.7717	9
9	1148.5259	574.7666			1130.5153	565.7613	L	873.5040	437.2556	856.4775	428.7424	855.4934	428.2504	8
10	1249.5735	625.2904			1231.5630	616.2851	T	760.4199	380.7136	743.3934	372.2003	742.4094	371.7083	7
11	1378.6161	689.8117			1360.6056	680.8064	E	659.3723	330.1898	642.3457	321.6765	641.3617	321.1845	6
12	1477.6846	739.3459			1459.6740	730.3406	V	530.3297	265.6685	513.3031	257.1552			5
13	1590.7686	795.8879			1572.7581	786.8827	L	431.2613	216.1343	414.2347	207.6210			4
14	1704.8115	852.9094	1687.7850	844.3961	1686.8010	843.9041	N	318.1772	159.5922	301.1506	151.0790			3
15	1761.8330	881.4201	1744.8065	872.9069	1743.8224	872.4149	G	204.1343	102.5708	187.1077	94.0575			2
16							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 23 ppm



RMS error 23 ppm

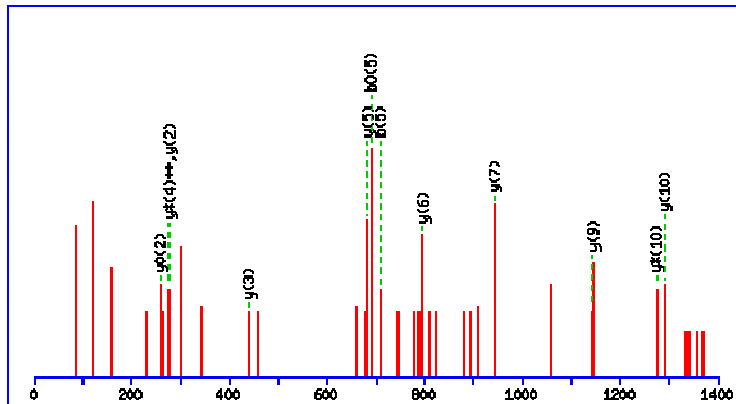
Peptide Number: 52623

MS/MS Fragmentation of **EYWNDVFSDFLNEYEK**Found in **IPI00026555** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TRMU Isoform 1 of Mitochondrial tRNA-specific 2-thiouridylase 1

Match to Query 15190: 2096.891592 from(699.971140,3+) index(34723)

Title: Elution from: 92.3166666666667 to 92.3166666666667 period: 0 cycle: 3517 experiment: 2 polarity: +

Data file 120212ry_aHDF1388-P9_3_4.mgf



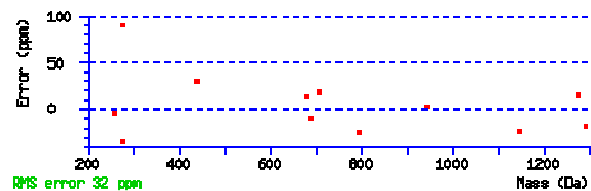
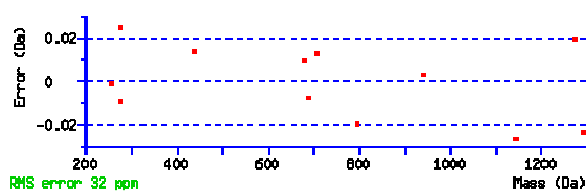
Monoisotopic mass of neutral peptide Mr(calc): 2096.9003

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 34 Expect: 0.0042

Matches : 12/172 fragment ions using 22 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							16
2	293.1132	147.0602			275.1026	138.0550	Y	1968.8650	984.9362	1951.8385	976.4229	1950.8545	975.9309	15
3	479.1925	240.0999			461.1819	231.0946	W	1805.8017	903.4045	1788.7752	894.8912	1787.7911	894.3992	14
4	593.2354	297.1214	576.2089	288.6081	575.2249	288.1161	N	1619.7224	810.3648	1602.6958	801.8516	1601.7118	801.3596	13
5	708.2624	354.6348	691.2358	346.1216	690.2518	345.6295	D	1505.6795	753.3434	1488.6529	744.8301	1487.6689	744.3381	12
6	807.3308	404.1690	790.3042	395.6558	789.3202	395.1638	V	1390.6525	695.8299	1373.6260	687.3166	1372.6420	686.8246	11
7	954.3992	477.7032	937.3727	469.1900	936.3886	468.6980	F	1291.5841	646.2957	1274.5576	637.7824	1273.5735	637.2904	10
8	1041.4312	521.2193	1024.4047	512.7060	1023.4207	512.2140	S	1144.5157	572.7615	1127.4891	564.2482	1126.5051	563.7562	9
9	1156.4582	578.7327	1139.4316	570.2195	1138.4476	569.7274	D	1057.4837	529.2455	1040.4571	520.7322	1039.4731	520.2402	8
10	1303.5266	652.2669	1286.5000	643.7537	1285.5160	643.2617	F	942.4567	471.7320	925.4302	463.2187	924.4462	462.7267	7
11	1416.6107	708.8090	1399.5841	700.2957	1398.6001	699.8037	L	795.3883	398.1978	778.3618	389.6845	777.3777	389.1925	6
12	1530.6536	765.8304	1513.6270	757.3172	1512.6430	756.8251	N	682.3042	341.6558	665.2777	333.1425	664.2937	332.6505	5
13	1659.6962	830.3517	1642.6696	821.8385	1641.6856	821.3464	E	568.2613	284.6343	551.2348	276.1210	550.2508	275.6290	4
14	1822.7595	911.8834	1805.7330	903.3701	1804.7489	902.8781	Y	439.2187	220.1130	422.1922	211.5997	421.2082	211.1077	3
15	1951.8021	976.4047	1934.7756	967.8914	1933.7915	967.3994	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
16							K	147.1128	74.0600	130.0863	65.5468			1



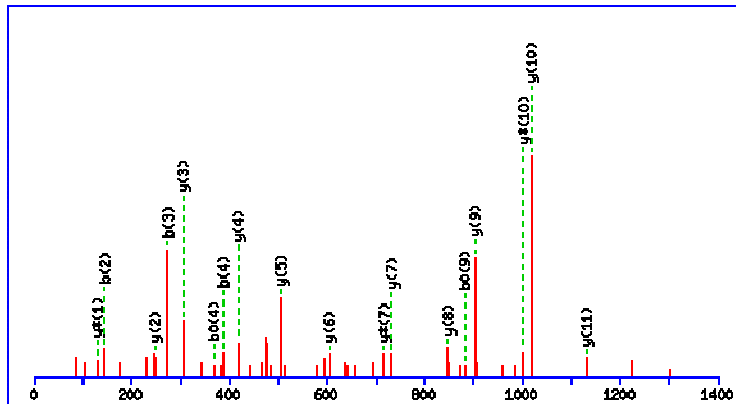
Peptide Number: 52707

MS/MS Fragmentation of **SGELNGDQVSLGTK**Found in **IPI00795249** in **IPI_human**, Tax_Id=9606 Gene_Symbol=C12orf43 Uncharacterized protein C12orf43

Match to Query 24078: 1403.696308 from(702.855430,2+) index(993)

Title: Elution from: 2.46666666666667 to 2.46666666666667 period: 0 cycle: 95 experiment: 10 polarity: +

Data file 120212ry_414C2-43_3_2.mgf



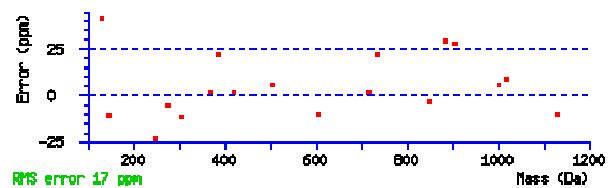
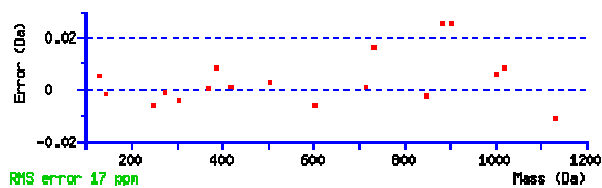
Monoisotopic mass of neutral peptide Mr(calc): 1403.6892

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 64 Expect: 2.7e-005

Matches : 18/146 fragment ions using 40 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							14
2	145.0608	73.0340			127.0502	64.0287	G	1317.6645	659.3359	1300.6379	650.8226	1299.6539	650.3306	13
3	274.1034	137.5553			256.0928	128.5500	E	1260.6430	630.8251	1243.6165	622.3119	1242.6325	621.8199	12
4	387.1874	194.0974			369.1769	185.0921	L	1131.6004	566.3039	1114.5739	557.7906	1113.5899	557.2986	11
5	501.2304	251.1188	484.2038	242.6055	483.2198	242.1135	N	1018.5164	509.7618	1001.4898	501.2485	1000.5058	500.7565	10
6	558.2518	279.6295	541.2253	271.1163	540.2413	270.6243	G	904.4734	452.7404	887.4469	444.2271	886.4629	443.7351	9
7	673.2788	337.1430	656.2522	328.6297	655.2682	328.1377	D	847.4520	424.2296	830.4254	415.7164	829.4414	415.2243	8
8	801.3373	401.1723	784.3108	392.6590	783.3268	392.1670	Q	732.4250	366.7162	715.3985	358.2029	714.4145	357.7109	7
9	900.4058	450.7065	883.3792	442.1932	882.3952	441.7012	V	604.3665	302.6869	587.3399	294.1736	586.3559	293.6816	6
10	987.4378	494.2225	970.4112	485.7093	969.4272	485.2172	S	505.2980	253.1527	488.2715	244.6394	487.2875	244.1474	5
11	1100.5218	550.7646	1083.4953	542.2513	1082.5113	541.7593	L	418.2660	209.6366	401.2395	201.1234	400.2554	200.6314	4
12	1157.5433	579.2753	1140.5168	570.7620	1139.5327	570.2700	G	305.1819	153.0946	288.1554	144.5813	287.1714	144.0893	3
13	1258.5910	629.7991	1241.5644	621.2859	1240.5804	620.7938	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
14							K	147.1128	74.0600	130.0863	65.5468			1



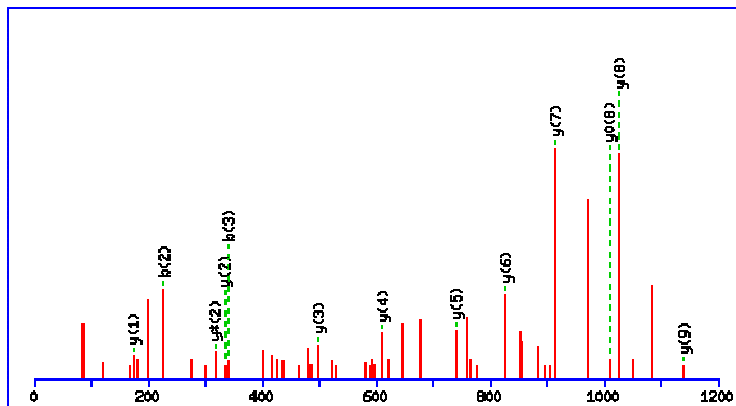
Peptide Number: 52837

MS/MS Fragmentation of **LLLSSELYCR**Found in **IPI00884928** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CAMSAP1 Isoform 3 of Calmodulin-regulated spectrin-associated protein 1

Match to Query 17082: 1252.653928 from(627.334240,2+) index(44684)

Title: Elution from: 108.416666666667 to 108.416666666667 period: 0 cycle: 4095 experiment: 7 polarity: +

Data file 120212ry_414C2-43_3_2.mgf



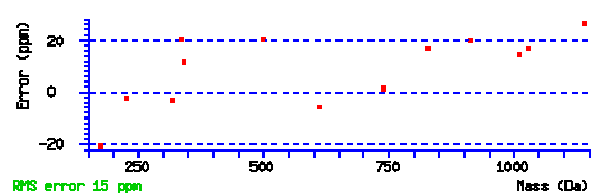
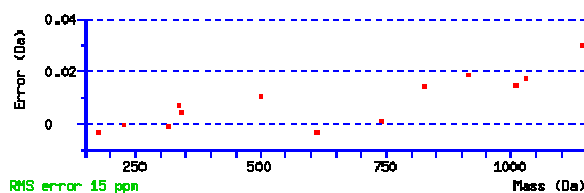
Monoisotopic mass of neutral peptide Mr(calc): 1252.6485

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 45 Expect: 0.0019

Matches : 13/76 fragment ions using 39 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							10
2	227.1754	114.0913			L	1140.5718	570.7895	1123.5452	562.2762	1122.5612	561.7842	9
3	340.2595	170.6334			L	1027.4877	514.2475	1010.4612	505.7342	1009.4771	505.2422	8
4	427.2915	214.1494	409.2809	205.1441	S	914.4036	457.7055	897.3771	449.1922	896.3931	448.7002	7
5	514.3235	257.6654	496.3130	248.6601	S	827.3716	414.1894	810.3451	405.6762	809.3610	405.1842	6
6	643.3661	322.1867	625.3556	313.1814	E	740.3396	370.6734	723.3130	362.1602	722.3290	361.6681	5
7	756.4502	378.7287	738.4396	369.7234	L	611.2970	306.1521	594.2704	297.6389			4
8	919.5135	460.2604	901.5029	451.2551	Y	498.2129	249.6101	481.1864	241.0968			3
9	1079.5442	540.2757	1061.5336	531.2704	C	335.1496	168.0784	318.1231	159.5652			2
10					R	175.1190	88.0631	158.0924	79.5498			1



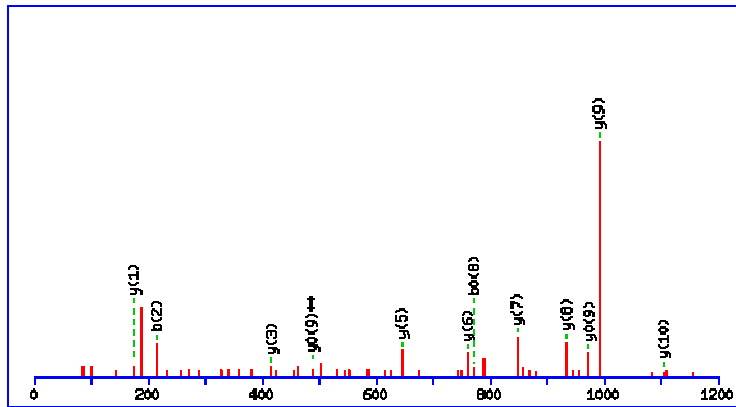
Peptide Number: 52950

MS/MS Fragmentation of **TLGSSDTQQLR**Found in **IPI00013743** in **IPI_human**, Tax_Id=9606 Gene_Symbol=BUD13 Isoform 1 of BUD13 homolog

Match to Query 19158: 1204.607968 from(603.311260,2+) index(18703)

Title: Elution from: 77.6166666666667 to 77.6166666666667 period: 0 cycle: 7928 experiment: 10 polarity:+

Data file 120214ry_32R1-32_4_1.mgf



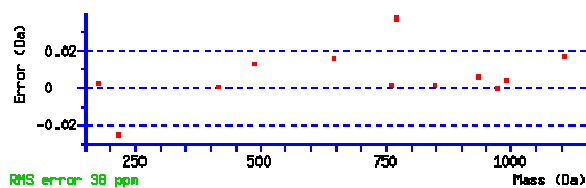
Monoisotopic mass of neutral peptide Mr(calc): 1204.6048

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

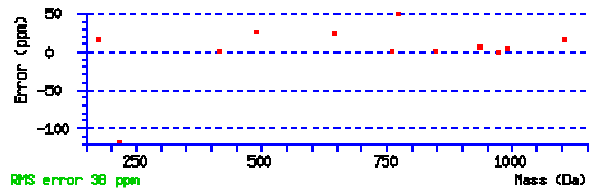
Ions Score: 59 Expect: 0.00012

Matches : 12/98 fragment ions using 22 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							11
2	215.1390	108.0731			197.1285	99.0679	L	1104.5644	552.7858	1087.5378	544.2726	1086.5538	543.7805	10
3	272.1605	136.5839			254.1499	127.5786	G	991.4803	496.2438	974.4538	487.7305	973.4697	487.2385	9
4	359.1925	180.0999			341.1819	171.0946	S	934.4588	467.7331	917.4323	459.2198	916.4483	458.7278	8
5	446.2245	223.6159			428.2140	214.6106	S	847.4268	424.2170	830.4003	415.7038	829.4163	415.2118	7
6	561.2515	281.1294			543.2409	272.1241	D	760.3948	380.7010	743.3682	372.1878	742.3842	371.6958	6
7	662.2992	331.6532			644.2886	322.6479	T	645.3679	323.1876	628.3413	314.6743	627.3573	314.1823	5
8	790.3577	395.6825	773.3312	387.1692	772.3472	386.6772	Q	544.3202	272.6637	527.2936	264.1504			4
9	918.4163	459.7118	901.3898	451.1985	900.4058	450.7065	Q	416.2616	208.6344	399.2350	200.1212			3
10	1031.5004	516.2538	1014.4738	507.7406	1013.4898	507.2485	L	288.2030	144.6051	271.1765	136.0919			2
11							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 38 ppm



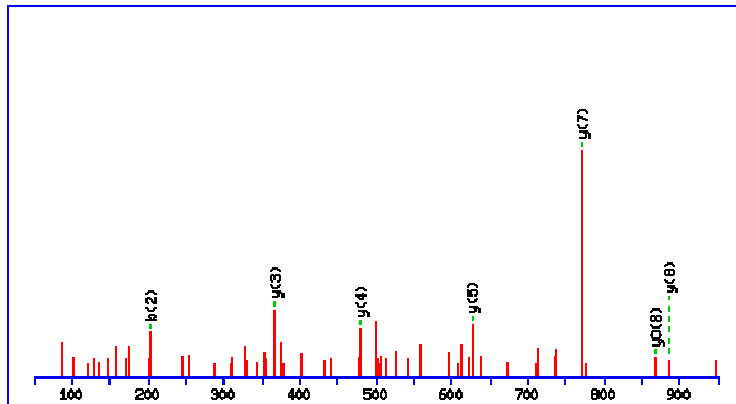
RMS error 38 ppm

Peptide Number: 53028MS/MS Fragmentation of **SDGSFIGYK**Found in **IPI00012870** in **IPI_human**, Tax_Id=9606 Gene_Symbol=AKT2 RAC-beta serine/threonine-protein kinase

Match to Query 5153: 972.461308 from(487.237930,2+) index(3790)

Title: Elution from: 9.61666666666667 to 9.61666666666667 period: 0 cycle: 368 experiment: 4 polarity: +

Data file 120208ry_Tig120slc-P8_3_2.mgf



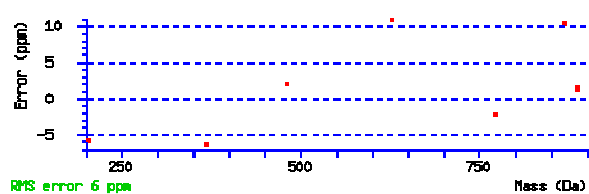
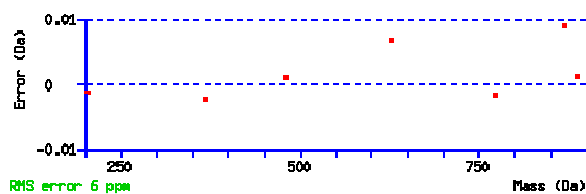
Monoisotopic mass of neutral peptide Mr(calc): 972.4553

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 41 Expect: 0.0024

Matches : 7/70 fragment ions using 9 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233	70.0287	35.5180	S							9
2	203.0662	102.0368	185.0557	93.0315	D	886.4305	443.7189	869.4040	435.2056	868.4199	434.7136	8
3	260.0877	130.5475	242.0771	121.5422	G	771.4036	386.2054	754.3770	377.6921	753.3930	377.2001	7
4	347.1197	174.0635	329.1092	165.0582	S	714.3821	357.6947	697.3556	349.1814	696.3715	348.6894	6
5	494.1882	247.5977	476.1776	238.5924	F	627.3501	314.1787	610.3235	305.6654			5
6	607.2722	304.1397	589.2617	295.1345	I	480.2817	240.6445	463.2551	232.1312			4
7	664.2937	332.6505	646.2831	323.6452	G	367.1976	184.1024	350.1710	175.5892			3
8	827.3570	414.1821	809.3464	405.1769	Y	310.1761	155.5917	293.1496	147.0784			2
9					K	147.1128	74.0600	130.0863	65.5468			1



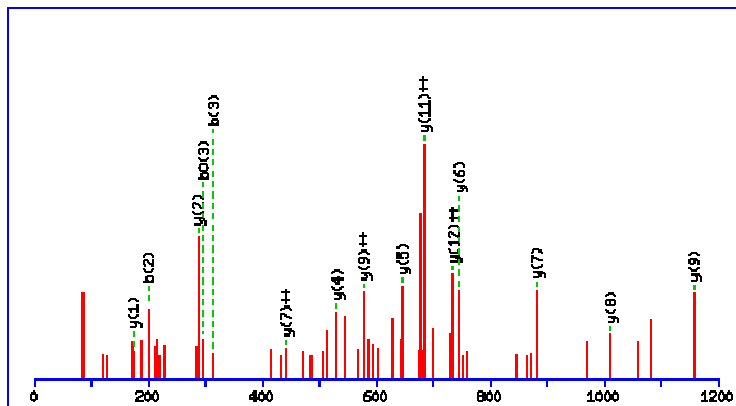
Peptide Number: 53407

MS/MS Fragmentation of **VTLVFEHVDQDLR**Found in **IPI00007811** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CDK4 Cyclin-dependent kinase 4

Match to Query 15883: 1569.813372 from(524.278400,3+) index(3456)

Title: Elution from: 8.55 to 8.55 period: 0 cycle: 316 experiment: 3 polarity: +

Data file 120124ry_414C2-43_1_3.mgf



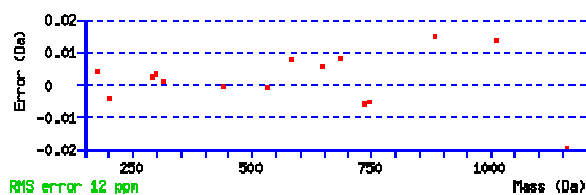
Monoisotopic mass of neutral peptide Mr(calc): 1569.8151

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

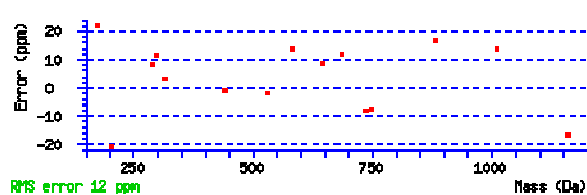
Ions Score: 44 Expect: 0.0026

Matches : 15/120 fragment ions using 30 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							13
2	201.1234	101.0653			183.1128	92.0600	T	1471.7540	736.3806	1454.7274	727.8673	1453.7434	727.3753	12
3	314.2074	157.6074			296.1969	148.6021	L	1370.7063	685.8568	1353.6797	677.3435	1352.6957	676.8515	11
4	413.2758	207.1416			395.2653	198.1363	V	1257.6222	629.3148	1240.5957	620.8015	1239.6117	620.3095	10
5	560.3443	280.6758			542.3337	271.6705	F	1158.5538	579.7805	1141.5273	571.2673	1140.5432	570.7753	9
6	689.3869	345.1971			671.3763	336.1918	E	1011.4854	506.2463	994.4588	497.7331	993.4748	497.2411	8
7	826.4458	413.7265			808.4352	404.7212	H	882.4428	441.7250	865.4163	433.2118	864.4322	432.7198	7
8	925.5142	463.2607			907.5036	454.2554	V	745.3839	373.1956	728.3573	364.6823	727.3733	364.1903	6
9	1040.5411	520.7742			1022.5306	511.7689	D	646.3155	323.6614	629.2889	315.1481	628.3049	314.6561	5
10	1168.5997	584.8035	1151.5732	576.2902	1150.5891	575.7982	Q	531.2885	266.1479	514.2620	257.6346	513.2780	257.1426	4
11	1283.6266	642.3170	1266.6001	633.8037	1265.6161	633.3117	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
12	1396.7107	698.8590	1379.6842	690.3457	1378.7001	689.8537	L	288.2030	144.6051	271.1765	136.0919			2
13							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 12 ppm



RMS error 12 ppm

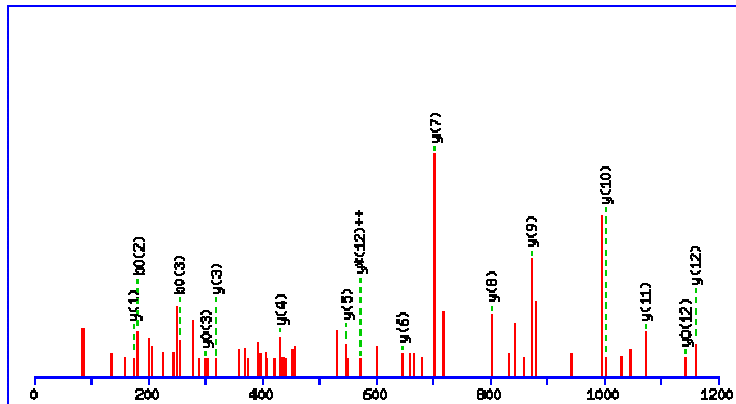
Peptide Number: 53490

MS/MS Fragmentation of **ISAEAVGVDISGR**Found in **IPI00304655** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CEP44 Isoform 1 of Centrosomal protein of 44 kDa

Match to Query 18845: 1272.660468 from(637.337510,2+) index(25471)

Title: Elution from: 61.0166666666667 to 61.0166666666667 period: 0 cycle: 2258 experiment: 9 polarity:+

Data file 120129ry_604A1-46_3_2.mgf



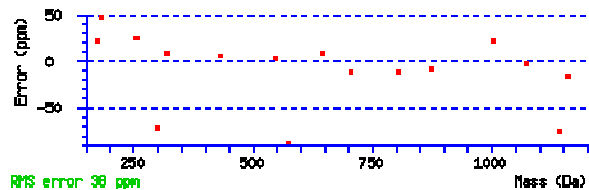
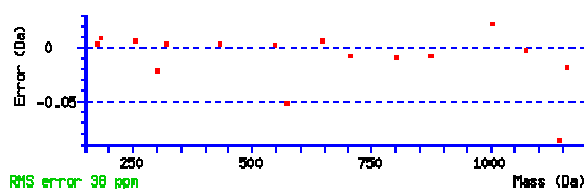
Monoisotopic mass of neutral peptide Mr(calc): 1272.6674

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 58 Expect: 0.00012

Matches : 16/114 fragment ions using 44 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			I							13
2	201.1234	101.0653	183.1128	92.0600	S	1160.5906	580.7989	1143.5640	572.2857	1142.5800	571.7937	12
3	272.1605	136.5839	254.1499	127.5786	A	1073.5586	537.2829	1056.5320	528.7696	1055.5480	528.2776	11
4	401.2031	201.1052	383.1925	192.0999	E	1002.5215	501.7644	985.4949	493.2511	984.5109	492.7591	10
5	472.2402	236.6237	454.2296	227.6184	A	873.4789	437.2431	856.4523	428.7298	855.4683	428.2378	9
6	571.3086	286.1579	553.2980	277.1527	V	802.4417	401.7245	785.4152	393.2112	784.4312	392.7192	8
7	628.3301	314.6687	610.3195	305.6634	G	703.3733	352.1903	686.3468	343.6770	685.3628	343.1850	7
8	727.3985	364.2029	709.3879	355.1976	V	646.3519	323.6796	629.3253	315.1663	628.3413	314.6743	6
9	842.4254	421.7163	824.4149	412.7111	D	547.2835	274.1454	530.2569	265.6321	529.2729	265.1401	5
10	955.5095	478.2584	937.4989	469.2531	I	432.2565	216.6319	415.2300	208.1186	414.2459	207.6266	4
11	1042.5415	521.7744	1024.5310	512.7691	S	319.1724	160.0899	302.1459	151.5766	301.1619	151.0846	3
12	1099.5630	550.2851	1081.5524	541.2798	G	232.1404	116.5738	215.1139	108.0606			2
13					R	175.1190	88.0631	158.0924	79.5498			1

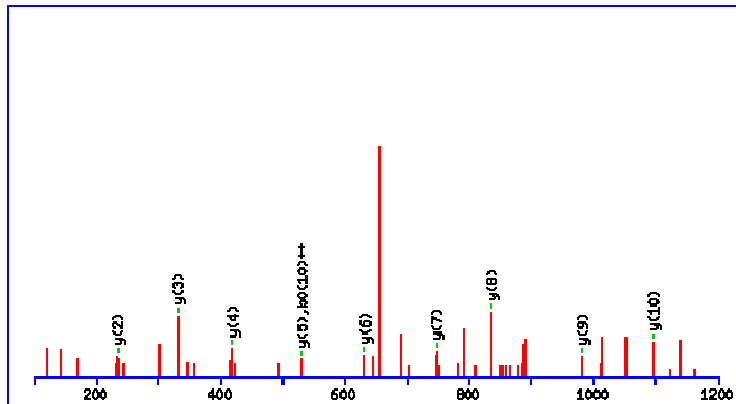


Peptide Number: 53614MS/MS Fragmentation of **ESDFSDTLSPSK**Found in **IPI00794566** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SLMAP Isoform 2 of Sarcolemmal membrane-associated protein

Match to Query 19503: 1311.594128 from(656.804340,2+) index(5460)

Title: Elution from: 13.5 to 13.5 period: 0 cycle: 516 experiment: 10 polarity: +

Data file 120212ry_aHDF1388-P9_2_2.mgf



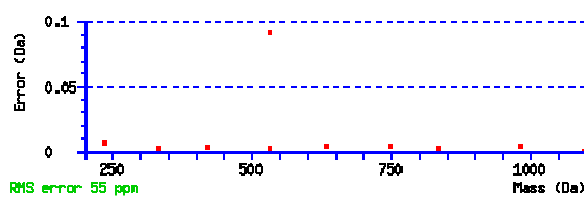
Monoisotopic mass of neutral peptide Mr(calcd): 1311.5830

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

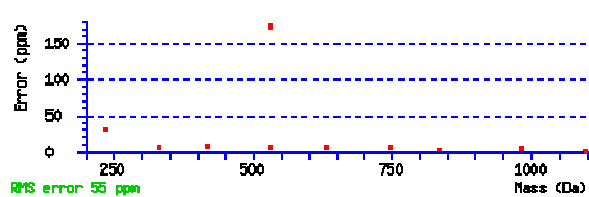
Ions Score: 43 Expect: 0.0016

Matches : 10/108 fragment ions using 30 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286	112.0393	56.5233	E							12
2	217.0819	109.0446	199.0713	100.0393	S	1183.5477	592.2775	1166.5212	583.7642	1165.5372	583.2722	11
3	332.1088	166.5581	314.0983	157.5528	D	1096.5157	548.7615	1079.4891	540.2482	1078.5051	539.7562	10
4	479.1773	240.0923	461.1667	231.0870	F	981.4888	491.2480	964.4622	482.7347	963.4782	482.2427	9
5	566.2093	283.6083	548.1987	274.6030	S	834.4203	417.7138	817.3938	409.2005	816.4098	408.7085	8
6	681.2362	341.1218	663.2257	332.1165	D	747.3883	374.1978	730.3618	365.6845	729.3777	365.1925	7
7	782.2839	391.6456	764.2733	382.6403	T	632.3614	316.6843	615.3348	308.1710	614.3508	307.6790	6
8	895.3680	448.1876	877.3574	439.1823	L	531.3137	266.1605	514.2871	257.6472	513.3031	257.1552	5
9	982.4000	491.7036	964.3894	482.6984	S	418.2296	209.6184	401.2031	201.1052	400.2191	200.6132	4
10	1079.4528	540.2300	1061.4422	531.2247	P	331.1976	166.1024	314.1710	157.5892	313.1870	157.0972	3
11	1166.4848	583.7460	1148.4742	574.7407	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
12					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 55 ppm



RMS error 55 ppm

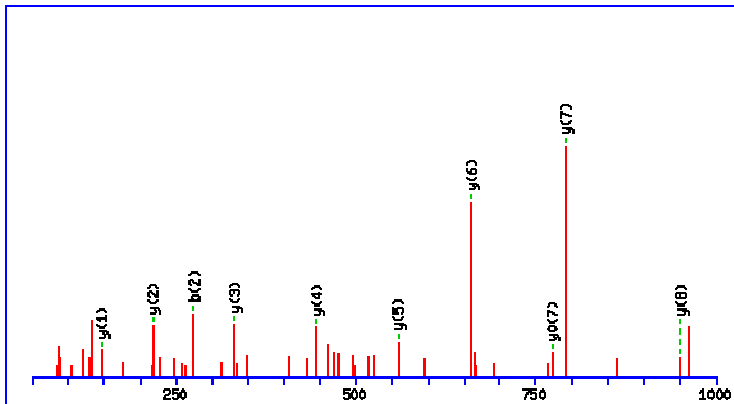
Peptide Number: 53798**MS/MS Fragmentation of NCMTDLLAK**

Found in **IPI00024670** in **IPI_human**, Tax_Id=9606 Gene_Symbol=REEP5 Receptor expression-enhancing protein 5

Match to Query 10376: 1064.491008 from(533.252780,2+) index(35826)

Title: Elution from: 85.8333333333333 to 85.8333333333333 period: 0 cycle: 3168 experiment: 7 polarity:+

Data file 120118ry_201B7-32_1_2.mgf



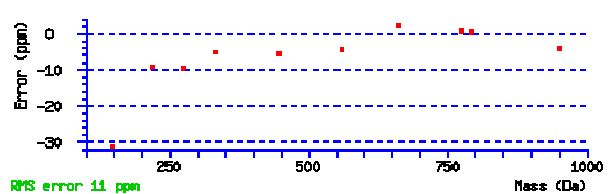
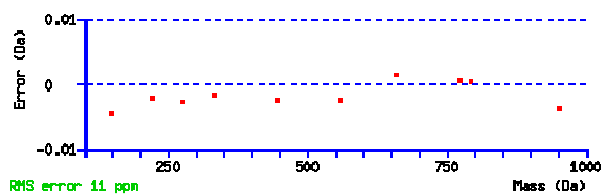
Monoisotopic mass of neutral peptide Mr(calc): 1064.4994

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 52 **Expect:** 0.0003

Matches : 10/82 fragment ions using 26 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							9
2	275.0809	138.0441	258.0543	129.5308			C	951.4638	476.2355	934.4373	467.7223	933.4532	467.2303	8
3	406.1213	203.5643	389.0948	195.0510			M	791.4332	396.2202	774.4066	387.7069	773.4226	387.2149	7
4	507.1690	254.0881	490.1425	245.5749	489.1585	245.0829	T	660.3927	330.7000	643.3661	322.1867	642.3821	321.6947	6
5	622.1960	311.6016	605.1694	303.0883	604.1854	302.5963	D	559.3450	280.1761	542.3184	271.6629	541.3344	271.1708	5
6	735.2800	368.1436	718.2535	359.6304	717.2695	359.1384	L	444.3180	222.6627	427.2915	214.1494			4
7	848.3641	424.6857	831.3375	416.1724	830.3535	415.6804	L	331.2340	166.1206	314.2074	157.6074			3
8	919.4012	460.2042	902.3747	451.6910	901.3906	451.1990	A	218.1499	109.5786	201.1234	101.0653			2
9							K	147.1128	74.0600	130.0863	65.5468			1



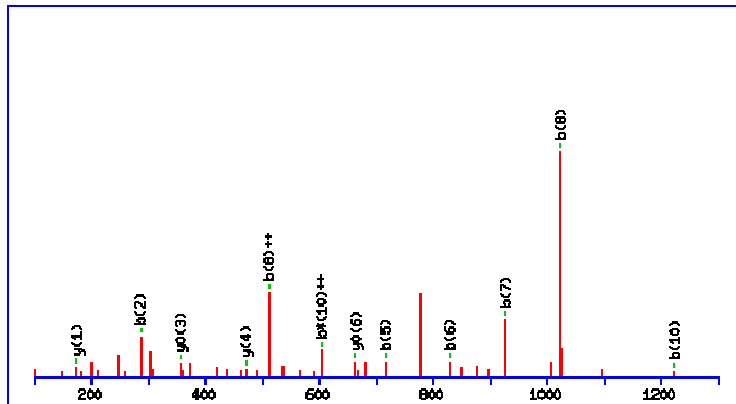
Peptide Number: 54407

MS/MS Fragmentation of **VWRDCLPPSLR**Found in **IPI00169381** in **IPI_human**, Tax_Id=9606 Gene_Symbol=HUS1B Checkpoint protein HUS1B

Match to Query 31466: 1397.699488 from(699.857020,2+) index(15820)

Title: Elution from: 38.0666666666667 to 38.0666666666667 period: 0 cycle: 1421 experiment: 6 polarity: +

Data file 120126ry_585A1-55_2_2.mgf



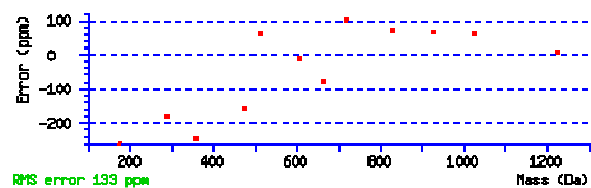
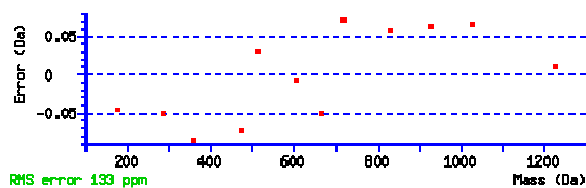
Monoisotopic mass of neutral peptide Mr(calc): 1397.7238

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 38 Expect: 0.01

Matches : 12/106 fragment ions using 20 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							11
2	286.1550	143.5811					W	1299.6627	650.3350	1282.6361	641.8217	1281.6521	641.3297	10
3	442.2561	221.6317	425.2296	213.1184			R	1113.5833	557.2953	1096.5568	548.7820	1095.5728	548.2900	9
4	557.2831	279.1452	540.2565	270.6319	539.2725	270.1399	D	957.4822	479.2448	940.4557	470.7315	939.4717	470.2395	8
5	717.3137	359.1605	700.2872	350.6472	699.3031	350.1552	C	842.4553	421.7313	825.4287	413.2180	824.4447	412.7260	7
6	830.3978	415.7025	813.3712	407.1892	812.3872	406.6972	L	682.4246	341.7160	665.3981	333.2027	664.4141	332.7107	6
7	927.4505	464.2289	910.4240	455.7156	909.4400	455.2236	P	569.3406	285.1739	552.3140	276.6606	551.3300	276.1686	5
8	1024.5033	512.7553	1007.4767	504.2420	1006.4927	503.7500	P	472.2878	236.6475	455.2613	228.1343	454.2772	227.6423	4
9	1111.5353	556.2713	1094.5088	547.7580	1093.5248	547.2660	S	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
10	1224.6194	612.8133	1207.5928	604.3001	1206.6088	603.8081	L	288.2030	144.6051	271.1765	136.0919			2
11							R	175.1190	88.0631	158.0924	79.5498			1



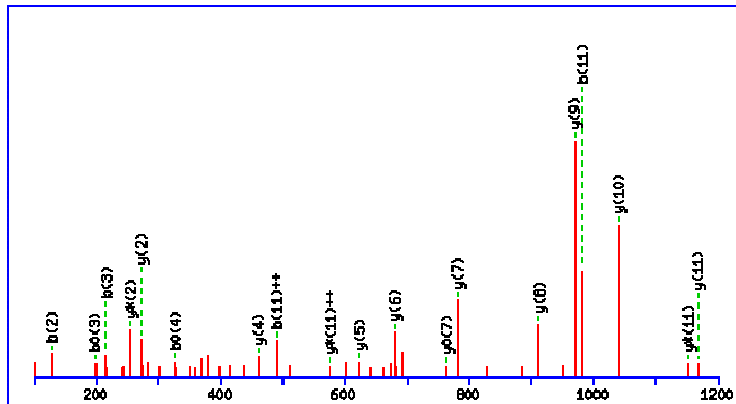
Peptide Number: 54442

MS/MS Fragmentation of **GASQAGMTGYGMPR**Found in **IPI00550363** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TAGLN2 Transgelin-2

Match to Query 24719: 1382.612088 from(692.313320,2+) index(7432)

Title: Elution from: 18.4333333333333 to 18.4333333333333 period: 0 cycle: 699 experiment: 9 polarity: +

Data file 120210ry_32R1-32_2_2.mgf



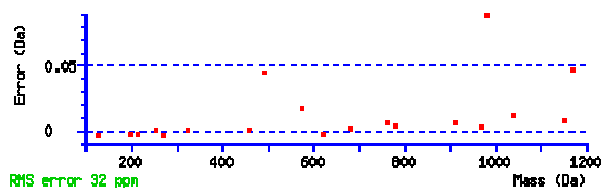
Monoisotopic mass of neutral peptide Mr(calc): 1382.6071

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

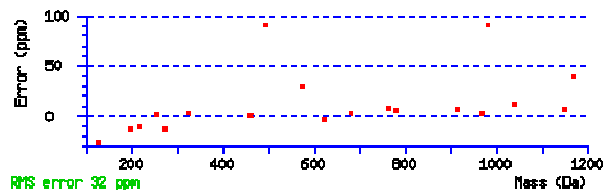
Ions Score: 68 Expect: 4.7e-006

Matches : 19/134 fragment ions using 29 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							14
2	129.0659	65.0366					A	1326.5929	663.8001	1309.5664	655.2868	1308.5824	654.7948	13
3	216.0979	108.5526			198.0873	99.5473	S	1255.5558	628.2815	1238.5293	619.7683	1237.5452	619.2763	12
4	344.1565	172.5819	327.1299	164.0686	326.1459	163.5766	Q	1168.5238	584.7655	1151.4972	576.2523	1150.5132	575.7602	11
5	415.1936	208.1004	398.1670	199.5872	397.1830	199.0951	A	1040.4652	520.7362	1023.4387	512.2230	1022.4546	511.7310	10
6	472.2150	236.6112	455.1885	228.0979	454.2045	227.6059	G	969.4281	485.2177	952.4015	476.7044	951.4175	476.2124	9
7	603.2555	302.1314	586.2290	293.6181	585.2450	293.1261	M	912.4066	456.7069	895.3801	448.1937	894.3961	447.7017	8
8	704.3032	352.6552	687.2767	344.1420	686.2926	343.6500	T	781.3661	391.1867	764.3396	382.6734	763.3556	382.1814	7
9	761.3247	381.1660	744.2981	372.6527	743.3141	372.1607	G	680.3185	340.6629	663.2919	332.1496			6
10	924.3880	462.6976	907.3614	454.1844	906.3774	453.6924	Y	623.2970	312.1521	606.2704	303.6389			5
11	981.4095	491.2084	964.3829	482.6951	963.3989	482.2031	G	460.2337	230.6205	443.2071	222.1072			4
12	1112.4499	556.7286	1095.4234	548.2153	1094.4394	547.7233	M	403.2122	202.1097	386.1857	193.5965			3
13	1209.5027	605.2550	1192.4762	596.7417	1191.4921	596.2497	P	272.1717	136.5895	255.1452	128.0762			2
14							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 32 ppm



RMS error 32 ppm

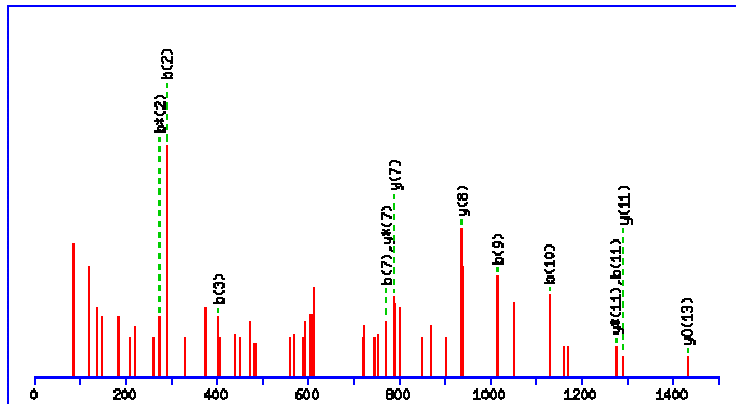
Peptide Number: 54893

MS/MS Fragmentation of **YQIPLSADQLFTQSVLDK**Found in **IPI00000897** in **IPI_human**, Tax_Id=9606 Gene_Symbol=HELZ HELZ protein

Match to Query 27339: 2065.071582 from(689.364470,3+) index(44886)

Title: Elution from: 115.016666666667 to 115.016666666667 period: 0 cycle: 4342 experiment: 8 polarity:+

Data file 120210ry_585A1-55_3_3.mgf



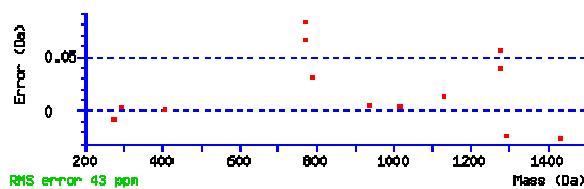
Monoisotopic mass of neutral peptide Mr(calc): 2065.0732

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

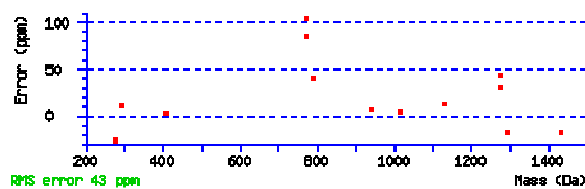
Ions Score: 40 Expect: 0.0067

Matches : 13/190 fragment ions using 14 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389					Y							18
2	292.1292	146.5682	275.1026	138.0550			Q	1903.0171	952.0122	1885.9906	943.4989	1885.0066	943.0069	17
3	405.2132	203.1103	388.1867	194.5970			I	1774.9585	887.9829	1757.9320	879.4696	1756.9480	878.9776	16
4	502.2660	251.6366	485.2395	243.1234			P	1661.8745	831.4409	1644.8479	822.9276	1643.8639	822.4356	15
5	615.3501	308.1787	598.3235	299.6654			L	1564.8217	782.9145	1547.7952	774.4012	1546.8112	773.9092	14
6	702.3821	351.6947	685.3556	343.1814	684.3715	342.6894	S	1451.7377	726.3725	1434.7111	717.8592	1433.7271	717.3672	13
7	773.4192	387.2132	756.3927	378.7000	755.4087	378.2080	A	1364.7056	682.8564	1347.6791	674.3432	1346.6951	673.8512	12
8	888.4462	444.7267	871.4196	436.2134	870.4356	435.7214	D	1293.6685	647.3379	1276.6420	638.8246	1275.6579	638.3326	11
9	1016.5047	508.7560	999.4782	500.2427	998.4942	499.7507	Q	1178.6416	589.8244	1161.6150	581.3111	1160.6310	580.8191	10
10	1129.5888	565.2980	1112.5623	556.7848	1111.5782	556.2928	L	1050.5830	525.7951	1033.5564	517.2819	1032.5724	516.7898	9
11	1276.6572	638.8322	1259.6307	630.3190	1258.6467	629.8270	F	937.4989	469.2531	920.4724	460.7398	919.4884	460.2478	8
12	1377.7049	689.3561	1360.6783	680.8428	1359.6943	680.3508	T	790.4305	395.7189	773.4040	387.2056	772.4199	386.7136	7
13	1505.7635	753.3854	1488.7369	744.8721	1487.7529	744.3801	Q	689.3828	345.1951	672.3563	336.6818	671.3723	336.1898	6
14	1592.7955	796.9014	1575.7690	788.3881	1574.7849	787.8961	S	561.3243	281.1658	544.2977	272.6525	543.3137	272.1605	5
15	1691.8639	846.4356	1674.8374	837.9223	1673.8534	837.4303	V	474.2922	237.6498	457.2657	229.1365	456.2817	228.6445	4
16	1804.9480	902.9776	1787.9214	894.4644	1786.9374	893.9723	L	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
17	1919.9749	960.4911	1902.9484	951.9778	1901.9644	951.4858	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
18							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 43 ppm



RMS error 43 ppm

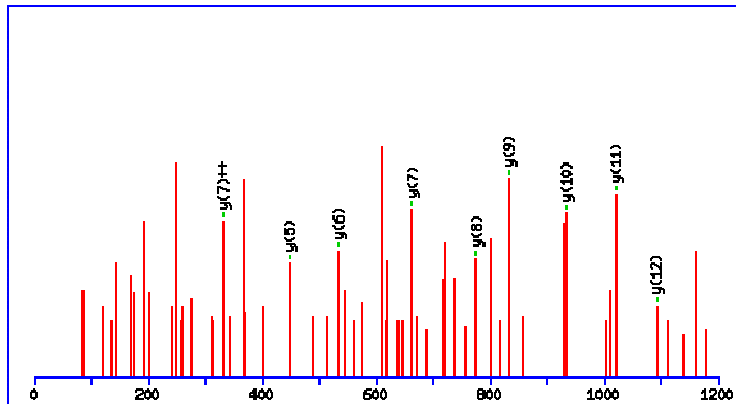
Peptide Number: 54903

MS/MS Fragmentation of **AFASTGLES GASGR**Found in **IPI00397015** in **IPI_human**, Tax_Id=9606 Gene_Symbol=AHDC1 AT-hook DNA-binding motif-containing protein 1

Match to Query 21450: 1309.607068 from(655.810810,2+) index(30996)

Title: Elution from: 115.233333333333 to 115.233333333333 period: 0 cycle: 8336 experiment: 10 polarity: +

Data file 120118ry_201B7-32_1_1.mgf



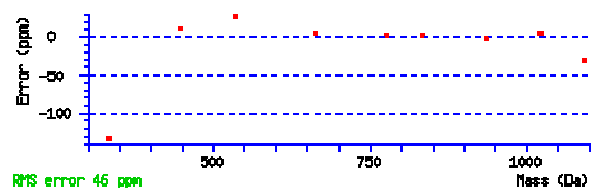
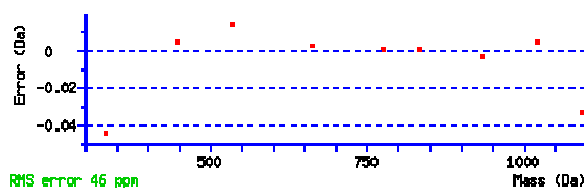
Monoisotopic mass of neutral peptide Mr(calc): 1309.6262

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 41 Expect: 0.0027

Matches : 9/120 fragment ions using 22 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258			A							14
2	219.1128	110.0600			F	1239.5964	620.3018	1222.5699	611.7886	1221.5858	611.2966	13
3	290.1499	145.5786			A	1092.5280	546.7676	1075.5014	538.2544	1074.5174	537.7624	12
4	377.1819	189.0946	359.1714	180.0893	S	1021.4909	511.2491	1004.4643	502.7358	1003.4803	502.2438	11
5	478.2296	239.6185	460.2191	230.6132	T	934.4589	467.7331	917.4323	459.2198	916.4483	458.7278	10
6	535.2511	268.1292	517.2405	259.1239	G	833.4112	417.2092	816.3846	408.6959	815.4006	408.2039	9
7	648.3352	324.6712	630.3246	315.6659	L	776.3897	388.6985	759.3632	380.1852	758.3791	379.6932	8
8	777.3777	389.1925	759.3672	380.1872	E	663.3056	332.1565	646.2791	323.6432	645.2951	323.1512	7
9	864.4098	432.7085	846.3992	423.7032	S	534.2631	267.6352	517.2365	259.1219	516.2525	258.6299	6
10	921.4312	461.2193	903.4207	452.2140	G	447.2310	224.1191	430.2045	215.6059	429.2205	215.1139	5
11	992.4684	496.7378	974.4578	487.7325	A	390.2096	195.6084	373.1830	187.0951	372.1990	186.6031	4
12	1079.5004	540.2538	1061.4898	531.2485	S	319.1724	160.0899	302.1459	151.5766	301.1619	151.0846	3
13	1136.5218	568.7646	1118.5113	559.7593	G	232.1404	116.5738	215.1139	108.0606			2
14					R	175.1190	88.0631	158.0924	79.5498			1



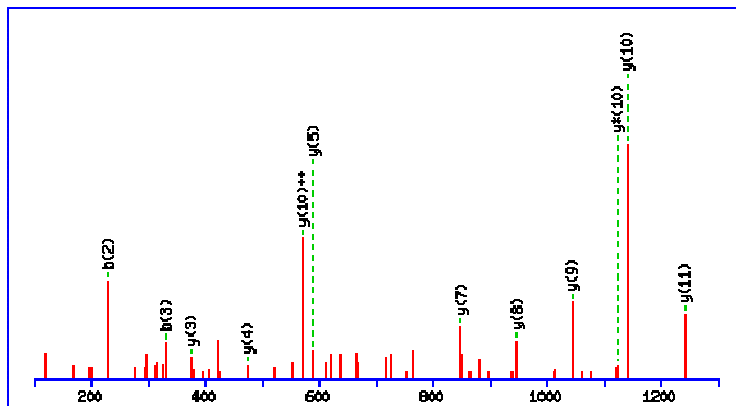
Peptide Number: 54916

MS/MS Fragmentation of **TQTPPVEENVTK**Found in **IPI00853093** in **IPI_human**, Tax_Id=9606 Gene_Symbol=METTL2B Isoform 1 of Methyltransferase-like protein 2B

Match to Query 24506: 1469.733588 from(735.874070,2+) index(18803)

Title: Elution from: 86.9166666666667 to 86.9166666666667 period: 0 cycle: 8582 experiment: 10 polarity:+

Data file 120210ry_32R1-32_3_1.mgf



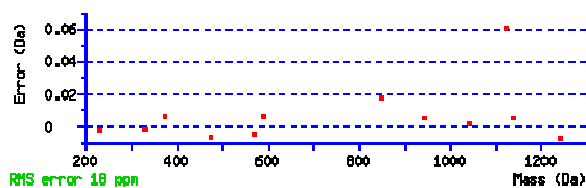
Monoisotopic mass of neutral peptide Mr(calc): 1469.7362

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

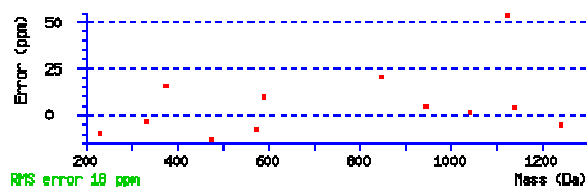
Ions Score: 52 Expect: 0.00047

Matches : 12/138 fragment ions using 24 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							13
2	230.1135	115.5604	213.0870	107.0471	212.1030	106.5551	Q	1369.6958	685.3515	1352.6692	676.8383	1351.6852	676.3462	12
3	331.1612	166.0842	314.1347	157.5710	313.1506	157.0790	T	1241.6372	621.3222	1224.6107	612.8090	1223.6266	612.3170	11
4	428.2140	214.6106	411.1874	206.0974	410.2034	205.6053	P	1140.5895	570.7984	1123.5630	562.2851	1122.5790	561.7931	10
5	525.2667	263.1370	508.2402	254.6237	507.2562	254.1317	P	1043.5368	522.2720	1026.5102	513.7587	1025.5262	513.2667	9
6	624.3352	312.6712	607.3086	304.1579	606.3246	303.6659	V	946.4840	473.7456	929.4575	465.2324	928.4734	464.7404	8
7	753.3777	377.1925	736.3512	368.6792	735.3672	368.1872	E	847.4156	424.2114	830.3890	415.6982	829.4050	415.2061	7
8	882.4203	441.7138	865.3938	433.2005	864.4098	432.7085	E	718.3730	359.6901	701.3464	351.1769	700.3624	350.6849	6
9	996.4633	498.7353	979.4367	490.2220	978.4527	489.7300	N	589.3304	295.1688	572.3039	286.6556	571.3198	286.1636	5
10	1095.5317	548.2695	1078.5051	539.7562	1077.5211	539.2642	V	475.2875	238.1474	458.2609	229.6341	457.2769	229.1421	4
11	1196.5794	598.7933	1179.5528	590.2800	1178.5688	589.7880	T	376.2191	188.6132	359.1925	180.0999	358.2085	179.6079	3
12	1324.6379	662.8226	1307.6114	654.3093	1306.6274	653.8173	Q	275.1714	138.0893	258.1448	129.5761			2
13							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 18 ppm



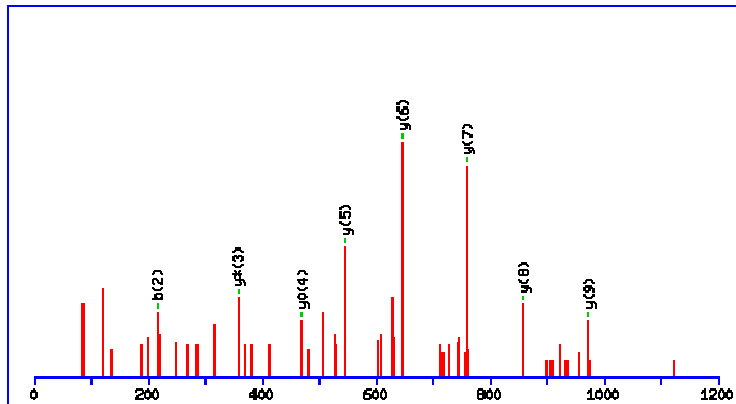
RMS error 18 ppm

Peptide Number: 55204MS/MS Fragmentation of **TDVLTGLSIR**Found in **IPI00395474** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SAMD1 Atherin

Match to Query 14608: 1073.592948 from(537.803750,2+) index(46525)

Title: Elution from: 115.9 to 115.9 period: 0 cycle: 4346 experiment: 6 polarity: +

Data file 120126ry_585A1-55_2_2.mgf



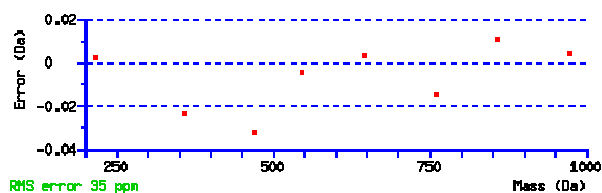
Monoisotopic mass of neutral peptide Mr(calc): 1073.6081

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

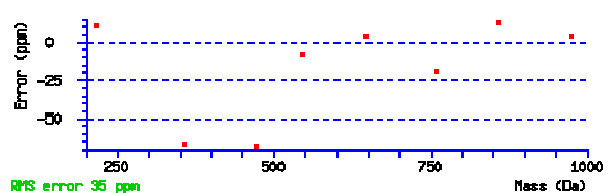
Ions Score: 45 Expect: 0.0032

Matches : 8/86 fragment ions using 9 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311	84.0444	42.5258	T							10
2	217.0819	109.0446	199.0713	100.0393	D	973.5677	487.2875	956.5411	478.7742	955.5571	478.2822	9
3	316.1503	158.5788	298.1397	149.5735	V	858.5407	429.7740	841.5142	421.2607	840.5302	420.7687	8
4	429.2344	215.1208	411.2238	206.1155	L	759.4723	380.2398	742.4458	371.7265	741.4618	371.2345	7
5	530.2821	265.6447	512.2715	256.6394	T	646.3883	323.6978	629.3617	315.1845	628.3777	314.6925	6
6	587.3035	294.1554	569.2930	285.1501	G	545.3406	273.1739	528.3140	264.6606	527.3300	264.1686	5
7	700.3876	350.6974	682.3770	341.6921	L	488.3191	244.6632	471.2926	236.1499	470.3085	235.6579	4
8	787.4196	394.2134	769.4090	385.2082	S	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
9	900.5037	450.7555	882.4931	441.7502	I	288.2030	144.6051	271.1765	136.0919			2
10					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 35 ppm



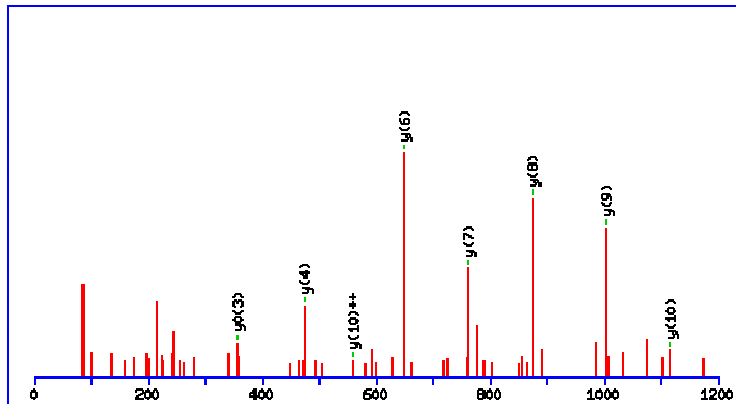
RMS error 35 ppm

Peptide Number: 55689**MS/MS Fragmentation of ELLQDIGDTLSR**Found in **IPI00426252** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TRIM27 Isoform Alpha of Zinc finger protein RFP

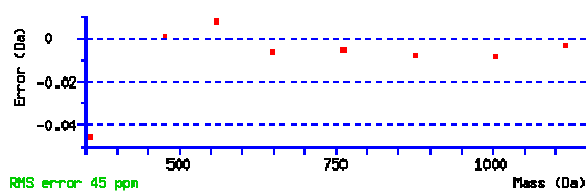
Match to Query 7730: 1358.688488 from(680.351520,2+) index(18398)

Title: Elution from: 45.4666666666667 to 45.4666666666667 period: 0 cycle: 1711 experiment: 6 polarity: +

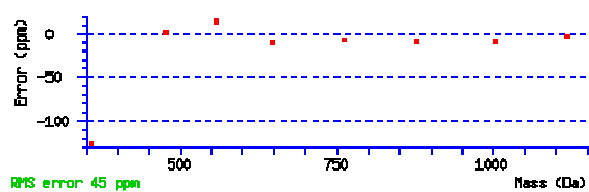
Data file 120210ry_32R1-32_3.mgf

**Monoisotopic mass of neutral peptide Mr(calcd):** 1358.7041**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 46 **Expect:** 0.0021**Matches :** 8/124 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							12
2	243.1339	122.0706			225.1234	113.0653	L	1230.6688	615.8381	1213.6423	607.3248	1212.6583	606.8328	11
3	356.2180	178.6126			338.2074	169.6074	L	1117.5848	559.2960	1100.5582	550.7828	1099.5742	550.2907	10
4	484.2766	242.6419	467.2500	234.1287	466.2660	233.6366	Q	1004.5007	502.7540	987.4742	494.2407	986.4901	493.7487	9
5	599.3035	300.1554	582.2770	291.6421	581.2930	291.1501	D	876.4421	438.7247	859.4156	430.2114	858.4316	429.7194	8
6	712.3876	356.6974	695.3610	348.1842	694.3770	347.6921	I	761.4152	381.2112	744.3886	372.6980	743.4046	372.2060	7
7	769.4090	385.2082	752.3825	376.6949	751.3985	376.2029	G	648.3311	324.6692	631.3046	316.1559	630.3206	315.6639	6
8	884.4360	442.7216	867.4094	434.2084	866.4254	433.7164	D	591.3097	296.1585	574.2831	287.6452	573.2991	287.1532	5
9	985.4837	493.2455	968.4571	484.7322	967.4731	484.2402	T	476.2827	238.6450	459.2562	230.1317	458.2722	229.6397	4
10	1098.5677	549.7875	1081.5412	541.2742	1080.5572	540.7822	L	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
11	1185.5998	593.3035	1168.5732	584.7902	1167.5892	584.2982	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
12							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 45 ppm



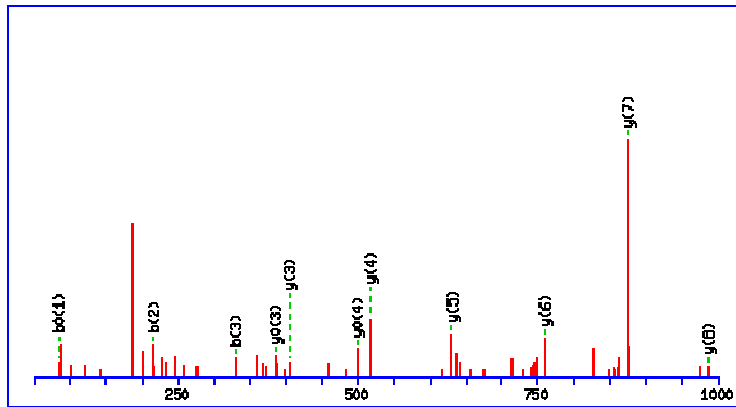
RMS error 45 ppm

Peptide Number: 55714MS/MS Fragmentation of **TLDEILQEK**Found in **IPI00219508** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CDK11A Isoform SV2 of Cyclin-dependent kinase 11A

Match to Query 9672: 1087.574768 from(544.794660,2+) index(28052)

Title: Elution from: 70.9 to 70.9 period: 0 cycle: 2700 experiment: 6 polarity:+

Data file 120210ry_585A1-55_3_2.mgf



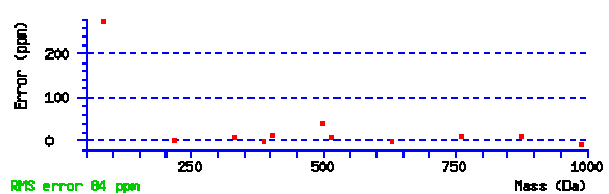
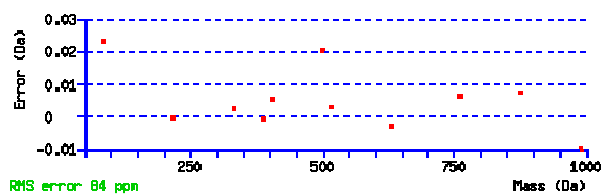
Monoisotopic mass of neutral peptide Mr(calc): 1087.5761

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 42 Expect: 0.0058

Matches : 11/82 fragment ions using 18 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							9
2	215.1390	108.0731			197.1285	99.0679	L	987.5357	494.2715	970.5092	485.7582	969.5251	485.2662	8
3	330.1660	165.5866			312.1554	156.5813	D	874.4516	437.7295	857.4251	429.2162	856.4411	428.7242	7
4	459.2086	230.1079			441.1980	221.1026	E	759.4247	380.2160	742.3981	371.7027	741.4141	371.2107	6
5	572.2926	286.6499			554.2821	277.6447	I	630.3821	315.6947	613.3556	307.1814	612.3715	306.6894	5
6	685.3767	343.1920			667.3661	334.1867	L	517.2980	259.1527	500.2715	250.6394	499.2875	250.1474	4
7	813.4353	407.2213	796.4087	398.7080	795.4247	398.2160	Q	404.2140	202.6106	387.1874	194.0974	386.2034	193.6053	3
8	942.4779	471.7426	925.4513	463.2293	924.4673	462.7373	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
9							K	147.1128	74.0600	130.0863	65.5468			1



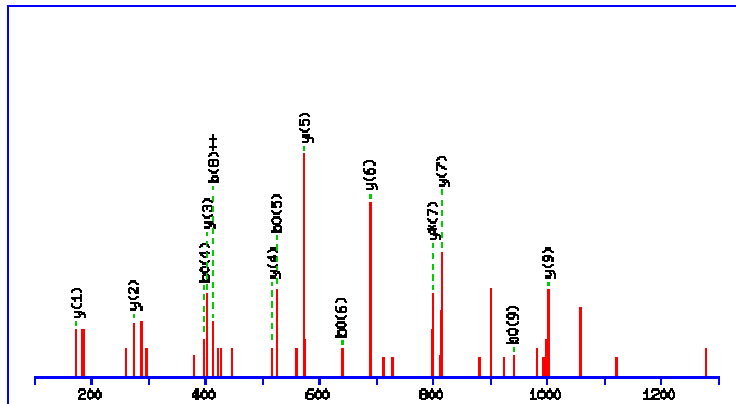
Peptide Number: 55796

MS/MS Fragmentation of **ETGQQIGDEV**RFound in **IPI00004928** in **IPI_human**, Tax_Id=9606 Gene_Symbol=EGLN1 Isoform 1 of Egl nine homolog 1

Match to Query 18160: 1230.582968 from(616.298760,2+) index(23268)

Title: Elution from: 91.6166666666667 to 91.6166666666667 period: 0 cycle: 7273 experiment: 5 polarity:+

Data file 120208ry_Tig120slc-P8_1_1.mgf



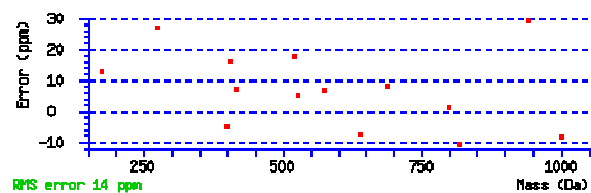
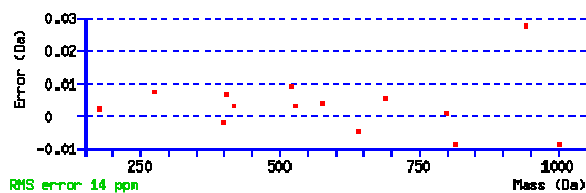
Monoisotopic mass of neutral peptide Mr(calc): 1230.5840

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 43 Expect: 0.0025

Matches : 14/110 fragment ions using 27 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							11
2	231.0975	116.0524			213.0870	107.0471	T	1102.5487	551.7780	1085.5222	543.2647	1084.5382	542.7727	10
3	288.1190	144.5631			270.1084	135.5579	G	1001.5011	501.2542	984.4745	492.7409	983.4905	492.2489	9
4	416.1776	208.5924	399.1510	200.0792	398.1670	199.5872	Q	944.4796	472.7434	927.4530	464.2302	926.4690	463.7381	8
5	544.2362	272.6217	527.2096	264.1084	526.2256	263.6164	Q	816.4210	408.7141	799.3945	400.2009	798.4104	399.7089	7
6	657.3202	329.1638	640.2937	320.6505	639.3097	320.1585	I	688.3624	344.6849	671.3359	336.1716	670.3519	335.6796	6
7	714.3417	357.6745	697.3151	349.1612	696.3311	348.6692	G	575.2784	288.1428	558.2518	279.6295	557.2678	279.1375	5
8	829.3686	415.1880	812.3421	406.6747	811.3581	406.1827	D	518.2569	259.6321	501.2304	251.1188	500.2463	250.6268	4
9	958.4112	479.7093	941.3847	471.1960	940.4007	470.7040	E	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
10	1057.4796	529.2435	1040.4531	520.7302	1039.4691	520.2382	V	274.1874	137.5973	257.1608	129.0840			2
11							R	175.1190	88.0631	158.0924	79.5498			1

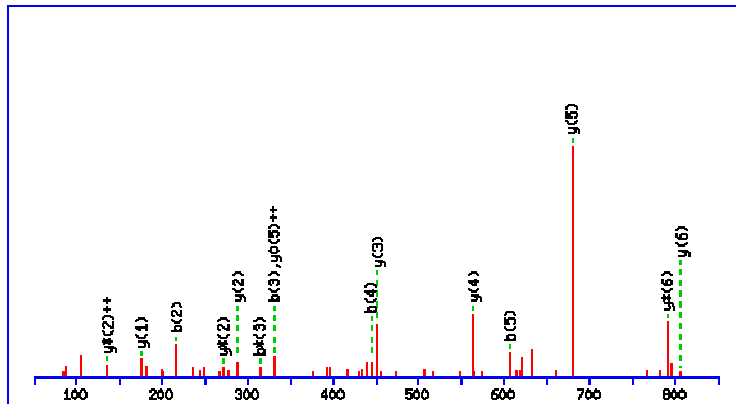


Peptide Number: 56076MS/MS Fragmentation of **SQDIYLR**Found in **IPI01020905** in **IPI_human**, Tax_Id=9606 Gene_Symbol=RPL18 Protein

Match to Query 6834: 893.460868 from(447.737710,2+) index(29582)

Title: Elution from: 105.166666666667 to 105.166666666667 period: 0 cycle: 8193 experiment: 4 polarity:+

Data file 120208ry_Tig120slc-P8_2_1.mgf



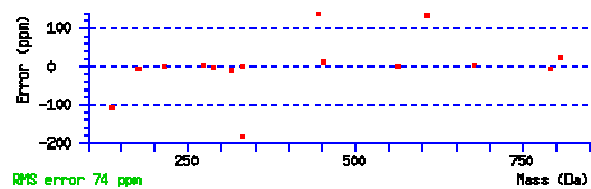
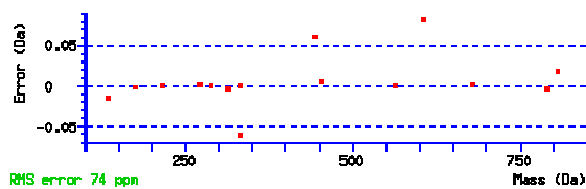
Monoisotopic mass of neutral peptide Mr(calcd): 893.4607

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 45 Expect: 0.0019

Matches : 15/62 fragment ions using 23 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							7
2	216.0979	108.5526	199.0713	100.0393	198.0873	99.5473	Q	807.4359	404.2216	790.4094	395.7083	789.4254	395.2163	6
3	331.1248	166.0661	314.0983	157.5528	313.1143	157.0608	D	679.3774	340.1923	662.3508	331.6790	661.3668	331.1870	5
4	444.2089	222.6081	427.1823	214.0948	426.1983	213.6028	I	564.3504	282.6788	547.3239	274.1656			4
5	607.2722	304.1397	590.2457	295.6265	589.2617	295.1345	Y	451.2663	226.1368	434.2398	217.6235			3
6	720.3563	360.6818	703.3297	352.1685	702.3457	351.6765	L	288.2030	144.6051	271.1765	136.0919			2
7							R	175.1190	88.0631	158.0924	79.5498			1



Peptide Number: 56092

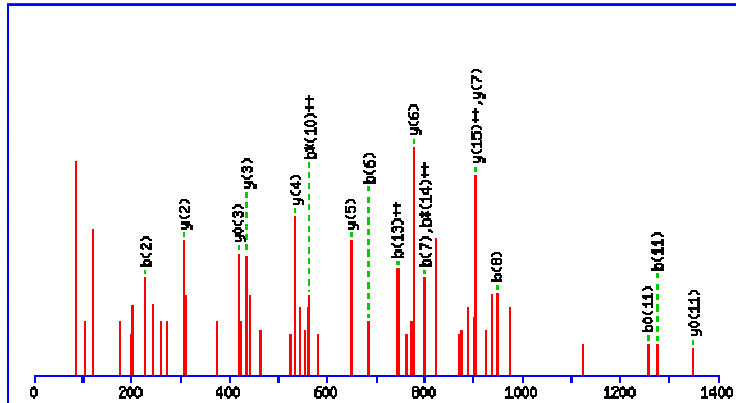
MS/MS Fragmentation of **ILESIEDFAQELVECK**

Found in **IPI00029144** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PPP2R3A Isoform PR130 of Serine/threonine-protein phosphatase 2A regulatory subunit B'' subunit alpha

Match to Query 11196: 1921.948032 from(641.656620,3+) index(23199)

Title: Elution from: 61.4666666666667 to 61.4666666666667 period: 0 cycle: 2332 experiment: 3 polarity: +

Data file 120206ry_aHDF1419-P10_2_4.mgf



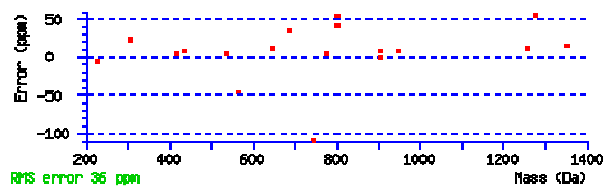
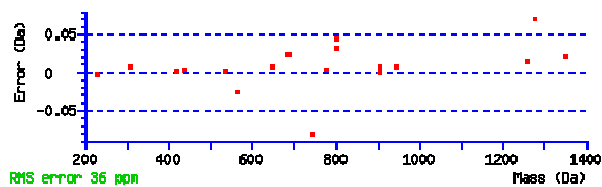
Monoisotopic mass of neutral peptide Mr(calc): 1921.9343

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 46 Expect: 0.0016

Matches : 18/154 fragment ions using 22 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							16
2	227.1754	114.0913					L	1809.8575	905.4324	1792.8310	896.9191	1791.8469	896.4271	15
3	356.2180	178.6126			338.2074	169.6074	E	1696.7734	848.8904	1679.7469	840.3771	1678.7629	839.8851	14
4	443.2500	222.1287			425.2395	213.1234	S	1567.7309	784.3691	1550.7043	775.8558	1549.7203	775.3638	13
5	556.3341	278.6707			538.3235	269.6654	I	1480.6988	740.8530	1463.6723	732.3398	1462.6883	731.8478	12
6	685.3767	343.1920			667.3661	334.1867	E	1367.6148	684.3110	1350.5882	675.7977	1349.6042	675.3057	11
7	800.4036	400.7055			782.3931	391.7002	D	1238.5722	619.7897	1221.5456	611.2764	1220.5616	610.7844	10
8	947.4720	474.2397			929.4615	465.2344	F	1123.5452	562.2762	1106.5187	553.7630	1105.5347	553.2710	9
9	1018.5092	509.7582			1000.4986	500.7529	A	976.4768	488.7420	959.4503	480.2288	958.4662	479.7368	8
10	1146.5677	573.7875	1129.5412	565.2742	1128.5572	564.7822	Q	905.4397	453.2235	888.4131	444.7102	887.4291	444.2182	7
11	1275.6103	638.3088	1258.5838	629.7955	1257.5998	629.3035	E	777.3811	389.1942	760.3546	380.6809	759.3706	380.1889	6
12	1388.6944	694.8508	1371.6678	686.3376	1370.6838	685.8455	L	648.3385	324.6729	631.3120	316.1596	630.3280	315.6676	5
13	1487.7628	744.3850	1470.7363	735.8718	1469.7522	735.3798	V	535.2545	268.1309	518.2279	259.6176	517.2439	259.1256	4
14	1616.8054	808.9063	1599.7788	800.3931	1598.7948	799.9011	E	436.1860	218.5967	419.1595	210.0834	418.1755	209.5914	3
15	1776.8360	888.9217	1759.8095	880.4084	1758.8255	879.9164	C	307.1435	154.0754	290.1169	145.5621			2
16							K	147.1128	74.0600	130.0863	65.5468			1



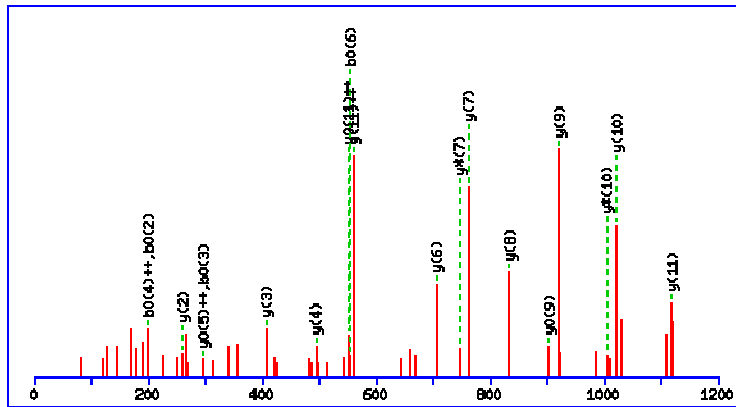
Peptide Number: 56180

MS/MS Fragmentation of **DTPTSAGPNSFNK**Found in **IPI00790305** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PCNP PEST proteolytic signal containing nuclear protein, isoform CRA_a

Match to Query 22049: 1334.610588 from(668.312570,2+) index(18424)

Title: Elution from: 85.7166666666667 to 85.7166666666667 period: 0 cycle: 7243 experiment: 10 polarity:+

Data file 120118ry_201B7-32_1_1.mgf



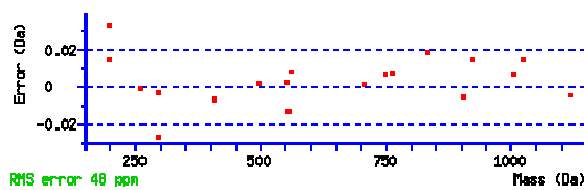
Monoisotopic mass of neutral peptide Mr(calc): 1334.6103

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

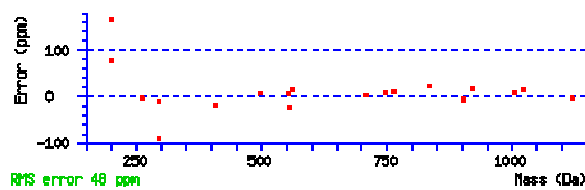
Ions Score: 50 Expect: 0.00036

Matches : 19/122 fragment ions using 37 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							13
2	217.0819	109.0446			199.0713	100.0393	T	1220.5906	610.7989	1203.5640	602.2857	1202.5800	601.7937	12
3	314.1347	157.5710			296.1241	148.5657	P	1119.5429	560.2751	1102.5164	551.7618	1101.5323	551.2698	11
4	415.1823	208.0948			397.1718	199.0895	T	1022.4901	511.7487	1005.4636	503.2354	1004.4796	502.7434	10
5	502.2144	251.6108			484.2038	242.6055	S	921.4425	461.2249	904.4159	452.7116	903.4319	452.2196	9
6	573.2515	287.1294			555.2409	278.1241	A	834.4104	417.7089	817.3839	409.1956	816.3999	408.7036	8
7	630.2729	315.6401			612.2624	306.6348	G	763.3733	382.1903	746.3468	373.6770	745.3628	373.1850	7
8	727.3257	364.1665			709.3151	355.1612	P	706.3519	353.6796	689.3253	345.1663	688.3413	344.6743	6
9	841.3686	421.1880	824.3421	412.6747	823.3581	412.1827	N	609.2991	305.1532	592.2726	296.6399	591.2885	296.1479	5
10	928.4007	464.7040	911.3741	456.1907	910.3901	455.6987	S	495.2562	248.1317	478.2296	239.6185	477.2456	239.1264	4
11	1075.4691	538.2382	1058.4425	529.7249	1057.4585	529.2329	F	408.2241	204.6157	391.1976	196.1024			3
12	1189.5120	595.2596	1172.4855	586.7464	1171.5014	586.2544	N	261.1557	131.0815	244.1292	122.5682			2
13							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 48 ppm



RMS error 48 ppm

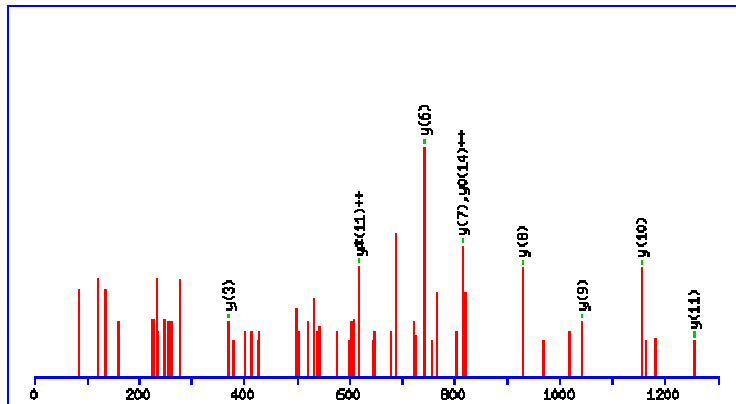
Peptide Number: 56541

MS/MS Fragmentation of **FLYIVNLDAPFEGHR**Found in **IPI00242841** in **IPI_human**, Tax_Id=9606 Gene_Symbol=WDR59 Isoform 1 of WD repeat-containing protein 59

Match to Query 27548: 1789.909062 from(597.643630,3+) index(40753)

Title: Elution from: 102.366666666667 to 102.366666666667 period: 0 cycle: 3817 experiment: 4 polarity: +

Data file 120126ry_585A1-55_2_3.mgf



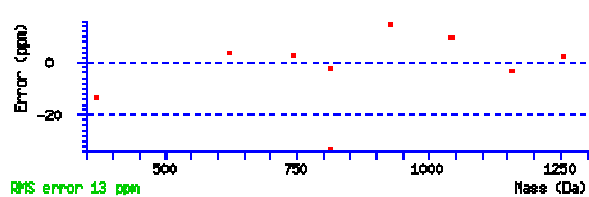
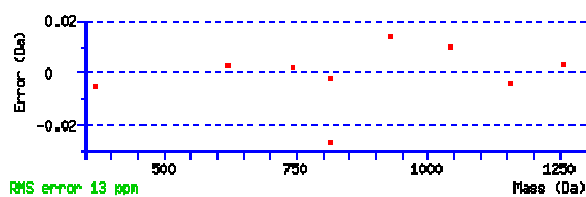
Monoisotopic mass of neutral peptide Mr(calc): 1789.9151

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 47 Expect: 0.0016

Matches : 9/138 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415					F							15
2	261.1598	131.0835					L	1643.8540	822.4306	1626.8275	813.9174	1625.8435	813.4254	14
3	424.2231	212.6152					Y	1530.7700	765.8886	1513.7434	757.3753	1512.7594	756.8833	13
4	537.3071	269.1572					I	1367.7066	684.3570	1350.6801	675.8437	1349.6961	675.3517	12
5	636.3756	318.6914					V	1254.6226	627.8149	1237.5960	619.3016	1236.6120	618.8096	11
6	750.4185	375.7129	733.3919	367.1996			N	1155.5541	578.2807	1138.5276	569.7674	1137.5436	569.2754	10
7	863.5026	432.2549	846.4760	423.7416			L	1041.5112	521.2592	1024.4847	512.7460	1023.5007	512.2540	9
8	978.5295	489.7684	961.5029	481.2551	960.5189	480.7631	D	928.4272	464.7172	911.4006	456.2039	910.4166	455.7119	8
9	1049.5666	525.2869	1032.5401	516.7737	1031.5560	516.2817	A	813.4002	407.2037	796.3737	398.6905	795.3896	398.1985	7
10	1146.6194	573.8133	1129.5928	565.3001	1128.6088	564.8080	P	742.3631	371.6852	725.3366	363.1719	724.3525	362.6799	6
11	1293.6878	647.3475	1276.6612	638.8343	1275.6772	638.3422	F	645.3103	323.1588	628.2838	314.6455	627.2998	314.1535	5
12	1422.7304	711.8688	1405.7038	703.3556	1404.7198	702.8635	E	498.2419	249.6246	481.2154	241.1113	480.2314	240.6193	4
13	1479.7518	740.3796	1462.7253	731.8663	1461.7413	731.3743	G	369.1993	185.1033	352.1728	176.5900			3
14	1616.8108	808.9090	1599.7842	800.3957	1598.8002	799.9037	H	312.1779	156.5926	295.1513	148.0793			2
15							R	175.1190	88.0631	158.0924	79.5498			1



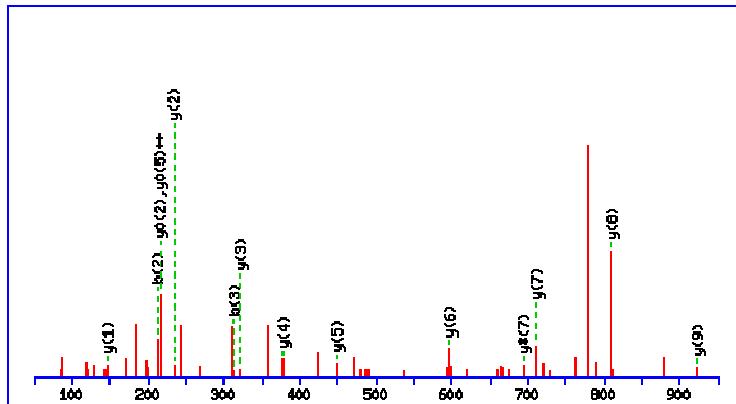
Peptide Number: 56815

MS/MS Fragmentation of **VIVDFAGSSK**Found in **IPI00180685** in **IPI_human**, Tax_Id=9606 Gene_Symbol=APTX Isoform 2 of Aprataxin

Match to Query 7366: 1021.540728 from(511.777640,2+) index(8644)

Title: Elution from: 20.6333333333333 to 20.6333333333333 period: 0 cycle: 779 experiment: 5 polarity:+

Data file 120214ry_414C2-43_4_2.mgf



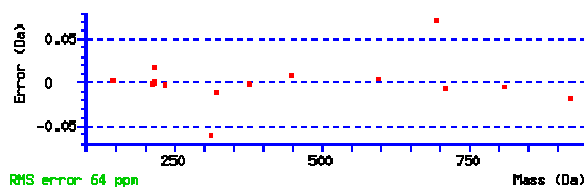
Monoisotopic mass of neutral peptide Mr(calc): 1021.5444

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

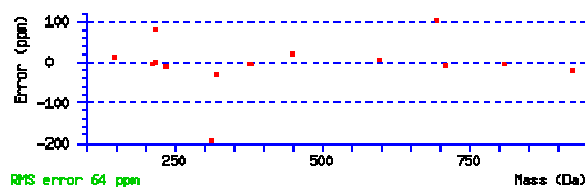
Ions Score: 48 Expect: 0.001

Matches : 14/82 fragment ions using 41 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415			V							10
2	213.1598	107.0835			I	923.4833	462.2453	906.4567	453.7320	905.4727	453.2400	9
3	312.2282	156.6177			V	810.3992	405.7032	793.3727	397.1900	792.3886	396.6980	8
4	427.2551	214.1312	409.2445	205.1259	D	711.3308	356.1690	694.3042	347.6558	693.3202	347.1638	7
5	574.3235	287.6654	556.3130	278.6601	F	596.3039	298.6556	579.2773	290.1423	578.2933	289.6503	6
6	645.3606	323.1840	627.3501	314.1787	A	449.2354	225.1214	432.2089	216.6081	431.2249	216.1161	5
7	702.3821	351.6947	684.3715	342.6894	G	378.1983	189.6028	361.1718	181.0895	360.1878	180.5975	4
8	789.4141	395.2107	771.4036	386.2054	S	321.1769	161.0921	304.1503	152.5788	303.1663	152.0868	3
9	876.4462	438.7267	858.4356	429.7214	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
10					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 64 ppm



RMS error 64 ppm

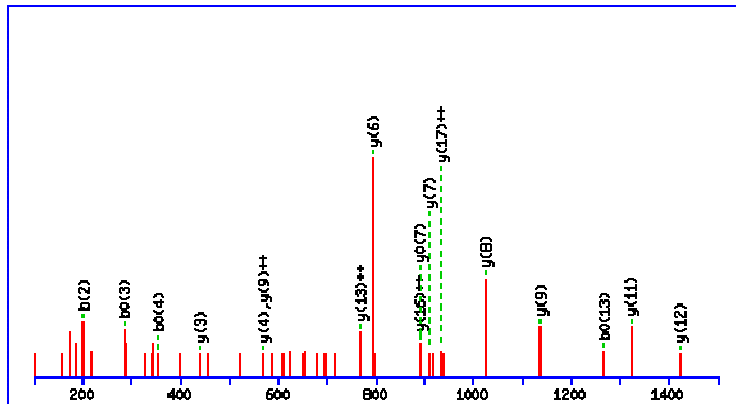
Peptide Number: 56849

MS/MS Fragmentation of **LSTAANTGQIDDPQEQHR**Found in **IPI00216826** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SLC41A3 Uncharacterized protein

Match to Query 30452: 1979.922912 from(660.981580,3+) index(27140)

Title: Elution from: 101.183333333333 to 101.183333333333 period: 0 cycle: 7639 experiment: 10 polarity:+

Data file 120208ry_Tig120slc-P8_1_1.mgf



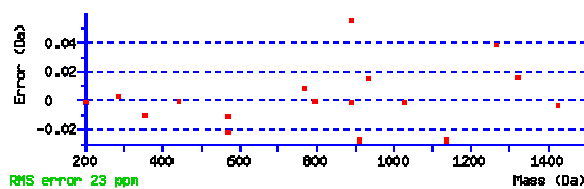
Monoisotopic mass of neutral peptide Mr(calc): 1979.9297

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

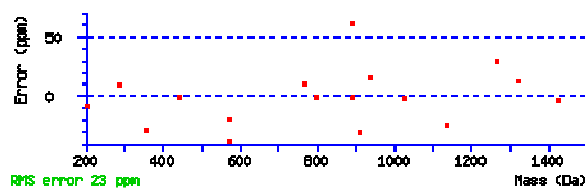
Ions Score: 55 Expect: 0.00014

Matches : 17/186 fragment ions using 23 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							18
2	201.1234	101.0653			183.1128	92.0600	S	1867.8529	934.4301	1850.8264	925.9168	1849.8423	925.4248	17
3	302.1710	151.5892			284.1605	142.5839	T	1780.8209	890.9141	1763.7943	882.4008	1762.8103	881.9088	16
4	373.2082	187.1077			355.1976	178.1024	A	1679.7732	840.3902	1662.7467	831.8770	1661.7626	831.3850	15
5	444.2453	222.6263			426.2347	213.6210	A	1608.7361	804.8717	1591.7095	796.3584	1590.7255	795.8664	14
6	558.2882	279.6477	541.2617	271.1345	540.2776	270.6425	N	1537.6990	769.3531	1520.6724	760.8399	1519.6884	760.3478	13
7	659.3359	330.1716	642.3093	321.6583	641.3253	321.1663	T	1423.6560	712.3317	1406.6295	703.8184	1405.6455	703.3264	12
8	716.3573	358.6823	699.3308	350.1690	698.3468	349.6770	G	1322.6084	661.8078	1305.5818	653.2945	1304.5978	652.8025	11
9	844.4159	422.7116	827.3894	414.1983	826.4054	413.7063	Q	1265.5869	633.2971	1248.5604	624.7838	1247.5763	624.2918	10
10	957.5000	479.2536	940.4734	470.7404	939.4894	470.2483	I	1137.5283	569.2678	1120.5018	560.7545	1119.5178	560.2625	9
11	1072.5269	536.7671	1055.5004	528.2538	1054.5164	527.7618	D	1024.4443	512.7258	1007.4177	504.2125	1006.4337	503.7205	8
12	1187.5539	594.2806	1170.5273	585.7673	1169.5433	585.2753	D	909.4173	455.2123	892.3908	446.6990	891.4068	446.2070	7
13	1284.6066	642.8070	1267.5801	634.2937	1266.5961	633.8017	P	794.3904	397.6988	777.3638	389.1856	776.3798	388.6935	6
14	1412.6652	706.8362	1395.6387	698.3230	1394.6547	697.8310	Q	697.3376	349.1724	680.3111	340.6592	679.3270	340.1672	5
15	1541.7078	771.3575	1524.6813	762.8443	1523.6972	762.3523	E	569.2790	285.1432	552.2525	276.6299	551.2685	276.1379	4
16	1669.7664	835.3868	1652.7398	826.8736	1651.7558	826.3815	Q	440.2364	220.6219	423.2099	212.1086			3
17	1806.8253	903.9163	1789.7987	895.4030	1788.8147	894.9110	H	312.1779	156.5926	295.1513	148.0793			2
18							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 23 ppm



RMS error 23 ppm

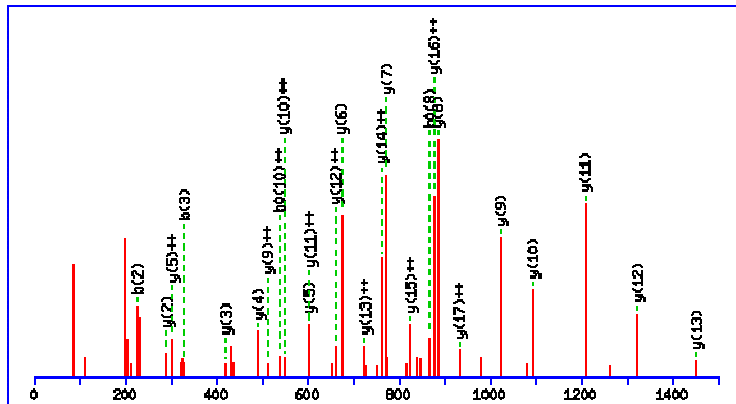
Peptide Number: 57032

MS/MS Fragmentation of **ILTEAIDAHLVALAERD**Found in **IPI00029623** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PSMA6 Proteasome subunit alpha type-6

Match to Query 22356: 1978.045722 from(660.355850,3+) index(31132)

Title: Elution from: 87 to 87 period: 0 cycle: 3346 experiment: 3 polarity:+

Data file 120208ry_Tig120slc-P8_1_3.mgf



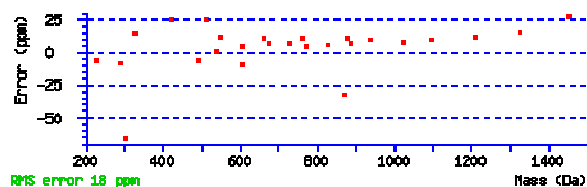
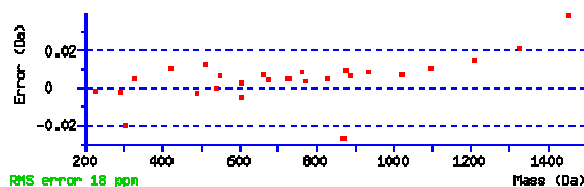
Monoisotopic mass of neutral peptide Mr(calc): 1978.0371

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 102 Expect: 3.3e-009

Matches : 26/166 fragment ions using 41 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							18
2	227.1754	114.0913					L	1865.9603	933.4838	1848.9338	924.9705	1847.9498	924.4785	17
3	328.2231	164.6152			310.2125	155.6099	T	1752.8763	876.9418	1735.8497	868.4285	1734.8657	867.9365	16
4	457.2657	229.1365			439.2551	220.1312	E	1651.8286	826.4179	1634.8020	817.9047	1633.8180	817.4127	15
5	528.3028	264.6550			510.2922	255.6498	A	1522.7860	761.8966	1505.7594	753.3834	1504.7754	752.8914	14
6	657.3454	329.1763			639.3348	320.1710	E	1451.7489	726.3781	1434.7223	717.8648	1433.7383	717.3728	13
7	770.4294	385.7184			752.4189	376.7131	I	1322.7063	661.8568	1305.6797	653.3435	1304.6957	652.8515	12
8	885.4564	443.2318			867.4458	434.2266	D	1209.6222	605.3148	1192.5957	596.8015	1191.6117	596.3095	11
9	956.4935	478.7504			938.4829	469.7451	A	1094.5953	547.8013	1077.5687	539.2880	1076.5847	538.7960	10
10	1093.5524	547.2798			1075.5419	538.2746	H	1023.5582	512.2827	1006.5316	503.7694	1005.5476	503.2774	9
11	1206.6365	603.8219			1188.6259	594.8166	L	886.4993	443.7533	869.4727	435.2400	868.4887	434.7480	8
12	1305.7049	653.3561			1287.6943	644.3508	V	773.4152	387.2112	756.3886	378.6980	755.4046	378.2060	7
13	1376.7420	688.8746			1358.7314	679.8694	A	674.3468	337.6770	657.3202	329.1638	656.3362	328.6717	6
14	1489.8261	745.4167			1471.8155	736.4114	L	603.3097	302.1585	586.2831	293.6452	585.2991	293.1532	5
15	1560.8632	780.9352			1542.8526	771.9299	A	490.2256	245.6164	473.1991	237.1032	472.2150	236.6112	4
16	1689.9058	845.4565			1671.8952	836.4512	E	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	3
17	1846.0069	923.5071	1828.9803	914.9938	1827.9963	914.5018	R	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
18							D	134.0448	67.5260			116.0342	58.5207	1



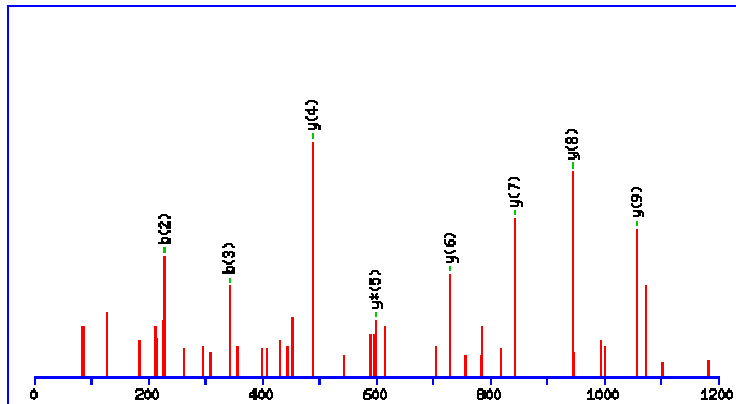
Peptide Number: 57093

MS/MS Fragmentation of **NNLTLDQPQDK**Found in **IPI00893511** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TANK Uncharacterized protein

Match to Query 19625: 1284.631208 from(643.322880,2+) index(29528)

Title: Elution from: 106.95 to 106.95 period: 0 cycle: 7858 experiment: 9 polarity: +

Data file 120208ry_Tig120slc-P8_1_1.mgf



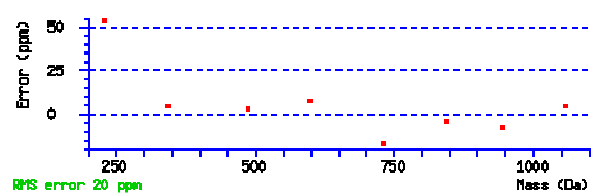
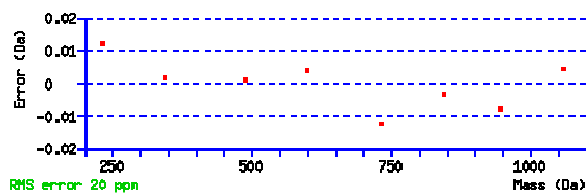
Monoisotopic mass of neutral peptide Mr(calc): 1284.6310

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 37 Expect: 0.01

Matches : 8/112 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							11
2	229.0931	115.0502	212.0666	106.5369			N	1171.5953	586.3013	1154.5688	577.7880	1153.5848	577.2960	10
3	342.1772	171.5922	325.1506	163.0790			L	1057.5524	529.2798	1040.5259	520.7666	1039.5419	520.2746	9
4	443.2249	222.1161	426.1983	213.6028	425.2143	213.1108	T	944.4684	472.7378	927.4418	464.2245	926.4578	463.7325	8
5	556.3089	278.6581	539.2824	270.1448	538.2984	269.6528	L	843.4207	422.2140	826.3941	413.7007	825.4101	413.2087	7
6	671.3359	336.1716	654.3093	327.6583	653.3253	327.1663	D	730.3366	365.6719	713.3101	357.1587	712.3260	356.6667	6
7	799.3945	400.2009	782.3679	391.6876	781.3839	391.1956	Q	615.3097	308.1585	598.2831	299.6452	597.2991	299.1532	5
8	896.4472	448.7272	879.4207	440.2140	878.4367	439.7220	P	487.2511	244.1292	470.2245	235.6159	469.2405	235.1239	4
9	1024.5058	512.7565	1007.4793	504.2433	1006.4952	503.7513	Q	390.1983	195.6028	373.1718	187.0895	372.1878	186.5975	3
10	1139.5327	570.2700	1122.5062	561.7567	1121.5222	561.2647	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
11							K	147.1128	74.0600	130.0863	65.5468			1



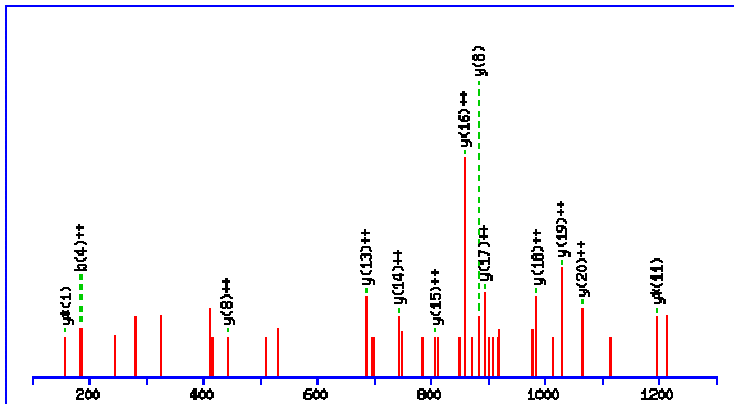
Peptide Number: 57246

MS/MS Fragmentation of **ALLASWATQDSATLDALLAALRR**Found in **IPI00027436** in **IPI_human**, Tax_Id=9606 Gene_Symbol=NGFR Tumor necrosis factor receptor superfamily member 16

Match to Query 20096: 2426.308062 from(809.776630,3+) index(34781)

Title: Elution from: 108.65 to 108.65 period: 0 cycle: 4110 experiment: 4 polarity: +

Data file 120129ry_604A1-46_2_4.mgf



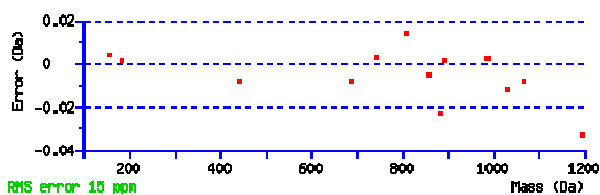
Monoisotopic mass of neutral peptide Mr(calc): 2426.3281

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

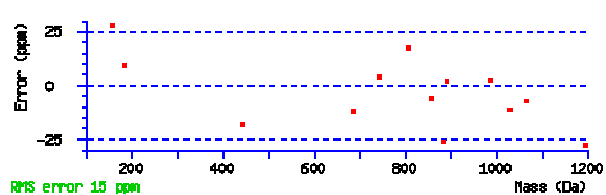
Ions Score: 45 Expect: 0.0012

Matches : 14/224 fragment ions using 27 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							23
2	185.1285	93.0679					L	2356.2983	1178.6528	2339.2718	1170.1395	2338.2878	1169.6475	22
3	298.2125	149.6099					L	2243.2143	1122.1108	2226.1877	1113.5975	2225.2037	1113.1055	21
4	369.2496	185.1285					A	2130.1302	1065.5687	2113.1036	1057.0555	2112.1196	1056.5635	20
5	456.2817	228.6445			438.2711	219.6392	S	2059.0931	1030.0502	2042.0665	1021.5369	2041.0825	1021.0449	19
6	642.3610	321.6841			624.3504	312.6788	W	1972.0611	986.5342	1955.0345	978.0209	1954.0505	977.5289	18
7	713.3981	357.2027			695.3875	348.1974	A	1785.9817	893.4945	1768.9552	884.9812	1767.9712	884.4892	17
8	814.4458	407.7265			796.4352	398.7212	T	1714.9446	857.9760	1697.9181	849.4627	1696.9341	848.9707	16
9	942.5043	471.7558	925.4778	463.2425	924.4938	462.7505	Q	1613.8969	807.4521	1596.8704	798.9388	1595.8864	798.4468	15
10	1057.5313	529.2693	1040.5047	520.7560	1039.5207	520.2640	D	1485.8384	743.4228	1468.8118	734.9095	1467.8278	734.4175	14
11	1144.5633	572.7853	1127.5368	564.2720	1126.5528	563.7800	S	1370.8114	685.9094	1353.7849	677.3961	1352.8009	676.9041	13
12	1215.6004	608.3039	1198.5739	599.7906	1197.5899	599.2986	A	1283.7794	642.3933	1266.7528	633.8801	1265.7688	633.3881	12
13	1316.6481	658.8277	1299.6216	650.3144	1298.6375	649.8224	T	1212.7423	606.8748	1195.7157	598.3615	1194.7317	597.8695	11
14	1429.7322	715.3697	1412.7056	706.8564	1411.7216	706.3644	L	1111.6946	556.3509	1094.6681	547.8377	1093.6840	547.3457	10
15	1544.7591	772.8832	1527.7326	764.3699	1526.7486	763.8779	D	998.6105	499.8089	981.5840	491.2956	980.6000	490.8036	9
16	1615.7962	808.4018	1598.7697	799.8885	1597.7857	799.3965	A	883.5836	442.2954	866.5570	433.7822			8
17	1728.8803	864.9438	1711.8537	856.4305	1710.8697	855.9385	L	812.5465	406.7769	795.5199	398.2636			7
18	1841.9644	921.4858	1824.9378	912.9725	1823.9538	912.4805	L	699.4624	350.2348	682.4359	341.7216			6
19	1913.0015	957.0044	1895.9749	948.4911	1894.9909	947.9991	A	586.3784	293.6928	569.3518	285.1795			5
20	1984.0386	992.5229	1967.0120	984.0097	1966.0280	983.5176	A	515.3412	258.1743	498.3147	249.6610			4
21	2097.1226	1049.0650	2080.0961	1040.5517	2079.1121	1040.0597	L	444.3041	222.6557	427.2776	214.1424			3
22	2253.2238	1127.1155	2236.1972	1118.6022	2235.2132	1118.1102	R	331.2201	166.1137	314.1935	157.6004			2
23							R	175.1190	88.0631	158.0924	79.5498			1



RMS error: 15 ppm



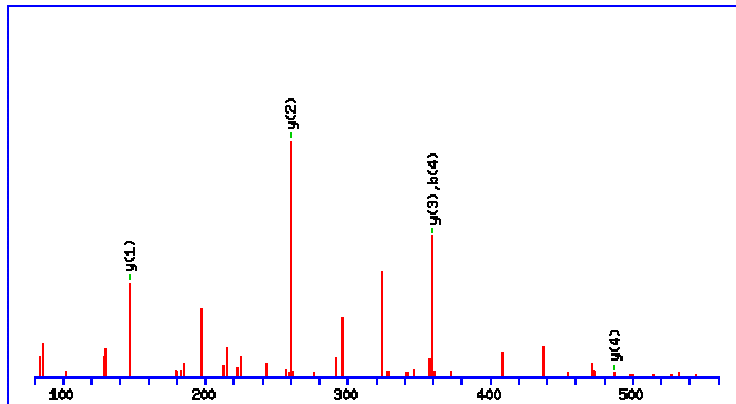
RMS error: 15 ppm

Peptide Number: 57257MS/MS Fragmentation of **LASSRSLKVLK**Found in **IPI01013367** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TIAM2 T-cell lymphoma invasion and metastasis 2 variant (Fragment)

Match to Query 17112: 1200.773256 from(301.200590,4+) index(17017)

Title: Elution from: 82.85 to 82.85 period: 0 cycle: 8175 experiment: 1 polarity:+

Data file 120212ry_aHDF1388-P9_2_1.mgf



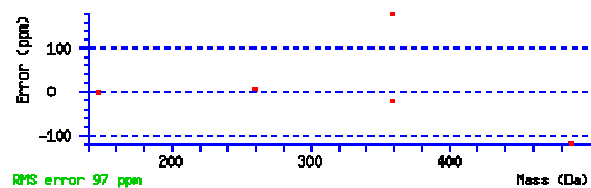
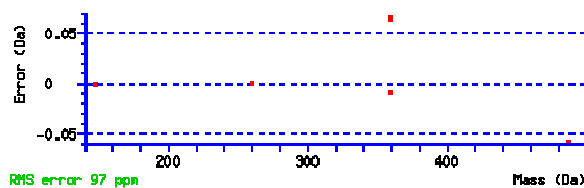
Monoisotopic mass of neutral peptide Mr(calc): 1200.7554

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 31 Expect: 0.0012

Matches : 5/98 fragment ions using 5 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							11
2	185.1285	93.0679					A	1088.6786	544.8429	1071.6521	536.3297	1070.6681	535.8377	10
3	272.1605	136.5839			254.1499	127.5786	S	1017.6415	509.3244	1000.6150	500.8111	999.6309	500.3191	9
4	359.1925	180.0999			341.1819	171.0946	S	930.6095	465.8084	913.5829	457.2951	912.5989	456.8031	8
5	515.2936	258.1504	498.2671	249.6372	497.2831	249.1452	R	843.5774	422.2924	826.5509	413.7791	825.5669	413.2871	7
6	602.3256	301.6665	585.2991	293.1532	584.3151	292.6612	S	687.4763	344.2418	670.4498	335.7285	669.4658	335.2365	6
7	715.4097	358.2085	698.3832	349.6952	697.3991	349.2032	L	600.4443	300.7258	583.4178	292.2125			5
8	843.5047	422.2560	826.4781	413.7427	825.4941	413.2507	K	487.3602	244.1838	470.3337	235.6705			4
9	942.5731	471.7902	925.5465	463.2769	924.5625	462.7849	V	359.2653	180.1363	342.2387	171.6230			3
10	1055.6572	528.3322	1038.6306	519.8189	1037.6466	519.3269	L	260.1969	130.6021	243.1703	122.0888			2
11							K	147.1128	74.0600	130.0863	65.5468			1



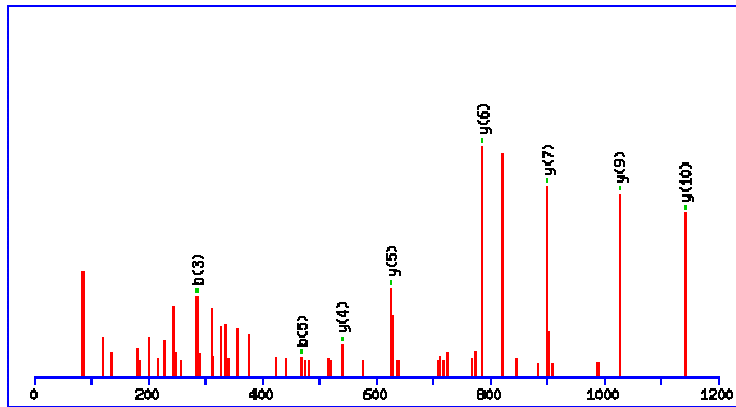
Peptide Number: 57540

MS/MS Fragmentation of **LDGALCSYTEK**Found in **IPI00004406** in **IPI_human**, Tax_Id=9606 Gene_Symbol=UPP1 Isoform 1 of Uridine phosphorylase 1

Match to Query 18591: 1255.567348 from(628.790950,2+) index(5517)

Title: Elution from: 12.95 to 12.95 period: 0 cycle: 493 experiment: 8 polarity: +

Data file 120214ry_32R1-32_4_2.mgf



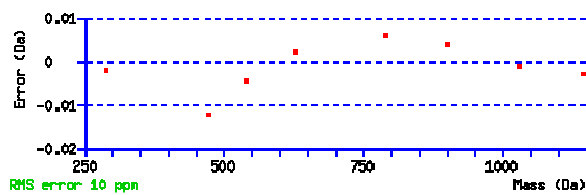
Monoisotopic mass of neutral peptide Mr(calc): 1255.5754

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

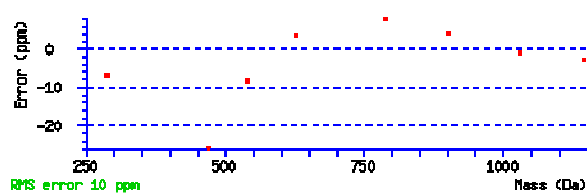
Ions Score: 47 Expect: 0.00064

Matches : 8/96 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							11
2	229.1183	115.0628	211.1077	106.0575	D	1143.4987	572.2530	1126.4721	563.7397	1125.4881	563.2477	10
3	286.1397	143.5735	268.1292	134.5682	G	1028.4717	514.7395	1011.4452	506.2262	1010.4612	505.7342	9
4	357.1769	179.0921	339.1663	170.0868	A	971.4503	486.2288	954.4237	477.7155	953.4397	477.2235	8
5	470.2609	235.6341	452.2504	226.6288	L	900.4131	450.7102	883.3866	442.1969	882.4026	441.7049	7
6	630.2916	315.6494	612.2810	306.6441	C	787.3291	394.1682	770.3025	385.6549	769.3185	385.1629	6
7	717.3236	359.1654	699.3130	350.1602	S	627.2984	314.1529	610.2719	305.6396	609.2879	305.1476	5
8	880.3869	440.6971	862.3764	431.6918	Y	540.2664	270.6368	523.2399	262.1236	522.2558	261.6316	4
9	981.4346	491.2209	963.4240	482.2157	T	377.2031	189.1052	360.1765	180.5919	359.1925	180.0999	3
10	1110.4772	555.7422	1092.4666	546.7370	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
11					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 10 ppm



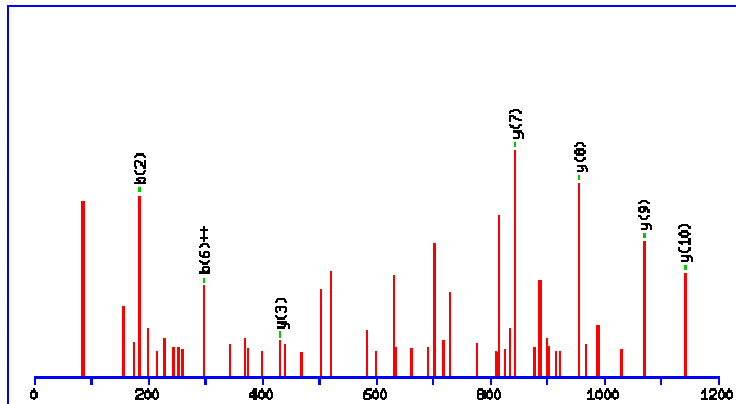
RMS error 10 ppm

Peptide Number: 57616MS/MS Fragmentation of **LALLALLDRTR**Found in **IPI00869136** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PCNXL3 Isoform 1 of Pecanex-like protein 3

Match to Query 4345: 1253.773148 from(627.893850,2+) index(33149)

Title: Elution from: 84.6 to 84.6 period: 0 cycle: 3214 experiment: 6 polarity: +

Data file 120206ry_aHDF1419-P10_3_3.mgf



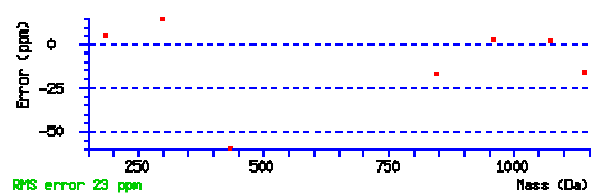
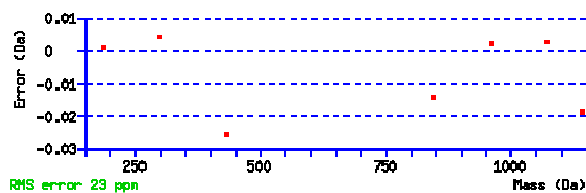
Monoisotopic mass of neutral peptide Mr(calc): 1253.7819

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 32 Expect: 0.0077

Matches : 8/88 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							11
2	185.1285	93.0679					A	1141.7052	571.3562	1124.6786	562.8429	1123.6946	562.3509	10
3	298.2125	149.6099					L	1070.6681	535.8377	1053.6415	527.3244	1052.6575	526.8324	9
4	411.2966	206.1519					L	957.5840	479.2956	940.5574	470.7824	939.5734	470.2904	8
5	482.3337	241.6705					A	844.4999	422.7536	827.4734	414.2403	826.4894	413.7483	7
6	595.4178	298.2125					L	773.4628	387.2350	756.4363	378.7218	755.4522	378.2298	6
7	708.5018	354.7546					L	660.3787	330.6930	643.3522	322.1797	642.3682	321.6877	5
8	823.5288	412.2680			805.5182	403.2627	D	547.2947	274.1510	530.2681	265.6377	529.2841	265.1457	4
9	979.6299	490.3186	962.6033	481.8053	961.6193	481.3133	R	432.2677	216.6375	415.2412	208.1242	414.2572	207.6322	3
10	1080.6776	540.8424	1063.6510	532.3291	1062.6670	531.8371	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
11							R	175.1190	88.0631	158.0924	79.5498			1



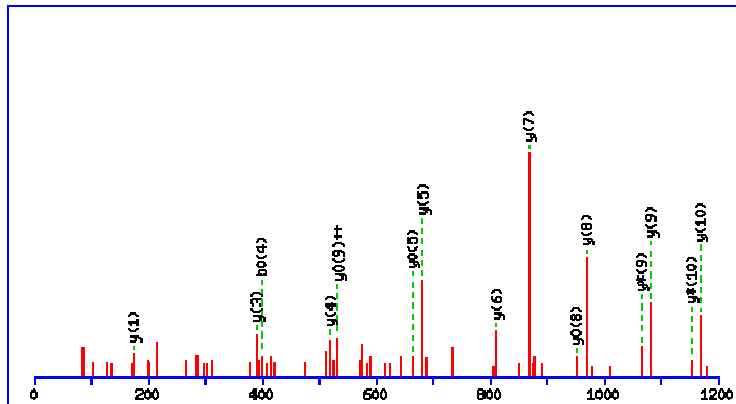
Peptide Number: 57842

MS/MS Fragmentation of **LSNTGEYESQR**Found in **IPI00001022** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PNKD Isoform 2 of Probable hydrolase PNKD

Match to Query 20248: 1282.577968 from(642.296260,2+) index(11179)

Title: Elution from: 62.3166666666667 to 62.3166666666667 period: 0 cycle: 6562 experiment: 8 polarity:+

Data file 120208ry_Tig120slc-P8_2_1.mgf



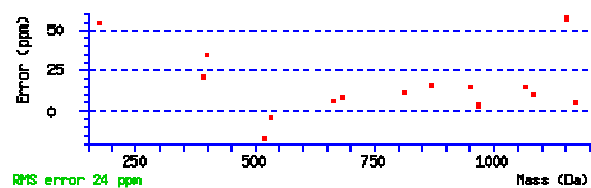
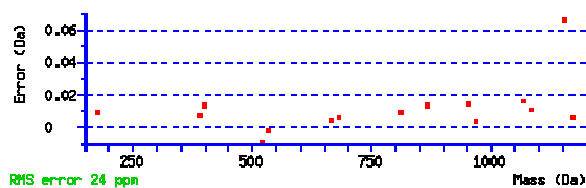
Monoisotopic mass of neutral peptide Mr(calc): 1282.5789

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 74 Expect: 1.4e-006

Matches : 15/110 fragment ions using 22 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							11
2	201.1234	101.0653			183.1128	92.0600	S	1170.5022	585.7547	1153.4756	577.2414	1152.4916	576.7494	10
3	315.1663	158.0868	298.1397	149.5735	297.1557	149.0815	N	1083.4701	542.2387	1066.4436	533.7254	1065.4596	533.2334	9
4	416.2140	208.6106	399.1874	200.0974	398.2034	199.6053	T	969.4272	485.2172	952.4007	476.7040	951.4167	476.2120	8
5	473.2354	237.1214	456.2089	228.6081	455.2249	228.1161	G	868.3795	434.6934	851.3530	426.1801	850.3690	425.6881	7
6	602.2780	301.6427	585.2515	293.1294	584.2675	292.6374	E	811.3581	406.1827	794.3315	397.6694	793.3475	397.1774	6
7	765.3414	383.1743	748.3148	374.6610	747.3308	374.1690	Y	682.3155	341.6614	665.2889	333.1481	664.3049	332.6561	5
8	894.3840	447.6956	877.3574	439.1823	876.3734	438.6903	E	519.2522	260.1297	502.2256	251.6164	501.2416	251.1244	4
9	981.4160	491.2116	964.3894	482.6984	963.4054	482.2063	S	390.2096	195.6084	373.1830	187.0951	372.1990	186.6031	3
10	1109.4746	555.2409	1092.4480	546.7276	1091.4640	546.2356	Q	303.1775	152.0924	286.1510	143.5791			2
11							R	175.1190	88.0631	158.0924	79.5498			1



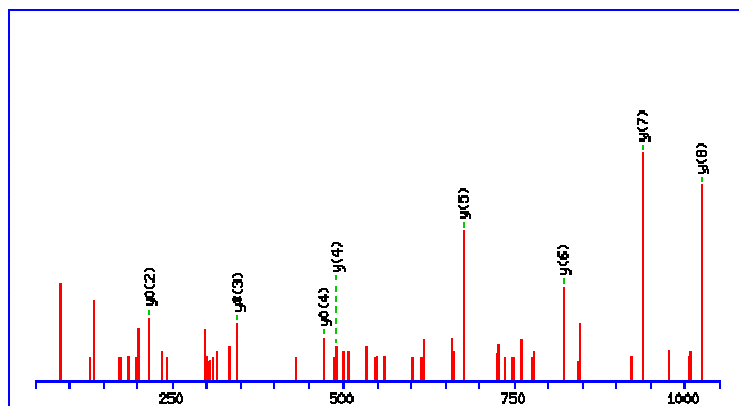
Peptide Number: 57876

MS/MS Fragmentation of **LSDFWQQSK**Found in **IPI00154910** in **IPI_human**, Tax_Id=9606 Gene_Symbol=UBASH3B Ubiquitin-associated and SH3 domain-containing protein B

Match to Query 11374: 1137.553728 from(569.784140,2+) index(27509)

Title: Elution from: 71.5 to 71.5 period: 0 cycle: 2729 experiment: 5 polarity: +

Data file 120206ry_aHDF1419-P10_2_2.mgf



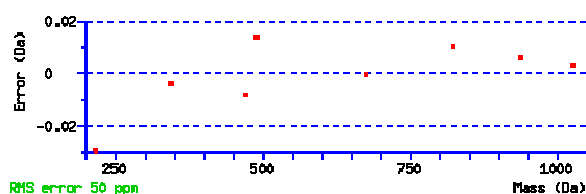
Monoisotopic mass of neutral peptide Mr(calc): 1137.5455

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

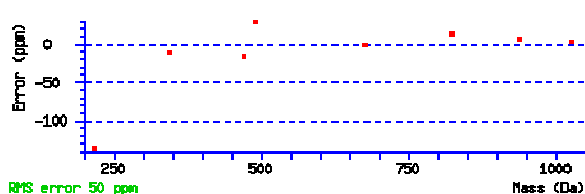
Ions Score: 39 Expect: 0.0064

Matches : 8/82 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							9
2	201.1234	101.0653			183.1128	92.0600	S	1025.4687	513.2380	1008.4421	504.7247	1007.4581	504.2327	8
3	316.1503	158.5788			298.1397	149.5735	D	938.4367	469.7220	921.4101	461.2087	920.4261	460.7167	7
4	463.2187	232.1130			445.2082	223.1077	F	823.4097	412.2085	806.3832	403.6952	805.3991	403.2032	6
5	649.2980	325.1527			631.2875	316.1474	W	676.3413	338.6743	659.3148	330.1610	658.3307	329.6690	5
6	777.3566	389.1819	760.3301	380.6687	759.3461	380.1767	Q	490.2620	245.6346	473.2354	237.1214	472.2514	236.6293	4
7	905.4152	453.2112	888.3886	444.6980	887.4046	444.2060	Q	362.2034	181.6053	345.1769	173.0921	344.1928	172.6001	3
8	992.4472	496.7272	975.4207	488.2140	974.4367	487.7220	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
9							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 50 ppm



RMS error 50 ppm

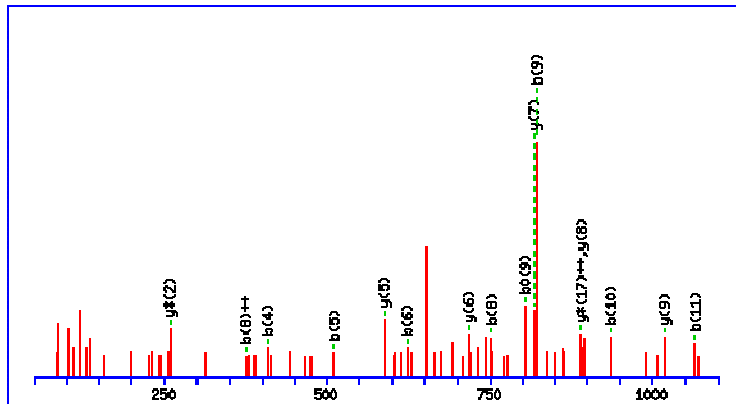
Peptide Number: 58018

MS/MS Fragmentation of **SALHTIAGALEATESLLQK**Found in **IPI00178512** in **IPI_human**, Tax_Id=9606 Gene_Symbol=C1orf112 Isoform 1 of Uncharacterized protein C1orf112

Match to Query 12341: 1952.065602 from(651.695810,3+) index(10745)

Title: Elution from: 26.6166666666667 to 26.6166666666667 period: 0 cycle: 1008 experiment: 1 polarity: +

Data file 120212ry_414C2-43_3_4.mgf



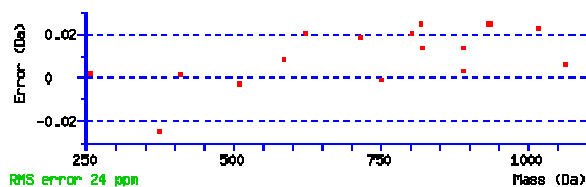
Monoisotopic mass of neutral peptide Mr(calc): 1952.0578

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

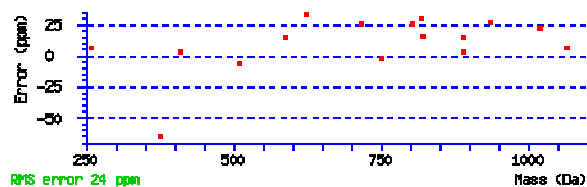
Ions Score: 39 Expect: 0.0042

Matches : 16/174 fragment ions using 28 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							19
2	159.0764	80.0418			141.0659	71.0366	A	1866.0331	933.5202	1849.0066	925.0069	1848.0225	924.5149	18
3	272.1605	136.5839			254.1499	127.5786	L	1794.9960	898.0016	1777.9694	889.4884	1776.9854	888.9964	17
4	409.2194	205.1133			391.2088	196.1081	H	1681.9119	841.4596	1664.8854	832.9463	1663.9014	832.4543	16
5	510.2671	255.6372			492.2565	246.6319	T	1544.8530	772.9301	1527.8265	764.4169	1526.8425	763.9249	15
6	623.3511	312.1792			605.3406	303.1739	I	1443.8053	722.4063	1426.7788	713.8930	1425.7948	713.4010	14
7	694.3883	347.6978			676.3777	338.6925	A	1330.7213	665.8643	1313.6947	657.3510	1312.7107	656.8590	13
8	751.4097	376.2085			733.3992	367.2032	G	1259.6842	630.3457	1242.6576	621.8324	1241.6736	621.3404	12
9	822.4468	411.7271			804.4363	402.7218	A	1202.6627	601.8350	1185.6361	593.3217	1184.6521	592.8297	11
10	935.5309	468.2691			917.5203	459.2638	L	1131.6256	566.3164	1114.5990	557.8032	1113.6150	557.3111	10
11	1064.5735	532.7904			1046.5629	523.7851	E	1018.5415	509.7744	1001.5150	501.2611	1000.5310	500.7691	9
12	1135.6106	568.3089			1117.6000	559.3037	A	889.4989	445.2531	872.4724	436.7398	871.4884	436.2478	8
13	1236.6583	618.8328			1218.6477	609.8275	T	818.4618	409.7345	801.4353	401.2213	800.4512	400.7293	7
14	1365.7009	683.3541			1347.6903	674.3488	E	717.4141	359.2107	700.3876	350.6974	699.4036	350.2054	6
15	1452.7329	726.8701			1434.7223	717.8648	S	588.3715	294.6894	571.3450	286.1761	570.3610	285.6841	5
16	1565.8170	783.4121			1547.8064	774.4068	L	501.3395	251.1734	484.3130	242.6601			4
17	1678.9010	839.9542			1660.8905	830.9489	L	388.2554	194.6314	371.2289	186.1181			3
18	1806.9596	903.9834	1789.9331	895.4702	1788.9490	894.9782	Q	275.1714	138.0893	258.1448	129.5761			2
19							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 24 ppm



RMS error 24 ppm

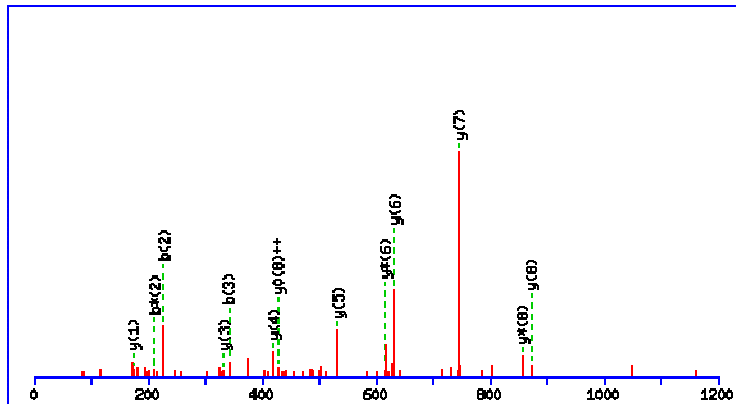
Peptide Number: 58463

MS/MS Fragmentation of **VQIVISSAR**Found in **IPI00736473** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CHTF8 Chromosome transmission fidelity protein 8 homolog

Match to Query 6629: 971.575368 from(486.794960,2+) index(2709)

Title: Elution from: 6.48333333333333 to 6.48333333333333 period: 0 cycle: 243 experiment: 5 polarity: +

Data file 120210ry_32R1-32_2_2.mgf



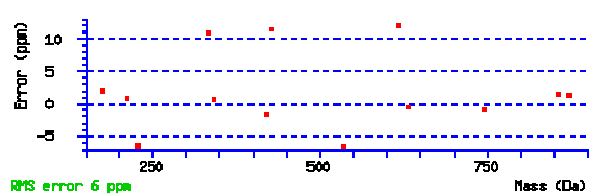
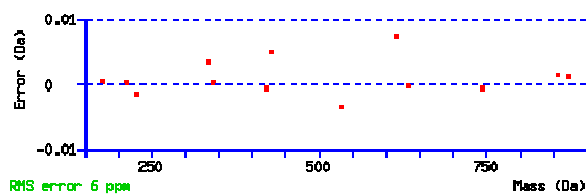
Monoisotopic mass of neutral peptide Mr(calc): 971.5764

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 41 Expect: 0.0042

Matches : 13/80 fragment ions using 32 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							9
2	228.1343	114.5708	211.1077	106.0575			Q	873.5152	437.2613	856.4887	428.7480	855.5047	428.2560	8
3	341.2183	171.1128	324.1918	162.5995			I	745.4567	373.2320	728.4301	364.7187	727.4461	364.2267	7
4	440.2867	220.6470	423.2602	212.1337			V	632.3726	316.6899	615.3461	308.1767	614.3620	307.6847	6
5	553.3708	277.1890	536.3443	268.6758			I	533.3042	267.1557	516.2776	258.6425	515.2936	258.1504	5
6	640.4028	320.7051	623.3763	312.1918	622.3923	311.6998	S	420.2201	210.6137	403.1936	202.1004	402.2096	201.6084	4
7	727.4349	364.2211	710.4083	355.7078	709.4243	355.2158	S	333.1881	167.0977	316.1615	158.5844	315.1775	158.0924	3
8	798.4720	399.7396	781.4454	391.2264	780.4614	390.7343	A	246.1561	123.5817	229.1295	115.0684			2
9							R	175.1190	88.0631	158.0924	79.5498			1



Peptide Number: 58522

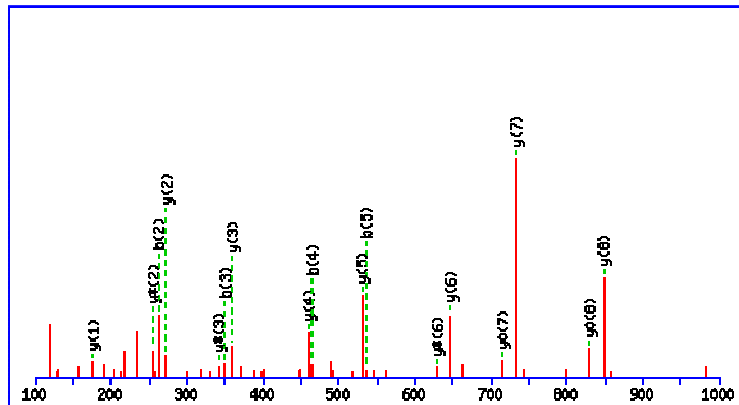
MS/MS Fragmentation of **FDSDATSPR**

Found in **IPI00887572** in **IPI_human**, Tax_Id=9606 Gene_Symbol=HLA-B;HLA-C;HLA-A;MICA;LOC441528 Major histocompatibility complex, class I, B

Match to Query 10230: 994.432668 from(498.223610,2+) index(11535)

Title: Elution from: 61.3 to 61.3 period: 0 cycle: 6104 experiment: 8 polarity:+

Data file 120208ry_Tig120slc-P8_1_1.mgf



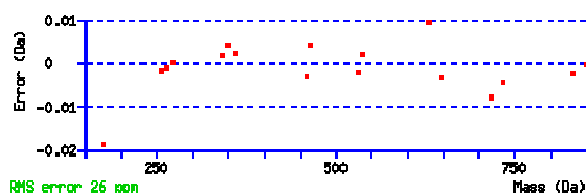
Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 994.4356

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

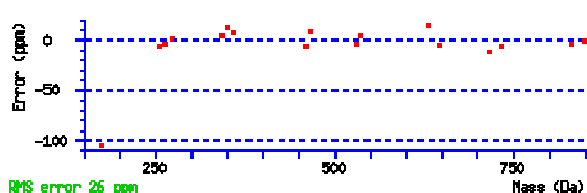
Ions Score: 63 Expect: 9.3e-006

Matches : 17/74 fragment ions using 31 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415			F							9
2	263.1026	132.0550	245.0921	123.0497	D	848.3745	424.6909	831.3479	416.1776	830.3639	415.6856	8
3	350.1347	175.5710	332.1241	166.5657	S	733.3475	367.1774	716.3210	358.6641	715.3369	358.1721	7
4	465.1616	233.0844	447.1510	224.0792	D	646.3155	323.6614	629.2889	315.1481	628.3049	314.6561	6
5	536.1987	268.6030	518.1882	259.5977	A	531.2885	266.1479	514.2620	257.6346	513.2780	257.1426	5
6	637.2464	319.1268	619.2358	310.1216	T	460.2514	230.6293	443.2249	222.1161	442.2409	221.6241	4
7	724.2784	362.6429	706.2679	353.6376	S	359.2037	180.1055	342.1772	171.5922	341.1932	171.1002	3
8	821.3312	411.1692	803.3206	402.1640	P	272.1717	136.5895	255.1452	128.0762			2
9					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 26 ppm



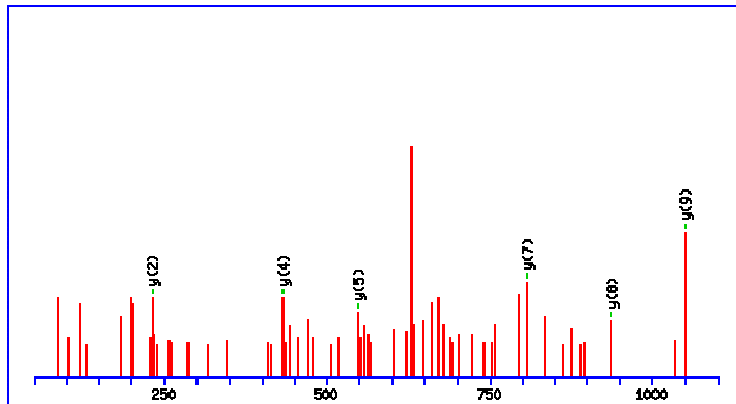
RMS error 26 ppm

Peptide Number: 58682MS/MS Fragmentation of **NLNEFLDAEGR**Found in **IPI00477223** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PNMAL1 Isoform 1 of PNMA-like protein 1

Match to Query 22035: 1276.608108 from(639.311330,2+) index(45800)

Title: Elution from: 110.116666666667 to 110.116666666667 period: 0 cycle: 4057 experiment: 8 polarity:+

Data file 120118ry_201B7-32_2_2.mgf



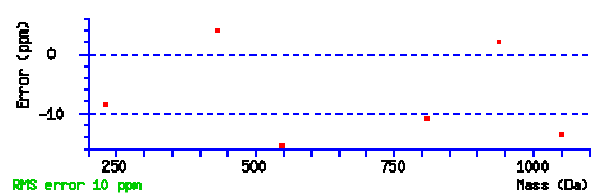
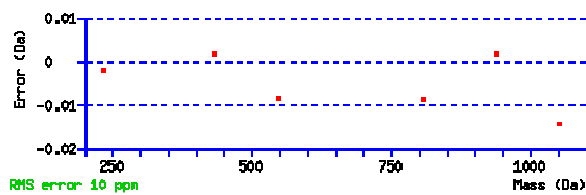
Monoisotopic mass of neutral peptide Mr(calc): 1276.6048

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 44 Expect: 0.0024

Matches : 6/110 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							11
2	228.1343	114.5708	211.1077	106.0575			L	1163.5691	582.2882	1146.5426	573.7749	1145.5586	573.2829	10
3	342.1772	171.5922	325.1506	163.0790			N	1050.4851	525.7462	1033.4585	517.2329	1032.4745	516.7409	9
4	471.2198	236.1135	454.1932	227.6003	453.2092	227.1082	E	936.4421	468.7247	919.4156	460.2114	918.4316	459.7194	8
5	618.2882	309.6477	601.2617	301.1345	600.2776	300.6425	F	807.3995	404.2034	790.3730	395.6901	789.3890	395.1981	7
6	731.3723	366.1898	714.3457	357.6765	713.3617	357.1845	L	660.3311	330.6692	643.3046	322.1559	642.3206	321.6639	6
7	846.3992	423.7032	829.3727	415.1900	828.3886	414.6980	D	547.2471	274.1272	530.2205	265.6139	529.2365	265.1219	5
8	917.4363	459.2218	900.4098	450.7085	899.4258	450.2165	A	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	4
9	1046.4789	523.7431	1029.4524	515.2298	1028.4683	514.7378	E	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	3
10	1103.5004	552.2538	1086.4738	543.7406	1085.4898	543.2485	G	232.1404	116.5738	215.1139	108.0606			2
11							R	175.1190	88.0631	158.0924	79.5498			1



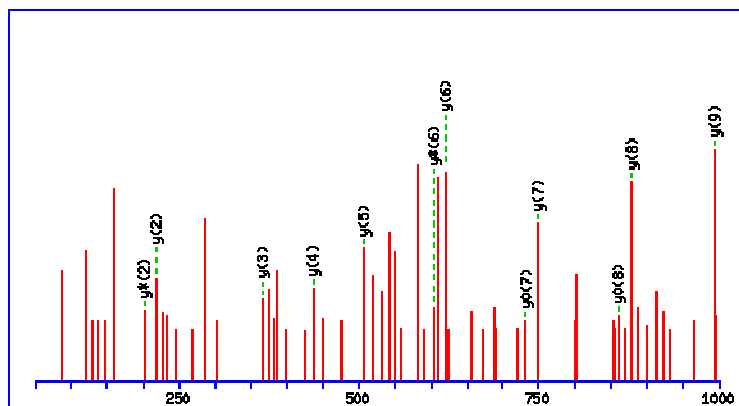
Peptide Number: 59299

MS/MS Fragmentation of **WDEELAAFAK**Found in **IPI00301143** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PI16 Isoform 1 of Peptidase inhibitor 16

Match to Query 3200: 1178.560368 from(590.287460,2+) index(5233)

Title: Elution from: 12.6166666666667 to 12.6166666666667 period: 0 cycle: 480 experiment: 5 polarity: +

Data file 120208ry_Tig120slc-P8_2_3.mgf



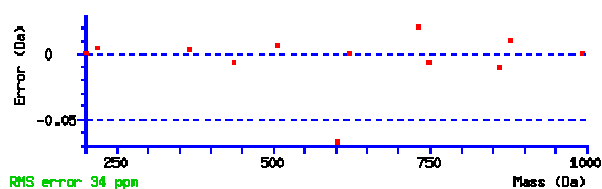
Monoisotopic mass of neutral peptide Mr(calc): 1178.5608

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

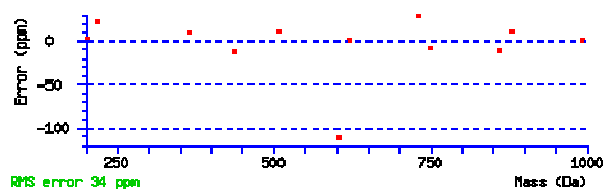
Ions Score: 47 Expect: 0.00098

Matches : 12/76 fragment ions using 29 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	187.0866	94.0469			W							10
2	302.1135	151.5604	284.1030	142.5551	D	993.4888	497.2480	976.4622	488.7347	975.4782	488.2427	9
3	431.1561	216.0817	413.1456	207.0764	E	878.4618	439.7345	861.4353	431.2213	860.4512	430.7293	8
4	560.1987	280.6030	542.1882	271.5977	E	749.4192	375.2132	732.3927	366.7000	731.4087	366.2080	7
5	673.2828	337.1450	655.2722	328.1397	L	620.3766	310.6920	603.3501	302.1787			6
6	744.3199	372.6636	726.3093	363.6583	A	507.2926	254.1499	490.2660	245.6366			5
7	815.3570	408.1821	797.3464	399.1769	A	436.2554	218.6314	419.2289	210.1181			4
8	962.4254	481.7164	944.4149	472.7111	F	365.2183	183.1128	348.1918	174.5995			3
9	1033.4625	517.2349	1015.4520	508.2296	A	218.1499	109.5786	201.1234	101.0653			2
10					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 34 ppm



RMS error 34 ppm

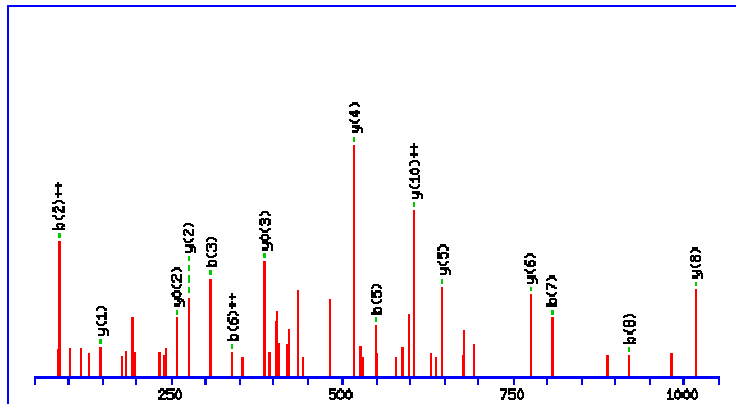
Peptide Number: 59351

MS/MS Fragmentation of **IGHLQEELEEK**Found in **IPI00655762** in **IPI_human**, Tax_Id=9606 Gene_Symbol=GOLGA4 Antigen MU-RMS-40.18 (Fragment)

Match to Query 19381: 1323.672432 from(442.231420,3+) index(1868)

Title: Elution from: 4.33333333333333 to 4.33333333333333 period: 0 cycle: 163 experiment: 1 polarity: +

Data file 120214ry_aHDF1419-P10_4_2.mgf



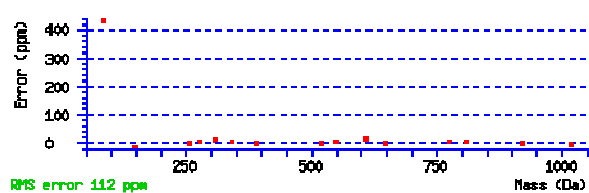
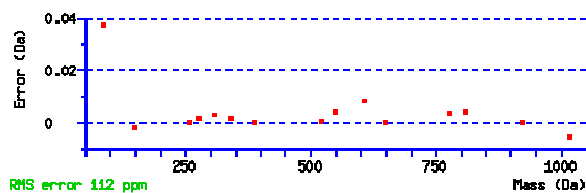
Monoisotopic mass of neutral peptide Mr(calcd): 1323.6670

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 50 Expect: 0.00073

Matches : 15/100 fragment ions using 18 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							11
2	171.1128	86.0600					G	1211.5903	606.2988	1194.5637	597.7855	1193.5797	597.2935	10
3	308.1717	154.5895					H	1154.5688	577.7880	1137.5422	569.2748	1136.5582	568.7828	9
4	421.2558	211.1315					L	1017.5099	509.2586	1000.4833	500.7453	999.4993	500.2533	8
5	549.3144	275.1608	532.2878	266.6475			Q	904.4258	452.7165	887.3993	444.2033	886.4153	443.7113	7
6	678.3570	339.6821	661.3304	331.1688	660.3464	330.6768	E	776.3672	388.6873	759.3407	380.1740	758.3567	379.6820	6
7	807.3995	404.2034	790.3730	395.6901	789.3890	395.1981	E	647.3246	324.1660	630.2981	315.6527	629.3141	315.1607	5
8	920.4836	460.7454	903.4571	452.2322	902.4730	451.7402	L	518.2821	259.6447	501.2555	251.1314	500.2715	250.6394	4
9	1049.5262	525.2667	1032.4997	516.7535	1031.5156	516.2615	E	405.1980	203.1026	388.1714	194.5894	387.1874	194.0974	3
10	1178.5688	589.7880	1161.5422	581.2748	1160.5582	580.7828	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
11							K	147.1128	74.0600	130.0863	65.5468			1



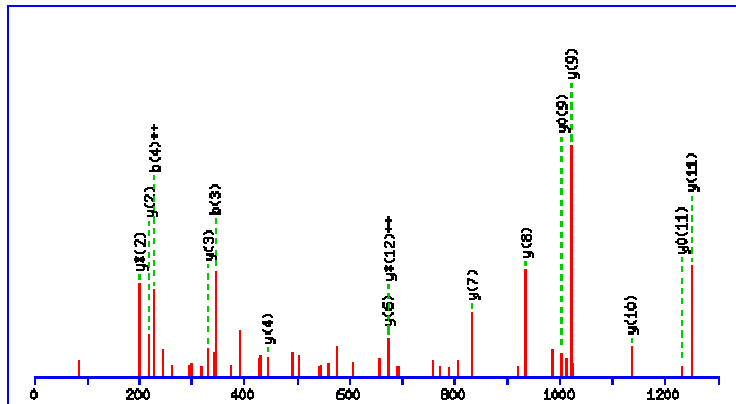
Peptide Number: 59432

MS/MS Fragmentation of **LDDLSTCNDLIAK**Found in **IPI00746936** in **IPI_human**, Tax_Id=9606 Gene_Symbol=OSBP2 Oxysterol-binding protein 2

Match to Query 24406: 1476.717348 from(739.365950,2+) index(17014)

Title: Elution from: 42.9333333333333 to 42.9333333333333 period: 0 cycle: 1641 experiment: 10 polarity: +

Data file 120208ry_Tig120slc-P8_3_2.mgf



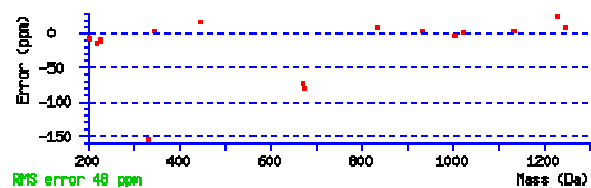
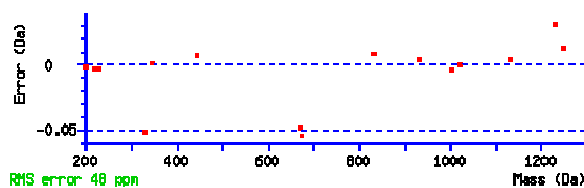
Monoisotopic mass of neutral peptide Mr(calc): 1476.7130

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 55 Expect: 0.00025

Matches : 16/120 fragment ions using 32 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							13
2	229.1183	115.0628			211.1077	106.0575	D	1364.6362	682.8217	1347.6097	674.3085	1346.6257	673.8165	12
3	344.1452	172.5763			326.1347	163.5710	D	1249.6093	625.3083	1232.5827	616.7950	1231.5987	616.3030	11
4	457.2293	229.1183			439.2187	220.1130	L	1134.5823	567.7948	1117.5558	559.2815	1116.5718	558.7895	10
5	544.2613	272.6343			526.2508	263.6290	S	1021.4983	511.2528	1004.4717	502.7395	1003.4877	502.2475	9
6	645.3090	323.1581			627.2984	314.1529	T	934.4662	467.7368	917.4397	459.2235	916.4557	458.7315	8
7	805.3396	403.1735			787.3291	394.1682	C	833.4186	417.2129	816.3920	408.6996	815.4080	408.2076	7
8	919.3826	460.1949	902.3560	451.6817	901.3720	451.1896	N	673.3879	337.1976	656.3614	328.6843	655.3774	328.1923	6
9	1034.4095	517.7084	1017.3830	509.1951	1016.3990	508.7031	D	559.3450	280.1761	542.3184	271.6629	541.3344	271.1708	5
10	1147.4936	574.2504	1130.4670	565.7372	1129.4830	565.2451	L	444.3180	222.6627	427.2915	214.1494			4
11	1260.5776	630.7925	1243.5511	622.2792	1242.5671	621.7872	I	331.2340	166.1206	314.2074	157.6074			3
12	1331.6148	666.3110	1314.5882	657.7977	1313.6042	657.3057	A	218.1499	109.5786	201.1234	101.0653			2
13							K	147.1128	74.0600	130.0863	65.5468			1



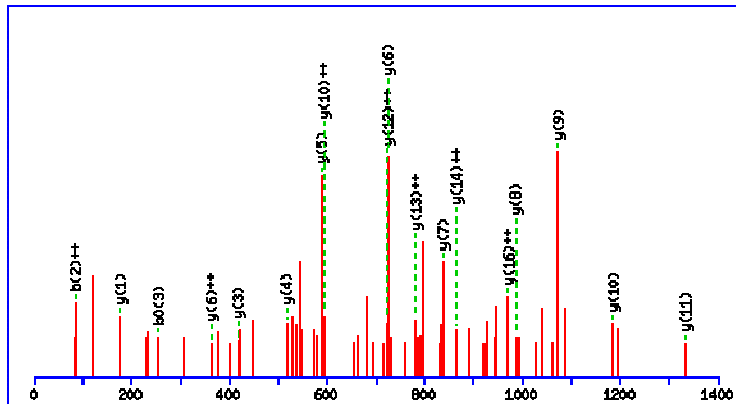
Peptide Number: 59604

MS/MS Fragmentation of **LGTTNYDDFLSFIHAVQDR**Found in **IPI00103521** in **IPI_human**, Tax_Id=9606 Gene_Symbol=STON2 Stonin-2

Match to Query 18295: 2211.084492 from(738.035440,3+) index(13248)

Title: Elution from: 32.65 to 32.65 period: 0 cycle: 1236 experiment: 7 polarity:+

Data file 120212ry_414C2-43_3_4.mgf



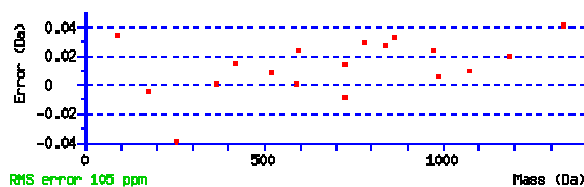
Monoisotopic mass of neutral peptide Mr(calc): 2211.0597

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

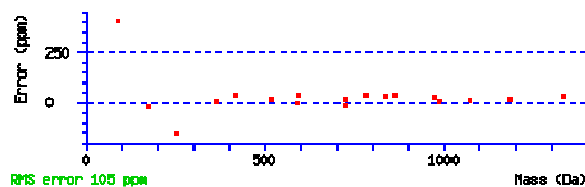
Ions Score: 48 Expect: 0.00088

Matches : 18/202 fragment ions using 42 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							19
2	171.1128	86.0600					G	2098.9829	1049.9951	2081.9563	1041.4818	2080.9723	1040.9898	18
3	272.1605	136.5839			254.1499	127.5786	T	2041.9614	1021.4843	2024.9348	1012.9711	2023.9508	1012.4791	17
4	373.2082	187.1077			355.1976	178.1024	T	1940.9137	970.9605	1923.8872	962.4472	1922.9032	961.9552	16
5	487.2511	244.1292	470.2245	235.6159	469.2405	235.1239	N	1839.8660	920.4367	1822.8395	911.9234	1821.8555	911.4314	15
6	650.3144	325.6608	633.2879	317.1476	632.3039	316.6556	Y	1725.8231	863.4152	1708.7966	854.9019	1707.8125	854.4099	14
7	765.3414	383.1743	748.3148	374.6610	747.3308	374.1690	D	1562.7598	781.8835	1545.7332	773.3703	1544.7492	772.8782	13
8	880.3683	440.6878	863.3418	432.1745	862.3577	431.6825	D	1447.7328	724.3701	1430.7063	715.8568	1429.7223	715.3648	12
9	1027.4367	514.2220	1010.4102	505.7087	1009.4262	505.2167	F	1332.7059	666.8566	1315.6793	658.3433	1314.6953	657.8513	11
10	1140.5208	570.7640	1123.4942	562.2508	1122.5102	561.7587	L	1185.6375	593.3224	1168.6109	584.8091	1167.6269	584.3171	10
11	1227.5528	614.2800	1210.5263	605.7668	1209.5422	605.2748	S	1072.5534	536.7803	1055.5269	528.2671	1054.5429	527.7751	9
12	1374.6212	687.8143	1357.5947	679.3010	1356.6107	678.8090	F	985.5214	493.2643	968.4948	484.7511	967.5108	484.2591	8
13	1487.7053	744.3563	1470.6787	735.8430	1469.6947	735.3510	I	838.4530	419.7301	821.4264	411.2169	820.4424	410.7248	7
14	1624.7642	812.8857	1607.7377	804.3725	1606.7536	803.8805	H	725.3689	363.1881	708.3424	354.6748	707.3583	354.1828	6
15	1695.8013	848.4043	1678.7748	839.8910	1677.7907	839.3990	A	588.3100	294.6586	571.2835	286.1454	570.2994	285.6534	5
16	1794.8697	897.9385	1777.8432	889.4252	1776.8592	888.9332	V	517.2729	259.1401	500.2463	250.6268	499.2623	250.1348	4
17	1922.9283	961.9678	1905.9018	953.4545	1904.9177	952.9625	Q	418.2045	209.6059	401.1779	201.0926	400.1939	200.6006	3
18	2037.9552	1019.4813	2020.9287	1010.9680	2019.9447	1010.4760	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
19							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 105 ppm



RMS error 105 ppm

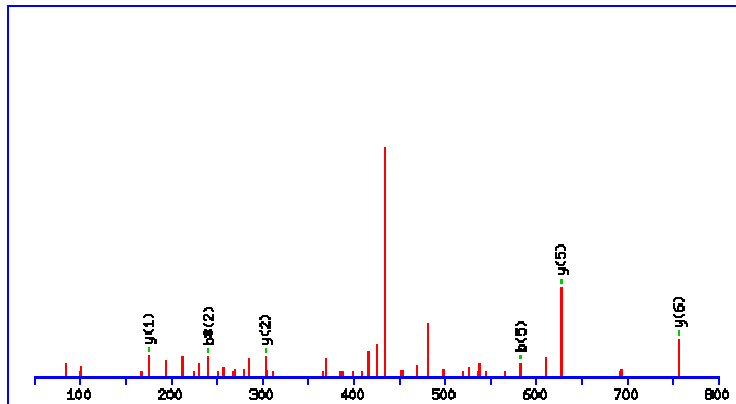
Peptide Number: 59906**MS/MS Fragmentation of QEDPLQR**

Found in **IPI00479643** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SRCIN1 Isoform 1 of SRC kinase signaling inhibitor 1

Match to Query 6526: 884.436728 from(443.225640,2+) index(8772)

Title: Elution from: 56.3333333333333 to 56.3333333333333 period: 0 cycle: 6331 experiment: 2 polarity: +

Data file 120208ry_Tig120slc-P8_2_1.mgf



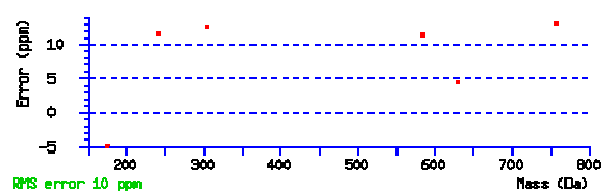
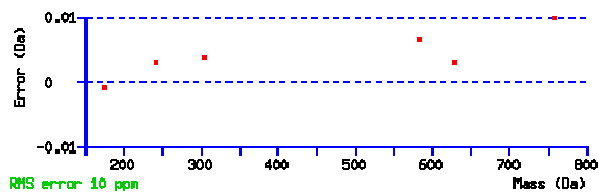
Monoisotopic mass of neutral peptide Mr(calcd): 884.4352

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 39 **Expect:** 0.0041

Matches : 6/62 fragment ions using 7 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.0659	65.0366	112.0393	56.5233			Q							7
2	258.1084	129.5579	241.0819	121.0446	240.0979	120.5526	E	757.3839	379.1956	740.3573	370.6823	739.3733	370.1903	6
3	373.1354	187.0713	356.1088	178.5581	355.1248	178.0661	D	628.3413	314.6743	611.3148	306.1610	610.3307	305.6690	5
4	470.1882	235.5977	453.1616	227.0844	452.1776	226.5924	P	513.3144	257.1608	496.2878	248.6475			4
5	583.2722	292.1397	566.2457	283.6265	565.2617	283.1345	L	416.2616	208.6344	399.2350	200.1212			3
6	711.3308	356.1690	694.3042	347.6558	693.3202	347.1638	Q	303.1775	152.0924	286.1510	143.5791			2
7							R	175.1190	88.0631	158.0924	79.5498			1



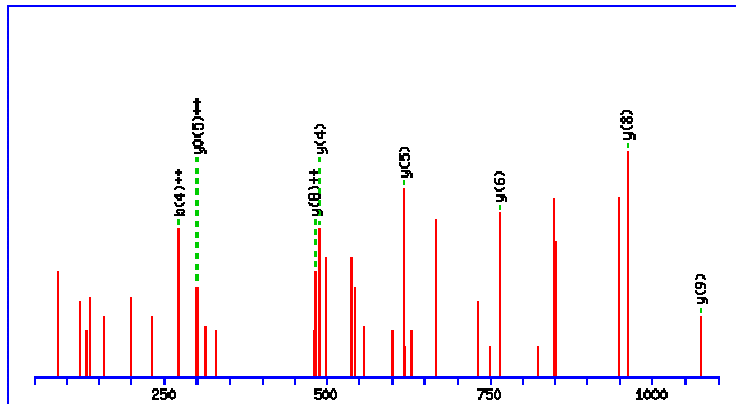
Peptide Number: 60184

MS/MS Fragmentation of **EYYSIPVMEFHGK**Found in **IPI00374192** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ANKAR Isoform 1 of Ankyrin and armadillo repeat-containing protein

Match to Query 12747: 1614.754812 from(539.258880,3+) index(38792)

Title: Elution from: 107.55 to 107.55 period: 0 cycle: 4125 experiment: 2 polarity: +

Data file 120208ry_Tig120slc-P8_1_3.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1614.7388

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

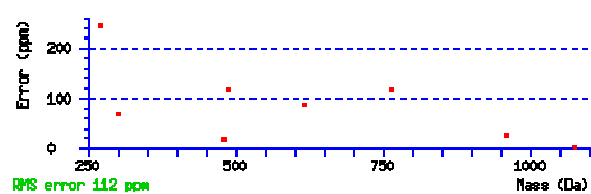
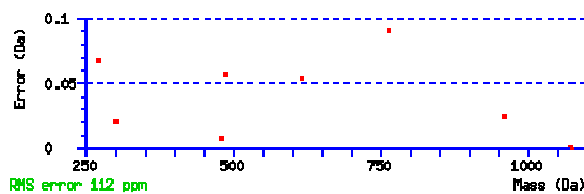
Variable modifications:

MS : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

Ions Score: 36 Expect: 0.01

Matches : 8/174 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286	112.0393	56.5233	E							13
2	293.1132	147.0602	275.1026	138.0550	Y	1486.7035	743.8554	1469.6770	735.3421	1468.6929	734.8501	12
3	456.1765	228.5919	438.1660	219.5866	Y	1323.6402	662.3237	1306.6136	653.8105	1305.6296	653.3184	11
4	543.2086	272.1079	525.1980	263.1026	S	1160.5769	580.7921	1143.5503	572.2788	1142.5663	571.7868	10
5	656.2926	328.6499	638.2821	319.6447	I	1073.5448	537.2761	1056.5183	528.7628	1055.5343	528.2708	9
6	753.3454	377.1763	735.3348	368.1710	P	960.4608	480.7340	943.4342	472.2207	942.4502	471.7287	8
7	852.4138	426.7105	834.4032	417.7053	V	863.4080	432.2076	846.3815	423.6944	845.3974	423.2024	7
8	999.4492	500.2282	981.4386	491.2230	M	764.3396	382.6734	747.3130	374.1602	746.3290	373.6681	6
9	1128.4918	564.7495	1110.4812	555.7443	E	617.3042	309.1557	600.2776	300.6425	599.2936	300.1504	5
10	1275.5602	638.2837	1257.5496	629.2785	F	488.2616	244.6344	471.2350	236.1212			4
11	1412.6191	706.8132	1394.6086	697.8079	H	341.1932	171.1002	324.1666	162.5870			3
12	1469.6406	735.3239	1451.6300	726.3186	G	204.1343	102.5708	187.1077	94.0575			2
13					K	147.1128	74.0600	130.0863	65.5468			1



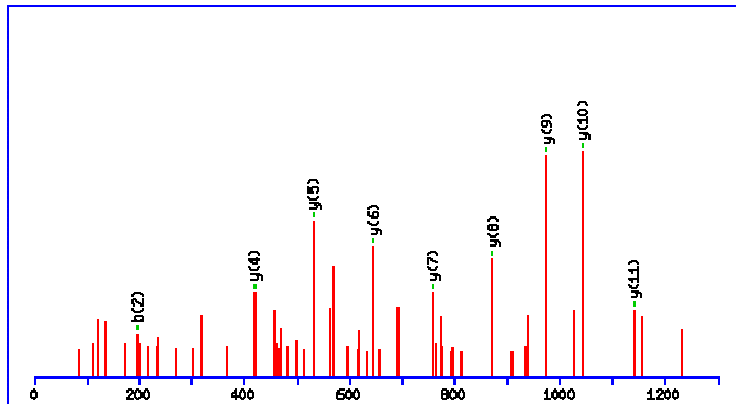
Peptide Number: 60454

MS/MS Fragmentation of **VPATNLILGEGR**Found in **IPI00420065** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ACAD11 Isoform 1 of Acyl-CoA dehydrogenase family member 11

Match to Query 15424: 1238.678468 from(620.346510,2+) index(29937)

Title: Elution from: 77.1833333333333 to 77.1833333333333 period: 0 cycle: 2952 experiment: 8 polarity:+

Data file 120208ry_Tig120slc-P8_1_2.mgf



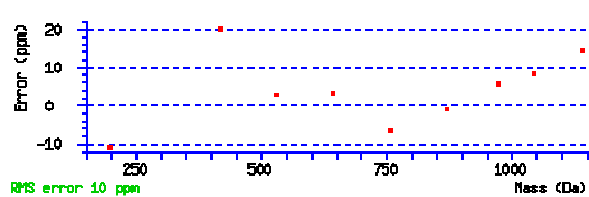
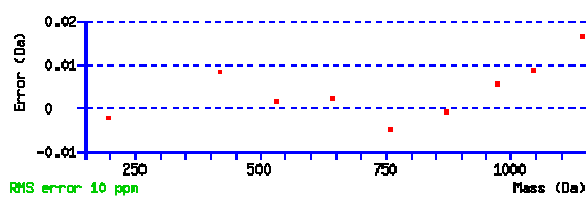
Monoisotopic mass of neutral peptide Mr(calc): 1238.6983

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 71 Expect: 3.4e-006

Matches : 9/114 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							12
2	197.1285	99.0679					P	1140.6371	570.8222	1123.6106	562.3089	1122.6266	561.8169	11
3	268.1656	134.5864					A	1043.5844	522.2958	1026.5578	513.7826	1025.5738	513.2905	10
4	369.2132	185.1103			351.2027	176.1050	T	972.5473	486.7773	955.5207	478.2640	954.5367	477.7720	9
5	483.2562	242.1317	466.2296	233.6185	465.2456	233.1264	N	871.4996	436.2534	854.4730	427.7402	853.4890	427.2482	8
6	596.3402	298.6738	579.3137	290.1605	578.3297	289.6685	L	757.4567	379.2320	740.4301	370.7187	739.4461	370.2267	7
7	709.4243	355.2158	692.3978	346.7025	691.4137	346.2105	I	644.3726	322.6899	627.3461	314.1767	626.3620	313.6847	6
8	822.5084	411.7578	805.4818	403.2445	804.4978	402.7525	L	531.2885	266.1479	514.2620	257.6346	513.2780	257.1426	5
9	879.5298	440.2686	862.5033	431.7553	861.5193	431.2633	G	418.2045	209.6059	401.1779	201.0926	400.1939	200.6006	4
10	1008.5724	504.7898	991.5459	496.2766	990.5619	495.7846	E	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	3
11	1065.5939	533.3006	1048.5673	524.7873	1047.5833	524.2953	G	232.1404	116.5738	215.1139	108.0606			2
12							R	175.1190	88.0631	158.0924	79.5498			1



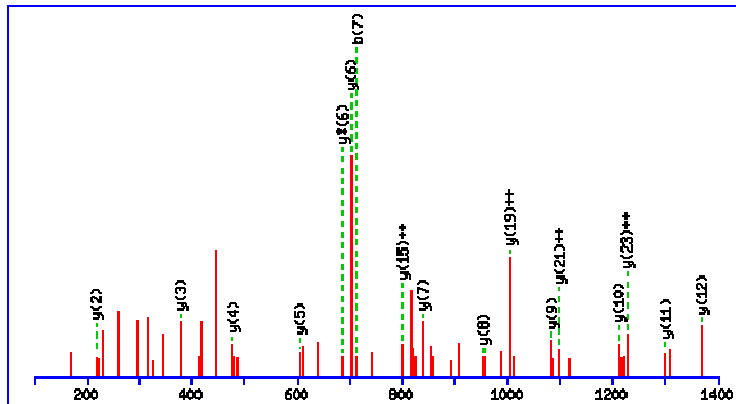
Peptide Number: 60505

MS/MS Fragmentation of **LGVPCEPAELGGDASEEDHPQVCAK**Found in **IPI01012706** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SALL2 cDNA FLJ58537, highly similar to Sal-like protein 2

Match to Query 47287: 2721.189072 from(908.070300,3+) index(28079)

Title: Elution from: 68.1666666666667 to 68.1666666666667 period: 0 cycle: 2580 experiment: 10 polarity:+

Data file 120210ry_32R1-32_3_2.mgf



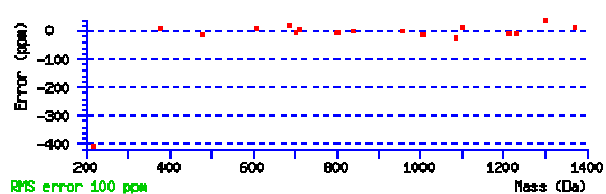
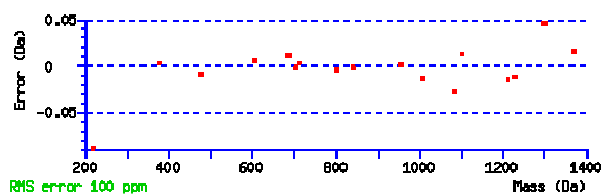
Monoisotopic mass of neutral peptide Mr(calc): 2721.2011

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 42 Expect: 0.00087

Matches : 17/232 fragment ions using 44 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							26
2	171.1128	86.0600					G	2609.1243	1305.0658	2592.0977	1296.5525	2591.1137	1296.0605	25
3	270.1812	135.5942					V	2552.1028	1276.5550	2535.0762	1268.0418	2534.0922	1267.5498	24
4	367.2340	184.1206					P	2453.0344	1227.0208	2436.0078	1218.5076	2435.0238	1218.0155	23
5	527.2646	264.1360					C	2355.9816	1178.4944	2338.9551	1169.9812	2337.9711	1169.4892	22
6	584.2861	292.6467					G	2195.9510	1098.4791	2178.9244	1089.9658	2177.9404	1089.4738	21
7	713.3287	357.1680			695.3181	348.1627	E	2138.9295	1069.9684	2121.9030	1061.4551	2120.9189	1060.9631	20
8	810.3815	405.6944			792.3709	396.6891	P	2009.8869	1005.4471	1992.8604	996.9338	1991.8763	996.4418	19
9	881.4186	441.2129			863.4080	432.2076	A	1912.8341	956.9207	1895.8076	948.4074	1894.8236	947.9154	18
10	1010.4612	505.7342			992.4506	496.7289	E	1841.7970	921.4022	1824.7705	912.8889	1823.7865	912.3969	17
11	1123.5452	562.2762			1105.5347	553.2710	L	1712.7544	856.8809	1695.7279	848.3676	1694.7439	847.8756	16
12	1180.5667	590.7870			1162.5561	581.7817	G	1599.6704	800.3388	1582.6438	791.8256	1581.6598	791.3335	15
13	1237.5882	619.2977			1219.5776	610.2924	G	1542.6489	771.8281	1525.6224	763.3148	1524.6383	762.8228	14
14	1352.6151	676.8112			1334.6045	667.8059	D	1485.6274	743.3174	1468.6009	734.8041	1467.6169	734.3121	13
15	1423.6522	712.3297			1405.6416	703.3245	A	1370.6005	685.8039	1353.5740	677.2906	1352.5899	676.7986	12
16	1510.6842	755.8458			1492.6737	746.8405	S	1299.5634	650.2853	1282.5368	641.7721	1281.5528	641.2801	11
17	1639.7268	820.3671			1621.7163	811.3618	E	1212.5314	606.7693	1195.5048	598.2560	1194.5208	597.7640	10
18	1768.7694	884.8883			1750.7589	875.8831	E	1083.4888	542.2480	1066.4622	533.7347	1065.4782	533.2427	9
19	1883.7964	942.4018			1865.7858	933.3965	D	954.4462	477.7267	937.4196	469.2135	936.4356	468.7214	8
20	2020.8553	1010.9313			2002.8447	1001.9260	H	839.4192	420.2133	822.3927	411.7000			7
21	2117.9080	1059.4577			2099.8975	1050.4524	P	702.3603	351.6838	685.3338	343.1705			6
22	2245.9666	1123.4869	2228.9401	1114.9737	2227.9561	1114.4817	Q	605.3076	303.1574	588.2810	294.6441			5
23	2345.0350	1173.0212	2328.0085	1164.5079	2327.0245	1164.0159	V	477.2490	239.1281	460.2224	230.6149			4
24	2505.0657	1253.0365	2488.0391	1244.5232	2487.0551	1244.0312	C	378.1806	189.5939	361.1540	181.0806			3
25	2576.1028	1288.5550	2559.0762	1280.0418	2558.0922	1279.5498	A	218.1499	109.5786	201.1234	101.0653			2
26							K	147.1128	74.0600	130.0863	65.5468			1

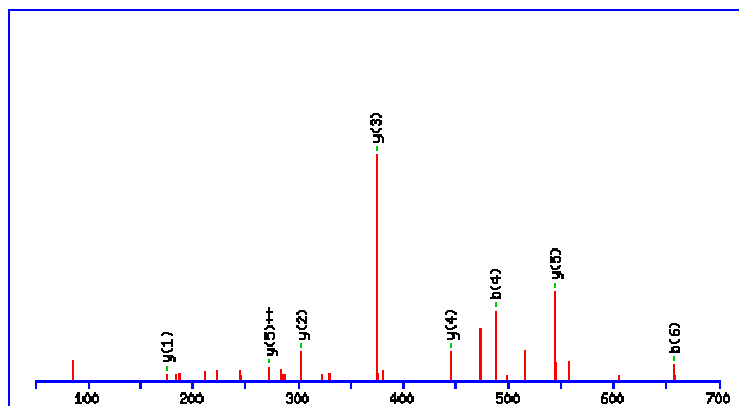


Peptide Number: 60557**MS/MS Fragmentation of CVVKVAAKR**Found in **IPI00165990** in **IPI_human**, Tax_Id=9606 Gene_Symbol=RFX4 Isoform 4 of Transcription factor RFX4

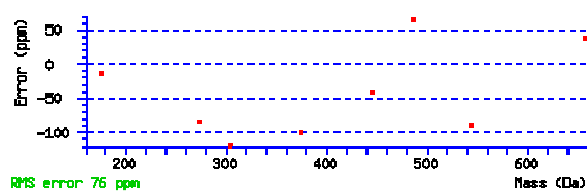
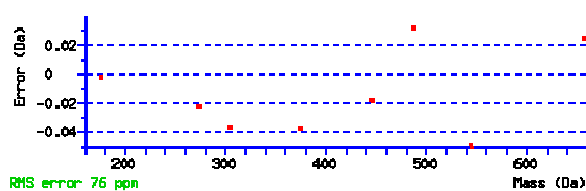
Match to Query 12293: 1029.595962 from(344.205930,3+) index(26552)

Title: Elution from: 63.9333333333333 to 63.9333333333333 period: 0 cycle: 2395 experiment: 1 polarity:+

Data file 120126ry_585A1-55_2.mgf

**Monoisotopic mass of neutral peptide Mr(calc):** 1029.6117**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 38 **Expect:** 0.0098**Matches :** 8/58 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	#
1	161.0379	81.0226			C					9
2	260.1063	130.5568			V	870.5883	435.7978	853.5618	427.2845	8
3	359.1748	180.0910			V	771.5199	386.2636	754.4934	377.7503	7
4	487.2697	244.1385	470.2432	235.6252	K	672.4515	336.7294	655.4250	328.2161	6
5	586.3381	293.6727	569.3116	285.1594	V	544.3566	272.6819	527.3300	264.1686	5
6	657.3752	329.1913	640.3487	320.6780	A	445.2881	223.1477	428.2616	214.6344	4
7	728.4124	364.7098	711.3858	356.1965	A	374.2510	187.6292	357.2245	179.1159	3
8	856.5073	428.7573	839.4808	420.2440	K	303.2139	152.1106	286.1874	143.5973	2
9					R	175.1190	88.0631	158.0924	79.5498	1



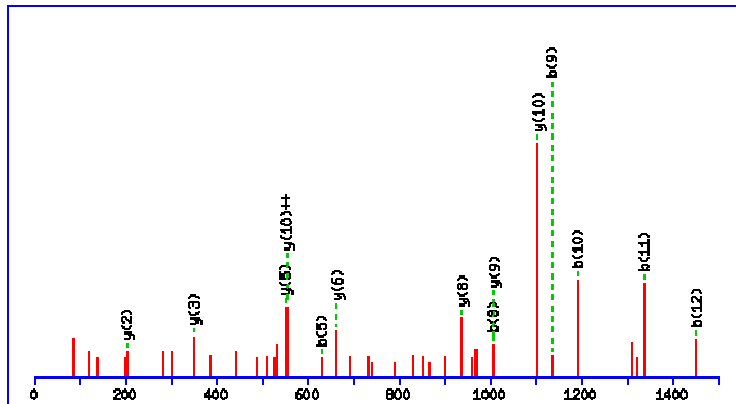
Peptide Number: 61183

MS/MS Fragmentation of **EYAEHCTDEGFIPACLLSLFGK**Found in **IPI00290547** in **IPI_human**, Tax_Id=9606 Gene_Symbol=NPAT Protein NPAT

Match to Query 25891: 2556.165252 from(853.062360,3+) index(31536)

Title: Elution from: 78.85 to 78.85 period: 0 cycle: 2947 experiment: 4 polarity: +

Data file 120118ry_201B7-32_1_4.mgf



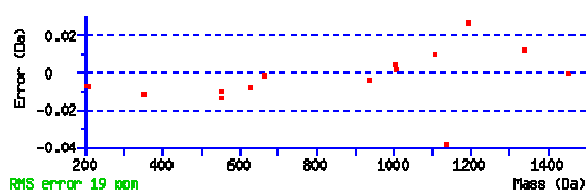
Monoisotopic mass of neutral peptide Mr(calc): 2556.1665

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

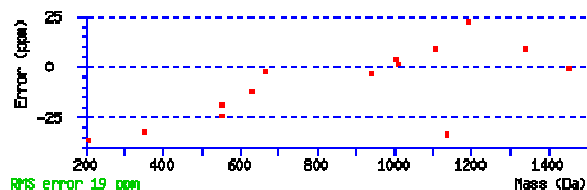
Ions Score: 47 Expect: 0.0007

Matches : 14/202 fragment ions using 26 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286	112.0393	56.5233	E							22
2	293.1132	147.0602	275.1026	138.0550	Y	2428.1312	1214.5692	2411.1046	1206.0560	2410.1206	1205.5639	21
3	364.1503	182.5788	346.1397	173.5735	A	2265.0679	1133.0376	2248.0413	1124.5243	2247.0573	1124.0323	20
4	493.1929	247.1001	475.1823	238.0948	E	2194.0307	1097.5190	2177.0042	1089.0057	2176.0202	1088.5137	19
5	630.2518	315.6295	612.2413	306.6243	H	2064.9881	1032.9977	2047.9616	1024.4844	2046.9776	1023.9924	18
6	790.2825	395.6449	772.2719	386.6396	C	1927.9292	964.4683	1910.9027	955.9550	1909.9187	955.4630	17
7	891.3301	446.1687	873.3196	437.1634	T	1767.8986	884.4529	1750.8720	875.9397	1749.8880	875.4476	16
8	1006.3571	503.6822	988.3465	494.6769	D	1666.8509	833.9291	1649.8244	825.4158	1648.8403	824.9238	15
9	1135.3997	568.2035	1117.3891	559.1982	E	1551.8240	776.4156	1534.7974	767.9023	1533.8134	767.4103	14
10	1192.4211	596.7142	1174.4106	587.7089	G	1422.7814	711.8943	1405.7548	703.3810	1404.7708	702.8890	13
11	1339.4896	670.2484	1321.4790	661.2431	F	1365.7599	683.3836	1348.7334	674.8703	1347.7493	674.3783	12
12	1452.5736	726.7904	1434.5631	717.7852	I	1218.6915	609.8494	1201.6649	601.3361	1200.6809	600.8441	11
13	1549.6264	775.3168	1531.6158	766.3115	P	1105.6074	553.3074	1088.5809	544.7941	1087.5969	544.3021	10
14	1620.6635	810.8354	1602.6529	801.8301	A	1008.5547	504.7810	991.5281	496.2677	990.5441	495.7757	9
15	1780.6942	890.8507	1762.6836	881.8454	C	937.5176	469.2624	920.4910	460.7491	919.5070	460.2571	8
16	1893.7782	947.3927	1875.7676	938.3875	L	777.4869	389.2471	760.4604	380.7338	759.4763	380.2418	7
17	2006.8623	1003.9348	1988.8517	994.9295	L	664.4028	332.7051	647.3763	324.1918	646.3923	323.6998	6
18	2093.8943	1047.4508	2075.8837	1038.4455	S	551.3188	276.1630	534.2922	267.6498	533.3082	267.1577	5
19	2206.9784	1103.9928	2188.9678	1094.9875	L	464.2867	232.6470	447.2602	224.1337			4
20	2354.0468	1177.5270	2336.0362	1168.5217	F	351.2027	176.1050	334.1761	167.5917			3
21	2411.0682	1206.0378	2393.0577	1197.0325	G	204.1343	102.5708	187.1077	94.0575			2
22					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 19 ppm



RMS error 19 ppm

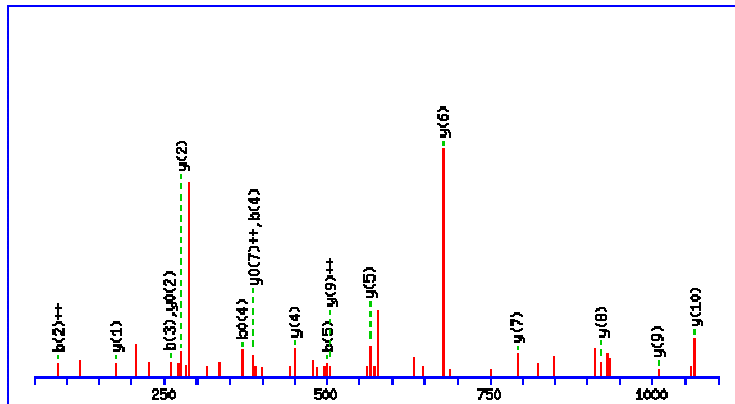
Peptide Number: 61529

MS/MS Fragmentation of **LGSEIDSSTR**Found in **IPI00396963** in **IPI_human**, Tax_Id=9606 Gene_Symbol=DSTYK Isoform 2 of Dual serine/threonine and tyrosine protein kinase

Match to Query 12098: 1176.614348 from(589.314450,2+) index(530)

Title: Elution from: 1.56666666666667 to 1.56666666666667 period: 0 cycle: 62 experiment: 6 polarity:+

Data file 120208ry_Tig120slc-P8_3_2.mgf



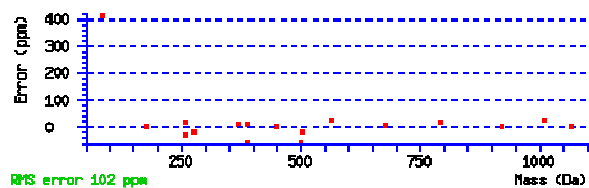
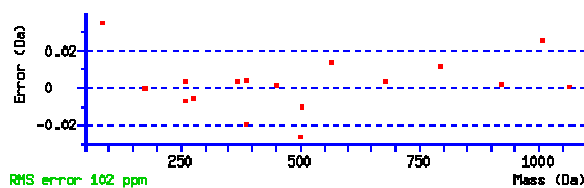
Monoisotopic mass of neutral peptide Mr(calc): 1176.5986

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 53 Expect: 0.00035

Matches : 17/94 fragment ions using 34 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							11
2	171.1128	86.0600			G	1064.5218	532.7646	1047.4953	524.2513	1046.5113	523.7593	10
3	258.1448	129.5761	240.1343	120.5708	S	1007.5004	504.2538	990.4738	495.7406	989.4898	495.2485	9
4	387.1874	194.0974	369.1769	185.0921	E	920.4684	460.7378	903.4418	452.2245	902.4578	451.7325	8
5	500.2715	250.6394	482.2609	241.6341	I	791.4258	396.2165	774.3992	387.7032	773.4152	387.2112	7
6	613.3556	307.1814	595.3450	298.1761	I	678.3417	339.6745	661.3151	331.1612	660.3311	330.6692	6
7	728.3825	364.6949	710.3719	355.6896	D	565.2576	283.1325	548.2311	274.6192	547.2471	274.1272	5
8	815.4145	408.2109	797.4040	399.2056	S	450.2307	225.6190	433.2041	217.1057	432.2201	216.6137	4
9	902.4466	451.7269	884.4360	442.7216	S	363.1987	182.1030	346.1721	173.5897	345.1881	173.0977	3
10	1003.4942	502.2508	985.4837	493.2455	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
11					R	175.1190	88.0631	158.0924	79.5498			1



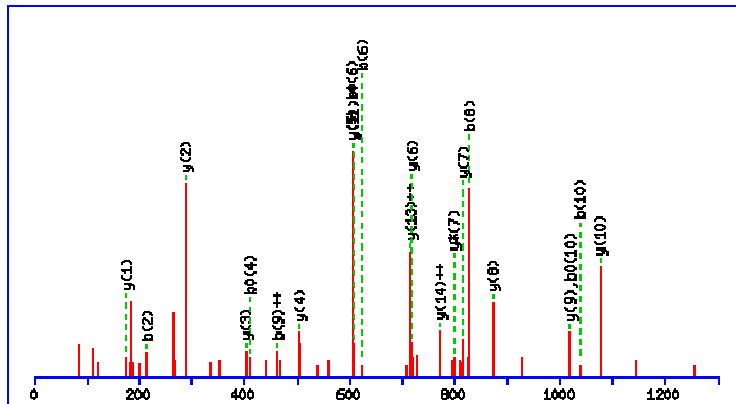
Peptide Number: 61562

MS/MS Fragmentation of **VLSEHGFGPITTDIR**Found in **IPI00006592** in **IPI_human**, Tax_Id=9606 Gene_Symbol=MSRA Isoform 1 of Mitochondrial peptide methionine sulfoxide reductase

Match to Query 30245: 1640.855892 from(547.959240,3+) index(37405)

Title: Elution from: 97.4666666666667 to 97.4666666666667 period: 0 cycle: 3737 experiment: 4 polarity: +

Data file 120208ry_Tig120slc-P8_1_2.mgf



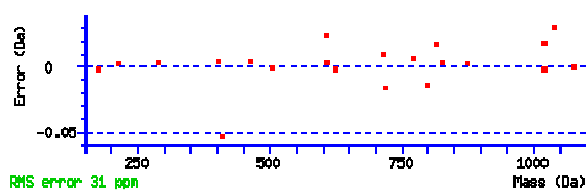
Monoisotopic mass of neutral peptide Mr(calc): 1640.8522

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

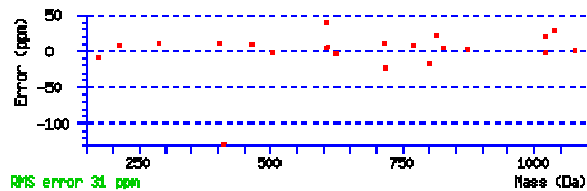
Ions Score: 64 Expect: 2.5e-005

Matches : 22/132 fragment ions using 37 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415			V							15
2	213.1598	107.0835			L	1542.7911	771.8992	1525.7645	763.3859	1524.7805	762.8939	14
3	300.1918	150.5995	282.1812	141.5942	S	1429.7070	715.3571	1412.6805	706.8439	1411.6965	706.3519	13
4	429.2344	215.1208	411.2238	206.1155	E	1342.6750	671.8411	1325.6484	663.3279	1324.6644	662.8359	12
5	566.2933	283.6503	548.2827	274.6450	H	1213.6324	607.3198	1196.6059	598.8066	1195.6218	598.3146	11
6	623.3148	312.1610	605.3042	303.1557	G	1076.5735	538.7904	1059.5469	530.2771	1058.5629	529.7851	10
7	770.3832	385.6952	752.3726	376.6899	F	1019.5520	510.2796	1002.5255	501.7664	1001.5415	501.2744	9
8	827.4046	414.2060	809.3941	405.2007	G	872.4836	436.7454	855.4571	428.2322	854.4730	427.7402	8
9	924.4574	462.7323	906.4468	453.7271	P	815.4621	408.2347	798.4356	399.7214	797.4516	399.2294	7
10	1037.5415	519.2744	1019.5309	510.2691	I	718.4094	359.7083	701.3828	351.1951	700.3988	350.7030	6
11	1138.5891	569.7982	1120.5786	560.7929	T	605.3253	303.1663	588.2988	294.6530	587.3148	294.1610	5
12	1239.6368	620.3220	1221.6263	611.3168	T	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	4
13	1354.6638	677.8355	1336.6532	668.8302	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
14	1467.7478	734.3775	1449.7373	725.3723	I	288.2030	144.6051	271.1765	136.0919			2
15					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 31 ppm



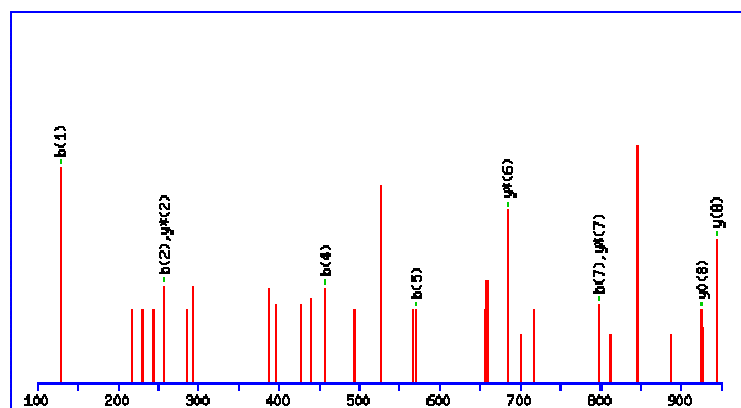
RMS error 31 ppm

Peptide Number: 61704MS/MS Fragmentation of **KELSLNQK**Found in **IPI00855790** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ZNF251 Zinc finger protein 251

Match to Query 12368: 1071.627468 from(536.821010,2+) index(5887)

Title: Elution from: 59.0833333333333 to 59.0833333333333 period: 0 cycle: 6205 experiment: 9 polarity:+

Data file 120129ry_604A1-46_3_1.mgf



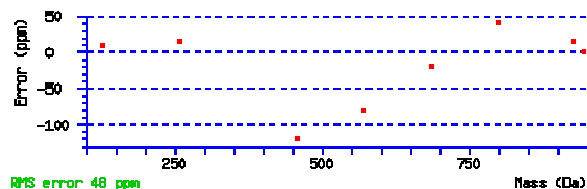
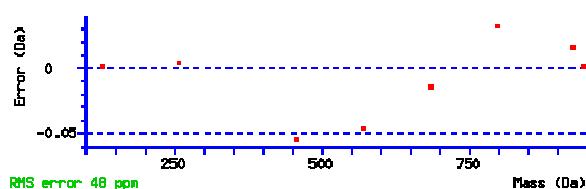
Monoisotopic mass of neutral peptide Mr(calc): 1071.6288

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 39 Expect: 0.0064

Matches : 11/84 fragment ions using 17 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.1022	65.0548	112.0757	56.5415			K							9
2	258.1448	129.5761	241.1183	121.0628	240.1343	120.5708	E	944.5411	472.7742	927.5146	464.2609	926.5306	463.7689	8
3	371.2289	186.1181	354.2023	177.6048	353.2183	177.1128	L	815.4985	408.2529	798.4720	399.7396	797.4880	399.2476	7
4	458.2609	229.6341	441.2344	221.1208	440.2504	220.6288	S	702.4145	351.7109	685.3879	343.1976	684.4039	342.7056	6
5	571.3450	286.1761	554.3184	277.6629	553.3344	277.1708	I	615.3824	308.1949	598.3559	299.6816			5
6	684.4291	342.7182	667.4025	334.2049	666.4185	333.7129	L	502.2984	251.6528	485.2718	243.1395			4
7	798.4720	399.7396	781.4454	391.2264	780.4614	390.7343	N	389.2143	195.1108	372.1878	186.5975			3
8	926.5306	463.7689	909.5040	455.2556	908.5200	454.7636	Q	275.1714	138.0893	258.1448	129.5761			2
9							K	147.1128	74.0600	130.0863	65.5468			1



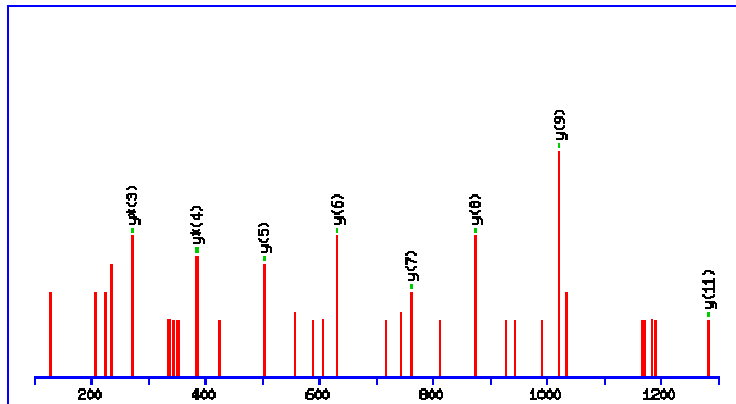
Peptide Number: 61765

MS/MS Fragmentation of **SFDDFFLEETLGGR**Found in **IPI00168291** in **IPI_human**, Tax_Id=9606 Gene_Symbol=UGT3A2 UDP-glucuronosyltransferase 3A2

Match to Query 3519: 1516.719648 from(759.367100,2+) index(9381)

Title: Elution from: 24.2166666666667 to 24.2166666666667 period: 0 cycle: 908 experiment: 6 polarity: +

Data file 120126ry_585A1-55_1_4.mgf



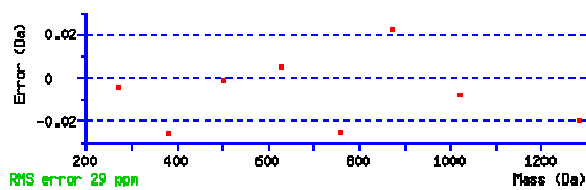
Monoisotopic mass of neutral peptide Mr(calc): 1516.7198

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

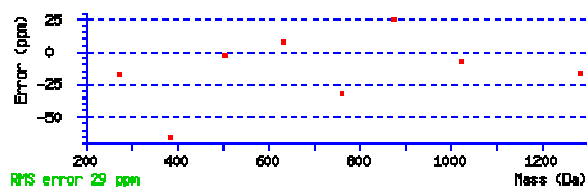
Ions Score: 41 Expect: 0.0035

Matches : 8/112 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233	70.0287	35.5180	S							13
2	235.1077	118.0575	217.0972	109.0522	F	1430.6951	715.8512	1413.6685	707.3379	1412.6845	706.8459	12
3	350.1347	175.5710	332.1241	166.5657	D	1283.6266	642.3170	1266.6001	633.8037	1265.6161	633.3117	11
4	497.2031	249.1052	479.1925	240.0999	F	1168.5997	584.8035	1151.5732	576.2902	1150.5891	575.7982	10
5	644.2715	322.6394	626.2609	313.6341	F	1021.5313	511.2693	1004.5047	502.7560	1003.5207	502.2640	9
6	757.3556	379.1814	739.3450	370.1761	L	874.4629	437.7351	857.4363	429.2218	856.4523	428.7298	8
7	886.3981	443.7027	868.3876	434.6974	E	761.3788	381.1930	744.3523	372.6798	743.3682	372.1878	7
8	1015.4407	508.2240	997.4302	499.2187	E	632.3362	316.6717	615.3097	308.1585	614.3257	307.6665	6
9	1116.4884	558.7478	1098.4779	549.7426	T	503.2936	252.1504	486.2671	243.6372	485.2831	243.1452	5
10	1229.5725	615.2899	1211.5619	606.2846	L	402.2459	201.6266	385.2194	193.1133			4
11	1286.5939	643.8006	1268.5834	634.7953	G	289.1619	145.0846	272.1353	136.5713			3
12	1343.6154	672.3113	1325.6048	663.3061	G	232.1404	116.5738	215.1139	108.0606			2
13					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 29 ppm



RMS error 29 ppm

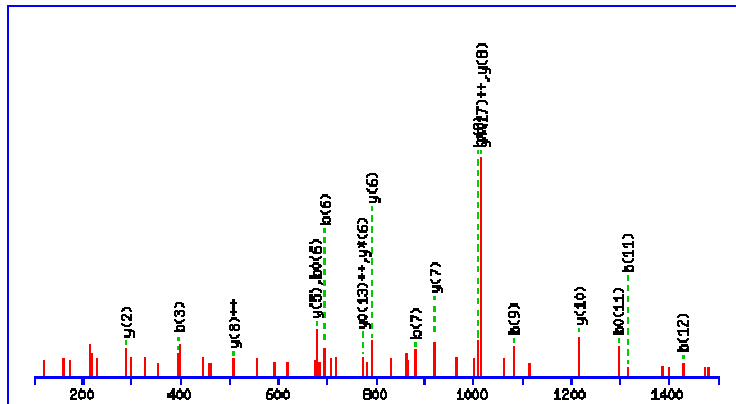
Peptide Number: 61846

MS/MS Fragmentation of **EHEIGWEAFSLPELQNFLR**Found in **IPI00176829** in **IPI_human**, Tax_Id=9606 Gene_Symbol=RASSF3 Isoform 1 of Ras association domain-containing protein 3

Match to Query 23853: 2443.217412 from(815.413080,3+) index(29208)

Title: Elution from: 73.6166666666667 to 73.6166666666667 period: 0 cycle: 2785 experiment: 2 polarity: +

Data file 120212ry_414C2-43_3_4.mgf



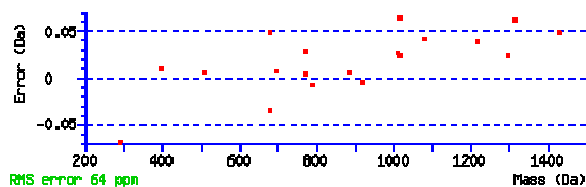
Monoisotopic mass of neutral peptide Mr(calc): 2443.1808

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

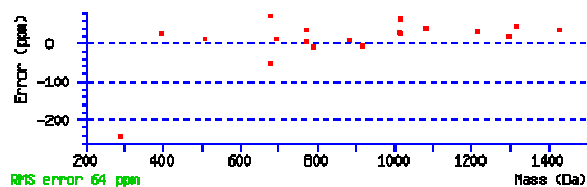
Ions Score: 51 Expect: 0.00058

Matches : 19/186 fragment ions using 27 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							20
2	267.1088	134.0580			249.0982	125.0527	H	2315.1455	1158.0764	2298.1190	1149.5631	2297.1349	1149.0711	19
3	396.1514	198.5793			378.1408	189.5740	E	2178.0866	1089.5469	2161.0600	1081.0337	2160.0760	1080.5417	18
4	509.2354	255.1214			491.2249	246.1161	I	2049.0440	1025.0256	2032.0175	1016.5124	2031.0334	1016.0204	17
5	566.2569	283.6321			548.2463	274.6268	G	1935.9599	968.4836	1918.9334	959.9703	1917.9494	959.4783	16
6	695.2995	348.1534			677.2889	339.1481	E	1878.9385	939.9729	1861.9119	931.4596	1860.9279	930.9676	15
7	881.3788	441.1930			863.3682	432.1878	W	1749.8959	875.4516	1732.8693	866.9383	1731.8853	866.4463	14
8	1010.4214	505.7143			992.4108	496.7091	E	1563.8166	782.4119	1546.7900	773.8986	1545.8060	773.4066	13
9	1081.4585	541.2329			1063.4480	532.2276	A	1434.7740	717.8906	1417.7474	709.3774	1416.7634	708.8853	12
10	1228.5269	614.7671			1210.5164	605.7618	F	1363.7369	682.3721	1346.7103	673.8588	1345.7263	673.3668	11
11	1315.5590	658.2831			1297.5484	649.2778	S	1216.6684	608.8379	1199.6419	600.3246	1198.6579	599.8326	10
12	1428.6430	714.8251			1410.6325	705.8199	L	1129.6364	565.3218	1112.6099	556.8086	1111.6259	556.3166	9
13	1525.6958	763.3515			1507.6852	754.3462	P	1016.5524	508.7798	999.5258	500.2665	998.5418	499.7745	8
14	1654.7384	827.8728			1636.7278	818.8675	E	919.4996	460.2534	902.4730	451.7402	901.4890	451.2482	7
15	1767.8224	884.4149			1749.8119	875.4096	L	790.4570	395.7321	773.4304	387.2189			6
16	1895.8810	948.4441	1878.8545	939.9309	1877.8705	939.4389	Q	677.3729	339.1901	660.3464	330.6768			5
17	2009.9239	1005.4656	1992.8974	996.9523	1991.9134	996.4603	N	549.3144	275.1608	532.2878	266.6475			4
18	2156.9924	1078.9998	2139.9658	1070.4865	2138.9818	1069.9945	F	435.2714	218.1394	418.2449	209.6261			3
19	2270.0764	1135.5419	2253.0499	1127.0286	2252.0659	1126.5366	L	288.2030	144.6051	271.1765	136.0919			2
20							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 64 ppm



RMS error 64 ppm

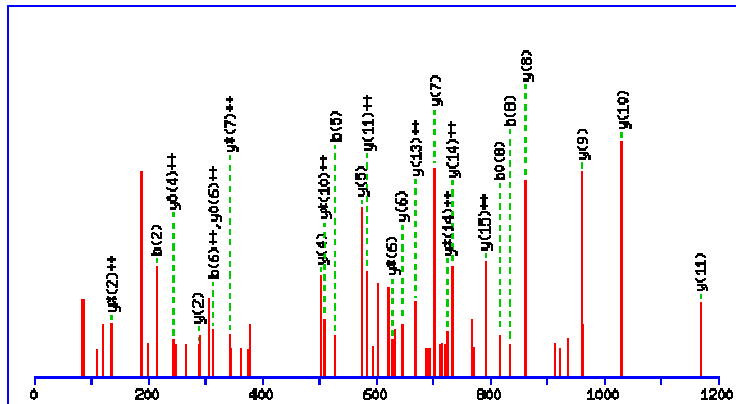
Peptide Number: 61959

MS/MS Fragmentation of **DVLEAVHAVCGAASQLR**Found in **IPI00161196** in **IPI_human**, Tax_Id=9606 Gene_Symbol=FBXL8 F-box/LRR-repeat protein 8

Match to Query 19893: 1794.901812 from(599.307880,3+) index(28526)

Title: Elution from: 71.25 to 71.25 period: 0 cycle: 2702 experiment: 3 polarity:+

Data file 120206ry_aHDF1419-P10_2_3.mgf



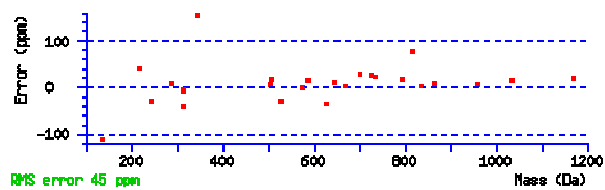
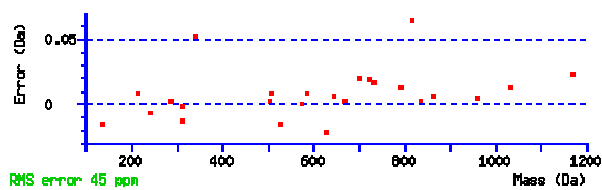
Monoisotopic mass of neutral peptide Mr(calc): 1794.9047

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 48 Expect: 0.001

Matches : 25/158 fragment ions using 46 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							17
2	215.1026	108.0550			197.0921	99.0497	V	1680.8850	840.9461	1663.8585	832.4329	1662.8744	831.9409	16
3	328.1867	164.5970			310.1761	155.5917	L	1581.8166	791.4119	1564.7900	782.8987	1563.8060	782.4066	15
4	457.2293	229.1183			439.2187	220.1130	E	1468.7325	734.8699	1451.7060	726.3566	1450.7220	725.8646	14
5	528.2664	264.6368			510.2558	255.6316	A	1339.6899	670.3486	1322.6634	661.8353	1321.6794	661.3433	13
6	627.3348	314.1710			609.3243	305.1658	V	1268.6528	634.8300	1251.6263	626.3168	1250.6423	625.8248	12
7	764.3937	382.7005			746.3832	373.6952	H	1169.5844	585.2958	1152.5579	576.7826	1151.5738	576.2906	11
8	835.4308	418.2191			817.4203	409.2138	A	1032.5255	516.7664	1015.4989	508.2531	1014.5149	507.7611	10
9	934.4993	467.7533			916.4887	458.7480	V	961.4884	481.2478	944.4618	472.7346	943.4778	472.2425	9
10	1094.5299	547.7686			1076.5193	538.7633	C	862.4200	431.7136	845.3934	423.2003	844.4094	422.7083	8
11	1151.5514	576.2793			1133.5408	567.2740	G	702.3893	351.6983	685.3628	343.1850	684.3787	342.6930	7
12	1222.5885	611.7979			1204.5779	602.7926	A	645.3679	323.1876	628.3413	314.6743	627.3573	314.1823	6
13	1293.6256	647.3164			1275.6150	638.3112	A	574.3307	287.6690	557.3042	279.1557	556.3202	278.6637	5
14	1380.6576	690.8325			1362.6471	681.8272	S	503.2936	252.1504	486.2671	243.6372	485.2831	243.1452	4
15	1508.7162	754.8617	1491.6897	746.3485	1490.7056	745.8565	Q	416.2616	208.6344	399.2350	200.1212			3
16	1621.8003	811.4038	1604.7737	802.8905	1603.7897	802.3985	L	288.2030	144.6051	271.1765	136.0919			2
17							R	175.1190	88.0631	158.0924	79.5498			1



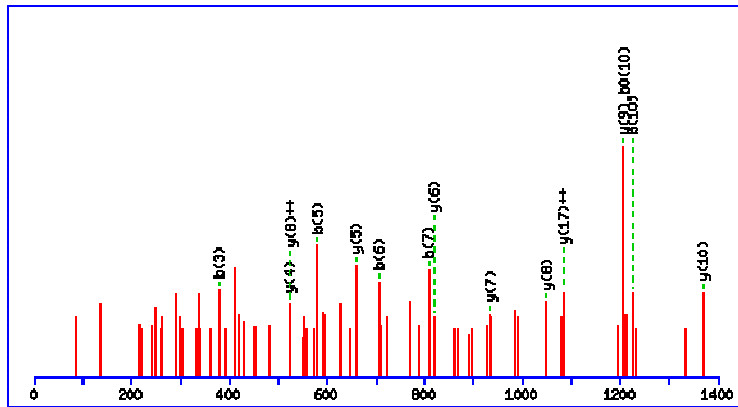
Peptide Number: 62121

MS/MS Fragmentation of **IQHAQQTCCECSTLFGEYYCDICHLFDK**Found in **IPI00552504** in **IPI_human**, Tax_Id=9606 Gene_Symbol=RCHY1 RING finger and CHY zinc finger domain-containing protein 1 isoform 2

Match to Query 39721: 3551.483976 from(888.878270,4+) index(25123)

Title: Elution from: 62.6 to 62.6 period: 0 cycle: 2336 experiment: 7 polarity:+

Data file 120129ry_604A1-46_1_4.mgf



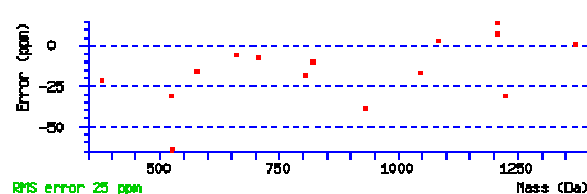
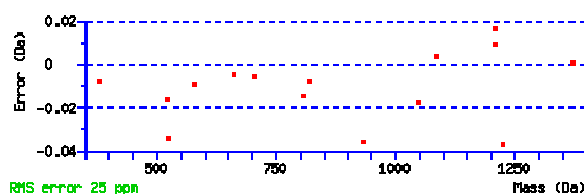
Monoisotopic mass of neutral peptide Mr(calcd): 3551.4891

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 26 Expect: 0.0097

Matches : 15/308 fragment ions using 35 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							28
2	242.1499	121.5786	225.1234	113.0653			Q	3439.4123	1720.2098	3422.3857	1711.6965	3421.4017	1711.2045	27
3	379.2088	190.1081	362.1823	181.5948			H	3311.3537	1656.1805	3294.3271	1647.6672	3293.3431	1647.1752	26
4	450.2459	225.6266	433.2194	217.1133			A	3174.2948	1587.6510	3157.2682	1579.1378	3156.2842	1578.6457	25
5	578.3045	289.6559	561.2780	281.1426			Q	3103.2577	1552.1325	3086.2311	1543.6192	3085.2471	1543.1272	24
6	706.3631	353.6852	689.3366	345.1719			Q	2975.1991	1488.1032	2958.1725	1479.5899	2957.1885	1479.0979	23
7	807.4108	404.2090	790.3842	395.6958	789.4002	395.2037	T	2847.1405	1424.0739	2830.1140	1415.5606	2829.1299	1415.0686	22
8	967.4414	484.2244	950.4149	475.7111	949.4309	475.2191	C	2746.0928	1373.5501	2729.0663	1365.0368	2728.0823	1364.5448	21
9	1096.4840	548.7456	1079.4575	540.2324	1078.4735	539.7404	E	2586.0622	1293.5347	2569.0356	1285.0215	2568.0516	1284.5294	20
10	1225.5266	613.2669	1208.5001	604.7537	1207.5160	604.2617	E	2457.0196	1229.0134	2439.9930	1220.5002	2439.0090	1220.0081	19
11	1385.5573	693.2823	1368.5307	684.7690	1367.5467	684.2770	C	2327.9770	1164.4921	2310.9504	1155.9789	2309.9664	1155.4869	18
12	1472.5893	736.7983	1455.5627	728.2850	1454.5787	727.7930	S	2167.9463	1084.4768	2150.9198	1075.9635	2149.9358	1075.4715	17
13	1573.6370	787.3221	1556.6104	778.8088	1555.6264	778.3168	T	2080.9143	1040.9608	2063.8878	1032.4475	2062.9037	1031.9555	16
14	1686.7210	843.8642	1669.6945	835.3509	1668.7105	834.8589	L	1979.8666	990.4370	1962.8401	981.9237	1961.8561	981.4317	15
15	1833.7894	917.3984	1816.7629	908.8851	1815.7789	908.3931	F	1866.7826	933.8949	1849.7560	925.3816	1848.7720	924.8896	14
16	1890.8109	945.9091	1873.7844	937.3958	1872.8003	936.9038	G	1719.7142	860.3607	1702.6876	851.8474	1701.7036	851.3554	13
17	2019.8535	1010.4304	2002.8270	1001.9171	2001.8429	1001.4251	E	1662.6927	831.8500	1645.6661	823.3367	1644.6821	822.8447	12
18	2182.9168	1091.9621	2165.8903	1083.4488	2164.9063	1082.9568	Y	1533.6501	767.3287	1516.6236	758.8154	1515.6395	758.3234	11
19	2345.9802	1173.4937	2328.9536	1164.9804	2327.9696	1164.4884	Y	1370.5868	685.7970	1353.5602	677.2837	1352.5762	676.7917	10
20	2506.0108	1253.5090	2488.9843	1244.9958	2488.0002	1244.5038	C	1207.5234	604.2654	1190.4969	595.7521	1189.5129	595.2601	9
21	2621.0378	1311.0225	2604.0112	1302.5092	2603.0272	1302.0172	D	1047.4928	524.2500	1030.4662	515.7368	1029.4822	515.2448	8
22	2734.1218	1367.5645	2717.0953	1359.0513	2716.1113	1358.5593	I	932.4658	466.7366	915.4393	458.2233	914.4553	457.7313	7
23	2894.1525	1447.5799	2877.1259	1439.0666	2876.1419	1438.5746	C	819.3818	410.1945	802.3552	401.6813	801.3712	401.1892	6
24	3031.2114	1516.1093	3014.1848	1507.5961	3013.2008	1507.1040	H	659.3511	330.1792	642.3246	321.6659	641.3406	321.1739	5
25	3144.2954	1572.6514	3127.2689	1564.1381	3126.2849	1563.6461	L	522.2922	261.6498	505.2657	253.1365	504.2817	252.6445	4
26	3291.3639	1646.1856	3274.3373	1637.6723	3273.3533	1637.1803	F	409.2082	205.1077	392.1816	196.5944	391.1976	196.1024	3
27	3406.3908	1703.6990	3389.3643	1695.1858	3388.3802	1694.6938	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
28							K	147.1128	74.0600	130.0863	65.5468			1

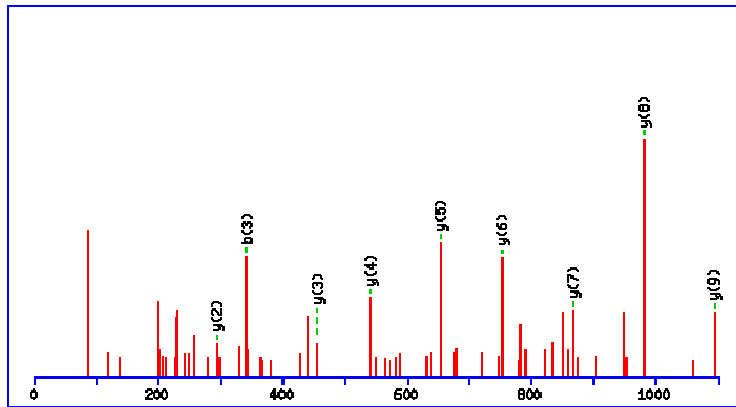


Peptide Number: 62225MS/MS Fragmentation of **ILDLVISCFK**Found in **IPI00027445** in **IPI_human**, Tax_Id=9606 Gene_Symbol=HARS2 Probable histidyl-tRNA synthetase, mitochondrial

Match to Query 3450: 1206.665348 from(604.339950,2+) index(30086)

Title: Elution from: 77.7 to 77.7 period: 0 cycle: 2949 experiment: 3 polarity: +

Data file 120212ry_aHDF1388-P9_3_3.mgf



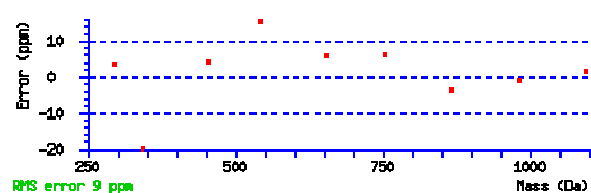
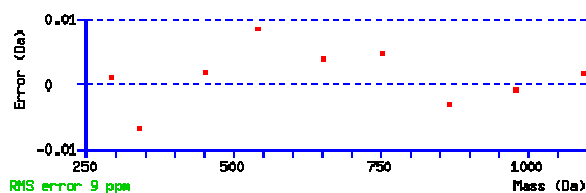
Monoisotopic mass of neutral peptide Mr(calc): 1206.6682

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 53 Expect: 0.00029

Matches : 9/80 fragment ions using 20 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			I							10
2	227.1754	114.0913			L	1094.5914	547.7994	1077.5649	539.2861	1076.5809	538.7941	9
3	342.2023	171.6048	324.1918	162.5995	D	981.5074	491.2573	964.4808	482.7441	963.4968	482.2520	8
4	455.2864	228.1468	437.2758	219.1416	L	866.4804	433.7439	849.4539	425.2306	848.4699	424.7386	7
5	554.3548	277.6811	536.3443	268.6758	V	753.3964	377.2018	736.3698	368.6886	735.3858	368.1965	6
6	667.4389	334.2231	649.4283	325.2178	I	654.3280	327.6676	637.3014	319.1543	636.3174	318.6623	5
7	754.4709	377.7391	736.4604	368.7338	S	541.2439	271.1256	524.2173	262.6123	523.2333	262.1203	4
8	914.5016	457.7544	896.4910	448.7491	C	454.2119	227.6096	437.1853	219.0963			3
9	1061.5700	531.2886	1043.5594	522.2833	F	294.1812	147.5942	277.1547	139.0810			2
10					K	147.1128	74.0600	130.0863	65.5468			1

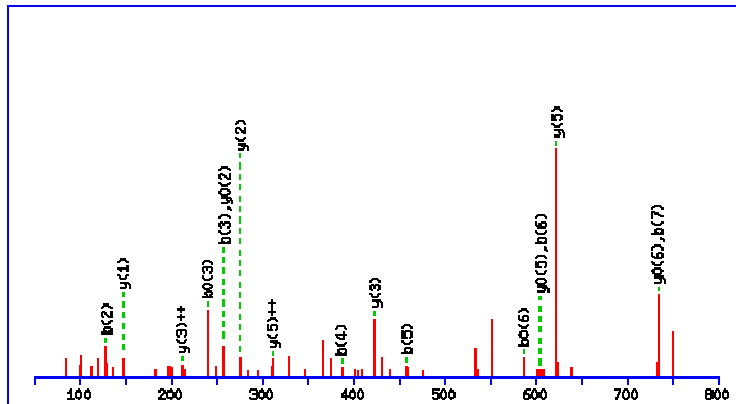


Peptide Number: 62265MS/MS Fragmentation of **AGEEAFEK**Found in **IPI00384617** in **IPI_human**, Tax_Id=9606 Gene_Symbol=NME9 Isoform 1 of Thioredoxin domain-containing protein 6

Match to Query 7055: 879.396268 from(440.705410,2+) index(20325)

Title: Elution from: 92.5666666666667 to 92.5666666666667 period: 0 cycle: 7846 experiment: 4 polarity:+

Data file 120118ry_201B7-32_2_1.mgf



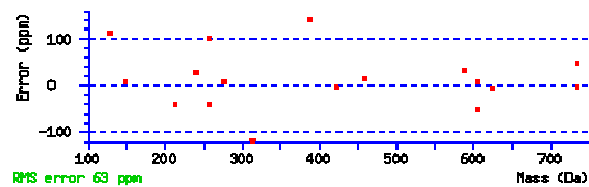
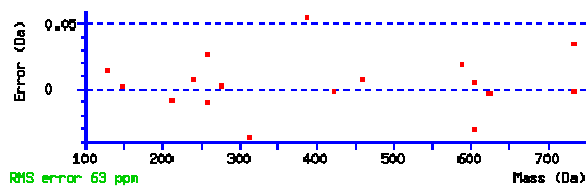
Monoisotopic mass of neutral peptide Mr(calc): 879.3974

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 37 Expect: 0.0084

Matches : 17/64 fragment ions using 31 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258			A							8
2	129.0659	65.0366			G	809.3676	405.1874	792.3410	396.6742	791.3570	396.1821	7
3	258.1084	129.5579	240.0979	120.5526	E	752.3461	376.6767	735.3196	368.1634	734.3355	367.6714	6
4	387.1510	194.0792	369.1405	185.0739	E	623.3035	312.1554	606.2770	303.6421	605.2930	303.1501	5
5	458.1882	229.5977	440.1776	220.5924	A	494.2609	247.6341	477.2344	239.1208	476.2504	238.6288	4
6	605.2566	303.1319	587.2460	294.1266	F	423.2238	212.1155	406.1973	203.6023	405.2132	203.1103	3
7	734.2992	367.6532	716.2886	358.6479	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
8					K	147.1128	74.0600	130.0863	65.5468			1

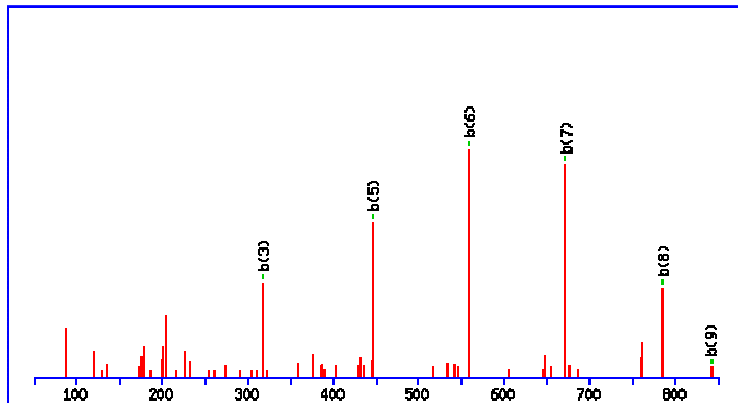


Peptide Number: 62330MS/MS Fragmentation of **AFVAGLLLGK**Found in **IPI00024263** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TAF1A Isoform 1 of TATA box-binding protein-associated factor RNA polymerase I subunit A

Match to Query 735: 987.596368 from(494.805460,2+) index(32843)

Title: Elution from: 86.8333333333333 to 86.8333333333333 period: 0 cycle: 3320 experiment: 1 polarity:+

Data file 120208ry_Tig120slc-P8_3_3.mgf



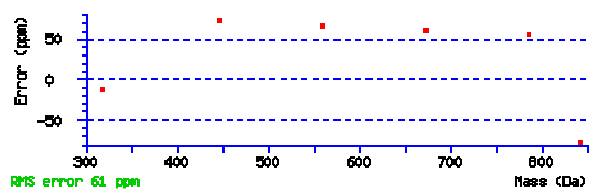
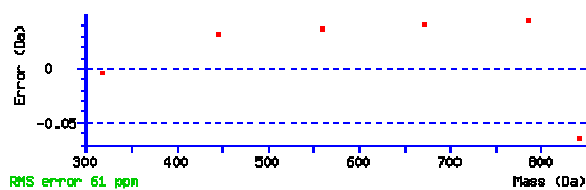
Monoisotopic mass of neutral peptide Mr(calc): 987.6117

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 54 Expect: 0.00014

Matches : 6/54 fragment ions using 8 most intense peaks ([help](#))

#	b	b ⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	#
1	72.0444	36.5258	A					10
2	219.1128	110.0600	F	917.5819	459.2946	900.5553	450.7813	9
3	318.1812	159.5942	V	770.5135	385.7604	753.4869	377.2471	8
4	389.2183	195.1128	A	671.4450	336.2262	654.4185	327.7129	7
5	446.2398	223.6235	G	600.4079	300.7076	583.3814	292.1943	6
6	559.3239	280.1656	L	543.3865	272.1969	526.3599	263.6836	5
7	672.4079	336.7076	L	430.3024	215.6548	413.2758	207.1416	4
8	785.4920	393.2496	L	317.2183	159.1128	300.1918	150.5995	3
9	842.5135	421.7604	G	204.1343	102.5708	187.1077	94.0575	2
10			K	147.1128	74.0600	130.0863	65.5468	1



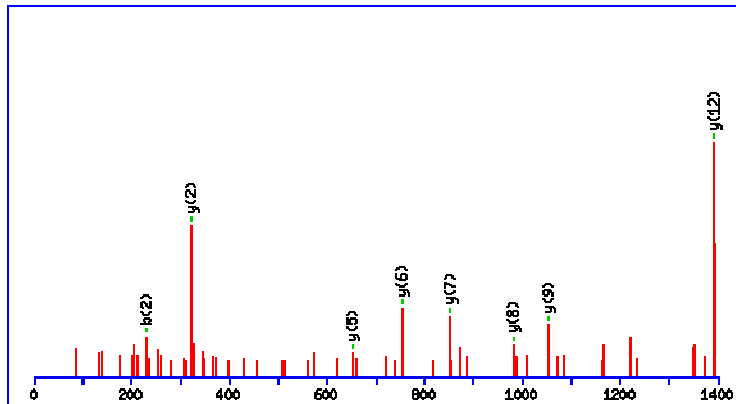
Peptide Number: 62575

MS/MS Fragmentation of **IDVCPENAEVTLTDFR**Found in **IPI00028030** in **IPI_human**, Tax_Id=9606 Gene_Symbol=COMP Cartilage oligomeric matrix protein

Match to Query 19867: 1877.902668 from(939.958610,2+) index(17959)

Title: Elution from: 46.6666666666667 to 46.6666666666667 period: 0 cycle: 1784 experiment: 9 polarity: +

Data file 120208ry_Tig120slc-P8_3_3.mgf



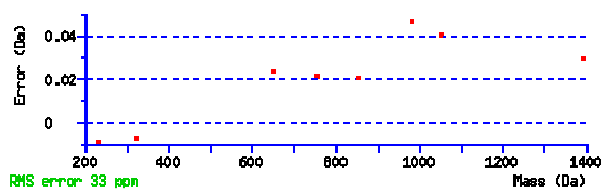
Monoisotopic mass of neutral peptide Mr(calc): 1877.8829

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

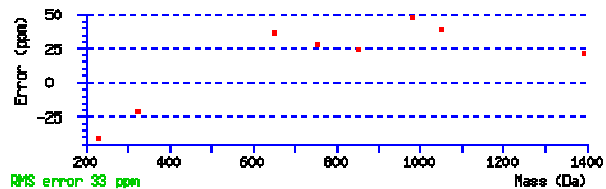
Ions Score: 43 Expect: 0.003

Matches : 8/162 fragment ions using 14 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							16
2	229.1183	115.0628			211.1077	106.0575	D	1765.8061	883.4067	1748.7796	874.8934	1747.7956	874.4014	15
3	328.1867	164.5970			310.1761	155.5917	V	1650.7792	825.8932	1633.7527	817.3800	1632.7686	816.8880	14
4	488.2173	244.6123			470.2068	235.6070	C	1551.7108	776.3590	1534.6842	767.8458	1533.7002	767.3537	13
5	585.2701	293.1387			567.2595	284.1334	P	1391.6801	696.3437	1374.6536	687.8304	1373.6696	687.3384	12
6	714.3127	357.6600			696.3021	348.6547	E	1294.6274	647.8173	1277.6008	639.3040	1276.6168	638.8120	11
7	828.3556	414.6815	811.3291	406.1682	810.3451	405.6762	N	1165.5848	583.2960	1148.5582	574.7828	1147.5742	574.2907	10
8	899.3927	450.2000	882.3662	441.6867	881.3822	441.1947	A	1051.5419	526.2746	1034.5153	517.7613	1033.5313	517.2693	9
9	1028.4353	514.7213	1011.4088	506.2080	1010.4248	505.7160	E	980.5047	490.7560	963.4782	482.2427	962.4942	481.7507	8
10	1127.5038	564.2555	1110.4772	555.7422	1109.4932	555.2502	V	851.4621	426.2347	834.4356	417.7214	833.4516	417.2294	7
11	1228.5514	614.7794	1211.5249	606.2661	1210.5409	605.7741	T	752.3937	376.7005	735.3672	368.1872	734.3832	367.6952	6
12	1341.6355	671.3214	1324.6089	662.8081	1323.6249	662.3161	L	651.3461	326.1767	634.3195	317.6634	633.3355	317.1714	5
13	1442.6832	721.8452	1425.6566	713.3320	1424.6726	712.8399	T	538.2620	269.6346	521.2354	261.1214	520.2514	260.6293	4
14	1557.7101	779.3587	1540.6836	770.8454	1539.6996	770.3534	D	437.2143	219.1108	420.1878	210.5975	419.2037	210.1055	3
15	1704.7785	852.8929	1687.7520	844.3796	1686.7680	843.8876	F	322.1874	161.5973	305.1608	153.0840			2
16							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 33 ppm



RMS error 33 ppm

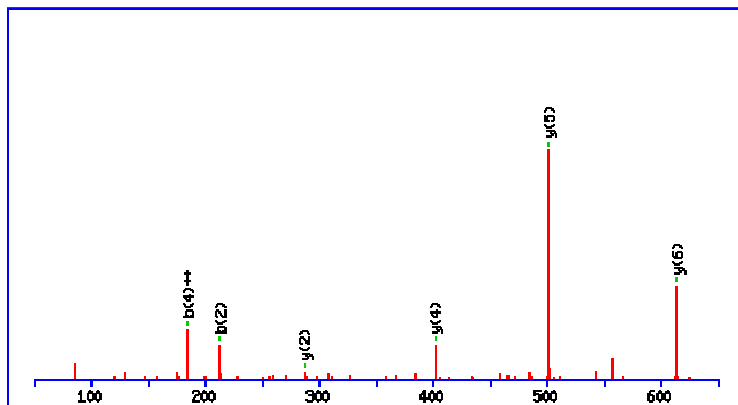
Peptide Number: 62634**MS/MS Fragmentation of VLVGGLR**

Found in **IPI00915412** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TRBC1;TRBV5-4;EPHB6;TRBV12-4;TRBV19 Isoform 1 of Ephrin type-B receptor 6

Match to Query 2032: 712.462188 from(357.238370,2+) index(31789)

Title: Elution from: 118.316666666667 to 118.316666666667 period: 0 cycle: 9775 experiment: 1 polarity: +

Data file 120210ry_32R1-32_3_1.mgf



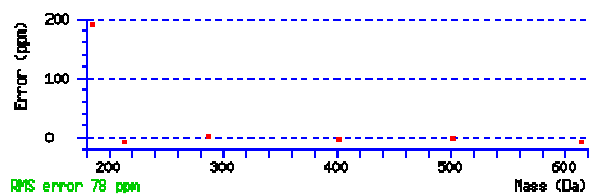
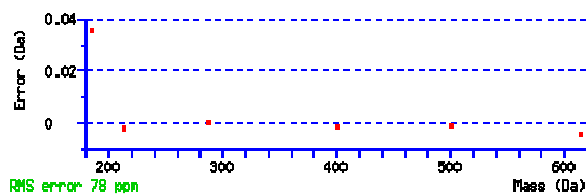
Monoisotopic mass of neutral peptide Mr(calc): 712.4596

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 43 **Expect:** 0.0013

Matches : 6/36 fragment ions using 6 most intense peaks ([help](#))

#	b	b ⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	#
1	100.0757	50.5415	V					7
2	213.1598	107.0835	L	614.3984	307.7028	597.3719	299.1896	6
3	312.2282	156.6177	V	501.3144	251.1608	484.2878	242.6475	5
4	369.2496	185.1285	G	402.2459	201.6266	385.2194	193.1133	4
5	426.2711	213.6392	G	345.2245	173.1159	328.1979	164.6026	3
6	539.3552	270.1812	L	288.2030	144.6051	271.1765	136.0919	2
7			R	175.1190	88.0631	158.0924	79.5498	1



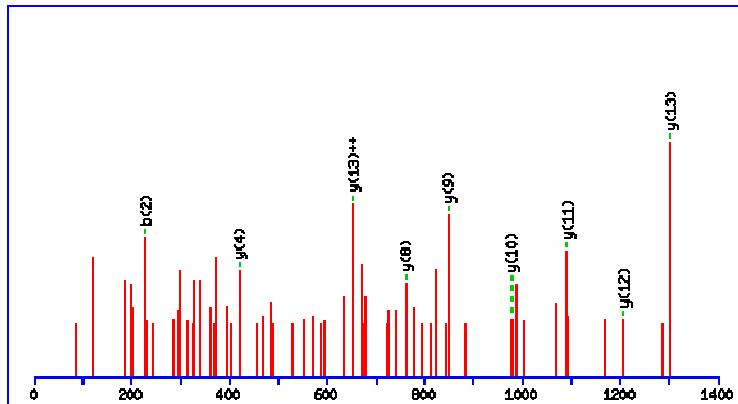
Peptide Number: 63264

MS/MS Fragmentation of **ILLSVVSMLAEPNDESGANVDASK**Found in **IPI00010142** in **IPI_human**, Tax_Id=9606 Gene_Symbol=UBE2G2 Ubiquitin-conjugating enzyme E2 G2

Match to Query 39150: 2458.197402 from(820.406410,3+) index(48149)

Title: Elution from: 118.216666666667 to 118.216666666667 period: 0 cycle: 4353 experiment: 8 polarity:+

Data file 120118ry_201B7-32_3_3.mgf



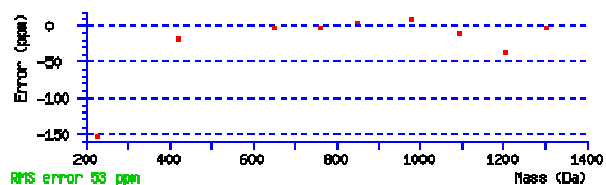
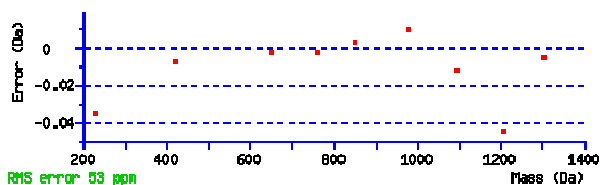
Monoisotopic mass of neutral peptide Mr(calc): 2458.2261

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 42 Expect: 0.0033

Matches : 9/244 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							24
2	227.1754	114.0913					L	2346.1493	1173.5783	2329.1228	1165.0650	2328.1388	1164.5730	23
3	340.2595	170.6334					L	2233.0653	1117.0363	2216.0387	1108.5230	2215.0547	1108.0310	22
4	427.2915	214.1494			409.2809	205.1441	S	2119.9812	1060.4942	2102.9547	1051.9810	2101.9706	1051.4890	21
5	526.3599	263.6836			508.3493	254.6783	V	2032.9492	1016.9782	2015.9226	1008.4650	2014.9386	1007.9729	20
6	625.4283	313.2178			607.4178	304.2125	V	1933.8808	967.4440	1916.8542	958.9307	1915.8702	958.4387	19
7	712.4604	356.7338			694.4498	347.7285	S	1834.8123	917.9098	1817.7858	909.3965	1816.8018	908.9045	18
8	843.5008	422.2541			825.4903	413.2488	M	1747.7803	874.3938	1730.7538	865.8805	1729.7698	865.3885	17
9	956.5849	478.7961			938.5743	469.7908	L	1616.7398	808.8736	1599.7133	800.3603	1598.7293	799.8683	16
10	1027.6220	514.3146			1009.6114	505.3094	A	1503.6558	752.3315	1486.6292	743.8182	1485.6452	743.3262	15
11	1156.6646	578.8359			1138.6540	569.8307	E	1432.6187	716.8130	1415.5921	708.2997	1414.6081	707.8077	14
12	1253.7174	627.3623			1235.7068	618.3570	P	1303.5761	652.2917	1286.5495	643.7784	1285.5655	643.2864	13
13	1367.7603	684.3838	1350.7337	675.8705	1349.7497	675.3785	N	1206.5233	603.7653	1189.4968	595.2520	1188.5127	594.7600	12
14	1482.7872	741.8973	1465.7607	733.3840	1464.7767	732.8920	D	1092.4804	546.7438	1075.4538	538.2305	1074.4698	537.7385	11
15	1611.8298	806.4186	1594.8033	797.9053	1593.8193	797.4133	E	977.4534	489.2304	960.4269	480.7171	959.4429	480.2251	10
16	1698.8619	849.9346	1681.8353	841.4213	1680.8513	840.9293	S	848.4108	424.7091	831.3843	416.1958	830.4003	415.7038	9
17	1755.8833	878.4453	1738.8568	869.9320	1737.8728	869.4400	G	761.3788	381.1930	744.3523	372.6798	743.3682	372.1878	8
18	1826.9204	913.9639	1809.8939	905.4506	1808.9099	904.9586	A	704.3573	352.6823	687.3308	344.1690	686.3468	343.6770	7
19	1940.9634	970.9853	1923.9368	962.4720	1922.9528	961.9800	N	633.3202	317.1638	616.2937	308.6505	615.3097	308.1585	6
20	2040.0318	1020.5195	2023.0052	1012.0063	2022.0212	1011.5142	V	519.2773	260.1423	502.2508	251.6290	501.2667	251.1370	5
21	2155.0587	1078.0330	2138.0322	1069.5197	2137.0482	1069.0277	D	420.2089	210.6081	403.1823	202.0948	402.1983	201.6028	4
22	2226.0958	1113.5516	2209.0693	1105.0383	2208.0853	1104.5463	A	305.1819	153.0946	288.1554	144.5813	287.1714	144.0893	3
23	2313.1279	1157.0676	2296.1013	1148.5543	2295.1173	1148.0623	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
24							K	147.1128	74.0600	130.0863	65.5468			1

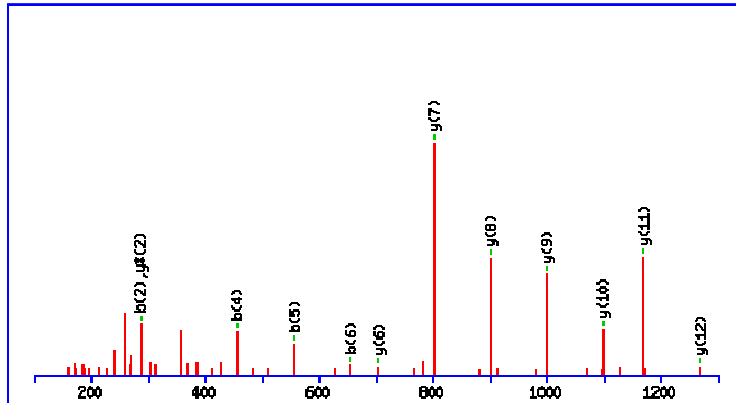


Peptide Number: 63657MS/MS Fragmentation of **WVAVVPSGQEQR**Found in **IPI00472882** in **IPI_human**, Tax_Id=9606 Gene_Symbol=HLA-B;HLA-C;HLA-A;MICA;LOC441528 HLA class I histocompatibility antigen, A-68 alpha chain

Match to Query 24413: 1453.762188 from(727.888370,2+) index(28605)

Title: Elution from: 74.1833333333333 to 74.1833333333333 period: 0 cycle: 2830 experiment: 9 polarity: +

Data file 120206ry_aHDF1419-P10_2.mgf



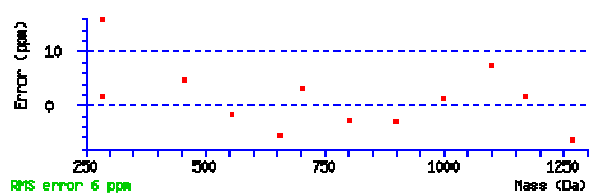
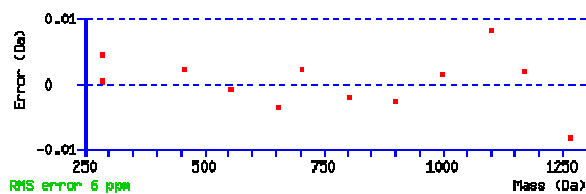
Monoisotopic mass of neutral peptide Mr(calc): 1453.7678

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 67 Expect: 1.3e-005

Matches : 12/108 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	187.0866	94.0469					W							13
2	286.1550	143.5811					V	1268.6957	634.8515	1251.6692	626.3382	1250.6852	625.8462	12
3	357.1921	179.0997					A	1169.6273	585.3173	1152.6008	576.8040	1151.6167	576.3120	11
4	456.2605	228.6339					V	1098.5902	549.7987	1081.5637	541.2855	1080.5796	540.7935	10
5	555.3289	278.1681					V	999.5218	500.2645	982.4952	491.7513	981.5112	491.2592	9
6	654.3974	327.7023					V	900.4534	450.7303	883.4268	442.2170	882.4428	441.7250	8
7	751.4501	376.2287					P	801.3850	401.1961	784.3584	392.6828	783.3744	392.1908	7
8	838.4822	419.7447			820.4716	410.7394	S	704.3322	352.6697	687.3056	344.1565	686.3216	343.6645	6
9	895.5036	448.2554			877.4931	439.2502	G	617.3002	309.1537	600.2736	300.6404	599.2896	300.1484	5
10	1023.5622	512.2847	1006.5356	503.7715	1005.5516	503.2795	Q	560.2787	280.6430	543.2522	272.1297	542.2681	271.6377	4
11	1152.6048	576.8060	1135.5782	568.2928	1134.5942	567.8007	E	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	3
12	1280.6634	640.8353	1263.6368	632.3220	1262.6528	631.8300	Q	303.1775	152.0924	286.1510	143.5791			2
13							R	175.1190	88.0631	158.0924	79.5498			1



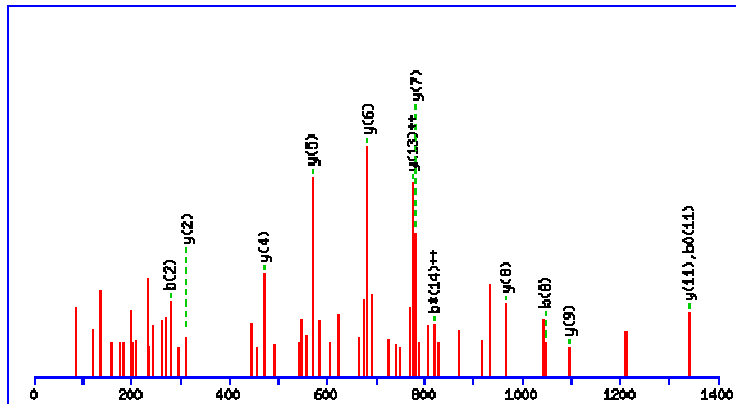
Peptide Number: 63787

MS/MS Fragmentation of **YNPLQDEWLVSAHR**Found in **IPI00013925** in **IPI_human**, Tax_Id=9606 Gene_Symbol=GALT Galactose-1-phosphate uridylyltransferase

Match to Query 20285: 1825.910922 from(609.644250,3+) index(26523)

Title: Elution from: 68.5833333333333 to 68.5833333333333 period: 0 cycle: 2603 experiment: 1 polarity: +

Data file 120212ry_aHDF1388-P9_3_3.mgf



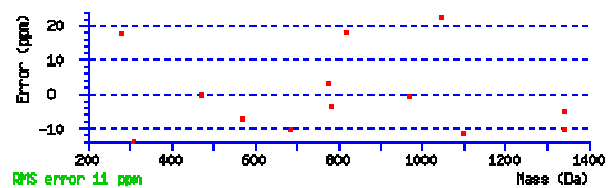
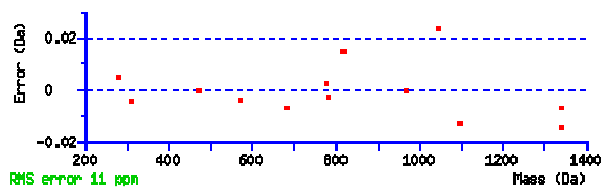
Monoisotopic mass of neutral peptide Mr(calc): 1825.9111

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 45 Expect: 0.0018

Matches : 13/150 fragment ions using 23 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389					Y							15
2	278.1135	139.5604	261.0870	131.0471			N	1663.8551	832.4312	1646.8285	823.9179	1645.8445	823.4259	14
3	375.1663	188.0868	358.1397	179.5735			P	1549.8122	775.4097	1532.7856	766.8964	1531.8016	766.4044	13
4	488.2504	244.6288	471.2238	236.1155			L	1452.7594	726.8833	1435.7328	718.3701	1434.7488	717.8781	12
5	616.3089	308.6581	599.2824	300.1448			Q	1339.6753	670.3413	1322.6488	661.8280	1321.6648	661.3360	11
6	731.3359	366.1716	714.3093	357.6583	713.3253	357.1663	D	1211.6167	606.3120	1194.5902	597.7987	1193.6062	597.3067	10
7	860.3785	430.6929	843.3519	422.1796	842.3679	421.6876	E	1096.5898	548.7985	1079.5633	540.2853	1078.5792	539.7933	9
8	1046.4578	523.7325	1029.4312	515.2193	1028.4472	514.7272	W	967.5472	484.2772	950.5207	475.7640	949.5366	475.2720	8
9	1145.5262	573.2667	1128.4997	564.7535	1127.5156	564.2615	V	781.4679	391.2376	764.4413	382.7243	763.4573	382.2323	7
10	1258.6103	629.8088	1241.5837	621.2955	1240.5997	620.8035	L	682.3995	341.7034	665.3729	333.1901	664.3889	332.6981	6
11	1357.6787	679.3430	1340.6521	670.8297	1339.6681	670.3377	V	569.3154	285.1613	552.2889	276.6481	551.3049	276.1561	5
12	1444.7107	722.8590	1427.6842	714.3457	1426.7001	713.8537	S	470.2470	235.6271	453.2205	227.1139	452.2364	226.6219	4
13	1515.7478	758.3775	1498.7213	749.8643	1497.7373	749.3723	A	383.2150	192.1111	366.1884	183.5979			3
14	1652.8067	826.9070	1635.7802	818.3937	1634.7962	817.9017	H	312.1779	156.5926	295.1513	148.0793			2
15							R	175.1190	88.0631	158.0924	79.5498			1

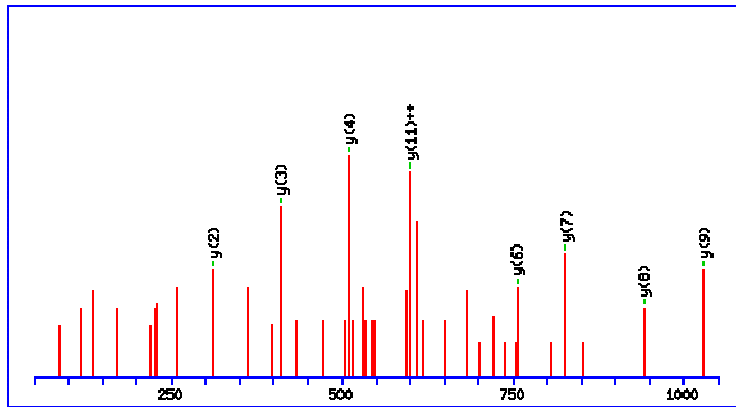


Peptide Number: 64924MS/MS Fragmentation of **VGLSDAFVVVHR**Found in **IPI00044369** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PLXDC2 Isoform 1 of Plexin domain-containing protein 2

Match to Query 9031: 1297.711272 from(433,577700,3+) index(512)

Title: Elution from: 1.18333333333333 to 1.18333333333333 period: 0 cycle: 44 experiment: 1 polarity: +

Data file 120126ry_585A1-55_1_3.mgf



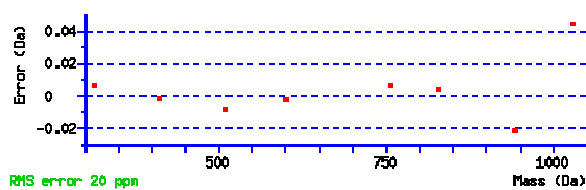
Monoisotopic mass of neutral peptide Mr(calc): 1297.7143

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

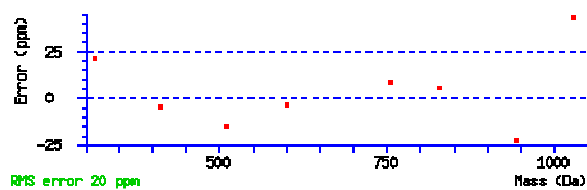
Ions Score: 62 Expect: 3.9e-005

Matches : 8/90 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415			V							12
2	157.0972	79.0522			G	1199.6531	600.3302	1182.6266	591.8169	1181.6426	591.3249	11
3	270.1812	135.5942			L	1142.6317	571.8195	1125.6051	563.3062	1124.6211	562.8142	10
4	357.2132	179.1103	339.2027	170.1050	S	1029.5476	515.2774	1012.5211	506.7642	1011.5370	506.2722	9
5	472.2402	236.6237	454.2296	227.6185	D	942.5156	471.7614	925.4890	463.2482	924.5050	462.7561	8
6	543.2773	272.1423	525.2667	263.1370	A	827.4886	414.2480	810.4621	405.7347			7
7	690.3457	345.6765	672.3352	336.6712	F	756.4515	378.7294	739.4250	370.2161			6
8	789.4141	395.2107	771.4036	386.2054	V	609.3831	305.1952	592.3566	296.6819			5
9	888.4825	444.7449	870.4720	435.7396	V	510.3147	255.6610	493.2881	247.1477			4
10	987.5510	494.2791	969.5404	485.2738	V	411.2463	206.1268	394.2197	197.6135			3
11	1124.6099	562.8086	1106.5993	553.8033	H	312.1779	156.5926	295.1513	148.0793			2
12					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 20 ppm



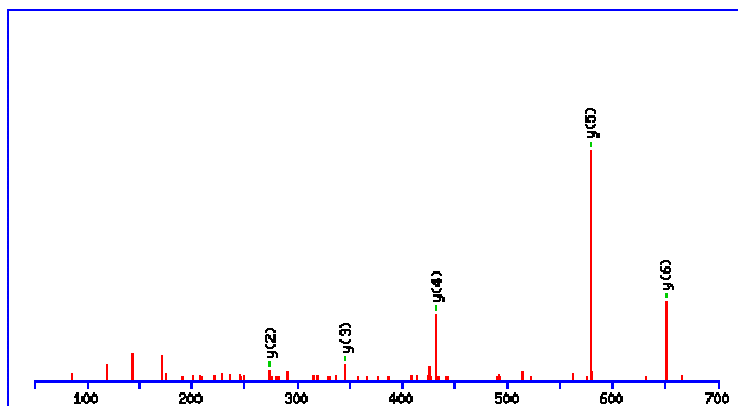
RMS error 20 ppm

Peptide Number: 65209MS/MS Fragmentation of **VAFSAVR**Found in **IPI00018396** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CBLN4 Cerebellin-4

Match to Query 2518: 748.420588 from(375.217570,2+) index(28487)

Title: Elution from: 109.55 to 109.55 period: 0 cycle: 8127 experiment: 1 polarity: +

Data file 120118ry_201B7-32_1_1.mgf



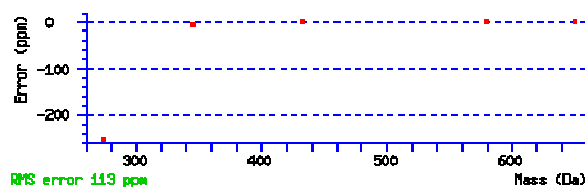
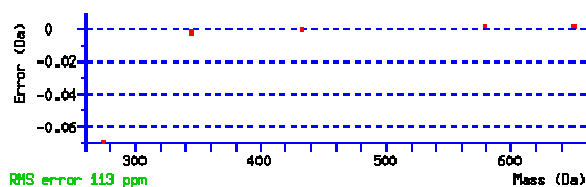
Monoisotopic mass of neutral peptide Mr(calc): 748.4232

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 51 Expect: 0.0005

Matches : 5/48 fragment ions using 6 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415			V							7
2	171.1128	86.0600			A	650.3620	325.6847	633.3355	317.1714	632.3515	316.6794	6
3	318.1812	159.5942			F	579.3249	290.1661	562.2984	281.6528	561.3144	281.1608	5
4	405.2132	203.1103	387.2027	194.1050	S	432.2565	216.6319	415.2300	208.1186	414.2459	207.6266	4
5	476.2504	238.6288	458.2398	229.6235	A	345.2245	173.1159	328.1979	164.6026			3
6	575.3188	288.1630	557.3082	279.1577	V	274.1874	137.5973	257.1608	129.0840			2
7					R	175.1190	88.0631	158.0924	79.5498			1



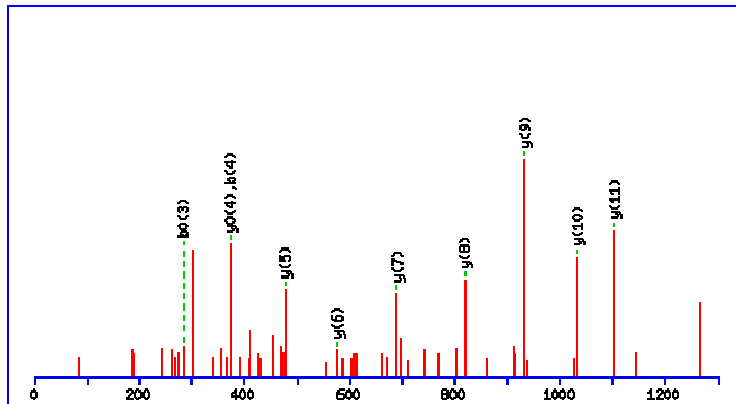
Peptide Number: 66101

MS/MS Fragmentation of **DGQAVLENVSEGGK**Found in **IPI00646161** in **IPI_human**, Tax_Id=9606 Gene_Symbol=RENBP Uncharacterized protein

Match to Query 22230: 1401.671968 from(701.843260,2+) index(9711)

Title: Elution from: 25.2666666666667 to 25.2666666666667 period: 0 cycle: 962 experiment: 8 polarity:+

Data file 120212ry_aHDF1388-P9_3_2.mgf



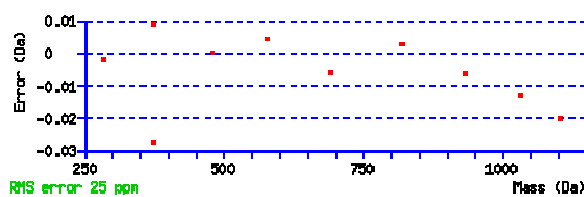
Monoisotopic mass of neutral peptide Mr(calc): 1401.6736

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

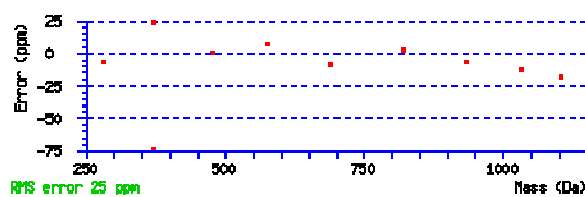
Ions Score: 57 Expect: 0.00012

Matches : 10/146 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							14
2	173.0557	87.0315			155.0451	78.0262	G	1287.6539	644.3306	1270.6274	635.8173	1269.6434	635.3253	13
3	301.1143	151.0608	284.0877	142.5475	283.1037	142.0555	Q	1230.6325	615.8199	1213.6059	607.3066	1212.6219	606.8146	12
4	372.1514	186.5793	355.1248	178.0661	354.1408	177.5740	A	1102.5739	551.7906	1085.5473	543.2773	1084.5633	542.7853	11
5	471.2198	236.1135	454.1932	227.6003	453.2092	227.1083	V	1031.5368	516.2720	1014.5102	507.7587	1013.5262	507.2667	10
6	584.3039	292.6556	567.2773	284.1423	566.2933	283.6503	L	932.4684	466.7378	915.4418	458.2245	914.4578	457.7325	9
7	713.3464	357.1769	696.3199	348.6636	695.3359	348.1716	E	819.3843	410.1958	802.3577	401.6825	801.3737	401.1905	8
8	827.3894	414.1983	810.3628	405.6850	809.3788	405.1930	N	690.3417	345.6745	673.3151	337.1612	672.3311	336.6692	7
9	926.4578	463.7325	909.4312	455.2193	908.4472	454.7272	V	576.2988	288.6530	559.2722	280.1397	558.2882	279.6477	6
10	1013.4898	507.2485	996.4633	498.7353	995.4792	498.2433	S	477.2304	239.1188	460.2038	230.6055	459.2198	230.1135	5
11	1142.5324	571.7698	1125.5059	563.2566	1124.5218	562.7646	E	390.1983	195.6028	373.1718	187.0895	372.1878	186.5975	4
12	1199.5539	600.2806	1182.5273	591.7673	1181.5433	591.2753	G	261.1557	131.0815	244.1292	122.5682			3
13	1256.5753	628.7913	1239.5488	620.2780	1238.5648	619.7860	G	204.1343	102.5708	187.1077	94.0575			2
14							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 25 ppm



RMS error 25 ppm

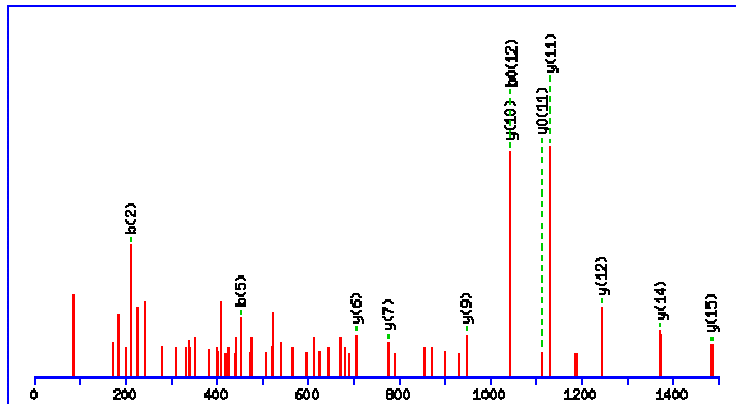
Peptide Number: 66142

MS/MS Fragmentation of **VLI~~GA~~LSPLAADFL~~LK~~**Found in **IPI01012884** in **IPI_human**, Tax_Id=9606 Gene_Symbol=MMAA Uncharacterized protein

Match to Query 7096: 1697.022128 from(849.518340,2+) index(18746)

Title: Elution from: 47.6833333333333 to 47.6833333333333 period: 0 cycle: 1806 experiment: 7 polarity:+

Data file 120212ry_aHDF1388-P9_2_4.mgf



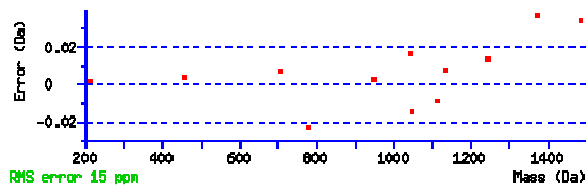
Monoisotopic mass of neutral peptide Mr(calc): 1697.0127

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

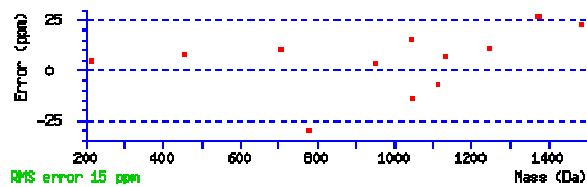
Ions Score: 40 Expect: 0.0011

Matches : 12/140 fragment ions using 27 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415			V							17
2	213.1598	107.0835			L	1598.9516	799.9794	1581.9251	791.4662	1580.9410	790.9742	16
3	326.2438	163.6255			I	1485.8675	743.4374	1468.8410	734.9241	1467.8570	734.4321	15
4	383.2653	192.1363			G	1372.7835	686.8954	1355.7569	678.3821	1354.7729	677.8901	14
5	454.3024	227.6548			A	1315.7620	658.3846	1298.7355	649.8714	1297.7515	649.3794	13
6	567.3865	284.1969			L	1244.7249	622.8661	1227.6984	614.3528	1226.7143	613.8608	12
7	654.4185	327.7129	636.4079	318.7076	S	1131.6408	566.3241	1114.6143	557.8108	1113.6303	557.3188	11
8	751.4713	376.2393	733.4607	367.2340	P	1044.6088	522.8080	1027.5823	514.2948	1026.5982	513.8028	10
9	808.4927	404.7500	790.4822	395.7447	G	947.5560	474.2817	930.5295	465.7684	929.5455	465.2764	9
10	921.5768	461.2920	903.5662	452.2867	L	890.5346	445.7709	873.5080	437.2577	872.5240	436.7656	8
11	992.6139	496.8106	974.6033	487.8053	A	777.4505	389.2289	760.4240	380.7156	759.4400	380.2236	7
12	1063.6510	532.3291	1045.6404	523.3239	A	706.4134	353.7103	689.3869	345.1971	688.4028	344.7051	6
13	1178.6780	589.8426	1160.6674	580.8373	D	635.3763	318.1918	618.3497	309.6785	617.3657	309.1865	5
14	1325.7464	663.3768	1307.7358	654.3715	F	520.3493	260.6783	503.3228	252.1650			4
15	1438.8304	719.9189	1420.8199	710.9136	L	373.2809	187.1441	356.2544	178.6308			3
16	1551.9145	776.4609	1533.9039	767.4556	L	260.1969	130.6021	243.1703	122.0888			2
17					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 15 ppm



RMS error 15 ppm

Peptide Number: 66261

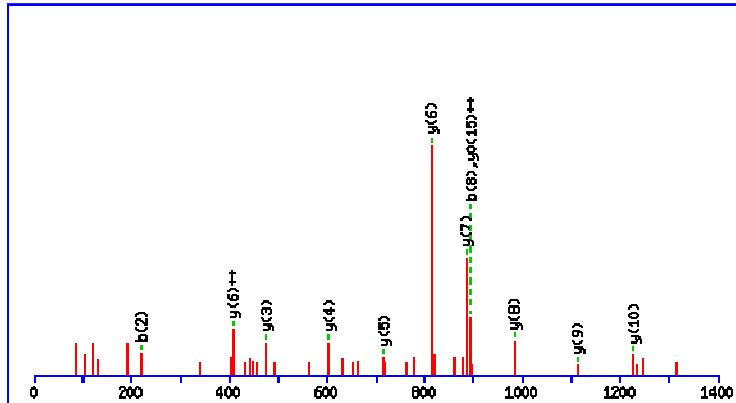
MS/MS Fragmentation of **AFLDGFNEVAPLEWLR**

Found in **IPI00902762** in **IPI_human**, Tax_Id=9606 Gene_Symbol=WWP2 cDNA FLJ44359 fis, clone TRACH3007479, highly similar to Homo sapiens Nedd-4-like ubiquitin-protein ligase

Match to Query 9874: 1875.955182 from(626.325670,3+) index(30084)

Title: Elution from: 77.8833333333333 to 77.8833333333333 period: 0 cycle: 2953 experiment: 4 polarity: +

Data file 120214ry_414C2-43_4_4.mgf



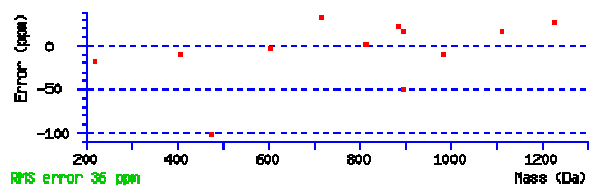
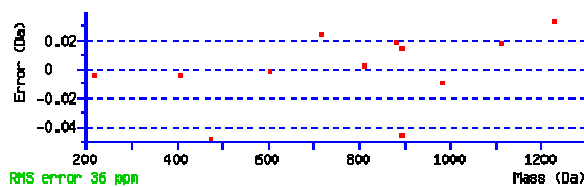
Monoisotopic mass of neutral peptide Mr(calc): 1875.9519

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 48 Expect: 0.0011

Matches : 12/156 fragment ions using 21 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							16
2	219.1128	110.0600					F	1805.9221	903.4647	1788.8955	894.9514	1787.9115	894.4594	15
3	332.1969	166.6021					L	1658.8537	829.9305	1641.8271	821.4172	1640.8431	820.9252	14
4	447.2238	224.1155			429.2132	215.1103	D	1545.7696	773.3884	1528.7431	764.8752	1527.7591	764.3832	13
5	504.2453	252.6263			486.2347	243.6210	G	1430.7427	715.8750	1413.7161	707.3617	1412.7321	706.8697	12
6	651.3137	326.1605			633.3031	317.1552	F	1373.7212	687.3642	1356.6947	678.8510	1355.7106	678.3590	11
7	765.3566	383.1819	748.3301	374.6687	747.3461	374.1767	N	1226.6528	613.8300	1209.6262	605.3168	1208.6422	604.8248	10
8	894.3992	447.7032	877.3727	439.1900	876.3886	438.6980	E	1112.6099	556.8086	1095.5833	548.2953	1094.5993	547.8033	9
9	993.4676	497.2374	976.4411	488.7242	975.4571	488.2322	V	983.5673	492.2873	966.5407	483.7740	965.5567	483.2820	8
10	1064.5047	532.7560	1047.4782	524.2427	1046.4942	523.7507	A	884.4989	442.7531	867.4723	434.2398	866.4883	433.7478	7
11	1161.5575	581.2824	1144.5310	572.7691	1143.5469	572.2771	P	813.4617	407.2345	796.4352	398.7212	795.4512	398.2292	6
12	1274.6416	637.8244	1257.6150	629.3111	1256.6310	628.8191	L	716.4090	358.7081	699.3824	350.1949	698.3984	349.7028	5
13	1403.6842	702.3457	1386.6576	693.8324	1385.6736	693.3404	E	603.3249	302.1661	586.2984	293.6528	585.3144	293.1608	4
14	1589.7635	795.3854	1572.7369	786.8721	1571.7529	786.3801	W	474.2823	237.6448	457.2558	229.1315			3
15	1702.8475	851.9274	1685.8210	843.4141	1684.8370	842.9221	L	288.2030	144.6051	271.1765	136.0919			2
16							R	175.1190	88.0631	158.0924	79.5498			1



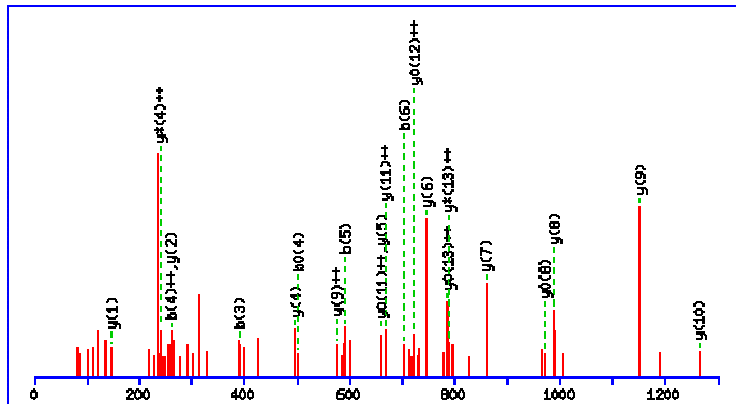
Peptide Number: 66380

MS/MS Fragmentation of **DFQQALYELSYHVIK**Found in **IPI00915022** in **IPI_human**, Tax_Id=9606 Gene_Symbol=THOC2 Isoform 1 of THO complex subunit 2

Match to Query 10031: 1852.919472 from(618.647100,3+) index(14637)

Title: Elution from: 36.6833333333333 to 36.6833333333333 period: 0 cycle: 1371 experiment: 1 polarity:+

Data file 120118ry_201B7-32_1_4.mgf



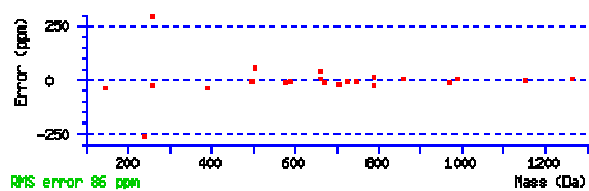
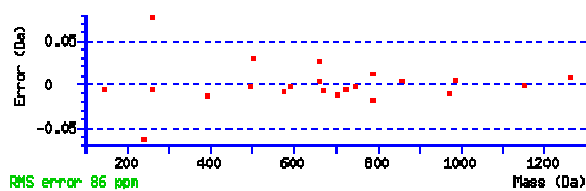
Monoisotopic mass of neutral peptide Mr(calc): 1852.9359

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 58 Expect: 0.0001

Matches : 22/154 fragment ions using 32 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							15
2	263.1026	132.0550			245.0921	123.0497	F	1738.9163	869.9618	1721.8897	861.4485	1720.9057	860.9565	14
3	391.1612	196.0842	374.1347	187.5710	373.1506	187.0790	Q	1591.8479	796.4276	1574.8213	787.9143	1573.8373	787.4223	13
4	519.2198	260.1135	502.1932	251.6003	501.2092	251.1083	Q	1463.7893	732.3983	1446.7627	723.8850	1445.7787	723.3930	12
5	590.2569	295.6321	573.2304	287.1188	572.2463	286.6268	A	1335.7307	668.3690	1318.7042	659.8557	1317.7202	659.3637	11
6	703.3410	352.1741	686.3144	343.6608	685.3304	343.1688	L	1264.6936	632.8504	1247.6671	624.3372	1246.6830	623.8452	10
7	866.4043	433.7058	849.3777	425.1925	848.3937	424.7005	Y	1151.6095	576.3084	1134.5830	567.7951	1133.5990	567.3031	9
8	995.4469	498.2271	978.4203	489.7138	977.4363	489.2218	E	988.5462	494.7767	971.5197	486.2635	970.5356	485.7715	8
9	1108.5310	554.7691	1091.5044	546.2558	1090.5204	545.7638	L	859.5036	430.2554	842.4771	421.7422	841.4931	421.2502	7
10	1195.5630	598.2851	1178.5364	589.7719	1177.5524	589.2798	S	746.4196	373.7134	729.3930	365.2001	728.4090	364.7081	6
11	1358.6263	679.8168	1341.5998	671.3035	1340.6157	670.8115	Y	659.3875	330.1974	642.3610	321.6841			5
12	1495.6852	748.3462	1478.6587	739.8330	1477.6747	739.3410	H	496.3242	248.6657	479.2976	240.1525			4
13	1594.7536	797.8805	1577.7271	789.3672	1576.7431	788.8752	V	359.2653	180.1363	342.2387	171.6230			3
14	1707.8377	854.4225	1690.8112	845.9092	1689.8271	845.4172	I	260.1969	130.6021	243.1703	122.0888			2
15							K	147.1128	74.0600	130.0863	65.5468			1



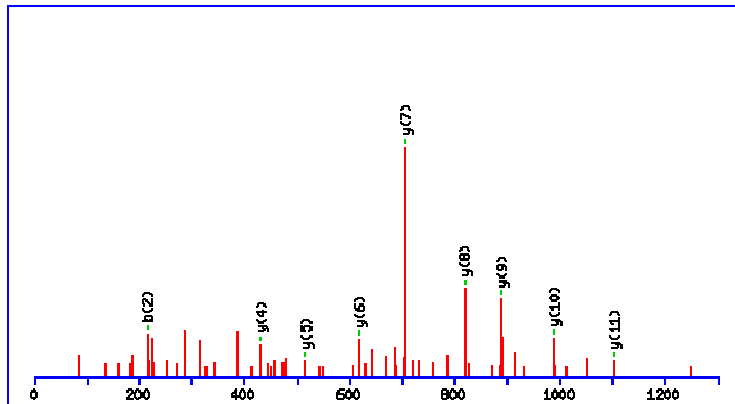
Peptide Number: 66443

MS/MS Fragmentation of **VDVAISTSALAR**Found in **IPI00101106** in **IPI_human**, Tax_Id=9606 Gene_Symbol=COMMD5 COMM domain-containing protein 5

Match to Query 13762: 1201.671908 from(601.843230,2+) index(24490)

Title: Elution from: 63.3833333333333 to 63.3833333333333 period: 0 cycle: 2423 experiment: 7 polarity: +

Data file 120208ry_Tig120slc-P8_1_2.mgf



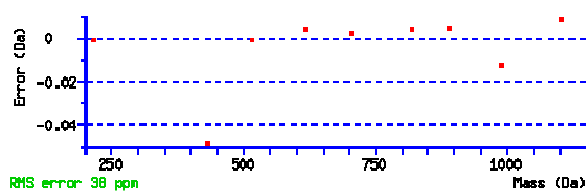
Monoisotopic mass of neutral peptide Mr(calc): 1201.6666

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

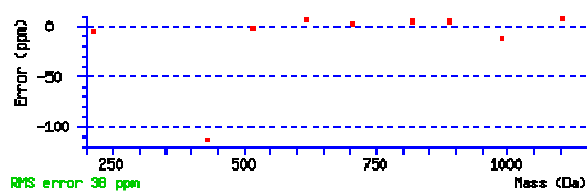
Ions Score: 76 Expect: 1.9e-006

Matches : 9/100 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415			V							12
2	215.1026	108.0550	197.0921	99.0497	D	1103.6055	552.3064	1086.5790	543.7931	1085.5949	543.3011	11
3	314.1710	157.5892	296.1605	148.5839	V	988.5786	494.7929	971.5520	486.2796	970.5680	485.7876	10
4	385.2082	193.1077	367.1976	184.1024	A	889.5102	445.2587	872.4836	436.7454	871.4996	436.2534	9
5	498.2922	249.6498	480.2817	240.6445	I	818.4730	409.7402	801.4465	401.2269	800.4625	400.7349	8
6	585.3243	293.1658	567.3137	284.1605	S	705.3890	353.1981	688.3624	344.6849	687.3784	344.1928	7
7	686.3719	343.6896	668.3614	334.6843	T	618.3570	309.6821	601.3304	301.1688	600.3464	300.6768	6
8	773.4040	387.2056	755.3934	378.2003	S	517.3093	259.1583	500.2827	250.6450	499.2987	250.1530	5
9	844.4411	422.7242	826.4305	413.7189	A	430.2772	215.6423	413.2507	207.1290			4
10	957.5251	479.2662	939.5146	470.2609	L		359.2401	180.1237	342.2136	171.6104		3
11	1028.5623	514.7848	1010.5517	505.7795	A		246.1561	123.5817	229.1295	115.0684		2
12					R		175.1190	88.0631	158.0924	79.5498		1



RMS error 38 ppm



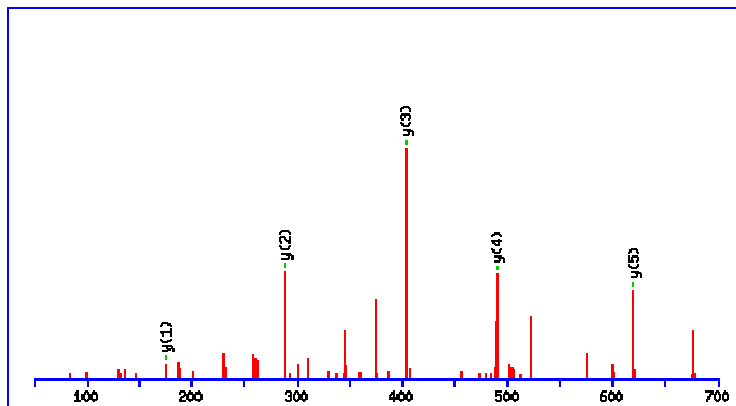
RMS error 38 ppm

Peptide Number: 66701MS/MS Fragmentation of **ILFEESDLR**Found in **IPI00374129** in **IPI_human**, Tax_Id=9606 Gene_Symbol=NLRP3 Isoform 1 of NACHT, LRR and PYD domains-containing protein 3

Match to Query 14955: 1120.558752 from(374.526860,3+) index(24192)

Title: Elution from: 98.2833333333333 to 98.2833333333333 period: 0 cycle: 8728 experiment: 3 polarity:+

Data file 120212ry_414C2-43_3_1.mgf



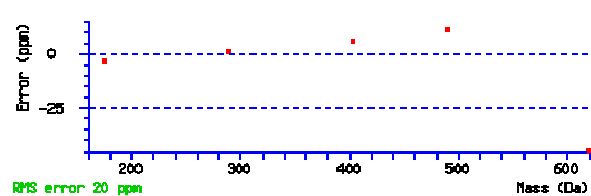
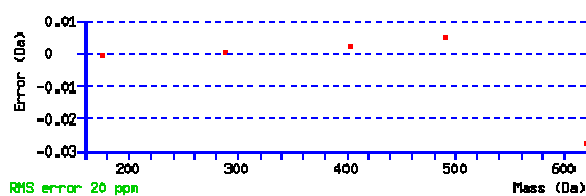
Monoisotopic mass of neutral peptide Mr(calc): 1120.5764

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 43 Expect: 0.0037

Matches : 5/70 fragment ions using 6 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			I							9
2	227.1754	114.0913			L	1008.4997	504.7535	991.4731	496.2402	990.4891	495.7482	8
3	374.2438	187.6255			F	895.4156	448.2114	878.3890	439.6982	877.4050	439.2061	7
4	503.2864	252.1468	485.2758	243.1416	E	748.3472	374.6772	731.3206	366.1640	730.3366	365.6719	6
5	632.3290	316.6681	614.3184	307.6629	E	619.3046	310.1559	602.2780	301.6427	601.2940	301.1506	5
6	719.3610	360.1842	701.3505	351.1789	S	490.2620	245.6346	473.2354	237.1214	472.2514	236.6293	4
7	834.3880	417.6976	816.3774	408.6923	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
8	947.4720	474.2397	929.4615	465.2344	L	288.2030	144.6051	271.1765	136.0919			2
9					R	175.1190	88.0631	158.0924	79.5498			1

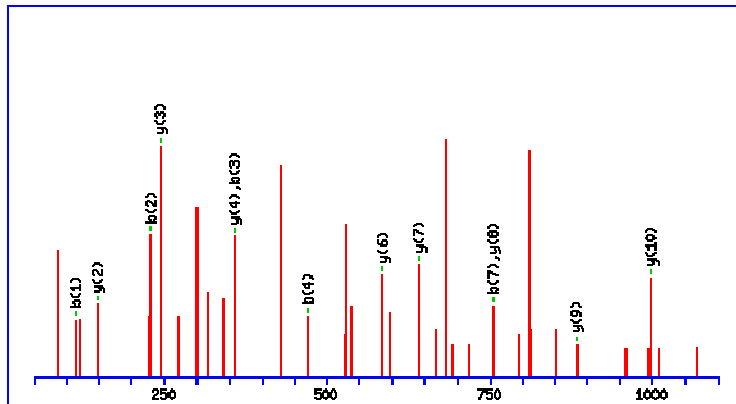


Peptide Number: 66787MS/MS Fragmentation of **LDKIGLNLPAQ**Found in **IPI00945156** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TFAP2A Uncharacterized protein

Match to Query 1963: 1109.634728 from(555.824640,2+) index(8858)

Title: Elution from: 23.2833333333333 to 23.2833333333333 period: 0 cycle: 894 experiment: 2 polarity: +

Data file 120208ry_Tig120slc-P8_1_3.mgf



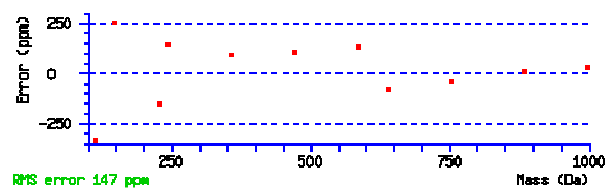
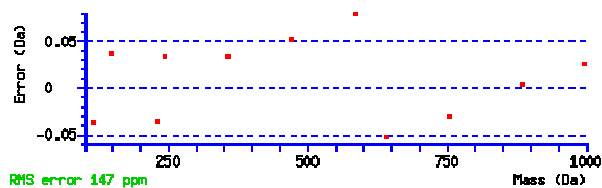
Monoisotopic mass of neutral peptide Mr(calc): 1109.6444

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 38 Expect: 0.0057

Matches : 13/88 fragment ions using 36 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							11
2	229.1183	115.0628			211.1077	106.0575	D	997.5677	499.2875	980.5411	490.7742	979.5571	490.2822	10
3	357.2132	179.1103	340.1867	170.5970	339.2027	170.1050	K	882.5407	441.7740	865.5142	433.2607			9
4	470.2973	235.6523	453.2708	227.1390	452.2867	226.6470	I	754.4458	377.7265	737.4192	369.2132			8
5	527.3188	264.1630	510.2922	255.6498	509.3082	255.1577	G	641.3617	321.1845	624.3352	312.6712			7
6	640.4028	320.7051	623.3763	312.1918	622.3923	311.6998	L	584.3402	292.6738	567.3137	284.1605			6
7	754.4458	377.7265	737.4192	369.2132	736.4352	368.7212	N	471.2562	236.1317	454.2296	227.6185			5
8	867.5298	434.2686	850.5033	425.7553	849.5193	425.2633	L	357.2132	179.1103					4
9	964.5826	482.7949	947.5560	474.2817	946.5720	473.7897	P	244.1292	122.5682					3
10	1035.6197	518.3135	1018.5932	509.8002	1017.6091	509.3082	A	147.0764	74.0418					2
11							G	76.0393	38.5233					1



Peptide Number: 67083

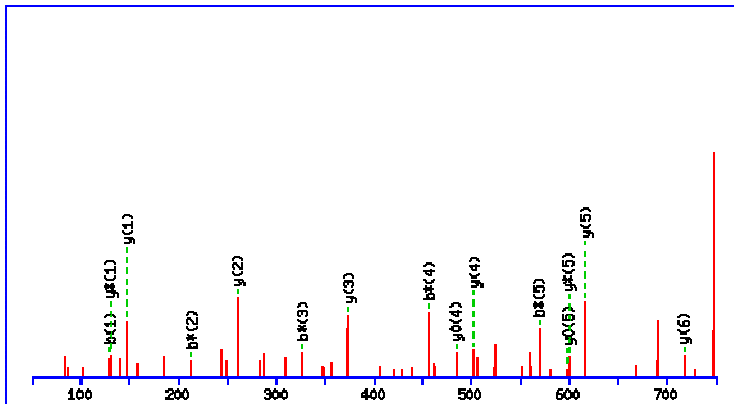
MS/MS Fragmentation of **KTNEILK**

Found in **IPI00024278** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ABCC9 Isoform SUR2A of ATP-binding cassette sub-family C member 9

Match to Query 5106: 844.510728 from(423.262640,2+) index(15162)

Title: Elution from: 79.2166666666667 to 79.2166666666667 period: 0 cycle: 8035 experiment: 4 polarity: +

Data file 120214ry_aHDF1419-P10_4_1.mgf



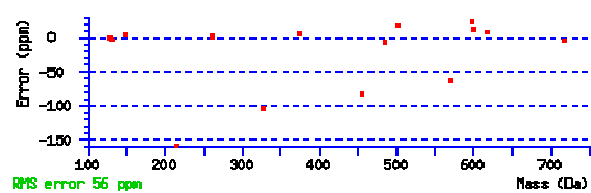
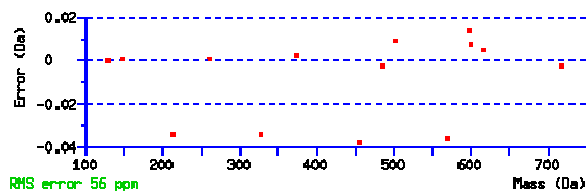
Monoisotopic mass of neutral peptide Mr(calc): 844.5018

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 40 Expect: 0.0058

Matches : 15/64 fragment ions using 28 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.1022	65.0548	112.0757	56.5415			K							7
2	230.1499	115.5786	213.1234	107.0653	212.1394	106.5733	T	717.4141	359.2107	700.3876	350.6974	699.4036	350.2054	6
3	344.1928	172.6001	327.1663	164.0868	326.1823	163.5948	N	616.3665	308.6869	599.3399	300.1736	598.3559	299.6816	5
4	473.2354	237.1214	456.2089	228.6081	455.2249	228.1161	E	502.3235	251.6654	485.2970	243.1521	484.3130	242.6601	4
5	586.3195	293.6634	569.2930	285.1501	568.3089	284.6581	I	373.2809	187.1441	356.2544	178.6308			3
6	699.4036	350.2054	682.3770	341.6921	681.3930	341.2001	L	260.1969	130.6021	243.1703	122.0888			2
7							K	147.1128	74.0600	130.0863	65.5468			1



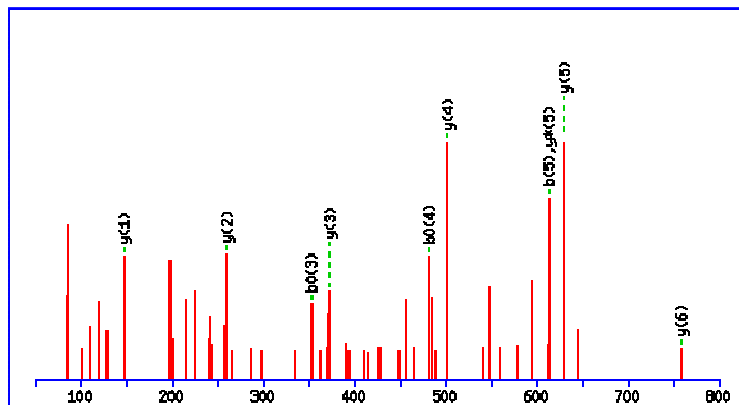
Peptide Number: 67169**MS/MS Fragmentation of LEQELLK**

Found in **IPI00910883** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CALCOCO2 cDNA FLJ55141, highly similar to Homo sapiens nuclear domain 10 protein (NDP52), mRNA

Match to Query 3285: 871.495168 from(436.754860,2+) index(17297)

Title: Elution from: 41.1666666666667 to 41.1666666666667 period: 0 cycle: 1520 experiment: 2 polarity: +

Data file 120118ry_201B7-32_1_2.mgf



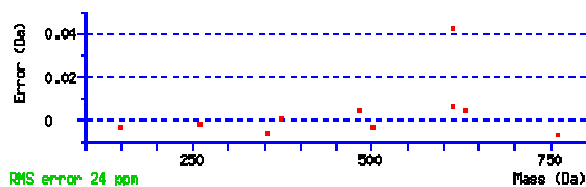
Monoisotopic mass of neutral peptide Mr(calc): 871.5014

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

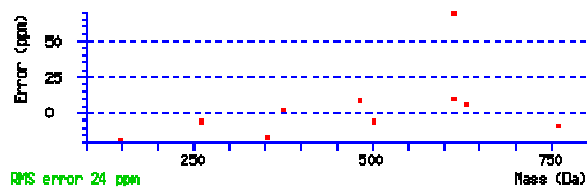
Ions Score: 51 **Expect:** 0.00054

Matches : 10/60 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							7
2	243.1339	122.0706			225.1234	113.0653	E	759.4247	380.2160	742.3981	371.7027	741.4141	371.2107	6
3	371.1925	186.0999	354.1660	177.5866	353.1819	177.0946	Q	630.3821	315.6947	613.3556	307.1814	612.3715	306.6894	5
4	500.2351	250.6212	483.2086	242.1079	482.2245	241.6159	E	502.3235	251.6654	485.2970	243.1521	484.3130	242.6601	4
5	613.3192	307.1632	596.2926	298.6499	595.3086	298.1579	L	373.2809	187.1441	356.2544	178.6308			3
6	726.4032	363.7053	709.3767	355.1920	708.3927	354.7000	L	260.1969	130.6021	243.1703	122.0888			2
7							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 24 ppm



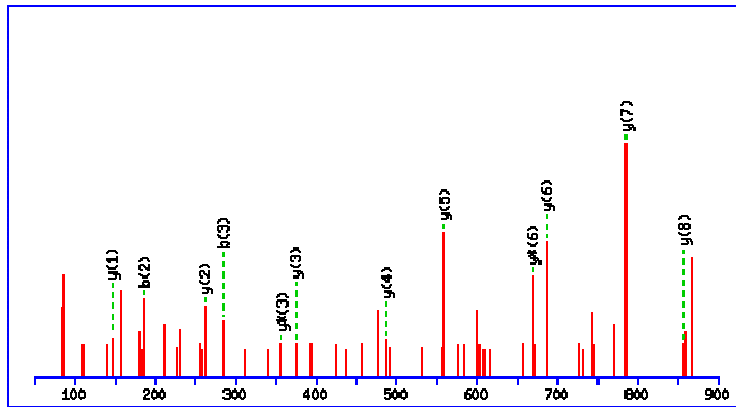
RMS error 24 ppm

Peptide Number: 67203MS/MS Fragmentation of **NAVQALIDK**Found in **IPI00984036** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TMEM68 Uncharacterized protein

Match to Query 6299: 970.530788 from(486.272670,2+) index(21165)

Title: Elution from: 50.65 to 50.65 period: 0 cycle: 1878 experiment: 7 polarity:+

Data file 120129ry_604A1-46_1_2.mgf



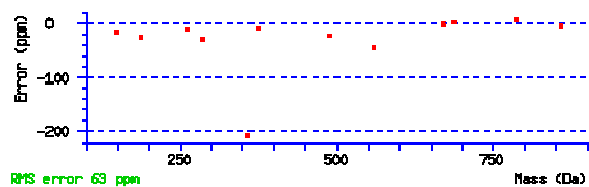
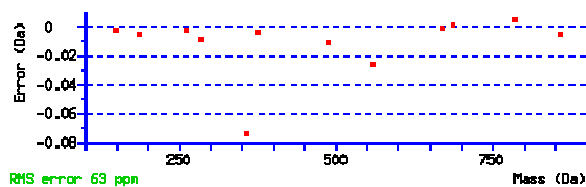
Monoisotopic mass of neutral peptide Mr(calc): 970.5447

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 43 Expect: 0.0028

Matches : 12/80 fragment ions using 39 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							9
2	186.0873	93.5473	169.0608	85.0340			A	857.5091	429.2582	840.4825	420.7449	839.4985	420.2529	8
3	285.1557	143.0815	268.1292	134.5682			V	786.4720	393.7396	769.4454	385.2264	768.4614	384.7343	7
4	413.2143	207.1108	396.1878	198.5975			Q	687.4036	344.2054	670.3770	335.6921	669.3930	335.2001	6
5	484.2514	242.6293	467.2249	234.1161			A	559.3450	280.1761	542.3184	271.6629	541.3344	271.1709	5
6	597.3355	299.1714	580.3089	290.6581			L	488.3079	244.6576	471.2813	236.1443	470.2973	235.6523	4
7	710.4196	355.7134	693.3930	347.2001			I	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
8	825.4465	413.2269	808.4199	404.7136	807.4359	404.2216	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
9							K	147.1128	74.0600	130.0863	65.5468			1



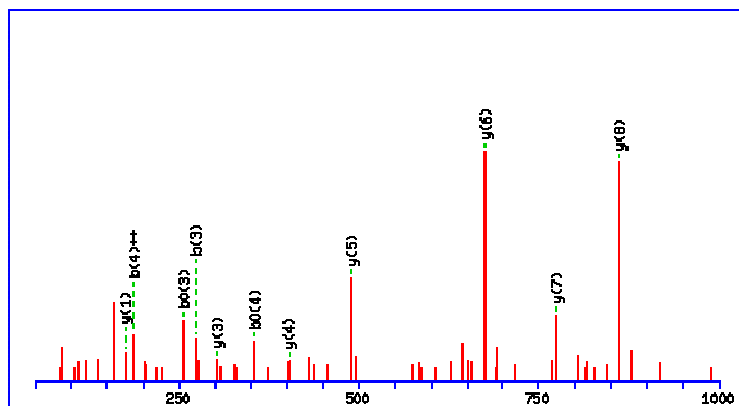
Peptide Number: 67375

MS/MS Fragmentation of **SVSVWSVAGR**Found in **IPI00074010** in **IPI_human**, Tax_Id=9606 Gene_Symbol=QTRTD1 48 kDa protein

Match to Query 9419: 1046.546768 from(524.280660,2+) index(29308)

Title: Elution from: 71.25 to 71.25 period: 0 cycle: 2699 experiment: 4 polarity:+

Data file 120210ry_32R1-32_3_2.mgf



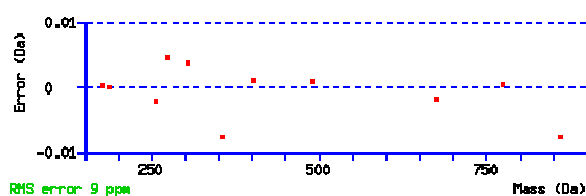
Monoisotopic mass of neutral peptide Mr(calc): 1046.5509

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

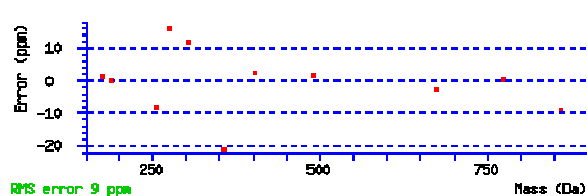
Ions Score: 41 Expect: 0.0066

Matches : 12/82 fragment ions using 26 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233	70.0287	35.5180	S							10
2	187.1077	94.0575	169.0972	85.0522	V	960.5261	480.7667	943.4996	472.2534	942.5156	471.7614	9
3	274.1397	137.5735	256.1292	128.5682	S	861.4577	431.2325	844.4312	422.7192	843.4472	422.2272	8
4	373.2082	187.1077	355.1976	178.1024	V	774.4257	387.7165	757.3992	379.2032	756.4151	378.7112	7
5	559.2875	280.1474	541.2769	271.1421	W	675.3573	338.1823	658.3307	329.6690	657.3467	329.1770	6
6	646.3195	323.6634	628.3089	314.6581	S	489.2780	245.1426	472.2514	236.6293	471.2674	236.1373	5
7	745.3879	373.1976	727.3773	364.1923	V	402.2459	201.6266	385.2194	193.1133			4
8	816.4250	408.7162	798.4145	399.7109	A	303.1775	152.0924	286.1510	143.5791			3
9	873.4465	437.2269	855.4359	428.2216	G	232.1404	116.5738	215.1139	108.0606			2
10					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 9 ppm



RMS error 9 ppm

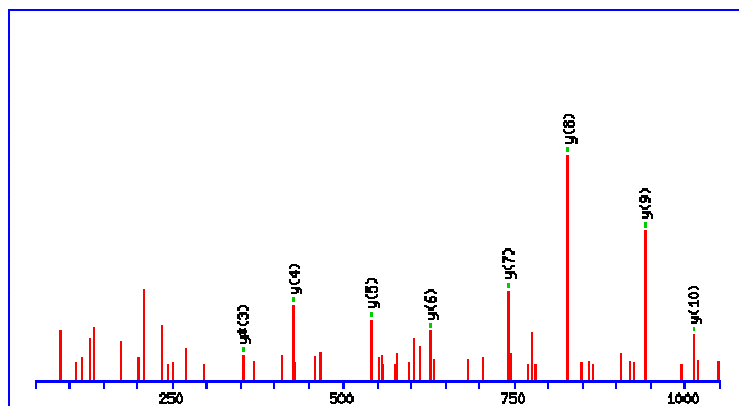
Peptide Number: 67546

MS/MS Fragmentation of **YALSNSIGPVR**Found in **IPI00026944** in **IPI_human**, Tax_Id=9606 Gene_Symbol=NID1 Isoform 1 of Nidogen-1

Match to Query 13043: 1175.614328 from(588.814440,2+) index(20117)

Title: Elution from: 47.9833333333333 to 47.9833333333333 period: 0 cycle: 1818 experiment: 9 polarity:+

Data file 120208ry_Tig120slc-P8_2_2.mgf



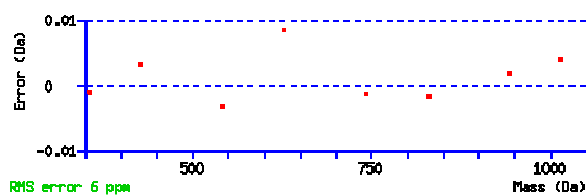
Monoisotopic mass of neutral peptide Mr(calc): 1175.6299

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

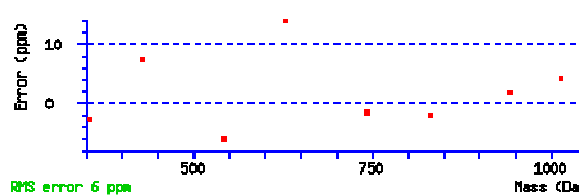
Ions Score: 64 Expect: 3.5e-005

Matches : 8/96 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389					Y							11
2	235.1077	118.0575					A	1013.5738	507.2905	996.5473	498.7773	995.5633	498.2853	10
3	348.1918	174.5995					L	942.5367	471.7720	925.5102	463.2587	924.5261	462.7667	9
4	435.2238	218.1155			417.2132	209.1103	S	829.4526	415.2300	812.4261	406.7167	811.4421	406.2247	8
5	549.2667	275.1370	532.2402	266.6237	531.2562	266.1317	N	742.4206	371.7139	725.3941	363.2007	724.4100	362.7087	7
6	636.2988	318.6530	619.2722	310.1397	618.2882	309.6477	S	628.3777	314.6925	611.3511	306.1792	610.3671	305.6872	6
7	749.3828	375.1951	732.3563	366.6818	731.3723	366.1898	I	541.3457	271.1765	524.3191	262.6632			5
8	806.4043	403.7058	789.3777	395.1925	788.3937	394.7005	G	428.2616	214.6344	411.2350	206.1212			4
9	903.4571	452.2322	886.4305	443.7189	885.4465	443.2269	P	371.2401	186.1237	354.2136	177.6104			3
10	1002.5255	501.7664	985.4989	493.2531	984.5149	492.7611	V	274.1874	137.5973	257.1608	129.0840			2
11							R	175.1190	88.0631	158.0924	79.5498			1



RMS error: 6 ppm



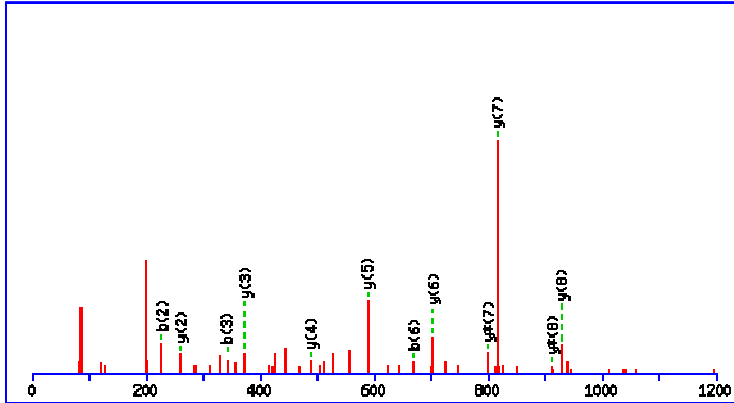
RMS error: 6 ppm

Peptide Number: 67783MS/MS Fragmentation of **LINLTDILK**Found in **IPI00031386** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PIK3CA Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit alpha isoform

Match to Query 1264: 1041.637728 from(521.826140,2+) index(35222)

Title: Elution from: 91.1333333333333 to 91.1333333333333 period: 0 cycle: 3459 experiment: 1 polarity: +

Data file 120212ry_aHDF1388-P9_3_3.mgf



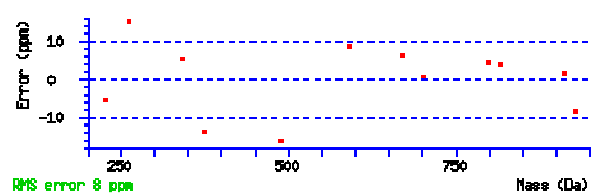
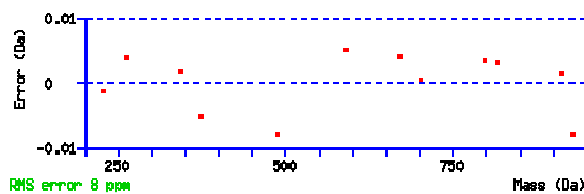
Monoisotopic mass of neutral peptide Mr(calc): 1041.6434

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 38 Expect: 0.0061

Matches : 12/78 fragment ions using 30 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							9
2	227.1754	114.0913					I	929.5666	465.2869	912.5401	456.7737	911.5560	456.2817	8
3	341.2183	171.1128	324.1918	162.5995			N	816.4825	408.7449	799.4560	400.2316	798.4720	399.7396	7
4	454.3024	227.6548	437.2758	219.1416			L	702.4396	351.7234	685.4131	343.2102	684.4291	342.7182	6
5	555.3501	278.1787	538.3235	269.6654	537.3395	269.1734	T	589.3556	295.1814	572.3290	286.6681	571.3450	286.1761	5
6	670.3770	335.6921	653.3505	327.1789	652.3665	326.6869	D	488.3079	244.6576	471.2813	236.1443	470.2973	235.6523	4
7	783.4611	392.2342	766.4345	383.7209	765.4505	383.2289	I	373.2809	187.1441	356.2544	178.6308			3
8	896.5451	448.7762	879.5186	440.2629	878.5346	439.7709	L	260.1969	130.6021	243.1703	122.0888			2
9							K	147.1128	74.0600	130.0863	65.5468			1



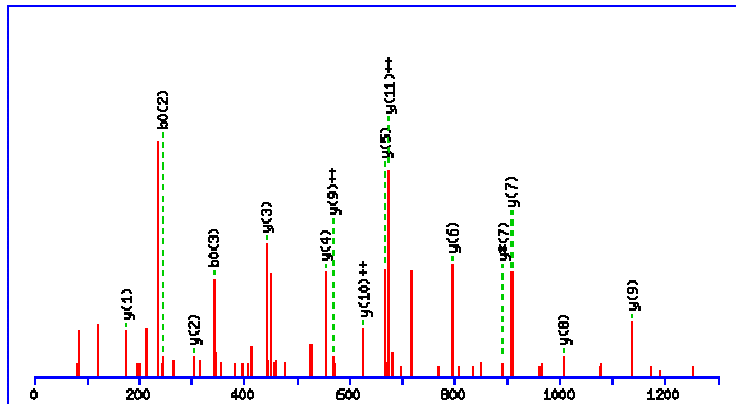
Peptide Number: 68022

MS/MS Fragmentation of **DFPDEVQLIHER**Found in **IPI00328276** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CDK5RAP1 Isoform 1 of CDK5 regulatory subunit-associated protein 1

Match to Query 5560: 1609.813962 from(537.611930,3+) index(8898)

Title: Elution from: 23.15 to 23.15 period: 0 cycle: 879 experiment: 1 polarity: +

Data file 120210ry_32R1-32_2_4.mgf



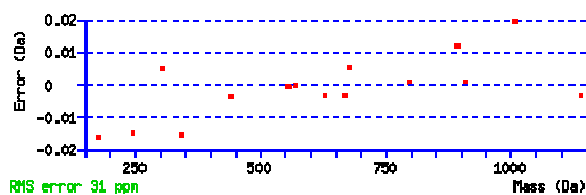
Monoisotopic mass of neutral peptide Mr(calc): 1609.8100

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

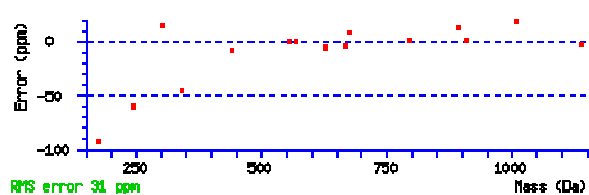
Ions Score: 45 Expect: 0.0022

Matches : 15/128 fragment ions using 34 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							13
2	263.1026	132.0550			245.0921	123.0497	F	1495.7904	748.3988	1478.7638	739.8855	1477.7798	739.3935	12
3	360.1554	180.5813			342.1448	171.5761	P	1348.7219	674.8646	1331.6954	666.3513	1330.7114	665.8593	11
4	475.1823	238.0948			457.1718	229.0895	D	1251.6692	626.3382	1234.6426	617.8250	1233.6586	617.3329	10
5	604.2249	302.6161			586.2144	293.6108	E	1136.6422	568.8248	1119.6157	560.3115	1118.6317	559.8195	9
6	703.2933	352.1503			685.2828	343.1450	V	1007.5996	504.3035	990.5731	495.7902	989.5891	495.2982	8
7	816.3774	408.6923			798.3668	399.6871	L	908.5312	454.7693	891.5047	446.2560	890.5207	445.7640	7
8	944.4360	472.7216	927.4094	464.2084	926.4254	463.7163	Q	795.4472	398.2272	778.4206	389.7139	777.4366	389.2219	6
9	1057.5201	529.2637	1040.4935	520.7504	1039.5095	520.2584	L	667.3886	334.1979	650.3620	325.6847	649.3780	325.1926	5
10	1170.6041	585.8057	1153.5776	577.2924	1152.5936	576.8004	I	554.3045	277.6559	537.2780	269.1426	536.2940	268.6506	4
11	1307.6630	654.3352	1290.6365	645.8219	1289.6525	645.3299	H	441.2205	221.1139	424.1939	212.6006	423.2099	212.1086	3
12	1436.7056	718.8564	1419.6791	710.3432	1418.6951	709.8512	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
13							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 31 ppm



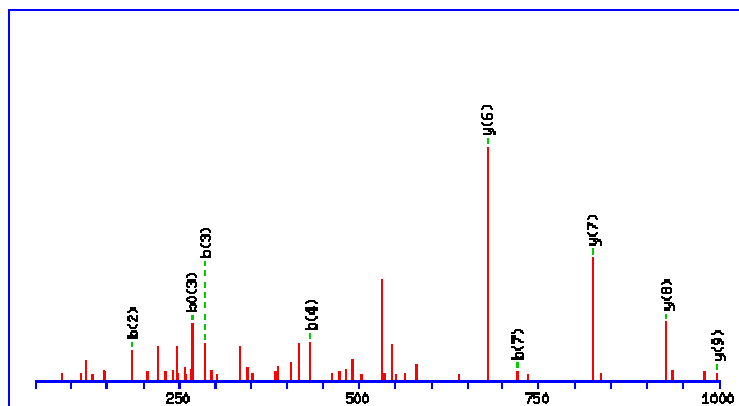
RMS error 31 ppm

Peptide Number: 68063MS/MS Fragmentation of **IATFSLSESR**Found in **IPI00645210** in **IPI_human**, Tax_Id=9606 Gene_Symbol=BTNL2 Isoform 2 of Butyrophilin-like protein 2

Match to Query 2724: 1109.577748 from(555.796150,2+) index(40450)

Title: Elution from: 102.016666666667 to 102.016666666667 period: 0 cycle: 3854 experiment: 1 polarity: +

Data file 120210ry_32R1-32_2_3.mgf



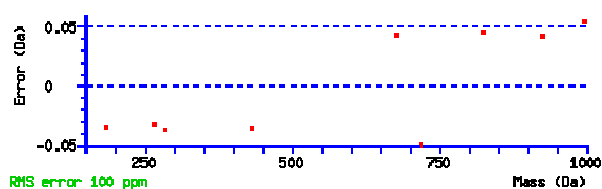
Monoisotopic mass of neutral peptide Mr(calc): 1109.5717

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

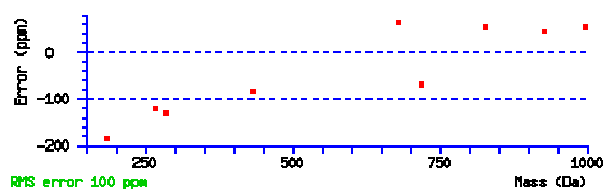
Ions Score: 40 Expect: 0.0052

Matches : 9/84 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			I							10
2	185.1285	93.0679			A	997.4949	499.2511	980.4684	490.7378	979.4843	490.2458	9
3	286.1761	143.5917	268.1656	134.5864	T	926.4578	463.7325	909.4312	455.2193	908.4472	454.7272	8
4	433.2445	217.1259	415.2340	208.1206	F	825.4101	413.2087	808.3836	404.6954	807.3995	404.2034	7
5	520.2766	260.6419	502.2660	251.6366	S	678.3417	339.6745	661.3151	331.1612	660.3311	330.6692	6
6	633.3606	317.1840	615.3501	308.1787	L	591.3097	296.1585	574.2831	287.6452	573.2991	287.1532	5
7	720.3927	360.7000	702.3821	351.6947	S	478.2256	239.6164	461.1991	231.1032	460.2150	230.6112	4
8	849.4353	425.2213	831.4247	416.2160	E	391.1936	196.1004	374.1670	187.5872	373.1830	187.0951	3
9	936.4673	468.7373	918.4567	459.7320	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
10					R	175.1190	88.0631	158.0924	79.5498			1



RMS error: 100 ppm



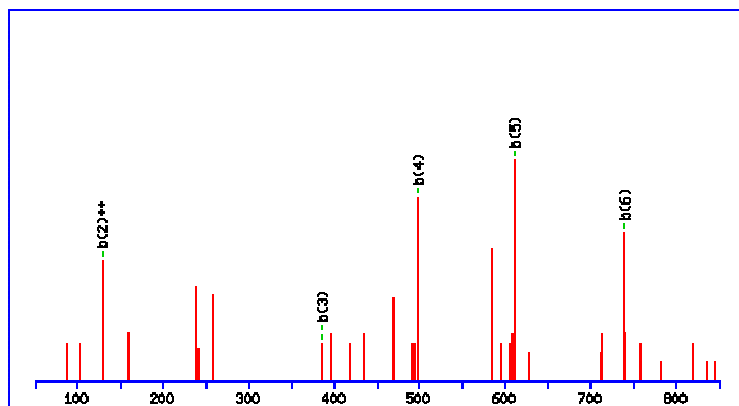
RMS error: 100 ppm

Peptide Number: 68122MS/MS Fragmentation of **QQQLLKK**Found in **IPI00022372** in **IPI_human**, Tax_Id=9606 Gene_Symbol=MYCN N-myc proto-oncogene protein

Match to Query 6837: 884.542848 from(443.278700,2+) index(7583)

Title: Elution from: 55.8833333333333 to 55.8833333333333 period: 0 cycle: 6899 experiment: 7 polarity:+

Data file 120210ry_32R1-32_2_1.mgf



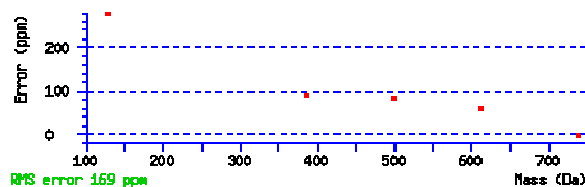
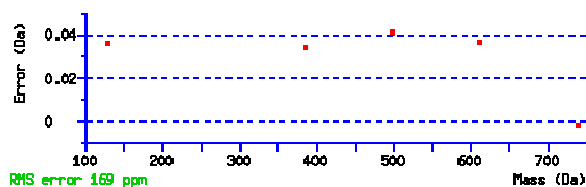
Monoisotopic mass of neutral peptide Mr(calc): 884.5443

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 39 Expect: 0.006

Matches : 6/48 fragment ions using 8 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	#
1	129.0659	65.0366	112.0393	56.5233	Q					7
2	257.1244	129.0659	240.0979	120.5526	Q	757.4931	379.2502	740.4665	370.7369	6
3	385.1830	193.0951	368.1565	184.5819	Q	629.4345	315.2209	612.4079	306.7076	5
4	498.2671	249.6372	481.2405	241.1239	L	501.3759	251.1916	484.3493	242.6783	4
5	611.3511	306.1792	594.3246	297.6659	L	388.2918	194.6496	371.2653	186.1363	3
6	739.4461	370.2267	722.4196	361.7134	K	275.2078	138.1075	258.1812	129.5942	2
7					K	147.1128	74.0600	130.0863	65.5468	1



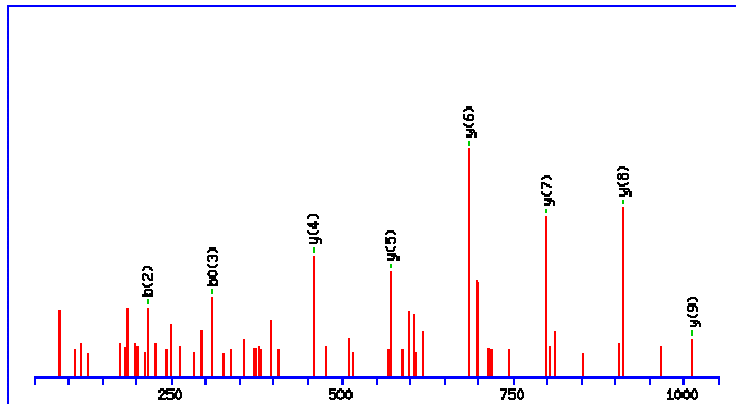
Peptide Number: 68212

MS/MS Fragmentation of **LTLILNPLTK**Found in **IPI00008495** in **IPI_human**, Tax_Id=9606 Gene_Symbol=MT-ND4 NADH-ubiquinone oxidoreductase chain 4

Match to Query 2252: 1124.724288 from(563.369420,2+) index(17101)

Title: Elution from: 43.5833333333333 to 43.5833333333333 period: 0 cycle: 1660 experiment: 4 polarity: +

Data file 120206ry_aHDF1419-P10_3_3.mgf



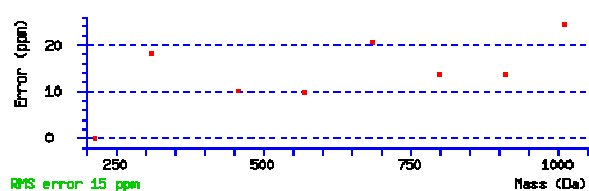
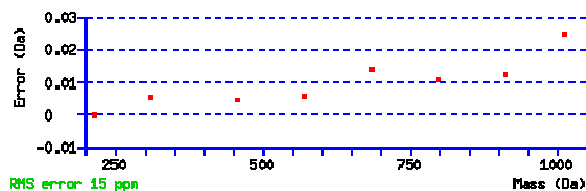
Monoisotopic mass of neutral peptide Mr(calc): 1124.7169

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 51 Expect: 5e-005

Matches : 8/94 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							10
2	215.1390	108.0731			197.1285	99.0679	T	1012.6401	506.8237	995.6136	498.3104	994.6295	497.8184	9
3	328.2231	164.6152			310.2125	155.6099	L	911.5924	456.2999	894.5659	447.7866	893.5819	447.2946	8
4	441.3071	221.1572			423.2966	212.1519	I	798.5084	399.7578	781.4818	391.2445	780.4978	390.7525	7
5	554.3912	277.6992			536.3806	268.6940	L	685.4243	343.2158	668.3978	334.7025	667.4137	334.2105	6
6	668.4341	334.7207	651.4076	326.2074	650.4236	325.7154	N	572.3402	286.6738	555.3137	278.1605	554.3297	277.6685	5
7	765.4869	383.2471	748.4604	374.7338	747.4763	374.2418	P	458.2973	229.6523	441.2708	221.1390	440.2867	220.6470	4
8	878.5710	439.7891	861.5444	431.2758	860.5604	430.7838	L	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
9	979.6186	490.3130	962.5921	481.7997	961.6081	481.3077	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
10							K	147.1128	74.0600	130.0863	65.5468			1



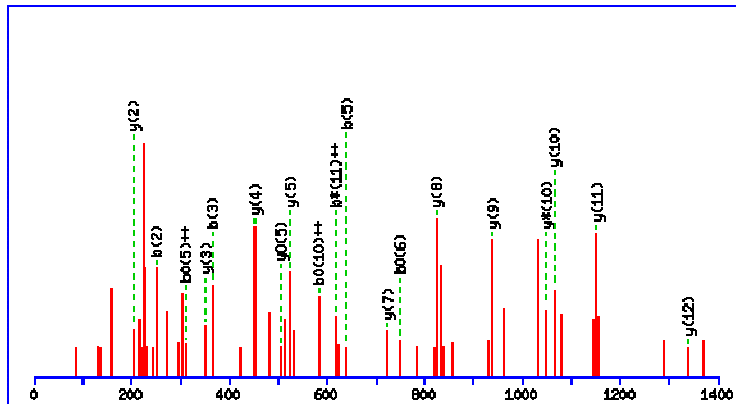
Peptide Number: 68488

MS/MS Fragmentation of **SYDWSQITTVATFGK**Found in **IPI00007778** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CTBS Di-N-acetylchitobiase

Match to Query 16465: 1702.812508 from(852.413530,2+) index(31602)

Title: Elution from: 82.1833333333333 to 82.1833333333333 period: 0 cycle: 3122 experiment: 8 polarity: +

Data file 120212ry_aHDF1388-P9_3_3.mgf



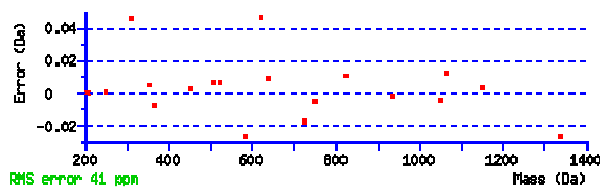
Monoisotopic mass of neutral peptide Mr(calc): 1702.8203

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

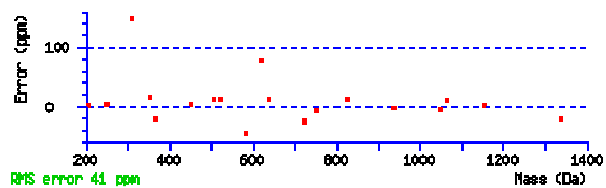
Ions Score: 41 Expect: 0.0042

Matches : 19/152 fragment ions using 56 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							15
2	251.1026	126.0550			233.0921	117.0497	Y	1616.7955	808.9014	1599.7690	800.3881	1598.7849	799.8961	14
3	366.1296	183.5684			348.1190	174.5631	D	1453.7322	727.3697	1436.7056	718.8565	1435.7216	718.3644	13
4	552.2089	276.6081			534.1983	267.6028	W	1338.7052	669.8563	1321.6787	661.3430	1320.6947	660.8510	12
5	639.2409	320.1241			621.2304	311.1188	S	1152.6259	576.8166	1135.5994	568.3033	1134.6154	567.8113	11
6	767.2995	384.1534	750.2729	375.6401	749.2889	375.1481	Q	1065.5939	533.3006	1048.5673	524.7873	1047.5833	524.2953	10
7	880.3836	440.6954	863.3570	432.1821	862.3730	431.6901	I	937.5353	469.2713	920.5088	460.7580	919.5247	460.2660	9
8	981.4312	491.2193	964.4047	482.7060	963.4207	482.2140	T	824.4512	412.7293	807.4247	404.2160	806.4407	403.7240	8
9	1082.4789	541.7431	1065.4524	533.2298	1064.4684	532.7378	T	723.4036	362.2054	706.3770	353.6921	705.3930	353.2001	7
10	1181.5473	591.2773	1164.5208	582.7640	1163.5368	582.2720	V	622.3559	311.6816	605.3293	303.1683	604.3453	302.6763	6
11	1252.5844	626.7959	1235.5579	618.2826	1234.5739	617.7906	A	523.2875	262.1474	506.2609	253.6341	505.2769	253.1421	5
12	1353.6321	677.3197	1336.6056	668.8064	1335.6216	668.3144	T	452.2504	226.6288	435.2238	218.1155	434.2398	217.6235	4
13	1500.7005	750.8539	1483.6740	742.3406	1482.6900	741.8486	F	351.2027	176.1050	334.1761	167.5917			3
14	1557.7220	779.3646	1540.6955	770.8514	1539.7114	770.3594	G	204.1343	102.5708	187.1077	94.0575			2
15							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 41 ppm



RMS error 41 ppm

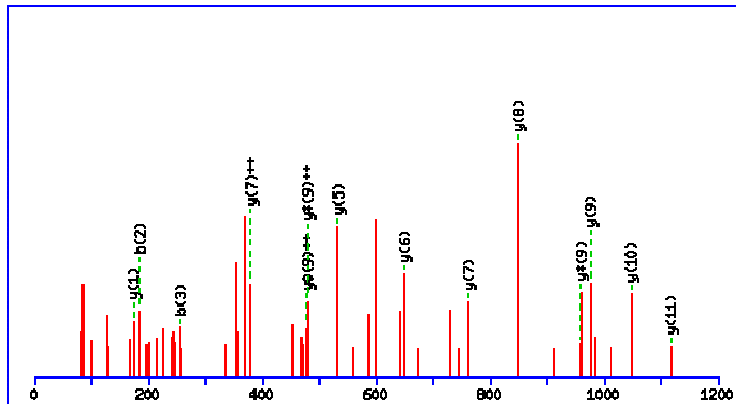
Peptide Number: 68556

MS/MS Fragmentation of **LAAQSLDTSGLR**Found in **IPI00010388** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CENPB Major centromere autoantigen B

Match to Query 14417: 1230.654568 from(616.334560,2+) index(8438)

Title: Elution from: 21.4333333333333 to 21.4333333333333 period: 0 cycle: 817 experiment: 8 polarity: +

Data file 120208ry_Tig120slc-P8_3_2.mgf



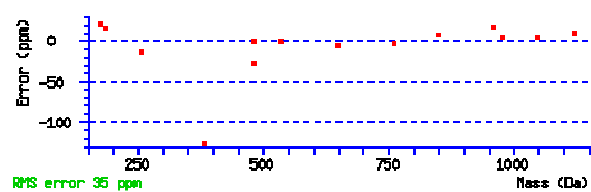
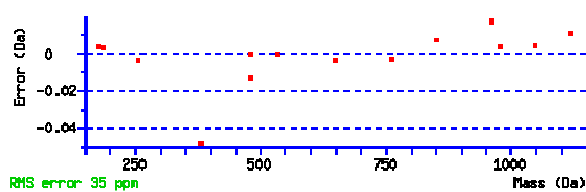
Monoisotopic mass of neutral peptide Mr(calc): 1230.6568

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 51 Expect: 0.00074

Matches : 14/112 fragment ions using 29 most intense peaks ([help](#))

#	b	b ⁺⁺	b [*]	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							12
2	185.1285	93.0679					A	1118.5800	559.7937	1101.5535	551.2804	1100.5695	550.7884	11
3	256.1656	128.5864					A	1047.5429	524.2751	1030.5164	515.7618	1029.5323	515.2698	10
4	384.2241	192.6157	367.1976	184.1024			Q	976.5058	488.7565	959.4793	480.2433	958.4952	479.7513	9
5	471.2562	236.1317	454.2296	227.6185	453.2456	227.1264	S	848.4472	424.7272	831.4207	416.2140	830.4367	415.7220	8
6	584.3402	292.6738	567.3137	284.1605	566.3297	283.6685	L	761.4152	381.2112	744.3886	372.6980	743.4046	372.2060	7
7	699.3672	350.1872	682.3406	341.6740	681.3566	341.1819	D	648.3311	324.6692	631.3046	316.1559	630.3206	315.6639	6
8	800.4149	400.7111	783.3883	392.1978	782.4043	391.7058	T	533.3042	267.1557	516.2776	258.6425	515.2936	258.1504	5
9	887.4469	444.2271	870.4203	435.7138	869.4363	435.2218	S	432.2565	216.6319	415.2300	208.1186	414.2459	207.6266	4
10	944.4684	472.7378	927.4418	464.2245	926.4578	463.7325	G	345.2245	173.1159	328.1979	164.6026			3
11	1057.5524	529.2798	1040.5259	520.7666	1039.5419	520.2746	L	288.2030	144.6051	271.1765	136.0919			2
12							R	175.1190	88.0631	158.0924	79.5498			1

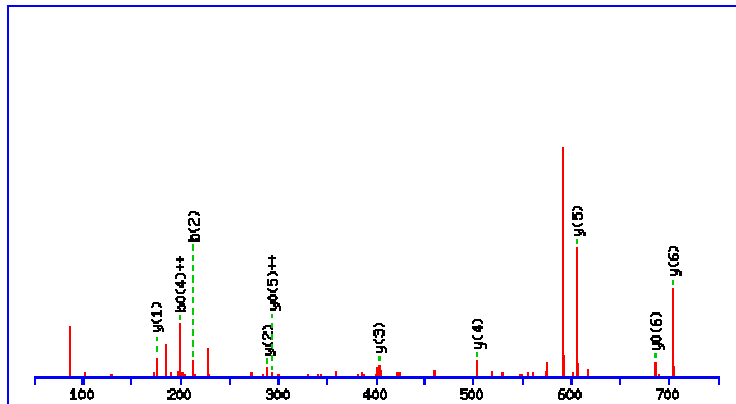


Peptide Number: 68589MS/MS Fragmentation of **IVTTDLR**Found in **IPI00020396** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PCSK6 Isoform PACE4A-I of Proprotein convertase subtilisin/kexin type 6

Match to Query 4426: 816.468548 from(409.241550,2+) index(19930)

Title: Elution from: 89.2333333333333 to 89.2333333333333 period: 0 cycle: 7373 experiment: 4 polarity:+

Data file 120118ry_201B7-32_1_1.mgf



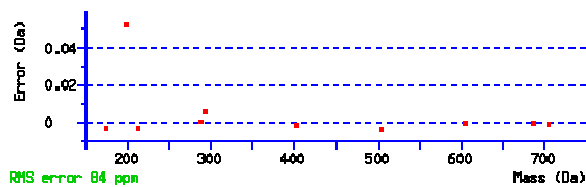
Monoisotopic mass of neutral peptide Mr(calc): 816.4705

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

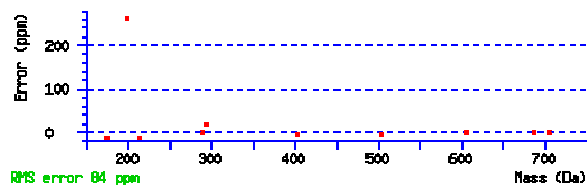
Ions Score: 41 Expect: 0.0078

Matches : 10/52 fragment ions using 21 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			I							7
2	213.1598	107.0835			V	704.3937	352.7005	687.3672	344.1872	686.3832	343.6952	6
3	314.2074	157.6074	296.1969	148.6021	T	605.3253	303.1663	588.2988	294.6530	587.3148	294.1610	5
4	415.2551	208.1312	397.2445	199.1259	T	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	4
5	530.2821	265.6447	512.2715	256.6394	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
6	643.3661	322.1867	625.3556	313.1814	L	288.2030	144.6051	271.1765	136.0919			2
7					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 84 ppm



RMS error 84 ppm

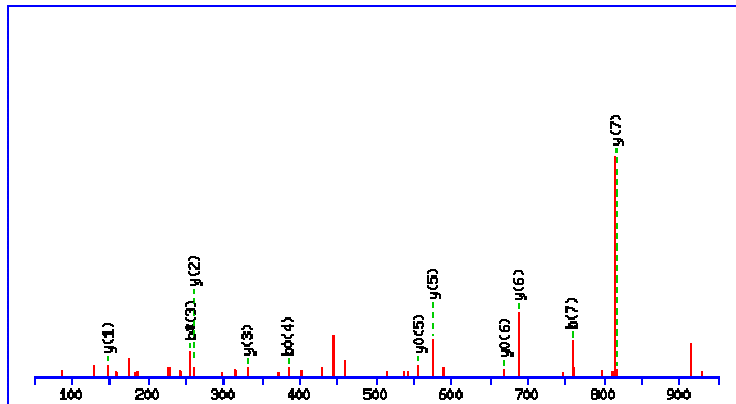
Peptide Number: 69019

MS/MS Fragmentation of **SQGEIDKAIK**Found in **IPI00412930** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TTC39B tetratricopeptide repeat protein 39B isoform 4 precursor

Match to Query 9260: 1087.586108 from(544.800330,2+) index(10514)

Title: Elution from: 27.5 to 27.5 period: 0 cycle: 1047 experiment: 5 polarity: +

Data file 120212ry_aHDF1388-P9_3_2.mgf



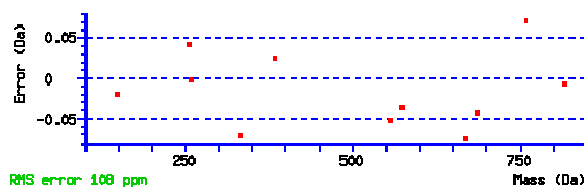
Monoisotopic mass of neutral peptide Mr(calc): 1087.5873

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

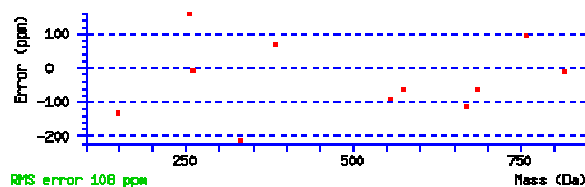
Ions Score: 40 Expect: 0.0085

Matches : 11/98 fragment ions using 18 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							10
2	216.0979	108.5526	199.0713	100.0393	198.0873	99.5473	Q	1001.5626	501.2849	984.5360	492.7717	983.5520	492.2796	9
3	273.1193	137.0633	256.0928	128.5500	255.1088	128.0580	G	873.5040	437.2556	856.4775	428.7424	855.4934	428.2504	8
4	402.1619	201.5846	385.1354	193.0713	384.1514	192.5793	E	816.4825	408.7449	799.4560	400.2316	798.4720	399.7396	7
5	515.2460	258.1266	498.2195	249.6134	497.2354	249.1214	I	687.4400	344.2236	670.4134	335.7103	669.4294	335.2183	6
6	630.2729	315.6401	613.2464	307.1268	612.2624	306.6348	D	574.3559	287.6816	557.3293	279.1683	556.3453	278.6763	5
7	758.3679	379.6876	741.3414	371.1743	740.3573	370.6823	K	459.3289	230.1681	442.3024	221.6548			4
8	829.4050	415.2061	812.3785	406.6929	811.3945	406.2009	A	331.2340	166.1206	314.2074	157.6074			3
9	942.4891	471.7482	925.4625	463.2349	924.4785	462.7429	I	260.1969	130.6021	243.1703	122.0888			2
10							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 108 ppm



RMS error 108 ppm

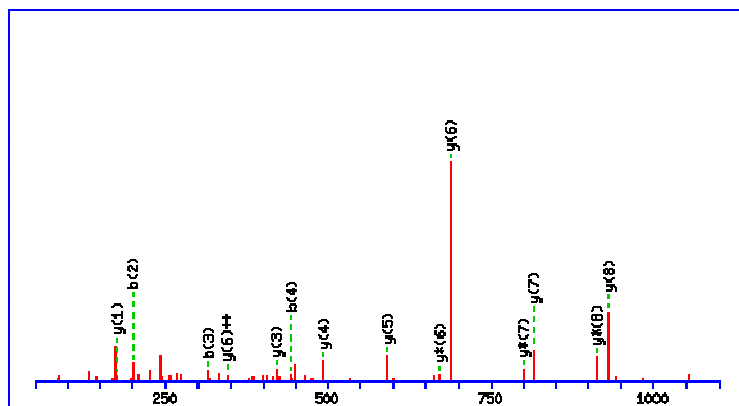
Peptide Number: 69218

MS/MS Fragmentation of **SINQPVAFVR**Found in **IPI01024994** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SLIRP Protein

Match to Query 13196: 1129.619108 from(565.816830,2+) index(19571)

Title: Elution from: 46.5666666666667 to 46.5666666666667 period: 0 cycle: 1720 experiment: 8 polarity: +

Data file 120118ry_201B7-32_1_2.mgf



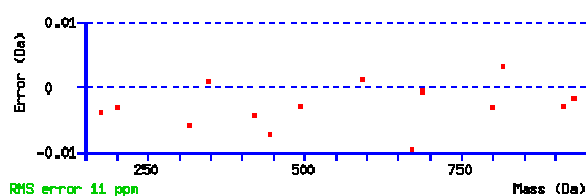
Monoisotopic mass of neutral peptide Mr(calc): 1129.6244

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

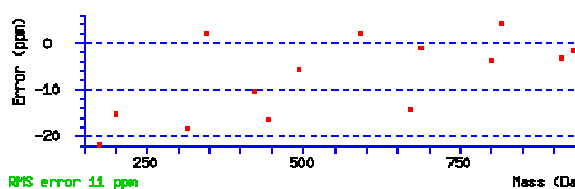
Ions Score: 47 Expect: 0.0015

Matches : 14/86 fragment ions using 25 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S					10
2	201.1234	101.0653			183.1128	92.0600	I	1043.5996	522.3035	1026.5731	513.7902	9
3	315.1663	158.0868	298.1397	149.5735	297.1557	149.0815	N	930.5156	465.7614	913.4890	457.2482	8
4	443.2249	222.1161	426.1983	213.6028	425.2143	213.1108	Q	816.4726	408.7400	799.4461	400.2267	7
5	540.2776	270.6425	523.2511	262.1292	522.2671	261.6372	P	688.4141	344.7107	671.3875	336.1974	6
6	639.3461	320.1767	622.3195	311.6634	621.3355	311.1714	V	591.3613	296.1843	574.3348	287.6710	5
7	710.3832	355.6952	693.3566	347.1819	692.3726	346.6899	A	492.2929	246.6501	475.2663	238.1368	4
8	857.4516	429.2294	840.4250	420.7162	839.4410	420.2241	F	421.2558	211.1315	404.2292	202.6183	3
9	956.5200	478.7636	939.4934	470.2504	938.5094	469.7584	V	274.1874	137.5973	257.1608	129.0840	2
10							R	175.1190	88.0631	158.0924	79.5498	1



RMS error 11 ppm



RMS error 11 ppm

Mass (Da)

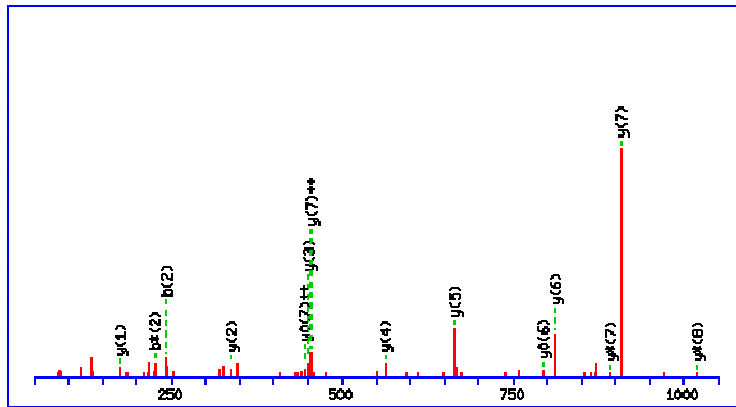
Peptide Number: 69916

MS/MS Fragmentation of **DQPFTILYR**Found in **IPI00294615** in **IPI_human**, Tax_Id=9606 Gene_Symbol=FBLN5 Fibulin-5

Match to Query 2464: 1151.600488 from(576.807520,2+) index(7078)

Title: Elution from: 18.45 to 18.45 period: 0 cycle: 708 experiment: 2 polarity: +

Data file 120208ry_Tig120slc-P8_1_3.mgf



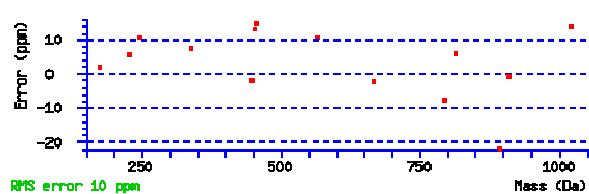
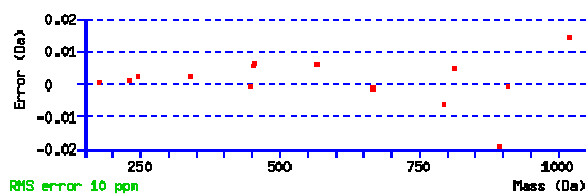
Monoisotopic mass of neutral peptide Mr(calc): 1151.5975

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 44 Expect: 0.0023

Matches : 14/86 fragment ions using 27 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							9
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	Q	1037.5778	519.2926	1020.5513	510.7793	1019.5673	510.2873	8
3	341.1456	171.0764	324.1190	162.5631	323.1350	162.0711	P	909.5193	455.2633	892.4927	446.7500	891.5087	446.2580	7
4	488.2140	244.6106	471.1874	236.0974	470.2034	235.6053	F	812.4665	406.7369	795.4400	398.2236	794.4559	397.7316	6
5	589.2617	295.1345	572.2351	286.6212	571.2511	286.1292	T	665.3981	333.2027	648.3715	324.6894	647.3875	324.1974	5
6	702.3457	351.6765	685.3192	343.1632	684.3352	342.6712	I	564.3504	282.6788	547.3239	274.1656			4
7	815.4298	408.2185	798.4032	399.7053	797.4192	399.2132	L	451.2663	226.1368	434.2398	217.6235			3
8	978.4931	489.7502	961.4666	481.2369	960.4825	480.7449	Y	338.1823	169.5948	321.1557	161.0815			2
9							R	175.1190	88.0631	158.0924	79.5498			1



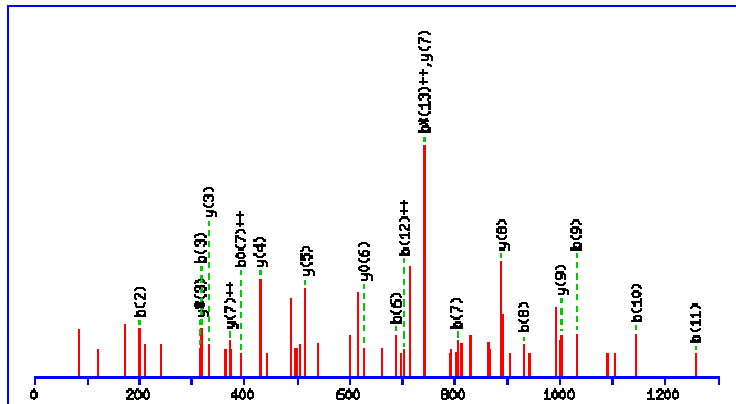
Peptide Number: 70271

MS/MS Fragmentation of **SLDPLYNQVLLFPESPQ GK**Found in **IPI00301500** in **IPI_human**, Tax_Id=9606 Gene_Symbol=RIMS4 Regulating synaptic membrane exocytosis protein 4

Match to Query 29280: 2144.121492 from(715.714440,3+) index(41358)

Title: Elution from: 103.483333333333 to 103.483333333333 period: 0 cycle: 3905 experiment: 3 polarity:+

Data file 120214ry_414C2-43_4_3.mgf



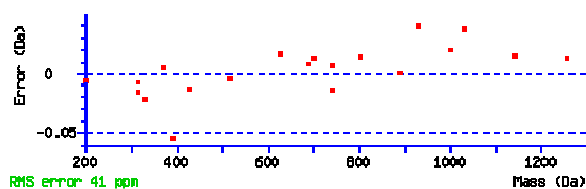
Monoisotopic mass of neutral peptide Mr(calcd): 2144.1154

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

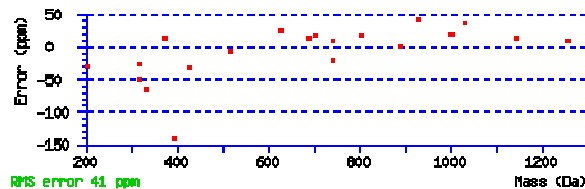
Ions Score: 39 Expect: 0.0082

Matches : 20/196 fragment ions using 41 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							19
2	201.1234	101.0653			183.1128	92.0600	L	2058.0906	1029.5489	2041.0641	1021.0357	2040.0801	1020.5437	18
3	316.1503	158.5788			298.1397	149.5735	D	1945.0066	973.0069	1927.9800	964.4936	1926.9960	964.0016	17
4	413.2031	207.1052			395.1925	198.0999	P	1829.9796	915.4934	1812.9531	906.9802	1811.9690	906.4882	16
5	526.2871	263.6472			508.2766	254.6419	L	1732.9268	866.9671	1715.9003	858.4538	1714.9163	857.9618	15
6	689.3505	345.1789			671.3399	336.1736	Y	1619.8428	810.4250	1602.8162	801.9118	1601.8322	801.4197	14
7	803.3934	402.2003	786.3668	393.6871	785.3828	393.1951	N	1456.7795	728.8934	1439.7529	720.3801	1438.7689	719.8881	13
8	931.4520	466.2296	914.4254	457.7164	913.4414	457.2243	Q	1342.7365	671.8719	1325.7100	663.3586	1324.7260	662.8666	12
9	1030.5204	515.7638	1013.4938	507.2506	1012.5098	506.7585	V	1214.6780	607.8426	1197.6514	599.3293	1196.6674	598.8373	11
10	1143.6045	572.3059	1126.5779	563.7926	1125.5939	563.3006	L	1115.6095	558.3084	1098.5830	549.7951	1097.5990	549.3031	10
11	1256.6885	628.8479	1239.6620	620.3346	1238.6779	619.8426	L	1002.5255	501.7664	985.4989	493.2531	984.5149	492.7611	9
12	1403.7569	702.3821	1386.7304	693.8688	1385.7464	693.3768	F	889.4414	445.2243	872.4149	436.7111	871.4308	436.2191	8
13	1500.8097	750.9085	1483.7831	742.3952	1482.7991	741.9032	P	742.3730	371.6901	725.3464	363.1769	724.3624	362.6849	7
14	1629.8523	815.4298	1612.8257	806.9165	1611.8417	806.4245	E	645.3202	323.1638	628.2937	314.6505	627.3097	314.1585	6
15	1716.8843	858.9458	1699.8578	850.4325	1698.8737	849.9405	S	516.2776	258.6425	499.2511	250.1292	498.2671	249.6372	5
16	1813.9371	907.4722	1796.9105	898.9589	1795.9265	898.4669	P	429.2456	215.1264	412.2191	206.6132			4
17	1941.9957	971.5015	1924.9691	962.9882	1923.9851	962.4962	Q	332.1928	166.6001	315.1663	158.0868			3
18	1999.0171	1000.0122	1981.9906	991.4989	1981.0066	991.0069	G	204.1343	102.5708	187.1077	94.0575			2
19							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 41 ppm



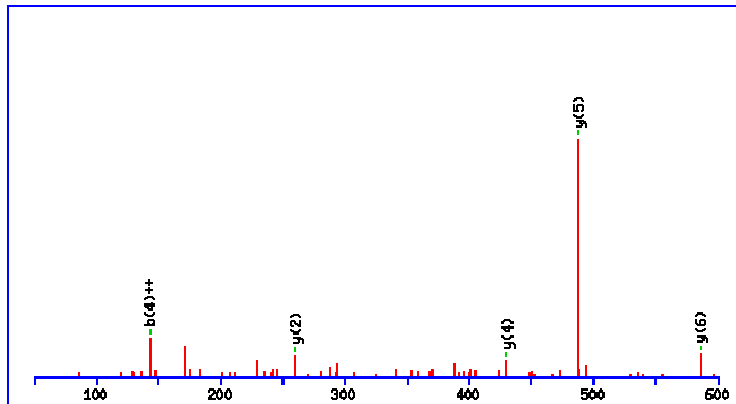
RMS error 41 ppm

Peptide Number: 70359MS/MS Fragmentation of **AVGGIIK**Found in **IPI00926670** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SATB2 Uncharacterized protein

Match to Query 986: 656.423308 from(329.218930,2+) index(11110)

Title: Elution from: 68.133333333333 to 68.133333333333 period: 0 cycle: 6659 experiment: 2 polarity: +

Data file 120212ry_aHDF1388-P9_3_1.mgf



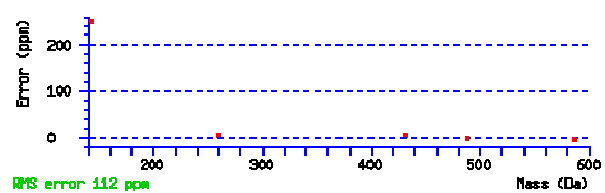
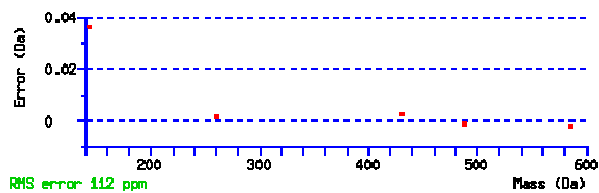
Monoisotopic mass of neutral peptide Mr(calc): 656.4221

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 37 Expect: 0.01

Matches : 5/36 fragment ions using 6 most intense peaks ([help](#))

#	b	b ⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	#
1	72.0444	36.5258	A					7
2	171.1128	86.0600	V	586.3923	293.6998	569.3657	285.1865	6
3	228.1343	114.5708	G	487.3239	244.1656	470.2973	235.6523	5
4	285.1557	143.0815	G	430.3024	215.6548	413.2758	207.1416	4
5	398.2398	199.6235	I	373.2809	187.1441	356.2544	178.6308	3
6	511.3239	256.1656	I	260.1969	130.6021	243.1703	122.0888	2
7			K	147.1128	74.0600	130.0863	65.5468	1



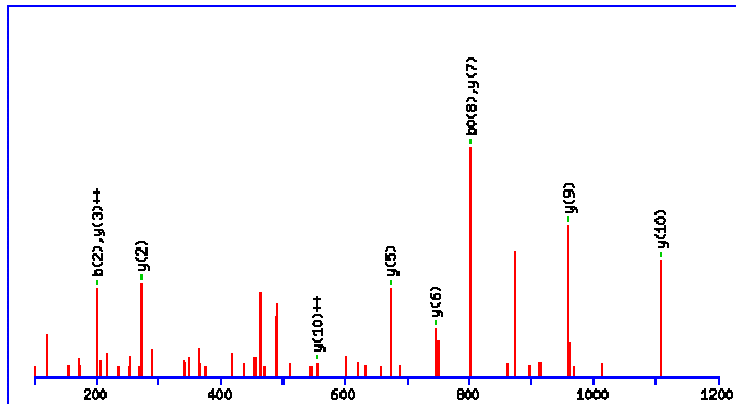
Peptide Number: 70376

MS/MS Fragmentation of **AEFSAGAWSEPR**Found in **IPI00167074** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ARL6IP6 ADP-ribosylation factor-like protein 6-interacting protein 6

Match to Query 18870: 1306.589748 from(654.302150,2+) index(26524)

Title: Elution from: 67.1166666666667 to 67.1166666666667 period: 0 cycle: 2559 experiment: 8 polarity: +

Data file 120210ry_585A1-55_3_2.mgf



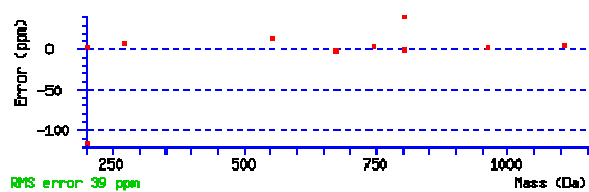
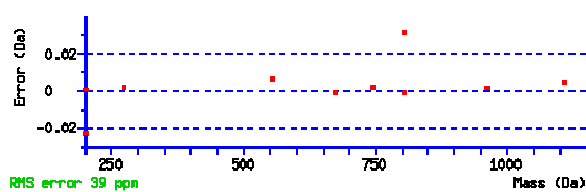
Monoisotopic mass of neutral peptide Mr(calc): 1306.5942

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 47 Expect: 0.00068

Matches : 10/104 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258			A							12
2	201.0870	101.0471	183.0764	92.0418	E	1236.5644	618.7858	1219.5378	610.2726	1218.5538	609.7805	11
3	348.1554	174.5813	330.1448	165.5761	F	1107.5218	554.2645	1090.4952	545.7513	1089.5112	545.2592	10
4	435.1874	218.0974	417.1769	209.0921	S	960.4534	480.7303	943.4268	472.2170	942.4428	471.7250	9
5	506.2245	253.6159	488.2140	244.6106	A	873.4213	437.2143	856.3948	428.7010	855.4108	428.2090	8
6	563.2460	282.1266	545.2354	273.1214	G	802.3842	401.6958	785.3577	393.1825	784.3737	392.6905	7
7	634.2831	317.6452	616.2726	308.6399	A	745.3628	373.1850	728.3362	364.6717	727.3522	364.1797	6
8	820.3624	410.6849	802.3519	401.6796	W	674.3257	337.6665	657.2991	329.1532	656.3151	328.6612	5
9	907.3945	454.2009	889.3839	445.1956	S	488.2463	244.6268	471.2198	236.1135	470.2358	235.6215	4
10	1036.4371	518.7222	1018.4265	509.7169	E	401.2143	201.1108	384.1878	192.5975	383.2037	192.1055	3
11	1133.4898	567.2485	1115.4793	558.2433	P	272.1717	136.5895	255.1452	128.0762			2
12					R	175.1190	88.0631	158.0924	79.5498			1



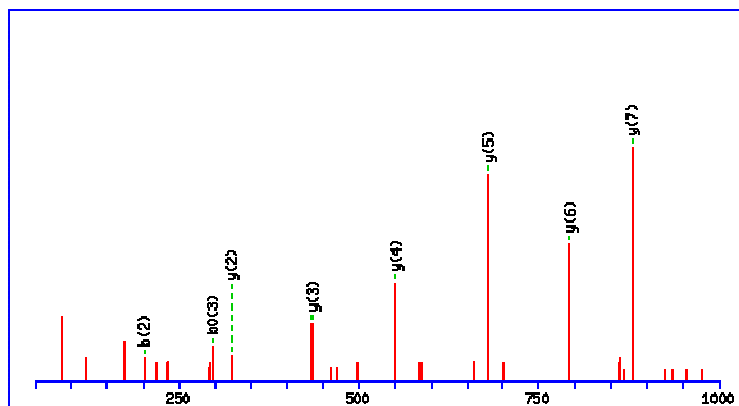
Peptide Number: 70740

MS/MS Fragmentation of **LSLEDLFR**Found in **IPI00166892** in **IPI_human**, Tax_Id=9606 Gene_Symbol=DPP10 inactive dipeptidyl peptidase 10 isoform c

Match to Query 436: 991.527308 from(496.770930,2+) index(1653)

Title: Elution from: 4.03333333333333 to 4.03333333333333 period: 0 cycle: 150 experiment: 1 polarity: +

Data file 120126ry_585A1-55_2_4.mgf



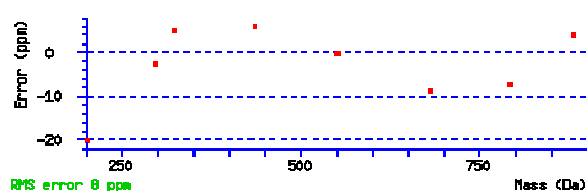
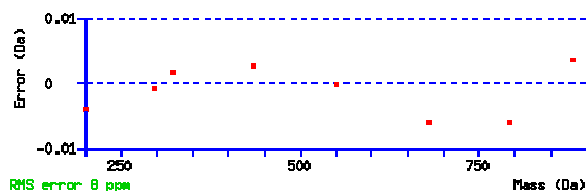
Monoisotopic mass of neutral peptide Mr(calc): 991.5338

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 40 Expect: 0.0074

Matches : 8/62 fragment ions using 17 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							8
2	201.1234	101.0653	183.1128	92.0600	S	879.4571	440.2322	862.4305	431.7189	861.4465	431.2269	7
3	314.2074	157.6074	296.1969	148.6021	L	792.4250	396.7162	775.3985	388.2029	774.4145	387.7109	6
4	443.2500	222.1287	425.2395	213.1234	E	679.3410	340.1741	662.3144	331.6608	661.3304	331.1688	5
5	558.2770	279.6421	540.2664	270.6368	D	550.2984	275.6528	533.2718	267.1396	532.2878	266.6475	4
6	671.3610	336.1842	653.3505	327.1789	L	435.2714	218.1394	418.2449	209.6261			3
7	818.4294	409.7184	800.4189	400.7131	F	322.1874	161.5973	305.1608	153.0840			2
8					R	175.1190	88.0631	158.0924	79.5498			1

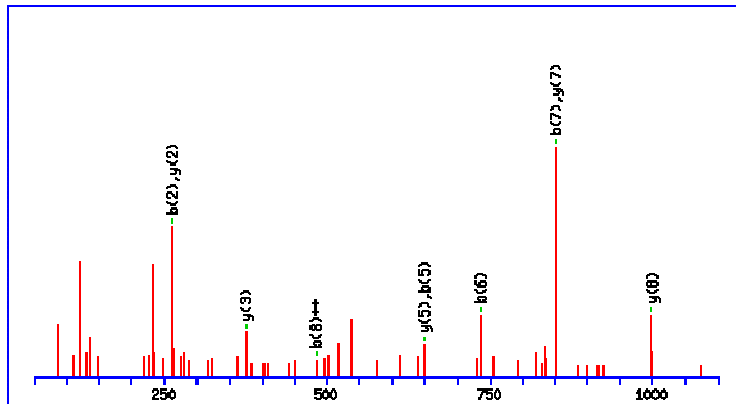


Peptide Number: 70903MS/MS Fragmentation of **LMMAWSDNK**Found in **IPI00151977** in **IPI_human**, Tax_Id=9606 Gene_Symbol=NLRP4 Isoform 1 of NACHT, LRR and PYD domains-containing protein 4

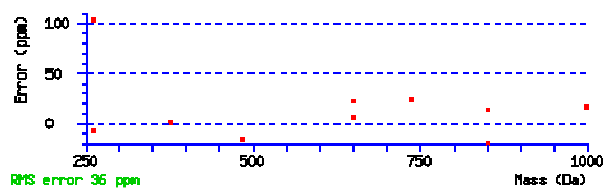
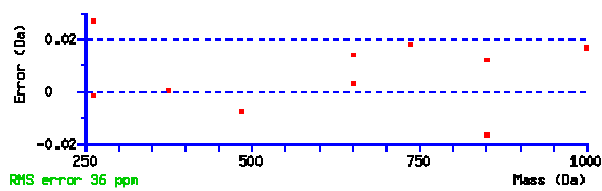
Match to Query 11529: 1110.500988 from(556.257770,2+) index(14128)

Title: Elution from: 33.9333333333333 to 33.9333333333333 period: 0 cycle: 1290 experiment: 8 polarity:+

Data file 120201ry_aHDF1388-P9_1_2.mgf

**Monoisotopic mass of neutral peptide Mr(calc):** 1110.4838**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Variable modifications:****M2** : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983**Ions Score:** 36 **Expect:** 0.0071**Matches** : 10/96 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							9
2	261.1267	131.0670					M	998.4070	499.7071	981.3805	491.1939	980.3964	490.7019	8
3	392.1672	196.5873					M	851.3716	426.1894	834.3451	417.6762	833.3610	417.1842	7
4	463.2043	232.1058					A	720.3311	360.6692	703.3046	352.1559	702.3206	351.6639	6
5	649.2837	325.1455					W	649.2940	325.1506	632.2675	316.6374	631.2835	316.1454	5
6	736.3157	368.6615			718.3051	359.6562	S	463.2147	232.1110	446.1882	223.5977	445.2041	223.1057	4
7	851.3426	426.1749			833.3321	417.1697	D	376.1827	188.5950	359.1561	180.0817	358.1721	179.5897	3
8	965.3855	483.1964	948.3590	474.6831	947.3750	474.1911	N	261.1557	131.0815	244.1292	122.5682			2
9							K	147.1128	74.0600	130.0863	65.5468			1



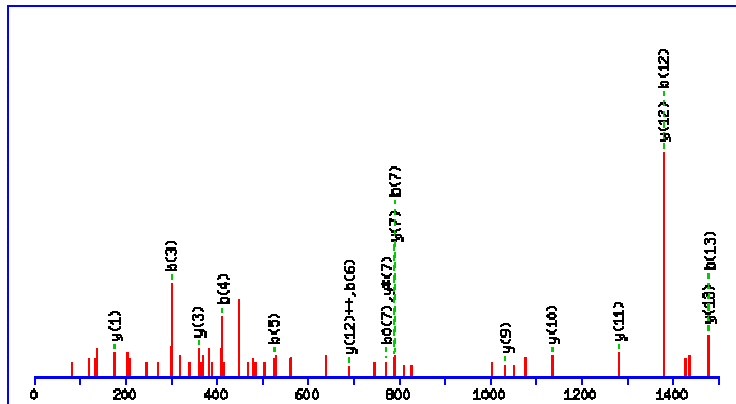
Peptide Number: 71049

MS/MS Fragmentation of **DGQLIYTPFTEDTETVGQR**Found in **IPI00289615** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PSEN1 Isoform 3 of Presenilin-1

Match to Query 30682: 2169.029588 from(1085.522070,2+) index(19236)

Title: Elution from: 45.9166666666667 to 45.9166666666667 period: 0 cycle: 1740 experiment: 9 polarity: +

Data file 120212ry_aHDF1388-P9_2_3.mgf



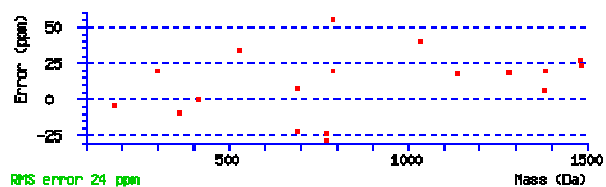
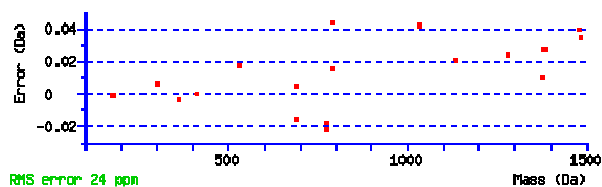
Monoisotopic mass of neutral peptide Mr(calc): 2169.0226

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 53 Expect: 0.00025

Matches : 18/204 fragment ions using 32 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							19
2	173.0557	87.0315			155.0451	78.0262	G	2055.0029	1028.0051	2037.9764	1019.4918	2036.9924	1018.9998	18
3	301.1143	151.0608	284.0877	142.5475	283.1037	142.0555	Q	1997.9815	999.4944	1980.9549	990.9811	1979.9709	990.4891	17
4	414.1983	207.6028	397.1718	199.0895	396.1878	198.5975	L	1869.9229	935.4651	1852.8963	926.9518	1851.9123	926.4598	16
5	527.2824	264.1448	510.2558	255.6316	509.2718	255.1396	I	1756.8388	878.9231	1739.8123	870.4098	1738.8283	869.9178	15
6	690.3457	345.6765	673.3192	337.1632	672.3352	336.6712	Y	1643.7548	822.3810	1626.7282	813.8677	1625.7442	813.3757	14
7	791.3934	396.2003	774.3668	387.6871	773.3828	387.1951	T	1480.6914	740.8494	1463.6649	732.3361	1462.6809	731.8441	13
8	888.4462	444.7267	871.4196	436.2134	870.4356	435.7214	P	1379.6438	690.3255	1362.6172	681.8122	1361.6332	681.3202	12
9	1035.5146	518.2609	1018.4880	509.7477	1017.5040	509.2556	F	1282.5910	641.7991	1265.5644	633.2859	1264.5804	632.7938	11
10	1136.5623	568.7848	1119.5357	560.2715	1118.5517	559.7795	T	1135.5226	568.2649	1118.4960	559.7517	1117.5120	559.2596	10
11	1265.6048	633.3061	1248.5783	624.7928	1247.5943	624.3008	E	1034.4749	517.7411	1017.4483	509.2278	1016.4643	508.7358	9
12	1380.6318	690.8195	1363.6052	682.3063	1362.6212	681.8143	D	905.4323	453.2198	888.4058	444.7065	887.4217	444.2145	8
13	1481.6795	741.3434	1464.6529	732.8301	1463.6689	732.3381	T	790.4054	395.7063	773.3788	387.1930	772.3948	386.7010	7
14	1610.7221	805.8647	1593.6955	797.3514	1592.7115	796.8594	E	689.3577	345.1825	672.3311	336.6692	671.3471	336.1772	6
15	1711.7697	856.3885	1694.7432	847.8752	1693.7592	847.3832	T	560.3151	280.6612	543.2885	272.1479	542.3045	271.6559	5
16	1810.8382	905.9227	1793.8116	897.4094	1792.8276	896.9174	V	459.2674	230.1373	442.2409	221.6241			4
17	1867.8596	934.4334	1850.8331	925.9202	1849.8491	925.4282	G	360.1990	180.6031	343.1724	172.0899			3
18	1995.9182	998.4627	1978.8916	989.9495	1977.9076	989.4575	Q	303.1775	152.0924	286.1510	143.5791			2
19							R	175.1190	88.0631	158.0924	79.5498			1



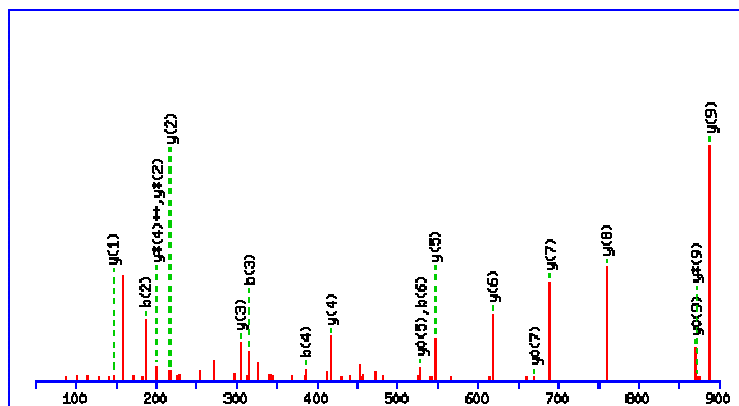
Peptide Number: 71160

MS/MS Fragmentation of **SVEAAAELSAK**Found in **IPI00550020** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PTMS Parathymosin

Match to Query 13043: 1074.555948 from(538.285250,2+) index(30255)

Title: Elution from: 108.883333333333 to 108.883333333333 period: 0 cycle: 7933 experiment: 2 polarity: +

Data file 120208ry_Tig120slc-P8_1_1.mgf



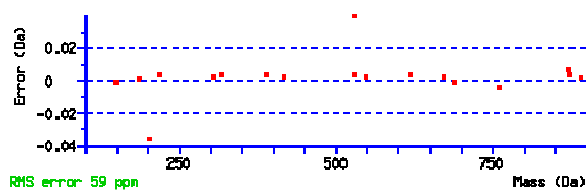
Monoisotopic mass of neutral peptide Mr(calcd): 1074.5557

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

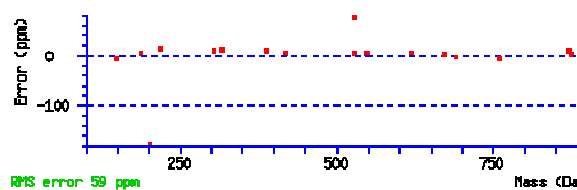
Ions Score: 59 Expect: 0.0001

Matches : 19/96 fragment ions using 37 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233	70.0287	35.5180	S							11
2	187.1077	94.0575	169.0972	85.0522	V	988.5310	494.7691	971.5044	486.2558	970.5204	485.7638	10
3	316.1503	158.5788	298.1397	149.5735	E	889.4625	445.2349	872.4360	436.7216	871.4520	436.2296	9
4	387.1874	194.0974	369.1769	185.0921	A	760.4199	380.7136	743.3934	372.2003	742.4094	371.7083	8
5	458.2245	229.6159	440.2140	220.6106	A	689.3828	345.1951	672.3563	336.6818	671.3723	336.1898	7
6	529.2617	265.1345	511.2511	256.1292	A	618.3457	309.6765	601.3192	301.1632	600.3352	300.6712	6
7	658.3042	329.6558	640.2937	320.6505	E	547.3086	274.1579	530.2821	265.6447	529.2980	265.1527	5
8	771.3883	386.1978	753.3777	377.1925	L	418.2660	209.6366	401.2395	201.1234	400.2554	200.6314	4
9	858.4203	429.7138	840.4098	420.7085	S	305.1819	153.0946	288.1554	144.5813	287.1714	144.0893	3
10	929.4575	465.2324	911.4469	456.2271	A	218.1499	109.5786	201.1234	101.0653			2
11					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 59 ppm



RMS error 59 ppm

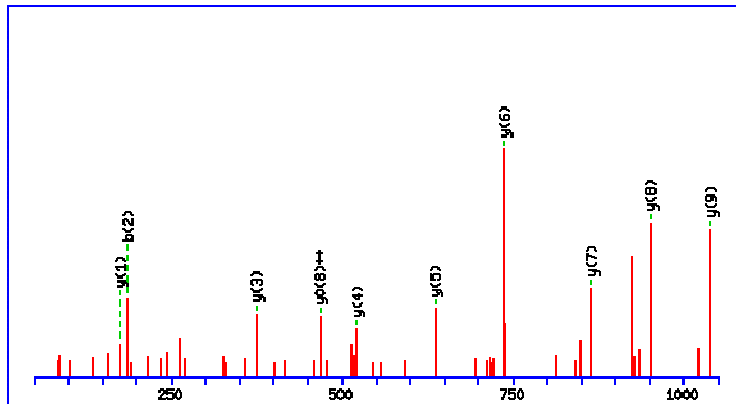
Peptide Number: 71364

MS/MS Fragmentation of **VSSQTNFLSR**Found in **IPI00169331** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SGMS2 Phosphatidylcholine:ceramide cholinephosphotransferase 2

Match to Query 10581: 1137.575188 from(569.794870,2+) index(2082)

Title: Elution from: 5.35 to 5.35 period: 0 cycle: 205 experiment: 6 polarity: +

Data file 120208ry_Tig120slc-P8_3_2.mgf



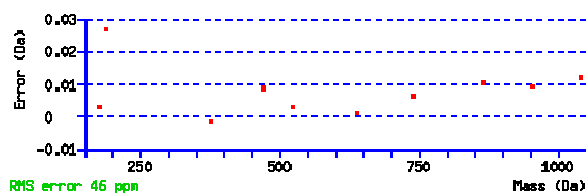
Monoisotopic mass of neutral peptide Mr(calc): 1137.5778

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

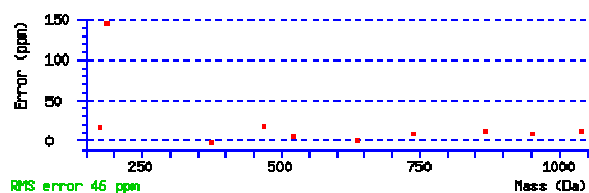
Ions Score: 90 Expect: 6.7e-008

Matches : 10/98 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							10
2	187.1077	94.0575			169.0972	85.0522	S	1039.5167	520.2620	1022.4901	511.7487	1021.5061	511.2567	9
3	274.1397	137.5735			256.1292	128.5682	S	952.4847	476.7460	935.4581	468.2327	934.4741	467.7407	8
4	402.1983	201.6028	385.1718	193.0895	384.1878	192.5975	Q	865.4526	433.2300	848.4261	424.7167	847.4421	424.2247	7
5	503.2460	252.1266	486.2195	243.6134	485.2354	243.1214	T	737.3941	369.2007	720.3675	360.6874	719.3835	360.1954	6
6	617.2889	309.1481	600.2624	300.6348	599.2784	300.1428	N	636.3464	318.6768	619.3198	310.1636	618.3358	309.6715	5
7	764.3573	382.6823	747.3308	374.1690	746.3468	373.6770	F	522.3035	261.6554	505.2769	253.1421	504.2929	252.6501	4
8	877.4414	439.2243	860.4149	430.7111	859.4308	430.2191	L	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
9	964.4734	482.7404	947.4469	474.2271	946.4629	473.7351	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
10							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 46 ppm



RMS error 46 ppm

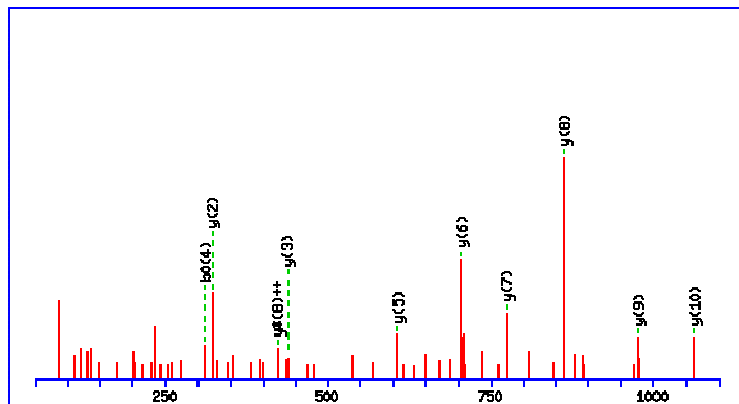
Peptide Number: 72049

MS/MS Fragmentation of **GALSISAPLGDFR**Found in **IPI00290570** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CDC42EP5 Cdc42 effector protein 5

Match to Query 5689: 1302.694728 from(652.354640,2+) index(14436)

Title: Elution from: 34.65 to 34.65 period: 0 cycle: 1312 experiment: 4 polarity: +

Data file 120208ry_Tig120slc-P8_2_3.mgf



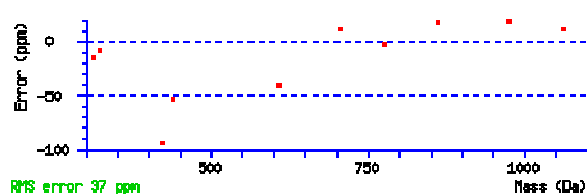
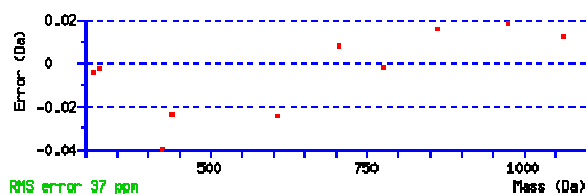
Monoisotopic mass of neutral peptide Mr(calc): 1302.6932

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 49 Expect: 0.001

Matches : 10/110 fragment ions using 20 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180			G							13
2	129.0659	65.0366			A	1246.6790	623.8431	1229.6525	615.3299	1228.6684	614.8379	12
3	242.1499	121.5786			L	1175.6419	588.3246	1158.6154	579.8113	1157.6313	579.3193	11
4	329.1819	165.0946	311.1714	156.0893	S	1062.5578	531.7826	1045.5313	523.2693	1044.5473	522.7773	10
5	442.2660	221.6366	424.2554	212.6314	I	975.5258	488.2665	958.4993	479.7533	957.5152	479.2613	9
6	529.2980	265.1527	511.2875	256.1474	S	862.4417	431.7245	845.4152	423.2112	844.4312	422.7192	8
7	600.3352	300.6712	582.3246	291.6659	A	775.4097	388.2085	758.3832	379.6952	757.3992	379.2032	7
8	697.3879	349.1976	679.3774	340.1923	P	704.3726	352.6899	687.3461	344.1767	686.3620	343.6847	6
9	810.4720	405.7396	792.4614	396.7343	L	607.3198	304.1636	590.2933	295.6503	589.3093	295.1583	5
10	867.4934	434.2504	849.4829	425.2451	G	494.2358	247.6215	477.2092	239.1083	476.2252	238.6162	4
11	982.5204	491.7638	964.5098	482.7585	D	437.2143	219.1108	420.1878	210.5975	419.2037	210.1055	3
12	1129.5888	565.2980	1111.5782	556.2928	F	322.1874	161.5973	305.1608	153.0840			2
13					R	175.1190	88.0631	158.0924	79.5498			1



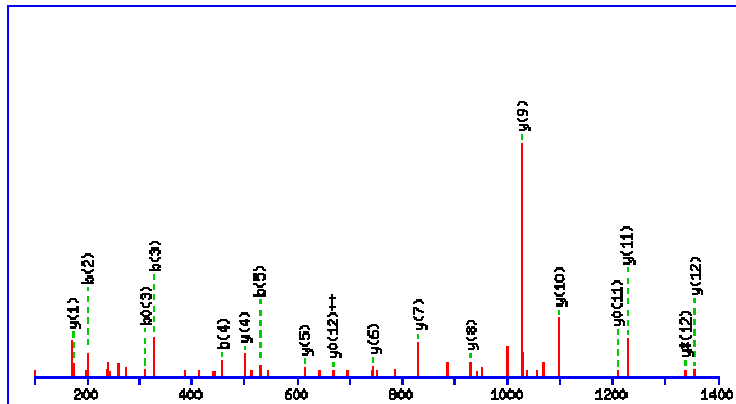
Peptide Number: 72138

MS/MS Fragmentation of **SIQEAPVSEDLVIR**Found in **IPI00936738** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TOR1AIP1 Isoform 1 of Torsin-1A-interacting protein 1

Match to Query 31292: 1554.816648 from(778.415600,2+) index(40091)

Title: Elution from: 98.3666666666667 to 98.3666666666667 period: 0 cycle: 3720 experiment: 7 polarity: +

Data file 120210ry_32R1-32_3_2.mgf



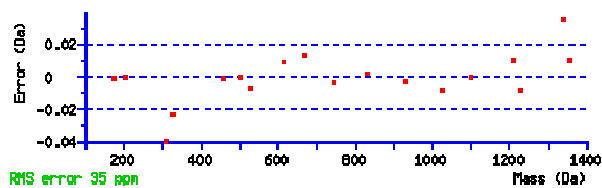
Monoisotopic mass of neutral peptide Mr(calc): 1554.8253

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

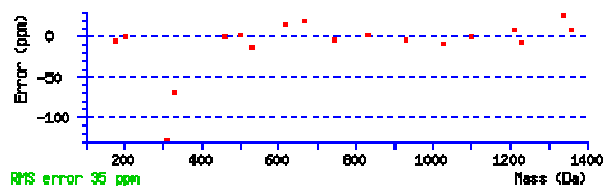
Ions Score: 86 Expect: 1.4e-007

Matches : 18/144 fragment ions using 24 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							14
2	201.1234	101.0653			183.1128	92.0600	I	1468.8006	734.9039	1451.7740	726.3907	1450.7900	725.8986	13
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	Q	1355.7165	678.3619	1338.6900	669.8486	1337.7060	669.3566	12
4	458.2245	229.6159	441.1980	221.1026	440.2140	220.6106	E	1227.6579	614.3326	1210.6314	605.8193	1209.6474	605.3273	11
5	529.2617	265.1345	512.2351	256.6212	511.2511	256.1292	A	1098.6153	549.8113	1081.5888	541.2980	1080.6048	540.8060	10
6	626.3144	313.6608	609.2879	305.1476	608.3039	304.6556	P	1027.5782	514.2928	1010.5517	505.7795	1009.5677	505.2875	9
7	725.3828	363.1951	708.3563	354.6818	707.3723	354.1898	V	930.5255	465.7664	913.4989	457.2531	912.5149	456.7611	8
8	812.4149	406.7111	795.3883	398.1978	794.4043	397.7058	S	831.4571	416.2322	814.4305	407.7189	813.4465	407.2269	7
9	941.4575	471.2324	924.4309	462.7191	923.4469	462.2271	E	744.4250	372.7162	727.3985	364.2029	726.4145	363.7109	6
10	1056.4844	528.7458	1039.4578	520.2326	1038.4738	519.7406	D	615.3824	308.1949	598.3559	299.6816	597.3719	299.1896	5
11	1169.5685	585.2879	1152.5419	576.7746	1151.5579	576.2826	L	500.3555	250.6814	483.3289	242.1681			4
12	1268.6369	634.8221	1251.6103	626.3088	1250.6263	625.8168	V	387.2714	194.1394	370.2449	185.6261			3
13	1381.7209	691.3641	1364.6944	682.8508	1363.7104	682.3588	I	288.2030	144.6051	271.1765	136.0919			2
14							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 35 ppm



RMS error 35 ppm

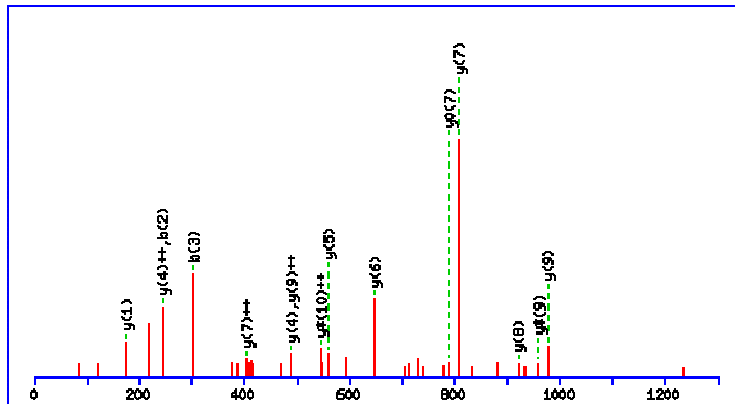
Peptide Number: 72402

MS/MS Fragmentation of **DEGLCSANVTR**Found in **IPI00009198** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TFPI2 Tissue factor pathway inhibitor 2

Match to Query 18224: 1220.552468 from(611.283510,2+) index(24652)

Title: Elution from: 103.283333333333 to 103.283333333333 period: 0 cycle: 8073 experiment: 10 polarity: +

Data file 120201ry_aHDF1388-P9_1_1.mgf



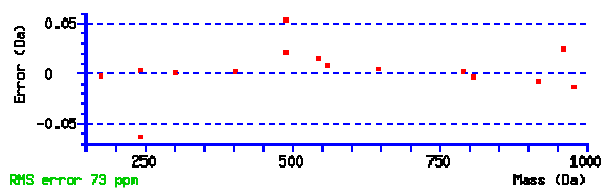
Monoisotopic mass of neutral peptide Mr(calc): 1220.5455

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

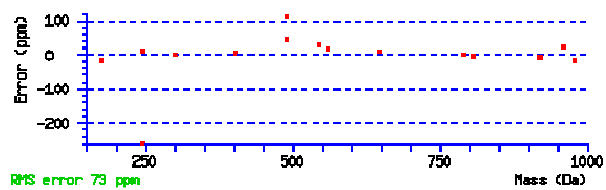
Ions Score: 49 Expect: 0.00045

Matches : 15/104 fragment ions using 24 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							11
2	245.0768	123.0420			227.0662	114.0368	E	1106.5259	553.7666	1089.4993	545.2533	1088.5153	544.7613	10
3	302.0983	151.5528			284.0877	142.5475	G	977.4833	489.2453	960.4567	480.7320	959.4727	480.2400	9
4	415.1823	208.0948			397.1718	199.0895	L	920.4618	460.7346	903.4353	452.2213	902.4513	451.7293	8
5	575.2130	288.1101			557.2024	279.1049	C	807.3778	404.1925	790.3512	395.6792	789.3672	395.1872	7
6	662.2450	331.6261			644.2345	322.6209	S	647.3471	324.1772	630.3206	315.6639	629.3365	315.1719	6
7	733.2821	367.1447			715.2716	358.1394	A	560.3151	280.6612	543.2885	272.1479	542.3045	271.6559	5
8	847.3251	424.1662	830.2985	415.6529	829.3145	415.1609	N	489.2780	245.1426	472.2514	236.6293	471.2674	236.1373	4
9	946.3935	473.7004	929.3669	465.1871	928.3829	464.6951	V	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
10	1047.4412	524.2242	1030.4146	515.7109	1029.4306	515.2189	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
11							R	175.1190	88.0631	158.0924	79.5498			1



RMS error: 73 ppm



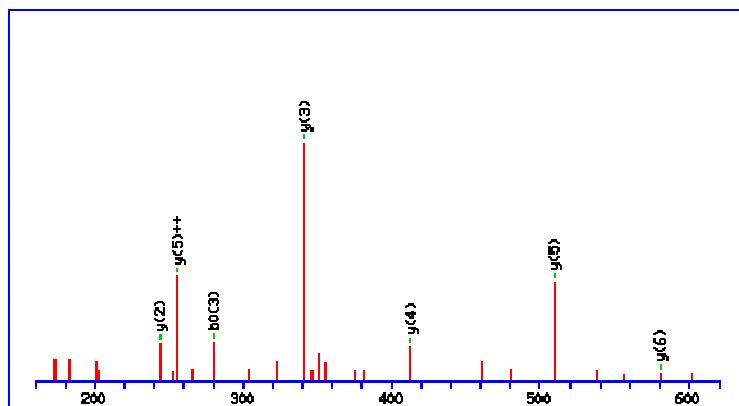
RMS error: 73 ppm

Peptide Number: 72939MS/MS Fragmentation of **EAPAPPK**Found in **IPI00021266** in **IPI_human**, Tax_Id=9606 Gene_Symbol=RPL23A;SNORD4A 60S ribosomal protein L23a

Match to Query 1827: 708.383948 from(355.199250,2+) index(2884)

Title: Elution from: 47.2 to 47.2 period: 0 cycle: 6938 experiment: 3 polarity:+

Data file 120214ry_414C2-43_4_1.mgf



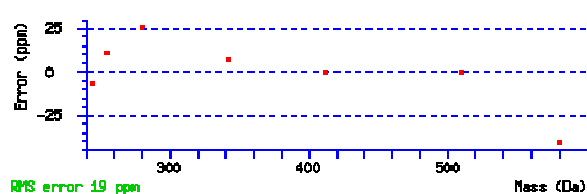
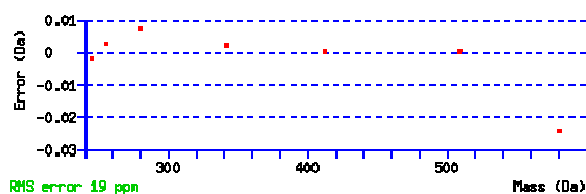
Monoisotopic mass of neutral peptide Mr(calc): 708.3806

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 42 Expect: 0.0017

Matches : 7/48 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	#
1	130.0499	65.5286	112.0393	56.5233	E					7
2	201.0870	101.0471	183.0764	92.0418	A	580.3453	290.6763	563.3188	282.1630	6
3	298.1397	149.5735	280.1292	140.5682	P	509.3082	255.1577	492.2817	246.6445	5
4	369.1769	185.0921	351.1663	176.0868	A	412.2554	206.6314	395.2289	198.1181	4
5	466.2296	233.6185	448.2191	224.6132	P	341.2183	171.1128	324.1918	162.5995	3
6	563.2824	282.1448	545.2718	273.1396	P	244.1656	122.5864	227.1390	114.0731	2
7					K	147.1128	74.0600	130.0863	65.5468	1

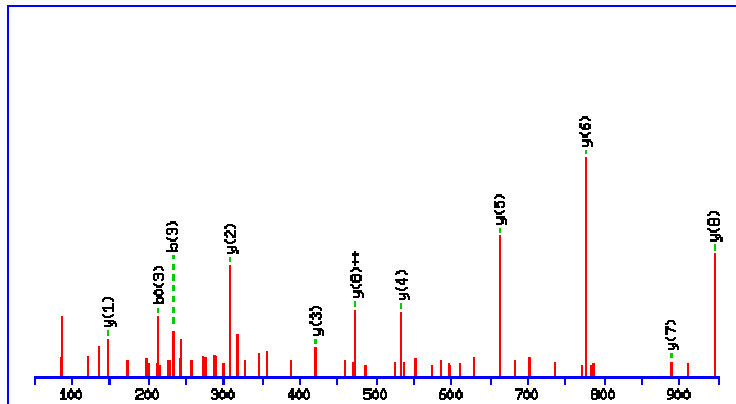


Peptide Number: 73028MS/MS Fragmentation of **SSGLLELICK**Found in **IPI00166835** in **IPI_human**, Tax_Id=9606 Gene_Symbol=FAM26E Protein FAM26E

Match to Query 2093: 1118.598648 from(560,306600,2+) index(15236)

Title: Elution from: 42.1333333333333 to 42.1333333333333 period: 0 cycle: 1628 experiment: 4 polarity:+

Data file 120208ry_Tig120slc-P8_1_3.mgf



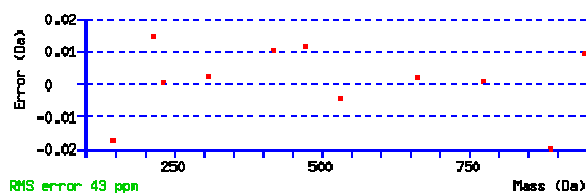
Monoisotopic mass of neutral peptide Mr(calc): 1118.6005

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

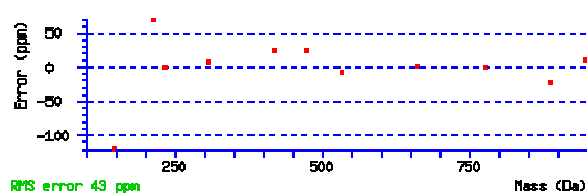
Ions Score: 70 Expect: 8.4e-006

Matches : 11/82 fragment ions using 17 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233	70.0287	35.5180	S							10
2	175.0713	88.0393	157.0608	79.0340	S	1032.5758	516.7915	1015.5492	508.2783	1014.5652	507.7863	9
3	232.0928	116.5500	214.0822	107.5448	G	945.5438	473.2755	928.5172	464.7622	927.5332	464.2702	8
4	345.1769	173.0921	327.1663	164.0868	L	888.5223	444.7648	871.4958	436.2515	870.5117	435.7595	7
5	458.2609	229.6341	440.2504	220.6288	L	775.4382	388.2228	758.4117	379.7095	757.4277	379.2175	6
6	587.3035	294.1554	569.2930	285.1501	E	662.3542	331.6807	645.3276	323.1675	644.3436	322.6754	5
7	700.3876	350.6974	682.3770	341.6921	L	533.3116	267.1594	516.2850	258.6462			4
8	813.4716	407.2395	795.4611	398.2342	I	420.2275	210.6174	403.2010	202.1041			3
9	973.5023	487.2548	955.4917	478.2495	C	307.1435	154.0754	290.1169	145.5621			2
10					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 43 ppm



RMS error 43 ppm

Mass (Da)

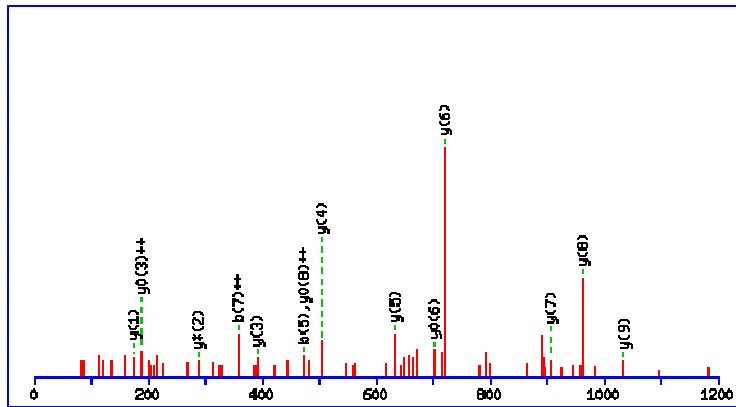
Peptide Number: 73102

MS/MS Fragmentation of **AAGWSELSE**RFound in **IPI00874020** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PCBD2 Pterin-4-alpha-carbinolamine dehydratase 2

Match to Query 17674: 1104.525848 from(553.270200,2+) index(23108)

Title: Elution from: 54.4 to 54.4 period: 0 cycle: 2038 experiment: 8 polarity: +

Data file 120126ry_585A1-55_1_2.mgf



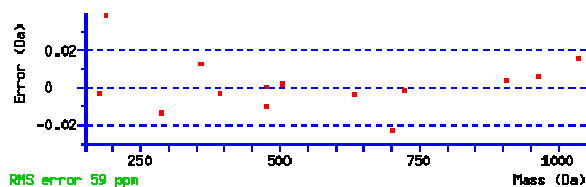
Monoisotopic mass of neutral peptide Mr(calc): 1104.5200

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

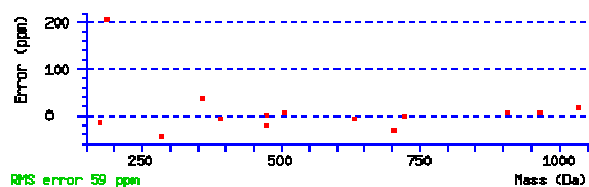
Ions Score: 40 Expect: 0.0056

Matches : 14/80 fragment ions using 38 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258			A							10
2	143.0815	72.0444			A	1034.4901	517.7487	1017.4636	509.2354	1016.4796	508.7434	9
3	200.1030	100.5551			G	963.4530	482.2302	946.4265	473.7169	945.4425	473.2249	8
4	386.1823	193.5948			W	906.4316	453.7194	889.4050	445.2061	888.4210	444.7141	7
5	473.2143	237.1108	455.2037	228.1055	S	720.3523	360.6798	703.3257	352.1665	702.3417	351.6745	6
6	602.2569	301.6321	584.2463	292.6268	E	633.3202	317.1638	616.2937	308.6505	615.3097	308.1585	5
7	715.3410	358.1741	697.3304	349.1688	L	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	4
8	802.3730	401.6901	784.3624	392.6849	S	391.1936	196.1004	374.1670	187.5872	373.1830	187.0951	3
9	931.4156	466.2114	913.4050	457.2061	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
10					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 59 ppm



RMS error 59 ppm

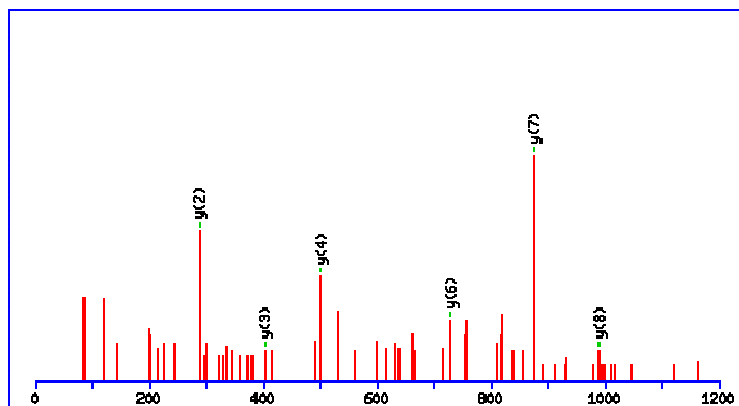
Peptide Number: 73321

MS/MS Fragmentation of **LLFNPDRLR**Found in **IPI00219990** in **IPI_human**, Tax_Id=9606 Gene_Symbol=DROSHA Isoform 2 of Ribonuclease 3

Match to Query 3994: 1101.585528 from(551.800040,2+) index(895)

Title: Elution from: 2.1 to 2.1 period: 0 cycle: 78 experiment: 6 polarity:+

Data file 120126ry_585A1-55_1_3.mgf



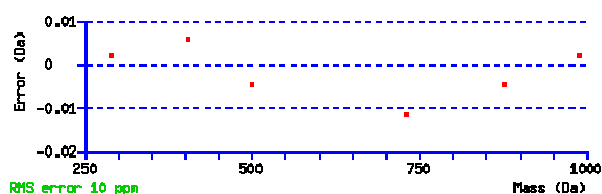
Monoisotopic mass of neutral peptide Mr(calc): 1101.5818

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

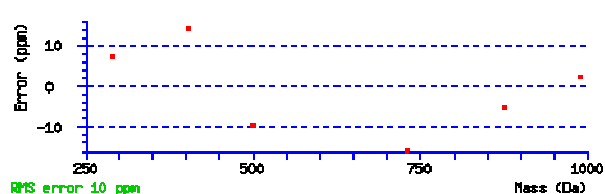
Ions Score: 44 Expect: 0.0041

Matches : 6/78 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							9
2	227.1754	114.0913					L	989.5051	495.2562	972.4785	486.7429	971.4945	486.2509	8
3	374.2438	187.6255					F	876.4210	438.7141	859.3945	430.2009	858.4104	429.7089	7
4	488.2867	244.6470	471.2602	236.1337			N	729.3526	365.1799	712.3260	356.6667	711.3420	356.1747	6
5	603.3137	302.1605	586.2871	293.6472	585.3031	293.1552	D	615.3097	308.1585	598.2831	299.6452	597.2991	299.1532	5
6	700.3665	350.6869	683.3399	342.1736	682.3559	341.6816	P	500.2827	250.6450	483.2562	242.1317	482.2722	241.6397	4
7	815.3934	408.2003	798.3668	399.6871	797.3828	399.1951	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
8	928.4775	464.7424	911.4509	456.2291	910.4669	455.7371	L	288.2030	144.6051	271.1765	136.0919			2
9							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 10 ppm



RMS error 10 ppm

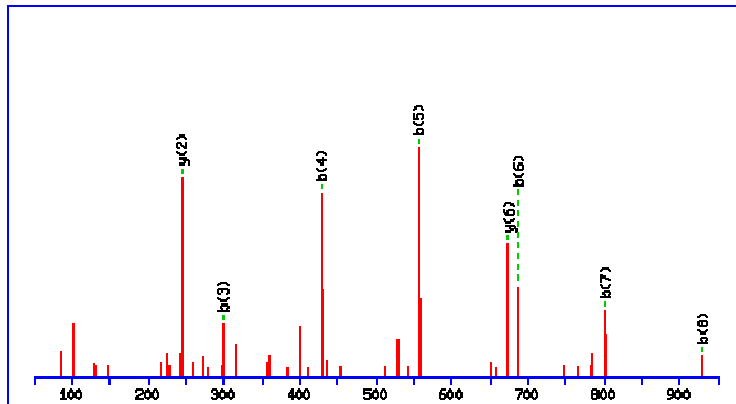
Peptide Number: 73389

MS/MS Fragmentation of **RAAEEDEADPK**Found in **IPI00550020** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PTMS Parathymosin

Match to Query 21494: 1358.594322 from(453.872050,3+) index(6009)

Title: Elution from: 45.7666666666667 to 45.7666666666667 period: 0 cycle: 5509 experiment: 1 polarity: +

Data file 120208ry_Tig120slc-P8_1_1.mgf



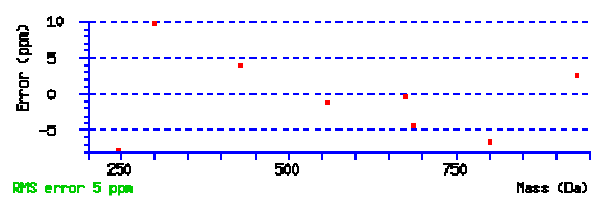
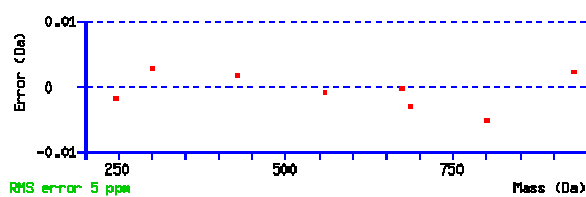
Monoisotopic mass of neutral peptide Mr(calc): 1358.5950

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 55 Expect: 6.6e-005

Matches : 8/122 fragment ions using 9 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	157.1084	79.0578	140.0818	70.5446			R							12
2	228.1455	114.5764	211.1190	106.0631			A	1203.5012	602.2542	1186.4746	593.7409	1185.4906	593.2489	11
3	299.1826	150.0949	282.1561	141.5817			A	1132.4641	566.7357	1115.4375	558.2224	1114.4535	557.7304	10
4	428.2252	214.6162	411.1987	206.1030	410.2146	205.6110	E	1061.4269	531.2171	1044.4004	522.7038	1043.4164	522.2118	9
5	557.2678	279.1375	540.2413	270.6243	539.2572	270.1323	E	932.3843	466.6958	915.3578	458.1825	914.3738	457.6905	8
6	686.3104	343.6588	669.2838	335.1456	668.2998	334.6536	E	803.3418	402.1745	786.3152	393.6612	785.3312	393.1692	7
7	801.3373	401.1723	784.3108	392.6590	783.3268	392.1670	D	674.2992	337.6532	657.2726	329.1399	656.2886	328.6479	6
8	930.3799	465.6936	913.3534	457.1803	912.3694	456.6883	E	559.2722	280.1397	542.2457	271.6265	541.2617	271.1345	5
9	1001.4170	501.2122	984.3905	492.6989	983.4065	492.2069	A	430.2296	215.6185	413.2031	207.1052	412.2191	206.6132	4
10	1116.4440	558.7256	1099.4174	550.2124	1098.4334	549.7203	D	359.1925	180.0999	342.1660	171.5866	341.1819	171.0946	3
11	1213.4968	607.2520	1196.4702	598.7387	1195.4862	598.2467	P	244.1656	122.5864	227.1390	114.0731			2
12							K	147.1128	74.0600	130.0863	65.5468			1

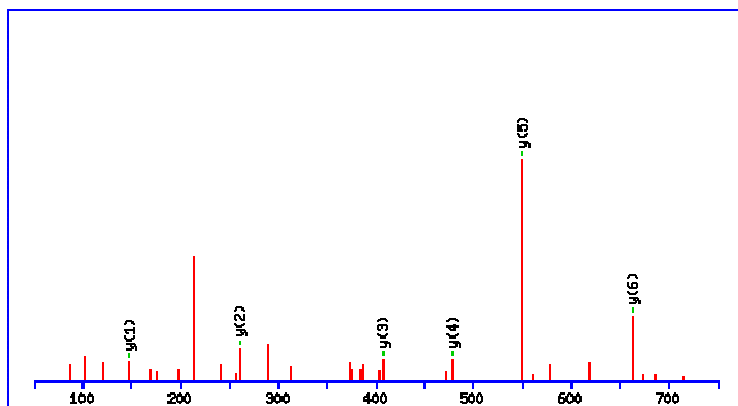


Peptide Number: 73654MS/MS Fragmentation of **KLAAMIK**Found in **IPI00007111** in **IPI_human**, Tax_Id=9606 Gene_Symbol=RASD1 Dexamethasone-induced Ras-related protein 1

Match to Query 1226: 789.475608 from(395.745080,2+) index(28229)

Title: Elution from: 72.95 to 72.95 period: 0 cycle: 2790 experiment: 1 polarity:+

Data file 120208ry_Tig120slc-P8_1_2.mgf



Monoisotopic mass of neutral peptide Mr(calc): 789.4782

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

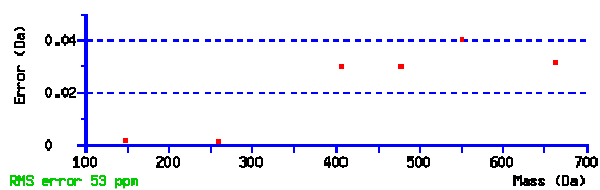
Variable modifications:

MS : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

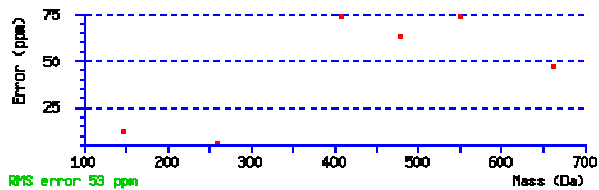
Ions Score: 41 Expect: 0.0027

Matches : 6/72 fragment ions using 14 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	#
1	129.1022	65.0548	112.0757	56.5415	K					7
2	242.1863	121.5968	225.1598	113.0835	L	662.3906	331.6989	645.3640	323.1856	6
3	313.2234	157.1153	296.1969	148.6021	A	549.3065	275.1569	532.2799	266.6436	5
4	384.2605	192.6339	367.2340	184.1206	A	478.2694	239.6383	461.2428	231.1251	4
5	531.2959	266.1516	514.2694	257.6383	M	407.2323	204.1198	390.2057	195.6065	3
6	644.3800	322.6936	627.3534	314.1804	I	260.1969	130.6021	243.1703	122.0888	2
7					K	147.1128	74.0600	130.0863	65.5468	1



RMS error 53 ppm



RMS error 53 ppm

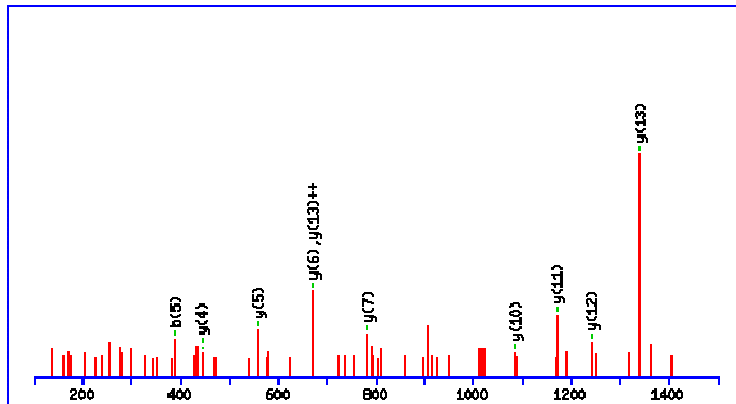
Peptide Number: 73745

MS/MS Fragmentation of **ASASAPAPASATEILLTPAR**Found in **IPI00916964** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ITM2C Uncharacterized protein

Match to Query 22363: 1894.015488 from(948.015020,2+) index(2717)

Title: Elution from: 6.93333333333333 to 6.93333333333333 period: 0 cycle: 265 experiment: 9 polarity:+

Data file 120214ry_aHDF1419-P10_4_3.mgf



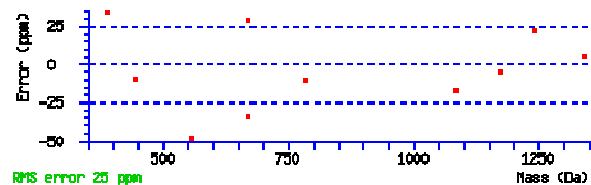
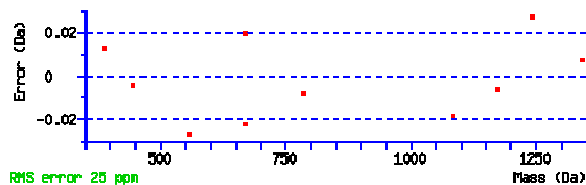
Monoisotopic mass of neutral peptide Mr(calc): 1894.0159

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 56 Expect: 0.00012

Matches : 10/182 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258			A							20
2	159.0764	80.0418	141.0659	71.0366	S	1823.9862	912.4967	1806.9596	903.9834	1805.9756	903.4914	19
3	230.1135	115.5604	212.1030	106.5551	A	1736.9541	868.9807	1719.9276	860.4674	1718.9436	859.9754	18
4	317.1456	159.0764	299.1350	150.0711	S	1665.9170	833.4621	1648.8905	824.9489	1647.9064	824.4569	17
5	388.1827	194.5950	370.1721	185.5897	A	1578.8850	789.9461	1561.8584	781.4329	1560.8744	780.9408	16
6	485.2354	243.1214	467.2249	234.1161	P	1507.8479	754.4276	1490.8213	745.9143	1489.8373	745.4223	15
7	556.2726	278.6399	538.2620	269.6346	A	1410.7951	705.9012	1393.7686	697.3879	1392.7845	696.8959	14
8	653.3253	327.1663	635.3148	318.1610	P	1339.7580	670.3826	1322.7314	661.8694	1321.7474	661.3774	13
9	724.3624	362.6849	706.3519	353.6796	A	1242.7052	621.8563	1225.6787	613.3430	1224.6947	612.8510	12
10	811.3945	406.2009	793.3839	397.1956	S	1171.6681	586.3377	1154.6416	577.8244	1153.6575	577.3324	11
11	882.4316	441.7194	864.4210	432.7141	A	1084.6361	542.8217	1067.6095	534.3084	1066.6255	533.8164	10
12	983.4793	492.2433	965.4687	483.2380	T	1013.5990	507.3031	996.5724	498.7898	995.5884	498.2978	9
13	1112.5218	556.7646	1094.5113	547.7593	E	912.5513	456.7793	895.5247	448.2660	894.5407	447.7740	8
14	1225.6059	613.3066	1207.5953	604.3013	I	783.5087	392.2580	766.4822	383.7447	765.4981	383.2527	7
15	1338.6900	669.8486	1320.6794	660.8433	L	670.4246	335.7160	653.3981	327.2027	652.4141	326.7107	6
16	1451.7740	726.3907	1433.7635	717.3854	L	557.3406	279.1739	540.3140	270.6606	539.3300	270.1686	5
17	1552.8217	776.9145	1534.8111	767.9092	T	444.2565	222.6319	427.2300	214.1186	426.2459	213.6266	4
18	1649.8745	825.4409	1631.8639	816.4356	P	343.2088	172.1081	326.1823	163.5948			3
19	1720.9116	860.9594	1702.9010	851.9542	A	246.1561	123.5817	229.1295	115.0684			2
20					R	175.1190	88.0631	158.0924	79.5498			1



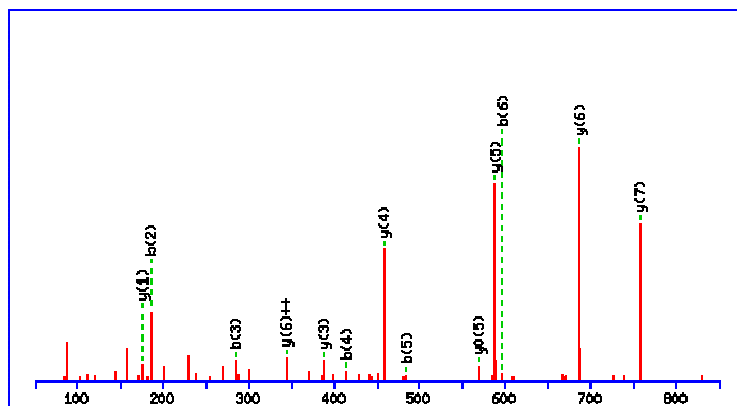
Peptide Number: 73853

MS/MS Fragmentation of **LAVEALVR**Found in **IPI00023768** in **IPI_human**, Tax_Id=9606 Gene_Symbol=HAS1 Hyaluronan synthase 1

Match to Query 2411: 869.533868 from(435.774210,2+) index(19907)

Title: Elution from: 50.05 to 50.05 period: 0 cycle: 1910 experiment: 1 polarity:+

Data file 120208ry_Tig120slc-P8_3_2.mgf



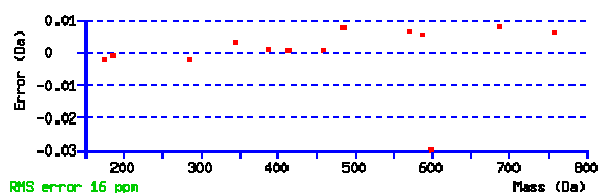
Monoisotopic mass of neutral peptide Mr(calc): 869.5334

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

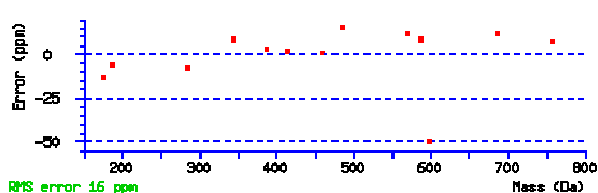
Ions Score: 46 Expect: 0.00065

Matches : 13/56 fragment ions using 22 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							8
2	185.1285	93.0679			A	757.4567	379.2320	740.4301	370.7187	739.4461	370.2267	7
3	284.1969	142.6021			V	686.4196	343.7134	669.3930	335.2001	668.4090	334.7081	6
4	413.2395	207.1234	395.2289	198.1181	E	587.3511	294.1792	570.3246	285.6659	569.3406	285.1739	5
5	484.2766	242.6419	466.2660	233.6366	A	458.3085	229.6579	441.2820	221.1446			4
6	597.3606	299.1840	579.3501	290.1787	L	387.2714	194.1394	370.2449	185.6261			3
7	696.4291	348.7182	678.4185	339.7129	V	274.1874	137.5973	257.1608	129.0840			2
8					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 16 ppm



RMS error 16 ppm

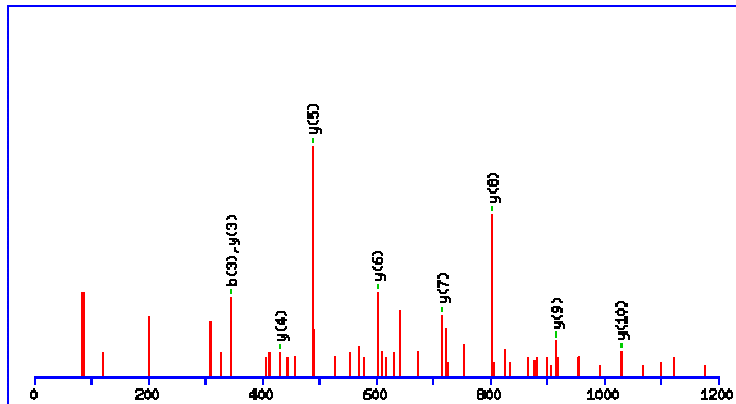
Peptide Number: 74028

MS/MS Fragmentation of **ESQILSLLSDIGSGIR**Found in **IPI00005104** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CHUK Inhibitor of nuclear factor kappa-B kinase subunit alpha

Match to Query 6993: 1686.918852 from(563.313560,3+) index(25909)

Title: Elution from: 67.1 to 67.1 period: 0 cycle: 2546 experiment: 1 polarity: +

Data file 120210ry_32R1-32_2_4.mgf



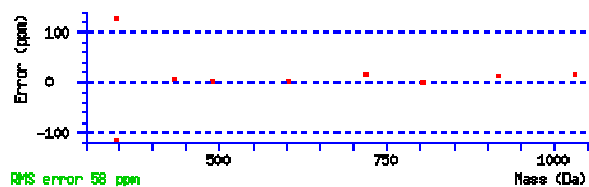
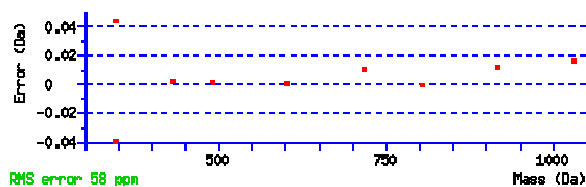
Monoisotopic mass of neutral peptide Mr(calc): 1686.9152

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 65 Expect: 1.8e-005

Matches : 9/170 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							16
2	217.0819	109.0446			199.0713	100.0393	S	1558.8799	779.9436	1541.8533	771.4303	1540.8693	770.9383	15
3	345.1405	173.0739	328.1139	164.5606	327.1299	164.0686	Q	1471.8479	736.4276	1454.8213	727.9143	1453.8373	727.4223	14
4	458.2245	229.6159	441.1980	221.1026	440.2140	220.6106	I	1343.7893	672.3983	1326.7627	663.8850	1325.7787	663.3930	13
5	571.3086	286.1579	554.2821	277.6447	553.2980	277.1527	L	1230.7052	615.8563	1213.6787	607.3430	1212.6947	606.8510	12
6	658.3406	329.6740	641.3141	321.1607	640.3301	320.6687	S	1117.6212	559.3142	1100.5946	550.8009	1099.6106	550.3089	11
7	771.4247	386.2160	754.3981	377.7027	753.4141	377.2107	L	1030.5891	515.7982	1013.5626	507.2849	1012.5786	506.7929	10
8	884.5088	442.7580	867.4822	434.2447	866.4982	433.7527	L	917.5051	459.2562	900.4785	450.7429	899.4945	450.2509	9
9	971.5408	486.2740	954.5142	477.7608	953.5302	477.2687	S	804.4210	402.7141	787.3945	394.2009	786.4104	393.7089	8
10	1086.5677	543.7875	1069.5412	535.2742	1068.5572	534.7822	D	717.3890	359.1981	700.3624	350.6849	699.3784	350.1928	7
11	1199.6518	600.3295	1182.6252	591.8163	1181.6412	591.3243	I	602.3620	301.6847	585.3355	293.1714	584.3515	292.6794	6
12	1256.6733	628.8403	1239.6467	620.3270	1238.6627	619.8350	G	489.2780	245.1426	472.2514	236.6293	471.2674	236.1373	5
13	1343.7053	672.3563	1326.6787	663.8430	1325.6947	663.3510	S	432.2565	216.6319	415.2300	208.1186	414.2459	207.6266	4
14	1400.7267	700.8670	1383.7002	692.3537	1382.7162	691.8617	G	345.2245	173.1159	328.1979	164.6026			3
15	1513.8108	757.4090	1496.7843	748.8958	1495.8002	748.4038	I	288.2030	144.6051	271.1765	136.0919			2
16							R	175.1190	88.0631	158.0924	79.5498			1



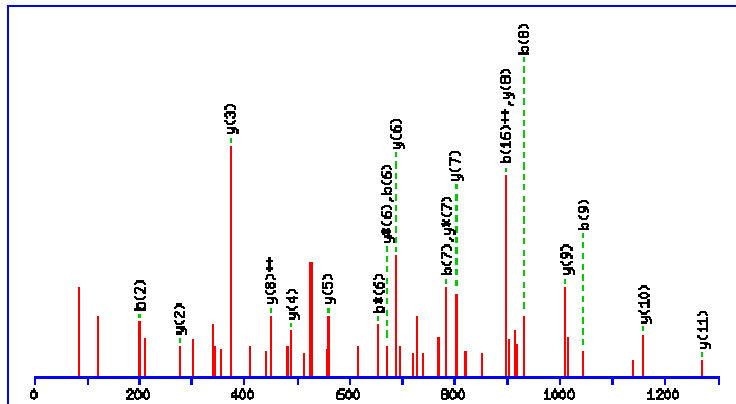
Peptide Number: 74040

MS/MS Fragmentation of **AEGLWNFLPLEADPEK**Found in **IPI00418639** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ACAD10 Isoform 1 of Acyl-CoA dehydrogenase family member 10

Match to Query 10189: 1941.001632 from(648.007820,3+) index(31648)

Title: Elution from: 91.4666666666667 to 91.4666666666667 period: 0 cycle: 3517 experiment: 1 polarity: +

Data file 120210ry_585A1-55_3_4.mgf



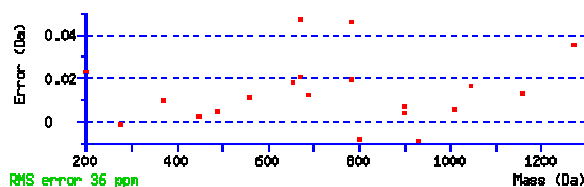
Monoisotopic mass of neutral peptide Mr(calc): 1940.9883

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

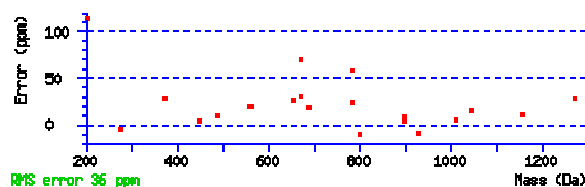
Ions Score: 59 Expect: 7.9e-005

Matches : 20/178 fragment ions using 32 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							17
2	201.0870	101.0471			183.0764	92.0418	E	1870.9585	935.9829	1853.9320	927.4696	1852.9480	926.9776	16
3	258.1084	129.5579			240.0979	120.5526	G	1741.9159	871.4616	1724.8894	862.9483	1723.9054	862.4563	15
4	371.1925	186.0999			353.1819	177.0946	L	1684.8945	842.9509	1667.8679	834.4376	1666.8839	833.9456	14
5	557.2718	279.1396			539.2613	270.1343	W	1571.8104	786.4088	1554.7839	777.8956	1553.7999	777.4036	13
6	671.3148	336.1610	654.2882	327.6477	653.3042	327.1557	N	1385.7311	693.3692	1368.7046	684.8559	1367.7205	684.3639	12
7	784.3988	392.7030	767.3723	384.1898	766.3883	383.6978	L	1271.6882	636.3477	1254.6616	627.8345	1253.6776	627.3424	11
8	931.4672	466.2373	914.4407	457.7240	913.4567	457.2320	F	1158.6041	579.8057	1141.5776	571.2924	1140.5936	570.8004	10
9	1044.5513	522.7793	1027.5247	514.2660	1026.5407	513.7740	L	1011.5357	506.2715	994.5092	497.7582	993.5251	497.2662	9
10	1141.6041	571.3057	1124.5775	562.7924	1123.5935	562.3004	P	898.4516	449.7295	881.4251	441.2162	880.4411	440.7242	8
11	1254.6881	627.8477	1237.6616	619.3344	1236.6776	618.8424	L	801.3989	401.2031	784.3723	392.6898	783.3883	392.1978	7
12	1383.7307	692.3690	1366.7042	683.8557	1365.7201	683.3637	E	688.3148	344.6610	671.2883	336.1478	670.3042	335.6558	6
13	1454.7678	727.8876	1437.7413	719.3743	1436.7573	718.8823	A	559.2722	280.1397	542.2457	271.6265	541.2617	271.1345	5
14	1569.7948	785.4010	1552.7682	776.8877	1551.7842	776.3957	D	488.2351	244.6212	471.2086	236.1079	470.2245	235.6159	4
15	1666.8475	833.9274	1649.8210	825.4141	1648.8370	824.9221	P	373.2082	187.1077	356.1816	178.5944	355.1976	178.1024	3
16	1795.8901	898.4487	1778.8636	889.9354	1777.8796	889.4434	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
17							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 36 ppm



RMS error 36 ppm

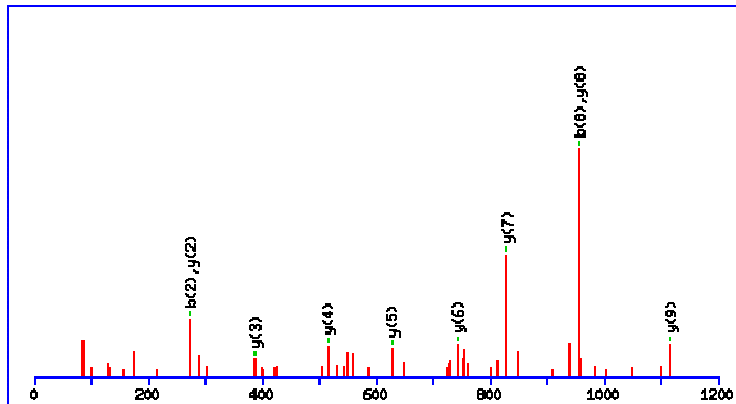
Peptide Number: 74085

MS/MS Fragmentation of **ICQSNLQLVR**Found in **IPI00014478** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ITGA7 Isoform Alpha-7X1X2B of Integrin alpha-7

Match to Query 15593: 1229.650728 from(615.832640,2+) index(9747)

Title: Elution from: 23.75 to 23.75 period: 0 cycle: 901 experiment: 7 polarity:+

Data file 120212ry_aHDF1388-P9_2_2.mgf



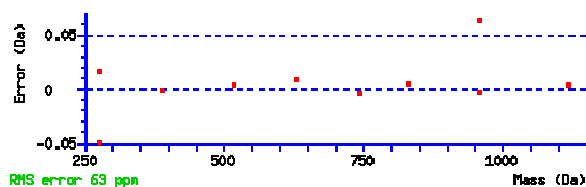
Monoisotopic mass of neutral peptide Mr(calc): 1229.6550

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

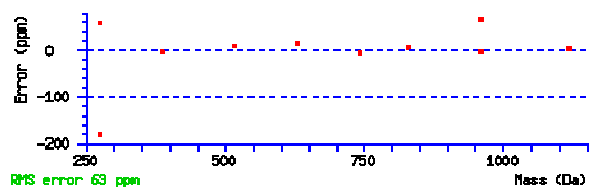
Ions Score: 72 Expect: 5.1e-006

Matches : 10/86 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							10
2	274.1220	137.5646					C	1117.5783	559.2928	1100.5517	550.7795	1099.5677	550.2875	9
3	402.1806	201.5939	385.1540	193.0806			Q	957.5476	479.2774	940.5211	470.7642	939.5370	470.2722	8
4	489.2126	245.1099	472.1860	236.5967	471.2020	236.1047	S	829.4890	415.2482	812.4625	406.7349	811.4785	406.2429	7
5	603.2555	302.1314	586.2290	293.6181	585.2450	293.1261	N	742.4570	371.7321	725.4305	363.2189			6
6	716.3396	358.6734	699.3130	350.1602	698.3290	349.6681	L	628.4141	314.7107	611.3875	306.1974			5
7	844.3982	422.7027	827.3716	414.1894	826.3876	413.6974	Q	515.3300	258.1686	498.3035	249.6554			4
8	957.4822	479.2448	940.4557	470.7315	939.4717	470.2395	L	387.2714	194.1394	370.2449	185.6261			3
9	1056.5506	528.7790	1039.5241	520.2657	1038.5401	519.7737	V	274.1874	137.5973	257.1608	129.0840			2
10							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 63 ppm



RMS error 63 ppm

Peptide Number: 74249

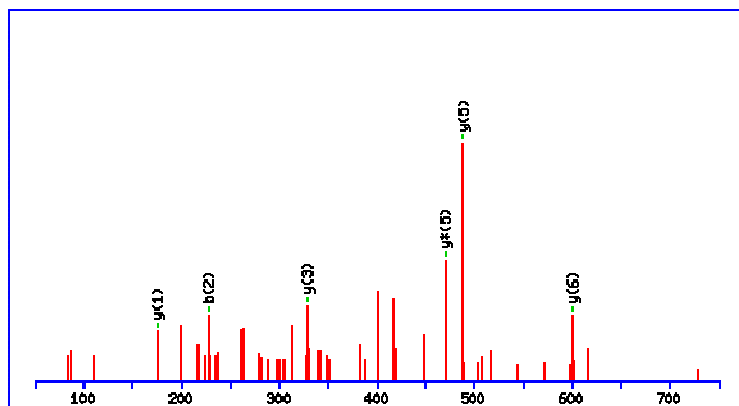
MS/MS Fragmentation of **LLGTPGR**

Found in **IPI00419784** in **IPI_human**, Tax_Id=9606 Gene_Symbol=THSD4 Isoform 3 of Thrombospondin type-1 domain-containing protein 4

Match to Query 1539: 712.429688 from(357.222120,2+) index(9558)

Title: Elution from: 66.6666666666667 to 66.6666666666667 period: 0 cycle: 5714 experiment: 1 polarity: +

Data file 120129ry_604A1-46_1_1.mgf



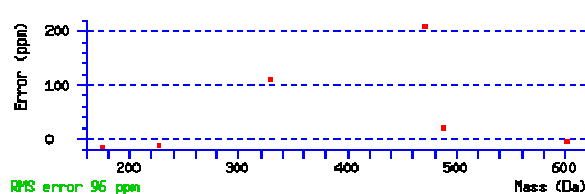
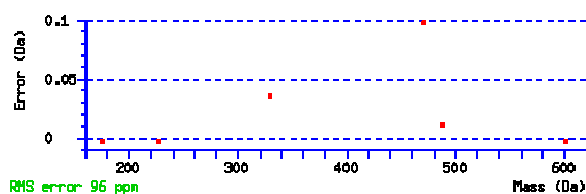
Monoisotopic mass of neutral peptide Mr(calc): 712.4232

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 40 Expect: 0.002

Matches : 6/48 fragment ions using 6 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							7
2	227.1754	114.0913			L	600.3464	300.6768	583.3198	292.1636	582.3358	291.6715	6
3	284.1969	142.6021			G	487.2623	244.1348	470.2358	235.6215	469.2518	235.1295	5
4	385.2445	193.1259	367.2340	184.1206	T	430.2409	215.6241	413.2143	207.1108	412.2303	206.6188	4
5	482.2973	241.6523	464.2867	232.6470	P	329.1932	165.1002	312.1666	156.5870			3
6	539.3188	270.1630	521.3082	261.1577	G	232.1404	116.5738	215.1139	108.0606			2
7					R	175.1190	88.0631	158.0924	79.5498			1



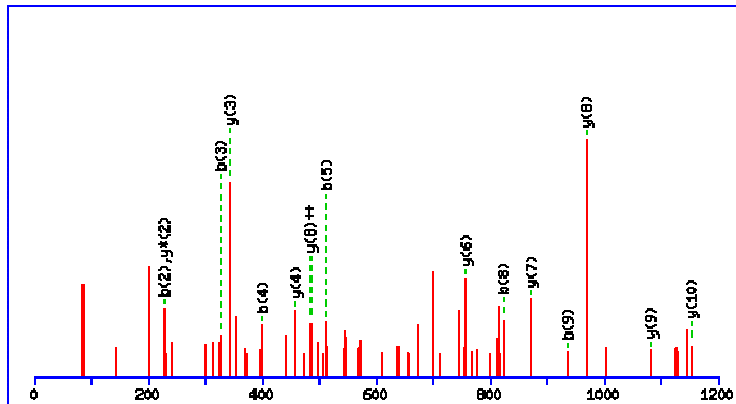
Peptide Number: 74740

MS/MS Fragmentation of **DLVALQLALPDWLDPAR**Found in **IPI00329757** in **IPI_human**, Tax_Id=9606 Gene_Symbol=RASGRP2 Isoform 1 of RAS guanyl-releasing protein 2

Match to Query 11222: 1905.026442 from(636.016090,3+) index(38881)

Title: Elution from: 103.016666666667 to 103.016666666667 period: 0 cycle: 3917 experiment: 1 polarity: +

Data file 120210ry_32R1-32_3_4.mgf



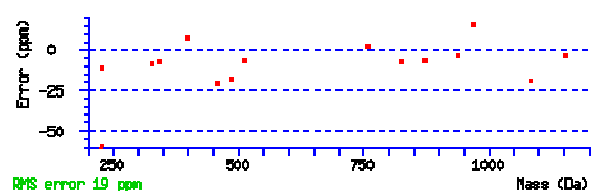
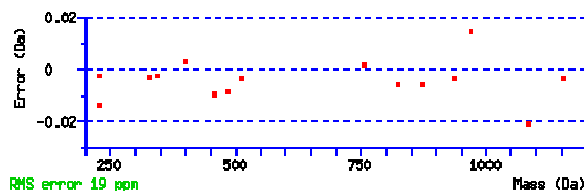
Monoisotopic mass of neutral peptide Mr(calc): 1905.0360

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 39 Expect: 0.0068

Matches : 15/176 fragment ions using 31 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							17
2	229.1183	115.0628			211.1077	106.0575	L	1791.0163	896.0118	1773.9898	887.4985	1773.0058	887.0065	16
3	328.1867	164.5970			310.1761	155.5917	V	1677.9323	839.4698	1660.9057	830.9565	1659.9217	830.4645	15
4	399.2238	200.1155			381.2132	191.1103	A	1578.8639	789.9356	1561.8373	781.4223	1560.8533	780.9303	14
5	512.3079	256.6576			494.2973	247.6523	L	1507.8267	754.4170	1490.8002	745.9037	1489.8162	745.4117	13
6	640.3665	320.6869	623.3399	312.1736	622.3559	311.6816	Q	1394.7427	697.8750	1377.7161	689.3617	1376.7321	688.8697	12
7	753.4505	377.2289	736.4240	368.7156	735.4400	368.2236	L	1266.6841	633.8457	1249.6576	625.3324	1248.6735	624.8404	11
8	824.4876	412.7475	807.4611	404.2342	806.4771	403.7422	A	1153.6000	577.3037	1136.5735	568.7904	1135.5895	568.2984	10
9	937.5717	469.2895	920.5451	460.7762	919.5611	460.2842	L	1082.5629	541.7851	1065.5364	533.2718	1064.5524	532.7798	9
10	1034.6245	517.8159	1017.5979	509.3026	1016.6139	508.8106	P	969.4789	485.2431	952.4523	476.7298	951.4683	476.2378	8
11	1149.6514	575.3293	1132.6249	566.8161	1131.6408	566.3241	D	872.4261	436.7167	855.3995	428.2034	854.4155	427.7114	7
12	1335.7307	668.3690	1318.7042	659.8557	1317.7202	659.3637	W	757.3991	379.2032	740.3726	370.6899	739.3886	370.1979	6
13	1448.8148	724.9110	1431.7882	716.3978	1430.8042	715.9057	L	571.3198	286.1636	554.2933	277.6503	553.3093	277.1583	5
14	1563.8417	782.4245	1546.8152	773.9112	1545.8312	773.4192	D	458.2358	229.6215	441.2092	221.1083	440.2252	220.6162	4
15	1660.8945	830.9509	1643.8679	822.4376	1642.8839	821.9456	P	343.2088	172.1081	326.1823	163.5948			3
16	1731.9316	866.4694	1714.9051	857.9562	1713.9210	857.4642	A	246.1561	123.5817	229.1295	115.0684			2
17							R	175.1190	88.0631	158.0924	79.5498			1

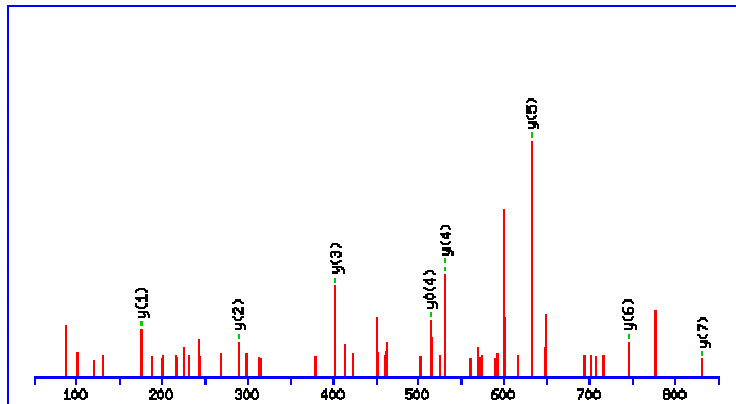


Peptide Number: 74909MS/MS Fragmentation of **ESLTEINR**Found in **IPI00016800** in **IPI_human**, Tax_Id=9606 Gene_Symbol=FAM65B Isoform 1 of Protein FAM65B

Match to Query 9195: 960.492348 from(481.253450,2+) index(24808)

Title: Elution from: 94.15 to 94.15 period: 0 cycle: 7774 experiment: 5 polarity: +

Data file 120208ry_Tig120slc-P8_2_1.mgf



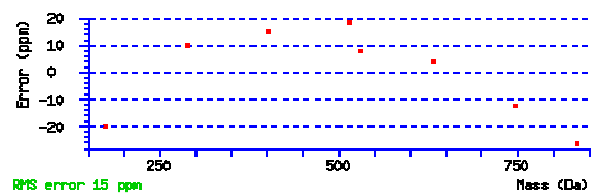
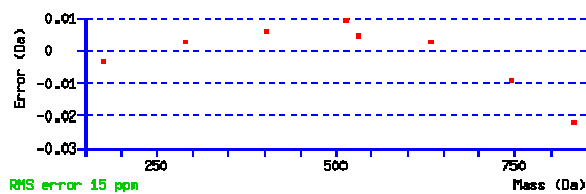
Monoisotopic mass of neutral peptide Mr(calc): 960.4876

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 40 Expect: 0.0092

Matches : 8/66 fragment ions using 22 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							8
2	217.0819	109.0446			199.0713	100.0393	S	832.4523	416.7298	815.4258	408.2165	814.4417	407.7245	7
3	330.1660	165.5866			312.1554	156.5813	L	745.4203	373.2138	728.3937	364.7005	727.4097	364.2085	6
4	431.2136	216.1105			413.2031	207.1052	T	632.3362	316.6717	615.3097	308.1585	614.3257	307.6665	5
5	560.2562	280.6318			542.2457	271.6265	E	531.2885	266.1479	514.2620	257.6346	513.2780	257.1426	4
6	673.3403	337.1738			655.3297	328.1685	I	402.2459	201.6266	385.2194	193.1133			3
7	787.3832	394.1953	770.3567	385.6820	769.3727	385.1900	N	289.1619	145.0846	272.1353	136.5713			2
8							R	175.1190	88.0631	158.0924	79.5498			1



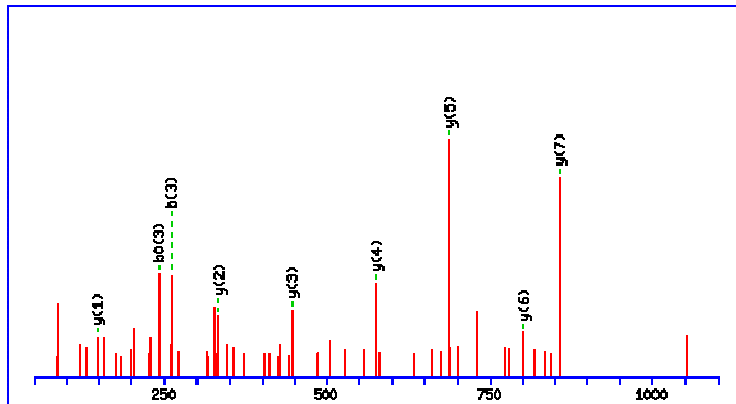
Peptide Number: 74940

MS/MS Fragmentation of **SDGLLQLWK**Found in **IPI00025463** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PHLDA1 Pleckstrin homology-like domain family A member 1

Match to Query 1403: 1058.581188 from(530.297870,2+) index(21798)

Title: Elution from: 55.35 to 55.35 period: 0 cycle: 2103 experiment: 3 polarity: +

Data file 120206ry_aHDF1419-P10_3_3.mgf



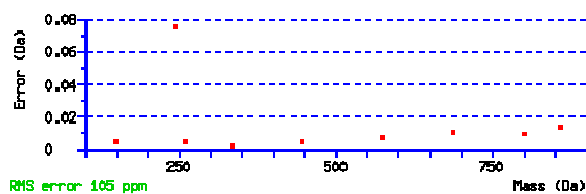
Monoisotopic mass of neutral peptide Mr(calc): 1058.5760

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

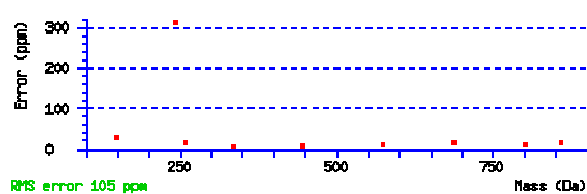
Ions Score: 49 Expect: 0.001

Matches : 9/72 fragment ions using 17 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							9
2	203.0662	102.0368			185.0557	93.0315	D	972.5513	486.7793	955.5247	478.2660	954.5407	477.7740	8
3	260.0877	130.5475			242.0771	121.5422	G	857.5244	429.2658	840.4978	420.7525			7
4	373.1718	187.0895			355.1612	178.0842	L	800.5029	400.7551	783.4763	392.2418			6
5	486.2558	243.6316			468.2453	234.6263	L	687.4188	344.2130	670.3923	335.6998			5
6	614.3144	307.6608	597.2879	299.1476	596.3039	298.6556	Q	574.3348	287.6710	557.3082	279.1577			4
7	727.3985	364.2029	710.3719	355.6896	709.3879	355.1976	L	446.2762	223.6417	429.2496	215.1285			3
8	913.4778	457.2425	896.4512	448.7293	895.4672	448.2373	W	333.1921	167.0997	316.1656	158.5864			2
9							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 105 ppm



RMS error 105 ppm

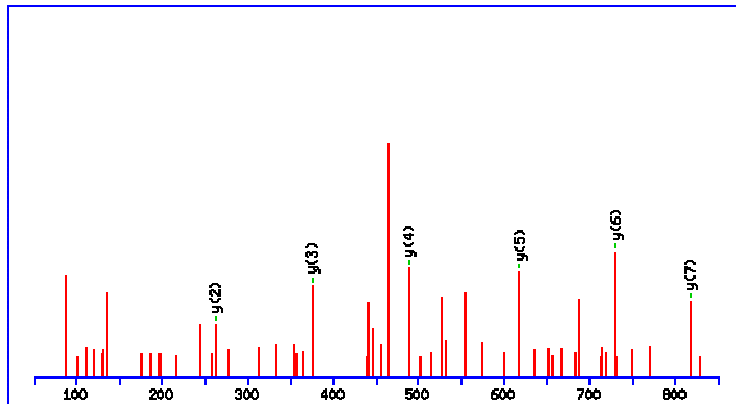
Peptide Number: 75357**MS/MS Fragmentation of QSLEISR**

Found in **IPI00030356** in **IPI_human**, Tax_Id=9606 Gene_Symbol=MCL1 Isoform 1 of Induced myeloid leukemia cell differentiation protein Mcl-1

Match to Query 4918: 944.526028 from(473.270290,2+) index(6404)

Title: Elution from: 16.8666666666667 to 16.8666666666667 period: 0 cycle: 645 experiment: 7 polarity: +

Data file 120210ry_585A1-55_3_2.mgf



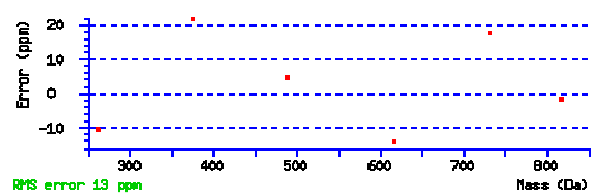
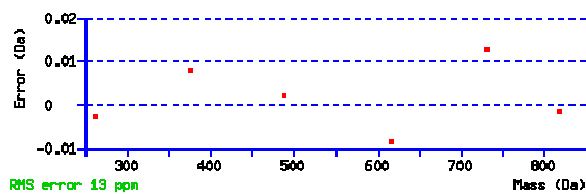
Monoisotopic mass of neutral peptide Mr(calc): 944.5291

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 58 **Expect:** 0.00015

Matches : 6/80 fragment ions using 8 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.0659	65.0366	112.0393	56.5233			Q							8
2	216.0979	108.5526	199.0713	100.0393	198.0873	99.5473	S	817.4778	409.2425	800.4512	400.7293	799.4672	400.2373	7
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	L	730.4458	365.7265	713.4192	357.2132	712.4352	356.7212	6
4	458.2245	229.6159	441.1980	221.1026	440.2140	220.6106	E	617.3617	309.1845	600.3352	300.6712	599.3511	300.1792	5
5	571.3086	286.1579	554.2821	277.6447	553.2980	277.1527	I	488.3191	244.6632	471.2926	236.1499	470.3085	235.6579	4
6	684.3927	342.7000	667.3661	334.1867	666.3821	333.6947	I	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
7	771.4247	386.2160	754.3981	377.7027	753.4141	377.2107	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
8							R	175.1190	88.0631	158.0924	79.5498			1



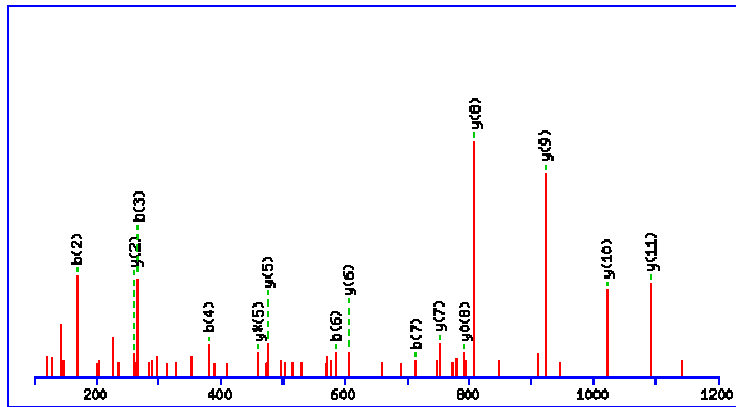
Peptide Number: 75380

MS/MS Fragmentation of **PAVLGFEGSANK**Found in **IPI00015809** in **IPI_human**, Tax_Id=9606 Gene_Symbol=OSGEP Probable tRNA threonylcarbamoyladenosine biosynthesis protein OSGEP

Match to Query 12551: 1188.609888 from(595.312220,2+) index(12075)

Title: Elution from: 30.7666666666667 to 30.7666666666667 period: 0 cycle: 1178 experiment: 7 polarity:+

Data file 120208ry_Tig120slc-P8_3_2.mgf



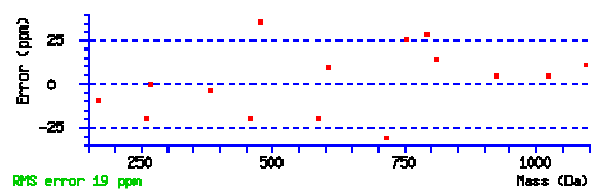
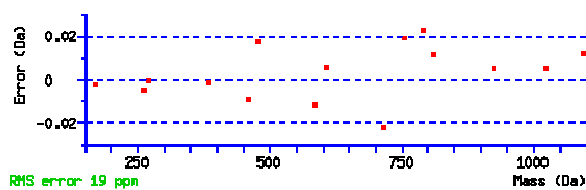
Monoisotopic mass of neutral peptide Mr(calc): 1188.6139

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 52 Expect: 0.00053

Matches : 15/94 fragment ions using 29 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	98.0600	49.5337					P							12
2	169.0972	85.0522					A	1092.5684	546.7878	1075.5419	538.2746	1074.5578	537.7826	11
3	268.1656	134.5864					V	1021.5313	511.2693	1004.5047	502.7560	1003.5207	502.2640	10
4	381.2496	191.1285					L	922.4629	461.7351	905.4363	453.2218	904.4523	452.7298	9
5	438.2711	219.6392					G	809.3788	405.1930	792.3523	396.6798	791.3682	396.1878	8
6	585.3395	293.1734					F	752.3573	376.6823	735.3308	368.1690	734.3468	367.6770	7
7	714.3821	357.6947			696.3715	348.6894	E	605.2889	303.1481	588.2624	294.6348	587.2784	294.1428	6
8	771.4036	386.2054			753.3930	377.2001	G	476.2463	238.6268	459.2198	230.1135	458.2358	229.6215	5
9	858.4356	429.7214			840.4250	420.7162	S	419.2249	210.1161	402.1983	201.6028	401.2143	201.1108	4
10	929.4727	465.2400			911.4621	456.2347	A	332.1928	166.6001	315.1663	158.0868			3
11	1043.5156	522.2615	1026.4891	513.7482	1025.5051	513.2562	N	261.1557	131.0815	244.1292	122.5682			2
12							K	147.1128	74.0600	130.0863	65.5468			1

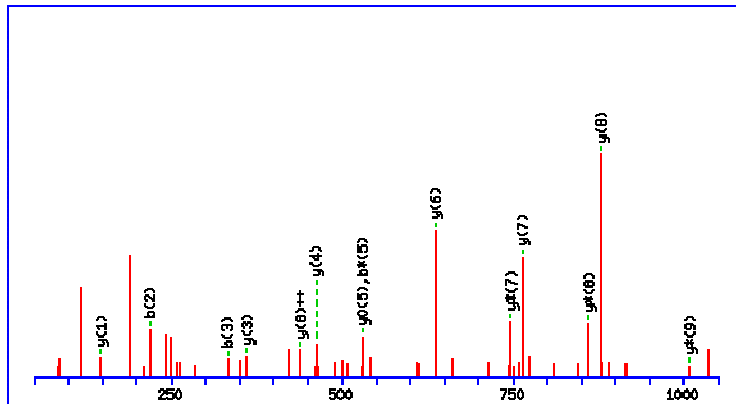


Peptide Number: 75394MS/MS Fragmentation of **AFNQSSTLTK**Found in **IPI00395321** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ZNF92 Isoform 1 of Zinc finger protein 92

Match to Query 13830: 1095.553168 from(548.783860,2+) index(14680)

Title: Elution from: 75.9 to 75.9 period: 0 cycle: 8017 experiment: 7 polarity:+

Data file 120214ry_414C2-43_4_1.mgf



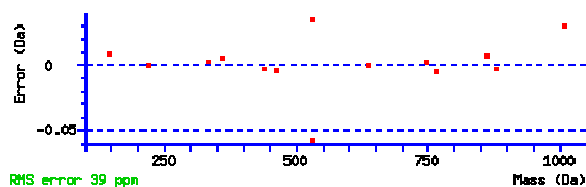
Monoisotopic mass of neutral peptide Mr(calc): 1095.5560

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

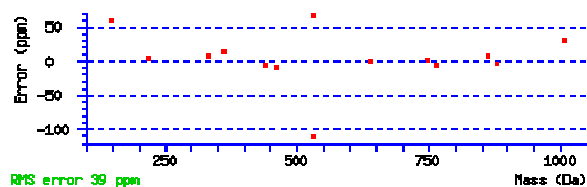
Ions Score: 45 Expect: 0.0016

Matches : 14/94 fragment ions using 20 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							10
2	219.1128	110.0600					F	1025.5262	513.2667	1008.4997	504.7535	1007.5156	504.2615	9
3	333.1557	167.0815	316.1292	158.5682			N	878.4578	439.7325	861.4312	431.2193	860.4472	430.7272	8
4	461.2143	231.1108	444.1878	222.5975			Q	764.4149	382.7111	747.3883	374.1978	746.4043	373.7058	7
5	548.2463	274.6268	531.2198	266.1135	530.2358	265.6215	S	636.3563	318.6818	619.3297	310.1685	618.3457	309.6765	6
6	635.2784	318.1428	618.2518	309.6295	617.2678	309.1375	S	549.3243	275.1658	532.2977	266.6525	531.3137	266.1605	5
7	736.3260	368.6667	719.2995	360.1534	718.3155	359.6614	T	462.2922	231.6498	445.2657	223.1365	444.2817	222.6445	4
8	849.4101	425.2087	832.3836	416.6954	831.3995	416.2034	L	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
9	950.4578	475.7325	933.4312	467.2193	932.4472	466.7272	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
10							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 39 ppm



RMS error 39 ppm

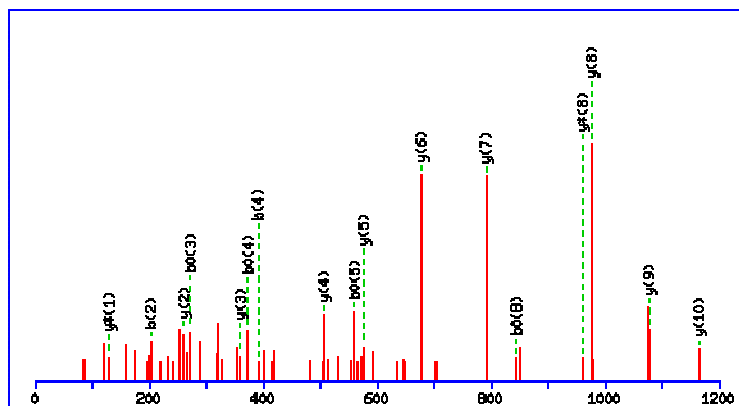
Peptide Number: 75709

MS/MS Fragmentation of **DSSTWLTAFLK**Found in **IPI00032258** in **IPI_human**, Tax_Id=9606 Gene_Symbol=C4A Complement C4-A

Match to Query 1657: 1366.718908 from(684.366730,2+) index(11071)

Title: Elution from: 28 to 28 period: 0 cycle: 1059 experiment: 2 polarity: +

Data file 120208ry_Tig120slc-P8_2_4.mgf



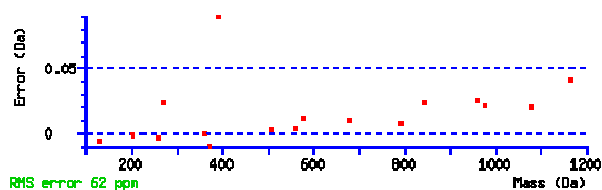
Monoisotopic mass of neutral peptide Mr(calc): 1366.7133

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

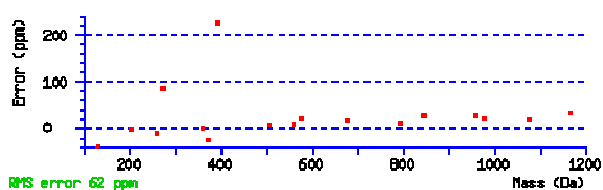
Ions Score: 43 Expect: 0.0031

Matches : 17/100 fragment ions using 47 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	98.0237	49.5155	D							12
2	203.0662	102.0368	185.0557	93.0315	S	1252.6936	626.8504	1235.6671	618.3372	1234.6830	617.8452	11
3	290.0983	145.5528	272.0877	136.5475	S	1165.6616	583.3344	1148.6350	574.8212	1147.6510	574.3291	10
4	391.1460	196.0766	373.1354	187.0713	T	1078.6295	539.8184	1061.6030	531.3051	1060.6190	530.8131	9
5	577.2253	289.1163	559.2147	280.1110	W	977.5819	489.2946	960.5553	480.7813	959.5713	480.2893	8
6	690.3093	345.6583	672.2988	336.6530	L	791.5026	396.2549	774.4760	387.7416	773.4920	387.2496	7
7	791.3570	396.1821	773.3464	387.1769	T	678.4185	339.7129	661.3919	331.1996	660.4079	330.7076	6
8	862.3941	431.7007	844.3836	422.6954	A	577.3708	289.1890	560.3443	280.6758			5
9	1009.4625	505.2349	991.4520	496.2296	F	506.3337	253.6705	489.3071	245.1572			4
10	1108.5310	554.7691	1090.5204	545.7638	V	359.2653	180.1363	342.2387	171.6230			3
11	1221.6150	611.3111	1203.6045	602.3059	L	260.1969	130.6021	243.1703	122.0888			2
12					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 62 ppm



RMS error 62 ppm

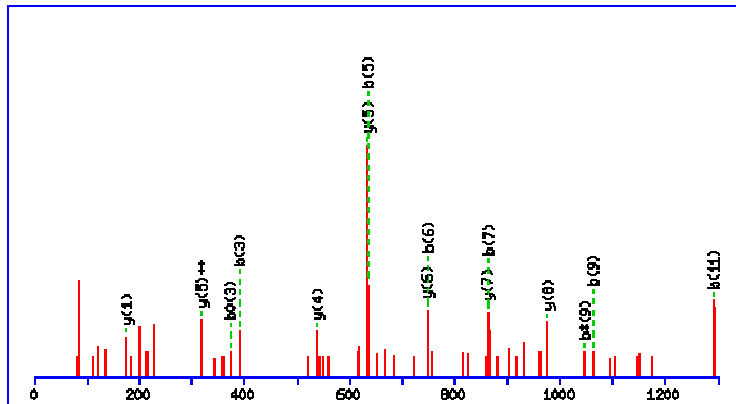
Peptide Number: 76357

MS/MS Fragmentation of **KFDPF~~LD~~SLDIP~~SQ~~FR**Found in **IPI00002330** in **IPI_human**, Tax_Id=9606 Gene_Symbol=USP3 Ubiquitin carboxyl-terminal hydrolase 3

Match to Query 13226: 2037.047832 from(680.023220,3+) index(13309)

Title: Elution from: 33.15 to 33.15 period: 0 cycle: 1257 experiment: 3 polarity:+

Data file 120214ry_414C2-43_4_4.mgf



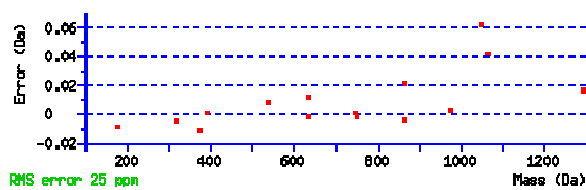
Monoisotopic mass of neutral peptide Mr(calc): 2037.0571

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

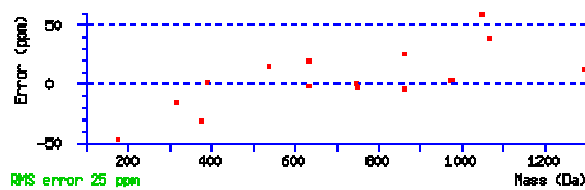
Ions Score: 48 Expect: 0.00096

Matches : 15/182 fragment ions using 23 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.1022	65.0548	112.0757	56.5415			K							17
2	276.1707	138.5890	259.1441	130.0757			F	1909.9694	955.4884	1892.9429	946.9751	1891.9589	946.4831	16
3	391.1976	196.1024	374.1710	187.5892	373.1870	187.0972	D	1762.9010	881.9542	1745.8745	873.4409	1744.8905	872.9489	15
4	488.2504	244.6288	471.2238	236.1155	470.2398	235.6235	P	1647.8741	824.4407	1630.8475	815.9274	1629.8635	815.4354	14
5	635.3188	318.1630	618.2922	309.6498	617.3082	309.1577	F	1550.8213	775.9143	1533.7948	767.4010	1532.8108	766.9090	13
6	748.4028	374.7051	731.3763	366.1918	730.3923	365.6998	L	1403.7529	702.3801	1386.7264	693.8668	1385.7423	693.3748	12
7	863.4298	432.2185	846.4032	423.7053	845.4192	423.2132	D	1290.6688	645.8381	1273.6423	637.3248	1272.6583	636.8328	11
8	976.5138	488.7606	959.4873	480.2473	958.5033	479.7553	L	1175.6419	588.3246	1158.6154	579.8113	1157.6313	579.3193	10
9	1063.5459	532.2766	1046.5193	523.7633	1045.5353	523.2713	S	1062.5578	531.7826	1045.5313	523.2693	1044.5473	522.7773	9
10	1176.6299	588.8186	1159.6034	580.3053	1158.6194	579.8133	L	975.5258	488.2665	958.4993	479.7533	957.5152	479.2613	8
11	1291.6569	646.3321	1274.6303	637.8188	1273.6463	637.3268	D	862.4417	431.7245	845.4152	423.2112	844.4312	422.7192	7
12	1404.7409	702.8741	1387.7144	694.3608	1386.7304	693.8688	I	747.4148	374.2110	730.3883	365.6978	729.4042	365.2058	6
13	1501.7937	751.4005	1484.7672	742.8872	1483.7831	742.3952	P	634.3307	317.6690	617.3042	309.1557	616.3202	308.6637	5
14	1588.8257	794.9165	1571.7992	786.4032	1570.8152	785.9112	S	537.2780	269.1426	520.2514	260.6293	519.2674	260.1373	4
15	1716.8843	858.9458	1699.8578	850.4325	1698.8737	849.9405	Q	450.2459	225.6266	433.2194	217.1133			3
16	1863.9527	932.4800	1846.9262	923.9667	1845.9422	923.4747	F	322.1874	161.5973	305.1608	153.0840			2
17							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 25 ppm



RMS error 25 ppm

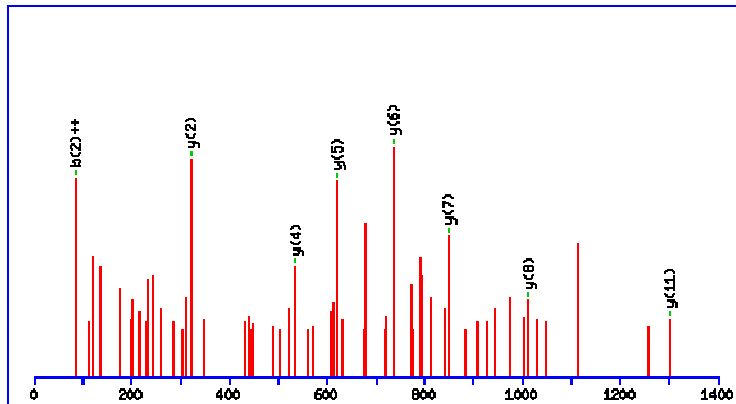
Peptide Number: 76532

MS/MS Fragmentation of **GLPTLEFSDSYLDSPDFR**Found in **IPI00902744** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ARHGAP42 Rho GTPase-activating protein 42

Match to Query 28279: 2057.987232 from(687.003020,3+) index(43386)

Title: Elution from: 105.7 to 105.7 period: 0 cycle: 3974 experiment: 3 polarity:+

Data file 120212ry_414C2-43_3_3.mgf



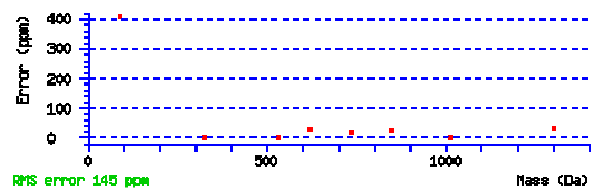
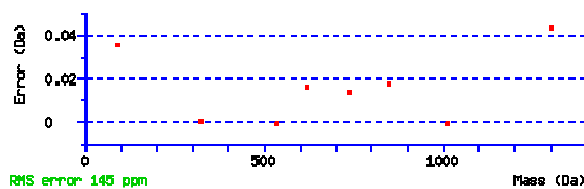
Monoisotopic mass of neutral peptide Mr(calc): 2057.9582

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 42 Expect: 0.0031

Matches : 8/160 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180			Q							18
2	171.1128	86.0600			L	2001.9440	1001.4756	1984.9175	992.9624	1983.9334	992.4704	17
3	268.1656	134.5864			P	1888.8600	944.9336	1871.8334	936.4203	1870.8494	935.9283	16
4	369.2132	185.1103	351.2027	176.1050	T	1791.8072	896.4072	1774.7806	887.8940	1773.7966	887.4019	15
5	482.2973	241.6523	464.2867	232.6470	L	1690.7595	845.8834	1673.7330	837.3701	1672.7489	836.8781	14
6	611.3399	306.1736	593.3293	297.1683	E	1577.6754	789.3414	1560.6489	780.8281	1559.6649	780.3361	13
7	758.4083	379.7078	740.3978	370.7025	F	1448.6329	724.8201	1431.6063	716.3068	1430.6223	715.8148	12
8	845.4403	423.2238	827.4298	414.2185	S	1301.5644	651.2859	1284.5379	642.7726	1283.5539	642.2806	11
9	960.4673	480.7373	942.4567	471.7320	D	1214.5324	607.7698	1197.5059	599.2566	1196.5218	598.7646	10
10	1047.4993	524.2533	1029.4888	515.2480	S	1099.5055	550.2564	1082.4789	541.7431	1081.4949	541.2511	9
11	1210.5626	605.7850	1192.5521	596.7797	Y	1012.4734	506.7404	995.4469	498.2271	994.4629	497.7351	8
12	1323.6467	662.3270	1305.6361	653.3217	L	849.4101	425.2087	832.3836	416.6954	831.3995	416.2034	7
13	1438.6737	719.8405	1420.6631	710.8352	D	736.3260	368.6667	719.2995	360.1534	718.3155	359.6614	6
14	1525.7057	763.3565	1507.6951	754.3512	S	621.2991	311.1532	604.2726	302.6399	603.2885	302.1479	5
15	1622.7584	811.8829	1604.7479	802.8776	P	534.2671	267.6372	517.2405	259.1239	516.2565	258.6319	4
16	1737.7854	869.3963	1719.7748	860.3910	D	437.2143	219.1108	420.1878	210.5975	419.2037	210.1055	3
17	1884.8538	942.9305	1866.8432	933.9253	F	322.1874	161.5973	305.1608	153.0840			2
18					R	175.1190	88.0631	158.0924	79.5498			1



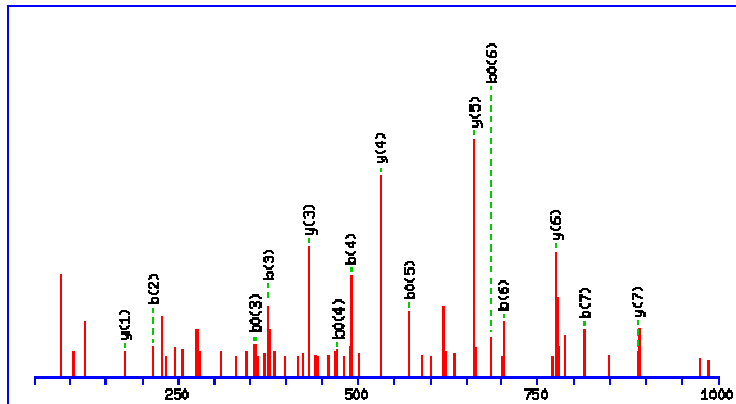
Peptide Number: 76766

MS/MS Fragmentation of **TLCDVILMVQER**Found in **IPI00186843** in **IPI_human**, Tax_Id=9606 Gene_Symbol=KLHL7 Isoform 1 of Kelch-like protein 7

Match to Query 9951: 1475.757582 from(492.926470,3+) index(33380)

Title: Elution from: 86.6833333333333 to 86.6833333333333 period: 0 cycle: 3283 experiment: 2 polarity: +

Data file 120210ry_585A1-55_3.mgf



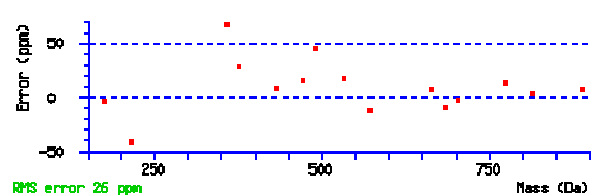
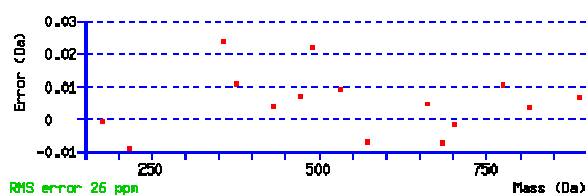
Monoisotopic mass of neutral peptide Mr(calc): 1475.7476

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 39 Expect: 0.0096

Matches : 15/112 fragment ions using 28 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							12
2	215.1390	108.0731			197.1285	99.0679	L	1375.7072	688.3572	1358.6807	679.8440	1357.6967	679.3520	11
3	375.1697	188.0885			357.1591	179.0832	C	1262.6232	631.8152	1245.5966	623.3019	1244.6126	622.8099	10
4	490.1966	245.6019			472.1860	236.5967	D	1102.5925	551.7999	1085.5660	543.2866	1084.5819	542.7946	9
5	589.2650	295.1362			571.2545	286.1309	V	987.5656	494.2864	970.5390	485.7731	969.5550	485.2811	8
6	702.3491	351.6782			684.3385	342.6729	I	888.4972	444.7522	871.4706	436.2389	870.4866	435.7469	7
7	815.4332	408.2202			797.4226	399.2149	L	775.4131	388.2102	758.3865	379.6969	757.4025	379.2049	6
8	946.4736	473.7405			928.4631	464.7352	M	662.3290	331.6681	645.3025	323.1549	644.3185	322.6629	5
9	1045.5421	523.2747			1027.5315	514.2694	V	531.2885	266.1479	514.2620	257.6346	513.2780	257.1426	4
10	1173.6006	587.3040	1156.5741	578.7907	1155.5901	578.2987	Q	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	3
11	1302.6432	651.8252	1285.6167	643.3120	1284.6327	642.8200	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
12							R	175.1190	88.0631	158.0924	79.5498			1



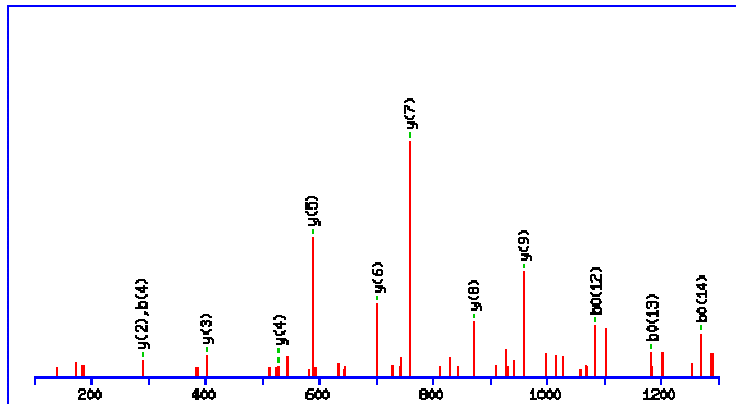
Peptide Number: 76947

MS/MS Fragmentation of **SSGGSEHSTEGSVSLGQGQLNR**Found in **IPI00043638** in **IPI_human**, Tax_Id=9606 Gene_Symbol=LARP4 Isoform 2 of La-related protein 4

Match to Query 31621: 2159.970162 from(720.997330,3+) index(33968)

Title: Elution from: 119.616666666667 to 119.616666666667 period: 0 cycle: 9319 experiment: 9 polarity:+

Data file 120210ry_32R1-32_2_1.mgf



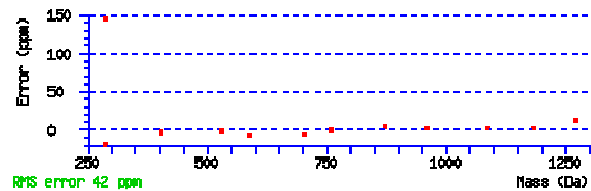
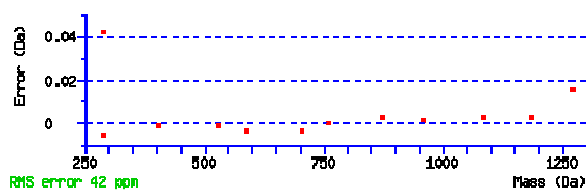
Monoisotopic mass of neutral peptide Mr(calc): 2159.9679

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 70 Expect: 3.3e-006

Matches : 12/206 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							22
2	175.0713	88.0393			157.0608	79.0340	S	2073.9432	1037.4752	2056.9166	1028.9620	2055.9326	1028.4699	21
3	232.0928	116.5500			214.0822	107.5448	G	1986.9112	993.9592	1969.8846	985.4459	1968.9006	984.9539	20
4	289.1143	145.0608			271.1037	136.0555	G	1929.8897	965.4485	1912.8631	956.9352	1911.8791	956.4432	19
5	376.1463	188.5768			358.1357	179.5715	S	1872.8682	936.9377	1855.8417	928.4245	1854.8577	927.9325	18
6	505.1889	253.0981			487.1783	244.0928	E	1785.8362	893.4217	1768.8096	884.9085	1767.8256	884.4165	17
7	642.2478	321.6275			624.2372	312.6223	H	1656.7936	828.9004	1639.7671	820.3872	1638.7830	819.8952	16
8	729.2798	365.1435			711.2693	356.1383	S	1519.7347	760.3710	1502.7081	751.8577	1501.7241	751.3657	15
9	830.3275	415.6674			812.3169	406.6621	T	1432.7027	716.8550	1415.6761	708.3417	1414.6921	707.8497	14
10	959.3701	480.1887			941.3595	471.1834	E	1331.6550	666.3311	1314.6284	657.8179	1313.6444	657.3258	13
11	1016.3916	508.6994			998.3810	499.6941	G	1202.6124	601.8098	1185.5858	593.2966	1184.6018	592.8046	12
12	1103.4236	552.2154			1085.4130	543.2101	S	1145.5909	573.2991	1128.5644	564.7858	1127.5804	564.2938	11
13	1202.4920	601.7496			1184.4814	592.7444	V	1058.5589	529.7831	1041.5323	521.2698	1040.5483	520.7778	10
14	1289.5240	645.2657			1271.5135	636.2604	S	959.4905	480.2489	942.4639	471.7356	941.4799	471.2436	9
15	1402.6081	701.8077			1384.5975	692.8024	L	872.4585	436.7329	855.4319	428.2196	854.4479	427.7276	8
16	1459.6296	730.3184			1441.6190	721.3131	G	759.3744	380.1908	742.3478	371.6776	741.3638	371.1856	7
17	1574.6565	787.8319			1556.6459	778.8266	D	702.3529	351.6801	685.3264	343.1668	684.3424	342.6748	6
18	1631.6780	816.3426			1613.6674	807.3373	G	587.3260	294.1666	570.2994	285.6534			5
19	1759.7365	880.3719	1742.7100	871.8586	1741.7260	871.3666	Q	530.3045	265.6559	513.2780	257.1426			4
20	1872.8206	936.9139	1855.7941	928.4007	1854.8100	927.9087	L	402.2459	201.6266	385.2194	193.1133			3
21	1986.8635	993.9354	1969.8370	985.4221	1968.8530	984.9301	N	289.1619	145.0846	272.1353	136.5713			2
22							R	175.1190	88.0631	158.0924	79.5498			1



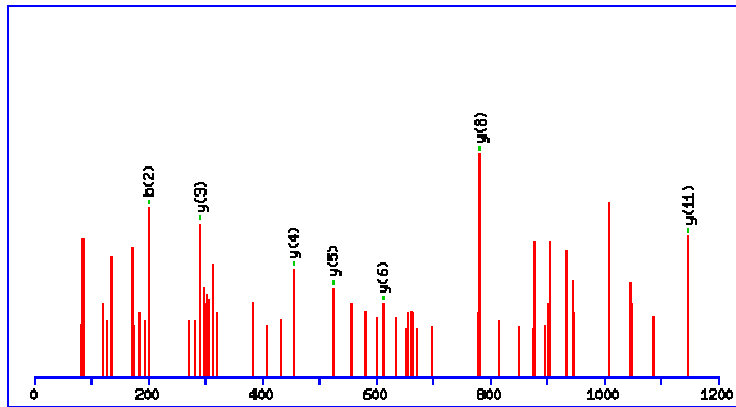
Peptide Number: 77035

MS/MS Fragmentation of **SLTTYGLSAYSGK**Found in **IPI00303053** in **IPI_human**, Tax_Id=9606 Gene_Symbol=EIF2AK3 Eukaryotic translation initiation factor 2-alpha kinase 3

Match to Query 20714: 1346.673848 from(674.344200,2+) index(27699)

Title: Elution from: 70.0166666666667 to 70.0166666666667 period: 0 cycle: 2667 experiment: 9 polarity:+

Data file 120210ry_585A1-55_3_2.mgf



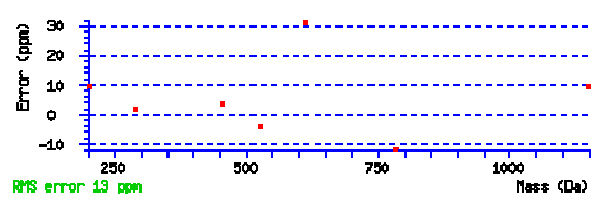
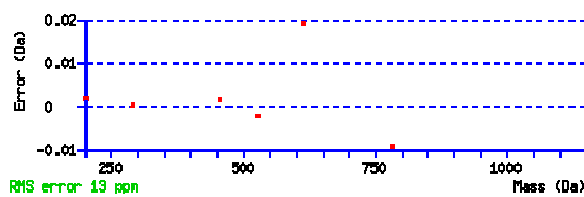
Monoisotopic mass of neutral peptide Mr(calc): 1346.6718

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 39 Expect: 0.0093

Matches : 7/116 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233	70.0287	35.5180	S							13
2	201.1234	101.0653	183.1128	92.0600	L	1260.6470	630.8272	1243.6205	622.3139	1242.6365	621.8219	12
3	302.1710	151.5892	284.1605	142.5839	T	1147.5630	574.2851	1130.5364	565.7719	1129.5524	565.2798	11
4	403.2187	202.1130	385.2082	193.1077	T	1046.5153	523.7613	1029.4888	515.2480	1028.5047	514.7560	10
5	566.2821	283.6447	548.2715	274.6394	Y	945.4676	473.2375	928.4411	464.7242	927.4571	464.2322	9
6	623.3035	312.1554	605.2930	303.1501	G	782.4043	391.7058	765.3777	383.1925	764.3937	382.7005	8
7	736.3876	368.6974	718.3770	359.6921	L	725.3828	363.1951	708.3563	354.6818	707.3723	354.1898	7
8	823.4196	412.2134	805.4090	403.2082	S	612.2988	306.6530	595.2722	298.1397	594.2882	297.6477	6
9	894.4567	447.7320	876.4462	438.7267	A	525.2667	263.1370	508.2402	254.6237	507.2562	254.1317	5
10	1057.5201	529.2637	1039.5095	520.2584	Y	454.2296	227.6185	437.2031	219.1052	436.2191	218.6132	4
11	1144.5521	572.7797	1126.5415	563.7744	S	291.1663	146.0868	274.1397	137.5735	273.1557	137.0815	3
12	1201.5735	601.2904	1183.5630	592.2851	G	204.1343	102.5708	187.1077	94.0575			2
13					K	147.1128	74.0600	130.0863	65.5468			1

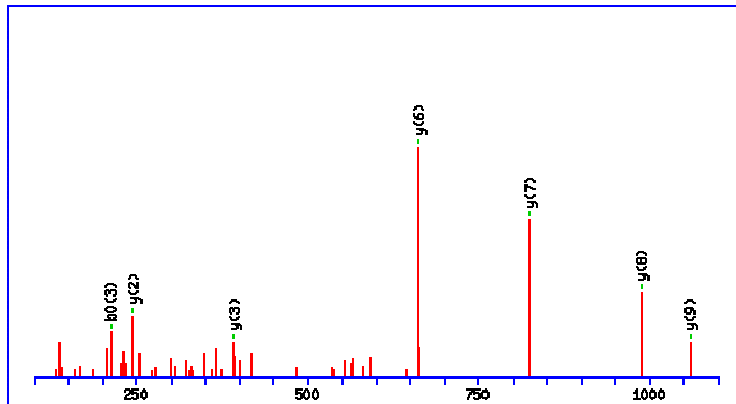


Peptide Number: 77123MS/MS Fragmentation of **ASAYYPSSFPK**Found in **IPI00296147** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TMEM119 Transmembrane protein 119

Match to Query 14424: 1216.576528 from(609.295540,2+) index(20700)

Title: Elution from: 53.5666666666667 to 53.5666666666667 period: 0 cycle: 2049 experiment: 6 polarity: +

Data file 120208ry_Tig120slc-P8_1_2.mgf



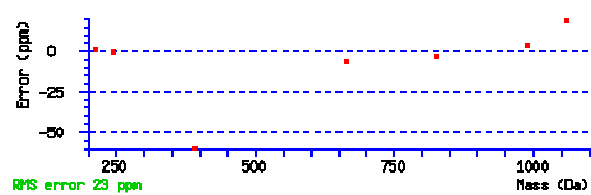
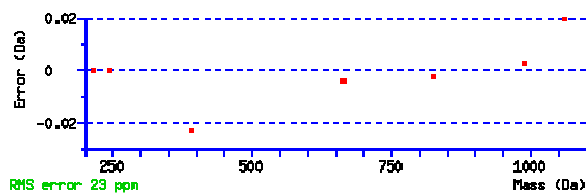
Monoisotopic mass of neutral peptide Mr(calc): 1216.5764

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 49 Expect: 0.00061

Matches : 7/92 fragment ions using 9 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258			A							11
2	159.0764	80.0418	141.0659	71.0366	S	1146.5466	573.7769	1129.5201	565.2637	1128.5360	564.7717	10
3	230.1135	115.5604	212.1030	106.5551	A	1059.5146	530.2609	1042.4880	521.7477	1041.5040	521.2556	9
4	393.1769	197.0921	375.1663	188.0868	Y	988.4775	494.7424	971.4509	486.2291	970.4669	485.7371	8
5	556.2402	278.6237	538.2296	269.6185	Y	825.4141	413.2107	808.3876	404.6974	807.4036	404.2054	7
6	653.2930	327.1501	635.2824	318.1448	P	662.3508	331.6790	645.3243	323.1658	644.3402	322.6738	6
7	740.3250	370.6661	722.3144	361.6608	S	565.2980	283.1527	548.2715	274.6394	547.2875	274.1474	5
8	827.3570	414.1821	809.3464	405.1769	S	478.2660	239.6366	461.2395	231.1234	460.2554	230.6314	4
9	974.4254	487.7163	956.4149	478.7111	F	391.2340	196.1206	374.2074	187.6074			3
10	1071.4782	536.2427	1053.4676	527.2374	P	244.1656	122.5864	227.1390	114.0731			2
11					K	147.1128	74.0600	130.0863	65.5468			1



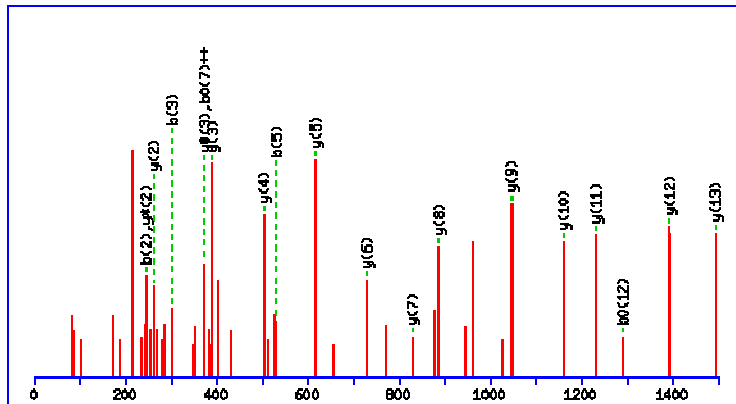
Peptide Number: 77246

MS/MS Fragmentation of **MLGETCADCGTILLQDK**Found in **IPI00977633** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SSSCA1 Protein

Match to Query 41306: 1923.874348 from(962.944450,2+) index(46244)

Title: Elution from: 110.033333333333 to 110.033333333333 period: 0 cycle: 4152 experiment: 9 polarity: +

Data file 120214ry_32R1-32_4_2.mgf



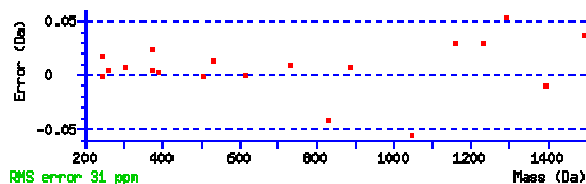
Monoisotopic mass of neutral peptide Mr(calc): 1923.8740

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

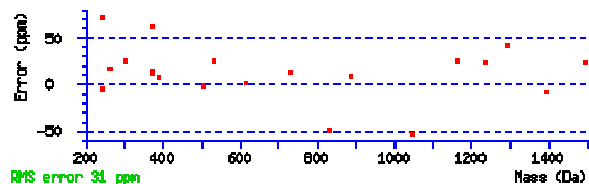
Ions Score: 82 Expect: 2.5e-007

Matches : 20/156 fragment ions using 35 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	132.0478	66.5275					M							17
2	245.1318	123.0696					L	1793.8408	897.4240	1776.8143	888.9108	1775.8302	888.4188	16
3	302.1533	151.5803					G	1680.7568	840.8820	1663.7302	832.3687	1662.7462	831.8767	15
4	431.1959	216.1016			413.1853	207.0963	E	1623.7353	812.3713	1606.7087	803.8580	1605.7247	803.3660	14
5	532.2436	266.6254			514.2330	257.6201	T	1494.6927	747.8500	1477.6661	739.3367	1476.6821	738.8447	13
6	692.2742	346.6407			674.2636	337.6355	C	1393.6450	697.3261	1376.6185	688.8129	1375.6344	688.3209	12
7	763.3113	382.1593			745.3008	373.1540	A	1233.6144	617.3108	1216.5878	608.7975	1215.6038	608.3055	11
8	878.3383	439.6728			860.3277	430.6675	D	1162.5773	581.7923	1145.5507	573.2790	1144.5667	572.7870	10
9	1038.3689	519.6881			1020.3584	510.6828	C	1047.5503	524.2788	1030.5238	515.7655	1029.5397	515.2735	9
10	1095.3904	548.1988			1077.3798	539.1935	G	887.5197	444.2635	870.4931	435.7502	869.5091	435.2582	8
11	1196.4381	598.7227			1178.4275	589.7174	T	830.4982	415.7527	813.4716	407.2395	812.4876	406.7475	7
12	1309.5221	655.2647			1291.5116	646.2594	I	729.4505	365.2289	712.4240	356.7156	711.4400	356.2236	6
13	1422.6062	711.8067			1404.5956	702.8014	L	616.3665	308.6869	599.3399	300.1736	598.3559	299.6816	5
14	1535.6903	768.3488			1517.6797	759.3435	L	503.2824	252.1448	486.2558	243.6316	485.2718	243.1395	4
15	1663.7488	832.3781	1646.7223	823.8648	1645.7383	823.3728	Q	390.1983	195.6028	373.1718	187.0895	372.1878	186.5975	3
16	1778.7758	889.8915	1761.7492	881.3782	1760.7652	880.8862	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
17							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 31 ppm



RMS error 31 ppm

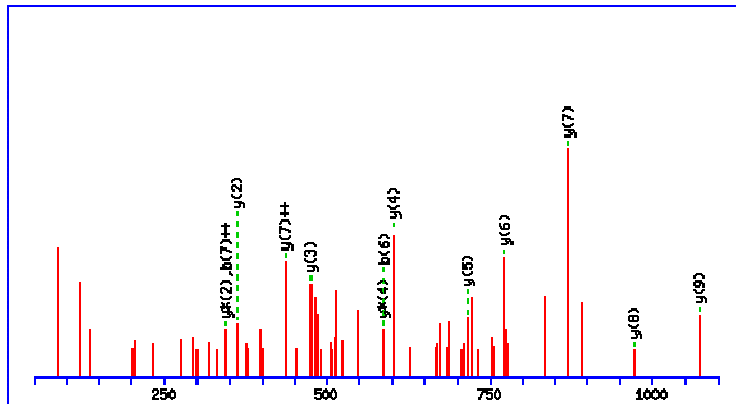
Peptide Number: 77386

MS/MS Fragmentation of **GSLNITTPGLQWR**Found in **IPI00218852** in **IPI_human**, Tax_Id=9606 Gene_Symbol=VIL1 Villin-1

Match to Query 13495: 1554.839922 from(519.287250,3+) index(25206)

Title: Elution from: 62.35 to 62.35 period: 0 cycle: 2347 experiment: 2 polarity: +

Data file 120210ry_32R1-32_3.mgf



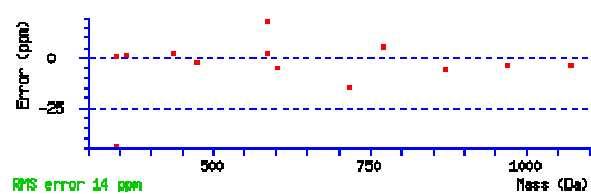
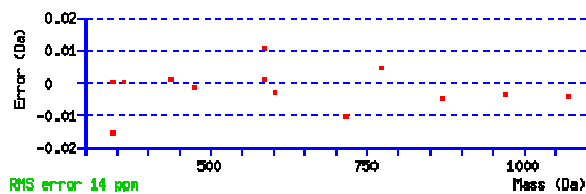
Monoisotopic mass of neutral peptide Mr(calc): 1554.8518

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 43 Expect: 0.0029

Matches : 13/134 fragment ions using 26 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							14
2	145.0608	73.0340			127.0502	64.0287	S	1498.8376	749.9225	1481.8111	741.4092	1480.8271	740.9172	13
3	258.1448	129.5761			240.1343	120.5708	L	1411.8056	706.4064	1394.7791	697.8932	1393.7950	697.4012	12
4	372.1878	186.5975	355.1612	178.0842	354.1772	177.5922	N	1298.7215	649.8644	1281.6950	641.3511	1280.7110	640.8591	11
5	485.2718	243.1395	468.2453	234.6263	467.2613	234.1343	I	1184.6786	592.8429	1167.6521	584.3297	1166.6681	583.8377	10
6	586.3195	293.6634	569.2930	285.1501	568.3089	284.6581	T	1071.5946	536.3009	1054.5680	527.7876	1053.5840	527.2956	9
7	687.3672	344.1872	670.3406	335.6740	669.3566	335.1819	T	970.5469	485.7771	953.5203	477.2638	952.5363	476.7718	8
8	784.4199	392.7136	767.3934	384.2003	766.4094	383.7083	P	869.4992	435.2532	852.4726	426.7400			7
9	841.4414	421.2243	824.4149	412.7111	823.4308	412.2191	G	772.4464	386.7269	755.4199	378.2136			6
10	954.5255	477.7664	937.4989	469.2531	936.5149	468.7611	L	715.4250	358.2161	698.3984	349.7028			5
11	1082.5841	541.7957	1065.5575	533.2824	1064.5735	532.7904	Q	602.3409	301.6741	585.3144	293.1608			4
12	1195.6681	598.3377	1178.6416	589.8244	1177.6575	589.3324	I	474.2823	237.6448	457.2558	229.1315			3
13	1381.7474	691.3774	1364.7209	682.8641	1363.7369	682.3721	W	361.1983	181.1028	344.1717	172.5895			2
14							R	175.1190	88.0631	158.0924	79.5498			1



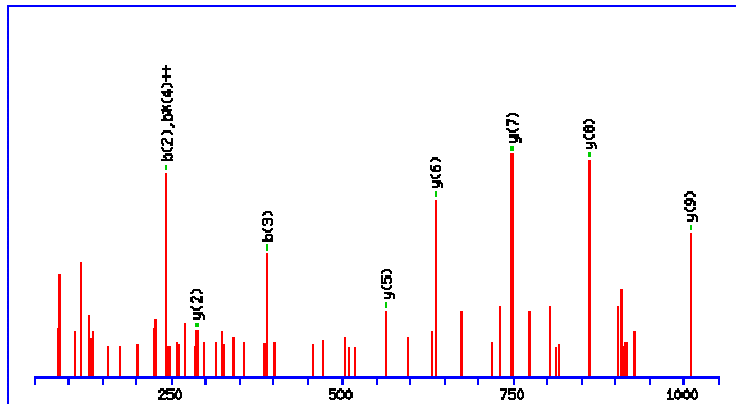
Peptide Number: 77500

MS/MS Fragmentation of **DQFIAYGGLR**Found in **IPI00020060** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SLC9A1 Isoform 1 of Sodium/hydrogen exchanger 1

Match to Query 4539: 1251.640168 from(626.827360,2+) index(12852)

Title: Elution from: 30.7833333333333 to 30.7833333333333 period: 0 cycle: 1164 experiment: 4 polarity:+

Data file 120208ry_Tig120slc-P8_2_3.mgf



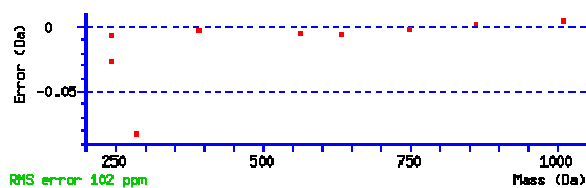
Monoisotopic mass of neutral peptide Mr(calc): 1251.6612

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

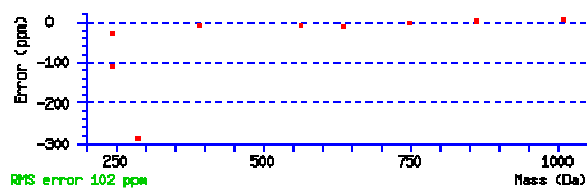
Ions Score: 50 Expect: 0.00073

Matches : 9/98 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	#
1	116.0342	58.5207			98.0237	49.5155	D					11
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	Q	1137.6415	569.3244	1120.6150	560.8111	10
3	391.1612	196.0842	374.1347	187.5710	373.1506	187.0790	F	1009.5829	505.2951	992.5564	496.7818	9
4	504.2453	252.6263	487.2187	244.1130	486.2347	243.6210	I	862.5145	431.7609	845.4880	423.2476	8
5	617.3293	309.1683	600.3028	300.6550	599.3188	300.1630	I	749.4305	375.2189	732.4039	366.7056	7
6	688.3665	344.6869	671.3399	336.1736	670.3559	335.6816	A	636.3464	318.6768	619.3198	310.1636	6
7	851.4298	426.2185	834.4032	417.7053	833.4192	417.2132	Y	565.3093	283.1583	548.2827	274.6450	5
8	908.4512	454.7293	891.4247	446.2160	890.4407	445.7240	G	402.2459	201.6266	385.2194	193.1133	4
9	965.4727	483.2400	948.4462	474.7267	947.4621	474.2347	G	345.2245	173.1159	328.1979	164.6026	3
10	1078.5568	539.7820	1061.5302	531.2688	1060.5462	530.7767	L	288.2030	144.6051	271.1765	136.0919	2
11							R	175.1190	88.0631	158.0924	79.5498	1



RMS error: 102 ppm



RMS error: 102 ppm

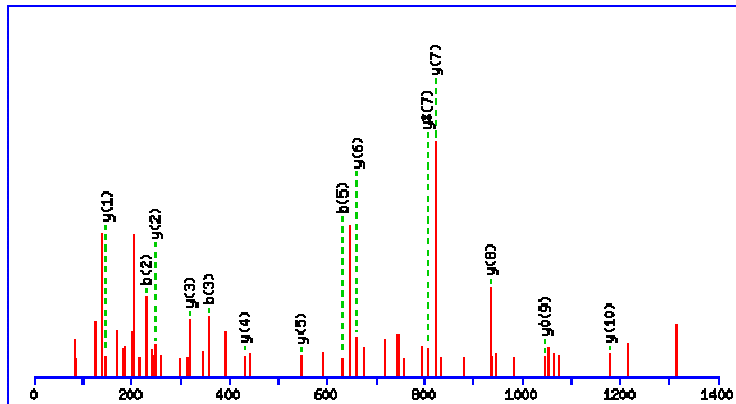
Peptide Number: 77728

MS/MS Fragmentation of **LDELCNDIATK**Found in **IPI00878545** in **IPI_human**, Tax_Id=9606 Gene_Symbol=BRD8 Protein

Match to Query 18798: 1290.619088 from(646.316820,2+) index(8218)

Title: Elution from: 19.9833333333333 to 19.9833333333333 period: 0 cycle: 754 experiment: 9 polarity: +

Data file 120212ry_414C2-43_3_2.mgf



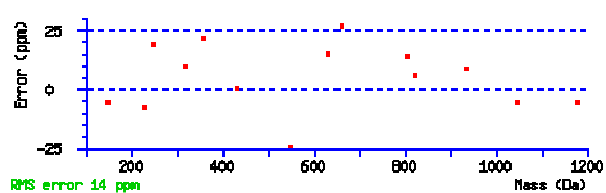
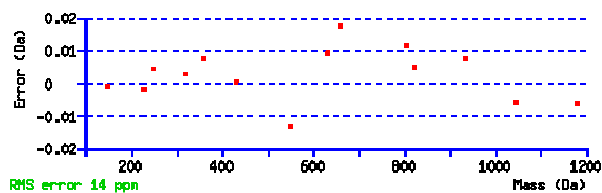
Monoisotopic mass of neutral peptide Mr(calcd): 1290.6125

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 40 Expect: 0.0063

Matches : 14/106 fragment ions using 46 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							11
2	229.1183	115.0628			211.1077	106.0575	D	1178.5358	589.7715	1161.5092	581.2583	1160.5252	580.7662	10
3	358.1609	179.5841			340.1503	170.5788	E	1063.5088	532.2581	1046.4823	523.7448	1045.4983	523.2528	9
4	471.2449	236.1261			453.2344	227.1208	L	934.4662	467.7368	917.4397	459.2235	916.4557	458.7315	8
5	631.2756	316.1414			613.2650	307.1362	C	821.3822	411.1947	804.3556	402.6815	803.3716	402.1894	7
6	745.3185	373.1629	728.2920	364.6496	727.3080	364.1576	N	661.3515	331.1794	644.3250	322.6661	643.3410	322.1741	6
7	860.3455	430.6764	843.3189	422.1631	842.3349	421.6711	D	547.3086	274.1579	530.2821	265.6447	529.2980	265.1527	5
8	973.4295	487.2184	956.4030	478.7051	955.4190	478.2131	I	432.2817	216.6445	415.2551	208.1312	414.2711	207.6392	4
9	1044.4666	522.7370	1027.4401	514.2237	1026.4561	513.7317	A	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	3
10	1145.5143	573.2608	1128.4878	564.7475	1127.5038	564.2555	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
11							K	147.1128	74.0600	130.0863	65.5468			1



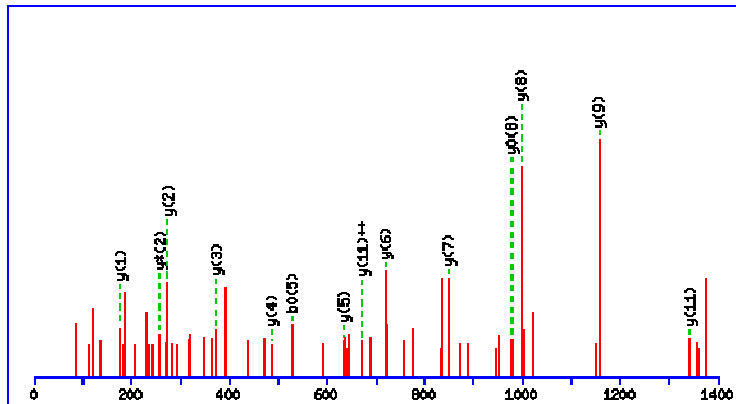
Peptide Number: 77830

MS/MS Fragmentation of **EAGQCFESFLVVR**Found in **IPI00444452** in **IPI_human**, Tax_Id=9606 Gene_Symbol=MOV10 Isoform 1 of Putative helicase MOV-10

Match to Query 13614: 1540.728168 from(771.371360,2+) index(24391)

Title: Elution from: 59.3333333333333 to 59.3333333333333 period: 0 cycle: 2192 experiment: 8 polarity: +

Data file 120118ry_201B7-32_1_3.mgf



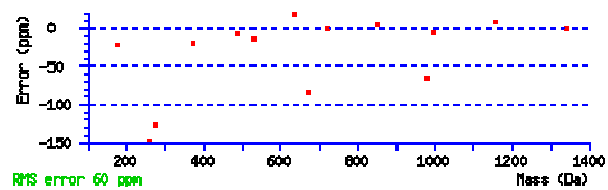
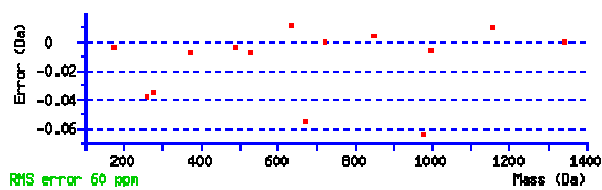
Monoisotopic mass of neutral peptide Mr(calc): 1540.7344

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 44 Expect: 0.0019

Matches : 14/128 fragment ions using 42 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							13
2	201.0870	101.0471			183.0764	92.0418	A	1412.6991	706.8532	1395.6725	698.3399	1394.6885	697.8479	12
3	258.1084	129.5579			240.0979	120.5526	G	1341.6620	671.3346	1324.6354	662.8214	1323.6514	662.3293	11
4	386.1670	193.5872	369.1405	185.0739	368.1565	184.5819	Q	1284.6405	642.8239	1267.6140	634.3106	1266.6300	633.8186	10
5	546.1977	273.6025	529.1711	265.0892	528.1871	264.5972	C	1156.5819	578.7946	1139.5554	570.2813	1138.5714	569.7893	9
6	693.2661	347.1367	676.2395	338.6234	675.2555	338.1314	F	996.5513	498.7793	979.5247	490.2660	978.5407	489.7740	8
7	822.3087	411.6580	805.2821	403.1447	804.2981	402.6527	E	849.4829	425.2451	832.4563	416.7318	831.4723	416.2398	7
8	909.3407	455.1740	892.3142	446.6607	891.3301	446.1687	S	720.4403	360.7238	703.4137	352.2105	702.4297	351.7185	6
9	1056.4091	528.7082	1039.3826	520.1949	1038.3986	519.7029	F	633.4083	317.2078	616.3817	308.6945			5
10	1169.4932	585.2502	1152.4666	576.7370	1151.4826	576.2449	L	486.3398	243.6736	469.3133	235.1603			4
11	1268.5616	634.7844	1251.5351	626.2712	1250.5510	625.7792	V	373.2558	187.1315	356.2292	178.6183			3
12	1367.6300	684.3186	1350.6035	675.8054	1349.6195	675.3134	V	274.1874	137.5973	257.1608	129.0840			2
13							R	175.1190	88.0631	158.0924	79.5498			1



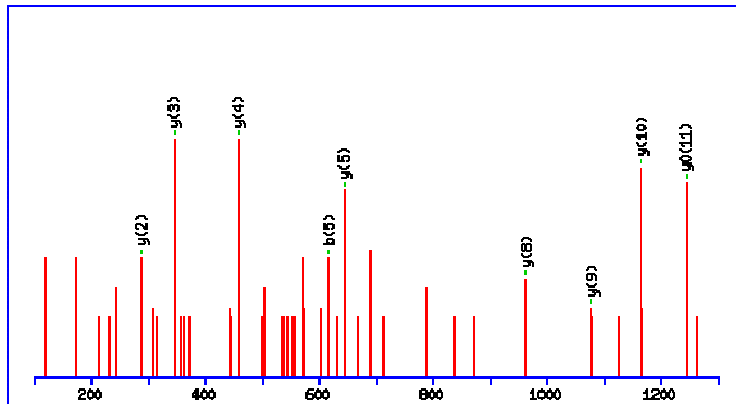
Peptide Number: 77958

MS/MS Fragmentation of **FIENTLPSDGDWFGLR**Found in **IPI00418125** in **IPI_human**, Tax_Id=9606 Gene_Symbol=LAYN Isoform 1 of Laylin

Match to Query 10353: 1991.033142 from(664.684990,3+) index(18715)

Title: Elution from: 58.2166666666667 to 58.2166666666667 period: 0 cycle: 2315 experiment: 3 polarity:+

Data file 120208ry_Tig120slc-P8_1_4.mgf



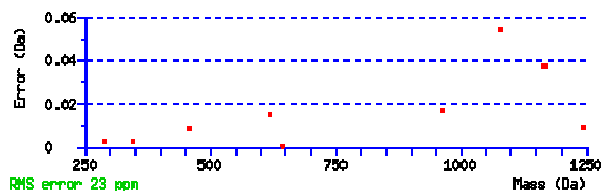
Monoisotopic mass of neutral peptide Mr(calc): 1991.0153

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

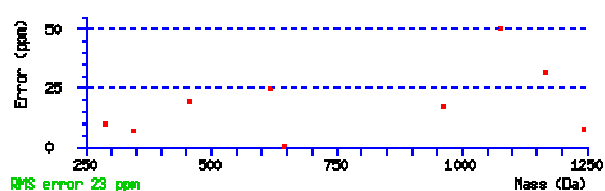
Ions Score: 52 Expect: 0.00044

Matches : 9/170 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415					F							17
2	261.1598	131.0835					I	1844.9541	922.9807	1827.9276	914.4674	1826.9436	913.9754	16
3	390.2023	195.6048			372.1918	186.5995	E	1731.8701	866.4387	1714.8435	857.9254	1713.8595	857.4334	15
4	504.2453	252.6263	487.2187	244.1130	486.2347	243.6210	N	1602.8275	801.9174	1585.8009	793.4041	1584.8169	792.9121	14
5	617.3293	309.1683	600.3028	300.6550	599.3188	300.1630	L	1488.7845	744.8959	1471.7580	736.3826	1470.7740	735.8906	13
6	730.4134	365.7103	713.3869	357.1971	712.4028	356.7051	L	1375.7005	688.3539	1358.6739	679.8406	1357.6899	679.3486	12
7	827.4662	414.2367	810.4396	405.7234	809.4556	405.2314	P	1262.6164	631.8118	1245.5899	623.2986	1244.6058	622.8066	11
8	914.4982	457.7527	897.4716	449.2395	896.4876	448.7475	S	1165.5636	583.2855	1148.5371	574.7722	1147.5531	574.2802	10
9	1029.5251	515.2662	1012.4986	506.7529	1011.5146	506.2609	D	1078.5316	539.7694	1061.5051	531.2562	1060.5211	530.7642	9
10	1086.5466	543.7769	1069.5201	535.2637	1068.5360	534.7717	G	963.5047	482.2560	946.4781	473.7427	945.4941	473.2507	8
11	1201.5735	601.2904	1184.5470	592.7771	1183.5630	592.2851	D	906.4832	453.7452	889.4567	445.2320	888.4726	444.7400	7
12	1348.6420	674.8246	1331.6154	666.3113	1330.6314	665.8193	F	791.4563	396.2318	774.4297	387.7185			6
13	1534.7213	767.8643	1517.6947	759.3510	1516.7107	758.8590	W	644.3879	322.6976	627.3613	314.1843			5
14	1647.8053	824.4063	1630.7788	815.8930	1629.7948	815.4010	I	458.3085	229.6579	441.2820	221.1446			4
15	1704.8268	852.9170	1687.8003	844.4038	1686.8162	843.9118	G	345.2245	173.1159	328.1979	164.6026			3
16	1817.9109	909.4591	1800.8843	900.9458	1799.9003	900.4538	L	288.2030	144.6051	271.1765	136.0919			2
17							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 23 ppm



RMS error 23 ppm

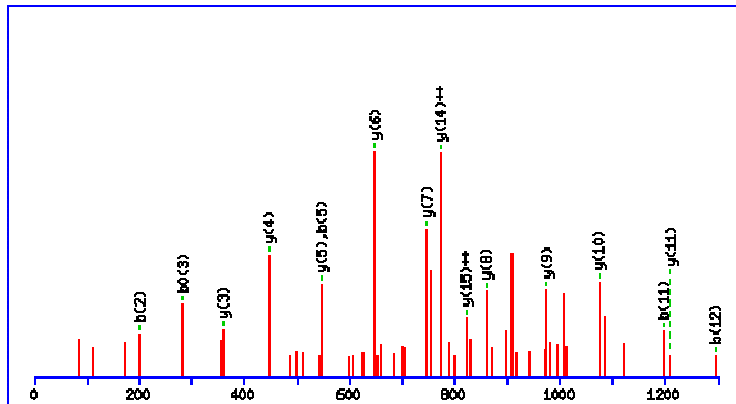
Peptide Number: 77991

MS/MS Fragmentation of **LSVVFGHEILLVTVSGQR**Found in **IPI00924667** in **IPI_human**, Tax_Id=9606 Gene_Symbol=C7orf59 UPF0539 protein C7orf59

Match to Query 26329: 1941.054912 from(648.025580,3+) index(28973)

Title: Elution from: 70.2833333333333 to 70.2833333333333 period: 0 cycle: 2632 experiment: 4 polarity:+

Data file 120201ry_aHDF1388-P9_1_3.mgf



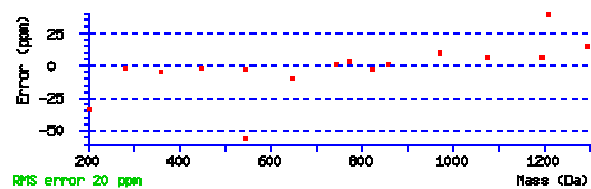
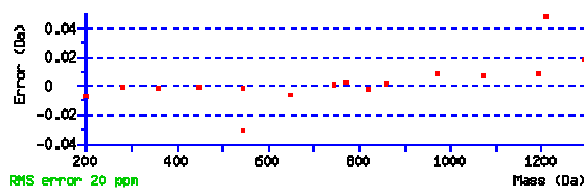
Monoisotopic mass of neutral peptide Mr(calc): 1941.0684

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 61 Expect: 4e-005

Matches : 16/164 fragment ions using 24 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							18
2	201.1234	101.0653			183.1128	92.0600	S	1828.9916	914.9994	1811.9650	906.4862	1810.9810	905.9941	17
3	300.1918	150.5995			282.1812	141.5942	V	1741.9595	871.4834	1724.9330	862.9701	1723.9490	862.4781	16
4	399.2602	200.1337			381.2496	191.1285	V	1642.8911	821.9492	1625.8646	813.4359	1624.8806	812.9439	15
5	546.3286	273.6679			528.3180	264.6627	F	1543.8227	772.4150	1526.7962	763.9017	1525.8122	763.4097	14
6	603.3501	302.1787			585.3395	293.1734	G	1396.7543	698.8808	1379.7278	690.3675	1378.7437	689.8755	13
7	732.3927	366.7000			714.3821	357.6947	E	1339.7328	670.3701	1322.7063	661.8568	1321.7223	661.3648	12
8	869.4516	435.2294			851.4410	426.2241	H	1210.6902	605.8488	1193.6637	597.3355	1192.6797	596.8435	11
9	970.4993	485.7533			952.4887	476.7480	T	1073.6313	537.3193	1056.6048	528.8060	1055.6208	528.3140	10
10	1083.5833	542.2953			1065.5728	533.2900	L	972.5837	486.7955	955.5571	478.2822	954.5731	477.7902	9
11	1196.6674	598.8373			1178.6568	589.8320	L	859.4996	430.2534	842.4730	421.7402	841.4890	421.2482	8
12	1295.7358	648.3715			1277.7252	639.3663	V	746.4155	373.7114	729.3890	365.1981	728.4050	364.7061	7
13	1396.7835	698.8954			1378.7729	689.8901	T	647.3471	324.1772	630.3206	315.6639	629.3365	315.1719	6
14	1495.8519	748.4296			1477.8413	739.4243	V	546.2994	273.6534	529.2729	265.1401	528.2889	264.6481	5
15	1582.8839	791.9456			1564.8734	782.9403	S	447.2310	224.1191	430.2045	215.6059	429.2205	215.1139	4
16	1639.9054	820.4563			1621.8948	811.4510	G	360.1990	180.6031	343.1724	172.0899			3
17	1767.9640	884.4856	1750.9374	875.9723	1749.9534	875.4803	Q	303.1775	152.0924	286.1510	143.5791			2
18							R	175.1190	88.0631	158.0924	79.5498			1



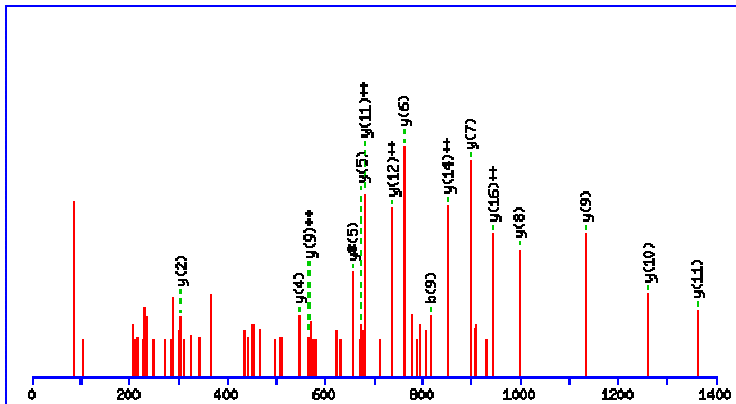
Peptide Number: 78051

MS/MS Fragmentation of **GSGNTVAIDLIVQHVHSQLEER**Found in **IPI00645413** in **IPI_human**, Tax_Id=9606 Gene_Symbol=UCKL1 uridine-cytidine kinase-like 1 isoform 2

Match to Query 34607: 2401.225896 from(601.313750,4+) index(37577)

Title: Elution from: 94.23333333333333 to 94.23333333333333 period: 0 cycle: 3562 experiment: 2 polarity: +

Data file 120214ry_414C2-43_4_3.mgf



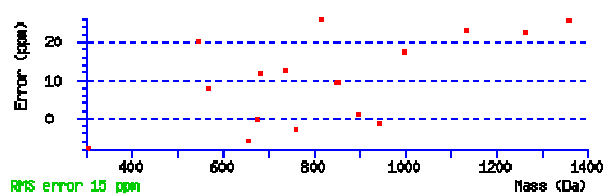
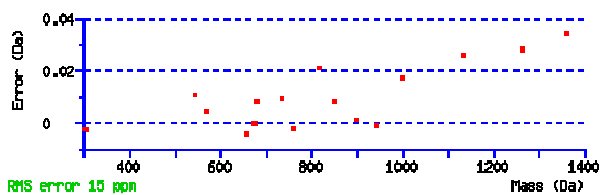
Monoisotopic mass of neutral peptide Mr(calc): 2401.2350

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 48 Expect: 0.001

Matches : 16/242 fragment ions using 30 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							22
2	145.0608	73.0340			127.0502	64.0287	S	2345.2208	1173.1140	2328.1942	1164.6008	2327.2102	1164.1088	21
3	202.0822	101.5448			184.0717	92.5395	G	2258.1888	1129.5980	2241.1622	1121.0847	2240.1782	1120.5927	20
4	316.1252	158.5662	299.0986	150.0529	298.1146	149.5609	N	2201.1673	1101.0873	2184.1408	1092.5740	2183.1567	1092.0820	19
5	417.1728	209.0901	400.1463	200.5768	399.1623	200.0848	T	2087.1244	1044.0658	2070.0978	1035.5526	2069.1138	1035.0605	18
6	516.2413	258.6243	499.2147	250.1110	498.2307	249.6190	V	1986.0767	993.5420	1969.0502	985.0287	1968.0661	984.5367	17
7	587.2784	294.1428	570.2518	285.6295	569.2678	285.1375	A	1887.0083	944.0078	1869.9817	935.4945	1868.9977	935.0025	16
8	700.3624	350.6849	683.3359	342.1716	682.3519	341.6796	I	1815.9712	908.4892	1798.9446	899.9760	1797.9606	899.4839	15
9	815.3894	408.1983	798.3628	399.6850	797.3788	399.1930	D	1702.8871	851.9472	1685.8606	843.4339	1684.8765	842.9419	14
10	928.4734	464.7404	911.4469	456.2271	910.4629	455.7351	L	1587.8602	794.4337	1570.8336	785.9204	1569.8496	785.4284	13
11	1041.5575	521.2824	1024.5310	512.7691	1023.5469	512.2771	I	1474.7761	737.8917	1457.7496	729.3784	1456.7655	728.8864	12
12	1140.6259	570.8166	1123.5994	562.3033	1122.6154	561.8113	V	1361.6920	681.3497	1344.6655	672.8364	1343.6815	672.3444	11
13	1268.6845	634.8459	1251.6579	626.3326	1250.6739	625.8406	Q	1262.6236	631.8154	1245.5971	623.3022	1244.6131	622.8102	10
14	1405.7434	703.3753	1388.7169	694.8621	1387.7328	694.3701	H	1134.5650	567.7862	1117.5385	559.2729	1116.5545	558.7809	9
15	1504.8118	752.9095	1487.7853	744.3963	1486.8013	743.9043	V	997.5061	499.2567	980.4796	490.7434	979.4956	490.2514	8
16	1641.8707	821.4390	1624.8442	812.9257	1623.8602	812.4337	H	898.4377	449.7225	881.4112	441.2092	880.4272	440.7172	7
17	1728.9028	864.9550	1711.8762	856.4417	1710.8922	855.9497	S	761.3788	381.1930	744.3523	372.6798	743.3682	372.1878	6
18	1856.9613	928.9843	1839.9348	920.4710	1838.9508	919.9790	Q	674.3468	337.6770	657.3202	329.1638	656.3362	328.6717	5
19	1970.0454	985.5263	1953.0189	977.0131	1952.0348	976.5211	L	546.2882	273.6477	529.2617	265.1345	528.2776	264.6425	4
20	2099.0880	1050.0476	2082.0614	1041.5344	2081.0774	1041.0424	E	433.2041	217.1057	416.1776	208.5924	415.1936	208.1004	3
21	2228.1306	1114.5689	2211.1040	1106.0557	2210.1200	1105.5636	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
22							R	175.1190	88.0631	158.0924	79.5498			1



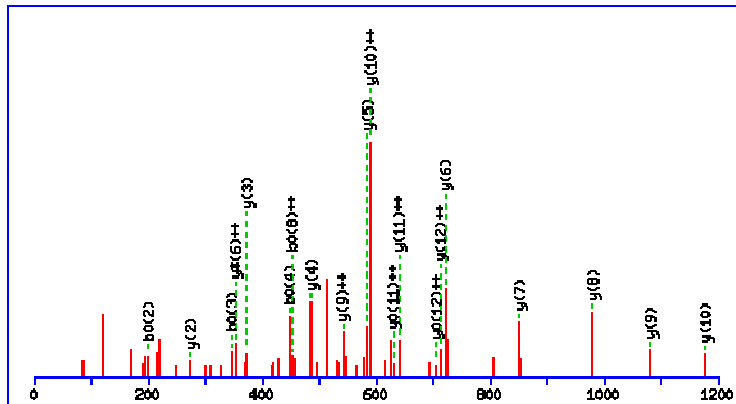
Peptide Number: 78438

MS/MS Fragmentation of **ESFTPTEEHVLVVR**Found in **IPI00910464** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SMPD4 sphingomyelin phosphodiesterase 4 isoform 3

Match to Query 34563: 1641.833772 from(548.285200,3+) index(30142)

Title: Elution from: 70.9666666666667 to 70.9666666666667 period: 0 cycle: 2682 experiment: 5 polarity:+

Data file 120214ry_32R1-32_4_2.mgf



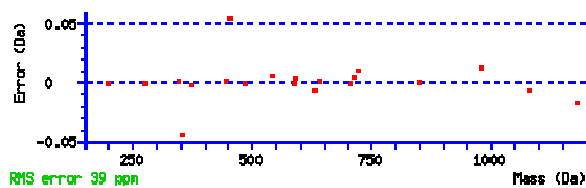
Monoisotopic mass of neutral peptide Mr(calc): 1641.8362

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

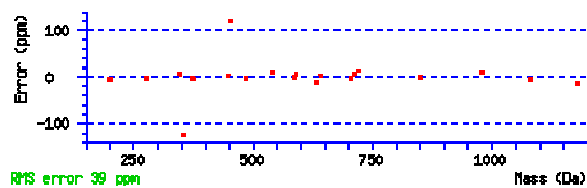
Ions Score: 45 Expect: 0.0021

Matches : 20/118 fragment ions using 39 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286	112.0393	56.5233	E							14
2	217.0819	109.0446	199.0713	100.0393	S	1513.8009	757.4041	1496.7744	748.8908	1495.7904	748.3988	13
3	364.1503	182.5788	346.1397	173.5735	F	1426.7689	713.8881	1409.7423	705.3748	1408.7583	704.8828	12
4	465.1980	233.1026	447.1874	224.0974	T	1279.7005	640.3539	1262.6739	631.8406	1261.6899	631.3486	11
5	562.2508	281.6290	544.2402	272.6237	P	1178.6528	589.8300	1161.6263	581.3168	1160.6422	580.8248	10
6	663.2984	332.1529	645.2879	323.1476	T	1081.6000	541.3037	1064.5735	532.7904	1063.5895	532.2984	9
7	792.3410	396.6742	774.3305	387.6689	E	980.5524	490.7798	963.5258	482.2665	962.5418	481.7745	8
8	921.3836	461.1954	903.3731	452.1902	E	851.5098	426.2585	834.4832	417.7452	833.4992	417.2532	7
9	1058.4425	529.7249	1040.4320	520.7196	H	722.4672	361.7372	705.4406	353.2239			6
10	1157.5109	579.2591	1139.5004	570.2538	V	585.4083	293.2078	568.3817	284.6945			5
11	1270.5950	635.8011	1252.5844	626.7959	L	486.3398	243.6736	469.3133	235.1603			4
12	1369.6634	685.3353	1351.6529	676.3301	V	373.2558	187.1315	356.2292	178.6183			3
13	1468.7318	734.8696	1450.7213	725.8643	V	274.1874	137.5973	257.1608	129.0840			2
14					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 39 ppm



RMS error 39 ppm

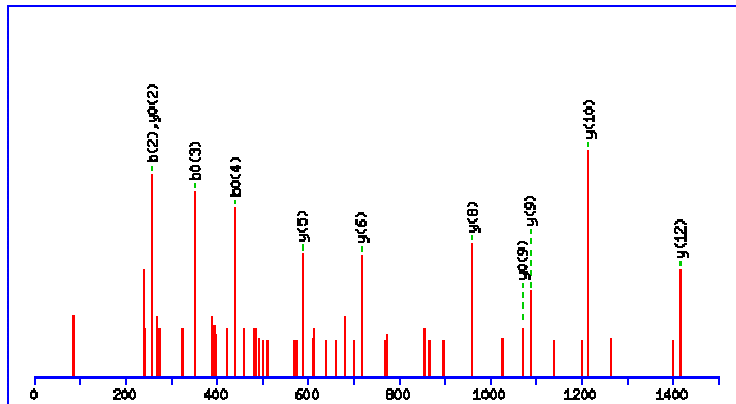
Peptide Number: 78484

MS/MS Fragmentation of **EQLSSLQEELESLEK**Found in **IPI00018111** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TAF7 Transcription initiation factor TFIID subunit 7

Match to Query 11554: 1873.922828 from(937.968690,2+) index(24273)

Title: Elution from: 59.8333333333333 to 59.8333333333333 period: 0 cycle: 2227 experiment: 10 polarity:+

Data file 120118ry_201B7-32_2_4.mgf



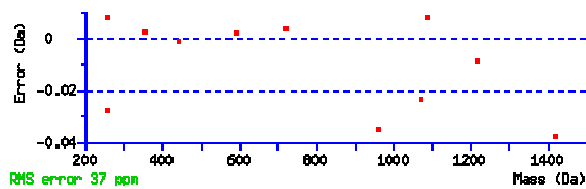
Monoisotopic mass of neutral peptide Mr(calc): 1873.9520

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

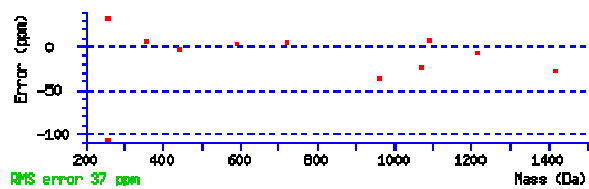
Ions Score: 43 Expect: 0.0031

Matches : 11/176 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							16
2	258.1084	129.5579	241.0819	121.0446	240.0979	120.5526	Q	1745.9167	873.4620	1728.8902	864.9487	1727.9062	864.4567	15
3	371.1925	186.0999	354.1660	177.5866	353.1819	177.0946	L	1617.8582	809.4327	1600.8316	800.9194	1599.8476	800.4274	14
4	458.2245	229.6159	441.1980	221.1026	440.2140	220.6106	S	1504.7741	752.8907	1487.7475	744.3774	1486.7635	743.8854	13
5	545.2566	273.1319	528.2300	264.6186	527.2460	264.1266	S	1417.7421	709.3747	1400.7155	700.8614	1399.7315	700.3694	12
6	658.3406	329.6740	641.3141	321.1607	640.3301	320.6687	L	1330.7100	665.8587	1313.6835	657.3454	1312.6995	656.8534	11
7	786.3992	393.7032	769.3727	385.1900	768.3886	384.6980	Q	1217.6260	609.3166	1200.5994	600.8034	1199.6154	600.3113	10
8	915.4418	458.2245	898.4153	449.7113	897.4312	449.2193	E	1089.5674	545.2873	1072.5408	536.7741	1071.5568	536.2821	9
9	1044.4844	522.7458	1027.4578	514.2326	1026.4738	513.7406	E	960.5248	480.7660	943.4983	472.2528	942.5142	471.7608	8
10	1157.5685	579.2879	1140.5419	570.7746	1139.5579	570.2826	L	831.4822	416.2447	814.4557	407.7315	813.4716	407.2395	7
11	1286.6111	643.8092	1269.5845	635.2959	1268.6005	634.8039	E	718.3981	359.7027	701.3716	351.1894	700.3876	350.6974	6
12	1373.6431	687.3252	1356.6165	678.8119	1355.6325	678.3199	S	589.3556	295.1814	572.3290	286.6681	571.3450	286.1761	5
13	1486.7271	743.8672	1469.7006	735.3539	1468.7166	734.8619	L	502.3235	251.6654	485.2970	243.1521	484.3130	242.6601	4
14	1599.8112	800.4092	1582.7847	791.8960	1581.8006	791.4040	L	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
15	1728.8538	864.9305	1711.8273	856.4173	1710.8432	855.9253	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
16							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 37 ppm



RMS error 37 ppm

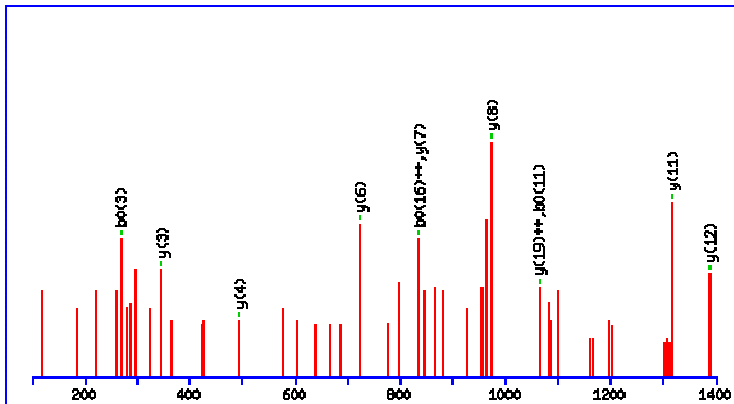
Peptide Number: 79057

MS/MS Fragmentation of **ANTVYGLGFASEQHLTQFAEK**Found in **IPI00395003** in **IPI_human**, Tax_Id=9606 Gene_Symbol=HOMER3 Isoform 2 of Homer protein homolog 3

Match to Query 29207: 2310.133962 from(771.051930,3+) index(15625)

Title: Elution from: 43.1333333333333 to 43.1333333333333 period: 0 cycle: 1666 experiment: 9 polarity:+

Data file 120208ry_Tig120slc-P8_1_3.mgf



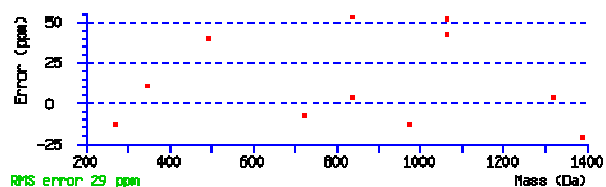
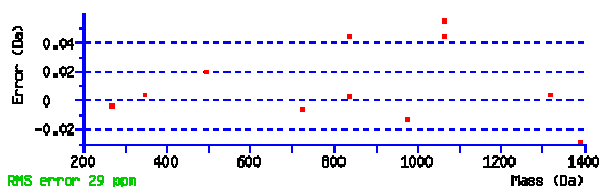
Monoisotopic mass of neutral peptide Mr(calc): 2310.1281

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 42 Expect: 0.0038

Matches : 11/232 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							21
2	186.0873	93.5473	169.0608	85.0340			N	2240.0982	1120.5528	2223.0717	1112.0395	2222.0877	1111.5475	20
3	287.1350	144.0711	270.1084	135.5579	269.1244	135.0659	T	2126.0553	1063.5313	2109.0287	1055.0180	2108.0447	1054.5260	19
4	386.2034	193.6053	369.1769	185.0921	368.1928	184.6001	V	2025.0076	1013.0074	2007.9811	1004.4942	2006.9971	1004.0022	18
5	549.2667	275.1370	532.2402	266.6237	531.2562	266.1317	Y	1925.9392	963.4732	1908.9127	954.9600	1907.9286	954.4680	17
6	606.2882	303.6477	589.2617	295.1345	588.2776	294.6425	G	1762.8759	881.9416	1745.8493	873.4283	1744.8653	872.9363	16
7	719.3723	360.1898	702.3457	351.6765	701.3617	351.1845	L	1705.8544	853.4308	1688.8279	844.9176	1687.8438	844.4256	15
8	776.3937	388.7005	759.3672	380.1872	758.3832	379.6952	G	1592.7703	796.8888	1575.7438	788.3755	1574.7598	787.8835	14
9	923.4621	462.2347	906.4356	453.7214	905.4516	453.2294	F	1535.7489	768.3781	1518.7223	759.8648	1517.7383	759.3728	13
10	994.4993	497.7533	977.4727	489.2400	976.4887	488.7480	A	1388.6805	694.8439	1371.6539	686.3306	1370.6699	685.8386	12
11	1081.5313	541.2693	1064.5047	532.7560	1063.5207	532.2640	S	1317.6434	659.3253	1300.6168	650.8120	1299.6328	650.3200	11
12	1210.5739	605.7906	1193.5473	597.2773	1192.5633	596.7853	E	1230.6113	615.8093	1213.5848	607.2960	1212.6008	606.8040	10
13	1338.6325	669.8199	1321.6059	661.3066	1320.6219	660.8146	Q	1101.5687	551.2880	1084.5422	542.7747	1083.5582	542.2827	9
14	1475.6914	738.3493	1458.6648	729.8360	1457.6808	729.3440	H	973.5102	487.2587	956.4836	478.7454	955.4996	478.2534	8
15	1588.7754	794.8914	1571.7489	786.3781	1570.7649	785.8861	L	836.4512	418.7293	819.4247	410.2160	818.4407	409.7240	7
16	1689.8231	845.4152	1672.7966	836.9019	1671.8125	836.4099	T	723.3672	362.1872	706.3406	353.6740	705.3566	353.1819	6
17	1817.8817	909.4445	1800.8551	900.9312	1799.8711	900.4392	Q	622.3195	311.6634	605.2930	303.1501	604.3089	302.6581	5
18	1964.9501	982.9787	1947.9236	974.4654	1946.9395	973.9734	F	494.2609	247.6341	477.2344	239.1208	476.2504	238.6288	4
19	2035.9872	1018.4972	2018.9607	1009.9840	2017.9767	1009.4920	A	347.1925	174.0999	330.1660	165.5866	329.1819	165.0946	3
20	2165.0298	1083.0185	2148.0033	1074.5053	2147.0192	1074.0133	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
21							K	147.1128	74.0600	130.0863	65.5468			1



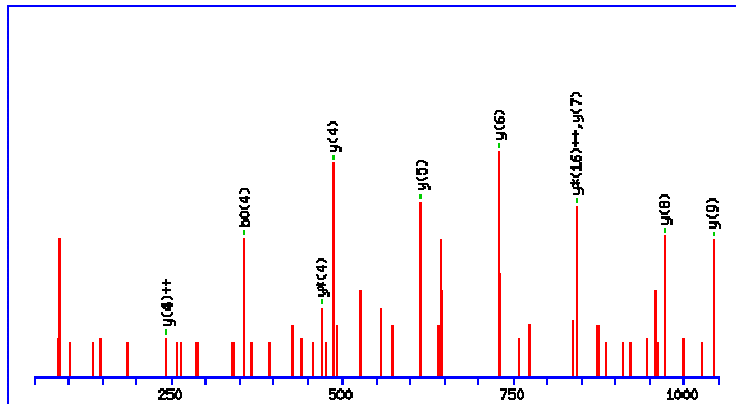
Peptide Number: 79520

MS/MS Fragmentation of **VSTSQAIAELLENIK**Found in **IPI00016922** in **IPI_human**, Tax_Id=9606 Gene_Symbol=DEPDC1 Isoform 2 of DEP domain-containing protein 1A

Match to Query 9051: 1799.023092 from(600.681640,3+) index(40030)

Title: Elution from: 100.866666666667 to 100.866666666667 period: 0 cycle: 3812 experiment: 1 polarity: +

Data file 120212ry_414C2-43_3_4.mgf



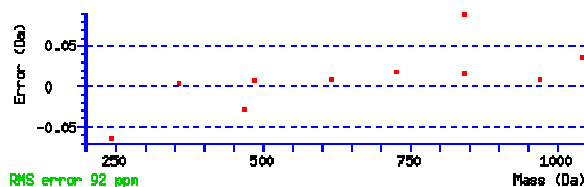
Monoisotopic mass of neutral peptide Mr(calc): 1799.0040

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

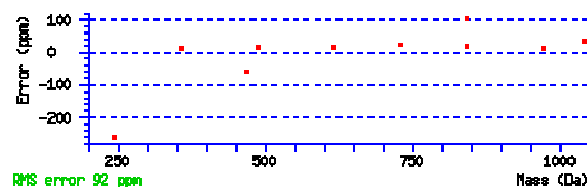
Ions Score: 45 Expect: 0.00073

Matches : 10/174 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							17
2	187.1077	94.0575			169.0972	85.0522	S	1700.9429	850.9751	1683.9163	842.4618	1682.9323	841.9698	16
3	288.1554	144.5813			270.1448	135.5761	T	1613.9109	807.4591	1596.8843	798.9458	1595.9003	798.4538	15
4	375.1874	188.0974			357.1769	179.0921	S	1512.8632	756.9352	1495.8366	748.4220	1494.8526	747.9299	14
5	503.2460	252.1266	486.2195	243.6134	485.2354	243.1214	Q	1425.8312	713.4192	1408.8046	704.9059	1407.8206	704.4139	13
6	574.2831	287.6452	557.2566	279.1319	556.2726	278.6399	A	1297.7726	649.3899	1280.7460	640.8767	1279.7620	640.3846	12
7	645.3202	323.1638	628.2937	314.6505	627.3097	314.1585	A	1226.7355	613.8714	1209.7089	605.3581	1208.7249	604.8661	11
8	758.4043	379.7058	741.3777	371.1925	740.3937	370.7005	I	1155.6984	578.3528	1138.6718	569.8395	1137.6878	569.3475	10
9	829.4414	415.2243	812.4149	406.7111	811.4308	406.2191	A	1042.6143	521.8108	1025.5877	513.2975	1024.6037	512.8055	9
10	958.4840	479.7456	941.4575	471.2324	940.4734	470.7404	E	971.5772	486.2922	954.5506	477.7789	953.5666	477.2869	8
11	1071.5681	536.2877	1054.5415	527.7744	1053.5575	527.2824	L	842.5346	421.7709	825.5080	413.2577	824.5240	412.7656	7
12	1184.6521	592.8297	1167.6256	584.3164	1166.6416	583.8244	L	729.4505	365.2289	712.4240	356.7156	711.4400	356.2236	6
13	1313.6947	657.3510	1296.6682	648.8377	1295.6842	648.3457	E	616.3665	308.6869	599.3399	300.1736	598.3559	299.6816	5
14	1427.7376	714.3725	1410.7111	705.8592	1409.7271	705.3672	N	487.3239	244.1656	470.2973	235.6523			4
15	1540.8217	770.9145	1523.7952	762.4012	1522.8111	761.9092	I	373.2809	187.1441	356.2544	178.6308			3
16	1653.9058	827.4565	1636.8792	818.9433	1635.8952	818.4512	I	260.1969	130.6021	243.1703	122.0888			2
17							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 92 ppm



RMS error 92 ppm

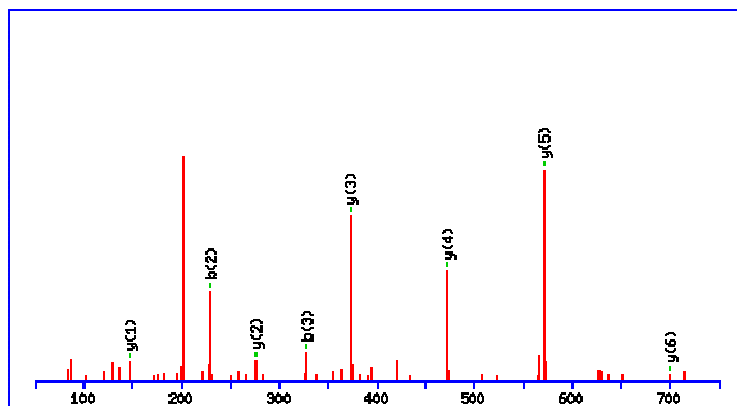
Peptide Number: 79658

MS/MS Fragmentation of **VEVVPEK**Found in **IPI00941965** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TTN Cellular titin isoform PEVK variant 1

Match to Query 3912: 798.451208 from(400.232880,2+) index(23060)

Title: Elution from: 96.05 to 96.05 period: 0 cycle: 8786 experiment: 2 polarity: +

Data file 120214ry_414C2-43_4_1.mgf



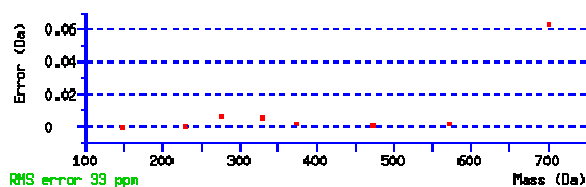
Monoisotopic mass of neutral peptide Mr(calc): 798.4487

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

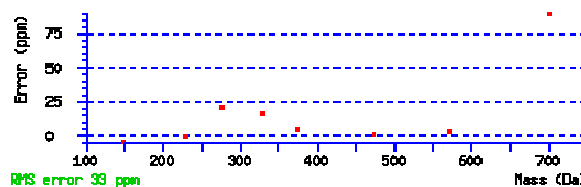
Ions Score: 37 Expect: 0.0071

Matches : 8/56 fragment ions using 20 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415			V							7
2	229.1183	115.0628	211.1077	106.0575	E	700.3876	350.6974	683.3610	342.1842	682.3770	341.6921	6
3	328.1867	164.5970	310.1761	155.5917	V	571.3450	286.1761	554.3184	277.6629	553.3344	277.1709	5
4	427.2551	214.1312	409.2445	205.1259	V	472.2766	236.6419	455.2500	228.1287	454.2660	227.6366	4
5	524.3079	262.6576	506.2973	253.6523	P	373.2082	187.1077	356.1816	178.5944	355.1976	178.1024	3
6	653.3505	327.1789	635.3399	318.1736	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
7					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 39 ppm



RMS error 39 ppm

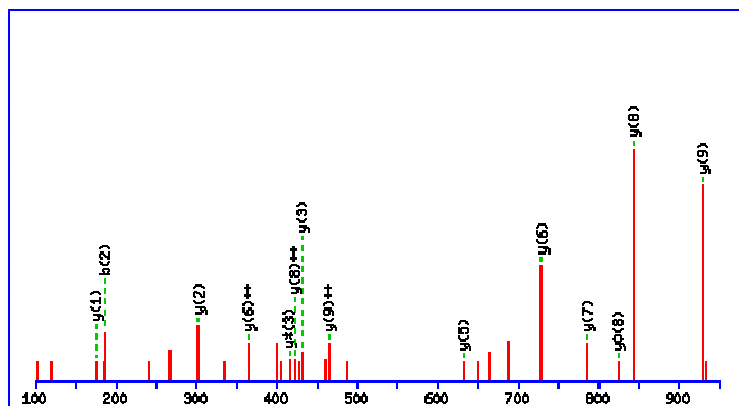
Peptide Number: 79750

MS/MS Fragmentation of **VSGGPSLEQR**Found in **IPI00465233** in **IPI_human**, Tax_Id=9606 Gene_Symbol=EIF3L Uncharacterized protein

Match to Query 11461: 1028.521948 from(515.268250,2+) index(17332)

Title: Elution from: 75.85 to 75.85 period: 0 cycle: 6662 experiment: 7 polarity: +

Data file 120208ry_Tig120slc-P8_1_1.mgf



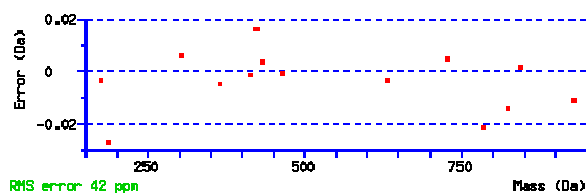
Monoisotopic mass of neutral peptide Mr(calc): 1028.5251

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

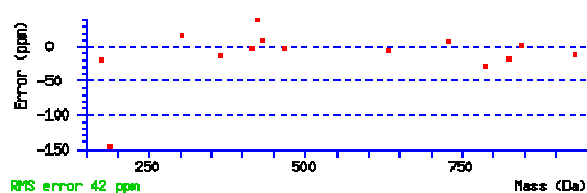
Ions Score: 63 Expect: 2.5e-005

Matches : 14/86 fragment ions using 24 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							10
2	187.1077	94.0575			169.0972	85.0522	S	930.4639	465.7356	913.4374	457.2223	912.4534	456.7303	9
3	244.1292	122.5682			226.1186	113.5629	G	843.4319	422.2196	826.4054	413.7063	825.4213	413.2143	8
4	301.1506	151.0790			283.1401	142.0737	G	786.4104	393.7089	769.3839	385.1956	768.3999	384.7036	7
5	398.2034	199.6053			380.1928	190.6001	P	729.3890	365.1981	712.3624	356.6849	711.3784	356.1928	6
6	485.2354	243.1214			467.2249	234.1161	S	632.3362	316.6717	615.3097	308.1585	614.3257	307.6665	5
7	598.3195	299.6634			580.3089	290.6581	L	545.3042	273.1557	528.2776	264.6425	527.2936	264.1504	4
8	727.3621	364.1847			709.3515	355.1794	E	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	3
9	855.4207	428.2140	838.3941	419.7007	837.4101	419.2087	Q	303.1775	152.0924	286.1510	143.5791			2
10							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 42 ppm



RMS error 42 ppm

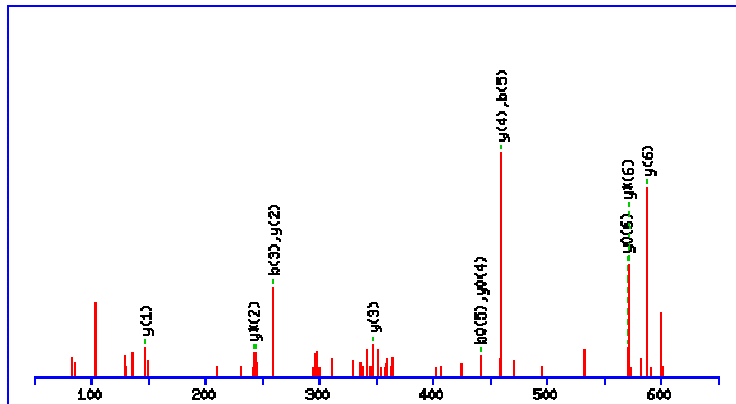
Mass (Da)

Peptide Number: 79838MS/MS Fragmentation of **MAGLSLK**Found in **IPI00008044** in **IPI_human**, Tax_Id=9606 Gene_Symbol=-- PRO3077

Match to Query 2010: 718.406548 from(360.210550,2+) index(19374)

Title: Elution from: 87.3 to 87.3 period: 0 cycle: 8697 experiment: 3 polarity:+

Data file 120206ry_aHDF1419-P10_3_1.mgf



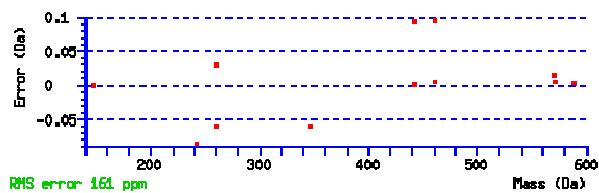
Monoisotopic mass of neutral peptide Mr(calc): 718.4047

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

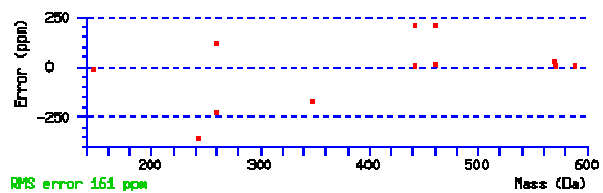
Ions Score: 48 Expect: 0.00098

Matches : 12/48 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	132.0478	66.5275			M							7
2	203.0849	102.0461			A	588.3715	294.6894	571.3450	286.1761	570.3610	285.6841	6
3	260.1063	130.5568			G	517.3344	259.1709	500.3079	250.6576	499.3239	250.1656	5
4	373.1904	187.0988			L	460.3130	230.6601	443.2864	222.1468	442.3024	221.6548	4
5	460.2224	230.6149	442.2119	221.6096	S	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
6	573.3065	287.1569	555.2959	278.1516	L	260.1969	130.6021	243.1703	122.0888			2
7					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 161 ppm



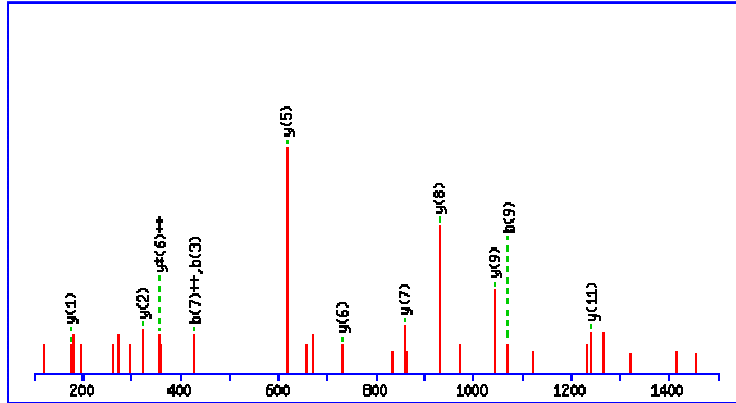
RMS error 161 ppm

Peptide Number: 79854MS/MS Fragmentation of **WIQGLQETNPTLAQIPVVFR**Found in **IPI00106506** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ECSIT Isoform 1 of Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial

Match to Query 15603: 2309.234622 from(770.752150,3+) index(2510)

Title: Elution from: 7.51666666666667 to 7.51666666666667 period: 0 cycle: 287 experiment: 6 polarity: +

Data file 120126ry_585A1-55_1_4.mgf



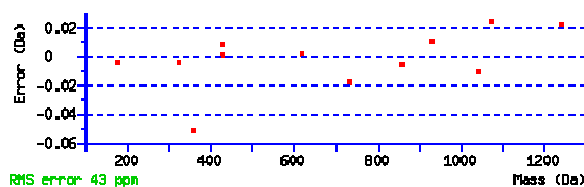
Monoisotopic mass of neutral peptide Mr(calc): 2309.2532

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

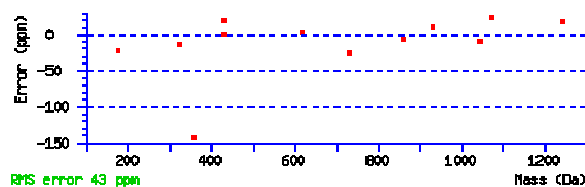
Ions Score: 43 Expect: 0.0019

Matches : 12/194 fragment ions using 22 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	187.0866	94.0469					W							20
2	300.1707	150.5890					I	2124.1812	1062.5942	2107.1546	1054.0809	2106.1706	1053.5889	19
3	428.2292	214.6183	411.2027	206.1050			Q	2011.0971	1006.0522	1994.0706	997.5389	1993.0865	997.0469	18
4	485.2507	243.1290	468.2241	234.6157			G	1883.0385	942.0229	1866.0120	933.5096	1865.0280	933.0176	17
5	598.3348	299.6710	581.3082	291.1577			L	1826.0171	913.5122	1808.9905	904.9989	1808.0065	904.5069	16
6	726.3933	363.7003	709.3668	355.1870			Q	1712.9330	856.9701	1695.9064	848.4569	1694.9224	847.9649	15
7	855.4359	428.2216	838.4094	419.7083	837.4254	419.2163	E	1584.8744	792.9408	1567.8479	784.4276	1566.8639	783.9356	14
8	956.4836	478.7454	939.4571	470.2322	938.4730	469.7402	T	1455.8318	728.4196	1438.8053	719.9063	1437.8213	719.4143	13
9	1070.5265	535.7669	1053.5000	527.2536	1052.5160	526.7616	N	1354.7841	677.8957	1337.7576	669.3824	1336.7736	668.8904	12
10	1167.5793	584.2933	1150.5528	575.7800	1149.5687	575.2880	P	1240.7412	620.8742	1223.7147	612.3610	1222.7307	611.8690	11
11	1268.6270	634.8171	1251.6004	626.3039	1250.6164	625.8118	T	1143.6885	572.3479	1126.6619	563.8346	1125.6779	563.3426	10
12	1381.7110	691.3592	1364.6845	682.8459	1363.7005	682.3539	L	1042.6408	521.8240	1025.6142	513.3108			9
13	1452.7482	726.8777	1435.7216	718.3644	1434.7376	717.8724	A	929.5567	465.2820	912.5302	456.7687			8
14	1580.8067	790.9070	1563.7802	782.3937	1562.7962	781.9017	Q	858.5196	429.7634	841.4931	421.2502			7
15	1693.8908	847.4490	1676.8642	838.9358	1675.8802	838.4438	I	730.4610	365.7341	713.4345	357.2209			6
16	1790.9436	895.9754	1773.9170	887.4621	1772.9330	886.9701	P	617.3770	309.1921	600.3504	300.6788			5
17	1890.0120	945.5096	1872.9854	936.9964	1872.0014	936.5043	V	520.3242	260.6657	503.2976	252.1525			4
18	1989.0804	995.0438	1972.0538	986.5306	1971.0698	986.0386	V	421.2558	211.1315	404.2292	202.6183			3
19	2136.1488	1068.5780	2119.1223	1060.0648	2118.1382	1059.5728	F	322.1874	161.5973	305.1608	153.0840			2
20							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 43 ppm



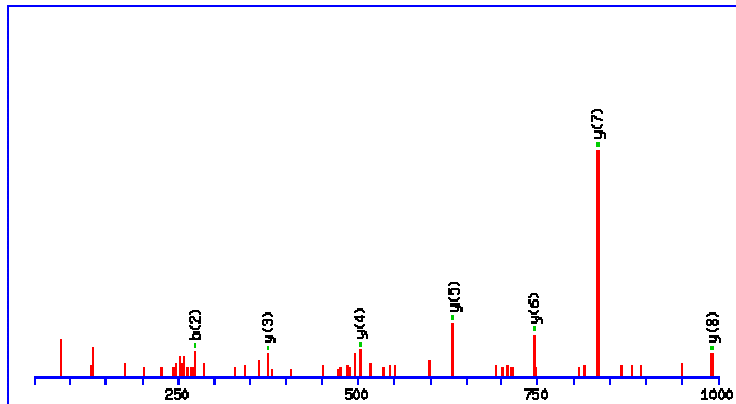
RMS error 43 ppm

Peptide Number: 79895MS/MS Fragmentation of **LCSLEEAQR**Found in **IPI00909164** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CARD17 cDNA FLJ58540, highly similar to Caspase-1

Match to Query 14274: 1104.522928 from(553.268740,2+) index(20820)

Title: Elution from: 85.1166666666667 to 85.1166666666667 period: 0 cycle: 7433 experiment: 8 polarity:+

Data file 120208ry_Tig120slc-P8_2_1.mgf



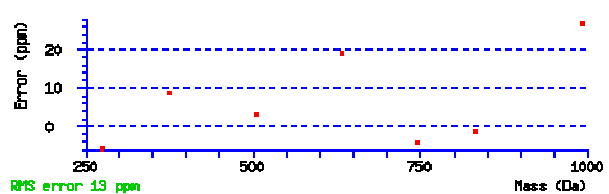
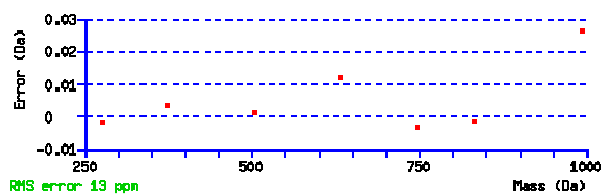
Monoisotopic mass of neutral peptide Mr(calc): 1104.5233

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 49 Expect: 0.00061

Matches : 7/72 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							9
2	274.1220	137.5646					C	992.4466	496.7269	975.4200	488.2136	974.4360	487.7216	8
3	361.1540	181.0806			343.1435	172.0754	S	832.4159	416.7116	815.3894	408.1983	814.4054	407.7063	7
4	474.2381	237.6227			456.2275	228.6174	L	745.3839	373.1956	728.3573	364.6823	727.3733	364.1903	6
5	603.2807	302.1440			585.2701	293.1387	E	632.2998	316.6536	615.2733	308.1403	614.2893	307.6483	5
6	732.3233	366.6653			714.3127	357.6600	E	503.2572	252.1323	486.2307	243.6190	485.2467	243.1270	4
7	803.3604	402.1838			785.3498	393.1785	A	374.2146	187.6110	357.1881	179.0977			3
8	931.4190	466.2131	914.3924	457.6998	913.4084	457.2078	Q	303.1775	152.0924	286.1510	143.5791			2
9							R	175.1190	88.0631	158.0924	79.5498			1



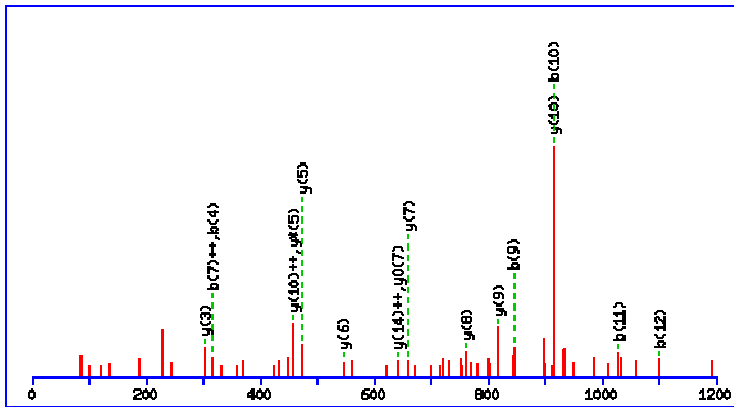
Peptide Number: 80707

MS/MS Fragmentation of **GSGDVCGVLALAPGTNAGDGAR**Found in **IPI00103059** in **IPI_human**, Tax_Id=9606 Gene_Symbol=NAT14 N-acetyltransferase 14

Match to Query 41133: 2013.968052 from(672.329960,3+) index(47977)

Title: Elution from: 114.183333333333 to 114.183333333333 period: 0 cycle: 4329 experiment: 7 polarity:+

Data file 120208ry_Tig120slc-P8_2_2.mgf



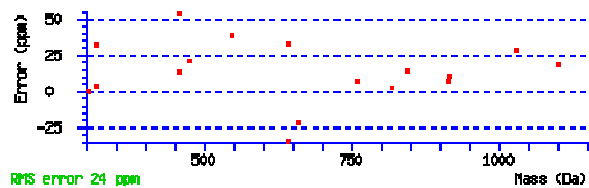
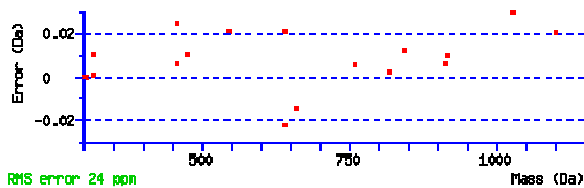
Monoisotopic mass of neutral peptide Mr(calc): 2013.9538

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 49 Expect: 0.00066

Matches : 17/214 fragment ions using 22 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							22
2	145.0608	73.0340			127.0502	64.0287	S	1957.9396	979.4734	1940.9131	970.9602	1939.9291	970.4682	21
3	202.0822	101.5448			184.0717	92.5395	G	1870.9076	935.9574	1853.8810	927.4442	1852.8970	926.9521	20
4	317.1092	159.0582			299.0986	150.0529	D	1813.8861	907.4467	1796.8596	898.9334	1795.8756	898.4414	19
5	416.1776	208.5924			398.1670	199.5872	V	1698.8592	849.9332	1681.8326	841.4200	1680.8486	840.9279	18
6	576.2082	288.6078			558.1977	279.6025	C	1599.7908	800.3990	1582.7642	791.8857	1581.7802	791.3937	17
7	633.2297	317.1185			615.2191	308.1132	G	1439.7601	720.3837	1422.7336	711.8704	1421.7496	711.3784	16
8	732.2981	366.6527			714.2876	357.6474	V	1382.7387	691.8730	1365.7121	683.3597	1364.7281	682.8677	15
9	845.3822	423.1947			827.3716	414.1894	L	1283.6702	642.3388	1266.6437	633.8255	1265.6597	633.3335	14
10	916.4193	458.7133			898.4087	449.7080	A	1170.5862	585.7967	1153.5596	577.2835	1152.5756	576.7914	13
11	1029.5034	515.2553			1011.4928	506.2500	L	1099.5491	550.2782	1082.5225	541.7649	1081.5385	541.2729	12
12	1100.5405	550.7739			1082.5299	541.7686	A	986.4650	493.7361	969.4384	485.2229	968.4544	484.7309	11
13	1197.5932	599.3003			1179.5827	590.2950	P	915.4279	458.2176	898.4013	449.7043	897.4173	449.2123	10
14	1254.6147	627.8110			1236.6041	618.8057	G	818.3751	409.6912	801.3486	401.1779	800.3646	400.6859	9
15	1355.6624	678.3348			1337.6518	669.3295	T	761.3537	381.1805	744.3271	372.6672	743.3431	372.1752	8
16	1469.7053	735.3563	1452.6788	726.8430	1451.6947	726.3510	N	660.3060	330.6566	643.2794	322.1434	642.2954	321.6513	7
17	1540.7424	770.8748	1523.7159	762.3616	1522.7319	761.8696	A	546.2631	273.6352	529.2365	265.1219	528.2525	264.6299	6
18	1597.7639	799.3856	1580.7373	790.8723	1579.7533	790.3803	G	475.2259	238.1166	458.1994	229.6033	457.2154	229.1113	5
19	1712.7908	856.8991	1695.7643	848.3858	1694.7803	847.8938	D	418.2045	209.6059	401.1779	201.0926	400.1939	200.6006	4
20	1769.8123	885.4098	1752.7857	876.8965	1751.8017	876.4045	G	303.1775	152.0924	286.1510	143.5791			3
21	1840.8494	920.9283	1823.8229	912.4151	1822.8388	911.9231	A	246.1561	123.5817	229.1295	115.0684			2
22							R	175.1190	88.0631	158.0924	79.5498			1

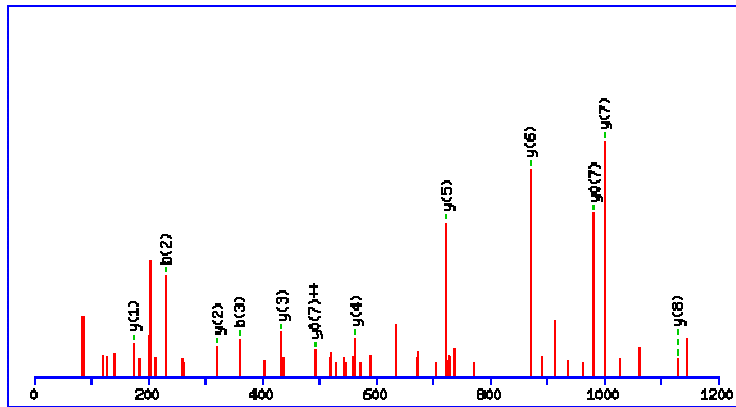


Peptide Number: 80806MS/MS Fragmentation of **TEEFCEIFR**Found in **IPI00300273** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CaMKV Isoform 2 of CaM kinase-like vesicle-associated protein

Match to Query 4518: 1229.527668 from(615.771110,2+) index(5074)

Title: Elution from: 12.5833333333333 to 12.5833333333333 period: 0 cycle: 475 experiment: 4 polarity: +

Data file 120210ry_32R1-32_3_3.mgf



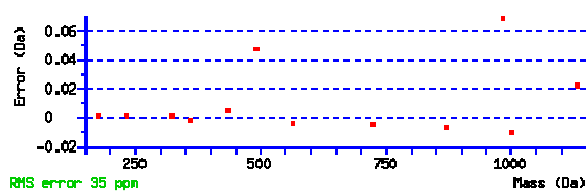
Monoisotopic mass of neutral peptide Mr(calc): 1229.5387

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

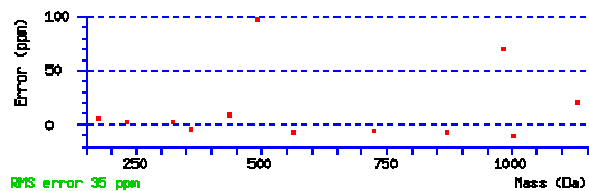
Ions Score: 58 Expect: 2.4e-005

Matches : 12/74 fragment ions using 21 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311	84.0444	42.5258	T							9
2	231.0975	116.0524	213.0870	107.0471	E	1129.4983	565.2528	1112.4717	556.7395	1111.4877	556.2475	8
3	360.1401	180.5737	342.1296	171.5684	E	1000.4557	500.7315	983.4291	492.2182	982.4451	491.7262	7
4	507.2086	254.1079	489.1980	245.1026	F	871.4131	436.2102	854.3865	427.6969	853.4025	427.2049	6
5	667.2392	334.1232	649.2286	325.1180	C	724.3447	362.6760	707.3181	354.1627	706.3341	353.6707	5
6	796.2818	398.6445	778.2712	389.6393	E	564.3140	282.6606	547.2875	274.1474	546.3035	273.6554	4
7	909.3659	455.1866	891.3553	446.1813	I	435.2714	218.1394	418.2449	209.6261			3
8	1056.4343	528.7208	1038.4237	519.7155	F	322.1874	161.5973	305.1608	153.0840			2
9					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 35 ppm



RMS error 35 ppm

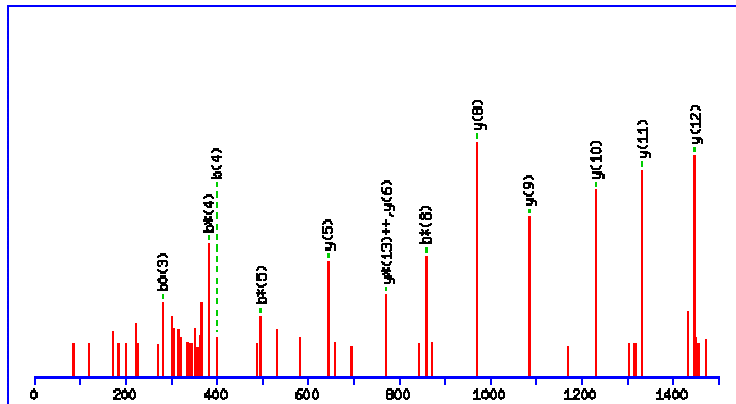
Peptide Number: 81094

MS/MS Fragmentation of **QATVLDFTLTPERPQED**Found in **IPI00031533** in **IPI_human**, Tax_Id=9606 Gene_Symbol=DBNDD1 Isoform 2 of Dysbindin domain-containing protein 1

Match to Query 27089: 1960.980788 from(981.497670,2+) index(38031)

Title: Elution from: 90.8666666666667 to 90.8666666666667 period: 0 cycle: 3421 experiment: 10 polarity: +

Data file 120214ry_32R1-32_4_3.mgf



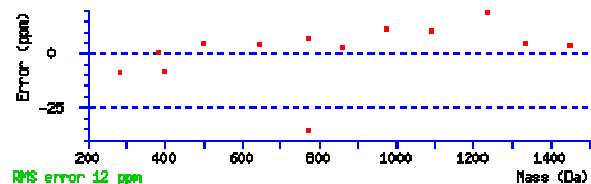
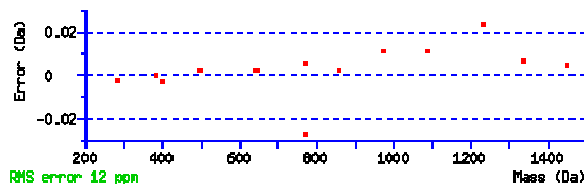
Monoisotopic mass of neutral peptide Mr(calc): 1960.9742

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 61 Expect: 5.8e-005

Matches : 13/184 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	129.0659	65.0366	112.0393	56.5233			Q							17
2	200.1030	100.5551	183.0764	92.0418			A	1833.9229	917.4651	1816.8963	908.9518	1815.9123	908.4598	16
3	301.1506	151.0790	284.1241	142.5657	283.1401	142.0737	T	1762.8858	881.9465	1745.8592	873.4333	1744.8752	872.9412	15
4	400.2191	200.6132	383.1925	192.0999	382.2085	191.6079	V	1661.8381	831.4227	1644.8115	822.9094	1643.8275	822.4174	14
5	513.3031	257.1552	496.2766	248.6419	495.2926	248.1499	L	1562.7697	781.8885	1545.7431	773.3752	1544.7591	772.8832	13
6	628.3301	314.6687	611.3035	306.1554	610.3195	305.6634	D	1449.6856	725.3464	1432.6591	716.8332	1431.6751	716.3412	12
7	729.3777	365.1925	712.3512	356.6792	711.3672	356.1872	T	1334.6587	667.8330	1317.6321	659.3197	1316.6481	658.8277	11
8	876.4462	438.7267	859.4196	430.2134	858.4356	429.7214	F	1233.6110	617.3091	1216.5844	608.7959	1215.6004	608.3039	10
9	989.5302	495.2688	972.5037	486.7555	971.5197	486.2635	L	1086.5426	543.7749	1069.5160	535.2617	1068.5320	534.7696	9
10	1090.5779	545.7926	1073.5514	537.2793	1072.5673	536.7873	T	973.4585	487.2329	956.4320	478.7196	955.4480	478.2276	8
11	1189.6463	595.3268	1172.6198	586.8135	1171.6358	586.3215	V	872.4108	436.7091	855.3843	428.1958	854.4003	427.7038	7
12	1318.6889	659.8481	1301.6624	651.3348	1300.6783	650.8428	E	773.3424	387.1748	756.3159	378.6616	755.3319	378.1696	6
13	1474.7900	737.8986	1457.7635	729.3854	1456.7795	728.8934	R	644.2998	322.6536	627.2733	314.1403	626.2893	313.6483	5
14	1571.8428	786.4250	1554.8162	777.9118	1553.8322	777.4197	P	488.1987	244.6030	471.1722	236.0897	470.1882	235.5977	4
15	1699.9014	850.4543	1682.8748	841.9410	1681.8908	841.4490	Q	391.1460	196.0766	374.1194	187.5633	373.1354	187.0713	3
16	1828.9440	914.9756	1811.9174	906.4623	1810.9334	905.9703	E	263.0874	132.0473			245.0768	123.0420	2
17							D	134.0448	67.5260			116.0342	58.5207	1



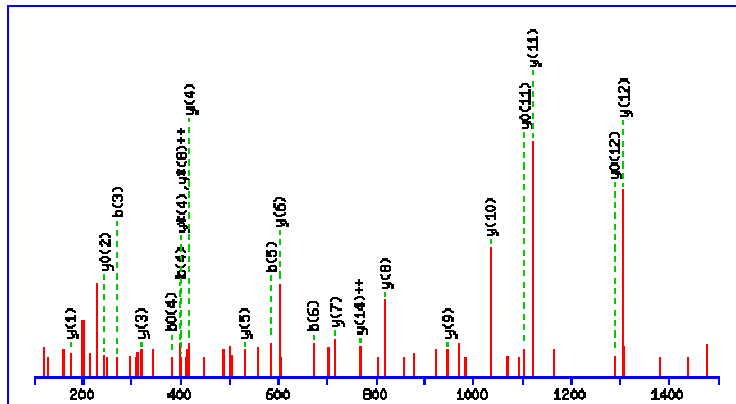
Peptide Number: 81297

MS/MS Fragmentation of **GDPEWSSETDALVGSR**Found in **IPI00334453** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TMEM179B Transmembrane protein 179B

Match to Query 32032: 1704.768708 from(853.391630,2+) index(40413)

Title: Elution from: 105.35 to 105.35 period: 0 cycle: 4039 experiment: 9 polarity: +

Data file 120208ry_Tig120slc-P8_1_2.mgf



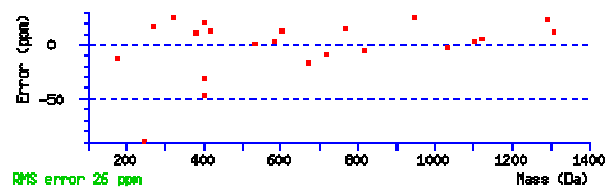
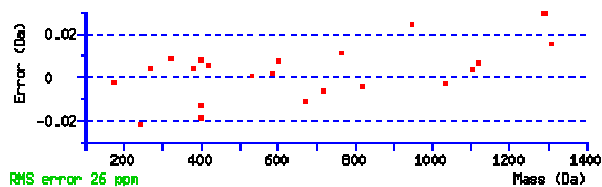
Monoisotopic mass of neutral peptide Mr(calc): 1704.7591

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 55 Expect: 8.1e-005

Matches : 22/146 fragment ions using 53 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180			G							16
2	173.0557	87.0315	155.0451	78.0262	D	1648.7449	824.8761	1631.7184	816.3628	1630.7344	815.8708	15
3	270.1084	135.5579	252.0979	126.5526	P	1533.7180	767.3626	1516.6914	758.8494	1515.7074	758.3573	14
4	399.1510	200.0792	381.1405	191.0739	E	1436.6652	718.8362	1419.6387	710.3230	1418.6546	709.8310	13
5	585.2304	293.1188	567.2198	284.1135	W	1307.6226	654.3149	1290.5961	645.8017	1289.6121	645.3097	12
6	672.2624	336.6348	654.2518	327.6295	S	1121.5433	561.2753	1104.5168	552.7620	1103.5327	552.2700	11
7	759.2944	380.1508	741.2838	371.1456	S	1034.5113	517.7593	1017.4847	509.2460	1016.5007	508.7540	10
8	888.3370	444.6721	870.3264	435.6669	E	947.4793	474.2433	930.4527	465.7300	929.4687	465.2380	9
9	989.3847	495.1960	971.3741	486.1907	T	818.4367	409.7220	801.4101	401.2087	800.4261	400.7167	8
10	1104.4116	552.7095	1086.4011	543.7042	D	717.3890	359.1981	700.3624	350.6849	699.3784	350.1928	7
11	1175.4487	588.2280	1157.4382	579.2227	A	602.3620	301.6847	585.3355	293.1714	584.3515	292.6794	6
12	1288.5328	644.7700	1270.5222	635.7648	L	531.3249	266.1661	514.2984	257.6528	513.3144	257.1608	5
13	1387.6012	694.3042	1369.5907	685.2990	V	418.2409	209.6241	401.2143	201.1108	400.2303	200.6188	4
14	1444.6227	722.8150	1426.6121	713.8097	G	319.1724	160.0899	302.1459	151.5766	301.1619	151.0846	3
15	1531.6547	766.3310	1513.6441	757.3257	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
16					R	175.1190	88.0631	158.0924	79.5498			1

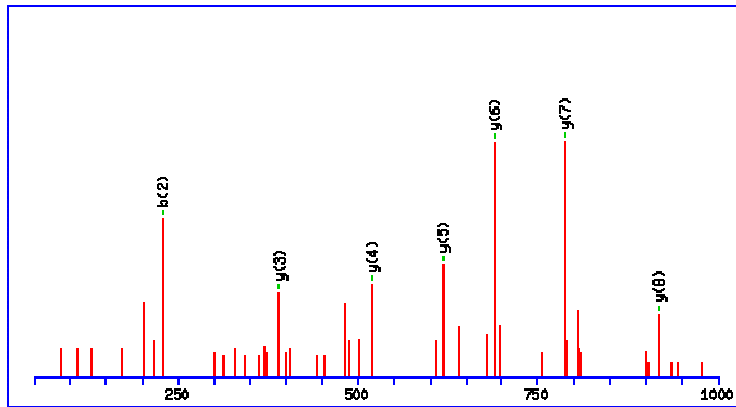


Peptide Number: 81513MS/MS Fragmentation of **VEVAVESQR**Found in **IPI00549666** in **IPI_human**, Tax_Id=9606 Gene_Symbol=GRPEL2 GrpE protein homolog 2, mitochondrial

Match to Query 11782: 1015.527768 from(508.771160,2+) index(12552)

Title: Elution from: 71.7833333333333 to 71.7833333333333 period: 0 cycle: 8004 experiment: 9 polarity: +

Data file 120210ry_32R1-32_3_1.mgf



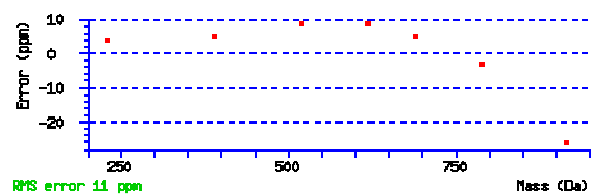
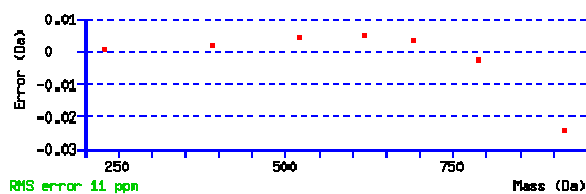
Monoisotopic mass of neutral peptide Mr(calc): 1015.5298

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 53 Expect: 0.00037

Matches : 7/76 fragment ions using 9 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							9
2	229.1183	115.0628			211.1077	106.0575	E	917.4687	459.2380	900.4421	450.7247	899.4581	450.2327	8
3	328.1867	164.5970			310.1761	155.5917	V	788.4261	394.7167	771.3995	386.2034	770.4155	385.7114	7
4	399.2238	200.1155			381.2132	191.1103	A	689.3577	345.1825	672.3311	336.6692	671.3471	336.1772	6
5	498.2922	249.6498			480.2817	240.6445	V	618.3206	309.6639	601.2940	301.1506	600.3100	300.6586	5
6	627.3348	314.1710			609.3243	305.1658	E	519.2522	260.1297	502.2256	251.6164	501.2416	251.1244	4
7	714.3668	357.6871			696.3563	348.6818	S	390.2096	195.6084	373.1830	187.0951	372.1990	186.6031	3
8	842.4254	421.7164	825.3989	413.2031	824.4149	412.7111	Q	303.1775	152.0924	286.1510	143.5791			2
9							R	175.1190	88.0631	158.0924	79.5498			1



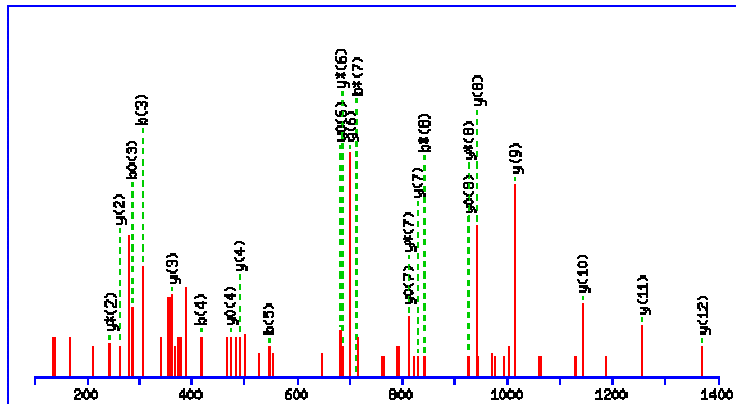
Peptide Number: 81805

MS/MS Fragmentation of **TSDIEANQPLETNK**Found in **IPI00401151** in **IPI_human**, Tax_Id=9606 Gene_Symbol=LOC729852 cDNA FLJ54628

Match to Query 25748: 1558.749188 from(780.381870,2+) index(21753)

Title: Elution from: 93.2 to 93.2 period: 0 cycle: 8923 experiment: 9 polarity: +

Data file 120206ry_aHDF1419-P10_3_1.mgf



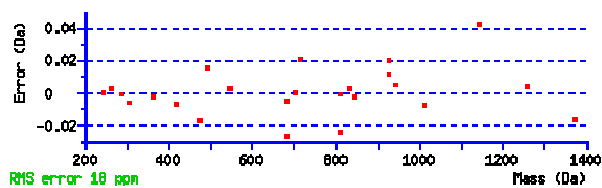
Monoisotopic mass of neutral peptide Mr(calc): 1558.7475

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

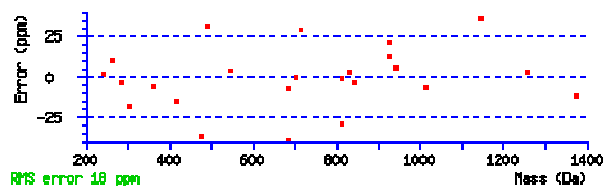
Ions Score: 63 Expect: 2.4e-005

Matches : 24/140 fragment ions using 45 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							14
2	189.0870	95.0471			171.0764	86.0418	S	1458.7071	729.8572	1441.6805	721.3439	1440.6965	720.8519	13
3	304.1139	152.5606			286.1034	143.5553	D	1371.6751	686.3412	1354.6485	677.8279	1353.6645	677.3359	12
4	417.1980	209.1026			399.1874	200.0974	I	1256.6481	628.8277	1239.6216	620.3144	1238.6375	619.8224	11
5	546.2406	273.6239			528.2300	264.6186	E	1143.5640	572.2857	1126.5375	563.7724	1125.5535	563.2804	10
6	617.2777	309.1425			599.2671	300.1372	A	1014.5215	507.7644	997.4949	499.2511	996.5109	498.7591	9
7	731.3206	366.1640	714.2941	357.6507	713.3101	357.1587	N	943.4843	472.2458	926.4578	463.7325	925.4738	463.2405	8
8	859.3792	430.1932	842.3527	421.6800	841.3686	421.1880	Q	829.4414	415.2243	812.4149	406.7111	811.4308	406.2191	7
9	956.4320	478.7196	939.4054	470.2063	938.4214	469.7143	P	701.3828	351.1951	684.3563	342.6818	683.3723	342.1898	6
10	1069.5160	535.2617	1052.4895	526.7484	1051.5055	526.2564	L	604.3301	302.6687	587.3035	294.1554	586.3195	293.6634	5
11	1198.5586	599.7829	1181.5321	591.2697	1180.5481	590.7777	E	491.2460	246.1266	474.2195	237.6134	473.2354	237.1214	4
12	1299.6063	650.3068	1282.5798	641.7935	1281.5957	641.3015	T	362.2034	181.6053	345.1769	173.0921	344.1928	172.6001	3
13	1413.6492	707.3283	1396.6227	698.8150	1395.6387	698.3230	N	261.1557	131.0815	244.1292	122.5682			2
14							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 18 ppm



RMS error 18 ppm

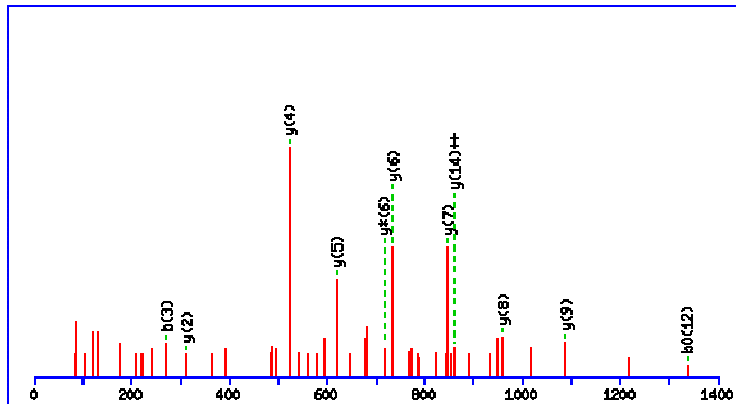
Peptide Number: 81952

MS/MS Fragmentation of **GVNLFQEILVPIHR**Found in **IPI00307683** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SENP2 cDNA FLJ54905, highly similar to Sentrin-specific protease 2

Match to Query 30470: 1876.045272 from(626.355700,3+) index(46150)

Title: Elution from: 115.65 to 115.65 period: 0 cycle: 4306 experiment: 3 polarity:+

Data file 120126ry_585A1-55_2_3.mgf



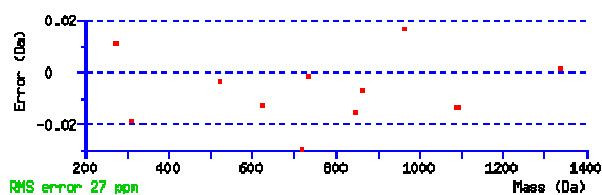
Monoisotopic mass of neutral peptide Mr(calc): 1876.0571

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

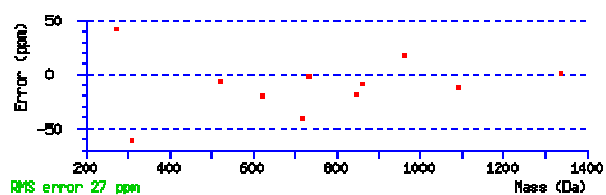
Ions Score: 36 Expect: 0.0072

Matches : 11/150 fragment ions using 22 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							16
2	157.0972	79.0522					V	1820.0429	910.5251	1803.0163	902.0118	1802.0323	901.5198	15
3	271.1401	136.0737	254.1135	127.5604			N	1720.9745	860.9909	1703.9479	852.4776	1702.9639	851.9856	14
4	384.2241	192.6157	367.1976	184.1024			L	1606.9315	803.9694	1589.9050	795.4561	1588.9210	794.9641	13
5	531.2926	266.1499	514.2660	257.6366			F	1493.8475	747.4274	1476.8209	738.9141	1475.8369	738.4221	12
6	660.3352	330.6712	643.3086	322.1579	642.3246	321.6659	E	1346.7791	673.8932	1329.7525	665.3799	1328.7685	664.8879	11
7	788.3937	394.7005	771.3672	386.1872	770.3832	385.6952	Q	1217.7365	609.3719	1200.7099	600.8586	1199.7259	600.3666	10
8	917.4363	459.2218	900.4098	450.7085	899.4258	450.2165	E	1089.6779	545.3426	1072.6513	536.8293	1071.6673	536.3373	9
9	1030.5204	515.7638	1013.4938	507.2506	1012.5098	506.7585	I	960.6353	480.8213	943.6087	472.3080			8
10	1143.6045	572.3059	1126.5779	563.7926	1125.5939	563.3006	I	847.5512	424.2793	830.5247	415.7660			7
11	1256.6885	628.8479	1239.6620	620.3346	1238.6779	619.8426	L	734.4672	367.7372	717.4406	359.2239			6
12	1355.7569	678.3821	1338.7304	669.8688	1337.7464	669.3768	V	621.3831	311.1952	604.3566	302.6819			5
13	1452.8097	726.9085	1435.7831	718.3952	1434.7991	717.9032	P	522.3147	261.6610	505.2881	253.1477			4
14	1565.8938	783.4505	1548.8672	774.9372	1547.8832	774.4452	I	425.2619	213.1346	408.2354	204.6213			3
15	1702.9527	851.9800	1685.9261	843.4667	1684.9421	842.9747	H	312.1779	156.5926	295.1513	148.0793			2
16							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 27 ppm



RMS error 27 ppm

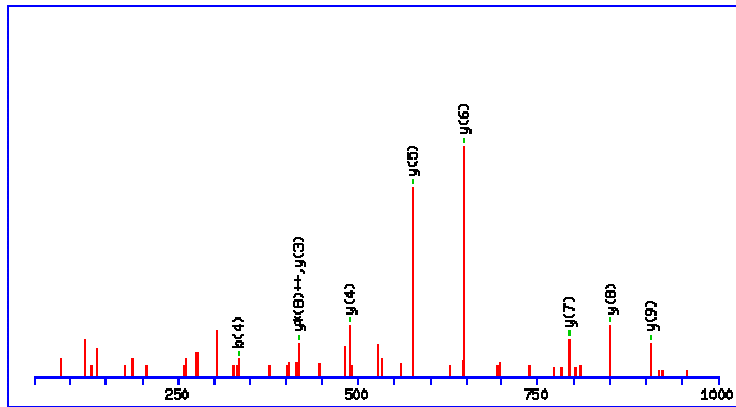
Peptide Number: 82801**MS/MS Fragmentation of AGGFASALER**

Found in **IPI00022276** in **IPI_human**, Tax_Id=9606 Gene_Symbol=MRPS28 28S ribosomal protein S28, mitochondrial

Match to Query 9639: 977.487468 from(489.751010,2+) index(15680)

Title: Elution from: 37.6333333333333 to 37.6333333333333 period: 0 cycle: 1404 experiment: 6 polarity: +

Data file 120126ry_585A1-55_2_2.mgf



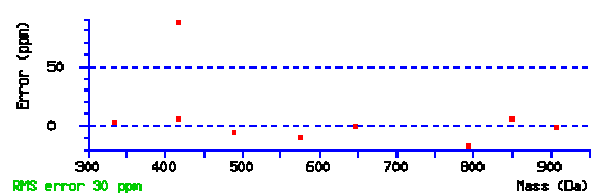
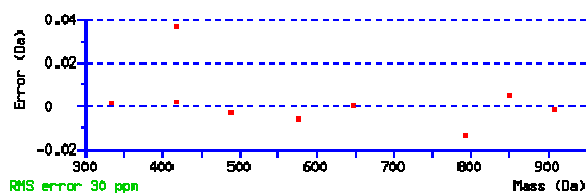
Monoisotopic mass of neutral peptide Mr(calcd): 977.4930

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 49 **Expect:** 0.0009

Matches: 9/78 fragment ions using 18 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258			A							10
2	129.0659	65.0366			G	907.4632	454.2352	890.4367	445.7220	889.4526	445.2300	9
3	186.0873	93.5473			G	850.4417	425.7245	833.4152	417.2112	832.4312	416.7192	8
4	333.1557	167.0815			F	793.4203	397.2138	776.3937	388.7005	775.4097	388.2085	7
5	404.1928	202.6001			A	646.3519	323.6796	629.3253	315.1663	628.3413	314.6743	6
6	491.2249	246.1161	473.2143	237.1108	S	575.3148	288.1610	558.2882	279.6477	557.3042	279.1557	5
7	562.2620	281.6346	544.2514	272.6293	A	488.2827	244.6450	471.2562	236.1317	470.2722	235.6397	4
8	675.3461	338.1767	657.3355	329.1714	L	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
9	804.3886	402.6980	786.3781	393.6927	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
10					R	175.1190	88.0631	158.0924	79.5498			1



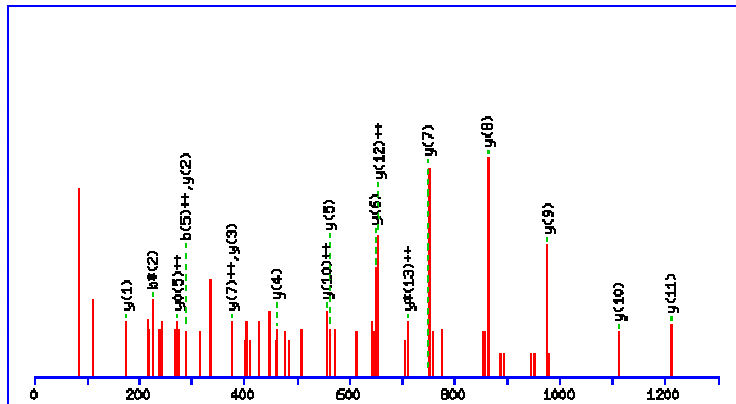
Peptide Number: 82900

MS/MS Fragmentation of **IQPVHILTSVSSLR**Found in **IPI00171252** in **IPI_human**, Tax_Id=9606 Gene_Symbol=EZH2 Isoform 3 of Histone-lysine N-methyltransferase EZH2

Match to Query 18537: 1548.893562 from(517.305130,3+) index(3087)

Title: Elution from: 7.36666666666667 to 7.36666666666667 period: 0 cycle: 274 experiment: 4 polarity:+

Data file 120126ry_585A1-55_1_3.mgf



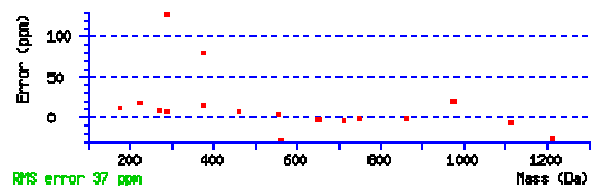
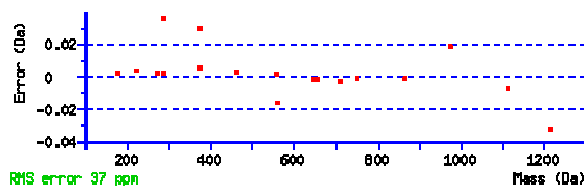
Monoisotopic mass of neutral peptide Mr(calcd): 1548.8988

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 67 Expect: 5e-006

Matches : 18/136 fragment ions using 37 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							14
2	242.1499	121.5786	225.1234	113.0653			Q	1436.8220	718.9146	1419.7954	710.4014	1418.8114	709.9094	13
3	339.2027	170.1050	322.1761	161.5917			P	1308.7634	654.8853	1291.7369	646.3721	1290.7528	645.8801	12
4	438.2711	219.6392	421.2445	211.1259			V	1211.7106	606.3590	1194.6841	597.8457	1193.7001	597.3537	11
5	575.3300	288.1686	558.3035	279.6554			H	1112.6422	556.8248	1095.6157	548.3115	1094.6317	547.8195	10
6	688.4141	344.7107	671.3875	336.1974			I	975.5833	488.2953	958.5568	479.7820	957.5728	479.2900	9
7	801.4981	401.2527	784.4716	392.7394			L	862.4993	431.7533	845.4727	423.2400	844.4887	422.7480	8
8	902.5458	451.7765	885.5193	443.2633	884.5353	442.7713	T	749.4152	375.2112	732.3886	366.6980	731.4046	366.2060	7
9	989.5778	495.2926	972.5513	486.7793	971.5673	486.2873	S	648.3675	324.6874	631.3410	316.1741	630.3569	315.6821	6
10	1088.6463	544.8268	1071.6197	536.3135	1070.6357	535.8215	V	561.3355	281.1714	544.3089	272.6581	543.3249	272.1661	5
11	1175.6783	588.3428	1158.6517	579.8295	1157.6677	579.3375	S	462.2671	231.6372	445.2405	223.1239	444.2565	222.6319	4
12	1262.7103	631.8588	1245.6838	623.3455	1244.6997	622.8535	S	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
13	1375.7944	688.4008	1358.7678	679.8876	1357.7838	679.3955	L	288.2030	144.6051	271.1765	136.0919			2
14							R	175.1190	88.0631	158.0924	79.5498			1



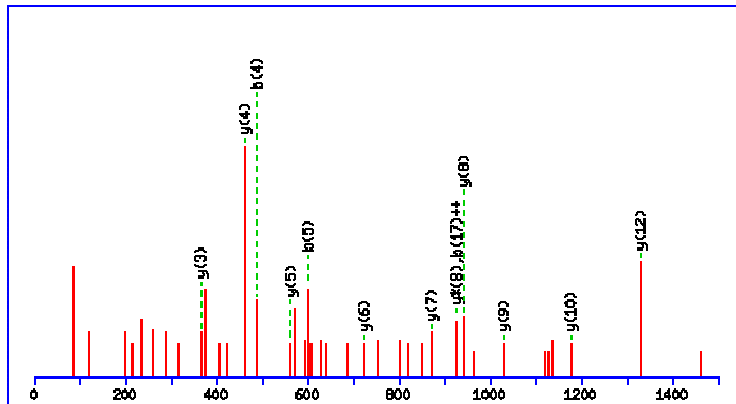
Peptide Number: 82913

MS/MS Fragmentation of **LLIIFIIPGNPGFSAFYVPFAK**Found in **IPI00030257** in **IPI_human**, Tax_Id=9606 Gene_Symbol=C2orf43 UPF0554 protein C2orf43

Match to Query 4919: 2310.268242 from(771.096690,3+) index(2810)

Title: Elution from: 8.38333333333333 to 8.38333333333333 period: 0 cycle: 346 experiment: 4 polarity: +

Data file 120201ry_aHDF1388-P9_1_5.mgf



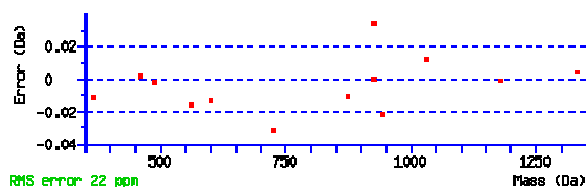
Monoisotopic mass of neutral peptide Mr(calc): 2310.2816

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

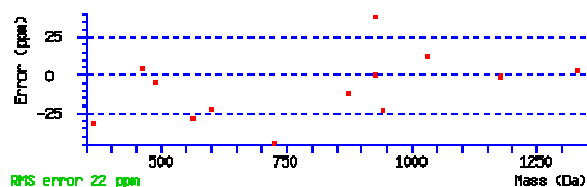
Ions Score: 38 Expect: 0.0047

Matches : 13/184 fragment ions using 32 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							21
2	227.1754	114.0913					L	2198.2049	1099.6061	2181.1783	1091.0928	2180.1943	1090.6008	20
3	340.2595	170.6334					I	2085.1208	1043.0640	2068.0942	1034.5508	2067.1102	1034.0588	19
4	487.3279	244.1676					F	1972.0367	986.5220	1955.0102	978.0087	1954.0262	977.5167	18
5	600.4119	300.7096					I	1824.9683	912.9878	1807.9418	904.4745	1806.9578	903.9825	17
6	713.4960	357.2516					I	1711.8843	856.4458	1694.8577	847.9325	1693.8737	847.4405	16
7	810.5488	405.7780					P	1598.8002	799.9037	1581.7736	791.3905	1580.7896	790.8985	15
8	867.5702	434.2888					G	1501.7474	751.3774	1484.7209	742.8641	1483.7369	742.3721	14
9	981.6132	491.3102	964.5866	482.7969			N	1444.7260	722.8666	1427.6994	714.3533	1426.7154	713.8613	13
10	1078.6659	539.8366	1061.6394	531.3233			P	1330.6830	665.8452	1313.6565	657.3319	1312.6725	656.8399	12
11	1135.6874	568.3473	1118.6608	559.8341			G	1233.6303	617.3188	1216.6037	608.8055	1215.6197	608.3135	11
12	1282.7558	641.8815	1265.7293	633.3683			F	1176.6088	588.8080	1159.5823	580.2948	1158.5982	579.8028	10
13	1369.7878	685.3976	1352.7613	676.8843	1351.7773	676.3923	S	1029.5404	515.2738	1012.5138	506.7606	1011.5298	506.2686	9
14	1440.8249	720.9161	1423.7984	712.4028	1422.8144	711.9108	A	942.5084	471.7578	925.4818	463.2445			8
15	1587.8934	794.4503	1570.8668	785.9370	1569.8828	785.4450	F	871.4713	436.2393	854.4447	427.7260			7
16	1750.9567	875.9820	1733.9301	867.4687	1732.9461	866.9767	Y	724.4028	362.7051	707.3763	354.1918			6
17	1850.0251	925.5162	1832.9986	917.0029	1832.0145	916.5109	V	561.3395	281.1734	544.3130	272.6601			5
18	1947.0779	974.0426	1930.0513	965.5293	1929.0673	965.0373	P	462.2711	231.6392	445.2445	223.1259			4
19	2094.1463	1047.5768	2077.1197	1039.0635	2076.1357	1038.5715	F	365.2183	183.1128	348.1918	174.5995			3
20	2165.1834	1083.0953	2148.1568	1074.5821	2147.1728	1074.0901	A	218.1499	109.5786	201.1234	101.0653			2
21							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 22 ppm



RMS error 22 ppm

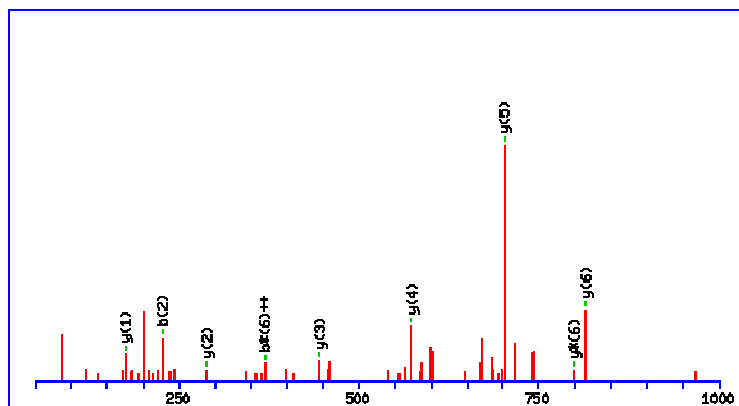
Peptide Number: 83342

MS/MS Fragmentation of **LLEERLR**Found in **IPI00010067** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SRPK3 Uncharacterized protein

Match to Query 4630: 927.533488 from(464.774020,2+) index(14809)

Title: Elution from: 35.4666666666667 to 35.4666666666667 period: 0 cycle: 1315 experiment: 4 polarity:+

Data file 120129ry_604A1-46_2_2.mgf



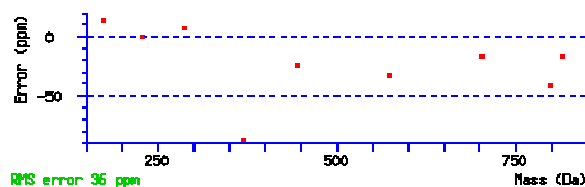
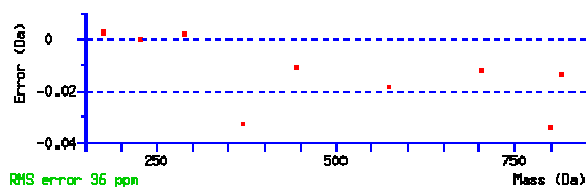
Monoisotopic mass of neutral peptide Mr(calcd): 927.5501

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 42 Expect: 0.0038

Matches : 9/54 fragment ions using 16 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							7
2	227.1754	114.0913					L	815.4734	408.2403	798.4468	399.7271	797.4628	399.2350	6
3	356.2180	178.6126			338.2074	169.6074	E	702.3893	351.6983	685.3628	343.1850	684.3787	342.6930	5
4	485.2606	243.1339			467.2500	234.1287	E	573.3467	287.1770	556.3202	278.6637	555.3362	278.1717	4
5	641.3617	321.1845	624.3352	312.6712	623.3511	312.1792	R	444.3041	222.6557	427.2776	214.1424			3
6	754.4458	377.7265	737.4192	369.2132	736.4352	368.7212	L	288.2030	144.6051	271.1765	136.0919			2
7							R	175.1190	88.0631	158.0924	79.5498			1

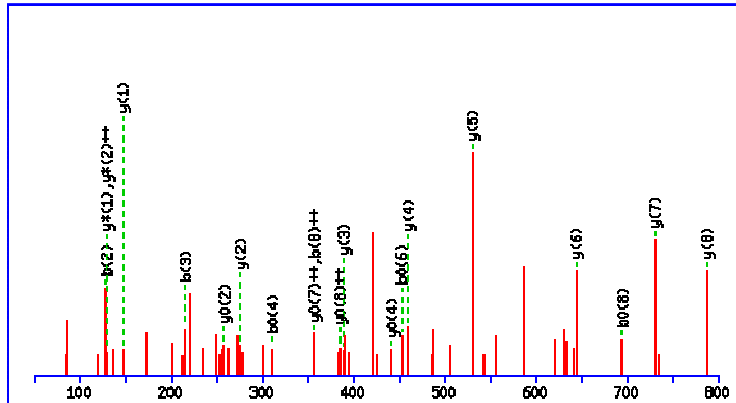


Peptide Number: 83491MS/MS Fragmentation of **AGSLAALEK**Found in **IPI00893850** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SMTN cDNA FLJ35365 fis, clone SKMUS2000873, highly similar to Smoothelin large isoform L2

Match to Query 5535: 858.480128 from(430.247340,2+) index(25349)

Title: Elution from: 104.666666666667 to 104.666666666667 period: 0 cycle: 9006 experiment: 3 polarity: +

Data file 120214ry_aHDF1419-P10_4_1.mgf



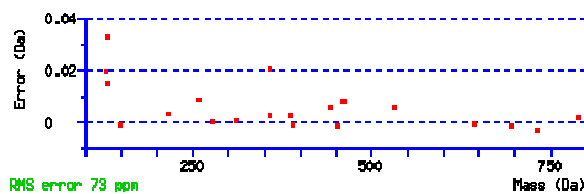
Monoisotopic mass of neutral peptide Mr(calc): 858.4810

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

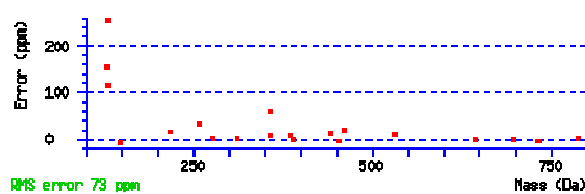
Ions Score: 52 Expect: 0.00074

Matches : 20/74 fragment ions using 41 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258			A							9
2	129.0659	65.0366			G	788.4512	394.7293	771.4247	386.2160	770.4407	385.7240	8
3	216.0979	108.5526	198.0873	99.5473	S	731.4298	366.2185	714.4032	357.7053	713.4192	357.2132	7
4	329.1819	165.0946	311.1714	156.0893	L	644.3978	322.7025	627.3712	314.1892	626.3872	313.6972	6
5	400.2191	200.6132	382.2085	191.6079	A	531.3137	266.1605	514.2871	257.6472	513.3031	257.1552	5
6	471.2562	236.1317	453.2456	227.1264	A	460.2766	230.6419	443.2500	222.1287	442.2660	221.6366	4
7	584.3402	292.6738	566.3297	283.6685	L	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
8	713.3828	357.1951	695.3723	348.1898	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
9					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 73 ppm



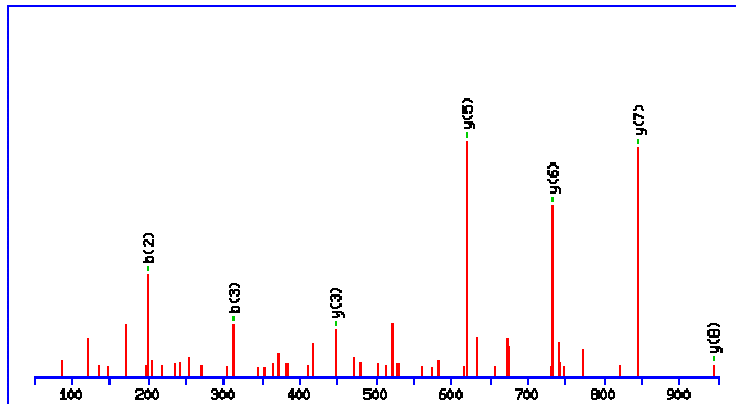
RMS error 73 ppm

Peptide Number: 83644MS/MS Fragmentation of **VVILGDNWK**Found in **IPI00892948** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SEC14L6 Putative SEC14-like protein 6

Match to Query 9062: 1042.598828 from(522.306690,2+) index(9520)

Title: Elution from: 22.4333333333333 to 22.4333333333333 period: 0 cycle: 848 experiment: 5 polarity: +

Data file 120214ry_32R1-32_4_2.mgf



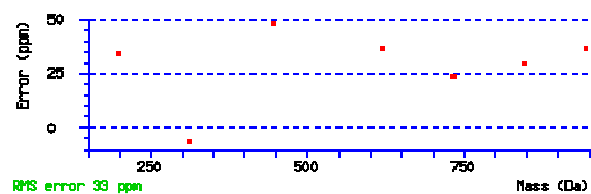
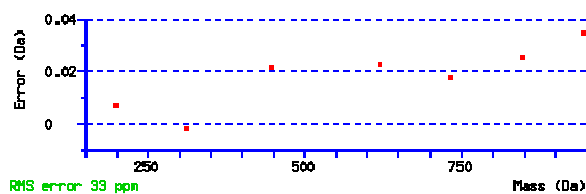
Monoisotopic mass of neutral peptide Mr(calc): 1042.5811

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 42 Expect: 0.0047

Matches : 7/68 fragment ions using 9 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							9
2	199.1441	100.0757					V	944.5200	472.7636	927.4934	464.2504	926.5094	463.7584	8
3	312.2282	156.6177					I	845.4516	423.2294	828.4250	414.7162	827.4410	414.2241	7
4	425.3122	213.1598					L	732.3675	366.6874	715.3410	358.1741	714.3569	357.6821	6
5	482.3337	241.6705					G	619.2835	310.1454	602.2569	301.6321	601.2729	301.1401	5
6	597.3606	299.1840			579.3501	290.1787	D	562.2620	281.6346	545.2354	273.1214	544.2514	272.6293	4
7	711.4036	356.2054	694.3770	347.6921	693.3930	347.2001	N	447.2350	224.1212	430.2085	215.6079			3
8	897.4829	449.2451	880.4563	440.7318	879.4723	440.2398	W	333.1921	167.0997	316.1656	158.5864			2
9							K	147.1128	74.0600	130.0863	65.5468			1



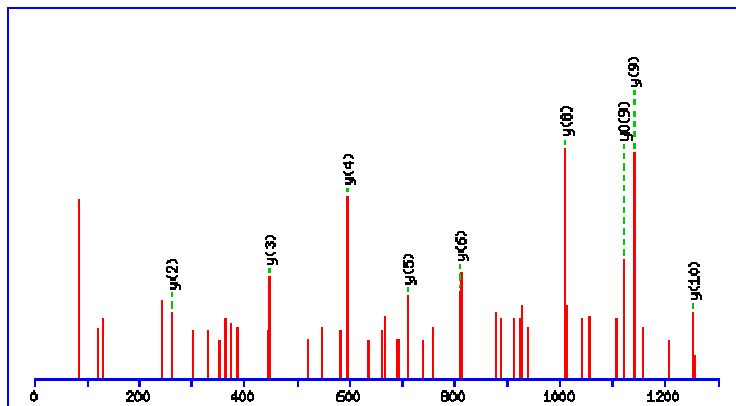
Peptide Number: 83825

MS/MS Fragmentation of **SAIESDVDFWDK**Found in **IPI00032931** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PEX5 Isoform 2 of Peroxisomal targeting signal 1 receptor

Match to Query 9681: 1410.633808 from(706.324180,2+) index(14715)

Title: Elution from: 36.5166666666667 to 36.5166666666667 period: 0 cycle: 1374 experiment: 6 polarity: +

Data file 120210ry_32R1-32_2_3.mgf



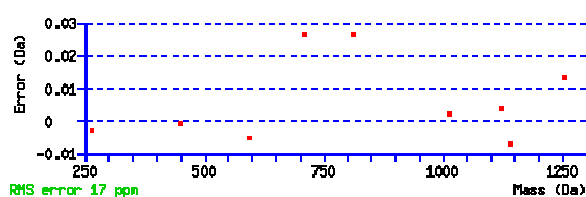
Monoisotopic mass of neutral peptide Mr(calc): 1410.6303

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

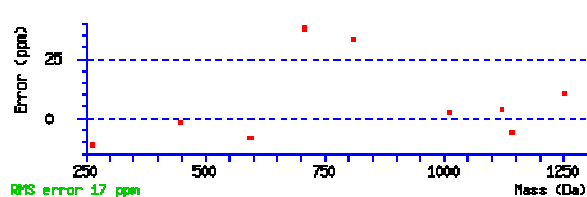
Ions Score: 42 Expect: 0.002

Matches : 9/108 fragment ions using 24 most intense peaks ([help](#))

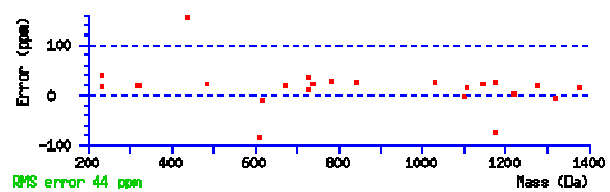
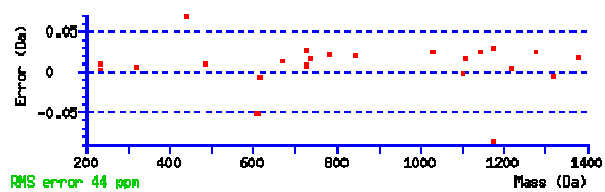
#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233	70.0287	35.5180	S							12
2	159.0764	80.0418	141.0659	71.0366	A	1324.6056	662.8064	1307.5790	654.2932	1306.5950	653.8011	11
3	272.1605	136.5839	254.1499	127.5786	I	1253.5685	627.2879	1236.5419	618.7746	1235.5579	618.2826	10
4	401.2031	201.1052	383.1925	192.0999	E	1140.4844	570.7458	1123.4578	562.2326	1122.4738	561.7406	9
5	488.2351	244.6212	470.2245	235.6159	S	1011.4418	506.2245	994.4153	497.7113	993.4312	497.2193	8
6	603.2620	302.1347	585.2515	293.1294	D	924.4098	462.7085	907.3832	454.1953	906.3992	453.7032	7
7	702.3305	351.6689	684.3199	342.6636	V	809.3828	405.1951	792.3563	396.6818	791.3723	396.1898	6
8	817.3574	409.1823	799.3468	400.1771	D	710.3144	355.6608	693.2879	347.1476	692.3039	346.6556	5
9	964.4258	482.7165	946.4153	473.7113	F	595.2875	298.1474	578.2609	289.6341	577.2769	289.1421	4
10	1150.5051	575.7562	1132.4946	566.7509	W	448.2191	224.6132	431.1925	216.0999	430.2085	215.6079	3
11	1265.5321	633.2697	1247.5215	624.2644	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
12					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 17 ppm



RMS error 17 ppm



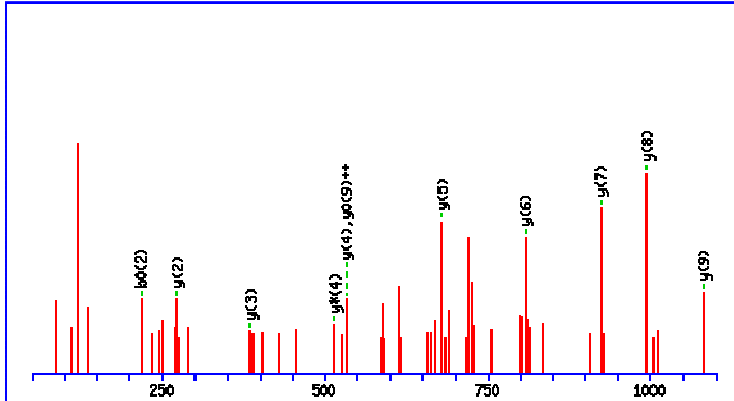
Peptide Number: 83917**MS/MS Fragmentation of FSADEFFIPR**

Found in **IPI00640902** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ZBTB8OS cDNA FLJ75987, highly similar to Homo sapiens zinc finger and BTB domain containing 8 opposite strand (ZBTB8OS), mRNA

Match to Query 4037: 1227.595328 from(614.804940,2+) index(26690)

Title: Elution from: 64.1666666666667 to 64.1666666666667 period: 0 cycle: 2430 experiment: 3 polarity:+

Data file 120208ry_Tig120slc-P8_2_3.mgf



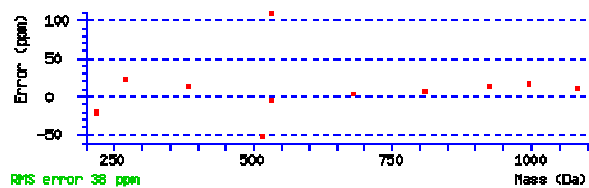
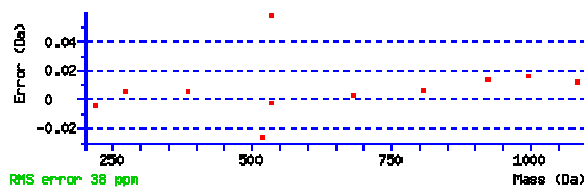
Monoisotopic mass of neutral peptide Mr(calc): 1227.5924

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 49 **Expect:** 0.00057

Matches : 11/78 fragment ions using 20 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415			F							10
2	235.1077	118.0575	217.0972	109.0522	S	1081.5313	541.2693	1064.5047	532.7560	1063.5207	532.2640	9
3	306.1448	153.5761	288.1343	144.5708	A	994.4993	497.7533	977.4727	489.2400	976.4887	488.7480	8
4	421.1718	211.0895	403.1612	202.0842	D	923.4621	462.2347	906.4356	453.7214	905.4516	453.2294	7
5	550.2144	275.6108	532.2038	266.6055	E	808.4352	404.7212	791.4087	396.2080	790.4246	395.7160	6
6	697.2828	349.1450	679.2722	340.1397	F	679.3926	340.1999	662.3661	331.6867			5
7	844.3512	422.6792	826.3406	413.6740	F	532.3242	266.6657	515.2976	258.1525			4
8	957.4353	479.2213	939.4247	470.2160	I	385.2558	193.1315	368.2292	184.6183			3
9	1054.4880	527.7477	1036.4775	518.7424	P	272.1717	136.5895	255.1452	128.0762			2
10					R	175.1190	88.0631	158.0924	79.5498			1



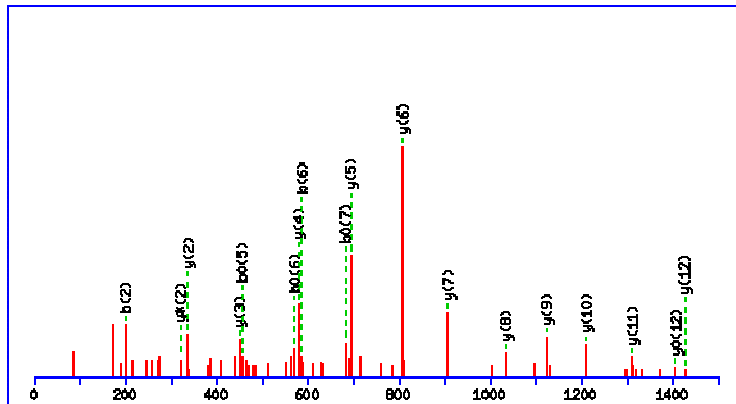
Peptide Number: 84558

MS/MS Fragmentation of **SIATTLIDDTSSSEVLDELYR**Found in **IPI00027627** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TNFAIP8 Isoform 1 of Tumor necrosis factor alpha-induced protein 8

Match to Query 15159: 2240.139012 from(747.720280,3+) index(30521)

Title: Elution from: 98.2833333333333 to 98.2833333333333 period: 0 cycle: 3859 experiment: 3 polarity:+

Data file 120208ry_Tig120slc-P8_1_4.mgf



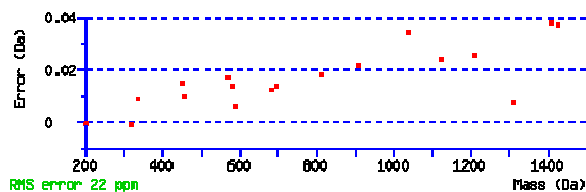
Monoisotopic mass of neutral peptide Mr(calc): 2240.1060

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

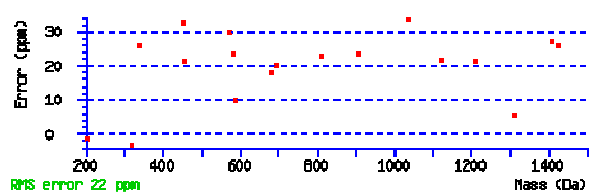
Ions Score: 80 Expect: 6.1e-007

Matches : 18/184 fragment ions using 27 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233	70.0287	35.5180	S							20
2	201.1234	101.0653	183.1128	92.0600	I	2154.0812	1077.5443	2137.0547	1069.0310	2136.0707	1068.5390	19
3	272.1605	136.5839	254.1499	127.5786	A	2040.9972	1021.0022	2023.9706	1012.4889	2022.9866	1011.9969	18
4	373.2082	187.1077	355.1976	178.1024	T	1969.9601	985.4837	1952.9335	976.9704	1951.9495	976.4784	17
5	474.2558	237.6316	456.2453	228.6263	T	1868.9124	934.9598	1851.8858	926.4466	1850.9018	925.9545	16
6	587.3399	294.1736	569.3293	285.1683	L	1767.8647	884.4360	1750.8382	875.9227	1749.8541	875.4307	15
7	700.4240	350.7156	682.4134	341.7103	I	1654.7806	827.8940	1637.7541	819.3807	1636.7701	818.8887	14
8	815.4509	408.2291	797.4403	399.2238	D	1541.6966	771.3519	1524.6700	762.8386	1523.6860	762.3466	13
9	930.4779	465.7426	912.4673	456.7373	D	1426.6696	713.8385	1409.6431	705.3252	1408.6591	704.8332	12
10	1031.5255	516.2664	1013.5150	507.2611	T	1311.6427	656.3250	1294.6161	647.8117	1293.6321	647.3197	11
11	1118.5576	559.7824	1100.5470	550.7771	S	1210.5950	605.8011	1193.5685	597.2879	1192.5844	596.7959	10
12	1205.5896	603.2984	1187.5790	594.2932	S	1123.5630	562.2851	1106.5364	553.7719	1105.5524	553.2798	9
13	1334.6322	667.8197	1316.6216	658.8144	E	1036.5310	518.7691	1019.5044	510.2558	1018.5204	509.7638	8
14	1433.7006	717.3539	1415.6900	708.3487	V	907.4884	454.2478	890.4618	445.7345	889.4778	445.2425	7
15	1546.7847	773.8960	1528.7741	764.8907	L	808.4199	404.7136	791.3934	396.2003	790.4094	395.7083	6
16	1661.8116	831.4094	1643.8010	822.4042	D	695.3359	348.1716	678.3093	339.6583	677.3253	339.1663	5
17	1790.8542	895.9307	1772.8436	886.9255	E	580.3089	290.6581	563.2824	282.1448	562.2984	281.6528	4
18	1903.9383	952.4728	1885.9277	943.4675	L	451.2663	226.1368	434.2398	217.6235			3
19	2067.0016	1034.0044	2048.9910	1024.9991	Y	338.1823	169.5948	321.1557	161.0815			2
20					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 22 ppm



RMS error 22 ppm

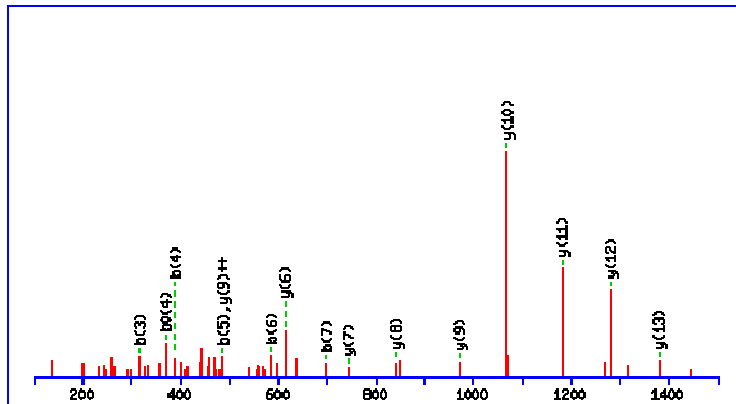
Peptide Number: 84609

MS/MS Fragmentation of **EGEAVVLPEVEPGLTAR**Found in **IPI00002441** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SDC1 Syndecan-1

Match to Query 16692: 1764.923688 from(883.469120,2+) index(3267)

Title: Elution from: 8.68333333333333 to 8.68333333333333 period: 0 cycle: 337 experiment: 9 polarity:+

Data file 120208ry_Tig120slc-P8_1_3.mgf



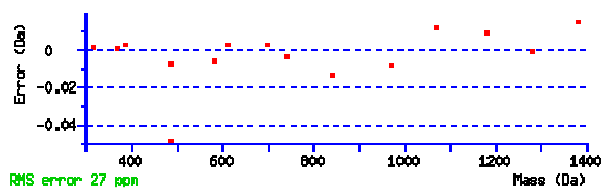
Monoisotopic mass of neutral peptide Mr(calc): 1764.9258

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

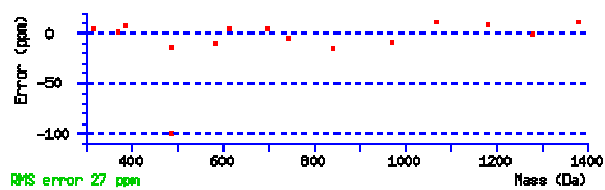
Ions Score: 50 Expect: 0.00071

Matches : 15/156 fragment ions using 24 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286	112.0393	56.5233	E							17
2	187.0713	94.0393	169.0608	85.0340	G	1636.8905	818.9489	1619.8639	810.4356	1618.8799	809.9436	16
3	316.1139	158.5606	298.1034	149.5553	E	1579.8690	790.4381	1562.8425	781.9249	1561.8584	781.4329	15
4	387.1510	194.0792	369.1405	185.0739	A	1450.8264	725.9168	1433.7999	717.4036	1432.8158	716.9116	14
5	486.2195	243.6134	468.2089	234.6081	V	1379.7893	690.3983	1362.7627	681.8850	1361.7787	681.3930	13
6	585.2879	293.1476	567.2773	284.1423	V	1280.7209	640.8641	1263.6943	632.3508	1262.7103	631.8588	12
7	698.3719	349.6896	680.3614	340.6843	L	1181.6525	591.3299	1164.6259	582.8166	1163.6419	582.3246	11
8	795.4247	398.2160	777.4141	389.2107	P	1068.5684	534.7878	1051.5419	526.2746	1050.5578	525.7826	10
9	924.4673	462.7373	906.4567	453.7320	E	971.5156	486.2615	954.4891	477.7482	953.5051	477.2562	9
10	1023.5357	512.2715	1005.5251	503.2662	V	842.4730	421.7402	825.4465	413.2269	824.4625	412.7349	8
11	1152.5783	576.7928	1134.5677	567.7875	E	743.4046	372.2060	726.3781	363.6927	725.3941	363.2007	7
12	1249.6311	625.3192	1231.6205	616.3139	P	614.3620	307.6847	597.3355	299.1714	596.3515	298.6794	6
13	1306.6525	653.8299	1288.6420	644.8246	G	517.3093	259.1583	500.2827	250.6450	499.2987	250.1530	5
14	1419.7366	710.3719	1401.7260	701.3666	L	460.2878	230.6475	443.2613	222.1343	442.2772	221.6423	4
15	1520.7843	760.8958	1502.7737	751.8905	T	347.2037	174.1055	330.1772	165.5922	329.1932	165.1002	3
16	1591.8214	796.4143	1573.8108	787.4090	A	246.1561	123.5817	229.1295	115.0684			2
17					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 27 ppm



RMS error 27 ppm

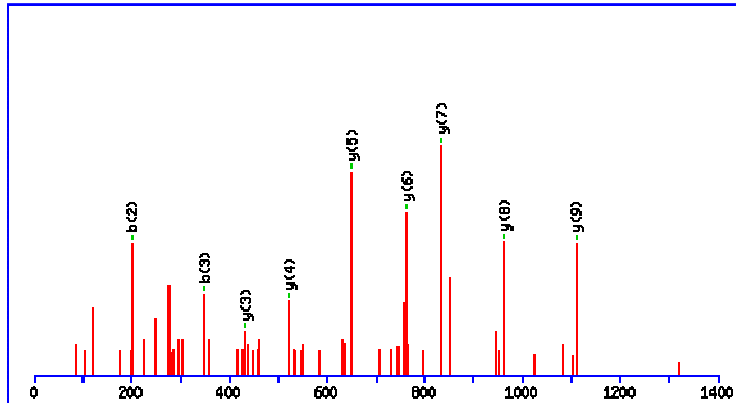
Peptide Number: 84763**MS/MS Fragmentation of AEFEALESEER**

Found in **IPI00472931** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ZC4H2 cDNA FLJ41769 fis, clone IMR322006886, highly similar to Hepatocellular carcinoma-associated antigen 127 homolog

Match to Query 22483: 1308.597228 from(655.305890,2+) index(20066)

Title: Elution from: 47.7166666666667 to 47.7166666666667 period: 0 cycle: 1763 experiment: 9 polarity: +

Data file 120118ry_201B7-32_1_2.mgf



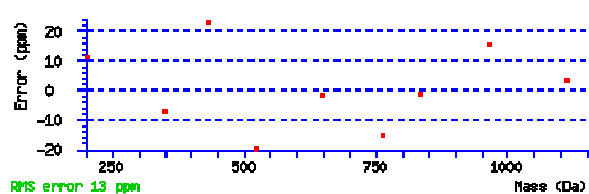
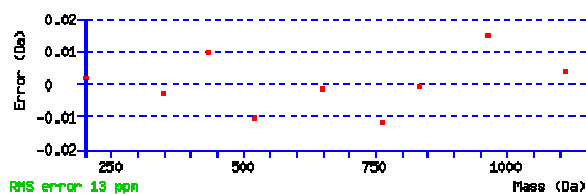
Monoisotopic mass of neutral peptide Mr(calc): 1308.5833

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 63 **Expect:** 1.8e-005

Matches : 9/96 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258			A							11
2	201.0870	101.0471	183.0764	92.0418	E	1238.5535	619.7804	1221.5270	611.2671	1220.5430	610.7751	10
3	348.1554	174.5813	330.1448	165.5761	F	1109.5109	555.2591	1092.4844	546.7458	1091.5004	546.2538	9
4	477.1980	239.1026	459.1874	230.0974	E	962.4425	481.7249	945.4160	473.2116	944.4320	472.7196	8
5	548.2351	274.6212	530.2245	265.6159	A	833.3999	417.2036	816.3734	408.6903	815.3894	408.1983	7
6	661.3192	331.1632	643.3086	322.1579	L	762.3628	381.6850	745.3363	373.1718	744.3523	372.6798	6
7	790.3618	395.6845	772.3512	386.6792	E	649.2788	325.1430	632.2522	316.6297	631.2682	316.1377	5
8	877.3938	439.2005	859.3832	430.1953	S	520.2362	260.6217	503.2096	252.1084	502.2256	251.6164	4
9	1006.4364	503.7218	988.4258	494.7165	E	433.2041	217.1057	416.1776	208.5924	415.1936	208.1004	3
10	1135.4790	568.2431	1117.4684	559.2378	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
11					R	175.1190	88.0631	158.0924	79.5498			1

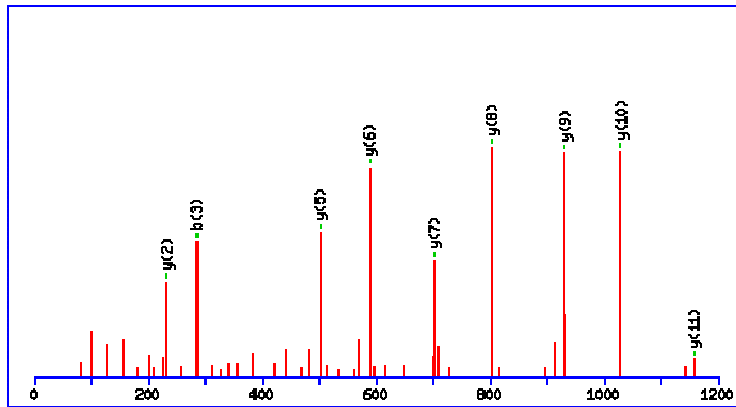


Peptide Number: 84874MS/MS Fragmentation of **GVQVETISPGDGR**Found in **IPI00759644** in **IPI_human**, Tax_Id=9606 Gene_Symbol=FKBP1A peptidyl-prolyl cis-trans isomerase FKBP1A isoform b

Match to Query 18676: 1313.657688 from(657.836120,2+) index(3840)

Title: Elution from: 10.1166666666667 to 10.1166666666667 period: 0 cycle: 389 experiment: 10 polarity:+

Data file 120208ry_Tig120slc-P8_1_2.mgf



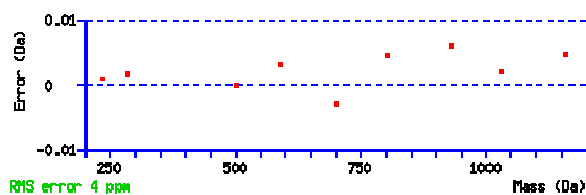
Monoisotopic mass of neutral peptide Mr(calc): 1313.6576

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

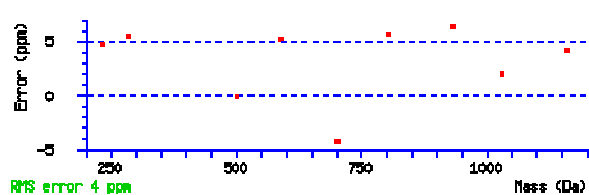
Ions Score: 76 Expect: 1.4e-006

Matches : 9/128 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							13
2	157.0972	79.0522					V	1257.6434	629.3253	1240.6168	620.8120	1239.6328	620.3200	12
3	285.1557	143.0815	268.1292	134.5682			Q	1158.5749	579.7911	1141.5484	571.2778	1140.5644	570.7858	11
4	384.2241	192.6157	367.1976	184.1024			V	1030.5164	515.7618	1013.4898	507.2485	1012.5058	506.7565	10
5	513.2667	257.1370	496.2402	248.6237	495.2562	248.1317	E	931.4480	466.2276	914.4214	457.7143	913.4374	457.2223	9
6	614.3144	307.6608	597.2879	299.1476	596.3039	298.6556	T	802.4054	401.7063	785.3788	393.1930	784.3948	392.7010	8
7	727.3985	364.2029	710.3719	355.6896	709.3879	355.1976	I	701.3577	351.1825	684.3311	342.6692	683.3471	342.1772	7
8	814.4305	407.7189	797.4040	399.2056	796.4199	398.7136	S	588.2736	294.6404	571.2471	286.1272	570.2630	285.6352	6
9	911.4833	456.2453	894.4567	447.7320	893.4727	447.2400	P	501.2416	251.1244	484.2150	242.6112	483.2310	242.1191	5
10	968.5047	484.7560	951.4782	476.2427	950.4942	475.7507	G	404.1888	202.5980	387.1623	194.0848	386.1783	193.5928	4
11	1083.5317	542.2695	1066.5051	533.7562	1065.5211	533.2642	D	347.1674	174.0873	330.1408	165.5740	329.1568	165.0820	3
12	1140.5531	570.7802	1123.5266	562.2669	1122.5426	561.7749	G	232.1404	116.5738	215.1139	108.0606			2
13							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 4 ppm



RMS error 4 ppm

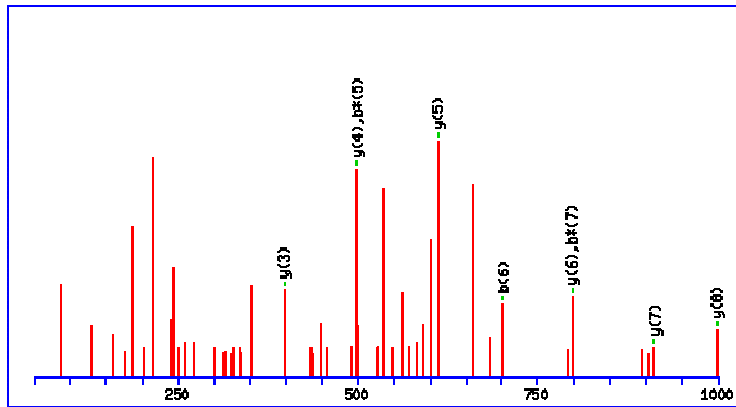
Peptide Number: 84928

MS/MS Fragmentation of **LEASNWLTHIK**Found in **IPI00102580** in **IPI_human**, Tax_Id=9606 Gene_Symbol=MTMR9 Myotubularin-related protein 9

Match to Query 18110: 1310.704152 from(437.908660,3+) index(41734)

Title: Elution from: 107.45 to 107.45 period: 0 cycle: 4101 experiment: 1 polarity: +

Data file 120206ry_aHDF1419-P10_3_2.mgf



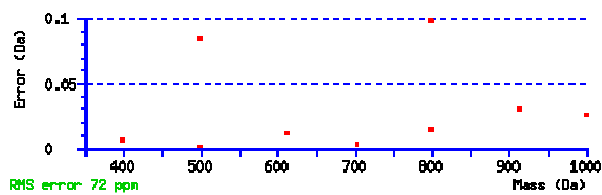
Monoisotopic mass of neutral peptide Mr(calc): 1310.6983

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

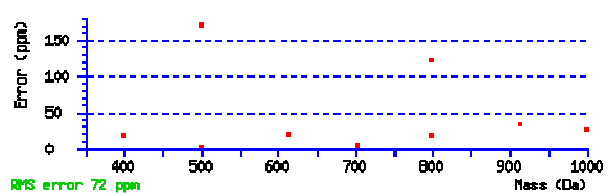
Ions Score: 44 Expect: 0.0022

Matches : 9/104 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							11
2	243.1339	122.0706			225.1234	113.0653	E	1198.6215	599.8144	1181.5949	591.3011	1180.6109	590.8091	10
3	314.1710	157.5892			296.1605	148.5839	A	1069.5789	535.2931	1052.5524	526.7798	1051.5683	526.2878	9
4	401.2031	201.1052			383.1925	192.0999	S	998.5418	499.7745	981.5152	491.2613	980.5312	490.7693	8
5	515.2460	258.1266	498.2195	249.6134	497.2354	249.1214	N	911.5098	456.2585	894.4832	447.7452	893.4992	447.2532	7
6	701.3253	351.1663	684.2988	342.6530	683.3148	342.1610	W	797.4668	399.2371	780.4403	390.7238	779.4563	390.2318	6
7	814.4094	407.7083	797.3828	399.1951	796.3988	398.7030	L	611.3875	306.1974	594.3610	297.6841	593.3770	297.1921	5
8	915.4571	458.2322	898.4305	449.7189	897.4465	449.2269	T	498.3035	249.6554	481.2769	241.1421	480.2929	240.6501	4
9	1052.5160	526.7616	1035.4894	518.2483	1034.5054	517.7563	H	397.2558	199.1315	380.2292	190.6183			3
10	1165.6000	583.3037	1148.5735	574.7904	1147.5895	574.2984	I	260.1969	130.6021	243.1703	122.0888			2
11							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 72 ppm



RMS error 72 ppm

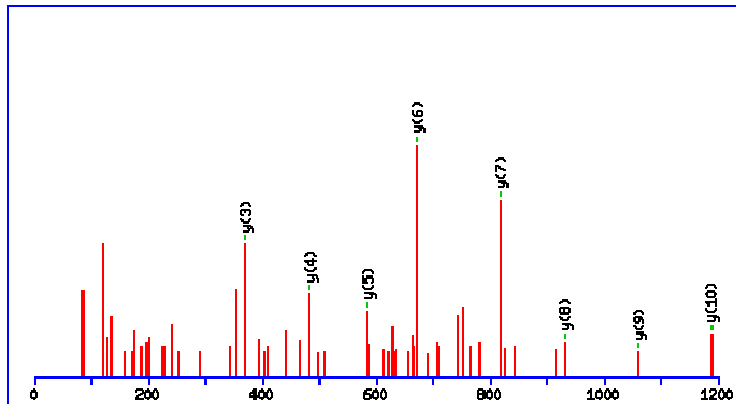
Peptide Number: 85178

MS/MS Fragmentation of **GTTVSQQLFSTLPVR**Found in **IPI00604708** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PMS2 Uncharacterized protein

Match to Query 7915: 1731.939162 from(578.320330,3+) index(177)

Title: Elution from: 0.416666666666667 to 0.416666666666667 period: 0 cycle: 16 experiment: 2 polarity: +

Data file 120210ry_32R1-32_2_4.mgf



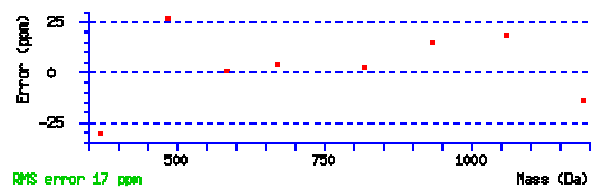
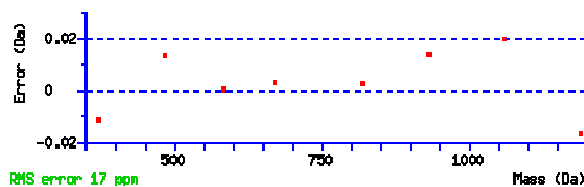
Monoisotopic mass of neutral peptide Mr(calc): 1731.9520

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 63 Expect: 2.7e-005

Matches : 8/158 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							16
2	159.0764	80.0418			141.0659	71.0366	T	1675.9377	838.4725	1658.9112	829.9592	1657.9272	829.4672	15
3	260.1241	130.5657			242.1135	121.5604	T	1574.8901	787.9487	1557.8635	779.4354	1556.8795	778.9434	14
4	359.1925	180.0999			341.1819	171.0946	V	1473.8424	737.4248	1456.8158	728.9116	1455.8318	728.4196	13
5	446.2245	223.6159			428.2140	214.6106	S	1374.7740	687.8906	1357.7474	679.3774	1356.7634	678.8853	12
6	545.2930	273.1501			527.2824	264.1448	V	1287.7419	644.3746	1270.7154	635.8613	1269.7314	635.3693	11
7	673.3515	337.1794	656.3250	328.6661	655.3410	328.1741	Q	1188.6735	594.8404	1171.6470	586.3271	1170.6630	585.8351	10
8	801.4101	401.2087	784.3836	392.6954	783.3995	392.2034	Q	1060.6150	530.8111	1043.5884	522.2978	1042.6044	521.8058	9
9	914.4942	457.7507	897.4676	449.2375	896.4836	448.7454	L	932.5564	466.7818	915.5298	458.2686	914.5458	457.7765	8
10	1061.5626	531.2849	1044.5360	522.7717	1043.5520	522.2796	F	819.4723	410.2398	802.4458	401.7265	801.4618	401.2345	7
11	1148.5946	574.8009	1131.5681	566.2877	1130.5841	565.7957	S	672.4039	336.7056	655.3774	328.1923	654.3933	327.7003	6
12	1249.6423	625.3248	1232.6157	616.8115	1231.6317	616.3195	T	585.3719	293.1896	568.3453	284.6763	567.3613	284.1843	5
13	1362.7264	681.8668	1345.6998	673.3535	1344.7158	672.8615	L	484.3242	242.6657	467.2976	234.1525			4
14	1459.7791	730.3932	1442.7526	721.8799	1441.7686	721.3879	P	371.2401	186.1237	354.2136	177.6104			3
15	1558.8475	779.9274	1541.8210	771.4141	1540.8370	770.9221	V	274.1874	137.5973	257.1608	129.0840			2
16							R	175.1190	88.0631	158.0924	79.5498			1



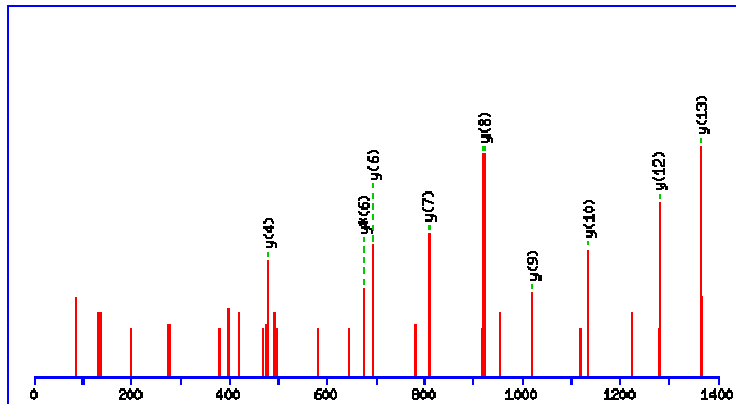
Peptide Number: 85307

MS/MS Fragmentation of **YGLSGSDVLDNVAYAR**Found in **IPI01010370** in **IPI_human**, Tax_Id=9606 Gene_Symbol=RAD51 Isoform 3 of DNA repair protein RAD51 homolog 1

Match to Query 18952: 1698.809088 from(850.411820,2+) index(12277)

Title: Elution from: 30.5 to 30.5 period: 0 cycle: 1147 experiment: 10 polarity: +

Data file 120210ry_32R1-32_2_3.mgf



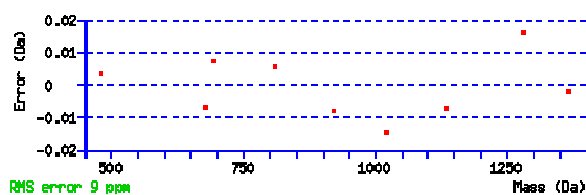
Monoisotopic mass of neutral peptide Mr(calc): 1698.8213

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

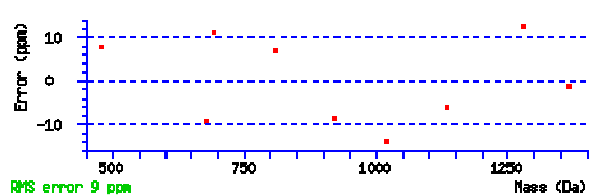
Ions Score: 62 Expect: 2.7e-005

Matches : 9/142 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389					Y							16
2	221.0921	111.0497					G	1536.7653	768.8863	1519.7387	760.3730	1518.7547	759.8810	15
3	334.1761	167.5917					L	1479.7438	740.3755	1462.7172	731.8623	1461.7332	731.3703	14
4	421.2082	211.1077			403.1976	202.1024	S	1366.6597	683.8335	1349.6332	675.3202	1348.6492	674.8282	13
5	478.2296	239.6185			460.2191	230.6132	G	1279.6277	640.3175	1262.6012	631.8042	1261.6171	631.3122	12
6	565.2617	283.1345			547.2511	274.1292	S	1222.6062	611.8068	1205.5797	603.2935	1204.5957	602.8015	11
7	680.2886	340.6479			662.2780	331.6427	D	1135.5742	568.2907	1118.5477	559.7775	1117.5636	559.2855	10
8	779.3570	390.1821			761.3464	381.1769	V	1020.5473	510.7773	1003.5207	502.2640	1002.5367	501.7720	9
9	892.4411	446.7242			874.4305	437.7189	L	921.4789	461.2431	904.4523	452.7298	903.4683	452.2378	8
10	1007.4680	504.2376			989.4575	495.2324	D	808.3948	404.7010	791.3682	396.1878	790.3842	395.6958	7
11	1121.5109	561.2591	1104.4844	552.7458	1103.5004	552.2538	N	693.3679	347.1876	676.3413	338.6743			6
12	1220.5794	610.7933	1203.5528	602.2800	1202.5688	601.7880	V	579.3249	290.1661	562.2984	281.6528			5
13	1291.6165	646.3119	1274.5899	637.7986	1273.6059	637.3066	A	480.2565	240.6319	463.2300	232.1186			4
14	1454.6798	727.8435	1437.6533	719.3303	1436.6692	718.8383	Y	409.2194	205.1133	392.1928	196.6001			3
15	1525.7169	763.3621	1508.6904	754.8488	1507.7063	754.3568	A	246.1561	123.5817	229.1295	115.0684			2
16							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 9 ppm



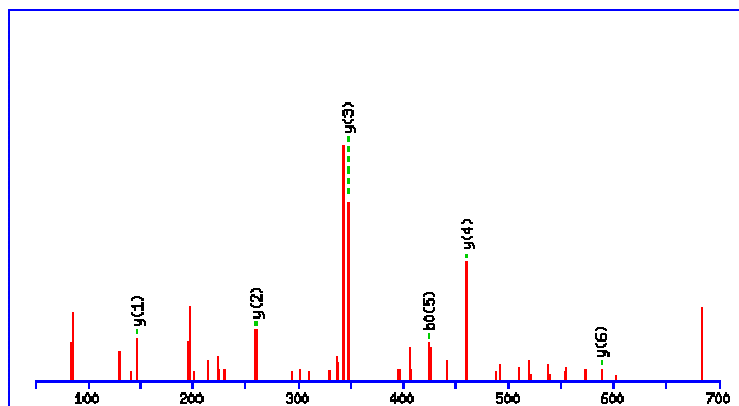
RMS error 9 ppm

Peptide Number: 85723MS/MS Fragmentation of **LAGLSLK**Found in **IPI00470917** in **IPI_human**, Tax_Id=9606 Gene_Symbol=C9orf174 KIAA1529 protein

Match to Query 323: 700.451808 from(351.233180,2+) index(12067)

Title: Elution from: 31.2333333333333 to 31.2333333333333 period: 0 cycle: 1196 experiment: 1 polarity: +

Data file 120208ry_Tig120slc-P8_1_2.mgf



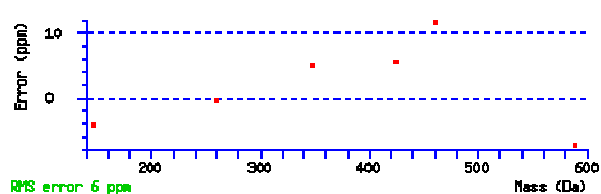
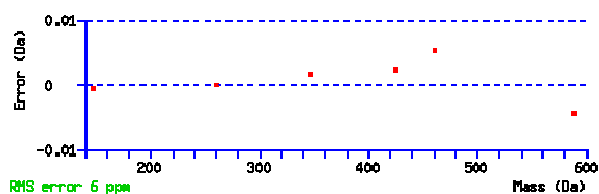
Monoisotopic mass of neutral peptide Mr(calc): 700.4483

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 37 Expect: 0.01

Matches : 6/48 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							7
2	185.1285	93.0679			A	588.3715	294.6894	571.3450	286.1761	570.3610	285.6841	6
3	242.1499	121.5786			G	517.3344	259.1709	500.3079	250.6576	499.3239	250.1656	5
4	355.2340	178.1206			L	460.3130	230.6601	443.2864	222.1468	442.3024	221.6548	4
5	442.2660	221.6366	424.2554	212.6314	S	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
6	555.3501	278.1787	537.3395	269.1734	L	260.1969	130.6021	243.1703	122.0888			2
7					K	147.1128	74.0600	130.0863	65.5468			1



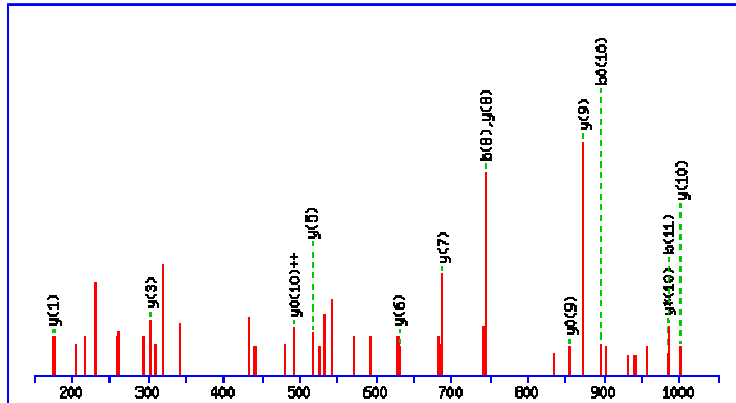
Peptide Number: 85844**MS/MS Fragmentation of ASQEGGDVLGAR**

Found in **IPI00386330** in **IPI_human**, Tax_Id=9606 Gene_Symbol=LDLRAP1 cDNA FLJ14335 fis, clone PLACE4000411, highly similar to Homo sapiens mRNA

Match to Query 16264: 1158.560608 from(580.287580,2+) index(19993)

Title: Elution from: 92.8 to 92.8 period: 0 cycle: 7678 experiment: 8 polarity: +

Data file 120201ry_aHDF1388-P9_1_1.mgf



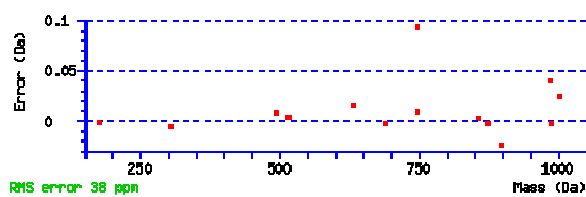
Monoisotopic mass of neutral peptide Mr(calc): 1158.5629

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

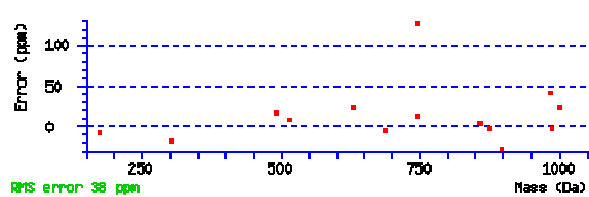
Ions Score: 44 **Expect:** 0.0018

Matches : 14/116 fragment ions using 31 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							12
2	159.0764	80.0418			141.0659	71.0366	S	1088.5331	544.7702	1071.5065	536.2569	1070.5225	535.7649	11
3	287.1350	144.0711	270.1084	135.5579	269.1244	135.0659	Q	1001.5011	501.2542	984.4745	492.7409	983.4905	492.2489	10
4	416.1776	208.5924	399.1510	200.0792	398.1670	199.5872	E	873.4425	437.2249	856.4159	428.7116	855.4319	428.2196	9
5	473.1991	237.1032	456.1725	228.5899	455.1885	228.0979	G	744.3999	372.7036	727.3733	364.1903	726.3893	363.6983	8
6	530.2205	265.6139	513.1940	257.1006	512.2100	256.6086	G	687.3784	344.1928	670.3519	335.6796	669.3679	335.1876	7
7	645.2475	323.1274	628.2209	314.6141	627.2369	314.1221	D	630.3570	315.6821	613.3304	307.1688	612.3464	306.6768	6
8	744.3159	372.6616	727.2893	364.1483	726.3053	363.6563	V	515.3300	258.1686	498.3035	249.6554			5
9	857.3999	429.2036	840.3734	420.6903	839.3894	420.1983	L	416.2616	208.6344	399.2350	200.1212			4
10	914.4214	457.7143	897.3949	449.2011	896.4108	448.7091	G	303.1775	152.0924	286.1510	143.5791			3
11	985.4585	493.2329	968.4320	484.7196	967.4480	484.2276	A	246.1561	123.5817	229.1295	115.0684			2
12							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 38 ppm



RMS error 38 ppm

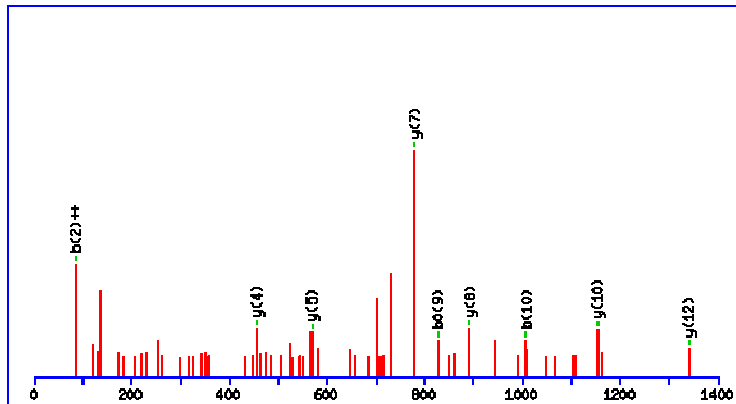
Peptide Number: 86106

MS/MS Fragmentation of **LGSDDISVYIPLIHGNK**Found in **IPI00736251** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PPM1H Protein phosphatase 1H

Match to Query 30283: 1996.048332 from(666.356720,3+) index(36133)

Title: Elution from: 87.9 to 87.9 period: 0 cycle: 3237 experiment: 5 polarity: +

Data file 120118ry_201B7-32_2_3.mgf



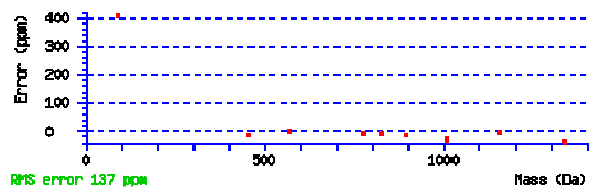
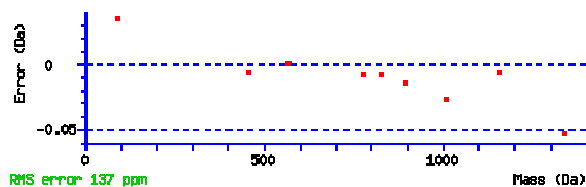
Monoisotopic mass of neutral peptide Mr(calc): 1996.0629

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 40 Expect: 0.0067

Matches : 9/156 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							19
2	171.1128	86.0600					G	1883.9862	942.4967	1866.9596	933.9834	1865.9756	933.4914	18
3	258.1448	129.5761			240.1343	120.5708	S	1826.9647	913.9860	1809.9381	905.4727	1808.9541	904.9807	17
4	315.1663	158.0868			297.1557	149.0815	G	1739.9327	870.4700	1722.9061	861.9567	1721.9221	861.4647	16
5	430.1932	215.6003			412.1827	206.5950	D	1682.9112	841.9592	1665.8846	833.4460	1664.9006	832.9540	15
6	545.2202	273.1137			527.2096	264.1084	D	1567.8843	784.4458	1550.8577	775.9325	1549.8737	775.4405	14
7	658.3042	329.6558			640.2937	320.6505	I	1452.8573	726.9323	1435.8308	718.4190	1434.8467	717.9270	13
8	745.3363	373.1718			727.3257	364.1665	S	1339.7732	670.3903	1322.7467	661.8770	1321.7627	661.3850	12
9	844.4047	422.7060			826.3941	413.7007	V	1252.7412	626.8742	1235.7147	618.3610			11
10	1007.4680	504.2376			989.4575	495.2324	Y	1153.6728	577.3400	1136.6463	568.8268			10
11	1106.5364	553.7719			1088.5259	544.7666	V	990.6095	495.8084	973.5829	487.2951			9
12	1219.6205	610.3139			1201.6099	601.3086	I	891.5411	446.2742	874.5145	437.7609			8
13	1316.6733	658.8403			1298.6627	649.8350	P	778.4570	389.7321	761.4304	381.2189			7
14	1429.7573	715.3823			1411.7468	706.3770	L	681.4042	341.2058	664.3777	332.6925			6
15	1542.8414	771.9243			1524.8308	762.9190	I	568.3202	284.6637	551.2936	276.1504			5
16	1679.9003	840.4538			1661.8897	831.4485	H	455.2361	228.1217	438.2096	219.6084			4
17	1736.9218	868.9645			1718.9112	859.9592	G	318.1772	159.5922	301.1506	151.0790			3
18	1850.9647	925.9860	1833.9381	917.4727	1832.9541	916.9807	N	261.1557	131.0815	244.1292	122.5682			2
19							K	147.1128	74.0600	130.0863	65.5468			1



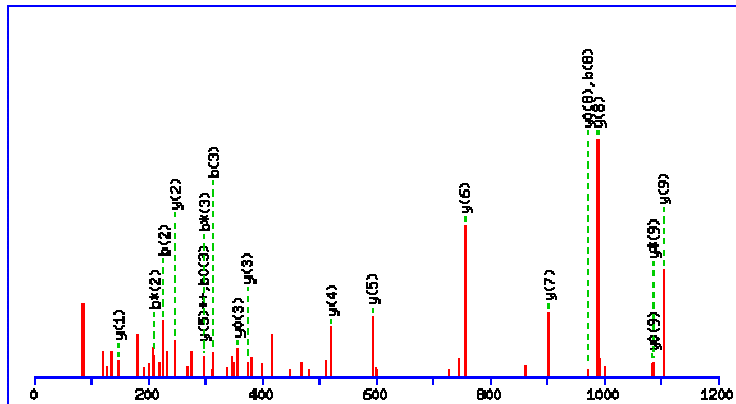
Peptide Number: 86137

MS/MS Fragmentation of **INSFYAFEVK**Found in **IPI00291695** in **IPI_human**, Tax_Id=9606 Gene_Symbol=GPX8 Probable glutathione peroxidase 8

Match to Query 3441: 1216.612988 from(609.313770,2+) index(3081)

Title: Elution from: 8.25 to 8.25 period: 0 cycle: 321 experiment: 6 polarity: +

Data file 120208ry_Tig120slc-P8_1_3.mgf



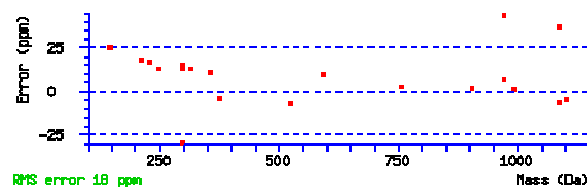
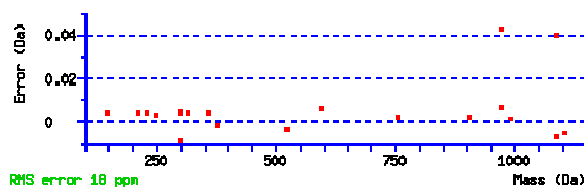
Monoisotopic mass of neutral peptide Mr(calc): 1216.6128

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 53 Expect: 0.00039

Matches : 20/98 fragment ions using 46 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							10
2	228.1343	114.5708	211.1077	106.0575			N	1104.5360	552.7717	1087.5095	544.2584	1086.5255	543.7664	9
3	315.1663	158.0868	298.1397	149.5735	297.1557	149.0815	S	990.4931	495.7502	973.4666	487.2369	972.4825	486.7449	8
4	462.2347	231.6210	445.2082	223.1077	444.2241	222.6157	F	903.4611	452.2342	886.4345	443.7209	885.4505	443.2289	7
5	625.2980	313.1527	608.2715	304.6394	607.2875	304.1474	Y	756.3927	378.7000	739.3661	370.1867	738.3821	369.6947	6
6	696.3352	348.6712	679.3086	340.1579	678.3246	339.6659	A	593.3293	297.1683	576.3028	288.6550	575.3188	288.1630	5
7	843.4036	422.2054	826.3770	413.6921	825.3930	413.2001	F	522.2922	261.6498	505.2657	253.1365	504.2817	252.6445	4
8	972.4462	486.7267	955.4196	478.2134	954.4356	477.7214	E	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
9	1071.5146	536.2609	1054.4880	527.7477	1053.5040	527.2556	V	246.1812	123.5942	229.1547	115.0810			2
10							K	147.1128	74.0600	130.0863	65.5468			1

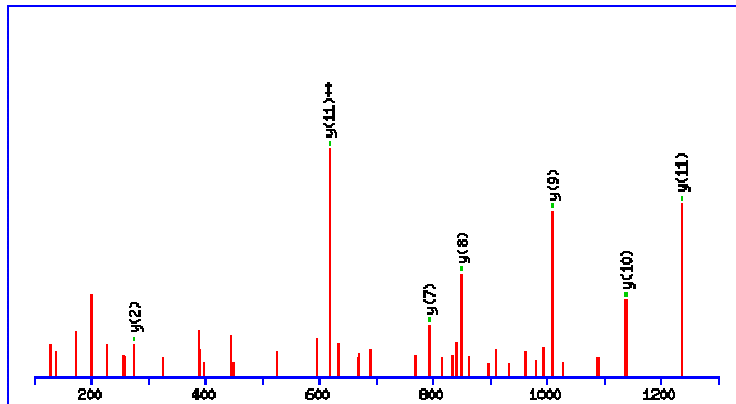


Peptide Number: 86299MS/MS Fragmentation of **TTPECGPTGYVEK**Found in **IPI00000912** in **IPI_human**, Tax_Id=9606 Gene_Symbol=JTB Isoform 2 of Protein JTB

Match to Query 23195: 1437.643888 from(719.829220,2+) index(30799)

Title: Elution from: 110.233333333333 to 110.233333333333 period: 0 cycle: 7985 experiment: 7 polarity:+

Data file 120208ry_Tig120slc-P8_1_1.mgf



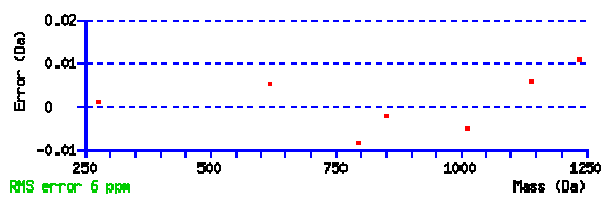
Monoisotopic mass of neutral peptide Mr(calc): 1437.6446

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

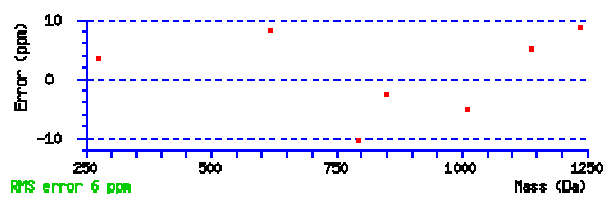
Ions Score: 40 Expect: 0.0028

Matches : 7/118 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311	84.0444	42.5258	T							13
2	203.1026	102.0550	185.0921	93.0497	T							12
3	300.1554	150.5813	282.1448	141.5761	P	1236.5565	618.7819	1219.5300	610.2686	1218.5460	609.7766	11
4	429.1980	215.1026	411.1874	206.0974	E	1139.5038	570.2555	1122.4772	561.7422	1121.4932	561.2502	10
5	589.2286	295.1180	571.2181	286.1127	C	1010.4612	505.7342	993.4346	497.2209	992.4506	496.7289	9
6	646.2501	323.6287	628.2395	314.6234	G	850.4305	425.7189	833.4040	417.2056	832.4199	416.7136	8
7	743.3029	372.1551	725.2923	363.1498	P	793.4090	397.2082	776.3825	388.6949	775.3985	388.2029	7
8	844.3505	422.6789	826.3400	413.6736	T	696.3563	348.6818	679.3297	340.1685	678.3457	339.6765	6
9	901.3720	451.1896	883.3614	442.1844	G	595.3086	298.1579	578.2821	289.6447	577.2980	289.1527	5
10	1064.4353	532.7213	1046.4248	523.7160	Y	538.2871	269.6472	521.2606	261.1339	520.2766	260.6419	4
11	1163.5038	582.2555	1145.4932	573.2502	V	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
12	1292.5463	646.7768	1274.5358	637.7715	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
13					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 6 ppm



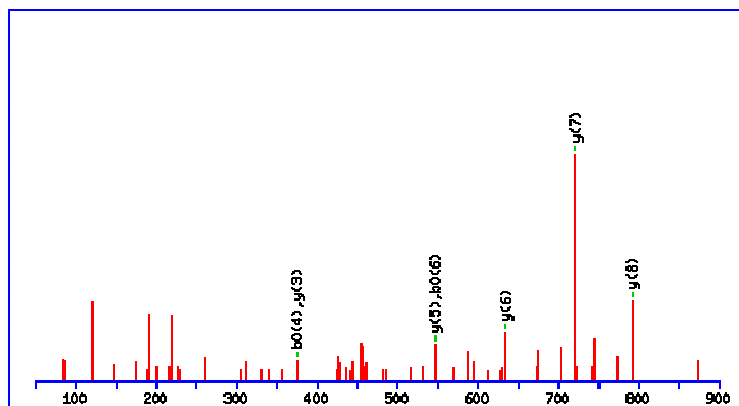
RMS error 6 ppm

Peptide Number: 86521MS/MS Fragmentation of **FASSGDDIK**Found in **IPI00169345** in **IPI_human**, Tax_Id=9606 Gene_Symbol=NEDD1 Protein NEDD1

Match to Query 8385: 938.435328 from(470.224940,2+) index(9824)

Title: Elution from: 64.0166666666667 to 64.0166666666667 period: 0 cycle: 7794 experiment: 7 polarity:+

Data file 120210ry_585A1-55_3_1.mgf



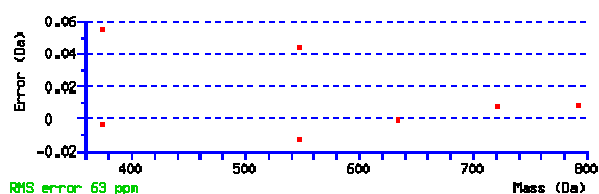
Monoisotopic mass of neutral peptide Mr(calc): 938.4345

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

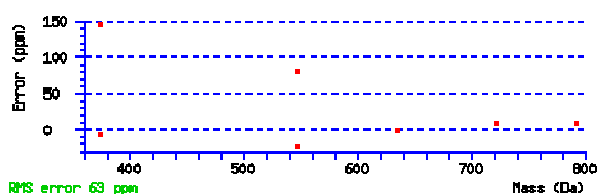
Ions Score: 37 Expect: 0.0078

Matches : 7/72 fragment ions using 8 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415			F							9
2	219.1128	110.0600			A	792.3734	396.6903	775.3468	388.1771	774.3628	387.6850	8
3	306.1448	153.5761	288.1343	144.5708	S	721.3363	361.1718	704.3097	352.6585	703.3257	352.1665	7
4	393.1769	197.0921	375.1663	188.0868	S	634.3042	317.6558	617.2777	309.1425	616.2937	308.6505	6
5	450.1983	225.6028	432.1878	216.5975	G	547.2722	274.1397	530.2457	265.6265	529.2617	265.1345	5
6	565.2253	283.1163	547.2147	274.1110	D	490.2508	245.6290	473.2242	237.1157	472.2402	236.6237	4
7	680.2522	340.6297	662.2416	331.6245	D	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
8	793.3363	397.1718	775.3257	388.1665	I	260.1969	130.6021	243.1703	122.0888			2
9					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 63 ppm



RMS error 63 ppm

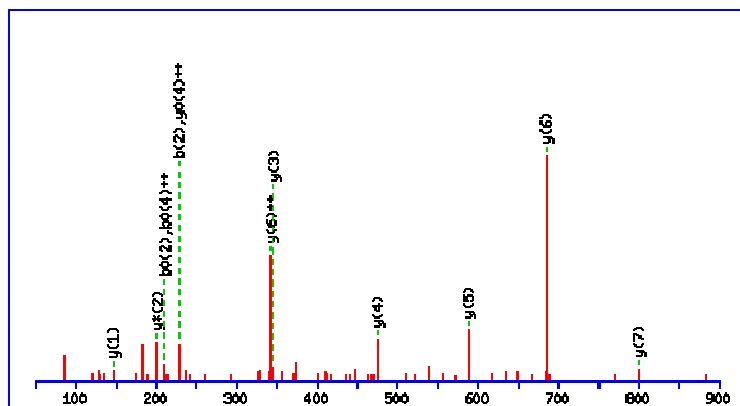
Peptide Number: 86538

MS/MS Fragmentation of **LDPLEQAK**Found in **IPI00007322** in **IPI_human**, Tax_Id=9606 Gene_Symbol=C1D Nuclear nucleic acid-binding protein C1D

Match to Query 8248: 912.488988 from(457.251770,2+) index(29727)

Title: Elution from: 102.883333333333 to 102.883333333333 period: 0 cycle: 8884 experiment: 1 polarity: +

Data file 120214ry_32R1-32_4_1.mgf



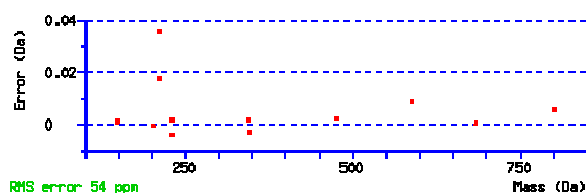
Monoisotopic mass of neutral peptide Mr(calc): 912.4916

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

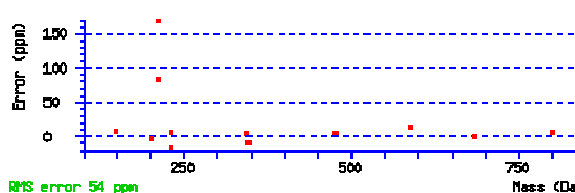
Ions Score: 37 Expect: 0.0098

Matches : 12/66 fragment ions using 23 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							8
2	229.1183	115.0628			211.1077	106.0575	D	800.4149	400.7111	783.3883	392.1978	782.4043	391.7058	7
3	326.1710	163.5892			308.1605	154.5839	P	685.3879	343.1976	668.3614	334.6843	667.3774	334.1923	6
4	439.2551	220.1312			421.2445	211.1259	L	588.3352	294.6712	571.3086	286.1579	570.3246	285.6659	5
5	568.2977	284.6525			550.2871	275.6472	E	475.2511	238.1292	458.2245	229.6159	457.2405	229.1239	4
6	696.3563	348.6818	679.3297	340.1685	678.3457	339.6765	Q	346.2085	173.6079	329.1819	165.0946			3
7	767.3934	384.2003	750.3668	375.6871	749.3828	375.1951	A	218.1499	109.5786	201.1234	101.0653			2
8							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 54 ppm



RMS error 54 ppm

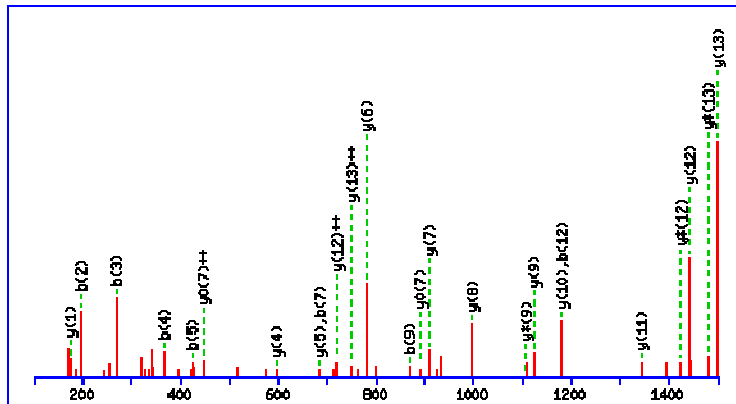
Peptide Number: 86540

MS/MS Fragmentation of **PVAVGPGYQSQPSCFDR**Found in **IPI00016046** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ROMO1 Isoform 1 of Reactive oxygen species modulator 1

Match to Query 39118: 1863.864408 from(932.939480,2+) index(24149)

Title: Elution from: 59.1333333333333 to 59.1333333333333 period: 0 cycle: 2233 experiment: 8 polarity:+

Data file 120210ry_32R1-32_2_2.mgf



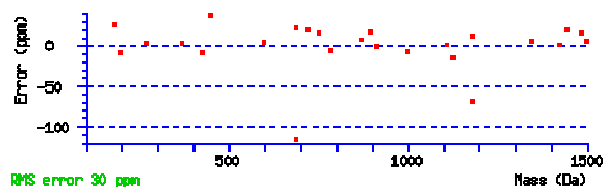
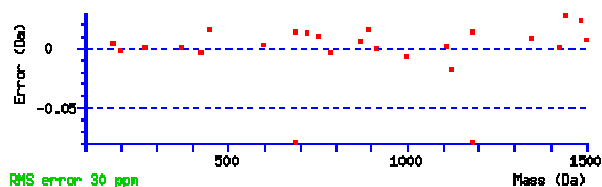
Monoisotopic mass of neutral peptide Mr(calc): 1863.8574

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 71 Expect: 4e-006

Matches : 25/156 fragment ions using 44 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	98.0600	49.5337					P							17
2	197.1285	99.0679					V	1767.8119	884.4096	1750.7853	875.8963	1749.8013	875.4043	16
3	268.1656	134.5864					A	1668.7435	834.8754	1651.7169	826.3621	1650.7329	825.8701	15
4	367.2340	184.1206					V	1597.7064	799.3568	1580.6798	790.8435	1579.6958	790.3515	14
5	424.2554	212.6314					G	1498.6380	749.8226	1481.6114	741.3093	1480.6274	740.8173	13
6	521.3082	261.1577					P	1441.6165	721.3119	1424.5899	712.7986	1423.6059	712.3066	12
7	684.3715	342.6894					Y	1344.5637	672.7855	1327.5372	664.2722	1326.5532	663.7802	11
8	741.3930	371.2001					G	1181.5004	591.2538	1164.4738	582.7406	1163.4898	582.2486	10
9	869.4516	435.2294	852.4250	426.7162			Q	1124.4789	562.7431	1107.4524	554.2298	1106.4684	553.7378	9
10	956.4836	478.7454	939.4571	470.2322	938.4730	469.7402	S	996.4204	498.7138	979.3938	490.2005	978.4098	489.7085	8
11	1084.5422	542.7747	1067.5156	534.2615	1066.5316	533.7694	Q	909.3883	455.1978	892.3618	446.6845	891.3778	446.1925	7
12	1181.5950	591.3011	1164.5684	582.7878	1163.5844	582.2958	P	781.3298	391.1685	764.3032	382.6552	763.3192	382.1632	6
13	1268.6270	634.8171	1251.6004	626.3039	1250.6164	625.8118	S	684.2770	342.6421	667.2504	334.1289	666.2664	333.6368	5
14	1428.6576	714.8325	1411.6311	706.3192	1410.6471	705.8272	C	597.2450	299.1261	580.2184	290.6128	579.2344	290.1208	4
15	1575.7260	788.3667	1558.6995	779.8534	1557.7155	779.3614	F	437.2143	219.1108	420.1878	210.5975	419.2037	210.1055	3
16	1690.7530	845.8801	1673.7264	837.3669	1672.7424	836.8748	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
17							R	175.1190	88.0631	158.0924	79.5498			1

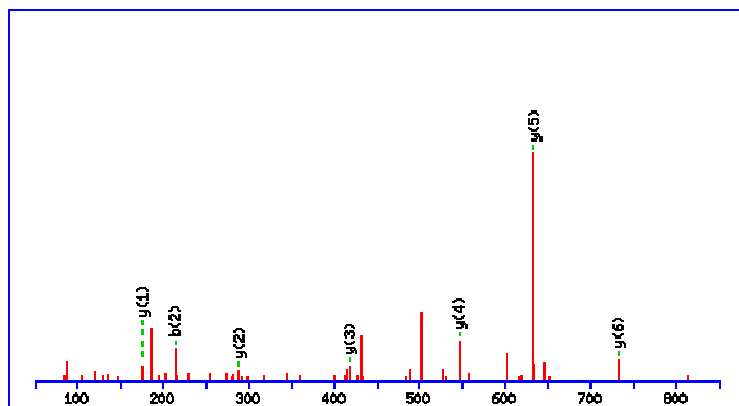


Peptide Number: 86943**MS/MS Fragmentation of LVSEELR**Found in **IPI00064935** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ALPK3 Alpha-protein kinase 3

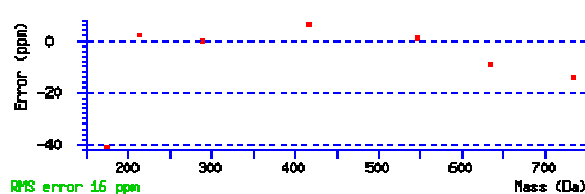
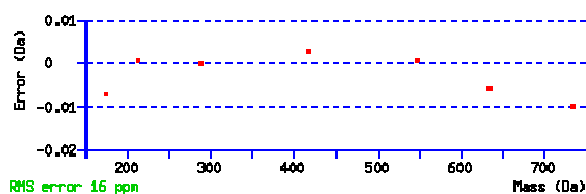
Match to Query 5278: 844.452028 from(423.233290,2+) index(14307)

Title: Elution from: 69.65 to 69.65 period: 0 cycle: 6840 experiment: 3 polarity:+

Data file 120208ry_Tig120slc-P8_2_1.mgf

**Monoisotopic mass of neutral peptide Mr(calc):** 844.4654**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 43 **Expect:** 0.0049**Matches :** 7/52 fragment ions using 14 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							7
2	213.1598	107.0835			V	732.3886	366.6980	715.3621	358.1847	714.3781	357.6927	6
3	300.1918	150.5995	282.1812	141.5942	S	633.3202	317.1638	616.2937	308.6505	615.3097	308.1585	5
4	429.2344	215.1208	411.2238	206.1155	E	546.2882	273.6477	529.2617	265.1345	528.2776	264.6425	4
5	558.2770	279.6421	540.2664	270.6368	E	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
6	671.3610	336.1842	653.3505	327.1789	L	288.2030	144.6051	271.1765	136.0919			2
7					R	175.1190	88.0631	158.0924	79.5498			1



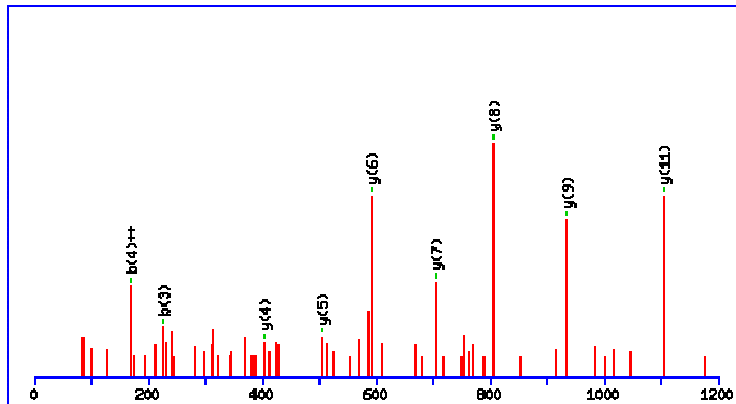
Peptide Number: 87046

MS/MS Fragmentation of **VAGLETISTATGR**Found in **IPI00019018** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TM7SF2 Isoform 1 of Delta(14)-sterol reductase

Match to Query 21947: 1274.668868 from(638.341710,2+) index(20460)

Title: Elution from: 48.7 to 48.7 period: 0 cycle: 1794 experiment: 10 polarity:+

Data file 120118ry_201B7-32_2_2.mgf



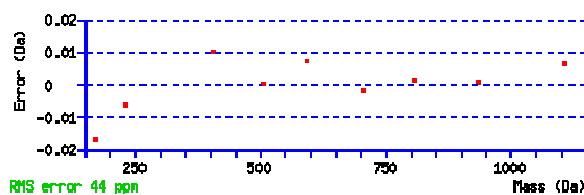
Monoisotopic mass of neutral peptide Mr(calc): 1274.6830

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

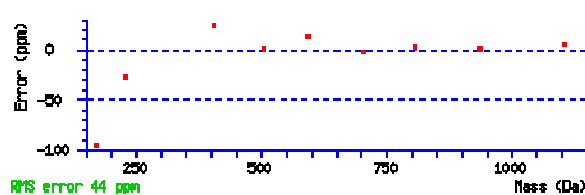
Ions Score: 62 Expect: 6e-005

Matches : 10/108 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415			V							13
2	171.1128	86.0600			A	1176.6219	588.8146	1159.5953	580.3013	1158.6113	579.8093	12
3	228.1343	114.5708			G	1105.5848	553.2960	1088.5582	544.7828	1087.5742	544.2907	11
4	341.2183	171.1128			L	1048.5633	524.7853	1031.5368	516.2720	1030.5528	515.7800	10
5	470.2609	235.6341	452.2504	226.6288	E	935.4793	468.2433	918.4527	459.7300	917.4687	459.2380	9
6	571.3086	286.1579	553.2980	277.1527	T	806.4367	403.7220	789.4101	395.2087	788.4261	394.7167	8
7	684.3927	342.7000	666.3821	333.6947	I	705.3890	353.1981	688.3624	344.6849	687.3784	344.1928	7
8	771.4247	386.2160	753.4141	377.2107	S	592.3049	296.6561	575.2784	288.1428	574.2944	287.6508	6
9	872.4724	436.7398	854.4618	427.7345	T	505.2729	253.1401	488.2463	244.6268	487.2623	244.1348	5
10	943.5095	472.2584	925.4989	463.2531	A	404.2252	202.6162	387.1987	194.1030	386.2146	193.6110	4
11	1044.5572	522.7822	1026.5466	513.7769	T	333.1881	167.0977	316.1615	158.5844	315.1775	158.0924	3
12	1101.5786	551.2930	1083.5681	542.2877	G	232.1404	116.5738	215.1139	108.0606			2
13					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 44 ppm



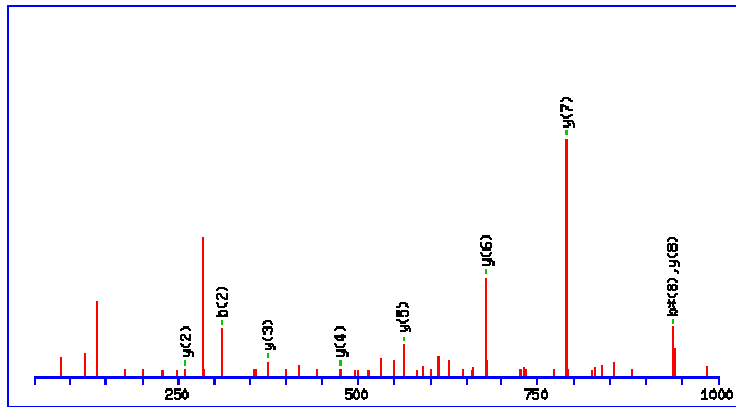
RMS error 44 ppm

Peptide Number: 87649MS/MS Fragmentation of **YFIDSTNLK**Found in **IPI00844193** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ZNF593 Zinc finger protein 593

Match to Query 10174: 1099.548788 from(550.781670,2+) index(23032)

Title: Elution from: 55.9333333333333 to 55.9333333333333 period: 0 cycle: 2116 experiment: 6 polarity:+

Data file 120214ry_414C2-43_4_2.mgf



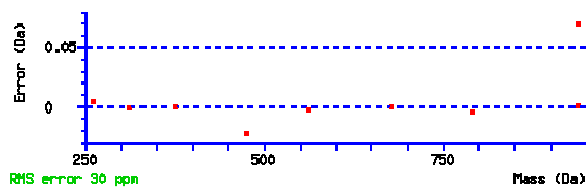
Monoisotopic mass of neutral peptide Mr(calc): 1099.5550

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

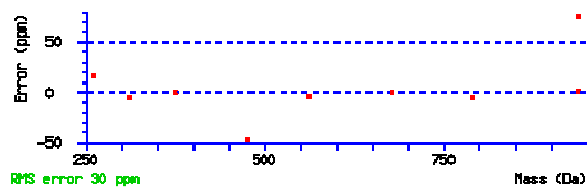
Ions Score: 44 Expect: 0.0022

Matches : 9/72 fragment ions using 19 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389					Y							9
2	311.1390	156.0731					F	937.4989	469.2531	920.4724	460.7398	919.4884	460.2478	8
3	424.2231	212.6152					I	790.4305	395.7189	773.4040	387.2056	772.4199	386.7136	7
4	539.2500	270.1287			521.2395	261.1234	D	677.3464	339.1769	660.3199	330.6636	659.3359	330.1716	6
5	626.2821	313.6447			608.2715	304.6394	S	562.3195	281.6634	545.2930	273.1501	544.3089	272.6581	5
6	727.3297	364.1685			709.3192	355.1632	T	475.2875	238.1474	458.2609	229.6341	457.2769	229.1421	4
7	841.3727	421.1900	824.3461	412.6767	823.3621	412.1847	N	374.2398	187.6235	357.2132	179.1103			3
8	954.4567	477.7320	937.4302	469.2187	936.4462	468.7267	L	260.1969	130.6021	243.1703	122.0888			2
9							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 30 ppm



RMS error 30 ppm

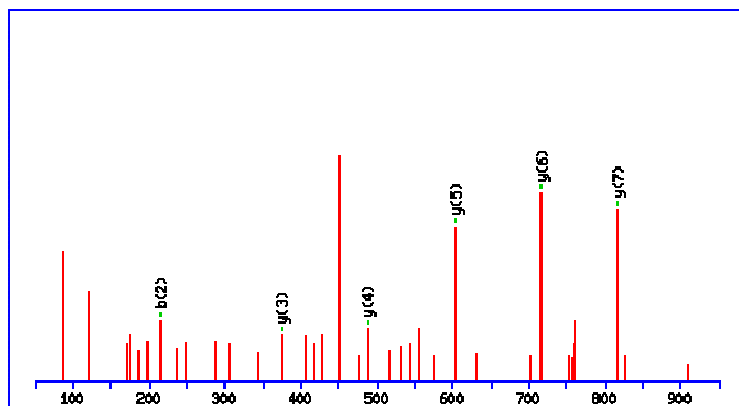
Peptide Number: 88116

MS/MS Fragmentation of **ITLDLLSR**Found in **IPI00396310** in **IPI_human**, Tax_Id=9606 Gene_Symbol=AFF1 AF4/FMR2 family member 1 isoform 1

Match to Query 1076: 929.554848 from(465.784700,2+) index(6062)

Title: Elution from: 15.05 to 15.05 period: 0 cycle: 562 experiment: 1 polarity: +

Data file 120126ry_585A1-55_2_3.mgf



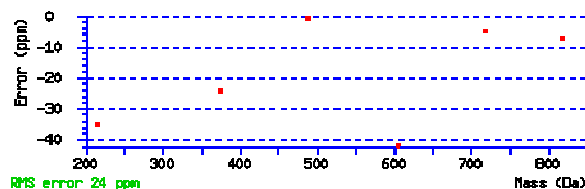
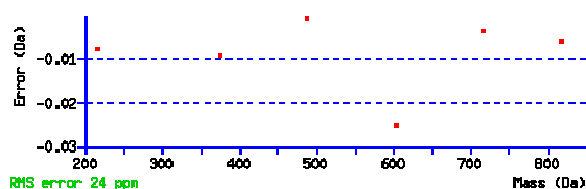
Monoisotopic mass of neutral peptide Mr(calc): 929.5546

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 37 Expect: 0.0084

Matches : 6/66 fragment ions using 9 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			I							8
2	215.1390	108.0731	197.1285	99.0679	T	817.4778	409.2425	800.4512	400.7293	799.4672	400.2373	7
3	328.2231	164.6152	310.2125	155.6099	L	716.4301	358.7187	699.4036	350.2054	698.4195	349.7134	6
4	443.2500	222.1287	425.2395	213.1234	D	603.3461	302.1767	586.3195	293.6634	585.3355	293.1714	5
5	556.3341	278.6707	538.3235	269.6654	L	488.3191	244.6632	471.2926	236.1499	470.3085	235.6579	4
6	669.4182	335.2127	651.4076	326.2074	L	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
7	756.4502	378.7287	738.4396	369.7234	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
8					R	175.1190	88.0631	158.0924	79.5498			1



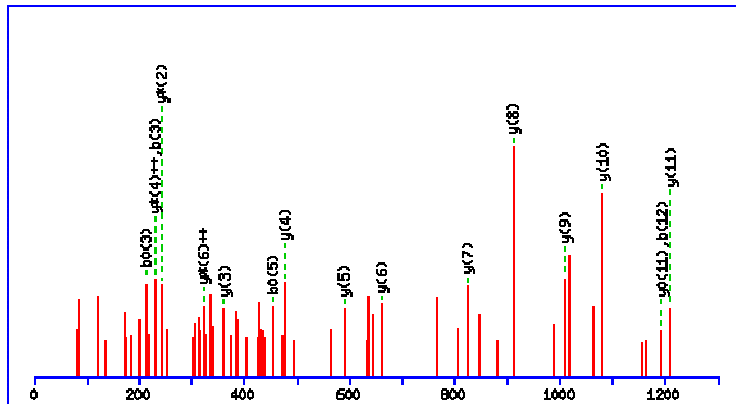
Peptide Number: 88231

MS/MS Fragmentation of **AASLEAVSYAIDTLK**Found in **IPI00005218** in **IPI_human**, Tax_Id=9606 Gene_Symbol=MOCS2 Molybdopterin synthase catalytic subunit

Match to Query 12238: 1550.815848 from(776.415200,2+) index(37315)

Title: Elution from: 89.4333333333333 to 89.4333333333333 period: 0 cycle: 3384 experiment: 7 polarity:+

Data file 120208ry_Tig120slc-P8_2_3.mgf



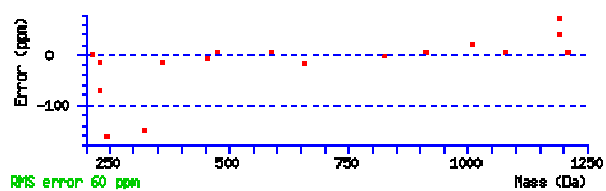
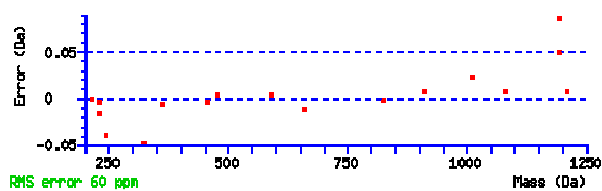
Monoisotopic mass of neutral peptide Mr(calc): 1550.8192

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 53 Expect: 0.0003

Matches : 17/132 fragment ions using 30 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258			A							15
2	143.0815	72.0444			A	1480.7894	740.8983	1463.7628	732.3850	1462.7788	731.8930	14
3	230.1135	115.5604	212.1030	106.5551	S	1409.7522	705.3798	1392.7257	696.8665	1391.7417	696.3745	13
4	343.1976	172.1024	325.1870	163.0972	L	1322.7202	661.8637	1305.6937	653.3505	1304.7096	652.8585	12
5	472.2402	236.6237	454.2296	227.6185	E	1209.6361	605.3217	1192.6096	596.8084	1191.6256	596.3164	11
6	543.2773	272.1423	525.2667	263.1370	A	1080.5936	540.8004	1063.5670	532.2871	1062.5830	531.7951	10
7	642.3457	321.6765	624.3352	312.6712	V	1009.5564	505.2819	992.5299	496.7686	991.5459	496.2766	9
8	729.3777	365.1925	711.3672	356.1872	S	910.4880	455.7477	893.4615	447.2344	892.4775	446.7424	8
9	892.4411	446.7242	874.4305	437.7189	Y	823.4560	412.2316	806.4294	403.7184	805.4454	403.2264	7
10	963.4782	482.2427	945.4676	473.2374	A	660.3927	330.7000	643.3661	322.1867	642.3821	321.6947	6
11	1076.5623	538.7848	1058.5517	529.7795	I	589.3556	295.1814	572.3290	286.6681	571.3450	286.1761	5
12	1191.5892	596.2982	1173.5786	587.2930	D	476.2715	238.6394	459.2449	230.1261	458.2609	229.6341	4
13	1292.6369	646.8221	1274.6263	637.8168	T	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
14	1405.7209	703.3641	1387.7104	694.3588	L	260.1969	130.6021	243.1703	122.0888			2
15					K	147.1128	74.0600	130.0863	65.5468			1

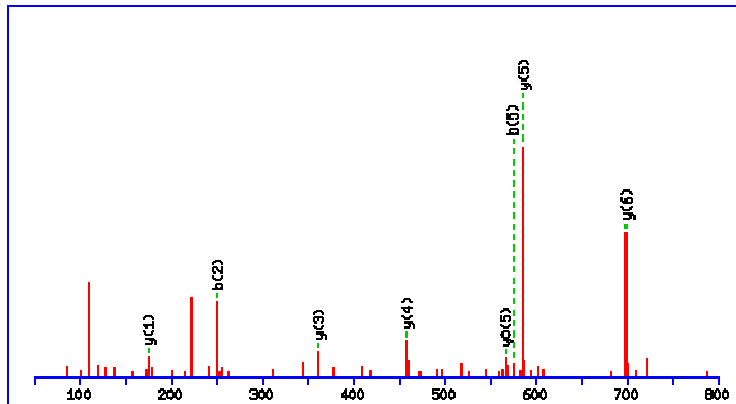


Peptide Number: 88385MS/MS Fragmentation of **HIKPVSR**Found in **IPI00087498** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ESCO2 N-acetyltransferase ESCO2

Match to Query 5319: 835.498908 from(418.756730,2+) index(19236)

Title: Elution from: 88 to 88 period: 0 cycle: 8624 experiment: 3 polarity:+

Data file 120210ry_32R1-32_3_1.mgf



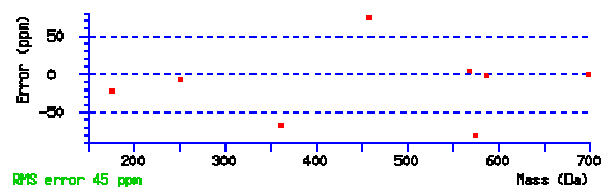
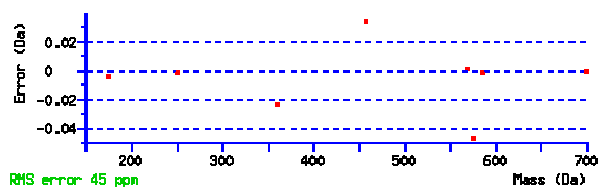
Monoisotopic mass of neutral peptide Mr(calc): 835.5028

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 34 Expect: 0.0066

Matches : 8/56 fragment ions using 15 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	138.0662	69.5367					H							7
2	251.1503	126.0788					I	699.4512	350.2292	682.4246	341.7160	681.4406	341.2239	6
3	379.2452	190.1262	362.2187	181.6130			K	586.3671	293.6872	569.3406	285.1739	568.3566	284.6819	5
4	476.2980	238.6526	459.2714	230.1394			P	458.2722	229.6397	441.2456	221.1264	440.2616	220.6344	4
5	575.3664	288.1868	558.3398	279.6736			V	361.2194	181.1133	344.1928	172.6001	343.2088	172.1081	3
6	662.3984	331.7028	645.3719	323.1896	644.3879	322.6976	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
7							R	175.1190	88.0631	158.0924	79.5498			1

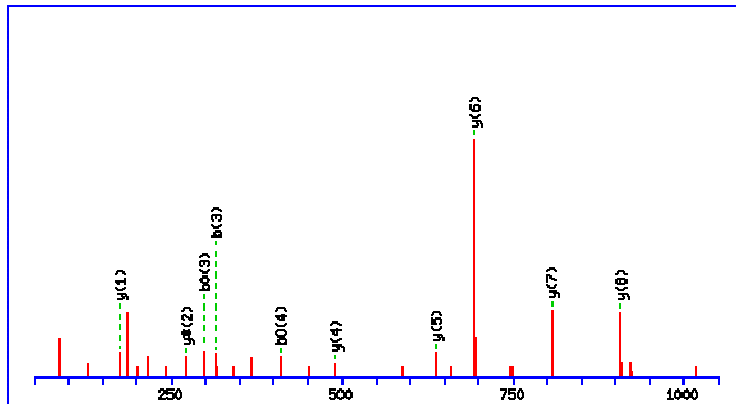


Peptide Number: 88585**MS/MS Fragmentation of DVTIGFSLDR**Found in **IPI00184474** in **IPI_human**, Tax_Id=9606 Gene_Symbol=GPR107 GPR107 protein (Fragment)

Match to Query 4575: 1121.565728 from(561.790140,2+) index(6646)

Title: Elution from: 16.4666666666667 to 16.4666666666667 period: 0 cycle: 614 experiment: 5 polarity: +

Data file 120126ry_585A1-55_2_3.mgf



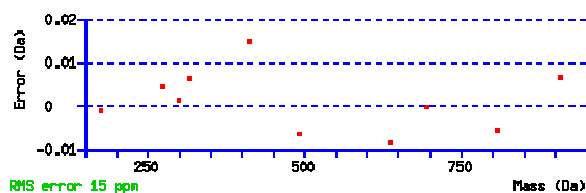
Monoisotopic mass of neutral peptide Mr(calc): 1121.5717

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

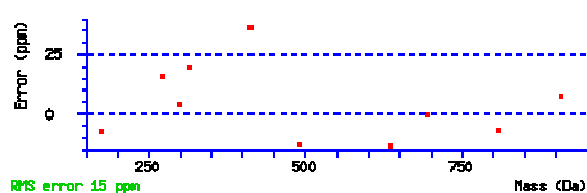
Ions Score: 41 Expect: 0.006

Matches : 10/88 fragment ions using 17 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	98.0237	49.5155	D							10
2	215.1026	108.0550	197.0921	99.0497	V	1007.5520	504.2796	990.5255	495.7664	989.5415	495.2744	9
3	316.1503	158.5788	298.1397	149.5735	T	908.4836	454.7454	891.4571	446.2322	890.4730	445.7402	8
4	429.2344	215.1208	411.2238	206.1155	I	807.4359	404.2216	790.4094	395.7083	789.4254	395.2163	7
5	486.2558	243.6316	468.2453	234.6263	G	694.3519	347.6796	677.3253	339.1663	676.3413	338.6743	6
6	633.3243	317.1658	615.3137	308.1605	F	637.3304	319.1688	620.3039	310.6556	619.3198	310.1636	5
7	720.3563	360.6818	702.3457	351.6765	S	490.2620	245.6346	473.2354	237.1214	472.2514	236.6293	4
8	833.4403	417.2238	815.4298	408.2185	L	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
9	948.4673	474.7373	930.4567	465.7320	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
10					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 15 ppm



RMS error 15 ppm

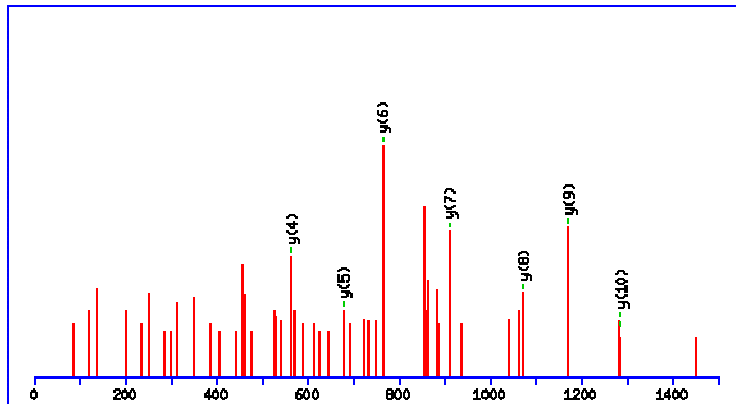
Peptide Number: 88592

MS/MS Fragmentation of **DGSLGNIDDLAQYADYNTCFSDVCER**Found in **IPI00478570** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SASH1 Uncharacterized protein

Match to Query 35804: 3288.403736 from(823.108210,4+) index(16748)

Title: Elution from: 46.35 to 46.35 period: 0 cycle: 1779 experiment: 7 polarity:+

Data file 120206ry_aHDF1419-P10_3_4.mgf



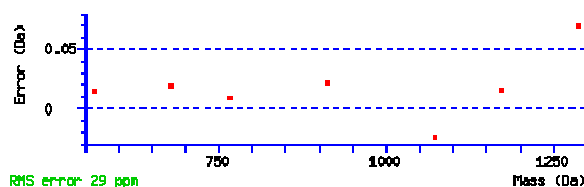
Monoisotopic mass of neutral peptide Mr(calc): 3288.3612

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

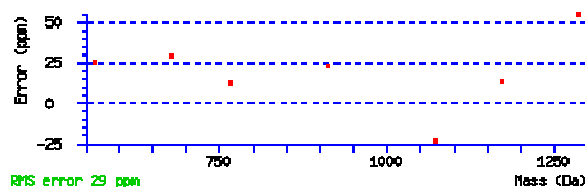
Ions Score: 31 Expect: 0.0067

Matches : 7/312 fragment ions using 14 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							28
2	173.0557	87.0315			155.0451	78.0262	G	3174.3415	1587.6744	3157.3150	1579.1611	3156.3310	1578.6691	27
3	260.0877	130.5475			242.0771	121.5422	S	3117.3201	1559.1637	3100.2935	1550.6504	3099.3095	1550.1584	26
4	373.1718	187.0895			355.1612	178.0842	L	3030.2880	1515.6477	3013.2615	1507.1344	3012.2775	1506.6424	25
5	430.1932	215.6003			412.1827	206.5950	G	2917.2040	1459.1056	2900.1774	1450.5923	2899.1934	1450.1003	24
6	544.2362	272.6217	527.2096	264.1084	526.2256	263.6164	N	2860.1825	1430.5949	2843.1560	1422.0816	2842.1719	1421.5896	23
7	657.3202	329.1638	640.2937	320.6505	639.3097	320.1585	I	2746.1396	1373.5734	2729.1130	1365.0602	2728.1290	1364.5681	22
8	772.3472	386.6772	755.3206	378.1640	754.3366	377.6719	D	2633.0555	1317.0314	2616.0290	1308.5181	2615.0449	1308.0261	21
9	887.3741	444.1907	870.3476	435.6774	869.3636	435.1854	D	2518.0286	1259.5179	2501.0020	1251.0046	2500.0180	1250.5126	20
10	1000.4582	500.7327	983.4316	492.2195	982.4476	491.7274	L	2403.0016	1202.0045	2385.9751	1193.4912	2384.9911	1192.9992	19
11	1071.4953	536.2513	1054.4687	527.7380	1053.4847	527.2460	A	2289.9176	1145.4624	2272.8910	1136.9491	2271.9070	1136.4571	18
12	1199.5539	600.2806	1182.5273	591.7673	1181.5433	591.2753	Q	2218.8804	1109.9439	2201.8539	1101.4306	2200.8699	1100.9386	17
13	1327.6125	664.3099	1310.5859	655.7966	1309.6019	655.3046	Q	2090.8219	1045.9146	2073.7953	1037.4013	2072.8113	1036.9093	16
14	1490.6758	745.8415	1473.6492	737.3283	1472.6652	736.8362	Y	1962.7633	981.8853	1945.7367	973.3720	1944.7527	972.8800	15
15	1561.7129	781.3601	1544.6863	772.8468	1543.7023	772.3548	A	1799.7000	900.3536	1782.6734	891.8403	1781.6894	891.3483	14
16	1676.7398	838.8736	1659.7133	830.3603	1658.7293	829.8683	D	1728.6628	864.8351	1711.6363	856.3218	1710.6523	855.8298	13
17	1839.8032	920.4052	1822.7766	911.8919	1821.7926	911.3999	Y	1613.6359	807.3216	1596.6094	798.8083	1595.6253	798.3163	12
18	2002.8665	1001.9369	1985.8399	993.4236	1984.8559	992.9316	Y	1450.5726	725.7899	1433.5460	717.2767	1432.5620	716.7846	11
19	2116.9094	1058.9583	2099.8829	1050.4451	2098.8989	1049.9531	N	1287.5092	644.2583	1270.4827	635.7450	1269.4987	635.2530	10
20	2217.9571	1109.4822	2200.9306	1100.9689	2199.9465	1100.4769	T	1173.4663	587.2368	1156.4398	578.7235	1155.4558	578.2315	9
21	2377.9877	1189.4975	2360.9612	1180.9842	2359.9772	1180.4922	C	1072.4186	536.7130	1055.3921	528.1997	1054.4081	527.7077	8
22	2525.0562	1263.0317	2508.0296	1254.5184	2507.0456	1254.0264	F	912.3880	456.6976	895.3614	448.1844	894.3774	447.6924	7
23	2612.0882	1306.5477	2595.0616	1298.0345	2594.0776	1297.5425	S	765.3196	383.1634	748.2930	374.6502	747.3090	374.1581	6
24	2727.1151	1364.0612	2710.0886	1355.5479	2709.1046	1355.0559	D	678.2876	339.6474	661.2610	331.1341	660.2770	330.6421	5
25	2826.1835	1413.5954	2809.1570	1405.0821	2808.1730	1404.5901	V	563.2606	282.1339	546.2341	273.6207	545.2500	273.1287	4
26	2986.2142	1493.6107	2969.1876	1485.0975	2968.2036	1484.6055	C	464.1922	232.5997	447.1656	224.0865	446.1816	223.5945	3
27	3115.2568	1558.1320	3098.2302	1549.6188	3097.2462	1549.1268	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
28							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 29 ppm



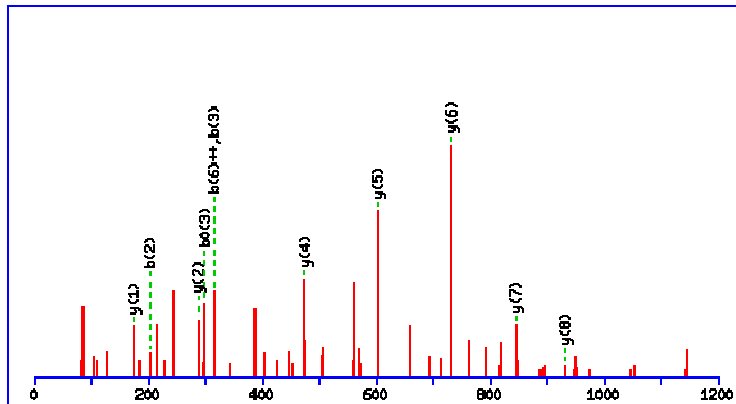
RMS error 29 ppm

Peptide Number: 88835MS/MS Fragmentation of **DSLEEGELR**Found in **IPI00071185** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CDK11B Isoform SV1 of Cyclin-dependent kinase 11B

Match to Query 12895: 1046.492408 from(524.253480,2+) index(29551)

Title: Elution from: 113.3 to 113.3 period: 0 cycle: 9584 experiment: 6 polarity: +

Data file 120210ry_32R1-32_3_1.mgf



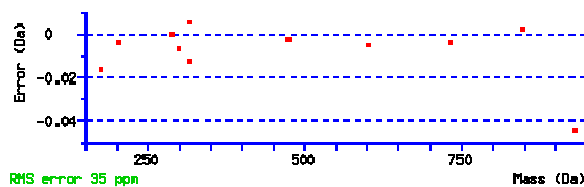
Monoisotopic mass of neutral peptide Mr(calc): 1046.4880

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

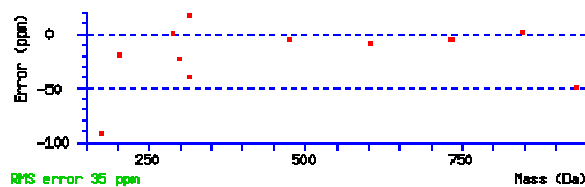
Ions Score: 39 Expect: 0.0058

Matches : 11/76 fragment ions using 27 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	98.0237	49.5155	D							9
2	203.0662	102.0368	185.0557	93.0315	S	932.4684	466.7378	915.4418	458.2245	914.4578	457.7325	8
3	316.1503	158.5788	298.1397	149.5735	L	845.4363	423.2218	828.4098	414.7085	827.4258	414.2165	7
4	445.1929	223.1001	427.1823	214.0948	E	732.3523	366.6798	715.3257	358.1665	714.3417	357.6745	6
5	574.2355	287.6214	556.2249	278.6161	E	603.3097	302.1585	586.2831	293.6452	585.2991	293.1532	5
6	631.2570	316.1321	613.2464	307.1268	G	474.2671	237.6372	457.2405	229.1239	456.2565	228.6319	4
7	760.2996	380.6534	742.2890	371.6481	E	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
8	873.3836	437.1954	855.3731	428.1902	L	288.2030	144.6051	271.1765	136.0919			2
9					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 35 ppm



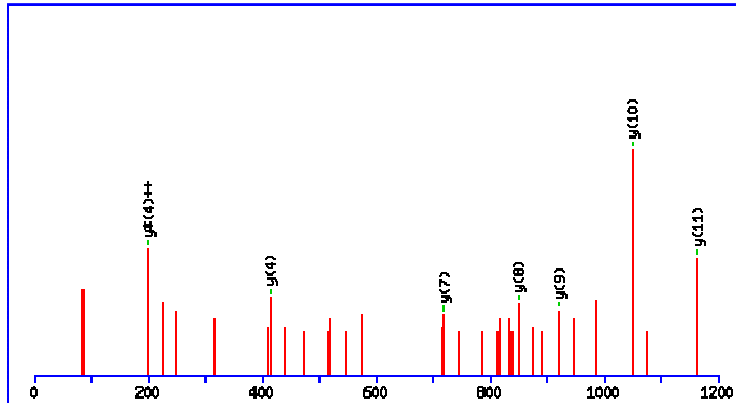
RMS error 35 ppm

Peptide Number: 88985MS/MS Fragmentation of **IIEAMGFTGPLK**Found in **IPI00219889** in **IPI_human**, Tax_Id=9606 Gene_Symbol=UQCC Isoform 2 of Ubiquinol-cytochrome c reductase complex chaperone CBP3 homolog

Match to Query 8444: 1275.674028 from(638.844290,2+) index(8611)

Title: Elution from: 21.2666666666667 to 21.2666666666667 period: 0 cycle: 791 experiment: 8 polarity: +

Data file 120126ry_585A1-55_2_3.mgf



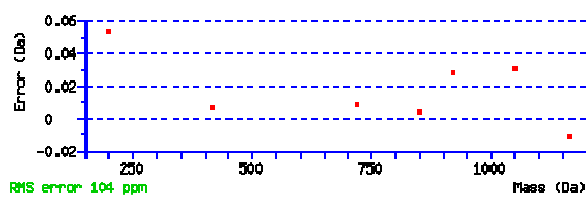
Monoisotopic mass of neutral peptide Mr(calc): 1275.6897

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

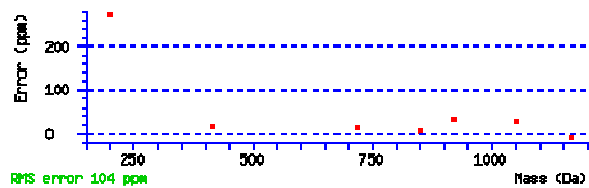
Ions Score: 46 Expect: 0.002

Matches : 7/98 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			I							12
2	227.1754	114.0913			I	1163.6129	582.3101	1146.5864	573.7968	1145.6023	573.3048	11
3	356.2180	178.6126	338.2074	169.6074	E	1050.5288	525.7681	1033.5023	517.2548	1032.5183	516.7628	10
4	427.2551	214.1312	409.2445	205.1259	A	921.4863	461.2468	904.4597	452.7335	903.4757	452.2415	9
5	558.2956	279.6514	540.2850	270.6462	M	850.4491	425.7282	833.4226	417.2149	832.4386	416.7229	8
6	615.3171	308.1622	597.3065	299.1569	G	719.4087	360.2080	702.3821	351.6947	701.3981	351.2027	7
7	762.3855	381.6964	744.3749	372.6911	F	662.3872	331.6972	645.3606	323.1840	644.3766	322.6920	6
8	863.4332	432.2202	845.4226	423.2149	T	515.3188	258.1630	498.2922	249.6498	497.3082	249.1577	5
9	920.4546	460.7309	902.4441	451.7257	G	414.2711	207.6392	397.2445	199.1259			4
10	1017.5074	509.2573	999.4968	500.2520	P	357.2496	179.1285	340.2231	170.6152			3
11	1130.5914	565.7994	1112.5809	556.7941	L	260.1969	130.6021	243.1703	122.0888			2
12					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 104 ppm



RMS error 104 ppm

Peptide Number: 89186

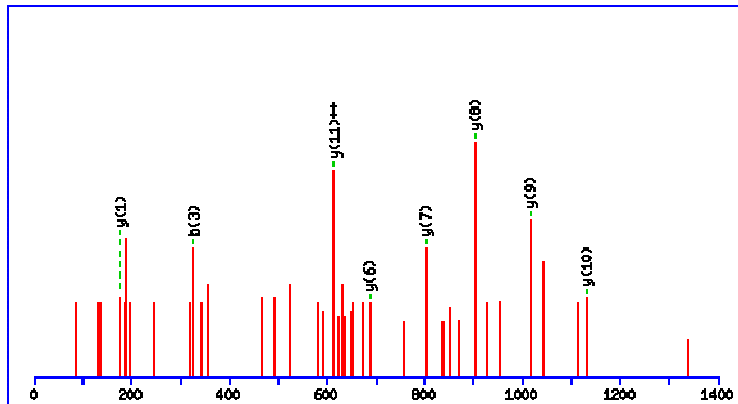
MS/MS Fragmentation of **IPDLTDVNAIDR**

Found in **IPI00003467** in **IPI_human**, Tax_Id=9606 Gene_Symbol=GABRB3 Isoform 1 of Gamma-aminobutyric acid receptor subunit beta-3

Match to Query 22376: 1340.673188 from(671.343870,2+) index(44479)

Title: Elution from: 108.25 to 108.25 period: 0 cycle: 4013 experiment: 8 polarity: +

Data file 120129ry_604A1-46_3_2.mgf



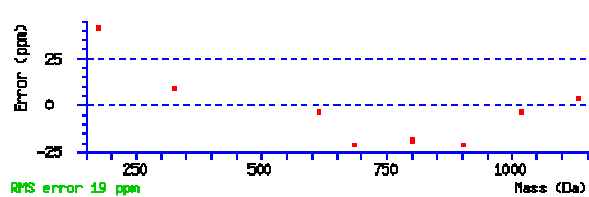
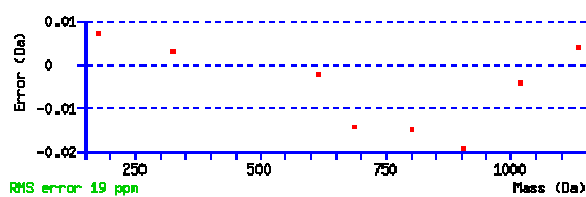
Monoisotopic mass of neutral peptide Mr(calc): 1340.6936

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 42 Expect: 0.0044

Matches : 8/112 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							12
2	211.1441	106.0757					P	1228.6168	614.8120	1211.5903	606.2988	1210.6062	605.8068	11
3	326.1710	163.5892			308.1605	154.5839	D	1131.5640	566.2857	1114.5375	557.7724	1113.5535	557.2804	10
4	439.2551	220.1312			421.2445	211.1259	L	1016.5371	508.7722	999.5106	500.2589	998.5265	499.7669	9
5	540.3028	270.6550			522.2922	261.6498	T	903.4530	452.2302	886.4265	443.7169	885.4425	443.2249	8
6	655.3297	328.1685			637.3192	319.1632	D	802.4054	401.7063	785.3788	393.1930	784.3948	392.7010	7
7	754.3981	377.7027			736.3876	368.6974	V	687.3784	344.1928	670.3519	335.6796	669.3678	335.1876	6
8	868.4411	434.7242	851.4145	426.2109	850.4305	425.7189	N	588.3100	294.6586	571.2835	286.1454	570.2994	285.6534	5
9	939.4782	470.2427	922.4516	461.7295	921.4676	461.2374	A	474.2671	237.6372	457.2405	229.1239	456.2565	228.6319	4
10	1052.5623	526.7848	1035.5357	518.2715	1034.5517	517.7795	I	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
11	1167.5892	584.2982	1150.5626	575.7850	1149.5786	575.2930	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
12							R	175.1190	88.0631	158.0924	79.5498			1



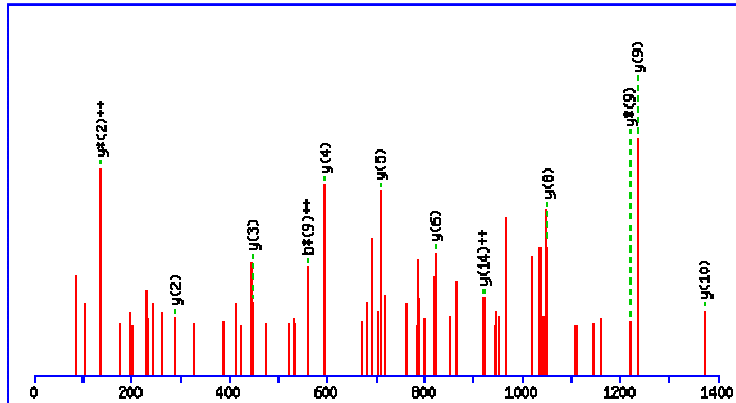
Peptide Number: 89469

MS/MS Fragmentation of **YGQDYSTHWNDLLFCLR**Found in **IPI00296379** in **IPI_human**, Tax_Id=9606 Gene_Symbol=TNFRSF10B Isoform Long of Tumor necrosis factor receptor superfamily member 10B

Match to Query 31260: 2186.996022 from(730.005950,3+) index(47761)

Title: Elution from: 114.2 to 114.2 period: 0 cycle: 4310 experiment: 2 polarity: +

Data file 120212ry_aHDF1388-P9_2_3.mgf



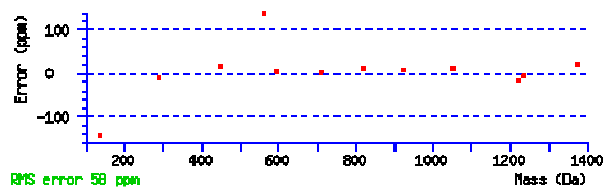
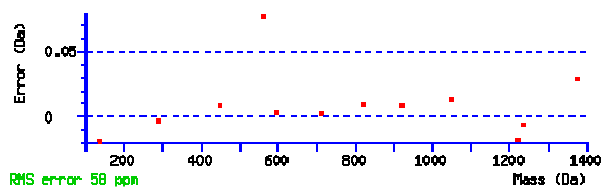
Monoisotopic mass of neutral peptide Mr(calc): 2186.9844

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 36 Expect: 0.009

Matches : 12/170 fragment ions using 25 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389					Y							17
2	221.0921	111.0497					G	2024.9283	1012.9678	2007.9018	1004.4545	2006.9178	1003.9625	16
3	349.1506	175.0790	332.1241	166.5657			Q	1967.9069	984.4571	1950.8803	975.9438	1949.8963	975.4518	15
4	464.1776	232.5924	447.1510	224.0792	446.1670	223.5872	D	1839.8483	920.4278	1822.8217	911.9145	1821.8377	911.4225	14
5	627.2409	314.1241	610.2144	305.6108	609.2304	305.1188	Y	1724.8213	862.9143	1707.7948	854.4010	1706.8108	853.9090	13
6	714.2729	357.6401	697.2464	349.1268	696.2624	348.6348	S	1561.7580	781.3826	1544.7315	772.8694	1543.7474	772.3774	12
7	815.3206	408.1640	798.2941	399.6507	797.3101	399.1587	T	1474.7260	737.8666	1457.6994	729.3534	1456.7154	728.8613	11
8	952.3795	476.6934	935.3530	468.1801	934.3690	467.6881	H	1373.6783	687.3428	1356.6518	678.8295	1355.6677	678.3375	10
9	1138.4589	569.7331	1121.4323	561.2198	1120.4483	560.7278	W	1236.6194	618.8133	1219.5928	610.3001	1218.6088	609.8081	9
10	1252.5018	626.7545	1235.4752	618.2413	1234.4912	617.7492	N	1050.5401	525.7737	1033.5135	517.2604	1032.5295	516.7684	8
11	1367.5287	684.2680	1350.5022	675.7547	1349.5182	675.2627	D	936.4971	468.7522	919.4706	460.2389	918.4866	459.7469	7
12	1480.6128	740.8100	1463.5862	732.2968	1462.6022	731.8047	L	821.4702	411.2387	804.4437	402.7255			6
13	1593.6968	797.3521	1576.6703	788.8388	1575.6863	788.3468	L	708.3861	354.6967	691.3596	346.1834			5
14	1740.7653	870.8863	1723.7387	862.3730	1722.7547	861.8810	F	595.3021	298.1547	578.2755	289.6414			4
15	1900.7959	950.9016	1883.7694	942.3883	1882.7853	941.8963	C	448.2337	224.6205	431.2071	216.1072			3
16	2013.8800	1007.4436	1996.8534	998.9304	1995.8694	998.4383	L	288.2030	144.6051	271.1765	136.0919			2
17							R	175.1190	88.0631	158.0924	79.5498			1

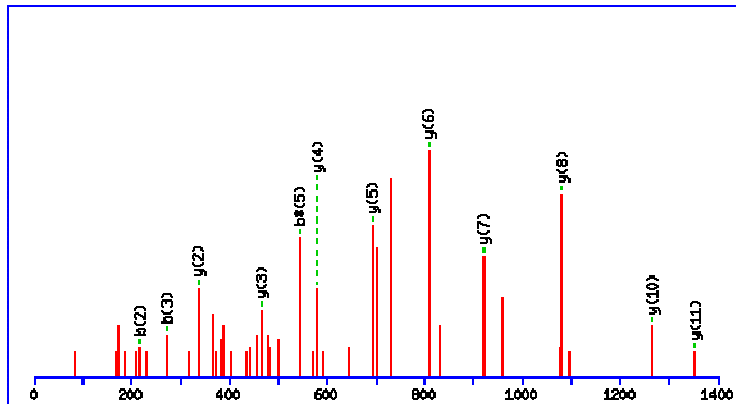


Peptide Number: 89560**MS/MS Fragmentation of QSGQCLDIDECR**Found in **IPI00294615** in **IPI_human**, Tax_Id=9606 Gene_Symbol=FBLN5 Fibulin-5

Match to Query 24904: 1479.610828 from(740.812690,2+) index(2913)

Title: Elution from: 7.85 to 7.85 period: 0 cycle: 303 experiment: 10 polarity: +

Data file 120208ry_Tig120slc-P8_1_2.mgf



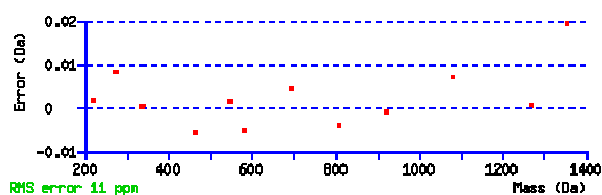
Monoisotopic mass of neutral peptide Mr(calc): 1479.6082

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

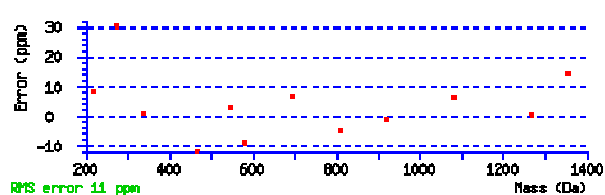
Ions Score: 62 Expect: 6.9e-006

Matches : 12/126 fragment ions using 24 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	129.0659	65.0366	112.0393	56.5233			Q							12
2	216.0979	108.5526	199.0713	100.0393	198.0873	99.5473	S	1352.5569	676.7821	1335.5304	668.2688	1334.5464	667.7768	11
3	273.1193	137.0633	256.0928	128.5500	255.1088	128.0580	G	1265.5249	633.2661	1248.4984	624.7528	1247.5143	624.2608	10
4	401.1779	201.0926	384.1514	192.5793	383.1674	192.0873	Q	1208.5034	604.7554	1191.4769	596.2421	1190.4929	595.7501	9
5	561.2086	281.1079	544.1820	272.5947	543.1980	272.1026	C	1080.4449	540.7261	1063.4183	532.2128	1062.4343	531.7208	8
6	674.2926	337.6500	657.2661	329.1367	656.2821	328.6447	L	920.4142	460.7107	903.3877	452.1975	902.4036	451.7055	7
7	789.3196	395.1634	772.2930	386.6502	771.3090	386.1581	D	807.3301	404.1687	790.3036	395.6554	789.3196	395.1634	6
8	902.4036	451.7055	885.3771	443.1922	884.3931	442.7002	I	692.3032	346.6552	675.2767	338.1420	674.2926	337.6500	5
9	1017.4306	509.2189	1000.4040	500.7057	999.4200	500.2136	D	579.2191	290.1132	562.1926	281.5999	561.2086	281.1079	4
10	1146.4732	573.7402	1129.4466	565.2270	1128.4626	564.7349	E	464.1922	232.5997	447.1656	224.0865	446.1816	223.5945	3
11	1306.5038	653.7556	1289.4773	645.2423	1288.4933	644.7503	C	335.1496	168.0784	318.1231	159.5652			2
12							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 11.11 ppm



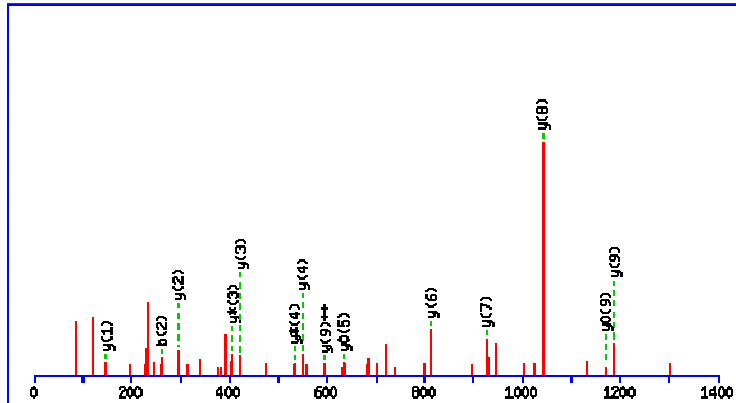
RMS error 11.11 ppm

Peptide Number: 89622MS/MS Fragmentation of **LFDDCTQQFK**Found in **IPI00442098** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PPP2R5C serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform isoform f

Match to Query 20820: 1300.572228 from(651.293390,2+) index(21055)

Title: Elution from: 49.55 to 49.55 period: 0 cycle: 1871 experiment: 9 polarity: +

Data file 120214ry_32R1-32_4.2.mgf



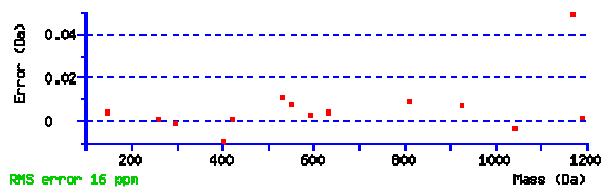
Monoisotopic mass of neutral peptide Mr(calc): 1300.5758

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

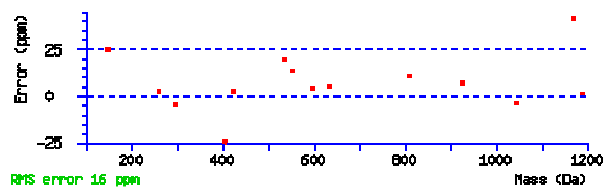
Ions Score: 40 Expect: 0.0021

Matches : 14/84 fragment ions using 33 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							10
2	261.1598	131.0835					F	1188.4990	594.7531	1171.4725	586.2399	1170.4884	585.7479	9
3	376.1867	188.5970			358.1761	179.5917	D	1041.4306	521.2189	1024.4040	512.7057	1023.4200	512.2136	8
4	491.2136	246.1105			473.2031	237.1052	D	926.4036	463.7055	909.3771	455.1922	908.3931	454.7002	7
5	651.2443	326.1258			633.2337	317.1205	C	811.3767	406.1920	794.3502	397.6787	793.3661	397.1867	6
6	752.2920	376.6496			734.2814	367.6443	T	651.3461	326.1767	634.3195	317.6634	633.3355	317.1714	5
7	880.3505	440.6789	863.3240	432.1656	862.3400	431.6736	Q	550.2984	275.6528	533.2718	267.1396			4
8	1008.4091	504.7082	991.3826	496.1949	990.3986	495.7029	Q	422.2398	211.6235	405.2132	203.1103			3
9	1155.4775	578.2424	1138.4510	569.7291	1137.4670	569.2371	F	294.1812	147.5942	277.1547	139.0810			2
10							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 16 ppm



RMS error 16 ppm

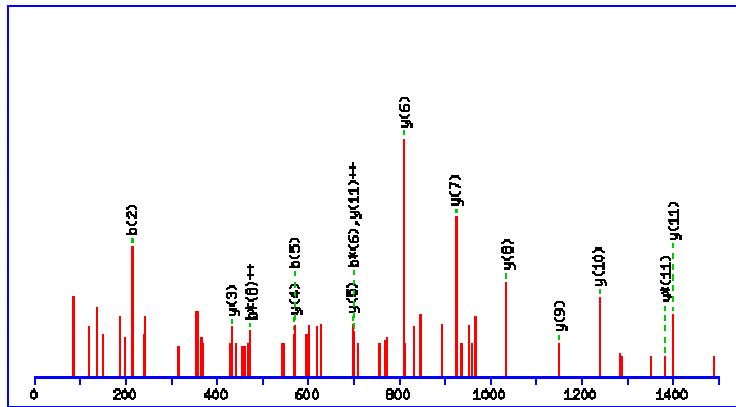
Peptide Number: 89632

MS/MS Fragmentation of **LTLENFYNSLILQHEER**Found in **IPI01011144** in **IPI_human**, Tax_Id=9606 Gene_Symbol=STK38L Uncharacterized protein

Match to Query 16462: 2118.075822 from(707.032550,3+) index(766)

Title: Elution from: 1.83333333333333 to 1.83333333333333 period: 0 cycle: 68 experiment: 5 polarity: +

Data file 120210ry_32R1-32_2_4.mgf



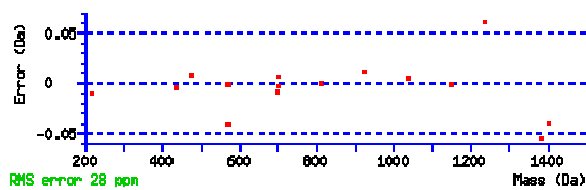
Monoisotopic mass of neutral peptide Mr(calcd): 2118.0745

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

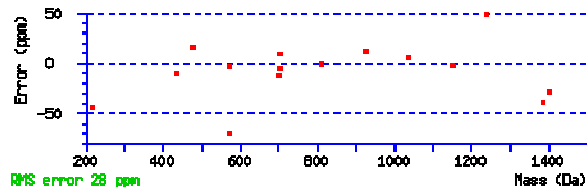
Ions Score: 49 Expect: 0.00097

Matches : 15/180 fragment ions using 27 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							17
2	215.1390	108.0731			197.1285	99.0679	T	2005.9978	1003.5025	1988.9712	994.9893	1987.9872	994.4972	16
3	328.2231	164.6152			310.2125	155.6099	L	1904.9501	952.9787	1887.9236	944.4654	1886.9395	943.9734	15
4	457.2657	229.1365			439.2551	220.1312	E	1791.8660	896.4367	1774.8395	887.9234	1773.8555	887.4314	14
5	571.3086	286.1579	554.2821	277.6447	553.2980	277.1527	N	1662.8234	831.9154	1645.7969	823.4021	1644.8129	822.9101	13
6	718.3770	359.6921	701.3505	351.1789	700.3665	350.6869	F	1548.7805	774.8939	1531.7540	766.3806	1530.7700	765.8886	12
7	881.4403	441.2238	864.4138	432.7105	863.4298	432.2185	Y	1401.7121	701.3597	1384.6856	692.8464	1383.7015	692.3544	11
8	968.4724	484.7398	951.4458	476.2266	950.4618	475.7345	S	1238.6488	619.8280	1221.6222	611.3148	1220.6382	610.8227	10
9	1082.5153	541.7613	1065.4888	533.2480	1064.5047	532.7560	N	1151.6167	576.3120	1134.5902	567.7987	1133.6062	567.3067	9
10	1195.5994	598.3033	1178.5728	589.7900	1177.5888	589.2980	L	1037.5738	519.2905	1020.5473	510.7773	1019.5633	510.2853	8
11	1308.6834	654.8454	1291.6569	646.3321	1290.6729	645.8401	I	924.4898	462.7485	907.4632	454.2352	906.4792	453.7432	7
12	1421.7675	711.3874	1404.7409	702.8741	1403.7569	702.3821	L	811.4057	406.2065	794.3791	397.6932	793.3951	397.2012	6
13	1549.8261	775.4167	1532.7995	766.9034	1531.8155	766.4114	Q	698.3216	349.6645	681.2951	341.1512	680.3111	340.6592	5
14	1686.8850	843.9461	1669.8584	835.4329	1668.8744	834.9408	H	570.2631	285.6352	553.2365	277.1219	552.2525	276.6299	4
15	1815.9276	908.4674	1798.9010	899.9542	1797.9170	899.4621	E	433.2041	217.1057	416.1776	208.5924	415.1936	208.1004	3
16	1944.9702	972.9887	1927.9436	964.4754	1926.9596	963.9834	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
17							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 28 ppm



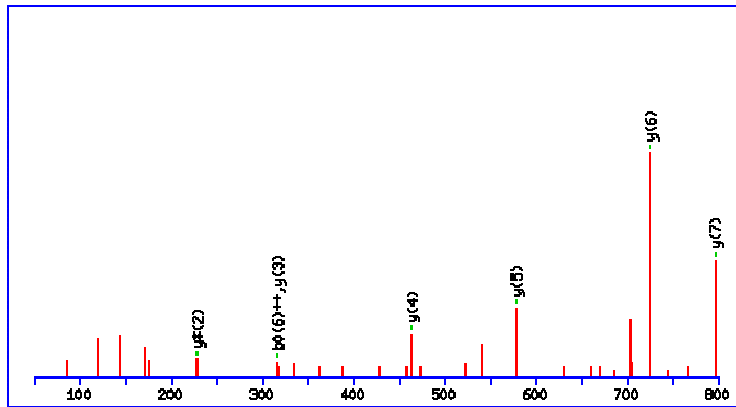
RMS error 28 ppm

Peptide Number: 89744MS/MS Fragmentation of **VAFDFAAR**Found in **IPI00747159** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ACAD8 Isobutyryl-CoA dehydrogenase, mitochondrial

Match to Query 5846: 895.454828 from(448.734690,2+) index(33326)

Title: Elution from: 80.1666666666667 to 80.1666666666667 period: 0 cycle: 3002 experiment: 3 polarity:+

Data file 120126ry_585A1-55_2_2.mgf



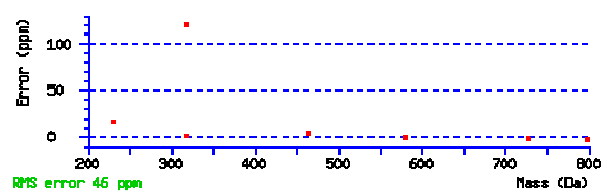
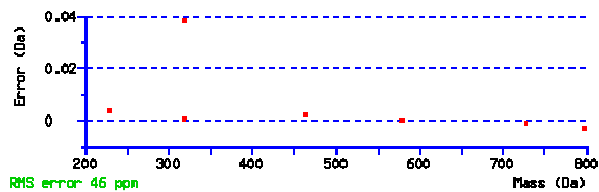
Monoisotopic mass of neutral peptide Mr(calc): 895.4552

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 43 Expect: 0.0024

Matches : 7/56 fragment ions using 8 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415			V							8
2	171.1128	86.0600			A	797.3941	399.2007	780.3675	390.6874	779.3835	390.1954	7
3	318.1812	159.5942			F	726.3570	363.6821	709.3304	355.1688	708.3464	354.6768	6
4	433.2082	217.1077	415.1976	208.1024	D	579.2885	290.1479	562.2620	281.6346	561.2780	281.1426	5
5	580.2766	290.6419	562.2660	281.6366	F	464.2616	232.6344	447.2350	224.1212			4
6	651.3137	326.1605	633.3031	317.1552	A	317.1932	159.1002	300.1666	150.5870			3
7	722.3508	361.6790	704.3402	352.6738	A		246.1561	123.5817	229.1295	115.0684		2
8					R	175.1190	88.0631	158.0924	79.5498			1



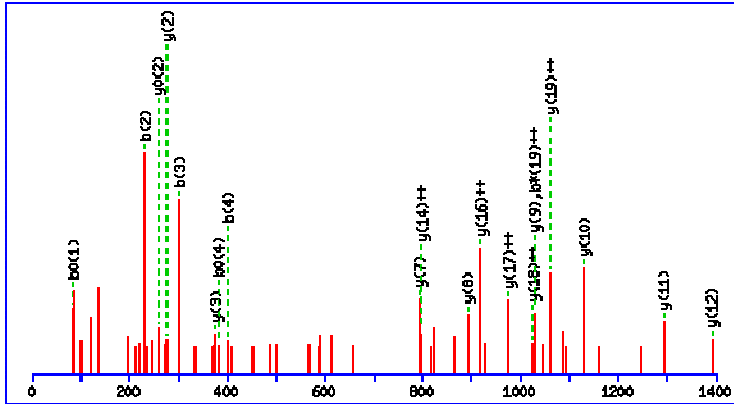
Peptide Number: 89949

MS/MS Fragmentation of **TQAVLDQSDVYTHVLSAFVEK**Found in **IPI00149964** in **IPI_human**, Tax_Id=9606 Gene_Symbol=C18orf8 Uncharacterized protein C18orf8

Match to Query 33955: 2349.208092 from(784.076640,3+) index(47746)

Title: Elution from: 118.25 to 118.25 period: 0 cycle: 4470 experiment: 7 polarity: +

Data file 120206ry_aHDF1419-P10_2_3.mgf



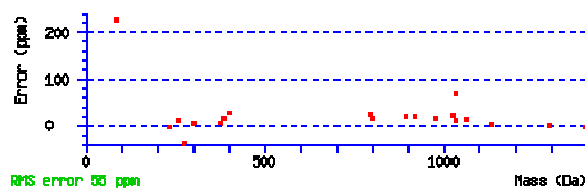
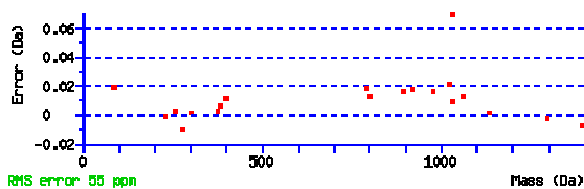
Monoisotopic mass of neutral peptide Mr(calc): 2349.1853

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 42 Expect: 0.0039

Matches : 20/236 fragment ions using 41 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							21
2	230.1135	115.5604	213.0870	107.0471	212.1030	106.5551	Q	2249.1448	1125.0761	2232.1183	1116.5628	2231.1343	1116.0708	20
3	301.1506	151.0790	284.1241	142.5657	283.1401	142.0737	A	2121.0863	1061.0468	2104.0597	1052.5335	2103.0757	1052.0415	19
4	400.2191	200.6132	383.1925	192.0999	382.2085	191.6079	V	2050.0491	1025.5282	2033.0226	1017.0149	2032.0386	1016.5229	18
5	513.3031	257.1552	496.2766	248.6419	495.2926	248.1499	L	1950.9807	975.9940	1933.9542	967.4807	1932.9702	966.9887	17
6	628.3301	314.6687	611.3035	306.1554	610.3195	305.6634	D	1837.8967	919.4520	1820.8701	910.9387	1819.8861	910.4467	16
7	756.3886	378.6980	739.3621	370.1847	738.3781	369.6927	Q	1722.8697	861.9385	1705.8432	853.4252	1704.8592	852.9332	15
8	843.4207	422.2140	826.3941	413.7007	825.4101	413.2087	S	1594.8112	797.9092	1577.7846	789.3959	1576.8006	788.9039	14
9	958.4476	479.7274	941.4211	471.2142	940.4371	470.7222	D	1507.7791	754.3932	1490.7526	745.8799	1489.7686	745.3879	13
10	1057.5160	529.2617	1040.4895	520.7484	1039.5055	520.2564	V	1392.7522	696.8797	1375.7256	688.3665	1374.7416	687.8744	12
11	1220.5794	610.7933	1203.5528	602.2800	1202.5688	601.7880	Y	1293.6838	647.3455	1276.6572	638.8322	1275.6732	638.3402	11
12	1321.6270	661.3172	1304.6005	652.8039	1303.6165	652.3119	T	1130.6204	565.8139	1113.5939	557.3006	1112.6099	556.8086	10
13	1458.6860	729.8466	1441.6594	721.3333	1440.6754	720.8413	H	1029.5728	515.2900	1012.5462	506.7767	1011.5622	506.2847	9
14	1557.7544	779.3808	1540.7278	770.8675	1539.7438	770.3755	V	892.5138	446.7606	875.4873	438.2473	874.5033	437.7553	8
15	1670.8384	835.9229	1653.8119	827.4096	1652.8279	826.9176	L	793.4454	397.2264	776.4189	388.7131	775.4349	388.2211	7
16	1757.8705	879.4389	1740.8439	870.9256	1739.8599	870.4336	S	680.3614	340.6843	663.3348	332.1710	662.3508	331.6790	6
17	1828.9076	914.9574	1811.8810	906.4441	1810.8970	905.9521	A	593.3293	297.1683	576.3028	288.6550	575.3188	288.1630	5
18	1975.9760	988.4916	1958.9494	979.9784	1957.9654	979.4863	F	522.2922	261.6498	505.2657	253.1365	504.2817	252.6445	4
19	2075.0444	1038.0258	2058.0178	1029.5126	2057.0338	1029.0206	V	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
20	2204.0870	1102.5471	2187.0604	1094.0339	2186.0764	1093.5419	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
21							K	147.1128	74.0600	130.0863	65.5468			1



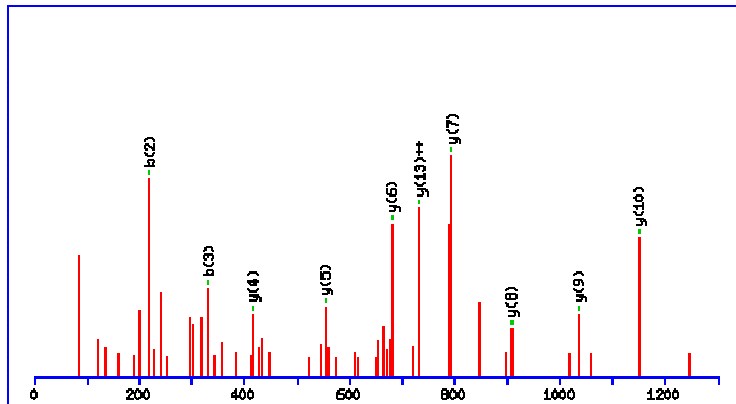
Peptide Number: 90033

MS/MS Fragmentation of **GCILDSLQIIQHLAGR**Found in **IPI00219849** in **IPI_human**, Tax_Id=9606 Gene_Symbol=RTEL1 Isoform 1 of Regulator of telomere elongation helicase 1

Match to Query 1753: 1907.993052 from(637.004960,3+) index(2937)

Title: Elution from: 12.0166666666667 to 12.0166666666667 period: 0 cycle: 474 experiment: 1 polarity: +

Data file 120210ry_32R1-32_2_5.mgf



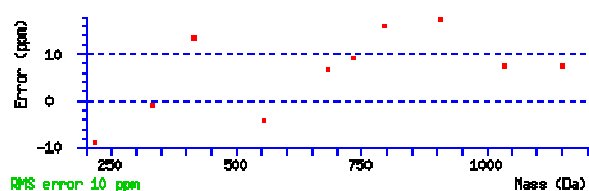
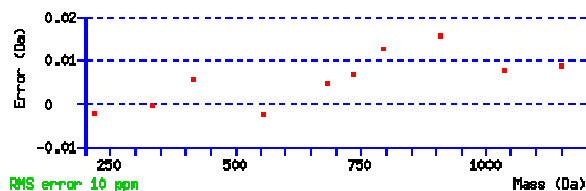
Monoisotopic mass of neutral peptide Mr(calc): 1907.9887

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 56 Expect: 0.00017

Matches : 10/150 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							17
2	218.0594	109.5333					C	1851.9745	926.4909	1834.9480	917.9776	1833.9640	917.4856	16
3	331.1435	166.0754					I	1691.9439	846.4756	1674.9173	837.9623	1673.9333	837.4703	15
4	444.2275	222.6174					L	1578.8598	789.9336	1561.8333	781.4203	1560.8493	780.9283	14
5	559.2545	280.1309			541.2439	271.1256	D	1465.7758	733.3915	1448.7492	724.8782	1447.7652	724.3862	13
6	646.2865	323.6469			628.2759	314.6416	S	1350.7488	675.8781	1333.7223	667.3648	1332.7383	666.8728	12
7	759.3706	380.1889			741.3600	371.1836	L	1263.7168	632.3620	1246.6902	623.8488	1245.7062	623.3568	11
8	874.3975	437.7024			856.3869	428.6971	D	1150.6327	575.8200	1133.6062	567.3067	1132.6222	566.8147	10
9	1002.4561	501.7317	985.4295	493.2184	984.4455	492.7264	Q	1035.6058	518.3065	1018.5792	509.7933			9
10	1115.5401	558.2737	1098.5136	549.7604	1097.5296	549.2684	I	907.5472	454.2772	890.5207	445.7640			8
11	1228.6242	614.8157	1211.5977	606.3025	1210.6136	605.8105	I	794.4631	397.7352	777.4366	389.2219			7
12	1356.6828	678.8450	1339.6562	670.3318	1338.6722	669.8397	Q	681.3791	341.1932	664.3525	332.6799			6
13	1493.7417	747.3745	1476.7151	738.8612	1475.7311	738.3692	H	553.3205	277.1639	536.2940	268.6506			5
14	1606.8258	803.9165	1589.7992	795.4032	1588.8152	794.9112	L	416.2616	208.6344	399.2350	200.1212			4
15	1677.8629	839.4351	1660.8363	830.9218	1659.8523	830.4298	A	303.1775	152.0924	286.1510	143.5791			3
16	1734.8843	867.9458	1717.8578	859.4325	1716.8738	858.9405	G	232.1404	116.5738	215.1139	108.0606			2
17							R	175.1190	88.0631	158.0924	79.5498			1



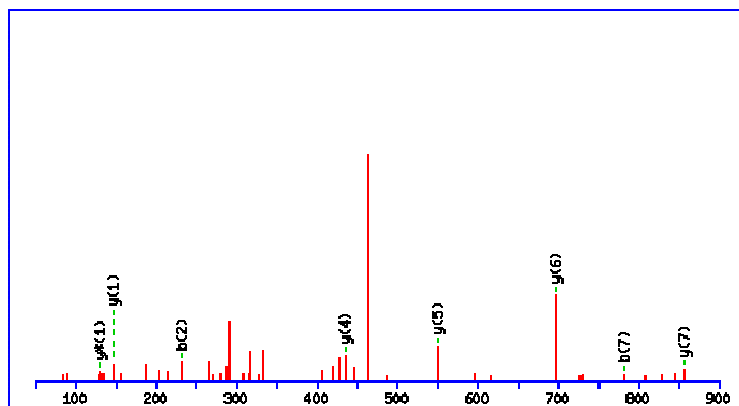
Peptide Number: 90723

MS/MS Fragmentation of **ACFDGAK**Found in **IPI00297322** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ARFGAP2 ADP-ribosylation factor GTPase-activating protein 2

Match to Query 7751: 927.362148 from(464.688350,2+) index(12244)

Title: Elution from: 62.9 to 62.9 period: 0 cycle: 6165 experiment: 5 polarity: +

Data file 120208ry_Tig120slc-P8_1_1.mgf



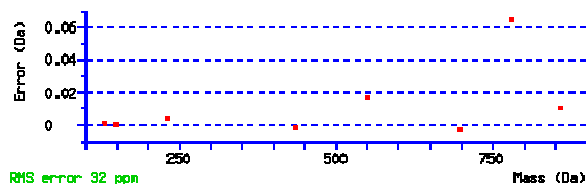
Monoisotopic mass of neutral peptide Mr(calc): 927.3579

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

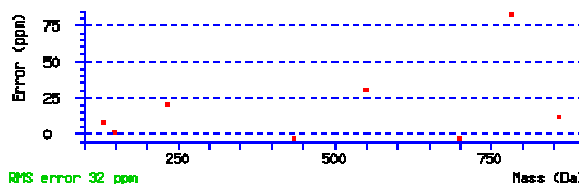
Ions Score: 27 Expect: 0.01

Matches : 8/56 fragment ions using 16 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258			A							8
2	232.0750	116.5412			C	857.3280	429.1677	840.3015	420.6544	839.3175	420.1624	7
3	379.1435	190.0754			F	697.2974	349.1523	680.2708	340.6391	679.2868	340.1470	6
4	494.1704	247.5888	476.1598	238.5836	D	550.2290	275.6181	533.2024	267.1049	532.2184	266.6128	5
5	654.2010	327.6042	636.1905	318.5989	C	435.2020	218.1047	418.1755	209.5914			4
6	711.2225	356.1149	693.2119	347.1096	G	275.1714	138.0893	258.1448	129.5761			3
7	782.2596	391.6334	764.2491	382.6282	A	218.1499	109.5786	201.1234	101.0653			2
8					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 32 ppm



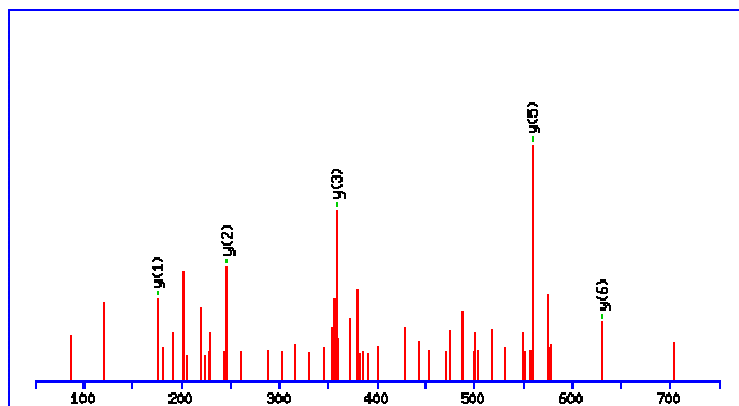
RMS error 32 ppm

Peptide Number: 90746MS/MS Fragmentation of **MASIIAR**Found in **IPI00166136** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ZCCHC12 Zinc finger CCHC domain-containing protein 12

Match to Query 2221: 776.409148 from(389.211850,2+) index(18394)

Title: Elution from: 87.8 to 87.8 period: 0 cycle: 7257 experiment: 3 polarity: +

Data file 120129ry_604A1-46_3_1.mgf



Monoisotopic mass of neutral peptide Mr(calc): 776.4214

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

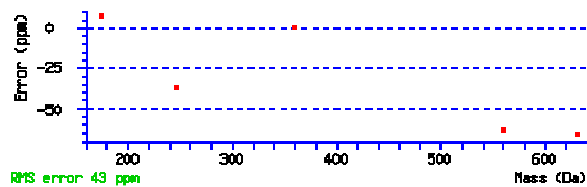
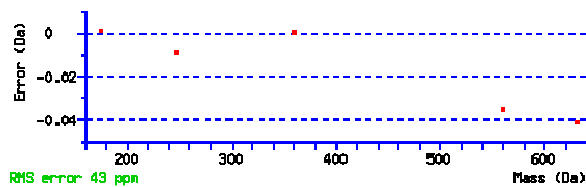
Variable modifications:

M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

Ions Score: 43 Expect: 0.0036

Matches : 5/68 fragment ions using 7 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	148.0427	74.5250			M							7
2	219.0798	110.0435			A	630.3933	315.7003	613.3668	307.1870	612.3828	306.6950	6
3	306.1118	153.5595	288.1013	144.5543	S	559.3562	280.1817	542.3297	271.6685	541.3457	271.1765	5
4	419.1959	210.1016	401.1853	201.0963	I	472.3242	236.6657	455.2976	228.1525			4
5	532.2799	266.6436	514.2694	257.6383	I	359.2401	180.1237	342.2136	171.6104			3
6	603.3171	302.1622	585.3065	293.1569	A	246.1561	123.5817	229.1295	115.0684			2
7					R	175.1190	88.0631	158.0924	79.5498			1



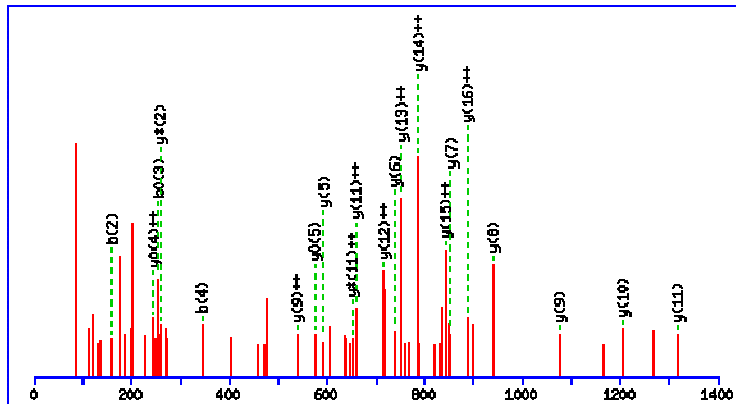
Peptide Number: 91168

MS/MS Fragmentation of **ASLAAILHSLFSTEQK**Found in **IPI00436705** in **IPI_human**, Tax_Id=9606 Gene_Symbol=MORC3 Uncharacterized protein

Match to Query 9909: 1843.955292 from(615.659040,3+) index(7208)

Title: Elution from: 19.1666666666667 to 19.1666666666667 period: 0 cycle: 738 experiment: 4 polarity:+

Data file 120210ry_32R1-32_3_4.mgf



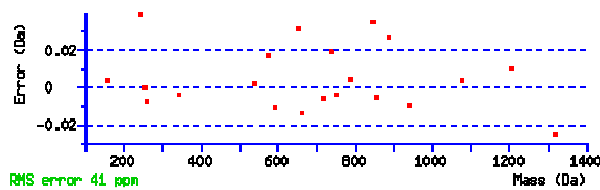
Monoisotopic mass of neutral peptide Mr(calc): 1843.9679

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

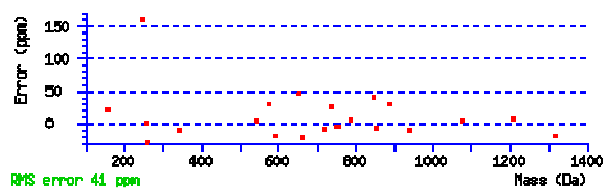
Ions Score: 45 Expect: 0.0024

Matches : 21/156 fragment ions using 45 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							17
2	159.0764	80.0418			141.0659	71.0366	S	1773.9381	887.4727	1756.9116	878.9594	1755.9276	878.4674	16
3	272.1605	136.5839			254.1499	127.5786	L	1686.9061	843.9567	1669.8796	835.4434	1668.8955	834.9514	15
4	343.1976	172.1024			325.1870	163.0972	A	1573.8220	787.4147	1556.7955	778.9014	1555.8115	778.4094	14
5	414.2347	207.6210			396.2241	198.6157	A	1502.7849	751.8961	1485.7584	743.3828	1484.7744	742.8908	13
6	527.3188	264.1630			509.3082	255.1577	I	1431.7478	716.3775	1414.7213	707.8643	1413.7373	707.3723	12
7	640.4028	320.7051			622.3923	311.6998	L	1318.6638	659.8355	1301.6372	651.3222	1300.6532	650.8302	11
8	769.4454	385.2264			751.4349	376.2211	E	1205.5797	603.2935	1188.5531	594.7802	1187.5691	594.2882	10
9	906.5043	453.7558			888.4938	444.7505	H	1076.5371	538.7722	1059.5106	530.2589	1058.5265	529.7669	9
10	993.5364	497.2718			975.5258	488.2665	S	939.4782	470.2427	922.4516	461.7295	921.4676	461.2374	8
11	1106.6204	553.8139			1088.6099	544.8086	L	852.4462	426.7267	835.4196	418.2134	834.4356	417.7214	7
12	1253.6888	627.3481			1235.6783	618.3428	F	739.3621	370.1847	722.3355	361.6714	721.3515	361.1794	6
13	1340.7209	670.8641			1322.7103	661.8588	S	592.2937	296.6505	575.2671	288.1372	574.2831	287.6452	5
14	1441.7686	721.3879			1423.7580	712.3826	T	505.2617	253.1345	488.2351	244.6212	487.2511	244.1292	4
15	1570.8111	785.9092			1552.8006	776.9039	E	404.2140	202.6106	387.1874	194.0974	386.2034	193.6053	3
16	1698.8697	849.9385	1681.8432	841.4252	1680.8592	840.9332	Q	275.1714	138.0893	258.1448	129.5761			2
17							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 41 ppm



RMS error 41 ppm

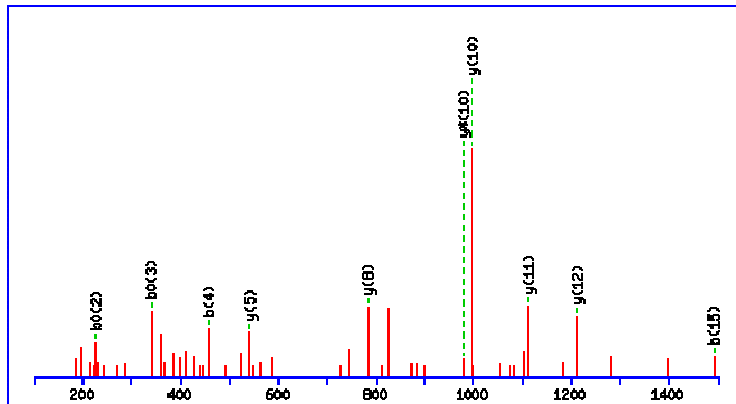
Peptide Number: 91221

MS/MS Fragmentation of **ELDVVDPDGSVPVGLR**Found in **IPI00414008** in **IPI_human**, Tax_Id=9606 Gene_Symbol=LMOD1 Isoform 1 of Leiomodin-1

Match to Query 14132: 1665.852008 from(833.933280,2+) index(4448)

Title: Elution from: 11.6 to 11.6 period: 0 cycle: 447 experiment: 10 polarity: +

Data file 120208ry_Tig120slc-P8_1_3.mgf



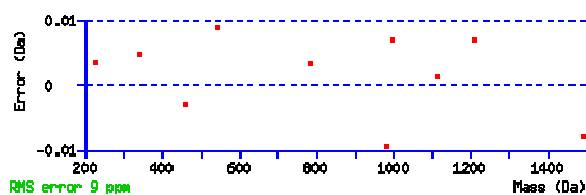
Monoisotopic mass of neutral peptide Mr(calc): 1665.8574

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

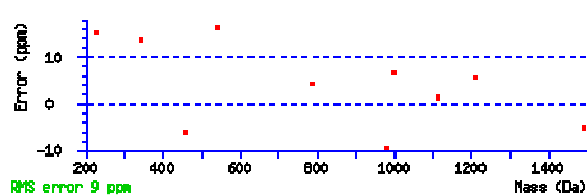
Ions Score: 40 Expect: 0.0058

Matches : 10/138 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286	112.0393	56.5233	E							16
2	243.1339	122.0706	225.1234	113.0653	L	1537.8220	769.4147	1520.7955	760.9014	1519.8115	760.4094	15
3	358.1609	179.5841	340.1503	170.5788	D	1424.7380	712.8726	1407.7114	704.3594	1406.7274	703.8673	14
4	457.2293	229.1183	439.2187	220.1130	V	1309.7110	655.3592	1292.6845	646.8459	1291.7005	646.3539	13
5	556.2977	278.6525	538.2871	269.6472	V	1210.6426	605.8250	1193.6161	597.3117	1192.6321	596.8197	12
6	671.3246	336.1660	653.3141	327.1607	D	1111.5742	556.2907	1094.5477	547.7775	1093.5636	547.2855	11
7	768.3774	384.6923	750.3668	375.6871	P	996.5473	498.7773	979.5207	490.2640	978.5367	489.7720	10
8	883.4044	442.2058	865.3938	433.2005	D	899.4945	450.2509	882.4680	441.7376	881.4839	441.2456	9
9	940.4258	470.7165	922.4153	461.7113	G	784.4676	392.7374	767.4410	384.2241	766.4570	383.7321	8
10	1027.4578	514.2326	1009.4473	505.2273	S	727.4461	364.2267	710.4196	355.7134	709.4355	355.2214	7
11	1126.5263	563.7668	1108.5157	554.7615	V	640.4141	320.7107	623.3875	312.1974			6
12	1223.5790	612.2932	1205.5685	603.2879	P	541.3457	271.1765	524.3191	262.6632			5
13	1322.6474	661.8274	1304.6369	652.8221	V	444.2929	222.6501	427.2663	214.1368			4
14	1379.6689	690.3381	1361.6583	681.3328	G	345.2245	173.1159	328.1979	164.6026			3
15	1492.7530	746.8801	1474.7424	737.8748	L	288.2030	144.6051	271.1765	136.0919			2
16					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 9 ppm



RMS error 9 ppm

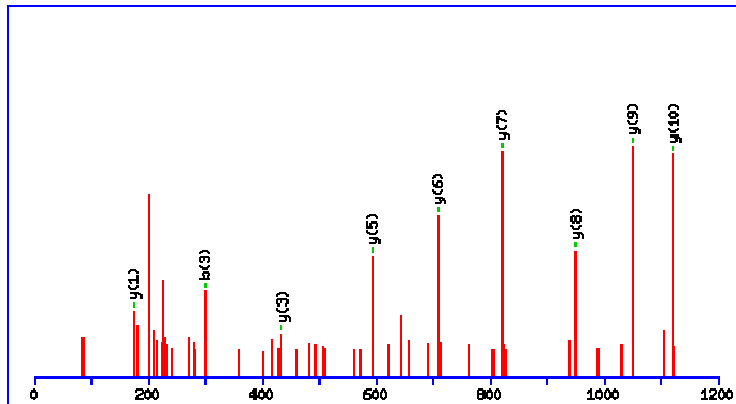
Peptide Number: 91428

MS/MS Fragmentation of **NLATQLDSAFIR**Found in **IPI00018031** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ALDH3B1 Isoform 1 of Aldehyde dehydrogenase family 3 member B1

Match to Query 6682: 1347.717048 from(674.865800,2+) index(25756)

Title: Elution from: 61.7666666666667 to 61.7666666666667 period: 0 cycle: 2341 experiment: 6 polarity:+

Data file 120212ry_aHDF1388-P9_2_3.mgf



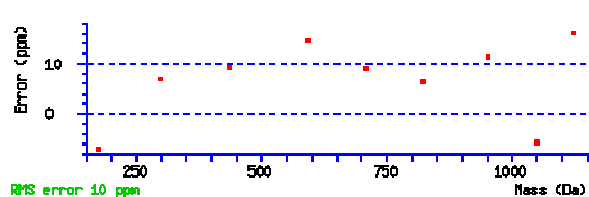
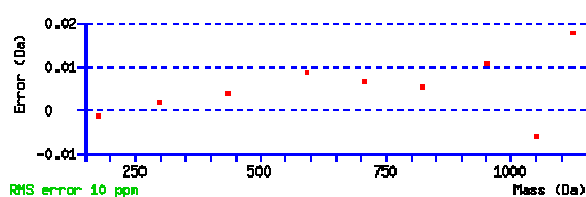
Monoisotopic mass of neutral peptide Mr(calc): 1347.7146

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 74 Expect: 2.7e-006

Matches : 9/118 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							12
2	228.1343	114.5708	211.1077	106.0575			L	1234.6790	617.8431	1217.6525	609.3299	1216.6684	608.8379	11
3	299.1714	150.0893	282.1448	141.5761			A	1121.5949	561.3011	1104.5684	552.7878	1103.5844	552.2958	10
4	400.2191	200.6132	383.1925	192.0999	382.2085	191.6079	T	1050.5578	525.7826	1033.5313	517.2693	1032.5473	516.7773	9
5	528.2776	264.6425	511.2511	256.1292	510.2671	255.6372	Q	949.5102	475.2587	932.4836	466.7454	931.4996	466.2534	8
6	641.3617	321.1845	624.3352	312.6712	623.3511	312.1792	L	821.4516	411.2294	804.4250	402.7162	803.4410	402.2241	7
7	756.3886	378.6980	739.3621	370.1847	738.3781	369.6927	D	708.3675	354.6874	691.3410	346.1741	690.3569	345.6821	6
8	843.4207	422.2140	826.3941	413.7007	825.4101	413.2087	S	593.3406	297.1739	576.3140	288.6606	575.3300	288.1686	5
9	914.4578	457.7325	897.4312	449.2193	896.4472	448.7272	A	506.3085	253.6579	489.2820	245.1446			4
10	1061.5262	531.2667	1044.4997	522.7535	1043.5156	522.2615	F	435.2714	218.1394	418.2449	209.6261			3
11	1174.6103	587.8088	1157.5837	579.2955	1156.5997	578.8035	I	288.2030	144.6051	271.1765	136.0919			2
12							R	175.1190	88.0631	158.0924	79.5498			1

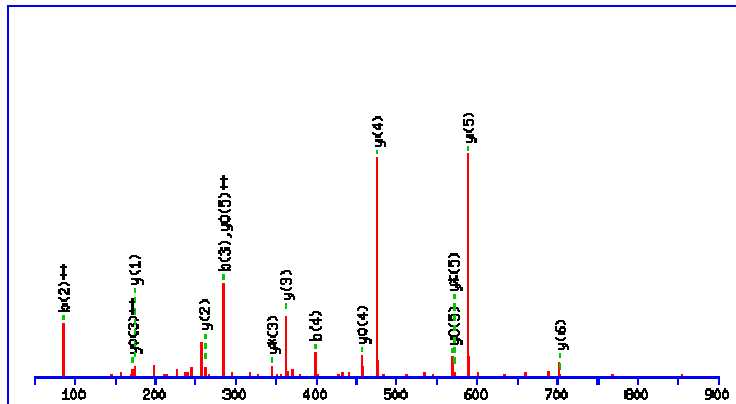


Peptide Number: 91470**MS/MS Fragmentation of GLDLLTSR**Found in **IPI00927055** in **IPI_human**, Tax_Id=9606 Gene_Symbol=C2orf80 16 kDa protein

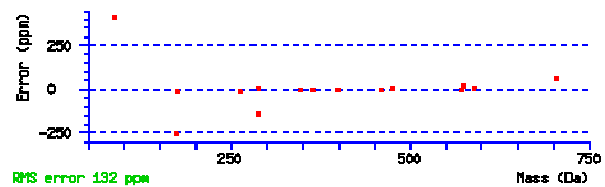
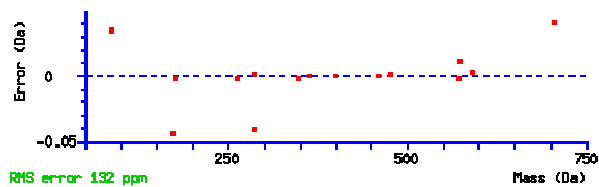
Match to Query 2752: 873.488388 from(437.751470,2+) index(9705)

Title: Elution from: 23.1 to 23.1 period: 0 cycle: 874 experiment: 3 polarity:+

Data file 120208ry_Tig120slc-P8_2_2.mgf

**Monoisotopic mass of neutral peptide Mr(calcd):** 873.4920**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)**Ions Score:** 48 **Expect:** 0.0015**Matches :** 15/64 fragment ions using 22 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180			Q							8
2	171.1128	86.0600			L	817.4778	409.2425	800.4512	400.7293	799.4672	400.2373	7
3	286.1397	143.5735	268.1292	134.5682	D	704.3937	352.7005	687.3672	344.1872	686.3832	343.6952	6
4	399.2238	200.1155	381.2132	191.1103	L	589.3668	295.1870	572.3402	286.6738	571.3562	286.1817	5
5	512.3079	256.6576	494.2973	247.6523	L	476.2827	238.6450	459.2562	230.1317	458.2722	229.6397	4
6	613.3556	307.1814	595.3450	298.1761	T	363.1987	182.1030	346.1721	173.5897	345.1881	173.0977	3
7	700.3876	350.6974	682.3770	341.6921	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
8					R	175.1190	88.0631	158.0924	79.5498			1



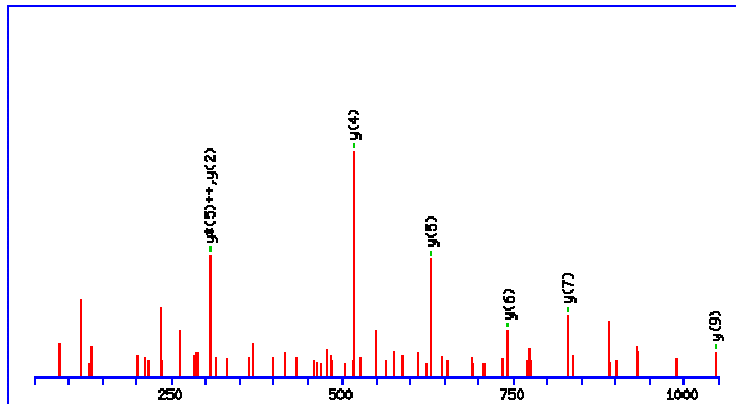
Peptide Number: 91487

MS/MS Fragmentation of **FDTSILPICK**Found in **IPI00005292** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SPOCK1 Testican-1

Match to Query 3061: 1192.615888 from(597.315220,2+) index(3841)

Title: Elution from: 10.1333333333333 to 10.1333333333333 period: 0 cycle: 392 experiment: 4 polarity: +

Data file 120208ry_Tig120slc-P8_1_3.mgf



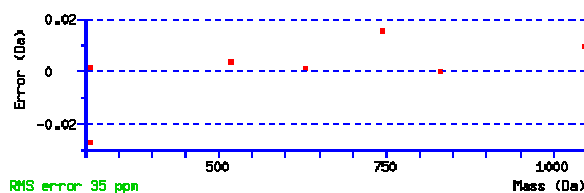
Monoisotopic mass of neutral peptide Mr(calc): 1192.6162

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

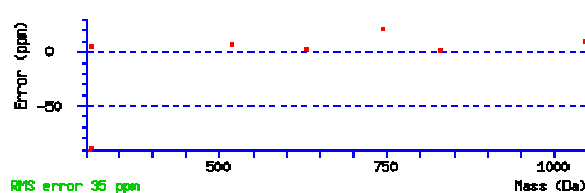
Ions Score: 43 Expect: 0.0035

Matches : 7/76 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415			F							10
2	263.1026	132.0550	245.0921	123.0497	D	1046.5551	523.7812	1029.5285	515.2679	1028.5445	514.7759	9
3	364.1503	182.5788	346.1397	173.5735	T	931.5281	466.2677	914.5016	457.7544	913.5176	457.2624	8
4	451.1823	226.0948	433.1718	217.0895	S	830.4804	415.7439	813.4539	407.2306	812.4699	406.7386	7
5	564.2664	282.6368	546.2558	273.6316	I	743.4484	372.2278	726.4219	363.7146			6
6	677.3505	339.1789	659.3399	330.1736	L	630.3643	315.6858	613.3378	307.1725			5
7	774.4032	387.7053	756.3927	378.7000	P	517.2803	259.1438	500.2537	250.6305			4
8	887.4873	444.2473	869.4767	435.2420	I	420.2275	210.6174	403.2010	202.1041			3
9	1047.5179	524.2626	1029.5074	515.2573	C	307.1435	154.0754	290.1169	145.5621			2
10					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 35 ppm



RMS error 35 ppm

Peptide Number: 92471

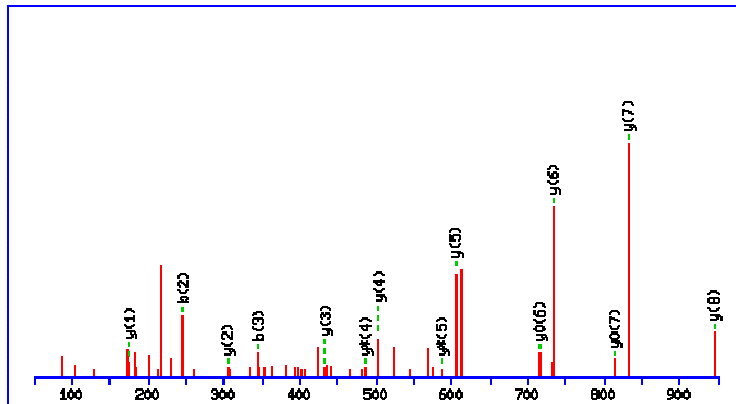
MS/MS Fragmentation of **MLVETAQER**

Found in **IPI00646420** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PSEN2 Presenilin 2 (Alzheimer disease 4), isoform CRA_b

Match to Query 13224: 1075.542648 from(538.778600,2+) index(17938)

Title: Elution from: 83.6 to 83.6 period: 0 cycle: 8312 experiment: 4 polarity:+

Data file 120214ry_414C2-43_4_1.mgf



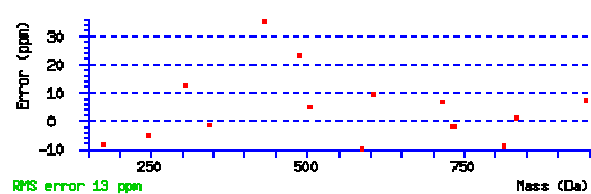
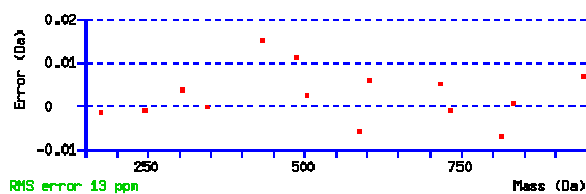
Monoisotopic mass of neutral peptide Mr(calc): 1075.5332

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 41 Expect: 0.0054

Matches : 14/76 fragment ions using 41 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	132.0478	66.5275					M							9
2	245.1318	123.0696					L	945.5000	473.2536	928.4734	464.7404	927.4894	464.2483	8
3	344.2002	172.6038					V	832.4159	416.7116	815.3894	408.1983	814.4054	407.7063	7
4	473.2428	237.1251			455.2323	228.1198	E	733.3475	367.1774	716.3210	358.6641	715.3369	358.1721	6
5	574.2905	287.6489			556.2799	278.6436	T	604.3049	302.6561	587.2784	294.1428	586.2944	293.6508	5
6	645.3276	323.1675			627.3171	314.1622	A	503.2572	252.1323	486.2307	243.6190	485.2467	243.1270	4
7	773.3862	387.1967	756.3597	378.6835	755.3756	378.1915	Q	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	3
8	902.4288	451.7180	885.4022	443.2048	884.4182	442.7128	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
9							R	175.1190	88.0631	158.0924	79.5498			1



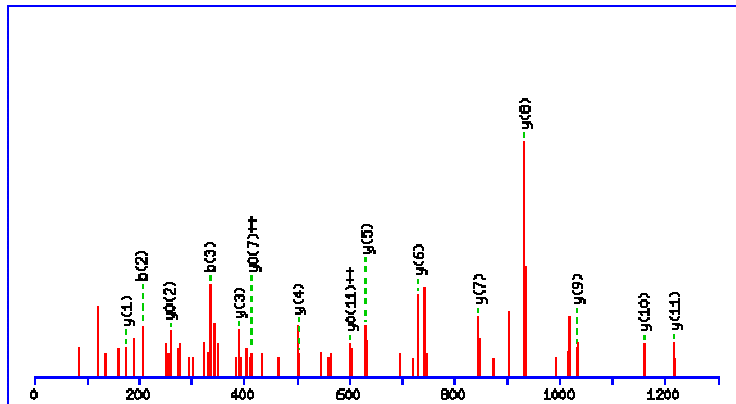
Peptide Number: 92509

MS/MS Fragmentation of **FGEVSDVEIIR**Found in **IPI00161085** in **IPI_human**, Tax_Id=9606 Gene_Symbol=NOL8 Isoform 1 of Nucleolar protein 8

Match to Query 31254: 1363.671128 from(682.842840,2+) index(48051)

Title: Elution from: 116.433333333333 to 116.433333333333 period: 0 cycle: 4362 experiment: 9 polarity:+

Data file 120126ry_585A1-55_1_2.mgf



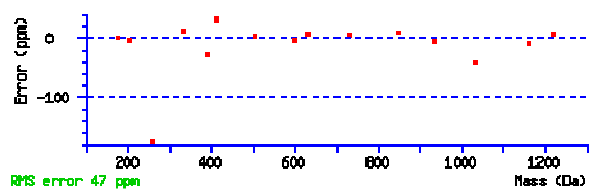
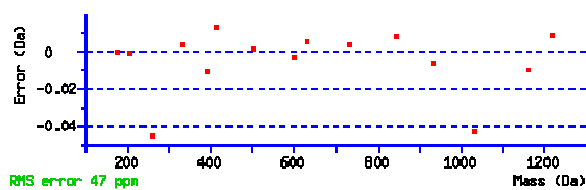
Monoisotopic mass of neutral peptide Mr(calc): 1363.6983

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 64 Expect: 3e-005

Matches : 15/104 fragment ions using 33 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415			F							12
2	205.0972	103.0522			G	1217.6372	609.3222	1200.6107	600.8090	1199.6266	600.3170	11
3	334.1397	167.5735	316.1292	158.5682	E	1160.6157	580.8115	1143.5892	572.2982	1142.6052	571.8062	10
4	433.2082	217.1077	415.1976	208.1024	V	1031.5732	516.2902	1014.5466	507.7769	1013.5626	507.2849	9
5	520.2402	260.6237	502.2296	251.6185	S	932.5047	466.7560	915.4782	458.2427	914.4942	457.7507	8
6	635.2671	318.1372	617.2566	309.1319	D	845.4727	423.2400	828.4462	414.7267	827.4621	414.2347	7
7	734.3355	367.6714	716.3250	358.6661	V	730.4458	365.7265	713.4192	357.2132	712.4352	356.7212	6
8	863.3781	432.1927	845.3676	423.1874	E	631.3774	316.1923	614.3508	307.6790	613.3668	307.1870	5
9	976.4622	488.7347	958.4516	479.7295	I	502.3348	251.6710	485.3082	243.1577	484.3242	242.6657	4
10	1089.5463	545.2768	1071.5357	536.2715	I	389.2507	195.1290	372.2241	186.6157	371.2401	186.1237	3
11	1190.5939	595.8006	1172.5834	586.7953	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
12					R	175.1190	88.0631	158.0924	79.5498			1

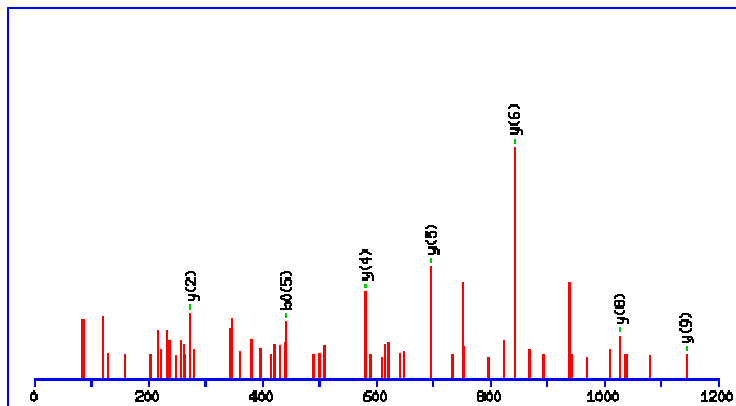


Peptide Number: 92642MS/MS Fragmentation of **TGDSVFLCFQK**Found in **IPI00016377** in **IPI_human**, Tax_Id=9606 Gene_Symbol=RAB28 Isoform S of Ras-related protein Rab-28

Match to Query 6166: 1300.603108 from(651.308830,2+) index(2579)

Title: Elution from: 6.35 to 6.35 period: 0 cycle: 237 experiment: 6 polarity: +

Data file 120210ry_32R1-32_3.mgf



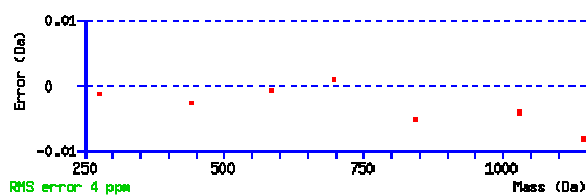
Monoisotopic mass of neutral peptide Mr(calc): 1300.6122

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

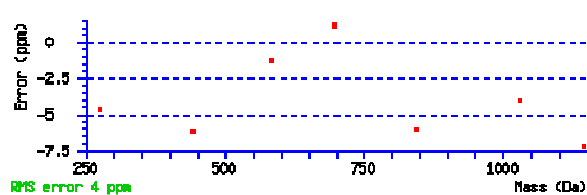
Ions Score: 38 Expect: 0.0051

Matches : 7/88 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							11
2	159.0764	80.0418			141.0659	71.0366	G	1200.5718	600.7895	1183.5452	592.2762	1182.5612	591.7842	10
3	274.1034	137.5553			256.0928	128.5500	D	1143.5503	572.2788	1126.5238	563.7655	1125.5397	563.2735	9
4	361.1354	181.0713			343.1248	172.0661	S	1028.5234	514.7653	1011.4968	506.2520	1010.5128	505.7600	8
5	460.2038	230.6055			442.1932	221.6003	V	941.4913	471.2493	924.4648	462.7360			7
6	607.2722	304.1397			589.2617	295.1345	F	842.4229	421.7151	825.3964	413.2018			6
7	720.3563	360.6818			702.3457	351.6765	L	695.3545	348.1809	678.3280	339.6676			5
8	880.3869	440.6971			862.3764	431.6918	C	582.2704	291.6389	565.2439	283.1256			4
9	1027.4553	514.2313			1009.4448	505.2260	F	422.2398	211.6235	405.2132	203.1103			3
10	1155.5139	578.2606	1138.4874	569.7473	1137.5034	569.2553	Q	275.1714	138.0893	258.1448	129.5761			2
11							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 4 ppm



RMS error 4 ppm

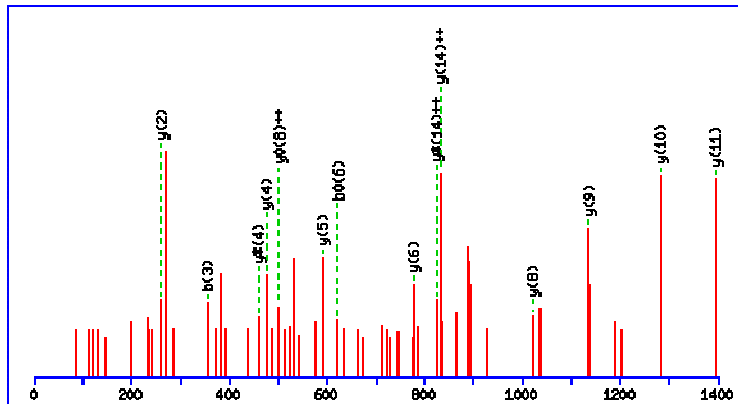
Peptide Number: 92668

MS/MS Fragmentation of **EQPGDLFNEWDSELK**Found in **IPI00161600** in **IPI_human**, Tax_Id=9606 Gene_Symbol=C17orf79 Cooperator of PRMT5

Match to Query 23855: 1920.843988 from(961.429270,2+) index(32153)

Title: Elution from: 76.7666666666667 to 76.7666666666667 period: 0 cycle: 2906 experiment: 9 polarity: +

Data file 120212ry_aHDF1388-P9_2_3.mgf



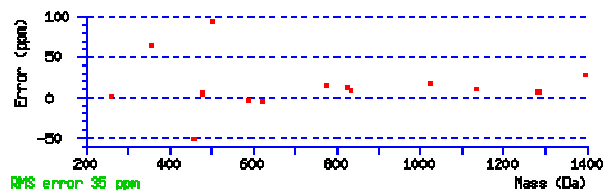
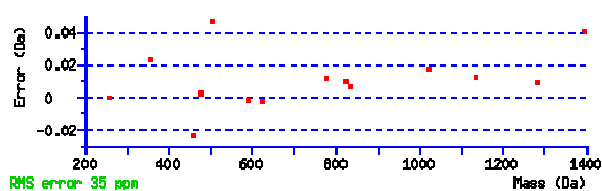
Monoisotopic mass of neutral peptide Mr(calc): 1920.8377

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 45 Expect: 0.00066

Matches : 14/174 fragment ions using 25 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							16
2	258.1084	129.5579	241.0819	121.0446	240.0979	120.5526	Q	1792.8024	896.9049	1775.7759	888.3916	1774.7919	887.8996	15
3	355.1612	178.0842	338.1347	169.5710	337.1506	169.0790	P	1664.7439	832.8756	1647.7173	824.3623	1646.7333	823.8703	14
4	412.1827	206.5950	395.1561	198.0817	394.1721	197.5897	G	1567.6911	784.3492	1550.6645	775.8359	1549.6805	775.3439	13
5	527.2096	264.1084	510.1831	255.5952	509.1991	255.1032	D	1510.6696	755.8385	1493.6431	747.3252	1492.6591	746.8332	12
6	640.2937	320.6505	623.2671	312.1372	622.2831	311.6452	L	1395.6427	698.3250	1378.6161	689.8117	1377.6321	689.3197	11
7	787.3621	394.1847	770.3355	385.6714	769.3515	385.1794	F	1282.5586	641.7829	1265.5321	633.2697	1264.5481	632.7777	10
8	901.4050	451.2061	884.3785	442.6929	883.3945	442.2009	N	1135.4902	568.2487	1118.4637	559.7355	1117.4796	559.2435	9
9	1030.4476	515.7274	1013.4211	507.2142	1012.4371	506.7222	E	1021.4473	511.2273	1004.4207	502.7140	1003.4367	502.2220	8
10	1145.4746	573.2409	1128.4480	564.7276	1127.4640	564.2356	D	892.4047	446.7060	875.3781	438.1927	874.3941	437.7007	7
11	1331.5539	666.2806	1314.5273	657.7673	1313.5433	657.2753	W	777.3777	389.1925	760.3512	380.6792	759.3672	380.1872	6
12	1446.5808	723.7940	1429.5543	715.2808	1428.5703	714.7888	D	591.2984	296.1529	574.2719	287.6396	573.2879	287.1476	5
13	1533.6128	767.3101	1516.5863	758.7968	1515.6023	758.3048	S	476.2715	238.6394	459.2449	230.1261	458.2609	229.6341	4
14	1662.6554	831.8314	1645.6289	823.3181	1644.6449	822.8261	E	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
15	1775.7395	888.3734	1758.7130	879.8601	1757.7289	879.3681	L	260.1969	130.6021	243.1703	122.0888			2
16							K	147.1128	74.0600	130.0863	65.5468			1



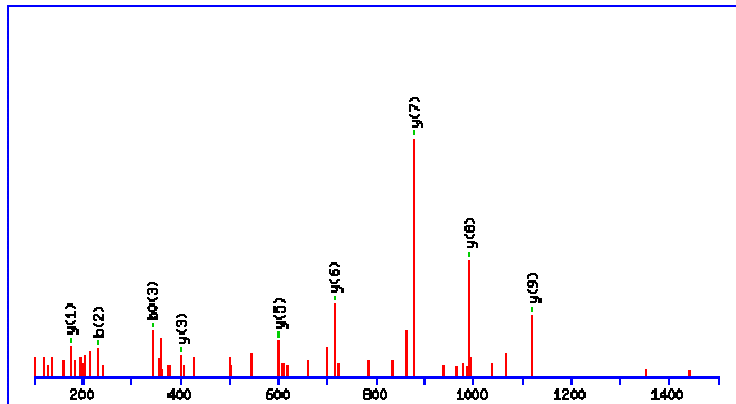
Peptide Number: 92795

MS/MS Fragmentation of **ETEIYNTVLLR**Found in **IPI01013348** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ACVRL1 Serine/threonine-protein kinase receptor R3

Match to Query 21305: 1349.726028 from(675.870290,2+) index(49620)

Title: Elution from: 119.433333333333 to 119.433333333333 period: 0 cycle: 4536 experiment: 7 polarity:+

Data file 120212ry_aHDF1388-P9_2_2.mgf



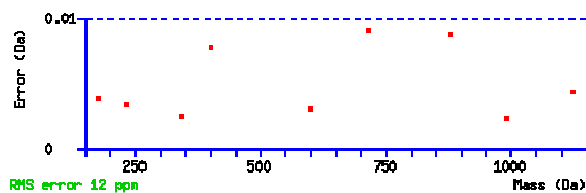
Monoisotopic mass of neutral peptide Mr(calc): 1349.7191

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

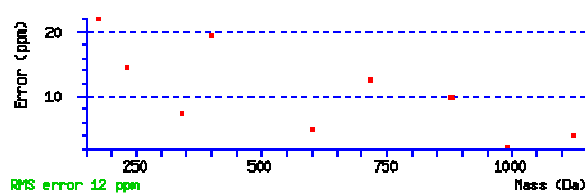
Ions Score: 62 Expect: 3.9e-005

Matches : 9/102 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							11
2	231.0975	116.0524			213.0870	107.0471	T	1221.6838	611.3455	1204.6572	602.8322	1203.6732	602.3402	10
3	360.1401	180.5737			342.1296	171.5684	E	1120.6361	560.8217	1103.6095	552.3084	1102.6255	551.8164	9
4	473.2242	237.1157			455.2136	228.1105	I	991.5935	496.3004	974.5669	487.7871	973.5829	487.2951	8
5	636.2875	318.6474			618.2770	309.6421	Y	878.5094	439.7584	861.4829	431.2451	860.4989	430.7531	7
6	750.3305	375.6689	733.3039	367.1556	732.3199	366.6636	N	715.4461	358.2267	698.4196	349.7134	697.4355	349.2214	6
7	851.3781	426.1927	834.3516	417.6794	833.3676	417.1874	T	601.4032	301.2052	584.3766	292.6919	583.3926	292.1999	5
8	950.4466	475.7269	933.4200	467.2136	932.4360	466.7216	V	500.3555	250.6814	483.3289	242.1681			4
9	1063.5306	532.2689	1046.5041	523.7557	1045.5201	523.2637	L	401.2871	201.1472	384.2605	192.6339			3
10	1176.6147	588.8110	1159.5881	580.2977	1158.6041	579.8057	L	288.2030	144.6051	271.1765	136.0919			2
11							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 12 ppm



RMS error 12 ppm

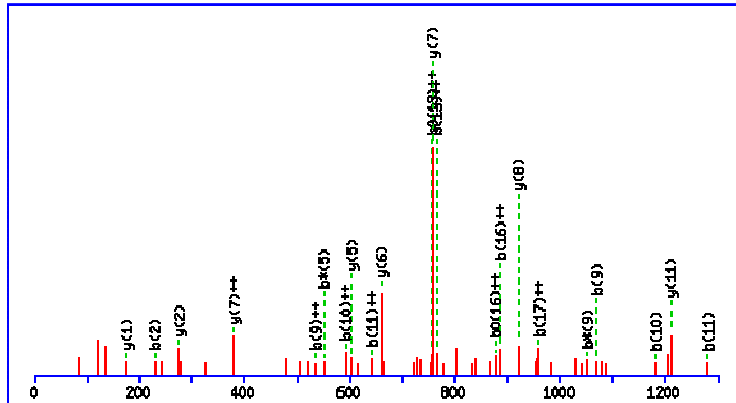
Peptide Number: 93184

MS/MS Fragmentation of **TQPLQHHNLLVCSVSGFYPGSIEVR**Found in **IPI00465279** in **IPI_human**, Tax_Id=9606 Gene_Symbol=HLA-DRB4;HLA-DRB3;LOC649783;HLA-DRB1;HLA-DRB5;LOC100507714;LOC100507709 HLA class II histocompatibility antigen, DRB1-7 beta chain

Match to Query 41853: 2837.433056 from(710.365540,4+) index(20194)

Title: Elution from: 48.2333333333333 to 48.2333333333333 period: 0 cycle: 1827 experiment: 5 polarity: +

Data file 120212ry_aHDF1388-P9_2.3.mgf



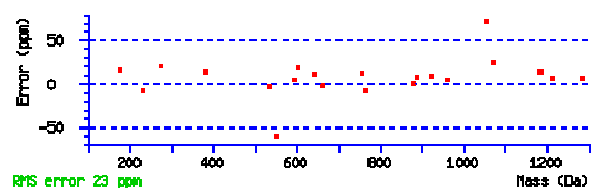
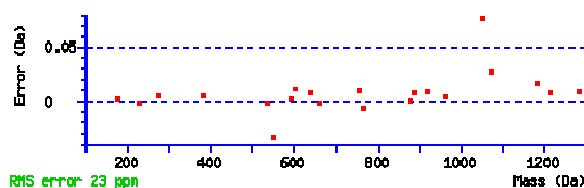
Monoisotopic mass of neutral peptide Mr(calc): 2837.4283

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 38 Expect: 0.0086

Matches : 22/282 fragment ions using 41 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							25
2	230.1135	115.5604	213.0870	107.0471	212.1030	106.5551	Q	2737.3879	1369.1976	2720.3613	1360.6843	2719.3773	1360.1923	24
3	327.1663	164.0868	310.1397	155.5735	309.1557	155.0815	P	2609.3293	1305.1683	2592.3028	1296.6550	2591.3187	1296.1630	23
4	440.2504	220.6288	423.2238	212.1155	422.2398	211.6235	L	2512.2765	1256.6419	2495.2500	1248.1286	2494.2660	1247.6366	22
5	568.3089	284.6581	551.2824	276.1448	550.2984	275.6528	Q	2399.1925	1200.0999	2382.1659	1191.5866	2381.1819	1191.0946	21
6	705.3679	353.1876	688.3413	344.6743	687.3573	344.1823	H	2271.1339	1136.0706	2254.1073	1127.5573	2253.1233	1127.0653	20
7	842.4268	421.7170	825.4002	413.2037	824.4162	412.7117	H	2134.0750	1067.5411	2117.0484	1059.0279	2116.0644	1058.5358	19
8	956.4697	478.7385	939.4431	470.2252	938.4591	469.7332	N	1997.0161	999.0117	1979.9895	990.4984	1979.0055	990.0064	18
9	1069.5538	535.2805	1052.5272	526.7672	1051.5432	526.2752	L	1882.9731	941.9902	1865.9466	933.4769	1864.9626	932.9849	17
10	1182.6378	591.8225	1165.6113	583.3093	1164.6273	582.8173	L	1769.8891	885.4482	1752.8625	876.9349	1751.8785	876.4429	16
11	1281.7062	641.3568	1264.6797	632.8435	1263.6957	632.3515	V	1656.8050	828.9061	1639.7785	820.3929	1638.7945	819.9009	15
12	1441.7369	721.3721	1424.7103	712.8588	1423.7263	712.3668	C	1557.7366	779.3719	1540.7101	770.8587	1539.7260	770.3667	14
13	1528.7689	764.8881	1511.7424	756.3748	1510.7583	755.8828	S	1397.7060	699.3566	1380.6794	690.8433	1379.6954	690.3513	13
14	1627.8373	814.4223	1610.8108	805.9090	1609.8268	805.4170	V	1310.6739	655.8406	1293.6474	647.3273	1292.6634	646.8353	12
15	1714.8694	857.9383	1697.8428	849.4250	1696.8588	848.9330	S	1211.6055	606.3064	1194.5790	597.7931	1193.5949	597.3011	11
16	1771.8908	886.4490	1754.8643	877.9358	1753.8803	877.4438	G	1124.5735	562.7904	1107.5469	554.2771	1106.5629	553.7851	10
17	1918.9592	959.9833	1901.9327	951.4700	1900.9487	950.9780	F	1067.5520	534.2796	1050.5255	525.7664	1049.5415	525.2744	9
18	2082.0226	1041.5149	2064.9960	1033.0016	2064.0120	1032.5096	Y	920.4836	460.7454	903.4571	452.2322	902.4730	451.7402	8
19	2179.0753	1090.0413	2162.0488	1081.5280	2161.0648	1081.0360	P	757.4203	379.2138	740.3937	370.7005	739.4097	370.2085	7
20	2236.0968	1118.5520	2219.0702	1110.0388	2218.0862	1109.5467	G	660.3675	330.6874	643.3410	322.1741	642.3570	321.6821	6
21	2323.1288	1162.0680	2306.1023	1153.5548	2305.1182	1153.0628	S	603.3461	302.1767	586.3195	293.6634	585.3355	293.1714	5
22	2436.2129	1218.6101	2419.1863	1210.0968	2418.2023	1209.6048	I	516.3140	258.6606	499.2875	250.1474	498.3035	249.6554	4
23	2565.2555	1283.1314	2548.2289	1274.6181	2547.2449	1274.1261	E	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
24	2664.3239	1332.6656	2647.2973	1324.1523	2646.3133	1323.6603	V	274.1874	137.5973	257.1608	129.0840			2
25							R	175.1190	88.0631	158.0924	79.5498			1



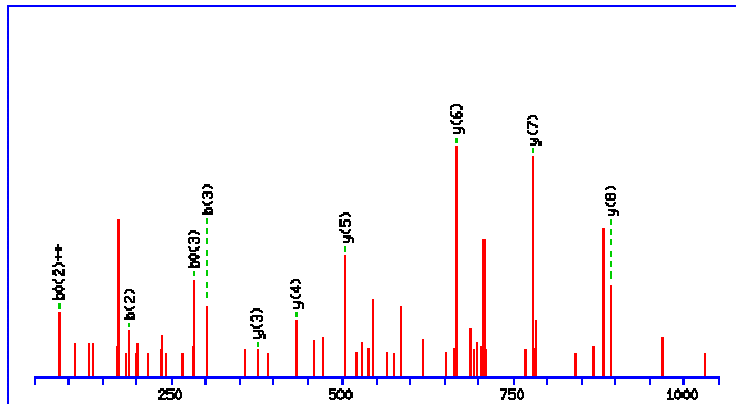
Peptide Number: 93651

MS/MS Fragmentation of **STILYAGNDK**Found in **IPI00442298** in **IPI_human**, Tax_Id=9606 Gene_Symbol=NTM Isoform 3 of Neurotrimin

Match to Query 13535: 1080.530568 from(541.272560,2+) index(26732)

Title: Elution from: 98.5833333333333 to 98.5833333333333 period: 0 cycle: 7943 experiment: 5 polarity:+

Data file 120208ry_Tig120slc-P8_2_1.mgf



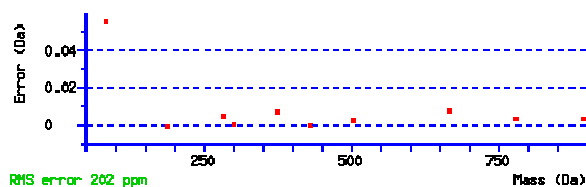
Monoisotopic mass of neutral peptide Mr(calc): 1080.5451

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

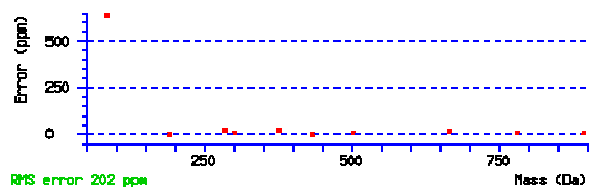
Ions Score: 37 Expect: 0.01

Matches : 10/92 fragment ions using 19 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							10
2	189.0870	95.0471			171.0764	86.0418	T	994.5204	497.7638	977.4938	489.2506	976.5098	488.7585	9
3	302.1710	151.5892			284.1605	142.5839	I	893.4727	447.2400	876.4462	438.7267	875.4621	438.2347	8
4	415.2551	208.1312			397.2445	199.1259	L	780.3886	390.6980	763.3621	382.1847	762.3781	381.6927	7
5	578.3184	289.6629			560.3079	280.6576	Y	667.3046	334.1559	650.2780	325.6427	649.2940	325.1506	6
6	649.3556	325.1814			631.3450	316.1761	A	504.2413	252.6243	487.2147	244.1110	486.2307	243.6190	5
7	706.3770	353.6921			688.3665	344.6869	G	433.2041	217.1057	416.1776	208.5924	415.1936	208.1004	4
8	820.4199	410.7136	803.3934	402.2003	802.4094	401.7083	N	376.1827	188.5950	359.1561	180.0817	358.1721	179.5897	3
9	935.4469	468.2271	918.4203	459.7138	917.4363	459.2218	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
10							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 202 ppm



RMS error 202 ppm

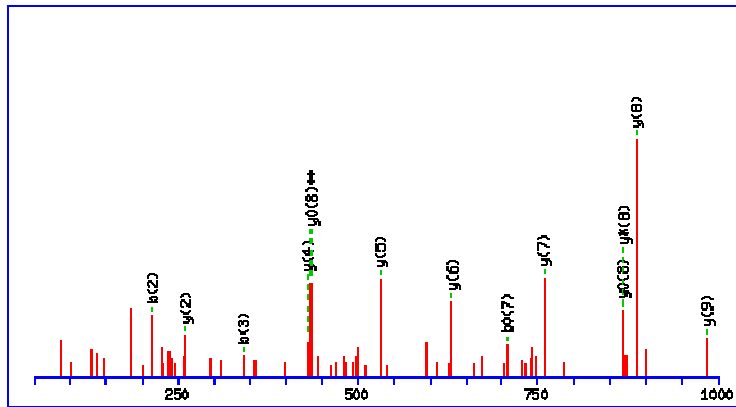
Peptide Number: 93710

MS/MS Fragmentation of **IVQQVTGILK**Found in **IPI00465310** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SLC30A5 Isoform 1 of Zinc transporter 5

Match to Query 9998: 1097.681108 from(549.847830,2+) index(19433)

Title: Elution from: 49.5 to 49.5 period: 0 cycle: 1883 experiment: 5 polarity: +

Data file 120210ry_585A1-55_3_2.mgf



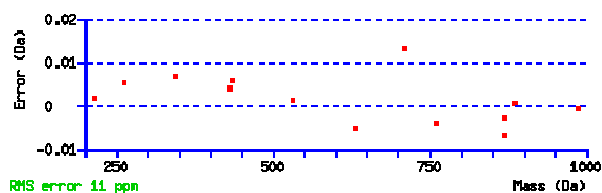
Monoisotopic mass of neutral peptide Mr(calc): 1097.6808

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

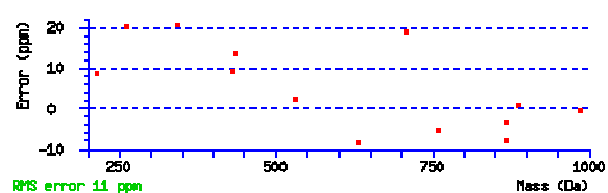
Ions Score: 59 Expect: 2.3e-005

Matches : 13/86 fragment ions using 18 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							10
2	213.1598	107.0835					V	985.6041	493.3057	968.5775	484.7924	967.5935	484.3004	9
3	341.2183	171.1128	324.1918	162.5995			Q	886.5356	443.7715	869.5091	435.2582	868.5251	434.7662	8
4	469.2769	235.1421	452.2504	226.6288			Q	758.4771	379.7422	741.4505	371.2289	740.4665	370.7369	7
5	568.3453	284.6763	551.3188	276.1630			V	630.4185	315.7129	613.3919	307.1996	612.4079	306.7076	6
6	669.3930	335.2001	652.3665	326.6869	651.3824	326.1949	T	531.3501	266.1787	514.3235	257.6654	513.3395	257.1734	5
7	726.4145	363.7109	709.3879	355.1976	708.4039	354.7056	G	430.3024	215.6548	413.2758	207.1416			4
8	839.4985	420.2529	822.4720	411.7396	821.4880	411.2476	I	373.2809	187.1441	356.2544	178.6308			3
9	952.5826	476.7949	935.5560	468.2817	934.5720	467.7897	L	260.1969	130.6021	243.1703	122.0888			2
10							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 11 ppm



RMS error 11 ppm

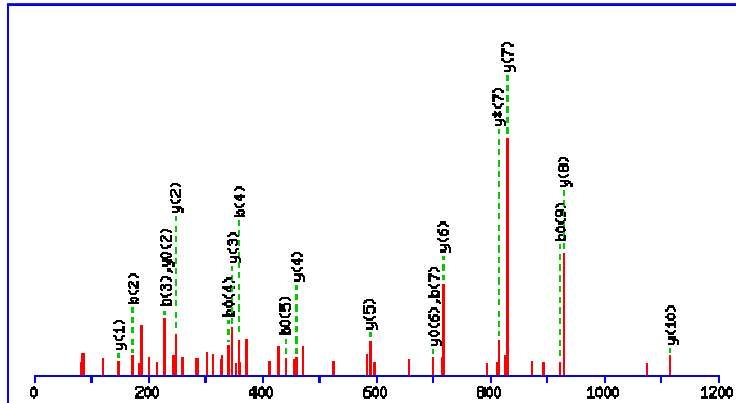
Peptide Number: 93790

MS/MS Fragmentation of **GDGEVLEEIVTK**Found in **IPI00883925** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ARL6IP4 Similar to 2-oxoglutarate and iron-dependent oxygenase domain-containing protein 2

Match to Query 22618: 1287.646228 from(644.830390,2+) index(47839)

Title: Elution from: 115.166666666667 to 115.166666666667 period: 0 cycle: 4244 experiment: 7 polarity: +

Data file 120118ry_201B7-32_2_2.mgf



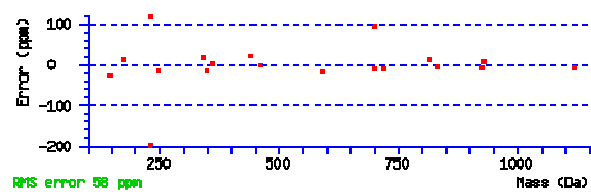
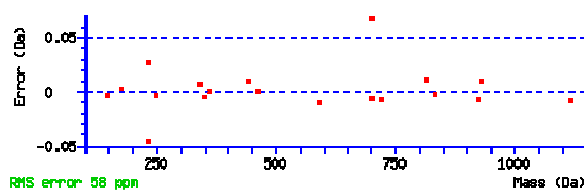
Monoisotopic mass of neutral peptide Mr(calc): 1287.6558

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 60 Expect: 7.8e-005

Matches : 19/106 fragment ions using 34 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180			G							12
2	173.0557	87.0315	155.0451	78.0262	D	1231.6416	616.3245	1214.6151	607.8112	1213.6311	607.3192	11
3	230.0771	115.5422	212.0666	106.5369	G	1116.6147	558.8110	1099.5881	550.2977	1098.6041	549.8057	10
4	359.1197	180.0635	341.1092	171.0582	E	1059.5932	530.3002	1042.5667	521.7870	1041.5827	521.2950	9
5	458.1882	229.5977	440.1776	220.5924	V	930.5506	465.7790	913.5241	457.2657	912.5401	456.7737	8
6	571.2722	286.1397	553.2617	277.1345	L	831.4822	416.2447	814.4557	407.7315	813.4716	407.2395	7
7	700.3148	350.6610	682.3042	341.6558	E	718.3981	359.7027	701.3716	351.1894	700.3876	350.6974	6
8	829.3574	415.1823	811.3468	406.1771	E	589.3556	295.1814	572.3290	286.6681	571.3450	286.1761	5
9	942.4415	471.7244	924.4309	462.7191	I	460.3130	230.6601	443.2864	222.1468	442.3024	221.6548	4
10	1041.5099	521.2586	1023.4993	512.2533	V	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
11	1142.5576	571.7824	1124.5470	562.7771	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
12					K	147.1128	74.0600	130.0863	65.5468			1



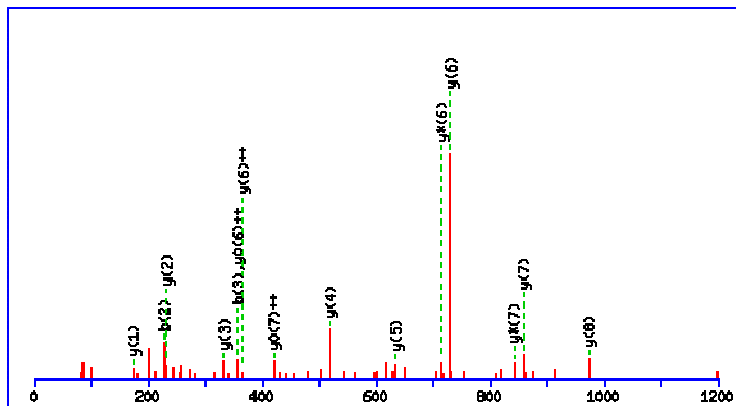
Peptide Number: 94038

MS/MS Fragmentation of **LDQPDWTGR**Found in **IPI00170916** in **IPI_human**, Tax_Id=9606 Gene_Symbol=NECAP1 Isoform 1 of Adaptin ear-binding coat-associated protein 1

Match to Query 10930: 1086.504788 from(544.259670,2+) index(10424)

Title: Elution from: 25.6 to 25.6 period: 0 cycle: 967 experiment: 7 polarity:+

Data file 120210ry_32R1-32_3_2.mgf



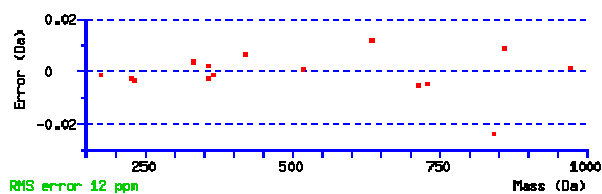
Monoisotopic mass of neutral peptide Mr(calc): 1086.5094

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

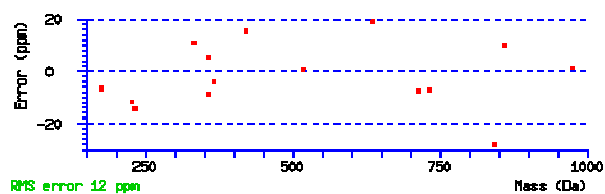
Ions Score: 59 Expect: 3.6e-005

Matches : 15/86 fragment ions using 26 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							9
2	229.1183	115.0628			211.1077	106.0575	D	974.4326	487.7200	957.4061	479.2067	956.4221	478.7147	8
3	357.1769	179.0921	340.1503	170.5788	339.1663	170.0868	Q	859.4057	430.2065	842.3791	421.6932	841.3951	421.2012	7
4	454.2296	227.6185	437.2031	219.1052	436.2191	218.6132	P	731.3471	366.1772	714.3206	357.6639	713.3366	357.1719	6
5	569.2566	285.1319	552.2300	276.6186	551.2460	276.1266	D	634.2944	317.6508	617.2678	309.1375	616.2838	308.6455	5
6	755.3359	378.1716	738.3093	369.6583	737.3253	369.1663	W	519.2674	260.1373	502.2409	251.6241	501.2568	251.1321	4
7	856.3836	428.6954	839.3570	420.1821	838.3730	419.6901	T	333.1881	167.0977	316.1615	158.5844	315.1775	158.0924	3
8	913.4050	457.2062	896.3785	448.6929	895.3945	448.2009	G	232.1404	116.5738	215.1139	108.0606			2
9							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 12 ppm



RMS error 12 ppm

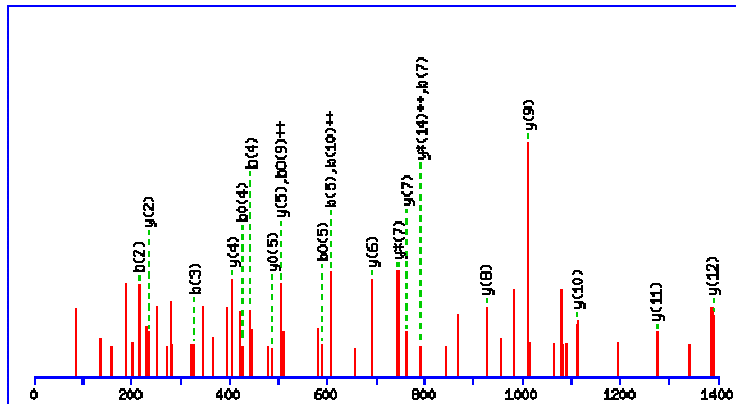
Peptide Number: 94054

MS/MS Fragmentation of **DVNDYVSYAWVGDSK**Found in **IPI00374574** in **IPI_human**, Tax_Id=9606 Gene_Symbol=INPP5K Isoform 1 of Inositol polyphosphate 5-phosphatase K

Match to Query 17272: 1716.756328 from(859.385440,2+) index(13506)

Title: Elution from: 34.3166666666667 to 34.3166666666667 period: 0 cycle: 1294 experiment: 10 polarity: +

Data file 120210ry_585A1-55_3_3.mgf



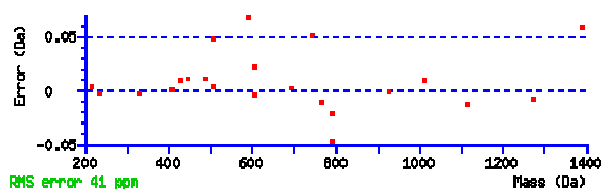
Monoisotopic mass of neutral peptide Mr(calcd): 1716.7631

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

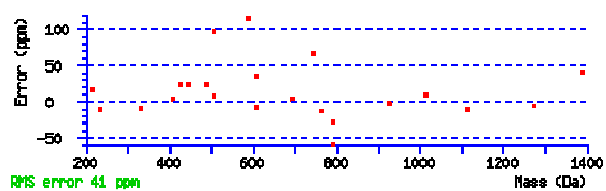
Ions Score: 47 Expect: 0.00039

Matches : 22/162 fragment ions using 49 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							15
2	215.1026	108.0550			197.0921	99.0497	V	1602.7435	801.8754	1585.7169	793.3621	1584.7329	792.8701	14
3	329.1456	165.0764	312.1190	156.5631	311.1350	156.0711	N	1503.6751	752.3412	1486.6485	743.8279	1485.6645	743.3359	13
4	444.1725	222.5899	427.1460	214.0766	426.1619	213.5846	D	1389.6321	695.3197	1372.6056	686.8064	1371.6216	686.3144	12
5	607.2358	304.1216	590.2093	295.6083	589.2253	295.1163	Y	1274.6052	637.8062	1257.5786	629.2930	1256.5946	628.8009	11
6	706.3042	353.6558	689.2777	345.1425	688.2937	344.6505	V	1111.5419	556.2746	1094.5153	547.7613	1093.5313	547.2693	10
7	793.3363	397.1718	776.3097	388.6585	775.3257	388.1665	S	1012.4734	506.7404	995.4469	498.2271	994.4629	497.7351	9
8	956.3996	478.7034	939.3731	470.1902	938.3890	469.6982	Y	925.4414	463.2243	908.4149	454.7111	907.4308	454.2191	8
9	1027.4367	514.2220	1010.4102	505.7087	1009.4262	505.2167	A	762.3781	381.6927	745.3515	373.1794	744.3675	372.6874	7
10	1213.5160	607.2617	1196.4895	598.7484	1195.5055	598.2564	W	691.3410	346.1741	674.3144	337.6608	673.3304	337.1688	6
11	1312.5844	656.7959	1295.5579	648.2826	1294.5739	647.7906	V	505.2617	253.1345	488.2351	244.6212	487.2511	244.1292	5
12	1369.6059	685.3066	1352.5794	676.7933	1351.5953	676.3013	G	406.1932	203.6003	389.1667	195.0870	388.1827	194.5950	4
13	1484.6329	742.8201	1467.6063	734.3068	1466.6223	733.8148	D	349.1718	175.0895	332.1452	166.5763	331.1612	166.0842	3
14	1571.6649	786.3361	1554.6383	777.8228	1553.6543	777.3308	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
15							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 41 ppm



RMS error 41 ppm

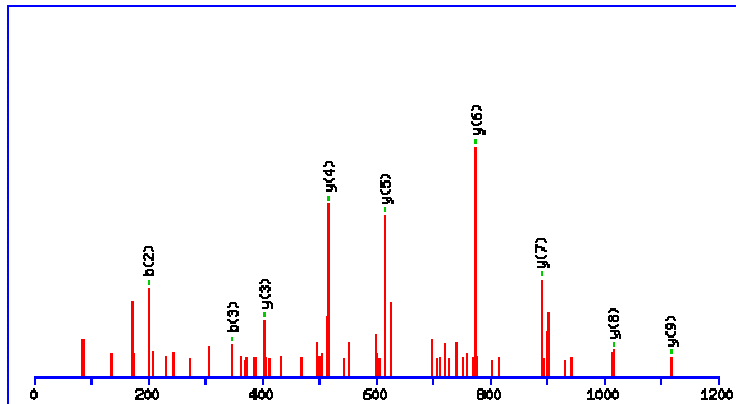
Peptide Number: 94072

MS/MS Fragmentation of **TVFSSTQLCVLND**RFound in **IPI00434539** in **IPI_human**, Tax_Id=9606 Gene_Symbol=NANOG Isoform 1 of Homeobox protein NANOG

Match to Query 16955: 1638.811212 from(547.277680,3+) index(4232)

Title: Elution from: 10.3666666666667 to 10.3666666666667 period: 0 cycle: 389 experiment: 4 polarity: +

Data file 120210ry_32R1-32_2_3.mgf



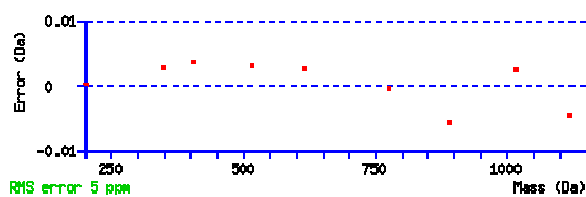
Monoisotopic mass of neutral peptide Mr(calc): 1638.8036

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

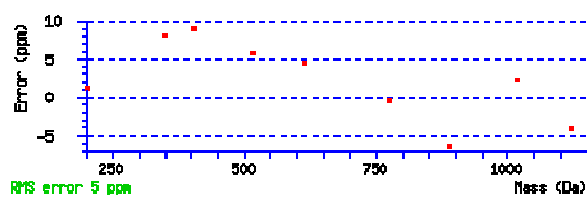
Ions Score: 58 Expect: 9.1e-005

Matches : 9/142 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							14
2	201.1234	101.0653			183.1128	92.0600	V	1538.7632	769.8852	1521.7366	761.3719	1520.7526	760.8799	13
3	348.1918	174.5995			330.1812	165.5942	F	1439.6947	720.3510	1422.6682	711.8377	1421.6842	711.3457	12
4	435.2238	218.1155			417.2132	209.1103	S	1292.6263	646.8168	1275.5998	638.3035	1274.6158	637.8115	11
5	522.2558	261.6316			504.2453	252.6263	S	1205.5943	603.3008	1188.5677	594.7875	1187.5837	594.2955	10
6	623.3035	312.1554			605.2930	303.1501	T	1118.5623	559.7848	1101.5357	551.2715	1100.5517	550.7795	9
7	751.3621	376.1847	734.3355	367.6714	733.3515	367.1794	Q	1017.5146	509.2609	1000.4880	500.7477	999.5040	500.2557	8
8	864.4462	432.7267	847.4196	424.2134	846.4356	423.7214	L	889.4560	445.2316	872.4295	436.7184	871.4454	436.2264	7
9	1024.4768	512.7420	1007.4503	504.2288	1006.4662	503.7368	C	776.3719	388.6896	759.3454	380.1763	758.3614	379.6843	6
10	1123.5452	562.2762	1106.5187	553.7630	1105.5347	553.2710	V	616.3413	308.6743	599.3148	300.1610	598.3307	299.6690	5
11	1236.6293	618.8183	1219.6027	610.3050	1218.6187	609.8130	L	517.2729	259.1401	500.2463	250.6268	499.2623	250.1348	4
12	1350.6722	675.8397	1333.6457	667.3265	1332.6616	666.8345	N	404.1888	202.5980	387.1623	194.0848	386.1783	193.5928	3
13	1465.6992	733.3532	1448.6726	724.8399	1447.6886	724.3479	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
14							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 5 ppm



RMS error 5 ppm

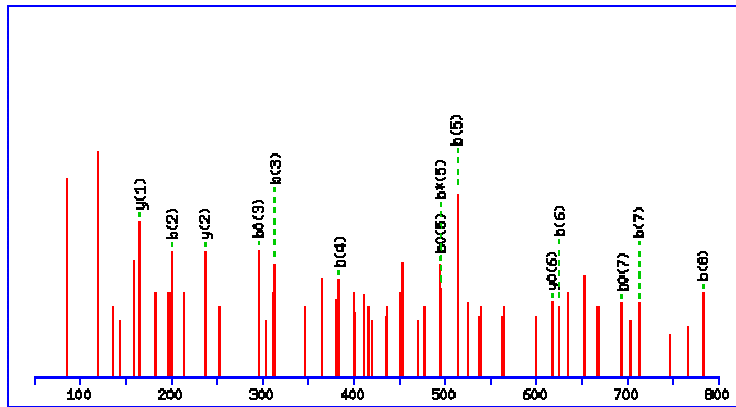
Peptide Number: 94245

MS/MS Fragmentation of **LSLAQLSAF**Found in **IPI00217858** in **IPI_human**, Tax_Id=9606 Gene_Symbol=LENG8 Isoform 2 of Leukocyte receptor cluster member 8

Match to Query 1364: 948.519128 from(475.266840,2+) index(42306)

Title: Elution from: 106.2 to 106.2 period: 0 cycle: 3959 experiment: 3 polarity: +

Data file 120126ry_585A1-55_2_3.mgf



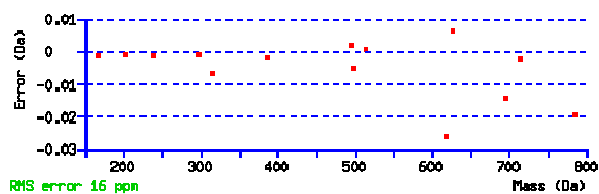
Monoisotopic mass of neutral peptide Mr(calc): 948.5280

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

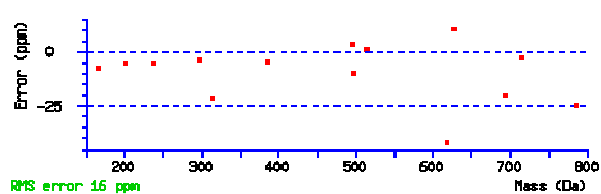
Ions Score: 45 Expect: 0.0019

Matches : 14/74 fragment ions using 28 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							9
2	201.1234	101.0653			183.1128	92.0600	S	836.4512	418.7293	819.4247	410.2160	818.4407	409.7240	8
3	314.2074	157.6074			296.1969	148.6021	L	749.4192	375.2132	732.3927	366.7000	731.4087	366.2080	7
4	385.2445	193.1259			367.2340	184.1206	A	636.3352	318.6712	619.3086	310.1579	618.3246	309.6659	6
5	513.3031	257.1552	496.2766	248.6419	495.2926	248.1499	Q	565.2980	283.1527	548.2715	274.6394	547.2875	274.1474	5
6	626.3872	313.6972	609.3606	305.1840	608.3766	304.6919	L	437.2395	219.1234			419.2289	210.1181	4
7	713.4192	357.2132	696.3927	348.7000	695.4087	348.2080	S	324.1554	162.5813			306.1448	153.5761	3
8	784.4563	392.7318	767.4298	384.2185	766.4458	383.7265	A	237.1234	119.0653					2
9							F	166.0863	83.5468					1



RMS error 16 ppm



RMS error 16 ppm

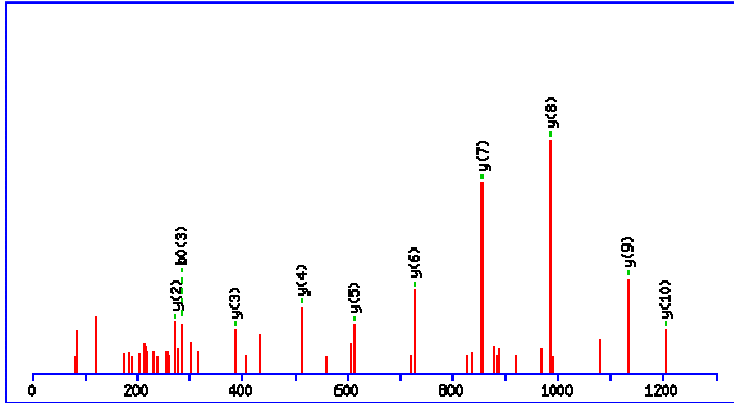
Peptide Number: 94620**MS/MS Fragmentation of ETAFEEVDVQLPR**

Found in **IPI00008239** in **IPI_human**, Tax_Id=9606 Gene_Symbol=GPRC5B cDNA FLJ55176, highly similar to G-protein coupled receptor family C group 5 member B

Match to Query 26975: 1432.691708 from(717.353130,2+) index(42144)

Title: Elution from: 100.016666666667 to 100.016666666667 period: 0 cycle: 3774 experiment: 7 polarity: +

Data file 120214ry_32R1-32_4_2.mgf



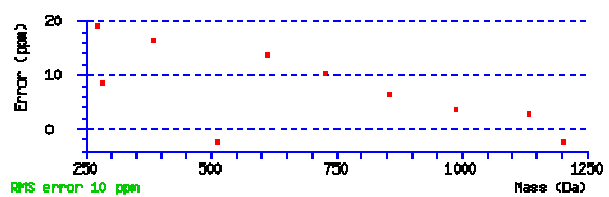
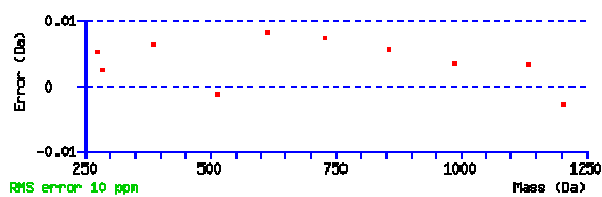
Monoisotopic mass of neutral peptide Mr(calc): 1432.6834

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 84 **Expect:** 2.2e-007

Matches : 10/106 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							12
2	231.0975	116.0524			213.0870	107.0471	T	1304.6481	652.8277	1287.6216	644.3144	1286.6375	643.8224	11
3	302.1347	151.5710			284.1241	142.5657	A	1203.6004	602.3039	1186.5739	593.7906	1185.5899	593.2986	10
4	449.2031	225.1052			431.1925	216.0999	F	1132.5633	566.7853	1115.5368	558.2720	1114.5528	557.7800	9
5	578.2457	289.6265			560.2351	280.6212	E	985.4949	493.2511	968.4684	484.7378	967.4843	484.2458	8
6	707.2883	354.1478			689.2777	345.1425	E	856.4523	428.7298	839.4258	420.2165	838.4417	419.7245	7
7	822.3152	411.6612			804.3046	402.6560	D	727.4097	364.2085	710.3832	355.6952	709.3991	355.2032	6
8	921.3836	461.1954			903.3731	452.1902	V	612.3828	306.6950	595.3562	298.1817			5
9	1049.4422	525.2247	1032.4156	516.7115	1031.4316	516.2195	Q	513.3144	257.1608	496.2878	248.6475			4
10	1162.5263	581.7668	1145.4997	573.2535	1144.5157	572.7615	L	385.2558	193.1315	368.2292	184.6183			3
11	1259.5790	630.2932	1242.5525	621.7799	1241.5685	621.2879	P	272.1717	136.5895	255.1452	128.0762			2
12							R	175.1190	88.0631	158.0924	79.5498			1



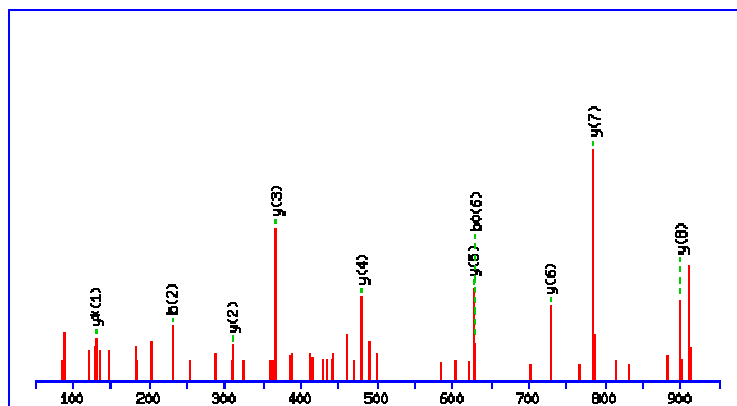
Peptide Number: 94696

MS/MS Fragmentation of **NDGTFIGYK**Found in **IPI00012866** in **IPI_human**, Tax_Id=9606 Gene_Symbol=AKT1 RAC-alpha serine/threonine-protein kinase

Match to Query 7800: 1013.474748 from(507.744650,2+) index(9233)

Title: Elution from: 22.3 to 22.3 period: 0 cycle: 851 experiment: 4 polarity: +

Data file 120201ry_aHDF1388-P9_1_2.mgf



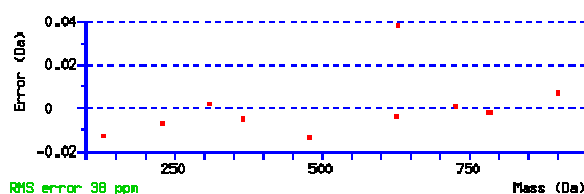
Monoisotopic mass of neutral peptide Mr(calc): 1013.4818

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

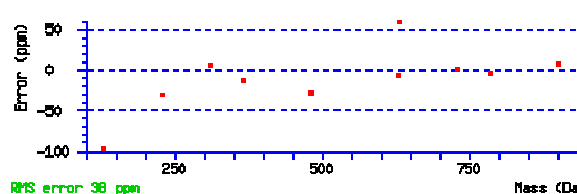
Ions Score: 53 Expect: 0.00013

Matches : 10/84 fragment ions using 18 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							9
2	230.0771	115.5422	213.0506	107.0289	212.0666	106.5369	D	900.4462	450.7267	883.4196	442.2134	882.4356	441.7214	8
3	287.0986	144.0529	270.0721	135.5397	269.0880	135.0477	G	785.4192	393.2132	768.3927	384.7000	767.4087	384.2080	7
4	388.1463	194.5768	371.1197	186.0635	370.1357	185.5715	T	728.3978	364.7025	711.3712	356.1892	710.3872	355.6972	6
5	535.2147	268.1110	518.1882	259.5977	517.2041	259.1057	F	627.3501	314.1787	610.3235	305.6654			5
6	648.2988	324.6530	631.2722	316.1397	630.2882	315.6477	I	480.2817	240.6445	463.2551	232.1312			4
7	705.3202	353.1638	688.2937	344.6505	687.3097	344.1585	G	367.1976	184.1024	350.1710	175.5892			3
8	868.3836	434.6954	851.3570	426.1821	850.3730	425.6901	Y	310.1761	155.5917	293.1496	147.0784			2
9							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 38 ppm



RMS error 38 ppm

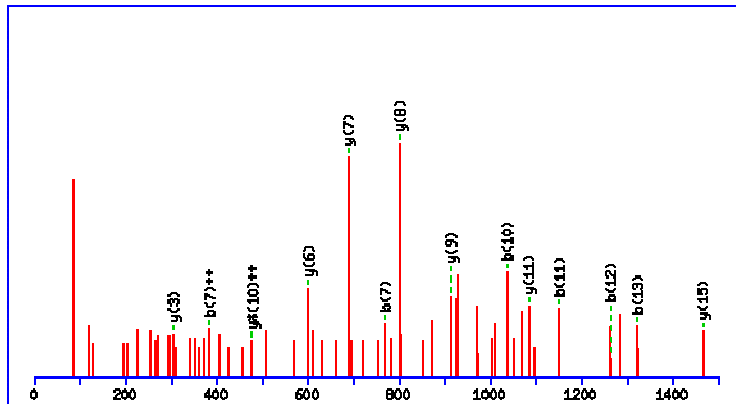
Peptide Number: 94747

MS/MS Fragmentation of **FGNTIVHGVNLINGLISALLG****TK**Found in **IPI00795857** in **IPI_human**, Tax_Id=9606 Gene_Symbol=RPP14 Hydroxyacyl-thioester dehydratase type 2, mitochondrial

Match to Query 15453: 2236.310142 from(746.443990,3+) index(36126)

Title: Elution from: 108.766666666667 to 108.766666666667 period: 0 cycle: 4181 experiment: 3 polarity:+

Data file 120210ry_585A1-55_3_4.mgf



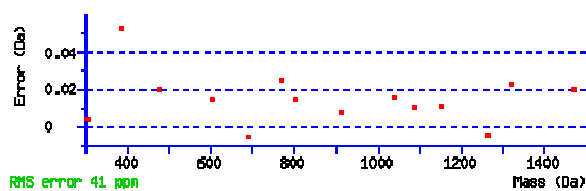
Monoisotopic mass of neutral peptide Mr(calc): 2236.2943

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

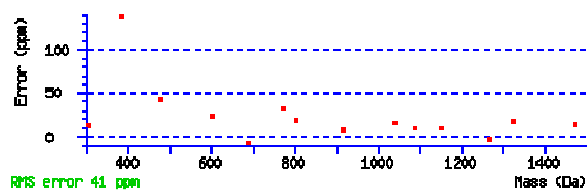
Ions Score: 33 Expect: 0.0036

Matches : 14/240 fragment ions using 27 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415					F							22
2	205.0972	103.0522					G	2090.2332	1045.6202	2073.2067	1037.1070	2072.2226	1036.6150	21
3	319.1401	160.0737	302.1135	151.5604			N	2033.2117	1017.1095	2016.1852	1008.5962	2015.2012	1008.1042	20
4	420.1878	210.5975	403.1612	202.0842	402.1772	201.5922	T	1919.1688	960.0880	1902.1423	951.5748	1901.1582	951.0828	19
5	533.2718	267.1396	516.2453	258.6263	515.2613	258.1343	I	1818.1211	909.5642	1801.0946	901.0509	1800.1106	900.5589	18
6	632.3402	316.6738	615.3137	308.1605	614.3297	307.6685	V	1705.0371	853.0222	1688.0105	844.5089	1687.0265	844.0169	17
7	769.3991	385.2032	752.3726	376.6899	751.3886	376.1979	H	1605.9687	803.4880	1588.9421	794.9747	1587.9581	794.4827	16
8	826.4206	413.7139	809.3941	405.2007	808.4100	404.7087	G	1468.9097	734.9585	1451.8832	726.4452	1450.8992	725.9532	15
9	925.4890	463.2482	908.4625	454.7349	907.4785	454.2429	V	1411.8883	706.4478	1394.8617	697.9345	1393.8777	697.4425	14
10	1038.5731	519.7902	1021.5465	511.2769	1020.5625	510.7849	L	1312.8199	656.9136	1295.7933	648.4003	1294.8093	647.9083	13
11	1151.6572	576.3322	1134.6306	567.8189	1133.6466	567.3269	I	1199.7358	600.3715	1182.7093	591.8583	1181.7252	591.3663	12
12	1265.7001	633.3537	1248.6735	624.8404	1247.6895	624.3484	N	1086.6517	543.8295	1069.6252	535.3162	1068.6412	534.8242	11
13	1322.7215	661.8644	1305.6950	653.3511	1304.7110	652.8591	G	972.6088	486.8080	955.5823	478.2948	954.5982	477.8028	10
14	1435.8056	718.4064	1418.7791	709.8932	1417.7950	709.4012	L	915.5873	458.2973	898.5608	449.7840	897.5768	449.2920	9
15	1548.8897	774.9485	1531.8631	766.4352	1530.8791	765.9432	I	802.5033	401.7553	785.4767	393.2420	784.4927	392.7500	8
16	1635.9217	818.4645	1618.8952	809.9512	1617.9111	809.4592	S	689.4192	345.2132	672.3927	336.7000	671.4087	336.2080	7
17	1706.9588	853.9830	1689.9323	845.4698	1688.9483	844.9778	A	602.3872	301.6972	585.3606	293.1840	584.3766	292.6919	6
18	1820.0429	910.5251	1803.0163	902.0118	1802.0323	901.5198	L	531.3501	266.1787	514.3235	257.6654	513.3395	257.1734	5
19	1933.1269	967.0671	1916.1004	958.5538	1915.1164	958.0618	L	418.2660	209.6366	401.2395	201.1234	400.2554	200.6314	4
20	1990.1484	995.5778	1973.1219	987.0646	1972.1378	986.5726	G	305.1819	153.0946	288.1554	144.5813	287.1714	144.0893	3
21	2091.1961	1046.1017	2074.1695	1037.5884	2073.1855	1037.0964	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
22							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 41 ppm



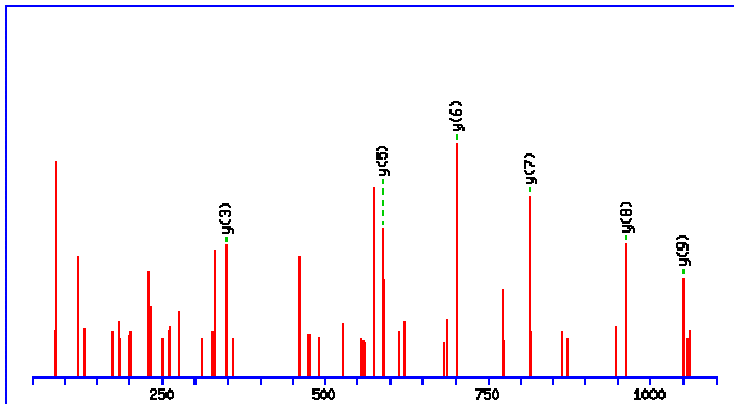
RMS error 41 ppm

Peptide Number: 94947MS/MS Fragmentation of **LSFLLLSIK**Found in **IPI00761051** in **IPI_human**, Tax_Id=9606 Gene_Symbol=C10orf137 Isoform 1 of Erythroid differentiation-related factor 1

Match to Query 3178: 1160.715868 from(581.365210,2+) index(42815)

Title: Elution from: 102.3 to 102.3 period: 0 cycle: 3847 experiment: 3 polarity:+

Data file 120214ry_32R1-32_4_3.mgf



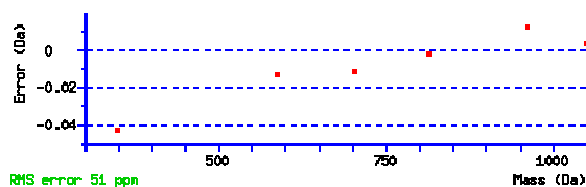
Monoisotopic mass of neutral peptide Mr(calc): 1160.7169

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

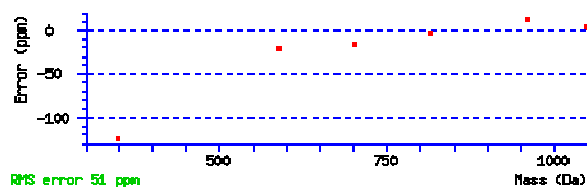
Ions Score: 42 Expect: 0.00067

Matches : 6/90 fragment ions using 10 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							10
2	201.1234	101.0653			183.1128	92.0600	S	1048.6401	524.8237	1031.6136	516.3104	1030.6295	515.8184	9
3	348.1918	174.5995			330.1812	165.5942	F	961.6081	481.3077	944.5815	472.7944	943.5975	472.3024	8
4	461.2758	231.1416			443.2653	222.1363	L	814.5397	407.7735	797.5131	399.2602	796.5291	398.7682	7
5	574.3599	287.6836			556.3493	278.6783	L	701.4556	351.2314	684.4291	342.7182	683.4450	342.2262	6
6	687.4440	344.2256			669.4334	335.2203	L	588.3715	294.6894	571.3450	286.1761	570.3610	285.6841	5
7	815.5026	408.2549	798.4760	399.7416	797.4920	399.2496	Q	475.2875	238.1474	458.2609	229.6341	457.2769	229.1421	4
8	902.5346	451.7709	885.5080	443.2577	884.5240	442.7656	S	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
9	1015.6186	508.3130	998.5921	499.7997	997.6081	499.3077	I	260.1969	130.6021	243.1703	122.0888			2
10							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 51 ppm



RMS error 51 ppm

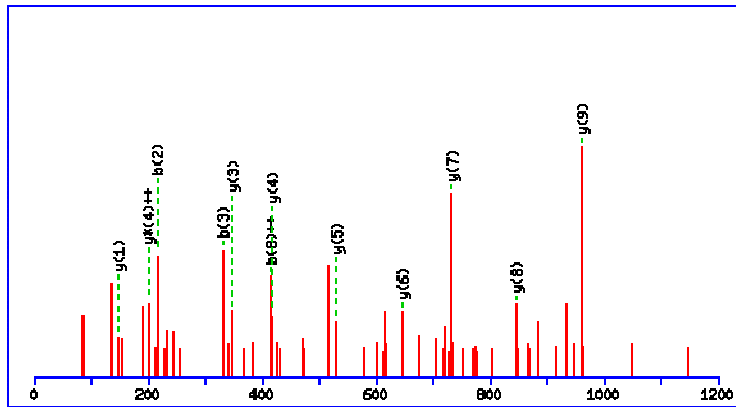
Peptide Number: 94990

MS/MS Fragmentation of **SEDLSDIASLK**Found in **IPI00014952** in **IPI_human**, Tax_Id=9606 Gene_Symbol=GDAP2 Isoform 1 of Ganglioside-induced differentiation-associated protein 2

Match to Query 13076: 1176.597048 from(589.305800,2+) index(37204)

Title: Elution from: 88.4333333333333 to 88.4333333333333 period: 0 cycle: 3355 experiment: 8 polarity:+

Data file 120208ry_Tig120slc-P8_2_2.mgf



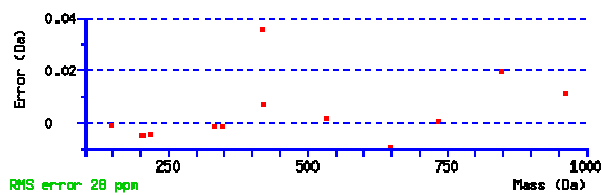
Monoisotopic mass of neutral peptide Mr(calc): 1176.5874

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

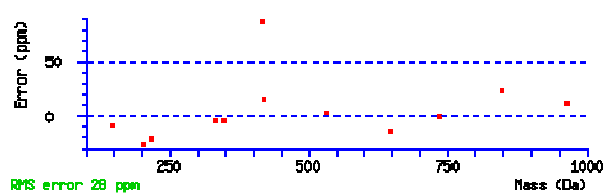
Ions Score: 48 Expect: 0.00096

Matches : 12/96 fragment ions using 29 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233	70.0287	35.5180	S							11
2	217.0819	109.0446	199.0713	100.0393	E	1090.5626	545.7850	1073.5361	537.2717	1072.5521	536.7797	10
3	332.1088	166.5581	314.0983	157.5528	D	961.5201	481.2637	944.4935	472.7504	943.5095	472.2584	9
4	445.1929	223.1001	427.1823	214.0948	L	846.4931	423.7502	829.4666	415.2369	828.4825	414.7449	8
5	532.2249	266.6161	514.2144	257.6108	S	733.4090	367.2082	716.3825	358.6949	715.3985	358.2029	7
6	647.2519	324.1296	629.2413	315.1243	D	646.3770	323.6921	629.3505	315.1789	628.3665	314.6869	6
7	760.3359	380.6716	742.3254	371.6663	I	531.3501	266.1787	514.3235	257.6654	513.3395	257.1734	5
8	831.3731	416.1902	813.3625	407.1849	A	418.2660	209.6366	401.2395	201.1234	400.2554	200.6314	4
9	918.4051	459.7062	900.3945	450.7009	S	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
10	1031.4891	516.2482	1013.4786	507.2429	L	260.1969	130.6021	243.1703	122.0888			2
11					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 28 ppm



RMS error 28 ppm

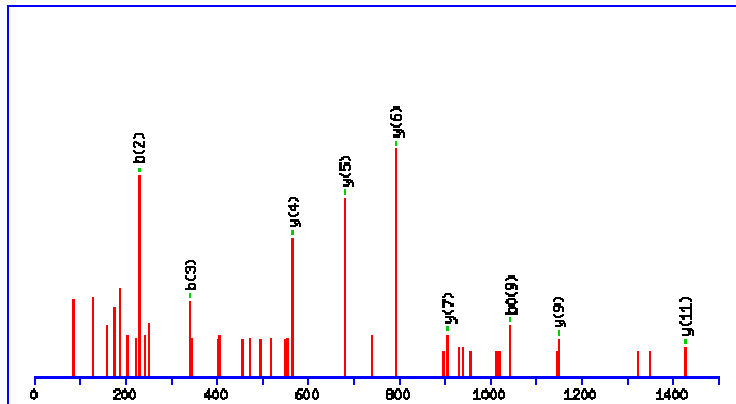
Peptide Number: 95009

MS/MS Fragmentation of **DNISDYDQIIDYVER**Found in **IPI01012794** in **IPI_human**, Tax_Id=9606 Gene_Symbol=GDAP1L1 38 kDa protein

Match to Query 14323: 1969.909602 from(657.643810,3+) index(27205)

Title: Elution from: 68.5833333333333 to 68.5833333333333 period: 0 cycle: 2563 experiment: 4 polarity: +

Data file 120118ry_201B7-32_3_4.mgf



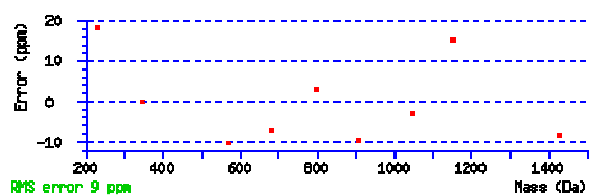
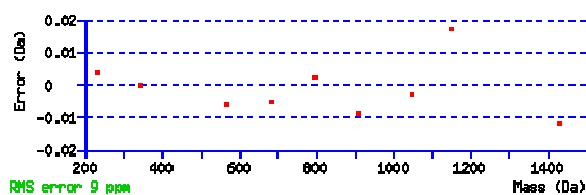
Monoisotopic mass of neutral peptide Mr(calc): 1969.9269

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 39 Expect: 0.005

Matches : 9/176 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							16
2	230.0771	115.5422	213.0506	107.0289	212.0666	106.5369	N	1855.9072	928.4573	1838.8807	919.9440	1837.8967	919.4520	15
3	343.1612	172.0842	326.1347	163.5710	325.1506	163.0790	I	1741.8643	871.4358	1724.8378	862.9225	1723.8537	862.4305	14
4	456.2453	228.6263	439.2187	220.1130	438.2347	219.6210	I	1628.7802	814.8938	1611.7537	806.3805	1610.7697	805.8885	13
5	543.2773	272.1423	526.2508	263.6290	525.2667	263.1370	S	1515.6962	758.3517	1498.6696	749.8385	1497.6856	749.3464	12
6	658.3042	329.6558	641.2777	321.1425	640.2937	320.6505	D	1428.6642	714.8357	1411.6376	706.3224	1410.6536	705.8304	11
7	821.3676	411.1874	804.3410	402.6742	803.3570	402.1821	Y	1313.6372	657.3222	1296.6107	648.8090	1295.6266	648.3170	10
8	936.3945	468.7009	919.3680	460.1876	918.3840	459.6956	D	1150.5739	575.7906	1133.5473	567.2773	1132.5633	566.7853	9
9	1064.4531	532.7302	1047.4265	524.2169	1046.4425	523.7249	Q	1035.5469	518.2771	1018.5204	509.7638	1017.5364	509.2718	8
10	1177.5372	589.2722	1160.5106	580.7589	1159.5266	580.2669	I	907.4884	454.2478	890.4618	445.7345	889.4778	445.2425	7
11	1290.6212	645.8142	1273.5947	637.3010	1272.6107	636.8090	I	794.4043	397.7058	777.3777	389.1925	776.3937	388.7005	6
12	1405.6482	703.3277	1388.6216	694.8144	1387.6376	694.3224	D	681.3202	341.1638	664.2937	332.6505	663.3097	332.1585	5
13	1568.7115	784.8594	1551.6849	776.3461	1550.7009	775.8541	Y	566.2933	283.6503	549.2667	275.1370	548.2827	274.6450	4
14	1667.7799	834.3936	1650.7534	825.8803	1649.7693	825.3883	V	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
15	1796.8225	898.9149	1779.7960	890.4016	1778.8119	889.9096	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
16							R	175.1190	88.0631	158.0924	79.5498			1



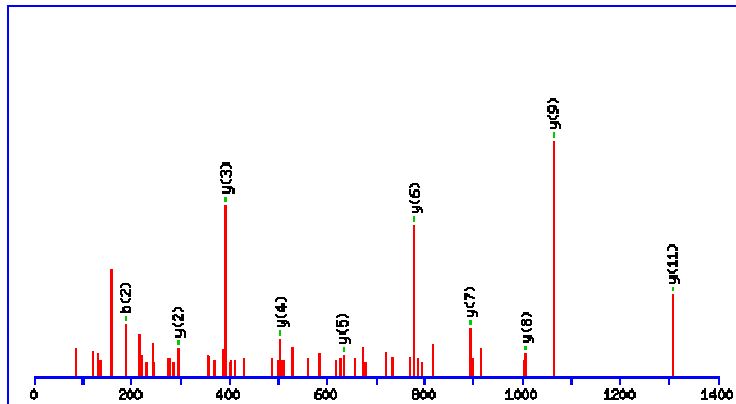
Peptide Number: 95621

MS/MS Fragmentation of **SVGWGNIFQLPFK**Found in **IPI00008490** in **IPI_human**, Tax_Id=9606 Gene_Symbol=UNC93B1 Protein unc-93 homolog B1

Match to Query 2896: 1491.792328 from(746.903440,2+) index(14772)

Title: Elution from: 40.8833333333333 to 40.8833333333333 period: 0 cycle: 1574 experiment: 2 polarity: +

Data file 120210ry_585A1-55_3_4.mgf



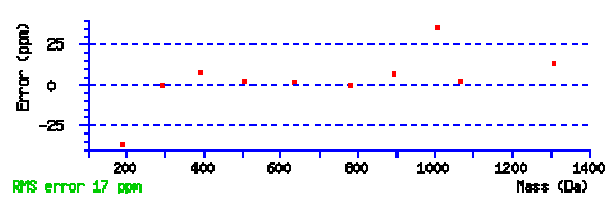
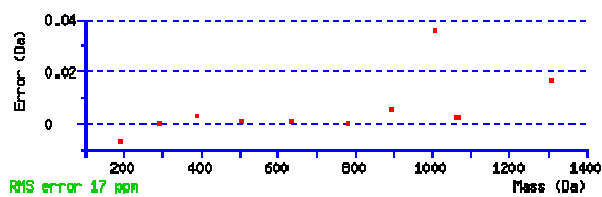
Monoisotopic mass of neutral peptide Mr(calc): 1491.7874

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 59 Expect: 8.8e-005

Matches : 10/110 fragment ions using 21 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S					13
2	187.1077	94.0575			169.0972	85.0522	V	1405.7627	703.3850	1388.7361	694.8717	12
3	244.1292	122.5682			226.1186	113.5629	G	1306.6943	653.8508	1289.6677	645.3375	11
4	430.2085	215.6079			412.1979	206.6026	W	1249.6728	625.3400	1232.6463	616.8268	10
5	487.2300	244.1186			469.2194	235.1133	G	1063.5935	532.3004	1046.5669	523.7871	9
6	601.2729	301.1401	584.2463	292.6268	583.2623	292.1348	N	1006.5720	503.7897	989.5455	495.2764	8
7	714.3570	357.6821	697.3304	349.1688	696.3464	348.6768	I	892.5291	446.7682	875.5026	438.2549	7
8	861.4254	431.2163	844.3988	422.7030	843.4148	422.2110	F	779.4450	390.2262	762.4185	381.7129	6
9	989.4839	495.2456	972.4574	486.7323	971.4734	486.2403	Q	632.3766	316.6920	615.3501	308.1787	5
10	1102.5680	551.7876	1085.5415	543.2744	1084.5574	542.7824	L	504.3180	252.6627	487.2915	244.1494	4
11	1199.6208	600.3140	1182.5942	591.8007	1181.6102	591.3087	P	391.2340	196.1206	374.2074	187.6074	3
12	1346.6892	673.8482	1329.6626	665.3350	1328.6786	664.8429	F	294.1812	147.5942	277.1547	139.0810	2
13							K	147.1128	74.0600	130.0863	65.5468	1



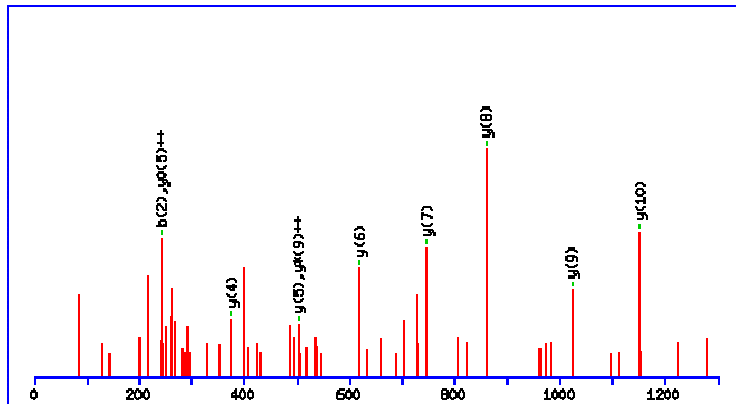
Peptide Number: 95645

MS/MS Fragmentation of **LEEYIQDELGGK**Found in **IPI00432655** in **IPI_human**, Tax_Id=9606 Gene_Symbol=FAM82A1 Isoform 1 of Regulator of microtubule dynamics protein 2

Match to Query 23005: 1392.678568 from(697.346560,2+) index(36216)

Title: Elution from: 87.5 to 87.5 period: 0 cycle: 3327 experiment: 9 polarity: +

Data file 120212ry_aHDF1388-P9_2_2.mgf



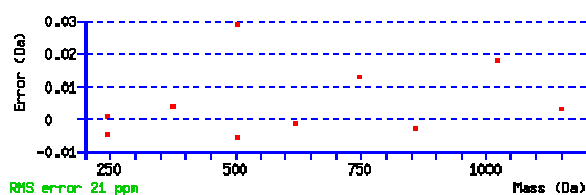
Monoisotopic mass of neutral peptide Mr(calc): 1392.6772

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

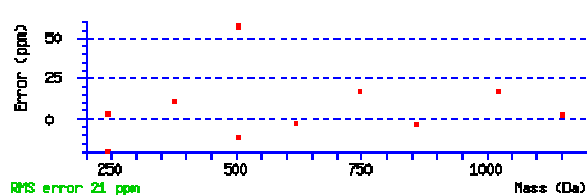
Ions Score: 53 Expect: 0.00033

Matches : 10/112 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							12
2	243.1339	122.0706			225.1234	113.0653	E	1280.6005	640.8039	1263.5739	632.2906	1262.5899	631.7986	11
3	372.1765	186.5919			354.1660	177.5866	E	1151.5579	576.2826	1134.5313	567.7693	1133.5473	567.2773	10
4	535.2399	268.1236			517.2293	259.1183	Y	1022.5153	511.7613	1005.4888	503.2480	1004.5047	502.7560	9
5	648.3239	324.6656			630.3134	315.6603	I	859.4520	430.2296	842.4254	421.7164	841.4414	421.2243	8
6	776.3825	388.6949	759.3559	380.1816	758.3719	379.6896	Q	746.3679	373.6876	729.3414	365.1743	728.3573	364.6823	7
7	891.4094	446.2084	874.3829	437.6951	873.3989	437.2031	D	618.3093	309.6583	601.2828	301.1450	600.2988	300.6530	6
8	1020.4520	510.7297	1003.4255	502.2164	1002.4415	501.7244	E	503.2824	252.1448	486.2558	243.6316	485.2718	243.1395	5
9	1133.5361	567.2717	1116.5095	558.7584	1115.5255	558.2664	L	374.2398	187.6235	357.2132	179.1103			4
10	1190.5576	595.7824	1173.5310	587.2691	1172.5470	586.7771	G	261.1557	131.0815	244.1292	122.5682			3
11	1247.5790	624.2932	1230.5525	615.7799	1229.5685	615.2879	G	204.1343	102.5708	187.1077	94.0575			2
12							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 21 ppm



RMS error 21 ppm

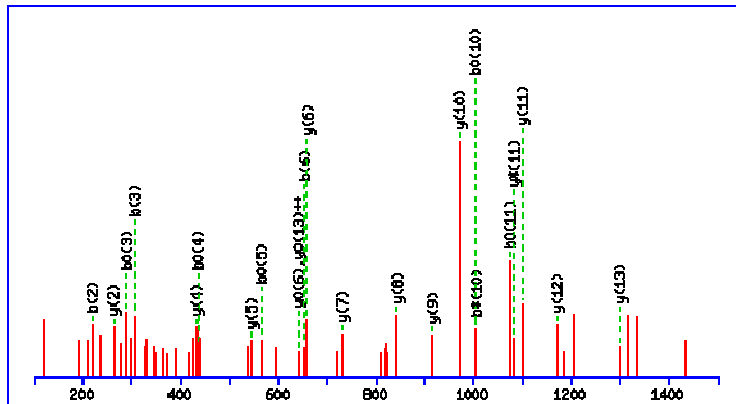
Peptide Number: 95675

MS/MS Fragmentation of **FASFEAQGALANIAVDK**Found in **IPI00005171** in **IPI_human**, Tax_Id=9606 Gene_Symbol=HLA-DRA HLA class II histocompatibility antigen, DR alpha chain

Match to Query 18628: 1750.888588 from(876.451570,2+) index(16160)

Title: Elution from: 38.7 to 38.7 period: 0 cycle: 1466 experiment: 6 polarity: +

Data file 120212ry_aHDF1388-P9_2_3.mgf



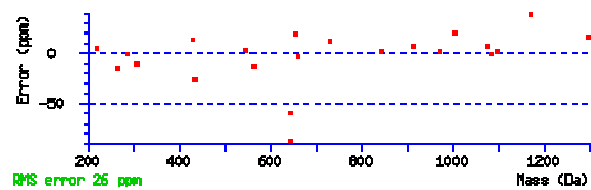
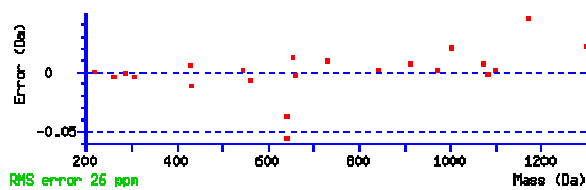
Monoisotopic mass of neutral peptide Mr(calc): 1750.8890

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 62 Expect: 4.5e-005

Matches : 23/174 fragment ions using 47 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415					F							17
2	219.1128	110.0600					A	1604.8279	802.9176	1587.8013	794.4043	1586.8173	793.9123	16
3	306.1448	153.5761			288.1343	144.5708	S	1533.7907	767.3990	1516.7642	758.8857	1515.7802	758.3937	15
4	453.2132	227.1103			435.2027	218.1050	F	1446.7587	723.8830	1429.7322	715.3697	1428.7482	714.8777	14
5	582.2558	291.6316			564.2453	282.6263	E	1299.6903	650.3488	1282.6638	641.8355	1281.6797	641.3435	13
6	653.2930	327.1501			635.2824	318.1448	A	1170.6477	585.8275	1153.6212	577.3142	1152.6371	576.8222	12
7	781.3515	391.1794	764.3250	382.6661	763.3410	382.1741	Q	1099.6106	550.3089	1082.5841	541.7957	1081.6000	541.3037	11
8	838.3730	419.6901	821.3464	411.1769	820.3624	410.6849	G	971.5520	486.2796	954.5255	477.7664	953.5415	477.2744	10
9	909.4101	455.2087	892.3836	446.6954	891.3995	446.2034	A	914.5306	457.7689	897.5040	449.2556	896.5200	448.7636	9
10	1022.4942	511.7507	1005.4676	503.2375	1004.4836	502.7454	L	843.4934	422.2504	826.4669	413.7371	825.4829	413.2451	8
11	1093.5313	547.2693	1076.5047	538.7560	1075.5207	538.2640	A	730.4094	365.7083	713.3828	357.1951	712.3988	356.7030	7
12	1207.5742	604.2907	1190.5477	595.7775	1189.5636	595.2855	N	659.3723	330.1898	642.3457	321.6765	641.3617	321.1845	6
13	1320.6583	660.8328	1303.6317	652.3195	1302.6477	651.8275	I	545.3293	273.1683	528.3028	264.6550	527.3188	264.1630	5
14	1391.6954	696.3513	1374.6688	687.8381	1373.6848	687.3461	A	432.2453	216.6263	415.2187	208.1130	414.2347	207.6210	4
15	1490.7638	745.8855	1473.7373	737.3723	1472.7532	736.8803	V	361.2082	181.1077	344.1816	172.5944	343.1976	172.1024	3
16	1605.7907	803.3990	1588.7642	794.8857	1587.7802	794.3937	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
17							K	147.1128	74.0600	130.0863	65.5468			1



Peptide Number: 95684

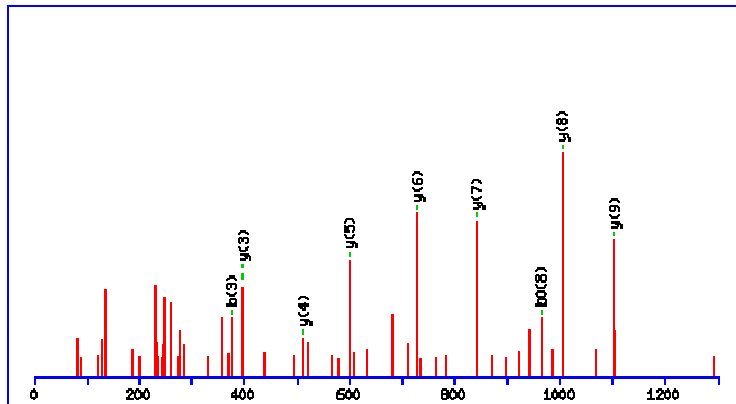
MS/MS Fragmentation of QFVYLESYDK

Found in IPI00295461 in IPI_human, Tax_Id=9606 Gene_Symbol=FAP Isoform 1 of Sepsae

Match to Query 21259: 1377.648228 from(689.831390,2+) index(32939)

Title: Elution from: 85.2333333333333 to 85.2333333333333 period: 0 cycle: 3262 experiment: 5 polarity:+

Data file 120208ry_Tig120slc-P8_1_2.mgf



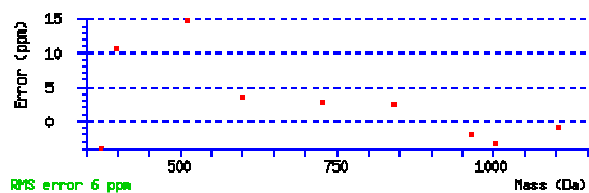
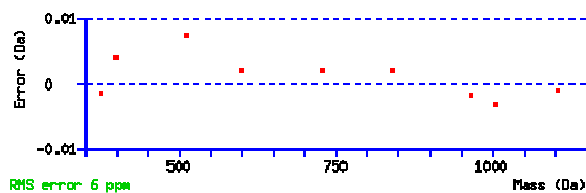
Monoisotopic mass of neutral peptide Mr(calc): 1377.6452

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 58 Expect: 7.9e-005

Matches : 9/108 fragment ions using 12 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.0659	65.0366	112.0393	56.5233			Q							11
2	276.1343	138.5708	259.1077	130.0575			F	1250.5939	625.8006	1233.5674	617.2873	1232.5834	616.7953	10
3	375.2027	188.1050	358.1761	179.5917			V	1103.5255	552.2664	1086.4990	543.7531	1085.5150	543.2611	9
4	538.2660	269.6366	521.2395	261.1234			Y	1004.4571	502.7322	987.4306	494.2189	986.4466	493.7269	8
5	651.3501	326.1787	634.3235	317.6654			L	841.3938	421.2005	824.3672	412.6873	823.3832	412.1953	7
6	780.3927	390.7000	763.3661	382.1867	762.3821	381.6947	E	728.3097	364.6585	711.2832	356.1452	710.2992	355.6532	6
7	867.4247	434.2160	850.3981	425.7027	849.4141	425.2107	S	599.2671	300.1372	582.2406	291.6239	581.2566	291.1319	5
8	982.4516	491.7295	965.4251	483.2162	964.4411	482.7242	D	512.2351	256.6212	495.2086	248.1079	494.2245	247.6159	4
9	1145.5150	573.2611	1128.4884	564.7478	1127.5044	564.2558	Y	397.2082	199.1077	380.1816	190.5944	379.1976	190.1024	3
10	1232.5470	616.7771	1215.5204	608.2639	1214.5364	607.7719	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
11							K	147.1128	74.0600	130.0863	65.5468			1

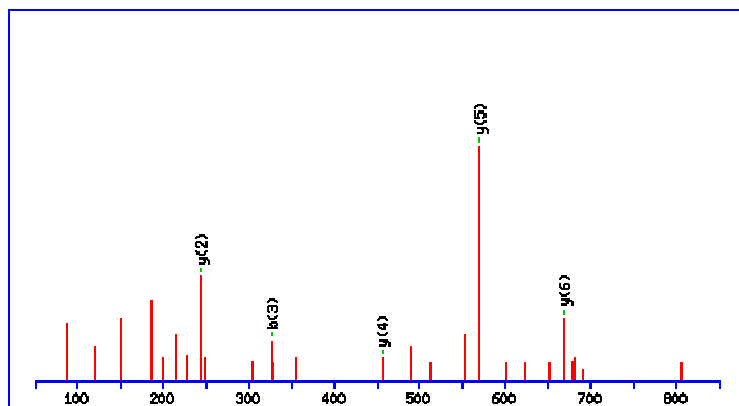


Peptide Number: 95816MS/MS Fragmentation of **LVNIVPK**Found in **IPI00410039** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PPHLN1 Isoform 1 of Periphilin-1

Match to Query 1772: 781.508388 from(391.761470,2+) index(5474)

Title: Elution from: 12.7666666666667 to 12.7666666666667 period: 0 cycle: 479 experiment: 2 polarity: +

Data file 120126ry_585A1-55_2_2.mgf



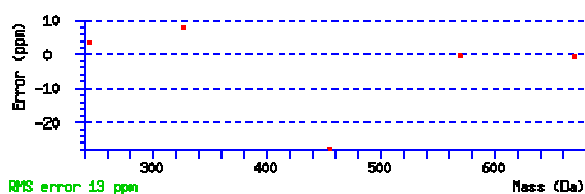
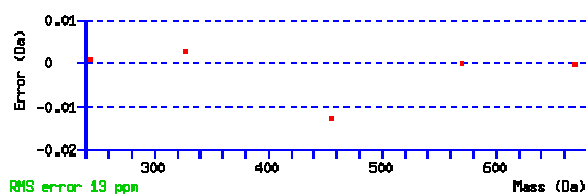
Monoisotopic mass of neutral peptide Mr(calc): 781.5062

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 31 Expect: 0.0029

Matches : 5/44 fragment ions using 7 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	#
1	114.0913	57.5493			L					7
2	213.1598	107.0835			V	669.4294	335.2183	652.4028	326.7051	6
3	327.2027	164.1050	310.1761	155.5917	N	570.3610	285.6841	553.3344	277.1709	5
4	440.2867	220.6470	423.2602	212.1337	I	456.3180	228.6627	439.2915	220.1494	4
5	539.3552	270.1812	522.3286	261.6679	V	343.2340	172.1206	326.2074	163.6074	3
6	636.4079	318.7076	619.3814	310.1943	P	244.1656	122.5864	227.1390	114.0731	2
7					K	147.1128	74.0600	130.0863	65.5468	1

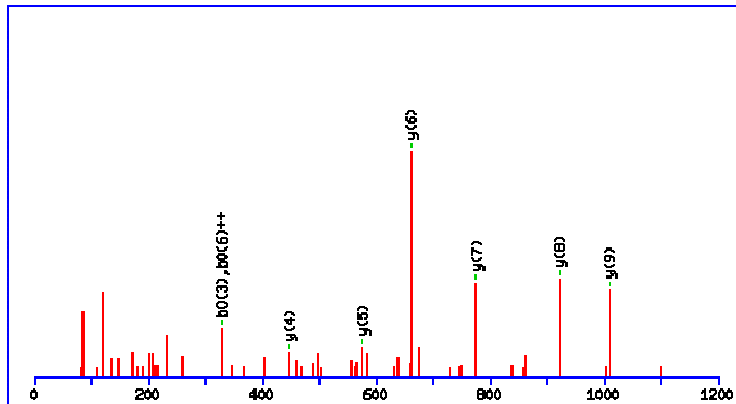


Peptide Number: 96087MS/MS Fragmentation of **LSFISEGEIK**Found in **IPI00956749** in **IPI_human**, Tax_Id=9606 Gene_Symbol=-- P40

Match to Query 12397: 1121.596908 from(561.805730,2+) index(39753)

Title: Elution from: 98.45 to 98.45 period: 0 cycle: 3726 experiment: 3 polarity:+

Data file 120210ry_32R1-32_2_2.mgf



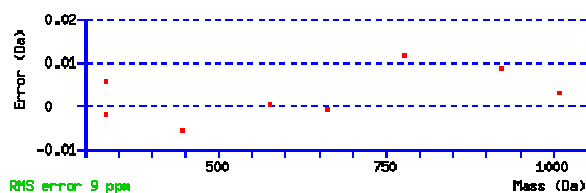
Monoisotopic mass of neutral peptide Mr(calc): 1121.5968

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

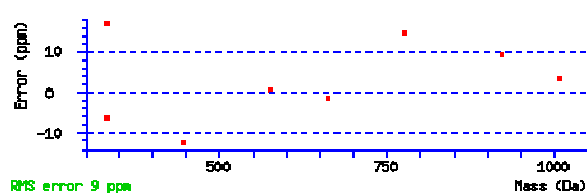
Ions Score: 41 Expect: 0.0049

Matches : 8/84 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							10
2	201.1234	101.0653	183.1128	92.0600	S	1009.5201	505.2637	992.4935	496.7504	991.5095	496.2584	9
3	348.1918	174.5995	330.1812	165.5942	F	922.4880	461.7477	905.4615	453.2344	904.4775	452.7424	8
4	461.2758	231.1416	443.2653	222.1363	I	775.4196	388.2134	758.3931	379.7002	757.4090	379.2082	7
5	548.3079	274.6576	530.2973	265.6523	S	662.3355	331.6714	645.3090	323.1581	644.3250	322.6661	6
6	677.3505	339.1789	659.3399	330.1736	E	575.3035	288.1554	558.2770	279.6421	557.2930	279.1501	5
7	734.3719	367.6896	716.3614	358.6843	G	446.2609	223.6341	429.2344	215.1208	428.2504	214.6288	4
8	863.4145	432.2109	845.4040	423.2056	E	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
9	976.4986	488.7529	958.4880	479.7476	I	260.1969	130.6021	243.1703	122.0888			2
10					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 9 ppm



RMS error 9 ppm

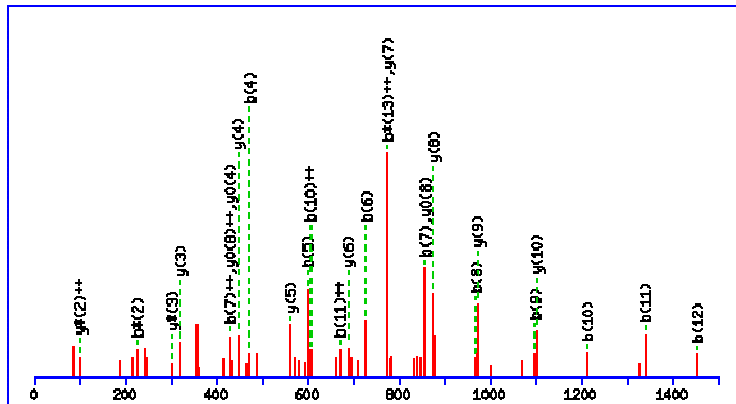
Peptide Number: 96107

MS/MS Fragmentation of **SRDLEQQQLQDELLEVVSSELQTAK**Found in **IPI00328842** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ARHGAP4 rho GTPase-activating protein 4 isoform 1

Match to Query 4551: 2670.389136 from(668.604560,4+) index(6576)

Title: Elution from: 35.9833333333333 to 35.9833333333333 period: 0 cycle: 1409 experiment: 1 polarity: +

Data file 120210ry_32R1-32_2_5.mgf



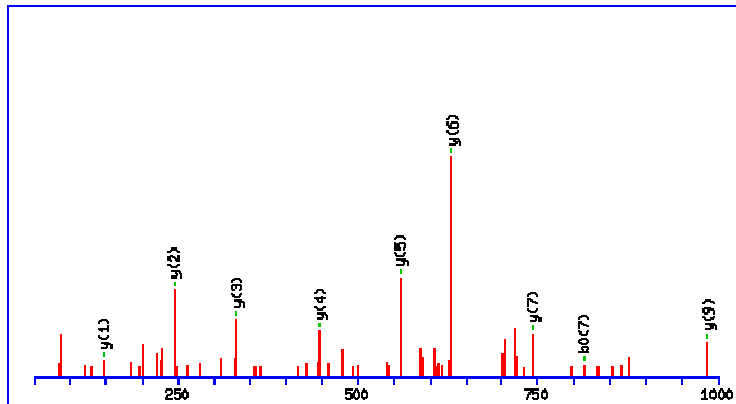
Peptide Number: 96364

MS/MS Fragmentation of **NLTFDQLALDSPK**Found in **IPI00375226** in **IPI_human**, Tax_Id=9606 Gene_Symbol=- Similar to ribosomal protein L18

Match to Query 10596: 1460.774502 from(487.932110,3+) index(24082)

Title: Elution from: 58.9833333333333 to 58.9833333333333 period: 0 cycle: 2182 experiment: 1 polarity: +

Data file 120129ry_604A1-46_1_3.mgf



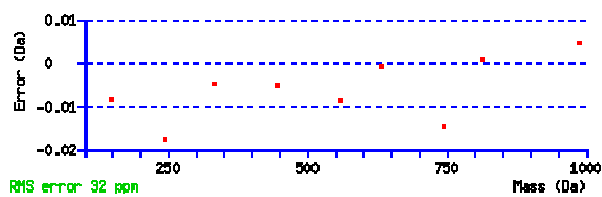
Monoisotopic mass of neutral peptide Mr(calc): 1460.7511

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

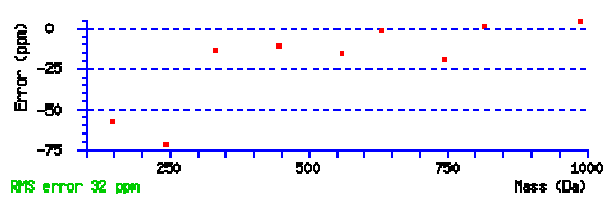
Ions Score: 50 Expect: 0.00063

Matches : 9/136 fragment ions using 17 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	115.0502	58.0287	98.0237	49.5155			N							13
2	228.1343	114.5708	211.1077	106.0575			L	1347.7155	674.3614	1330.6889	665.8481	1329.7049	665.3561	12
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	T	1234.6314	617.8193	1217.6048	609.3061	1216.6208	608.8141	11
4	476.2504	238.6288	459.2238	230.1155	458.2398	229.6235	F	1133.5837	567.2955	1116.5572	558.7822	1115.5732	558.2902	10
5	591.2773	296.1423	574.2508	287.6290	573.2667	287.1370	D	986.5153	493.7613	969.4888	485.2480	968.5047	484.7560	9
6	719.3359	360.1716	702.3093	351.6583	701.3253	351.1663	Q	871.4884	436.2478	854.4618	427.7345	853.4778	427.2425	8
7	832.4199	416.7136	815.3934	408.2003	814.4094	407.7083	L	743.4298	372.2185	726.4032	363.7053	725.4192	363.2132	7
8	903.4571	452.2322	886.4305	443.7189	885.4465	443.2269	A	630.3457	315.6765	613.3192	307.1632	612.3352	306.6712	6
9	1016.5411	508.7742	999.5146	500.2609	998.5306	499.7689	L	559.3086	280.1579	542.2821	271.6447	541.2980	271.1527	5
10	1131.5681	566.2877	1114.5415	557.7744	1113.5575	557.2824	D	446.2245	223.6159	429.1980	215.1026	428.2140	214.6106	4
11	1218.6001	609.8037	1201.5735	601.2904	1200.5895	600.7984	S	331.1976	166.1024	314.1710	157.5892	313.1870	157.0972	3
12	1315.6529	658.3301	1298.6263	649.8168	1297.6423	649.3248	P	244.1656	122.5864	227.1390	114.0731			2
13							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 32 ppm



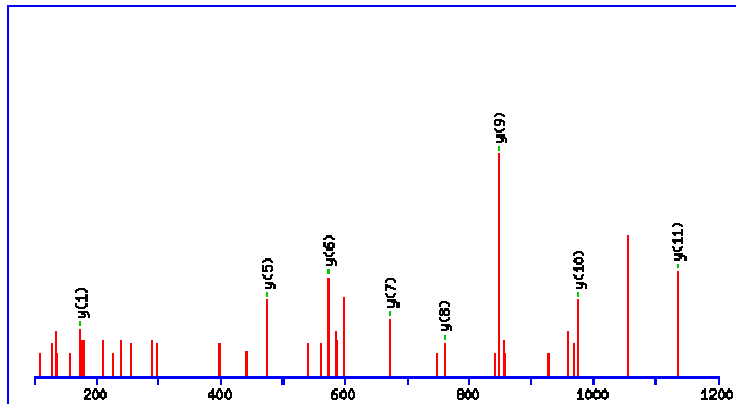
RMS error 32 ppm

Peptide Number: 96704MS/MS Fragmentation of **GVCQSSVVAGTAR**Found in **IPI00029819** in **IPI_human**, Tax_Id=9606 Gene_Symbol=NOTCH3 Neurogenic locus notch homolog protein 3

Match to Query 19824: 1290.630728 from(646.322640,2+) index(20220)

Title: Elution from: 83.4333333333333 to 83.4333333333333 period: 0 cycle: 6954 experiment: 9 polarity:+

Data file 120208ry_Tig120slc-P8_1_1.mgf



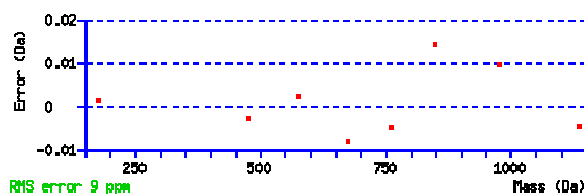
Monoisotopic mass of neutral peptide Mr(calc): 1290.6351

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

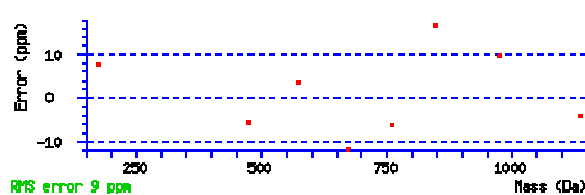
Ions Score: 69 Expect: 8.2e-006

Matches : 8/126 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							13
2	157.0972	79.0522					V	1234.6208	617.8141	1217.5943	609.3008	1216.6103	608.8088	12
3	317.1278	159.0675					C	1135.5524	568.2799	1118.5259	559.7666	1117.5419	559.2746	11
4	445.1864	223.0968	428.1598	214.5836			Q	975.5218	488.2645	958.4952	479.7513	957.5112	479.2592	10
5	532.2184	266.6128	515.1919	258.0996	514.2078	257.6076	S	847.4632	424.2352	830.4367	415.7220	829.4526	415.2300	9
6	619.2504	310.1289	602.2239	301.6156	601.2399	301.1236	S	760.4312	380.7192	743.4046	372.2060	742.4206	371.7139	8
7	718.3189	359.6631	701.2923	351.1498	700.3083	350.6578	V	673.3992	337.2032	656.3726	328.6899	655.3886	328.1979	7
8	817.3873	409.1973	800.3607	400.6840	799.3767	400.1920	V	574.3307	287.6690	557.3042	279.1557	556.3202	278.6637	6
9	888.4244	444.7158	871.3978	436.2026	870.4138	435.7105	A	475.2623	238.1348	458.2358	229.6215	457.2518	229.1295	5
10	945.4458	473.2266	928.4193	464.7133	927.4353	464.2213	G	404.2252	202.6162	387.1987	194.1030	386.2146	193.6110	4
11	1046.4935	523.7504	1029.4670	515.2371	1028.4830	514.7451	T	347.2037	174.1055	330.1772	165.5922	329.1932	165.1002	3
12	1117.5306	559.2690	1100.5041	550.7557	1099.5201	550.2637	A	246.1561	123.5817	229.1295	115.0684			2
13							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 9 ppm



RMS error 9 ppm

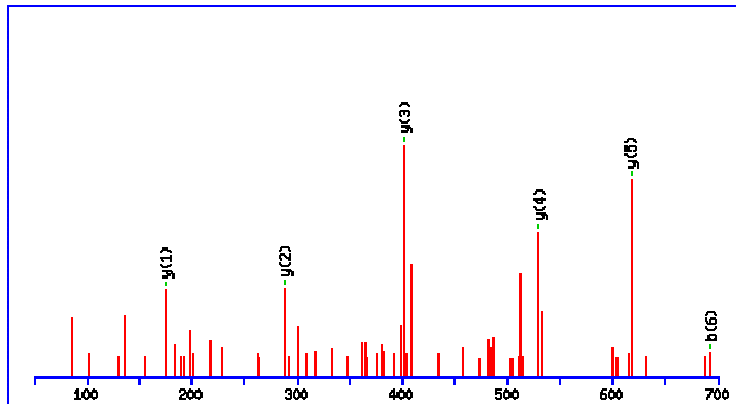
Peptide Number: 97040

MS/MS Fragmentation of **ECGKAFRGNSELLR**Found in **IPI00064885** in **IPI_human**, Tax_Id=9606 Gene_Symbol=ZFP3 Zinc finger protein 3 homolog

Match to Query 25303: 1635.787296 from(409.954100,4+) index(21027)

Title: Elution from: 86.8833333333333 to 86.8833333333333 period: 0 cycle: 8119 experiment: 4 polarity:+

Data file 120206ry_aHDF1419-P10_2_1.mgf



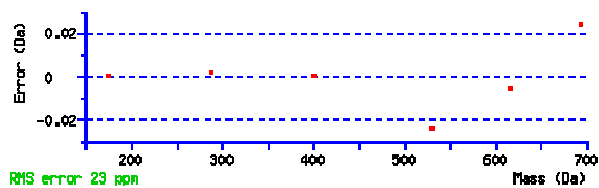
Monoisotopic mass of neutral peptide Mr(calc): 1635.8151

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

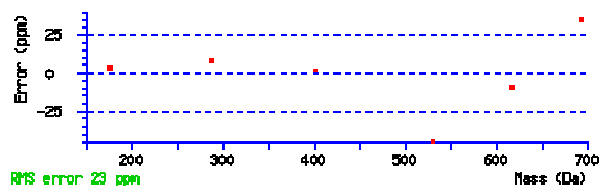
Ions Score: 39 Expect: 0.0085

Matches : 6/144 fragment ions using 7 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							14
2	290.0805	145.5439			272.0700	136.5386	C	1507.7798	754.3935	1490.7533	745.8803	1489.7692	745.3883	13
3	347.1020	174.0546			329.0914	165.0493	G	1347.7492	674.3782	1330.7226	665.8649	1329.7386	665.3729	12
4	475.1969	238.1021	458.1704	229.5888	457.1864	229.0968	K	1290.7277	645.8675	1273.7011	637.3542	1272.7171	636.8622	11
5	546.2341	273.6207	529.2075	265.1074	528.2235	264.6154	A	1162.6327	581.8200	1145.6062	573.3067	1144.6222	572.8147	10
6	693.3025	347.1549	676.2759	338.6416	675.2919	338.1496	F	1091.5956	546.3014	1074.5691	537.7882	1073.5851	537.2962	9
7	849.4036	425.2054	832.3770	416.6922	831.3930	416.2001	R	944.5272	472.7672	927.5007	464.2540	926.5166	463.7620	8
8	906.4250	453.7162	889.3985	445.2029	888.4145	444.7109	G	788.4261	394.7167	771.3995	386.2034	770.4155	385.7114	7
9	1020.4680	510.7376	1003.4414	502.2244	1002.4574	501.7323	N	731.4046	366.2060	714.3781	357.6927	713.3941	357.2007	6
10	1107.5000	554.2536	1090.4735	545.7404	1089.4894	545.2484	S	617.3617	309.1845	600.3352	300.6712	599.3511	300.1792	5
11	1236.5426	618.7749	1219.5160	610.2617	1218.5320	609.7697	E	530.3297	265.6685	513.3031	257.1552	512.3191	256.6632	4
12	1349.6267	675.3170	1332.6001	666.8037	1331.6161	666.3117	L	401.2871	201.1472	384.2605	192.6339			3
13	1462.7107	731.8590	1445.6842	723.3457	1444.7002	722.8537	L	288.2030	144.6051	271.1765	136.0919			2
14							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 23 ppm

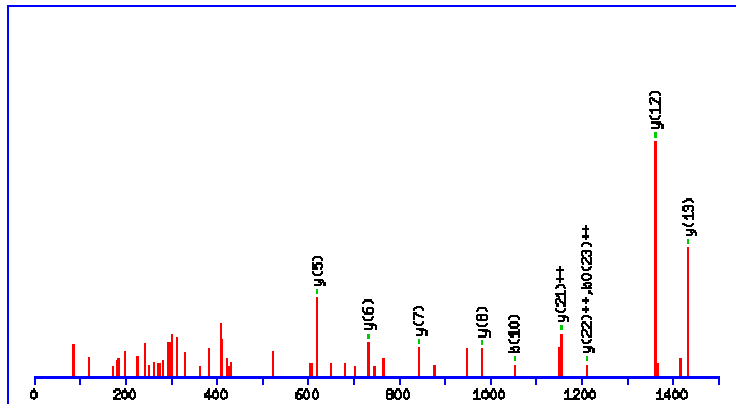


RMS error 23 ppm

Peptide Number: 97067

MS/MS Fragmentation of **FDCNSVSTAALLADILPTLVIKLLAPLGLHLLPYSPR**
 Found in **IPI00010906** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CLN3 CLN3 protein

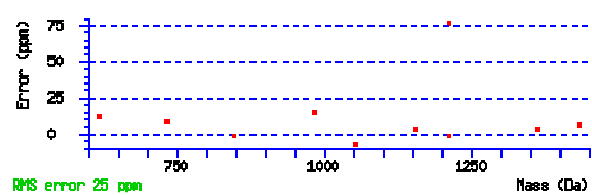
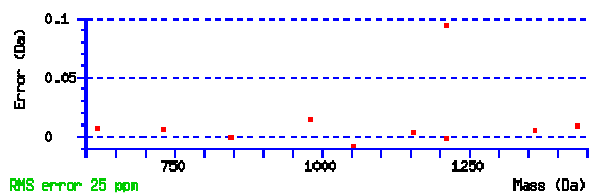
Match to Query 15977: 4100.288936 from(1026.079510,4+) index(16355)
 Title: Elution from: 41.8166666666667 to 41.8166666666667 period: 0 cycle: 1572 experiment: 2 polarity:+
 Data file 120206ry_aHDF1419-P10_2_5.mgf



Monoisotopic mass of neutral peptide Mr(calc): 4100.3112
 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
 Ions Score: 29 Expect: 0.0067
 Matches : 10/432 fragment ions using 14 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415					F							38
2	263.1026	132.0550			245.0921	123.0497	D	3954.2500	1977.6287	3937.2235	1969.1154	3936.2395	1968.6234	37
3	423.1333	212.0703			405.1227	203.0650	C	3839.2231	1920.1152	3822.1966	1911.6019	3821.2125	1911.1099	36
4	537.1762	269.0917	520.1497	260.5785	519.1656	260.0865	N	3679.1925	1840.0999	3662.1659	1831.5866	3661.1819	1831.0946	35
5	624.2082	312.6078	607.1817	304.0945	606.1977	303.6025	S	3565.1495	1783.0784	3548.1230	1774.5651	3547.1390	1774.0731	34
6	723.2767	362.1420	706.2501	353.6287	705.2661	353.1367	V	3478.1175	1739.5624	3461.0909	1731.0491	3460.1069	1730.5571	33
7	810.3087	405.6580	793.2821	397.1447	792.2981	396.6527	S	3379.0491	1690.0282	3362.0225	1681.5149	3361.0385	1681.0229	32
8	911.3564	456.1818	894.3298	447.6685	893.3458	447.1765	T	3292.0171	1646.5122	3274.9905	1637.9989	3274.0065	1637.5069	31
9	982.3935	491.7004	965.3669	483.1871	964.3829	482.6951	A	3190.9694	1595.9883	3173.9428	1587.4751	3172.9588	1586.9830	30
10	1053.4306	527.2189	1036.4040	518.7057	1035.4200	518.2136	A	3119.9323	1560.4698	3102.9057	1551.9565	3101.9217	1551.4645	29
11	1152.4990	576.7531	1135.4725	568.2399	1134.4884	567.7479	V	3048.8951	1524.9512	3031.8686	1516.4379	3030.8846	1515.9459	28
12	1265.5831	633.2952	1248.5565	624.7819	1247.5725	624.2899	L	2949.8267	1475.4170	2932.8002	1466.9037	2931.8162	1466.4117	27
13	1378.6671	689.8372	1361.6406	681.3239	1360.6566	680.8319	L	2836.7427	1418.8750	2819.7161	1410.3617	2818.7321	1409.8697	26
14	1449.7042	725.3558	1432.6777	716.8425	1431.6937	716.3505	A	2723.6586	1362.3329	2706.6321	1353.8197	2705.6480	1353.3277	25
15	1564.7312	782.8692	1547.7046	774.3560	1546.7206	773.8639	D	2652.6215	1326.8144	2635.5949	1318.3011	2634.6109	1317.8091	24
16	1677.8152	839.4113	1660.7887	830.8980	1659.8047	830.4060	I	2537.5946	1269.3009	2520.5680	1260.7876	2519.5840	1260.2956	23
17	1790.8993	895.9533	1773.8728	887.4400	1772.8887	886.9480	L	2424.5105	1212.7589	2407.4839	1204.2456	2406.4999	1203.7536	22
18	1887.9521	944.4797	1870.9255	935.9664	1869.9415	935.4744	P	2311.4264	1156.2168	2294.3999	1147.7036	2293.4159	1147.2116	21
19	1988.9998	995.0035	1971.9732	986.4902	1970.9892	985.9982	T	2214.3737	1107.6905	2197.3471	1099.1772	2196.3631	1098.6852	20
20	2102.0838	1051.5455	2085.0573	1043.0323	2084.0733	1042.5403	L	2113.3260	1057.1666	2096.2994	1048.6534	2095.3154	1048.1613	19
21	2201.1522	1101.0798	2184.1257	1092.5665	2183.1417	1092.0745	V	2000.2419	1000.6246	1983.2154	992.1113	1982.2314	991.6193	18
22	2314.2363	1157.6218	2297.2097	1149.1085	2296.2257	1148.6165	I	1901.1735	951.0904	1884.1470	942.5771	1883.1629	942.0851	17
23	2442.3313	1221.6693	2425.3047	1213.1560	2424.3207	1212.6640	K	1788.0894	894.5484	1771.0629	886.0351	1770.0789	885.5431	16
24	2555.4153	1278.2113	2538.3888	1269.6980	2537.4048	1269.2060	L	1659.9945	830.5009	1642.9679	821.9876	1641.9839	821.4956	15
25	2668.4994	1334.7533	2651.4728	1326.2401	2650.4888	1325.7480	L	1546.9104	773.9588	1529.8839	765.4456	1528.8998	764.9536	14
26	2739.5365	1370.2719	2722.5100	1361.7586	2721.5259	1361.2666	A	1433.8263	717.4168	1416.7998	708.9035	1415.8158	708.4115	13
27	2836.5893	1418.7983	2819.5627	1410.2850	2818.5787	1409.7930	P	1362.7892	681.8983	1345.7627	673.3850	1344.7787	672.8930	12
28	2949.6733	1475.3403	2932.6468	1466.8270	2931.6628	1466.3350	L	1265.7365	633.3719	1248.7099	624.8586	1247.7259	624.3666	11
29	3006.6948	1503.8510	2989.6682	1495.3378	2988.6842	1494.8458	G	1152.6524	576.8298	1135.6259	568.3166	1134.6418	567.8246	10
30	3119.7789	1560.3931	3102.7523	1551.8798	3101.7683	1551.3878	L	1095.6309	548.3191	1078.6044	539.8058	1077.6204	539.3138	9
31	3256.8378	1628.9225	3239.8112	1620.4092	3238.8272	1619.9172	H	982.5469	491.7771	965.5203	483.2638	964.5363	482.7718	8
32	3369.9218	1685.4646	3352.8953	1676.9513	3351.9113	1676.4593	L	845.4880	423.2476	828.4614	414.7343	827.4774	414.2423	7
33	3483.0059	1742.0066	3465.9794	1733.4933	3464.9953	1733.0013	L	732.4039	366.7056	715.3774	358.1923	714.3933	357.7003	6
34	3580.0587	1790.5330	3563.0321	1782.0197	3562.0481	1781.5277	P	619.3198	310.1636	602.2933	301.6503	601.3093	301.1583	5
35	3743.1220	1872.0646	3726.0954	1863.5514	3725.1114	1863.0594	Y	522.2671	261.6372	505.2405	253.1239	504.2565	252.6319	4

36	3830.1540	1915.5806	3813.1275	1907.0674	3812.1435	1906.5754	S	359.2037	180.1055	342.1772	171.5922	341.1932	171.1002	3
37	3927.2068	1964.1070	3910.1802	1955.5938	3909.1962	1955.1017	P	272.1717	136.5895	255.1452	128.0762			2
38							R	175.1190	88.0631	158.0924	79.5498			1



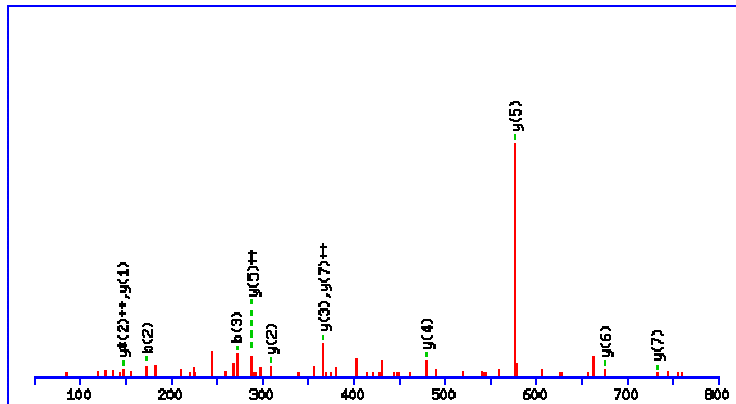
Peptide Number: 97107

MS/MS Fragmentation of **DGVPIGYK**Found in **IPI00007346** in **IPI_human**, Tax_Id=9606 Gene_Symbol=PPIH Peptidyl-prolyl cis-trans isomerase H

Match to Query 5722: 847.442788 from(424.728670,2+) index(29065)

Title: Elution from: 112.166666666667 to 112.166666666667 period: 0 cycle: 9542 experiment: 2 polarity:+

Data file 120210ry_32R1-32_3_1.mgf



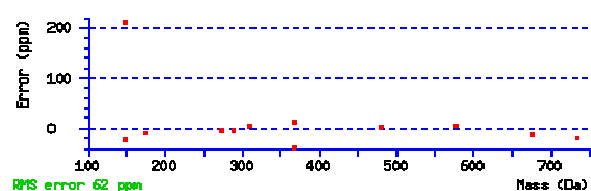
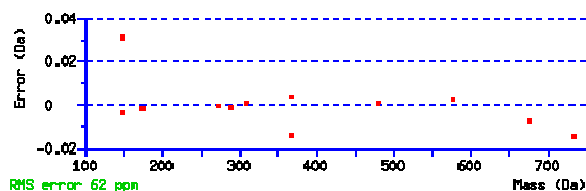
Monoisotopic mass of neutral peptide Mr(calc): 847.4440

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 52 Expect: 0.00066

Matches : 12/56 fragment ions using 21 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	#
1	116.0342	58.5207	98.0237	49.5155	D					8
2	173.0557	87.0315	155.0451	78.0262	G	733.4243	367.2158	716.3978	358.7025	7
3	272.1241	136.5657	254.1135	127.5604	V	676.4028	338.7051	659.3763	330.1918	6
4	369.1769	185.0921	351.1663	176.0868	P	577.3344	289.1709	560.3079	280.6576	5
5	482.2609	241.6341	464.2504	232.6288	I	480.2817	240.6445	463.2551	232.1312	4
6	539.2824	270.1448	521.2718	261.1396	G	367.1976	184.1024	350.1710	175.5892	3
7	702.3457	351.6765	684.3352	342.6712	Y	310.1761	155.5917	293.1496	147.0784	2
8					K	147.1128	74.0600	130.0863	65.5468	1



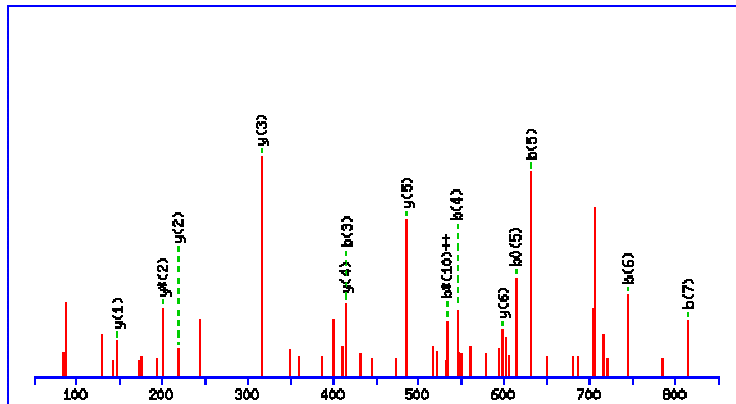
Peptide Number: 97627

MS/MS Fragmentation of **REEESLAVPAK**Found in **IPI00847400** in **IPI_human**, Tax_Id=9606 Gene_Symbol=C19orf47 Isoform 3 of Uncharacterized protein C19orf47

Match to Query 20004: 1227.640302 from(410.220710,3+) index(17767)

Title: Elution from: 75.4666666666667 to 75.4666666666667 period: 0 cycle: 7845 experiment: 4 polarity:+

Data file 120214ry_32R1-32_4_1.mgf



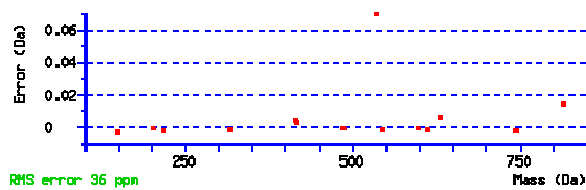
Monoisotopic mass of neutral peptide Mr(calc): 1227.6459

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

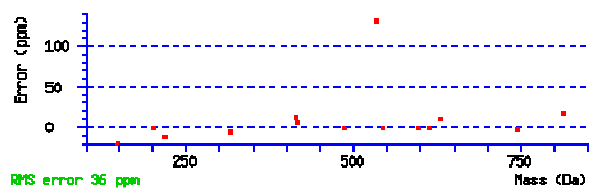
Ions Score: 43 Expect: 0.003

Matches : 14/106 fragment ions using 23 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	157.1084	79.0578	140.0818	70.5446			R							11
2	286.1510	143.5791	269.1244	135.0659	268.1404	134.5738	E	1072.5521	536.7797	1055.5255	528.2664	1054.5415	527.7744	10
3	415.1936	208.1004	398.1670	199.5872	397.1830	199.0951	E	943.5095	472.2584	926.4829	463.7451	925.4989	463.2531	9
4	544.2362	272.6217	527.2096	264.1084	526.2256	263.6164	E	814.4669	407.7371	797.4403	399.2238	796.4563	398.7318	8
5	631.2682	316.1377	614.2416	307.6245	613.2576	307.1325	S	685.4243	343.2158	668.3978	334.7025	667.4137	334.2105	7
6	744.3523	372.6798	727.3257	364.1665	726.3417	363.6745	L	598.3923	299.6998	581.3657	291.1865			6
7	815.3894	408.1983	798.3628	399.6850	797.3788	399.1930	A	485.3082	243.1577	468.2817	234.6445			5
8	914.4578	457.7325	897.4312	449.2193	896.4472	448.7272	V	414.2711	207.6392	397.2445	199.1259			4
9	1011.5106	506.2589	994.4840	497.7456	993.5000	497.2536	P	315.2027	158.1050	298.1761	149.5917			3
10	1082.5477	541.7775	1065.5211	533.2642	1064.5371	532.7722	A	218.1499	109.5786	201.1234	101.0653			2
11							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 36 ppm



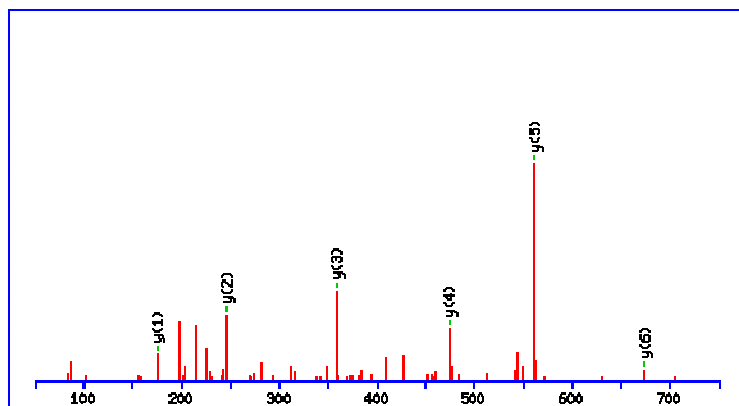
RMS error 36 ppm

Peptide Number: 97669MS/MS Fragmentation of **EISDIAR**Found in **IPI00784201** in **IPI_human**, Tax_Id=9606 Gene_Symbol=CEP290 291 kDa protein

Match to Query 3956: 802.416708 from(402.215630,2+) index(22853)

Title: Elution from: 96.1166666666667 to 96.1166666666667 period: 0 cycle: 7631 experiment: 2 polarity: +

Data file 120118ry_201B7-32_1_1.mgf



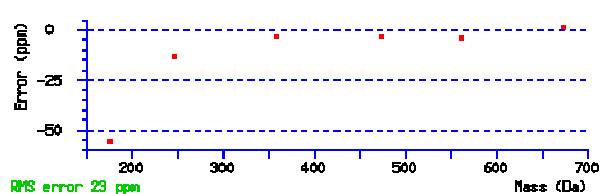
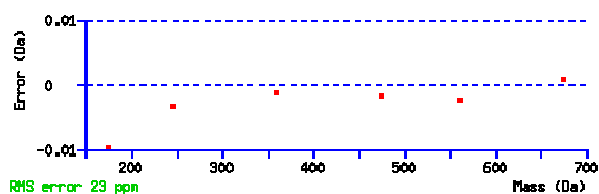
Monoisotopic mass of neutral peptide Mr(calc): 802.4185

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 62 Expect: 6.3e-005

Matches : 6/54 fragment ions using 7 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286	112.0393	56.5233	E							7
2	243.1339	122.0706	225.1234	113.0653	I	674.3832	337.6952	657.3566	329.1819	656.3726	328.6899	6
3	330.1660	165.5866	312.1554	156.5813	S	561.2991	281.1532	544.2726	272.6399	543.2885	272.1479	5
4	445.1929	223.1001	427.1823	214.0948	D	474.2671	237.6372	457.2405	229.1239	456.2565	228.6319	4
5	558.2770	279.6421	540.2664	270.6368	I	359.2401	180.1237	342.2136	171.6104			3
6	629.3141	315.1607	611.3035	306.1554	A	246.1561	123.5817	229.1295	115.0684			2
7					R	175.1190	88.0631	158.0924	79.5498			1



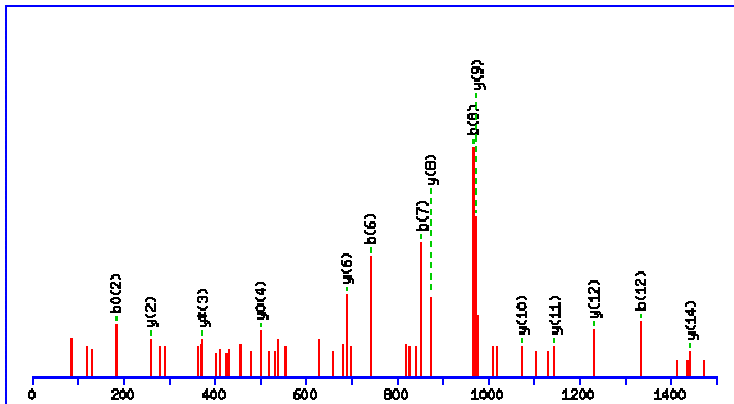
Peptide Number: 98042

MS/MS Fragmentation of **TVEFQHIIPIISAVTGEGIEELK**Found in **IPI00167638** in **IPI_human**, Tax_Id=9606 Gene_Symbol=GTPBP10 Isoform 1 of GTP-binding protein 10

Match to Query 36534: 2409.279072 from(804.100300,3+) index(41414)

Title: Elution from: 104.416666666667 to 104.416666666667 period: 0 cycle: 3944 experiment: 7 polarity: +

Data file 120210ry_32R1-32_2_3.mgf



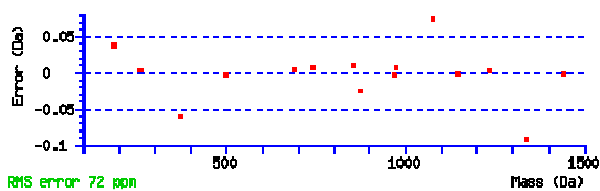
Monoisotopic mass of neutral peptide Mr(calc): 2409.2791

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

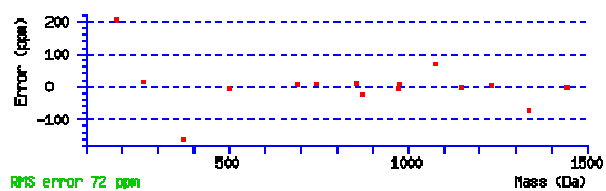
Ions Score: 42 Expect: 0.0028

Matches : 15/240 fragment ions using 27 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b* ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.0550	51.5311			84.0444	42.5258	T							22
2	201.1234	101.0653			183.1128	92.0600	V	2309.2387	1155.1230	2292.2122	1146.6097	2291.2282	1146.1177	21
3	330.1660	165.5866			312.1554	156.5813	E	2210.1703	1105.5888	2193.1438	1097.0755	2192.1598	1096.5835	20
4	477.2344	239.1208			459.2238	230.1155	F	2081.1277	1041.0675	2064.1012	1032.5542	2063.1172	1032.0622	19
5	605.2930	303.1501	588.2664	294.6368	587.2824	294.1448	Q	1934.0593	967.5333	1917.0328	959.0200	1916.0488	958.5280	18
6	742.3519	371.6796	725.3253	363.1663	724.3413	362.6743	H	1806.0007	903.5040	1788.9742	894.9907	1787.9902	894.4987	17
7	855.4359	428.2216	838.4094	419.7083	837.4254	419.2163	I	1668.9418	834.9746	1651.9153	826.4613	1650.9313	825.9693	16
8	968.5200	484.7636	951.4934	476.2504	950.5094	475.7584	I	1555.8578	778.4325	1538.8312	769.9192	1537.8472	769.4272	15
9	1065.5728	533.2900	1048.5462	524.7767	1047.5622	524.2847	P	1442.7737	721.8905	1425.7472	713.3772	1424.7631	712.8852	14
10	1178.6568	589.8320	1161.6303	581.3188	1160.6463	580.8268	I	1345.7209	673.3641	1328.6944	664.8508	1327.7104	664.3588	13
11	1265.6889	633.3481	1248.6623	624.8348	1247.6783	624.3428	S	1232.6369	616.8221	1215.6103	608.3088	1214.6263	607.8168	12
12	1336.7260	668.8666	1319.6994	660.3533	1318.7154	659.8613	A	1145.6048	573.3061	1128.5783	564.7928	1127.5943	564.3008	11
13	1435.7944	718.4008	1418.7678	709.8876	1417.7838	709.3955	V	1074.5677	537.7875	1057.5412	529.2742	1056.5572	528.7822	10
14	1536.8421	768.9247	1519.8155	760.4114	1518.8315	759.9194	T	975.4993	488.2533	958.4728	479.7400	957.4888	479.2480	9
15	1593.8635	797.4354	1576.8370	788.9221	1575.8530	788.4301	G	874.4516	437.7295	857.4251	429.2162	856.4411	428.7242	8
16	1722.9061	861.9567	1705.8796	853.4434	1704.8955	852.9514	E	817.4302	409.2187	800.4036	400.7055	799.4196	400.2134	7
17	1779.9276	890.4674	1762.9010	881.9542	1761.9170	881.4621	G	688.3876	344.6974	671.3610	336.1842	670.3770	335.6921	6
18	1893.0116	947.0095	1875.9851	938.4962	1875.0011	938.0042	I	631.3661	316.1867	614.3396	307.6734	613.3556	307.1814	5
19	2022.0542	1011.5308	2005.0277	1003.0175	2004.0437	1002.5255	E	518.2821	259.6447	501.2555	251.1314	500.2715	250.6394	4
20	2151.0968	1076.0521	2134.0703	1067.5388	2133.0863	1067.0468	E	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
21	2264.1809	1132.5941	2247.1543	1124.0808	2246.1703	1123.5888	L	260.1969	130.6021	243.1703	122.0888			2
22							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 72 ppm



RMS error 72 ppm

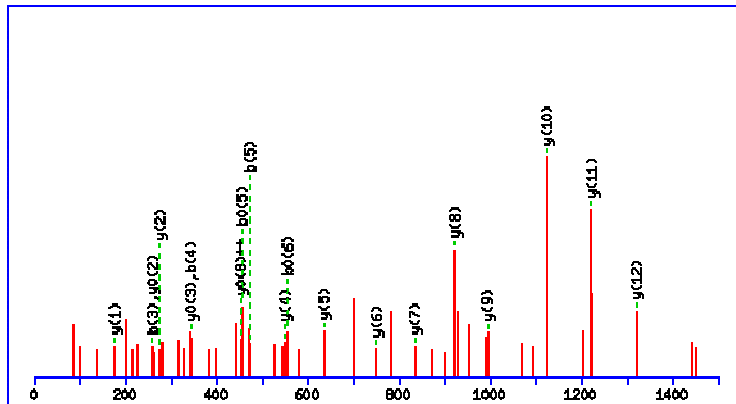
Peptide Number: 98163

MS/MS Fragmentation of **SGLSEVVEASSLSWSTR**Found in **IPI00029002** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SFT2D2 Vesicle transport protein SFT2B

Match to Query 19880: 1793.898668 from(897.956610,2+) index(26896)

Title: Elution from: 67.3166666666667 to 67.3166666666667 period: 0 cycle: 2552 experiment: 7 polarity: +

Data file 120206ry_aHDF1419-P10_2_3.mgf



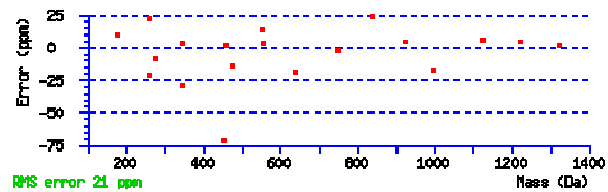
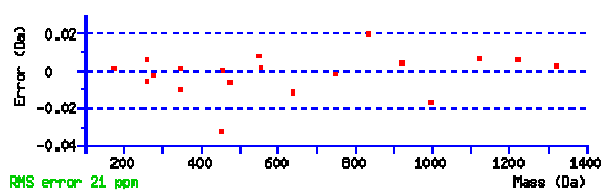
Monoisotopic mass of neutral peptide Mr(calc): 1793.8795

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 45 Expect: 0.0022

Matches : 19/158 fragment ions using 55 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233	70.0287	35.5180	S							17
2	145.0608	73.0340	127.0502	64.0287	Q	1707.8548	854.4310	1690.8283	845.9178	1689.8442	845.4258	16
3	258.1448	129.5761	240.1343	120.5708	L	1650.8333	825.9203	1633.8068	817.4070	1632.8228	816.9150	15
4	345.1769	173.0921	327.1663	164.0868	S	1537.7493	769.3783	1520.7227	760.8650	1519.7387	760.3730	14
5	474.2195	237.6134	456.2089	228.6081	E	1450.7172	725.8623	1433.6907	717.3490	1432.7067	716.8570	13
6	573.2879	287.1476	555.2773	278.1423	V	1321.6747	661.3410	1304.6481	652.8277	1303.6641	652.3357	12
7	672.3563	336.6818	654.3457	327.6765	V	1222.6062	611.8068	1205.5797	603.2935	1204.5957	602.8015	11
8	801.3989	401.2031	783.3883	392.1978	E	1123.5378	562.2726	1106.5113	553.7593	1105.5273	553.2673	10
9	872.4360	436.7216	854.4254	427.7163	A	994.4952	497.7513	977.4687	489.2380	976.4847	488.7460	9
10	959.4680	480.2376	941.4575	471.2324	S	923.4581	462.2327	906.4316	453.7194	905.4476	453.2274	8
11	1046.5000	523.7537	1028.4895	514.7484	S	836.4261	418.7167	819.3995	410.2034	818.4155	409.7114	7
12	1159.5841	580.2957	1141.5735	571.2904	L	749.3941	375.2007	732.3675	366.6874	731.3835	366.1954	6
13	1246.6161	623.8117	1228.6056	614.8064	S	636.3100	318.6586	619.2835	310.1454	618.2994	309.6534	5
14	1432.6954	716.8514	1414.6849	707.8461	W	549.2780	275.1426	532.2514	266.6293	531.2674	266.1373	4
15	1519.7275	760.3674	1501.7169	751.3621	S	363.1987	182.1030	346.1721	173.5897	345.1881	173.0977	3
16	1620.7752	810.8912	1602.7646	801.8859	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
17					R	175.1190	88.0631	158.0924	79.5498			1



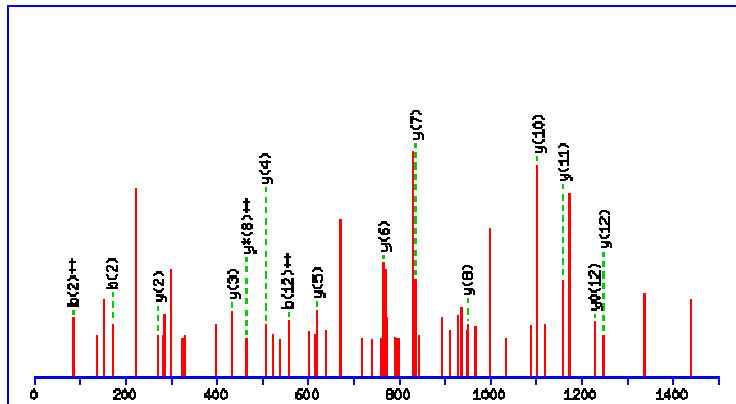
Peptide Number: 98359

MS/MS Fragmentation of **VAESGPGLAFIAYPR**Found in **IPI00007582** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SLC6A8 Sodium- and chloride-dependent creatine transporter 1

Match to Query 12036: 1546.806428 from(774.410490,2+) index(11561)

Title: Elution from: 28.6166666666667 to 28.6166666666667 period: 0 cycle: 1079 experiment: 10 polarity:+

Data file 120214ry_414C2-43_4_3.mgf



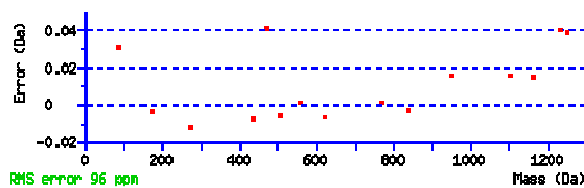
Monoisotopic mass of neutral peptide Mr(calc): 1546.8144

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

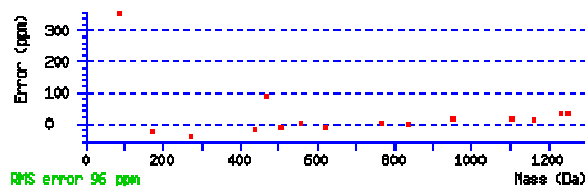
Ions Score: 42 Expect: 0.0049

Matches : 15/114 fragment ions using 45 most intense peaks ([help](#))

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415			V							15
2	171.1128	86.0600			A	1448.7532	724.8803	1431.7267	716.3670	1430.7427	715.8750	14
3	300.1554	150.5813	282.1448	141.5761	E	1377.7161	689.3617	1360.6896	680.8484	1359.7056	680.3564	13
4	387.1874	194.0974	369.1769	185.0921	S	1248.6735	624.8404	1231.6470	616.3271	1230.6630	615.8351	12
5	444.2089	222.6081	426.1983	213.6028	G	1161.6415	581.3244	1144.6150	572.8111			11
6	541.2617	271.1345	523.2511	262.1292	P	1104.6200	552.8137	1087.5935	544.3004			10
7	598.2831	299.6452	580.2726	290.6399	G	1007.5673	504.2873	990.5407	495.7740			9
8	711.3672	356.1872	693.3566	347.1819	L	950.5458	475.7765	933.5193	467.2633			8
9	782.4043	391.7058	764.3937	382.7005	A	837.4618	419.2345	820.4352	410.7212			7
10	929.4727	465.2400	911.4621	456.2347	F	766.4246	383.7160	749.3981	375.2027			6
11	1042.5568	521.7820	1024.5462	512.7767	I	619.3562	310.1817	602.3297	301.6685			5
12	1113.5939	557.3006	1095.5833	548.2953	A	506.2722	253.6397	489.2456	245.1264			4
13	1276.6572	638.8322	1258.6467	629.8270	Y	435.2350	218.1212	418.2085	209.6079			3
14	1373.7100	687.3586	1355.6994	678.3533	P	272.1717	136.5895	255.1452	128.0762			2
15					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 96 ppm



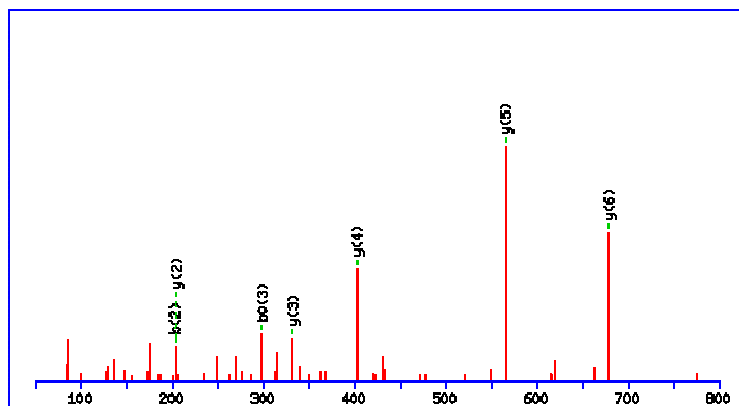
RMS error 96 ppm

Peptide Number: 98638MS/MS Fragmentation of **DSLYAQGK**Found in **IPI00220344** in **IPI_human**, Tax_Id=9606 Gene_Symbol=RPL36A 60S ribosomal protein L36a isoform a

Match to Query 6790: 880.427308 from(441.220930,2+) index(9530)

Title: Elution from: 64.8166666666667 to 64.8166666666667 period: 0 cycle: 7744 experiment: 4 polarity:+

Data file 120210ry_32R1-32_3_1.mgf



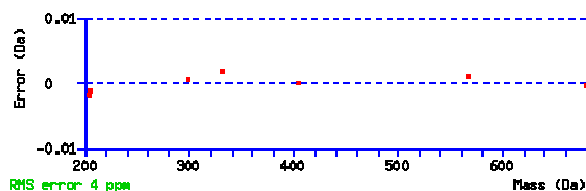
Monoisotopic mass of neutral peptide Mr(calc): 880.4290

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

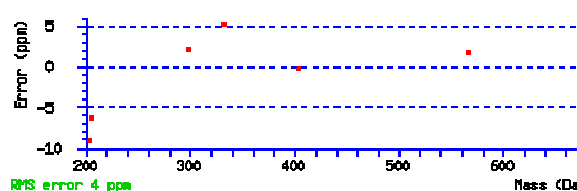
Ions Score: 38 Expect: 0.0077

Matches : 7/62 fragment ions using 13 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							8
2	203.0662	102.0368			185.0557	93.0315	S	766.4094	383.7083	749.3828	375.1951	748.3988	374.7030	7
3	316.1503	158.5788			298.1397	149.5735	L	679.3774	340.1923	662.3508	331.6790			6
4	479.2136	240.1105			461.2031	231.1052	Y	566.2933	283.6503	549.2667	275.1370			5
5	550.2508	275.6290			532.2402	266.6237	A	403.2300	202.1186	386.2034	193.6053			4
6	678.3093	339.6583	661.2828	331.1450	660.2988	330.6530	Q	332.1928	166.6001	315.1663	158.0868			3
7	735.3308	368.1690	718.3042	359.6558	717.3202	359.1638	G	204.1343	102.5708	187.1077	94.0575			2
8							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 4 ppm



RMS error 4 ppm

Peptide Number: 98766

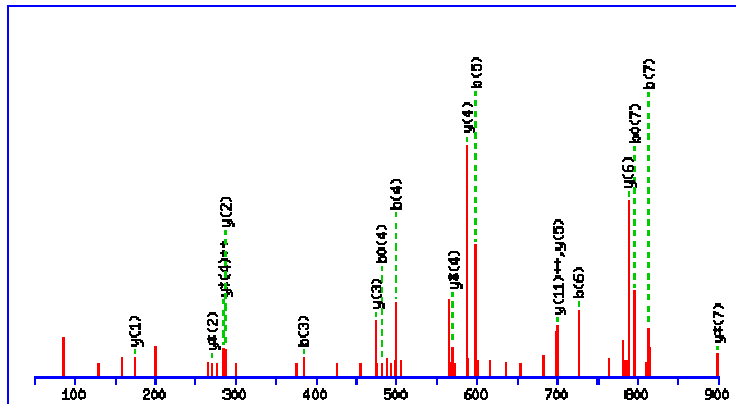
MS/MS Fragmentation of **LRDDVQSINWLR**

Found in **IPI00956390** in **IPI_human**, Tax_Id=9606 Gene_Symbol=FGFR1 basic fibroblast growth factor receptor 1 isoform 14 precursor

Match to Query 29776: 1513.795122 from(505.605650,3+) index(47406)

Title: Elution from: 116.6 to 116.6 period: 0 cycle: 4408 experiment: 2 polarity: +

Data file 120210ry_32R1-32_3_2.mgf



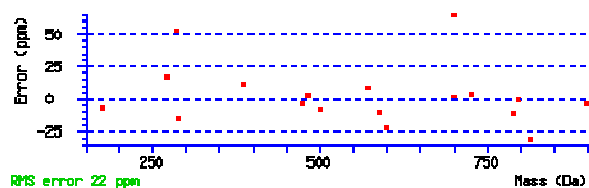
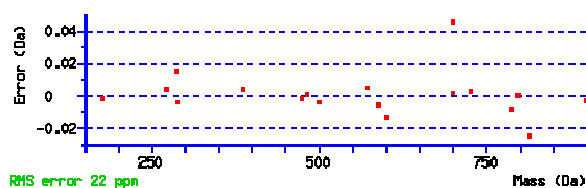
Monoisotopic mass of neutral peptide Mr(calc): 1513.8001

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 48 Expect: 0.00095

Matches : 18/116 fragment ions using 25 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							12
2	270.1925	135.5999	253.1659	127.0866			R	1401.7233	701.3653	1384.6968	692.8520	1383.7128	692.3600	11
3	385.2194	193.1133	368.1928	184.6001	367.2088	184.1081	D	1245.6222	623.3148	1228.5957	614.8015	1227.6117	614.3095	10
4	500.2463	250.6268	483.2198	242.1135	482.2358	241.6215	D	1130.5953	565.8013	1113.5687	557.2880	1112.5847	556.7960	9
5	599.3148	300.1610	582.2882	291.6477	581.3042	291.1557	V	1015.5683	508.2878	998.5418	499.7745	997.5578	499.2825	8
6	727.3733	364.1903	710.3468	355.6770	709.3628	355.1850	Q	916.4999	458.7536	899.4734	450.2403	898.4894	449.7483	7
7	814.4054	407.7063	797.3788	399.1930	796.3948	398.7010	S	788.4413	394.7243	771.4148	386.2110	770.4308	385.7190	6
8	927.4894	464.2483	910.4629	455.7351	909.4789	455.2431	I	701.4093	351.2083	684.3828	342.6950			5
9	1041.5323	521.2698	1024.5058	512.7565	1023.5218	512.2645	N	588.3253	294.6663	571.2987	286.1530			4
10	1227.6117	614.3095	1210.5851	605.7962	1209.6011	605.3042	W	474.2823	237.6448	457.2558	229.1315			3
11	1340.6957	670.8515	1323.6692	662.3382	1322.6852	661.8462	L	288.2030	144.6051	271.1765	136.0919			2
12							R	175.1190	88.0631	158.0924	79.5498			1



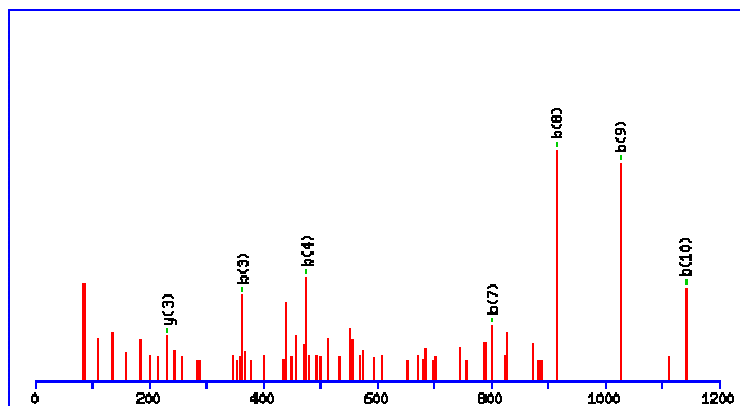
Peptide Number: 99475

MS/MS Fragmentation of **LHIPINNIVGG**Found in **IPI00006072** in **IPI_human**, Tax_Id=9606 Gene_Symbol=SEC61G Protein transport protein Sec61 subunit gamma

Match to Query 6494: 1371.829308 from(686.921930,2+) index(25648)

Title: Elution from: 71.2666666666667 to 71.2666666666667 period: 0 cycle: 2741 experiment: 8 polarity:+

Data file 120208ry_Tig120slc-P8_1_3.mgf



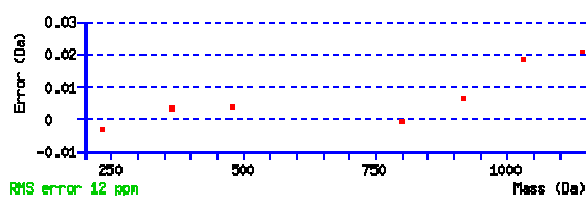
Monoisotopic mass of neutral peptide Mr(calc): 1371.8238

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

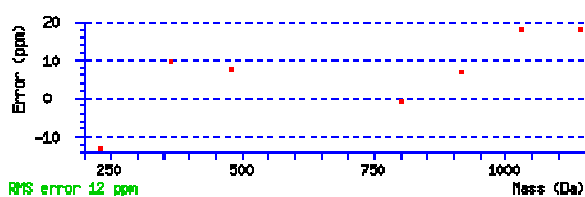
Ions Score: 41 Expect: 0.00077

Matches : 7/74 fragment ions using 11 most intense peaks ([help](#))

#	b	b ⁺⁺	b*	b ⁺⁺ *	Seq.	y	y ⁺⁺	y*	y ⁺⁺ *	#
1	114.0913	57.5493			L					13
2	227.1754	114.0913			I	1259.7470	630.3772	1242.7205	621.8639	12
3	364.2343	182.6208			H	1146.6630	573.8351	1129.6364	565.3218	11
4	477.3184	239.1628			I	1009.6041	505.3057	992.5775	496.7924	10
5	574.3711	287.6892			P	896.5200	448.7636	879.4934	440.2504	9
6	687.4552	344.2312			I	799.4672	400.2373	782.4407	391.7240	8
7	801.4981	401.2527	784.4716	392.7394	N	686.3832	343.6952	669.3566	335.1819	7
8	915.5411	458.2742	898.5145	449.7609	N	572.3402	286.6738	555.3137	278.1605	6
9	1028.6251	514.8162	1011.5986	506.3029	I	458.2973	229.6523			5
10	1141.7092	571.3582	1124.6826	562.8450	I	345.2132	173.1103			4
11	1240.7776	620.8924	1223.7511	612.3792	V	232.1292	116.5682			3
12	1297.7991	649.4032	1280.7725	640.8899	G	133.0608	67.0340			2
13					G	76.0393	38.5233			1



RMS error 12 ppm



RMS error 12 ppm

Peptide View

Peptide: 257.

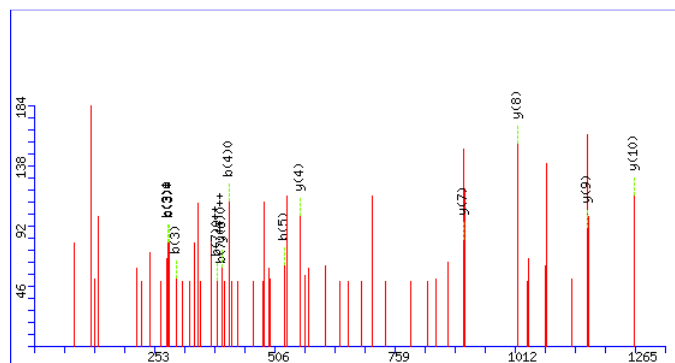
MS/MS Fragmentation of **EGNEVFLPFTWVEK**:

Found in **IP100433284**

Title: 4.1.1.854.5

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120212ry¥120212ry_aHDF1388-P9_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							14
2	187.0713	94.0393	0	0	169.0608	85.0340	G	1565.7999	783.4036	1548.7733	774.8903	1547.7893	774.3983	13
3	301.1143	151.0608	284.0877	142.5475	283.1037	142.0555	N	1508.7784	754.8928	1491.7518	746.3796	1490.7678	745.8876	12
4	430.1569	215.5821	413.1303	207.0688	412.1463	206.5768	E	1394.7355	697.8714	1377.7089	689.3581	1376.7249	688.8661	11
5	529.2253	265.1163	512.1987	256.6030	511.2147	256.1110	V	1265.6929	633.3501	1248.6663	624.8368	1247.6823	624.3448	10
6	676.2937	338.6505	659.2671	330.1372	658.2831	329.6452	F	1166.6245	583.8159	1149.5979	575.3026	1148.6139	574.8106	9
7	789.3777	395.1925	772.3512	386.6792	771.3672	386.1872	L	1019.5560	510.2817	1002.5295	501.7684	1001.5455	501.2764	8
8	886.4305	443.7189	869.4040	435.2056	868.4199	434.7136	P	906.4720	453.7396	889.4454	445.2264	888.4614	444.7343	7
9	1033.4989	517.2531	1016.4724	508.7398	1015.4884	508.2478	F	809.4192	405.2132	792.3927	396.7000	791.4087	396.2080	6
10	1134.5466	567.7769	1117.5201	559.2637	1116.5360	558.7717	T	662.3508	331.6790	645.3243	323.1658	644.3402	322.6738	5
11	1320.6259	660.8166	1303.5994	652.3033	1302.6154	651.8113	W	561.3031	281.1552	544.2766	272.6419	543.2926	272.1499	4
12	1419.6943	710.3508	1402.6678	701.8375	1401.6838	701.3455	V	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
13	1548.7369	774.8721	1531.7104	766.3588	1530.7264	765.8668	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 403.

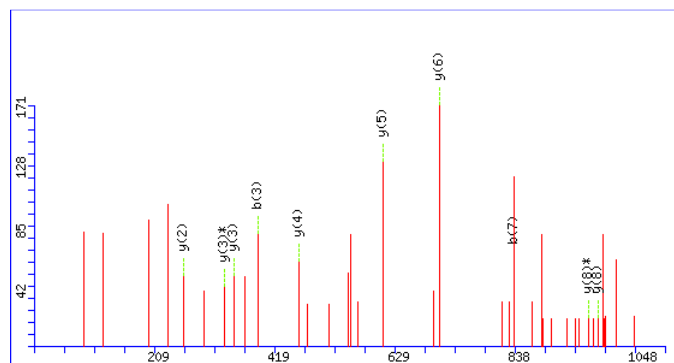
MS/MS Fragmentation of **NFEVFLSSR**:

Found in **IP100384909,IP100885052,IP100885055,IP100945293,IP100945435,IP100946906**

Title: 3.1.1.647.6

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							9
2	262.1186	131.5629	245.0921	123.0497	0	0	F	984.5149	492.7611	967.4884	484.2478	966.5043	483.7558	8
3	391.1612	196.0842	374.1347	187.5710	373.1506	187.0790	E	837.4465	419.2269	820.4199	410.7136	819.4359	410.2216	7
4	490.2296	245.6185	473.2031	237.1052	472.2191	236.6132	V	708.4039	354.7056	691.3774	346.1923	690.3933	345.7003	6
5	637.2980	319.1527	620.2715	310.6394	619.2875	310.1474	F	609.3355	305.1714	592.3089	296.6581	591.3249	296.1661	5
6	750.3821	375.6947	733.3556	367.1814	732.3715	366.6894	L	462.2671	231.6372	445.2405	223.1239	444.2565	222.6319	4
7	837.4141	419.2107	820.3876	410.6974	819.4036	410.2054	S	349.1830	175.0951	332.1565	166.5819	331.1724	166.0899	3
8	924.4462	462.7267	907.4196	454.2134	906.4356	453.7214	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
9							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 633.

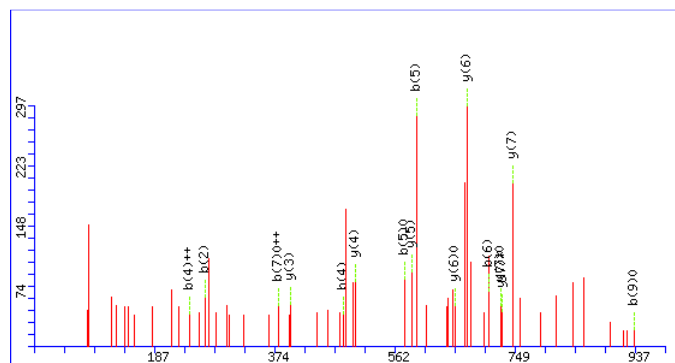
MS/MS Fragmentation of **HEDTNLASSTLLR**:

Found in **IP100003917;IP100293857;IP100336017;IP100644870;IP100937605;IP100982457;IP101015395**

Title: 2.1.1.1214.5

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	138.0662	69.5367	0	0	0	0	H							13
2	267.1088	134.0580	0	0	249.0982	125.0527	E	1319.6801	660.3437	1302.6536	651.8304	1301.6696	651.3384	12
3	382.1357	191.5715	0	0	364.1252	182.5662	D	1190.6375	595.8224	1173.6110	587.3091	1172.6270	586.8171	11
4	483.1834	242.0953	0	0	465.1728	233.0901	T	1075.6106	538.3089	1058.5840	529.7957	1057.6000	529.3037	10
5	597.2263	299.1168	580.1998	290.6035	579.2158	290.1115	N	974.5629	487.7851	957.5364	479.2718	956.5524	478.7798	9
6	710.3104	355.6588	693.2838	347.1456	692.2998	346.6536	L	860.5200	430.7636	843.4934	422.2504	842.5094	421.7584	8
7	781.3475	391.1774	764.3210	382.6641	763.3369	382.1721	A	747.4359	374.2216	730.4094	365.7083	729.4254	365.2163	7
8	868.3795	434.6934	851.3530	426.1801	850.3690	425.6881	S	676.3988	338.7030	659.3723	330.1898	658.3883	329.6978	6
9	955.4116	478.2094	938.3850	469.6961	937.4010	469.2041	S	589.3668	295.1870	572.3402	286.6738	571.3562	286.1817	5
10	1056.4592	528.7333	1039.4327	520.2200	1038.4487	519.7280	T	502.3348	251.6710	485.3082	243.1577	484.3242	242.6657	4
11	1169.5433	585.2753	1152.5168	576.7620	1151.5327	576.2700	L	401.2871	201.1472	384.2605	192.6339	0	0	3
12	1282.6274	641.8173	1265.6008	633.3040	1264.6168	632.8120	L	288.2030	144.6051	271.1765	136.0919	0	0	2
13							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 684.

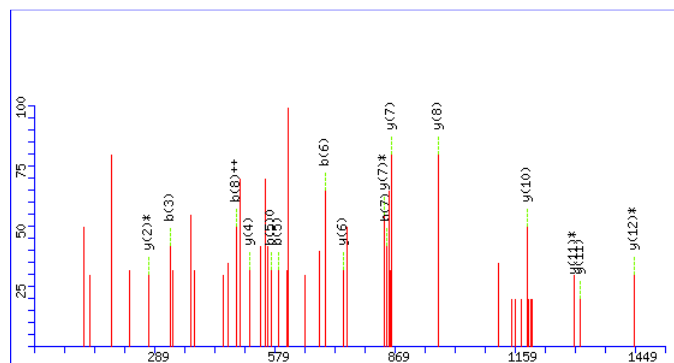
MS/MS Fragmentation of **TINDFLQSQIDNINLFK**:

Found in **IP100023299;IP100332293;IP100657836;IP100658184;IP100784410;IP100872853;IP100942296;IP101015216;IP101015699**

Title: 4.1.1.1889.5

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							18
2	215.1390	108.0731	0	0	197.1285	99.0679	I	2069.0702	1035.0387	2052.0437	1026.5255	2051.0597	1026.0335	17
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	N	1955.9862	978.4967	1938.9596	969.9834	1937.9756	969.4914	16
4	444.2089	222.6081	427.1823	214.0948	426.1983	213.6028	D	1841.9432	921.4753	1824.9167	912.9620	1823.9327	912.4700	15
5	591.2773	296.1423	574.2508	287.6290	573.2667	287.1370	F	1726.9163	863.9618	1709.8897	855.4485	1708.9057	854.9565	14
6	704.3614	352.6843	687.3348	344.1710	686.3508	343.6790	L	1579.8479	790.4276	1562.8213	781.9143	1561.8373	781.4223	13
7	851.4298	426.2185	834.4032	417.7053	833.4192	417.2132	F	1466.7638	733.8855	1449.7373	725.3723	1448.7532	724.8803	12
8	979.4884	490.2478	962.4618	481.7345	961.4778	481.2425	Q	1319.6954	660.3513	1302.6688	651.8381	1301.6848	651.3461	11
9	1066.5204	533.7638	1049.4938	525.2506	1048.5098	524.7585	S	1191.6368	596.3220	1174.6103	587.8088	1173.6262	587.3168	10
10	1194.5790	597.7931	1177.5524	589.2798	1176.5684	588.7878	Q	1104.6048	552.8060	1087.5782	544.2928	1086.5942	543.8007	9
11	1307.6630	654.3352	1290.6365	645.8219	1289.6525	645.3299	I	976.5462	488.7767	959.5197	480.2635	958.5356	479.7715	8
12	1422.6900	711.8486	1405.6634	703.3353	1404.6794	702.8433	D	863.4621	432.2347	846.4356	423.7214	845.4516	423.2294	7
13	1536.7329	768.8701	1519.7063	760.3568	1518.7223	759.8648	N	748.4352	374.7212	731.4087	366.2080	0	0	6
14	1649.8170	825.4121	1632.7904	816.8988	1631.8064	816.4068	I	634.3923	317.6998	617.3657	309.1865	0	0	5
15	1763.8599	882.4336	1746.8333	873.9203	1745.8493	873.4283	N	521.3082	261.1577	504.2817	252.6445	0	0	4
16	1876.9440	938.9756	1859.9174	930.4623	1858.9334	929.9703	L	407.2653	204.1363	390.2387	195.6230	0	0	3
17	2024.0124	1012.5098	2006.9858	1003.9965	2006.0018	1003.5045	F	294.1812	147.5942	277.1547	139.0810	0	0	2
18							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 828.

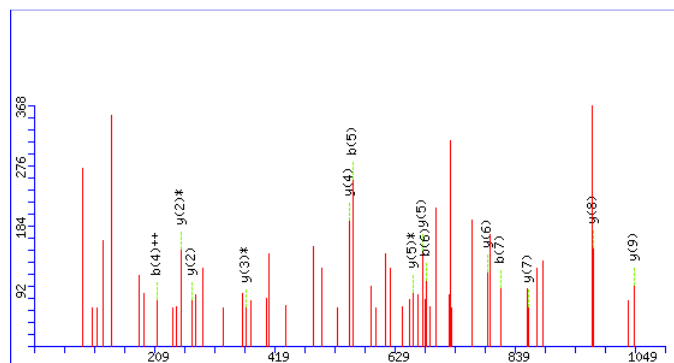
MS/MS Fragmentation of **EEAVQQMADALQYLQK**:

Found in **IP100017695;IP100815683;IP100816476;IP100816771;IP100909459;IP101012444**

Title: 3.1.1.3841.4

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120206ry¥120206ry_aHDF1419-P10_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							16
2	259.0925	130.0499	0	0	241.0819	121.0446	E	1735.8683	868.4378	1718.8418	859.9245	1717.8578	859.4325	15
3	330.1296	165.5684	0	0	312.1190	156.5631	A	1606.8258	803.9165	1589.7992	795.4032	1588.8152	794.9112	14
4	429.1980	215.1026	0	0	411.1874	206.0974	V	1535.7886	768.3980	1518.7621	759.8847	1517.7781	759.3927	13
5	557.2566	279.1319	540.2300	270.6186	539.2460	270.1266	Q	1436.7202	718.8638	1419.6937	710.3505	1418.7097	709.8585	12
6	685.3151	343.1612	668.2886	334.6479	667.3046	334.1559	Q	1308.6617	654.8345	1291.6351	646.3212	1290.6511	645.8292	11
7	816.3556	408.6815	799.3291	400.1682	798.3451	399.6762	M	1180.6031	590.8052	1163.5765	582.2919	1162.5925	581.7999	10
8	887.3927	444.2000	870.3662	435.6867	869.3822	435.1947	A	1049.5626	525.2849	1032.5360	516.7717	1031.5520	516.2796	9
9	1002.4197	501.7135	985.3931	493.2002	984.4091	492.7082	D	978.5255	489.7664	961.4989	481.2531	960.5149	480.7611	8
10	1073.4568	537.2320	1056.4303	528.7188	1055.4462	528.2268	A	863.4985	432.2529	846.4720	423.7396	0	0	7
11	1186.5409	593.7741	1169.5143	585.2608	1168.5303	584.7688	L	792.4614	396.7343	775.4349	388.2211	0	0	6
12	1314.5994	657.8034	1297.5729	649.2901	1296.5889	648.7981	Q	679.3774	340.1923	662.3508	331.6790	0	0	5
13	1477.6628	739.3350	1460.6362	730.8217	1459.6522	730.3297	Y	551.3188	276.1630	534.2922	267.6498	0	0	4
14	1590.7468	795.8771	1573.7203	787.3638	1572.7363	786.8718	L	388.2554	194.6314	371.2289	186.1181	0	0	3
15	1718.8054	859.9063	1701.7789	851.3931	1700.7949	850.9011	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
16							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 896.

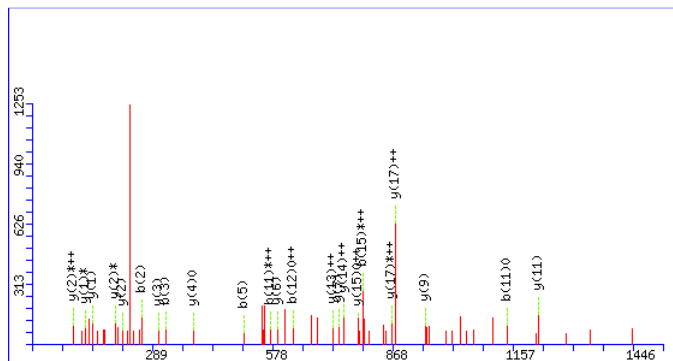
MS/MS Fragmentation of **TYGTSGLDNRPLFGETSAK**:

Found in **IPI00013331:IPI00926699**

Title: 2.1.1.2747.10

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							19
2	265.1183	133.0628	0	0	247.1077	124.0575	Y	1912.9399	956.9736	1895.9134	948.4603	1894.9294	947.9683	18
3	322.1397	161.5735	0	0	304.1292	152.5682	G	1749.8766	875.4419	1732.8501	866.9287	1731.8660	866.4367	17
4	423.1874	212.0974	0	0	405.1769	203.0921	T	1692.8551	846.9312	1675.8286	838.4179	1674.8446	837.9259	16
5	510.2195	255.6134	0	0	492.2089	246.6081	S	1591.8075	796.4074	1574.7809	787.8941	1573.7969	787.4021	15
6	567.2409	284.1241	0	0	549.2304	275.1188	G	1504.7754	752.8914	1487.7489	744.3781	1486.7649	743.8861	14
7	680.3250	340.6661	0	0	662.3144	331.6608	L	1447.7540	724.3806	1430.7274	715.8673	1429.7434	715.3753	13
8	795.3519	398.1796	0	0	777.3144	389.1743	D	1334.6699	667.8386	1317.6434	659.3253	1316.6593	658.8333	12
9	909.3949	455.2011	892.3683	446.6878	891.3843	446.1958	N	1219.6430	610.3251	1202.6164	601.8118	1201.6324	601.3198	11
10	1065.4960	533.2516	1048.4694	524.7383	1047.4854	524.2463	R	1105.6000	553.3037	1088.5735	544.7904	1087.5895	544.2984	10
11	1162.5487	581.7780	1145.5222	573.2647	1144.5382	572.7727	P	949.4989	475.2531	932.4724	466.7398	931.4884	466.2478	9
12	1275.6328	638.3200	1258.6062	629.8068	1257.6222	629.3148	L	852.4462	426.7267	835.4196	418.2134	834.4356	417.7214	8
13	1422.7012	711.8542	1405.6747	703.3410	1404.6906	702.8490	F	739.3621	370.1847	722.3355	361.6714	721.3515	361.1794	7
14	1479.7227	740.3650	1462.6961	731.8517	1461.7121	731.3597	G	592.2937	296.6505	575.2671	288.1372	574.2831	287.6452	6
15	1608.7653	804.8863	1591.7387	796.3730	1590.7547	795.8810	E	535.2722	268.1397	518.2457	259.6265	517.2617	259.1345	5
16	1709.8129	855.4101	1692.7864	846.8968	1691.8024	846.4048	T	406.2296	203.6185	389.2031	195.1052	388.2191	194.6132	4
17	1796.8450	898.9261	1779.8184	890.4128	1778.8344	889.9208	S	305.1819	153.0946	288.1554	144.5813	287.1714	144.0893	3
18	1867.8821	934.4447	1850.8555	925.9314	1849.8715	925.4394	A	218.1499	109.5786	201.1234	101.0653	0	0	2
19							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 924.

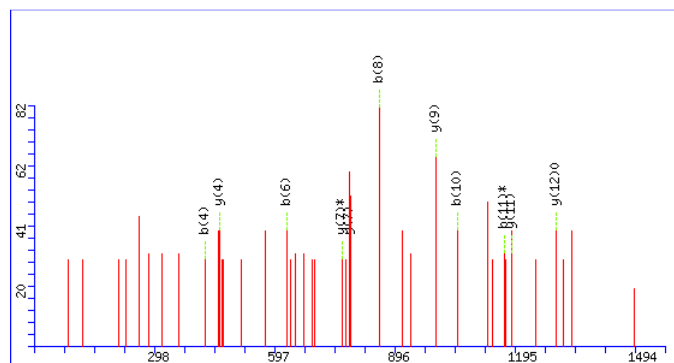
MS/MS Fragmentation of **ALQIAMCAPVMVELEGETDPLLIAMK: 57.021465@C:7**

Found in **IP100015119;IP100877920;IP100879602;IP100880079**

Title: 4.1.1.3654.10

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120214ry¥120214ry_32R1-32_4.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							26
2	185.1285	93.0679	0	0	0	0	L	2772.4054	1386.7064	2755.3789	1378.1931	2754.3949	1377.7011	25
3	313.1870	157.0972	296.1605	148.5839	0	0	Q	2659.3214	1330.1643	2642.2948	1321.6510	2641.3108	1321.1590	24
4	426.2711	213.6392	409.2445	205.1259	0	0	I	2531.2628	1266.1350	2514.2362	1257.6218	2513.2522	1257.1298	23
5	497.3082	249.1577	480.2817	240.6445	0	0	A	2418.1787	1209.5930	2401.1522	1201.0797	2400.1682	1200.5877	22
6	628.3487	314.6780	611.3221	306.1647	0	0	M	2347.1416	1174.0744	2330.1151	1165.5612	2329.1310	1165.0692	21
7	788.3793	394.6933	771.3528	386.1800	0	0	C	2216.1011	1108.5542	2199.0746	1100.0409	2198.0906	1099.5489	20
8	859.4165	430.2119	842.3899	421.6986	0	0	A	2056.0705	1028.5389	2039.0439	1020.0256	2038.0599	1019.5336	19
9	956.4692	478.7382	939.4427	470.2250	0	0	P	1985.0334	993.0203	1968.0068	984.5070	1967.0228	984.0150	18
10	1055.5378	528.2725	1038.5111	519.7592	0	0	V	1887.9806	944.4939	1870.9541	935.9807	1869.9700	935.4887	17
11	1186.5781	593.7927	1169.5516	585.2794	0	0	M	1788.9122	894.9597	1771.8856	886.4465	1770.9016	885.9544	16
12	1285.6465	643.3269	1268.6200	634.8136	0	0	V	1657.8717	829.4395	1640.8452	820.9262	1639.8611	820.4342	15
13	1414.6891	707.8482	1397.6626	699.3349	1396.6786	698.8429	E	1558.8033	779.9053	1541.7767	771.3920	1540.7927	770.9000	14
14	1527.7732	764.3902	1510.7466	755.8770	1509.7626	755.3850	L	1429.7607	715.3840	1412.7341	706.8707	1411.7501	706.3787	13
15	1656.8158	828.9115	1639.7892	820.3983	1638.8052	819.9062	E	1316.6766	658.8420	1299.6501	650.3287	1298.6661	649.8367	12
16	1713.8373	857.4223	1696.8107	848.9090	1695.8267	848.4170	G	1187.6340	594.3207	1170.6075	585.8074	1169.6235	585.3154	11
17	1842.8798	921.9436	1825.8533	913.4303	1824.8693	912.9383	E	1130.6126	565.8099	1113.5860	557.2967	1112.6020	556.8046	10
18	1943.9275	972.4674	1926.9010	963.9541	1925.9170	963.4621	T	1001.5700	501.2886	984.5434	492.7754	983.5594	492.2833	9
19	2058.9545	1029.9809	2041.9279	1021.4676	2040.9439	1020.9756	D	900.5223	450.7648	883.4958	442.2515	882.5117	441.7595	8
20	2156.0072	1078.5073	2138.9807	1069.9940	2137.9967	1069.5020	P	785.4954	393.2513	768.4688	384.7380	0	0	7
21	2269.0913	1135.0493	2252.0647	1126.5360	2251.0807	1126.0440	L	688.4426	344.7249	671.4160	336.2117	0	0	6
22	2382.1754	1191.5913	2365.1488	1183.0780	2364.1648	1182.5860	L	575.3585	288.1829	558.3320	279.6696	0	0	5
23	2495.2594	1248.1333	2478.2329	1239.6201	2477.2489	1239.1281	I	462.2745	231.6409	445.2479	223.1276	0	0	4
24	2566.2965	1283.6519	2549.2700	1275.1386	2548.2860	1274.6466	A	349.1904	175.0988	332.1639	166.5856	0	0	3
25	2697.3370	1349.1721	2680.3105	1340.6589	2679.3265	1340.1669	M	278.1533	139.5803	261.1267	131.0670	0	0	2
26							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 1109.

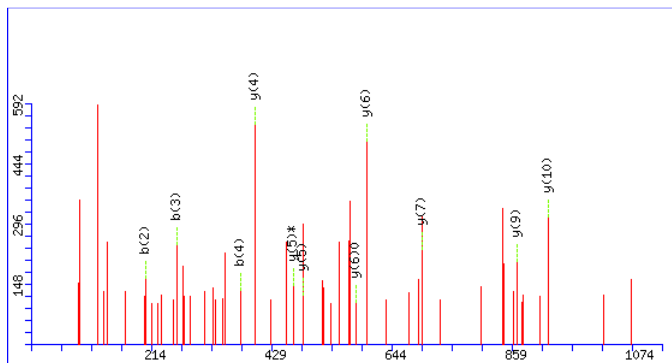
MS/MS Fragmentation of **FGGLVLSPVGK**:

Found in **IP100011693**

Title: 2.1.1.4190.6

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							11
2	205.0972	103.0522	0	0	0	0	G	928.5669	463.7871	909.5404	455.2738	908.5564	454.7818	10
3	262.1186	131.5629	0	0	0	0	G	869.5455	435.2764	852.5189	426.7631	851.5349	426.2711	9
4	375.2027	188.1050	0	0	0	0	L	812.5240	406.7656	795.4975	398.2524	794.5135	397.7604	8
5	474.2711	237.6392	0	0	0	0	V	699.4400	350.2236	682.4134	341.7103	681.4294	341.2183	7
6	587.3552	294.1812	0	0	0	0	L	600.3715	300.6894	583.3450	292.1761	582.3610	291.6841	6
7	674.3872	337.6972	0	0	656.3766	328.6919	S	487.2875	244.1474	470.2609	235.6341	469.2769	235.1421	5
8	771.4400	386.2236	0	0	753.4294	377.2183	P	400.2554	200.6314	383.2289	192.1181	0	0	4
9	870.5084	435.7578	0	0	852.4978	426.7525	V	303.2027	152.1050	286.1761	143.5917	0	0	3
10	927.5298	464.2686	0	0	909.5193	455.2633	G	204.1343	102.5708	187.1077	94.0575	0	0	2
11							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

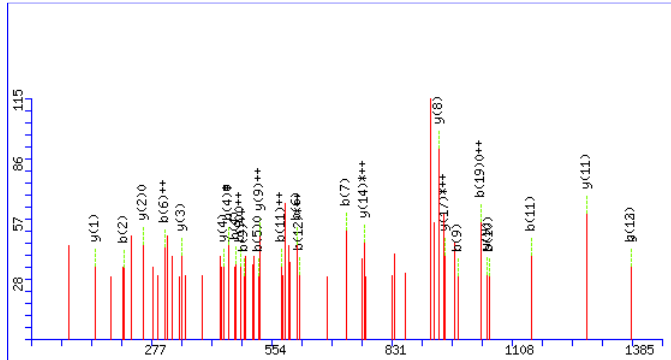
Peptide: 1187.

MS/MS Fragmentation of **QSWAAALQEAVTETLSDYEVAEK:**
Found in **IP100103380;IP100965073;IP100965334**

Title: 5.1.1.1061.4

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3.5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233	0	0	Q							23
2	216.0979	108.5526	199.0713	100.0393	198.0873	99.5473	S	2411.1613	1206.0843	2394.1347	1197.5710	2393.1507	1197.0790	22
3	402.1772	201.5922	385.1506	193.0790	384.1666	192.5870	W	2324.1293	1162.5683	2307.1027	1154.0550	2306.1187	1153.5630	21
4	473.2143	237.1108	456.1878	228.5975	455.2037	228.1055	A	2138.0499	1069.5286	2121.0234	1061.0153	2120.0394	1060.5233	20
5	544.2514	272.6293	527.2249	264.1161	526.2409	263.6241	A	2067.0128	1034.0100	2049.9863	1025.4968	2049.0023	1025.0048	19
6	615.2885	308.1479	598.2620	299.6346	597.2780	299.1426	A	1995.9757	998.4915	1978.9492	989.9782	1977.9651	989.4862	18
7	728.3728	364.6899	711.3461	356.1767	710.3620	355.6847	L	1924.9386	962.9729	1907.9120	954.4597	1906.9280	953.9677	17
8	856.4312	428.7192	839.4046	420.2060	838.4206	419.7139	Q	1811.8545	906.4309	1794.8280	897.9176	1793.8440	897.4256	16
9	985.4738	493.2405	968.4472	484.7272	967.4632	484.2352	E	1683.7960	842.4016	1666.7694	833.8883	1665.7854	833.3963	15
10	1056.5109	528.7591	1039.4843	520.2458	1038.5003	519.7538	A	1554.7534	777.8803	1537.7268	769.3670	1536.7428	768.8750	14
11	1155.5793	578.2933	1138.5528	569.7800	1137.5687	569.2880	V	1483.7162	742.3618	1466.6897	733.8485	1465.7057	733.3565	13
12	1256.6270	628.8171	1239.6004	620.3039	1238.6164	619.8118	T	1384.6478	692.8276	1367.6213	684.3143	1366.6373	683.8223	12
13	1385.6696	693.3384	1368.6430	684.8251	1367.6590	684.3331	E	1283.6002	642.3037	1266.5736	633.7904	1265.5896	633.2984	11
14	1486.7173	743.8623	1469.6907	735.3490	1468.7067	734.8570	T	1154.5576	577.7824	1137.5310	569.2691	1136.5470	568.7771	10
15	1599.8013	800.4043	1582.7748	791.8910	1581.7908	791.3990	L	1053.5099	527.2586	1036.4833	518.7453	1035.4993	518.2533	9
16	1686.8333	843.9203	1669.8068	835.4070	1668.8228	834.9150	S	940.4258	470.7165	923.3993	462.2033	922.4153	461.7113	8
17	1801.8603	901.4338	1784.8337	892.9205	1783.8497	892.4285	D	853.3938	427.2005	836.3672	418.6873	835.3832	418.1953	7
18	1964.9236	982.9654	1947.8971	974.4522	1946.9131	973.9602	Y	738.3668	369.6871	721.3403	361.1738	720.3563	360.6818	6
19	2093.9662	1047.4867	2076.9397	1038.9735	2075.9556	1038.4815	E	575.3035	288.1554	558.2770	279.6421	557.2930	279.1501	5
20	2193.0346	1097.0209	2176.0081	1088.5077	2175.0241	1088.0157	V	446.2609	223.6341	429.2344	215.1208	428.2504	214.6288	4
21	2264.0717	1132.5395	2247.0452	1124.0262	2246.0612	1123.5342	A	347.1925	174.0999	330.1660	165.5866	329.1819	165.0946	3
22	2393.1143	1197.0608	2376.0878	1188.5475	2375.1038	1188.0555	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
23							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 1215.

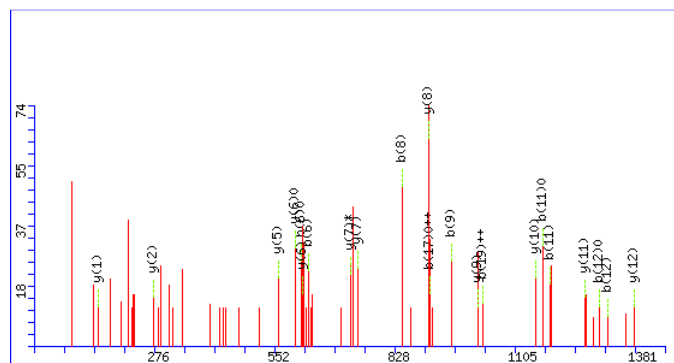
MS/MS Fragmentation of **SGTTWVSQILDMIYQGGDLEK**:

Found in **IP100030730;IP100300026;IP100300027;IP100446834;IP100640414;IP100647709;IP100976309**

Title: 5.1.1.1915.2

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120118ry¥120118ry_201B7-32_2_5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							21
2	145.0608	73.0340	0	0	127.0502	64.0287	G	2254.1060	1127.5566	2237.0795	1119.0434	2236.0954	1118.5514	20
3	246.1084	123.5579	0	0	228.0979	114.5526	T	2197.0845	1099.0459	2180.0580	1090.5326	2179.0740	1090.0406	19
4	347.1561	174.0817	0	0	329.1456	165.0764	T	2096.0369	1048.5221	2079.0103	1040.0088	2078.0263	1039.5168	18
5	533.2354	267.1214	0	0	515.2249	258.1161	W	1994.9892	997.9982	1977.9626	989.4850	1976.9786	988.9930	17
6	632.3039	316.6556	0	0	614.2933	307.6503	V	1808.9099	904.9586	1791.8833	896.4453	1790.8993	895.9533	16
7	719.3359	360.1716	0	0	701.3253	351.1663	S	1709.8415	855.4244	1692.8149	846.9111	1691.8309	846.4191	15
8	847.3945	424.2009	830.3679	415.6876	829.3839	415.1956	Q	1622.8094	811.9084	1605.7829	803.3951	1604.7989	802.9031	14
9	960.4785	480.7429	943.4520	472.2296	942.4680	471.7376	I	1494.7509	747.8791	1477.7243	739.3658	1476.7403	738.8738	13
10	1073.5626	537.2849	1056.5360	528.7717	1055.5520	528.2796	L	1381.6668	691.3370	1364.6402	682.8238	1363.6562	682.3318	12
11	1188.5895	594.7984	1171.5630	586.2851	1170.5790	585.7931	D	1268.5827	634.7950	1251.5562	626.2817	1250.5722	625.7897	11
12	1319.6300	660.3186	1302.6035	651.8054	1301.6195	651.3134	M	1153.5558	577.2815	1136.5292	568.7683	1135.5452	568.2762	10
13	1432.7141	716.8607	1415.6875	708.3474	1414.7035	707.8554	I	1022.5153	511.7613	1005.4888	503.2480	1004.5047	502.7560	9
14	1595.7774	798.3923	1578.7509	789.8791	1577.7668	789.3871	Y	909.4312	455.2193	892.4047	446.7060	891.4207	446.2140	8
15	1723.8360	862.4216	1706.8094	853.9084	1705.8254	853.4163	Q	746.3679	373.6876	729.3414	365.1743	728.3573	364.6823	7
16	1780.8575	890.9324	1763.8309	882.4191	1762.8469	881.9271	G	618.3093	309.6583	601.2828	301.1450	600.2988	300.6530	6
17	1837.8789	919.4431	1820.8524	910.9298	1819.8683	910.4378	G	561.2879	281.1476	544.2613	272.6343	543.2773	272.1423	5
18	1952.9059	976.9566	1935.8793	968.4433	1934.8953	967.9513	D	504.2664	252.6368	487.2399	244.1236	486.2558	243.6316	4
19	2065.9899	1033.4986	2048.9634	1024.9853	2047.9794	1024.4933	L	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
20	2195.0325	1098.0199	2178.0060	1089.5066	2177.0219	1089.0146	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
21							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 1427.

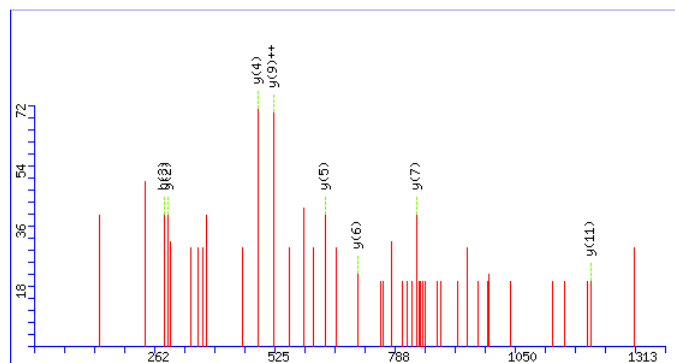
MS/MS Fragmentation of **LGDPLEAFPVFK**:

Found in **IP100328847;IP101012996;IP101013870**

Title: 3.1.1.4102.4

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_1_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							12
2	171.1128	86.0600	0	0	0	0	G	1219.6358	610.3215	1202.6092	601.8082	1201.6252	601.3162	11
3	286.1397	143.5735	0	0	268.1292	134.5682	D	1162.6143	581.8108	1145.5877	573.2975	1144.6037	572.8055	10
4	383.1925	192.0999	0	0	365.1819	183.0946	P	1047.5873	524.2973	1030.5608	515.7840	1029.5768	515.2920	9
5	496.2766	248.6419	0	0	478.2660	239.6366	L	950.5346	475.7709	933.5080	467.2577	932.5240	466.7656	8
6	625.3192	313.1632	0	0	607.3086	304.1579	E	837.4505	419.2289	820.4240	410.7156	819.4400	410.2236	7
7	696.3563	348.6818	0	0	678.3457	339.6765	A	708.4079	354.7076	691.3814	346.1943	0	0	6
8	843.4247	422.2160	0	0	825.4141	413.2107	F	637.3708	319.1890	620.3443	310.6758	0	0	5
9	940.4775	470.7424	0	0	922.4669	461.7371	P	490.3024	245.6548	473.2758	237.1416	0	0	4
10	1039.5459	520.2766	0	0	1021.5353	511.2713	V	393.2496	197.1285	376.2231	188.6152	0	0	3
11	1186.6143	593.8108	0	0	1168.6037	584.8055	F	294.1812	147.5942	277.1547	139.0810	0	0	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 1640.

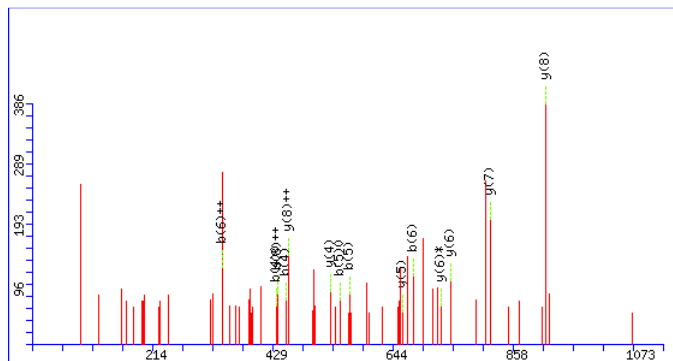
MS/MS Fragmentation of **EDPLIIPVPA**SENPR:

Found in **IPI00030058**

Title: 3.1.1.3275.3

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_1_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							16
2	245.0768	123.0420	0	0	227.0662	114.0368	D	1664.9006	832.9540	1647.8741	824.4407	1646.8901	823.9487	15
3	342.1296	171.5684	0	0	324.1190	162.5631	P	1549.8737	775.4405	1532.8471	766.9272	1531.8631	766.4352	14
4	455.2136	228.1105	0	0	437.2031	219.1052	L	1452.8209	726.9141	1435.7944	718.4008	1434.8104	717.9088	13
5	568.2977	284.6525	0	0	550.2871	275.6472	I	1339.7369	670.3721	1322.7103	661.8588	1321.7263	661.3668	12
6	681.3818	341.1945	0	0	663.3712	332.1892	I	1226.6528	613.8300	1209.6262	605.3168	1208.6422	604.8248	11
7	778.4345	389.7209	0	0	760.4240	380.7156	P	1113.5687	557.2880	1096.5422	548.7747	1095.5582	548.2827	10
8	877.5029	439.2551	0	0	859.4924	430.2498	V	1016.5160	508.7616	999.4894	500.2483	998.5054	499.7563	9
9	974.5557	487.7815	0	0	956.5451	478.7762	P	917.4476	459.2274	900.4210	450.7141	899.4370	450.2221	8
10	1045.5928	523.3001	0	0	1027.5823	514.2948	A	820.3948	410.7010	803.3682	402.1878	802.3842	401.6958	7
11	1132.6249	566.8161	0	0	1114.6143	557.8108	S	749.3577	375.1825	732.3311	366.6692	731.3471	366.1772	6
12	1261.6674	631.3374	0	0	1243.6569	622.3321	E	662.3256	331.6665	645.2991	323.1532	644.3151	322.6612	5
13	1375.7104	688.3588	1358.6838	679.8455	1357.6998	679.3535	N	533.2831	267.1452	516.2565	258.6319	0	0	4
14	1472.7631	736.8852	1455.7366	728.3719	1454.7526	727.8799	P	419.2401	210.1237	402.1363	201.6104	0	0	3
15	1619.8316	810.4194	1602.8050	801.9061	1601.8210	801.4141	F	322.1874	161.5973	305.1608	153.0840	0	0	2
16							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 1688.

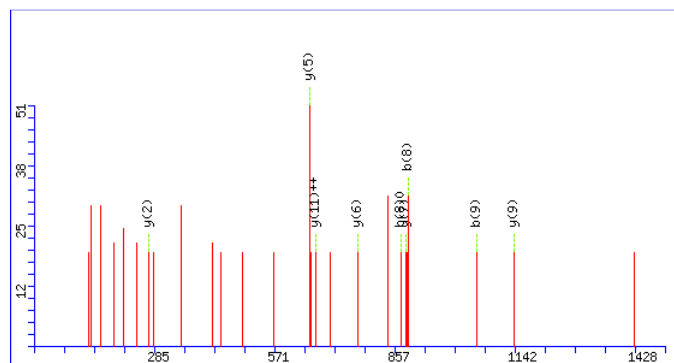
MS/MS Fragmentation of **DTTKPISFYLSLELLAWKPR**:

Found in **IP100168838;IP100874016;IP100889689;IP101018828**

Title: 5.1.1.699.2

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							22
2	217.0819	109.0446	0	0	199.0713	100.0393	T	2479.3595	1240.1834	2462.3330	1231.6701	2461.3490	1231.1781	21
3	318.1296	159.5684	0	0	300.1190	150.5631	T	2378.3118	1189.6596	2361.2853	1181.1463	2360.3013	1180.6543	20
4	446.2245	223.6159	429.1980	215.1026	428.2140	214.6106	K	2277.2642	1139.1357	2260.2376	1130.6224	2259.2536	1130.1304	19
5	543.2773	272.1423	526.2508	263.6290	525.2667	263.1370	P	2149.1692	1075.0882	2132.1427	1066.5750	2131.1586	1066.0830	18
6	656.3614	328.6843	639.3348	320.1710	638.3508	319.6790	I	2052.1164	1026.5619	2035.0899	1018.0486	2034.1059	1017.5566	17
7	743.3934	372.2003	726.3668	363.6871	725.3828	363.1951	S	1939.0324	970.0198	1922.0058	961.5066	1921.0218	961.0145	16
8	890.4618	445.7345	873.4353	437.2213	872.4512	436.7293	F	1852.0003	926.5038	1834.9738	917.9905	1833.9898	917.4985	15
9	1053.5251	527.2662	1036.4986	518.7529	1035.5146	518.2609	Y	1704.9319	852.9696	1687.9054	844.4563	1686.9214	843.9643	14
10	1166.6092	583.8082	1149.5827	575.2950	1148.5986	574.8030	L	1541.8686	771.4379	1524.8421	762.9247	1523.8580	762.4327	13
11	1253.6412	627.3243	1236.6147	618.8110	1235.6307	618.3190	S	1428.7845	714.8959	1411.7580	706.3826	1410.7740	705.8906	12
12	1340.6733	670.8403	1323.6467	662.3270	1322.6627	661.8350	S	1341.7525	671.3799	1324.7260	662.8666	1323.7419	662.3746	11
13	1453.7573	727.3823	1436.7308	718.8690	1435.7468	718.3770	L	1254.7205	627.8639	1237.6939	619.3506	1236.7099	618.8586	10
14	1582.7999	791.9036	1565.7734	783.3903	1564.7894	782.8983	E	1141.6364	571.3218	1124.6099	562.8086	1123.6259	562.3166	9
15	1711.8425	856.4249	1694.8160	847.9116	1693.8319	847.4196	E	1012.5938	506.8006	995.5673	498.2873	994.5833	497.7953	8
16	1824.9266	912.9669	1807.9000	904.4536	1806.9160	903.9616	L	883.5512	442.2793	866.5247	433.7660	0	0	7
17	1938.0106	969.5090	1920.9841	960.9957	1920.0001	960.5037	L	770.4672	385.7372	753.4406	377.2239	0	0	6
18	2009.0478	1005.0275	1992.0212	996.5142	1991.0372	996.0222	A	657.3831	329.1952	640.3566	320.6819	0	0	5
19	2195.1271	1098.0672	2178.1005	1089.5539	2177.1165	1089.0619	W	586.3460	293.6766	569.3194	285.1634	0	0	4
20	2323.2220	1162.1147	2306.1955	1153.6014	2305.2115	1153.1094	K	400.2667	200.6370	383.2401	192.1237	0	0	3
21	2420.2748	1210.6410	2403.2482	1202.1278	2402.2642	1201.6358	P	272.1717	136.5895	255.1452	128.0762	0	0	2
22							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 1753.

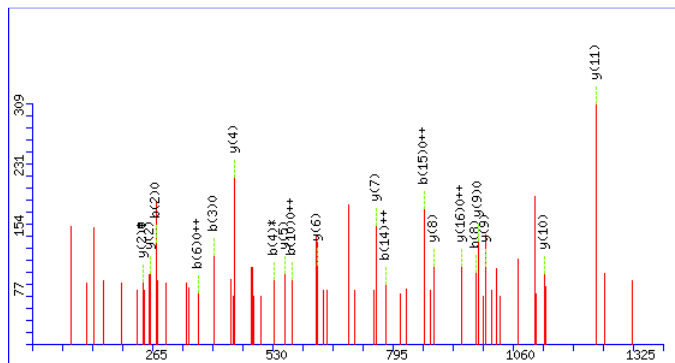
MS/MS Fragmentation of **EYQENSDIVSDSPVWQDQILENEEAIALSR**:

Found in **IPI00028099:IPI00641814**

Title: 4.1.1.428.7

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10 3 4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							30
2	293.1132	147.0602	0	0	275.1026	138.0550	Y	3348.5866	1674.7970	3331.5601	1666.2837	3330.5761	1665.7917	29
3	421.1718	211.0895	404.1452	202.5763	403.1612	202.0842	Q	3185.5233	1593.2653	3168.4968	1584.7520	3167.5127	1584.2600	28
4	550.2144	275.6108	533.1878	267.0975	532.2038	266.6055	E	3057.4647	1529.2360	3040.4382	1520.7227	3039.4542	1520.2307	27
5	664.2573	332.6323	647.2307	324.1190	646.2467	323.6270	N	2928.4221	1464.7147	2911.3956	1456.2014	2910.4116	1455.7094	26
6	751.2893	376.1483	734.2628	367.6350	733.2788	367.1430	S	2814.3792	1407.6932	2797.3527	1399.1800	2796.3686	1398.6880	25
7	866.3163	433.6618	849.2897	425.1485	848.3057	424.6565	D	2727.3472	1364.1772	2710.3206	1355.6640	2709.3366	1355.1719	24
8	979.4003	490.2038	962.3738	481.6905	961.3898	481.1985	I	2612.3202	1306.6638	2595.2937	1298.1505	2594.3097	1297.6585	23
9	1078.4687	539.7380	1061.4422	531.2247	1060.4582	530.7327	V	2499.2362	1250.1217	2482.2096	1241.6084	2481.2256	1241.1164	22
10	1165.5008	583.2540	1148.4742	574.7407	1147.4902	574.2487	S	2400.1678	1200.5875	2383.1412	1192.0742	2382.1572	1191.5822	21
11	1280.5277	640.7675	1263.5012	632.2542	1262.5172	631.7622	D	2313.1357	1157.0715	2296.1092	1148.5582	2295.1252	1148.0662	20
12	1367.5597	684.2835	1350.5332	675.7702	1349.5492	675.2782	S	2198.1088	1099.5580	2181.0822	1091.0448	2180.0982	1090.5527	19
13	1464.6125	732.8099	1447.5860	724.2966	1446.6019	723.8046	P	2111.0768	1056.0420	2094.0502	1047.5287	2093.0662	1047.0367	18
14	1563.6809	782.3441	1546.6544	773.8308	1545.6704	773.3388	V	2014.0240	1007.5156	1996.9974	999.0024	1996.0134	998.5104	17
15	1749.7602	875.3838	1732.7337	866.8705	1731.7497	866.3785	W	1914.9556	957.9814	1897.9290	949.4682	1896.9450	948.9761	16
16	1877.8188	939.4130	1860.7923	930.8998	1859.8082	930.4078	Q	1728.8763	864.9418	1711.8497	856.4285	1710.8657	855.9365	15
17	1992.8458	996.9265	1975.8192	988.4132	1974.8352	987.9212	D	1600.8177	800.9125	1583.7911	792.3992	1582.8071	791.9072	14
18	2120.9403	1060.9558	2103.8778	1052.4425	2102.8938	1051.9505	Q	1485.7907	743.3990	1468.7642	734.8857	1467.7802	734.3937	13
19	2233.9884	1117.4978	2216.9618	1108.9846	2215.9738	1108.4926	I	1357.7322	679.3697	1340.7056	670.8564	1339.7216	670.3644	12
20	2347.0725	1174.0399	2330.0459	1165.5266	2329.0619	1165.0346	L	1244.6481	622.8277	1227.6216	614.3144	1226.6375	613.8224	11
21	2476.1151	1238.5612	2459.0885	1230.0479	2458.1045	1229.5559	E	1131.5640	566.2857	1114.5375	557.7724	1113.5535	557.2804	10
22	2590.1580	1295.5826	2573.1314	1287.0694	2572.1474	1286.5773	N	1002.5214	501.7644	985.4949	493.2511	984.5109	492.7591	9

Peptide View

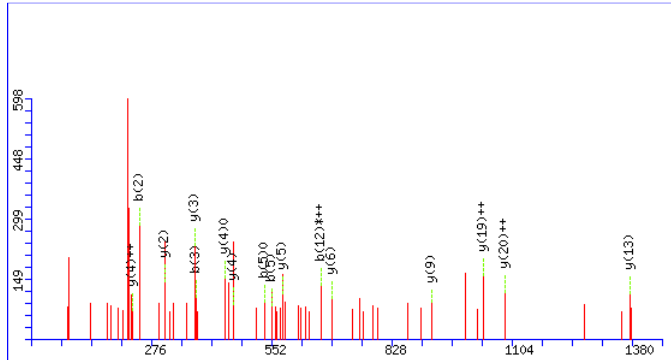
Peptide: 1914.

MS/MS Fragmentation of **SYESSLPQTQQVDLDSRPLFTSAALLSACK: 57.021465@C:30**
 Found in **IP100001641**

Title: 4.1.1.765.6

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120214ry¥120214ry_32R1-32_4.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							31
2	251.1028	126.0550	0	0	233.0921	117.0497	Y	3338.6937	1669.8505	3321.6671	1661.3372	3320.6831	1660.8452	30
3	380.1452	190.5763	0	0	362.1347	181.5710	E	3175.6304	1588.3188	3158.6038	1579.8055	3157.6198	1579.3135	29
4	467.1773	234.0923	0	0	449.1667	225.0870	S	3046.5878	1523.7975	3029.5612	1515.2842	3028.5772	1514.7922	28
5	554.2093	277.6083	0	0	536.1987	268.6030	S	2959.5557	1480.2815	2942.5292	1471.7682	2941.5452	1471.2762	27
6	667.2933	334.1503	0	0	649.2828	325.1450	L	2872.5237	1436.7655	2855.4972	1428.2522	2854.5131	1427.7602	26
7	764.3461	382.6767	0	0	746.3355	373.6714	P	2759.4396	1380.2235	2742.4131	1371.7102	2741.4291	1371.2182	25
8	892.4047	446.7060	875.3781	438.1927	874.3941	437.7007	Q	2662.3869	1331.6971	2645.3603	1323.1838	2644.3763	1322.6918	24
9	993.4524	497.2298	976.4258	488.7165	975.4418	488.2245	T	2534.3283	1267.6678	2517.3018	1259.1545	2516.3177	1258.6625	23
10	1121.5109	561.2591	1104.4844	552.7458	1103.5004	552.2538	Q	2433.2806	1217.1439	2416.2541	1208.6307	2415.2701	1208.1387	22
11	1249.5695	625.2884	1232.5430	616.7751	1231.5590	616.2831	Q	2305.2220	1153.1147	2288.1955	1144.6014	2287.2115	1144.1094	21
12	1348.6379	674.8226	1331.6114	666.3093	1330.6274	665.8173	V	2177.1635	1089.0854	2160.1369	1080.5721	2159.1529	1080.0801	20
13	1463.6649	732.3361	1446.6383	723.8228	1445.6543	723.3308	D	2078.0951	1039.5512	2061.0685	1031.0379	2060.0845	1030.5459	19
14	1576.7489	788.8781	1559.7224	780.3648	1558.7384	779.8728	L	1963.0681	982.0377	1946.0416	973.5244	1945.0575	973.0324	18
15	1691.7759	846.3916	1674.7493	837.8783	1673.7653	837.3863	D	1849.9840	925.4957	1832.9575	916.9824	1831.9735	916.4904	17
16	1804.8600	902.9336	1787.8334	894.4203	1786.8494	893.9283	L	1734.9571	867.9822	1717.9306	859.4689	1716.9465	858.9769	16
17	1891.8920	946.4496	1874.8654	937.9364	1873.8814	937.4443	S	1621.8730	811.4402	1604.8465	802.9269	1603.8625	802.4349	15
18	2047.9931	1024.5002	2030.9665	1015.9869	2029.9825	1015.4949	R	1534.8410	767.9241	1517.8145	759.4109	1516.8304	758.9189	14
19	2145.0459	1073.0266	2128.0193	1064.5133	2127.0353	1064.0213	P	1378.7399	689.8736	1361.7134	681.3603	1360.7293	680.8683	13
20	2258.1299	1129.5686	2241.1034	1121.0553	2240.1194	1120.5633	L	1281.6871	641.3472	1264.6606	632.8339	1263.6766	632.3419	12
21	2405.1983	1203.1028	2388.1718	1194.5895	2387.1878	1194.0975	F	1168.6031	584.8052	1151.5765	576.2919	1150.5925	575.7999	11
22	2506.2460	1253.6266	2489.2195	1245.1134	2488.2354	1244.6214	T	1021.5347	511.2710	1004.5081	502.7577	1003.5241	502.2657	10
23	2593.2780	1297.1427	2576.2515	1288.6294	2575.2675	1288.1374	S	920.4870	460.7471	903.4604	452.2339	902.4764	451.7418	9
24	2664.3152	1332.6612	2647.2886	1324.1479	2646.3046	1323.6559	A	833.4550	417.2311	816.4284	408.7178	815.4444	408.2258	8
25	2735.3523	1368.1798	2718.3257	1359.6665	2717.3417	1359.1745	A	762.4178	381.7126	745.3913	373.1993	744.4073	372.7073	7
26	2848.4363	1424.7218	2831.4098	1416.2085	2830.4258	1415.7165	L	691.3807	346.1940	674.3542	337.6807	673.3702	337.1887	6
27	2961.5204	1481.2638	2944.4938	1472.7506	2943.5098	1472.2586	L	578.2967	289.6520	561.2701	281.1387	560.2861	280.6467	5
28	3048.5524	1524.7798	3031.5259	1516.2666	3030.5419	1515.7746	S	465.2126	233.1099	448.1860	224.5967	447.2020	224.1047	4
29	3119.5895	1560.2984	3102.5630	1551.7851	3101.5790	1551.2931	A	378.1806	189.5939	361.1540	181.0806	0	0	3
30	3279.6202	1640.3137	3262.5936	1631.8005	3261.6096	1631.3084	C	307.1435	154.0754	290.1169	145.5621	0	0	2
31							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 2166.

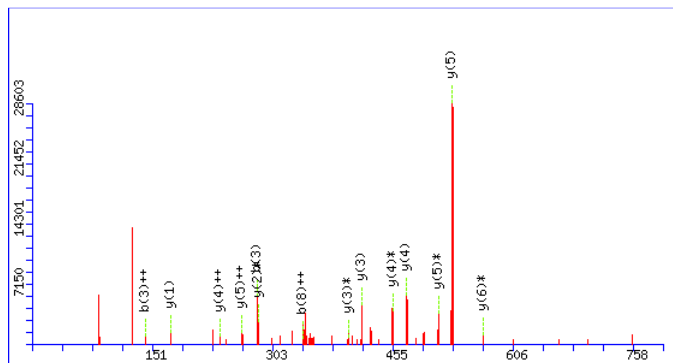
MS/MS Fragmentation of **GRAGGRAGGGLQR**:

Found in **IP100431745**

Title: 1.1.1.8412.5

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							13
2	214.1299	107.5686	197.1033	99.0553	0	0	R	1155.6454	578.3263	1138.6188	569.8130	0	0	12
3	285.1670	143.0871	268.1404	134.5738	0	0	A	999.5443	500.2758	982.5177	491.7625	0	0	11
4	342.1884	171.5979	325.1619	163.0846	0	0	G	928.5071	464.7572	911.4806	456.2439	0	0	10
5	399.2099	200.1086	382.1833	191.5953	0	0	G	871.4857	436.2465	854.4591	427.7332	0	0	9
6	555.3110	278.1591	538.2845	269.6459	0	0	R	814.4642	407.7357	797.4377	399.2225	0	0	8
7	626.3481	313.6777	609.3216	305.1644	0	0	A	658.3631	329.6852	641.3366	321.1719	0	0	7
8	683.3696	342.1884	666.3430	333.6752	0	0	G	587.3260	294.1666	570.2994	285.6534	0	0	6
9	740.3910	370.6992	723.3645	362.1859	0	0	G	530.3045	265.6559	513.2780	257.1426	0	0	5
10	797.4125	399.2099	780.3860	390.6966	0	0	G	473.2831	237.1452	456.2565	228.6319	0	0	4
11	910.4966	455.7519	893.4700	447.2387	0	0	L	416.2616	208.6344	399.2350	200.1212	0	0	3
12	1038.5552	519.7812	1021.5286	511.2679	0	0	Q	303.1775	152.0924	286.1510	143.5791	0	0	2
13							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 2257.

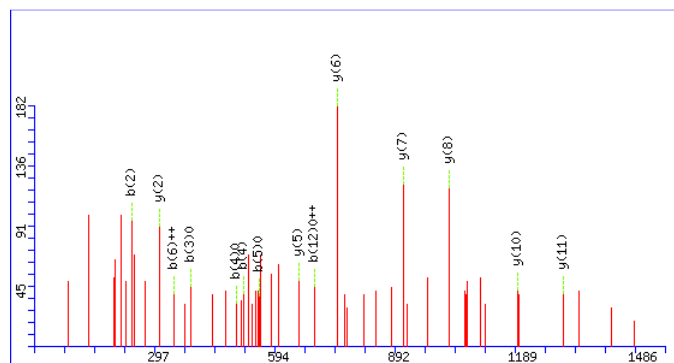
MS/MS Fragmentation of **ELYLGLLYPTEDYK**:

Found in **IP100007819;IP100644084**

Title: 3.1.1.3809.8

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							14
2	243.1339	122.0706	0	0	225.1234	113.0653	L	1587.8305	794.4189	1570.8039	785.9056	1569.8199	785.4136	13
3	406.1973	203.6023	0	0	388.1867	194.5970	Y	1474.7464	737.8769	1457.7199	729.3636	1456.7359	728.8716	12
4	519.2813	260.1443	0	0	501.2708	251.1390	L	1311.6831	656.3452	1294.6565	647.8319	1293.6725	647.3399	11
5	576.3028	288.6550	0	0	558.2922	279.6498	G	1198.5990	599.8032	1181.5725	591.2899	1180.5885	590.7979	10
6	689.3869	345.1971	0	0	671.3763	336.1918	L	1141.5776	571.2924	1124.5510	562.7791	1123.5670	562.2871	9
7	802.4709	401.7391	0	0	784.4604	392.7338	L	1028.4935	514.7504	1011.4670	506.2371	1010.4829	505.7451	8
8	965.5342	483.2708	0	0	947.5237	474.2655	Y	915.4094	458.2084	898.3829	449.6951	897.3989	449.2031	7
9	1062.5870	531.7971	0	0	1044.5764	522.7919	P	752.3461	376.6767	735.3196	368.1634	734.3355	367.6714	6
10	1163.6347	582.3210	0	0	1145.6241	573.3157	T	655.2933	328.1503	638.2668	319.6370	637.2828	319.1450	5
11	1292.6773	646.8423	0	0	1274.6667	637.8370	E	554.2457	277.6265	537.2191	269.1132	536.2351	268.6212	4
12	1407.7042	704.3558	0	0	1389.6937	695.3505	D	425.2031	213.1052	408.1765	204.5919	407.1925	204.0999	3
13	1570.7676	785.8874	0	0	1552.7570	776.8821	Y	310.1761	155.5917	293.1496	147.0784	0	0	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 2438.

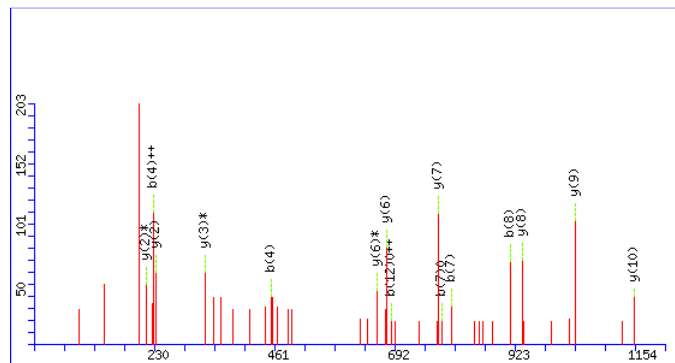
MS/MS Fragmentation of **DIDLDEILTYVQDSLK**:

Found in **IP100021008**

Title: 5.1.1.1369.2

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2.5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							18
2	229.1183	115.0628	0	0	211.1077	106.0575	I	1953.0063	977.0068	1935.9797	968.4935	1934.9957	968.0015	17
3	344.1452	172.5763	0	0	326.1347	163.5710	D	1839.9222	920.4647	1822.8957	911.9515	1821.9117	911.4595	16
4	457.2293	229.1183	0	0	439.2187	220.1130	L	1724.8953	862.9513	1707.8687	854.4380	1706.8847	853.9460	15
5	558.2770	279.6421	0	0	540.2664	270.6368	T	1611.8112	806.4092	1594.7847	797.8960	1593.8006	797.4040	14
6	673.3039	337.1556	0	0	655.2933	328.1503	D	1510.7635	755.8854	1493.7370	747.3721	1492.7530	746.8801	13
7	802.3465	401.6769	0	0	784.3359	392.6716	E	1395.7366	698.3719	1378.7100	689.8587	1377.7260	689.3666	12
8	915.4306	458.2189	0	0	897.4200	449.2136	I	1266.6940	633.8506	1249.6674	625.3374	1248.6834	624.8454	11
9	1028.5146	514.7610	0	0	1010.5041	505.7557	L	1153.6099	577.3086	1136.5834	568.7953	1135.5994	568.3033	10
10	1129.5623	565.2848	0	0	1111.5517	556.2795	T	1040.5259	520.7666	1023.4993	512.2533	1022.5153	511.7613	9
11	1292.6256	646.8165	0	0	1274.6151	637.8112	Y	939.4782	470.2427	922.4516	461.7295	921.4676	461.2374	8
12	1391.6941	696.3507	0	0	1373.6835	687.3454	V	776.4149	388.7111	759.3883	380.1978	758.4043	379.7058	7
13	1519.7526	760.3800	1502.7261	751.8667	1501.7421	751.3747	Q	677.3464	339.1769	660.3199	330.6636	659.3359	330.1716	6
14	1634.7796	817.8934	1617.7530	809.3802	1616.7690	808.8881	D	549.2879	275.1476	532.2613	266.6343	531.2773	266.1423	5
15	1721.8116	861.4094	1704.7851	852.8962	1703.8010	852.4042	S	434.2609	217.6341	417.2344	209.1208	416.2504	208.6288	4
16	1834.8957	917.9515	1817.8691	909.4382	1816.8851	908.9462	L	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
17	1921.9277	961.4675	1904.9011	952.9542	1903.9171	952.4622	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
18							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 2612.

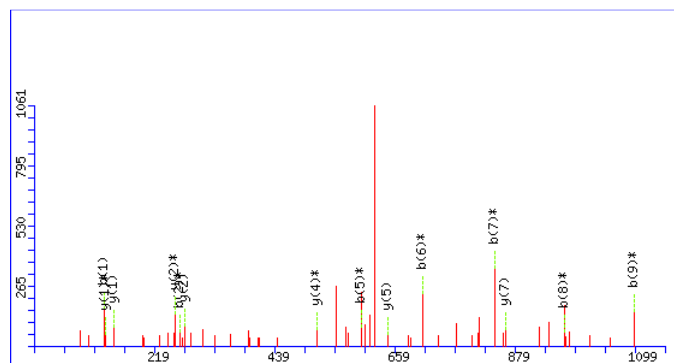
MS/MS Fragmentation of **QRDSEIMQKQK: -17.026549@N-term(Q)**

Found in **IP100024781;IP100179265;IP100894485;IP100979802**

Title: 1.1.1.8033.10

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120214ry¥120214ry_414C2-43_4_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233	0	0	Q							10
2	285.1670	143.0871	268.1404	134.5738	0	0	R	1134.5572	567.7822	1117.5306	559.2690	1116.5466	558.7769	9
3	400.1939	200.6006	383.1674	192.0873	382.1833	191.5953	D	978.4561	489.7317	961.4295	481.2184	960.4455	480.7264	8
4	487.2259	244.1166	470.1994	235.6033	469.2154	235.1113	S	863.4291	432.2182	846.4026	423.7049	845.4186	423.2129	7
5	616.2685	308.6379	599.2420	300.1246	598.2580	299.6326	E	776.3971	388.7022	759.3706	380.1889	758.3865	379.6969	6
6	729.3526	365.1799	712.3260	356.6667	711.3420	356.1747	I	647.3545	324.1809	630.3280	315.6676	0	0	5
7	860.3931	430.7002	843.3665	422.1869	842.3825	421.6949	M	534.2704	267.6389	517.2439	259.1256	0	0	4
8	988.4517	494.7295	971.4251	486.2162	970.4411	485.7242	Q	403.2300	202.1186	386.2034	193.6053	0	0	3
9	1116.5102	558.7588	1099.4837	550.2455	1098.4997	549.7535	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
10							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 2657.

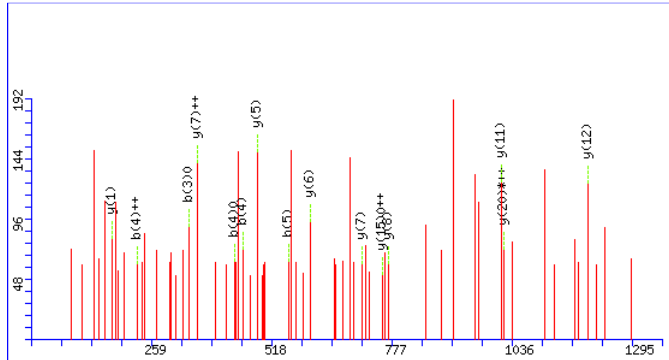
MS/MS Fragmentation of **EVEVVPSNMWGGQGLLGASVR: 0.984015@N:8**

Found in **IP100011074;IP100456615;IP100456616;IP100790902;IP100924764;IP100926571;IP100926998;IP100927125**

Title: 3.1.1.3355.5

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_3_3.mgf

ProteinPilot Peptide Confidence > 99%

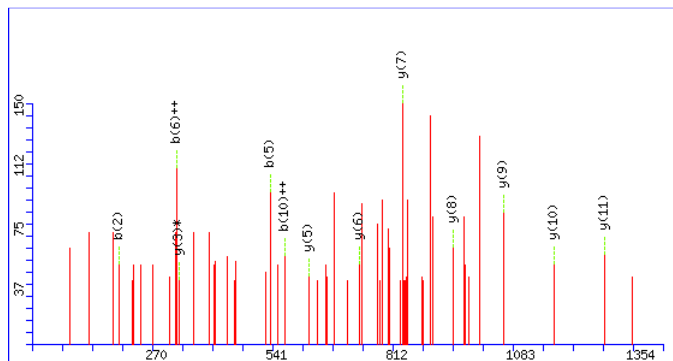


#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							21
2	229.1183	115.0628	0	0	211.1077	106.0575	V	2057.0484	1029.0279	2040.0219	1020.5146	2039.0379	1020.0226	20
3	358.1609	179.5841	0	0	340.1503	170.5788	E	1957.9800	979.4936	1940.9535	970.9804	1939.9695	970.4884	19
4	457.2293	229.1183	0	0	439.2187	220.1130	V	1828.9374	914.9724	1811.9109	906.4591	1810.9269	905.9671	18
5	556.2977	278.6525	0	0	538.2871	269.6472	V	1729.8690	865.4381	1712.8425	856.9249	1711.8585	856.4329	17
6	653.3505	327.1789	0	0	635.3399	318.1736	P	1630.8006	815.9039	1613.7741	807.3907	1612.7900	806.8987	16
7	740.3825	370.6949	0	0	722.3719	361.6896	S	1533.7478	767.3776	1516.7213	758.8643	1515.7373	758.3723	15
8	855.4094	428.2084	838.3829	419.6951	837.3989	419.2031	N	1446.7158	723.8615	1429.6893	715.3483	1428.7052	714.8563	14
9	986.4499	493.7286	969.4234	485.2153	968.4394	484.7233	M	1331.6889	666.3481	1314.6623	657.8348	1313.6783	657.3428	13
10	1172.5292	586.7683	1155.5027	578.2550	1154.5187	577.7630	W	1200.6484	600.8278	1183.6218	592.3146	1182.6378	591.8225	12
11	1229.5507	615.2790	1212.5242	606.7657	1211.5401	606.2737	G	1014.5691	507.7882	997.5425	499.2749	996.5585	498.7829	11
12	1286.5722	643.7897	1269.5456	635.2764	1268.5616	634.7844	G	957.5476	479.2774	940.5211	470.7642	939.5370	470.2722	10
13	1414.6307	707.8190	1397.6042	699.3057	1396.6202	698.8137	Q	900.5261	450.7667	883.4996	442.2534	882.5156	441.7614	9
14	1471.6522	736.3297	1454.6257	727.8165	1453.6416	727.3245	G	772.4676	386.7374	755.4410	378.2241	754.4570	377.7321	8
15	1584.7363	792.8718	1567.7097	784.3585	1566.7257	783.8665	L	715.4461	358.2267	698.4196	349.7134	697.4355	349.2214	7
16	1697.8203	849.4138	1680.7938	840.9005	1679.8098	840.4085	L	602.3620	301.6847	585.3355	293.1714	584.3515	292.6794	6
17	1754.8418	877.9245	1737.8152	869.4113	1736.8312	868.9193	G	489.2780	245.1426	472.2514	236.6293	471.2674	236.1373	5
18	1825.8789	913.4431	1808.8524	904.9298	1807.8683	904.4378	A	432.2565	216.6319	415.2300	208.1186	414.2459	207.6266	4
19	1912.9109	956.9591	1895.8844	948.4458	1894.9004	947.9538	S	361.2194	181.1133	344.1928	172.6001	343.2088	172.1081	3
20	2011.9794	1006.4933	1994.9528	997.9800	1993.9688	997.4880	V	274.1874	137.5973	257.1608	129.0840	0	0	2
21							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 2686.

MS/MS Fragmentation of **VPIDIVNCDDSK: 57.021465@C:9**
 Found in **IP100023586;IP100747900;IP100941249;IP100965131;IP100966088;IP100967649**
 Title: 2.1.1.3612.11
 Data file: Y:\TT5600(CiRA1)\¥2012-01¥120118ry¥120118ry_201B7-32_1_2.mgf
 ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							13
2	197.1285	99.0679	0	0	0	0	P	1388.6726	694.8399	1371.6461	686.3267	1370.6620	685.8347	12
3	310.2125	155.6099	0	0	0	0	I	1291.6198	646.3136	1274.5933	637.8003	1273.6093	637.3083	11
4	425.2395	213.1234	0	0	407.2289	204.1181	D	1178.5358	589.7715	1161.5092	581.2583	1160.5252	580.7662	10
5	538.3235	269.6654	0	0	520.3130	260.6601	I	1063.5088	532.2581	1046.4823	523.7448	1045.4983	523.2528	9
6	651.4076	326.2074	0	0	633.3970	317.2022	I	950.4248	475.7160	933.3982	467.2027	932.4142	466.7107	8
7	750.4760	375.7416	0	0	732.4654	366.7364	V	837.3407	419.1740	820.3142	410.6607	819.3301	410.1687	7
8	864.5189	432.7631	847.4924	424.2498	846.5084	423.7578	N	738.2723	369.6398	721.2457	361.1265	720.2617	360.6345	6
9	1024.5496	512.7784	1007.5230	504.2652	1006.5390	503.7731	C	624.2294	312.6183	607.2028	304.1050	606.2188	303.6130	5
10	1139.5765	570.2919	1122.5500	561.7786	1121.5660	561.2866	D	464.1987	232.6030	447.1722	224.0897	446.1882	223.5977	4
11	1254.6035	627.8054	1237.5769	619.2921	1236.5929	618.8001	D	349.1718	175.0895	332.1452	166.5763	331.1612	166.0842	3
12	1341.6355	671.3214	1324.6089	662.8081	1323.6249	662.3161	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 2762.

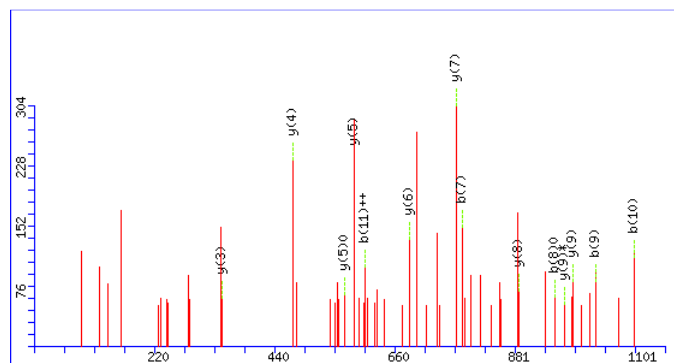
MS/MS Fragmentation of **FVTHVSDWGALATISTLEAVR**:

Found in **IP100021997**

Title: 4.1.1.608.4

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							21
2	247.1441	124.0757	0	0	0	0	V	2126.1240	1063.5657	2109.0975	1055.0524	2108.1135	1054.5604	20
3	348.1918	174.5995	0	0	330.1812	165.5942	T	2027.0556	1014.0315	2010.0291	1005.5182	2009.0451	1005.0262	19
4	485.2507	243.1290	0	0	467.2401	234.1237	H	1926.0080	963.5076	1908.9814	954.9943	1907.9974	954.5023	18
5	584.3191	292.6632	0	0	566.3085	283.6579	V	1788.9490	894.9782	1771.9225	886.4649	1770.9385	885.9729	17
6	671.3511	336.1792	0	0	653.3406	327.1739	S	1689.8806	845.4440	1672.8541	836.9307	1671.8701	836.4387	16
7	786.3781	393.6927	0	0	768.3675	384.6874	D	1602.8486	801.9279	1585.8220	793.4147	1584.8380	792.9227	15
8	972.4574	486.7323	0	0	954.4468	477.7271	W	1487.8217	744.4145	1470.7951	735.9012	1469.8111	735.4092	14
9	1029.4789	515.2431	0	0	1011.4683	506.2378	G	1301.7423	651.3748	1284.7158	642.8615	1283.7318	642.3695	13
10	1100.5160	550.7616	0	0	1082.5054	541.7563	A	1244.7209	622.8641	1227.6943	614.3508	1226.7103	613.8588	12
11	1213.6000	607.3037	0	0	1195.5895	598.2984	L	1173.6838	587.3455	1156.6572	578.8322	1155.6732	578.3402	11
12	1284.6371	642.8222	0	0	1266.6266	633.8169	A	1060.5997	530.8035	1043.5732	522.2902	1042.5891	521.7982	10
13	1385.6848	693.3461	0	0	1367.6743	684.3408	T	989.5626	495.2849	972.5360	486.7717	971.5520	486.2796	9
14	1498.7689	749.8881	0	0	1480.7583	740.8828	I	888.5149	444.7611	871.4884	436.2478	870.5043	435.7558	8
15	1585.8009	793.4041	0	0	1567.7904	784.3988	S	775.4308	388.2191	758.4043	379.7058	757.4203	379.2138	7
16	1686.8486	843.9279	0	0	1668.8380	834.9227	T	688.3988	344.7030	671.3723	336.1898	670.3883	335.6978	6
17	1799.9327	900.4700	0	0	1781.9221	891.4647	L	587.3511	294.1792	570.3246	285.6659	569.3406	285.1739	5
18	1928.9753	964.9913	0	0	1910.9647	955.9860	E	474.2671	237.6372	457.2405	229.1239	456.2565	228.6319	4
19	2000.0124	1000.5098	0	0	1982.0018	991.5045	A	345.2245	173.1159	328.1979	164.6026	0	0	3
20	2099.0808	1050.0440	0	0	2081.0702	1041.0387	V	274.1874	137.5973	257.1608	129.0840	0	0	2
21							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 2797.

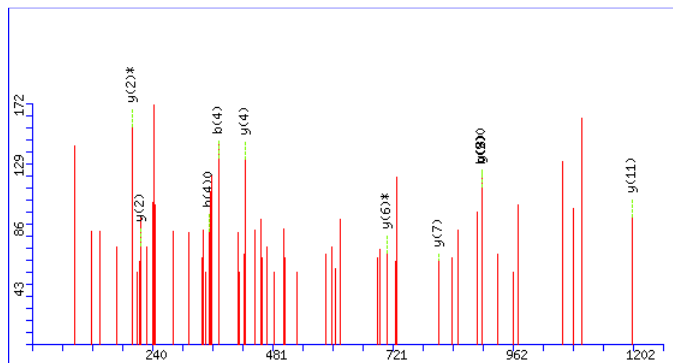
MS/MS Fragmentation of **SGLDSVSSWLPLAK**:

Found in **IP100100193**

Title: 3.1.1.3953.8

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2.3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							14
2	145.0608	73.0340	0	0	127.0502	64.0287	G	1372.7471	686.8772	1355.7205	678.3639	1354.7365	677.8719	13
3	258.1448	129.5761	0	0	240.1343	120.5708	L	1315.7256	658.3665	1298.6991	649.8532	1297.7151	649.3612	12
4	373.1718	187.0895	0	0	355.1612	178.0842	D	1202.6416	601.8244	1185.6150	593.3111	1184.6310	592.8191	11
5	460.2038	230.6055	0	0	442.1932	221.6003	S	1087.6146	544.3109	1070.5881	535.7977	1069.6041	535.3057	10
6	559.2722	280.1397	0	0	541.2617	271.1345	V	1000.5826	500.7949	983.5560	492.2817	982.5720	491.7897	9
7	646.3042	323.6558	0	0	628.2937	314.6505	S	901.5142	451.2607	884.4876	442.7475	883.5036	442.2554	8
8	733.3363	367.1718	0	0	715.3257	358.1665	S	814.4822	407.7447	797.4556	399.2314	796.4716	398.7394	7
9	919.4156	460.2114	0	0	901.4050	451.2061	W	727.4501	364.2287	710.4236	355.7154	0	0	6
10	1032.4997	516.7535	0	0	1014.4891	507.7482	L	541.3708	271.1890	524.3443	262.6758	0	0	5
11	1129.5524	565.2798	0	0	1111.5418	556.2746	P	428.2867	214.6470	411.2602	206.1337	0	0	4
12	1242.6365	621.8219	0	0	1224.6259	612.8166	L	331.2340	166.1206	314.2074	157.6074	0	0	3
13	1313.6736	657.3404	0	0	1295.6630	648.3352	A	218.1499	109.5786	201.1234	101.0653	0	0	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 3246.

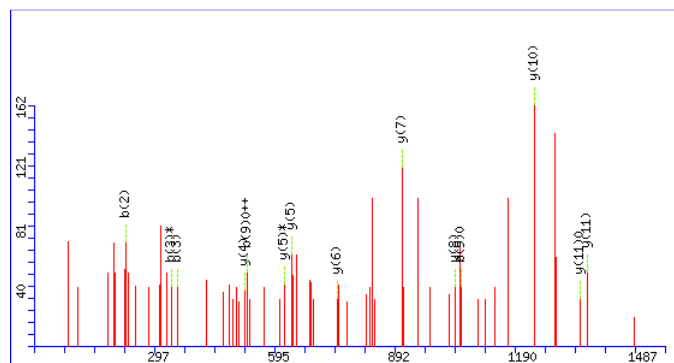
MS/MS Fragmentation of **NIEPTEYIDDLFK**:

Found in **IP100291839;IP100337694;IP100337696;IP100853219;IP100872771;IP100943807;IP100965119;IP100966076;IP100966410;IP100968195**

Title: 4.1.1.256.6

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							13
2	228.1343	114.5708	211.1077	106.0575	0	0	I	1482.7363	741.8718	1465.7097	733.3585	1464.7257	732.8665	12
3	357.1769	179.0921	340.1503	170.5788	339.1663	170.0868	E	1369.6522	685.3297	1352.6256	676.8165	1351.6416	676.3245	11
4	454.2296	227.6185	437.2031	219.1052	436.2191	218.6132	P	1240.6096	620.8084	1223.5830	612.2952	1222.5990	611.8032	10
5	555.2773	278.1423	538.2508	269.6290	537.2667	269.1370	T	1143.5568	572.2821	1126.5303	563.7688	1125.5463	563.2768	9
6	684.3199	342.6636	667.2933	334.1503	666.3093	333.6583	E	1042.5092	521.7582	1025.4826	513.2449	1024.4986	512.7529	8
7	847.3832	424.1953	830.3567	415.6820	829.3727	415.1900	Y	913.4666	457.2369	896.4400	448.7236	895.4560	448.2316	7
8	960.4673	480.7373	943.4407	472.2240	942.4567	471.7320	I	750.4032	375.7053	733.3767	367.1920	732.3927	366.7000	6
9	1075.4942	538.2508	1058.4677	529.7375	1057.4837	529.2455	D	637.3192	319.1632	620.2926	310.6499	619.3086	310.1579	5
10	1190.5212	595.7642	1173.4946	587.2510	1172.5106	586.7589	D	522.2922	261.6498	505.2657	253.1365	504.2817	252.6445	4
11	1303.6052	652.3063	1286.5787	643.7930	1285.5947	643.3010	L	407.2653	204.1363	390.2387	195.6230	0	0	3
12	1450.6737	725.8405	1433.6471	717.3272	1432.6631	716.8352	F	294.1812	147.5942	277.1547	139.0810	0	0	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 3269.

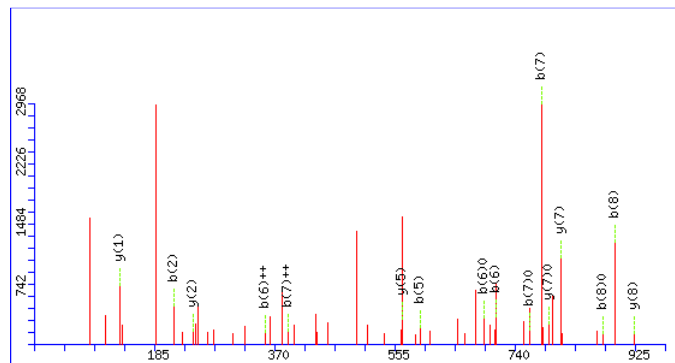
MS/MS Fragmentation of **TIDEHDAII**:

Found in **IP100217366;IP100395888;IP100976631**

Title: 2.1.1.1439.5

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2.2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							9
2	215.1390	108.0731	0	0	197.1285	99.0679	I	925.4625	463.2349	0	0	907.4520	454.2296	8
3	330.1660	165.5866	0	0	312.1554	156.5813	D	812.3785	406.6929	0	0	794.3679	397.6876	7
4	459.2086	230.1079	0	0	441.1980	221.1026	E	697.3515	349.1794	0	0	679.3410	340.1741	6
5	596.2675	298.6374	0	0	578.2569	289.6321	H	568.3089	284.6581	0	0	550.2984	275.6528	5
6	711.2944	356.1508	0	0	693.2838	347.1456	D	431.2500	216.1287	0	0	413.2395	207.1234	4
7	782.3315	391.6694	0	0	764.3210	382.6641	A	316.2231	158.6152	0	0	0	0	3
8	895.4156	448.2114	0	0	877.4050	439.2061	I	245.1860	123.0966	0	0	0	0	2
9							I	132.1019	66.5546	0	0	0	0	1

Peptide View

Peptide: 3297.

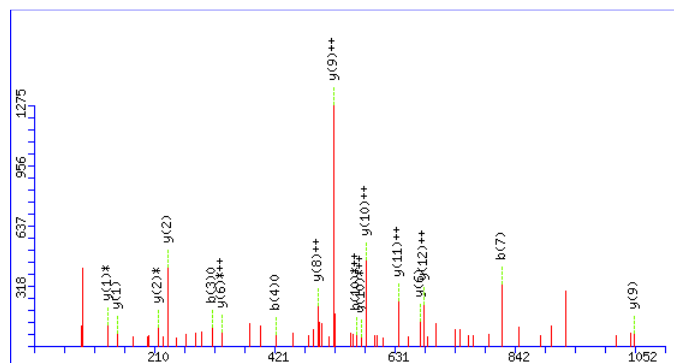
MS/MS Fragmentation of **ESLIGYRPTEDSK**:

Found in **IP100010808,IP101010137**

Title: 2.1.1.461.6

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_3.2.mgf

ProteinPilot Peptide Confidence > 99%

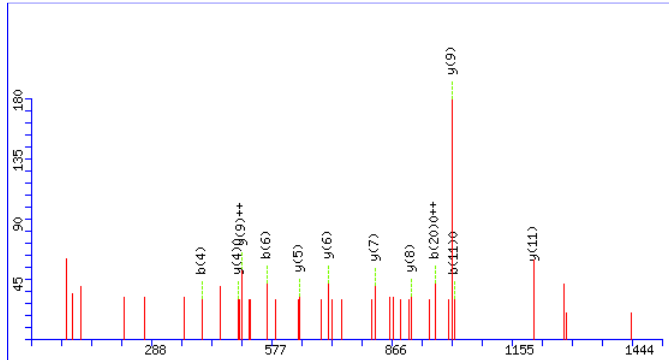


#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							13
2	217.0819	109.0446	0	0	199.0713	100.0393	S	1365.7009	683.3541	1348.6743	674.8408	1347.6903	674.3488	12
3	330.1660	165.5866	0	0	312.1554	156.5813	L	1278.6688	639.8381	1261.6423	631.3248	1260.6583	630.8328	11
4	443.2500	222.1287	0	0	425.2395	213.1234	I	1165.5848	583.2960	1148.5582	574.7828	1147.5742	574.2907	10
5	500.2715	250.6394	0	0	482.2609	241.6341	G	1052.5007	526.7540	1035.4742	518.2407	1034.4902	517.7487	9
6	663.3348	332.1710	0	0	645.3243	323.1658	Y	995.4793	498.2433	978.4527	489.7300	977.4687	489.2380	8
7	819.4359	410.2216	802.4094	401.7083	801.4254	401.2163	R	832.4159	416.7116	815.3894	408.1983	814.4054	407.7063	7
8	916.4887	458.7480	899.4621	450.2347	898.4781	449.7427	P	676.3148	338.6610	659.2883	330.1478	658.3042	329.6558	6
9	1017.5364	509.2718	1000.5098	500.7585	999.5258	500.2665	T	579.2620	290.1347	562.2355	281.6214	561.2515	281.1294	5
10	1146.5790	573.7931	1129.5524	565.2798	1128.5684	564.7878	E	478.2144	239.6108	461.1878	231.0975	460.2038	230.6055	4
11	1261.6059	631.3066	1244.5794	622.7933	1243.5953	622.3013	D	349.1718	175.0895	332.1452	166.5763	331.1612	166.0842	3
12	1348.6379	674.8226	1331.6114	666.3093	1330.6274	665.8173	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 3349.

MS/MS Fragmentation of **SPLLVGVPVSVSFPVPSLAIVER**:
 Found in **IP100027090;IP100654619;IP100746600;IP100873139;IP100903154;IP101011505**
 Title: 4.1.1.2456.8
 Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_4.mgf
 ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							24
2	185.0921	93.0497	0	0	167.0815	84.0444	P	2392.3486	1196.6779	2375.3221	1188.1647	2374.3381	1187.6727	23
3	298.1761	149.5917	0	0	280.1656	140.5864	L	2295.2959	1148.1516	2278.2693	1139.6383	2277.2853	1139.1463	22
4	411.2602	206.1337	0	0	393.2496	197.1285	L	2182.2118	1091.6095	2165.1852	1083.0963	2164.2012	1082.6043	21
5	510.3286	255.6679	0	0	492.3180	246.6627	V	2069.1277	1035.0675	2052.1012	1026.5542	2051.1172	1026.0622	20
6	567.3501	284.1787	0	0	549.3395	275.1734	G	1970.0593	985.5333	1953.0328	977.0200	1952.0488	976.5280	19
7	664.4028	332.7051	0	0	646.3923	323.6998	P	1913.0379	957.0226	1896.0113	948.5093	1895.0273	948.0173	18
8	763.4713	382.2393	0	0	745.4607	373.2340	V	1815.9851	908.4962	1798.9585	899.9829	1797.9745	899.4909	17
9	850.5033	425.7553	0	0	832.4927	416.7500	S	1716.9167	858.9620	1699.8901	850.4487	1698.9061	849.9567	16
10	949.5717	475.2895	0	0	931.5611	466.2842	V	1629.8846	815.4460	1612.8581	806.9327	1611.8741	806.4407	15
11	1036.6037	518.8055	0	0	1018.5932	509.8002	S	1530.8162	765.9118	1513.7897	757.3985	1512.8057	756.9065	14
12	1183.6721	592.3397	0	0	1165.6616	583.3344	F	1443.7842	722.3957	1426.7577	713.8825	1425.7736	713.3905	13
13	1270.7042	635.8557	0	0	1252.6936	626.8504	S	1296.7158	648.8615	1279.6892	640.3483	1278.7052	639.8563	12
14	1367.7569	684.3821	0	0	1349.7464	675.3768	P	1209.6838	605.3455	1192.6572	596.8322	1191.6732	596.3402	11
15	1466.8253	733.9163	0	0	1448.8148	724.9110	V	1112.6310	556.8191	1095.6045	548.3059	1094.6204	547.8139	10
16	1563.8781	782.4427	0	0	1545.8675	773.4374	P	1013.5626	507.2849	996.5360	498.7717	995.5520	498.2796	9
17	1650.9101	825.9587	0	0	1632.8996	816.9534	S	916.5098	458.7585	899.4833	450.2453	898.4993	449.7533	8
18	1763.9942	882.5007	0	0	1745.9836	873.4955	L	829.4778	415.2425	812.4512	406.7293	811.4672	406.2373	7
19	1835.0313	918.0193	0	0	1817.0207	909.0140	A	716.3937	358.7005	699.3672	350.1872	698.3832	349.6952	6
20	1964.0739	982.5406	0	0	1946.0633	973.5353	E	645.3566	323.1819	628.3301	314.6687	627.3461	314.1767	5
21	2077.1580	1039.0826	0	0	2059.1474	1030.0773	I	516.3140	258.6606	499.2875	250.1474	498.3035	249.6554	4
22	2176.2264	1088.6168	0	0	2158.2158	1079.6115	V	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
23	2305.2690	1153.1381	0	0	2287.2584	1144.1328	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
24							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 3404.

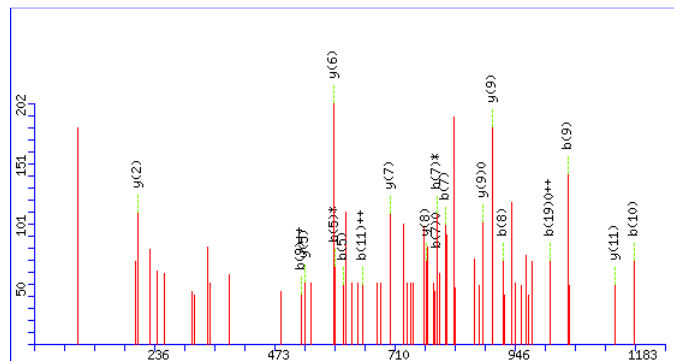
MS/MS Fragmentation of **VHEENTTIEELEALGESLGK**:

Found in **IP100021146;IP100644341;IP100647857**

Title: 4.1.1.263.4

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							20
2	237.1346	119.0709	0	0	0	0	H	2099.0139	1050.0106	2081.9873	1041.4973	2081.0033	1041.0053	19
3	366.1772	183.5922	0	0	348.1666	174.5870	E	1961.9550	981.4811	1944.9284	972.9678	1943.9444	972.4758	18
4	495.2198	248.1135	0	0	477.2092	239.1082	E	1832.9124	916.9598	1815.8858	908.4466	1814.9018	907.9545	17
5	609.2627	305.1350	592.2362	296.6217	591.2522	296.1297	N	1703.8698	852.4385	1686.8432	843.9253	1685.8592	843.4332	16
6	710.3104	355.6588	693.2838	347.1456	692.2998	346.6536	T	1589.8269	795.4171	1572.8003	786.9038	1571.8163	786.4118	15
7	811.3581	406.1827	794.3315	397.6694	793.3475	397.1774	T	1488.7792	744.8932	1471.7526	736.3800	1470.7686	735.8879	14
8	924.4421	462.7247	907.4156	454.2114	906.4316	453.7194	I	1387.7315	694.3694	1370.7050	685.8561	1369.7209	685.3641	13
9	1053.4847	527.2460	1036.4582	518.7327	1035.4742	518.2407	E	1274.6474	637.8274	1257.6209	629.3141	1256.6369	628.8221	12
10	1182.5273	591.7673	1165.5008	583.2540	1164.5168	582.7620	E	1145.6048	573.3061	1128.5783	564.7928	1127.5943	564.3008	11
11	1295.6114	648.3093	1278.5848	639.7961	1277.6008	639.3040	L	1016.5623	508.7848	999.5357	500.2715	998.5517	499.7795	10
12	1424.6540	712.8306	1407.6274	704.3174	1406.6434	703.8253	E	903.4782	452.2427	886.4516	443.7295	885.4676	443.2374	9
13	1495.6911	748.3492	1478.6645	739.8359	1477.6805	739.3439	A	774.4356	387.7214	757.4090	379.2082	756.4250	378.7162	8
14	1608.7752	804.8912	1591.7486	796.3779	1590.7646	795.8859	L	703.3985	352.2029	686.3719	343.6896	685.3879	343.1976	7
15	1665.7966	833.4019	1648.7701	824.8887	1647.7861	824.3967	G	590.3144	295.6608	573.2879	287.1476	572.3039	286.6556	6
16	1794.8392	897.9232	1777.8127	889.4100	1776.8287	888.9180	E	533.2930	267.1501	516.2664	258.6368	515.2824	258.1448	5
17	1881.8712	941.4393	1864.8447	932.9260	1863.8607	932.4340	S	404.2504	202.6288	387.2238	194.1155	386.2398	193.6235	4
18	1994.9553	997.9813	1977.9288	989.4680	1976.9447	988.9760	L	317.2183	159.1128	300.1918	150.5995	0	0	3
19	2051.9768	1026.4920	2034.9502	1017.9787	2033.9662	1017.4867	G	204.1343	102.5708	187.1077	94.0575	0	0	2
20							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 3454.

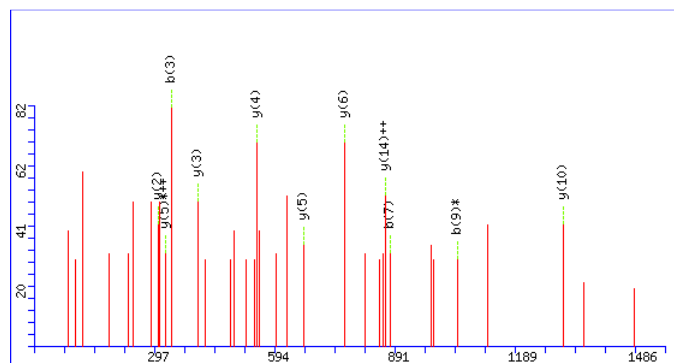
MS/MS Fragmentation of **ELPELWLQGNEFDFTDFVCK: 57.021465@C:20**

Found in **IP100019175;IP100216547**

Title: 5.1.1.64.8

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							21
2	243.1339	122.0706	0	0	225.1234	113.0653	L	2489.1516	1245.0794	2472.1250	1236.5662	2471.1410	1236.0741	20
3	340.1867	170.5970	0	0	322.1761	161.5917	P	2376.0675	1188.5374	2359.0410	1180.0241	2358.0570	1179.5321	19
4	469.2293	235.1183	0	0	451.2187	226.1130	E	2279.0148	1140.0110	2261.9882	1131.4977	2261.0042	1131.0057	18
5	582.3134	291.6603	0	0	564.3028	282.6550	L	2149.9722	1075.4897	2132.9456	1066.9764	2131.9616	1066.4844	17
6	768.3927	384.7000	0	0	750.3821	375.6947	W	2036.8881	1018.9477	2019.8615	1010.4344	2018.8775	1009.9424	16
7	881.4767	441.2420	0	0	863.4662	432.2367	L	1850.8088	925.9080	1833.7822	917.3948	1832.7982	916.9027	15
8	938.4982	469.7527	0	0	920.4876	460.7475	G	1737.7247	869.3660	1720.6982	860.8527	1719.7142	860.3607	14
9	1066.5568	533.7820	1049.5302	525.2687	1048.5462	524.7767	Q	1680.7033	840.8553	1663.6767	832.3420	1662.6927	831.8500	13
10	1180.5997	590.8035	1163.5732	582.2902	1162.5891	581.7982	N	1552.6447	776.8260	1535.6181	768.3127	1534.6341	767.8207	12
11	1309.6423	655.3248	1292.6157	646.8115	1291.6317	646.3195	E	1438.6018	719.8045	1421.5752	711.2912	1420.5912	710.7992	11
12	1456.7107	728.8590	1439.6842	720.3457	1438.7001	719.8537	F	1309.5592	655.2832	1292.5326	646.7699	1291.5486	646.2779	10
13	1571.7377	786.3725	1554.7111	777.8592	1553.7271	777.3672	D	1162.4907	581.7490	1145.4642	573.2357	1144.4802	572.7437	9
14	1718.8061	859.9067	1701.7795	851.3934	1700.7955	850.9014	F	1047.4638	524.2355	1030.4373	515.7223	1029.4532	515.2303	8
15	1849.8465	925.4269	1832.8200	916.9136	1831.8360	916.4216	M	900.3954	450.7013	883.3688	442.1881	882.3848	441.6961	7
16	1950.8942	975.9508	1933.8677	967.4375	1932.8837	966.9455	T	769.3549	385.1811	752.3284	376.6678	751.3443	376.1758	6
17	2065.9212	1033.4642	2048.8946	1024.9509	2047.9106	1024.4589	D	668.3072	334.6573	651.2807	326.1440	650.2967	325.6520	5
18	2212.9896	1106.9984	2195.9630	1098.4852	2194.9790	1097.9931	F	553.2803	277.1438	536.2537	268.6305	0	0	4
19	2312.0580	1156.5326	2295.0314	1148.0194	2294.0474	1147.5274	V	406.2119	203.6096	389.1853	195.0963	0	0	3
20	2472.0886	1236.5480	2455.0621	1228.0347	2454.0781	1227.5427	C	307.1435	154.0754	290.1169	145.5621	0	0	2
21							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 3624.

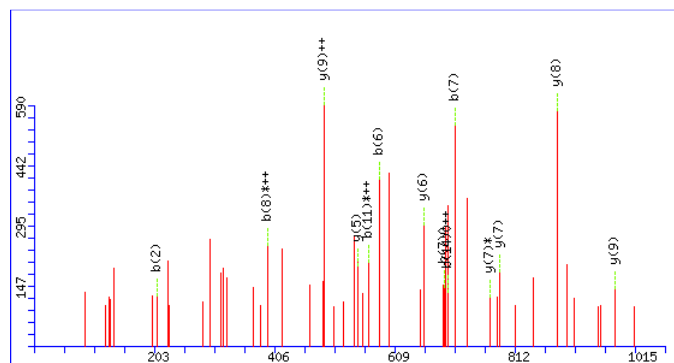
MS/MS Fragmentation of **AHSTGEQPPQLSLATR**:

Found in **IP100032388;IP100788867;IP100788897;IP100909107;IP101009658**

Title: 2.1.1.628.7

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120208ry¥120208ry_Tig120slc-P8_2.2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							16
2	209.1033	105.0553	0	0	0	0	H	1621.8293	811.4183	1604.8027	802.9050	1603.8187	802.4130	15
3	296.1353	148.5713	0	0	278.1248	139.5660	S	1484.7703	742.8888	1467.7438	734.3755	1466.7598	733.8835	14
4	397.1830	199.0951	0	0	379.1724	190.0899	T	1397.7383	699.3728	1380.7118	690.8595	1379.7278	690.3675	13
5	454.2045	227.6059	0	0	436.1939	218.6006	G	1296.6906	648.8490	1279.6641	640.3357	1278.6801	639.8437	12
6	583.2471	292.1272	0	0	565.2365	283.1219	E	1239.6692	620.3382	1222.6426	611.8250	1221.6586	611.3329	11
7	711.3056	356.1565	694.2791	347.6432	693.2951	347.1512	Q	1110.6266	555.8169	1093.6000	547.3037	1092.6160	546.8116	10
8	808.3584	404.6828	791.3319	396.1696	790.3478	395.6776	P	982.5680	491.7876	965.5415	483.2744	964.5574	482.7824	9
9	905.4112	453.2092	888.3846	444.6959	887.4006	444.2039	P	885.5152	443.2613	868.4887	434.7480	867.5047	434.2560	8
10	1033.4698	517.2385	1016.4432	508.7252	1015.4592	508.2332	Q	788.4625	394.7349	771.4359	386.2216	770.4519	385.7296	7
11	1146.5538	573.7805	1129.5273	565.2673	1128.5432	564.7753	L	660.4039	330.7056	643.3774	322.1923	642.3933	321.7003	6
12	1233.5858	617.2966	1216.5593	608.7833	1215.5753	608.2913	S	547.3198	274.1636	530.2933	265.6503	529.3093	265.1583	5
13	1346.6699	673.8386	1329.6434	665.3253	1328.6593	664.8333	L	460.2878	230.6475	443.2613	222.1343	442.2772	221.6423	4
14	1417.7070	709.3571	1400.6805	700.8439	1399.6965	700.3519	A	347.2037	174.1055	330.1772	165.5922	329.1932	165.1002	3
15	1518.7547	759.8810	1501.7281	751.3677	1500.7441	750.8757	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
16							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 4004.

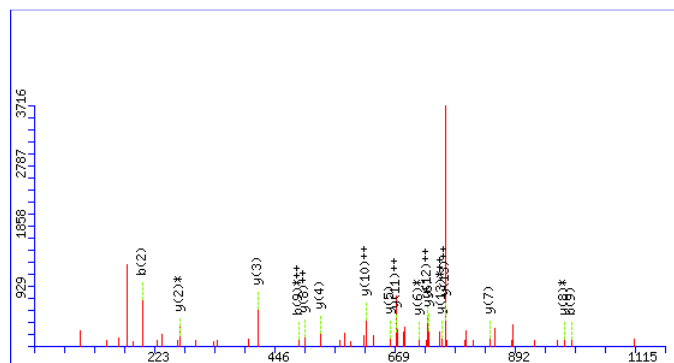
MS/MS Fragmentation of **SLALDIDRDAEDQNR**:

Found in **IP100009772;IP100396263;IP100746666;IP100939527;IP100984435**

Title: 2.1.1.1926.7

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							15
2	201.1234	101.0653	0	0	183.1128	92.0600	L	1643.7984	822.4028	1626.7718	813.8895	1625.7878	813.3975	14
3	272.1605	136.5839	0	0	254.1499	127.5786	A	1530.7143	765.8608	1513.6877	757.3475	1512.7037	756.8555	13
4	385.2445	193.1259	0	0	367.2340	184.1206	L	1459.6772	730.3422	1442.6506	721.8290	1441.6666	721.3369	12
5	500.2715	250.6394	0	0	482.2609	241.6341	D	1346.5931	673.8002	1329.5666	665.2869	1328.5825	664.7949	11
6	613.3556	307.1814	0	0	595.3450	298.1761	I	1231.5662	616.2867	1214.5396	607.7734	1213.5556	607.2814	10
7	728.3825	364.6949	0	0	710.3719	355.6896	D	1118.4821	559.7447	1101.4556	551.2314	1100.4715	550.7394	9
8	884.4836	442.7454	867.4571	434.2322	866.4730	433.7402	R	1003.4552	502.2312	986.4286	493.7179	985.4446	493.2259	8
9	999.5106	500.2589	982.4840	491.7456	981.5000	491.2536	D	847.3540	424.1807	830.3275	415.6674	829.3435	415.1754	7
10	1070.5477	535.7775	1053.5211	527.2642	1052.5371	526.7722	A	732.3271	366.6672	715.3006	358.1539	714.3165	357.6619	6
11	1199.5903	600.2988	1182.5637	591.7855	1181.5797	591.2935	E	661.2900	331.1486	644.2634	322.6354	643.2794	322.1434	5
12	1314.6172	657.8122	1297.5907	649.2990	1296.6066	648.8070	D	532.2474	266.6273	515.2209	258.1141	514.2368	257.6221	4
13	1442.6758	721.8415	1425.6492	713.3283	1424.6652	712.8362	Q	417.2205	209.1139	400.1939	200.6006	0	0	3
14	1556.7187	778.8630	1539.6922	770.3497	1538.7081	769.8577	N	289.1619	145.0846	272.1353	136.5713	0	0	2
15							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 4149.

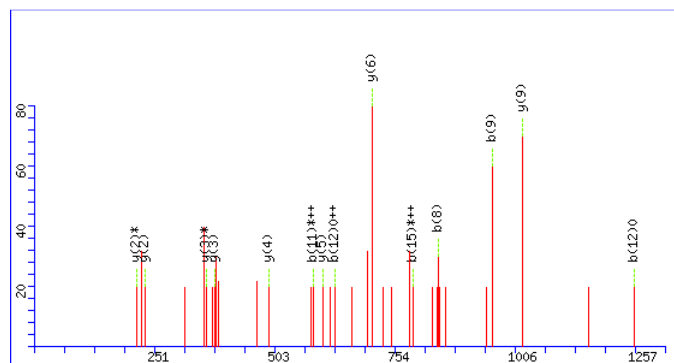
MS/MS Fragmentation of **RLSQPAGGLDSITNIFGR**: 79.966331@S:3

Found in **IP100432751;IP100446614;IP100470446;IP100871602;IP100979030**

Title: 4.1.1.2404.4

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120208ry¥120208ry_Tig120slc-P8_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	157.1084	79.0578	140.0818	70.5446	0	0	R							19
2	270.1925	135.5999	253.1659	127.0866	0	0	L	1938.9685	969.9879	1921.9419	961.4746	1920.9579	960.9826	18
3	437.1908	219.0990	420.1643	210.5858	419.1802	210.0938	S	1825.8844	913.4458	1808.8579	904.9326	1807.8738	904.4406	17
4	565.2494	283.1283	548.2228	274.6151	547.2388	274.1230	Q	1658.8860	829.9467	1641.8595	821.4334	1640.8755	820.9414	16
5	662.3022	331.6547	645.2756	323.1414	644.2916	322.6494	P	1530.8275	765.9174	1513.8009	757.4041	1512.8169	756.9121	15
6	733.3393	367.1733	716.3127	358.6600	715.3287	358.1680	A	1433.7747	717.3910	1416.7482	708.8777	1415.7641	708.3857	14
7	790.3607	395.6840	773.3342	387.1707	772.3502	386.6787	G	1362.7376	681.8724	1345.7110	673.3592	1344.7270	672.8672	13
8	847.3822	424.1947	830.3556	415.6815	829.3716	415.1895	G	1305.7161	653.3617	1288.6896	644.8484	1287.7056	644.3564	12
9	960.4663	480.7368	943.4397	472.2235	942.4557	471.7315	L	1248.6947	624.8510	1231.6681	616.3377	1230.6841	615.8457	11
10	1073.5503	537.2788	1056.5238	528.7655	1055.5398	528.2735	L	1135.6106	568.3089	1118.5840	559.7957	1117.6000	559.3037	10
11	1188.5773	594.7923	1171.5507	586.2790	1170.5667	585.7870	D	1022.5265	511.7669	1005.5000	503.2536	1004.5160	502.7616	9
12	1275.6093	638.3083	1258.5827	629.7950	1257.5987	629.3030	S	907.4996	454.2534	890.4730	445.7402	889.4890	445.2482	8
13	1388.6934	694.8503	1371.6668	686.3370	1370.6828	685.8450	I	820.4676	410.7374	803.4410	402.2241	802.4570	401.7321	7
14	1489.7410	745.3742	1472.7145	736.8609	1471.7305	736.3689	T	707.3835	354.1954	690.3570	345.6821	689.3729	345.1901	6
15	1603.7840	802.3956	1586.7574	793.8823	1585.7734	793.3903	N	606.3358	303.6715	589.3093	295.1583	0	0	5
16	1716.8680	858.9377	1699.8415	850.4244	1698.8575	849.9324	I	492.2929	246.6501	475.2663	238.1368	0	0	4
17	1863.9364	932.4719	1846.9099	923.9586	1845.9259	923.4666	F	379.2088	190.1081	362.1823	181.5948	0	0	3
18	1920.9579	960.9826	1903.9314	952.4693	1902.9473	951.9773	G	232.1404	116.5738	215.1139	108.0606	0	0	2
19							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 4193.

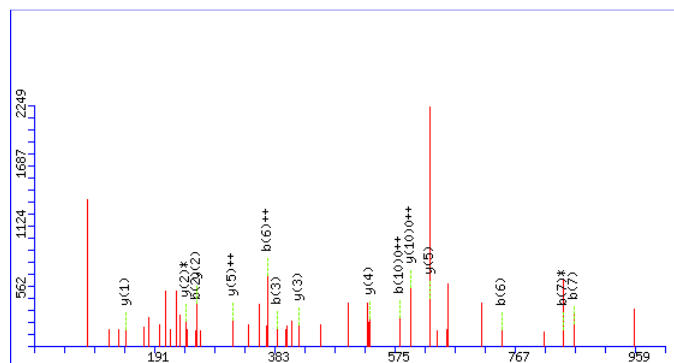
MS/MS Fragmentation of **LFQEDNDIPLYLK**:

Found in **IP100306720;IP100796142**

Title: 3.1.1.1826.3

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							13
2	261.1598	131.0835	0	0	0	0	F	1494.7475	747.8774	1477.7209	739.3641	1476.7369	738.8721	12
3	389.2183	195.1128	372.1918	186.5995	0	0	Q	1347.6791	674.3432	1330.6525	665.8299	1329.6685	665.3379	11
4	518.2609	259.6341	501.2344	251.1208	500.2504	250.6288	E	1219.6205	610.3139	1202.5939	601.8006	1201.6099	601.3086	10
5	633.2879	317.1476	616.2613	308.6343	615.2773	308.1423	D	1090.5779	545.7926	1073.5514	537.2793	1072.5673	536.7873	9
6	747.3308	374.1690	730.3042	365.6558	729.3202	365.1638	N	975.5510	488.2791	958.5244	479.7658	957.5404	479.2738	8
7	862.3577	431.6825	845.3312	423.1692	844.3472	422.6772	D	861.5080	431.2577	844.4815	422.7444	843.4975	422.2524	7
8	975.4418	488.2245	958.4153	479.7113	957.4312	479.2193	I	746.4811	373.7442	729.4545	365.2309	0	0	6
9	1072.4946	536.7509	1055.4680	528.2376	1054.4840	527.7456	P	633.3970	317.2022	616.3705	308.6889	0	0	5
10	1185.5786	593.2930	1168.5521	584.7797	1167.5681	584.2877	L	536.3443	268.6758	519.3177	260.1625	0	0	4
11	1348.6420	674.8246	1331.6154	666.3113	1330.6314	665.8193	Y	423.2602	212.1337	406.2336	203.6205	0	0	3
12	1461.7260	731.3666	1444.6995	722.8534	1443.7155	722.3614	L	260.1969	130.6021	243.1703	122.0888	0	0	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 4243.

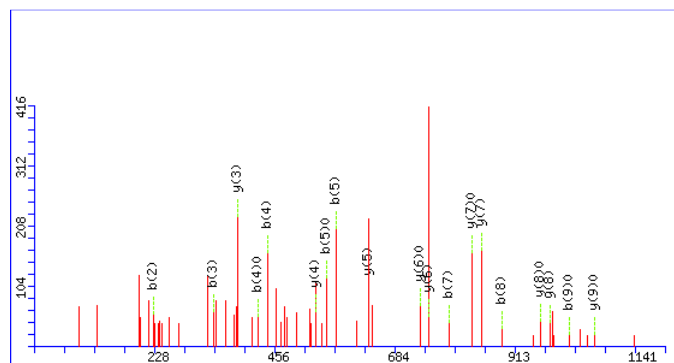
MS/MS Fragmentation of **LLDTMVDTFLLQK**:

Found in **IP100178359;IP100446176;IP100513817;IP100514558;IP100549361;IP100983677;IP100984909**

Title: 3.1.1.4073.2

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							12
2	227.1754	114.0913	0	0	0	0	L	1310.6661	655.8367	1293.6395	647.3234	1292.6555	646.8314	11
3	342.2023	171.6048	0	0	324.1918	162.5995	D	1197.5820	599.2946	1180.5555	590.7814	1179.5714	590.2894	10
4	443.2500	222.1287	0	0	425.2395	213.1234	T	1082.5551	541.7812	1065.5285	533.2679	1064.5445	532.7759	9
5	574.2905	287.6489	0	0	556.2799	278.6436	M	981.5074	491.2573	964.4808	482.7441	963.4968	482.2520	8
6	673.3589	337.1831	0	0	655.3484	328.1778	V	850.4669	425.7371	833.4403	417.2238	832.4563	416.7318	7
7	788.3859	394.6966	0	0	770.3753	385.6913	D	751.3985	376.2029	734.3719	367.6896	733.3879	367.1976	6
8	889.4335	445.2204	0	0	871.4230	436.2151	T	636.3715	318.6894	619.3450	310.1761	618.3610	309.6841	5
9	1036.5020	518.7546	0	0	1018.4914	509.7493	F	535.3239	268.1656	518.2973	259.6523	0	0	4
10	1149.5860	575.2967	0	0	1131.5755	566.2914	L	388.2554	194.6314	371.2289	186.1181	0	0	3
11	1277.6446	639.3259	1260.6181	630.8127	1259.6340	630.3207	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 4245.

MS/MS Fragmentation of **AVTELGRPDAEYWNSQK**:

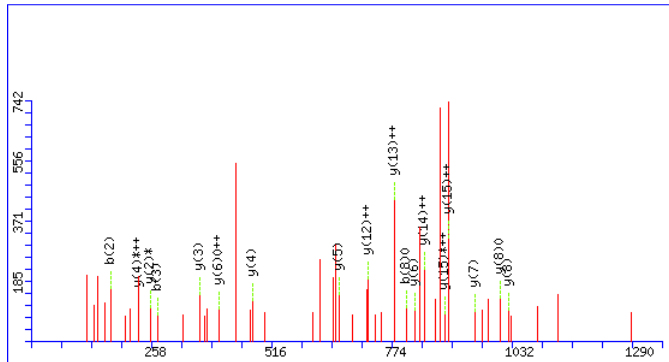
Found in

IP100010397,IP100107714,IP100472169,IP100473139,IP100738107,IP100887633,IP100929265,IP100955414,IP100956491,IP100976091,IP101018156,IP101019012,IP101019101

Title: 2.1.1.2492.10

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120201ry¥120201ry_aHDF1388-P9_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							17
2	171.1128	86.0600	0	0	0	0	V	1892.9137	946.9605	1875.8872	938.4472	1874.9032	937.9552	16
3	272.1605	136.5839	0	0	254.1499	127.5786	T	1793.8453	897.4263	1776.8188	888.9130	1775.8347	888.4210	15
4	401.2031	201.1052	0	0	383.1925	192.0999	E	1692.7976	846.9025	1675.7711	838.3892	1674.7871	837.8972	14
5	514.2871	257.6472	0	0	496.2766	248.6419	L	1563.7550	782.3812	1546.7285	773.8679	1545.7445	773.3759	13
6	571.3086	286.1579	0	0	553.2980	277.1527	G	1450.6710	725.8391	1433.6444	717.3258	1432.6604	716.8338	12
7	727.4097	364.2085	710.3832	355.6952	709.3992	355.2032	R	1393.6495	697.3284	1376.6230	688.8151	1375.6389	688.3231	11
8	824.4625	412.7349	807.4359	404.2216	806.4519	403.7296	P	1237.5484	619.2778	1220.5218	610.7646	1219.5378	610.2726	10
9	939.4894	470.2483	922.4629	461.7351	921.4789	461.2431	D	1140.4956	570.7515	1123.4691	562.2382	1122.4851	561.7462	9
10	1010.5265	505.7669	993.5000	497.2536	992.5160	496.7616	A	1025.4687	513.2380	1008.4421	504.7247	1007.4581	504.2327	8
11	1139.5691	570.2882	1122.5426	561.7749	1121.5586	561.2829	E	954.4316	477.7194	937.4050	469.2061	936.4210	468.7141	7
12	1302.6325	651.8199	1285.6059	643.3066	1284.6219	642.8146	Y	825.3890	413.1981	808.3624	404.6849	807.3784	404.1928	6
13	1488.7118	744.8595	1471.6852	736.3462	1470.7012	735.8542	W	662.3256	331.6665	645.2991	323.1532	644.3151	322.6612	5
14	1602.7547	801.8810	1585.7281	793.3677	1584.7441	792.8757	N	476.2463	238.6268	459.2198	230.1135	458.2358	229.6215	4
15	1689.7867	845.3970	1672.7602	836.8837	1671.7762	836.3917	S	362.2034	181.6053	345.1769	173.0921	344.1928	172.6001	3
16	1817.8453	909.4263	1800.8188	900.9130	1799.8347	900.4210	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
17							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 4604.

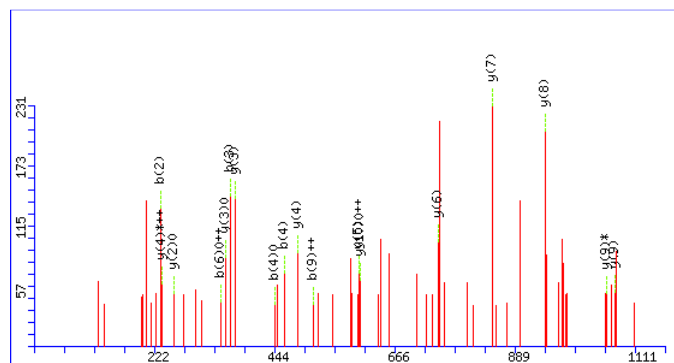
MS/MS Fragmentation of **SFEVVFNDPEK**:

Found in **IP100007956;IP100909604**

Title: 2.1.1.4090.11

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120212ry¥120212ry_aHDF1388-P9_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							11
2	235.1077	118.0575	0	0	217.0972	109.0522	F	1223.5943	612.3008	1206.5677	603.7875	1205.5837	603.2955	10
3	364.1503	182.5788	0	0	346.1397	173.5735	E	1076.5259	538.7666	1059.4993	530.2533	1058.5153	529.7613	9
4	463.2187	232.1130	0	0	445.2082	223.1077	V	947.4833	474.2453	930.4567	465.7320	929.4727	465.2400	8
5	562.2871	281.6472	0	0	544.2766	272.6419	V	848.4149	424.7111	831.3883	416.1978	830.4043	415.7058	7
6	709.3556	355.1814	0	0	691.3450	346.1761	F	749.3464	375.1769	732.3199	366.6636	731.3359	366.1716	6
7	823.3985	412.2029	806.3719	403.6896	805.3879	403.1976	N	602.2780	301.6427	585.2515	293.1294	584.2675	292.6374	5
8	938.4254	469.7163	921.3989	461.2031	920.4149	460.7111	D	488.2351	244.6212	471.2086	236.1079	470.2245	235.6159	4
9	1035.4782	518.2427	1018.4516	509.7295	1017.4676	509.2374	P	373.2082	187.1077	356.1816	178.5944	355.1976	178.1024	3
10	1164.5208	582.7640	1147.4942	574.2508	1146.5102	573.7587	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
11							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 4694.

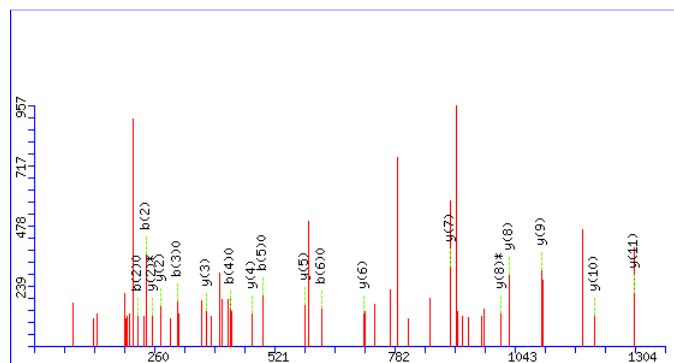
MS/MS Fragmentation of **EISDAQWEDVVQK**:

Found in **IP100157176**

Title: 2.1.1.3713.8

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							13
2	243.1339	122.0706	0	0	225.1234	113.0653	I	1417.6958	709.3515	1400.6692	700.8383	1399.6852	700.3462	12
3	330.1660	165.5866	0	0	312.1554	156.5813	S	1304.6117	652.8095	1287.5852	644.2962	1286.6012	643.8042	11
4	445.1929	223.1001	0	0	427.1823	214.0948	D	1217.5797	609.2935	1200.5531	600.7802	1199.5691	600.2882	10
5	516.2300	258.6186	0	0	498.2195	249.6134	A	1102.5528	551.7800	1085.5262	543.2667	1084.5422	542.7747	9
6	644.2886	322.6479	627.2620	314.1347	626.2780	313.6427	Q	1031.5156	516.2615	1014.4891	507.7482	1013.5051	507.2562	8
7	830.3679	415.6876	813.3414	407.1743	812.3573	406.6823	W	903.4571	452.2322	886.4305	443.7189	885.4465	443.2269	7
8	959.4105	480.2089	942.3840	471.6956	941.3999	471.2036	E	717.3777	359.1925	700.3512	350.6792	699.3672	350.1872	6
9	1074.4374	537.7224	1057.4109	529.2091	1056.4269	528.7171	D	588.3352	294.6712	571.3086	286.1579	570.3246	285.6659	5
10	1173.5059	587.2566	1156.4793	578.7433	1155.4953	578.2513	V	473.3082	237.1577	456.2817	228.6445	0	0	4
11	1272.5743	636.7908	1255.5477	628.2775	1254.5637	627.7855	V	374.2398	187.6235	357.2132	179.1103	0	0	3
12	1400.6329	700.8201	1383.6063	692.3068	1382.6223	691.8148	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 4787.

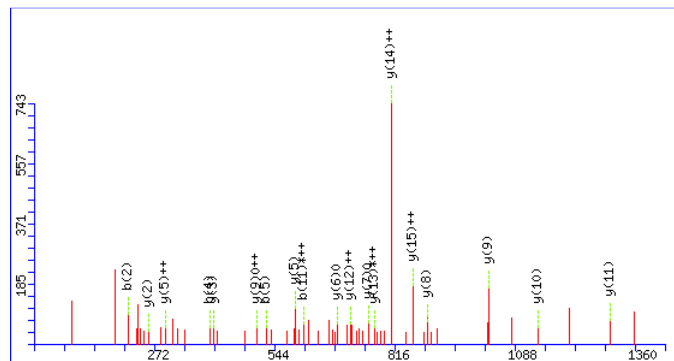
MS/MS Fragmentation of **LVGQQYLHDALGEFIK**:

Found in **IP100006854;IP100946817**

Title: 3.1.1.4335.3

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4.3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							16
2	213.1598	107.0835	0	0	0	0	V	1717.8908	859.4490	1700.8642	850.9358	1699.8802	850.4438	15
3	270.1812	135.5942	0	0	0	0	G	1618.8224	809.9148	1601.7958	801.4016	1600.8118	800.9095	14
4	398.2398	199.6235	381.2132	191.1103	0	0	Q	1561.8009	781.4041	1544.7744	772.8908	1543.7904	772.3988	13
5	526.2984	263.6528	509.2718	255.1396	0	0	Q	1433.7423	717.3748	1416.7158	708.8615	1415.7318	708.3695	12
6	689.3617	345.1845	672.3352	336.6712	0	0	Y	1305.6838	653.3455	1288.6572	644.8322	1287.6732	644.3402	11
7	802.4458	401.7265	785.4192	393.2132	0	0	L	1142.6204	571.8139	1125.5939	563.3006	1124.6099	562.8086	10
8	939.5047	470.2560	922.4781	461.7427	0	0	H	1029.5364	515.2718	1012.5098	506.7585	1011.5258	506.2665	9
9	1054.5316	527.7694	1037.5051	519.2562	1036.5211	518.7642	D	892.4775	446.7424	875.4509	438.2291	874.4669	437.7371	8
10	1125.5687	563.2880	1108.5422	554.7747	1107.5582	554.2827	A	777.4505	389.2289	760.4240	380.7156	759.4400	380.2236	7
11	1238.6528	619.8300	1221.6263	611.3168	1220.6422	610.8248	L	706.4134	353.7103	689.3869	345.1971	688.4028	344.7051	6
12	1295.6743	648.3408	1278.6477	639.8275	1277.6637	639.3355	G	593.3293	297.1683	576.3028	288.6550	575.3188	288.1630	5
13	1424.7169	712.8621	1407.6903	704.3488	1406.7063	703.8568	E	536.3079	268.6576	519.2813	260.1443	518.2973	259.6523	4
14	1571.7853	786.3963	1554.7587	777.8830	1553.7747	777.3910	F	407.2653	204.1363	390.2387	195.6230	0	0	3
15	1684.8693	842.9383	1667.8428	834.4250	1666.8588	833.9330	I	260.1969	130.6021	243.1703	122.0888	0	0	2
16							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 4831.

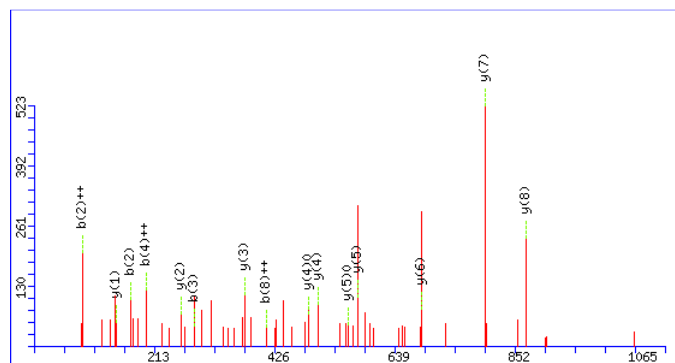
MS/MS Fragmentation of **VAILAELDK**:

Found in **IP100000330;IP100829819**

Title: 2.1.1.3963.2

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							9
2	171.1128	86.0600	0	0	0	0	A	872.5088	436.7580	855.4822	428.2447	854.4982	427.7527	8
3	284.1969	142.6021	0	0	0	0	I	801.4716	401.2395	784.4451	392.7262	783.4611	392.2342	7
4	397.2809	199.1441	0	0	0	0	L	688.3876	344.6974	671.3610	336.1842	670.3770	335.6921	6
5	468.3180	234.6627	0	0	0	0	A	575.3035	288.1554	558.2770	279.6421	557.2930	279.1501	5
6	597.3606	299.1840	0	0	579.3501	290.1787	E	504.2664	252.6368	487.2399	244.1236	486.2558	243.6316	4
7	710.4447	355.7260	0	0	692.4341	346.7207	L	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
8	825.4716	413.2395	0	0	807.4611	404.2342	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
9							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 4950.

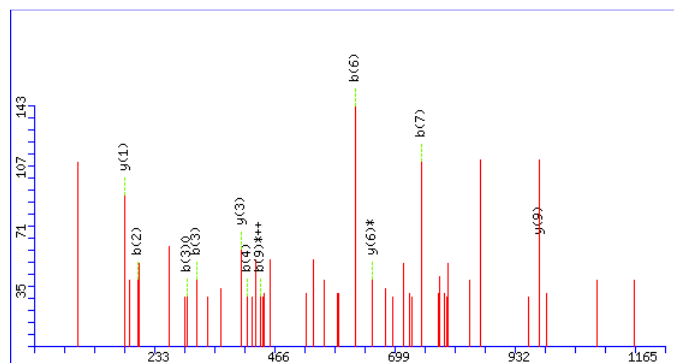
MS/MS Fragmentation of **SLDPLPQAAMPR: 0.984016@Q:7**

Found in **IP100062237**

Title: 4.1.1.803.3

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							12
2	201.1234	101.0653	0	0	183.1128	92.0600	L	1209.6296	605.3184	1192.6031	596.8052	1191.6191	596.3132	11
3	316.1503	158.5788	0	0	298.1397	149.5735	D	1096.5456	548.7764	1079.5190	540.2631	1078.5350	539.7711	10
4	413.2031	207.1052	0	0	395.1925	198.0999	P	981.5186	491.2629	964.4921	482.7497	0	0	9
5	526.2871	263.6472	0	0	508.2766	254.6419	L	884.4659	442.7366	867.4393	434.2233	0	0	8
6	623.3399	312.1736	0	0	605.3293	303.1683	P	771.3818	386.1945	754.3552	377.6813	0	0	7
7	752.3825	376.6949	735.3559	368.1816	734.3719	367.6896	Q	674.3290	337.6681	657.3025	329.1549	0	0	6
8	823.4196	412.2134	806.3931	403.7002	805.4090	403.2082	A	545.2864	273.1469	528.2599	264.6336	0	0	5
9	894.4567	447.7320	877.4302	439.2187	876.4462	438.7267	A	474.2493	237.6283	457.2228	229.1150	0	0	4
10	1025.4972	513.2522	1008.4707	504.7390	1007.4866	504.2470	M	403.2122	202.1097	386.1857	193.5965	0	0	3
11	1122.5500	561.7786	1105.5234	553.2654	1104.5394	552.7733	P	272.1717	136.5895	255.1452	128.0762	0	0	2
12							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 4988.

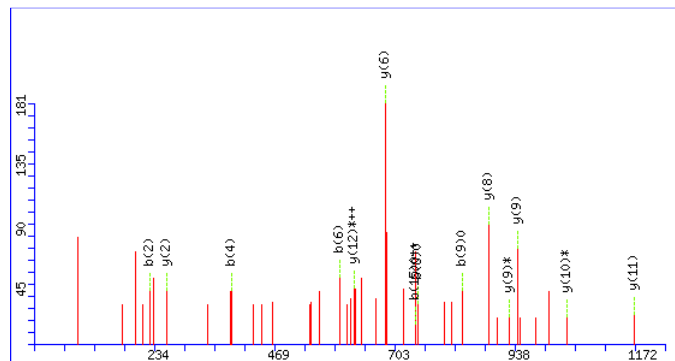
MS/MS Fragmentation of **LLGTPDIGSISNLLIK**:

Found in **IP100009286;IP100218500;IP100982112**

Title: 4.1.1.374.2

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							16
2	227.1754	114.0913	0	0	0	0	L	1540.8945	770.9509	1523.8679	762.4376	1522.8839	761.9456	15
3	284.1969	142.6021	0	0	0	0	G	1427.8104	714.4088	1410.7839	705.8956	1409.7999	705.4036	14
4	385.2445	193.1259	0	0	367.2340	184.1206	T	1370.7890	685.8981	1353.7624	677.3848	1352.7784	676.8928	13
5	482.2973	241.6523	0	0	464.2867	232.6470	P	1269.7413	635.3743	1252.7147	626.8610	1251.7307	626.3690	12
6	597.3243	299.1658	0	0	579.3137	290.1605	D	1172.6885	586.8479	1155.6620	578.3346	1154.6779	577.8426	11
7	710.4083	355.7078	0	0	692.3978	346.7025	I	1057.6616	529.3344	1040.6350	520.8211	1039.6510	520.3291	10
8	767.4298	384.2185	0	0	749.4192	375.2132	G	944.5775	472.7924	927.5510	464.2791	926.5669	463.7871	9
9	854.4618	427.7345	0	0	836.4512	418.7293	S	887.5560	444.2817	870.5295	435.7684	869.5455	435.2764	8
10	967.5459	484.2766	0	0	949.5353	475.2713	I	800.5240	400.7656	783.4975	392.2524	782.5135	391.7604	7
11	1054.5779	527.7926	0	0	1036.5673	518.7873	S	687.4400	344.2236	670.4134	335.7103	669.4294	335.2183	6
12	1168.6208	584.8141	1151.5943	576.3008	1150.6103	575.8088	N	600.4079	300.7076	583.3814	292.1943	0	0	5
13	1281.7049	641.3561	1264.6783	632.8428	1263.6943	632.3508	L	486.3650	243.6861	469.3384	235.1729	0	0	4
14	1394.7890	697.8981	1377.7624	689.3848	1376.7784	688.8928	L	373.2809	187.1441	356.2544	178.6308	0	0	3
15	1507.8730	754.4401	1490.8465	745.9269	1489.8625	745.4349	I	260.1969	130.6021	243.1703	122.0888	0	0	2
16							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 5020.

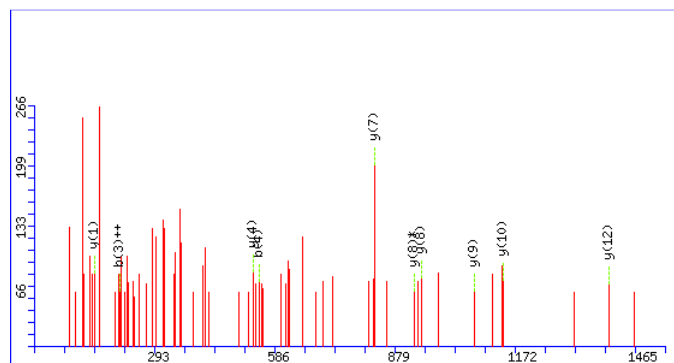
MS/MS Fragmentation of **SFWEEAELPAELFQK**:

Found in **IP100216142;IP100816670;IP100816801;IP101022599**

Title: 4.1.1.746.11

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							15
2	235.1077	118.0575	0	0	217.0972	109.0522	F	1736.8530	868.9301	1719.8265	860.4169	1718.8425	859.9249	14
3	421.1870	211.0972	0	0	403.1765	202.0919	W	1589.7846	795.3959	1572.7581	786.8827	1571.7740	786.3907	13
4	550.2296	275.6185	0	0	532.2191	266.6132	E	1403.7053	702.3563	1386.6787	693.8430	1385.6947	693.3510	12
5	679.2722	340.1397	0	0	661.2617	331.1345	E	1274.6627	637.8350	1257.6361	629.3217	1256.6521	628.8297	11
6	750.3093	375.6583	0	0	732.2988	366.6530	A	1145.6201	573.3137	1128.5936	564.8004	1127.6095	564.3084	10
7	879.3519	440.1796	0	0	861.3414	431.1743	E	1074.5830	537.7951	1057.5564	529.2819	1056.5724	528.7898	9
8	992.4360	496.7216	0	0	974.4254	487.7163	L	945.5404	473.2738	928.5138	464.7606	927.5298	464.2686	8
9	1089.4888	545.2480	0	0	1071.4782	536.2427	P	832.4563	416.7318	815.4298	408.2185	814.4458	407.7265	7
10	1160.5259	580.7666	0	0	1142.5153	571.7613	A	735.4036	368.2054	718.3770	359.6921	717.3930	359.2001	6
11	1289.5685	645.2879	0	0	1271.5579	636.2826	E	664.3665	332.6869	647.3399	324.1736	646.3559	323.6816	5
12	1402.6525	701.8299	0	0	1384.6420	692.8246	L	535.3239	268.1656	518.2973	259.6523	0	0	4
13	1549.7209	775.3641	0	0	1531.7104	766.3588	F	422.2398	211.6235	405.2132	203.1103	0	0	3
14	1677.7795	839.3934	1660.7530	830.8801	1659.7690	830.3881	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
15							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 5037.

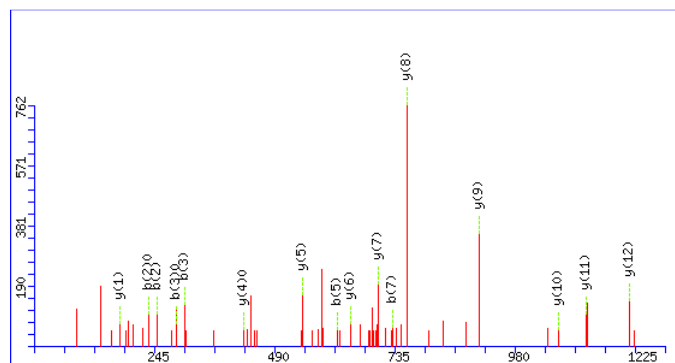
MS/MS Fragmentation of **YSGYFGGVLTALSR**:

Found in **IP100030128;IP100945621;IP100946167**

Title: 2.1.1.4390.10

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	164.0706	82.5389	0	0	0	0	Y							13
2	251.1028	126.0550	0	0	233.0921	117.0497	S	1214.6164	607.8118	1197.5899	599.2986	1196.6058	598.8066	12
3	308.1241	154.5657	0	0	290.1135	145.5604	G	1127.5844	564.2958	1110.5578	555.7826	1109.5738	555.2905	11
4	471.1874	236.0974	0	0	453.1769	227.0921	Y	1070.5629	535.7851	1053.5364	527.2718	1052.5524	526.7798	10
5	618.2558	309.6316	0	0	600.2453	300.6263	F	907.4996	454.2534	890.4730	445.7402	889.4890	445.2482	9
6	675.2773	338.1423	0	0	657.2667	329.1370	G	760.4312	380.7192	743.4046	372.2060	742.4206	371.7139	8
7	732.2988	366.6530	0	0	714.2882	357.6477	G	703.4097	352.2085	686.3832	343.6952	685.3992	343.2032	7
8	831.3672	416.1872	0	0	813.3566	407.1819	V	646.3883	323.6978	629.3617	315.1845	628.3777	314.6925	6
9	932.4149	466.7111	0	0	914.4043	457.7058	T	547.3198	274.1636	530.2933	265.6503	529.3093	265.1583	5
10	1003.4520	502.2296	0	0	985.4414	493.2243	A	446.2722	223.6397	429.2456	215.1264	428.2616	214.6344	4
11	1116.5360	558.7717	0	0	1098.5255	549.7664	L	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
12	1203.5681	602.2877	0	0	1185.5575	593.2824	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
13							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 5050.

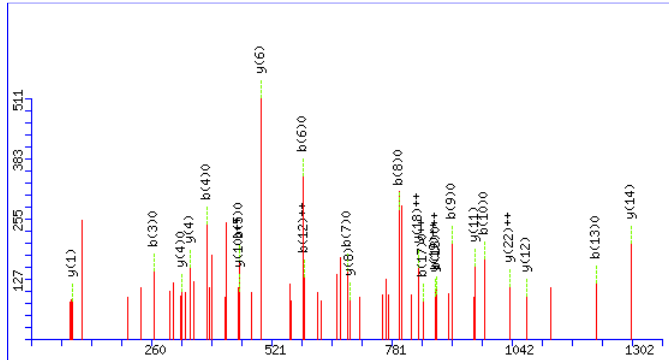
MS/MS Fragmentation of **EGPDAHPILAADGHPELQPDGHPGPQTA:**

Found in **IP100014478;IP100220749;IP100220751;IP100220755;IP100220757;IP100411446;IP100973410;IP101025617;IP101026519**

Title: 2.1.1.2279.9

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120212ry¥120212ry_aHDF1388-P9_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							28
2	187.0713	94.0393	0	0	169.0608	85.0340	G	2553.2117	1277.1095	0	0	2535.2011	1268.1042	27
3	284.1241	142.5657	0	0	266.1135	133.5604	P	2496.1902	1248.5988	0	0	2478.1797	1239.5935	26
4	399.1510	200.0792	0	0	381.1405	191.0739	D	2399.1375	1200.0724	0	0	2381.1269	1191.0671	25
5	470.1882	235.5977	0	0	452.1776	226.5924	A	2284.1105	1142.5589	0	0	2266.1000	1133.5536	24
6	607.2471	304.1272	0	0	589.2365	295.1219	H	2213.0734	1107.0403	0	0	2195.0628	1098.0351	23
7	704.2998	352.6536	0	0	686.2893	343.6483	P	2076.0145	1038.5109	0	0	2058.0039	1029.5056	22
8	817.3839	409.1956	0	0	799.3733	400.1903	I	1978.9617	989.9845	0	0	1960.9512	980.9792	21
9	930.4680	465.7376	0	0	912.4574	456.7323	L	1865.8777	933.4425	0	0	1847.8671	924.4372	20
10	1001.5051	501.2562	0	0	983.4945	492.2509	A	1752.7936	876.9004	0	0	1734.7830	867.8952	19
11	1072.5422	536.7747	0	0	1054.5316	527.7694	A	1681.7565	841.3819	0	0	1663.7459	832.3766	18
12	1187.5691	594.2882	0	0	1169.5586	585.2829	D	1610.7194	805.8633	0	0	1592.7088	796.8580	17
13	1244.5906	622.7989	0	0	1226.5800	613.7937	G	1495.6924	748.3499	0	0	1477.6819	739.3446	16
14	1381.6495	691.3284	0	0	1363.6389	682.3231	H	1438.6710	719.8391	0	0	1420.6604	710.8338	15
15	1478.7023	739.8548	0	0	1460.6917	730.8495	P	1301.6121	651.3097	0	0	1283.6015	642.3044	14
16	1607.7449	804.3761	0	0	1589.7343	795.3708	E	1204.5593	602.7833	0	0	1186.5487	593.7780	13
17	1720.8289	860.9181	0	0	1702.8184	851.9128	L	1075.5167	538.2620	0	0	1057.5061	529.2567	12
18	1777.8504	889.4288	0	0	1759.8398	880.4236	G	962.4326	481.7200	0	0	944.4221	472.7147	11
19	1874.9032	937.9552	0	0	1856.8926	928.9499	P	905.4112	453.2092	0	0	887.4006	444.2039	10
20	1989.9301	995.4687	0	0	1971.9195	986.4634	D	808.3584	404.6828	0	0	790.3478	395.6776	9
21	2046.9516	1023.9794	0	0	2028.9410	1014.9741	G	693.3315	347.1694	0	0	675.3209	338.1641	8
22	2184.0105	1092.5089	0	0	2165.9999	1083.5036	H	636.3100	318.6586	0	0	618.2994	309.6534	7
23	2281.0632	1141.0353	0	0	2263.0527	1132.0300	P	499.2511	250.1292	0	0	481.2405	241.1239	6
24	2338.0847	1169.5460	0	0	2320.0741	1160.5407	G	402.1983	201.6028	0	0	384.1878	192.5975	5
25	2435.1375	1218.0724	0	0	2417.1269	1209.0671	P	345.1769	173.0921	0	0	327.1663	164.0868	4
26	2492.1589	1246.5831	0	0	2474.1484	1237.5778	G	248.1241	124.5657	0	0	230.1135	115.5604	3
27	2593.2066	1297.1069	0	0	2575.1960	1288.1017	T	191.1026	96.0550	0	0	173.0921	87.0497	2
28							A	90.0550	45.5311	0	0	0	0	1

Peptide View

Peptide: **5442.**

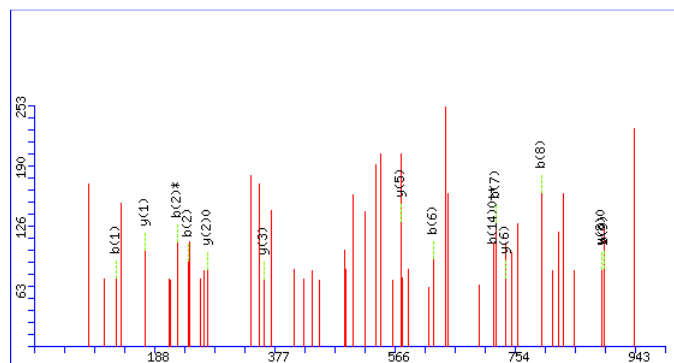
MS/MS Fragmentation of **KLGVQTVAVYSEADR**:

Found in **IP100024580;IP100945717;IP100985037**

Title: 2.1.1.1642.6

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120206ry¥120206ry_aHDF1419-P10_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	129.1022	65.0548	112.0757	56.5415	0	0	K							15
2	242.1863	121.5968	225.1598	113.0835	0	0	L	1507.7751	754.3912	1490.7486	745.8779	1489.7645	745.3859	14
3	299.2078	150.1075	282.1812	141.5942	0	0	G	1394.6910	697.8492	1377.6645	689.3359	1376.6805	688.8439	13
4	398.2762	199.6417	381.2496	191.1285	0	0	V	1337.6696	669.3384	1320.6430	660.8251	1319.6590	660.3331	12
5	526.3348	263.6710	509.3082	255.1577	0	0	Q	1238.6012	619.8042	1221.5746	611.2909	1220.5906	610.7989	11
6	627.3824	314.1949	610.3559	305.6816	609.3719	305.1896	T	1110.5426	555.7749	1093.5160	547.2617	1092.5320	546.7696	10
7	726.4509	363.7291	709.4243	355.2158	708.4403	354.7238	V	1009.4949	505.2511	992.4684	496.7378	991.4843	496.2458	9
8	797.4880	399.2476	780.4614	390.7343	779.4774	390.2423	A	910.4265	455.7169	893.3999	447.2036	892.4159	446.7116	8
9	896.5564	448.7818	879.5298	440.2686	878.5458	439.7765	V	839.3894	420.1983	822.3628	411.6850	821.3788	411.1930	7
10	1059.6197	530.3135	1042.5932	521.8002	1041.6091	521.3082	Y	740.3210	370.6641	723.2944	362.1508	722.3104	361.6588	6
11	1146.6517	573.8295	1129.6252	565.3162	1128.6412	564.8242	S	577.2576	289.1325	560.2311	280.6192	559.2471	280.1272	5
12	1275.6943	638.3508	1258.6678	629.8375	1257.6838	629.3455	E	490.2256	245.6164	473.1991	237.1032	472.2150	236.6112	4
13	1346.7314	673.8694	1329.7049	665.3561	1328.7209	664.8641	A	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	3
14	1461.7584	731.3828	1444.7318	722.8696	1443.7478	722.3775	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
15							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 5530.

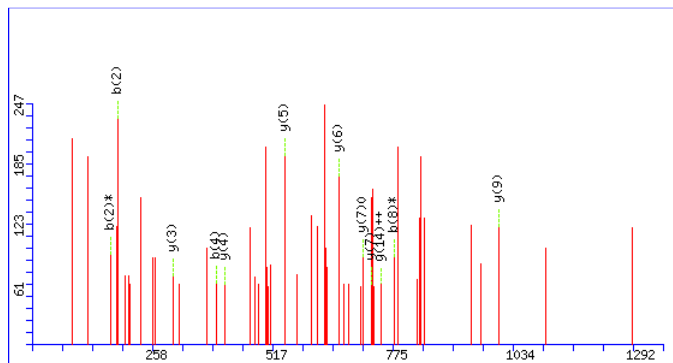
MS/MS Fragmentation of **QQLPISVTCIADEIGAR**: 57.021465@C:9

Found in **IP100240345**

Title: 3.1.1.3815.3

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2.3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							17
2	186.0873	93.5473	169.0608	85.0340	0	0	Q	1742.9105	871.9589	1725.8840	863.4456	1724.9000	862.9536	16
3	299.1714	150.0893	282.1448	141.5761	0	0	L	1614.8520	807.9296	1597.8254	799.4163	1596.8414	798.9243	15
4	396.2241	198.6157	379.1976	190.1024	0	0	P	1501.7679	751.3876	1484.7414	742.8743	1483.7573	742.3823	14
5	509.3082	255.1577	492.2817	246.6445	0	0	I	1404.7151	702.8612	1387.6886	694.3479	1386.7046	693.8559	13
6	596.3402	298.6738	579.3137	290.1605	578.3297	289.6685	S	1291.6311	646.3192	1274.6045	637.8059	1273.6205	637.3139	12
7	695.4087	348.2080	678.3821	339.6947	677.3981	339.2027	V	1204.5991	602.8032	1187.5725	594.2899	1186.5885	593.7979	11
8	796.4563	398.7318	779.4298	390.2185	778.4458	389.7265	T	1105.5306	553.2690	1088.5041	544.7557	1087.5201	544.2637	10
9	956.4870	478.7471	939.4604	470.2339	938.4764	469.7418	C	1004.4830	502.7451	987.4564	494.2318	986.4724	493.7398	9
10	1069.5710	535.2892	1052.5445	526.7759	1051.5605	526.2839	I	844.4523	422.7298	827.4258	414.2165	826.4417	413.7245	8
11	1140.6082	570.8077	1123.5816	562.2944	1122.5976	561.8024	A	731.3682	366.1878	714.3417	357.6745	713.3577	357.1825	7
12	1255.6351	628.3212	1238.6086	619.8079	1237.6245	619.3159	D	660.3311	330.6692	643.3046	322.1559	642.3206	321.6639	6
13	1384.6777	692.8425	1367.6511	684.3292	1366.6671	683.8372	E	545.3042	273.1557	528.2776	264.6425	527.2936	264.1504	5
14	1497.7618	749.3845	1480.7352	740.8712	1479.7512	740.3792	I	416.2616	208.6344	399.2350	200.1212	0	0	4
15	1554.7832	777.8952	1537.7567	769.3820	1536.7727	768.8900	G	303.1775	152.0924	286.1510	143.5791	0	0	3
16	1625.8203	813.4138	1608.7938	804.9005	1607.8098	804.4085	A	246.1561	123.5817	229.1295	115.0684	0	0	2
17							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 5540.

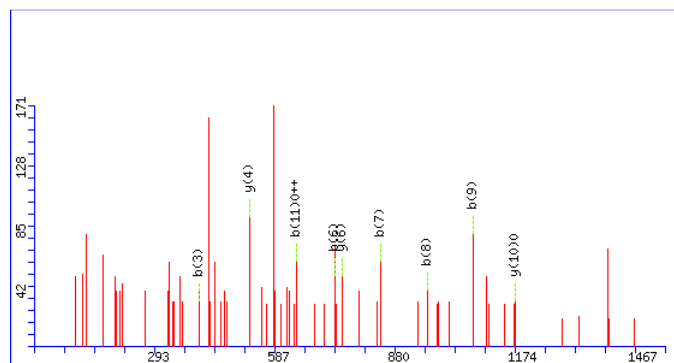
MS/MS Fragmentation of **TFRKNSILLSHQR**:

Found in **IP100412024,IP100796662**

Title: 4.1.1.1332.8

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							13
2	249.1234	125.0653	0	0	231.1128	116.0600	F	1498.8601	749.9337	1481.8336	741.4204	1480.8495	740.9284	12
3	405.2245	203.1159	388.1979	194.6026	387.2139	194.1106	R	1351.7917	676.3995	1334.7651	667.8862	1333.7811	667.3942	11
4	533.3194	267.1634	516.2929	258.6501	515.3089	258.1581	K	1195.6906	598.3489	1178.6640	589.8357	1177.6800	589.3436	10
5	647.3624	324.1848	630.3358	315.6715	629.3518	315.1795	N	1067.5956	534.3014	1050.5691	525.7882	1049.5851	525.2962	9
6	734.3944	367.7008	717.3678	359.1876	716.3838	358.6956	S	953.5527	477.2800	936.5261	468.7667	935.5421	468.2747	8
7	847.4785	424.2429	830.4519	415.7296	829.4679	415.2376	I	866.5207	433.7640	849.4941	425.2507	848.5101	424.7587	7
8	960.5625	480.7849	943.5360	472.2716	942.5520	471.7796	L	753.4366	377.2219	736.4100	368.7087	735.4260	368.2167	6
9	1073.6466	537.3269	1056.6200	528.8137	1055.6360	528.3217	L	640.3525	320.6799	623.3260	312.1666	622.3420	311.6746	5
10	1160.6786	580.8429	1143.6521	572.3297	1142.6681	571.8377	S	527.2685	264.1379	510.2419	255.6246	509.2579	255.1326	4
11	1297.7375	649.3724	1280.7110	640.8591	1279.7270	640.3671	H	440.2364	220.6219	423.2099	212.1086	0	0	3
12	1425.7961	713.4017	1408.7696	704.8884	1407.7855	704.3964	Q	303.1775	152.0924	286.1510	143.5791	0	0	2
13							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 5655.

MS/MS Fragmentation of **SRPSFHPLSDELVNYVNK**:

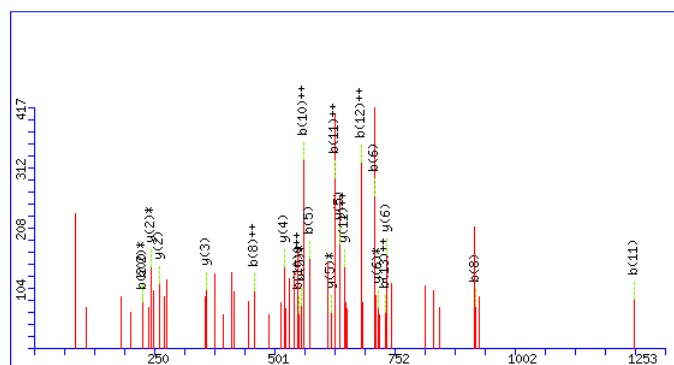
Found in

IP100295741;IP100975638;IP100976313;IP100976781;IP100978088;IP100978678;IP100980515;IP100981711;IP100982206;IP100982855;IP100983365;IP100983480;IP100984

Title: 3.1.1.625.3

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120214ry¥120214ry_aHDF1419-P10_4_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							18
2	244.1404	122.5738	227.1139	114.0606	226.1299	113.5686	R	2015.0345	1008.0209	1998.0080	999.5076	1997.0239	999.0156	17
3	341.1932	171.1002	324.1666	162.5870	323.1826	162.0949	P	1858.9334	929.9703	1841.9068	921.4571	1840.9228	920.9651	16
4	428.2252	214.6162	411.1987	206.1030	410.2146	205.6110	S	1761.8806	881.4440	1744.8541	872.9307	1743.8701	872.4387	15
5	575.2936	288.1504	558.2671	279.6372	557.2831	279.1452	F	1674.8486	837.9279	1657.8220	829.4147	1656.8380	828.9227	14
6	712.3525	356.6799	695.3260	348.1666	694.3420	347.6746	H	1527.7802	764.3937	1510.7536	755.8805	1509.7696	755.3884	13
7	809.4053	405.2063	792.3787	396.6930	791.3947	396.2010	P	1390.7213	695.8643	1373.6947	687.3510	1372.7107	686.8590	12
8	922.4894	461.7483	905.4628	453.2350	904.4788	452.7430	L	1293.6685	647.3379	1276.6420	638.8246	1275.6579	638.3326	11
9	1009.5214	505.2643	992.4948	496.7511	991.5108	496.2591	S	1180.5844	590.7959	1163.5579	582.2826	1162.5739	581.7906	10
10	1124.5483	562.7778	1107.5218	554.2645	1106.5378	553.7725	D	1093.5524	547.2798	1076.5259	538.7666	1075.5419	538.2746	9
11	1253.5909	627.2991	1236.5644	618.7858	1235.5804	618.2938	E	978.5255	489.7664	961.4989	481.2531	960.5149	480.7611	8
12	1366.6750	683.8411	1349.6484	675.3279	1348.6644	674.8359	L	849.4829	425.2451	832.4563	416.7318	0	0	7
13	1465.7434	733.3753	1448.7169	724.8621	1447.7328	724.3701	V	736.3988	368.7030	719.3723	360.1898	0	0	6
14	1579.7863	790.3968	1562.7598	781.8835	1561.7758	781.3915	N	637.3304	319.1688	620.3039	310.6556	0	0	5
15	1742.8497	871.9285	1725.8231	863.4152	1724.8391	862.9232	Y	523.2875	262.1474	506.2609	253.6341	0	0	4
16	1841.9181	921.4627	1824.8915	912.9494	1823.9075	912.4574	V	360.2241	180.6157	343.1976	172.1024	0	0	3
17	1955.9610	978.4841	1938.9345	969.9709	1937.9504	969.4789	N	261.1557	131.0815	244.1292	122.5682	0	0	2
18							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 5681.

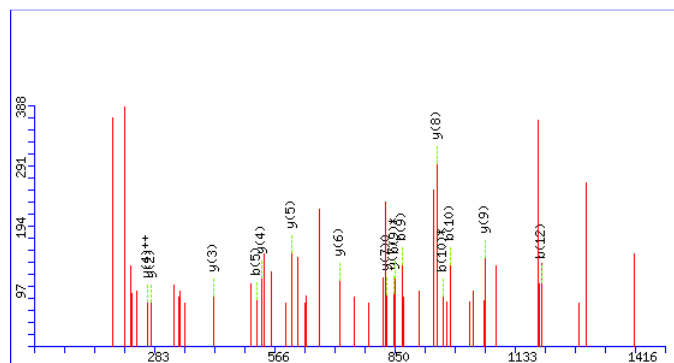
MS/MS Fragmentation of **APQETLNGGITDMLTELANFEK**:

Found in **IP100219538;IP100973464;IP100981347;IP100981942**

Title: 4.1.1.3803.6

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120214ry¥120214ry_414C2-43_4.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							22
2	169.0972	85.0522	0	0	0	0	P	2321.1330	1161.0701	2304.1064	1152.5568	2303.1224	1152.0648	21
3	297.1557	149.0815	280.1292	140.5682	0	0	Q	2224.0802	1112.5437	2207.0536	1104.0305	2206.0696	1103.5385	20
4	426.1983	213.6028	409.1718	205.0895	408.1878	204.5975	E	2096.0216	1048.5144	2078.9951	1040.0012	2078.0110	1039.5092	19
5	527.2460	264.1266	510.2195	255.6134	509.2354	255.1214	T	1966.9790	983.9931	1949.9525	975.4799	1948.9685	974.9879	18
6	640.3301	320.6687	623.3035	312.1554	622.3195	311.6634	L	1865.9313	933.4693	1848.9048	924.9560	1847.9208	924.4640	17
7	754.3730	377.6901	737.3464	369.1769	736.3624	368.6849	N	1752.8473	876.9273	1735.8207	868.4140	1734.8367	867.9220	16
8	811.3945	406.2009	794.3679	397.6876	793.3839	397.1956	G	1638.8044	819.9058	1621.7778	811.3925	1620.7938	810.9005	15
9	868.4159	434.7116	851.3894	426.1983	850.4054	425.7063	G	1581.7829	791.3951	1564.7563	782.8818	1563.7723	782.3898	14
10	981.5000	491.2536	964.4734	482.7404	963.4894	482.2483	I	1524.7614	762.8843	1507.7349	754.3711	1506.7509	753.8791	13
11	1082.5477	541.7775	1065.5211	533.2642	1064.5371	532.7722	T	1411.6774	706.3423	1394.6508	697.8290	1393.6668	697.3370	12
12	1197.5746	599.2909	1180.5481	590.7777	1179.5640	590.2857	D	1310.6297	655.8185	1293.6031	647.3052	1292.6191	646.8132	11
13	1328.6151	664.8112	1311.5885	656.2979	1310.6045	655.8059	M	1195.6027	598.3050	1178.5762	589.7917	1177.5922	589.2997	10
14	1441.6992	721.3532	1424.6726	712.8399	1423.6886	712.3479	L	1064.5623	532.7848	1047.5357	524.2715	1046.5517	523.7795	9
15	1542.7468	771.8771	1525.7203	763.3638	1524.7363	762.8718	T	951.4782	476.2427	934.4516	467.7295	933.4676	467.2374	8
16	1671.7894	836.3984	1654.7629	827.8851	1653.7789	827.3931	E	850.4305	425.7189	833.4040	417.2056	832.4199	416.7136	7
17	1784.8735	892.9404	1767.8469	884.4271	1766.8629	883.9351	L	721.3879	361.1976	704.3614	352.6843	703.3774	352.1923	6
18	1855.9106	928.4589	1838.8841	919.9457	1837.9000	919.4537	A	608.3039	304.6556	591.2773	296.1423	590.2933	295.6503	5
19	1969.9535	985.4804	1952.9270	976.9671	1951.9430	976.4751	N	537.2667	269.1370	520.2402	260.6237	519.2562	260.1317	4
20	2117.0219	1059.0146	2099.9954	1050.5013	2099.0114	1050.0093	F	423.2238	212.1155	406.1973	203.6023	405.2132	203.1103	3
21	2246.0645	1123.5359	2229.0380	1115.0226	2228.0540	1114.5306	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
22							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

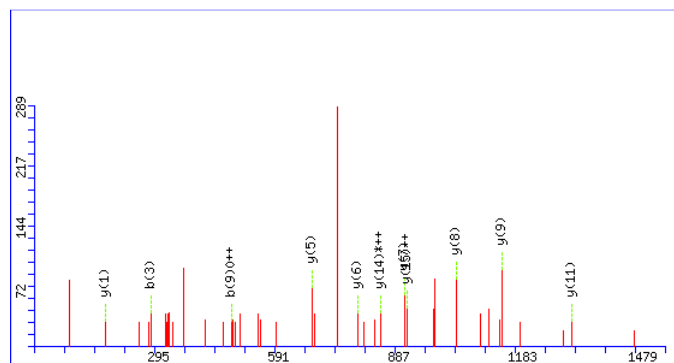
Peptide: 6083.

MS/MS Fragmentation of **ACGLLNCEAVLQLLTCHLR**: 57.021465@C:2,57.021465@C:7,57.021465@C:16
Found in **IP100043327:IP100444617**

Title: 4.1.1.1973.5

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_3.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							19
2	232.0750	116.5412	0	0	0	0	C	2170.0930	1085.5501	2153.0664	1077.0368	2152.0824	1076.5448	18
3	289.0965	145.0519	0	0	0	0	G	2010.0623	1005.5348	1993.0358	997.0215	1992.0518	996.5295	17
4	402.1806	201.5939	0	0	0	0	L	1953.0409	977.0241	1936.0143	968.5108	1935.0303	968.0188	16
5	515.2646	258.1360	0	0	0	0	L	1839.9568	920.4820	1822.9302	911.9688	1821.9462	911.4768	15
6	629.3076	315.1574	612.2810	306.6441	0	0	N	1726.8727	863.9400	1709.8462	855.4267	1708.8622	854.9347	14
7	789.3382	395.1727	772.3117	386.6595	0	0	C	1612.8298	806.9185	1595.8032	798.4053	1594.8192	797.9133	13
8	918.3808	459.6940	901.3543	451.1808	900.3702	450.6888	E	1452.7991	726.9032	1435.7726	718.3899	1434.7886	717.8979	12
9	989.4179	495.2126	972.3914	486.6993	971.4074	486.2073	A	1323.7566	662.3819	1306.7300	653.8686	1305.7460	653.3766	11
10	1088.4863	544.7468	1071.4598	536.2335	1070.4758	535.7415	V	1252.7194	626.8634	1235.6929	618.3501	1234.7089	617.8581	10
11	1201.5704	601.2888	1184.5438	592.7756	1183.5598	592.2836	L	1153.6510	577.3292	1136.6245	568.8159	1135.6405	568.3239	9
12	1329.6290	665.3181	1312.6024	656.8048	1311.6184	656.3128	Q	1040.5670	520.7871	1023.5404	512.2738	1022.5564	511.7818	8
13	1442.7130	721.8602	1425.6865	713.3469	1424.7025	712.8549	L	912.5084	456.7578	895.4818	448.2446	894.4978	447.7525	7
14	1555.7971	778.4022	1538.7706	769.8889	1537.7865	769.3969	L	799.4243	400.2158	782.3978	391.7025	781.4138	391.2105	6
15	1656.8448	828.9260	1639.8182	820.4128	1638.8342	819.9207	T	686.3403	343.6738	669.3137	335.1605	668.3297	334.6685	5
16	1816.8754	908.9414	1799.8489	900.4281	1798.8649	899.9361	C	585.2926	293.1499	568.2660	284.6367	0	0	4
17	1953.9343	977.4708	1936.9078	968.9575	1935.9238	968.4655	H	425.2619	213.1346	408.2354	204.6213	0	0	3
18	2067.0184	1034.0128	2049.9919	1025.4996	2049.0078	1025.0076	L	288.2030	144.6051	271.1765	136.0919	0	0	2
19							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 6246.

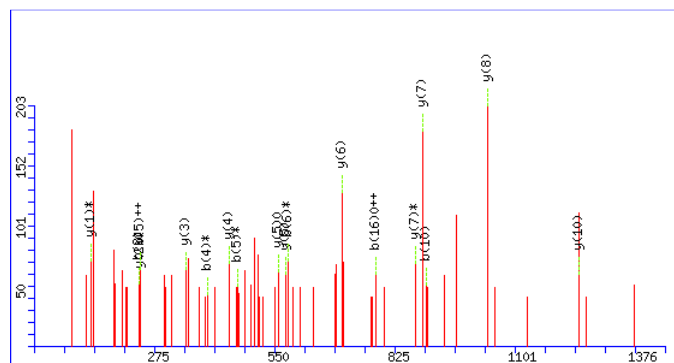
MS/MS Fragmentation of **LQGDALSVGGYEANPIFWEEVSDK:**

Found in **IP100034308;IP100642619;IP101011174;IP101012557**

Title: 3.1.1.4250.9

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120210ry¥120210ry_585A1-55_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							24
2	242.1499	121.5786	225.1234	113.0653	0	0	Q	2511.1674	1256.0874	2494.1409	1247.5741	2493.1569	1247.0821	23
3	299.1714	150.0893	282.1448	141.5761	0	0	G	2383.1088	1192.0581	2366.0823	1183.5448	2365.0983	1183.0528	22
4	414.1983	207.6028	397.1718	199.0895	396.1878	198.5975	D	2326.0874	1163.5473	2309.0608	1155.0341	2308.0768	1154.5420	21
5	485.2354	243.1214	468.2089	234.6081	467.2249	234.1161	A	2211.0604	1106.0339	2194.0339	1097.5206	2193.0499	1097.0286	20
6	598.3195	299.6634	581.2930	291.1501	580.3089	290.6581	L	2140.0233	1070.5153	2122.9968	1062.0020	2122.0128	1061.5100	19
7	685.3515	343.1794	668.3250	334.6661	667.3410	334.1741	S	2026.9393	1013.9733	2009.9127	1005.4600	2008.9287	1004.9680	18
8	784.4199	392.7136	767.3934	384.2003	766.4094	383.7083	V	1939.9072	970.4573	1922.8807	961.9440	1921.8967	961.4520	17
9	841.4414	421.2243	824.4149	412.7111	823.4308	412.2191	G	1840.8388	920.9230	1823.8123	912.4098	1822.8283	911.9178	16
10	898.4629	449.7351	881.4363	441.2218	880.4523	440.7298	G	1783.8174	892.4123	1766.7908	883.8990	1765.8068	883.4070	15
11	1061.5262	531.2667	1044.4997	522.7535	1043.5156	522.2615	Y	1726.7959	863.9016	1709.7693	855.3883	1708.7853	854.8963	14
12	1190.5688	595.7880	1173.5422	587.2748	1172.5582	586.7828	E	1563.7326	782.3699	1546.7060	773.8566	1545.7220	773.3646	13
13	1261.6059	631.3066	1244.5794	622.7933	1243.5953	622.3013	A	1434.6900	717.8486	1417.6634	709.3353	1416.6794	708.8433	12
14	1375.6488	688.3281	1358.6223	679.8148	1357.6383	679.3228	N	1363.6529	682.3301	1346.6263	673.8168	1345.6423	673.3248	11
15	1472.7016	736.8544	1455.6751	728.3412	1454.6910	727.8492	P	1249.6099	625.3086	1232.5834	616.7953	1231.5994	616.3033	10
16	1585.7857	793.3965	1568.7591	784.8832	1567.7751	784.3912	I	1152.5572	576.7822	1135.5306	568.2689	1134.5466	567.7769	9
17	1732.8541	866.9307	1715.8275	858.4174	1714.8435	857.9254	F	1039.4731	520.2402	1022.4466	511.7269	1021.4625	511.2349	8
18	1918.9334	959.9703	1901.9068	951.4571	1900.9228	950.9651	W	892.4047	446.7060	875.3781	438.1927	874.3941	437.7007	7
19	2047.9760	1024.4916	2030.9494	1015.9784	2029.9654	1015.4863	E	706.3254	353.6663	689.2988	345.1531	688.3148	344.6610	6
20	2177.0186	1089.0129	2159.9920	1080.4997	2159.0080	1080.0076	E	577.2828	289.1450	560.2562	280.6318	559.2722	280.1397	5
21	2276.0870	1138.5471	2259.0604	1130.0339	2258.0764	1129.5419	V	448.2402	224.6237	431.2136	216.1105	430.2296	215.6185	4
22	2363.1190	1182.0631	2346.0925	1173.5499	2345.1085	1173.0579	S	349.1718	175.0895	332.1452	166.5763	331.1612	166.0842	3
23	2478.1460	1239.5766	2461.1194	1231.0633	2460.1354	1230.5713	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
24							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 6314.

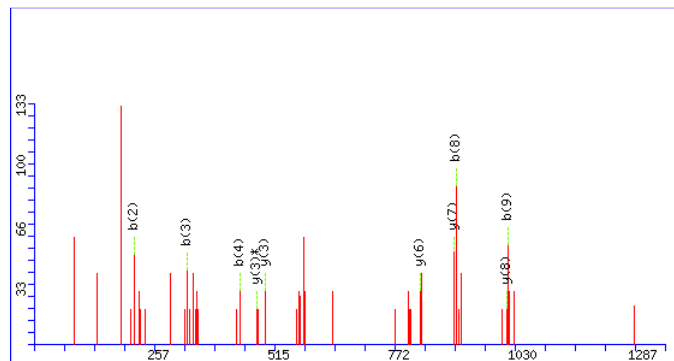
MS/MS Fragmentation of **DVLLLVHNLPGNLAGYIWK**:

Found in **IP100002903;IP100300046;IP100332814;IP100414259;IP100477046;IP100640684;IP100893034;IP100893298;IP100893420;IP100894522;IP100930527**

Title: 4.1.1.3082.3

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120208ry¥120208ry_Tig120slc-P8_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							20
2	215.1028	108.0550	0	0	197.0921	99.0497	V	2254.2747	1127.6410	2237.2481	1119.1277	0	0	19
3	328.1867	164.5970	0	0	310.1761	155.5917	L	2155.2063	1078.1068	2138.1797	1069.5935	0	0	18
4	441.2708	221.1390	0	0	423.2602	212.1337	L	2042.1222	1021.5647	2025.0956	1013.0515	0	0	17
5	554.3548	277.6811	0	0	536.3443	268.6758	L	1929.0381	965.0227	1912.0116	956.5094	0	0	16
6	653.4232	327.2153	0	0	635.4127	318.2100	V	1815.9541	908.4807	1798.9275	899.9674	0	0	15
7	790.4822	395.7447	0	0	772.4716	386.7394	H	1716.8857	858.9465	1699.8591	850.4332	0	0	14
8	904.5251	452.7662	887.4985	444.2529	886.5145	443.7609	N	1579.8267	790.4170	1562.8002	781.9037	0	0	13
9	1017.6091	509.3082	1000.5826	500.7949	999.5986	500.3029	L	1465.7838	733.3955	1448.7573	724.8823	0	0	12
10	1114.6619	557.8346	1097.6354	549.3213	1096.6513	548.8293	P	1352.6997	676.8535	1335.6732	668.3402	0	0	11
11	1242.7205	621.8639	1225.6939	613.3506	1224.7099	612.8586	Q	1255.6470	628.3271	1238.6204	619.8139	0	0	10
12	1356.7634	678.8853	1339.7369	670.3721	1338.7528	669.8801	N	1127.5884	564.2978	1110.5619	555.7846	0	0	9
13	1469.8475	735.4274	1452.8209	726.9141	1451.8369	726.4221	L	1013.5455	507.2764	996.5189	498.7631	0	0	8
14	1540.8846	770.9459	1523.8580	762.4327	1522.8740	761.9407	A	900.4614	450.7343	883.4349	442.2211	0	0	7
15	1597.9061	799.4567	1580.8795	790.9434	1579.8955	790.4514	G	829.4243	415.2158	812.3978	406.7025	0	0	6
16	1760.9694	880.9883	1743.9428	872.4751	1742.9588	871.9830	Y	772.4028	386.7051	755.3763	378.1918	0	0	5
17	1874.0534	937.5304	1857.0269	929.0171	1856.0429	928.5251	I	609.3395	305.1734	592.3130	296.6601	0	0	4
18	2060.1328	1030.5700	2043.1062	1022.0567	2042.1222	1021.5647	W	496.2554	248.6314	479.2289	240.1181	0	0	3
19	2223.1961	1112.1017	2206.1695	1103.5884	2205.1855	1103.0964	Y	310.1761	155.5917	293.1496	147.0784	0	0	2
20							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: **6456.**

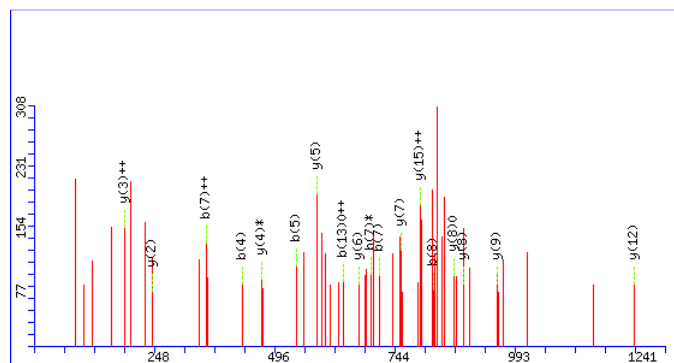
MS/MS Fragmentation of **SVNEILGLAESSPEPK:**

Found in **IP100303812:IP100954120**

Title: 3.1.1.933.5

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							17
2	187.1077	94.0575	0	0	169.0972	85.0522	V	1696.8752	848.9412	1679.8487	840.4280	1678.8646	839.9360	16
3	301.1506	151.0790	284.1241	142.5657	283.1401	142.0737	N	1597.8068	799.4070	1580.7802	790.8938	1579.7962	790.4018	15
4	430.1932	215.6003	413.1667	207.0870	412.1827	206.5950	E	1483.7639	742.3856	1466.7373	733.8723	1465.7533	733.3803	14
5	543.2773	272.1423	526.2508	263.6290	525.2667	263.1370	I	1354.7213	677.8643	1337.6947	669.3510	1336.7107	668.8590	13
6	656.3614	328.6843	639.3348	320.1710	638.3508	319.6790	L	1241.6372	621.3222	1224.6107	612.8090	1223.6266	612.3170	12
7	713.3828	357.1951	696.3563	348.6818	695.3723	348.1898	G	1128.5531	564.7802	1111.5266	556.2669	1110.5426	555.7749	11
8	826.4669	413.7371	809.4403	405.2238	808.4563	404.7318	L	1071.5317	536.2695	1054.5051	527.7562	1053.5211	527.2642	10
9	897.5040	449.2556	880.4775	440.7424	879.4934	440.2504	A	958.4476	479.7274	941.4211	471.2142	940.4371	470.7222	9
10	1026.5466	513.7769	1009.5201	505.2637	1008.5360	504.7717	E	887.4105	444.2089	870.3840	435.6956	869.3999	435.2036	8
11	1113.5786	557.2930	1096.5521	548.7797	1095.5681	548.2877	S	758.3679	379.6876	741.3414	371.1743	740.3573	370.6823	7
12	1200.6107	600.8090	1183.5841	592.2957	1182.6001	591.8037	S	671.3359	336.1716	654.3093	327.6583	653.3253	327.1663	6
13	1297.6634	649.3353	1280.6369	640.8221	1279.6529	640.3301	P	584.3039	292.6556	567.2773	284.1423	566.2933	283.6503	5
14	1411.7063	706.3568	1394.6798	697.8435	1393.6958	697.3515	N	487.2511	244.1292	470.2245	235.6159	469.2405	235.1239	4
15	1540.7489	770.8781	1523.7224	762.3648	1522.7384	761.8728	E	373.2082	187.1077	356.1816	178.5944	355.1976	178.1024	3
16	1637.8017	819.4045	1620.7752	810.8912	1619.7911	810.3992	P	244.1656	122.5864	227.1390	114.0731	0	0	2
17							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 6536.

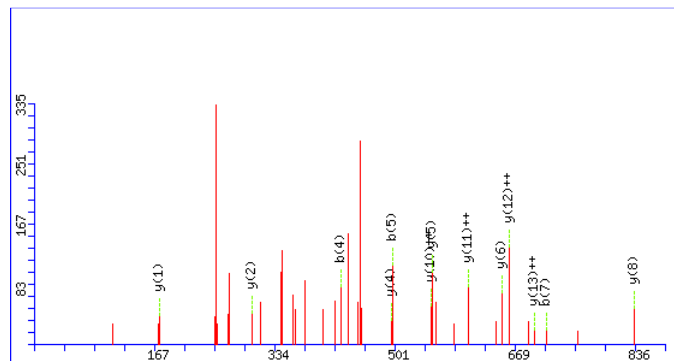
MS/MS Fragmentation of **REAAANTNRPSPGGHER**:

Found in **IP100029073;IP100783813**

Title: 1.1.1.4887.9

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_3_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	157.1084	79.0578	140.0818	70.5446	0	0	R							17
2	286.1510	143.5791	269.1244	135.0659	268.1404	134.5738	E	1663.7895	832.3984	1646.7630	823.8851	1645.7790	823.3931	16
3	357.1881	179.0977	340.1615	170.5844	339.1775	170.0924	A	1534.7469	767.8771	1517.7204	759.3638	1516.7364	758.8718	15
4	428.2252	214.6162	411.1987	206.1030	410.2146	205.6110	A	1463.7098	732.3585	1446.6833	723.8453	1445.6992	723.3533	14
5	499.2623	250.1348	482.2358	241.6215	481.2518	241.1295	A	1392.6727	696.8400	1375.6461	688.3267	1374.6621	687.8347	13
6	613.3052	307.1563	596.2787	298.6430	595.2947	298.1510	N	1321.6356	661.3214	1304.6090	652.8082	1303.6250	652.3161	12
7	714.3529	357.6801	697.3264	349.1668	696.3424	348.6748	T	1207.5927	604.3000	1190.5661	595.7867	1189.5821	595.2947	11
8	828.3959	414.7016	811.3693	406.1883	810.3853	405.6963	N	1106.5450	553.7761	1089.5184	545.2629	1088.5344	544.7708	10
9	984.4970	492.7521	967.4704	484.2388	966.4864	483.7468	R	992.5021	496.7547	975.4755	488.2414	974.4915	487.7494	9
10	1081.5497	541.2785	1064.5232	532.7652	1063.5392	532.2732	P	836.4009	418.7041	819.3744	410.1908	818.3904	409.6988	8
11	1168.5818	584.7945	1151.5552	576.2812	1150.5712	575.7892	S	739.3482	370.1777	722.3216	361.6645	721.3376	361.1724	7
12	1265.6345	633.3209	1248.6080	624.8076	1247.6240	624.3156	P	652.3161	326.6617	635.2896	318.1484	634.3056	317.6564	6
13	1322.6560	661.8316	1305.6294	653.3184	1304.6454	652.8263	G	555.2634	278.1353	538.2368	269.6221	537.2528	269.1300	5
14	1379.6775	690.3424	1362.6509	681.8291	1361.6669	681.3371	G	498.2419	249.6246	481.2154	241.1113	480.2314	240.6193	4
15	1516.7364	758.8718	1499.7098	750.3585	1498.7258	749.8665	H	441.2205	221.1139	424.1939	212.6006	423.2099	212.1086	3
16	1645.7790	823.3931	1628.7524	814.8798	1627.7684	814.3878	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
17							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 6632.

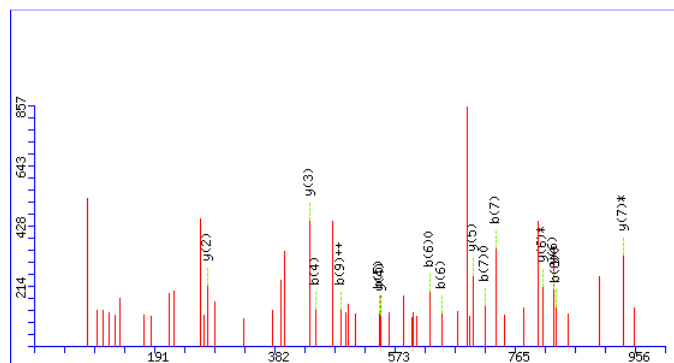
MS/MS Fragmentation of **DPVHTVSLQQFIYEK**:

Found in **IP100301107;IP100552710;IP100913938**

Title: 3.1.1.1400.6

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120212ry¥120212ry_414C2-43_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							15
2	213.0870	107.0471	0	0	195.0764	98.0418	P	1688.9006	844.9540	1671.8741	836.4407	1670.8901	835.9487	14
3	312.1554	156.5813	0	0	294.1448	147.5761	V	1591.8479	796.4276	1574.8213	787.9143	1573.8373	787.4223	13
4	449.2143	225.1108	0	0	431.2037	216.1055	H	1492.7795	746.8934	1475.7529	738.3801	1474.7689	737.8881	12
5	550.2620	275.6346	0	0	532.2514	266.6293	T	1355.7205	678.3639	1338.6940	669.8506	1337.7100	669.3586	11
6	649.3304	325.1688	0	0	631.3198	316.1636	V	1254.6729	627.8401	1237.6463	619.3268	1236.6623	618.8348	10
7	736.3624	368.6849	0	0	718.3519	359.6796	S	1155.6045	578.3059	1138.5779	569.7926	1137.5939	569.3006	9
8	849.4465	425.2269	0	0	831.4359	416.2216	L	1068.5724	534.7898	1051.5459	526.2766	1050.5619	525.7846	8
9	977.5051	489.2562	960.4785	480.7429	959.4945	480.2509	Q	955.4884	478.2478	938.4618	469.7345	937.4778	469.2425	7
10	1105.5637	553.2855	1088.5371	544.7722	1087.5531	544.2802	Q	827.4298	414.2185	810.4032	405.7053	809.4192	405.2132	6
11	1252.6321	626.8197	1235.6055	618.3064	1234.6215	617.8144	F	699.3712	350.1892	682.3447	341.6760	681.3606	341.1840	5
12	1365.7161	683.3617	1348.6896	674.8484	1347.7056	674.3564	I	552.3028	276.6550	535.2762	268.1418	534.2922	267.6498	4
13	1528.7795	764.8934	1511.7529	756.3801	1510.7689	755.8881	Y	439.2187	220.1130	422.1922	211.5997	421.2082	211.1077	3
14	1657.8221	829.4147	1640.7955	820.9014	1639.8115	820.4094	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
15							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 7175.

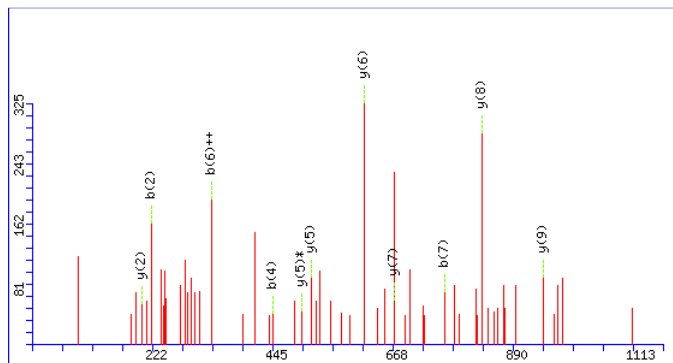
MS/MS Fragmentation of **GYLLYGPPGCGK: 57.021465@C:10**

Found in **IP100003985;IP100925726;IP100927724**

Title: 2.1.1.2782.6

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							12
2	221.0921	111.0497	0	0	0	0	Y	1224.6082	612.8077	1207.5816	604.2944	0	0	11
3	334.1761	167.5917	0	0	0	0	L	1061.5448	531.2761	1044.5183	522.7628	0	0	10
4	447.2602	224.1337	0	0	0	0	L	948.4608	474.7340	931.4342	466.2207	0	0	9
5	610.3235	305.6654	0	0	0	0	Y	835.3767	418.1920	818.3502	409.6787	0	0	8
6	667.3450	334.1761	0	0	0	0	G	672.3134	336.6603	655.2868	328.1471	0	0	7
7	764.3978	382.7025	0	0	0	0	P	615.2919	308.1496	598.2654	299.6363	0	0	6
8	861.4505	431.2289	0	0	0	0	P	518.2391	259.6232	501.2126	251.1099	0	0	5
9	918.4720	459.7396	0	0	0	0	G	421.1864	211.0968	404.1598	202.5836	0	0	4
10	1078.5026	539.7550	0	0	0	0	C	364.1649	182.5861	347.1384	174.0728	0	0	3
11	1135.5241	568.2657	0	0	0	0	G	204.1343	102.5708	187.1077	94.0575	0	0	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 7227.

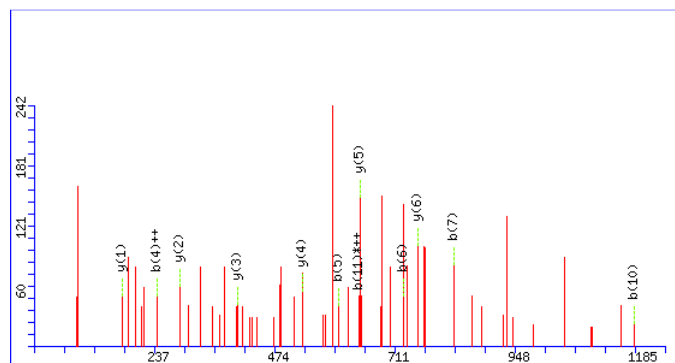
MS/MS Fragmentation of **KLNMDQVLDQILR**:

Found in **IP100456676;IP100456677;IP100456678**

Title: 3.1.1.4096.2

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120118ry¥120118ry_201B7-32_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	129.1022	65.0548	112.0757	56.5415	0	0	K							13
2	242.1863	121.5968	225.1598	113.0835	0	0	L	1457.7781	729.3927	1440.7515	720.8794	1439.7675	720.3874	12
3	356.2292	178.6183	339.2027	170.1050	0	0	N	1344.6940	672.8506	1327.6675	664.3374	1326.6834	663.8454	11
4	487.2697	244.1385	470.2432	235.6252	0	0	M	1230.6511	615.8292	1213.6245	607.3159	1212.6405	606.8239	10
5	602.2967	301.6520	585.2701	293.1387	584.2861	292.6467	D	1099.6106	550.3089	1082.5841	541.7957	1081.6000	541.3037	9
6	730.3552	365.6813	713.3287	357.1680	712.3447	356.6760	Q	984.5837	492.7955	967.5571	484.2822	966.5731	483.7902	8
7	829.4237	415.2155	812.3971	406.7022	811.4131	406.2102	V	856.5251	428.7662	839.4985	420.2529	838.5145	419.7609	7
8	942.5077	471.7575	925.4812	463.2442	924.4971	462.7522	L	757.4567	379.2320	740.4301	370.7187	739.4461	370.2267	6
9	1057.5347	529.2710	1040.5081	520.7577	1039.5241	520.2657	D	644.3726	322.6899	627.3461	314.1767	626.3620	313.6847	5
10	1185.5932	593.3003	1168.5667	584.7870	1167.5827	584.2950	Q	529.3457	265.1765	512.3191	256.6632	0	0	4
11	1298.6773	649.8423	1281.6507	641.3290	1280.6667	640.8370	I	401.2871	201.1472	384.2605	192.6339	0	0	3
12	1411.7614	706.3843	1394.7348	697.8710	1393.7508	697.3790	L	288.2030	144.6051	271.1765	136.0919	0	0	2
13							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 7410.

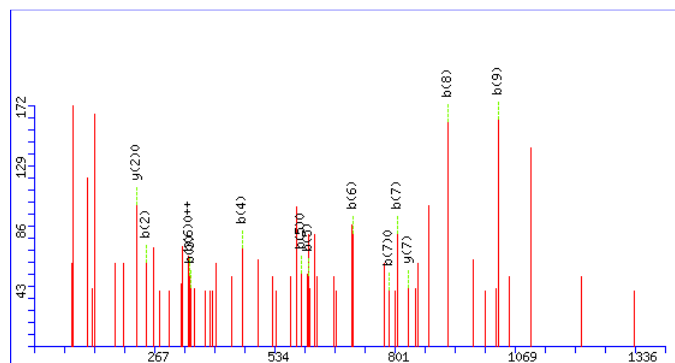
MS/MS Fragmentation of **IHVDFPVILYEV**:

Found in **IP100027248**

Title: 4.1.1.1167.6

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							12
2	251.1503	126.0788	0	0	0	0	H	1330.7042	665.8557	0	0	1312.6936	656.8504	11
3	350.2187	175.6130	0	0	0	0	V	1193.6453	597.3263	0	0	1175.6347	588.3210	10
4	465.2456	233.1264	0	0	447.2350	224.1212	D	1094.5768	547.7921	0	0	1076.5663	538.7868	9
5	612.3140	306.6606	0	0	594.3035	297.6554	F	979.5499	490.2786	0	0	961.5393	481.2733	8
6	708.3668	355.1870	0	0	691.3562	346.1817	P	832.4815	416.7444	0	0	814.4709	407.7391	7
7	808.4352	404.7212	0	0	790.4246	395.7160	V	735.4287	368.2180	0	0	717.4182	359.2127	6
8	921.5193	461.2633	0	0	903.5087	452.2580	I	636.3603	318.6838	0	0	618.3497	309.6785	5
9	1034.6033	517.8053	0	0	1016.5928	508.8000	L	523.2762	262.1418	0	0	505.2657	253.1365	4
10	1197.6667	599.3370	0	0	1179.6561	590.3317	Y	410.1922	205.5997	0	0	392.1816	196.5944	3
11	1326.7093	663.8583	0	0	1308.6987	654.8530	E	247.1288	124.0681	0	0	229.1183	115.0628	2
12							V	118.0863	59.5468	0	0	0	0	1

Peptide View

Peptide: 7499.

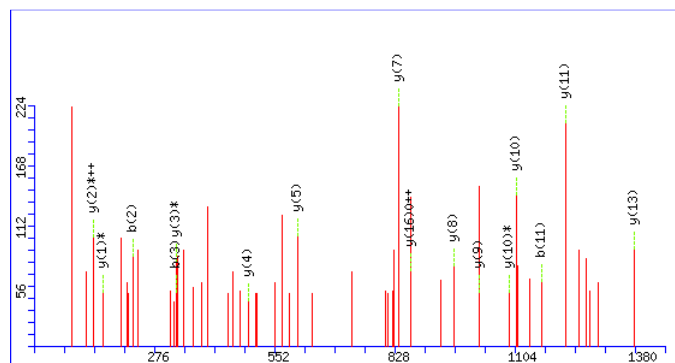
MS/MS Fragmentation of **LLVISAPNDEDWAYSQQLSALSQGACNFGLR: 57.021465@C:26**

Found in **IP100260630,IP100844310,IP100946343**

Title: 4.1.1.1373.10

Data file: Y:\TT5600(CiRA1)\2012-02\120201ry\120201ry_aHDF1388-P9_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							31
2	227.1754	114.0913	0	0	0	0	L	3310.5797	1655.7935	3293.5532	1647.2802	3292.5692	1646.7882	30
3	326.2438	163.6255	0	0	0	0	V	3197.4957	1599.2515	3180.4691	1590.7382	3179.4851	1590.2462	29
4	439.3279	220.1676	0	0	0	0	I	3098.4272	1549.7173	3081.4007	1541.2040	3080.4167	1540.7120	28
5	526.3599	263.6836	0	0	508.3493	254.6783	S	2985.3432	1493.1752	2968.3166	1484.6620	2967.3326	1484.1699	27
6	597.3970	299.2022	0	0	579.3865	290.1969	A	2898.3111	1449.6592	2881.2846	1441.1459	2880.3006	1440.6539	26
7	694.4498	347.7285	0	0	676.4392	338.7232	P	2827.2740	1414.1407	2810.2475	1405.6274	2809.2635	1405.1354	25
8	808.4927	404.7500	791.4662	396.2367	790.4822	395.7447	N	2730.2213	1365.6143	2713.1947	1357.1010	2712.2107	1356.6090	24
9	923.5197	462.2635	906.4931	453.7502	905.5091	453.2582	D	2616.1783	1308.5928	2599.1518	1300.0795	2598.1678	1299.5875	23
10	1052.5623	526.7848	1035.5357	518.2715	1034.5517	517.7795	E	2501.1514	1251.0793	2484.1249	1242.5661	2483.1408	1242.0741	22
11	1167.5892	584.2982	1150.5626	575.7850	1149.5786	575.2930	D	2372.1088	1186.5580	2355.0823	1178.0448	2354.0982	1177.5528	21
12	1353.6685	677.3379	1336.6420	668.8246	1335.6579	668.3326	W	2257.0819	1129.0446	2240.0553	1120.5313	2239.0713	1120.0393	20
13	1424.7056	712.8564	1407.6791	704.3432	1406.6951	703.8512	A	2071.0026	1036.0049	2053.9760	1027.4916	2052.9920	1026.9996	19
14	1587.7690	794.3881	1570.7424	785.8748	1569.7584	785.3828	Y	1999.9654	1000.4864	1982.9389	991.9731	1981.9549	991.4811	18
15	1674.8010	837.9041	1657.7744	829.3909	1656.7904	828.8988	S	1836.9021	918.9547	1819.8756	910.4414	1818.8915	909.9494	17
16	1802.8596	901.9334	1785.8330	893.4201	1784.8490	892.9281	Q	1749.8701	875.4387	1732.8435	866.9254	1731.8595	866.4334	16
17	1930.9181	965.9627	1913.8916	957.4494	1912.9076	956.9574	Q	1621.8115	811.4094	1604.7850	802.8961	1603.8009	802.4041	15
18	2044.0022	1022.5047	2026.9756	1013.9915	2025.9916	1013.4995	L	1493.7529	747.3801	1476.7264	738.8668	1475.7424	738.3748	14
19	2131.0342	1066.0208	2114.0077	1057.5075	2113.0237	1057.0155	S	1380.6689	690.8381	1363.6423	682.3248	1362.6583	681.8328	13
20	2202.0713	1101.5393	2185.0448	1093.0260	2184.0608	1092.5340	A	1293.6368	647.3221	1276.6103	638.8088	1275.6263	638.3168	12
21	2315.1554	1158.0813	2298.1289	1149.5681	2297.1448	1149.0761	L	1222.5997	611.8035	1205.5732	603.2902	1204.5892	602.7982	11
22	2402.1874	1201.5974	2385.1609	1193.0841	2384.1769	1192.5921	S	1109.5157	555.2615	1092.4891	546.7482	1091.5051	546.2562	10
23	2459.2089	1230.1081	2442.1823	1221.5948	2441.1983	1221.1028	G	1022.4836	511.7455	1005.4571	503.2322	0	0	9
24	2587.2675	1294.1374	2570.2409	1285.6241	2569.2569	1285.1321	Q	965.4622	483.2347	948.4356	474.7214	0	0	8
25	2658.3046	1329.6559	2641.2780	1321.1427	2640.2940	1320.6506	A	837.4036	419.2054	820.3770	410.6922	0	0	7
26	2818.3352	1409.6713	2801.3087	1401.1580	2800.3247	1400.6660	C	766.3665	383.6869	749.3399	375.1736	0	0	6
27	2932.3782	1466.6927	2915.3516	1458.1794	2914.3676	1457.6874	N	606.3358	303.6715	589.3093	295.1583	0	0	5
28	3079.4466	1540.2269	3062.4200	1531.7137	3061.4360	1531.2216	F	492.2929	246.6501	475.2663	238.1368	0	0	4
29	3136.4680	1568.7377	3119.4415	1560.2244	3118.4575	1559.7324	G	345.2245	173.1159	328.1979	164.6026	0	0	3
30	3249.5521	1625.2797	3232.5256	1616.7664	3231.5415	1616.2744	L	288.2030	144.6051	271.1765	136.0919	0	0	2
31							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 7515.

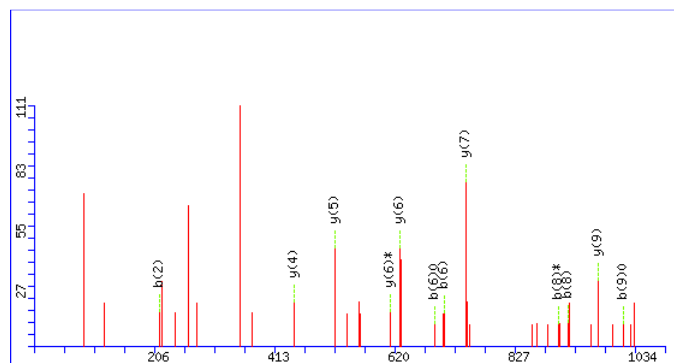
MS/MS Fragmentation of **ESFLDDVNLILANSVK**:

Found in **IP100009891;IP100100867;IP100149098;IP100645793;IP100828032;IP100877098;IP100939191;IP100965956;IP101024734**

Title: 4.1.1.3804.3

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120129ry¥120129ry_604A1-46_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							16
2	217.0819	109.0446	0	0	199.0713	100.0393	S	1647.8952	824.4512	1630.8687	815.9380	1629.8846	815.4460	15
3	364.1503	182.5788	0	0	346.1397	173.5735	F	1560.8632	780.9352	1543.8366	772.4220	1542.8526	771.9299	14
4	477.2344	239.1208	0	0	459.2238	230.1155	L	1413.7948	707.4010	1396.7682	698.8877	1395.7842	698.3957	13
5	592.2613	296.6343	0	0	574.2508	287.6290	D	1300.7107	650.8590	1283.6842	642.3457	1282.7001	641.8537	12
6	707.2883	354.1478	0	0	689.2777	345.1425	D	1185.6838	593.3455	1168.6572	584.8322	1167.6732	584.3402	11
7	806.3567	403.6820	0	0	788.3461	394.6767	V	1070.6568	535.8320	1053.6303	527.3188	1052.6463	526.8268	10
8	920.3996	460.7034	903.3731	452.1902	902.3890	451.6982	N	971.5884	486.2978	954.5619	477.7846	953.5778	477.2926	9
9	1033.4837	517.2455	1016.4571	508.7322	1015.4731	508.2402	L	857.5455	429.2764	840.5189	420.7631	839.5349	420.2711	8
10	1146.5677	573.7875	1129.5412	565.2742	1128.5572	564.7822	I	744.4614	372.7343	727.4349	364.2211	726.4509	363.7291	7
11	1259.6518	630.3295	1242.6252	621.8163	1241.6412	621.3243	L	631.3774	316.1923	614.3508	307.6790	613.3668	307.1870	6
12	1330.6889	665.8481	1313.6624	657.3348	1312.6783	656.8428	A	518.2933	259.6503	501.2667	251.1370	500.2827	250.6450	5
13	1444.7318	722.8696	1427.7053	714.3563	1426.7213	713.8643	N	447.2562	224.1317	430.2296	215.6184	429.2456	215.1264	4
14	1531.7639	766.3856	1514.7373	757.8723	1513.7533	757.3803	S	333.2132	167.1103	316.1867	158.5970	315.2027	158.1050	3
15	1630.8323	815.9198	1613.8057	807.4065	1612.8217	806.9145	V	246.1812	123.5942	229.1547	115.0810	0	0	2
16							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 7556.

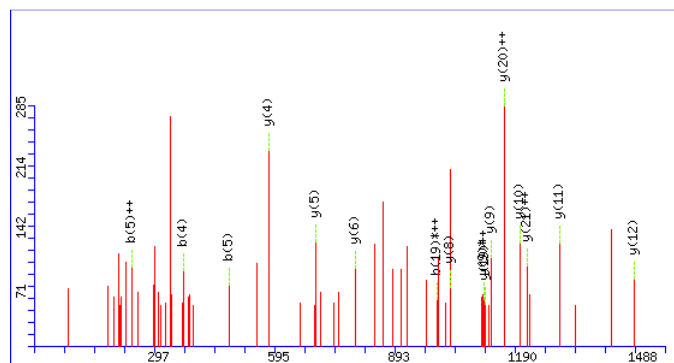
MS/MS Fragmentation of **AAVQLPSGEDQNDWVAVHVVDFFNR**:

Found in **IP100335089**

Title: 4.1.1.1555.10

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_3.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							25
2	143.0815	72.0444	0	0	0	0	A	2742.3271	1371.6672	2725.3005	1363.1539	2724.3165	1362.6619	24
3	242.1499	121.5786	0	0	0	0	V	2671.2899	1336.1486	2654.2634	1327.6353	2653.2794	1327.1433	23
4	370.2085	185.6079	353.1819	177.0946	0	0	Q	2572.2215	1286.6144	2555.1950	1278.1011	2554.2110	1277.6091	22
5	483.2926	242.1499	466.2660	233.6366	0	0	L	2444.1629	1222.5851	2427.1364	1214.0718	2426.1524	1213.5798	21
6	580.3453	290.6763	563.3188	282.1630	0	0	P	2331.0789	1166.0431	2314.0523	1157.5298	2313.0683	1157.0378	20
7	667.3774	334.1923	650.3508	325.6790	649.3668	325.1870	S	2234.0261	1117.5167	2216.9996	1109.0034	2216.0156	1108.5114	19
8	724.3988	362.7030	707.3723	354.1898	706.3883	353.6978	G	2146.9941	1074.0007	2129.9675	1065.4874	2128.9835	1064.9954	18
9	853.4414	427.2243	836.4149	418.7111	835.4308	418.2191	E	2089.9726	1045.4900	2072.9461	1036.9767	2071.9621	1036.4847	17
10	968.4684	484.7378	951.4418	476.2245	950.4578	475.7325	D	1960.9300	980.9687	1943.9035	972.4554	1942.9195	971.9634	16
11	1096.5269	548.7671	1079.5004	540.2538	1078.5164	539.7618	Q	1845.9031	923.4552	1828.8765	914.9419	1827.8925	914.4499	15
12	1210.5699	605.7886	1193.5433	597.2753	1192.5593	596.7833	N	1717.8445	859.4259	1700.8180	850.9126	1699.8340	850.4206	14
13	1325.5968	663.3020	1308.5703	654.7888	1307.5862	654.2968	D	1603.8016	802.4044	1586.7750	793.8912	1585.7910	793.3991	13
14	1511.6761	756.3417	1494.6496	747.8284	1493.6655	747.3364	W	1488.7746	744.8910	1471.7481	736.3777	1470.7641	735.8857	12
15	1610.7445	805.8759	1593.7180	797.3626	1592.7340	796.8706	V	1302.6953	651.8513	1285.6688	643.3380	1284.6848	642.8460	11
16	1681.7816	841.3945	1664.7551	832.8812	1663.7711	832.3892	A	1203.6269	602.3171	1186.6004	593.8038	1185.6164	593.3118	10
17	1780.8501	890.9287	1763.8235	882.4154	1762.8395	881.9234	V	1132.5898	566.7985	1115.5633	558.2853	1114.5792	557.7933	9
18	1917.9090	959.4581	1900.8824	950.9448	1899.8984	950.4528	H	1033.5214	517.2643	1016.4948	508.7511	1015.5108	508.2591	8
19	2016.9774	1008.9923	1999.9508	1000.4791	1998.9668	999.9870	V	896.4625	448.7349	879.4359	440.2216	878.4519	439.7296	7
20	2116.0458	1058.5265	2099.0192	1050.0133	2098.0352	1049.5213	V	797.3941	399.2007	780.3675	390.6874	779.3835	390.1954	6
21	2231.0727	1116.0400	2214.0462	1107.5267	2213.0622	1107.0347	D	698.3256	349.6665	681.2991	341.1532	680.3151	340.6612	5
22	2378.1412	1189.5742	2361.1146	1181.0609	2360.1306	1180.5689	F	583.2987	292.1530	566.2722	283.6397	0	0	4
23	2525.2096	1263.1084	2508.1830	1254.5951	2507.1990	1254.1031	F	436.2303	218.6188	419.2037	210.1055	0	0	3
24	2639.2525	1320.1299	2622.2259	1311.6166	2621.2419	1311.1246	N	289.1619	145.0846	272.1353	136.5713	0	0	2
25							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 7663.

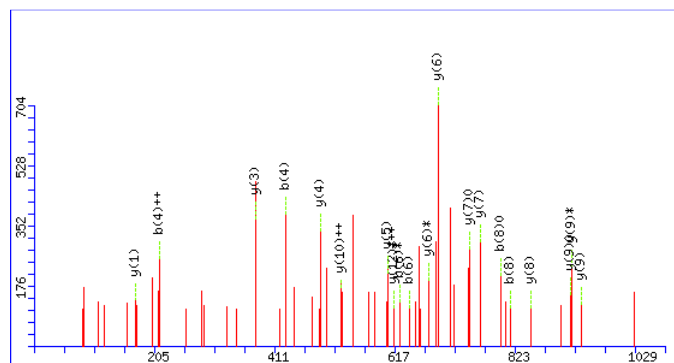
MS/MS Fragmentation of **SQNTPDSSASNLGFR**:

Found in **IP100301144;IP100332413;IP100785161;IP100909551;IP100909612**

Title: 2.1.1.713.8

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120208ry¥120208ry_Tig120slc-P8_2.2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							15
2	216.0979	108.5526	199.0713	100.0393	198.0873	99.5473	Q	1493.6979	747.3526	1476.6714	738.8393	1475.6873	738.3473	14
3	330.1408	165.5740	313.1143	157.0608	312.1302	156.5688	N	1365.6393	683.3233	1348.6128	674.8100	1347.6288	674.3180	13
4	431.1885	216.0979	414.1619	207.5846	413.1779	207.0926	T	1251.5964	626.3018	1234.5699	617.7886	1233.5858	617.2966	12
5	528.2413	264.6243	511.2147	256.1110	510.2307	255.6190	P	1150.5487	575.7780	1133.5222	567.2647	1132.5382	566.7727	11
6	643.2682	322.1377	626.2416	313.6245	625.2576	313.1325	D	1053.4960	527.2516	1036.4694	518.7383	1035.4854	518.2463	10
7	730.3002	365.6537	713.2737	357.1405	712.2897	356.6485	S	938.4690	469.7381	921.4425	461.2249	920.4585	460.7329	9
8	817.3323	409.1698	800.3057	400.6565	799.3217	400.1645	S	851.4370	426.2221	834.4104	417.7089	833.4264	417.2169	8
9	888.3694	444.6883	871.3428	436.1750	870.3588	435.6830	A	764.4050	382.7061	747.3784	374.1928	746.3944	373.7008	7
10	975.4014	488.2043	958.3748	479.6911	957.3908	479.1991	S	693.3678	347.1876	676.3413	338.6743	675.3573	338.1823	6
11	1089.4443	545.2258	1072.4178	536.7125	1071.4338	536.2205	N	606.3358	303.6715	589.3093	295.1583	0	0	5
12	1202.5284	601.7678	1185.5018	593.2546	1184.5178	592.7625	L	492.2929	246.6501	475.2663	238.1368	0	0	4
13	1259.5498	630.2786	1242.5233	621.7653	1241.5393	621.2733	G	379.2088	190.1081	362.1823	181.5948	0	0	3
14	1406.6183	703.8128	1389.5917	695.2995	1388.6077	694.8075	F	322.1874	161.5973	305.1608	153.0840	0	0	2
15							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 8026.

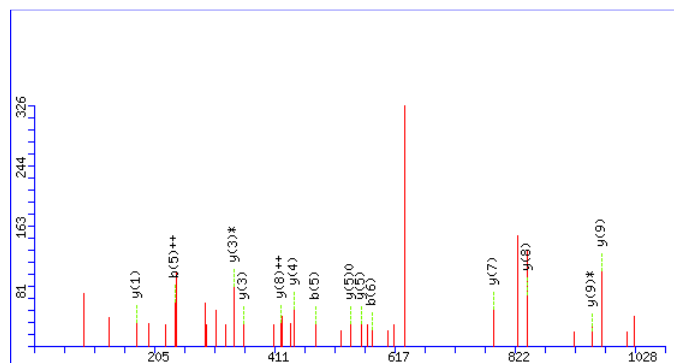
MS/MS Fragmentation of **LAIQGPEDSPSR**:

Found in **IP100023095**

Title: 2.1.1.407.10

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							12
2	185.1285	93.0679	0	0	0	0	A	1156.5593	578.7833	1139.5327	570.2700	1138.5487	569.7780	11
3	298.2125	149.6099	0	0	0	0	I	1085.5222	543.2647	1068.4956	534.7515	1067.5116	534.2594	10
4	426.2711	213.6392	409.2445	205.1259	0	0	Q	972.4381	486.7227	955.4116	478.2094	954.4275	477.7174	9
5	483.2926	242.1499	466.2660	233.6366	0	0	G	844.3795	422.6934	827.3530	414.1801	826.3690	413.6881	8
6	580.3453	290.6763	563.3188	282.1630	0	0	P	787.3581	394.1827	770.3315	385.6694	769.3475	385.1774	7
7	709.3879	355.1976	692.3614	346.6843	691.3774	346.1923	E	690.3053	345.6563	673.2788	337.1430	672.2947	336.6510	6
8	824.4149	412.7111	807.3883	404.1978	806.4043	403.7058	D	561.2627	281.1350	544.2362	272.6217	543.2522	272.1297	5
9	911.4469	456.2271	894.4203	447.7138	893.4363	447.2218	S	446.2358	223.6215	429.2092	215.1082	428.2252	214.6162	4
10	1008.4997	504.7535	991.4731	496.2402	990.4891	495.7482	P	359.2037	180.1055	342.1772	171.5922	341.1932	171.1002	3
11	1095.5317	548.2695	1078.5051	539.7562	1077.5211	539.2642	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
12							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 8080.

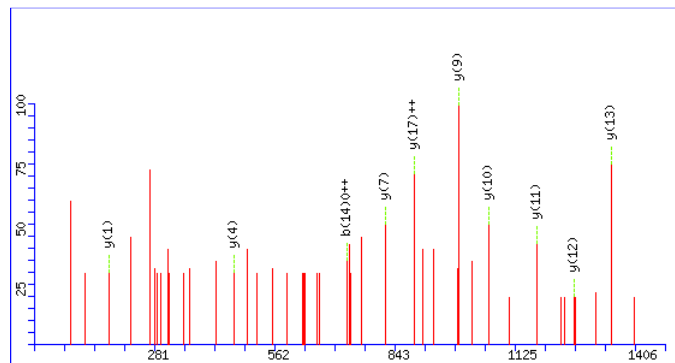
MS/MS Fragmentation of **WIAQDLSSLAGLLDQHGVK**:

Found in **IP100152199;IP100383997;IP100643409;IP100908363;IP100910916;IP100976876;IP101008862**

Title: 4.1.1.1789.5

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	187.0866	94.0469	0	0	0	0	W							19
2	300.1707	150.5890	0	0	0	0	I	1893.0189	947.0131	1875.9923	938.4998	1875.0083	938.0078	18
3	371.2078	186.1075	0	0	0	0	A	1779.9348	890.4710	1762.9082	881.9578	1761.9242	881.4657	17
4	499.2663	250.1368	482.2398	241.6235	0	0	Q	1708.8977	854.9525	1691.8711	846.4392	1690.8871	845.9472	16
5	614.2933	307.6503	597.2667	299.1370	596.2827	298.6450	D	1580.8391	790.9232	1563.8125	782.4099	1562.8285	781.9179	15
6	727.3774	364.1923	710.3508	355.6790	709.3668	355.1870	L	1465.8122	733.4097	1448.7856	724.8964	1447.8016	724.4044	14
7	814.4094	407.7083	797.3828	399.1951	796.3988	398.7030	S	1352.7281	676.8677	1335.7015	668.3544	1334.7175	667.8624	13
8	901.4414	451.2243	884.4149	442.7111	883.4308	442.2191	S	1265.6961	633.3517	1248.6695	624.8384	1247.6855	624.3464	12
9	1014.5255	507.7664	997.4989	499.2531	996.5149	498.7611	L	1178.6640	589.8357	1161.6375	581.3224	1160.6535	580.8304	11
10	1085.5626	543.2849	1068.5360	534.7717	1067.5520	534.2796	A	1065.5800	533.2936	1048.5534	524.7803	1047.5694	524.2883	10
11	1142.5841	571.7957	1125.5575	563.2824	1124.5735	562.7904	G	994.5429	497.7751	977.5163	489.2618	976.5323	488.7698	9
12	1255.6681	628.3377	1238.6416	619.8244	1237.6575	619.3324	L	937.5214	469.2643	920.4948	460.7511	919.5108	460.2591	8
13	1368.7522	684.8797	1351.7256	676.3665	1350.7416	675.8744	L	824.4373	412.7223	807.4108	404.2090	806.4268	403.7170	7
14	1483.7791	742.3932	1466.7526	733.8799	1465.7686	733.3879	D	711.3533	356.1803	694.3267	347.6670	693.3427	347.1750	6
15	1611.8377	806.4225	1594.8111	797.9092	1593.8271	797.4172	Q	596.3263	298.6668	579.2998	290.1535	0	0	5
16	1748.8966	874.9519	1731.8701	866.4387	1730.8860	865.9467	H	468.2677	234.6375	451.2412	226.1242	0	0	4
17	1805.9181	903.4627	1788.8915	894.9494	1787.9075	894.4574	G	331.2088	166.1081	314.1823	157.5948	0	0	3
18	1904.9865	952.9969	1887.9599	944.4836	1886.9759	943.9916	V	274.1874	137.5973	257.1608	129.0840	0	0	2
19							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 8135.

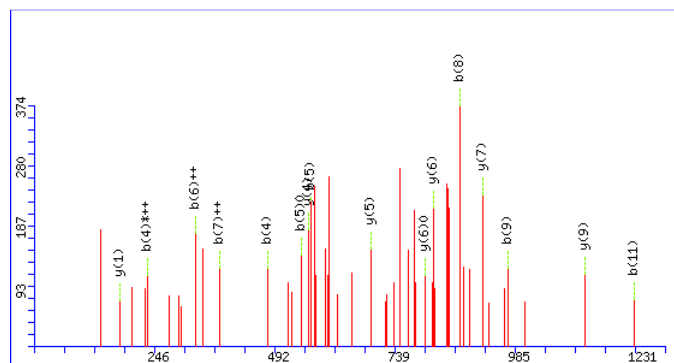
MS/MS Fragmentation of **RPPESPPIVEEWSR**:

Found in **IP100027798**

Title: 2.1.1.3253.5

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	157.1084	79.0578	140.0818	70.5446	0	0	R							15
2	254.1612	127.5842	237.1346	119.0709	0	0	P	1636.7966	818.9019	1619.7700	810.3886	1618.7860	809.8966	14
3	351.2139	176.1106	334.1874	167.5973	0	0	P	1539.7438	770.3755	1522.7172	761.8623	1521.7332	761.3703	13
4	480.2565	240.6319	463.2300	232.1186	462.2459	231.6266	E	1442.6910	721.8492	1425.6645	713.3359	1424.6805	712.8439	12
5	567.2885	284.1479	550.2620	275.6346	549.2780	275.1426	S	1313.6484	657.3279	1296.6219	648.8146	1295.6379	648.3226	11
6	664.3413	332.6743	647.3148	324.1610	646.3307	323.6690	P	1226.6164	613.8118	1209.5899	605.2986	1208.6058	604.8066	10
7	761.3941	381.2007	744.3675	372.6874	743.3835	372.1954	P	1129.5636	565.2855	1112.5371	556.7722	1111.5531	556.2802	9
8	874.4781	437.7427	857.4516	429.2294	856.4676	428.7374	I	1032.5109	516.7591	1015.4843	508.2458	1014.5003	507.7538	8
9	973.5465	487.2769	956.5200	478.7636	955.5360	478.2716	V	919.4268	460.2170	902.4003	451.7038	901.4163	451.2118	7
10	1102.5891	551.7982	1085.5626	543.2849	1084.5786	542.7929	E	820.3584	410.6828	803.3319	402.1696	802.3478	401.6776	6
11	1231.6317	616.3195	1214.6052	607.8062	1213.6212	607.3142	E	691.3158	346.1615	674.2893	337.6483	673.3052	337.1563	5
12	1417.7110	709.3592	1400.6845	700.8459	1399.7005	700.3539	W	562.2732	281.6402	545.2467	273.1270	544.2627	272.6350	4
13	1531.7540	766.3806	1514.7274	757.8673	1513.7434	757.3753	N	376.1939	188.6006	359.1674	180.0873	358.1833	179.5953	3
14	1618.7860	809.8966	1601.7594	801.3834	1600.7754	800.8914	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
15							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 8214.

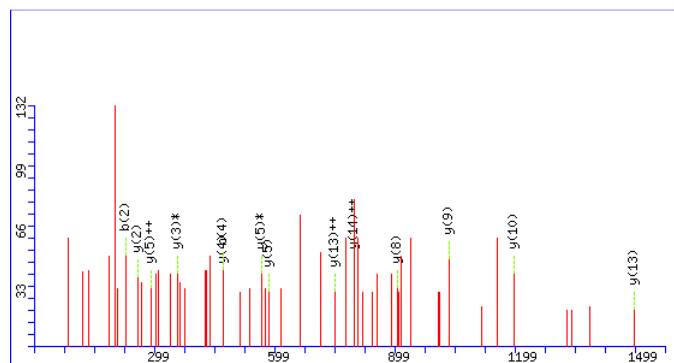
MS/MS Fragmentation of **DIELPSTTYEALHLPDIK**:

Found in **IP100012438;IP100981277**

Title: 4.1.1.1965.5

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							18
2	229.1183	115.0628	0	0	211.1077	106.0575	I	1952.0739	976.5406	1935.0474	968.0273	1934.0633	967.5353	17
3	358.1609	179.5841	0	0	340.1503	170.5788	E	1838.9898	919.9986	1821.9633	911.4853	1820.9793	910.9933	16
4	471.2449	236.1261	0	0	453.2344	227.1208	L	1709.9472	855.4773	1692.9207	846.9640	1691.9367	846.4720	15
5	568.2977	284.6525	0	0	550.2871	275.6472	P	1596.8632	798.9352	1579.8366	790.4220	1578.8526	789.9299	14
6	655.3297	328.1685	0	0	637.3192	319.1632	S	1499.8104	750.4088	1482.7839	741.8956	1481.7999	741.4036	13
7	756.3774	378.6923	0	0	738.3668	369.6871	T	1412.7784	706.8928	1395.7518	698.3796	1394.7678	697.8876	12
8	869.4615	435.2344	0	0	851.4509	426.2291	I	1311.7307	656.3690	1294.7042	647.8557	1293.7202	647.3637	11
9	1032.5248	516.7660	0	0	1014.5142	507.7608	Y	1198.6467	599.8270	1181.6201	591.3137	1180.6361	590.8217	10
10	1161.5674	581.2873	0	0	1143.5568	572.2821	E	1035.5833	518.2953	1018.5568	509.7820	1017.5728	509.2900	9
11	1232.6045	616.8059	0	0	1214.5939	607.8006	A	906.5407	453.7740	889.5142	445.2607	888.5302	444.7687	8
12	1345.6886	673.3479	0	0	1327.6780	664.3426	L	835.5036	418.2554	818.4771	409.7422	817.4931	409.2502	7
13	1482.7475	741.8774	0	0	1464.7369	732.8721	H	722.4196	361.7134	705.3930	353.2001	704.4090	352.7081	6
14	1595.8316	798.4194	0	0	1577.8210	789.4141	L	585.3606	293.1840	568.3341	284.6707	567.3501	284.1787	5
15	1692.8843	846.9458	0	0	1674.8738	837.9405	P	472.2766	236.6419	455.2500	228.1287	454.2660	227.6366	4
16	1807.9113	904.4593	0	0	1789.9007	895.4540	D	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
17	1920.9953	961.0013	0	0	1902.9848	951.9960	I	260.1969	130.6021	243.1703	122.0888	0	0	2
18							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 8246.

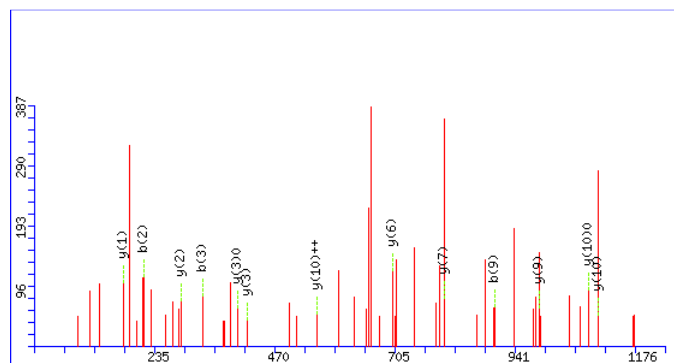
MS/MS Fragmentation of **TIDSVTSAQLR**:

Found in **IP100025803;IP100220325**

Title: 2.1.1.581.9

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							12
2	215.1390	108.0731	0	0	197.1285	99.0679	I	1218.6325	609.8199	1201.6059	601.3066	1200.6219	600.8146	11
3	330.1660	165.5866	0	0	312.1554	156.5813	D	1105.5484	553.2778	1088.5218	544.7646	1087.5378	544.2726	10
4	417.1980	209.1026	0	0	399.1874	200.0974	S	990.5214	495.7644	973.4949	487.2511	972.5109	486.7591	9
5	516.2664	258.6368	0	0	498.2558	249.6316	V	903.4894	452.2483	886.4629	443.7351	885.4789	443.2431	8
6	617.3141	309.1607	0	0	599.3035	300.1554	T	804.4210	402.7141	787.3945	394.2009	786.4104	393.7089	7
7	704.3461	352.6767	0	0	686.3355	343.6714	S	703.3733	352.1903	686.3468	343.6770	685.3628	343.1850	6
8	775.3832	388.1953	0	0	757.3727	379.1900	A	616.3413	308.6743	599.3148	300.1610	598.3307	299.6690	5
9	903.4418	452.2245	886.4153	443.7113	885.4312	443.2193	Q	545.3042	273.1557	528.2776	264.6425	527.2936	264.1504	4
10	1032.4844	516.7458	1015.4578	508.2326	1014.4738	507.7406	E	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
11	1145.5685	573.2879	1128.5419	564.7746	1127.5579	564.2826	L	288.2030	144.6051	271.1765	136.0919	0	0	2
12							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 8272.

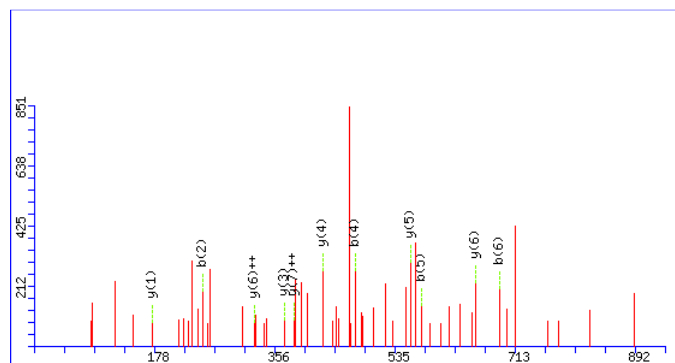
MS/MS Fragmentation of **HLLLVDPGQVVR**:

Found in **IP100021326;IP100165135;IP100643176;IP100643863;IP100786975;IP100943132;IP100973146;IP101014876**

Title: 2.1.1.4146.2

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	138.0662	69.5367	0	0	0	0	H							12
2	251.1503	126.0788	0	0	0	0	L	1209.7201	605.3637	1192.6936	596.8504	1191.7096	596.3584	11
3	364.2343	182.6208	0	0	0	0	L	1096.6361	548.8217	1079.6095	540.3084	1078.6255	539.8164	10
4	477.3184	239.1628	0	0	0	0	L	983.5520	492.2796	966.5255	483.7664	965.5415	483.2744	9
5	576.3868	288.6970	0	0	0	0	V	870.4680	435.7376	853.4414	427.2243	852.4574	426.7323	8
6	691.4137	346.2105	0	0	673.4032	337.2052	D	771.3995	386.2034	754.3730	377.6901	753.3890	377.1981	7
7	788.4665	394.7369	0	0	770.4559	385.7316	P	656.3726	328.6899	639.3461	320.1767	638.3620	319.6847	6
8	917.5091	459.2582	0	0	899.4985	450.2529	E	559.3198	280.1636	542.2933	271.6503	541.3093	271.1583	5
9	974.5306	487.7689	0	0	956.5200	478.7636	G	430.2772	215.6423	413.2507	207.1290	0	0	4
10	1073.5990	537.3031	0	0	1055.5884	528.2978	V	373.2558	187.1315	356.2292	178.6183	0	0	3
11	1172.6674	586.8373	0	0	1154.6568	577.8320	V	274.1874	137.5973	257.1608	129.0840	0	0	2
12							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 8445.

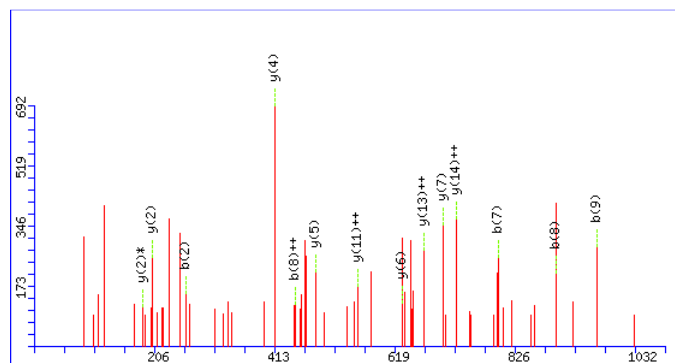
MS/MS Fragmentation of **FLLDHGDVAFAPLGK**:

Found in **IP100246842;IP100328322;IP100944587;IP100944618;IP101011153**

Title: 3.1.1.1707.3

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_3.mgf

ProteinPilot Peptide Confidence > 99%

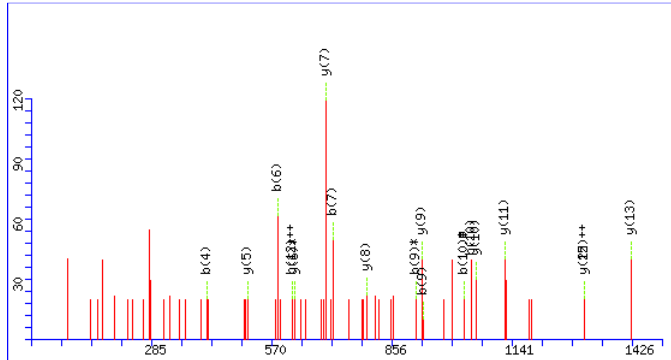


#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							15
2	261.1598	131.0835	0	0	0	0	L	1452.7845	726.8959	1435.7580	718.3826	1434.7740	717.8906	14
3	374.2438	187.6255	0	0	0	0	L	1339.7005	670.3539	1322.6739	661.8406	1321.6899	661.3486	13
4	489.2708	245.1390	0	0	471.2602	236.1337	D	1226.6164	613.8118	1209.5899	605.2986	1208.6058	604.8066	12
5	626.3297	313.6685	0	0	608.3191	304.6632	H	1111.5895	556.2984	1094.5629	547.7851	1093.5789	547.2931	11
6	683.3511	342.1792	0	0	665.3406	333.1739	G	974.5306	487.7689	957.5040	479.2556	956.5200	478.7636	10
7	798.3781	399.6927	0	0	780.3675	390.6874	D	917.5091	459.2582	900.4825	450.7449	899.4985	450.2529	9
8	897.4465	449.2269	0	0	879.4359	440.2216	V	802.4822	401.7447	785.4556	393.2314	0	0	8
9	968.4836	484.7454	0	0	950.4730	475.7402	A	703.4137	352.2105	686.3872	343.6972	0	0	7
10	1115.5520	558.2796	0	0	1097.5415	549.2744	F	632.3766	316.6919	615.3501	308.1787	0	0	6
11	1186.5891	593.7982	0	0	1168.5786	584.7929	A	485.3082	243.1577	468.2817	234.6445	0	0	5
12	1283.6419	642.3246	0	0	1265.6313	633.3193	P	414.2711	207.6392	397.2445	199.1259	0	0	4
13	1396.7260	698.8666	0	0	1378.7154	689.8613	L	317.2183	159.1128	300.1918	150.5995	0	0	3
14	1453.7474	727.3774	0	0	1435.7369	718.3721	G	204.1343	102.5708	187.1077	94.0575	0	0	2
15							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 8480.

MS/MS Fragmentation of **HPALPAMVNDPPVPALLWAGEVGQVLAGR**:
 Found in **IP100479357;IP100877791;IP100877921;IP100982052;IP100982665;IP101015540**
 Title: 5.1.1.649.3
 Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_5.mgf
 ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	138.0662	69.5367	0	0	0	0	H							29
2	235.1190	118.0631	0	0	0	0	P	2909.5706	1455.2889	2892.5440	1446.7757	2891.5600	1446.2837	28
3	306.1561	153.5817	0	0	0	0	A	2812.5178	1406.7626	2795.4913	1398.2493	2794.5073	1397.7573	27
4	419.2401	210.1237	0	0	0	0	L	2741.4807	1371.2440	2724.4542	1362.7307	2723.4702	1362.2387	26
5	516.2929	258.6501	0	0	0	0	P	2628.3967	1314.7020	2611.3701	1306.1887	2610.3861	1305.6967	25
6	587.3300	294.1686	0	0	0	0	A	2531.3439	1266.1756	2514.3173	1257.6623	2513.3333	1257.1703	24
7	718.3705	359.6889	0	0	0	0	M	2460.3068	1230.6570	2443.2802	1222.1438	2442.2962	1221.6517	23
8	817.4389	409.2231	0	0	0	0	V	2329.2663	1165.1368	2312.2397	1156.6235	2311.2557	1156.1315	22
9	931.4818	466.2446	914.4553	457.7313	0	0	N	2230.1979	1115.6026	2213.1713	1107.0893	2212.1873	1106.5973	21
10	1046.5088	523.7580	1029.4822	515.2448	1028.4982	514.7527	D	2116.1550	1058.5811	2099.1284	1050.0678	2098.1444	1049.5758	20
11	1143.5615	572.2844	1126.5350	563.7711	1125.5510	563.2791	P	2001.1280	1001.0676	1984.1015	992.5544	1983.1174	992.0624	19
12	1240.6143	620.8108	1223.5878	612.2975	1222.6037	611.8055	P	1904.0752	952.5413	1887.0487	944.0280	1886.0647	943.5360	18
13	1339.6827	670.3450	1322.6562	661.8317	1321.6722	661.3397	V	1807.0225	904.0149	1789.9959	895.5016	1789.0119	895.0096	17
14	1436.7355	718.8714	1419.7089	710.3581	1418.7249	709.8661	P	1707.9541	854.4807	1690.9275	845.9674	1689.9435	845.4754	16
15	1507.7726	754.3899	1490.7460	745.8767	1489.7620	745.3847	A	1610.9013	805.9543	1593.8748	797.4410	1592.8907	796.9490	15
16	1620.8567	810.9320	1603.8301	802.4187	1602.8461	801.9267	L	1539.8642	770.4357	1522.8376	761.9225	1521.8536	761.4305	14
17	1733.9407	867.4740	1716.9142	858.9607	1715.9302	858.4687	L	1426.7801	713.8937	1409.7536	705.3804	1408.7696	704.8884	13
18	1920.0200	960.5137	1902.9935	952.0004	1902.0095	951.5084	W	1313.6961	657.3517	1296.6695	648.8384	1295.6855	648.3464	12
19	1991.0572	996.0322	1974.0306	987.5189	1973.0466	987.0269	A	1127.6167	564.3120	1110.5902	555.7987	1109.6062	555.3067	11
20	2119.1157	1060.0615	2102.0892	1051.5482	2101.1052	1051.0562	Q	1056.5796	528.7935	1039.5531	520.2802	1038.5691	519.7882	10
21	2248.1583	1124.5828	2231.1318	1116.0695	2230.1478	1115.5775	E	928.5211	464.7642	911.4945	456.2509	910.5105	455.7589	9
22	2347.2267	1174.1170	2330.2002	1165.6037	2329.2162	1165.1117	V	799.4785	400.2429	782.4519	391.7296	0	0	8
23	2404.2482	1202.6277	2387.2217	1194.1145	2386.2376	1193.6225	G	700.4100	350.7087	683.3835	342.1954	0	0	7
24	2532.3068	1266.6570	2515.2802	1258.1438	2514.2962	1257.6517	Q	643.3886	322.1979	626.3620	313.6847	0	0	6
25	2631.3752	1316.1912	2614.3486	1307.6780	2613.3646	1307.1860	V	515.3300	258.1686	498.3035	249.6554	0	0	5
26	2744.4593	1372.7333	2727.4327	1364.2200	2726.4487	1363.7280	L	416.2616	208.6344	399.2350	200.1212	0	0	4
27	2815.4964	1408.2518	2798.4698	1399.7385	2797.4858	1399.2465	A	303.1775	152.0924	286.1510	143.5791	0	0	3
28	2872.5178	1436.7626	2855.4913	1428.2493	2854.5073	1427.7573	G	232.1404	116.5738	215.1139	108.0606	0	0	2
29							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 8631.

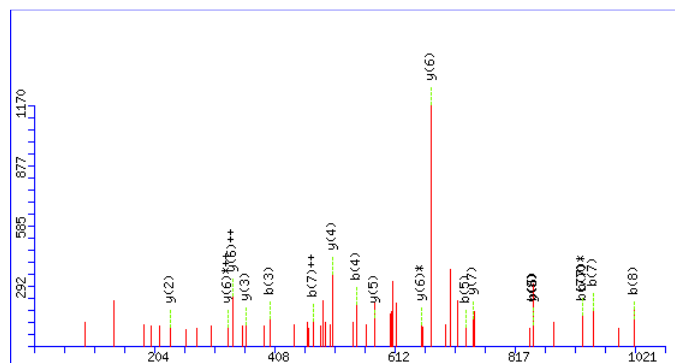
MS/MS Fragmentation of **RDEFWDTAPAFEGR**:

Found in **IP100017227;IP100157729**

Title: 3.1.1.523.4

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120206ry¥120206ry_aHDF1419-P10_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	157.1084	79.0578	140.0818	70.5446	0	0	R							14
2	272.1353	136.5713	255.1088	128.0580	254.1248	127.5660	D	1540.6703	770.8388	1523.6438	762.3255	1522.6597	761.8335	13
3	401.1779	201.0926	384.1514	192.5793	383.1674	192.0873	E	1425.6434	713.3253	1408.6168	704.8120	1407.6328	704.3200	12
4	548.2463	274.6268	531.2198	266.1135	530.2358	265.6215	F	1296.6008	648.8040	1279.5742	640.2907	1278.5902	639.7987	11
5	734.3257	367.6665	717.2991	359.1532	716.3151	358.6612	W	1149.5323	575.2698	1132.5058	566.7565	1131.5218	566.2645	10
6	849.3526	425.1799	832.3260	416.6667	831.3420	416.1747	D	963.4530	482.2302	946.4265	473.7169	945.4425	473.2249	9
7	950.4003	475.7038	933.3737	467.1905	932.3897	466.6985	T	848.4261	424.7167	831.3995	416.2034	830.4155	415.7114	8
8	1021.4374	511.2223	1004.4108	502.7091	1003.4268	502.2170	A	747.3784	374.1928	730.3519	365.6796	729.3679	365.1876	7
9	1118.4902	559.7487	1101.4636	551.2354	1100.4796	550.7434	P	676.3413	338.6743	659.3148	330.1610	658.3307	329.6690	6
10	1189.5273	595.2673	1172.5007	586.7540	1171.5167	586.2620	A	579.2885	290.1479	562.2620	281.6346	561.2780	281.1426	5
11	1336.5957	668.8015	1319.5691	660.2882	1318.5851	659.7962	F	508.2514	254.6293	491.2249	246.1161	490.2409	245.6241	4
12	1465.6383	733.3228	1448.6117	724.8095	1447.6277	724.3175	E	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	3
13	1522.6597	761.8335	1505.6332	753.3202	1504.6492	752.8282	G	232.1404	116.5738	215.1139	108.0606	0	0	2
14							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 8633.

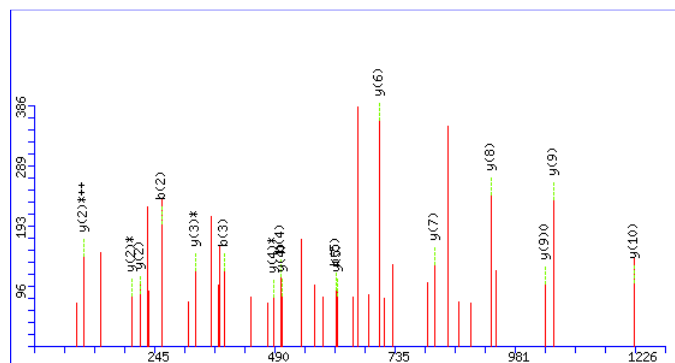
MS/MS Fragmentation of **PYENISLCQAK: 57.021465@C:8**

Found in **IP100655885;IP100872094;IP101015250;IP101025263;IP101025383;IP101025612**

Title: 2.1.1.848.10

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	98.0600	49.5337	0	0	0	0	P							11
2	261.1234	131.0653	0	0	0	0	Y	1225.5882	613.2977	1208.5616	604.7844	1207.5776	604.2924	10
3	390.1660	195.5866	0	0	372.1554	186.5813	E	1062.5248	531.7660	1045.4983	523.2528	1044.5143	522.7608	9
4	504.2089	252.6081	487.1823	244.0948	486.1983	243.6028	N	933.4822	467.2448	916.4557	458.7315	915.4717	458.2395	8
5	617.2930	309.1501	600.2664	300.6368	599.2824	300.1448	I	819.4393	410.2233	802.4128	401.7100	801.4287	401.2180	7
6	704.3250	352.6661	687.2984	344.1529	686.3144	343.6608	S	706.3552	353.6813	689.3287	345.1680	688.3447	344.6760	6
7	817.4090	409.2082	800.3825	400.6949	799.3985	400.2029	L	619.3232	310.1652	602.2967	301.6520	0	0	5
8	977.4397	489.2235	960.4131	480.7102	959.4291	480.2182	C	506.2391	253.6232	489.2126	245.1099	0	0	4
9	1105.4983	553.2528	1088.4717	544.7395	1087.4877	544.2475	Q	346.2085	173.6079	329.1819	165.0946	0	0	3
10	1176.5354	588.7713	1159.5088	580.2581	1158.5248	579.7660	A	218.1499	109.5786	201.1234	101.0653	0	0	2
11							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 8966.

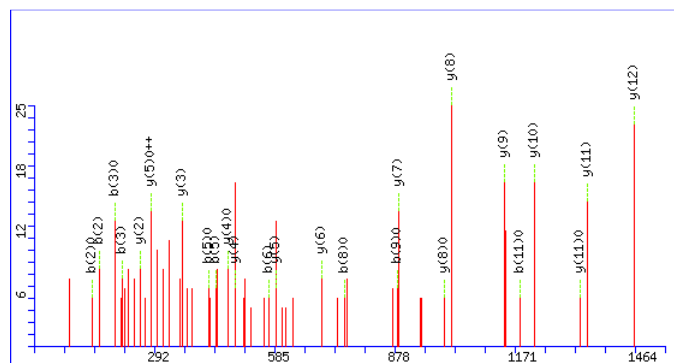
MS/MS Fragmentation of **GTGLDEAMEWLVELK**:

Found in **IP100219518;IP100791961;IP100908516;IP101011723;IP101022233**

Title: 5.1.1.2475.2

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_3_5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							16
2	159.0764	80.0418	0	0	141.0659	71.0366	T	1734.8619	867.9346	1717.8353	859.4213	1716.8513	858.9293	15
3	216.0979	108.5526	0	0	198.0873	99.5473	G	1633.8142	817.4107	1616.7876	808.8975	1615.8036	808.4054	14
4	329.1819	165.0946	0	0	311.1714	156.0893	L	1576.7927	788.9000	1559.7662	780.3867	1558.7822	779.8947	13
5	444.2089	222.6081	0	0	426.1983	213.6028	D	1463.7087	732.3580	1446.6821	723.8447	1445.6981	723.3527	12
6	573.2515	287.1294	0	0	555.2409	278.1241	E	1348.6817	674.8445	1331.6552	666.3312	1330.6712	665.8392	11
7	644.2886	322.6479	0	0	626.2780	313.6427	A	1219.6391	610.3232	1202.6126	601.8099	1201.6286	601.3179	10
8	775.3291	388.1682	0	0	757.3185	379.1629	M	1148.6020	574.8046	1131.5755	566.2914	1130.5914	565.7994	9
9	904.3717	452.6895	0	0	886.3611	443.6842	E	1017.5615	509.2844	1000.5350	500.7711	999.5510	500.2791	8
10	1090.4510	545.7291	0	0	1072.4404	536.7238	W	888.5189	444.7631	871.4924	436.2498	870.5084	435.7578	7
11	1203.5351	602.2712	0	0	1185.5245	593.2659	L	702.4396	351.7234	685.4131	343.2102	684.4291	342.7182	6
12	1302.6035	651.8054	0	0	1284.5929	642.8001	V	589.3556	295.1814	572.3290	286.6681	571.3450	286.1761	5
13	1431.6461	716.3267	0	0	1413.6355	707.3214	E	490.2871	245.6472	473.2606	237.1339	472.2766	236.6419	4
14	1532.6937	766.8505	0	0	1514.6832	757.8452	T	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
15	1645.7778	823.3925	0	0	1627.7672	814.3873	L	260.1969	130.6021	243.1703	122.0888	0	0	2
16							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 8989.

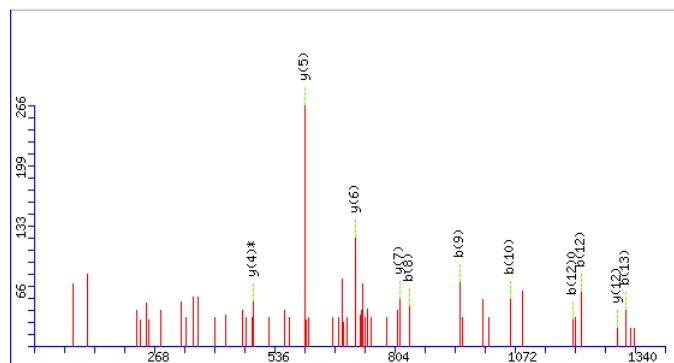
MS/MS Fragmentation of **VLGDIHTLLSAVIPNAFR**:

Found in **IP100306658;IP100513926;IP100844379;IP101012794;IP101014016**

Title: 4.1.1.619.4

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120210ry¥120210ry_32R1-32_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							19
2	213.1598	107.0835	0	0	0	0	L	1938.0807	969.5440	1921.0542	961.0307	1920.0702	960.5387	18
3	270.1812	135.5942	0	0	0	0	G	1824.9967	913.0020	1807.9701	904.4887	1806.9861	903.9967	17
4	385.2082	193.1077	0	0	367.1976	184.1024	D	1767.9752	884.4912	1750.9486	875.9780	1749.9646	875.4860	16
5	498.2922	249.6498	0	0	480.2817	240.6445	I	1652.9483	826.9778	1635.9217	818.4645	1634.9377	817.9725	15
6	635.3511	318.1792	0	0	617.3406	309.1739	H	1539.8642	770.4357	1522.8376	761.9225	1521.8536	761.4305	14
7	736.3988	368.7030	0	0	718.3883	359.6978	T	1402.8053	701.9063	1385.7787	693.3930	1384.7947	692.9010	13
8	837.4465	419.2269	0	0	819.4359	410.2216	T	1301.7576	651.3824	1284.7310	642.8692	1283.7470	642.3772	12
9	950.5306	475.7689	0	0	932.5200	466.7636	L	1200.7099	600.8586	1183.6834	592.3453	1182.6994	591.8533	11
10	1063.6146	532.3109	0	0	1045.6041	523.3057	L	1087.6259	544.3166	1070.5993	535.8033	1069.6153	535.3113	10
11	1150.6467	575.8270	0	0	1132.6361	566.8217	S	974.5418	487.7745	957.5152	479.2613	956.5312	478.7693	9
12	1221.6838	611.3455	0	0	1203.6732	602.3402	A	887.5098	444.2585	870.4832	435.7452	0	0	8
13	1320.7522	660.8797	0	0	1302.7416	651.8744	V	816.4726	408.7400	799.4461	400.2267	0	0	7
14	1433.8362	717.4218	0	0	1415.8257	708.4165	I	717.4042	359.2058	700.3777	350.6925	0	0	6
15	1530.8890	765.9481	0	0	1512.8784	756.9429	P	604.3202	302.6637	587.2936	294.1504	0	0	5
16	1644.9319	822.9696	1627.9054	814.4563	1626.9214	813.9643	N	507.2674	254.1373	490.2409	245.6241	0	0	4
17	1715.9690	858.4882	1698.9425	849.9749	1697.9585	849.4829	A	393.2245	197.1159	376.1979	188.6026	0	0	3
18	1863.0375	932.0224	1846.0109	923.5091	1845.0269	923.0171	F	322.1874	161.5973	305.1608	153.0840	0	0	2
19							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 9003.

MS/MS Fragmentation of **VTNQLQYLHK**:

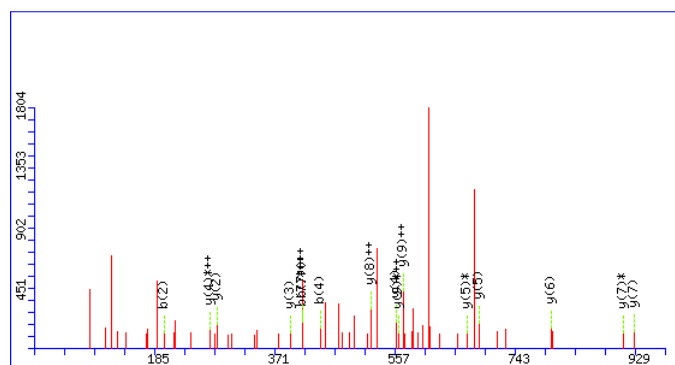
Found in

IP100014414;IP100440502;IP100794051;IP100797929;IP100893088;IP100893552;IP100893622;IP100893701;IP100894013;IP100894298;IP100894424;IP100981776;IP1009821

Title: 1.1.1.9297.2

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120210ry¥120210ry_32R1-32_2_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							10
2	201.1234	101.0653	0	0	183.1128	92.0600	T	1144.6109	572.8091	1127.5844	564.2958	1126.6004	563.8038	9
3	315.1663	158.0868	298.1397	149.5735	297.1557	149.0815	N	1043.5633	522.2853	1026.5367	513.7720	0	0	8
4	443.2249	222.1161	426.1983	213.6028	425.2143	213.1108	Q	929.5203	465.2638	912.4938	456.7505	0	0	7
5	556.3089	278.6581	539.2824	270.1448	538.2984	269.6528	L	801.4618	401.2345	784.4352	392.7212	0	0	6
6	684.3675	342.6874	667.3410	334.1741	666.3570	333.6821	Q	688.3777	344.6925	671.3511	336.1792	0	0	5
7	847.4308	424.2191	830.4043	415.7058	829.4203	415.2138	Y	560.3191	280.6632	543.2926	272.1499	0	0	4
8	960.5149	480.7611	943.4884	472.2478	942.5043	471.7558	L	397.2558	199.1315	380.2292	190.6183	0	0	3
9	1097.5738	549.2905	1080.5473	540.7773	1079.5633	540.2853	H	284.1717	142.5895	267.1452	134.0762	0	0	2
10							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 9178.

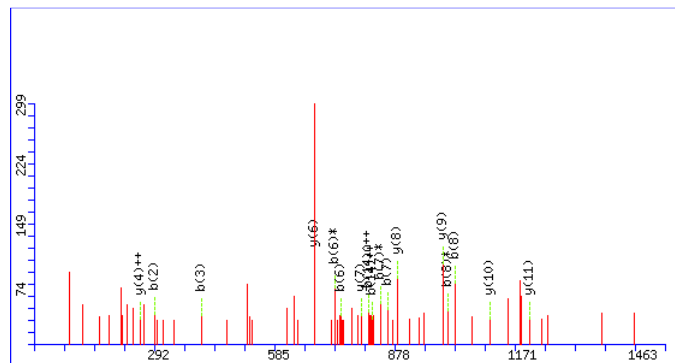
MS/MS Fragmentation of **FFNLQVLYPLSDPALNLR**:

Found in **IP100012402,IP100554552,IP100644538**

Title: 4.1.1.4369.3

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							19
2	295.1441	148.0757	0	0	0	0	F	2086.1695	1043.5884	2069.1430	1035.0751	2068.1590	1034.5831	18
3	409.1870	205.0972	392.1605	196.5839	0	0	N	1939.1011	970.0542	1922.0746	961.5409	1921.0906	961.0489	17
4	522.2711	261.6392	505.2445	253.1259	0	0	L	1825.0582	913.0327	1808.0316	904.5195	1807.0476	904.0275	16
5	650.3297	325.6685	633.3031	317.1552	0	0	Q	1711.9741	856.4907	1694.9476	847.9774	1693.9636	847.4854	15
6	749.3981	375.2027	732.3715	366.6894	0	0	V	1583.9156	792.4614	1566.8890	783.9481	1565.9050	783.4561	14
7	862.4822	431.7447	845.4556	423.2314	0	0	L	1484.8471	742.9272	1467.8206	734.4139	1466.8366	733.9219	13
8	1025.5455	513.2764	1008.5189	504.7631	0	0	Y	1371.7631	686.3852	1354.7365	677.8719	1353.7525	677.3799	12
9	1122.5982	561.8028	1105.5717	553.2895	0	0	P	1208.6997	604.8535	1191.6732	596.3402	1190.6892	595.8482	11
10	1235.6823	618.3448	1218.6558	609.8315	0	0	L	1111.6470	556.3271	1094.6204	547.8139	1093.6364	547.3218	10
11	1348.7664	674.8868	1331.7398	666.3735	0	0	L	998.5629	499.7851	981.5364	491.2718	980.5524	490.7798	9
12	1435.7984	718.4028	1418.7719	709.8896	1417.7878	709.3976	S	885.4789	443.2431	868.4523	434.7298	867.4683	434.2378	8
13	1550.8253	775.9163	1533.7988	767.4030	1532.8148	766.9110	D	798.4468	399.7271	781.4203	391.2138	780.4363	390.7218	7
14	1647.8781	824.4427	1630.8516	815.9294	1629.8675	815.4374	P	683.4199	342.2136	666.3933	333.7003	0	0	6
15	1718.9152	859.9612	1701.8887	851.4480	1700.9047	850.9560	A	586.3671	293.6872	569.3406	285.1739	0	0	5
16	1831.9993	916.5033	1814.9727	907.9900	1813.9887	907.4980	L	515.3300	258.1686	498.3035	249.6554	0	0	4
17	1946.0422	973.5247	1929.0157	965.0115	1928.0316	964.5195	N	402.2459	201.6266	385.2194	193.1133	0	0	3
18	2059.1263	1030.0668	2042.0997	1021.5535	2041.1157	1021.0615	L	288.2030	144.6051	271.1765	136.0919	0	0	2
19							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 9381.

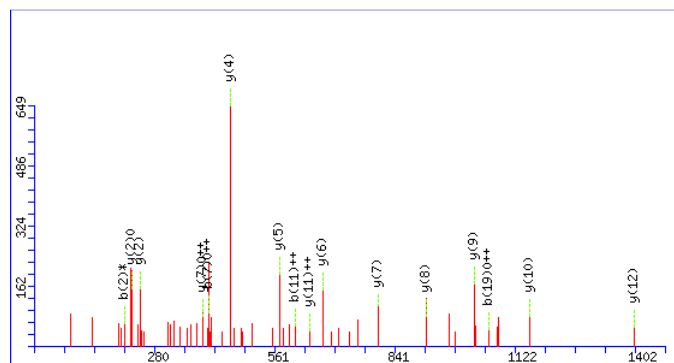
MS/MS Fragmentation of **DNYVPEISALDQEIIIVDPDTK: 0.984016@Q:12**

Found in **IP100018483**

Title: 3.1.1.4309.8

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							22
2	230.0771	115.5422	213.0506	107.0289	212.0666	106.5369	N	2389.1657	1195.0865	2372.1391	1186.5732	2371.1551	1186.0812	21
3	393.1405	197.0739	376.1139	188.5606	375.1299	188.0686	Y	2275.1228	1138.0650	2258.0962	1129.5517	2257.1122	1129.0597	20
4	492.2089	246.6081	475.1823	238.0948	474.1983	237.6028	V	2112.0594	1056.5334	2095.0329	1048.0201	2094.0489	1047.5281	19
5	589.2617	295.1345	572.2351	286.6212	571.2511	286.1292	P	2012.9910	1006.9992	1995.9645	998.4859	1994.9805	997.9939	18
6	718.3042	359.6558	701.2777	351.1425	700.2937	350.6505	E	1915.9383	958.4728	1898.9117	949.9595	1897.9277	949.4675	17
7	831.3883	416.1978	814.3618	407.6845	813.3777	407.1925	I	1786.8957	893.9515	1769.8691	885.4382	1768.8851	884.9462	16
8	918.4203	459.7138	901.3938	451.2005	900.4098	450.7085	S	1673.8116	837.4094	1656.7851	828.8962	1655.8010	828.4042	15
9	989.4575	495.2324	972.4309	486.7191	971.4469	486.2271	A	1586.7796	793.8934	1569.7530	785.3802	1568.7690	784.8881	14
10	1102.5415	551.7744	1085.5150	543.2611	1084.5310	542.7691	L	1515.7425	758.3749	1498.7159	749.8616	1497.7319	749.3696	13
11	1217.5685	609.2879	1200.5419	600.7746	1199.5579	600.2826	D	1402.6584	701.8328	1385.6318	693.3196	1384.6478	692.8276	12
12	1346.6111	673.8092	1329.5845	665.2959	1328.6005	664.8039	Q	1287.6315	644.3194	1270.6049	635.8061	1269.6209	635.3141	11
13	1475.6536	738.3305	1458.6271	729.8172	1457.6431	729.3252	E	1158.5889	579.7981	1141.5623	571.2848	1140.5783	570.7928	10
14	1588.7377	794.8725	1571.7112	786.3592	1570.7271	785.8672	I	1029.5463	515.2768	1012.5197	506.7635	1011.5357	506.2715	9
15	1701.8218	851.4145	1684.7952	842.9013	1683.8112	842.4092	I	918.4622	458.7347	899.4357	450.2215	898.4516	449.7295	8
16	1830.8644	915.9358	1813.8378	907.4225	1812.8538	906.9305	E	803.3781	402.1927	786.3516	393.6794	785.3676	393.1874	7
17	1929.9328	965.4700	1912.9062	956.9568	1911.9222	956.4647	V	674.3355	337.6714	657.3090	329.1581	656.3250	328.6661	6
18	2044.9597	1022.9835	2027.9332	1014.4702	2026.9492	1013.9782	D	575.2671	288.1372	558.2406	279.6239	557.2566	279.1319	5
19	2142.0125	1071.5099	2124.9859	1062.9966	2124.0019	1062.5046	P	460.2402	230.6237	443.2136	222.1105	442.2296	221.6185	4
20	2257.0394	1129.0234	2240.0129	1120.5101	2239.0289	1120.0181	D	363.1874	182.0974	346.1609	173.5841	345.1769	173.0921	3
21	2358.0871	1179.5472	2341.0606	1171.0339	2340.0765	1170.5419	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
22							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 9514.

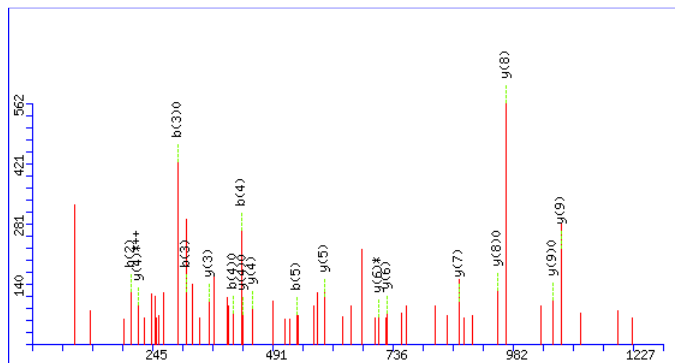
MS/MS Fragmentation of **DSLILPFQFSSEK**:

Found in **IPI00328185;IPI00829707**

Title: 3.1.1.3512.7

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							13
2	203.0662	102.0368	0	0	185.0557	93.0315	S	1395.7518	698.3796	1378.7253	689.8663	1377.7413	689.3743	12
3	316.1503	158.5788	0	0	298.1397	149.5735	L	1308.7198	654.8635	1291.6933	646.3503	1290.7093	645.8583	11
4	429.2344	215.1208	0	0	411.2238	206.1155	I	1195.6358	598.3215	1178.6092	589.8082	1177.6252	589.3162	10
5	542.3184	271.6629	0	0	524.3079	262.6576	L	1082.5517	541.7795	1065.5251	533.2662	1064.5411	532.7742	9
6	639.3712	320.1892	0	0	621.3606	311.1840	P	969.4676	485.2374	952.4411	476.7242	951.4571	476.2322	8
7	786.4396	393.7234	0	0	768.4291	384.7182	F	872.4149	436.7111	855.3883	428.1978	854.4043	427.7058	7
8	914.4982	457.7527	897.4716	449.2395	896.4876	448.7475	Q	725.3464	363.1769	708.3199	354.6636	707.3359	354.1716	6
9	1061.5666	531.2869	1044.5401	522.7737	1043.5560	522.2817	F	597.2879	299.1476	580.2613	290.6343	579.2773	290.1423	5
10	1148.5986	574.8030	1131.5721	566.2897	1130.5881	565.7977	S	450.2195	225.6134	433.1929	217.1001	432.2089	216.6081	4
11	1235.6307	618.3190	1218.6041	609.8057	1217.6201	609.3137	S	363.1874	182.0974	346.1609	173.5841	345.1769	173.0921	3
12	1364.6733	682.8403	1347.6467	674.3270	1346.6627	673.8350	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 9536.

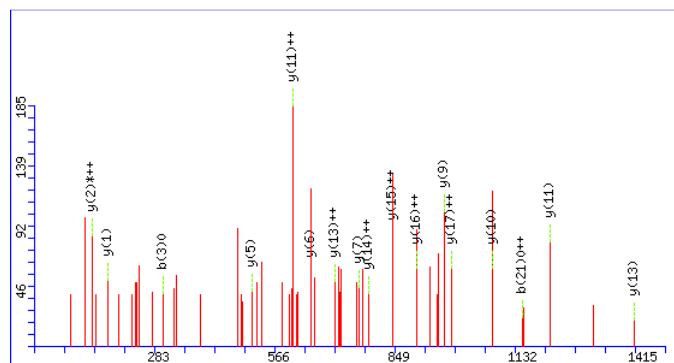
MS/MS Fragmentation of **SSFTTYLNYYVHLEADHGIGLR**:

Found in **IP100164352;IP100955853;IP100982616**

Title: 4.1.1.1376.2

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							22
2	175.0713	88.0393	0	0	157.0608	79.0340	S	2405.2248	1203.1160	2388.1983	1194.6028	2387.2143	1194.1108	21
3	322.1397	161.5735	0	0	304.1292	152.5682	F	2318.1928	1159.6000	2301.1662	1151.0868	2300.1822	1150.5948	20
4	423.1874	212.0974	0	0	405.1769	203.0921	T	2171.1244	1086.0658	2154.0978	1077.5526	2153.1138	1077.0605	19
5	524.2351	262.6212	0	0	506.2245	253.6159	T	2070.0767	1035.5420	2053.0502	1027.0287	2052.0661	1026.5367	18
6	687.2984	344.1529	0	0	669.2879	335.1476	Y	1969.0290	985.0181	1952.0025	976.5049	1951.0185	976.0129	17
7	800.3825	400.6949	0	0	782.3719	391.6896	L	1805.9657	903.4865	1788.9391	894.9732	1787.9551	894.4812	16
8	914.4254	457.7164	897.3989	449.2031	896.4149	448.7111	N	1692.8816	846.9445	1675.8551	838.4312	1674.8711	837.9392	15
9	1077.4888	539.2480	1060.4622	530.7347	1059.4782	530.2427	Y	1578.8387	789.9230	1561.8122	781.4097	1560.8281	780.9177	14
10	1176.5572	588.7822	1159.5306	580.2689	1158.5466	579.7769	V	1415.7754	708.3913	1398.7488	699.8781	1397.7648	699.3860	13
11	1275.6256	638.3164	1258.5990	629.8032	1257.6150	629.3111	V	1316.7070	658.8571	1299.6804	650.3438	1298.6964	649.8518	12
12	1412.6845	706.8459	1395.6579	698.3326	1394.6739	697.8406	H	1217.6385	609.3229	1200.6120	600.8096	1199.6280	600.3176	11
13	1525.7686	763.3879	1508.7420	754.8746	1507.7580	754.3826	L	1080.5796	540.7935	1063.5531	532.2802	1062.5691	531.7882	10
14	1654.8112	827.9092	1637.7846	819.3959	1636.8006	818.9039	E	967.4956	484.2514	950.4690	475.7381	949.4850	475.2461	9
15	1725.8483	863.4278	1708.8217	854.9145	1707.8377	854.4225	A	838.4530	419.7301	821.4264	411.2169	820.4424	410.7248	8
16	1840.8752	920.9412	1823.8487	912.4280	1822.8646	911.9360	D	767.4159	384.2116	750.3893	375.6983	749.4053	375.2063	7
17	1977.9341	989.4707	1960.9076	980.9574	1959.9236	980.4654	H	652.3889	326.6981	635.3624	318.1848	0	0	6
18	2034.9556	1017.9814	2017.9290	1009.4682	2016.9450	1008.9761	G	515.3300	258.1686	498.3035	249.6554	0	0	5
19	2148.0396	1074.5235	2131.0131	1066.0102	2130.0291	1065.5182	I	458.3085	229.6579	441.2820	221.1446	0	0	4
20	2205.0611	1103.0342	2188.0346	1094.5209	2187.0505	1094.0289	G	345.2245	173.1159	328.1979	164.6026	0	0	3
21	2318.1452	1159.5762	2301.1186	1151.0630	2300.1346	1150.5709	L	288.2030	144.6051	271.1765	136.0919	0	0	2
22							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 9638.

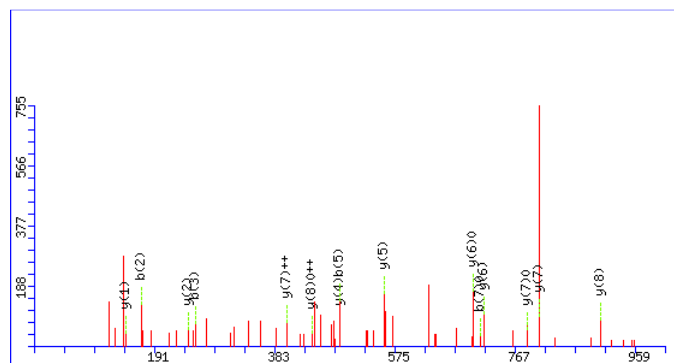
MS/MS Fragmentation of **AVSCAEIVK: 57.021465@C:4**

Found in **IP100166873**

Title: 1.1.1.7937.8

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_1.mgf

ProteinPilot Peptide Confidence > 99%

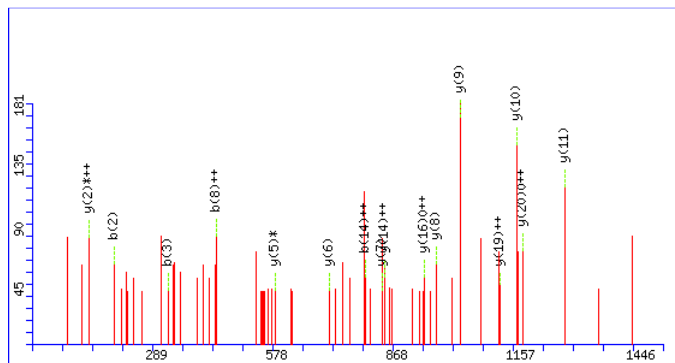


#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							9
2	171.1128	86.0600	0	0	0	0	V	905.4761	453.2417	888.4495	444.7284	887.4655	444.2364	8
3	258.1448	129.5761	0	0	240.1343	120.5708	S	806.4077	403.7075	789.3811	395.1942	788.3971	394.7022	7
4	418.1755	209.5914	0	0	400.1649	200.5861	C	719.3756	360.1915	702.3491	351.6782	701.3651	351.1862	6
5	489.2126	245.1099	0	0	471.2020	236.1047	A	559.3450	280.1761	542.3184	271.6629	541.3344	271.1709	5
6	618.2552	309.6312	0	0	600.2446	300.6260	E	488.3079	244.6576	471.2813	236.1443	470.2973	235.6523	4
7	731.3393	366.1733	0	0	713.3287	357.1680	I	359.2653	180.1363	342.2387	171.6230	0	0	3
8	830.4077	415.7075	0	0	812.3971	406.7022	V	246.1812	123.5942	229.1547	115.0810	0	0	2
9							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 9919.

MS/MS Fragmentation of **TPEDLNTIYSYLHGMEILSNLR: 0.984015@N:6**
 Found in **IP100291839;IP100337694;IP100337696;IP100943807;IP100943887;IP100966410;IP100968195**
 Title: 4.1.1.2967.10
 Data file: Y:\TT5600(CiRA1)\¥2012-02¥120214ry¥120214ry_32R1-32_4_4.mgf
 ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							22
2	199.1077	100.0575	0	0	181.0972	91.0522	P	2479.2174	1240.1123	2462.1908	1231.5990	2461.2068	1231.1070	21
3	328.1503	164.5788	0	0	310.1397	155.5735	E	2382.1646	1191.5859	2365.1380	1183.0727	2364.1540	1182.5806	20
4	443.1773	222.0923	0	0	425.1667	213.0870	D	2253.1220	1127.0646	2236.0954	1118.5514	2235.1114	1118.0594	19
5	556.2613	278.6343	0	0	538.2508	269.6290	L	2138.0951	1069.5512	2121.0685	1061.0379	2120.0845	1060.5459	18
6	671.2883	336.1478	654.2617	327.6345	653.2777	327.1425	N	2025.0110	1013.0091	2007.9844	1004.4959	2007.0004	1004.0038	17
7	772.3359	386.6716	755.3094	378.1583	754.3254	377.6663	T	1909.9840	955.4957	1892.9575	946.9824	1891.9735	946.4904	16
8	885.4200	443.2136	868.3935	434.7004	867.4094	434.2084	I	1808.9364	904.9718	1791.9098	896.4585	1790.9258	895.9665	15
9	1048.4833	524.7453	1031.4568	516.2320	1030.4728	515.7400	Y	1695.8523	848.4298	1678.8258	839.9165	1677.8417	839.4245	14
10	1135.5154	568.2613	1118.4888	559.7480	1117.5048	559.2560	S	1532.7890	766.8981	1515.7624	758.3849	1514.7784	757.8928	13
11	1298.5787	649.7930	1281.5521	641.2797	1280.5681	640.7877	Y	1445.7569	723.3821	1428.7304	714.8688	1427.7464	714.3768	12
12	1411.6628	706.3350	1394.6362	697.8217	1393.6522	697.3297	L	1282.6936	641.8504	1265.6671	633.3372	1264.6831	632.8452	11
13	1548.7217	774.8645	1531.6951	766.3512	1530.7111	765.8592	H	1169.6096	585.3084	1152.5830	576.7951	1151.5990	576.3031	10
14	1605.7431	803.3752	1588.7166	794.8619	1587.7326	794.3699	G	1032.5506	516.7790	1015.5241	508.2657	1014.5401	507.7737	9
15	1736.7836	868.8954	1719.7571	860.3822	1718.7731	859.8902	M	975.5292	488.2682	958.5026	479.7550	957.5186	479.2629	8
16	1865.8262	933.4167	1848.7997	924.9035	1847.8156	924.4115	E	844.4887	422.7480	827.4621	414.2347	826.4781	413.7427	7
17	1978.9103	989.9588	1961.8837	981.4455	1960.8997	980.9535	I	715.4461	358.2267	698.4195	349.7134	697.4355	349.2214	6
18	2091.9943	1046.5008	2074.9678	1037.9875	2073.9838	1037.4955	L	602.3620	301.6847	585.3355	293.1714	584.3515	292.6794	5
19	2179.0264	1090.0168	2161.9998	1081.5035	2161.0158	1081.0115	S	489.2780	245.1426	472.2514	236.6293	471.2674	236.1373	4
20	2293.0693	1147.0383	2276.0427	1138.5250	2275.0587	1138.0330	N	402.2459	201.6266	385.2194	193.1133	0	0	3
21	2406.1534	1203.5803	2389.1268	1195.0670	2388.1428	1194.5750	L	288.2030	144.6051	281.1765	136.0919	0	0	2
22							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 10009.

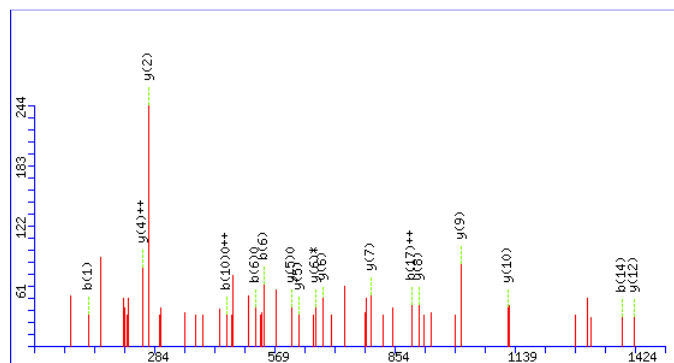
MS/MS Fragmentation of **EAGEASPGDDPQQLWLVLVDGIQDPR**:

Found in **IP100784477**

Title: 4.1.1.1218.10

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							25
2	201.0870	101.0471	0	0	183.0764	92.0418	A	2577.2580	1289.1326	2560.2314	1280.6194	2559.2474	1280.1273	24
3	258.1084	129.5579	0	0	240.0979	120.5526	G	2506.2209	1253.6141	2489.1943	1245.1008	2488.2103	1244.6088	23
4	387.1510	194.0792	0	0	369.1405	185.0739	E	2449.1994	1225.1033	2432.1728	1216.5901	2431.1888	1216.0981	22
5	458.1882	229.5977	0	0	440.1776	220.5924	A	2320.1568	1160.5820	2303.1303	1152.0688	2302.1462	1151.5768	21
6	545.2202	273.1137	0	0	527.2096	264.1084	S	2249.1197	1125.0635	2232.0931	1116.5502	2231.1091	1116.0582	20
7	642.2729	321.6401	0	0	624.2624	312.6348	P	2162.0877	1081.5475	2145.0611	1073.0342	2144.0771	1072.5422	19
8	699.2944	350.1508	0	0	681.2838	341.1456	G	2065.0349	1033.0211	2048.0083	1024.5078	2047.0243	1024.0158	18
9	814.3214	407.6643	0	0	796.3108	398.6590	D	2008.0134	1004.5104	1990.9869	995.9971	1990.0029	995.5051	17
10	929.3483	465.1778	0	0	911.3377	456.1725	D	1892.9865	946.9969	1875.9599	938.4836	1874.9759	937.9916	16
11	1026.4011	513.7042	0	0	1008.3905	504.6989	P	1777.9595	889.4834	1760.9330	880.9701	1759.9490	880.4781	15
12	1154.4596	577.7335	1137.4331	569.2202	1136.4491	568.7282	Q	1680.9068	840.9570	1663.8802	832.4438	1662.8962	831.9517	14
13	1282.5182	641.7627	1265.4917	633.2495	1264.5077	632.7575	Q	1552.8482	776.9277	1535.8217	768.4145	1534.8376	767.9225	13
14	1395.6023	698.3048	1378.5757	689.7915	1377.5917	689.2995	L	1424.7896	712.8985	1407.7631	704.3852	1406.7791	703.8932	12
15	1581.6816	791.3444	1564.6550	782.8312	1563.6710	782.3392	W	1311.7056	656.3564	1294.6790	647.8431	1293.6950	647.3511	11
16	1694.7657	847.8865	1677.7391	839.3732	1676.7551	838.8812	L	1125.6262	563.3168	1108.5997	554.8035	1107.6157	554.3115	10
17	1793.8341	897.4207	1776.8075	888.9074	1775.8235	888.4154	V	1012.5422	506.7747	995.5156	498.2615	994.5316	497.7694	9
18	1906.9181	953.9627	1889.8916	945.4494	1888.9076	944.9574	L	913.4738	457.2405	896.4472	448.7272	895.4632	448.2352	8
19	2021.9451	1011.4762	2004.9185	1002.9629	2003.9345	1002.4709	D	800.3897	400.6985	783.3632	392.1852	782.3791	391.6932	7
20	2078.9665	1039.9869	2061.9400	1031.4736	2060.9560	1030.9816	G	685.3628	343.1850	668.3362	334.6717	667.3522	334.1797	6
21	2192.0506	1096.5289	2175.0241	1088.0157	2174.0400	1087.5237	I	628.3413	314.6743	611.3148	306.1610	610.3307	305.6690	5
22	2320.1092	1160.5582	2303.0826	1152.0450	2302.0986	1151.5529	Q	515.2572	258.1323	498.2307	249.6190	497.2467	249.1270	4
23	2435.1361	1218.0717	2418.1096	1209.5584	2417.1256	1209.0664	D	387.1987	194.1030	370.1721	185.5897	369.1881	185.0977	3
24	2532.1889	1266.5981	2515.1623	1258.0848	2514.1783	1257.5928	P	272.1717	136.5895	255.1452	128.0762	0	0	2
25							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 10068.

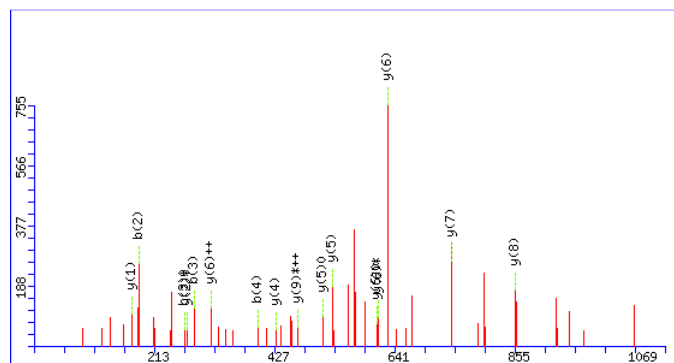
MS/MS Fragmentation of **GEVLDPTAANR**:

Found in **IP100305627;IP100908670;IP100909885**

Title: 1.1.1.8576.11

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							11
2	187.0713	94.0393	0	0	169.0608	85.0340	E	1085.5586	543.2829	1068.5320	534.7696	1067.5480	534.2776	10
3	286.1397	143.5735	0	0	268.1292	134.5682	V	956.5160	478.7616	939.4894	470.2483	938.5054	469.7563	9
4	399.2238	200.1155	0	0	381.2132	191.1103	L	857.4476	429.2274	840.4210	420.7141	839.4370	420.2221	8
5	514.2508	257.6290	0	0	496.2402	248.6237	D	744.3635	372.6854	727.3369	364.1721	726.3529	363.6801	7
6	611.3035	306.1554	0	0	593.2930	297.1501	P	629.3365	315.1719	612.3100	306.6586	611.3260	306.1666	6
7	712.3512	356.6792	0	0	694.3406	347.6740	T	532.2838	266.6455	515.2572	258.1323	514.2732	257.6402	5
8	783.3883	392.1978	0	0	765.3777	383.1925	A	431.2361	216.1217	414.2096	207.6084	0	0	4
9	854.4254	427.7164	0	0	836.4149	418.7111	A	360.1990	180.6031	343.1724	172.0899	0	0	3
10	968.4684	484.7378	951.4418	476.2245	950.4578	475.7325	N	289.1619	145.0846	272.1353	136.5713	0	0	2
11							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

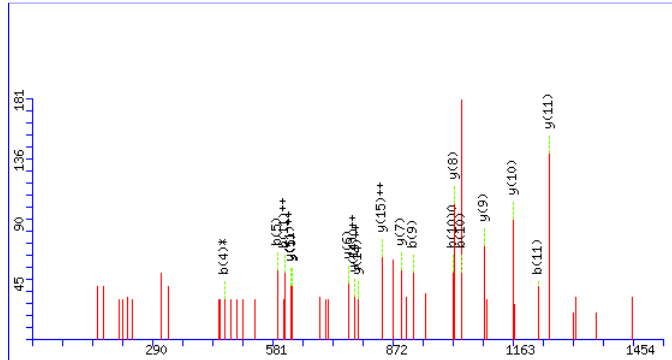
Peptide: 10475.

MS/MS Fragmentation of **NACHTGGLDWIDQSLSAEEHLEVL**R: 57.021465@C:3
Found in **IP100023540:IP100791365**

Title: 4.1.1.3119.9

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_3.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	A							27
2	186.0873	93.5473	169.0608	85.0340	0	0	A	2920.4258	1460.7165	2903.3992	1452.2033	2902.4152	1451.7112	26
3	346.1180	173.5626	329.0914	165.0493	0	0	C	2849.3887	1425.1980	2832.3621	1416.6847	2831.3781	1416.1927	25
4	483.1769	242.0921	466.1503	233.5788	0	0	H	2689.3580	1345.1826	2672.3315	1336.6694	2671.3475	1336.1774	24
5	596.2609	298.6341	579.2344	290.1208	0	0	L	2552.2991	1276.6532	2535.2726	1268.1399	2534.2885	1267.6479	23
6	697.3086	349.1579	680.2821	340.6447	679.2981	340.1527	T	2439.2150	1220.1112	2422.1885	1211.5979	2421.2045	1211.1059	22
7	754.3301	377.6687	737.3035	369.1554	736.3195	368.6634	G	2338.1674	1169.5873	2321.1408	1161.0740	2320.1568	1160.5820	21
8	811.3516	406.1794	794.3250	397.6661	793.3410	397.1741	G	2281.1459	1141.0766	2264.1194	1132.5633	2263.1353	1132.0713	20
9	924.4356	462.7214	907.4091	454.2082	906.4250	453.7162	L	2224.1244	1112.5659	2207.0979	1104.0526	2206.1139	1103.5606	19
10	1039.4626	520.2349	1022.4360	511.7216	1021.4520	511.2296	D	2111.0404	1056.0238	2094.0138	1047.5106	2093.0298	1047.0185	18
11	1225.5419	613.2746	1208.5153	604.7613	1207.5313	604.2693	W	1996.0134	998.5104	1978.9869	989.9971	1978.0029	989.5051	17
12	1338.6259	669.8166	1321.5994	661.3033	1320.6154	660.8113	I	1809.9341	905.4707	1792.9076	896.9574	1791.9236	896.4654	16
13	1453.6529	727.3301	1436.6263	718.8168	1435.6423	718.3248	D	1696.8501	848.9287	1679.8235	840.4154	1678.8395	839.9234	15
14	1581.7115	791.3594	1564.6849	782.8461	1563.7009	782.3541	Q	1581.8231	791.4152	1564.7966	782.9019	1563.8125	782.4099	14
15	1668.7435	834.8754	1651.7169	826.3621	1650.7329	825.8701	S	1453.7645	727.3859	1436.7380	718.8726	1435.7540	718.3806	13
16	1781.8275	891.4174	1764.8010	882.9041	1763.8170	882.4121	L	1366.7325	683.8699	1349.7060	675.3566	1348.7219	674.8646	12
17	1868.8596	934.9334	1851.8330	926.4202	1850.8490	925.9281	S	1253.6484	627.3279	1236.6219	618.8146	1235.6379	618.3226	11
18	1939.8967	970.4520	1922.8701	961.9387	1921.8861	961.4467	A	1166.6164	583.8118	1149.5899	575.2986	1148.6058	574.8066	10
19	2010.9338	1005.9705	1993.9073	997.4573	1992.9232	996.9653	A	1095.5793	548.2933	1078.5527	539.7800	1077.5687	539.2880	9
20	2139.9764	1070.4918	2122.9498	1061.9786	2121.9658	1061.4866	E	1024.5422	512.7747	1007.5156	504.2615	1006.5316	503.7694	8
21	2269.0190	1135.0131	2251.9924	1126.4999	2251.0084	1126.0079	E	895.4996	448.2534	878.4730	439.7402	877.4890	439.2482	7
22	2406.0779	1203.5426	2389.0514	1195.0293	2388.0673	1194.5373	H	766.4570	383.7321	749.4304	375.2189	748.4464	374.7269	6
23	2519.1620	1260.0846	2502.1354	1251.5713	2501.1514	1251.0793	L	629.3981	315.2027	612.3715	306.6894	611.3875	306.1974	5
24	2648.2046	1324.6059	2631.1780	1316.0926	2630.1940	1315.6006	E	516.3140	258.6606	499.2875	250.1474	498.3035	249.6554	4
25	2747.2730	1374.1401	2730.2464	1365.6268	2729.2624	1365.1348	V	387.2714	194.1394	370.2449	185.6261	0	0	3
26	2860.3570	1430.6822	2843.3305	1422.1689	2842.3465	1421.6769	L	288.2030	144.6051	271.1765	136.0919	0	0	2
27							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 10563.

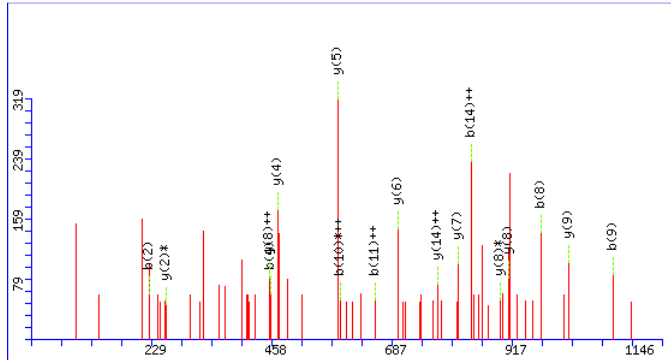
MS/MS Fragmentation of **LLETKPEYHSLQLQELGVDPPDLLPVTR**:

Found in **IP100299911;IP100796187;IP101015078;IP101018936**

Title: 3.1.1.4355.10

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120214ry¥120214ry_414C2-43_4_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							26
2	227.1754	114.0913	0	0	0	0	L	2864.4676	1432.7375	2847.4411	1424.2242	2846.4571	1423.7322	25
3	356.2180	178.6126	0	0	338.2074	169.6074	E	2751.3836	1376.1954	2734.3570	1367.6821	2733.3730	1367.1901	24
4	457.2657	229.1365	0	0	439.2551	220.1312	T	2622.3410	1311.6741	2605.3144	1303.1609	2604.3304	1302.6688	23
5	585.3606	293.1840	568.3341	284.6707	567.3501	284.1787	K	2521.2933	1261.1503	2504.2667	1252.6370	2503.2827	1252.1450	22
6	682.4134	341.7103	665.3869	333.1971	664.4028	332.7051	P	2393.1983	1197.1028	2376.1718	1188.5895	2375.1878	1188.0975	21
7	811.4560	406.2316	794.4294	397.7184	793.4454	397.2264	E	2296.1456	1148.5764	2279.1190	1140.0631	2278.1350	1139.5711	20
8	974.5193	487.7633	957.4928	479.2500	956.5088	478.7580	Y	2167.1030	1084.0551	2150.0764	1075.5419	2149.0924	1075.0498	19
9	1111.5782	556.2928	1094.5517	547.7795	1093.5677	547.2875	H	2004.0396	1002.5235	1987.0131	994.0102	1986.0291	993.5182	18
10	1198.6103	599.8088	1181.5837	591.2955	1180.5997	590.8035	S	1866.9807	933.9940	1849.9542	925.4807	1848.9702	924.9887	17
11	1311.6943	656.3508	1294.6678	647.8375	1293.6838	647.3455	L	1779.9487	890.4780	1762.9222	881.9647	1761.9381	881.4727	16
12	1424.7784	712.8928	1407.7518	704.3796	1406.7678	703.8876	L	1666.8646	833.9360	1649.8381	825.4227	1648.8541	824.9307	15
13	1552.8370	776.9221	1535.8104	768.4088	1534.8264	767.9168	Q	1553.7806	777.3939	1536.7540	768.8807	1535.7700	768.3886	14
14	1681.8796	841.4434	1664.8530	832.9301	1663.8690	832.4381	E	1425.7220	713.3646	1408.6955	704.8514	1407.7114	704.3594	13
15	1794.9636	897.9855	1777.9371	889.4722	1776.9531	888.9802	L	1296.6794	648.8433	1279.6529	640.3301	1278.6688	639.8381	12
16	1851.9851	926.4962	1834.9585	917.9829	1833.9745	917.4909	G	1183.5953	592.3013	1166.5688	583.7880	1165.5848	583.2960	11
17	1951.0535	976.0304	1934.0270	967.5171	1933.0429	967.0251	V	1126.5739	563.7906	1109.5473	555.2773	1108.5633	554.7853	10
18	2066.0804	1033.5439	2049.0539	1025.0306	2048.0699	1024.5386	D	1027.5055	514.2564	1010.4789	505.7431	1009.4949	505.2511	9
19	2163.1332	1082.0702	2146.1067	1073.5570	2145.1226	1073.0650	P	912.4785	456.7429	895.4520	448.2296	894.4680	447.7376	8
20	2278.1602	1139.5837	2261.1336	1131.0704	2260.1496	1130.5784	D	815.4258	408.2165	798.3992	399.7032	797.4152	399.2112	7
21	2393.1871	1197.0972	2376.1605	1188.5839	2375.1765	1188.0919	D	700.3988	350.7030	683.3723	342.1898	682.3883	341.6978	6
22	2506.2712	1253.6392	2489.2446	1245.1259	2488.2606	1244.6339	L	585.3719	293.1896	568.3453	284.6763	567.3613	284.1843	5
23	2603.3239	1302.1656	2586.2974	1293.6523	2585.3134	1293.1603	P	472.2878	236.6475	455.2613	228.1343	454.2772	227.6423	4
24	2702.3923	1351.6998	2685.3658	1343.1865	2684.3818	1342.6945	V	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
25	2803.4400	1402.2236	2786.4135	1393.7104	2785.4295	1393.2184	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
26							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 10622.

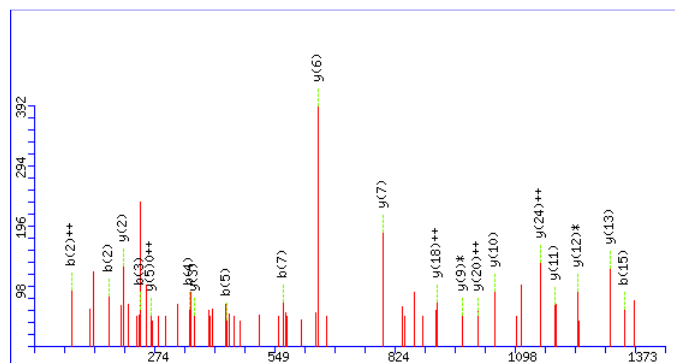
MS/MS Fragmentation of **LGALSGAAALGFASYGAHGAQFPDAYGK**:

Found in **IP100166483**

Title: 3.1.1.2806.9

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1.3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							28
2	171.1128	86.0600	0	0	0	0	G	2555.2314	1278.1193	2538.2048	1269.6060	2537.2208	1269.1140	27
3	242.1499	121.5786	0	0	0	0	A	2498.2099	1249.6086	2481.1834	1241.0953	2480.1993	1240.6033	26
4	355.2340	178.1206	0	0	0	0	L	2427.1728	1214.0900	2410.1462	1205.5768	2409.1622	1205.0848	25
5	442.2660	221.6366	0	0	424.2554	212.6314	S	2314.0887	1157.5480	2297.0622	1149.0347	2296.0782	1148.5427	24
6	499.2875	250.1474	0	0	481.2769	241.1421	G	2227.0567	1114.0320	2210.0301	1105.5187	2209.0461	1105.0267	23
7	570.3246	285.6659	0	0	552.3140	276.6606	A	2170.0352	1085.5213	2153.0087	1077.0080	2152.0247	1076.5160	22
8	641.3617	321.1845	0	0	623.3511	312.1792	A	2098.9981	1050.0027	2081.9716	1041.4894	2080.9876	1040.9974	21
9	712.3988	356.7030	0	0	694.3883	347.6978	A	2027.9610	1014.4841	2010.9345	1005.9709	2009.9504	1005.4789	20
10	825.4829	413.2451	0	0	807.4723	404.2398	L	1956.9239	978.9656	1939.8973	970.4523	1938.9133	969.9603	19
11	882.5043	441.7558	0	0	864.4938	432.7505	G	1843.8398	922.4236	1826.8133	913.9103	1825.8293	913.4183	18
12	1029.5728	515.2900	0	0	1011.5622	506.2847	F	1786.8184	893.9128	1769.7918	885.3995	1768.8078	884.9075	17
13	1100.6099	550.8086	0	0	1082.5993	541.8033	A	1639.7499	820.3786	1622.7234	811.8653	1621.7394	811.3733	16
14	1187.6419	594.3246	0	0	1169.6313	585.3193	S	1568.7128	784.8601	1551.6863	776.3468	1550.7023	775.8548	15
15	1350.7052	675.8563	0	0	1332.6947	666.8510	Y	1481.6808	741.3440	1464.6543	732.8308	1463.6702	732.3388	14
16	1407.7267	704.3670	0	0	1389.7161	695.3617	G	1318.6175	659.8124	1301.5909	651.2991	1300.6069	650.8071	13
17	1478.7638	739.8855	0	0	1460.7532	730.8803	A	1261.5960	631.3016	1244.5695	622.7884	1243.5854	622.2964	12
18	1615.8227	808.4150	0	0	1597.8122	799.4097	H	1190.5589	595.7831	1173.5324	587.2698	1172.5483	586.7778	11
19	1672.8442	836.9257	0	0	1654.8336	827.9204	G	1053.5000	527.2536	1036.4734	518.7404	1035.4894	518.2483	10
20	1743.8813	872.4443	0	0	1725.8707	863.4390	A	996.4785	498.7429	979.4520	490.2296	978.4680	489.7376	9
21	1871.9399	936.4736	1854.9133	927.9603	1853.9293	927.4683	Q	925.4414	463.2243	908.4149	454.7111	907.4308	454.2191	8
22	2019.0083	1010.0078	2001.9817	1001.4945	2000.9977	1001.0025	F	797.3828	399.1951	780.3563	390.6818	779.3723	390.1898	7
23	2116.0611	1058.5342	2099.0345	1050.0209	2098.0505	1049.5289	P	650.3144	325.6608	633.2879	317.1476	632.3039	316.6556	6
24	2231.0880	1116.0476	2214.0614	1107.5344	2213.0774	1107.0424	D	553.2617	277.1345	536.2351	268.6212	535.2511	268.1292	5
25	2302.1251	1151.5662	2285.0986	1143.0529	2284.1145	1142.5609	A	438.2347	219.6210	421.2082	211.1077	0	0	4
26	2465.1884	1233.0979	2448.1619	1224.5846	2447.1779	1224.0926	Y	367.1976	184.1024	350.1710	175.5892	0	0	3
27	2522.2099	1261.6086	2505.1834	1253.0953	2504.1993	1252.6033	G	204.1343	102.5708	187.1077	94.0575	0	0	2
28							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 10911.

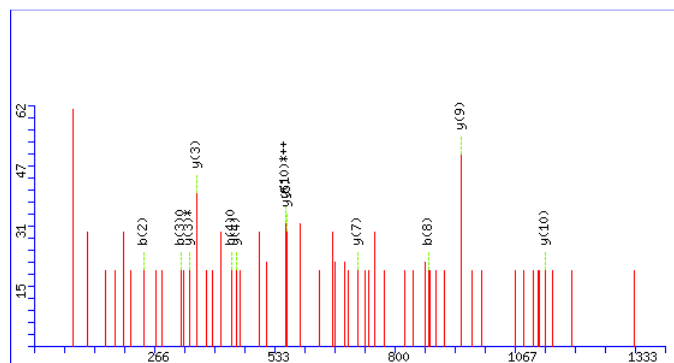
MS/MS Fragmentation of **ELTISPAYLLWDLAISQSK:**

Found in **IP100382432:IP100735667**

Title: 5.1.1.259.5

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4.5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	L							20
2	243.1339	122.0706	0	0	225.1234	113.0653	L	2106.1481	1053.5777	2089.1216	1045.0644	2088.1376	1044.5724	19
3	344.1816	172.5944	0	0	326.1710	163.5892	T	1993.0641	997.0357	1976.0375	988.5224	1975.0535	988.0304	18
4	457.2657	229.1365	0	0	439.2551	220.1312	I	1892.0164	946.5118	1874.9898	937.9986	1874.0058	937.5066	17
5	544.2977	272.6525	0	0	526.2871	263.6472	S	1778.9323	889.9698	1761.9058	881.4565	1760.9218	880.9645	16
6	641.3505	321.1789	0	0	623.3399	312.1736	P	1691.9003	846.4538	1674.8737	837.9405	1673.8897	837.4485	15
7	712.3876	356.6974	0	0	694.3770	347.6921	A	1594.8475	797.9274	1577.8210	789.4141	1576.8370	788.9221	14
8	875.4509	438.2291	0	0	857.4403	429.2238	Y	1523.8104	762.4088	1506.7839	753.8956	1505.7999	753.4036	13
9	988.5350	494.7711	0	0	970.5244	485.7658	L	1360.7471	680.8772	1343.7205	672.3639	1342.7365	671.8719	12
10	1101.6190	551.3132	0	0	1083.6085	542.3079	L	1247.6630	624.3352	1230.6365	615.8219	1229.6525	615.3299	11
11	1287.6984	644.3528	0	0	1269.6878	635.3475	W	1134.5790	567.7931	1117.5524	559.2798	1116.5684	558.7878	10
12	1402.7253	701.8663	0	0	1384.7147	692.8610	D	948.4997	474.7535	931.4731	466.2402	930.4891	465.7482	9
13	1515.8094	758.4083	0	0	1497.7988	749.4030	L	833.4727	417.2400	816.4462	408.7267	815.4621	408.2347	8
14	1602.8414	801.9243	0	0	1584.8308	792.9190	S	720.3886	360.6980	703.3621	352.1847	702.3781	351.6927	7
15	1673.8785	837.4429	0	0	1655.8679	828.4376	A	633.3566	317.1819	616.3301	308.6687	615.3461	308.1767	6
16	1786.9626	893.9849	0	0	1768.9520	884.9796	I	562.3195	281.6634	545.2930	273.1501	544.3089	272.6581	5
17	1873.9946	937.5009	0	0	1855.9840	928.4957	S	449.2354	225.1214	432.2089	216.6081	431.2249	216.1161	4
18	2002.0532	1001.5302	1985.0266	993.0169	1984.0426	992.5249	Q	362.2034	181.6053	345.1769	173.0921	344.1928	172.6001	3
19	2089.0852	1045.0462	2072.0586	1036.5330	2071.0746	1036.0410	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
20							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 11069.

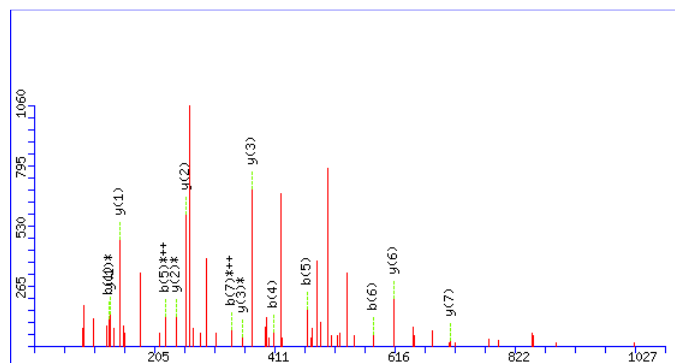
MS/MS Fragmentation of **QPQGGILK**:

Found in **IP100844022;IP100915784;IP100917968**

Title: 2.1.1.4381.2

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2.2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233	0	0	Q							8
2	226.1186	113.5629	209.0921	105.0497	0	0	P	712.4352	356.7212	695.4087	348.2080	0	0	7
3	354.1772	177.5922	337.1506	169.0790	0	0	Q	615.3824	308.1949	598.3559	299.6816	0	0	6
4	411.1987	206.1030	394.1721	197.5897	0	0	G	487.3239	244.1656	470.2973	235.6523	0	0	5
5	468.2201	234.6137	451.1936	226.1004	0	0	G	430.3024	215.6548	413.2758	207.1416	0	0	4
6	581.3042	291.1557	564.2776	282.6425	0	0	I	373.2809	187.1441	356.2544	178.6308	0	0	3
7	694.3883	347.6978	677.3617	339.1845	0	0	L	260.1969	130.6021	243.1703	122.0888	0	0	2
8							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 11095.

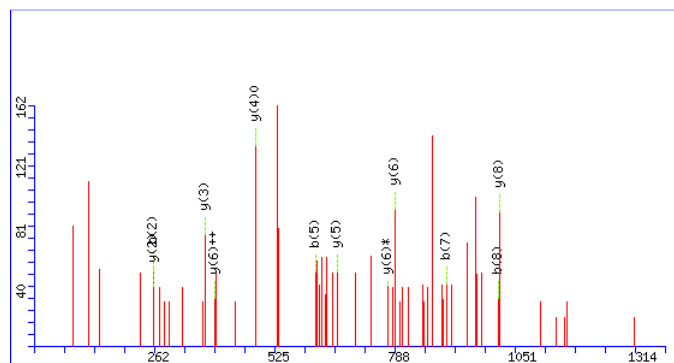
MS/MS Fragmentation of **FLNIQCQLSR: 57.021465@C:6**

Found in **IP100216873**

Title: 2.1.1.3915.8

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							10
2	261.1598	131.0835	0	0	0	0	L	1131.5939	566.3006	1114.5674	557.7873	1113.5833	557.2953	9
3	375.2027	188.1050	358.1761	179.5917	0	0	N	1018.5098	509.7586	1001.4833	501.2453	1000.4993	500.7533	8
4	488.2867	244.6470	471.2602	236.1337	0	0	I	904.4669	452.7371	887.4404	444.2238	886.4563	443.7318	7
5	616.3453	308.6763	599.3188	300.1630	0	0	Q	791.3828	396.1951	774.3563	387.6818	773.3723	387.1898	6
6	776.3760	388.6916	759.3494	380.1783	0	0	C	663.3243	332.1658	646.2977	323.6525	645.3137	323.1605	5
7	904.4346	452.7209	887.4080	444.2076	0	0	Q	503.2936	252.1504	486.2671	243.6372	485.2831	243.1452	4
8	1017.5186	509.2629	1000.4921	500.7497	0	0	L	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
9	1104.5506	552.7790	1087.5241	544.2657	1086.5401	543.7737	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 11201.

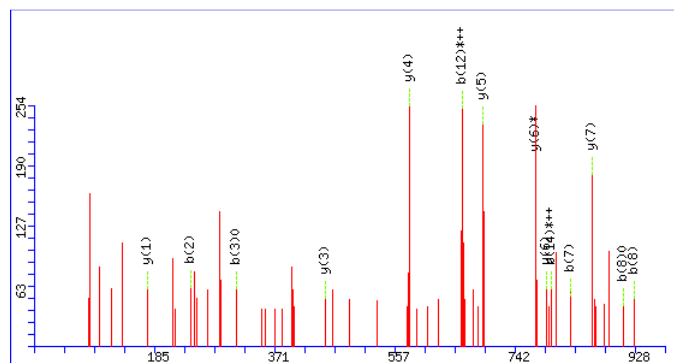
MS/MS Fragmentation of **EISKEELVAVLELYR**:

Found in **IP100164366;IP100795880;IP101015452**

Title: 3.1.1.4316.4

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							15
2	243.1339	122.0706	0	0	225.1234	113.0653	I	1661.9472	831.4773	1644.9207	822.9640	1643.9367	822.4720	14
3	330.1660	165.5866	0	0	312.1554	156.5813	S	1548.8632	774.9352	1531.8366	766.4220	1530.8526	765.9299	13
4	458.2609	229.6341	441.2344	221.1208	440.2504	220.6288	K	1461.8312	731.4192	1444.8046	722.9059	1443.8206	722.4139	12
5	587.3035	294.1554	570.2770	285.6421	569.2930	285.1501	E	1333.7362	667.3717	1316.7096	658.8585	1315.7256	658.3665	11
6	716.3461	358.6767	699.3196	350.1634	698.3355	349.6714	E	1204.6936	602.8504	1187.6671	594.3372	1186.6830	593.8452	10
7	829.4302	415.2187	812.4036	406.7055	811.4196	406.2134	L	1075.6510	538.3291	1058.6245	529.8159	1057.6404	529.3239	9
8	928.4986	464.7529	911.4720	456.2397	910.4880	455.7476	V	962.5669	481.7871	945.5404	473.2738	944.5564	472.7818	8
9	999.5357	500.2715	982.5092	491.7582	981.5251	491.2662	A	863.4985	432.2529	846.4720	423.7396	845.4880	423.2476	7
10	1098.6041	549.8057	1081.5776	541.2924	1080.5936	540.8004	V	792.4614	396.7343	775.4349	388.2211	774.4509	387.7291	6
11	1211.6882	606.3477	1194.6616	597.8345	1193.6776	597.3424	L	693.3930	347.2001	676.3665	338.6869	675.3824	338.1949	5
12	1340.7308	670.8690	1323.7042	662.3557	1322.7202	661.8637	E	580.3089	290.6581	563.2824	282.1448	562.2984	281.6528	4
13	1453.8148	727.4111	1436.7883	718.8978	1435.8043	718.4058	L	451.2663	226.1368	434.2398	217.6235	0	0	3
14	1616.8782	808.9427	1599.8516	800.4294	1598.8676	799.9374	Y	338.1823	169.5948	321.1557	161.0815	0	0	2
15							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 11663.

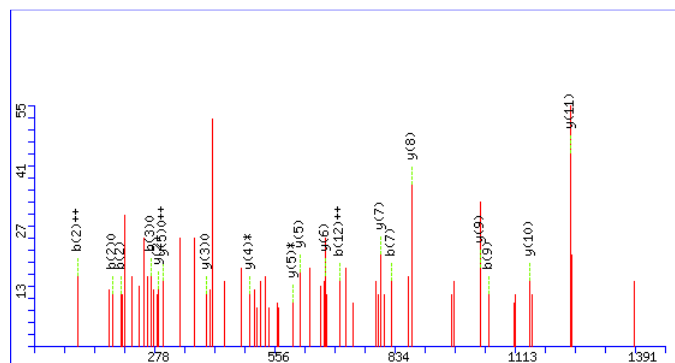
MS/MS Fragmentation of **SLSEPWQILTFDFQQPVLQPLCAEGTVELR: 0.984016@Q:20.57.021485@C:23**

Found in **IP100004567;IP100219090;IP100909654**

Title: 4.1.1.4074.3

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							31
2	201.1234	101.0653	0	0	183.1128	92.0600	L	3512.7770	1756.8922	3495.7505	1748.3789	3494.7665	1747.8869	30
3	288.1554	144.5813	0	0	270.1448	135.5761	S	3399.6930	1700.3501	3382.6664	1691.8368	3381.6824	1691.3448	29
4	417.1980	209.1026	0	0	399.1874	200.0974	E	3312.6609	1656.8341	3295.6344	1648.3208	3294.6504	1647.8288	28
5	514.2508	257.6290	0	0	496.2402	248.6237	P	3183.6183	1592.3128	3166.5918	1583.7995	3165.6078	1583.3075	27
6	700.3301	350.6687	0	0	682.3195	341.6634	W	3086.5656	1543.7864	3069.5390	1535.2732	3068.5550	1534.7811	26
7	828.3886	414.6980	811.3621	406.1847	810.3781	405.6927	Q	2900.4863	1450.7468	2883.4597	1442.2335	2882.4757	1441.7415	25
8	941.4727	471.2400	924.4462	462.7267	923.4621	462.2347	I	2772.4277	1386.7175	2755.4011	1378.2042	2754.4171	1377.7122	24
9	1054.5568	527.7820	1037.5302	519.2687	1036.5462	518.7767	L	2659.3436	1330.1754	2642.3171	1321.6622	2641.3331	1321.1702	23
10	1155.6045	578.3059	1138.5779	569.7926	1137.5939	569.3006	T	2546.2596	1273.6334	2529.2330	1265.1201	2528.2490	1264.6281	22
11	1302.6729	651.8401	1285.6463	643.3268	1284.6623	642.8348	F	2445.2119	1223.1096	2428.1853	1214.5963	2427.2013	1214.1043	21
12	1417.6998	709.3535	1400.6733	700.8403	1399.6892	700.3483	D	2298.1435	1149.5754	2281.1169	1141.0621	2280.1329	1140.5701	20
13	1564.7682	782.8877	1547.7417	774.3745	1546.7577	773.8825	F	2183.1165	1092.0619	2166.0900	1083.5486	2165.1060	1083.0566	19
14	1692.8268	846.9170	1675.8003	838.4038	1674.8162	837.9118	Q	2036.0481	1018.5277	2019.0216	1010.0144	2018.0375	1009.5224	18
15	1820.8854	910.9463	1803.8588	902.4331	1802.8748	901.9410	Q	1907.9895	954.4984	1890.9630	945.9851	1889.9790	945.4931	17
16	1917.9381	959.4727	1900.9116	950.9594	1899.9276	950.4674	P	1779.9310	890.4691	1762.9044	881.9558	1761.9204	881.4638	16
17	2017.0066	1009.0069	1999.9800	1000.4936	1998.9960	1000.0016	V	1682.8782	841.9427	1665.8516	833.4295	1664.8676	832.9374	15
18	2114.0593	1057.5333	2097.0328	1049.0200	2096.0488	1048.5280	P	1583.8098	792.4085	1566.7832	783.8952	1565.7992	783.4032	14
19	2227.1434	1114.0753	2210.1168	1105.5621	2209.1328	1105.0700	L	1486.7570	743.8821	1469.7305	735.3689	1468.7464	734.8769	13
20	2356.1860	1178.5966	2339.1594	1170.0834	2338.1754	1169.5913	Q	1373.6729	687.3401	1356.6464	678.8268	1355.6624	678.3348	12
21	2453.2387	1227.1230	2436.2122	1218.6097	2435.2282	1218.1177	P	1244.6304	622.8188	1227.6038	614.3055	1226.6198	613.8135	11
22	2566.3228	1283.6650	2549.2963	1275.1518	2548.3122	1274.6598	L	1147.5776	574.2924	1130.5510	565.7792	1129.5670	565.2871	10
23	2726.3535	1363.6804	2709.3269	1355.1671	2708.3429	1354.6751	C	1034.4935	517.7504	1017.4670	509.2371	1016.4830	508.7451	9
24	2797.3906	1399.1989	2780.3640	1390.6856	2779.3800	1390.1936	A	874.4629	437.7351	857.4363	429.2218	856.4523	428.7298	8
25	2926.4332	1463.7202	2909.4066	1455.2069	2908.4226	1454.7149	E	803.4258	402.2165	786.3992	393.7032	785.4152	393.2112	7
26	2983.4546	1492.2310	2966.4281	1483.7177	2965.4441	1483.2257	G	674.3832	337.6952	657.3566	329.1819	656.3726	328.6899	6
27	3084.5023	1542.7548	3067.4758	1534.2415	3066.4917	1533.7495	T	617.3617	309.1845	600.3352	300.6712	599.3511	300.1792	5
28	3183.5707	1592.2890	3166.5442	1583.7757	3165.5602	1583.2837	V	516.3140	258.6606	499.2875	250.1474	498.3035	249.6554	4
29	3312.6133	1656.8103	3295.5868	1648.2970	3294.6027	1647.8050	E	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
30	3425.6974	1713.3523	3408.6708	1704.8391	3407.6868	1704.3470	L	288.2030	144.6051	271.1765	136.0919	0	0	2
31							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 11777.

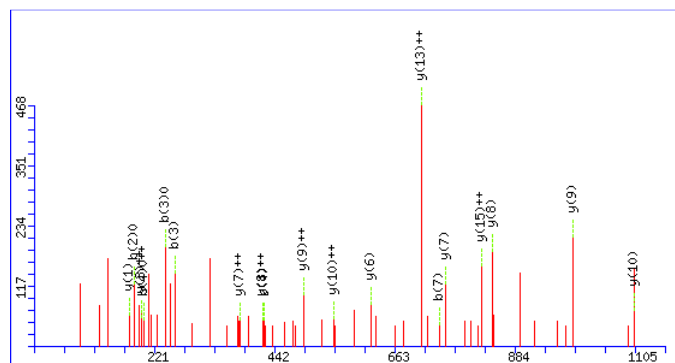
MS/MS Fragmentation of **DSGYPLIIFSHGLGAFR**:

Found in **IP100015388;IP100641128;IP100642198**

Title: 4.1.1.773.2

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							17
2	203.0662	102.0368	0	0	185.0557	93.0315	S	1734.9326	867.9699	1717.9061	859.4567	1716.9220	858.9647	16
3	260.0877	130.5475	0	0	242.0771	121.5422	G	1647.9006	824.4539	1630.8740	815.9407	1629.8900	815.4486	15
4	423.1510	212.0792	0	0	405.1405	203.0739	Y	1590.8791	795.9432	1573.8526	787.4299	1572.8685	786.9379	14
5	520.2038	260.6055	0	0	502.1932	251.6003	P	1427.8158	714.4115	1410.7892	705.8983	1409.8052	705.4062	13
6	633.2879	317.1476	0	0	615.2773	308.1423	L	1330.7630	665.8851	1313.7365	657.3719	1312.7525	656.8799	12
7	746.3719	373.6896	0	0	728.3614	364.6843	I	1217.6790	609.3431	1200.6524	600.8298	1199.6684	600.3378	11
8	859.4560	430.2316	0	0	841.4454	421.2264	I	1104.5949	552.8011	1087.5683	544.2878	1086.5843	543.7958	10
9	1006.5244	503.7658	0	0	988.5138	494.7606	F	991.5108	496.2591	974.4843	487.7458	973.5003	487.2538	9
10	1093.5564	547.2819	0	0	1075.5459	538.2766	S	844.4424	422.7248	827.4159	414.2116	826.4318	413.7196	8
11	1230.6154	615.8113	0	0	1212.6048	606.8060	H	757.4104	379.2088	740.3838	370.6956	0	0	7
12	1287.6368	644.3220	0	0	1269.6262	635.3168	G	620.3515	310.6794	603.3249	302.1661	0	0	6
13	1400.7209	700.8641	0	0	1382.7103	691.8588	L	563.3300	282.1686	546.3035	273.6554	0	0	5
14	1457.7423	729.3748	0	0	1439.7318	720.3695	G	450.2459	225.6266	433.2194	217.1133	0	0	4
15	1528.7795	764.8934	0	0	1510.7689	755.8881	A	393.2245	197.1159	376.1979	188.6026	0	0	3
16	1675.8479	838.4276	0	0	1657.8373	829.4223	F	322.1874	161.5973	305.1608	153.0840	0	0	2
17							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 11821.

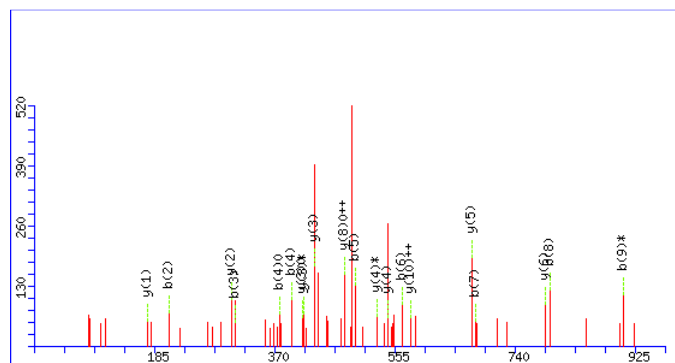
MS/MS Fragmentation of **AHTSVANNEIQER**:

Found in **IP100465189;IP100827592;IP100827642**

Title: 1.1.1.7403.7

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							13
2	209.1033	105.0553	0	0	0	0	H	1397.6768	699.3420	1380.6502	690.8288	1379.6662	690.3367	12
3	310.1510	155.5791	0	0	292.1404	146.5738	T	1260.6179	630.8126	1243.5913	622.2993	1242.6073	621.8073	11
4	397.1830	199.0951	0	0	379.1724	190.0899	S	1159.5702	580.2887	1142.5436	571.7755	1141.5596	571.2835	10
5	496.2514	248.6293	0	0	478.2409	239.6241	V	1072.5382	536.7727	1055.5116	528.2594	1054.5276	527.7674	9
6	567.2885	284.1479	0	0	549.2780	275.1426	A	973.4697	487.2385	956.4432	478.7252	955.4592	478.2332	8
7	681.3315	341.1694	664.3049	332.6561	663.3209	332.1641	N	902.4326	451.7200	885.4061	443.2067	884.4221	442.7147	7
8	795.3744	398.1908	778.3478	389.6776	777.3638	389.1856	N	788.3897	394.6985	771.3632	386.1852	770.3791	385.6932	6
9	924.4170	462.7121	907.3904	454.1989	906.4064	453.7068	E	674.3468	337.6770	657.3202	329.1638	656.3362	328.6717	5
10	1037.5010	519.2542	1020.4745	510.7409	1019.4905	510.2489	I	545.3042	273.1557	528.2776	264.6425	527.2936	264.1504	4
11	1165.5596	583.2835	1148.5331	574.7702	1147.5491	574.2782	Q	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	3
12	1294.6022	647.8047	1277.5757	639.2915	1276.5917	638.7995	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
13							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 12041.

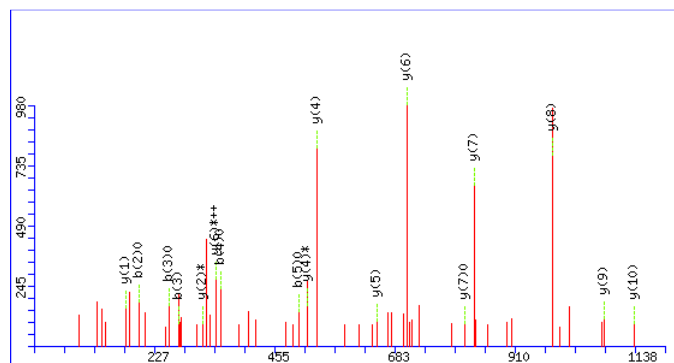
MS/MS Fragmentation of **ESGVFEGIPTYR**:

Found in **IP100177968;IP100291007;IP100375570;IP100447020;IP100939960;IP101008855;IP101009964;IP101011638**

Title: 2.1.1.4218.7

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2.2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							12
2	217.0819	109.0446	0	0	199.0713	100.0393	S	1225.6212	613.3142	1208.5946	604.8009	1207.6106	604.3089	11
3	274.1034	137.5553	0	0	256.0928	128.5500	G	1138.5891	569.7982	1121.5626	561.2849	1120.5786	560.7929	10
4	373.1718	187.0895	0	0	355.1612	178.0842	V	1081.5677	541.2875	1064.5411	532.7742	1063.5571	532.2822	9
5	520.2402	260.6237	0	0	502.2296	251.6185	F	982.4993	491.7533	965.4727	483.2400	964.4887	482.7480	8
6	649.2828	325.1450	0	0	631.2722	316.1397	E	835.4308	418.2191	818.4043	409.7058	817.4203	409.2138	7
7	706.3042	353.6558	0	0	688.2937	344.6505	G	706.3883	353.6978	689.3617	345.1845	688.3777	344.6925	6
8	819.3883	410.1978	0	0	801.3777	401.1925	I	649.3668	325.1870	632.3402	316.6738	631.3562	316.1817	5
9	916.4411	458.7242	0	0	898.4305	449.7189	P	536.2827	268.6450	519.2562	260.1317	518.2722	259.6397	4
10	1017.4888	509.2480	0	0	999.4782	500.2427	T	439.2300	220.1186	422.2034	211.6053	421.2194	211.1133	3
11	1180.5521	590.7797	0	0	1162.5415	581.7744	Y	338.1823	169.5948	321.1557	161.0815	0	0	2
12							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 12259.

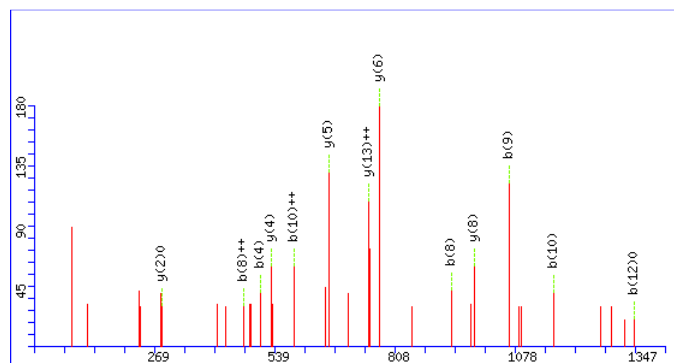
MS/MS Fragmentation of **EHQLENGEEVTLLEDLER**:

Found in **IP100019520;IP100909082**

Title: 4.1.1.1434.7

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							19
2	267.1088	134.0580	0	0	249.0982	125.0527	H	2123.0615	1062.0344	2106.0350	1053.5211	2105.0509	1053.0291	18
3	395.1674	198.0873	378.1408	189.5740	377.1568	189.0820	Q	1986.0026	993.5049	1968.9760	984.9917	1967.9920	984.4997	17
4	508.2514	254.6293	491.2249	246.1161	490.2409	245.6241	L	1857.9440	929.4756	1840.9175	920.9624	1839.9334	920.4704	16
5	637.2940	319.1506	620.2675	310.6374	619.2835	310.1454	E	1744.8599	872.9336	1727.8334	864.4203	1726.8494	863.9283	15
6	751.3369	376.1721	734.3104	367.6588	733.3264	367.1668	N	1615.8174	808.4123	1598.7908	799.8990	1597.8068	799.4070	14
7	808.3584	404.6828	791.3319	396.1696	790.3478	395.6776	G	1501.7744	751.3909	1484.7479	742.8776	1483.7639	742.3856	13
8	937.4010	469.2041	920.3745	460.6909	919.3904	460.1989	E	1444.7530	722.8801	1427.7264	714.3668	1426.7424	713.8748	12
9	1066.4436	533.7254	1049.4170	525.2122	1048.4330	524.7202	E	1315.7104	658.3588	1298.6838	649.8455	1297.6998	649.3535	11
10	1165.5120	583.2596	1148.4855	574.7464	1147.5014	574.2544	V	1186.6678	593.8375	1169.6412	585.3243	1168.6572	584.8322	10
11	1264.5804	632.7938	1247.5539	624.2806	1246.5699	623.7886	V	1087.5994	544.3033	1070.5728	535.7900	1069.5888	535.2980	9
12	1365.6281	683.3177	1348.6016	674.8044	1347.6175	674.3124	T	988.5310	494.7691	971.5044	486.2558	970.5204	485.7638	8
13	1478.7122	739.8597	1461.6856	731.3464	1460.7016	730.8544	L	887.4833	444.2453	870.4567	435.7320	869.4727	435.2400	7
14	1591.7962	796.4018	1574.7697	787.8885	1573.7857	787.3965	L	774.3992	387.7032	757.3727	379.1900	756.3886	378.6980	6
15	1720.8388	860.9230	1703.8123	852.4098	1702.8283	851.9178	E	661.3151	331.1612	644.2886	322.6479	643.3046	322.1559	5
16	1835.8658	918.4365	1818.8392	909.9232	1817.8552	909.4312	D	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
17	1948.9498	974.9786	1931.9233	966.4653	1930.9393	965.9733	L	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
18	2077.9924	1039.4998	2060.9659	1030.9866	2059.9819	1030.4946	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
19							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 12939.

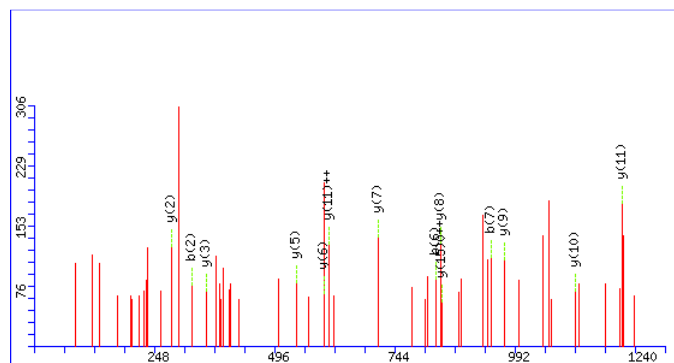
MS/MS Fragmentation of **YYECDVLPFMEIGSVAHK: 57.021465@C:4**

Found in **IP100171444;IP100384961;IP100640315;IP100641938;IP100656079;IP100974133;IP100978086;IP100984161;IP100984799;IP101014060**

Title: 3.1.1.3976.6

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120214ry¥120214ry_aHDF1419-P10_4.3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	164.0706	82.5389	0	0	0	0	Y							18
2	327.1339	164.0706	0	0	0	0	Y	1994.9350	997.9712	1977.9085	989.4579	1976.9245	988.9659	17
3	456.1765	228.5919	0	0	438.1660	219.5866	E	1831.8717	916.4395	1814.8452	907.9262	1813.8612	907.4342	16
4	616.2072	308.6072	0	0	598.1966	299.6019	C	1702.8291	851.9182	1685.8026	843.4049	1684.8186	842.9129	15
5	731.2341	366.1207	0	0	713.2236	357.1154	D	1542.7985	771.9029	1525.7719	763.3896	1524.7879	762.8976	14
6	830.3025	415.6549	0	0	812.2920	406.6496	V	1427.7715	714.3894	1410.7450	705.8761	1409.7610	705.3841	13
7	943.3866	472.1969	0	0	925.3760	463.1917	L	1328.7031	664.8552	1311.6766	656.3419	1310.6926	655.8499	12
8	1040.4394	520.7233	0	0	1022.4288	511.7180	P	1215.6191	608.3132	1198.5925	599.7999	1197.6085	599.3079	11
9	1187.5078	594.2575	0	0	1169.4972	585.2522	F	1118.5663	559.7868	1101.5397	551.2735	1100.5557	550.7815	10
10	1318.5483	659.7778	0	0	1300.5377	650.7725	M	971.4979	486.2526	954.4713	477.7393	953.4873	477.2473	9
11	1447.5909	724.2991	0	0	1429.5803	715.2938	E	840.4574	420.7323	823.4308	412.2191	822.4468	411.7271	8
12	1560.6749	780.8411	0	0	1542.6644	771.8358	I	711.4148	356.2110	694.3883	347.6978	693.4042	347.2058	7
13	1617.6964	809.3518	0	0	1599.6858	800.3465	G	598.3307	299.6690	581.3042	291.1557	580.3202	290.6637	6
14	1704.7284	852.8678	0	0	1686.7178	843.8626	S	541.3093	271.1583	524.2827	262.6450	523.2987	262.1530	5
15	1803.7968	902.4021	0	0	1785.7863	893.3968	V	454.2772	227.6423	437.2507	219.1290	0	0	4
16	1874.8339	937.9206	0	0	1856.8234	928.9153	A	355.2088	178.1081	338.1823	169.5948	0	0	3
17	2011.8929	1006.4501	0	0	1993.8823	997.4448	H	284.1717	142.5895	267.1452	134.0762	0	0	2
18							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 12946.

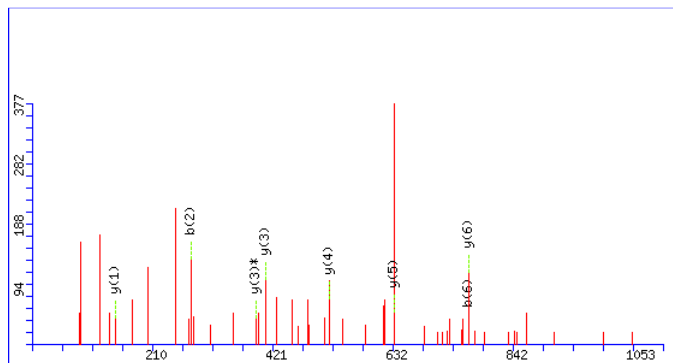
MS/MS Fragmentation of **FMLINFK: 0.984015@N:5**

Found in **IP100457355**

Title: 3.1.1.2505.2

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							7
2	279.1162	140.0617	0	0	0	0	M	766.4168	383.7120	749.3902	375.1987	0	0	6
3	392.2002	196.6038	0	0	0	0	L	635.3763	318.1918	618.3497	309.6785	0	0	5
4	505.2843	253.1458	0	0	0	0	I	522.2922	261.6497	505.2657	253.1365	0	0	4
5	620.3112	310.6593	603.2847	302.1460	0	0	N	409.2082	205.1077	392.1816	196.5944	0	0	3
6	767.3797	384.1935	750.3531	375.6802	0	0	F	294.1812	147.5942	277.1547	139.0810	0	0	2
7							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 13228.

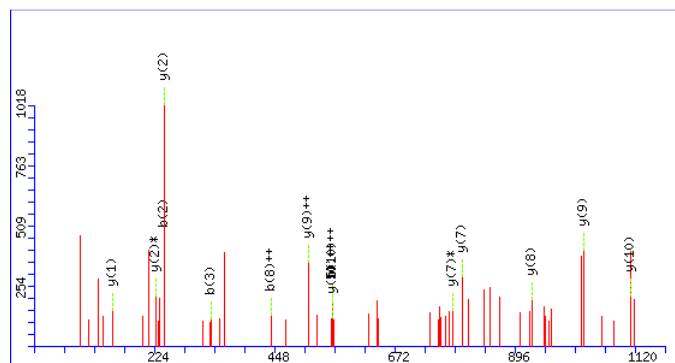
MS/MS Fragmentation of **IESPEEISLLPK**:

Found in **IP100220567;IP100795982;IP100797997**

Title: 3.1.1.49.9

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							12
2	243.1339	122.0706	0	0	225.1234	113.0653	E	1241.6624	621.3348	1224.6358	612.8215	1223.6518	612.3295	11
3	330.1660	165.5866	0	0	312.1554	156.5813	S	1112.6198	556.8135	1095.5932	548.3002	1094.6092	547.8082	10
4	427.2187	214.1130	0	0	409.2082	205.1077	P	1025.5877	513.2975	1008.5612	504.7842	1007.5772	504.2922	9
5	556.2613	278.6343	0	0	538.2508	269.6290	E	928.5350	464.7711	911.5084	456.2579	910.5244	455.7658	8
6	685.3039	343.1556	0	0	667.2933	334.1503	E	799.4924	400.2498	782.4658	391.7366	781.4818	391.2445	7
7	798.3880	399.6976	0	0	780.3774	390.6923	I	670.4498	335.7285	653.4232	327.2153	652.4392	326.7232	6
8	885.4200	443.2136	0	0	867.4094	434.2084	S	557.3657	279.1865	540.3392	270.6732	539.3552	270.1812	5
9	998.5041	499.7557	0	0	980.4935	490.7504	L	470.3337	235.6705	453.3071	227.1572	0	0	4
10	1111.5881	556.2977	0	0	1093.5776	547.2924	L	357.2496	179.1285	340.2231	170.6152	0	0	3
11	1208.6409	604.8241	0	0	1190.6303	595.8188	P	244.1656	122.5864	227.1390	114.0731	0	0	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 13268.

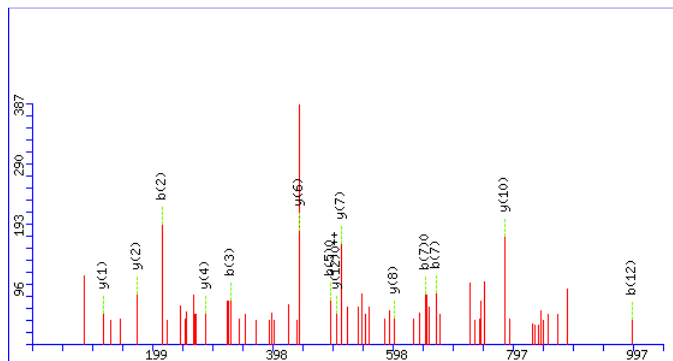
MS/MS Fragmentation of **SELPSSAPGGGGV**:

Found in **IP100067920**

Title: 2.1.1.440.6

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							13
2	217.0819	109.0446	0	0	199.0713	100.0393	E	1027.5055	514.2564	0	0	1009.4949	505.2511	12
3	330.1660	165.5866	0	0	312.1554	156.5813	L	898.4629	449.7351	0	0	880.4523	440.7298	11
4	427.2187	214.1130	0	0	409.2082	205.1077	P	785.3788	393.1930	0	0	767.3682	384.1878	10
5	514.2508	257.6290	0	0	496.2402	248.6237	S	688.3260	344.6667	0	0	670.3155	335.6614	9
6	601.2828	301.1450	0	0	583.2722	292.1397	S	601.2940	301.1506	0	0	583.2835	292.1454	8
7	672.3199	336.6636	0	0	654.3093	327.6583	A	514.2620	257.6346	0	0	0	0	7
8	769.3727	385.1900	0	0	751.3621	376.1847	P	443.2249	222.1161	0	0	0	0	6
9	826.3941	413.7007	0	0	808.3836	404.6954	G	346.1721	173.5897	0	0	0	0	5
10	883.4156	442.2114	0	0	865.4050	433.2061	G	289.1506	145.0790	0	0	0	0	4
11	940.4371	470.7222	0	0	922.4265	461.7169	G	232.1292	116.5682	0	0	0	0	3
12	997.4585	499.2329	0	0	979.4480	490.2276	G	175.1077	88.0575	0	0	0	0	2
13							V	118.0863	59.5468	0	0	0	0	1

Peptide View

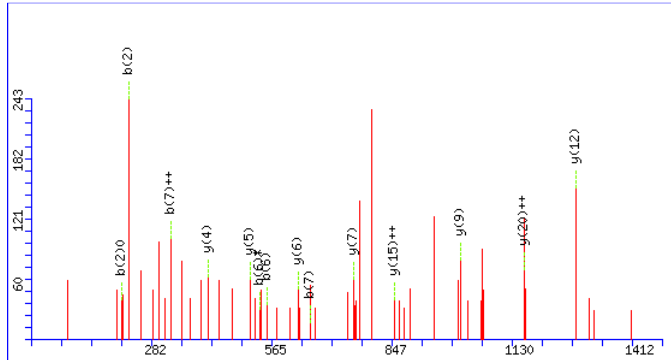
Peptide: 13555.

MS/MS Fragmentation of **DNVAGVTLPVFEHYHEGTDSELTGLAR**
 Found in **IP100001568;IP101025217;IP101025474;IP101025577;IP101026536**

Title: 3.1.1.3141.8

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_1_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							28
2	230.0771	115.5422	213.0506	107.0289	212.0666	106.5369	N	2975.4534	1488.2303	2958.4268	1479.7171	2957.4428	1479.2250	27
3	329.1456	165.0764	312.1190	156.5631	311.1350	156.0711	V	2861.4105	1431.2089	2844.3839	1422.6956	2843.3999	1422.2036	26
4	400.1827	200.5950	383.1561	192.0817	382.1721	191.5897	A	2762.3420	1381.6747	2745.3155	1373.1614	2744.3315	1372.6694	25
5	457.2041	229.1057	440.1776	220.5924	439.1936	220.1004	G	2691.3049	1346.1561	2674.2784	1337.6428	2673.2944	1337.1508	24
6	556.2726	278.6399	539.2460	270.1266	538.2620	269.6346	V	2634.2835	1317.6454	2617.2569	1309.1321	2616.2729	1308.6401	23
7	657.3202	329.1638	640.2937	320.6505	639.3097	320.1585	T	2535.2150	1268.1112	2518.1885	1259.5979	2517.2045	1259.1059	22
8	770.4043	385.7058	753.3777	377.1925	752.3937	376.7005	L	2434.1674	1217.5873	2417.1408	1209.0740	2416.1568	1208.5820	21
9	867.4571	434.2322	850.4305	425.7189	849.4465	425.2269	P	2321.0833	1161.0453	2304.0568	1152.5320	2303.0727	1152.0400	20
10	966.5255	483.7664	949.4989	475.2531	948.5149	474.7611	V	2224.0305	1112.5189	2207.0040	1104.0056	2206.0200	1103.5136	19
11	1113.5939	557.3006	1096.5673	548.7873	1095.5833	548.2953	F	2124.9621	1062.9847	2107.9356	1054.4714	2106.9516	1053.9794	18
12	1242.6365	621.8219	1225.6099	613.3086	1224.6259	612.8166	E	1977.8937	989.4505	1960.8672	980.9372	1959.8831	980.4452	17
13	1379.6954	690.3513	1362.6688	681.8381	1361.6848	681.3461	H	1848.8511	924.9292	1831.8246	916.4159	1830.8406	915.9239	16
14	1542.7587	771.8830	1525.7322	763.3697	1524.7482	762.8777	Y	1711.7922	856.3997	1694.7657	847.8865	1693.7816	847.3945	15
15	1679.8176	840.4125	1662.7911	831.8992	1661.8071	831.4072	H	1548.7289	774.8681	1531.7023	766.3548	1530.7183	765.8628	14
16	1808.8602	904.9338	1791.8337	896.4205	1790.8497	895.9285	E	1411.6700	706.3386	1394.6434	697.8253	1393.6594	697.3333	13
17	1865.8817	933.4445	1848.8551	924.9312	1847.8711	924.4392	G	1282.6274	641.8173	1265.6008	633.3040	1264.6168	632.8120	12
18	1966.9294	983.9683	1949.9028	975.4550	1948.9188	974.9630	T	1225.6059	613.3066	1208.5794	604.7933	1207.5953	604.3013	11
19	2081.9563	1041.4818	2064.9298	1032.9685	2063.9457	1032.4765	D	1124.5582	562.7828	1107.5317	554.2695	1106.5477	553.7775	10
20	2168.9883	1084.9978	2151.9618	1076.4845	2150.9778	1075.9925	S	1009.5313	505.2693	992.5047	496.7560	991.5207	496.2640	9
21	2332.0517	1166.5295	2315.0251	1158.0162	2314.0411	1157.5242	Y	922.4993	461.7533	905.4727	453.2400	904.4887	452.7480	8
22	2461.0943	1231.0508	2444.0677	1222.5375	2443.0837	1222.0455	E	759.4359	380.2216	742.4094	371.7083	741.4254	371.2163	7
23	2574.1783	1287.5928	2557.1518	1279.0795	2556.1678	1278.5875	L	630.3933	315.7003	613.3668	307.1870	612.3828	306.6950	6
24	2675.2260	1338.1166	2658.1995	1329.6034	2657.2154	1329.1114	T	517.3093	259.1583	500.2827	250.6450	499.2987	250.1530	5
25	2732.2475	1366.6274	2715.2209	1358.1141	2714.2369	1357.6221	G	416.2616	208.6344	399.2350	200.1212	0	0	4
26	2845.3315	1423.1694	2828.3050	1414.6561	2827.3210	1414.1641	L	359.2401	180.1237	342.2136	171.6104	0	0	3
27	2916.3686	1458.6880	2899.3421	1450.1747	2898.3581	1449.6827	A	246.1561	123.5817	229.1295	115.0684	0	0	2
28							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 13657.

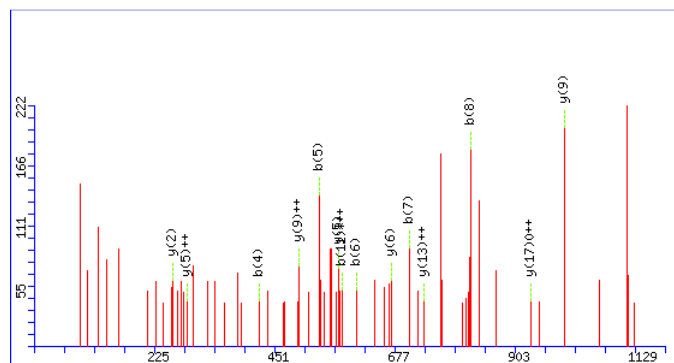
MS/MS Fragmentation of **TALHLAVDLQNPDLVSLLLK**:

Found in **IP100018330;IP101025114**

Title: 4.1.1.1614.6

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120208ry¥120208ry_Tig120slc-P8_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							20
2	173.0921	87.0497	0	0	155.0815	78.0444	A	2072.2114	1036.6093	2055.1849	1028.0961	2054.2008	1027.6041	19
3	286.1761	143.5917	0	0	268.1656	134.5864	L	2001.1743	1001.0908	1984.1477	992.5775	1983.1637	992.0855	18
4	423.2350	212.1212	0	0	405.2245	203.1159	H	1888.0902	944.5488	1871.0637	936.0355	1870.0797	935.5435	17
5	538.3191	268.6632	0	0	518.3085	259.6579	L	1751.0313	876.0193	1734.0048	867.5060	1733.0207	867.0140	16
6	607.3562	304.1817	0	0	589.3457	295.1765	A	1637.9472	819.4773	1620.9207	810.9640	1619.9367	810.4720	15
7	706.4246	353.7160	0	0	688.4141	344.7107	V	1566.9101	783.9587	1549.8836	775.4454	1548.8996	774.9534	14
8	821.4516	411.2294	0	0	803.4410	402.2241	D	1467.8417	734.4245	1450.8152	725.9112	1449.8312	725.4192	13
9	934.5356	467.7715	0	0	916.5251	458.7662	L	1352.8148	676.9110	1335.7882	668.3978	1334.8042	667.9057	12
10	1062.5942	531.8007	1045.5677	523.2875	1044.5837	522.7955	Q	1239.7307	620.3690	1222.7042	611.8557	1221.7201	611.3637	11
11	1176.6371	588.8222	1159.6106	580.3089	1158.6266	579.8169	N	1111.6721	556.3397	1094.6456	547.8264	1093.6616	547.3344	10
12	1273.6899	637.3486	1256.6634	628.8353	1255.6793	628.3433	P	997.6292	499.3182	980.6027	490.8050	979.6186	490.3130	9
13	1388.7169	694.8621	1371.6903	686.3488	1370.7063	685.8568	D	900.5764	450.7919	883.5499	442.2786	882.5659	441.7866	8
14	1501.8009	751.4041	1484.7744	742.8908	1483.7904	742.3988	L	785.5495	393.2784	768.5230	384.7651	767.5389	384.2731	7
15	1600.8693	800.9383	1583.8428	792.4250	1582.8588	791.9330	V	672.4654	336.7364	655.4389	328.2231	654.4549	327.7311	6
16	1687.9014	844.4543	1670.8748	835.9410	1669.8908	835.4490	S	573.3970	287.2021	556.3705	278.6889	555.3865	278.1969	5
17	1800.9854	900.9964	1783.9589	892.4831	1782.9749	891.9911	L	486.3650	243.6861	469.3384	235.1729	0	0	4
18	1914.0695	957.5384	1897.0429	949.0251	1896.0589	948.5331	L	373.2809	187.1441	356.2544	178.6308	0	0	3
19	2027.1536	1014.0804	2010.1270	1005.5671	2009.1430	1005.0751	L	260.1969	130.6021	243.1703	122.0888	0	0	2
20							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 13750.

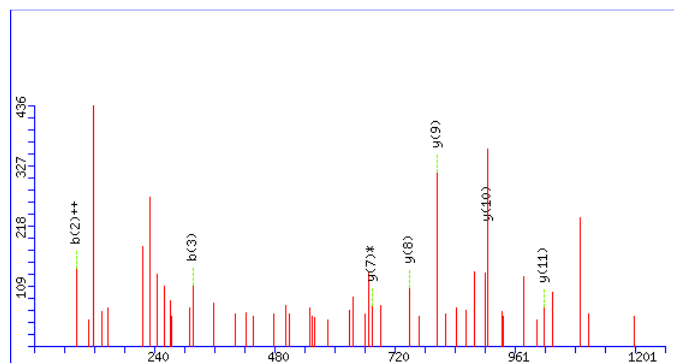
MS/MS Fragmentation of **VAFITGGSGIGFR**:

Found in **IP100010190;IP100444050;IP100856119;IP100877954**

Title: 3.1.1.502.2

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4.3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							14
2	171.1128	86.0600	0	0	0	0	A	1239.6480	620.3277	1222.6215	611.8144	1221.6375	611.3224	13
3	318.1812	159.5942	0	0	0	0	F	1168.6109	584.8091	1151.5844	576.2958	1150.6004	575.8038	12
4	431.2653	216.1363	0	0	0	0	I	1021.5425	511.2749	1004.5160	502.7616	1003.5320	502.2696	11
5	532.3130	266.6601	0	0	514.3024	257.6548	T	908.4585	454.7329	891.4319	446.2196	890.4479	445.7276	10
6	589.3344	295.1709	0	0	571.3239	286.1656	G	807.4108	404.2090	790.3842	395.6958	789.4002	395.2037	9
7	646.3559	323.6816	0	0	628.3453	314.6763	G	750.3893	375.6983	733.3628	367.1850	732.3787	366.6930	8
8	703.3774	352.1923	0	0	685.3668	343.1870	G	693.3678	347.1876	676.3413	338.6743	675.3573	338.1823	7
9	790.4094	395.7083	0	0	772.3988	386.7030	S	636.3464	318.6768	619.3198	310.1636	618.3358	309.6715	6
10	847.4308	424.2191	0	0	829.4203	415.2138	G	549.3144	275.1608	532.2878	266.6475	0	0	5
11	960.5149	480.7611	0	0	942.5043	471.7558	I	492.2929	246.6501	475.2663	238.1368	0	0	4
12	1017.5364	509.2718	0	0	999.5258	500.2665	G	379.2088	190.1081	362.1823	181.5948	0	0	3
13	1164.6048	582.8060	0	0	1146.5942	573.8007	F	322.1874	161.5973	305.1608	153.0840	0	0	2
14							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 13958.

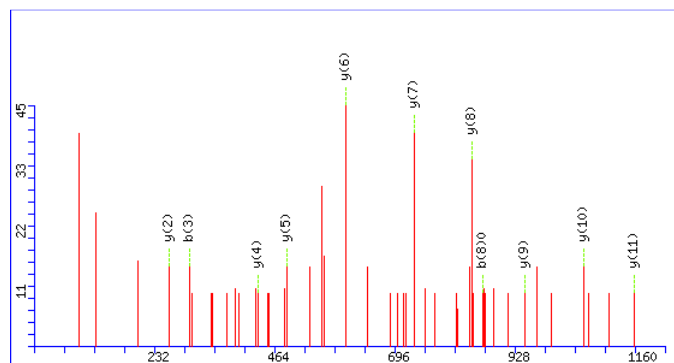
MS/MS Fragmentation of **DALCLVLTLMNGGDLK: 57.021465@C:4**

Found in **IP100017330;IP100180426;IP100182614;IP100217944;IP100220242;IP100337306;IP100414058;IP100465441;IP100873801;IP100908958;IP100966567;IP100967360**

Title: 5.1.1.183.2

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120210ry¥120210ry_32R1-32_2_5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							16
2	187.0713	94.0393	0	0	169.0608	85.0340	A	1617.8703	809.4388	1600.8437	800.9255	1599.8597	800.4335	15
3	300.1554	150.5813	0	0	282.1448	141.5761	L	1546.8331	773.9202	1529.8066	765.4069	1528.8226	764.9149	14
4	460.1860	230.5967	0	0	442.1755	221.5914	C	1433.7491	717.3782	1416.7225	708.8649	1415.7385	708.3729	13
5	573.2701	287.1387	0	0	555.2595	278.1334	L	1273.7184	637.3629	1256.6919	628.8496	1255.7079	628.3576	12
6	672.3385	336.6729	0	0	654.3280	327.6676	V	1160.6344	580.8208	1143.6078	572.3075	1142.6238	571.8155	11
7	785.4226	393.2149	0	0	767.4120	384.2097	L	1061.5660	531.2866	1044.5394	522.7733	1043.5554	522.2813	10
8	886.4703	443.7388	0	0	868.4597	434.7335	T	948.4819	474.7446	931.4553	466.2313	930.4713	465.7393	9
9	999.5543	500.2808	0	0	981.5438	491.2755	L	847.4342	424.2207	830.4077	415.7075	829.4237	415.2155	8
10	1130.5948	565.8010	0	0	1112.5843	556.7958	M	734.3502	367.6787	717.3236	359.1654	716.3396	358.6734	7
11	1244.6377	622.8225	1227.6112	614.3092	1226.6272	613.8172	N	603.3097	302.1585	586.2831	293.6452	585.2991	293.1532	6
12	1301.6592	651.3332	1284.6327	642.8200	1283.6486	642.3280	G	489.2667	245.1370	472.2402	236.6237	471.2562	236.1317	5
13	1358.6807	679.8440	1341.6541	671.3307	1340.6701	670.8387	G	432.2453	216.6263	415.2187	208.1130	414.2347	207.6210	4
14	1473.7076	737.3574	1456.6811	728.8442	1455.6971	728.3522	D	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
15	1586.7917	793.8995	1569.7651	785.3862	1568.7811	784.8942	L	260.1969	130.6021	243.1703	122.0888	0	0	2
16							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 14035.

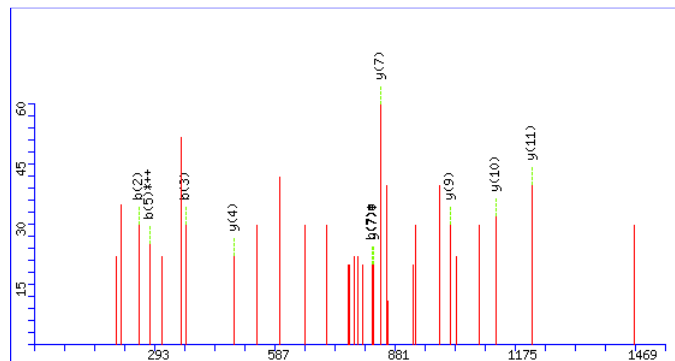
MS/MS Fragmentation of **AWNVDLQAYAGLVSLGNPDFIEVK**:

Found in **IP100182304;IP100477740;IP100923558;IP100969408**

Title: 4.1.1.3291.11

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							25
2	258.1237	129.5655	0	0	0	0	W	2748.3879	1374.6976	2731.3614	1366.1843	2730.3774	1365.6923	24
3	372.1666	186.5870	355.1401	178.0737	0	0	N	2562.3086	1281.6579	2545.2821	1273.1447	2544.2980	1272.6527	23
4	471.2350	236.1212	454.2085	227.6079	0	0	V	2448.2657	1224.6365	2431.2391	1216.1232	2430.2551	1215.6312	22
5	586.2620	293.6346	569.2354	285.1214	568.2514	284.6293	D	2349.1973	1175.1023	2332.1707	1166.5890	2331.1867	1166.0970	21
6	715.3046	358.1559	698.2780	349.6427	697.2940	349.1506	E	2234.1703	1117.5888	2217.1438	1109.0755	2216.1598	1108.5835	20
7	828.3886	414.6980	811.3621	406.1847	810.3781	405.6927	L	2105.1277	1053.0675	2088.1012	1044.5542	2087.1172	1044.0622	19
8	956.4472	478.7272	939.4207	470.2140	938.4367	469.7220	Q	1992.0437	996.5255	1975.0171	988.0122	1974.0331	987.5202	18
9	1027.4843	514.2458	1010.4578	505.7325	1009.4738	505.2405	A	1863.9851	932.4962	1846.9585	923.9829	1845.9745	923.4909	17
10	1190.5477	595.7775	1173.5211	587.2642	1172.5371	586.7722	Y	1792.9480	896.9776	1775.9214	888.4644	1774.9374	887.9723	16
11	1261.5848	631.2960	1244.5582	622.7828	1243.5742	622.2907	A	1629.8846	815.4460	1612.8581	806.9327	1611.8741	806.4407	15
12	1389.6434	695.3253	1372.6168	686.8120	1371.6328	686.3200	Q	1558.8475	779.9274	1541.8210	771.4141	1540.8370	770.9221	14
13	1502.7274	751.8673	1485.7009	743.3541	1484.7169	742.8621	L	1430.7890	715.8981	1413.7624	707.3848	1412.7784	706.8928	13
14	1601.7958	801.4016	1584.7693	792.8883	1583.7853	792.3963	V	1317.7049	659.3561	1300.6783	650.8428	1299.6943	650.3508	12
15	1688.8279	844.9176	1671.8013	836.4043	1670.8173	835.9123	S	1218.6365	609.8219	1201.6099	601.3086	1200.6259	600.8166	11
16	1801.9119	901.4596	1784.8854	892.9463	1783.9014	892.4543	L	1131.6045	566.3059	1114.5779	557.7926	1113.5939	557.3006	10
17	1858.9334	929.9703	1841.9068	921.4571	1840.9228	920.9651	G	1018.5204	509.7638	1001.4938	501.2506	1000.5098	500.7585	9
18	1972.9763	986.9918	1955.9498	978.4785	1954.9658	977.9865	N	961.4989	481.2531	944.4724	472.7398	943.4884	472.2478	8
19	2070.0291	1035.5182	2053.0025	1027.0049	2052.0185	1026.5129	P	847.4560	424.2316	830.4294	415.7184	829.4454	415.2264	7
20	2185.0560	1093.0317	2168.0295	1084.5184	2167.0455	1084.0264	D	750.4032	375.7053	733.3767	367.1920	732.3927	366.7000	6
21	2332.1244	1166.5659	2315.0979	1158.0526	2314.1139	1157.5606	F	635.3763	318.1918	618.3497	309.6785	617.3657	309.1865	5
22	2445.2085	1223.1079	2428.1820	1214.5946	2427.1979	1214.1026	I	488.3079	244.6576	471.2813	236.1443	470.2973	235.6523	4
23	2574.2511	1287.6292	2557.2245	1279.1159	2556.2405	1278.6239	E	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
24	2673.3195	1337.1634	2656.2930	1328.6501	2655.3089	1328.1581	V	246.1812	123.5942	229.1547	115.0810	0	0	2
25							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 14405.

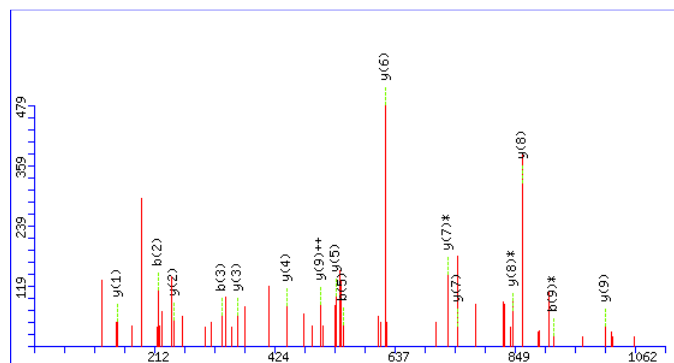
MS/MS Fragmentation of **AFNQSSSLTK**:

Found in **IP100384789;IP100396397;IP100552967;IP101010008**

Title: 1.1.1.7648.11

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							10
2	219.1128	110.0600	0	0	0	0	F	1011.5105	506.2589	994.4840	497.7456	993.5000	497.2536	9
3	333.1557	167.0815	316.1292	158.5682	0	0	N	864.4421	432.7247	847.4156	424.2114	846.4316	423.7194	8
4	461.2143	231.1108	444.1878	222.5975	0	0	Q	750.3992	375.7032	733.3727	367.1900	732.3886	366.6980	7
5	548.2463	274.6268	531.2198	266.1135	530.2358	265.6215	S	622.3406	311.6740	605.3141	303.1607	604.3301	302.6687	6
6	635.2784	318.1428	618.2518	309.6295	617.2678	309.1375	S	535.3086	268.1579	518.2821	259.6447	517.2980	259.1527	5
7	722.3104	361.6588	705.2838	353.1456	704.2998	352.6536	S	448.2766	224.6419	431.2500	216.1287	430.2660	215.6366	4
8	835.3945	418.2009	818.3679	409.6876	817.3839	409.1956	L	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
9	936.4421	468.7247	919.4156	460.2114	918.4316	459.7194	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
10							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 14518.

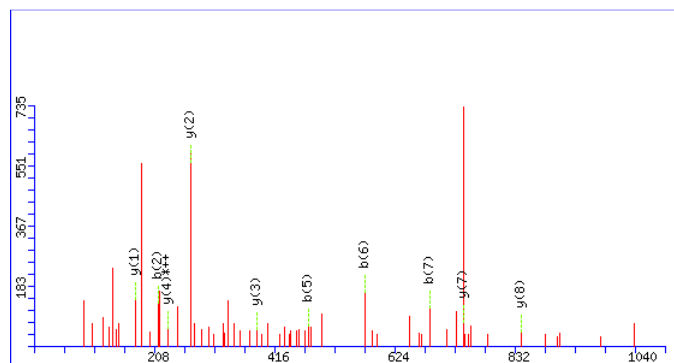
MS/MS Fragmentation of **LTSSSPIPR**:

Found in **IP100216674**

Title: 2.1.1.1244.4

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							9
2	215.1390	108.0731	0	0	197.1285	99.0679	T	844.4523	422.7298	827.4258	414.2165	826.4417	413.7245	8
3	302.1710	151.5892	0	0	284.1605	142.5839	S	743.4046	372.2060	726.3781	363.6927	725.3941	363.2007	7
4	389.2031	195.1052	0	0	371.1925	186.0999	S	656.3726	328.6899	639.3461	320.1767	638.3620	319.6847	6
5	476.2351	238.6212	0	0	458.2245	229.6159	S	569.3406	285.1739	552.3140	276.6606	551.3300	276.1686	5
6	573.2879	287.1476	0	0	555.2773	278.1423	P	482.3085	241.6579	465.2820	233.1446	0	0	4
7	686.3719	343.6896	0	0	668.3614	334.6843	I	385.2558	193.1315	368.2292	184.6183	0	0	3
8	783.4247	392.2160	0	0	765.4141	383.2107	P	272.1717	136.5895	255.1452	128.0762	0	0	2
9							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 14657.

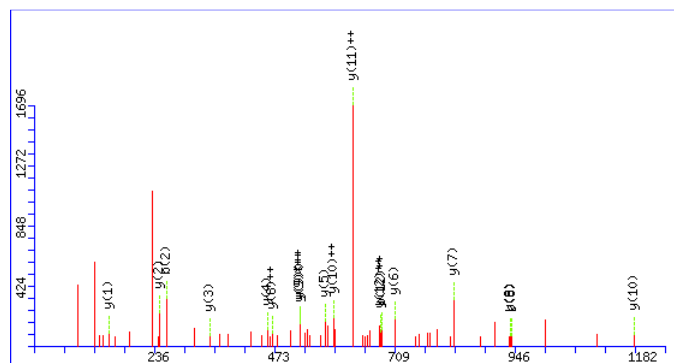
MS/MS Fragmentation of **FIADQLDHLNVTK**:

Found in **IP100031485**

Title: 2.1.1.3963.5

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2.2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							13
2	261.1598	131.0835	0	0	0	0	I	1366.7325	683.8699	1349.7060	675.3566	1348.7219	674.8646	12
3	332.1969	166.6021	0	0	0	0	A	1253.6484	627.3279	1236.6219	618.8146	1235.6379	618.3226	11
4	447.2238	224.1155	0	0	429.2132	215.1103	D	1182.6113	591.8093	1165.5848	583.2960	1164.6008	582.8040	10
5	575.2824	288.1448	558.2558	279.6316	557.2718	279.1396	Q	1067.5844	534.2958	1050.5578	525.7826	1049.5738	525.2905	9
6	688.3665	344.6869	671.3399	336.1736	670.3559	335.6816	L	939.5258	470.2665	922.4993	461.7533	921.5152	461.2613	8
7	803.3934	402.2003	786.3668	393.6871	785.3828	393.1951	D	826.4417	413.7245	809.4152	405.2112	808.4312	404.7192	7
8	940.4523	470.7298	923.4258	462.2165	922.4417	461.7245	H	711.4148	356.2110	694.3883	347.6978	693.4042	347.2058	6
9	1053.5364	527.2718	1036.5098	518.7585	1035.5258	518.2665	L	574.3559	287.6816	557.3293	279.1683	556.3453	278.6763	5
10	1167.5793	584.2933	1150.5527	575.7800	1149.5687	575.2880	N	461.2718	231.1395	444.2453	222.6263	443.2613	222.1343	4
11	1266.6477	633.8275	1249.6212	625.3142	1248.6371	624.8222	V	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
12	1367.6954	684.3513	1350.6688	675.8381	1349.6848	675.3461	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 14769.

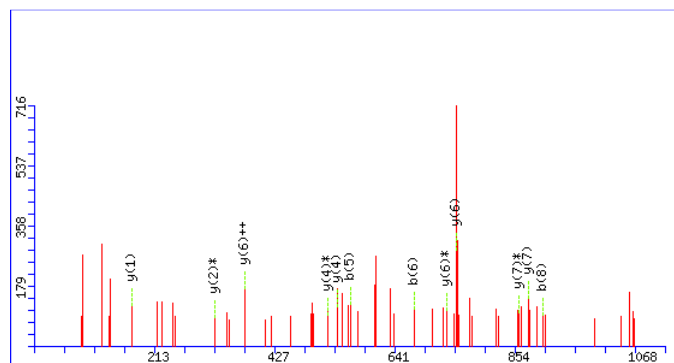
MS/MS Fragmentation of **VTSYIINNLPDTTYR**:

Found in **IP100456630;IP100549232;IP100945165;IP100945320**

Title: 2.1.1.4503.8

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120206ry¥120206ry_aHDF1419-P10_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							16
2	201.1234	101.0653	0	0	183.1128	92.0600	T	1798.8970	899.9521	1781.8705	891.4389	1780.8864	890.9469	15
3	288.1554	144.5813	0	0	270.1448	135.5761	S	1697.8493	849.4283	1680.8228	840.9150	1679.8388	840.4230	14
4	451.2187	226.1130	0	0	433.2082	217.1077	Y	1610.8173	805.9123	1593.7907	797.3990	1592.8067	796.9070	13
5	564.3028	282.6550	0	0	546.2922	273.6498	I	1447.7540	724.3806	1430.7274	715.8673	1429.7434	715.3753	12
6	677.3869	339.1971	0	0	659.3763	330.1918	I	1334.6699	667.8386	1317.6434	659.3253	1316.6593	658.8333	11
7	791.4298	396.2185	774.4032	387.7053	773.4192	387.2132	N	1221.5858	611.2966	1204.5593	602.7833	1203.5753	602.2913	10
8	905.4727	453.2400	888.4462	444.7267	887.4621	444.2347	N	1107.5429	554.2751	1090.5164	545.7618	1089.5324	545.2698	9
9	1018.5568	509.7820	1001.5302	501.2687	1000.5462	500.7767	L	993.5000	497.2536	976.4734	488.7404	975.4894	488.2483	8
10	1146.6154	573.8113	1129.5888	565.2980	1128.6048	564.8060	Q	880.4159	440.7116	863.3894	432.1983	862.4054	431.7063	7
11	1243.6681	622.3377	1226.6416	613.8244	1225.6575	613.3324	P	752.3573	376.6823	735.3308	368.1690	734.3468	367.6770	6
12	1358.6951	679.8512	1341.6685	671.3379	1340.6845	670.8459	D	655.3046	328.1559	638.2780	319.6427	637.2940	319.1506	5
13	1459.7427	730.3750	1442.7162	721.8617	1441.7322	721.3697	T	540.2776	270.6425	523.2511	262.1292	522.2671	261.6372	4
14	1560.7904	780.8988	1543.7639	772.3856	1542.7799	771.8936	T	439.2300	220.1186	422.2034	211.6053	421.2194	211.1133	3
15	1723.8537	862.4305	1706.8272	853.9172	1705.8432	853.4252	Y	338.1823	169.5948	321.1557	161.0815	0	0	2
16							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

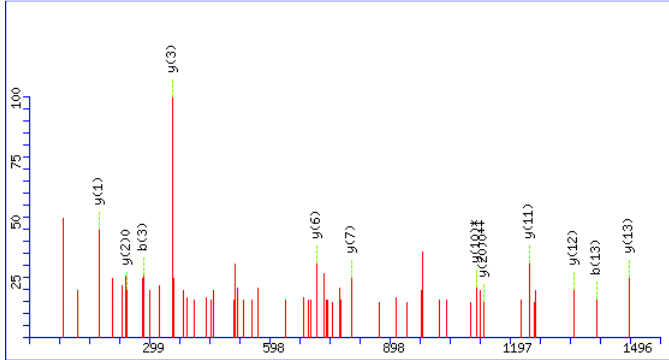
Peptide: 15781.

MS/MS Fragmentation of **TALFPQCTPPSVLPSPDITTYHLIQLSPFPDPSR**: 0.984016@Q:6,57.021465@C:7
Found in **IP100101923:IP100798078:IP101009685**

Title: 5.1.1.1368.8

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_2_5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							33
2	173.0921	87.0497	0	0	155.0815	78.0444	A	3597.8298	1799.4185	3580.8032	1790.9053	3579.8192	1790.4132	32
3	286.1761	143.5917	0	0	268.1656	134.5864	L	3526.7927	1763.9000	3509.7661	1755.3867	3508.7821	1754.8947	31
4	433.2445	217.1259	0	0	415.2340	208.1206	F	3413.7086	1707.3579	3396.6821	1698.8447	3395.6980	1698.3527	30
5	530.2973	265.6523	0	0	512.2867	256.6470	P	3266.6402	1633.8237	3249.6136	1625.3105	3248.6296	1624.8185	29
6	659.3399	330.1736	642.3134	321.6603	641.3293	321.1683	Q	3169.5874	1585.2974	3152.5609	1576.7841	3151.5769	1576.2921	28
7	819.3706	410.1889	802.3440	401.6756	801.3600	401.1836	C	3040.5448	1520.7761	3023.5183	1512.2628	3022.5343	1511.7708	27
8	920.4182	460.7128	903.3917	452.1995	902.4077	451.7075	T	2880.5142	1440.7607	2863.4876	1432.2475	2862.5036	1431.7554	26
9	1017.4710	509.2391	1000.4444	500.7259	999.4604	500.2339	P	2779.4665	1390.2369	2762.4400	1381.7236	2761.4559	1381.2316	25
10	1114.5238	557.7655	1097.4972	549.2522	1096.5132	548.7602	P	2682.4137	1341.7105	2665.3872	1333.1972	2664.4032	1332.7052	24
11	1201.5558	601.2815	1184.5292	592.7683	1183.5452	592.2763	S	2585.3610	1293.1841	2568.3344	1284.6709	2567.3504	1284.1788	23
12	1300.6242	650.8157	1283.5977	642.3025	1282.6136	641.8105	V	2498.3290	1249.6681	2481.3024	1241.1548	2480.3184	1240.6628	22
13	1413.7083	707.3578	1396.6817	698.8445	1395.6977	698.3525	L	2399.2605	1200.1339	2382.2340	1191.6206	2381.2500	1191.1286	21
14	1510.7610	755.8842	1493.7345	747.3709	1492.7505	746.8789	P	2286.1765	1143.5919	2269.1499	1135.0786	2268.1659	1134.5866	20
15	1597.7931	799.4002	1580.7665	790.8869	1579.7825	790.3949	S	2189.1237	1095.0655	2172.0972	1086.5522	2171.1131	1086.0602	19
16	1712.8200	856.9136	1695.7935	848.4004	1694.8094	847.9084	D	2102.0917	1051.5495	2085.0651	1043.0362	2084.0811	1042.5442	18
17	1825.9041	913.4557	1808.8775	904.9424	1807.8935	904.4504	I	1987.0647	994.0360	1970.0382	985.5227	1969.0542	985.0307	17
18	1926.9517	963.9795	1909.9252	955.4662	1908.9412	954.9742	T	1873.9807	937.4940	1856.9541	928.9807	1855.9701	928.4887	16
19	2040.0358	1020.5215	2023.0093	1012.0083	2022.0252	1011.5163	I	1772.9330	886.9701	1755.9064	878.4569	1754.9224	877.9649	15
20	2203.0991	1102.0532	2186.0726	1093.5399	2185.0886	1093.0479	Y	1659.8489	830.4281	1642.8224	821.9148	1641.8384	821.4228	14
21	2340.1581	1170.5827	2323.1315	1162.0694	2322.1475	1161.5774	H	1496.7856	748.8964	1479.7591	740.3832	1478.7750	739.8912	13
22	2453.2421	1227.1247	2436.2156	1218.6114	2435.2316	1218.1194	L	1359.7267	680.3670	1342.7001	671.8537	1341.7161	671.3617	12
23	2566.3262	1283.6667	2549.2996	1275.1535	2548.3156	1274.6614	I	1246.6426	623.8250	1229.6161	615.3117	1228.6321	614.8197	11
24	2694.3848	1347.6960	2677.3582	1339.1827	2676.3742	1338.6907	Q	1133.5586	567.2829	1116.5320	558.7696	1115.5480	558.2776	10
25	2781.4168	1391.2120	2764.3902	1382.6988	2763.4062	1382.2067	S	1005.5000	503.2536	988.4734	494.7404	987.4894	494.2483	9
26	2894.5008	1447.7541	2877.4743	1439.2408	2876.4903	1438.7488	L	918.4680	459.7376	901.4414	451.2243	900.4574	450.7323	8
27	2981.5329	1491.2701	2964.5063	1482.7568	2963.5223	1482.2648	S	805.3839	403.1956	788.3573	394.6823	787.3733	394.1903	7
28	3078.5856	1539.7965	3061.5591	1531.2832	3060.5751	1530.7912	P	718.3519	359.6796	701.3253	351.1663	700.3413	350.6743	6
29	3225.6541	1613.3307	3208.6275	1604.8174	3207.6435	1604.3254	F	621.2991	311.1532	604.2726	302.6399	603.2885	302.1479	5
30	3340.6810	1670.8441	3323.6544	1662.3309	3322.6704	1661.8389	D	474.2307	237.6190	457.2041	229.1057	456.2201	228.6137	4
31	3437.7338	1719.3705	3420.7072	1710.8572	3419.7232	1710.3652	P	359.2037	180.1055	342.1772	171.5922	341.1932	171.1002	3
32	3524.7658	1762.8865	3507.7392	1754.3733	3506.7552	1753.8813	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
33							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 15808.

MS/MS Fragmentation of **TLSGCPAVDSVVSLLDGVEEK: 57.021465@C:5**

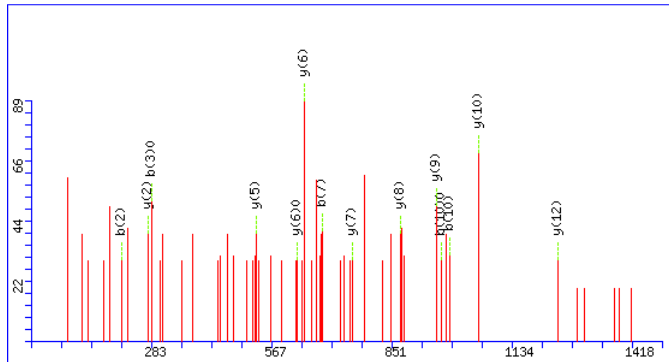
Found in

IP100419963;IP100556323;IP100607605;IP100845303;IP100845323;IP100910834;IP100963954;IP100964423;IP100964682;IP100965383;IP100965418;IP100965662;IP100965

Title: 4.1.1.3585.4

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120214ry¥120214ry_414C2-43_4_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							21
2	215.1390	108.0731	0	0	197.1285	99.0679	L	2044.0631	1022.5352	2027.0365	1014.0219	2026.0525	1013.5299	20
3	302.1710	151.5892	0	0	284.1605	142.5839	S	1930.9790	965.9931	1913.9525	957.4799	1912.9685	956.9879	19
4	359.1925	180.0999	0	0	341.1819	171.0946	G	1843.9470	922.4771	1826.9204	913.9639	1825.9364	913.4719	18
5	519.2232	260.1152	0	0	501.2126	251.1099	C	1786.9255	893.9664	1769.8990	885.4531	1768.9150	884.9611	17
6	616.2759	308.6416	0	0	598.2654	299.6363	P	1626.8949	813.9511	1609.8683	805.4378	1608.8843	804.9458	16
7	687.3130	344.1602	0	0	669.3025	335.1549	A	1529.8421	765.4247	1512.8156	756.9114	1511.8316	756.4194	15
8	786.3815	393.6944	0	0	768.3709	384.6891	V	1458.8050	729.9061	1441.7785	721.3929	1440.7944	720.9009	14
9	901.4084	451.2078	0	0	883.3978	442.2026	D	1359.7366	680.3719	1342.7100	671.8587	1341.7260	671.3666	13
10	988.4404	494.7239	0	0	970.4299	485.7186	S	1244.7096	622.8585	1227.6831	614.3452	1226.6991	613.8532	12
11	1087.5088	544.2581	0	0	1069.4983	535.2528	V	1157.6776	579.3424	1140.6511	570.8292	1139.6671	570.3372	11
12	1186.5773	593.7923	0	0	1168.5667	584.7870	V	1058.6092	529.8082	1041.5827	521.2950	1040.5986	520.8030	10
13	1273.6093	637.3083	0	0	1255.5987	628.3030	S	959.5408	480.2740	942.5142	471.7608	941.5302	471.2687	9
14	1386.6933	693.8503	0	0	1368.6828	684.8450	L	872.5088	436.7580	855.4822	428.2447	854.4982	427.7527	8
15	1499.7774	750.3923	0	0	1481.7668	741.3871	L	759.4247	380.2160	742.3981	371.7027	741.4141	371.2107	7
16	1614.8044	807.9058	0	0	1596.7938	798.9005	D	646.3406	323.6740	629.3141	315.1607	628.3301	314.6687	6
17	1671.8258	836.4165	0	0	1653.8153	827.4113	G	531.3137	266.1605	514.2871	257.6472	513.3031	257.1552	5
18	1770.8942	885.9508	0	0	1752.8837	876.9455	V	474.2922	237.6498	457.2657	229.1365	456.2817	228.6445	4
19	1869.9626	935.4850	0	0	1851.9521	926.4797	V	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
20	1999.0052	1000.0063	0	0	1980.9947	991.0010	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
21							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 15951.

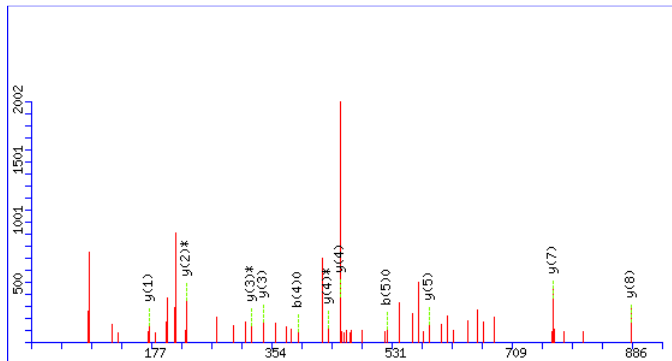
MS/MS Fragmentation of **IDPSMLPAR**:

Found in **IP100163550;IP100478161;IP101011202**

Title: 2.1.1.1017.10

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120212ry¥120212ry_414C2-43_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							9
2	229.1183	115.0628	0	0	211.1077	106.0575	D	886.4451	443.7262	869.4186	435.2129	868.4345	434.7209	8
3	326.1710	163.5892	0	0	308.1605	154.5839	P	771.4182	386.2127	754.3916	377.6994	753.4076	377.2074	7
4	413.2031	207.1052	0	0	395.1925	198.0999	S	674.3654	337.6863	657.3389	329.1731	656.3548	328.6811	6
5	544.2436	272.6254	0	0	526.2330	263.6201	M	587.3334	294.1703	570.3068	285.6571	0	0	5
6	657.3276	329.1675	0	0	639.3171	320.1622	L	456.2929	228.6501	439.2663	220.1368	0	0	4
7	754.3804	377.6938	0	0	736.3698	368.6885	P	343.2088	172.1081	326.1823	163.5948	0	0	3
8	825.4175	413.2124	0	0	807.4069	404.2071	A	246.1561	123.5817	229.1295	115.0684	0	0	2
9							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 16173.

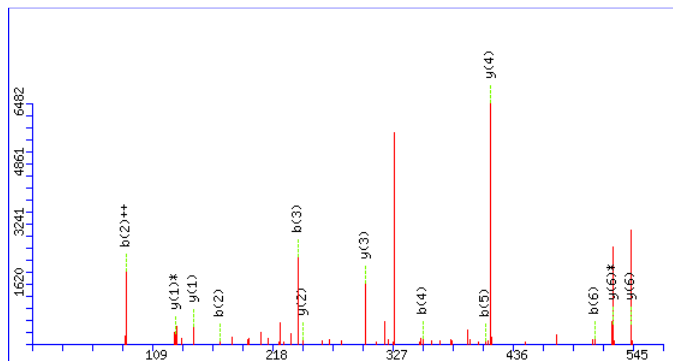
MS/MS Fragmentation of **IGALGVK**:

Found in **IP100304549;IP100552934**

Title: 1.1.1.7723.2

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							7
2	171.1128	86.0600	0	0	0	0	G	544.3453	272.6763	527.3188	264.1630	0	0	6
3	242.1499	121.5786	0	0	0	0	A	487.3239	244.1656	470.2973	235.6523	0	0	5
4	355.2340	178.1206	0	0	0	0	L	416.2867	208.6470	399.2602	200.1337	0	0	4
5	412.2554	206.6314	0	0	0	0	G	303.2027	152.1050	286.1761	143.5917	0	0	3
6	511.3239	256.1656	0	0	0	0	V	246.1812	123.5942	229.1547	115.0810	0	0	2
7							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

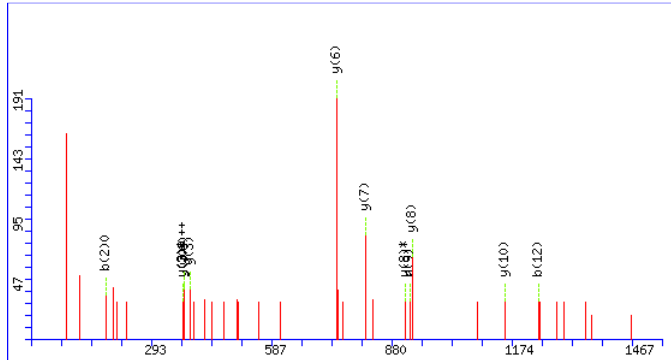
Peptide: 16334.

MS/MS Fragmentation of **ISDDGGAHAPGCLLEGAFINLLAPLFNEK: 57.021465@C:4,57.021465@C:12**
 Found in **IP100329038;IP100329039;IP100384417;IP100384418;IP100746700**

Title: 4.1.1.3792.9

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							29
2	201.1234	101.0653	0	0	183.1128	92.0600	S	3045.4081	1523.2077	3028.3815	1514.6944	3027.3975	1514.2024	28
3	316.1503	158.5788	0	0	298.1397	149.5735	D	2958.3761	1479.6917	2941.3495	1471.1784	2940.3655	1470.6864	27
4	476.1810	238.5941	0	0	458.1704	229.5888	C	2843.3491	1422.1782	2826.3226	1413.6649	2825.3386	1413.1729	26
5	591.2079	296.1076	0	0	573.1973	287.1023	D	2683.3185	1342.1629	2666.2919	1333.6496	2665.3079	1333.1576	25
6	648.2294	324.6183	0	0	630.2188	315.6130	G	2568.2915	1284.6494	2551.2650	1276.1361	2550.2810	1275.6441	24
7	719.2665	360.1369	0	0	701.2559	351.1316	A	2511.2701	1256.1387	2494.2435	1247.6254	2493.2595	1247.1334	23
8	856.3254	428.6663	0	0	838.3148	419.6611	H	2440.2329	1220.6201	2423.2064	1212.1068	2422.2224	1211.6148	22
9	927.3625	464.1849	0	0	909.3519	455.1796	A	2303.1740	1152.0907	2286.1475	1143.5774	2285.1635	1143.0854	21
10	1024.4153	512.7113	0	0	1006.4047	503.7060	P	2232.1369	1116.5721	2215.1104	1108.0588	2214.1264	1107.5668	20
11	1081.4367	541.2220	0	0	1063.4262	532.2167	G	2135.0842	1068.0457	2118.0576	1059.5324	2117.0736	1059.0404	19
12	1241.4674	621.2373	0	0	1223.4568	612.2320	C	2078.0627	1039.5350	2061.0361	1031.0217	2060.0521	1030.5297	18
13	1354.5515	677.7794	0	0	1336.5409	668.7741	L	1918.0320	959.5197	1901.0055	951.0064	1900.0215	950.5144	17
14	1483.5940	742.3007	0	0	1465.5835	733.2954	E	1804.9480	902.9776	1787.9214	894.4644	1786.9374	893.9723	16
15	1612.6366	806.8220	0	0	1594.6261	797.8167	E	1675.9054	838.4563	1658.8788	829.9431	1657.8948	829.4510	15
16	1669.6581	835.3327	0	0	1651.6475	826.3274	G	1546.8628	773.9350	1529.8362	765.4218	1528.8522	764.9298	14
17	1740.6952	870.8512	0	0	1722.6846	861.8460	A	1489.8413	745.4243	1472.8148	736.9110	1471.8308	736.4190	13
18	1887.7636	944.3855	0	0	1869.7531	935.3802	F	1418.8042	709.9057	1401.7777	701.3925	1400.7936	700.9005	12
19	2000.8477	1000.9275	0	0	1982.8371	991.9222	I	1271.7358	636.3715	1254.7092	627.8583	1253.7252	627.3663	11
20	2114.8906	1057.9489	2097.8641	1049.4357	2096.8801	1048.9437	N	1158.6517	579.8295	1141.6252	571.3162	1140.6412	570.8242	10
21	2227.9747	1114.4910	2210.9481	1105.9777	2209.9641	1105.4857	L	1044.6088	522.8080	1027.5823	514.2948	1026.5982	513.8028	9
22	2341.0587	1171.0330	2324.0322	1162.5197	2323.0482	1162.0277	L	931.5247	466.2660	914.4982	457.7527	913.5142	457.2607	8
23	2412.0959	1206.5516	2395.0693	1198.0383	2394.0853	1197.5463	A	818.4407	409.7240	801.4141	401.2107	800.4301	400.7187	7
24	2509.1486	1255.0780	2492.1221	1246.5647	2491.1381	1246.0727	P	747.4036	374.2054	730.3770	365.6921	729.3930	365.2001	6
25	2622.2327	1311.6200	2605.2061	1303.1067	2604.2221	1302.6147	L	650.3508	325.6790	633.3243	317.1658	632.3402	316.6738	5
26	2769.3011	1385.1542	2752.2746	1376.6409	2751.2905	1376.1489	F	537.2667	269.1370	520.2402	260.6237	519.2562	260.1317	4
27	2883.3440	1442.1757	2866.3175	1433.6624	2865.3335	1433.1704	N	390.1983	195.6028	373.1718	187.0895	372.1878	186.5975	3
28	3012.3866	1506.6969	2995.3601	1498.1837	2994.3761	1497.6917	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
29							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 16341.

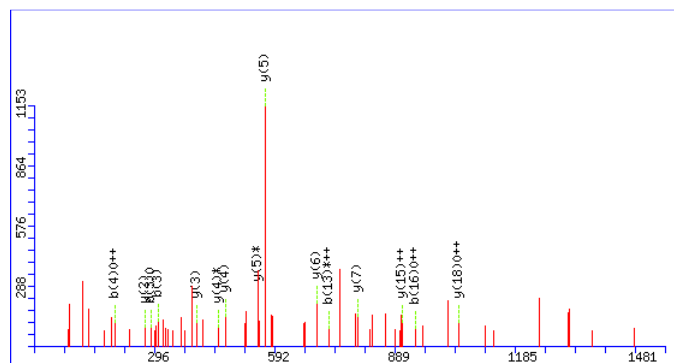
MS/MS Fragmentation of **AFSLYANIDILRPYFDVEPAQVR**:

Found in **IP100329688;IP100963891;IP100965871;IP100967180;IP100967418;IP100968007;IP101013772**

Title: 4.1.1.2011.5

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120206ry¥120206ry_aHDF1419-P10_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							23
2	219.1128	110.0600	0	0	0	0	F	2626.3664	1313.6868	2609.3399	1305.1736	2608.3558	1304.6816	22
3	306.1448	153.5761	0	0	288.1343	144.5708	S	2479.2980	1240.1526	2462.2714	1231.6394	2461.2874	1231.1473	21
4	419.2289	210.1181	0	0	401.2183	201.1128	L	2392.2660	1196.6366	2375.2394	1188.1233	2374.2554	1187.6313	20
5	582.2922	291.6498	0	0	564.2817	282.6445	Y	2279.1819	1140.0946	2262.1553	1131.5813	2261.1713	1131.0893	19
6	653.3293	327.1683	0	0	635.3188	318.1630	A	2116.1186	1058.5629	2099.0920	1050.0496	2098.1080	1049.5576	18
7	767.3723	384.1898	750.3457	375.6765	749.3617	375.1845	N	2045.0815	1023.0444	2028.0549	1014.5311	2027.0709	1014.0391	17
8	880.4563	440.7318	863.4298	432.2185	862.4458	431.7265	I	1931.0385	966.0229	1914.0120	957.5096	1913.0280	957.0176	16
9	995.4833	498.2453	978.4567	489.7320	977.4727	489.2400	D	1817.9545	909.4809	1800.9279	900.9676	1799.9439	900.4756	15
10	1108.5673	554.7873	1091.5408	546.2740	1090.5568	545.7820	I	1702.9275	851.9674	1685.9010	843.4541	1684.9170	842.9621	14
11	1221.6514	611.3293	1204.6249	602.8161	1203.6408	602.3241	L	1589.8435	795.4254	1572.8169	786.9121	1571.8329	786.4201	13
12	1377.7525	689.3799	1360.7260	680.8666	1359.7419	680.3746	R	1476.7594	738.8833	1459.7328	730.3701	1458.7488	729.8781	12
13	1474.8053	737.9063	1457.7787	729.3930	1456.7947	728.9010	P	1320.6583	660.8328	1303.6317	652.3195	1302.6477	651.8275	11
14	1637.8686	819.4379	1620.8421	810.9247	1619.8580	810.4327	Y	1223.6055	612.3064	1206.5790	603.7931	1205.5950	603.3011	10
15	1784.9370	892.9721	1767.9105	884.4589	1766.9265	883.9669	F	1060.5422	530.7747	1043.5156	522.2615	1042.5316	521.7694	9
16	1899.9640	950.4856	1882.9374	941.9723	1881.9534	941.4803	D	913.4738	457.2405	896.4472	448.7272	895.4632	448.2352	8
17	1999.0324	1000.0198	1982.0058	991.5066	1981.0218	991.0145	V	798.4468	399.7271	781.4203	391.2138	780.4363	390.7218	7
18	2128.0750	1064.5411	2111.0484	1056.0278	2110.0644	1055.5358	E	699.3784	350.1928	682.3519	341.6796	681.3679	341.1876	6
19	2225.1277	1113.0675	2208.1012	1104.5542	2207.1172	1104.0622	P	570.3358	285.6715	553.3093	277.1583	0	0	5
20	2296.1648	1148.5861	2279.1383	1140.0728	2278.1543	1139.5808	A	473.2831	237.1452	456.2565	228.6319	0	0	4
21	2424.2234	1212.6154	2407.1969	1204.1021	2406.2129	1203.6101	Q	402.2459	201.6266	385.2194	193.1133	0	0	3
22	2523.2918	1262.1496	2506.2653	1253.6363	2505.2813	1253.1443	V	274.1874	137.5973	257.1608	129.0840	0	0	2
23							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 16487.

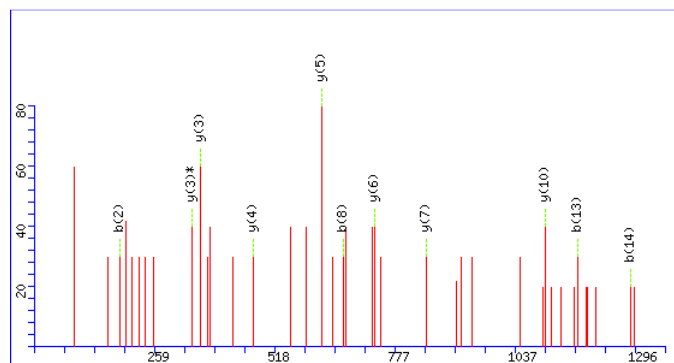
MS/MS Fragmentation of **IAAGLQPSYSGSLLLFDAIR**:

Found in **IP100004489**

Title: 4.1.1.1604.4

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_3.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							20
2	185.1285	93.0679	0	0	0	0	A	1908.0225	954.5149	1890.9960	946.0016	1890.0120	945.5096	19
3	256.1656	128.5864	0	0	0	0	A	1836.9854	918.9964	1819.9589	910.4831	1818.9749	909.9911	18
4	313.1870	157.0972	0	0	0	0	G	1765.9483	883.4778	1748.9218	874.9645	1747.9377	874.4725	17
5	426.2711	213.6392	0	0	0	0	L	1708.9268	854.9671	1691.9003	846.4538	1690.9163	845.9618	16
6	483.2926	242.1499	0	0	0	0	G	1595.8428	798.4250	1578.8162	789.9118	1577.8322	789.4197	15
7	580.3453	290.6763	0	0	0	0	P	1538.8213	769.9143	1521.7948	761.4010	1520.8108	760.9090	14
8	667.3774	334.1923	0	0	649.3668	325.1870	S	1441.7686	721.3879	1424.7420	712.8746	1423.7580	712.3826	13
9	830.4407	415.7240	0	0	812.4301	406.7187	Y	1354.7365	677.8719	1337.7100	669.3586	1336.7260	668.8666	12
10	917.4727	459.2400	0	0	899.4621	450.2347	S	1191.6732	596.3402	1174.6466	587.8270	1173.6626	587.3350	11
11	974.4942	487.7507	0	0	956.4836	478.7454	G	1104.6412	552.8242	1087.6146	544.3109	1086.6306	543.8189	10
12	1061.5262	531.2667	0	0	1043.5156	522.2615	S	1047.6197	524.3135	1030.5932	515.8002	1029.6091	515.3082	9
13	1174.6103	587.8088	0	0	1156.5997	578.8035	L	960.5877	480.7975	943.5611	472.2842	942.5771	471.7922	8
14	1287.6943	644.3508	0	0	1269.6838	635.3455	L	847.5036	424.2554	830.4771	415.7422	829.4931	415.2502	7
15	1400.7784	700.8928	0	0	1382.7678	691.8876	L	734.4196	367.7134	717.3930	359.2001	716.4090	358.7081	6
16	1547.8468	774.4270	0	0	1529.8362	765.4218	F	621.3355	311.1714	604.3089	302.6581	603.3249	302.1661	5
17	1662.8738	831.9405	0	0	1644.8632	822.9352	D	474.2671	237.6372	457.2405	229.1239	456.2565	228.6319	4
18	1733.9109	867.4591	0	0	1715.9003	858.4538	A	359.2401	180.1237	342.2136	171.6104	0	0	3
19	1846.9949	924.0011	0	0	1828.9844	914.9958	L	288.2030	144.6051	271.1765	136.0919	0	0	2
20							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 16630.

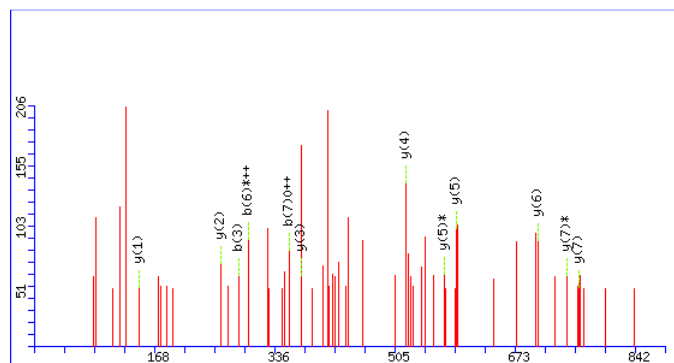
MS/MS Fragmentation of **DGNAFLDK**:

Found in **IP100290514;IP100871167;IP100974179;IP100976000;IP100976472;IP100979150;IP100981334;IP101011387**

Title: 1.1.1.8995.5

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120212ry¥120212ry_414C2-43.3.1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							8
2	173.0557	87.0315	0	0	155.0451	78.0262	G	764.3937	382.7005	747.3672	374.1872	746.3832	373.6952	7
3	287.0986	144.0529	270.0721	135.5397	269.0880	135.0477	N	707.3723	354.1898	690.3457	345.6765	689.3617	345.1845	6
4	358.1357	179.5715	341.1092	171.0582	340.1252	170.5662	A	593.3293	297.1683	576.3028	288.6550	575.3188	288.1630	5
5	505.2041	253.1057	488.1776	244.5924	487.1936	244.1004	F	522.2922	261.6498	505.2657	253.1365	504.2817	252.6445	4
6	618.2882	309.6477	601.2617	301.1345	600.2776	300.6425	L	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
7	733.3151	367.1612	716.2886	358.6479	715.3046	358.1559	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
8							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 16677.

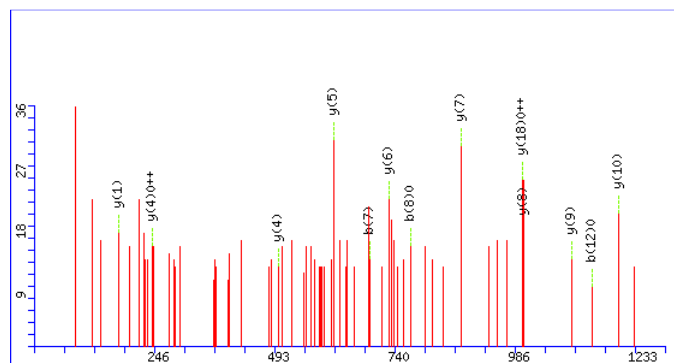
MS/MS Fragmentation of **ISGSDTETLGGFPVFLIQVTR**:

Found in **IP100445335,IP100465041,IP100844013,IP100946841,IP100946960,IP101012571**

Title: 4.1.1.3276.4

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120118ry¥120118ry_201B7-32_2.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							22
2	201.1234	101.0653	0	0	183.1128	92.0600	S	2253.1398	1127.0735	2236.1132	1118.5602	2235.1292	1118.0682	21
3	258.1448	129.5761	0	0	240.1343	120.5708	G	2166.1077	1083.5575	2149.0812	1075.0442	2148.0972	1074.5522	20
4	345.1769	173.0921	0	0	327.1663	164.0868	S	2109.0863	1055.0468	2092.0597	1046.5335	2091.0757	1046.0415	19
5	460.2038	230.6055	0	0	442.1932	221.6003	D	2022.0542	1011.5308	2005.0277	1003.0175	2004.0437	1002.5255	18
6	561.2515	281.1294	0	0	543.2409	272.1241	T	1907.0273	954.0173	1890.0007	945.5040	1889.0167	945.0120	17
7	690.2941	345.6507	0	0	672.2835	336.6454	E	1805.9796	903.4934	1788.9531	894.9802	1787.9690	894.4882	16
8	791.3418	396.1745	0	0	773.3312	387.1692	T	1676.9370	838.9721	1659.9105	830.4589	1658.9265	829.9669	15
9	904.4258	452.7165	0	0	886.4153	443.7113	L	1575.8893	788.4483	1558.8628	779.9350	1557.8788	779.4430	14
10	961.4473	481.2273	0	0	943.4367	472.2220	G	1462.8053	731.9063	1445.7787	723.3930	1444.7947	722.9010	13
11	1018.4687	509.7380	0	0	1000.4582	500.7327	G	1405.7838	703.3955	1388.7573	694.8823	1387.7732	694.3903	12
12	1165.5372	583.2722	0	0	1147.5266	574.2669	F	1348.7623	674.8848	1331.7358	666.3715	1330.7518	665.8795	11
13	1262.5899	631.7986	0	0	1244.5794	622.7933	P	1201.6939	601.3506	1184.6674	592.8373	1183.6834	592.3453	10
14	1361.6583	681.3328	0	0	1343.6478	672.3275	V	1104.6412	552.8242	1087.6146	544.3109	1086.6306	543.8189	9
15	1490.7009	745.8541	0	0	1472.6904	736.8488	E	1005.5728	503.2900	988.5462	494.7767	987.5622	494.2847	8
16	1637.7693	819.3883	0	0	1619.7588	810.3830	F	876.5302	438.7687	859.5036	430.2554	858.5196	429.7634	7
17	1750.8534	875.9303	0	0	1732.8428	866.9251	L	729.4618	365.2345	712.4352	356.7212	711.4512	356.2292	6
18	1863.9375	932.4724	0	0	1845.9269	923.4671	I	616.3777	308.6925	599.3511	300.1792	598.3671	299.6872	5
19	1991.9961	996.5017	1974.9695	987.9884	1973.9855	987.4964	Q	503.2936	252.1504	486.2671	243.6372	485.2831	243.1452	4
20	2091.0645	1046.0359	2074.0379	1037.5226	2073.0539	1037.0306	V	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
21	2192.1121	1096.5597	2175.0856	1088.0464	2174.1016	1087.5544	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
22							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 16722.

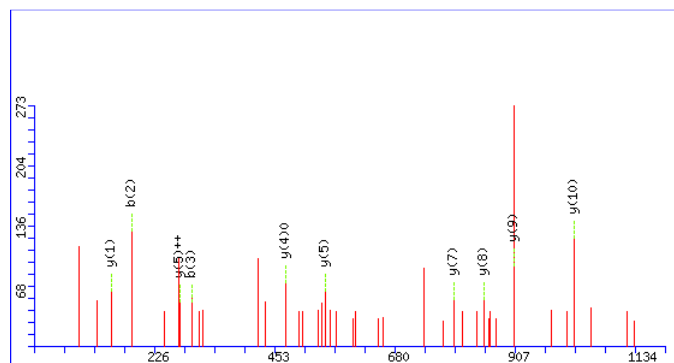
MS/MS Fragmentation of **LALIGGLEGLSK:**

Found in **IP100171925;IP100926491;IP101013759**

Title: 4.1.1.782.6

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							13
2	185.1285	93.0679	0	0	0	0	A	1204.6936	602.8504	1187.6671	594.3372	1186.6830	593.8452	12
3	298.2125	149.6099	0	0	0	0	L	1133.6565	567.3319	1116.6299	558.8186	1115.6459	558.3266	11
4	411.2966	206.1519	0	0	0	0	I	1020.5724	510.7898	1003.5459	502.2766	1002.5619	501.7846	10
5	468.3180	234.6627	0	0	0	0	G	907.4884	454.2478	890.4618	445.7345	889.4778	445.2425	9
6	525.3395	263.1734	0	0	0	0	G	850.4669	425.7371	833.4403	417.2238	832.4563	416.7318	8
7	638.4236	319.7154	0	0	0	0	L	793.4454	397.2264	776.4189	388.7131	775.4349	388.2211	7
8	767.4662	384.2367	0	0	749.4556	375.2314	E	680.3614	340.6843	663.3348	332.1710	662.3508	331.6790	6
9	824.4876	412.7475	0	0	806.4771	403.7422	G	551.3188	276.1630	534.2922	267.6498	533.3082	267.1577	5
10	971.5560	486.2817	0	0	953.5455	477.2764	F	494.2973	247.6523	477.2708	239.1390	476.2867	238.6470	4
11	1084.6401	542.8237	0	0	1066.6295	533.8184	L	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
12	1171.6721	586.3397	0	0	1153.6616	577.3344	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 16900.

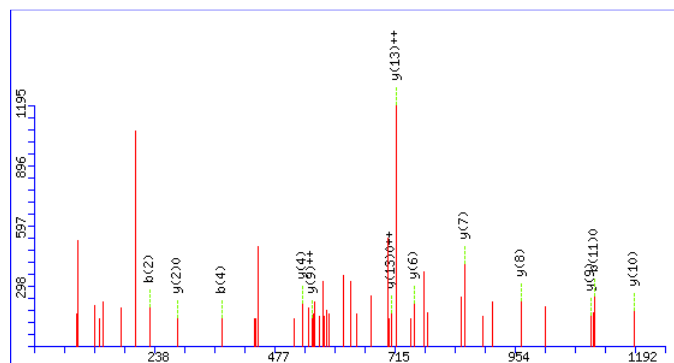
MS/MS Fragmentation of **DLGSVSHLTGYETER**:

Found in **IP100032633;IP100328619;IP101025995;IP101026416;IP101026589**

Title: 2.1.1.2483.6

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							15
2	229.1183	115.0628	0	0	211.1077	106.0575	L	1548.7653	774.8863	1531.7387	766.3730	1530.7547	765.8810	14
3	286.1397	143.5735	0	0	268.1292	134.5682	G	1435.6812	718.3442	1418.6546	709.8310	1417.6706	709.3390	13
4	373.1718	187.0895	0	0	355.1612	178.0842	S	1378.6597	689.8335	1361.6332	681.3202	1360.6492	680.8282	12
5	472.2402	236.6237	0	0	454.2296	227.6185	V	1291.6277	646.3175	1274.6012	637.8042	1273.6171	637.3122	11
6	559.2722	280.1397	0	0	541.2617	271.1345	S	1192.5593	596.7833	1175.5327	588.2700	1174.5487	587.7780	10
7	696.3311	348.6692	0	0	678.3206	339.6639	H	1105.5273	553.2673	1088.5007	544.7540	1087.5167	544.2620	9
8	809.4152	405.2112	0	0	791.4046	396.2060	L	968.4684	484.7378	951.4418	476.2245	950.4578	475.7325	8
9	910.4629	455.7351	0	0	892.4523	446.7298	T	855.3843	428.1958	838.3577	419.6825	837.3737	419.1905	7
10	967.4843	484.2458	0	0	949.4738	475.2405	G	754.3366	377.6719	737.3101	369.1587	736.3260	368.6667	6
11	1130.5477	565.7775	0	0	1112.5371	556.7722	Y	697.3151	349.1612	680.2886	340.6479	679.3046	340.1559	5
12	1259.5903	630.2988	0	0	1241.5797	621.2935	E	534.2518	267.6295	517.2253	259.1163	516.2413	258.6243	4
13	1360.6379	680.8226	0	0	1342.6274	671.8173	T	405.2092	203.1082	388.1827	194.5950	387.1987	194.1030	3
14	1489.6805	745.3439	0	0	1471.6700	736.3386	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
15							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 17129.

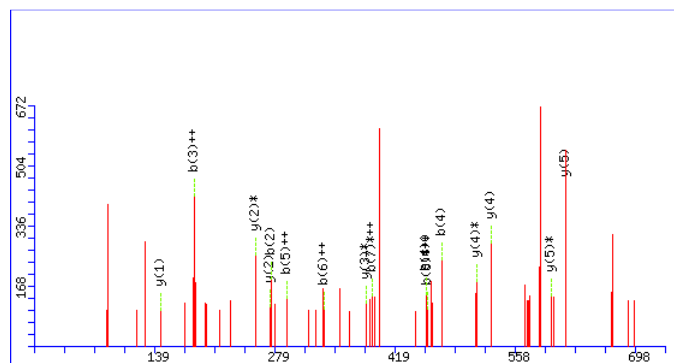
MS/MS Fragmentation of **FKPTLSQQQK**:

Found in **IP100218192;IP100896413;IP100896419;IP100944960;IP101010866;IP101018048**

Title: 1.1.1.5923.7

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_3_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							10
2	276.1707	138.5890	259.1441	130.0757	0	0	K	1057.6000	529.3037	1040.5735	520.7904	1039.5895	520.2984	9
3	373.2234	187.1153	356.1969	178.6021	0	0	P	929.5051	465.2562	912.4785	456.7429	911.4945	456.2509	8
4	474.2711	237.6392	457.2445	229.1259	456.2605	228.6339	T	832.4523	416.7298	815.4258	408.2165	814.4417	407.7245	7
5	587.3552	294.1812	570.3286	285.6679	569.3446	285.1759	L	731.4046	366.2060	714.3781	357.6927	713.3941	357.2007	6
6	674.3872	337.6972	657.3606	329.1840	656.3766	328.6919	S	618.3206	309.6639	601.2940	301.1506	600.3100	300.6586	5
7	802.4458	401.7265	785.4192	393.2132	784.4352	392.7212	Q	531.2885	266.1479	514.2620	257.6346	0	0	4
8	930.5043	465.7558	913.4778	457.2425	912.4938	456.7505	Q	403.2300	202.1186	386.2034	193.6053	0	0	3
9	1058.5629	529.7851	1041.5364	521.2718	1040.5524	520.7798	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
10							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 17379.

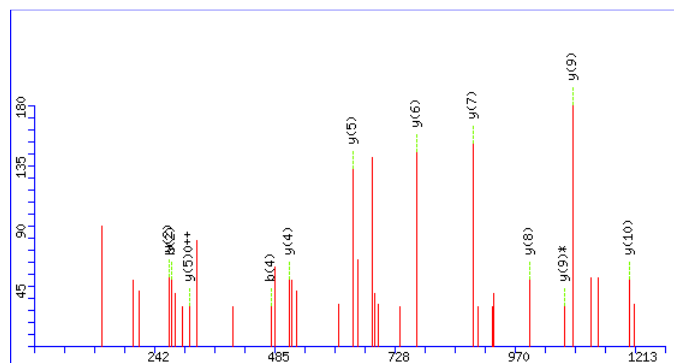
MS/MS Fragmentation of **YNSNLEEIVR**:

Found in **IP100169294;IP100607715;IP101011827;IP101014695**

Title: 2.1.1.2408.9

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	164.0706	82.5389	0	0	0	0	Y							11
2	278.1135	139.5604	261.0870	131.0471	0	0	N	1202.6012	601.8042	1185.5746	593.2909	1184.5906	592.7989	10
3	365.1456	183.0764	348.1190	174.5631	347.1350	174.0711	S	1088.5582	544.7828	1071.5317	536.2695	1070.5477	535.7775	9
4	479.1885	240.0979	462.1619	231.5846	461.1779	231.0926	N	1001.5262	501.2667	984.4997	492.7535	983.5156	492.2615	8
5	592.2726	296.6399	575.2460	288.1266	574.2620	287.6346	L	887.4833	444.2453	870.4567	435.7320	869.4727	435.2400	7
6	721.3151	361.1612	704.2886	352.6479	703.3046	352.1559	E	774.3992	387.7032	757.3727	379.1900	756.3886	378.6980	6
7	850.3577	425.6825	833.3312	417.1692	832.3472	416.6772	E	645.3566	323.1819	628.3301	314.6687	627.3461	314.1767	5
8	979.4003	490.2038	962.3738	481.6905	961.3898	481.1985	E	516.3140	258.6606	499.2875	250.1474	498.3035	249.6554	4
9	1092.4844	546.7458	1075.4578	538.2326	1074.4738	537.7406	I	387.2714	194.1394	370.2449	185.6261	0	0	3
10	1191.5528	596.2800	1174.5263	587.7668	1173.5422	587.2748	V	274.1874	137.5973	257.1608	129.0840	0	0	2
11							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 17450.

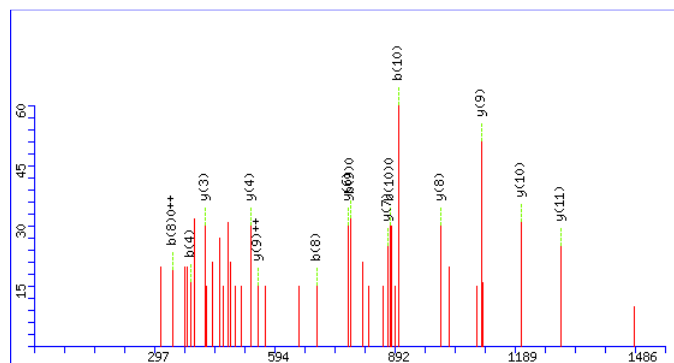
MS/MS Fragmentation of **AEEGGEGATVPSAAATTTEVVTEVELLYK**:

Found in **IP100465100:IP100478854**

Title: 5.1.1.1187.8

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							30
2	201.0870	101.0471	0	0	183.0764	92.0418	E	2964.4936	1482.7504	2947.4670	1474.2372	2946.4830	1473.7451	29
3	330.1296	165.5684	0	0	312.1190	156.5631	E	2835.4510	1418.2291	2818.4244	1409.7159	2817.4404	1409.2238	28
4	387.1510	194.0792	0	0	369.1405	185.0739	G	2706.4084	1353.7078	2689.3818	1345.1946	2688.3978	1344.7025	27
5	444.1725	222.5899	0	0	426.1619	213.5846	G	2649.3869	1325.1971	2632.3604	1316.6838	2631.3764	1316.1918	26
6	573.2151	287.1112	0	0	555.2045	278.1059	E	2592.3655	1296.6864	2575.3389	1288.1731	2574.3549	1287.6811	25
7	630.2366	315.6219	0	0	612.2260	306.6166	G	2463.3229	1232.1651	2446.2963	1223.6518	2445.3123	1223.1598	24
8	701.2737	351.1405	0	0	683.2631	342.1352	A	2406.3014	1203.6543	2389.2749	1195.1411	2388.2908	1194.6491	23
9	802.3214	401.6643	0	0	784.3108	392.6590	T	2335.2643	1168.1358	2318.2377	1159.6225	2317.2537	1159.1305	22
10	901.3898	451.1985	0	0	883.3792	442.1932	V	2234.2166	1117.6119	2217.1901	1109.0987	2216.2060	1108.6067	21
11	998.4425	499.7249	0	0	980.4320	490.7196	P	2135.1482	1068.0777	2118.1216	1059.5645	2117.1376	1059.0725	20
12	1085.4746	543.2409	0	0	1067.4640	534.2356	S	2038.0954	1019.5514	2021.0689	1011.0381	2020.0849	1010.5461	19
13	1156.5117	578.7595	0	0	1138.5011	569.7542	A	1951.0634	976.0353	1934.0369	967.5221	1933.0528	967.0301	18
14	1227.5488	614.2780	0	0	1209.5382	605.2727	A	1880.0263	940.5168	1862.9997	932.0035	1862.0157	931.5115	17
15	1298.5859	649.7966	0	0	1280.5753	640.7913	A	1808.9892	904.9982	1791.9626	896.4850	1790.9786	895.9929	16
16	1399.6336	700.3204	0	0	1381.6230	691.3151	T	1737.9521	869.4797	1720.9255	860.9664	1719.9415	860.4744	15
17	1500.6813	750.8443	0	0	1482.6707	741.8390	T	1636.9044	818.9558	1619.8778	810.4426	1618.8938	809.9505	14
18	1601.7289	801.3681	0	0	1583.7184	792.3628	T	1535.8567	768.4320	1518.8302	759.9187	1517.8461	759.4267	13
19	1730.7715	865.8894	0	0	1712.7610	856.8841	E	1434.8090	717.9082	1417.7825	709.3949	1416.7985	708.9029	12
20	1829.8399	915.4236	0	0	1811.8294	906.4183	V	1305.7664	653.3869	1288.7399	644.8736	1287.7559	644.3816	11
21	1928.9084	964.9578	0	0	1910.8978	955.9525	V	1206.6980	603.8526	1189.6715	595.3394	1188.6875	594.8474	10
22	2029.9560	1015.4817	0	0	2011.9455	1006.4764	T	1107.6296	554.3184	1090.6031	545.8052	1089.6190	545.3132	9
23	2158.9986	1080.0030	0	0	2140.9881	1070.9977	E	1006.5819	503.7946	989.5554	495.2813	988.5714	494.7893	8
24	2258.0670	1129.5372	0	0	2240.0565	1120.5319	V	877.5393	439.2733	860.5128	430.7600	859.5288	430.2680	7
25	2387.1096	1194.0585	0	0	2369.0991	1185.0532	E	778.4709	389.7391	761.4444	381.2258	760.4604	380.7338	6
26	2500.1937	1250.6005	0	0	2482.1831	1241.5952	L	649.4283	325.2178	632.4018	316.7045	0	0	5
27	2613.2778	1307.1425	0	0	2595.2672	1298.1372	L	536.3443	268.6758	519.3177	260.1625	0	0	4
28	2726.3618	1363.6846	0	0	2708.3513	1354.6793	L	423.2602	212.1337	406.2336	203.6205	0	0	3
29	2889.4252	1445.2162	0	0	2871.4146	1436.2109	Y	310.1761	155.5917	293.1496	147.0784	0	0	2
30							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 17514.

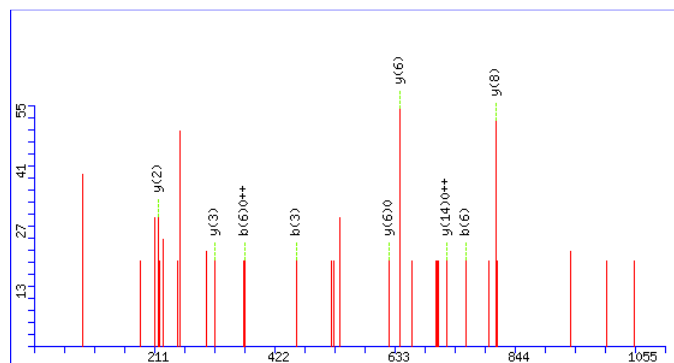
MS/MS Fragmentation of **DWCLLAMNLGLPDLVAK: 57.021465@C:3**

Found in **IP100021250;IP100947196;IP101010067**

Title: 4.1.1.3649.2

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							17
2	302.1135	151.5604	0	0	284.1030	142.5551	W	1813.9703	907.4888	1796.9438	898.9755	1795.9597	898.4835	16
3	462.1442	231.5757	0	0	444.1336	222.5704	C	1627.8910	814.4491	1610.8644	805.9359	1609.8804	805.4439	15
4	575.2282	288.1178	0	0	557.2177	279.1125	L	1467.8603	734.4338	1450.8338	725.9205	1449.8498	725.4285	14
5	688.3123	344.6598	0	0	670.3017	335.6545	L	1354.7763	677.8918	1337.7497	669.3785	1336.7657	668.8865	13
6	759.3494	380.1784	0	0	741.3389	371.1731	A	1241.6922	621.3497	1224.6657	612.8365	1223.6817	612.3445	12
7	890.3899	445.6986	0	0	872.3793	436.6933	M	1170.6551	585.8312	1153.6286	577.3179	1152.6445	576.8259	11
8	1004.4328	502.7201	987.4063	494.2068	986.4223	493.7148	N	1039.6146	520.3109	1022.5881	511.7977	1021.6041	511.3057	10
9	1117.5169	559.2621	1100.4904	550.7488	1099.5063	550.2568	L	925.5717	463.2895	908.5451	454.7762	907.5611	454.2842	9
10	1174.5384	587.7728	1157.5118	579.2595	1156.5278	578.7675	G	812.4876	406.7475	795.4611	398.2342	794.4771	397.7422	8
11	1287.6224	644.3149	1270.5959	635.8016	1269.6119	635.3096	L	755.4662	378.2367	738.4396	369.7234	737.4556	369.2314	7
12	1384.6752	692.8412	1367.6486	684.3280	1366.6646	683.8360	P	642.3821	321.6947	625.3556	313.1814	624.3715	312.6894	6
13	1499.7021	750.3547	1482.6756	741.8414	1481.6916	741.3494	D	545.3293	273.1683	528.3028	264.6550	527.3188	264.1630	5
14	1612.7862	806.8967	1595.7596	798.3835	1594.7756	797.8915	L	430.3024	215.6548	413.2758	207.1416	0	0	4
15	1711.8546	856.4309	1694.8281	847.9177	1693.8440	847.4257	V	317.2183	159.1128	300.1918	150.5995	0	0	3
16	1782.8917	891.9495	1765.8652	883.4362	1764.8812	882.9442	A	218.1499	109.5786	201.1234	101.0653	0	0	2
17							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 17689.

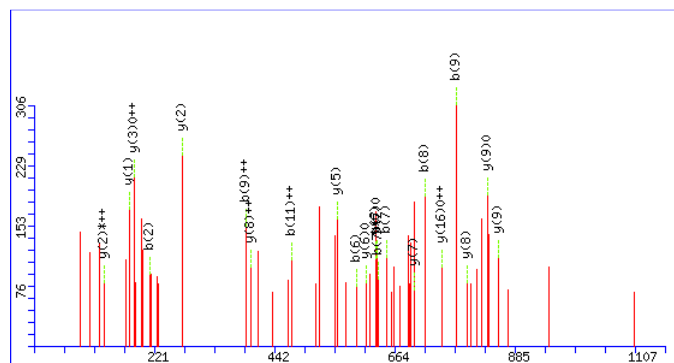
MS/MS Fragmentation of **GRPGPEGAGPAAGLDVR**:

Found in **IP100011115**

Title: 1.1.1.9604.8

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							17
2	214.1299	107.5686	197.1033	99.0553	0	0	R	1519.7976	760.4024	1502.7710	751.8891	1501.7870	751.3971	16
3	311.1826	156.0949	294.1561	147.5817	0	0	P	1363.6965	682.3519	1346.6699	673.8386	1345.6859	673.3466	15
4	368.2041	184.6057	351.1775	176.0924	0	0	G	1266.6437	633.8255	1249.6171	625.3122	1248.6331	624.8202	14
5	465.2568	233.1321	448.2303	224.6188	0	0	P	1209.6222	605.3148	1192.5957	596.8015	1191.6117	596.3095	13
6	594.2994	297.6534	577.2729	289.1401	576.2889	288.6481	E	1112.5695	556.7884	1095.5429	548.2751	1094.5589	547.7831	12
7	651.3209	326.1641	634.2944	317.6508	633.3103	317.1588	G	983.5269	492.2671	966.5003	483.7538	965.5163	483.2618	11
8	722.3580	361.6826	705.3315	353.1694	704.3474	352.6774	A	926.5054	463.7563	909.4789	455.2431	908.4948	454.7511	10
9	779.3795	390.1934	762.3529	381.6801	761.3689	381.1881	G	855.4683	428.2378	838.4417	419.7245	837.4577	419.2325	9
10	876.4322	438.7198	859.4057	430.2065	858.4217	429.7145	P	798.4468	399.7271	781.4203	391.2138	780.4363	390.7218	8
11	947.4694	474.2383	930.4428	465.7250	929.4588	465.2330	A	701.3941	351.2007	684.3675	342.6874	683.3835	342.1954	7
12	1018.5065	509.7569	1001.4799	501.2436	1000.4959	500.7516	A	630.3570	315.6821	613.3304	307.1688	612.3464	306.6768	6
13	1075.5279	538.2676	1058.5014	529.7543	1057.5174	529.2623	G	559.3198	280.1636	542.2933	271.6503	541.3093	271.1583	5
14	1188.6120	594.8096	1171.5854	586.2964	1170.6014	585.8044	L	502.2984	251.6528	485.2718	243.1395	484.2878	242.6475	4
15	1303.6389	652.3231	1286.6124	643.8098	1285.6284	643.3178	D	389.2143	195.1108	372.1878	186.5975	371.2037	186.1055	3
16	1402.7074	701.8573	1385.6808	693.3440	1384.6968	692.8520	V	274.1874	137.5973	257.1608	129.0840	0	0	2
17							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 18034.

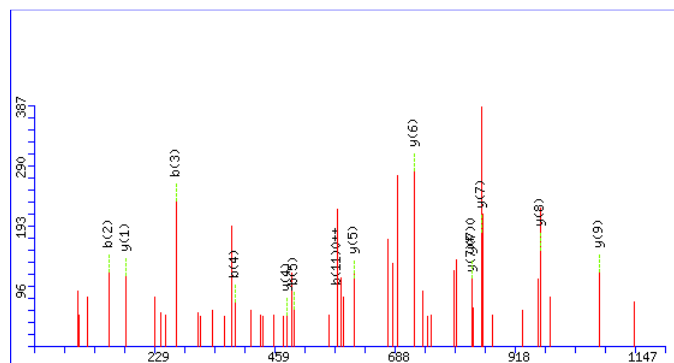
MS/MS Fragmentation of **AAELLQDEYSGR**:

Found in **IP100306049;IP100642805;IP100855996;IP100856007;IP100856061;IP100908498**

Title: 2.1.1.1349.10

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							12
2	143.0815	72.0444	0	0	0	0	A	1280.6117	640.8095	1263.5852	632.2962	1262.6012	631.8042	11
3	272.1241	136.5657	0	0	254.1135	127.5604	E	1209.5746	605.2909	1192.5481	596.7777	1191.5640	596.2857	10
4	385.2082	193.1077	0	0	367.1976	184.1024	L	1080.5320	540.7696	1063.5055	532.2564	1062.5215	531.7644	9
5	498.2922	249.6498	0	0	480.2817	240.6445	L	967.4480	484.2276	950.4214	475.7143	949.4374	475.2223	8
6	626.3508	313.6790	609.3243	305.1658	608.3402	304.6738	Q	854.3639	427.6856	837.3373	419.1723	836.3533	418.6803	7
7	741.3777	371.1925	724.3512	362.6792	723.3672	362.1872	D	726.3053	363.6563	709.2788	355.1430	708.2947	354.6510	6
8	870.4203	435.7138	853.3938	427.2005	852.4098	426.7085	E	611.2784	306.1428	594.2518	297.6295	593.2678	297.1375	5
9	1033.4837	517.2455	1016.4571	508.7322	1015.4731	508.2402	Y	482.2358	241.6215	465.2092	233.1082	464.2252	232.6162	4
10	1120.5157	560.7615	1103.4891	552.2482	1102.5051	551.7562	S	319.1724	160.0899	302.1459	151.5766	301.1619	151.0846	3
11	1177.5372	589.2722	1160.5106	580.7589	1159.5266	580.2669	G	232.1404	116.5738	215.1139	108.0606	0	0	2
12							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 18603.

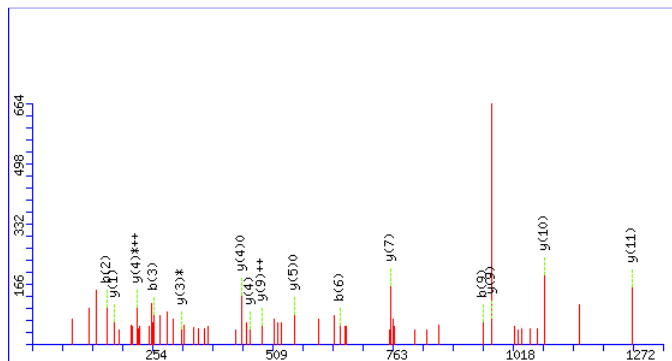
MS/MS Fragmentation of **SAVWLPSVLEASR**:

Found in **IP100013378,IP100221295,IP101011812,IP101012294**

Title: 3.1.1.2335.7

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120212ry¥120212ry_414C2-43_3_3.mgf

ProteinPilot Peptide Confidence > 99%

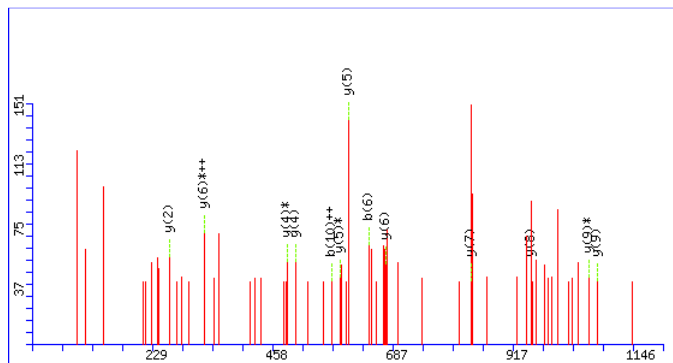


#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							14
2	159.0764	80.0418	0	0	141.0659	71.0366	A	1442.7638	721.8855	1425.7373	713.3723	1424.7532	712.8803	13
3	258.1448	129.5761	0	0	240.1343	120.5708	V	1371.7267	686.3670	1354.7001	677.8537	1353.7161	677.3617	12
4	444.2241	222.6157	0	0	426.2136	213.6104	W	1272.6583	636.8328	1255.6317	628.3195	1254.6477	627.8275	11
5	557.3082	279.1577	0	0	539.2976	270.1525	L	1086.5790	543.7931	1069.5524	535.2798	1068.5684	534.7878	10
6	654.3610	327.6841	0	0	636.3504	318.6788	P	973.4949	487.2511	956.4684	478.7378	955.4843	478.2458	9
7	769.3879	385.1976	0	0	751.3774	376.1923	D	876.4421	438.7247	859.4156	430.2114	858.4316	429.7194	8
8	856.4199	428.7136	0	0	838.4094	419.7083	S	761.4152	381.2112	744.3886	372.6980	743.4046	372.2060	7
9	955.4884	478.2478	0	0	937.4778	469.2425	V	674.3832	337.6952	657.3566	329.1819	656.3726	328.6899	6
10	1068.5724	534.7898	0	0	1050.5619	525.7846	L	575.3148	288.1610	558.2882	279.6477	557.3042	279.1557	5
11	1197.6150	599.3111	0	0	1179.6045	590.3059	E	462.2307	231.6190	445.2041	223.1057	444.2201	222.6137	4
12	1268.6521	634.8297	0	0	1250.6416	625.8244	A	333.1881	167.0977	316.1615	158.5844	315.1775	158.0924	3
13	1355.6842	678.3457	0	0	1337.6736	669.3404	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
14							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 19048.

MS/MS Fragmentation of **TDLVSQMQLYATLESR**: 0.984016@Q:8
 Found in **IP100604481;IP100607712;IP100744557;IP100745165;IP100884900;IP101010779**
 Title: 4.1.1.2840.4
 Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4.4.mgf
 ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							17
2	217.0819	109.0446	0	0	199.0713	100.0393	D	1882.9215	941.9644	1865.8950	933.4511	1864.9109	932.9591	16
3	330.1660	165.5866	0	0	312.1554	156.5813	L	1767.8946	884.4509	1750.8680	875.9376	1749.8840	875.4456	15
4	429.2344	215.1208	0	0	411.2238	206.1155	V	1654.8105	827.9089	1637.7840	819.3956	1636.7999	818.9036	14
5	516.2664	258.6368	0	0	498.2558	249.6316	S	1555.7421	778.3747	1538.7155	769.8614	1537.7315	769.3694	13
6	644.3250	322.6661	627.2984	314.1529	626.3144	313.6608	Q	1468.7101	734.8587	1451.6835	726.3454	1450.6995	725.8534	12
7	775.3655	388.1864	758.3389	379.6731	757.3549	379.1811	M	1340.6515	670.8294	1323.6249	662.3161	1322.6409	661.8241	11
8	904.4081	452.7077	887.3815	444.1944	886.3975	443.7024	Q	1209.6110	605.3091	1192.5844	596.7959	1191.6004	596.3039	10
9	1032.4666	516.7370	1015.4401	508.2237	1014.4561	507.7317	Q	1080.5684	540.7878	1063.5419	532.2746	1062.5578	531.7826	9
10	1145.5507	573.2790	1128.5242	564.7657	1127.5401	564.2737	L	952.5098	476.7585	935.4833	468.2453	934.4993	467.7533	8
11	1308.6140	654.8107	1291.5875	646.2974	1290.6035	645.8054	Y	839.4258	420.2165	822.3992	411.7032	821.4152	411.2112	7
12	1379.6511	690.3292	1362.6246	681.8159	1361.6406	681.3239	A	676.3624	338.6849	659.3359	330.1716	658.3519	329.6796	6
13	1480.6988	740.8531	1463.6723	732.3398	1462.6883	731.8478	T	605.3253	303.1663	588.2988	294.6530	587.3148	294.1610	5
14	1593.7829	797.3951	1576.7563	788.8818	1575.7723	788.3898	L	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	4
15	1722.8255	861.9164	1705.7989	853.4031	1704.8149	852.9111	E	391.1936	196.1004	374.1670	187.5871	373.1830	187.0951	3
16	1809.8575	905.4324	1792.8310	896.9191	1791.8469	896.4271	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
17							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 19217.

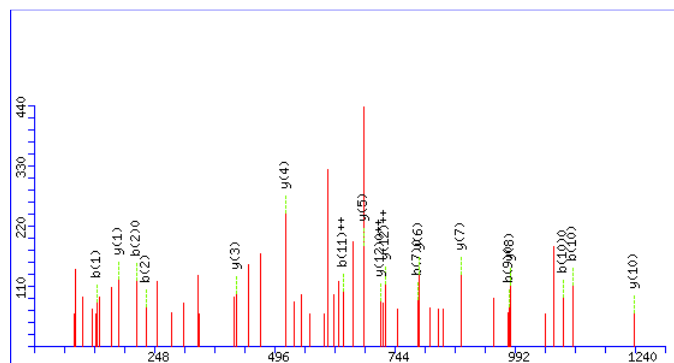
MS/MS Fragmentation of **ETIPLQETSLYTQDR**:

Found in **IP100002412;IP100514424;IP100514996;IP100908718;IP101018677**

Title: 2.1.1.3932.6

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4.2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							15
2	231.0975	116.0524	0	0	213.0870	107.0471	T	1664.8490	832.9281	1647.8224	824.4149	1646.8384	823.9229	14
3	344.1816	172.5944	0	0	326.1710	163.5892	I	1563.8013	782.4043	1546.7748	773.8910	1545.7908	773.3990	13
4	441.2344	221.1208	0	0	423.2238	212.1155	P	1450.7173	725.8623	1433.6907	717.3490	1432.7067	716.8570	12
5	554.3184	277.6629	0	0	536.3079	268.6576	L	1353.6645	677.3359	1336.6379	668.8226	1335.6539	668.3306	11
6	682.3770	341.6921	665.3505	333.1789	664.3665	332.6869	Q	1240.5804	620.7938	1223.5539	612.2806	1222.5699	611.7886	10
7	811.4196	406.2134	794.3931	397.7002	793.4090	397.2082	E	1112.5218	556.7646	1095.4953	548.2513	1094.5113	547.7593	9
8	912.4673	456.7373	895.4407	448.2240	894.4567	447.7320	T	983.4793	492.2433	966.4527	483.7300	965.4687	483.2380	8
9	999.4993	500.2533	982.4728	491.7400	981.4888	491.2480	S	882.4316	441.7194	865.4050	433.2061	864.4210	432.7141	7
10	1112.5834	556.7953	1095.5568	548.2821	1094.5728	547.7900	L	795.3995	398.2034	778.3730	389.6901	777.3890	389.1981	6
11	1275.6467	638.3270	1258.6202	629.8137	1257.6361	629.3217	Y	682.3155	341.6614	665.2889	333.1481	664.3049	332.6561	5
12	1376.6944	688.8508	1359.6678	680.3376	1358.6838	679.8456	T	519.2522	260.1297	502.2256	251.6164	501.2416	251.1244	4
13	1504.7530	752.8801	1487.7264	744.3668	1486.7424	743.8748	Q	418.2045	209.6059	401.1779	201.0926	400.1939	200.6006	3
14	1619.7799	810.3936	1602.7534	801.8803	1601.7693	801.3883	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
15							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 19227.

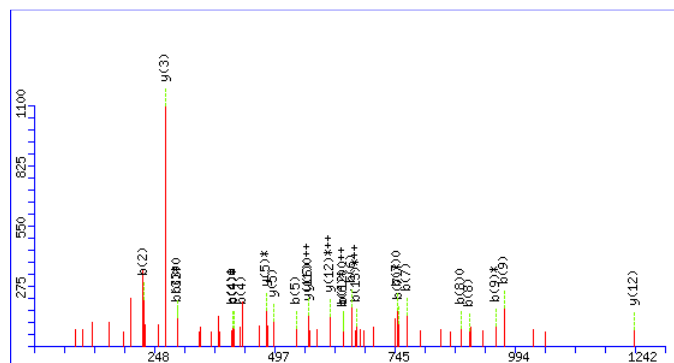
MS/MS Fragmentation of **NLSDIDLMA PQGV**:

Found in **IP100386294**

Title: 3.1.1.2122.9

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_2.3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							14
2	228.1343	114.5708	211.1077	106.0575	0	0	L	1355.6875	678.3474	1338.6610	669.8341	1337.6770	669.3421	13
3	315.1663	158.0868	298.1397	149.5735	297.1557	149.0815	S	1242.6035	621.8054	1225.5769	613.2921	1224.5929	612.8001	12
4	430.1932	215.6003	413.1667	207.0870	412.1827	206.5950	D	1155.5714	578.2894	1138.5449	569.7761	1137.5609	569.2841	11
5	543.2773	272.1423	526.2508	263.6290	525.2667	263.1370	I	1040.5445	520.7759	1023.5179	512.2626	1022.5339	511.7706	10
6	658.3042	329.6558	641.2777	321.1425	640.2937	320.6505	D	927.4604	464.2339	910.4339	455.7206	909.4499	455.2286	9
7	771.3883	386.1978	754.3618	377.6845	753.3777	377.1925	L	812.4335	406.7204	795.4069	398.2071	0	0	8
8	902.4288	451.7180	885.4022	443.2048	884.4182	442.7128	M	699.3494	350.1783	682.3229	341.6651	0	0	7
9	973.4659	487.2366	956.4394	478.7233	955.4553	478.2313	A	568.3089	284.6581	551.2824	276.1448	0	0	6
10	1070.5187	535.7630	1053.4921	527.2497	1052.5081	526.7577	P	497.2718	249.1396	480.2453	240.6263	0	0	5
11	1198.5773	599.7923	1181.5507	591.2790	1180.5667	590.7870	Q	400.2191	200.6132	383.1925	192.0999	0	0	4
12	1295.6300	648.3186	1278.6035	639.8054	1277.6194	639.3134	P	272.1605	136.5839	0	0	0	0	3
13	1352.6515	676.8294	1335.6249	668.3161	1334.6409	667.8241	G	175.1077	88.0575	0	0	0	0	2
14							V	118.0863	59.5468	0	0	0	0	1

Peptide View

Peptide: 19244.

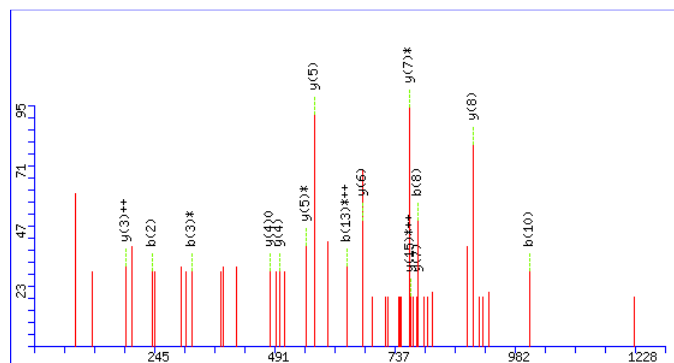
MS/MS Fragmentation of **QLVSGAETLNLVAEILK**:

Found in **IP100093725;IP100432355;IP100514920;IP100646391;IP100888891**

Title: 4.1.1.2945.2

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120206ry¥120206ry_aHDF1419-P10_2_4.mgf

ProteinPilot Peptide Confidence > 99%

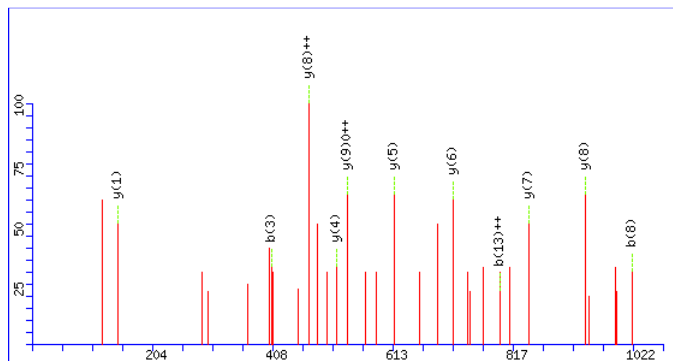


#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233	0	0	Q							17
2	242.1499	121.5786	225.1234	113.0653	0	0	L	1669.9735	835.4904	1652.9469	826.9771	1651.9629	826.4851	16
3	341.2183	171.1128	324.1918	162.5995	0	0	V	1556.8894	778.9483	1539.8629	770.4351	1538.8788	769.9431	15
4	428.2504	214.6288	411.2238	206.1155	410.2398	205.6235	S	1457.8210	729.4141	1440.7944	720.9009	1439.8104	720.4088	14
5	485.2718	243.1396	468.2453	234.6263	467.2613	234.1343	G	1370.7890	685.8981	1353.7624	677.3848	1352.7784	676.8928	13
6	556.3089	278.6581	539.2824	270.1448	538.2984	269.6528	A	1313.7675	657.3874	1296.7409	648.8741	1295.7569	648.3821	12
7	685.3515	343.1794	668.3250	334.6661	667.3410	334.1741	E	1242.7304	621.8688	1225.7038	613.3556	1224.7198	612.8635	11
8	766.3992	393.7032	769.3727	385.1900	768.3886	384.6980	T	1113.6878	557.3475	1096.6612	548.8343	1095.6772	548.3422	10
9	899.4833	450.2453	882.4567	441.7320	881.4727	441.2400	L	1012.6401	506.8237	995.6136	498.3104	994.6295	497.8184	9
10	1013.5262	507.2667	996.4997	498.7535	995.5156	498.2615	N	899.5560	450.2817	882.5295	441.7684	881.5455	441.2764	8
11	1126.6103	563.8088	1109.5837	555.2955	1108.5997	554.8035	L	785.5131	393.2602	768.4866	384.7469	767.5026	384.2549	7
12	1225.6787	613.3430	1208.6521	604.8297	1207.6681	604.3377	V	672.4291	336.7182	655.4025	328.2049	654.4185	327.7129	6
13	1296.7158	648.8615	1279.6892	640.3483	1278.7052	639.8563	A	573.3606	287.1840	556.3341	278.6707	555.3501	278.1787	5
14	1425.7584	713.3828	1408.7318	704.8696	1407.7478	704.3775	E	502.3235	251.6654	485.2970	243.1521	484.3130	242.6601	4
15	1538.8425	769.9249	1521.8159	761.4116	1520.8319	760.9196	I	373.2809	187.1441	356.2544	178.6308	0	0	3
16	1651.9265	826.4669	1634.9000	817.9536	1633.9159	817.4616	L	260.1969	130.6021	243.1703	122.0888	0	0	2
17							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 19310.

MS/MS Fragmentation of **VFCELFPEVVEIK**: 57.021465@C:3
 Found in **IP100335071;IP100375728;IP100455911;IP100514050;IP100873186;IP101013764**
 Title: 4.1.1.375.4
 Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_1_4.mgf
 ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							14
2	247.1441	124.0757	0	0	0	0	F	1638.8084	819.9078	1621.7818	811.3946	1620.7978	810.9025	13
3	407.1748	204.0910	0	0	0	0	C	1491.7400	746.3736	1474.7134	737.8603	1473.7294	737.3683	12
4	536.2173	268.6123	0	0	518.2068	259.6070	E	1331.7093	666.3583	1314.6828	657.8450	1313.6987	657.3530	11
5	649.3014	325.1543	0	0	631.2908	316.1491	L	1202.6667	601.8370	1185.6402	593.3237	1184.6562	592.8317	10
6	796.3698	398.6886	0	0	778.3593	389.6833	F	1089.5827	545.2950	1072.5561	536.7817	1071.5721	536.2897	9
7	893.4226	447.2149	0	0	875.4120	438.2097	P	942.5142	471.7608	925.4877	463.2475	924.5037	462.7555	8
8	1022.4652	511.7362	0	0	1004.4546	502.7309	E	845.4615	423.2344	828.4349	414.7211	827.4509	414.2291	7
9	1121.5336	561.2704	0	0	1103.5230	552.2652	V	716.4189	358.7131	699.3923	350.1998	698.4083	349.7078	6
10	1220.6020	610.8046	0	0	1202.5914	601.7994	V	617.3505	309.1789	600.3239	300.6656	599.3399	300.1736	5
11	1349.6446	675.3259	0	0	1331.6340	666.3207	E	518.2821	259.6447	501.2555	251.1314	500.2715	250.6394	4
12	1478.6872	739.8472	0	0	1460.6766	730.8420	E	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
13	1591.7713	796.3893	0	0	1573.7607	787.3840	I	260.1969	130.6021	243.1703	122.0888	0	0	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 19517.

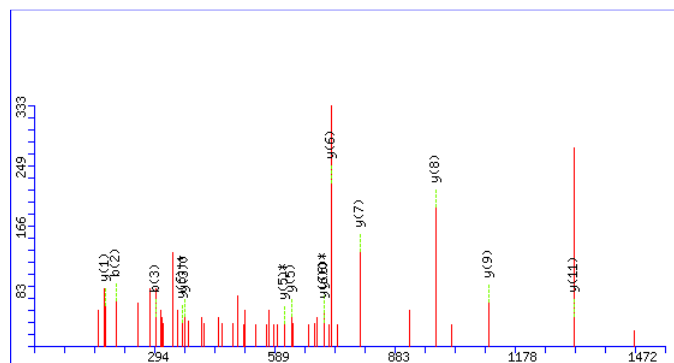
MS/MS Fragmentation of **SLVLPWSFPLEWAPQNLTR**:

Found in **IP100007096**

Title: 4.1.1.3907.4

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							19
2	201.1234	101.0653	0	0	183.1128	92.0600	L	2167.1699	1084.0886	2150.1433	1075.5753	2149.1593	1075.0833	18
3	300.1918	150.5995	0	0	282.1812	141.5942	V	2054.0858	1027.5465	2037.0593	1019.0333	2036.0752	1018.5413	17
4	413.2758	207.1416	0	0	395.2653	198.1363	L	1955.0174	978.0123	1937.9908	969.4991	1937.0068	969.0071	16
5	510.3286	255.6679	0	0	492.3180	246.6627	P	1841.9333	921.4703	1824.9068	912.9570	1823.9228	912.4650	15
6	696.4079	348.7076	0	0	678.3974	339.7023	W	1744.8806	872.9439	1727.8540	864.4306	1726.8700	863.9386	14
7	783.4400	392.2236	0	0	765.4294	383.2183	S	1558.8013	779.9043	1541.7747	771.3910	1540.7907	770.8990	13
8	930.5084	465.7578	0	0	912.4978	456.7525	F	1471.7692	736.3883	1454.7427	727.8750	1453.7587	727.3830	12
9	1027.5611	514.2842	0	0	1009.5506	505.2789	P	1324.7008	662.8540	1307.6743	654.3408	1306.6902	653.8488	11
10	1140.6452	570.8262	0	0	1122.6346	561.8210	L	1227.6480	614.3277	1210.6215	605.8144	1209.6375	605.3224	10
11	1269.6878	635.3475	0	0	1251.6772	626.3422	E	1114.5640	557.7856	1097.5374	549.2724	1096.5534	548.7803	9
12	1455.7671	728.3872	0	0	1437.7565	719.3819	W	985.5214	493.2643	968.4948	484.7511	967.5108	484.2591	8
13	1526.8042	763.9057	0	0	1508.7936	754.9005	A	799.4421	400.2247	782.4155	391.7114	781.4315	391.2194	7
14	1623.8570	812.4321	0	0	1605.8464	803.4268	P	728.4050	364.7061	711.3784	356.1928	710.3944	355.7008	6
15	1751.9156	876.4614	1734.8890	867.9481	1733.9050	867.4561	Q	631.3522	316.1797	614.3257	307.6665	613.3416	307.1745	5
16	1865.9585	933.4829	1848.9319	924.9696	1847.9479	924.4776	N	503.2936	252.1504	486.2671	243.6372	485.2831	243.1452	4
17	1979.0425	990.0249	1962.0160	981.5116	1961.0320	981.0196	L	389.2507	195.1290	372.2241	186.6157	371.2401	186.1237	3
18	2080.0902	1040.5488	2063.0637	1032.0355	2062.0797	1031.5435	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
19							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 19739.

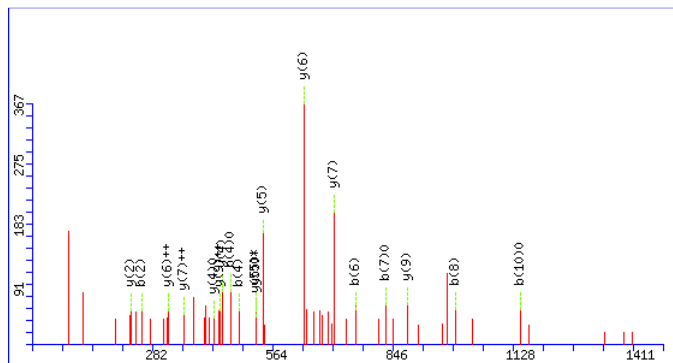
MS/MS Fragmentation of **EENIYSFLGLAPPPDSK**:

Found in **IP100026538;IP100418589;IP100657640;IP100893869;IP100925150**

Title: 4.1.1.2443.5

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							18
2	259.0925	130.0499	0	0	241.0819	121.0446	E	1860.9742	930.9907	1843.9476	922.4775	1842.9636	921.9855	17
3	373.1354	187.0713	356.1088	178.5581	355.1248	178.0661	N	1731.9316	866.4694	1714.9050	857.9562	1713.9210	857.4642	16
4	486.2195	243.6134	469.1929	235.1001	468.2089	234.6081	I	1617.8887	809.4480	1600.8621	800.9347	1599.8781	800.4427	15
5	599.3035	300.1554	582.2770	291.6421	581.2930	291.1501	I	1504.8046	752.9059	1487.7781	744.3927	1486.7940	743.9007	14
6	762.3668	381.6871	745.3403	373.1738	744.3563	372.6818	Y	1391.7205	696.3639	1374.6940	687.8506	1373.7100	687.3586	13
7	849.3989	425.2031	832.3723	416.6898	831.3883	416.1978	S	1228.6572	614.8322	1211.6307	606.3190	1210.6467	605.8270	12
8	996.4673	498.7373	979.4407	490.2240	978.4567	489.7320	F	1141.6252	571.3162	1124.5986	562.8030	1123.6146	562.3109	11
9	1109.5514	555.2793	1092.5248	546.7660	1091.5408	546.2740	L	994.5568	497.7820	977.5302	489.2687	976.5462	488.7767	10
10	1166.5728	583.7900	1149.5463	575.2768	1148.5623	574.7848	G	881.4727	441.2400	864.4462	432.7267	863.4621	432.2347	9
11	1279.6569	640.3321	1262.6303	631.8188	1261.6463	631.3268	L	824.4512	412.7293	807.4247	404.2160	806.4407	403.7240	8
12	1350.6940	675.8506	1333.6674	667.3374	1332.6834	666.8454	A	711.3672	356.1872	694.3406	347.6740	693.3566	347.1819	7
13	1447.7468	724.3770	1430.7202	715.8637	1429.7362	715.3717	P	640.3301	320.6687	623.3035	312.1554	622.3195	311.6634	6
14	1544.7995	772.9034	1527.7730	764.3901	1526.7890	763.8981	P	543.2773	272.1423	526.2508	263.6290	525.2667	263.1370	5
15	1641.8523	821.4298	1624.8257	812.9165	1623.8417	812.4245	P	446.2245	223.6159	429.1980	215.1026	428.2140	214.6106	4
16	1756.8792	878.9433	1739.8527	870.4300	1738.8687	869.9380	D	349.1718	175.0895	332.1452	166.5763	331.1612	166.0842	3
17	1843.9113	922.4593	1826.8847	913.9460	1825.9007	913.4540	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
18							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 19788.

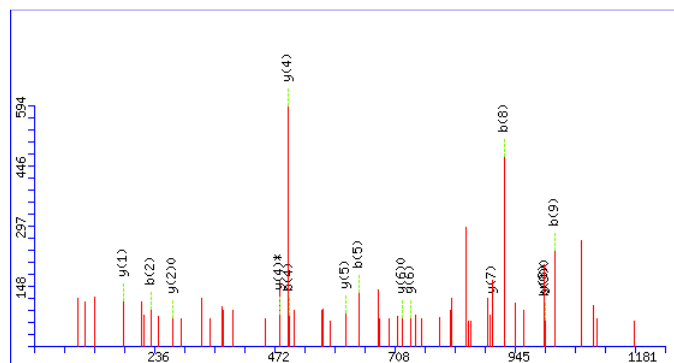
MS/MS Fragmentation of **TQICHTLAVTCQLPIDR**: 57.021465@C:4,57.021465@C:11,0.984016@Q:12

Found in **IP100032201;IP100553199;IP100980924;IP101010370**

Title: 2.1.1.3586.9

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							17
2	230.1135	115.5604	213.0870	107.0471	212.1030	106.5551	Q	1925.9572	963.4822	1908.9306	954.9690	1907.9466	954.4769	16
3	343.1976	172.1024	326.1710	163.5892	325.1870	163.0972	I	1797.8986	899.4529	1780.8721	890.9397	1779.8880	890.4477	15
4	503.2282	252.1178	486.2017	243.6045	485.2177	243.1125	C	1684.8145	842.9109	1667.7880	834.3976	1666.8040	833.9056	14
5	640.2872	320.6472	623.2606	312.1339	622.2766	311.6419	H	1524.7839	762.8956	1507.7573	754.3823	1506.7733	753.8903	13
6	741.3348	371.1711	724.3083	362.6578	723.3243	362.1658	T	1387.7250	694.3661	1370.6984	685.8529	1369.7144	685.3608	12
7	854.4189	427.7131	837.3924	419.1998	836.4083	418.7078	L	1286.6773	643.8423	1269.6508	635.3290	1268.6667	634.8370	11
8	925.4560	463.2316	908.4295	454.7184	907.4455	454.2264	A	1173.5932	587.3003	1156.5667	578.7870	1155.5827	578.2950	10
9	1024.5244	512.7659	1007.4979	504.2526	1006.5139	503.7606	V	1102.5561	551.7817	1085.5296	543.2684	1084.5456	542.7764	9
10	1125.5721	563.2897	1108.5456	554.7764	1107.5615	554.2844	T	1003.4877	502.2475	986.4612	493.7342	985.4771	493.2422	8
11	1285.6028	643.3050	1268.5762	634.7917	1267.5922	634.2997	C	902.4400	451.7237	885.4135	443.2104	884.4295	442.7184	7
12	1414.6454	707.8263	1397.6188	699.3130	1396.6348	698.8210	Q	742.4094	371.7083	725.3828	363.1951	724.3988	362.7030	6
13	1527.7294	764.3683	1510.7029	755.8551	1509.7189	755.3631	L	613.3668	307.1870	596.3402	298.6738	595.3562	298.1817	5
14	1624.7822	812.8947	1607.7556	804.3815	1606.7716	803.8894	P	500.2827	250.6450	483.2562	242.1317	482.2722	241.6397	4
15	1737.8662	869.4368	1720.8397	860.9235	1719.8557	860.4315	I	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
16	1852.8932	926.9502	1835.8666	918.4370	1834.8826	917.9449	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
17							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 19908.

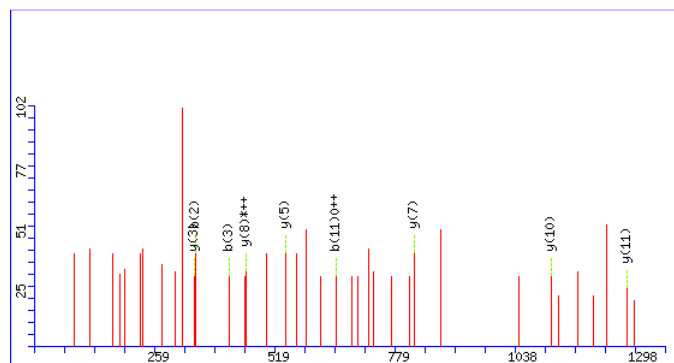
MS/MS Fragmentation of **WYALLYDPVISK**:

Found in **IP100220477;IP100479000;IP100655820;IP101021496;IP101026237**

Title: 3.1.1.3480.8

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	187.0866	94.0469	0	0	0	0	W							12
2	350.1499	175.5786	0	0	0	0	Y	1281.7089	641.3581	1264.6824	632.8448	1263.6984	632.3528	11
3	421.1870	211.0972	0	0	0	0	A	1118.6456	559.8264	1101.6190	551.3132	1100.6350	550.8211	10
4	534.2711	267.6392	0	0	0	0	L	1047.6085	524.3079	1030.5819	515.7946	1029.5979	515.3026	9
5	647.3552	324.1812	0	0	0	0	L	934.5244	467.7658	917.4979	459.2526	916.5138	458.7606	8
6	810.4185	405.7129	0	0	0	0	Y	821.4403	411.2238	804.4138	402.7105	803.4298	402.2185	7
7	925.4454	463.2264	0	0	907.4349	454.2211	D	658.3770	329.6921	641.3505	321.1789	640.3665	320.6869	6
8	1022.4982	511.7527	0	0	1004.4876	502.7475	P	543.3501	272.1787	526.3235	263.6654	525.3395	263.1734	5
9	1121.5666	561.2869	0	0	1103.5560	552.2817	V	446.2973	223.6523	429.2708	215.1390	428.2867	214.6470	4
10	1234.6507	617.8290	0	0	1216.6401	608.8237	I	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
11	1321.6827	661.3450	0	0	1303.6721	652.3397	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 20106.

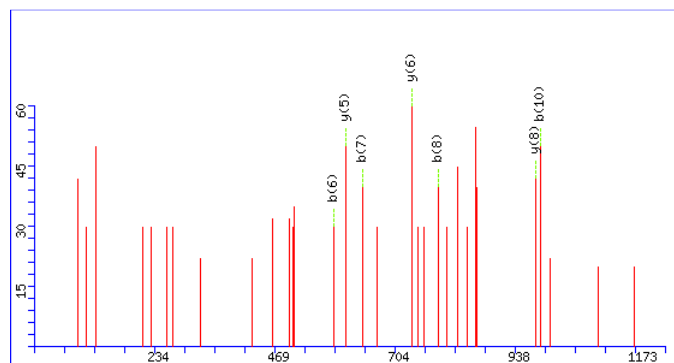
MS/MS Fragmentation of **ASDVVLGFALEGYLQK**:

Found in **IP100060200;IP100382746;IP100916994;IP100917237**

Title: 4.1.1.1500.5

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120118ry¥120118ry_201B7-32_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							17
2	159.0764	80.0418	0	0	141.0659	71.0366	S	1767.9163	884.4618	1750.8898	875.9485	1749.9058	875.4565	16
3	274.1034	137.5553	0	0	256.0928	128.5500	D	1680.8843	840.9458	1663.8578	832.4325	1662.8738	831.9405	15
4	373.1718	187.0895	0	0	355.1612	178.0842	V	1565.8574	783.4323	1548.8308	774.9190	1547.8468	774.4270	14
5	472.2402	236.6237	0	0	454.2296	227.6185	V	1466.7890	733.8981	1449.7624	725.3848	1448.7784	724.8928	13
6	585.3243	293.1658	0	0	567.3137	284.1605	L	1367.7205	684.3639	1350.6940	675.8506	1349.7100	675.3586	12
7	642.3457	321.6765	0	0	624.3352	312.6712	G	1254.6365	627.8219	1237.6099	619.3086	1236.6259	618.8166	11
8	789.4141	395.2107	0	0	771.4036	386.2054	F	1197.6150	599.3111	1180.5885	590.7979	1179.6045	590.3059	10
9	860.4512	430.7293	0	0	842.4407	421.7240	A	1050.5466	525.7769	1033.5201	517.2637	1032.5360	516.7717	9
10	989.4938	495.2506	0	0	971.4833	486.2453	E	979.5095	490.2584	962.4829	481.7451	961.4989	481.2531	8
11	1102.5779	551.7926	0	0	1084.5673	542.7873	L	850.4669	425.7371	833.4403	417.2238	832.4563	416.7318	7
12	1231.6205	616.3139	0	0	1213.6099	607.3086	E	737.3828	369.1951	720.3563	360.6818	719.3723	360.1898	6
13	1288.6420	644.8246	0	0	1270.6314	635.8193	G	608.3402	304.6738	591.3137	296.1605	0	0	5
14	1451.7053	726.3563	0	0	1433.6947	717.3510	Y	551.3188	276.1630	534.2922	267.6498	0	0	4
15	1564.7894	782.8983	0	0	1546.7788	773.8930	L	388.2554	194.6314	371.2289	186.1181	0	0	3
16	1692.8479	846.9276	1675.8214	838.4143	1674.8374	837.9223	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
17							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 20363.

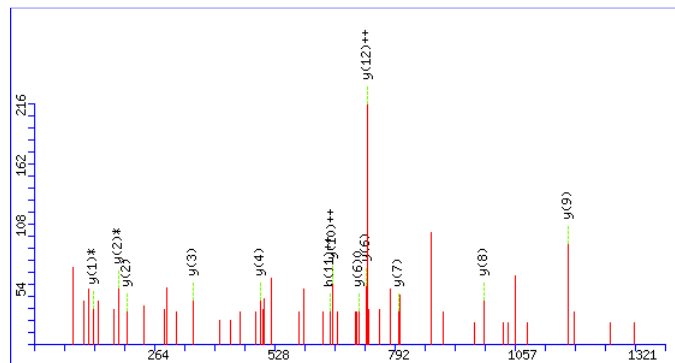
MS/MS Fragmentation of **ADPGHWWASFFFGK**:

Found in **IP100013278;IP100218175;IP100607900**

Title: 4.1.1.2550.2

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							14
2	187.0713	94.0393	0	0	169.0608	85.0340	D	1581.7274	791.3673	1564.7008	782.8540	1563.7168	782.3620	13
3	284.1241	142.5657	0	0	266.1135	133.5604	P	1466.7004	733.8538	1449.6739	725.3406	1448.6899	724.8486	12
4	341.1456	171.0764	0	0	323.1350	162.0711	G	1369.6477	685.3275	1352.6211	676.8142	1351.6371	676.3222	11
5	478.2045	239.6059	0	0	460.1939	230.6006	H	1312.6262	656.8167	1295.5996	648.3035	1294.6156	647.8115	10
6	664.2838	332.6455	0	0	646.2732	323.6402	W	1175.5673	588.2873	1158.5407	579.7740	1157.5567	579.2820	9
7	850.3631	425.6852	0	0	832.3525	416.6799	W	989.4880	495.2476	972.4614	486.7343	971.4774	486.2423	8
8	921.4002	461.2037	0	0	903.3896	452.1985	A	803.4087	402.2080	786.3821	393.6947	785.3981	393.2027	7
9	1008.4322	504.7198	0	0	990.4217	495.7145	S	732.3715	366.6894	715.3450	358.1761	714.3610	357.6841	6
10	1155.5007	578.2540	0	0	1137.4901	569.2487	F	645.3395	323.1734	628.3130	314.6601	0	0	5
11	1302.5691	651.7882	0	0	1284.5585	642.7829	F	498.2711	249.6392	481.2445	241.1259	0	0	4
12	1449.6375	725.3224	0	0	1431.6269	716.3171	F	351.2027	176.1050	334.1761	167.5917	0	0	3
13	1506.6589	753.8331	0	0	1488.6484	744.8278	G	204.1343	102.5708	187.1077	94.0575	0	0	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

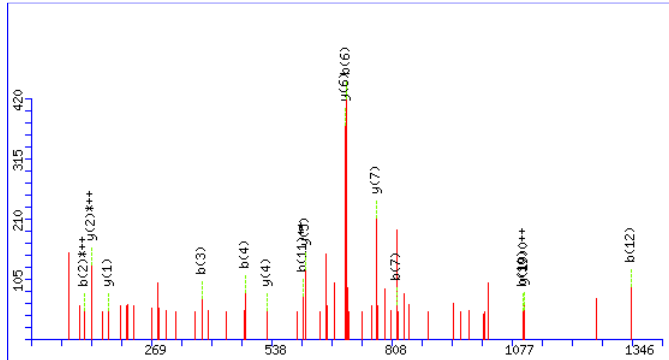
Peptide View

Peptide: 20373.

MS/MS Fragmentation of **RVEPPELPADLQHWISYNEASSQLLR**
Found in **IP100171421,IP100978773**

Title: 4.1.1.637.6

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_3.4.mgf
ProteinPilot Peptide Confidence > 99%

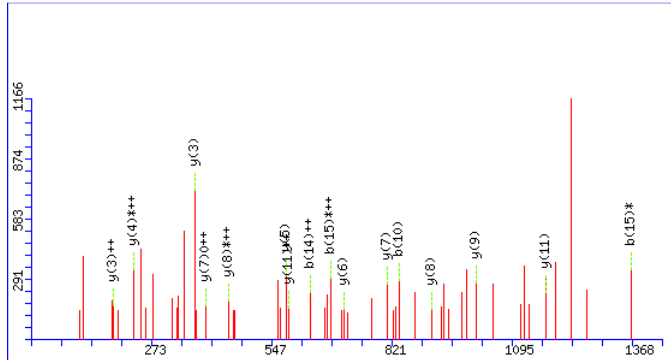


#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	157.1084	79.0578	140.0818	70.5446	0	0	R							26
2	256.1768	128.5920	239.1503	120.0788	0	0	V	2892.4526	1446.7300	2875.4261	1438.2167	2874.4421	1437.7247	25
3	385.2194	193.1133	368.1928	184.6001	367.2088	184.1081	E	2793.3842	1397.1958	2776.3577	1388.6825	2775.3737	1388.1905	24
4	482.2722	241.6397	465.2456	233.1264	464.2616	232.6344	P	2664.3416	1332.6745	2647.3151	1324.1612	2646.3311	1323.6692	23
5	579.3249	290.1661	562.2984	281.6528	561.3144	281.1608	P	2567.2889	1284.1481	2550.2623	1275.6348	2549.2783	1275.1428	22
6	708.3875	354.6874	691.3410	346.1741	690.3570	345.6821	E	2470.2361	1235.6217	2453.2096	1227.1084	2452.2255	1226.6164	21
7	821.4516	411.2294	804.4250	402.7162	803.4410	402.2241	L	2341.1935	1171.1004	2324.1670	1162.5871	2323.1830	1162.0951	20
8	918.5043	459.7558	901.4778	451.2425	900.4938	450.7505	P	2228.1095	1114.5584	2211.0829	1106.0451	2210.0989	1105.5531	19
9	989.5415	495.2744	972.5149	486.7611	971.5309	486.2691	A	2131.0567	1066.0320	2114.0301	1057.5187	2113.0461	1057.0267	18
10	1104.5684	552.7878	1087.5419	544.2746	1086.5578	543.7826	D	2060.0196	1030.5134	2042.9930	1022.0002	2042.0090	1021.5081	17
11	1217.6525	609.3299	1200.6259	600.8166	1199.6419	600.3246	L	1944.9926	973.0000	1927.9661	964.4867	1926.9821	963.9947	16
12	1345.7110	673.3592	1328.6845	664.8459	1327.7005	664.3539	Q	1831.9086	916.4579	1814.8820	907.9446	1813.8980	907.4526	15
13	1482.7700	741.8886	1465.7434	733.3753	1464.7594	732.8833	H	1703.8500	852.4286	1686.8234	843.9154	1685.8394	843.4234	14
14	1668.8493	834.9283	1651.8227	826.4150	1650.8387	825.9230	W	1566.7911	783.8992	1549.7645	775.3859	1548.7805	774.8939	13
15	1781.9333	891.4703	1764.9068	882.9570	1763.9228	882.4650	I	1380.7118	690.8595	1363.6852	682.3462	1362.7012	681.8542	12
16	1868.9654	934.9863	1851.9388	926.4730	1850.9548	925.9810	S	1267.6277	634.3175	1250.6012	625.8042	1249.6171	625.3122	11
17	2032.0287	1016.5180	2015.0021	1008.0047	2014.0181	1007.5127	Y	1180.5957	590.8015	1163.5691	582.2882	1162.5851	581.7962	10
18	2146.0716	1073.5394	2129.0451	1065.0262	2128.0611	1064.5342	N	1017.5323	509.2698	1000.5058	500.7565	999.5218	500.2645	9
19	2275.1142	1138.0607	2258.0877	1129.5475	2257.1036	1129.0555	E	903.4894	452.2483	886.4629	443.7351	885.4789	443.2431	8
20	2346.1513	1173.5793	2329.1248	1165.0660	2328.1408	1164.5740	A	774.4468	387.7271	757.4203	379.2138	756.4363	378.7218	7
21	2433.1834	1217.0953	2416.1568	1208.5820	2415.1728	1208.0900	S	703.4097	352.2085	686.3832	343.6952	685.3991	343.2032	6
22	2520.2154	1260.6113	2503.1888	1252.0981	2502.2048	1251.6060	S	616.3777	308.6925	599.3511	300.1792	598.3671	299.6872	5
23	2648.2740	1324.6406	2631.2474	1316.1273	2630.2634	1315.6353	Q	529.3457	265.1765	512.3191	256.6632	0	0	4
24	2761.3580	1381.1826	2744.3315	1372.6694	2743.3475	1372.1774	L	401.2871	201.1472	384.2605	192.6339	0	0	3
25	2874.4421	1437.7247	2857.4155	1429.2114	2856.4315	1428.7194	L	288.2030	144.6051	271.1765	136.0919	0	0	2
26							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 20547.

MS/MS Fragmentation of **VGGTKPAGGDFGEVLNSAANASATTTLEPLPEK**:
 Found in **IP100619958;IP100873344;IP100896474;IP100941154;IP100977108;IP100978200;IP100978805;IP100984852**
 Title: 3.1.1.587.9
 Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3.mgf
 ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							32
2	157.0972	79.0522	0	0	0	0	G	2987.4593	1494.2333	2970.4327	1485.7200	2969.4487	1485.2280	31
3	214.1186	107.5629	0	0	0	0	G	2930.4378	1465.7225	2913.4112	1457.2093	2912.4272	1456.7173	30
4	315.1663	158.0868	0	0	297.1557	149.0815	T	2873.4163	1437.2118	2856.3898	1428.6985	2855.4058	1428.2065	29
5	443.2613	222.1343	426.2347	213.6210	425.2507	213.1290	K	2772.3686	1386.6880	2755.3421	1378.1747	2754.3581	1377.6827	28
6	540.3140	270.6607	523.2875	262.1474	522.3035	261.6554	P	2644.2737	1322.6405	2627.2471	1314.1272	2626.2631	1313.6352	27
7	611.3511	306.1792	594.3246	297.6659	593.3406	297.1739	A	2547.2209	1274.1141	2530.1944	1265.6008	2529.2104	1265.1088	26
8	668.3726	334.6899	651.3461	326.1767	650.3620	325.6847	G	2476.1838	1238.5955	2459.1573	1230.0823	2458.1732	1229.5903	25
9	725.3941	363.2007	708.3675	354.6874	707.3835	354.1954	G	2419.1623	1210.0848	2402.1358	1201.5715	2401.1518	1201.0795	24
10	840.4210	420.7141	823.3945	412.2009	822.4104	411.7089	D	2362.1409	1181.5741	2345.1143	1173.0608	2344.1303	1172.5688	23
11	987.4894	494.2483	970.4629	485.7351	969.4789	485.2431	F	2247.1139	1124.0606	2230.0874	1115.5473	2229.1034	1115.0553	22
12	1044.5109	522.7591	1027.4843	514.2458	1026.5003	513.7538	G	2100.0455	1050.5264	2083.0190	1042.0131	2082.0350	1041.5211	21
13	1173.5535	587.2804	1156.5269	578.7671	1155.5429	578.2751	E	2043.0241	1022.0157	2025.9975	1013.5024	2025.0135	1013.0104	20
14	1272.6219	636.8146	1255.5953	628.3013	1254.6113	627.8093	V	1913.9815	957.4944	1896.9549	948.9811	1895.9709	948.4891	19
15	1385.7060	693.3566	1368.6794	684.8433	1367.6954	684.3513	L	1814.9130	907.9602	1797.8865	899.4469	1796.9025	898.9549	18
16	1499.7489	750.3781	1482.7223	741.8648	1481.7383	741.3728	N	1701.8290	851.4181	1684.8024	842.9049	1683.8184	842.4128	17
17	1586.7809	793.8941	1569.7544	785.3808	1568.7703	784.8888	S	1587.7861	794.3967	1570.7595	785.8834	1569.7755	785.3914	16
18	1657.8180	829.4127	1640.7915	820.8994	1639.8075	820.4074	A	1500.7540	750.8807	1483.7275	742.3674	1482.7435	741.8754	15
19	1728.8551	864.9312	1711.8286	856.4179	1710.8446	855.9259	A	1429.7169	715.3621	1412.6904	706.8488	1411.7064	706.3568	14
20	1842.8981	921.9527	1825.8715	913.4394	1824.8875	912.9474	N	1358.6798	679.8435	1341.6533	671.3303	1340.6692	670.8383	13
21	1913.9352	957.4712	1896.9086	948.9580	1895.9246	948.4659	A	1244.6369	622.8221	1227.6103	614.3088	1226.6263	613.8168	12
22	2000.9672	1000.9872	1983.9407	992.4740	1982.9566	991.9820	S	1173.5998	587.3035	1156.5732	578.7902	1155.5892	578.2982	11
23	2072.0043	1036.5058	2054.9778	1027.9925	2053.9938	1027.5005	A	1086.5677	543.7875	1069.5412	535.2742	1068.5572	534.7822	10
24	2173.0520	1087.0296	2156.0255	1078.5164	2155.0414	1078.0244	T	1015.5306	508.2689	998.5041	499.7557	997.5201	499.2637	9
25	2274.0997	1137.5535	2257.0731	1129.0402	2256.0891	1128.5482	T	914.4829	457.7451	897.4564	449.2318	896.4724	448.7398	8
26	2375.1474	1188.0773	2358.1208	1179.5640	2357.1368	1179.0720	T	813.4353	407.2213	796.4087	398.7080	795.4247	398.2160	7
27	2504.1900	1252.5986	2487.1634	1244.0853	2486.1794	1243.5933	E	712.3876	356.6974	695.3610	348.1842	694.3770	347.6921	6
28	2601.2427	1301.1250	2584.2162	1292.6117	2583.2322	1292.1197	P	583.3450	292.1761	566.3184	283.6629	565.3344	283.1709	5
29	2714.3268	1357.6670	2697.3002	1349.1538	2696.3162	1348.6617	L	486.2922	243.6498	469.2657	235.1365	468.2817	234.6445	4
30	2811.3795	1406.1934	2794.3530	1397.6801	2793.3690	1397.1881	P	373.2082	187.1077	356.1816	178.5944	355.1976	178.1024	3
31	2940.4221	1470.7147	2923.3956	1462.2014	2922.4116	1461.7094	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
32							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

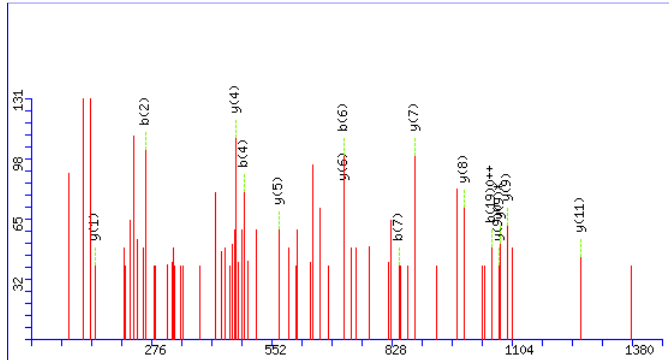
Peptide: 20643.

MS/MS Fragmentation of **YVIDVEQPFSCSLDAVVNYFVSHTK: 57.021465@C:11**
Found in **IP100015096;IP100383883**

Title: 5.1.1.114.5

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4.5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	164.0706	82.5389	0	0	0	0	Y							26
2	263.1390	132.0731	0	0	0	0	V	2855.3920	1428.1997	2838.3655	1419.6864	2837.3815	1419.1944	25
3	376.2231	188.6152	0	0	0	0	I	2756.3236	1378.6654	2739.2971	1370.1522	2738.3130	1369.6602	24
4	491.2500	246.1287	0	0	473.2395	237.1234	D	2643.2395	1322.1234	2626.2130	1313.6101	2625.2290	1313.1181	23
5	590.3184	295.6629	0	0	572.3079	286.6576	V	2528.2126	1264.6099	2511.1861	1256.0967	2510.2020	1255.6047	22
6	719.3610	360.1842	0	0	701.3505	351.1789	E	2429.1442	1215.0757	2412.1176	1206.5625	2411.1336	1206.0705	21
7	847.4196	424.2134	830.3931	415.7002	829.4090	415.2082	Q	2300.1016	1150.5544	2283.0750	1142.0412	2282.0910	1141.5492	20
8	944.4724	472.7398	927.4458	464.2266	926.4618	463.7345	P	2172.0430	1086.5251	2155.0165	1078.0119	2154.0325	1077.5199	19
9	1091.5408	546.2740	1074.5142	537.7608	1073.5302	537.2688	F	2074.9903	1037.9988	2057.9637	1029.4855	2056.9797	1028.9935	18
10	1178.5728	589.7900	1161.5463	581.2768	1160.5623	580.7848	S	1927.9218	964.4646	1910.8953	955.9513	1909.9113	955.4593	17
11	1338.6035	669.8054	1321.5769	661.2921	1320.5929	660.8001	C	1840.8898	920.9485	1823.8633	912.4353	1822.8792	911.9433	16
12	1439.6511	720.3292	1422.6246	711.8159	1421.6406	711.3239	T	1680.8592	840.9332	1663.8326	832.4199	1662.8486	831.9279	15
13	1526.6832	763.8452	1509.6566	755.3320	1508.6726	754.8399	S	1579.8115	790.4094	1562.7849	781.8961	1561.8009	781.4041	14
14	1639.7672	820.3873	1622.7407	811.8740	1621.7567	811.3820	L	1492.7795	746.8934	1475.7529	738.3801	1474.7689	737.8881	13
15	1754.7942	877.9007	1737.7676	869.3875	1736.7836	868.8954	D	1379.6954	690.3513	1362.6688	681.8381	1361.6848	681.3461	12
16	1825.8313	913.4193	1808.8047	904.9060	1807.8207	904.4140	A	1264.6684	632.8379	1247.6419	624.3246	1246.6579	623.8326	11
17	1924.8997	962.9535	1907.8732	954.4402	1906.8891	953.9482	V	1193.6313	597.3193	1176.6048	588.8060	1175.6208	588.3140	10
18	2023.9681	1012.4877	2006.9416	1003.9744	2005.9576	1003.4824	V	1094.5629	547.7851	1077.5364	539.2718	1076.5524	538.7798	9
19	2138.0111	1069.5092	2120.9845	1060.9959	2120.0005	1060.5039	N	995.4945	498.2509	978.4680	489.7376	977.4839	489.2456	8
20	2301.0744	1151.0408	2284.0478	1142.5276	2283.0638	1142.0355	Y	881.4516	441.2294	864.4250	432.7162	863.4410	432.2241	7
21	2448.1428	1224.5750	2431.1162	1216.0618	2430.1322	1215.5698	F	718.3883	359.6978	701.3617	351.1845	700.3777	350.6925	6
22	2547.2112	1274.1092	2530.1847	1265.5960	2529.2006	1265.1040	V	571.3198	286.1636	554.2933	277.6503	553.3093	277.1583	5
23	2634.2432	1317.6253	2617.2167	1309.1120	2616.2327	1308.6200	S	472.2514	236.6293	455.2249	228.1161	454.2409	227.6241	4
24	2771.3021	1386.1547	2754.2756	1377.6414	2753.2916	1377.1494	H	385.2194	193.1133	368.1928	184.6001	367.2088	184.1081	3
25	2872.3498	1436.6786	2855.3233	1428.1653	2854.3393	1427.6733	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
26							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 20741.

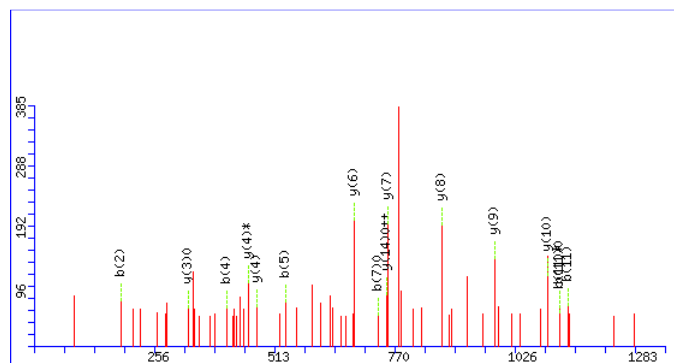
MS/MS Fragmentation of **LAEPQSQGNSQVLLDAPIQLSK:**

Found in **IP100465160,IP100925118**

Title: 3.1.1.975.7

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							22
2	185.1285	93.0679	0	0	0	0	A	2223.1616	1112.0844	2206.1350	1103.5711	2205.1510	1103.0791	21
3	314.1710	157.5892	0	0	296.1605	148.5839	E	2152.1244	1076.5659	2135.0979	1068.0526	2134.1139	1067.5606	20
4	411.2238	206.1155	0	0	393.2132	197.1103	P	2023.0818	1012.0446	2006.0553	1003.5313	2005.0713	1003.0393	19
5	539.2824	270.1448	522.2558	261.6316	521.2718	261.1396	Q	1926.0291	963.5182	1909.0025	955.0049	1908.0185	954.5129	18
6	626.3144	313.6608	609.2879	305.1476	608.3039	304.6556	S	1797.9705	899.4889	1780.9440	890.9756	1779.9599	890.4836	17
7	754.3730	377.6901	737.3464	369.1769	736.3624	368.6849	Q	1710.9385	855.9729	1693.9119	847.4596	1692.9279	846.9676	16
8	811.3945	406.2009	794.3679	397.6876	793.3839	397.1956	G	1582.8799	791.9436	1565.8533	783.4303	1564.8693	782.9383	15
9	925.4374	463.2223	908.4108	454.7091	907.4268	454.2170	N	1525.8584	763.4329	1508.8319	754.9196	1507.8479	754.4276	14
10	1012.4694	506.7383	995.4429	498.2251	994.4588	497.7331	S	1411.8155	706.4114	1394.7890	697.8981	1393.8049	697.4061	13
11	1140.5280	570.7676	1123.5014	562.2544	1122.5174	561.7624	Q	1324.7835	662.8954	1307.7569	654.3821	1306.7729	653.8901	12
12	1239.5964	620.3018	1222.5699	611.7886	1221.5858	611.2966	V	1196.7249	598.8661	1179.6984	590.3528	1178.7143	589.8608	11
13	1352.6805	676.8439	1335.6539	668.3306	1334.6699	667.8386	L	1097.6565	549.3319	1080.6299	540.8186	1079.6459	540.3266	10
14	1465.7645	733.3859	1448.7380	724.8726	1447.7540	724.3806	L	984.5724	492.7898	967.5459	484.2766	966.5619	483.7846	9
15	1580.7915	790.8994	1563.7649	782.3861	1562.7809	781.8941	D	871.4884	436.2478	854.4618	427.7345	853.4778	427.2425	8
16	1651.8286	826.4179	1634.8020	817.9047	1633.8180	817.4127	A	756.4614	378.7343	739.4349	370.2211	738.4509	369.7291	7
17	1748.8814	874.9443	1731.8548	866.4310	1730.8708	865.9390	P	685.4243	343.2158	668.3978	334.7025	667.4137	334.2105	6
18	1861.9654	931.4863	1844.9389	922.9731	1843.9549	922.4811	I	588.3715	294.6894	571.3450	286.1761	570.3610	285.6841	5
19	1990.0240	995.5156	1972.9974	987.0024	1972.0134	986.5104	Q	475.2875	238.1474	458.2609	229.6341	457.2769	229.1421	4
20	2103.1081	1052.0577	2086.0815	1043.5444	2085.0975	1043.0524	L	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
21	2190.1401	1095.5737	2173.1135	1087.0604	2172.1295	1086.5684	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
22							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 20891.

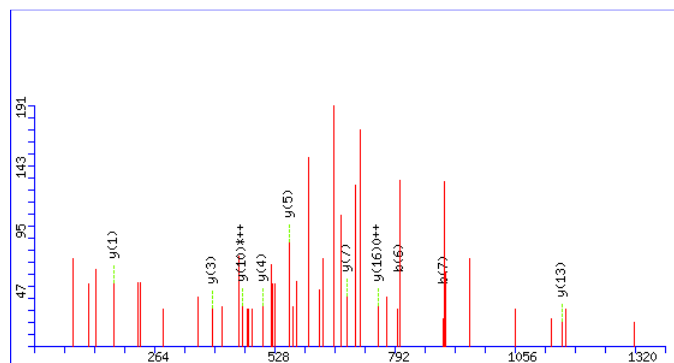
MS/MS Fragmentation of **LLLWFMPCLAGTGSVAGGIESR: 57.021465@C:8**

Found in **IP100100369**

Title: 4.1.1.2357.3

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120201ry¥120201ry_aHDF1388-P9_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							22
2	227.1754	114.0913	0	0	0	0	L	2222.1097	1111.5585	2205.0831	1103.0452	2204.0991	1102.5532	21
3	340.2595	170.6334	0	0	0	0	L	2109.0256	1055.0164	2091.9990	1046.5032	2091.0150	1046.0112	20
4	526.3388	263.6730	0	0	0	0	W	1995.9415	998.4744	1978.9150	989.9611	1977.9310	989.4691	19
5	673.4072	337.2072	0	0	0	0	F	1809.8622	905.4347	1792.8357	896.9215	1791.8517	896.4295	18
6	804.4477	402.7275	0	0	0	0	M	1662.7938	831.9005	1645.7673	823.3873	1644.7832	822.8953	17
7	901.5004	451.2539	0	0	0	0	P	1531.7533	766.3803	1514.7268	757.8670	1513.7428	757.3750	16
8	1061.5311	531.2692	0	0	0	0	C	1434.7006	717.8539	1417.6740	709.3406	1416.6900	708.8486	15
9	1174.6152	587.8112	0	0	0	0	L	1274.6699	637.8386	1257.6434	629.3253	1256.6593	628.8333	14
10	1245.6523	623.3298	0	0	0	0	A	1161.5858	581.2966	1144.5593	572.7833	1143.5753	572.2913	13
11	1302.6737	651.8405	0	0	0	0	G	1090.5487	545.7780	1073.5222	537.2647	1072.5382	536.7727	12
12	1403.7214	702.3643	0	0	1385.7109	693.3591	T	1033.5273	517.2673	1016.5007	508.7540	1015.5167	508.2620	11
13	1460.7429	730.8751	0	0	1442.7323	721.8698	G	932.4796	466.7434	915.4530	458.2302	914.4690	457.7381	10
14	1547.7749	774.3911	0	0	1529.7643	765.3858	S	875.4581	438.2327	858.4316	429.7194	857.4476	429.2274	9
15	1646.8433	823.9253	0	0	1628.8328	814.9200	V	788.4261	394.7167	771.3995	386.2034	770.4155	385.7114	8
16	1717.8804	859.4439	0	0	1699.8699	850.4386	A	689.3577	345.1825	672.3311	336.6692	671.3471	336.1772	7
17	1774.9019	887.9546	0	0	1756.8913	878.9493	G	618.3206	309.6639	601.2940	301.1506	600.3100	300.6586	6
18	1831.9234	916.4653	0	0	1813.9128	907.4600	G	561.2991	281.1532	544.2726	272.6399	543.2885	272.1479	5
19	1945.0074	973.0074	0	0	1926.9969	964.0021	I	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	4
20	2074.0500	1037.5286	0	0	2056.0395	1028.5234	E	391.1936	196.1004	374.1670	187.5871	373.1830	187.0951	3
21	2161.0820	1081.0447	0	0	2143.0715	1072.0394	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
22							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 20903.

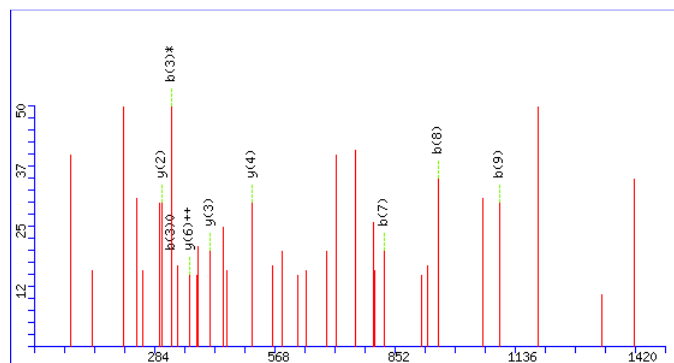
MS/MS Fragmentation of **ERGLSFHQFPTDTIQR**:

Found in **IP100885067;IP100965798;IP100966112;IP100966611**

Title: 5.1.1.280.8

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4.5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							16
2	286.1510	143.5791	269.1244	135.0659	268.1404	134.5738	R	1802.9296	901.9685	1785.9031	893.4552	1784.9191	892.9632	15
3	343.1724	172.0899	326.1459	163.5766	325.1619	163.0846	G	1646.8285	823.9179	1629.8020	815.4046	1628.8180	814.9126	14
4	456.2565	228.6319	439.2300	220.1186	438.2459	219.6266	L	1589.8071	795.4072	1572.7805	786.8939	1571.7965	786.4019	13
5	543.2885	272.1479	526.2620	263.6346	525.2780	263.1426	S	1476.7230	738.8651	1459.6965	730.3519	1458.7124	729.8599	12
6	690.3570	345.6821	673.3304	337.1688	672.3464	336.6768	F	1389.6910	695.3491	1372.6644	686.8359	1371.6804	686.3438	11
7	827.4159	414.2116	810.3893	405.6983	809.4053	405.2063	H	1242.6226	621.8149	1225.5960	613.3016	1224.6120	612.8096	10
8	955.4744	478.2409	938.4479	469.7276	937.4639	469.2356	Q	1105.5637	553.2855	1088.5371	544.7722	1087.5531	544.2802	9
9	1102.5429	551.7751	1085.5163	543.2618	1084.5323	542.7698	F	977.5051	489.2562	960.4785	480.7429	959.4945	480.2509	8
10	1199.5956	600.3014	1182.5691	591.7882	1181.5851	591.2962	P	830.4367	415.7220	813.4101	407.2087	812.4261	406.7167	7
11	1300.6433	650.8253	1283.6167	642.3120	1282.6327	641.8200	T	733.3839	367.1956	716.3573	358.6823	715.3733	358.1903	6
12	1415.6702	708.3388	1398.6437	699.8255	1397.6597	699.3335	D	632.3362	316.6717	615.3097	308.1585	614.3257	307.6665	5
13	1516.7179	758.8626	1499.6914	750.3493	1498.7074	749.8573	T	517.3093	259.1583	500.2827	250.6450	499.2987	250.1530	4
14	1629.8020	815.4046	1612.7754	806.8914	1611.7914	806.3993	I	416.2616	208.6344	399.2350	200.1212	0	0	3
15	1757.8606	879.4339	1740.8340	870.9206	1739.8500	870.4286	Q	303.1775	152.0924	286.1510	143.5791	0	0	2
16							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 20973.

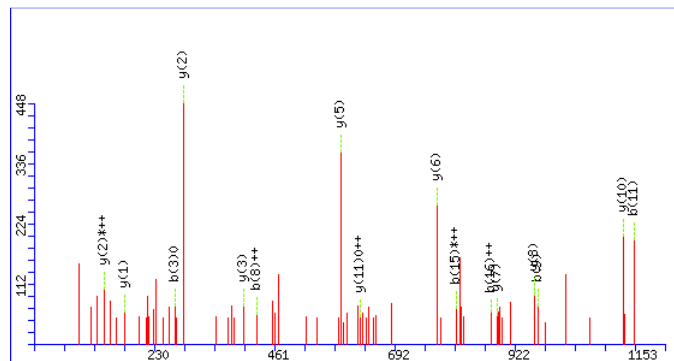
MS/MS Fragmentation of **SSLEELHGDANWGEDLR**:

Found in **IP100295940;IP100878697;IP100879049;IP100879539;IP100879581;IP100879752;IP100879913**

Title: 2.1.1.4226.7

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120201ry¥120201ry_aHDF1388-P9_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							17
2	175.0713	88.0393	0	0	157.0608	79.0340	S	1840.8460	920.9267	1823.8195	912.4134	1822.8355	911.9214	16
3	288.1554	144.5813	0	0	270.1448	135.5761	L	1753.8140	877.4106	1736.7875	868.8974	1735.8034	868.4054	15
4	417.1980	209.1026	0	0	399.1874	200.0974	E	1640.7299	820.8686	1623.7034	812.3553	1622.7194	811.8633	14
5	546.2406	273.6239	0	0	528.2300	264.6186	E	1511.6873	756.3473	1494.6608	747.8340	1493.6768	747.3420	13
6	659.3246	330.1660	0	0	641.3141	321.1607	L	1382.6448	691.8260	1365.6182	683.3127	1364.6342	682.8207	12
7	796.3836	398.6954	0	0	778.3730	389.6901	H	1269.5607	635.2840	1252.5341	626.7707	1251.5501	626.2787	11
8	853.4050	427.2061	0	0	835.3945	418.2009	G	1132.5018	566.7545	1115.4752	558.2413	1114.4912	557.7492	10
9	968.4320	484.7196	0	0	950.4214	475.7143	D	1075.4803	538.2438	1058.4538	529.7305	1057.4697	529.2385	9
10	1039.4691	520.2382	0	0	1021.4585	511.2329	A	960.4534	480.7303	943.4268	472.2170	942.4428	471.7250	8
11	1153.5120	577.2596	1136.4855	568.7464	1135.5014	568.2544	N	889.4163	445.2118	872.3897	436.6985	871.4057	436.2065	7
12	1339.5913	670.2993	1322.5648	661.7860	1321.5808	661.2940	W	775.3733	388.1903	758.3468	379.6770	757.3628	379.1850	6
13	1396.6128	698.8100	1379.5862	690.2968	1378.6022	689.8047	G	589.2940	295.1506	572.2675	286.6374	571.2835	286.1454	5
14	1525.6554	763.3313	1508.6288	754.8181	1507.6448	754.3260	E	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
15	1640.6823	820.8448	1623.6558	812.3315	1622.6718	811.8395	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
16	1753.7664	877.3868	1736.7398	868.8736	1735.7558	868.3815	L	288.2030	144.6051	271.1765	136.0919	0	0	2
17							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 21575.

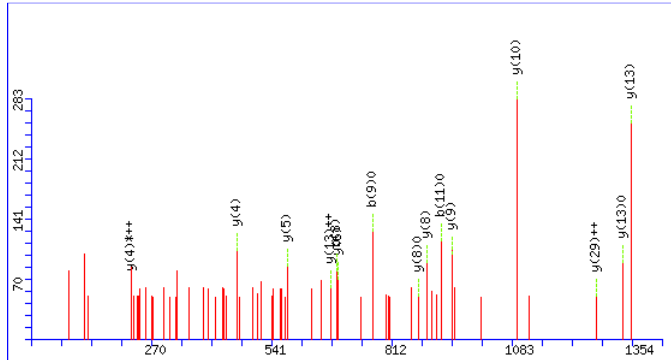
MS/MS Fragmentation of **FIGAGAATVGAGSGAGIGTVFGSLIIGYAR**:

Found in **IP100008727;IP100009075;IP100028482;IP100456749;IP100790579;IP100792819;IP100796559;IP100963825;IP100977456**

Title: 5.1.1.1598.9

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120214ry¥120214ry_414C2-43_4_5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							31
2	261.1598	131.0835	0	0	0	0	I	2663.4515	1332.2294	2646.4250	1323.7161	2645.4410	1323.2241	30
3	318.1812	159.5942	0	0	0	0	G	2550.3675	1275.6874	2533.3409	1267.1741	2532.3569	1266.6821	29
4	389.2183	195.1128	0	0	0	0	A	2493.3460	1247.1766	2476.3195	1238.6634	2475.3354	1238.1714	28
5	446.2398	223.6235	0	0	0	0	G	2422.3089	1211.6581	2405.2823	1203.1448	2404.2983	1202.6528	27
6	517.2769	259.1421	0	0	0	0	A	2365.2874	1183.1474	2348.2609	1174.6341	2347.2769	1174.1421	26
7	588.3140	294.6607	0	0	0	0	A	2294.2503	1147.6288	2277.2238	1139.1155	2276.2397	1138.6235	25
8	689.3617	345.1845	0	0	671.3511	336.1792	T	2223.2132	1112.1102	2206.1866	1103.5970	2205.2026	1103.1050	24
9	788.4301	394.7187	0	0	770.4196	385.7134	V	2122.1655	1061.5864	2105.1390	1053.0731	2104.1550	1052.5811	23
10	845.4516	423.2294	0	0	827.4410	414.2241	G	2023.0971	1012.0522	2006.0706	1003.5389	2005.0865	1003.0469	22
11	944.5200	472.7636	0	0	926.5094	463.7584	V	1966.0756	983.5415	1949.0491	975.0282	1948.0651	974.5362	21
12	1015.5571	508.2822	0	0	997.5465	499.2769	A	1867.0072	934.0073	1849.9807	925.4940	1848.9967	925.0020	20
13	1072.5786	536.7929	0	0	1054.5680	527.7876	G	1795.9701	898.4887	1778.9436	889.9754	1777.9595	889.4834	19
14	1159.6106	580.3089	0	0	1141.6000	571.3037	S	1738.9486	869.9780	1721.9221	861.4647	1720.9381	860.9727	18
15	1216.6321	608.8197	0	0	1198.6215	599.8144	G	1651.9166	826.4619	1634.8901	817.9487	1633.9061	817.4567	17
16	1287.6692	644.3382	0	0	1269.6586	635.3329	A	1594.8952	797.9512	1577.8686	789.4379	1576.8846	788.9459	16
17	1344.6906	672.8490	0	0	1326.6801	663.8437	G	1523.8580	762.4327	1506.8315	753.9194	1505.8475	753.4274	15
18	1457.7747	729.3910	0	0	1439.7641	720.3857	I	1466.8366	733.9219	1449.8100	725.4087	1448.8260	724.9166	14
19	1514.7962	757.9017	0	0	1496.7856	748.8964	G	1353.7525	677.3799	1336.7260	668.8666	1335.7419	668.3746	13
20	1615.8439	808.4256	0	0	1597.8333	799.4203	T	1296.7310	648.8692	1279.7045	640.3559	1278.7205	639.8639	12
21	1714.9123	857.9598	0	0	1696.9017	848.9545	V	1195.6834	598.3453	1178.6568	589.8320	1177.6728	589.3400	11
22	1861.9807	931.4940	0	0	1843.9701	922.4887	F	1096.6150	548.8111	1079.5884	540.2978	1078.6044	539.8058	10
23	1919.0021	960.0047	0	0	1900.9916	950.9994	G	949.5465	475.2769	932.5200	466.7636	931.5360	466.2716	9
24	2006.0342	1003.5207	0	0	1988.0236	994.5154	S	892.5251	446.7662	875.4985	438.2529	874.5145	437.7609	8
25	2119.1182	1060.0628	0	0	2101.1077	1051.0575	L	805.4931	403.2502	788.4665	394.7369	0	0	7
26	2232.2023	1116.6048	0	0	2214.1917	1107.5995	I	692.4090	346.7081	675.3824	338.1949	0	0	6
27	2345.2864	1173.1468	0	0	2327.2758	1164.1415	I	579.3249	290.1661	562.2984	281.6528	0	0	5
28	2402.3078	1201.6576	0	0	2384.2973	1192.6523	G	466.2409	233.6241	449.2143	225.1108	0	0	4
29	2565.3712	1283.1892	0	0	2547.3606	1274.1839	Y	409.2194	205.1133	392.1928	196.6001	0	0	3
30	2636.4083	1318.7078	0	0	2618.3977	1309.7025	A	246.1561	123.5817	229.1295	115.0684	0	0	2
31							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

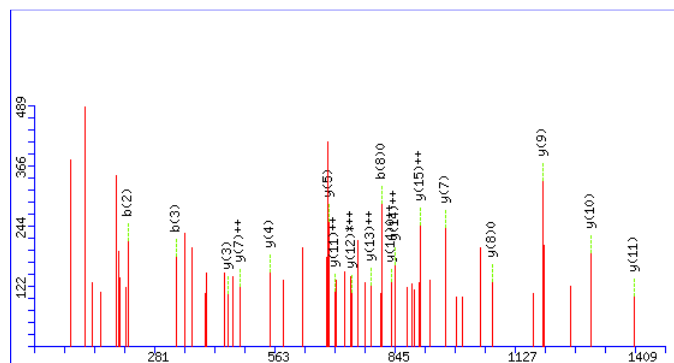
Peptide: 22124.

MS/MS Fragmentation of **GYLIDATTITECLHTFCK: 57.021465@C:12,57.021465@C:17**
Found in **IP100030334,IP100063571**

Title: 3.1.1.4383.3

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							18
2	221.0921	111.0497	0	0	0	0	Y	2085.9984	1043.5028	2068.9718	1034.9896	2067.9878	1034.4975	17
3	334.1761	167.5917	0	0	0	0	L	1922.9351	961.9712	1905.9085	953.4579	1904.9245	952.9659	16
4	447.2602	224.1337	0	0	0	0	I	1809.8510	905.4291	1792.8244	896.9159	1791.8404	896.4238	15
5	562.2871	281.6472	0	0	544.2766	272.6419	D	1696.7669	848.8871	1679.7404	840.3738	1678.7564	839.8818	14
6	633.3243	317.1658	0	0	615.3137	308.1605	A	1581.7400	791.3736	1564.7134	782.8604	1563.7294	782.3683	13
7	734.3719	367.6896	0	0	716.3614	358.6843	T	1510.7029	755.8551	1493.6763	747.3418	1492.6923	746.8498	12
8	835.4196	418.2134	0	0	817.4090	409.2082	T	1409.6552	705.3312	1392.6286	696.8180	1391.6446	696.3259	11
9	948.5037	474.7555	0	0	930.4931	465.7502	I	1308.6075	654.8074	1291.5810	646.2941	1290.5969	645.8021	10
10	1049.5514	525.2793	0	0	1031.5408	516.2740	T	1195.5234	598.2654	1178.4969	589.7521	1177.5129	589.2601	9
11	1178.5939	589.8006	0	0	1160.5834	580.7953	E	1094.4758	547.7415	1077.4492	539.2282	1076.4652	538.7362	8
12	1338.6246	669.8159	0	0	1320.6140	660.8107	C	965.4332	483.2202	948.4066	474.7069	947.4226	474.2149	7
13	1451.7087	726.3580	0	0	1433.6981	717.3527	L	805.4025	403.2049	788.3760	394.6916	787.3920	394.1996	6
14	1588.7676	794.8874	0	0	1570.7570	785.8821	H	692.3185	346.6629	675.2919	338.1496	674.3079	337.6576	5
15	1689.8153	845.4113	0	0	1671.8047	836.4060	T	555.2595	278.1334	538.2330	269.6201	537.2490	269.1281	4
16	1836.8837	918.9455	0	0	1818.8731	909.9402	F	454.2119	227.6096	437.1853	219.0963	0	0	3
17	1996.9143	998.9608	0	0	1978.9038	989.9555	C	307.1435	154.0754	290.1169	145.5621	0	0	2
18							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 22264.

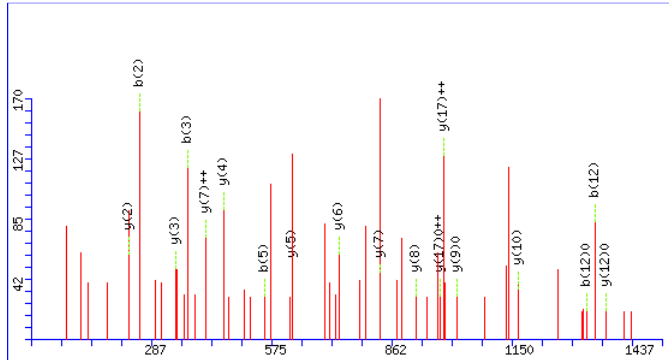
MS/MS Fragmentation of **IFLVSPITIVHEIDEDSPLYDLSK**:

Found in **IP100007614**

Title: 4.1.1.4399.2

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							24
2	261.1598	131.0835	0	0	0	0	F	2630.3600	1315.6836	2613.3334	1307.1704	2612.3494	1306.6783	23
3	374.2438	187.6255	0	0	0	0	L	2483.2916	1242.1494	2466.2650	1233.6361	2465.2810	1233.1441	22
4	473.3122	237.1598	0	0	0	0	V	2370.2075	1185.6074	2353.1809	1177.0941	2352.1969	1176.6021	21
5	560.3443	280.6758	0	0	542.3337	271.6705	S	2271.1391	1136.0732	2254.1125	1127.5599	2253.1285	1127.0679	20
6	657.3970	329.2022	0	0	639.3865	320.1969	P	2184.1071	1092.5572	2167.0805	1084.0439	2166.0965	1083.5519	19
7	770.4811	385.7442	0	0	752.4705	376.7389	I	2087.0543	1044.0308	2070.0277	1035.5175	2069.0437	1035.0255	18
8	871.5288	436.2680	0	0	853.5182	427.2627	T	1973.9702	987.4888	1956.9437	978.9755	1955.9597	978.4835	17
9	984.6128	492.8101	0	0	966.6023	483.8048	I	1872.9225	936.9649	1855.8960	928.4516	1854.9120	927.9596	16
10	1083.6812	542.3443	0	0	1065.6707	533.3390	V	1759.8385	880.4229	1742.8119	871.9096	1741.8279	871.4176	15
11	1220.7402	610.8737	0	0	1202.7296	601.8684	H	1660.7701	830.8887	1643.7435	822.3754	1642.7595	821.8834	14
12	1349.7828	675.3950	0	0	1331.7722	666.3897	E	1523.7112	762.3592	1506.6846	753.8459	1505.7006	753.3539	13
13	1462.8668	731.9370	0	0	1444.8562	722.9318	I	1394.6686	697.8379	1377.6420	689.3246	1376.6580	688.8326	12
14	1577.8938	789.4505	0	0	1559.8832	780.4452	D	1281.5845	641.2959	1264.5580	632.7826	1263.5739	632.2906	11
15	1706.9364	853.9718	0	0	1688.9258	844.9665	E	1166.5576	583.7824	1149.5310	575.2691	1148.5470	574.7771	10
16	1821.9633	911.4853	0	0	1803.9527	902.4800	D	1037.5150	519.2611	1020.4884	510.7478	1019.5044	510.2558	9
17	1908.9953	955.0013	0	0	1890.9848	945.9960	S	922.4880	461.7476	905.4615	453.2344	904.4775	452.7424	8
18	2006.0481	1003.5277	0	0	1988.0375	994.5224	P	835.4560	418.2316	818.4294	409.7184	817.4454	409.2264	7
19	2119.1321	1060.0697	0	0	2101.1216	1051.0644	L	738.4032	369.7053	721.3767	361.1920	720.3927	360.7000	6
20	2282.1955	1141.6014	0	0	2264.1849	1132.5961	Y	625.3192	313.1632	608.2926	304.6499	607.3086	304.1579	5
21	2397.2224	1199.1148	0	0	2379.2119	1190.1096	D	462.2558	231.6316	445.2293	223.1183	444.2453	222.6263	4
22	2510.3065	1255.6569	0	0	2492.2959	1246.6516	L	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
23	2597.3385	1299.1729	0	0	2579.3279	1290.1676	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
24							K	147.1128	74.0600	130.0863	65.5468	0	0	1

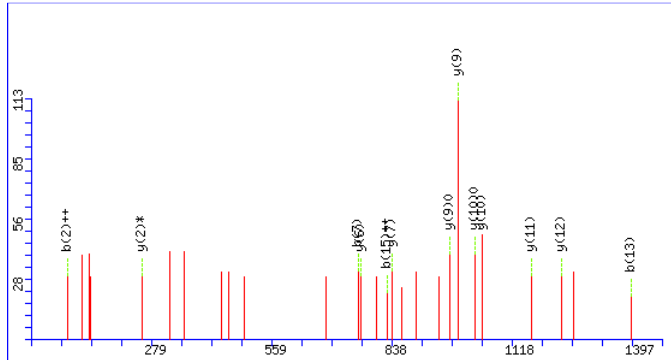
Peptide View

Peptide: 22276.

MS/MS Fragmentation of **IGTLSCEIDAYGDFLQALGPQATVEYTR**: 57.021465@C:6
Found in **IP100021943**

Title: 4.1.1.2557.10

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_2.4.mgf
ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							28
2	171.1128	86.0600	0	0	0	0	G	2904.3720	1452.6896	2887.3455	1444.1764	2886.3615	1443.6844	27
3	272.1605	136.5839	0	0	254.1499	127.5786	T	2847.3506	1424.1789	2830.3240	1415.6656	2829.3400	1415.1736	26
4	385.2445	193.1259	0	0	367.2340	184.1206	L	2746.3029	1373.6551	2729.2763	1365.1418	2728.2923	1364.6498	25
5	472.2766	236.6419	0	0	454.2660	227.6366	S	2633.2188	1317.1130	2616.1923	1308.5998	2615.2082	1308.1078	24
6	632.3072	316.6573	0	0	614.2967	307.6520	C	2546.1868	1273.5970	2529.1602	1265.0838	2528.1762	1264.5917	23
7	761.3498	381.1785	0	0	743.3393	372.1733	E	2386.1561	1193.5817	2369.1296	1185.0684	2368.1456	1184.5764	22
8	874.4339	437.7206	0	0	856.4233	428.7153	I	2257.1135	1129.0604	2240.0870	1120.5471	2239.1030	1120.0551	21
9	989.4608	495.2341	0	0	971.4503	486.2288	D	2144.0295	1072.5184	2127.0029	1064.0051	2126.0189	1063.5131	20
10	1060.4979	530.7526	0	0	1042.4874	521.7473	A	2029.0025	1015.0049	2011.9760	1006.4916	2010.9920	1005.9996	19
11	1223.5613	612.2843	0	0	1205.5507	603.2790	Y	1957.9654	979.4863	1940.9389	970.9731	1939.9549	970.4811	18
12	1280.5827	640.7950	0	0	1262.5722	631.7897	G	1794.9021	897.9547	1777.8755	889.4414	1776.8915	888.9494	17
13	1395.6097	698.3085	0	0	1377.5991	689.3032	D	1737.8806	869.4440	1720.8541	860.9307	1719.8701	860.4387	16
14	1542.6781	771.8427	0	0	1524.6675	762.8374	F	1622.8537	811.9305	1605.8271	803.4172	1604.8431	802.9252	15
15	1655.7622	828.3847	0	0	1637.7516	819.3794	L	1475.7853	738.3963	1458.7587	729.8830	1457.7747	729.3910	14
16	1783.8207	892.4140	1766.7942	883.9007	1765.8102	883.4087	Q	1362.7012	681.8542	1345.6747	673.3410	1344.6906	672.8490	13
17	1854.8578	927.9326	1837.8313	919.4193	1836.8473	918.9273	A	1234.6426	617.8250	1217.6161	609.3117	1216.6321	608.8197	12
18	1967.9419	984.4746	1950.9154	975.9613	1949.9313	975.4693	L	1163.6055	582.3064	1146.5790	573.7931	1145.5950	573.3011	11
19	2024.9634	1012.9853	2007.9368	1004.4720	2006.9528	1003.9800	G	1050.5215	525.7644	1033.4949	517.2511	1032.5109	516.7591	10
20	2122.0161	1061.5117	2104.9896	1052.9984	2104.0056	1052.5064	P	993.5000	497.2536	976.4734	488.7404	975.4894	488.2483	9
21	2179.0376	1090.0224	2162.0111	1081.5092	2161.0270	1081.0172	G	896.4472	448.7272	879.4207	440.2140	878.4367	439.7220	8
22	2250.0747	1125.5410	2233.0482	1117.0277	2232.0642	1116.5357	A	839.4258	420.2165	822.3992	411.7032	821.4152	411.2112	7
23	2351.1224	1176.0648	2334.0958	1167.5516	2333.1118	1167.0596	T	768.3886	384.6980	751.3621	376.1847	750.3781	375.6927	6
24	2450.1908	1225.5990	2433.1643	1217.0858	2432.1802	1216.5938	V	667.3410	334.1741	650.3144	325.6608	649.3304	325.1688	5
25	2579.2334	1290.1203	2562.2069	1281.6071	2561.2228	1281.1151	E	568.2726	284.6399	551.2460	276.1266	550.2620	275.6346	4
26	2742.2967	1371.6520	2725.2702	1363.1387	2724.2862	1362.6467	Y	439.2300	220.1186	422.2034	211.6053	421.2194	211.1133	3
27	2843.3444	1422.1758	2826.3179	1413.6626	2825.3338	1413.1706	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
28							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

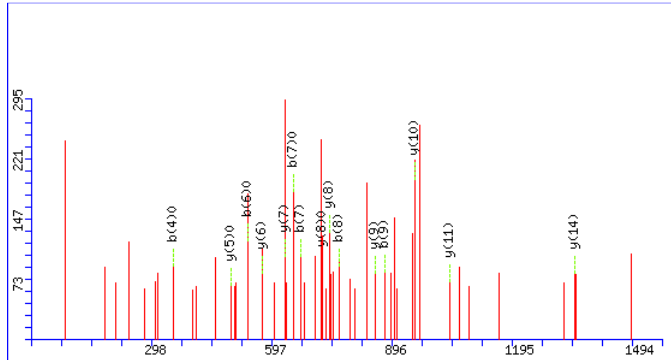
Peptide: 22628.

MS/MS Fragmentation of **ATSLPSIPNPFPELCSPPSQSPILGGPSSAR: 57.021465@C:15**
 Found in **IP100293948,IP100448767,IP100791383,IP100839546**

Title: 4.1.1.129.8

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							31
2	173.0921	87.0497	0	0	155.0815	78.0444	T	3090.5565	1545.7819	3073.5299	1537.2686	3072.5459	1536.7766	30
3	260.1241	130.5657	0	0	242.1135	121.5604	S	2989.5088	1495.2580	2972.4822	1486.7448	2971.4982	1486.2527	29
4	373.2082	187.1077	0	0	355.1976	178.1024	L	2902.4768	1451.7420	2885.4502	1443.2287	2884.4662	1442.7367	28
5	470.2609	235.6341	0	0	452.2504	226.6288	P	2789.3927	1395.2000	2772.3661	1386.6867	2771.3821	1386.1947	27
6	557.2930	279.1501	0	0	539.2824	270.1448	S	2692.3399	1346.6736	2675.3134	1338.1603	2674.3294	1337.6683	26
7	670.3770	335.6921	0	0	652.3665	326.6869	I	2605.3079	1303.1576	2588.2814	1294.6443	2587.2973	1294.1523	25
8	767.4298	384.2185	0	0	749.4192	375.2132	P	2492.2238	1246.6156	2475.1973	1238.1023	2474.2133	1237.6103	24
9	881.4727	441.2400	864.4462	432.7267	863.4621	432.2347	N	2395.1711	1198.0892	2378.1445	1189.5759	2377.1605	1189.0839	23
10	978.5255	489.7664	961.4989	481.2531	960.5149	480.7611	P	2281.1281	1141.0677	2264.1016	1132.5544	2263.1176	1132.0624	22
11	1125.5939	563.3006	1108.5673	554.7873	1107.5833	554.2953	F	2184.0754	1092.5413	2167.0488	1084.0281	2166.0648	1083.5360	21
12	1222.6467	611.8270	1205.6201	603.3137	1204.6361	602.8217	P	2037.0070	1019.0071	2019.9804	1010.4938	2018.9964	1010.0018	20
13	1351.6892	676.3483	1334.6627	667.8350	1333.6787	667.3430	E	1939.9542	970.4807	1922.9277	961.9675	1921.9436	961.4755	19
14	1464.7733	732.8903	1447.7468	724.3770	1446.7627	723.8850	L	1810.9116	905.9594	1793.8851	897.4462	1792.9010	896.9542	18
15	1624.8040	812.9056	1607.7774	804.3923	1606.7934	803.9003	C	1697.8275	849.4174	1680.8010	840.9041	1679.8170	840.4121	17
16	1711.8360	856.4216	1694.8094	847.9084	1693.8254	847.4163	S	1537.7969	769.4021	1520.7703	760.8888	1519.7863	760.3968	16
17	1808.8887	904.9480	1791.8622	896.4347	1790.8782	895.9427	P	1450.7649	725.8861	1433.7383	717.3728	1432.7543	716.8808	15
18	1905.9415	953.4744	1888.9150	944.9611	1887.9309	944.4691	P	1353.7121	677.3597	1336.6856	668.8464	1335.7015	668.3544	14
19	1992.9735	996.9904	1975.9470	988.4771	1974.9630	987.9851	S	1256.6593	628.8333	1239.6328	620.3200	1238.6488	619.8280	13
20	2121.0321	1061.0197	2104.0056	1052.5064	2103.0216	1052.0144	Q	1169.6273	585.3173	1152.6008	576.8040	1151.6167	576.3120	12
21	2208.0641	1104.5357	2191.0376	1096.0224	2190.0536	1095.5304	S	1041.5887	521.2880	1024.5422	512.7747	1023.5582	512.2827	11
22	2305.1169	1153.0621	2288.0904	1144.5488	2287.1063	1144.0568	P	954.5367	477.7720	937.5102	469.2587	936.5261	468.7667	10
23	2418.2010	1209.6041	2401.1744	1201.0909	2400.1904	1200.5988	I	857.4839	429.2456	840.4574	420.7323	839.4734	420.2403	9
24	2531.2850	1266.1462	2514.2585	1257.6329	2513.2745	1257.1409	L	744.3999	372.7036	727.3733	364.1903	726.3893	363.6983	8
25	2588.3065	1294.6569	2571.2800	1286.1436	2570.2959	1285.6516	G	631.3158	316.1615	614.2893	307.6483	613.3052	307.1563	7
26	2645.3280	1323.1676	2628.3014	1314.6543	2627.3174	1314.1623	G	574.2943	287.6508	557.2678	279.1375	556.2838	278.6455	6
27	2742.3807	1371.6940	2725.3542	1363.1807	2724.3702	1362.6887	P	517.2729	259.1401	500.2463	250.6268	499.2623	250.1348	5
28	2829.4128	1415.2100	2812.3862	1406.6967	2811.4022	1406.2047	S	420.2201	210.6137	403.1936	202.1004	402.2096	201.6084	4
29	2916.4448	1458.7260	2899.4182	1450.2128	2898.4342	1449.7207	S	333.1881	167.0977	316.1615	158.5844	315.1775	158.0924	3
30	2987.4819	1494.2446	2970.4554	1485.7313	2969.4713	1485.2393	A	246.1561	123.5817	229.1295	115.0684	0	0	2
31							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 22812.

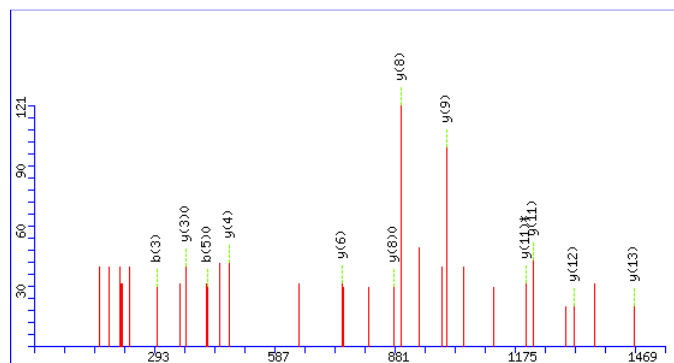
MS/MS Fragmentation of **SVLAAATEYFTPLLSQQFSES**R:

Found in **IP100018726**

Title: 4.1.1.2882.8

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							22
2	187.1077	94.0575	0	0	169.0972	85.0522	V	2287.1605	1144.0839	2270.1339	1135.5706	2269.1499	1135.0786	21
3	300.1918	150.5995	0	0	282.1812	141.5942	L	2188.0921	1094.5497	2171.0655	1086.0364	2170.0815	1085.5444	20
4	371.2289	186.1181	0	0	353.2183	177.1128	A	2075.0080	1038.0076	2057.9815	1029.4944	2056.9974	1029.0024	19
5	442.2660	221.6366	0	0	424.2554	212.6314	A	2003.9709	1002.4891	1986.9443	993.9758	1985.9603	993.4838	18
6	513.3031	257.1552	0	0	495.2926	248.1499	A	1932.9338	966.9705	1915.9072	958.4573	1914.9232	957.9652	17
7	614.3508	307.6790	0	0	596.3402	298.6738	T	1861.8967	931.4520	1844.8701	922.9387	1843.8861	922.4467	16
8	743.3934	372.2003	0	0	725.3828	363.1951	E	1760.8490	880.9281	1743.8224	872.4149	1742.8384	871.9229	15
9	906.4567	453.7320	0	0	888.4462	444.7267	Y	1631.8064	816.4068	1614.7798	807.8936	1613.7958	807.4016	14
10	1053.5251	527.2662	0	0	1035.5146	518.2609	F	1468.7431	734.8752	1451.7165	726.3619	1450.7325	725.8699	13
11	1154.5728	577.7900	0	0	1136.5623	568.7848	T	1321.6747	661.3410	1304.6481	652.8277	1303.6641	652.3357	12
12	1251.6256	626.3164	0	0	1233.6150	617.3111	P	1220.6270	610.8171	1203.6004	602.3039	1202.6164	601.8118	11
13	1364.7096	682.8585	0	0	1346.6991	673.8532	L	1123.5742	562.2907	1106.5477	553.7775	1105.5636	553.2855	10
14	1477.7937	739.4005	0	0	1459.7831	730.3952	L	1010.4901	505.7487	993.4636	497.2354	992.4796	496.7434	9
15	1564.8257	782.9165	0	0	1546.8152	773.9112	S	897.4061	449.2067	880.3795	440.6934	879.3955	440.2014	8
16	1621.8472	811.4272	0	0	1603.8366	802.4220	G	810.3741	405.6907	793.3475	397.1774	792.3635	396.6854	7
17	1749.9058	875.4565	1732.8792	866.9433	1731.8952	866.4512	Q	753.3526	377.1799	736.3260	368.6667	735.3420	368.1747	6
18	1896.9742	948.9907	1879.9476	940.4775	1878.9636	939.9855	F	625.2940	313.1506	608.2675	304.6374	607.2835	304.1454	5
19	1984.0062	992.5067	1966.9797	983.9935	1965.9957	983.5015	S	478.2256	239.6164	461.1991	231.1032	460.2150	230.6112	4
20	2113.0488	1057.0280	2096.0223	1048.5148	2095.0383	1048.0228	E	391.1936	196.1004	374.1670	187.5871	373.1830	187.0951	3
21	2200.0808	1100.5441	2183.0543	1092.0308	2182.0703	1091.5388	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
22							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 23088.

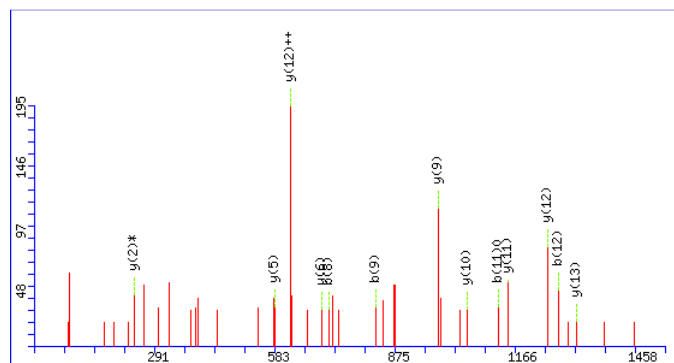
MS/MS Fragmentation of **AQLGPGDFDWEELLAPPAGQDLVLK:**

Found in **IP100783299**

Title: 4.1.1.3854.9

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							27
2	129.0659	65.0366	0	0	0	0	G	2747.4291	1374.2182	2730.4025	1365.7049	2729.4185	1365.2129	26
3	242.1499	121.5786	0	0	0	0	L	2690.4076	1345.7074	2673.3810	1337.1942	2672.3970	1336.7022	25
4	299.1714	150.0893	0	0	0	0	G	2577.3235	1289.1654	2560.2970	1280.6521	2559.3130	1280.1601	24
5	396.2241	198.6157	0	0	0	0	P	2520.3021	1260.6547	2503.2755	1252.1414	2502.2915	1251.6494	23
6	453.2456	227.1264	0	0	0	0	G	2423.2493	1212.1283	2406.2228	1203.6150	2405.2387	1203.1230	22
7	568.2726	284.6399	0	0	550.2620	275.6346	D	2366.2278	1183.6176	2349.2013	1175.1043	2348.2173	1174.6123	21
8	715.3410	358.1741	0	0	697.3304	349.1688	F	2251.2009	1126.1041	2234.1743	1117.5908	2233.1903	1117.0988	20
9	830.3679	415.6876	0	0	812.3573	406.6823	D	2104.1325	1052.5699	2087.1059	1044.0566	2086.1219	1043.5646	19
10	1016.4472	508.7272	0	0	998.4367	499.7220	W	1989.1055	995.0564	1972.0790	986.5431	1971.0950	986.0511	18
11	1145.4898	573.2485	0	0	1127.4793	564.2433	E	1803.0262	902.0168	1785.9997	893.5035	1785.0157	893.0115	17
12	1274.5324	637.7698	0	0	1256.5218	628.7646	E	1673.9836	837.4955	1656.9571	828.9822	1655.9731	828.4902	16
13	1387.6165	694.3119	0	0	1369.6059	685.3066	L	1544.9410	772.9742	1527.9145	764.4609	1526.9305	763.9689	15
14	1500.7005	750.8539	0	0	1482.6900	741.8486	L	1431.8570	716.4321	1414.8304	707.9189	1413.8464	707.4268	14
15	1571.7377	786.3725	0	0	1553.7271	777.3672	A	1318.7729	659.8901	1301.7464	651.3768	1300.7624	650.8848	13
16	1668.7904	834.8988	0	0	1650.7799	825.8936	P	1247.7358	624.3715	1230.7093	615.8583	1229.7252	615.3663	12
17	1765.8432	883.4252	0	0	1747.8326	874.4199	P	1150.6830	575.8452	1133.6565	567.3319	1132.6725	566.8399	11
18	1836.8803	918.9438	0	0	1818.8697	909.9385	A	1053.6303	527.3188	1036.6037	518.8055	1035.6197	518.3135	10
19	1933.9331	967.4702	0	0	1915.9225	958.4649	P	982.5932	491.8002	965.5666	483.2869	964.5826	482.7949	9
20	1990.9545	995.9809	0	0	1972.9440	986.9756	G	885.5404	443.2738	868.5138	434.7606	867.5298	434.2686	8
21	2119.0131	1060.0102	2101.9865	1051.4969	2101.0025	1051.0049	Q	828.5189	414.7631	811.4924	406.2498	810.5084	405.7578	7
22	2234.0400	1117.5237	2217.0135	1109.0104	2216.0295	1108.5184	D	700.4604	350.7338	683.4338	342.2205	682.4498	341.7285	6
23	2347.1241	1174.0657	2330.0976	1165.5524	2329.1135	1165.0604	L	585.4334	293.2203	568.4069	284.7071	0	0	5
24	2446.1925	1223.5999	2429.1660	1215.0866	2428.1820	1214.5946	V	472.3493	236.6783	455.3228	228.1650	0	0	4
25	2559.2766	1280.1419	2542.2500	1271.6287	2541.2660	1271.1366	I	373.2809	187.1441	356.2544	178.6308	0	0	3
26	2672.3606	1336.6840	2655.3341	1328.1707	2654.3501	1327.6787	L	260.1969	130.6021	243.1703	122.0888	0	0	2
27							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 23220.

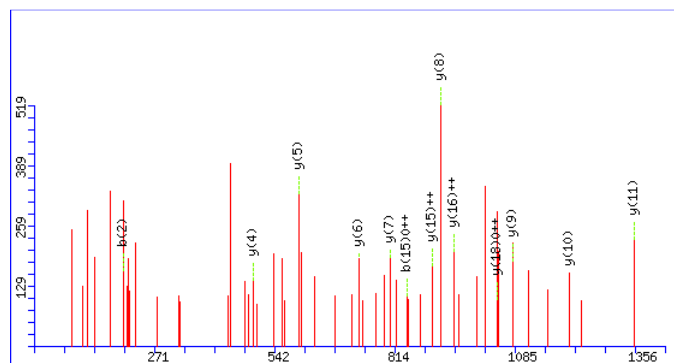
MS/MS Fragmentation of **SLTPDDVVFQYLAHTYASR**:

Found in **IP100026270;IP101021170;IP101022469**

Title: 3.1.1.4512.6

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							19
2	201.1234	101.0653	0	0	183.1128	92.0600	L	2112.0033	1056.5053	2094.9767	1047.9920	2093.9927	1047.5000	18
3	302.1710	151.5892	0	0	284.1605	142.5839	T	1998.9192	999.9632	1981.8926	991.4500	1980.9086	990.9580	17
4	399.2238	200.1155	0	0	381.2132	191.1103	P	1897.8715	949.4394	1880.8450	940.9261	1879.8610	940.4341	16
5	514.2508	257.6290	0	0	496.2402	248.6237	D	1800.8188	900.9130	1783.7922	892.3997	1782.8082	891.9077	15
6	629.2777	315.1425	0	0	611.2671	306.1372	D	1685.7918	843.3995	1668.7653	834.8863	1667.7812	834.3943	14
7	744.3046	372.6560	0	0	726.2941	363.6507	D	1570.7649	785.8861	1553.7383	777.3728	1552.7543	776.8808	13
8	843.3731	422.1902	0	0	825.3625	413.1849	V	1455.7379	728.3726	1438.7114	719.8593	1437.7274	719.3673	12
9	990.4415	495.7244	0	0	972.4309	486.7191	F	1356.6695	678.8384	1339.6430	670.3251	1338.6589	669.8331	11
10	1118.5000	559.7537	1101.4735	551.2404	1100.4895	550.7484	Q	1209.6011	605.3042	1192.5745	596.7909	1191.5905	596.2989	10
11	1281.5634	641.2853	1264.5368	632.7721	1263.5528	632.2800	Y	1081.5425	541.2749	1064.5160	532.7616	1063.5320	532.2696	9
12	1394.6474	697.8274	1377.6209	689.3141	1376.6369	688.8221	L	918.4792	459.7432	901.4526	451.2300	900.4686	450.7380	8
13	1465.6846	733.3459	1448.6580	724.8326	1447.6740	724.3406	A	805.3951	403.2012	788.3686	394.6879	787.3846	394.1959	7
14	1602.7435	801.8754	1585.7169	793.3621	1584.7329	792.8701	H	734.3580	367.6826	717.3315	359.1694	716.3474	358.6774	6
15	1703.7911	852.3992	1686.7646	843.8859	1685.7806	843.3939	T	597.2991	299.1532	580.2726	290.6399	579.2885	290.1479	5
16	1866.8545	933.9309	1849.8279	925.4176	1848.8439	924.9256	Y	496.2514	248.6293	479.2249	240.1161	478.2409	239.6241	4
17	1937.8916	969.4494	1920.8650	960.9362	1919.8810	960.4441	A	333.1881	167.0977	316.1615	158.5844	315.1775	158.0924	3
18	2024.9236	1012.9654	2007.8971	1004.4522	2006.9131	1003.9602	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
19							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 23244.

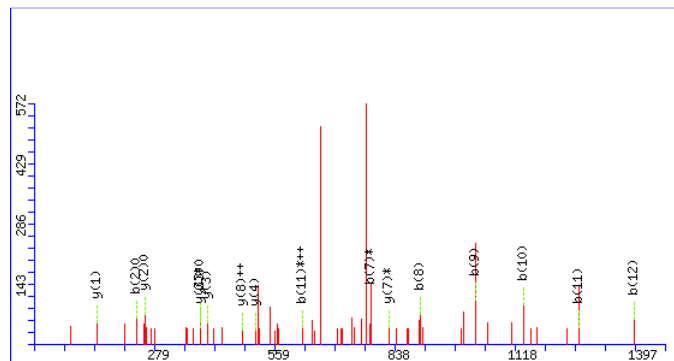
MS/MS Fragmentation of **KEGEEVPETQEK**:

Found in **IP100784739;IP100878852**

Title: 2.1.1.3774.9

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	129.1022	65.0548	112.0757	56.5415	0	0	K							13
2	258.1448	129.5761	241.1183	121.0628	240.1343	120.5708	E	1415.6536	708.3305	1398.6271	699.8172	1397.6431	699.3252	12
3	315.1663	158.0868	298.1397	149.5735	297.1557	149.0815	G	1286.6111	643.8092	1269.5845	635.2959	1268.6005	634.8039	11
4	444.2089	222.6081	427.1823	214.0948	426.1983	213.6028	E	1229.5896	615.2984	1212.5630	606.7852	1211.5790	606.2932	10
5	573.2515	287.1294	556.2249	278.6161	555.2409	278.1241	E	1100.5470	550.7771	1083.5204	542.2639	1082.5364	541.7719	9
6	702.2941	351.6507	685.2675	343.1374	684.2835	342.6454	E	971.5044	486.2558	954.4779	477.7426	953.4938	477.2506	8
7	801.3625	401.1849	784.3359	392.6716	783.3519	392.1796	V	842.4618	421.7345	825.4353	413.2213	824.4512	412.7293	7
8	898.4153	449.7113	881.3887	441.1980	880.4047	440.7060	P	743.3934	372.2003	726.3668	363.6871	725.3828	363.1951	6
9	1027.4578	514.2326	1010.4313	505.7193	1009.4473	505.2273	E	646.3406	323.6740	629.3141	315.1607	628.3301	314.6687	5
10	1140.5419	570.7746	1123.5154	562.2613	1122.5313	561.7693	I	517.2980	259.1527	500.2715	250.6394	499.2875	250.1474	4
11	1268.6005	634.8039	1251.5739	626.2906	1250.5899	625.7986	Q	404.2140	202.6106	387.1874	194.0974	386.2034	193.6053	3
12	1397.6431	699.3252	1380.6165	690.8119	1379.6325	690.3199	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 23355.

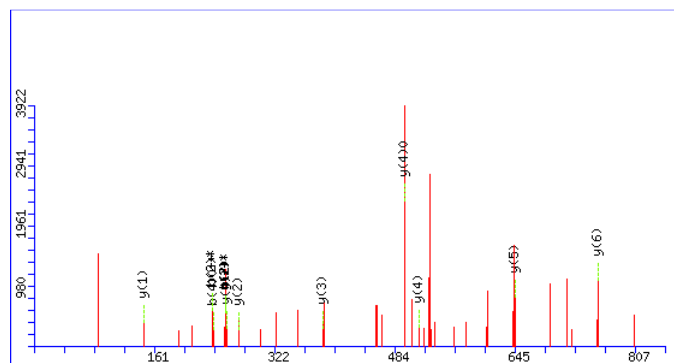
MS/MS Fragmentation of **KQLEEIQK**:

Found in **IP100217002**

Title: 2.1.1.2982.4

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_3.2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	129.1022	65.0548	112.0757	56.5415	0	0	K							8
2	257.1608	129.0840	240.1343	120.5708	0	0	Q	887.4833	444.2453	870.4567	435.7320	869.4727	435.2400	7
3	370.2449	185.6261	353.2183	177.1128	0	0	L	759.4247	380.2160	742.3981	371.7027	741.4141	371.2107	6
4	499.2875	250.1474	482.2609	241.6341	481.2769	241.1421	E	646.3406	323.6740	629.3141	315.1607	628.3301	314.6687	5
5	628.3301	314.6687	611.3035	306.1554	610.3195	305.6634	E	517.2980	259.1527	500.2715	250.6394	499.2875	250.1474	4
6	741.4141	371.2107	724.3876	362.6974	723.4036	362.2054	I	388.2554	194.6314	371.2289	186.1181	0	0	3
7	869.4727	435.2400	852.4462	426.7267	851.4621	426.2347	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
8							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 23375.

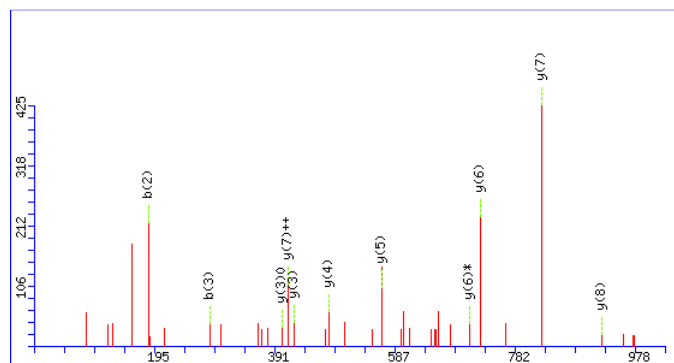
MS/MS Fragmentation of **SVVCSGFEEK: 57.021465@C:4**

Found in **IP100446798**

Title: 1.1.1.8391.9

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_2_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							9
2	187.1077	94.0575	0	0	169.0972	85.0522	V	925.4448	463.2260	908.4182	454.7128	907.4342	454.2207	8
3	286.1761	143.5917	0	0	268.1656	134.5864	V	826.3764	413.6918	809.3498	405.1785	808.3658	404.6865	7
4	446.2068	223.6070	0	0	428.1962	214.6017	C	727.3080	364.1576	710.2814	355.6443	709.2974	355.1523	6
5	533.2388	267.1230	0	0	515.2282	258.1178	S	567.2773	284.1423	550.2508	275.6290	549.2667	275.1370	5
6	590.2603	295.6338	0	0	572.2497	286.6285	G	480.2453	240.6263	463.2187	232.1130	462.2347	231.6210	4
7	737.3287	369.1680	0	0	719.3181	360.1627	F	423.2238	212.1155	406.1973	203.6023	405.2132	203.1103	3
8	866.3713	433.6893	0	0	848.3607	424.6840	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
9							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 23439.

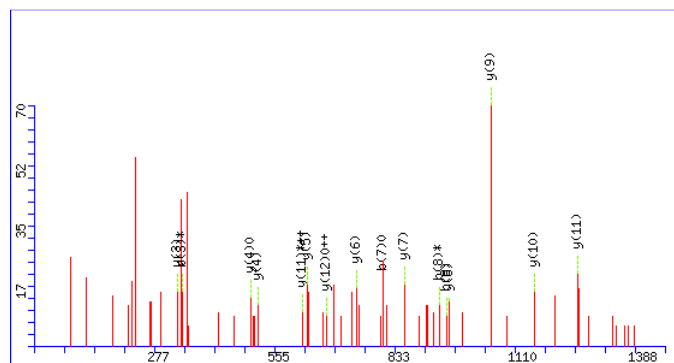
MS/MS Fragmentation of **NFPLEPQELTPTLLWGEK**:

Found in **IP100015658**

Title: 4.1.1.2154.4

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							20
2	262.1186	131.5629	245.0921	123.0497	0	0	F	2212.1900	1106.5986	2195.1635	1098.0854	2194.1794	1097.5934	19
3	359.1714	180.0893	342.1448	171.5761	0	0	P	2065.1216	1033.0644	2048.0950	1024.5512	2047.1110	1024.0591	18
4	472.2554	236.6314	455.2289	228.1181	0	0	L	1968.0688	984.5380	1951.0423	976.0248	1950.0583	975.5328	17
5	601.2980	301.1527	584.2715	292.6394	583.2875	292.1474	E	1854.9848	927.9960	1837.9582	919.4827	1836.9742	918.9907	16
6	698.3508	349.6790	681.3243	341.1658	680.3402	340.6738	P	1725.9422	863.4747	1708.9156	854.9614	1707.9316	854.4694	15
7	826.4094	413.7083	809.3828	405.1951	808.3988	404.7030	Q	1628.8894	814.9483	1611.8629	806.4351	1610.8788	805.9431	14
8	955.4520	478.2296	938.4254	469.7163	937.4414	469.2243	E	1500.8308	750.9190	1483.8043	742.4058	1482.8203	741.9138	13
9	1068.5360	534.7717	1051.5095	526.2584	1050.5255	525.7664	L	1371.7882	686.3978	1354.7617	677.8845	1353.7777	677.3925	12
10	1169.5837	585.2955	1152.5572	576.7822	1151.5732	576.2902	T	1258.7042	629.8557	1241.6776	621.3424	1240.6936	620.8504	11
11	1270.6314	635.8193	1253.6048	627.3061	1252.6208	626.8141	T	1157.6565	579.3319	1140.6299	570.8186	1139.6459	570.3266	10
12	1367.6842	684.3457	1350.6576	675.8324	1349.6736	675.3404	P	1056.6088	528.8080	1039.5823	520.2948	1038.5982	519.8028	9
13	1468.7318	734.8696	1451.7053	726.3563	1450.7213	725.8643	T	959.5560	480.2817	942.5295	471.7684	941.5455	471.2764	8
14	1581.8159	791.4116	1564.7894	782.8983	1563.8053	782.4063	L	858.5084	429.7578	841.4818	421.2445	840.4978	420.7525	7
15	1694.9000	847.9536	1677.8734	839.4403	1676.8894	838.9483	L	745.4243	373.2158	728.3978	364.7025	727.4137	364.2105	6
16	1807.9840	904.4957	1790.9575	895.9824	1789.9735	895.4904	L	632.3402	316.6738	615.3137	308.1605	614.3297	307.6685	5
17	1994.0633	997.5353	1977.0368	989.0220	1976.0528	988.5300	W	519.2562	260.1317	502.2296	251.6185	501.2456	251.1264	4
18	2051.0848	1026.0460	2034.0583	1017.5328	2033.0742	1017.0408	G	333.1769	167.0921	316.1503	158.5788	315.1663	158.0868	3
19	2180.1274	1090.5673	2163.1009	1082.0541	2162.1168	1081.5621	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
20							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 23685.

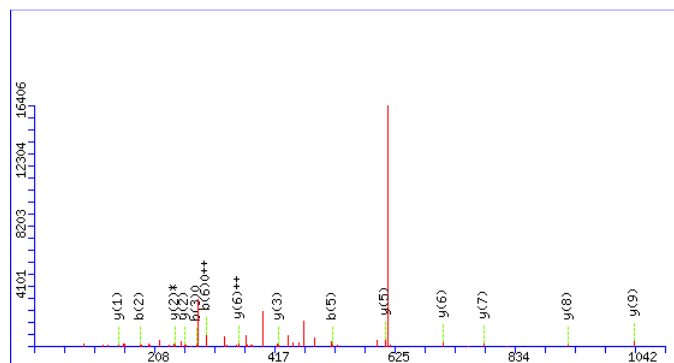
MS/MS Fragmentation of **ALDFAVGEYNK**:

Found in **IP100032293**

Title: 2.1.1.3488.7

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							11
2	185.1285	93.0679	0	0	0	0	L	1155.5681	578.2877	1138.5415	569.7744	1137.5575	569.2824	10
3	300.1554	150.5813	0	0	282.1448	141.5761	D	1042.4840	521.7456	1025.4575	513.2324	1024.4734	512.7404	9
4	447.2238	224.1155	0	0	429.2132	215.1103	F	927.4571	464.2322	910.4305	455.7189	909.4465	455.2269	8
5	518.2609	259.6341	0	0	500.2504	250.6288	A	780.3886	390.6980	763.3621	382.1847	762.3781	381.6927	7
6	617.3293	309.1683	0	0	599.3188	300.1630	V	709.3515	355.1794	692.3250	346.6661	691.3410	346.1741	6
7	674.3508	337.6790	0	0	656.3402	328.6738	G	610.2831	305.6452	593.2566	297.1319	592.2726	296.6399	5
8	803.3934	402.2003	0	0	785.3828	393.1951	E	553.2617	277.1345	536.2351	268.6212	535.2511	268.1292	4
9	966.4567	483.7320	0	0	948.4462	474.7267	Y	424.2191	212.6132	407.1925	204.0999	0	0	3
10	1080.4997	540.7535	1063.4731	532.2402	1062.4891	531.7482	N	261.1557	131.0815	244.1292	122.5682	0	0	2
11							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 23745.

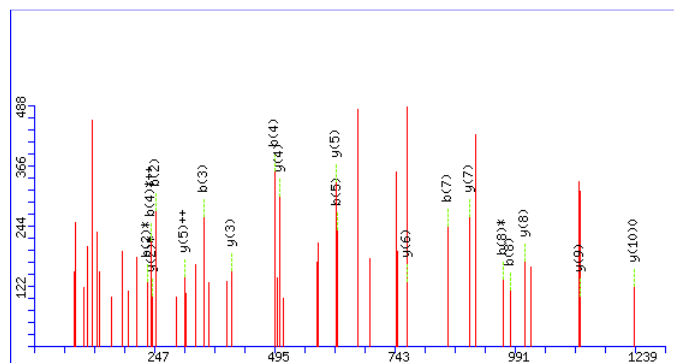
MS/MS Fragmentation of **HNVFQNDEFDVFSR**:

Found in **IP100549736;IP100892912;IP101015732**

Title: 3.1.1.1370.7

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	138.0662	69.5367	0	0	0	0	H							14
2	252.1091	126.5582	235.0826	118.0449	0	0	N	1616.7340	808.8706	1599.7074	800.3573	1598.7234	799.8653	13
3	351.1775	176.0924	334.1510	167.5791	0	0	V	1502.6910	751.8492	1485.6645	743.3359	1484.6805	742.8439	12
4	498.2459	249.6266	481.2194	241.1133	0	0	F	1403.6226	702.3149	1386.5961	693.8017	1385.6121	693.3097	11
5	628.3045	313.6559	609.2780	305.1426	0	0	Q	1256.5542	628.7807	1239.5277	620.2675	1238.5436	619.7755	10
6	740.3474	370.6774	723.3209	362.1641	0	0	N	1128.4956	564.7515	1111.4691	556.2382	1110.4851	555.7462	9
7	855.3744	428.1908	838.3478	419.6776	837.3638	419.1856	D	1014.4527	507.7300	997.4262	499.2167	996.4421	498.7247	8
8	984.4170	492.7121	967.3904	484.1989	966.4064	483.7068	E	899.4258	450.2165	882.3992	441.7032	881.4152	441.2112	7
9	1131.4854	566.2463	1114.4588	557.7331	1113.4748	557.2411	F	770.3832	385.6952	753.3566	377.1819	752.3726	376.6899	6
10	1246.5123	623.7598	1229.4858	615.2465	1228.5018	614.7545	D	623.3148	312.1610	606.2882	303.6477	605.3042	303.1557	5
11	1345.5808	673.2940	1328.5542	664.7807	1327.5702	664.2887	V	508.2878	254.6475	491.2613	246.1343	490.2772	245.6423	4
12	1492.6492	746.8282	1475.6226	738.3149	1474.6386	737.8229	F	409.2194	205.1133	392.1928	196.6001	391.2088	196.1081	3
13	1579.6812	790.3442	1562.6546	781.8310	1561.6706	781.3390	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
14							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 24587.

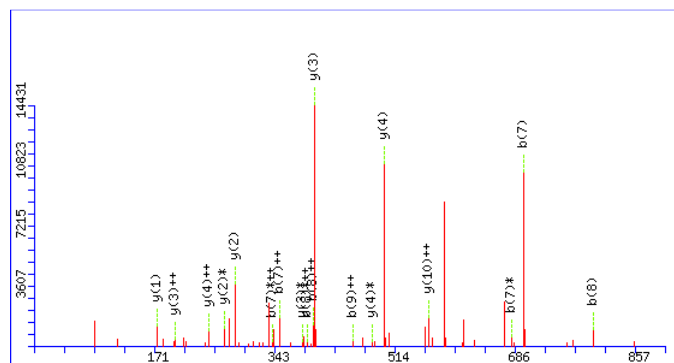
MS/MS Fragmentation of **AAKIVTDVLLR**:

Found in **IP100167547,IP100843754,IP100844073,IP100844236,IP100844349**

Title: 2.1.1.4387.2

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_3_2.mgf

ProteinPilot Peptide Confidence > 99%

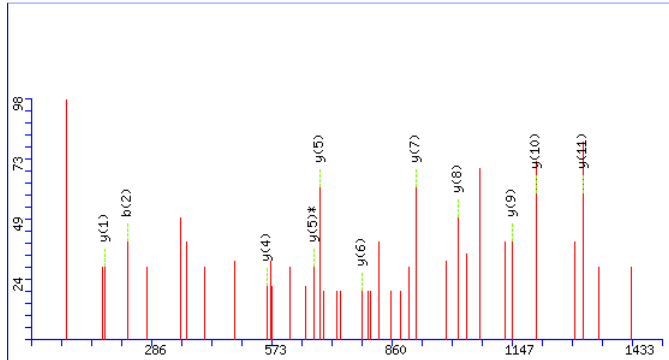


#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							11
2	143.0815	72.0444	0	0	0	0	A	1127.7147	564.3610	1110.6881	555.8477	1109.7041	555.3557	10
3	271.1765	136.0919	254.1499	127.5786	0	0	K	1056.6776	528.8424	1039.6510	520.3291	1038.6670	519.8371	9
4	384.2605	192.6339	367.2340	184.1206	0	0	I	928.5826	464.7949	911.5560	456.2817	910.5720	455.7897	8
5	483.3289	242.1681	466.3024	233.6548	0	0	V	815.4985	408.2529	798.4720	399.7396	797.4880	399.2476	7
6	584.3766	292.6920	567.3501	284.1787	566.3661	283.6867	T	716.4301	358.7187	699.4036	350.2054	698.4196	349.7134	6
7	699.4036	350.2054	682.3770	341.6921	681.3930	341.2001	D	615.3824	308.1949	598.3559	299.6816	597.3719	299.1896	5
8	798.4720	399.7396	781.4454	391.2264	780.4614	390.7343	V	500.3555	250.6814	483.3289	242.1681	0	0	4
9	911.5560	456.2817	894.5295	447.7684	893.5455	447.2764	L	401.2871	201.1472	384.2605	192.6339	0	0	3
10	1024.6401	512.8237	1007.6136	504.3104	1006.6295	503.8184	L	288.2030	144.6051	271.1765	136.0919	0	0	2
11							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 24718.

MS/MS Fragmentation of **NDAPEEAGEGCVAAILGETEVQQFLR: 57.021465@C:11**
 Found in **IP100644486;IP100791699;IP100908859**
 Title: 4.1.1.2008.10
 Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_4.mgf
 ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							26
2	230.0771	115.5422	213.0506	107.0289	212.0666	106.5369	D	2689.2774	1345.1423	2672.2508	1336.6291	2671.2668	1336.1371	25
3	301.1143	151.0608	284.0877	142.5475	283.1037	142.0555	A	2574.2504	1287.6289	2557.2239	1279.1156	2556.2399	1278.6236	24
4	398.1670	199.5872	381.1405	191.0739	380.1565	190.5819	P	2503.2133	1252.1103	2486.1868	1243.5970	2485.2028	1243.1050	23
5	527.2096	264.1084	510.1831	255.5952	509.1991	255.1032	E	2406.1606	1203.5839	2389.1340	1195.0706	2388.1500	1194.5786	22
6	656.2522	328.6297	639.2257	320.1165	638.2416	319.6245	E	2277.1180	1139.0626	2260.0914	1130.5494	2259.1074	1130.0573	21
7	727.2893	364.1483	710.2628	355.6350	709.2788	355.1430	A	2148.0754	1074.5413	2131.0488	1066.0281	2130.0648	1065.5360	20
8	784.3108	392.6590	767.2842	384.1458	766.3002	383.6537	G	2077.0383	1039.0228	2060.0117	1030.5095	2059.0277	1030.0175	19
9	913.3534	457.1803	896.3268	448.6671	895.3428	448.1750	E	2020.0168	1010.5120	2002.9903	1001.9988	2002.0062	1001.5068	18
10	970.3748	485.6911	953.3483	477.1778	952.3643	476.6858	G	1890.9742	945.9907	1873.9477	937.4775	1872.9636	936.9855	17
11	1130.4055	565.7064	1113.3789	557.1931	1112.3949	556.7011	C	1833.9527	917.4800	1816.9262	908.9667	1815.9422	908.4747	16
12	1229.4739	615.2406	1212.4474	606.7273	1211.4633	606.2353	V	1673.9221	837.4647	1656.8955	828.9514	1655.9115	828.4594	15
13	1300.5110	650.7591	1283.4845	642.2459	1282.5005	641.7539	A	1574.8537	787.9305	1557.8271	779.4172	1556.8431	778.9252	14
14	1371.5481	686.2777	1354.5216	677.7644	1353.5376	677.2724	A	1503.8166	752.4119	1486.7900	743.8986	1485.8060	743.4066	13
15	1484.6322	742.8197	1467.6057	734.3065	1466.6216	733.8145	I	1432.7795	716.8934	1415.7529	708.3801	1414.7689	707.8881	12
16	1597.7163	799.3618	1580.6897	790.8485	1579.7057	790.3565	L	1319.6954	660.3513	1302.6688	651.8381	1301.6848	651.3461	11
17	1654.7377	827.8725	1637.7112	819.3592	1636.7272	818.8672	G	1206.6113	603.8093	1189.5848	595.2960	1188.6008	594.8040	10
18	1783.7803	892.3938	1766.7538	883.8805	1765.7698	883.3885	E	1149.5899	575.2986	1132.5633	566.7853	1131.5793	566.2933	9
19	1884.8280	942.9176	1867.8015	934.4044	1866.8174	933.9124	T	1020.5473	510.7773	1003.5207	502.2640	1002.5367	501.7720	8
20	2013.8706	1007.4389	1996.8440	998.9257	1995.8600	998.4337	E	919.4996	460.2534	902.4730	451.7402	901.4890	451.2482	7
21	2112.9390	1056.9731	2095.9125	1048.4599	2094.9284	1047.9679	V	790.4570	395.7321	773.4305	387.2189	0	0	6
22	2240.9976	1121.0024	2223.9710	1112.4892	2222.9870	1111.9971	Q	691.3886	346.1979	674.3620	337.6847	0	0	5
23	2369.0562	1185.0317	2352.0296	1176.5184	2351.0456	1176.0264	Q	563.3300	282.1686	546.3035	273.6554	0	0	4
24	2516.1246	1258.5659	2499.0980	1250.0527	2498.1140	1249.5606	F	435.2714	218.1394	418.2449	209.6261	0	0	3
25	2629.2086	1315.1080	2612.1821	1306.5947	2611.1981	1306.1027	L	288.2030	144.6051	271.1765	136.0919	0	0	2
26							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 24975.

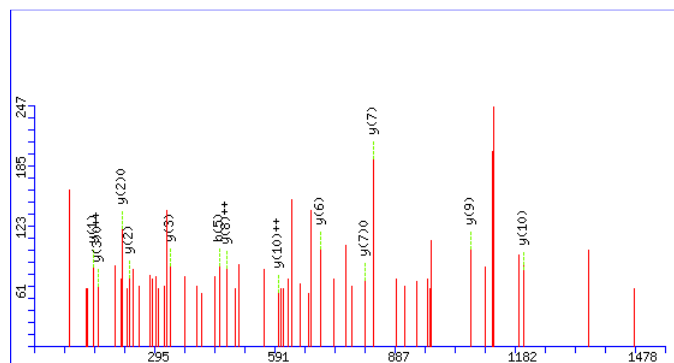
MS/MS Fragmentation of **SAGLEEIEQELTSK**:

Found in **IP100332095;IP100332097;IP100411606;IP100783452;IP100902682;IP100902702;IP100909771;IP100973013**

Title: 3.1.1.2503.7

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							14
2	159.0764	80.0418	0	0	141.0659	71.0366	A	1446.7322	723.8698	1429.7057	715.3565	1428.7217	714.8645	13
3	216.0979	108.5526	0	0	198.0873	99.5473	G	1375.6951	688.3512	1358.6686	679.8379	1357.6846	679.3459	12
4	329.1819	165.0946	0	0	311.1714	156.0893	L	1318.6737	659.8405	1301.6471	651.3272	1300.6631	650.8352	11
5	458.2245	229.6159	0	0	440.2140	220.6106	E	1205.5896	603.2984	1188.5630	594.7852	1187.5790	594.2932	10
6	587.2671	294.1372	0	0	569.2566	285.1319	E	1076.5470	538.7771	1059.5204	530.2639	1058.5364	529.7719	9
7	700.3512	350.6792	0	0	682.3406	341.6740	I	947.5044	474.2558	930.4779	465.7426	929.4938	465.2506	8
8	829.3938	415.2005	0	0	811.3832	406.1953	E	834.4203	417.7138	817.3938	409.2005	816.4098	408.7085	7
9	957.4524	479.2298	940.4258	470.7165	939.4418	470.2245	Q	705.3777	353.1925	688.3512	344.6792	687.3672	344.1872	6
10	1086.4950	543.7511	1069.4684	535.2378	1068.4844	534.7458	E	577.3192	289.1632	560.2926	280.6499	559.3086	280.1579	5
11	1199.5790	600.2932	1182.5525	591.7799	1181.5685	591.2879	L	448.2766	224.6419	431.2500	216.1287	430.2660	215.6366	4
12	1300.6267	650.8170	1283.6002	642.3037	1282.6161	641.8117	T	335.1925	168.0999	318.1660	159.5866	317.1819	159.0946	3
13	1387.6587	694.3330	1370.6322	685.8197	1369.6482	685.3277	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 25065.

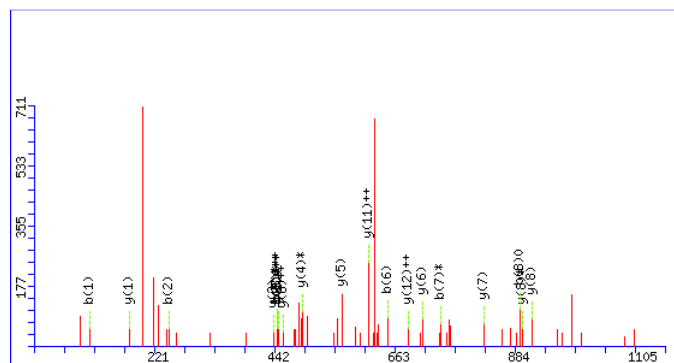
MS/MS Fragmentation of **TFSDISNFGAHQR**:

Found in **IP100301583;IP100395807;IP100642841**

Title: 2.1.1.2048.6

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							13
2	249.1234	125.0653	0	0	231.1128	116.0600	F	1378.6498	689.8286	1361.6233	681.3153	1360.6393	680.8233	12
3	336.1554	168.5813	0	0	318.1448	159.5761	S	1231.5814	616.2943	1214.5549	607.7811	1213.5709	607.2891	11
4	451.1823	226.0948	0	0	433.1718	217.0895	D	1144.5494	572.7783	1127.5228	564.2651	1126.5388	563.7731	10
5	564.2664	282.6368	0	0	546.2558	273.6316	I	1029.5225	515.2649	1012.4959	506.7516	1011.5119	506.2596	9
6	651.2984	326.1529	0	0	633.2879	317.1476	S	916.4384	458.7228	899.4118	450.2096	898.4278	449.7176	8
7	765.3414	383.1743	748.3148	374.6610	747.3308	374.1690	N	829.4064	415.2068	812.3798	406.6935	0	0	7
8	912.4098	456.7085	895.3832	448.1952	894.3992	447.7032	F	715.3634	358.1854	698.3369	349.6721	0	0	6
9	969.4312	485.2193	952.4047	476.7060	951.4207	476.2140	G	568.2950	284.6511	551.2685	276.1379	0	0	5
10	1040.4684	520.7378	1023.4418	512.2245	1022.4578	511.7325	A	511.2736	256.1404	494.2470	247.6271	0	0	4
11	1177.5273	589.2673	1160.5007	580.7540	1159.5167	580.2620	H	440.2364	220.6219	423.2099	212.1086	0	0	3
12	1305.5858	653.2966	1288.5593	644.7833	1287.5753	644.2913	Q	303.1775	152.0924	286.1510	143.5791	0	0	2
13							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 25363.

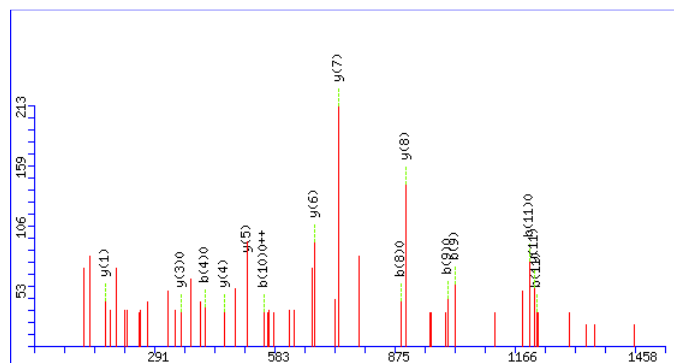
MS/MS Fragmentation of **EGDMPHHELLSLYGYGSTVR**:

Found in **IP100477825,IP100478280,IP100479032,IP100640919,IP100646985,IP100655630,IP100655783,IP100655845,IP100656079,IP100656089,IP100925194**

Title: 4.1.1.778.8

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							20
2	187.0713	94.0393	0	0	169.0608	85.0340	G	2108.0481	1054.5277	2091.0216	1046.0144	2090.0375	1045.5224	19
3	302.0983	151.5528	0	0	284.0877	142.5475	D	2051.0266	1026.0170	2034.0001	1017.5037	2033.0161	1017.0117	18
4	433.1388	217.0730	0	0	415.1282	208.0677	M	1935.9997	968.5035	1918.9731	959.9902	1917.9891	959.4982	17
5	530.1915	265.5994	0	0	512.1810	256.5941	P	1804.9592	902.9832	1787.9327	894.4700	1786.9486	893.9780	16
6	643.2756	322.1414	0	0	625.2650	313.1362	I	1707.9064	854.4569	1690.8799	845.9436	1689.8959	845.4516	15
7	780.3345	390.6709	0	0	762.3239	381.6656	H	1594.8224	797.9148	1577.7958	789.4016	1576.8118	788.9095	14
8	909.3771	455.1922	0	0	891.3665	446.1869	E	1457.7635	729.3854	1440.7369	720.8721	1439.7529	720.3801	13
9	1022.4612	511.7342	0	0	1004.4506	502.7289	L	1328.7209	664.8641	1311.6943	656.3508	1310.7103	655.8588	12
10	1135.5452	568.2762	0	0	1117.5347	559.2710	L	1215.6368	608.3220	1198.6103	599.8088	1197.6263	599.3168	11
11	1222.5773	611.7923	0	0	1204.5667	602.7870	S	1102.5528	551.7800	1085.5262	543.2667	1084.5422	542.7747	10
12	1335.6613	668.3343	0	0	1317.6507	659.3290	L	1015.5207	508.2640	998.4942	499.7507	997.5102	499.2587	9
13	1498.7246	749.8660	0	0	1480.7141	740.8607	Y	902.4367	451.7220	885.4101	443.2087	884.4261	442.7167	8
14	1555.7461	778.3767	0	0	1537.7355	769.3714	G	739.3733	370.1903	722.3468	361.6770	721.3628	361.1850	7
15	1718.8094	859.9084	0	0	1700.7989	850.9031	Y	682.3519	341.6796	665.3253	333.1663	664.3413	332.6743	6
16	1775.8309	888.4191	0	0	1757.8203	879.4138	G	519.2885	260.1479	502.2620	251.6346	501.2780	251.1426	5
17	1862.8629	931.9351	0	0	1844.8524	922.9298	S	462.2671	231.6372	445.2405	223.1239	444.2565	222.6319	4
18	1963.9106	982.4589	0	0	1945.9000	973.4537	T	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
19	2062.9790	1031.9931	0	0	2044.9685	1022.9879	V	274.1874	137.5973	257.1608	129.0840	0	0	2
20							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 25553.

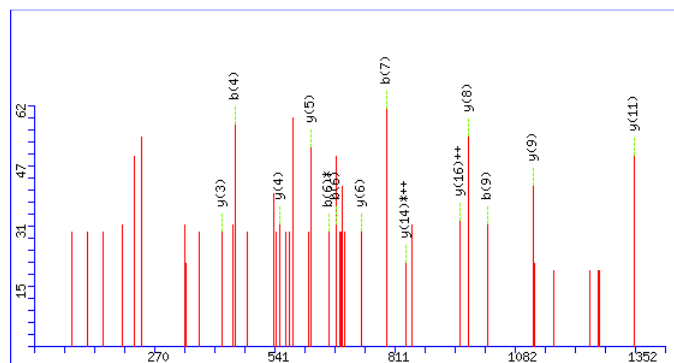
MS/MS Fragmentation of **NLPQNLLNIFNQIAEFEK**:

Found in **IP100550503**

Title: 5.1.1.804.5

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4.5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							18
2	228.1343	114.5708	211.1077	106.0575	0	0	L	2031.0910	1016.0491	2014.0644	1007.5358	2013.0804	1007.0438	17
3	325.1870	163.0972	308.1605	154.5839	0	0	P	1918.0069	959.5071	1900.9803	950.9938	1899.9963	950.5018	16
4	453.2456	227.1264	436.2191	218.6132	0	0	Q	1820.9541	910.9807	1803.9276	902.4674	1802.9436	901.9754	15
5	567.2885	284.1479	550.2620	275.6346	0	0	N	1692.8955	846.9514	1675.8690	838.4381	1674.8850	837.9461	14
6	680.3726	340.6899	663.3461	332.1767	0	0	L	1578.8526	789.9299	1561.8261	781.4167	1560.8421	780.9247	13
7	793.4567	397.2320	776.4301	388.7187	0	0	L	1465.7686	733.3879	1448.7420	724.8746	1447.7580	724.3826	12
8	907.4996	454.2534	890.4730	445.7402	0	0	N	1352.6845	676.8459	1335.6579	668.3326	1334.6739	667.8406	11
9	1020.5837	510.7955	1003.5571	502.2822	0	0	I	1238.6416	619.8244	1221.6150	611.3111	1220.6310	610.8191	10
10	1167.6521	584.3297	1150.6255	575.8164	0	0	F	1125.5575	563.2824	1108.5310	554.7691	1107.5469	554.2771	9
11	1281.6950	641.3511	1264.6684	632.8379	0	0	N	978.4891	489.7482	961.4625	481.2349	960.4785	480.7429	8
12	1409.7536	705.3804	1392.7270	696.8672	0	0	Q	864.4462	432.7267	847.4196	424.2134	846.4356	423.7214	7
13	1522.8376	761.9225	1505.8111	753.4092	0	0	I	736.3876	368.6974	719.3610	360.1842	718.3770	359.6921	6
14	1593.8748	797.4410	1576.8482	788.9277	0	0	A	623.3035	312.1554	606.2770	303.6421	605.2930	303.1501	5
15	1722.9173	861.9623	1705.8908	853.4490	1704.9068	852.9570	E	552.2664	276.6368	535.2399	268.1236	534.2558	267.6316	4
16	1869.9858	935.4965	1852.9592	926.9832	1851.9752	926.4912	F	423.2238	212.1155	406.1973	203.6023	405.2132	203.1103	3
17	1999.0284	1000.0178	1982.0018	991.5045	1981.0178	991.0125	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
18							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 25719.

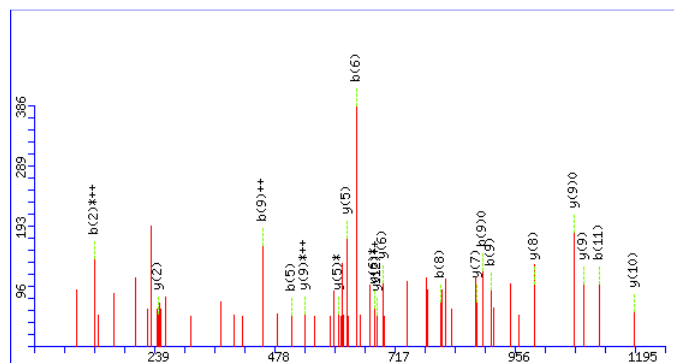
MS/MS Fragmentation of **RVSGLEPATVDWAFDLTK**:

Found in **IP100328847;IP100908915;IP100910984;IP101013870**

Title: 3.1.1.3261.10

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	157.1084	79.0578	140.0818	70.5446	0	0	R							18
2	256.1768	128.5920	239.1503	120.0788	0	0	V	1848.9378	924.9725	1831.9113	916.4593	1830.9272	915.9673	17
3	343.2088	172.1081	326.1823	163.5948	325.1983	163.1028	S	1749.8694	875.4383	1732.8428	866.9251	1731.8588	866.4331	16
4	400.2303	200.6188	383.2037	192.1055	382.2197	191.6135	G	1662.8374	831.9223	1645.8108	823.4090	1644.8268	822.9170	15
5	513.3144	257.1608	496.2878	248.6475	495.3038	248.1555	L	1605.8159	803.4116	1588.7894	794.8983	1587.8053	794.4063	14
6	642.3570	321.6821	625.3304	313.1688	624.3464	312.6768	E	1492.7318	746.8696	1475.7053	738.3563	1474.7213	737.8643	13
7	739.4097	370.2085	722.3832	361.6952	721.3991	361.2032	P	1363.6892	682.3483	1346.6627	673.8350	1345.6787	673.3430	12
8	810.4468	405.7271	793.4203	397.2138	792.4363	396.7218	A	1266.6365	633.8219	1249.6099	625.3086	1248.6259	624.8166	11
9	911.4945	456.2509	894.4680	447.7376	893.4839	447.2456	T	1195.5994	598.3033	1178.5728	589.7900	1177.5888	589.2980	10
10	1010.5629	505.7851	993.5364	497.2718	992.5524	496.7798	V	1094.5517	547.7795	1077.5251	539.2662	1076.5411	538.7742	9
11	1125.5899	563.2986	1108.5633	554.7853	1107.5793	554.2933	D	995.4833	498.2453	978.4567	489.7320	977.4727	489.2400	8
12	1311.6692	656.3382	1294.6426	647.8250	1293.6586	647.3329	W	880.4563	440.7318	863.4298	432.2185	862.4458	431.7265	7
13	1382.7063	691.8568	1365.6797	683.3435	1364.6957	682.8515	A	694.3770	347.6921	677.3505	339.1789	676.3665	338.6869	6
14	1529.7747	765.3910	1512.7482	756.8777	1511.7641	756.3857	F	623.3399	312.1736	606.3134	303.6603	605.3293	303.1683	5
15	1644.8016	822.9045	1627.7751	814.3912	1626.7911	813.8992	D	476.2715	238.6394	459.2449	230.1261	458.2609	229.6341	4
16	1757.8857	879.4465	1740.8592	870.9332	1739.8751	870.4412	L	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
17	1858.9334	929.9703	1841.9068	921.4571	1840.9228	920.9651	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
18							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 25875.

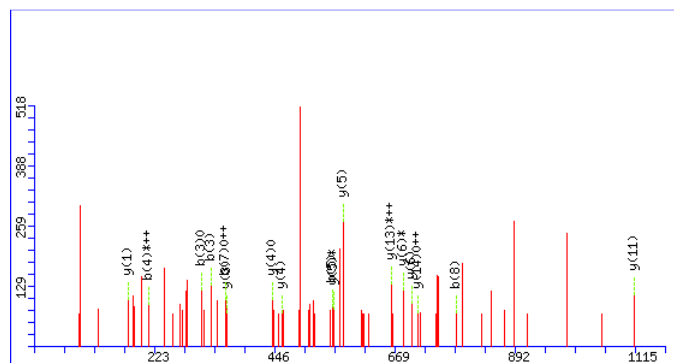
MS/MS Fragmentation of **LTNILDGGAQNTALR**:

Found in **IP100293125;IP100796345;IP100797502**

Title: 2.1.1.3016.6

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_3.2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							15
2	215.1390	108.0731	0	0	197.1285	99.0679	T	1443.7550	722.3812	1426.7285	713.8679	1425.7445	713.3759	14
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	N	1342.7074	671.8573	1325.6808	663.3440	1324.6968	662.8520	13
4	442.2660	221.6366	425.2395	213.1234	424.2554	212.6314	I	1228.6644	614.8359	1211.6379	606.3226	1210.6539	605.8306	12
5	555.3501	278.1787	538.3235	269.6654	537.3395	269.1734	L	1115.5804	558.2938	1098.5538	549.7805	1097.5698	549.2885	11
6	670.3770	335.6921	653.3505	327.1789	652.3665	326.6869	D	1002.4963	501.7518	985.4697	493.2385	984.4857	492.7465	10
7	727.3985	364.2029	710.3719	355.6896	709.3879	355.1976	G	887.4694	444.2383	870.4428	435.7250	869.4588	435.2330	9
8	784.4199	392.7136	767.3934	384.2003	766.4094	383.7083	G	830.4479	415.7276	813.4213	407.2143	812.4373	406.7223	8
9	855.4571	428.2322	838.4305	419.7189	837.4465	419.2269	A	773.4264	387.2169	756.3999	378.7036	755.4159	378.2116	7
10	983.5156	492.2615	966.4891	483.7482	965.5051	483.2562	Q	702.3893	351.6983	685.3628	343.1850	684.3787	342.6930	6
11	1097.5586	549.2829	1080.5320	540.7696	1079.5480	540.2776	N	574.3307	287.6690	557.3042	279.1557	556.3202	278.6637	5
12	1198.6062	599.8068	1181.5797	591.2935	1180.5957	590.8015	T	460.2878	230.6475	443.2613	222.1343	442.2772	221.6423	4
13	1269.6434	635.3253	1252.6168	626.8120	1251.6328	626.3200	A	359.2401	180.1237	342.2136	171.6104	0	0	3
14	1382.7274	691.8673	1365.7009	683.3541	1364.7169	682.8621	L	288.2030	144.6051	271.1765	136.0919	0	0	2
15							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 25920.

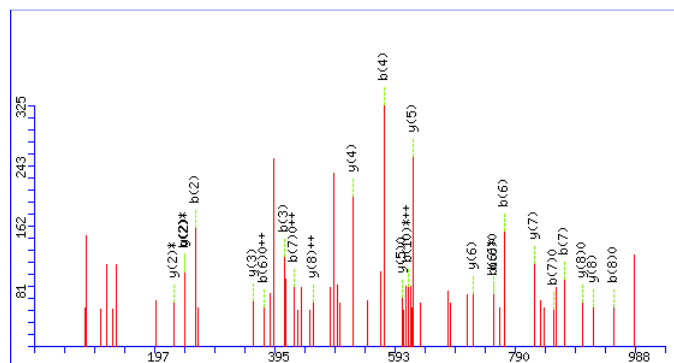
MS/MS Fragmentation of **HQFYPTVVYLTK**:

Found in **IP100166996;IP100172510;IP100396584;IP100902504;IP100977251;IP100977943;IP100983104**

Title: 2.1.1.3990.4

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	138.0662	69.5367	0	0	0	0	H							12
2	266.1248	133.5660	249.0982	125.0527	0	0	Q	1358.7355	679.8714	1341.7089	671.3581	1340.7249	670.8661	11
3	413.1932	207.1002	396.1666	198.5870	0	0	F	1230.6769	615.8421	1213.6503	607.3288	1212.6663	606.8368	10
4	576.2565	288.6319	559.2300	280.1186	0	0	Y	1083.6085	542.3079	1066.5819	533.7946	1065.5979	533.3026	9
5	673.3093	337.1583	656.2827	328.6450	0	0	P	920.5451	460.7762	903.5186	452.2629	902.5346	451.7709	8
6	774.3570	387.6821	757.3304	379.1688	756.3464	378.6768	T	823.4924	412.2498	806.4658	403.7366	805.4818	403.2445	7
7	873.4254	437.2163	856.3988	428.7030	855.4148	428.2110	V	722.4447	361.7260	705.4182	353.2127	704.4341	352.7207	6
8	972.4938	486.7505	955.4672	478.2373	954.4832	477.7452	V	623.3763	312.1918	606.3497	303.6785	605.3657	303.1865	5
9	1135.5571	568.2822	1118.5306	559.7689	1117.5465	559.2769	Y	524.3079	262.6576	507.2813	254.1443	506.2973	253.6523	4
10	1248.6412	624.8242	1231.6146	616.3109	1230.6306	615.8189	L	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
11	1349.6889	675.3481	1332.6623	666.8348	1331.6783	666.3428	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 26047.

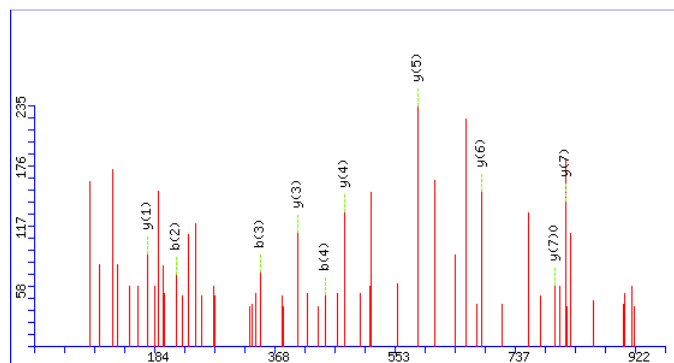
MS/MS Fragmentation of **AFEVIATER**:

Found in **IP100179452;IP100180725;IP100332991;IP100552577;IP100941084;IP101014558;IP101018277**

Title: 2.1.1.1225.8

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							9
2	219.1128	110.0600	0	0	0	0	F	964.5098	482.7585	947.4833	474.2453	946.4993	473.7533	8
3	348.1554	174.5813	0	0	330.1448	165.5761	E	817.4414	409.2243	800.4149	400.7111	799.4308	400.2191	7
4	447.2238	224.1155	0	0	429.2132	215.1103	V	688.3988	344.7030	671.3723	336.1898	670.3883	335.6978	6
5	560.3079	280.6576	0	0	542.2973	271.6523	I	589.3304	295.1688	572.3039	286.6556	571.3198	286.1636	5
6	631.3450	316.1761	0	0	613.3344	307.1709	A	476.2463	238.6268	459.2198	230.1135	458.2358	229.6215	4
7	732.3927	366.7000	0	0	714.3821	357.6947	T	405.2092	203.1082	388.1827	194.5950	387.1987	194.1030	3
8	861.4353	431.2213	0	0	843.4247	422.2160	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
9							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 26309.

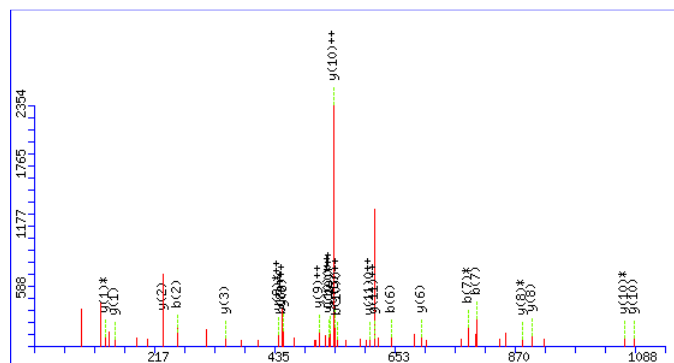
MS/MS Fragmentation of **LFGEVTRPTNSK**:

Found in **IP100654654,IP100945880,IP101010059**

Title: 1.1.1.8931.5

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							12
2	261.1598	131.0835	0	0	0	0	F	1235.6379	618.3226	1218.6113	609.8093	1217.6273	609.3173	11
3	318.1812	159.5942	0	0	0	0	G	1088.5695	544.7884	1071.5429	536.2751	1070.5589	535.7831	10
4	447.2238	224.1155	0	0	429.2132	215.1103	E	1031.5480	516.2776	1014.5214	507.7644	1013.5374	507.2724	9
5	546.2922	273.6498	0	0	528.2817	264.6445	V	902.5054	451.7563	885.4789	443.2431	884.4948	442.7511	8
6	647.3399	324.1736	0	0	629.3293	315.1683	T	803.4370	402.2221	786.4104	393.7089	785.4264	393.2169	7
7	803.4410	402.2241	786.4145	393.7109	785.4305	393.2189	R	702.3893	351.6983	685.3628	343.1850	684.3787	342.6930	6
8	900.4938	450.7505	883.4672	442.2373	882.4832	441.7452	P	546.2882	273.6477	529.2617	265.1345	528.2776	264.6425	5
9	1001.5415	501.2744	984.5149	492.7611	983.5309	492.2691	T	449.2354	225.1214	432.2089	216.6081	431.2249	216.1161	4
10	1115.5844	558.2958	1098.5578	549.7826	1097.5738	549.2905	N	348.1878	174.5975	331.1612	166.0842	330.1772	165.5922	3
11	1202.6164	601.8118	1185.5899	593.2986	1184.6058	592.8066	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 26322.

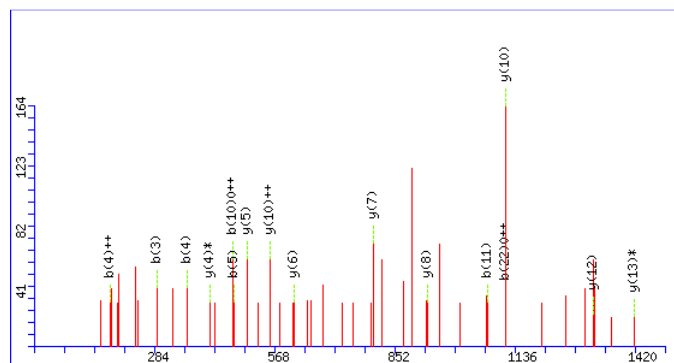
MS/MS Fragmentation of **FAAALAQDLGLIPSQWLAVADK: 0.984016@Q:7**

Found in **IP100152739,IP100917437**

Title: 4.1.1.3039.8

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							23
2	219.1128	110.0600	0	0	0	0	A	2249.2176	1125.1124	2232.1911	1116.5992	2231.2070	1116.1072	22
3	290.1499	145.5786	0	0	0	0	A	2178.1805	1089.5939	2161.1539	1081.0806	2160.1699	1080.5886	21
4	361.1870	181.0972	0	0	0	0	A	2107.1434	1054.0753	2090.1168	1045.5621	2089.1328	1045.0700	20
5	474.2711	237.6392	0	0	0	0	L	2036.1063	1018.5568	2019.0797	1010.0435	2018.0957	1009.5515	19
6	545.3082	273.1577	0	0	0	0	A	1923.0222	962.0147	1905.9957	953.5015	1905.0116	953.0095	18
7	674.3508	337.6790	657.3243	329.1658	0	0	Q	1851.9851	926.4962	1834.9585	917.9829	1833.9745	917.4909	17
8	789.3777	395.1925	772.3512	386.6792	771.3672	386.1872	D	1722.9425	861.9749	1705.9159	853.4616	1704.9319	852.9696	16
9	902.4618	451.7345	885.4353	443.2213	884.4512	442.7293	L	1607.9156	804.4614	1590.8890	795.9481	1589.9050	795.4561	15
10	959.4833	480.2453	942.4567	471.7320	941.4727	471.2400	G	1494.8315	747.9194	1477.8049	739.4061	1476.8209	738.9141	14
11	1072.5673	536.7873	1055.5408	528.2740	1054.5568	527.7820	L	1437.8100	719.4087	1420.7835	710.8954	1419.7995	710.4034	13
12	1169.6201	585.3137	1152.5936	576.8004	1151.6095	576.3084	P	1324.7260	662.8666	1307.6994	654.3533	1306.7154	653.8613	12
13	1282.7042	641.8557	1265.6776	633.3424	1264.6936	632.8504	I	1227.6732	614.3402	1210.6467	605.8270	1209.6626	605.3350	11
14	1379.7569	690.3821	1362.7304	681.8688	1361.7464	681.3768	P	1114.5891	557.7982	1097.5626	549.2849	1096.5786	548.7929	10
15	1466.7890	733.8981	1449.7624	725.3848	1448.7784	724.8928	S	1017.5364	509.2718	1000.5098	500.7585	999.5258	500.2665	9
16	1594.8475	797.9274	1577.8210	789.4141	1576.8370	788.9221	Q	930.5043	465.7558	913.4778	457.2425	912.4938	456.7505	8
17	1780.9269	890.9671	1763.9003	882.4538	1762.9163	881.9618	W	802.4458	401.7265	785.4192	393.2132	784.4352	392.7212	7
18	1894.0109	947.5091	1876.9844	938.9958	1876.0003	938.5038	L	616.3665	308.6869	599.3399	300.1736	598.3559	299.6816	6
19	1965.0480	983.0277	1948.0215	974.5144	1947.0375	974.0224	A	503.2824	252.1448	486.2558	243.6316	485.2718	243.1396	5
20	2064.1164	1032.5619	2047.0899	1024.0486	2046.1059	1023.5566	V	432.2453	216.6263	415.2187	208.1130	414.2347	207.6210	4
21	2135.1536	1068.0804	2118.1270	1059.5671	2117.1430	1059.0751	A	333.1769	167.0921	316.1503	158.5788	315.1663	158.0868	3
22	2250.1805	1125.5939	2233.1539	1117.0806	2232.1699	1116.5886	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
23							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 26478.

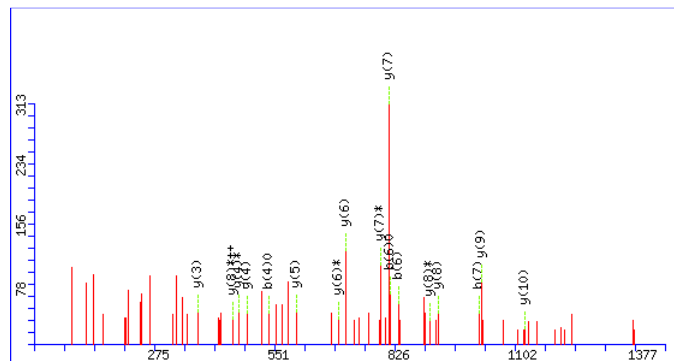
MS/MS Fragmentation of **EYYTFMWVTLPIDLNK**:

Found in **IP100908968;IP100910883;IP100963985;IP100965684;IP100966087;IP100966998**

Title: 4.1.1.3457.4

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120214ry¥120214ry_aHDF1419-P10_4.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							17
2	293.1132	147.0602	0	0	275.1026	138.0550	Y	2018.0092	1009.5082	2000.9826	1000.9950	1999.9986	1000.5030	16
3	456.1765	228.5919	0	0	438.1660	219.5866	Y	1854.9459	927.9766	1837.9193	919.4633	1836.9353	918.9713	15
4	557.2242	279.1157	0	0	539.2136	270.1105	T	1691.8825	846.4449	1674.8560	837.9316	1673.8720	837.4396	14
5	704.2926	352.6499	0	0	686.2821	343.6447	F	1590.8349	795.9211	1573.8083	787.4078	1572.8243	786.9158	13
6	835.3331	418.1702	0	0	817.3225	409.1649	M	1443.7664	722.3869	1426.7399	713.8736	1425.7559	713.3816	12
7	1021.4124	511.2098	0	0	1003.4019	502.2046	W	1312.7260	656.8666	1295.6994	648.3533	1294.7154	647.8613	11
8	1120.4808	560.7441	0	0	1102.4703	551.7388	V	1126.6466	563.8270	1109.6201	555.3137	1108.6361	554.8217	10
9	1221.5285	611.2679	0	0	1203.5179	602.2626	T	1027.5782	514.2928	1010.5517	505.7795	1009.5677	505.2875	9
10	1334.6126	667.8099	0	0	1316.6020	658.8046	L	926.5306	463.7689	909.5040	455.2556	908.5200	454.7636	8
11	1431.6653	716.3363	0	0	1413.6548	707.3310	P	813.4465	407.2269	796.4199	398.7136	795.4359	398.2216	7
12	1544.7494	772.8783	0	0	1526.7388	763.8731	I	716.3937	358.7005	699.3672	350.1872	698.3832	349.6952	6
13	1659.7763	830.3918	0	0	1641.7658	821.3865	D	603.3097	302.1585	586.2831	293.6452	585.2991	293.1532	5
14	1772.8604	886.9338	0	0	1754.8498	877.9286	L	488.2827	244.6450	471.2562	236.1317	0	0	4
15	1886.9033	943.9553	1869.8768	935.4420	1868.8928	934.9500	N	375.1987	188.1030	358.1721	179.5897	0	0	3
16	2000.9463	1000.9768	1983.9197	992.4635	1982.9357	991.9715	N	261.1557	131.0815	244.1292	122.5682	0	0	2
17							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 26702.

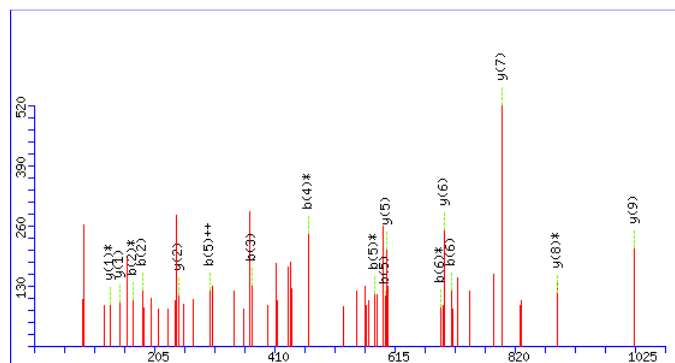
MS/MS Fragmentation of **GQWINLPVLQLTK**:

Found in **IP100024143;IP100747361;IP101021618;IP101022961**

Title: 3.1.1.4390.2

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							13
2	186.0873	93.5473	169.0608	85.0340	0	0	Q	1452.8573	726.9323	1435.8308	718.4190	1434.8467	717.9270	12
3	372.1666	186.5870	355.1401	178.0737	0	0	W	1324.7987	662.9030	1307.7722	654.3897	1306.7882	653.8977	11
4	485.2507	243.1290	468.2241	234.6157	0	0	I	1138.7194	569.8633	1121.6929	561.3501	1120.7089	560.8581	10
5	599.2936	300.1504	582.2671	291.6372	0	0	N	1025.6354	513.3213	1008.6088	504.8080	1007.6248	504.3160	9
6	712.3777	356.6925	695.3511	348.1792	0	0	L	911.5924	456.2999	894.5659	447.7866	893.5819	447.2946	8
7	809.4305	405.2189	792.4039	396.7056	0	0	P	798.5084	399.7578	781.4818	391.2445	780.4978	390.7525	7
8	908.4989	454.7531	891.4723	446.2398	0	0	V	701.4556	351.2314	684.4291	342.7182	683.4450	342.2262	6
9	1021.5829	511.2951	1004.5564	502.7818	0	0	L	602.3872	301.6972	585.3606	293.1840	584.3766	292.6920	5
10	1149.6415	575.3244	1132.6150	566.8111	0	0	Q	489.3031	245.1552	472.2766	236.6419	471.2926	236.1499	4
11	1262.7256	631.8664	1245.6990	623.3531	0	0	L	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
12	1363.7732	682.3903	1346.7467	673.8770	1345.7627	673.3850	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 26752.

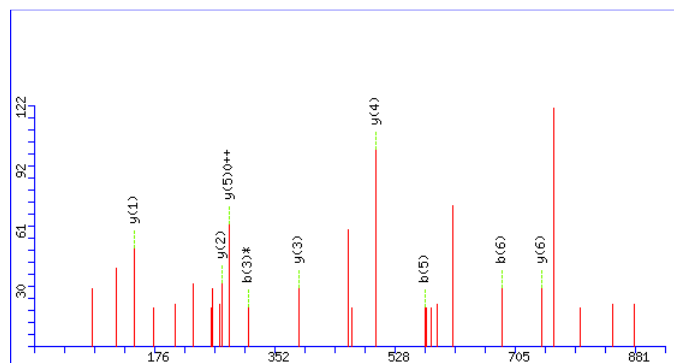
MS/MS Fragmentation of **NTDRSLLEK**:

Found in **IP100008581**

Title: 4.1.1.2502.3

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							9
2	216.0979	108.5526	199.0713	100.0393	198.0873	99.5473	T	961.5313	481.2693	944.5047	472.7560	943.5207	472.2640	8
3	331.1248	166.0661	314.0983	157.5528	313.1143	157.0608	D	860.4836	430.7454	843.4571	422.2322	842.4730	421.7402	7
4	487.2259	244.1166	470.1994	235.6033	469.2154	235.1113	R	745.4567	373.2320	728.4301	364.7187	727.4461	364.2267	6
5	574.2580	287.6326	557.2314	279.1193	556.2474	278.6273	S	589.3556	295.1814	572.3290	286.6681	571.3450	286.1761	5
6	687.3420	344.1747	670.3155	335.6614	669.3315	335.1694	L	502.3235	251.6654	485.2970	243.1521	484.3130	242.6601	4
7	800.4261	400.7167	783.3995	392.2034	782.4155	391.7114	L	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
8	929.4687	465.2380	912.4421	456.7247	911.4581	456.2327	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
9							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 26777.

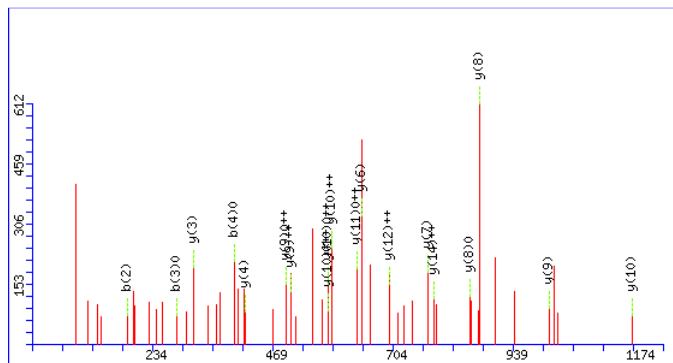
MS/MS Fragmentation of **EGLLLYHTENNVGLK**:

Found in **IPI00027437,IPI00880170**

Title: 2.1.1.3519.4

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							15
2	187.0713	94.0393	0	0	169.0608	85.0340	G	1570.8588	785.9330	1553.8322	777.4197	1552.8482	776.9277	14
3	300.1554	150.5813	0	0	282.1448	141.5761	L	1513.8373	757.4223	1496.8108	748.9090	1495.8267	748.4170	13
4	413.2395	207.1234	0	0	395.2289	198.1181	L	1400.7532	700.8803	1383.7267	692.3670	1382.7427	691.8750	12
5	526.3235	263.6654	0	0	508.3130	254.6601	L	1287.6692	644.3382	1270.6426	635.8250	1269.6586	635.3329	11
6	689.3869	345.1971	0	0	671.3763	336.1918	Y	1174.5851	587.7962	1157.5586	579.2829	1156.5745	578.7909	10
7	826.4458	413.7265	0	0	808.4352	404.7212	H	1011.5218	506.2645	994.4952	497.7513	993.5112	497.2592	9
8	927.4934	464.2504	0	0	909.4829	455.2451	T	874.4629	437.7351	857.4363	429.2218	856.4523	428.7298	8
9	1056.5360	528.7717	0	0	1038.5255	519.7664	E	773.4152	387.2112	756.3886	378.6980	755.4046	378.2060	7
10	1170.5790	585.7931	1153.5524	577.2798	1152.5684	576.7878	N	644.3726	322.6899	627.3461	314.1767	0	0	6
11	1284.6219	642.8146	1267.5953	634.3013	1266.6113	633.8093	N	530.3297	265.6685	513.3031	257.1552	0	0	5
12	1383.6903	692.3488	1366.6638	683.8355	1365.6797	683.3435	V	416.2867	208.6470	399.2602	200.1337	0	0	4
13	1440.7118	720.8595	1423.6852	712.3462	1422.7012	711.8542	G	317.2183	159.1128	300.1918	150.5995	0	0	3
14	1553.7958	777.4016	1536.7693	768.8883	1535.7853	768.3963	L	260.1969	130.6021	243.1703	122.0888	0	0	2
15							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 26852.

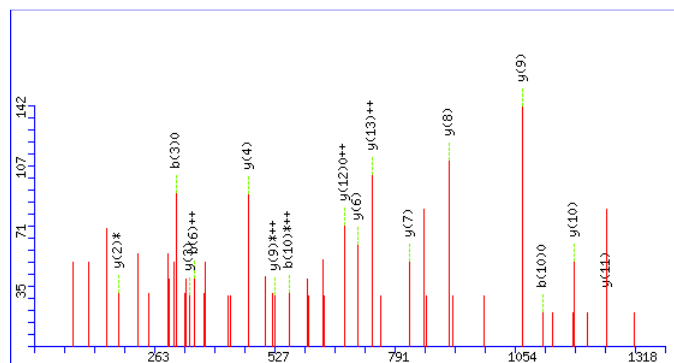
MS/MS Fragmentation of **GSWVFQALCSILEEHGK: 57.021465@C:9**

Found in **IP100216675;IP100221307;IP100910107;IP101010205**

Title: 4.1.1.3242.5

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120201ry¥120201ry_aHDF1388-P9_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							17
2	145.0608	73.0340	0	0	127.0502	64.0287	S	1903.9371	952.4722	1886.9105	943.9589	1885.9265	943.4669	16
3	331.1401	166.0737	0	0	313.1295	157.0684	W	1816.9051	908.9562	1799.8785	900.4429	1798.8945	899.9509	15
4	478.2085	239.6079	0	0	460.1979	230.6026	F	1630.8258	815.9165	1613.7992	807.4032	1612.8152	806.9112	14
5	577.2769	289.1421	0	0	559.2663	280.1368	V	1483.7573	742.3823	1466.7308	733.8690	1465.7468	733.3770	13
6	705.3355	353.1714	688.3089	344.6581	687.3249	344.1661	Q	1384.6889	692.8481	1367.6624	684.3348	1366.6784	683.8428	12
7	776.3726	388.6899	759.3461	380.1767	758.3620	379.6847	A	1256.6303	628.8188	1239.6038	620.3055	1238.6198	619.8135	11
8	889.4567	445.2320	872.4301	436.7187	871.4461	436.2267	L	1185.5932	593.3003	1168.5667	584.7870	1167.5827	584.2950	10
9	1049.4873	525.2473	1032.4608	516.7340	1031.4768	516.2420	C	1072.5092	536.7582	1055.4826	528.2449	1054.4986	527.7529	9
10	1136.5193	568.7633	1119.4928	560.2500	1118.5088	559.7580	S	912.4785	456.7429	895.4520	448.2296	894.4680	447.7376	8
11	1249.6034	625.3053	1232.5769	616.7921	1231.5928	616.3001	I	825.4465	413.2269	808.4199	404.7136	807.4359	404.2216	7
12	1362.6875	681.8474	1345.6609	673.3341	1344.6769	672.8421	L	712.3624	356.6849	695.3359	348.1716	694.3519	347.6796	6
13	1491.7301	746.3687	1474.7035	737.8554	1473.7195	737.3634	E	599.2784	300.1428	582.2518	291.6295	581.2678	291.1375	5
14	1620.7727	810.8900	1603.7461	802.3767	1602.7621	801.8847	E	470.2358	235.6215	453.2092	227.1082	452.2252	226.6162	4
15	1757.8316	879.4194	1740.8050	870.9061	1739.8210	870.4141	H	341.1932	171.1002	324.1666	162.5870	0	0	3
16	1814.8530	907.9302	1797.8265	899.4169	1796.8425	898.9249	G	204.1343	102.5708	187.1077	94.0575	0	0	2
17							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 26858.

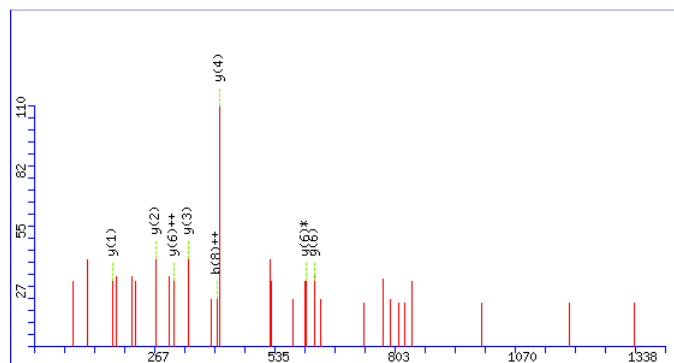
MS/MS Fragmentation of **GSACRLPAAPR: 57.021465@C:4**

Found in **IP100892939;IP100937866**

Title: 5.1.1.620.2

Data file: Y:\TT5600(CiRA1)\2012-01\120124ry\120124ry_414C2-43_1_5.mgf

ProteinPilot Peptide Confidence > 99%

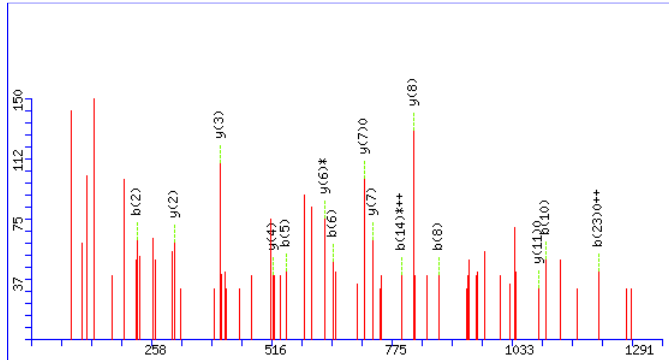


#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							11
2	145.0608	73.0340	0	0	127.0502	64.0287	S	1098.5837	549.7955	1081.5571	541.2822	1080.5731	540.7902	10
3	216.0979	108.5526	0	0	198.0873	99.5473	A	1011.5516	506.2795	994.5251	497.7662	0	0	9
4	376.1285	188.5679	0	0	358.1180	179.5626	C	940.5145	470.7609	923.4880	462.2476	0	0	8
5	532.2296	266.6185	515.2031	258.1052	514.2191	257.6132	R	780.4839	390.7456	763.4573	382.2323	0	0	7
6	645.3137	323.1605	628.2872	314.6472	627.3031	314.1552	L	624.3828	312.6950	607.3562	304.1817	0	0	6
7	742.3665	371.6869	725.3399	363.1736	724.3559	362.6816	P	511.2987	256.1530	494.2722	247.6397	0	0	5
8	813.4036	407.2054	796.3770	398.6922	795.3930	398.2001	A	414.2459	207.6266	397.2194	199.1133	0	0	4
9	884.4407	442.7240	867.4141	434.2107	866.4301	433.7187	A	343.2088	172.1081	326.1823	163.5948	0	0	3
10	981.4935	491.2504	964.4669	482.7371	963.4829	482.2451	P	272.1717	136.5895	255.1452	128.0762	0	0	2
11							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 26994.

MS/MS Fragmentation of **DLPHSVINDNDNYLNFSSLSGALPYK**:
 Found in **IP100168459;IP100333825;IP100410259;IP100657763;IP100789057;IP100847736**
 Title: 3.1.1.4467.5
 Data file: Y:\TT5600(CiRA1)\¥2012-02¥120214ry¥120214ry_aHDF1419-P10_4.3.mgf
 ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							26
2	229.1183	115.0628	0	0	211.1077	106.0575	L	2751.3624	1376.1849	2734.3359	1367.6716	2733.3519	1367.1796	25
3	326.1710	163.5892	0	0	308.1605	154.5839	P	2638.2784	1319.6428	2621.2518	1311.1295	2620.2678	1310.6375	24
4	463.2300	232.1186	0	0	445.2194	223.1133	H	2541.2256	1271.1164	2524.1991	1262.6032	2523.2150	1262.1112	23
5	550.2620	275.6346	0	0	532.2514	266.6293	S	2404.1667	1202.5870	2387.1401	1194.0737	2386.1561	1193.5817	22
6	649.3304	325.1688	0	0	631.3198	316.1636	V	2317.1347	1159.0710	2300.1081	1150.5577	2299.1241	1150.0657	21
7	762.4145	381.7109	0	0	744.4039	372.7056	I	2218.0663	1109.5368	2201.0397	1101.0235	2200.0557	1100.5315	20
8	877.4414	439.2243	0	0	859.4308	430.2191	D	2104.9822	1052.9947	2087.9556	1044.4815	2086.9716	1043.9895	19
9	991.4843	496.2458	974.4578	487.7325	973.4738	487.2405	N	1989.9552	995.4813	1972.9287	986.9680	1971.9447	986.4760	18
10	1106.5113	553.7593	1089.4847	545.2460	1088.5007	544.7540	D	1875.9123	938.4598	1858.8858	929.9465	1857.9018	929.4545	17
11	1220.5542	610.7807	1203.5277	602.2675	1202.5436	601.7755	N	1760.8854	880.9463	1743.8588	872.4331	1742.8748	871.9410	16
12	1383.6175	692.3124	1366.5910	683.7991	1365.6070	683.3071	Y	1646.8424	823.9249	1629.8159	815.4116	1628.8319	814.9196	15
13	1496.7016	748.8544	1479.6750	740.3412	1478.6910	739.8492	L	1483.7791	742.3932	1466.7526	733.8799	1465.7686	733.3879	14
14	1610.7445	805.8759	1593.7180	797.3626	1592.7340	796.8706	N	1370.6951	685.8512	1353.6685	677.3379	1352.6845	676.8459	13
15	1757.8129	879.4101	1740.7864	870.8968	1739.8024	870.4048	F	1256.6521	628.8297	1239.6256	620.3164	1238.6416	619.8244	12
16	1844.8450	922.9261	1827.8184	914.4128	1826.8344	913.9208	S	1109.5837	555.2955	1092.5572	546.7822	1091.5732	546.2902	11
17	1931.8770	966.4421	1914.8504	957.9289	1913.8664	957.4369	S	1022.5517	511.7795	1005.5251	503.2662	1004.5411	502.7742	10
18	2044.9611	1022.9842	2027.9345	1014.4709	2026.9505	1013.9789	L	935.5197	468.2635	918.4931	459.7502	917.5091	459.2582	9
19	2131.9931	1066.5002	2114.9665	1057.9869	2113.9825	1057.4949	S	822.4356	411.7214	805.4090	403.2082	804.4250	402.7162	8
20	2219.0251	1110.0162	2201.9986	1101.5029	2201.0146	1101.0109	S	735.4036	368.2054	718.3770	359.6921	717.3930	359.2001	7
21	2276.0466	1138.5269	2259.0200	1130.0137	2258.0360	1129.5216	G	648.3715	324.6894	631.3450	316.1761	0	0	6
22	2347.0837	1174.0455	2330.0571	1165.5322	2329.0731	1165.0402	A	591.3501	296.1787	574.3235	287.6654	0	0	5
23	2460.1678	1230.5875	2443.1412	1222.0742	2442.1572	1221.5822	L	520.3130	260.6601	503.2864	252.1468	0	0	4
24	2557.2205	1279.1139	2540.1940	1270.6006	2539.2100	1270.1086	P	407.2289	204.1181	390.2023	195.6048	0	0	3
25	2720.2839	1360.6456	2703.2573	1352.1323	2702.2733	1351.6403	Y	310.1761	155.5917	293.1496	147.0784	0	0	2
26							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 27036.

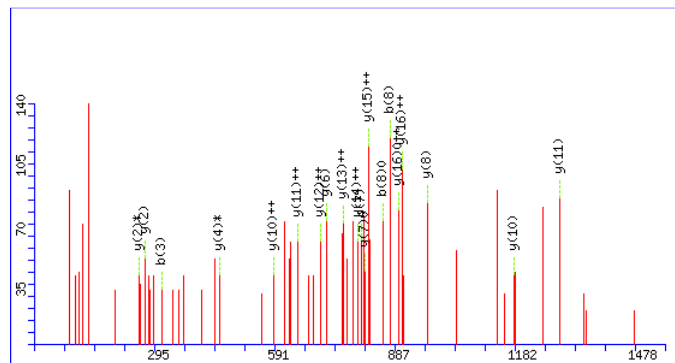
MS/MS Fragmentation of **VDTVEDFAYGANILVNHLDESLQK**:

Found in **IP100006231**

Title: 4.1.1.2904.4

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							24
2	215.1026	108.0550	0	0	197.0921	99.0497	D	2591.2624	1296.1348	2574.2358	1287.6216	2573.2518	1287.1296	23
3	316.1503	158.5788	0	0	298.1397	149.5735	T	2476.2354	1238.6214	2459.2089	1230.1081	2458.2249	1229.6161	22
4	415.2187	208.1130	0	0	397.2082	199.1077	V	2375.1878	1188.0975	2358.1612	1179.5842	2357.1772	1179.0922	21
5	544.2613	272.6343	0	0	526.2508	263.6290	E	2276.1194	1138.5633	2259.0928	1130.0500	2258.1088	1129.5580	20
6	659.2883	330.1478	0	0	641.2777	321.1425	D	2147.0768	1074.0420	2130.0502	1065.5287	2129.0662	1065.0367	19
7	806.3567	403.6820	0	0	788.3461	394.6767	F	2032.0498	1016.5285	2015.0233	1008.0153	2014.0393	1007.5233	18
8	877.3938	439.2005	0	0	859.3832	430.1953	A	1884.9814	942.9943	1867.9549	934.4811	1866.9708	933.9891	17
9	1040.4571	520.7322	0	0	1022.4466	511.7269	Y	1813.9443	907.4758	1796.9177	898.9625	1795.9337	898.4705	16
10	1097.4786	549.2429	0	0	1079.4680	540.2376	G	1650.8810	825.9441	1633.8544	817.4308	1632.8704	816.9388	15
11	1168.5157	584.7615	0	0	1150.5051	575.7562	A	1593.8595	797.4334	1576.8329	788.9201	1575.8489	788.4281	14
12	1282.5586	641.7830	1265.5321	633.2697	1264.5481	632.7777	N	1522.8224	761.9148	1505.7958	753.4016	1504.8118	752.9095	13
13	1395.6427	698.3250	1378.6161	689.8117	1377.6321	689.3197	I	1408.7795	704.8934	1391.7529	696.3801	1390.7689	695.8881	12
14	1508.7268	754.8670	1491.7002	746.3537	1490.7162	745.8617	L	1295.6954	648.3513	1278.6688	639.8381	1277.6848	639.3461	11
15	1607.7952	804.4012	1590.7686	795.8879	1589.7846	795.3959	V	1182.6113	591.8093	1165.5848	583.2960	1164.6008	582.8040	10
16	1721.8381	861.4227	1704.8115	852.9094	1703.8275	852.4174	N	1083.5429	542.2751	1066.5164	533.7618	1065.5323	533.2698	9
17	1858.8970	929.9521	1841.8705	921.4389	1840.8864	920.9469	H	969.5000	485.2536	952.4734	476.7404	951.4894	476.2483	8
18	1971.9811	986.4942	1954.9545	977.9809	1953.9705	977.4889	L	832.4411	416.7242	815.4145	408.2109	814.4305	407.7189	7
19	2087.0080	1044.0076	2069.9815	1035.4944	2068.9974	1035.0024	D	719.3570	360.1821	702.3305	351.6689	701.3464	351.1769	6
20	2216.0506	1108.5289	2199.0241	1100.0157	2198.0400	1099.5237	E	604.3301	302.6687	587.3035	294.1554	586.3195	293.6634	5
21	2303.0826	1152.0450	2286.0561	1143.5317	2285.0721	1143.0397	S	475.2875	238.1474	458.2609	229.6341	457.2769	229.1421	4
22	2416.1667	1208.5870	2399.1401	1200.0737	2398.1561	1199.5817	L	388.2554	194.6314	371.2289	186.1181	0	0	3
23	2544.2253	1272.6163	2527.1987	1264.1030	2526.2147	1263.6110	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
24							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 27312.

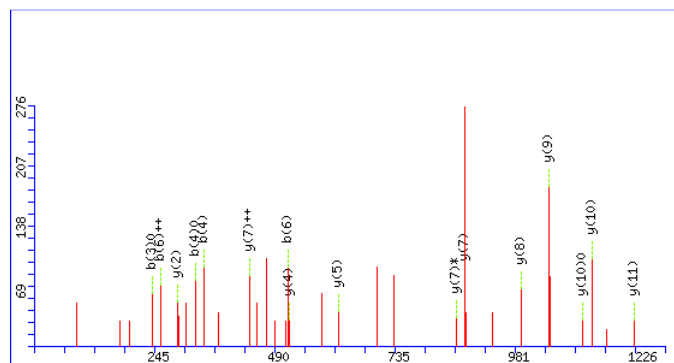
MS/MS Fragmentation of **GDSSGDPCTDLFK: 57.021465@C:8**

Found in **IP100013829**

Title: 2.1.1.2619.11

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							13
2	173.0557	87.0315	0	0	155.0451	78.0262	D	1341.5627	671.2850	1324.5362	662.7717	1323.5522	662.2797	12
3	260.0877	130.5475	0	0	242.0771	121.5422	S	1226.5358	613.7715	1209.5092	605.2583	1208.5252	604.7662	11
4	347.1197	174.0635	0	0	329.1092	165.0582	S	1139.5038	570.2555	1122.4772	561.7422	1121.4932	561.2502	10
5	404.1412	202.5742	0	0	386.1306	193.5690	G	1052.4717	526.7395	1035.4452	518.2262	1034.4612	517.7342	9
6	519.1681	260.0877	0	0	501.1576	251.0824	D	995.4503	498.2288	978.4237	489.7155	977.4397	489.2235	8
7	616.2209	308.6141	0	0	598.2103	299.6088	P	880.4233	440.7153	863.3968	432.2020	862.4128	431.7100	7
8	776.2516	388.6294	0	0	758.2410	379.6241	C	783.3706	392.1889	766.3440	383.6756	765.3600	383.1836	6
9	877.2992	439.1533	0	0	859.2887	430.1480	T	623.3399	312.1736	606.3134	303.6603	605.3293	303.1683	5
10	992.3262	496.6667	0	0	974.3156	487.6614	D	522.2922	261.6498	505.2657	253.1365	504.2817	252.6445	4
11	1105.4102	553.2088	0	0	1087.3997	544.2035	L	407.2653	204.1363	390.2387	195.6230	0	0	3
12	1252.4787	626.7430	0	0	1234.4681	617.7377	F	294.1812	147.5942	277.1547	139.0810	0	0	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 27450.

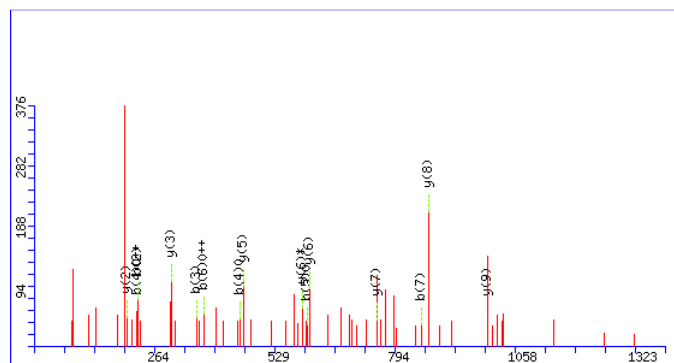
MS/MS Fragmentation of **DLEDFFSAVGK**:

Found in **IP100168431;IP100376960;IP100376962;IP100376963;IP100386141;IP100977373;IP101010168;IP101025465;IP101025820;IP101026224**

Title: 3.1.1.4054.4

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							11
2	229.1183	115.0628	0	0	211.1077	106.0575	L	1112.5623	556.7848	1095.5357	548.2715	1094.5517	547.7795	10
3	358.1609	179.5841	0	0	340.1503	170.5788	E	999.4782	500.2427	982.4516	491.7295	981.4676	491.2374	9
4	473.1878	237.0975	0	0	455.1773	228.0923	D	870.4356	435.7214	853.4090	427.2082	852.4250	426.7162	8
5	620.2562	310.6318	0	0	602.2457	301.6265	F	755.4087	378.2080	738.3821	369.6947	737.3981	369.2027	7
6	767.3246	384.1660	0	0	749.3141	375.1607	F	608.3402	304.6738	591.3137	296.1605	590.3297	295.6685	6
7	854.3567	427.6820	0	0	836.3461	418.6767	S	461.2718	231.1395	444.2453	222.6263	443.2613	222.1343	5
8	925.3938	463.2005	0	0	907.3832	454.1953	A	374.2398	187.6235	357.2132	179.1103	0	0	4
9	1024.4622	512.7347	0	0	1006.4516	503.7295	V	303.2027	152.1050	286.1761	143.5917	0	0	3
10	1081.4837	541.2455	0	0	1063.4731	532.2402	G	204.1343	102.5708	187.1077	94.0575	0	0	2
11							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 27469.

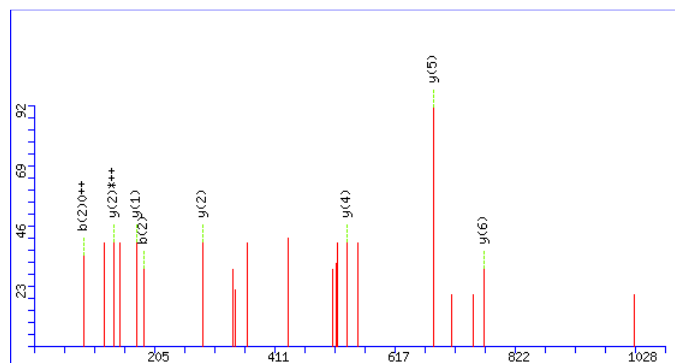
MS/MS Fragmentation of **TSFTFLR**:

Found in **IP100797834;IP100908939;IP100966780;IP101011342**

Title: 2.1.1.3609.2

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							7
2	189.0870	95.0471	0	0	171.0764	86.0418	S	770.4196	385.7134	753.3930	377.2001	752.4090	376.7081	6
3	336.1554	168.5813	0	0	318.1448	159.5761	F	683.3875	342.1974	666.3610	333.6841	665.3770	333.1921	5
4	437.2031	219.1052	0	0	419.1925	210.0999	T	536.3191	268.6632	519.2926	260.1499	518.3085	259.6579	4
5	584.2715	292.6394	0	0	566.2609	283.6341	F	435.2714	218.1394	418.2449	209.6261	0	0	3
6	697.3556	349.1814	0	0	679.3450	340.1761	L	288.2030	144.6051	271.1765	136.0919	0	0	2
7							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 27648.

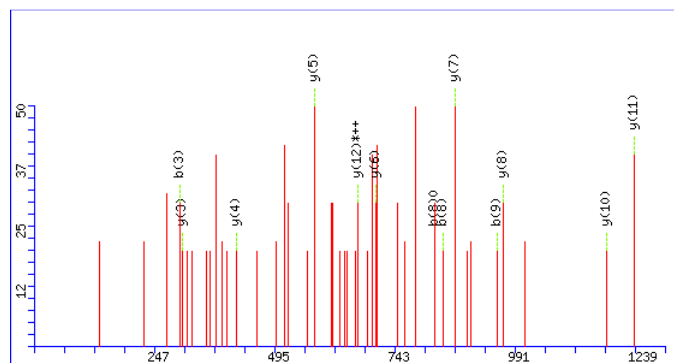
MS/MS Fragmentation of **ADLWSIGTTVYQCLTGK: 57.021465@C:13**

Found in **IP100289357:IP101009875**

Title: 5.1.1.814.2

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2.5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							17
2	187.0713	94.0393	0	0	169.0608	85.0340	D	1853.9466	927.4769	1836.9201	918.9637	1835.9360	918.4717	16
3	300.1554	150.5813	0	0	282.1448	141.5761	L	1738.9197	869.9635	1721.8931	861.4502	1720.9091	860.9582	15
4	486.2347	243.6210	0	0	468.2241	234.6157	W	1625.8356	813.4214	1608.8090	804.9082	1607.8250	804.4162	14
5	573.2667	287.1370	0	0	555.2562	278.1317	S	1439.7563	720.3818	1422.7297	711.8685	1421.7457	711.3765	13
6	686.3508	343.6790	0	0	668.3402	334.6738	I	1352.7243	676.8658	1335.6977	668.3525	1334.7137	667.8605	12
7	743.3723	372.1898	0	0	725.3617	363.1845	G	1239.6402	620.3237	1222.6136	611.8105	1221.6296	611.3185	11
8	844.4199	422.7136	0	0	826.4094	413.7083	T	1182.6187	591.8130	1165.5922	583.2997	1164.6082	582.8077	10
9	957.5040	479.2556	0	0	939.4934	470.2504	I	1081.5710	541.2892	1064.5445	532.7759	1063.5605	532.2839	9
10	1056.5724	528.7898	0	0	1038.5619	519.7846	V	968.4870	484.7471	951.4604	476.2339	950.4764	475.7418	8
11	1219.6358	610.3215	0	0	1201.6252	601.3162	Y	869.4186	435.2129	852.3920	426.6996	851.4080	426.2076	7
12	1347.6943	674.3508	1330.6678	665.8375	1329.6838	665.3455	Q	706.3552	353.6813	689.3287	345.1680	688.3447	344.6760	6
13	1507.7250	754.3661	1490.6984	745.8529	1489.7144	745.3608	C	578.2967	289.6520	561.2701	281.1387	560.2861	280.6467	5
14	1620.8090	810.9082	1603.7825	802.3949	1602.7985	801.9029	L	418.2660	209.6366	401.2395	201.1234	400.2554	200.6314	4
15	1721.8567	861.4320	1704.8302	852.9187	1703.8462	852.4267	T	305.1819	153.0946	288.1554	144.5813	287.1714	144.0893	3
16	1778.8782	889.9427	1761.8516	881.4295	1760.8676	880.9374	G	204.1343	102.5708	187.1077	94.0575	0	0	2
17							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

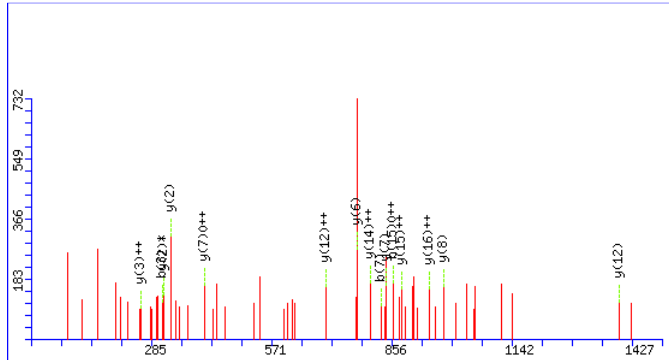
Peptide: 27785.

MS/MS Fragmentation of **VPDSCCLEFSESCGLHAPGTWWK**: 57.021465@C:5,57.021465@C:6,57.021465@C:13
Found in **IP100024174;IP100619895;IP100916272;IP100973982;IP100976972**

Title: 3.1.1.2433.11

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2.3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							23
2	197.1285	99.0679	0	0	0	0	P	2624.1003	1312.5538	2607.0737	1304.0405	2606.0897	1303.5485	22
3	312.1554	156.5813	0	0	294.1448	147.5761	D	2527.0475	1264.0274	2510.0210	1255.5141	2509.0370	1255.0221	21
4	399.1874	200.0974	0	0	381.1769	191.0921	S	2412.0206	1206.5139	2394.9940	1198.0007	2394.0100	1197.5087	20
5	559.2181	280.1127	0	0	541.2075	271.1074	C	2324.9886	1162.9979	2307.9620	1154.4846	2306.9780	1153.9926	19
6	719.2487	360.1280	0	0	701.2382	351.1227	C	2164.9579	1082.9826	2147.9314	1074.4693	2146.9473	1073.9773	18
7	832.3328	416.6700	0	0	814.3222	407.6648	L	2004.9273	1002.9673	1987.9007	994.4540	1986.9167	993.9620	17
8	961.3754	481.1913	0	0	943.3648	472.1860	E	1891.8432	946.4252	1874.8166	937.9120	1873.8326	937.4200	16
9	1108.4438	554.7255	0	0	1090.4332	545.7203	F	1762.8006	881.9039	1745.7741	873.3907	1744.7900	872.8987	15
10	1195.4758	598.2416	0	0	1177.4653	589.2363	S	1615.7322	808.3697	1598.7056	799.8565	1597.7216	799.3645	14
11	1324.5184	662.7628	0	0	1306.5079	653.7576	E	1528.7002	764.8537	1511.6736	756.3404	1510.6896	755.8484	13
12	1411.5504	706.2789	0	0	1393.5399	697.2736	S	1399.6576	700.3324	1382.6310	691.8191	1381.6470	691.3271	12
13	1571.5811	786.2942	0	0	1553.5705	777.2889	C	1312.6255	656.8164	1295.5990	648.3031	1294.6150	647.8111	11
14	1628.6026	814.8049	0	0	1610.5920	805.7996	G	1152.5949	576.8011	1135.5683	568.2878	1134.5843	567.7958	10
15	1741.6866	871.3469	0	0	1723.6761	862.3417	L	1095.5734	548.2904	1078.5469	539.7771	1077.5629	539.2851	9
16	1878.7455	939.8764	0	0	1860.7350	930.8711	H	982.4894	491.7483	965.4628	483.2350	964.4788	482.7430	8
17	1949.7826	975.3950	0	0	1931.7721	966.3897	A	845.4305	423.2189	828.4039	414.7056	827.4199	414.2136	7
18	2046.8354	1023.9213	0	0	2028.8248	1014.9161	P	774.3933	387.7003	757.3668	379.1870	756.3828	378.6950	6
19	2103.8569	1052.4321	0	0	2085.8463	1043.4268	G	677.3406	339.1739	660.3140	330.6606	659.3300	330.1686	5
20	2204.9046	1102.9559	0	0	2186.8940	1093.9506	T	620.3191	310.6632	603.2926	302.1499	602.3085	301.6579	4
21	2390.9839	1195.9956	0	0	2372.9733	1186.9903	W	519.2714	260.1394	502.2449	251.6261	0	0	3
22	2577.0632	1289.0352	0	0	2559.0526	1280.0299	W	333.1921	167.0997	316.1656	158.5864	0	0	2
23							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 27912.

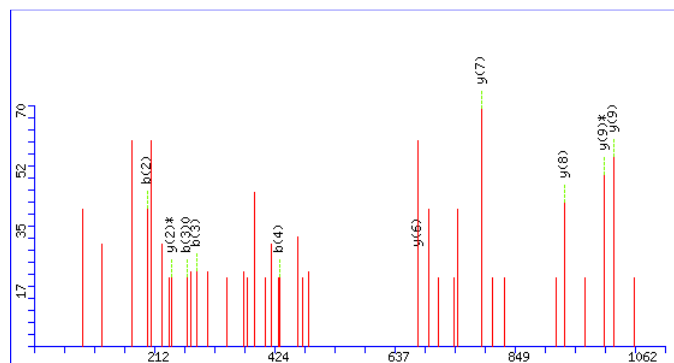
MS/MS Fragmentation of **SLSFLGTILK**:

Found in **IP100023500;IP100219736;IP100394961;IP100909196**

Title: 4.1.1.731.3

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120208ry¥120208ry_Tig120slc-P8_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							11
2	201.1234	101.0653	0	0	183.1128	92.0600	L	1138.6871	569.8472	1121.6605	561.3339	1120.6765	560.8419	10
3	288.1554	144.5813	0	0	270.1448	135.5761	S	1025.6030	513.3051	1008.5764	504.7919	1007.5924	504.2999	9
4	435.2238	218.1155	0	0	417.2132	209.1103	F	938.5710	469.7891	921.5444	461.2758	920.5604	460.7838	8
5	548.3079	274.6576	0	0	530.2973	265.6523	L	791.5028	396.2549	774.4760	387.7416	773.4920	387.2496	7
6	605.3293	303.1683	0	0	587.3188	294.1630	G	678.4185	339.7129	661.3919	331.1996	660.4079	330.7076	6
7	706.3770	353.6921	0	0	688.3665	344.6869	T	621.3970	311.2022	604.3705	302.6889	603.3865	302.1969	5
8	853.4454	427.2264	0	0	835.4349	418.2211	F	520.3493	260.6783	503.3228	252.1650	0	0	4
9	966.5295	483.7684	0	0	948.5189	474.7631	I	373.2809	187.1441	356.2544	178.6308	0	0	3
10	1079.6136	540.3104	0	0	1061.6030	531.3051	L	260.1969	130.6021	243.1703	122.0888	0	0	2
11							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 28005.

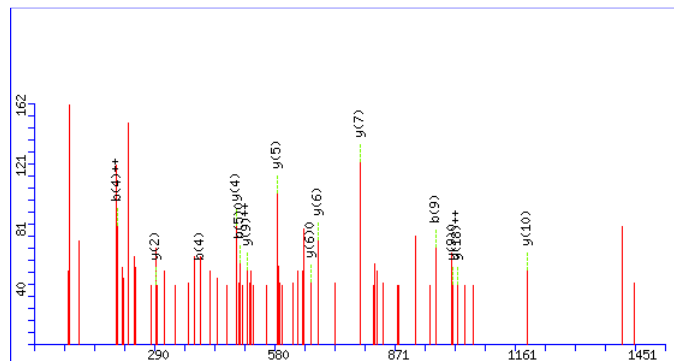
MS/MS Fragmentation of **ISAEDLIDLCELTVTGHFK: 57.021465@C:10**

Found in **IP100062810;IP100291665;IP100791217**

Title: 4.1.1.1216.4

Data file: Y:\TT5600(CiRA1)\2012-02\120201ry\120201ry_aHDF1388-P9_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							19
2	201.1234	101.0653	0	0	183.1128	92.0600	S	2048.0005	1024.5039	2030.9739	1015.9906	2029.9899	1015.4986	18
3	272.1605	136.5839	0	0	254.1499	127.5786	A	1960.9685	980.9879	1943.9419	972.4746	1942.9579	971.9826	17
4	401.2031	201.1052	0	0	383.1925	192.0999	E	1889.9313	945.4693	1872.9048	936.9560	1871.9208	936.4640	16
5	516.2300	258.6186	0	0	498.2195	249.6134	D	1760.8888	880.9480	1743.8622	872.4347	1742.8782	871.9427	15
6	629.3141	315.1607	0	0	611.3035	306.1554	L	1645.8618	823.4345	1628.8353	814.9213	1627.8512	814.4293	14
7	742.3981	371.7027	0	0	724.3876	362.6974	I	1532.7777	766.8925	1515.7512	758.3792	1514.7672	757.8872	13
8	857.4251	429.2162	0	0	839.4145	420.2109	D	1419.6937	710.3505	1402.6671	701.8372	1401.6831	701.3452	12
9	970.5092	485.7582	0	0	952.4986	476.7529	L	1304.6667	652.8370	1287.6402	644.3237	1286.6562	643.8317	11
10	1130.5398	565.7735	0	0	1112.5292	556.7683	C	1191.5827	596.2950	1174.5561	587.7817	1173.5721	587.2897	10
11	1259.5824	630.2948	0	0	1241.5718	621.2896	E	1031.5520	516.2796	1014.5255	507.7664	1013.5415	507.2744	9
12	1372.6665	686.8369	0	0	1354.6559	677.8316	L	902.5094	451.7584	885.4829	443.2451	884.4989	442.7531	8
13	1473.7141	737.3607	0	0	1455.7036	728.3554	T	789.4254	395.2163	772.3988	386.7030	771.4148	386.2110	7
14	1572.7826	786.8949	0	0	1554.7720	777.8896	V	688.3777	344.6925	671.3511	336.1792	670.3671	335.6872	6
15	1673.8302	837.4188	0	0	1655.8197	828.4135	T	589.3093	295.1583	572.2827	286.6450	571.2987	286.1530	5
16	1730.8517	865.9295	0	0	1712.8411	856.9242	G	488.2616	244.6344	471.2350	236.1212	0	0	4
17	1867.9106	934.4589	0	0	1849.9000	925.4537	H	431.2401	216.1237	414.2136	207.6104	0	0	3
18	2014.9790	1007.9931	0	0	1996.9685	998.9879	F	294.1812	147.5942	277.1547	139.0810	0	0	2
19							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 28074.

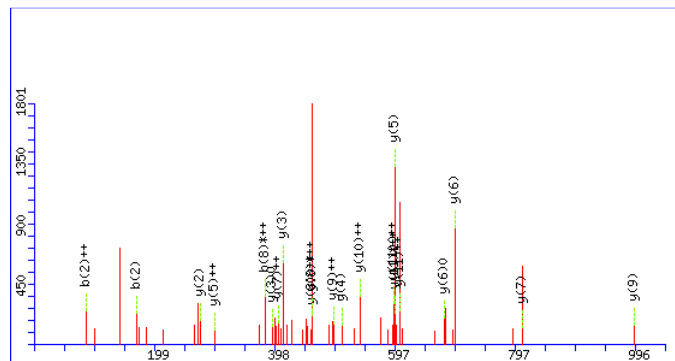
MS/MS Fragmentation of **AVESGQLVSVHEK**:

Found in **IP100031612**

Title: 1.1.1.8333.7

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							13
2	171.1128	86.0600	0	0	0	0	V	1311.6903	656.3488	1294.6638	647.8355	1293.6797	647.3435	12
3	300.1554	150.5813	0	0	282.1448	141.5761	E	1212.6219	606.8146	1195.5953	598.3013	1194.6113	597.8093	11
4	387.1874	194.0974	0	0	369.1769	185.0921	S	1083.5793	542.2933	1066.5527	533.7800	1065.5687	533.2880	10
5	444.2089	222.6081	0	0	426.1983	213.6028	G	996.5473	498.7773	979.5207	490.2640	978.5367	489.7720	9
6	572.2675	286.6374	555.2409	278.1241	554.2569	277.6321	Q	939.5258	470.2665	922.4993	461.7533	921.5152	461.2613	8
7	685.3515	343.1794	668.3250	334.6661	667.3410	334.1741	L	811.4672	406.2373	794.4407	397.7240	793.4567	397.2320	7
8	784.4199	392.7136	767.3934	384.2003	766.4094	383.7083	V	698.3832	349.6952	681.3566	341.1819	680.3726	340.6899	6
9	871.4520	436.2296	854.4254	427.7163	853.4414	427.2243	S	599.3148	300.1610	582.2882	291.6477	581.3042	291.1557	5
10	970.5204	485.7638	953.4938	477.2506	952.5098	476.7585	V	512.2827	256.6450	495.2562	248.1317	494.2722	247.6397	4
11	1107.5793	554.2933	1090.5527	545.7800	1089.5687	545.2880	H	413.2143	207.1108	396.1878	198.5975	395.2037	198.1055	3
12	1236.6219	618.8146	1219.5953	610.3013	1218.6113	609.8093	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 28100.

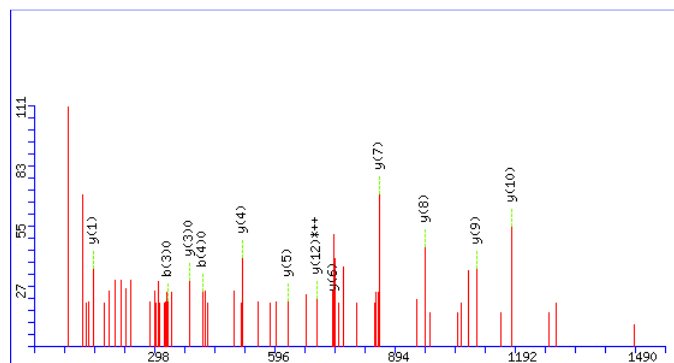
MS/MS Fragmentation of **DSFSQLINLLEEK**:

Found in **IP100005163**

Title: 4.1.1.2565.4

Data file: Y:\TT5600(CiRA1)\2012-02\120201ry\120201ry_aHDF1388-P9_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							13
2	203.0662	102.0368	0	0	185.0557	93.0315	S	1420.7682	710.8877	1403.7417	702.3745	1402.7577	701.8825	12
3	350.1347	175.5710	0	0	332.1241	166.5657	F	1333.7362	667.3717	1316.7096	658.8585	1315.7256	658.3665	11
4	437.1667	219.0870	0	0	419.1561	210.0817	S	1186.6678	593.8375	1169.6412	585.3243	1168.6572	584.8322	10
5	565.2253	283.1163	548.1987	274.6030	547.2147	274.1110	Q	1099.6358	550.3215	1082.6092	541.8082	1081.6252	541.3162	9
6	678.3093	339.6583	661.2828	331.1450	660.2988	330.6530	L	971.5772	486.2922	954.5506	477.7789	953.5666	477.2869	8
7	791.3934	396.2003	774.3668	387.6871	773.3828	387.1951	I	858.4931	429.7502	841.4666	421.2369	840.4825	420.7449	7
8	905.4363	453.2218	888.4098	444.7085	887.4258	444.2165	N	745.4090	373.2082	728.3825	364.6949	727.3985	364.2029	6
9	1018.5204	509.7638	1001.4938	501.2506	1000.5098	500.7585	L	631.3661	316.1867	614.3396	307.6734	613.3556	307.1814	5
10	1131.6045	566.3059	1114.5779	557.7926	1113.5939	557.3006	L	518.2821	259.6447	501.2555	251.1314	500.2715	250.6394	4
11	1260.6470	630.8272	1243.6205	622.3139	1242.6365	621.8219	E	405.1980	203.1026	388.1714	194.5894	387.1874	194.0974	3
12	1389.6896	695.3485	1372.6631	686.8352	1371.6791	686.3432	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 28269.

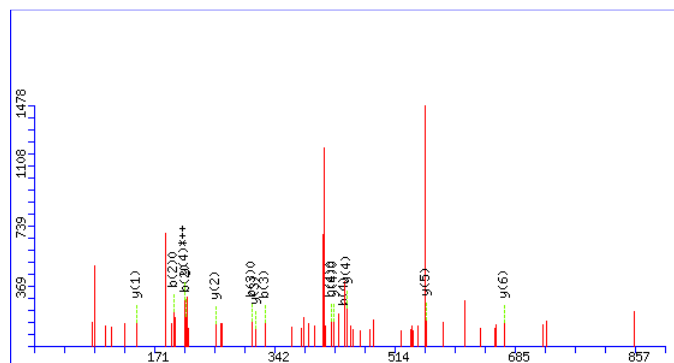
MS/MS Fragmentation of **ESIEGIK**:

Found in **IP100885176;IP100979376**

Title: 2.1.1.837.8

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							8
2	217.0819	109.0446	0	0	199.0713	100.0393	S	759.4611	380.2342	742.4345	371.7209	741.4505	371.2289	7
3	330.1660	165.5866	0	0	312.1554	156.5813	I	672.4291	336.7182	655.4025	328.2049	654.4185	327.7129	6
4	443.2500	222.1287	0	0	425.2395	213.1234	I	559.3450	280.1761	542.3184	271.6629	541.3344	271.1709	5
5	572.2926	286.6499	0	0	554.2821	277.6447	E	446.2609	223.6341	429.2344	215.1208	428.2504	214.6288	4
6	629.3141	315.1607	0	0	611.3035	306.1554	G	317.2183	159.1128	300.1918	150.5995	0	0	3
7	742.3981	371.7027	0	0	724.3876	362.6974	I	260.1969	130.6021	243.1703	122.0888	0	0	2
8							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 28362.

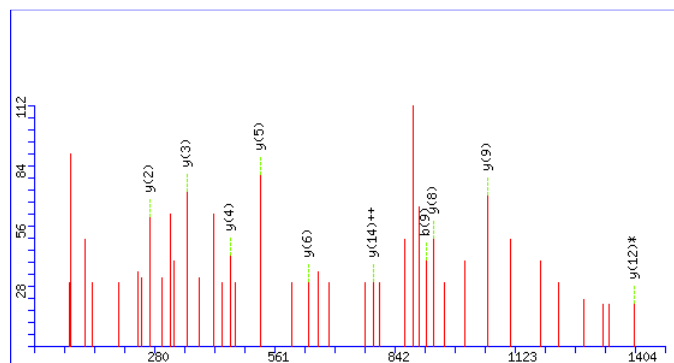
MS/MS Fragmentation of **ELCGLSSVANLMQCMLAVSPR**: 57.021465@C:3,57.021465@C:14

Found in **IP100010334;IP100789859;IP100847504**

Title: 4.1.1.4108.6

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							21
2	243.1339	122.0706	0	0	225.1234	113.0653	L	2207.0804	1104.0438	2190.0538	1095.5305	2189.0698	1095.0385	20
3	403.1646	202.0859	0	0	385.1540	193.0806	C	2093.9963	1047.5018	2076.9697	1038.9885	2075.9857	1038.4965	19
4	460.1860	230.5967	0	0	442.1755	221.5914	G	1933.9656	967.4865	1916.9391	958.9732	1915.9551	958.4812	18
5	573.2701	287.1387	0	0	555.2595	278.1334	L	1876.9442	938.9757	1859.9176	930.4624	1858.9336	929.9704	17
6	660.3021	330.6547	0	0	642.2916	321.6494	S	1763.8601	882.4337	1746.8336	873.9204	1745.8495	873.4284	16
7	747.3342	374.1707	0	0	729.3236	365.1654	S	1676.8281	838.9177	1659.8015	830.4044	1658.8175	829.9124	15
8	846.4026	423.7049	0	0	828.3920	414.6996	V	1589.7961	795.4017	1572.7695	786.8884	1571.7855	786.3964	14
9	917.4397	459.2235	0	0	899.4291	450.2182	A	1490.7276	745.8675	1473.7011	737.3542	1472.7171	736.8622	13
10	1031.4826	516.2449	1014.4561	507.7317	1013.4721	507.2397	N	1419.6905	710.3489	1402.6640	701.8356	1401.6800	701.3436	12
11	1144.5667	572.7870	1127.5401	564.2737	1126.5561	563.7817	L	1305.6476	653.3274	1288.6210	644.8142	1287.6370	644.3222	11
12	1275.6072	638.3072	1258.5806	629.7939	1257.5966	629.3019	M	1192.5635	596.7854	1175.5370	588.2721	1174.5530	587.7801	10
13	1403.6657	702.3365	1386.6392	693.8232	1385.6552	693.3312	Q	1061.5230	531.2652	1044.4965	522.7519	1043.5125	522.2599	9
14	1563.6964	782.3518	1546.6698	773.8386	1545.6858	773.3466	C	933.4645	467.2359	916.4379	458.7226	915.4539	458.2306	8
15	1694.7369	847.8721	1677.7103	839.3588	1676.7263	838.8668	M	773.4338	387.2205	756.4073	378.7073	755.4233	378.2153	7
16	1807.8209	904.4141	1790.7944	895.9008	1789.8104	895.4088	L	642.3933	321.7003	625.3668	313.1870	624.3828	312.6950	6
17	1878.8581	939.9327	1861.8315	931.4194	1860.8475	930.9274	A	529.3093	265.1583	512.2827	256.6450	511.2987	256.1530	5
18	1977.9265	989.4669	1960.8999	980.9536	1959.9159	980.4616	V	458.2722	229.6397	441.2456	221.1264	440.2616	220.6344	4
19	2064.9585	1032.9829	2047.9320	1024.4696	2046.9479	1023.9776	S	359.2037	180.1055	342.1772	171.5922	341.1932	171.1002	3
20	2162.0113	1081.5093	2144.9847	1072.9960	2144.0007	1072.5040	P	272.1717	136.5895	255.1452	128.0762	0	0	2
21							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 28641.

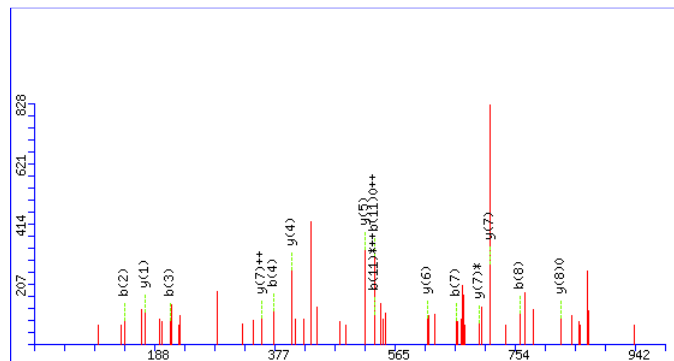
MS/MS Fragmentation of **AAAYSQVQPVDGATR: 0.984016@Q:9**

Found in **IP100011997:IP100867735**

Title: 1.1.1.9092.7

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120214ry¥120214ry_32R1-32_4_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							16
2	143.0815	72.0444	0	0	0	0	A	1534.7496	767.8784	1517.7231	759.3652	1516.7391	758.8732	15
3	214.1186	107.5629	0	0	0	0	A	1463.7125	732.3599	1446.6860	723.8466	1445.7019	723.3546	14
4	377.1819	189.0946	0	0	0	0	Y	1392.6754	696.8413	1375.6488	688.3281	1374.6648	687.8360	13
5	464.2140	232.6106	0	0	446.2034	223.6053	S	1229.6121	615.3097	1212.5855	606.7964	1211.6015	606.3044	12
6	535.2511	268.1292	0	0	517.2405	259.1239	A	1142.5800	571.7937	1125.5535	563.2804	1124.5695	562.7884	11
7	663.3097	332.1585	646.2831	323.6452	645.2991	323.1532	Q	1071.5429	536.2751	1054.5164	527.7618	1053.5324	527.2698	10
8	762.3781	381.6927	745.3515	373.1794	744.3675	372.6874	V	943.4843	472.2458	926.4578	463.7325	925.4738	463.2405	9
9	891.4207	446.2140	874.3941	437.7007	873.4101	437.2087	Q	844.4159	422.7116	827.3894	414.1983	826.4054	413.7063	8
10	988.4734	494.7404	971.4469	486.2271	970.4629	485.7351	P	715.3733	358.1903	698.3468	349.6770	697.3628	349.1850	7
11	1087.5419	544.2746	1070.5153	535.7613	1069.5313	535.2693	V	618.3206	309.6639	601.2940	301.1506	600.3100	300.6586	6
12	1202.5688	601.7880	1185.5422	593.2748	1184.5582	592.7828	D	519.2522	260.1297	502.2256	251.6164	501.2416	251.1244	5
13	1259.5903	630.2988	1242.5637	621.7855	1241.5797	621.2935	G	404.2252	202.6162	387.1987	194.1030	386.2146	193.6110	4
14	1330.6274	665.8173	1313.6008	657.3041	1312.6168	656.8120	A	347.2037	174.1055	330.1772	165.5922	329.1932	165.1002	3
15	1431.6751	716.3412	1414.6485	707.8279	1413.6645	707.3359	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
16							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 28690.

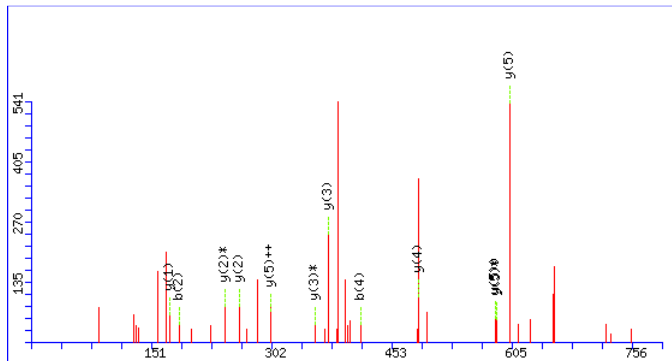
MS/MS Fragmentation of **VSDLISR**:

Found in **IP100065435;IP100554726;IP100980605;IP100982642;IP100983851;IP101021852;IP101022310**

Title: 2.1.1.3085.2

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							7
2	187.1077	94.0575	0	0	169.0972	85.0522	S	690.3781	345.6927	673.3515	337.1794	672.3675	336.6874	6
3	302.1347	151.5710	0	0	284.1241	142.5657	D	603.3461	302.1767	586.3195	293.6634	585.3355	293.1714	5
4	415.2187	208.1130	0	0	397.2082	199.1077	L	488.3191	244.6632	471.2926	236.1499	470.3085	235.6579	4
5	528.3028	264.6550	0	0	510.2922	255.6498	I	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
6	615.3348	308.1710	0	0	597.3243	299.1658	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
7							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 28945.

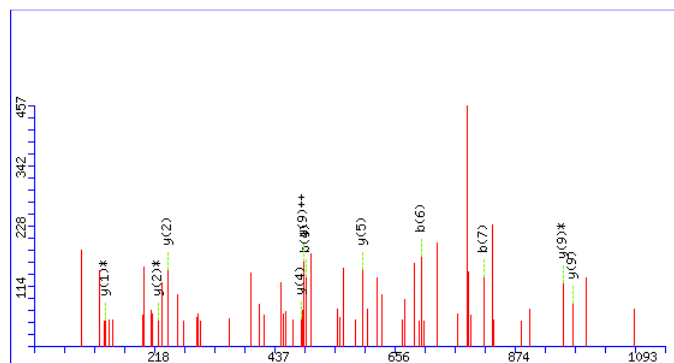
MS/MS Fragmentation of **DLEHPLLPGILEIPK**:

Found in **IP100017203;IP100654894**

Title: 3.1.1.3781.2

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_1_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							16
2	229.1183	115.0628	0	0	211.1077	106.0575	L	1683.9680	842.4876	1666.9414	833.9744	1665.9574	833.4823	15
3	358.1609	179.5841	0	0	340.1503	170.5788	E	1570.8839	785.9456	1553.8574	777.4323	1552.8734	776.9403	14
4	495.2198	248.1135	0	0	477.2092	239.1082	H	1441.8413	721.4243	1424.8148	712.9110	1423.8308	712.4190	13
5	592.2726	296.6399	0	0	574.2620	287.6346	P	1304.7824	652.8948	1287.7559	644.3816	1286.7719	643.8896	12
6	705.3566	353.1819	0	0	687.3461	344.1767	L	1207.7297	604.3685	1190.7031	595.8552	1189.7191	595.3632	11
7	818.4407	409.7240	0	0	800.4301	400.7187	L	1094.6456	547.8264	1077.6190	539.3132	1076.6350	538.8211	10
8	915.4934	458.2504	0	0	897.4829	449.2451	P	981.5615	491.2844	964.5350	482.7711	963.5510	482.2791	9
9	1030.5204	515.7638	0	0	1012.5098	506.7585	D	884.5088	442.7580	867.4822	434.2447	866.4982	433.7527	8
10	1087.5419	544.2746	0	0	1069.5313	535.2693	G	769.4818	385.2445	752.4553	376.7313	751.4713	376.2393	7
11	1200.6259	600.8166	0	0	1182.6154	591.8113	I	712.4604	356.7338	695.4338	348.2205	694.4498	347.7285	6
12	1313.7100	657.3586	0	0	1295.6994	648.3533	L	599.3763	300.1918	582.3497	291.6785	581.3657	291.1865	5
13	1442.7526	721.8799	0	0	1424.7420	712.8746	E	486.2922	243.6498	469.2657	235.1365	468.2817	234.6445	4
14	1555.8366	778.4220	0	0	1537.8261	769.4167	I	357.2496	179.1285	340.2231	170.6152	0	0	3
15	1652.8894	826.9483	0	0	1634.8788	817.9431	P	244.1656	122.5864	227.1390	114.0731	0	0	2
16							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 29146.

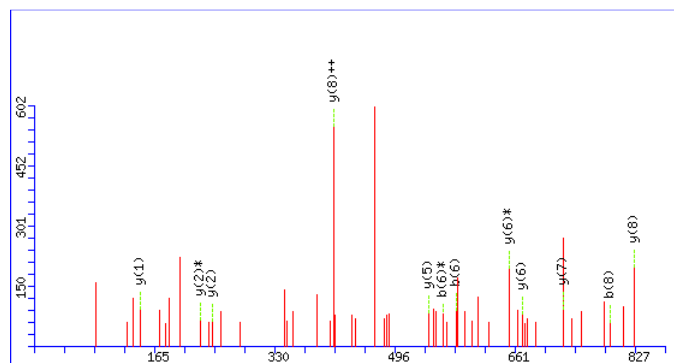
MS/MS Fragmentation of **LPGQANLVK**:

Found in **IP100010448;IP100166301;IP100783816;IP100829821;IP100964885;IP100967419**

Title: 1.1.1.8922.6

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_2_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							9
2	211.1441	106.0757	0	0	0	0	P	826.4781	413.7427	809.4516	405.2294	0	0	8
3	268.1656	134.5864	0	0	0	0	G	729.4254	365.2163	712.3988	356.7030	0	0	7
4	396.2241	198.6157	379.1976	190.1024	0	0	Q	672.4039	336.7056	655.3774	328.1923	0	0	6
5	467.2613	234.1343	450.2347	225.6210	0	0	A	544.3453	272.6763	527.3188	264.1630	0	0	5
6	581.3042	291.1557	564.2776	282.6425	0	0	N	473.3082	237.1577	456.2817	228.6445	0	0	4
7	694.3883	347.6978	677.3617	339.1845	0	0	L	359.2653	180.1363	342.2387	171.6230	0	0	3
8	793.4567	397.2320	776.4301	388.7187	0	0	V	246.1812	123.5942	229.1547	115.0810	0	0	2
9							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 29166.

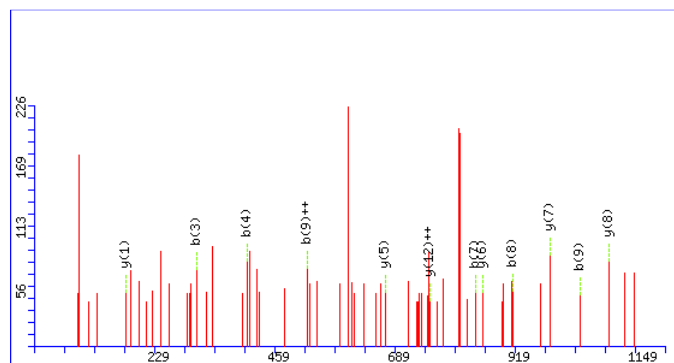
MS/MS Fragmentation of **DPVPYICAEPLPSNILEWHYVVR**: 57.021465@C:7.0.984015@N:14

Found in **IP100335071;IP100455911;IP100963927;IP100967274;IP101014819**

Title: 4.1.1.850.9

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120214ry¥120214ry_32R1-32_4.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							23
2	213.0870	107.0471	0	0	195.0764	98.0418	P	2653.3483	1327.1778	2636.3218	1318.6645	2635.3377	1318.1725	22
3	312.1554	156.5813	0	0	294.1448	147.5761	V	2556.2955	1278.6514	2539.2690	1270.1381	2538.2850	1269.6461	21
4	409.2082	205.1077	0	0	391.1976	196.1024	P	2457.2271	1229.1172	2440.2006	1220.6039	2439.2166	1220.1119	20
5	572.2715	286.6394	0	0	554.2609	277.6341	Y	2360.1744	1180.5908	2343.1478	1172.0775	2342.1638	1171.5855	19
6	685.3556	343.1814	0	0	667.3450	334.1761	I	2197.1110	1099.0592	2180.0845	1090.5459	2179.1005	1090.0539	18
7	845.3862	423.1967	0	0	827.3756	414.1915	C	2084.0270	1042.5171	2067.0004	1034.0039	2066.0164	1033.5118	17
8	916.4233	458.7153	0	0	898.4128	449.7100	A	1923.9963	962.5018	1906.9698	953.9885	1905.9858	953.4965	16
9	1045.4659	523.2366	0	0	1027.4553	514.2313	E	1852.9592	926.9832	1835.9327	918.4700	1834.9486	917.9780	15
10	1142.5187	571.7630	0	0	1124.5081	562.7577	P	1723.9166	862.4619	1706.8901	853.9487	1705.9061	853.4567	14
11	1255.6027	628.3050	0	0	1237.5922	619.2997	L	1626.8639	813.9356	1609.8373	805.4223	1608.8533	804.9303	13
12	1352.6555	676.8314	0	0	1334.6449	667.8261	P	1513.7798	757.3935	1496.7532	748.8803	1495.7692	748.3883	12
13	1439.6875	720.3474	0	0	1421.6770	711.3421	S	1416.7270	708.8672	1399.7005	700.3539	1398.7165	699.8619	11
14	1554.7145	777.8609	1537.6879	769.3476	1536.7039	768.8556	N	1329.6950	665.3511	1312.6684	656.8379	1311.6844	656.3459	10
15	1667.7985	834.4029	1650.7720	825.8896	1649.7880	825.3976	I	1214.6681	607.8377	1197.6415	599.3244	1196.6575	598.8324	9
16	1780.8826	890.9449	1763.8561	882.4317	1762.8720	881.9397	L	1101.5840	551.2956	1084.5574	542.7824	1083.5734	542.2904	8
17	1909.9252	955.4662	1892.8986	946.9530	1891.9146	946.4610	E	988.4999	494.7536	971.4734	486.2403	970.4894	485.7483	7
18	2096.0045	1048.5059	2078.9780	1039.9926	2077.9939	1039.5006	W	859.4573	430.2323	842.4308	421.7190	0	0	6
19	2233.0634	1117.0353	2216.0369	1108.5221	2215.0529	1108.0301	H	673.3780	337.1926	656.3515	328.6794	0	0	5
20	2396.1267	1198.5670	2379.1002	1190.0537	2378.1162	1189.5617	Y	536.3191	268.6632	519.2926	260.1499	0	0	4
21	2495.1952	1248.1012	2478.1686	1239.5879	2477.1846	1239.0959	V	373.2558	187.1315	356.2292	178.6183	0	0	3
22	2594.2636	1297.6354	2577.2370	1289.1222	2576.2530	1288.6301	V	274.1874	137.5973	257.1608	129.0840	0	0	2
23							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 29219.

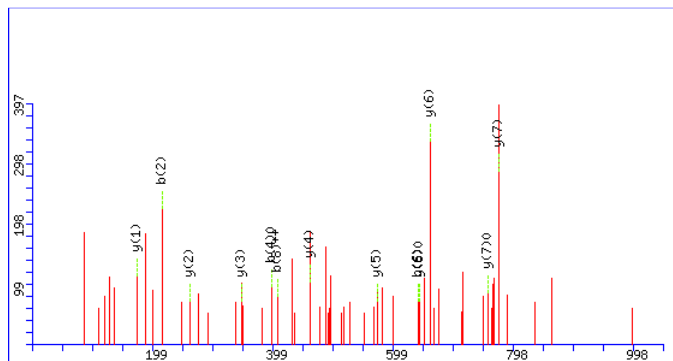
MS/MS Fragmentation of **SELSLISSR**:

Found in **IP100374068;IP100550741;IP100896415**

Title: 2.1.1.1706.4

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							9
2	217.0819	109.0446	0	0	199.0713	100.0393	E	904.5098	452.7585	887.4833	444.2453	886.4993	443.7533	8
3	330.1660	165.5866	0	0	312.1554	156.5813	L	775.4672	388.2373	758.4407	379.7240	757.4567	379.2320	7
4	417.1980	209.1026	0	0	399.1874	200.0974	S	662.3832	331.6952	645.3566	323.1819	644.3726	322.6899	6
5	530.2821	265.6447	0	0	512.2715	256.6394	L	575.3511	288.1792	558.3246	279.6659	557.3406	279.1739	5
6	643.3661	322.1867	0	0	625.3556	313.1814	I	462.2671	231.6372	445.2405	223.1239	444.2565	222.6319	4
7	730.3981	365.7027	0	0	712.3876	356.6974	S	349.1830	175.0951	332.1565	166.5819	331.1724	166.0899	3
8	817.4302	409.2187	0	0	799.4196	400.2134	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
9							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 29479.

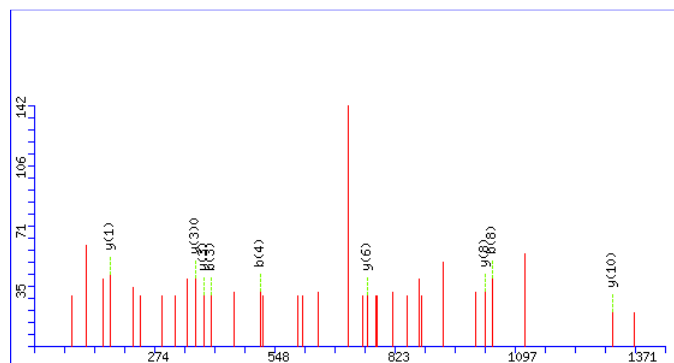
MS/MS Fragmentation of **LCMLRAMRPDR: 57.021465@C:2.15.994915@M:7**

Found in **IP100005823;IP100302453;IP100795394;IP100922629;IP100985458**

Title: 3.1.1.4527.6

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4.3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							11
2	274.1220	137.5646	0	0	0	0	C	1321.6286	661.3179	1304.6020	652.8047	1303.6180	652.3127	10
3	405.1625	203.0849	0	0	0	0	M	1161.5979	581.3026	1144.5714	572.7893	1143.5874	572.2973	9
4	518.2465	259.6269	0	0	0	0	L	1030.5575	515.7824	1013.5309	507.2691	1012.5469	506.7771	8
5	674.3477	337.6775	657.3211	329.1642	0	0	R	917.4734	459.2403	900.4468	450.7271	899.4628	450.2351	7
6	745.3848	373.1960	728.3582	364.6827	0	0	A	761.3723	381.1898	744.3457	372.6765	743.3617	372.1845	6
7	892.4202	446.7137	875.3936	438.2004	0	0	M	690.3352	345.6712	673.3086	337.1579	672.3246	336.6659	5
8	1048.5213	524.7643	1031.4947	516.2510	0	0	R	543.2998	272.1535	526.2732	263.6402	525.2892	263.1482	4
9	1145.5740	573.2907	1128.5475	564.7774	0	0	P	387.1987	194.1030	370.1721	185.5897	369.1881	185.0977	3
10	1260.6010	630.8041	1243.5744	622.2909	1242.5904	621.7988	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
11							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 29582.

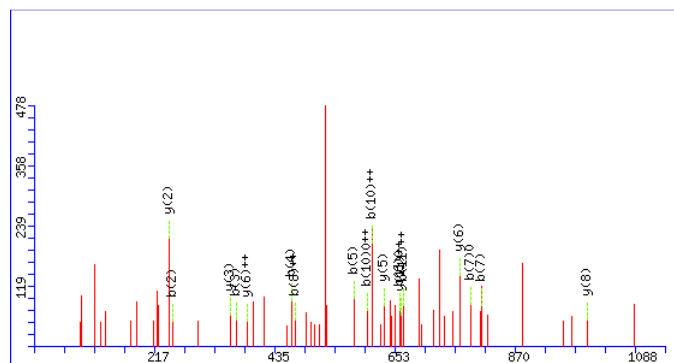
MS/MS Fragmentation of **HLDLTLEHYDIPK**:

Found in **IP100022402**

Title: 2.1.1.1855.5

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	138.0662	69.5367	0	0	0	0	H							13
2	251.1503	126.0788	0	0	0	0	L	1444.7318	722.8696	1427.7053	714.3563	1426.7213	713.8643	12
3	366.1772	183.5922	0	0	348.1666	174.5870	D	1331.6478	666.3275	1314.6212	657.8143	1313.6372	657.3222	11
4	467.2249	234.1161	0	0	449.2143	225.1108	T	1216.6208	608.8141	1199.5943	600.3008	1198.6103	599.8088	10
5	580.3089	290.6581	0	0	562.2984	281.6528	L	1115.5732	558.2902	1098.5466	549.7769	1097.5626	549.2849	9
6	681.3566	341.1819	0	0	663.3461	332.1767	T	1002.4891	501.7482	985.4625	493.2349	984.4785	492.7429	8
7	810.3992	405.7032	0	0	792.3886	396.6980	E	901.4414	451.2243	884.4149	442.7111	883.4308	442.2191	7
8	947.4581	474.2327	0	0	929.4476	465.2274	H	772.3988	386.7030	755.3723	378.1898	754.3883	377.6978	6
9	1110.5215	555.7644	0	0	1092.5109	546.7591	Y	635.3399	318.1736	618.3134	309.6603	617.3293	309.1683	5
10	1225.5484	613.2778	0	0	1207.5378	604.2726	D	472.2766	236.6419	455.2500	228.1287	454.2660	227.6366	4
11	1338.6325	669.8199	0	0	1320.6219	660.8146	I	357.2496	179.1285	340.2231	170.6152	0	0	3
12	1435.6852	718.3462	0	0	1417.6747	709.3410	P	244.1656	122.5864	227.1390	114.0731	0	0	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 29753.

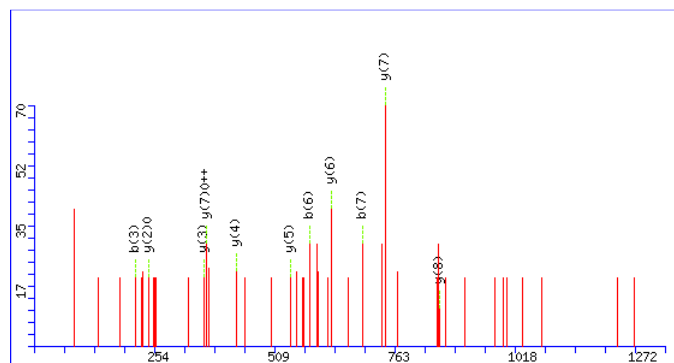
MS/MS Fragmentation of **AAAPCIIFFDELDLAPSR: 57.021465@C:5**

Found in **IP100299182:IP100383261**

Title: 4.1.1.3163.4

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120129ry¥120129ry_604A1-46_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							19
2	143.0815	72.0444	0	0	0	0	A	2022.0001	1011.5037	2004.9735	1002.9904	2003.9895	1002.4984	18
3	214.1186	107.5629	0	0	0	0	A	1950.9630	975.9851	1933.9364	967.4719	1932.9524	966.9798	17
4	311.1714	156.0893	0	0	0	0	P	1879.9259	940.4666	1862.8993	931.9533	1861.9153	931.4613	16
5	471.2020	236.1047	0	0	0	0	C	1782.8731	891.9402	1765.8465	883.4269	1764.8625	882.9349	15
6	584.2861	292.6467	0	0	0	0	I	1622.8424	811.9249	1605.8159	803.4116	1604.8319	802.9196	14
7	697.3702	349.1887	0	0	0	0	I	1509.7584	755.3828	1492.7318	746.8696	1491.7478	746.3775	13
8	844.4386	422.7229	0	0	0	0	F	1396.6743	698.8408	1379.6478	690.3275	1378.6638	689.8355	12
9	991.5070	496.2571	0	0	0	0	F	1249.6059	625.3066	1232.5794	616.7933	1231.5953	616.3013	11
10	1106.5339	553.7706	0	0	1088.5234	544.7653	D	1102.5375	551.7724	1085.5109	543.2591	1084.5269	542.7671	10
11	1235.5765	618.2919	0	0	1217.5660	609.2866	E	987.5105	494.2589	970.4840	485.7456	969.5000	485.2536	9
12	1348.6606	674.8339	0	0	1330.6500	665.8286	L	858.4680	429.7376	841.4414	421.2243	840.4574	420.7323	8
13	1463.6875	732.3474	0	0	1445.6770	723.3421	D	745.3839	373.1956	728.3573	364.6823	727.3733	364.1903	7
14	1550.7196	775.8634	0	0	1532.7090	766.8581	S	630.3569	315.6821	613.3304	307.1688	612.3464	306.6768	6
15	1663.8036	832.4054	0	0	1645.7931	823.4002	L	543.3249	272.1661	526.2984	263.6528	525.3144	263.1608	5
16	1734.8407	867.9240	0	0	1716.8302	858.9187	A	430.2409	215.6241	413.2143	207.1108	412.2303	206.6188	4
17	1831.8935	916.4504	0	0	1813.8829	907.4451	P	359.2037	180.1055	342.1772	171.5922	341.1932	171.1002	3
18	1918.9255	959.9664	0	0	1900.9150	950.9611	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
19							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 29796.

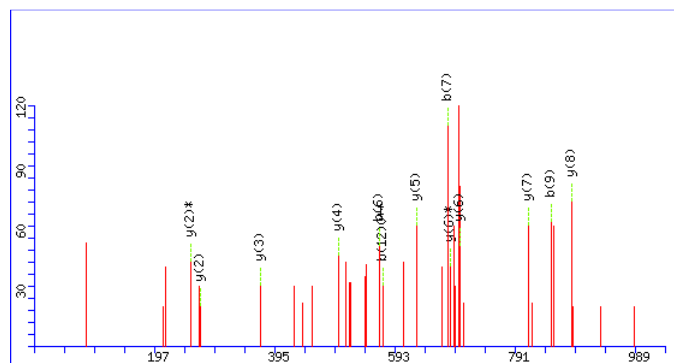
MS/MS Fragmentation of **AGDPLDLVALAEQVQK**:

Found in **IP100012198**

Title: 4.1.1.146.2

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120210ry¥120210ry_585A1-55_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							16
2	129.0659	65.0366	0	0	0	0	G	1595.8639	798.4356	1578.8374	789.9223	1577.8534	789.4303	15
3	244.0928	122.5500	0	0	226.0822	113.5448	D	1538.8425	769.9249	1521.8159	761.4116	1520.8319	760.9196	14
4	341.1456	171.0764	0	0	323.1350	162.0711	P	1423.8155	712.4114	1406.7890	703.8981	1405.8049	703.4061	13
5	454.2296	227.6185	0	0	436.2191	218.6132	L	1326.7627	663.8850	1309.7362	655.3717	1308.7522	654.8797	12
6	569.2566	285.1319	0	0	551.2460	276.1266	D	1213.6787	607.3430	1196.6521	598.8297	1195.6681	598.3377	11
7	682.3406	341.6740	0	0	664.3301	332.6687	L	1098.6517	549.8295	1081.6252	541.3162	1080.6412	540.8242	10
8	781.4090	391.2082	0	0	763.3985	382.2029	V	985.5677	493.2875	968.5411	484.7742	967.5571	484.2822	9
9	852.4462	426.7267	0	0	834.4356	417.7214	A	886.4993	443.7533	869.4727	435.2400	868.4887	434.7480	8
10	965.5302	483.2688	0	0	947.5197	474.2635	L	815.4621	408.2347	798.4356	399.7214	797.4516	399.2294	7
11	1036.5673	518.7873	0	0	1018.5568	509.7820	A	702.3781	351.6927	685.3515	343.1794	684.3675	342.6874	6
12	1165.6099	583.3086	0	0	1147.5994	574.3033	E	631.3410	316.1741	614.3144	307.6608	613.3304	307.1688	5
13	1293.6685	647.3379	1276.6420	638.8246	1275.6579	638.3326	Q	502.2984	251.6528	485.2718	243.1396	0	0	4
14	1392.7369	696.8721	1375.7104	688.3588	1374.7264	687.8668	V	374.2398	187.6235	357.2132	179.1103	0	0	3
15	1520.7955	760.9014	1503.7690	752.3881	1502.7849	751.8961	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
16							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 29887.

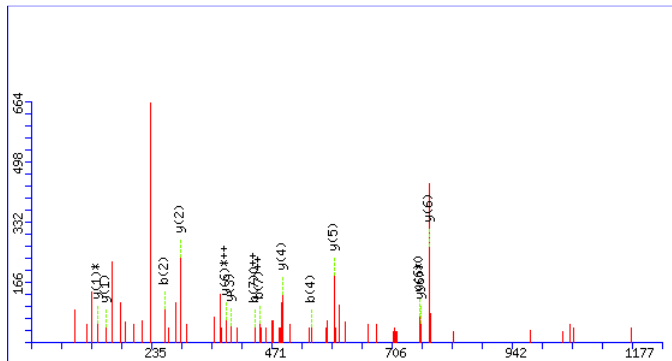
MS/MS Fragmentation of **DFWTTVFK**:

Found in **IP100329125,IP100384047,IP101025821**

Title: 4.1.1.120.3

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120210ry¥120210ry_32R1-32_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							8
2	263.1026	132.0550	0	0	245.0921	123.0497	F	928.4927	464.7500	911.4662	456.2367	910.4822	455.7447	7
3	449.1819	225.0946	0	0	431.1714	216.0893	W	781.4243	391.2158	764.3978	382.7025	763.4137	382.2105	6
4	550.2296	275.6185	0	0	532.2191	266.6132	T	595.3450	298.1761	578.3184	289.6629	577.3344	289.1709	5
5	651.2773	326.1423	0	0	633.2667	317.1370	T	494.2973	247.6523	477.2708	239.1390	476.2867	238.6470	4
6	750.3457	375.6765	0	0	732.3352	366.6712	V	393.2496	197.1285	376.2231	188.6152	0	0	3
7	897.4141	449.2107	0	0	879.4036	440.2054	F	294.1812	147.5942	277.1547	139.0810	0	0	2
8							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 29906.

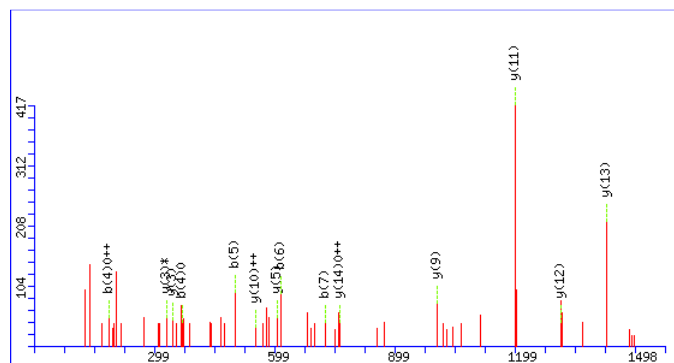
MS/MS Fragmentation of **ATSELILLPVTGLECVGDR: 57.021465@C:15**

Found in **IP100019714;IP100797612;IP100902960;IP100909651;IP100924672;IP100927196;IP100927338;IP100927558;IP101012533**

Title: 3.1.1.4473.11

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120210ry¥120210ry_585A1-55_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							19
2	173.0921	87.0497	0	0	155.0815	78.0444	T	1972.0420	986.5246	1955.0154	978.0113	1954.0314	977.5193	18
3	260.1241	130.5657	0	0	242.1135	121.5604	S	1870.9943	936.0008	1853.9677	927.4875	1852.9837	926.9955	17
4	389.1667	195.0870	0	0	371.1561	186.0817	E	1783.9622	892.4848	1766.9357	883.9715	1765.9517	883.4795	16
5	502.2508	251.6290	0	0	484.2402	242.6237	L	1654.9197	827.9635	1637.8931	819.4502	1636.9091	818.9582	15
6	615.3348	308.1710	0	0	597.3243	299.1658	I	1541.8356	771.4214	1524.8090	762.9082	1523.8250	762.4162	14
7	728.4189	364.7131	0	0	710.4083	355.7078	L	1428.7515	714.8794	1411.7250	706.3661	1410.7410	705.8741	13
8	841.5029	421.2551	0	0	823.4924	412.2498	L	1315.6675	658.3374	1298.6409	649.8241	1297.6569	649.3321	12
9	938.5557	469.7815	0	0	920.5451	460.7762	P	1202.5834	601.7953	1185.5569	593.2821	1184.5728	592.7901	11
10	1037.6241	519.3157	0	0	1019.6136	510.3104	V	1105.5306	553.2690	1088.5041	544.7557	1087.5201	544.2637	10
11	1138.6718	569.8395	0	0	1120.6612	560.8343	T	1006.4622	503.7347	989.4357	495.2215	988.4517	494.7295	9
12	1195.6933	598.3503	0	0	1177.6827	589.3450	G	905.4145	453.2109	888.3880	444.6976	887.4040	444.2056	8
13	1308.7773	654.8923	0	0	1290.7668	645.8870	L	848.3931	424.7002	831.3665	416.1869	830.3825	415.6949	7
14	1437.8199	719.4136	0	0	1419.8094	710.4083	E	735.3090	368.1581	718.2825	359.6449	717.2985	359.1529	6
15	1597.8506	799.4289	0	0	1579.8400	790.4236	C	606.2664	303.6368	589.2399	295.1236	588.2559	294.6316	5
16	1696.9190	848.9631	0	0	1678.9084	839.9578	V	446.2358	223.6215	429.2092	215.1082	428.2252	214.6162	4
17	1753.9405	877.4739	0	0	1735.9299	868.4686	G	347.1674	174.0873	330.1408	165.5740	329.1568	165.0820	3
18	1868.9674	934.9873	0	0	1850.9568	925.9821	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
19							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 30008.

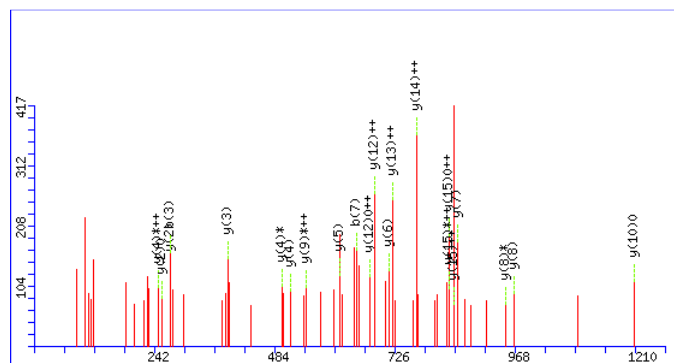
MS/MS Fragmentation of **AAMFTAGSNFNHVVQNEK**:

Found in **IP100031458;IP101015532**

Title: 2.1.1.2672.5

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_2.mgf

ProteinPilot Peptide Confidence > 99%



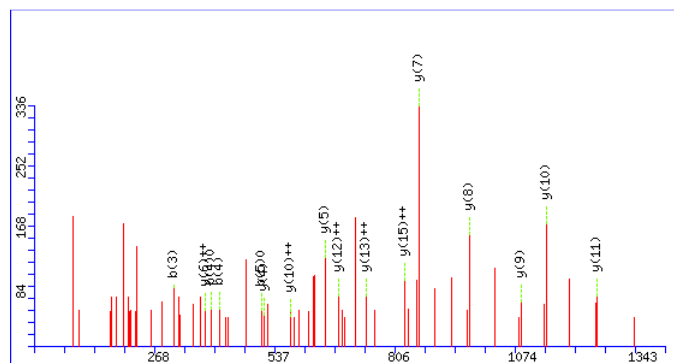
#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							18
2	143.0815	72.0444	0	0	0	0	A	1893.8912	947.4492	1876.8647	938.9360	1875.8806	938.4440	17
3	274.1220	137.5646	0	0	0	0	M	1822.8541	911.9307	1805.8275	903.4174	1804.8435	902.9254	16
4	421.1904	211.0988	0	0	0	0	F	1691.8136	846.4104	1674.7871	837.8972	1673.8030	837.4052	15
5	522.2381	261.6227	0	0	504.2275	252.6174	T	1544.7452	772.8762	1527.7186	764.3630	1526.7346	763.8710	14
6	593.2752	297.1412	0	0	575.2646	288.1360	A	1443.6975	722.3524	1426.6710	713.8391	1425.6870	713.3471	13
7	650.2967	325.6520	0	0	632.2861	316.6467	G	1372.6604	686.8338	1355.6339	678.3206	1354.6498	677.8286	12
8	737.3287	369.1680	0	0	719.3181	360.1627	S	1315.6389	658.3231	1298.6124	649.8098	1297.6284	649.3178	11
9	851.3716	426.1894	834.3451	417.6762	833.3611	417.1842	N	1228.6069	614.8071	1211.5804	606.2938	1210.5963	605.8018	10
10	998.4400	499.7237	981.4135	491.2104	980.4295	490.7184	F	1114.5640	557.7856	1097.5374	549.2724	1096.5534	548.7803	9
11	1112.4830	556.7451	1095.4564	548.2318	1094.4724	547.7398	N	967.4956	484.2514	950.4690	475.7381	949.4850	475.2461	8
12	1249.5419	625.2746	1232.5153	616.7613	1231.5313	616.2693	H	853.4526	427.2300	836.4261	418.7167	835.4421	418.2247	7
13	1348.6103	674.8088	1331.5837	666.2955	1330.5997	665.8035	V	716.3937	358.7005	699.3672	350.1872	698.3832	349.6952	6
14	1447.6787	724.3430	1430.6521	715.8297	1429.6681	715.3377	V	617.3253	309.1663	600.2988	300.6530	599.3148	300.1610	5
15	1575.7373	788.3723	1558.7107	779.8590	1557.7267	779.3670	Q	518.2569	259.6321	501.2304	251.1188	500.2463	250.6268	4
16	1689.7802	845.3937	1672.7537	836.8805	1671.7696	836.3885	N	390.1983	195.6028	373.1718	187.0895	372.1878	186.5975	3
17	1818.8228	909.9150	1801.7962	901.4018	1800.8122	900.9098	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
18							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 30474.

MS/MS Fragmentation of **LAQTLGLEVLGDIPHLNIR**
 Found in **IP100384517;IP100977678;IP100980159;IP101022620**
 Title: 4.1.1.1841.4

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120118ry¥120118ry_201B7-32_2.4.mgf
 ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							20
2	185.1285	93.0679	0	0	0	0	A	2072.1863	1036.5968	2055.1597	1028.0835	2054.1757	1027.5915	19
3	313.1870	157.0972	296.1605	148.5839	0	0	Q	2001.1491	1001.0782	1984.1226	992.5649	1983.1386	992.0729	18
4	414.2347	207.6210	397.2082	199.1077	396.2241	198.6157	T	1873.0906	937.0489	1856.0640	928.5356	1855.0800	928.0436	17
5	527.3188	264.1630	510.2922	255.6498	509.3082	255.1577	L	1772.0429	886.5251	1755.0163	878.0118	1754.0323	877.5198	16
6	584.3402	292.6738	567.3137	284.1605	566.3297	283.6685	G	1658.9588	829.9830	1641.9323	821.4698	1640.9483	820.9778	15
7	697.4243	349.2158	680.3978	340.7025	679.4137	340.2105	L	1601.9374	801.4723	1584.9108	792.9590	1583.9268	792.4670	14
8	826.4669	413.7371	809.4403	405.2238	808.4563	404.7318	E	1488.8533	744.9303	1471.8267	736.4170	1470.8427	735.9250	13
9	925.5353	463.2713	908.5088	454.7580	907.5247	454.2660	V	1359.8107	680.4090	1342.7841	671.8957	1341.8001	671.4037	12
10	1038.6194	519.8133	1021.5928	511.3001	1020.6088	510.8080	L	1260.7423	630.8748	1243.7157	622.3615	1242.7317	621.8695	11
11	1095.6408	548.3241	1078.6143	539.8108	1077.6303	539.3188	G	1147.6582	574.3327	1130.6317	565.8195	1129.6477	565.3275	10
12	1210.6678	605.8375	1193.6412	597.3243	1192.6572	596.8322	D	1090.6368	545.8220	1073.6102	537.3087	1072.6262	536.8167	9
13	1323.7518	662.3796	1306.7253	653.8663	1305.7413	653.3743	I	975.6098	488.3085	958.5833	479.7953	0	0	8
14	1420.8046	710.9059	1403.7781	702.3927	1402.7940	701.9007	P	862.5257	431.7665	845.4992	423.2532	0	0	7
15	1533.8887	767.4480	1516.8621	758.9347	1515.8781	758.4427	L	765.4730	383.2401	748.4464	374.7269	0	0	6
16	1670.9476	835.9774	1653.9210	827.4642	1652.9370	826.9721	H	652.3889	326.6981	635.3624	318.1848	0	0	5
17	1784.0316	892.5195	1767.0051	884.0062	1766.0211	883.5142	L	515.3300	258.1686	498.3035	249.6554	0	0	4
18	1898.0746	949.5409	1881.0480	941.0277	1880.0640	940.5356	N	402.2459	201.6266	385.2194	193.1133	0	0	3
19	2011.1586	1006.0830	1994.1321	997.5697	1993.1481	997.0777	I	288.2030	144.6051	271.1765	136.0919	0	0	2
20							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 30579.

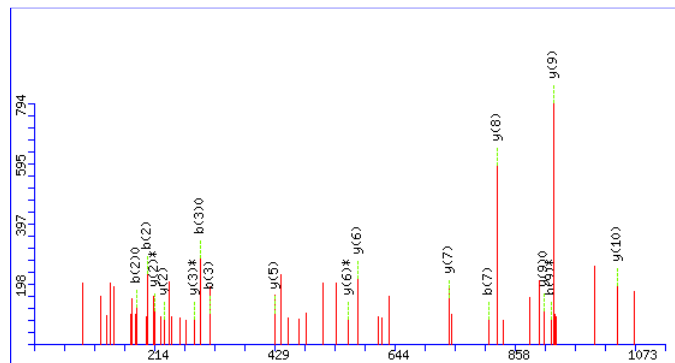
MS/MS Fragmentation of **NSITSYFGAAGR**:

Found in **IP100216510;IP100291983;IP100644804;IP100973456**

Title: 2.1.1.3547.7

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							12
2	202.0822	101.5448	185.0557	93.0315	184.0717	92.5395	S	1129.5636	565.2855	1112.5371	556.7722	1111.5531	556.2802	11
3	315.1663	158.0868	298.1397	149.5735	297.1557	149.0815	I	1042.5316	521.7694	1025.5051	513.2562	1024.5211	512.7642	10
4	416.2140	208.6106	399.1874	200.0974	398.2034	199.6053	T	929.4476	465.2274	912.4210	456.7141	911.4370	456.2221	9
5	503.2460	252.1266	486.2195	243.6134	485.2354	243.1214	S	828.3999	414.7036	811.3733	406.1903	810.3893	405.6983	8
6	666.3093	333.6583	649.2828	325.1450	648.2988	324.6530	Y	741.3679	371.1876	724.3413	362.6743	0	0	7
7	813.3777	407.1925	796.3512	398.6792	795.3672	398.1872	F	578.3045	289.6559	561.2780	281.1426	0	0	6
8	870.3992	435.7032	853.3727	427.1900	852.3886	426.6980	G	431.2361	216.1217	414.2096	207.6084	0	0	5
9	941.4363	471.2218	924.4098	462.7085	923.4258	462.2165	A	374.2146	187.6110	357.1881	179.0977	0	0	4
10	1012.4734	506.7404	995.4469	498.2271	994.4629	497.7351	A	303.1775	152.0924	286.1510	143.5791	0	0	3
11	1069.4949	535.2511	1052.4684	526.7378	1051.4843	526.2458	G	232.1404	116.5738	215.1139	108.0606	0	0	2
12							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 30962.

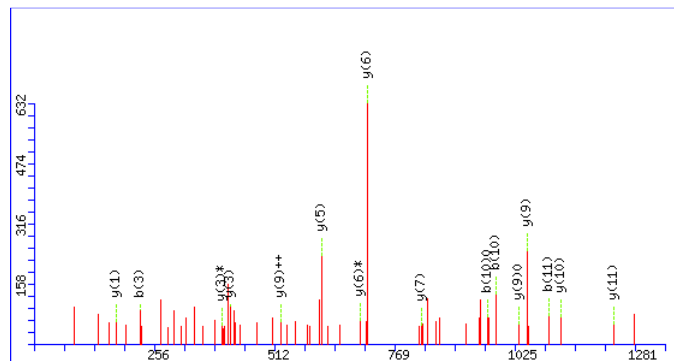
MS/MS Fragmentation of **GAPAEQPVFTILAPDPPVPFR**:

Found in **IP100298662;IP100789616**

Title: 4.1.1.751.5

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							22
2	129.0659	65.0366	0	0	0	0	A	2278.1754	1139.5913	2261.1489	1131.0781	2260.1648	1130.5861	21
3	226.1186	113.5629	0	0	0	0	P	2207.1383	1104.0728	2190.1117	1095.5595	2189.1277	1095.0675	20
4	297.1557	149.0815	0	0	0	0	A	2110.0855	1055.5464	2093.0590	1047.0331	2092.0750	1046.5411	19
5	426.1983	213.6028	0	0	408.1878	204.5975	E	2039.0484	1020.0278	2022.0219	1011.5146	2021.0379	1011.0226	18
6	541.2253	271.1163	0	0	523.2147	262.1110	D	1910.0058	955.5066	1892.9793	946.9933	1891.9953	946.5013	17
7	638.2780	319.6427	0	0	620.2675	310.6374	P	1794.9789	897.9931	1777.9523	889.4798	1776.9683	888.9878	16
8	737.3464	369.1769	0	0	719.3359	360.1716	V	1697.9261	849.4667	1680.8996	840.9534	1679.9156	840.4614	15
9	884.4149	442.7111	0	0	866.4043	433.7058	F	1598.8577	799.9325	1581.8312	791.4192	1580.8471	790.9272	14
10	985.4625	493.2349	0	0	967.4520	484.2296	T	1451.7893	726.3983	1434.7627	717.8850	1433.7787	717.3930	13
11	1098.5466	549.7769	0	0	1080.5360	540.7717	I	1350.7416	675.8744	1333.7151	667.3612	1332.7310	666.8692	12
12	1211.6307	606.3190	0	0	1193.6201	597.3137	L	1237.6575	619.3324	1220.6310	610.8191	1219.6470	610.3271	11
13	1282.6678	641.8375	0	0	1264.6572	632.8322	A	1124.5735	562.7904	1107.5469	554.2771	1106.5629	553.7851	10
14	1379.7205	690.3639	0	0	1361.7100	681.3586	P	1053.5364	527.2718	1036.5098	518.7585	1035.5258	518.2665	9
15	1508.7631	754.8852	0	0	1490.7526	745.8799	E	956.4836	478.7454	939.4571	470.2322	938.4730	469.7402	8
16	1623.7901	812.3987	0	0	1605.7795	803.3934	D	827.4410	414.2241	810.4145	405.7109	809.4305	405.2189	7
17	1720.8428	860.9251	0	0	1702.8323	851.9198	P	712.4141	356.7107	695.3875	348.1974	0	0	6
18	1817.8956	909.4514	0	0	1799.8850	900.4462	P	615.3613	308.1843	598.3348	299.6710	0	0	5
19	1916.9640	958.9856	0	0	1898.9535	949.9804	V	518.3085	259.6579	501.2820	251.1446	0	0	4
20	2014.0168	1007.5120	0	0	1996.0062	998.5067	P	419.2401	210.1237	402.2136	201.6104	0	0	3
21	2161.0852	1081.0462	0	0	2143.0746	1072.0410	F	322.1874	161.5973	305.1608	153.0840	0	0	2
22							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 31371.

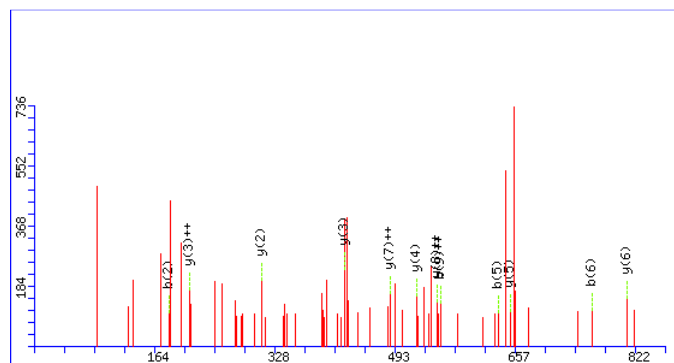
MS/MS Fragmentation of **SPQYQQVIHR: 57.021465@C:5**

Found in **IP100012303;IP100852768;IP100852953;IP100892906;IP100965813;IP101011716;IP101021263**

Title: 1.1.1.8562.4

Data file: Y:\TT5600(CiRA1)\2012-02\120201ry\120201ry_aHDF1388-P9_1_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							10
2	185.0921	93.0497	0	0	167.0815	84.0444	P	1200.5942	600.8008	1183.5677	592.2875	0	0	9
3	313.1506	157.0790	296.1241	148.5657	295.1401	148.0737	Q	1103.5415	552.2744	1086.5149	543.7611	0	0	8
4	476.2140	238.6106	459.1874	230.0974	458.2034	229.6053	Y	975.4829	488.2451	958.4563	479.7318	0	0	7
5	636.2446	318.6260	619.2181	310.1127	618.2341	309.6207	C	812.4196	406.7134	795.3930	398.2001	0	0	6
6	764.3032	382.6552	747.2767	374.1420	746.2926	373.6500	Q	652.3889	326.6981	635.3624	318.1848	0	0	5
7	863.3716	432.1894	846.3451	423.6762	845.3611	423.1842	V	524.3303	262.6688	507.3038	254.1555	0	0	4
8	976.4557	488.7315	959.4291	480.2182	958.4451	479.7262	I	425.2619	213.1346	408.2354	204.6213	0	0	3
9	1113.5146	557.2609	1096.4880	548.7477	1095.5040	548.2557	H	312.1779	156.5926	295.1513	148.0793	0	0	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 31542.

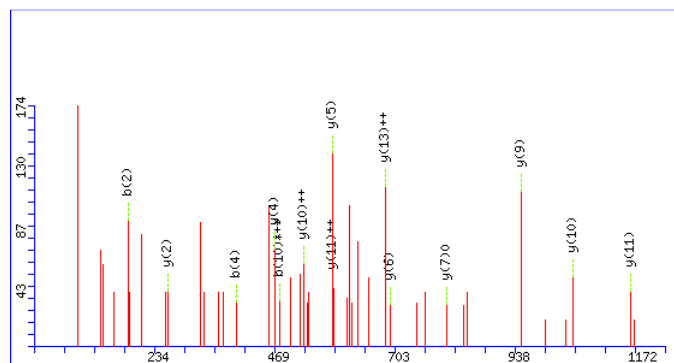
MS/MS Fragmentation of **ALPLIVGAQLIHADK**:

Found in **IP100448752;IP100642238;IP100744429;IP100877866;IP100980952**

Title: 3.1.1.2003.3

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_1_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							15
2	185.1285	93.0679	0	0	0	0	L	1487.8944	744.4509	1470.8679	735.9376	1469.8839	735.4456	14
3	282.1812	141.5942	0	0	0	0	P	1374.8104	687.9088	1357.7838	679.3955	1356.7998	678.9035	13
4	395.2653	198.1363	0	0	0	0	L	1277.7576	639.3824	1260.7310	630.8692	1259.7470	630.3772	12
5	508.3493	254.6783	0	0	0	0	I	1164.6735	582.8404	1147.6470	574.3271	1146.6630	573.8351	11
6	607.4178	304.2125	0	0	0	0	V	1051.5895	526.2984	1034.5629	517.7851	1033.5789	517.2931	10
7	664.4392	332.7233	0	0	0	0	G	952.5211	476.7642	935.4945	468.2509	934.5105	467.7589	9
8	735.4763	368.2418	0	0	0	0	A	895.4996	448.2534	878.4730	439.7402	877.4890	439.2482	8
9	863.5349	432.2711	846.5084	423.7578	0	0	Q	824.4625	412.7349	807.4359	404.2216	806.4519	403.7296	7
10	976.6190	488.8131	959.5924	480.2999	0	0	L	696.4039	348.7056	679.3774	340.1923	678.3933	339.7003	6
11	1089.7030	545.3552	1072.6765	536.8419	0	0	I	583.3198	292.1636	566.2933	283.6503	565.3093	283.1583	5
12	1226.7620	613.8846	1209.7354	605.3713	0	0	H	470.2358	235.6215	453.2092	227.1082	452.2252	226.6162	4
13	1297.7991	649.4032	1280.7725	640.8899	0	0	A	333.1769	167.0921	316.1503	158.5788	315.1663	158.0868	3
14	1412.8260	706.9166	1395.7995	698.4034	1394.8154	697.9114	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
15							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 31614.

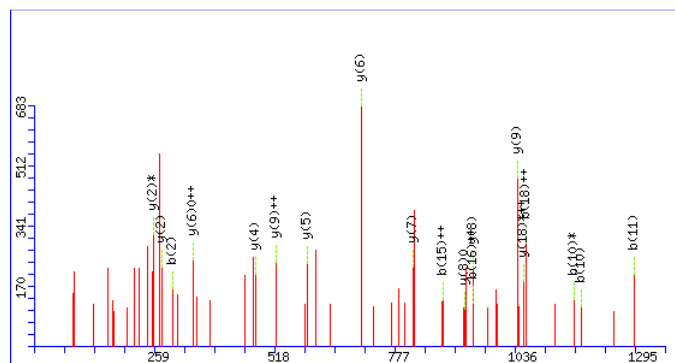
MS/MS Fragmentation of **WINAGHEEDELKPFVEPELDSQK:**

Found in **IP100183118,IP100220505,IP100220506,IP100220507,IP100220508,IP100220509,IP100827718,IP101025908**

Title: 3.1.1.2352.8

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	187.0866	94.0469	0	0	0	0	W							25
2	300.1707	150.5890	0	0	0	0	I	2752.3312	1376.6692	2735.3046	1368.1560	2734.3206	1367.6640	24
3	414.2136	207.6104	397.1870	199.0972	0	0	N	2639.2471	1320.1272	2622.2206	1311.6139	2621.2366	1311.1219	23
4	485.2507	243.1290	468.2241	234.6157	0	0	A	2525.2042	1263.1057	2508.1777	1254.5925	2507.1936	1254.1005	22
5	542.2722	271.6397	525.2456	263.1264	0	0	G	2454.1671	1227.5872	2437.1405	1219.0739	2436.1565	1218.5819	21
6	679.3311	340.1692	662.3045	331.6559	0	0	H	2397.1456	1199.0765	2380.1191	1190.5632	2379.1351	1190.0712	20
7	808.3737	404.6905	791.3471	396.1772	790.3631	395.6852	E	2260.0867	1130.5470	2243.0602	1122.0337	2242.0762	1121.5417	19
8	937.4163	469.2118	920.3897	460.6985	919.4057	460.2065	E	2131.0441	1066.0257	2114.0176	1057.5124	2113.0336	1057.0204	18
9	1052.4432	526.7252	1035.4166	518.2120	1034.4326	517.7200	D	2002.0015	1001.5044	1984.9750	992.9911	1983.9910	992.4991	17
10	1181.4858	591.2465	1164.4592	582.7333	1163.4752	582.2413	E	1886.9746	943.9909	1869.9480	935.4777	1868.9640	934.9856	16
11	1294.5699	647.7886	1277.5433	639.2753	1276.5593	638.7833	L	1757.9320	879.4696	1740.9054	870.9564	1739.9214	870.4644	15
12	1422.6648	711.8360	1405.6383	703.3228	1404.6543	702.8308	K	1644.8479	822.9276	1627.8214	814.4143	1626.8374	813.9223	14
13	1519.7176	760.3624	1502.6910	751.8492	1501.7070	751.3571	P	1516.7530	758.8801	1499.7264	750.3668	1498.7424	749.8748	13
14	1666.7860	833.8966	1649.7594	825.3834	1648.7754	824.8914	F	1419.7002	710.3537	1402.6737	701.8405	1401.6896	701.3485	12
15	1765.8544	883.4308	1748.8279	874.9176	1747.8438	874.4256	V	1272.6318	636.8195	1255.6052	628.3063	1254.6212	627.8142	11
16	1894.8970	947.9521	1877.8705	939.4389	1876.8864	938.9469	E	1173.5634	587.2853	1156.5368	578.7721	1155.5528	578.2800	10
17	1991.9498	996.4785	1974.9232	987.9652	1973.9392	987.4732	P	1044.5208	522.7640	1027.4942	514.2508	1026.5102	513.7587	9
18	2120.9924	1060.9998	2103.9658	1052.4865	2102.9818	1051.9945	E	947.4680	474.2376	930.4415	465.7244	929.4575	465.2324	8
19	2234.0764	1117.5419	2217.0499	1109.0286	2216.0659	1108.5366	L	818.4254	409.7163	801.3989	401.2031	800.4149	400.7111	7
20	2349.1034	1175.0553	2332.0768	1166.5420	2331.0928	1166.0500	D	705.3414	353.1743	688.3148	344.6610	687.3308	344.1690	6
21	2462.1874	1231.5974	2445.1609	1223.0841	2444.1769	1222.5921	I	590.3144	295.6608	573.2879	287.1476	572.3039	286.6556	5
22	2549.2195	1275.1134	2532.1929	1266.6001	2531.2089	1266.1081	S	477.2304	239.1188	460.2038	230.6055	459.2198	230.1135	4
23	2664.2464	1332.6268	2647.2199	1324.1136	2646.2358	1323.6216	D	390.1983	195.6028	373.1718	187.0895	372.1878	186.5975	3
24	2792.3050	1396.6561	2775.2784	1388.1429	2774.2944	1387.6508	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
25							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: **31622**.

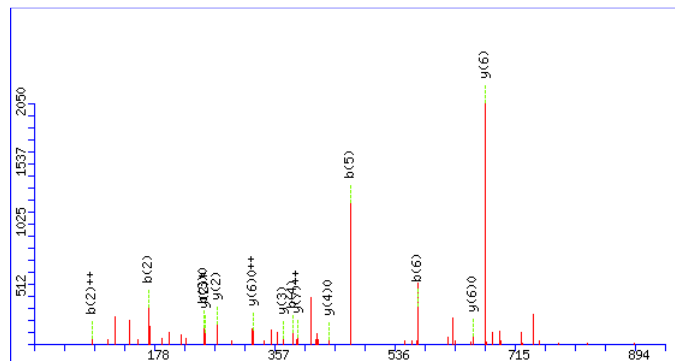
MS/MS Fragmentation of **GITLSVRP**:

Found in **IP101025580**

Title: 2.1.1.446.6

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							8
2	171.1128	86.0600	0	0	0	0	I	785.4880	393.2476	768.4614	384.7343	767.4774	384.2423	7
3	272.1605	136.5839	0	0	254.1499	127.5786	T	672.4039	336.7056	655.3774	328.1923	654.3933	327.7003	6
4	385.2445	193.1259	0	0	367.2340	184.1206	L	571.3562	286.1817	554.3297	277.6685	553.3457	277.1765	5
5	472.2766	236.6419	0	0	454.2660	227.6366	S	458.2722	229.6397	441.2456	221.1264	440.2616	220.6344	4
6	571.3450	286.1761	0	0	553.3344	277.1709	V	371.2401	186.1237	354.2136	177.6104	0	0	3
7	727.4461	364.2267	710.4196	355.7134	709.4355	355.2214	R	272.1717	136.5895	255.1452	128.0762	0	0	2
8							P	116.0706	58.5389	0	0	0	0	1

Peptide View

Peptide: 31641.

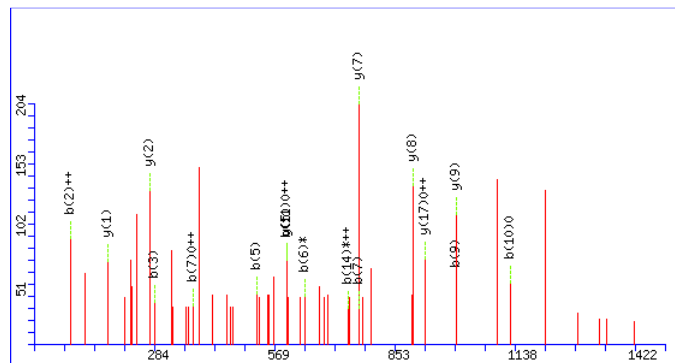
MS/MS Fragmentation of **GLNEDELDFAAALTEGLPLDVR**:

Found in **IP100180672;IP100289462;IP100289463;IP100413557;IP100514315;IP100746947;IP100925345;IP100926940**

Title: 4.1.1.3685.6

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							22
2	171.1128	86.0600	0	0	0	0	L	2343.2078	1172.1076	2326.1813	1163.5943	2325.1973	1163.1023	21
3	285.1557	143.0815	268.1292	134.5682	0	0	N	2230.1238	1115.5655	2213.0972	1107.0522	2212.1132	1106.5602	20
4	414.1983	207.6028	397.1718	199.0895	396.1878	198.5975	E	2116.0808	1058.5441	2099.0543	1050.0308	2098.0703	1049.5388	19
5	529.2253	265.1163	512.1987	256.6030	511.2147	256.1110	D	1987.0382	994.0228	1970.0117	985.5095	1969.0277	985.0175	18
6	658.2679	329.6376	641.2413	321.1243	640.2573	320.6323	E	1872.0113	936.5093	1854.9848	927.9960	1854.0007	927.5040	17
7	771.3519	386.1796	754.3254	377.6663	753.3414	377.1743	L	1742.9687	871.9880	1725.9422	863.4747	1724.9581	862.9827	16
8	884.4360	442.7216	867.4094	434.2084	866.4254	433.7163	L	1629.8846	815.4460	1612.8581	806.9327	1611.8741	806.4407	15
9	999.4629	500.2351	982.4364	491.7218	981.4524	491.2298	D	1516.8006	758.9039	1499.7740	750.3907	1498.7900	749.8986	14
10	1146.5313	573.7693	1129.5048	565.2560	1128.5208	564.7640	F	1401.7736	701.3905	1384.7471	692.8772	1383.7631	692.3852	13
11	1217.5685	609.2879	1200.5419	600.7746	1199.5579	600.2826	A	1254.7052	627.8563	1237.6787	619.3430	1236.6947	618.8510	12
12	1288.6056	644.8064	1271.5790	636.2931	1270.5950	635.8011	A	1183.6681	592.3377	1166.6416	583.8244	1165.6576	583.3324	11
13	1401.6896	701.3485	1384.6631	692.8352	1383.6791	692.3432	L	1112.6310	556.8191	1095.6045	548.3059	1094.6204	547.8139	10
14	1502.7373	751.8723	1485.7108	743.3590	1484.7268	742.8670	T	999.5469	500.2771	982.5204	491.7638	981.5364	491.2718	9
15	1631.7799	816.3936	1614.7534	807.8803	1613.7693	807.3883	E	898.4993	449.7533	881.4727	441.2400	880.4887	440.7480	8
16	1688.8014	844.9043	1671.7748	836.3910	1670.7908	835.8990	G	769.4567	385.2320	752.4301	376.7187	751.4461	376.2267	7
17	1801.8854	901.4464	1784.8589	892.9331	1783.8749	892.4411	L	712.4352	356.7212	695.4087	348.2080	694.4246	347.7160	6
18	1898.9382	949.9727	1881.9117	941.4595	1880.9276	940.9675	P	599.3511	300.1792	582.3246	291.6659	581.3406	291.1739	5
19	2012.0223	1006.5148	1994.9957	998.0015	1994.0117	997.5095	L	502.2984	251.6528	485.2718	243.1395	484.2878	242.6475	4
20	2127.0492	1064.0282	2110.0227	1055.5150	2109.0386	1055.0230	D	389.2143	195.1108	372.1878	186.5975	371.2037	186.1055	3
21	2226.1176	1113.5624	2209.0911	1105.0492	2208.1071	1104.5572	V	274.1874	137.5973	257.1608	129.0840	0	0	2
22							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 31671.

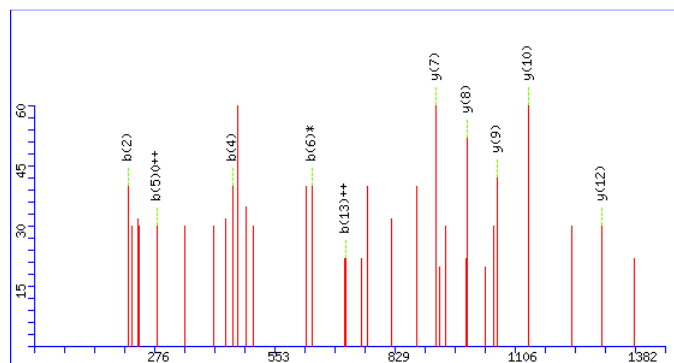
MS/MS Fragmentation of **TNIQQAVAAAPWWLPVK**:

Found in **IP100301144;IP100332413;IP100432718;IP100785161;IP101009479**

Title: 4.1.1.442.10

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							17
2	216.0979	108.5526	199.0713	100.0393	198.0873	99.5473	N	1791.9905	896.4989	1774.9639	887.9856	0	0	16
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	I	1677.9475	839.4774	1660.9210	830.9641	0	0	15
4	457.2405	229.1239	440.2140	220.6106	439.2300	220.1186	Q	1564.8635	782.9354	1547.8369	774.4221	0	0	14
5	585.2991	293.1532	568.2726	284.6399	567.2885	284.1479	Q	1436.8049	718.9061	1419.7783	710.3928	0	0	13
6	656.3362	328.6717	639.3097	320.1585	638.3257	319.6665	A	1308.7463	654.8768	1291.7198	646.3635	0	0	12
7	755.4046	378.2060	738.3781	369.6927	737.3941	369.2007	V	1237.7092	619.3582	1220.6826	610.8450	0	0	11
8	826.4417	413.7245	809.4152	405.2112	808.4312	404.7192	A	1138.6408	569.8240	1121.6142	561.3108	0	0	10
9	897.4789	449.2431	880.4523	440.7298	879.4683	440.2378	A	1067.6037	534.3055	1050.5771	525.7922	0	0	9
10	968.5160	484.7616	951.4894	476.2483	950.5054	475.7563	A	996.5665	498.7869	979.5400	490.2736	0	0	8
11	1065.5687	533.2880	1048.5422	524.7747	1047.5582	524.2827	P	925.5294	463.2684	908.5029	454.7551	0	0	7
12	1251.6480	626.3277	1234.6215	617.8144	1233.6375	617.3224	W	828.4767	414.7420	811.4501	406.2287	0	0	6
13	1437.7274	719.3673	1420.7008	710.8540	1419.7168	710.3620	W	642.3974	321.7023	625.3708	313.1890	0	0	5
14	1550.8114	775.9094	1533.7849	767.3961	1532.8009	766.9041	L	456.3180	228.6627	439.2915	220.1494	0	0	4
15	1647.8642	824.4357	1630.8376	815.9225	1629.8536	815.4305	P	343.2340	172.1206	326.2074	163.6074	0	0	3
16	1746.9326	873.9699	1729.9061	865.4567	1728.9220	864.9647	V	246.1812	123.5942	229.1547	115.0810	0	0	2
17							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 31755.

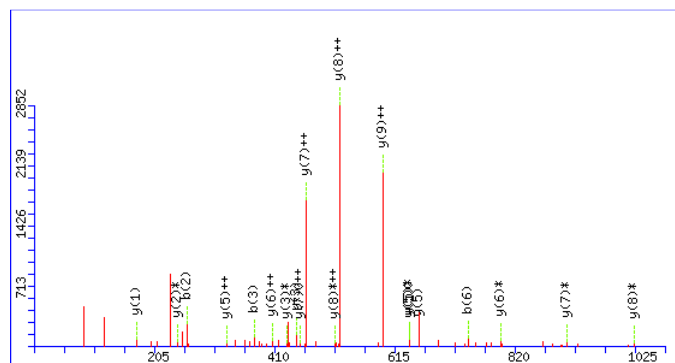
MS/MS Fragmentation of **LFDIRPIWSR**:

Found in **IP100411531;IP100514820;IP100641212;IP100642443;IP100844182;IP100871523;IP100879210;IP100940853**

Title: 3.1.1.2364.2

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							10
2	261.1598	131.0835	0	0	0	0	F	1189.6477	595.3275	1172.6211	586.8142	1171.6371	586.3222	9
3	376.1867	188.5970	0	0	358.1761	179.5917	D	1042.5792	521.7933	1025.5527	513.2800	1024.5687	512.7880	8
4	489.2708	245.1390	0	0	471.2602	236.1337	I	927.5523	464.2798	910.5257	455.7665	909.5417	455.2745	7
5	645.3719	323.1896	628.3453	314.6763	627.3613	314.1843	R	814.4682	407.7378	797.4417	399.2245	796.4577	398.7325	6
6	742.4246	371.7160	725.3981	363.2027	724.4141	362.7107	P	658.3671	329.6872	641.3406	321.1739	640.3566	320.6819	5
7	855.5087	428.2580	838.4822	419.7447	837.4981	419.2527	I	561.3144	281.1608	544.2878	272.6475	543.3038	272.1555	4
8	1041.5880	521.2976	1024.5615	512.7844	1023.5774	512.2924	W	448.2303	224.6188	431.2037	216.1055	430.2197	215.6135	3
9	1128.6200	564.8137	1111.5935	556.3004	1110.6095	555.8084	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

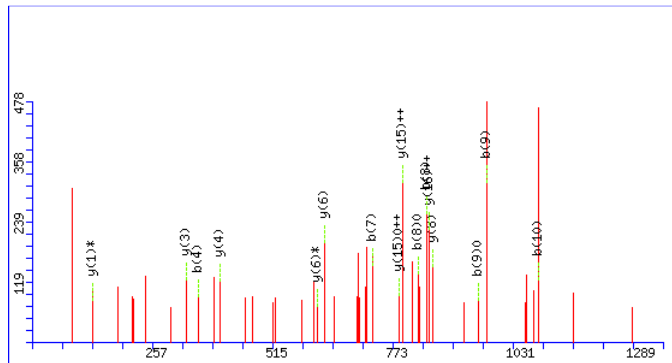
Peptide: 31789.

MS/MS Fragmentation of **GSGREEDDELLGNDDSDKTELLAGQK: 0.984015@N:13**
Found in **IPI00177912;IPI01011242;IPI01012314**

Title: 2.1.1.2532.9

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							26
2	145.0608	73.0340	0	0	127.0502	64.0287	S	2735.2490	1368.1281	2718.2224	1359.6149	2717.2384	1359.1228	25
3	202.0822	101.5448	0	0	184.0717	92.5395	G	2648.2170	1324.6121	2631.1904	1316.0988	2630.2064	1315.6068	24
4	358.1833	179.5953	341.1568	171.0820	340.1728	170.5900	R	2591.1955	1296.1014	2574.1689	1287.5881	2573.1849	1287.0961	23
5	487.2259	244.1166	470.1994	235.6033	469.2154	235.1113	E	2435.0944	1218.0508	2418.0678	1209.5376	2417.0838	1209.0455	22
6	616.2685	308.6379	599.2420	300.1246	598.2580	299.6326	E	2306.0518	1153.5295	2289.0252	1145.0163	2288.0412	1144.5242	21
7	731.2955	366.1514	714.2689	357.6381	713.2849	357.1461	D	2177.0092	1089.0082	2159.9826	1080.4950	2158.9986	1080.0030	20
8	846.3224	423.6648	829.2959	415.1516	828.3119	414.6596	D	2061.9828	1031.4948	2044.9557	1022.9815	2043.9717	1022.4895	19
9	975.3650	488.1861	958.3385	479.6729	957.3544	479.1809	E	1946.9553	973.9813	1929.9288	965.4680	1928.9447	964.9760	18
10	1088.4491	544.7282	1071.4225	536.2149	1070.4385	535.7229	L	1817.9127	909.4600	1800.8862	900.9467	1799.9021	900.4547	17
11	1201.5331	601.2702	1184.5066	592.7569	1183.5226	592.2649	L	1704.8286	852.9180	1687.8021	844.4047	1686.8181	843.9127	16
12	1258.5546	629.7809	1241.5281	621.2677	1240.5440	620.7757	G	1591.7446	796.3759	1574.7180	787.8627	1573.7340	787.3706	15
13	1373.5815	687.2944	1356.5550	678.7811	1355.5710	678.2891	N	1534.7231	767.8652	1517.6966	759.3519	1516.7126	758.8599	14
14	1488.6085	744.8079	1471.5819	736.2946	1470.5979	735.8026	D	1419.6962	710.3517	1402.6696	701.8385	1401.6856	701.3464	13
15	1603.6354	802.3214	1586.6089	793.8081	1585.6249	793.3161	D	1304.6692	652.8383	1287.6427	644.3250	1286.6587	643.8330	12
16	1690.6675	845.8374	1673.6409	837.3241	1672.6569	836.8321	S	1189.6423	595.3248	1172.6157	586.8115	1171.6317	586.3195	11
17	1805.6944	903.3508	1788.6678	894.8376	1787.6838	894.3456	D	1102.6103	551.8088	1085.5837	543.2955	1084.5997	542.8035	10
18	1933.7894	967.3983	1916.7628	958.8850	1915.7788	958.3930	K	987.5833	494.2953	970.5568	485.7820	969.5728	485.2900	9
19	2034.8370	1017.9222	2017.8105	1009.4089	2016.8265	1008.9169	T	859.4884	430.2478	842.4618	421.7345	841.4778	421.2425	8
20	2163.8796	1082.4435	2146.8531	1073.9302	2145.8691	1073.4382	E	758.4407	379.7240	741.4141	371.2107	740.4301	370.7187	7
21	2276.9637	1138.9855	2259.9371	1130.4722	2258.9531	1129.9802	L	629.3981	315.2027	612.3715	306.6894	0	0	6
22	2390.0478	1195.5275	2373.0212	1187.0142	2372.0372	1186.5222	L	516.3140	258.6606	499.2875	250.1474	0	0	5
23	2461.0849	1231.0461	2444.0583	1222.5328	2443.0743	1222.0408	A	403.2300	202.1186	386.2034	193.6053	0	0	4
24	2518.1063	1259.5568	2501.0798	1251.0435	2500.0958	1250.5515	G	332.1928	166.6001	315.1663	158.0868	0	0	3
25	2646.1649	1323.5861	2629.1384	1315.0728	2628.1544	1314.5808	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
26							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 31900.

MS/MS Fragmentation of **MYGCDLGPDGR: 57.021465@C:4**

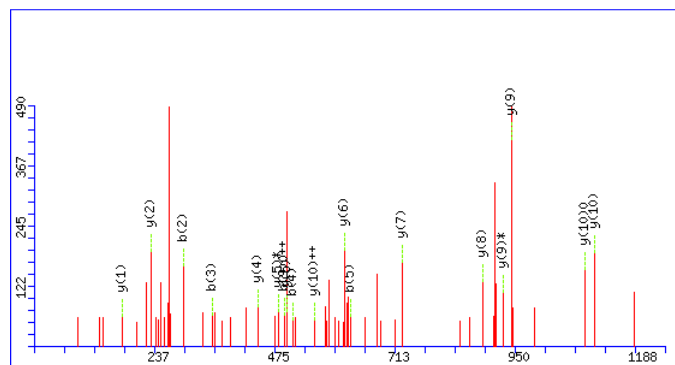
Found in

IP100471951;IP100471955;IP100472138;IP100472416;IP100472456;IP100472605;IP100472903;IP100473006;IP100655604;IP100657976;IP100743716;IP100788914;IP1007891

Title: 2.1.1.578.10

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120201ry¥120201ry_aHDF1388-P9_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	132.0478	66.5275	0	0	0	0	M							11
2	295.1111	148.0592	0	0	0	0	Y	1109.4680	555.2377	1092.4415	546.7244	1091.4575	546.2324	10
3	352.1326	176.5699	0	0	0	0	G	946.4047	473.7060	929.3782	465.1927	928.3941	464.7007	9
4	512.1632	256.5852	0	0	0	0	C	889.3832	445.1953	872.3567	436.6820	871.3727	436.1900	8
5	627.1901	314.0987	0	0	609.1796	305.0934	D	729.3526	365.1799	712.3260	356.6667	711.3420	356.1747	7
6	740.2742	370.6407	0	0	722.2636	361.6355	L	614.3257	307.6665	597.2991	299.1532	596.3151	298.6612	6
7	797.2957	399.1515	0	0	779.2851	390.1462	G	501.2416	251.1244	484.2150	242.6112	483.2310	242.1191	5
8	894.3484	447.6779	0	0	876.3379	438.6726	P	444.2201	222.6137	427.1936	214.1004	426.2096	213.6084	4
9	1009.3754	505.1913	0	0	991.3648	496.1860	D	347.1674	174.0873	330.1408	165.5740	329.1568	165.0820	3
10	1066.3968	533.7021	0	0	1048.3863	524.6968	G	232.1404	116.5738	215.1139	108.0606	0	0	2
11							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 31914.

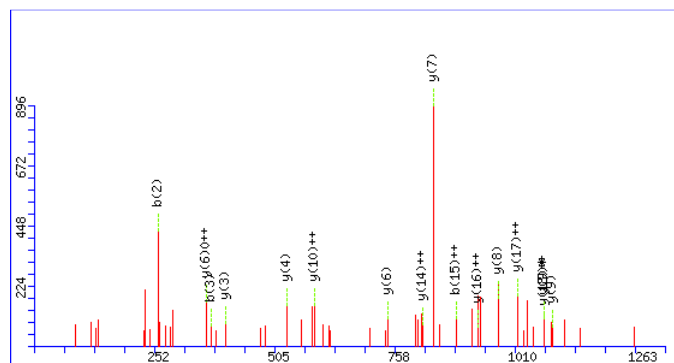
MS/MS Fragmentation of **LFLYSFNDNNSIHPLVEVQR**:

Found in **IP100030511**

Title: 3.1.1.2851.9

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120212ry¥120212ry_414C2-43_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							20
2	261.1598	131.0835	0	0	0	0	F	2292.1408	1146.5740	2275.1142	1138.0607	2274.1302	1137.5687	19
3	374.2438	187.6255	0	0	0	0	L	2145.0723	1073.0398	2128.0458	1064.5265	2127.0618	1064.0345	18
4	537.3071	269.1572	0	0	0	0	Y	2031.9883	1016.4978	2014.9617	1007.9845	2013.9777	1007.4925	17
5	624.3392	312.6732	0	0	606.3286	303.6679	S	1868.9249	934.9661	1851.8984	926.4528	1850.9144	925.9608	16
6	771.4076	386.2074	0	0	753.3970	377.2022	F	1781.8929	891.4501	1764.8664	882.9368	1763.8824	882.4448	15
7	885.4505	443.2289	868.4240	434.7156	867.4400	434.2236	N	1634.8245	817.9159	1617.7980	809.4026	1616.8139	808.9106	14
8	1000.4775	500.7424	983.4509	492.2291	982.4669	491.7371	D	1520.7816	760.8944	1503.7550	752.3812	1502.7710	751.8891	13
9	1114.5204	557.7638	1097.4938	549.2506	1096.5098	548.7585	N	1405.7546	703.3810	1388.7281	694.8677	1387.7441	694.3757	12
10	1228.5633	614.7853	1211.5368	606.2720	1210.5527	605.7800	N	1291.7117	646.3595	1274.6852	637.8462	1273.7011	637.3542	11
11	1315.5953	658.3013	1298.5688	649.7880	1297.5848	649.2960	S	1177.6688	589.3380	1160.6422	580.8248	1159.6582	580.3327	10
12	1428.6794	714.8433	1411.6529	706.3301	1410.6688	705.8381	I	1090.6368	545.8220	1073.6102	537.3087	1072.6262	536.8167	9
13	1565.7383	783.3728	1548.7118	774.8595	1547.7278	774.3675	H	977.5527	489.2800	960.5261	480.7667	959.5421	480.2747	8
14	1662.7911	831.8992	1645.7645	823.3859	1644.7805	822.8939	P	840.4938	420.7505	823.4672	412.2373	822.4832	411.7452	7
15	1775.8751	888.4412	1758.8486	879.9279	1757.8646	879.4359	L	743.4410	372.2241	726.4145	363.7109	725.4305	363.2189	6
16	1874.9436	937.9754	1857.9170	929.4621	1856.9330	928.9701	V	630.3570	315.6821	613.3304	307.1688	612.3464	306.6768	5
17	2003.9862	1002.4967	1986.9596	993.9834	1985.9756	993.4914	E	531.2885	266.1479	514.2620	257.6346	513.2780	257.1426	4
18	2103.0546	1052.0309	2086.0280	1043.5176	2085.0440	1043.0256	V	402.2459	201.6266	385.2194	193.1133	0	0	3
19	2231.1131	1116.0602	2214.0866	1107.5469	2213.1026	1107.0549	Q	303.1775	152.0924	286.1510	143.5791	0	0	2
20							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 31944.

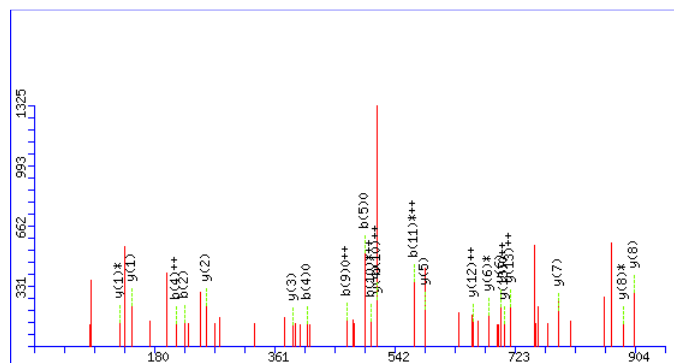
MS/MS Fragmentation of **ILTTSEDSNAQEIK**:

Found in **IP100030257;IP100658115;IP100940583;IP101018725**

Title: 1.1.1.8782.7

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120212ry¥120212ry_414C2-43_3_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							14
2	227.1754	114.0913	0	0	0	0	L	1435.6911	718.3492	1418.6645	709.8359	1417.6805	709.3439	13
3	328.2231	164.6152	0	0	310.2125	155.6099	T	1322.6070	661.8072	1305.5805	653.2939	1304.5965	652.8019	12
4	429.2708	215.1390	0	0	411.2602	206.1337	T	1221.5594	611.2833	1204.5328	602.7700	1203.5488	602.2780	11
5	516.3028	258.6550	0	0	498.2922	249.6498	S	1120.5117	560.7595	1103.4851	552.2462	1102.5011	551.7542	10
6	645.3454	323.1763	0	0	627.3348	314.1710	E	1033.4796	517.2435	1016.4531	508.7302	1015.4691	508.2382	9
7	760.3723	380.6898	0	0	742.3618	371.6845	D	904.4371	452.7222	887.4105	444.2089	886.4265	443.7169	8
8	847.4044	424.2058	0	0	829.3938	415.2005	S	789.4101	395.2087	772.3836	386.6954	771.3995	386.2034	7
9	961.4473	481.2273	944.4207	472.7140	943.4367	472.2220	N	702.3781	351.6927	685.3515	343.1794	684.3675	342.6874	6
10	1032.4844	516.7458	1015.4578	508.2326	1014.4738	507.7406	A	588.3352	294.6712	571.3086	286.1579	570.3246	285.6659	5
11	1160.5430	580.7751	1143.5164	572.2618	1142.5324	571.7698	Q	517.2980	259.1527	500.2715	250.6394	499.2875	250.1474	4
12	1289.5856	645.2964	1272.5590	636.7831	1271.5750	636.2911	E	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
13	1402.6696	701.8385	1385.6431	693.3252	1384.6591	692.8332	I	260.1969	130.6021	243.1703	122.0888	0	0	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 31974.

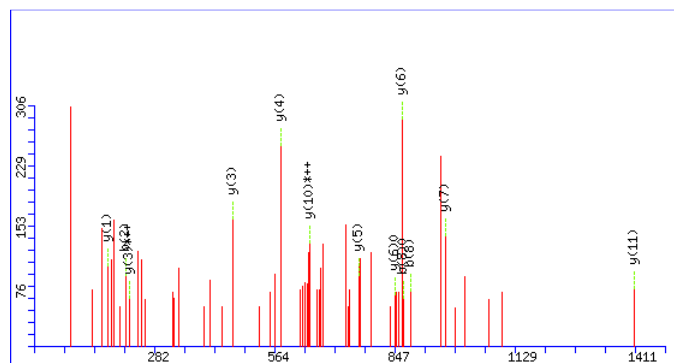
MS/MS Fragmentation of **DVPLETDDLTTWLYQR**:

Found in **IP100022447**

Title: 4.1.1.535.3

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120212ry¥120212ry_aHDF1388-P9_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							16
2	215.1028	108.0550	0	0	197.0921	99.0497	V	1849.9331	925.4702	1832.9065	916.9569	1831.9225	916.4649	15
3	312.1554	156.5813	0	0	294.1448	147.5761	P	1750.8646	875.9360	1733.8381	867.4227	1732.8541	866.9307	14
4	425.2395	213.1234	0	0	407.2289	204.1181	L	1653.8119	827.4096	1636.7853	818.8963	1635.8013	818.4043	13
5	554.2821	277.6447	0	0	536.2715	268.6394	E	1540.7278	770.8675	1523.7013	762.3543	1522.7173	761.8623	12
6	655.3297	328.1685	0	0	637.3192	319.1632	T	1411.6852	706.3462	1394.6587	697.8330	1393.6747	697.3410	11
7	770.3567	385.6820	0	0	752.3461	376.6767	D	1310.6375	655.8224	1293.6110	647.3091	1292.6270	646.8171	10
8	885.3836	443.1954	0	0	867.3731	434.1902	D	1195.6106	598.3089	1178.5841	589.7957	1177.6000	589.3037	9
9	998.4677	499.7375	0	0	980.4571	490.7322	L	1080.5837	540.7955	1063.5571	532.2822	1062.5731	531.7902	8
10	1099.5154	550.2613	0	0	1081.5048	541.2560	T	967.4996	484.2534	950.4730	475.7402	949.4890	475.2482	7
11	1200.5630	600.7852	0	0	1182.5525	591.7799	T	866.4519	433.7296	849.4254	425.2163	848.4414	424.7243	6
12	1386.6424	693.8248	0	0	1368.6318	684.8195	W	765.4042	383.2058	748.3777	374.6925	0	0	5
13	1499.7264	750.3668	0	0	1481.7159	741.3616	L	579.3249	290.1661	562.2984	281.6528	0	0	4
14	1662.7897	831.8985	0	0	1644.7792	822.8932	Y	466.2409	233.6241	449.2143	225.1108	0	0	3
15	1790.8483	895.9278	1773.8218	887.4145	1772.8378	886.9225	Q	303.1775	152.0924	286.1510	143.5791	0	0	2
16							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 32067.

MS/MS Fragmentation of **SGGGPVLSWQR**:

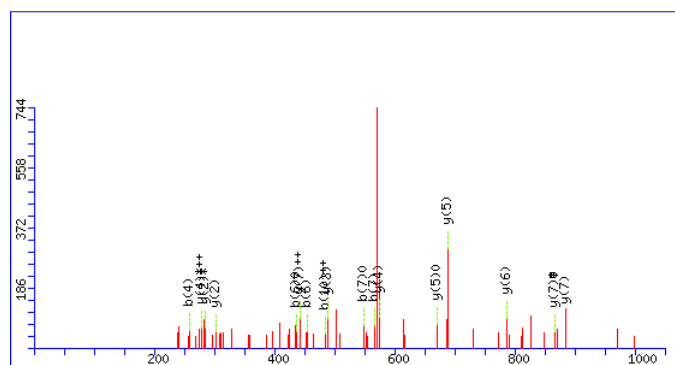
Found in

IP100064457;IP100167358;IP100792479;IP100976043;IP100977906;IP100979036;IP100980428;IP100981114;IP100981723;IP100982403;IP100983041;IP100984071;IP100984

Title: 2.1.1.2075.7

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120212ry¥120212ry_aHDF1388-P9_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							11
2	145.0608	73.0340	0	0	127.0502	64.0287	G	1056.5585	528.7829	1039.5320	520.2696	1038.5479	519.7776	10
3	202.0822	101.5448	0	0	184.0717	92.5395	G	999.5370	500.2722	982.5105	491.7589	981.5265	491.2669	9
4	259.1037	130.0555	0	0	241.0931	121.0502	G	942.5156	471.7614	925.4890	463.2482	924.5050	462.7561	8
5	356.1565	178.5819	0	0	338.1459	169.5766	P	885.4941	443.2507	868.4676	434.7374	867.4835	434.2454	7
6	455.2249	228.1161	0	0	437.2143	219.1108	V	788.4413	394.7243	771.4148	386.2110	770.4308	385.7190	6
7	568.3089	284.6581	0	0	550.2984	275.6528	L	689.3729	345.1901	672.3464	336.6768	671.3624	336.1848	5
8	655.3410	328.1741	0	0	637.3304	319.1688	S	576.2889	288.6481	559.2623	280.1348	558.2783	279.6428	4
9	841.4203	421.2138	0	0	823.4097	412.2085	W	489.2568	245.1321	472.2303	236.6188	0	0	3
10	969.4789	485.2431	952.4523	476.7298	951.4683	476.2378	Q	303.1775	152.0924	286.1510	143.5791	0	0	2
11							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 32377.

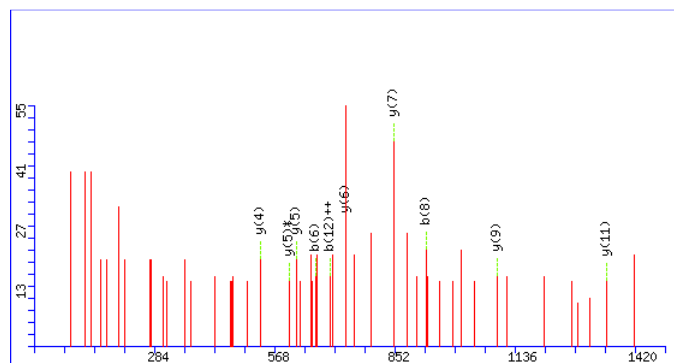
MS/MS Fragmentation of **FYSPATIFIDEIDSICSR: 57.021465@C:16**

Found in **IP100013075:IP100384339**

Title: 4.1.1.4401.4

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							18
2	311.1390	156.0731	0	0	0	0	Y	1986.9477	993.9775	1969.9212	985.4642	1968.9372	984.9722	17
3	398.1710	199.5892	0	0	380.1605	190.5839	S	1823.8844	912.4458	1806.8578	903.9326	1805.8738	903.4406	16
4	495.2238	248.1155	0	0	477.2132	239.1103	P	1736.8524	868.9298	1719.8258	860.4165	1718.8418	859.9245	15
5	566.2609	283.6341	0	0	548.2504	274.6288	A	1639.7996	820.4034	1622.7731	811.8902	1621.7890	811.3982	14
6	667.3086	334.1579	0	0	649.2980	325.1527	T	1568.7625	784.8849	1551.7359	776.3716	1550.7519	775.8796	13
7	780.3927	390.7000	0	0	762.3821	381.6947	I	1467.7148	734.3610	1450.6883	725.8478	1449.7042	725.3558	12
8	927.4611	464.2342	0	0	909.4505	455.2289	F	1354.6307	677.8190	1337.6042	669.3057	1336.6202	668.8137	11
9	1040.5451	520.7762	0	0	1022.5346	511.7709	I	1207.5623	604.2848	1190.5358	595.7715	1189.5518	595.2795	10
10	1155.5721	578.2897	0	0	1137.5615	569.2844	D	1094.4783	547.7428	1077.4517	539.2295	1076.4677	538.7375	9
11	1284.6147	642.8110	0	0	1266.6041	633.8057	E	979.4513	490.2293	962.4248	481.7160	961.4408	481.2240	8
12	1397.6987	699.3530	0	0	1379.6882	690.3477	I	850.4087	425.7080	833.3822	417.1947	832.3982	416.7027	7
13	1512.7257	756.8665	0	0	1494.7151	747.8612	D	737.3247	369.1660	720.2981	360.6527	719.3141	360.1607	6
14	1599.7577	800.3825	0	0	1581.7472	791.3772	S	622.2977	311.6525	605.2712	303.1392	604.2872	302.6472	5
15	1712.8418	856.9245	0	0	1694.8312	847.9192	I	535.2657	268.1365	518.2391	259.6232	517.2551	259.1312	4
16	1872.8724	936.9399	0	0	1854.8619	927.9346	C	422.1816	211.5945	405.1551	203.0812	404.1711	202.5892	3
17	1959.9045	980.4559	0	0	1941.8939	971.4506	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
18							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 32424.

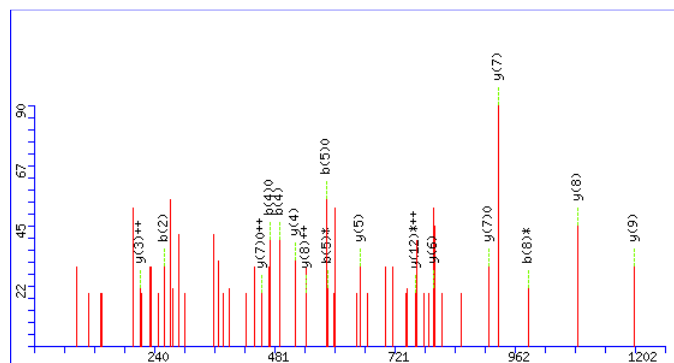
MS/MS Fragmentation of **NFQTILCEFETLYK: 57.021465@C:7**

Found in **IP100465237**

Title: 4.1.1.3559.4

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							14
2	262.1186	131.5629	245.0921	123.0497	0	0	F	1691.8349	846.4211	1674.8084	837.9078	1673.8244	837.4158	13
3	390.1772	195.5922	373.1506	187.0790	0	0	Q	1544.7665	772.8869	1527.7400	764.3736	1526.7559	763.8816	12
4	491.2249	246.1161	474.1983	237.6028	473.2143	237.1108	T	1416.7079	708.8576	1399.6814	700.3443	1398.6974	699.8523	11
5	604.3089	302.6581	587.2824	294.1448	586.2984	293.6528	I	1315.6603	658.3338	1298.6337	649.8205	1297.6497	649.3285	10
6	717.3930	359.2001	700.3665	350.6869	699.3824	350.1949	L	1202.5762	601.7917	1185.5496	593.2785	1184.5656	592.7865	9
7	877.4237	439.2155	860.3971	430.7022	859.4131	430.2102	C	1089.4921	545.2497	1072.4656	536.7364	1071.4816	536.2444	8
8	1006.4662	503.7368	989.4397	495.2235	988.4557	494.7315	E	929.4615	465.2344	912.4349	456.7211	911.4509	456.2291	7
9	1153.5347	577.2710	1136.5081	568.7577	1135.5241	568.2657	F	800.4189	400.7131	783.3923	392.1998	782.4083	391.7078	6
10	1282.5773	641.7923	1265.5507	633.2790	1264.5667	632.7870	E	653.3505	327.1789	636.3239	318.6656	635.3399	318.1736	5
11	1383.6249	692.3161	1366.5984	683.8028	1365.6144	683.3108	T	524.3079	262.6576	507.2813	254.1443	506.2973	253.6523	4
12	1496.7090	748.8581	1479.6824	740.3449	1478.6984	739.8529	L	423.2602	212.1337	406.2336	203.6205	0	0	3
13	1659.7723	830.3898	1642.7458	821.8765	1641.7618	821.3845	Y	310.1761	155.5917	293.1496	147.0784	0	0	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: **32559.**

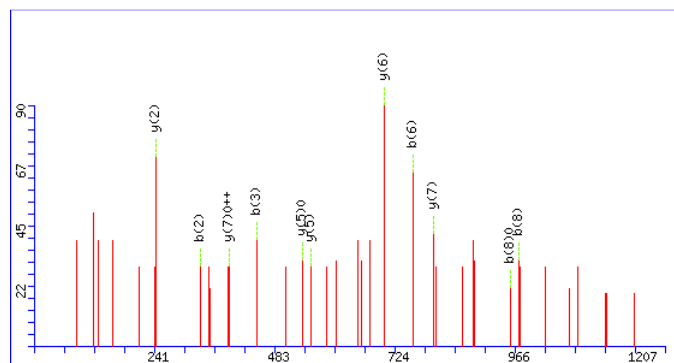
MS/MS Fragmentation of **FWLEQQVDSSVFEALPK:**

Found in **IP100328703,IP100979582**

Title: 4.1.1.764.2

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							17
2	334.1550	167.5811	0	0	0	0	W	1804.9116	902.9594	1787.8850	894.4462	1786.9010	893.9542	16
3	447.2391	224.1232	0	0	0	0	L	1618.8323	809.9198	1601.8057	801.4065	1600.8217	800.9145	15
4	576.2817	288.6445	0	0	558.2711	279.6392	E	1505.7482	753.3777	1488.7217	744.8645	1487.7377	744.3725	14
5	704.3402	352.6738	687.3137	344.1605	686.3297	343.6685	Q	1376.7056	688.8564	1359.6791	680.3432	1358.6951	679.8512	13
6	761.3617	381.1845	744.3352	372.6712	743.3511	372.1792	G	1248.6470	624.8272	1231.6205	616.3139	1230.6365	615.8219	12
7	860.4301	430.7187	843.4036	422.2054	842.4196	421.7134	V	1191.6256	596.3164	1174.5990	587.8032	1173.6150	587.3111	11
8	975.4571	488.2322	958.4305	479.7189	957.4465	479.2269	D	1092.5572	546.7822	1075.5306	538.2689	1074.5466	537.7769	10
9	1062.4891	531.7482	1045.4625	523.2349	1044.4785	522.7429	S	977.5302	489.2687	960.5037	480.7555	959.5197	480.2635	9
10	1149.5211	575.2642	1132.4946	566.7509	1131.5106	566.2589	S	890.4982	445.7527	873.4716	437.2395	872.4876	436.7475	8
11	1248.5895	624.7984	1231.5630	616.2851	1230.5790	615.7931	V	803.4662	402.2367	786.4396	393.7234	785.4556	393.2314	7
12	1395.6579	698.3326	1378.6314	689.8193	1377.6474	689.3273	F	704.3978	352.7025	687.3712	344.1892	686.3872	343.6972	6
13	1524.7005	762.8539	1507.6740	754.3406	1506.6900	753.8486	E	557.3293	279.1683	540.3028	270.6550	539.3188	270.1630	5
14	1595.7377	798.3725	1578.7111	789.8592	1577.7271	789.3672	A	428.2867	214.6470	411.2602	206.1337	0	0	4
15	1708.8217	854.9145	1691.7952	846.4012	1690.8111	845.9092	L	357.2496	179.1285	340.2231	170.6152	0	0	3
16	1805.8745	903.4409	1788.8479	894.9276	1787.8639	894.4356	P	244.1656	122.5864	227.1390	114.0731	0	0	2
17							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: **32594**.

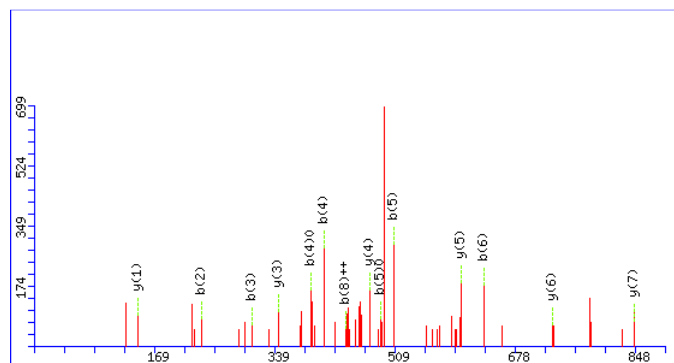
MS/MS Fragmentation of **HVATVQNEEEAQK**:

Found in **IP100006599**

Title: 1.1.1.7235.9

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	138.0662	69.5367	0	0	0	0	H							13
2	237.1346	119.0709	0	0	0	0	V	1345.6594	673.3333	1328.6329	664.8201	1327.6488	664.3281	12
3	308.1717	154.5895	0	0	0	0	A	1246.5910	623.7991	1229.5644	615.2859	1228.5804	614.7938	11
4	409.2194	205.1133	0	0	391.2088	196.1081	T	1175.5539	588.2806	1158.5273	579.7673	1157.5433	579.2753	10
5	508.2878	254.6475	0	0	490.2772	245.6423	V	1074.5062	537.7567	1057.4796	529.2435	1056.4956	528.7515	9
6	636.3464	318.6768	619.3198	310.1636	618.3358	309.6715	Q	975.4378	488.2225	958.4112	479.7093	957.4272	479.2172	8
7	750.3893	375.6983	733.3628	367.1850	732.3787	366.6930	N	847.3792	424.1932	830.3527	415.6800	829.3686	415.1880	7
8	879.4319	440.2196	862.4054	431.7063	861.4213	431.2143	E	733.3363	367.1718	716.3097	358.6585	715.3257	358.1665	6
9	1008.4745	504.7409	991.4480	496.2276	990.4639	495.7356	E	604.2937	302.6505	587.2671	294.1372	586.2831	293.6452	5
10	1137.5171	569.2622	1120.4905	560.7489	1119.5065	560.2569	E	475.2511	238.1292	458.2245	229.6159	457.2405	229.1239	4
11	1208.5542	604.7807	1191.5277	596.2675	1190.5436	595.7755	A	346.2085	173.6079	329.1819	165.0946	0	0	3
12	1336.6128	668.8100	1319.5862	660.2968	1318.6022	659.8047	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 32830.

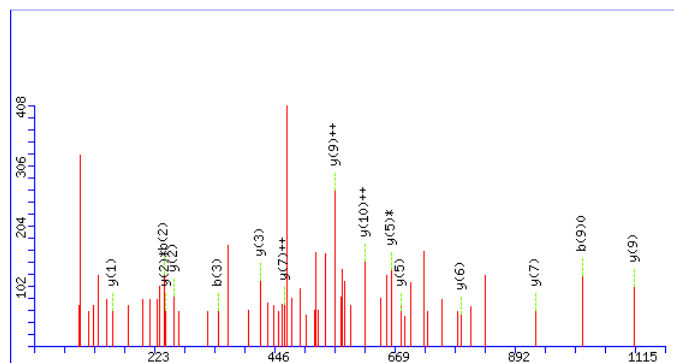
MS/MS Fragmentation of **IEVLPSHLFLONK: 57.021485@C:11**

Found in **IP100152642**

Title: 3.1.1.1077.4

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_2.3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							13
2	243.1339	122.0706	0	0	225.1234	113.0653	E	1456.7617	728.8845	1439.7351	720.3712	1438.7511	719.8792	12
3	342.2023	171.6048	0	0	324.1918	162.5995	V	1327.7191	664.3632	1310.6926	655.8499	1309.7085	655.3579	11
4	455.2864	228.1468	0	0	437.2758	219.1416	L	1228.6507	614.8290	1211.6241	606.3157	1210.6401	605.8237	10
5	552.3392	276.6732	0	0	534.3286	267.6679	P	1115.5666	558.2870	1098.5401	549.7737	1097.5561	549.2817	9
6	639.3712	320.1892	0	0	621.3606	311.1840	S	1018.5139	509.7606	1001.4873	501.2473	1000.5033	500.7553	8
7	776.4301	388.7187	0	0	758.4196	379.7134	H	931.4818	466.2446	914.4553	457.7313	0	0	7
8	889.5142	445.2607	0	0	871.5036	436.2554	L	794.4229	397.7151	777.3964	389.2018	0	0	6
9	1036.5826	518.7949	0	0	1018.5720	509.7897	F	681.3389	341.1731	664.3123	332.6598	0	0	5
10	1149.6667	575.3370	0	0	1131.6561	566.3317	L	534.2704	267.6389	517.2439	259.1256	0	0	4
11	1309.6973	655.3523	0	0	1291.6867	646.3470	C	421.1864	211.0968	404.1598	202.5836	0	0	3
12	1423.7402	712.3738	1406.7137	703.8605	1405.7297	703.3685	N	261.1557	131.0815	244.1292	122.5682	0	0	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 32967.

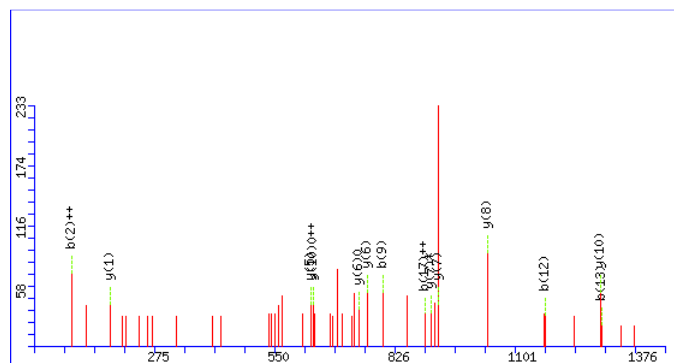
MS/MS Fragmentation of **LGDAETAAIEEEIYQSLFLR**:

Found in **IP100014455;IP100166825**

Title: 5.1.1.86.6

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3.5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							21
2	171.1128	86.0600	0	0	0	0	G	2226.0925	1113.5499	2209.0659	1105.0366	2208.0819	1104.5446	20
3	286.1397	143.5735	0	0	268.1292	134.5682	D	2169.0710	1085.0391	2152.0445	1076.5259	2151.0604	1076.0339	19
4	357.1769	179.0921	0	0	339.1663	170.0868	A	2054.0441	1027.5257	2037.0175	1019.0124	2036.0335	1018.5204	18
5	486.2195	243.6134	0	0	468.2089	234.6081	E	1983.0069	992.0071	1965.9804	983.4938	1964.9964	983.0018	17
6	587.2671	294.1372	0	0	569.2566	285.1319	T	1853.9644	927.4858	1836.9378	918.9725	1835.9538	918.4805	16
7	658.3042	329.6558	0	0	640.2937	320.6505	A	1752.9167	876.9620	1735.8901	868.4487	1734.9061	867.9567	15
8	729.3414	365.1743	0	0	711.3308	356.1690	A	1681.8796	841.4434	1664.8530	832.9301	1663.8690	832.4381	14
9	800.3785	400.6929	0	0	782.3679	391.6876	A	1610.8424	805.9249	1593.8159	797.4116	1592.8319	796.9196	13
10	913.4625	457.2349	0	0	895.4520	448.2296	I	1539.8053	770.4063	1522.7788	761.8930	1521.7948	761.4010	12
11	1042.5051	521.7562	0	0	1024.4946	512.7509	E	1426.7213	713.8643	1409.6947	705.3510	1408.7107	704.8590	11
12	1171.5477	586.2775	0	0	1153.5372	577.2722	E	1297.6787	649.3430	1280.6521	640.8297	1279.6681	640.3377	10
13	1300.5903	650.7988	0	0	1282.5798	641.7935	E	1168.6361	584.8217	1151.6095	576.3084	1150.6255	575.8164	9
14	1413.6744	707.3408	0	0	1395.6638	698.3355	I	1039.5935	520.3004	1022.5669	511.7871	1021.5829	511.2951	8
15	1576.7377	788.8725	0	0	1558.7271	779.8672	Y	928.5094	463.7584	909.4829	455.2451	908.4989	454.7531	7
16	1704.7963	852.9018	1687.7697	844.3885	1686.7857	843.8965	Q	763.4461	382.2267	746.4196	373.7134	745.4355	373.2214	6
17	1791.8283	896.4178	1774.8018	887.9045	1773.8178	887.4125	S	635.3875	318.1974	618.3610	309.6841	617.3770	309.1921	5
18	1904.9124	952.9598	1887.8858	944.4466	1886.9018	943.9545	L	548.3555	274.6814	531.3289	266.1681	0	0	4
19	2051.9808	1026.4940	2034.9542	1017.9808	2033.9702	1017.4888	F	435.2714	218.1394	418.2449	209.6261	0	0	3
20	2165.0649	1083.0361	2148.0383	1074.5228	2147.0543	1074.0308	L	288.2030	144.6051	271.1765	136.0919	0	0	2
21							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 33010.

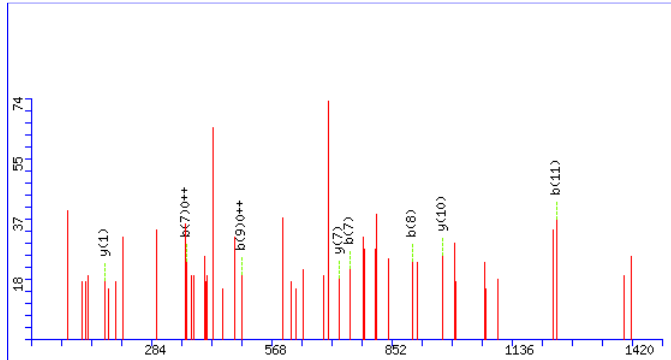
MS/MS Fragmentation of **RTDEPGVFILDLLEGGLAAQDGR**:

Found in **IP100171047**

Title: 5.1.1.300.3

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_3_5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	157.1084	79.0578	140.0818	70.5446	0	0	R							23
2	258.1561	129.5817	241.1295	121.0684	240.1455	120.5764	T	2286.1612	1143.5842	2269.1347	1135.0710	2268.1507	1134.5790	22
3	373.1830	187.0951	356.1565	178.5819	355.1724	178.0899	D	2185.1135	1093.0604	2168.0870	1084.5471	2167.1030	1084.0551	21
4	502.2256	251.6164	485.1991	243.1032	484.2150	242.6112	E	2070.0866	1035.5469	2053.0600	1027.0337	2052.0760	1026.5417	20
5	599.2784	300.1428	582.2518	291.6295	581.2678	291.1375	P	1941.0440	971.0256	1924.0175	962.5124	1923.0334	962.0204	19
6	656.2998	328.6536	639.2733	320.1403	638.2893	319.6483	G	1843.9912	922.4993	1826.9647	913.9860	1825.9807	913.4940	18
7	755.3682	378.1878	738.3417	369.6745	737.3577	369.1825	V	1786.9698	893.9885	1769.9432	885.4753	1768.9592	884.9832	17
8	902.4367	451.7220	885.4101	443.2087	884.4261	442.7167	F	1687.9014	844.4543	1670.8748	835.9410	1669.8908	835.4490	16
9	1015.5207	508.2640	998.4942	499.7507	997.5102	499.2587	I	1540.8329	770.9201	1523.8064	762.4068	1522.8224	761.9148	15
10	1128.6048	564.8060	1111.5782	556.2928	1110.5942	555.8007	L	1427.7489	714.3781	1410.7223	705.8648	1409.7383	705.3728	14
11	1243.6317	622.3195	1226.6052	613.8062	1225.6212	613.3142	D	1314.6648	657.8360	1297.6383	649.3228	1296.6543	648.8308	13
12	1356.7158	678.8615	1339.6892	670.3483	1338.7052	669.8563	L	1199.6379	600.3226	1182.6113	591.8093	1181.6273	591.3173	12
13	1469.7999	735.4036	1452.7733	726.8903	1451.7893	726.3983	L	1086.5538	543.7805	1069.5273	535.2673	1068.5432	534.7753	11
14	1598.8425	799.9249	1581.8159	791.4116	1580.8319	790.9196	E	973.4697	487.2385	956.4432	478.7252	955.4592	478.2332	10
15	1655.8639	828.4356	1638.8374	819.9223	1637.8533	819.4303	G	844.4272	422.7172	827.4006	414.2039	826.4166	413.7119	9
16	1712.8854	856.9463	1695.8588	848.4331	1694.8748	847.9410	G	787.4057	394.2065	770.3791	385.6932	769.3951	385.2012	8
17	1825.9694	913.4884	1808.9429	904.9751	1807.9589	904.4831	L	730.3842	365.6958	713.3577	357.1825	712.3737	356.6905	7
18	1897.0066	949.0069	1879.9800	940.4936	1878.9960	940.0016	A	617.3002	309.1537	600.2736	300.6404	599.2896	300.1484	6
19	1968.0437	984.5255	1951.0171	976.0122	1950.0331	975.5202	A	546.2631	273.6352	529.2365	265.1219	528.2525	264.6299	5
20	2096.1022	1048.5548	2079.0757	1040.0415	2078.0917	1039.5495	Q	475.2259	238.1166	458.1994	229.6033	457.2154	229.1113	4
21	2211.1292	1106.0682	2194.1026	1097.5550	2193.1186	1097.0630	D	347.1674	174.0873	330.1408	165.5740	329.1568	165.0820	3
22	2268.1507	1134.5790	2251.1241	1126.0657	2250.1401	1125.5737	G	232.1404	116.5738	215.1139	108.0606	0	0	2
23							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 33013.

MS/MS Fragmentation of **APQGVHLICYSQGGLVCR**: 57.021465@C:9,57.021465@C:17

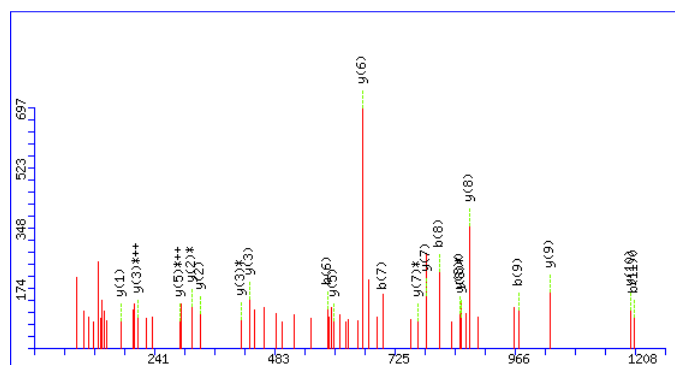
Found in

IP100021421;IP100216441;IP100453232;IP100552460;IP100646292;IP100647927;IP100654792;IP100783827;IP100789091;IP100853212;IP100893015;IP100942563;IP1009761

Title: 2.1.1.3251.10

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120212ry¥120212ry_414C2-43_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							18
2	169.0972	85.0522	0	0	0	0	P	1943.9579	972.4826	1926.9313	963.9693	1925.9473	963.4773	17
3	297.1557	149.0815	280.1292	140.5682	0	0	Q	1846.9051	923.9562	1829.8785	915.4429	1828.8945	914.9509	16
4	354.1772	177.5922	337.1506	169.0790	0	0	G	1718.8465	859.9269	1701.8200	851.4136	1700.8359	850.9216	15
5	453.2456	227.1264	436.2191	218.6132	0	0	V	1661.8250	831.4162	1644.7985	822.9029	1643.8145	822.4109	14
6	590.3045	295.6559	573.2780	287.1426	0	0	H	1562.7566	781.8820	1545.7301	773.3687	1544.7461	772.8767	13
7	703.3886	352.1979	686.3620	343.6847	0	0	L	1425.6977	713.3525	1408.6712	704.8392	1407.6872	704.3472	12
8	816.4727	408.7400	799.4461	400.2267	0	0	I	1312.6137	656.8105	1295.5871	648.2972	1294.6031	647.8052	11
9	976.5033	488.7553	959.4768	480.2420	0	0	C	1199.5296	600.2684	1182.5030	591.7552	1181.5190	591.2632	10
10	1139.5666	570.2870	1122.5401	561.7737	0	0	Y	1039.4989	520.2531	1022.4724	511.7398	1021.4884	511.2478	9
11	1226.5987	613.8030	1209.5721	605.2897	1208.5881	604.7977	S	876.4356	438.7214	859.4091	430.2082	858.4250	429.7162	8
12	1354.6572	677.8323	1337.6307	669.3190	1336.6467	668.8270	Q	789.4036	395.2054	772.3770	386.6922	0	0	7
13	1411.6787	706.3430	1394.6521	697.8297	1393.6681	697.3377	G	661.3450	331.1761	644.3185	322.6629	0	0	6
14	1468.7002	734.8537	1451.6736	726.3404	1450.6896	725.8484	G	604.3235	302.6654	587.2970	294.1521	0	0	5
15	1581.7842	791.3958	1564.7577	782.8825	1563.7737	782.3905	L	547.3021	274.1547	530.2755	265.6414	0	0	4
16	1680.8526	840.9300	1663.8261	832.4167	1662.8421	831.9247	V	434.2180	217.6126	417.1915	209.0994	0	0	3
17	1840.8833	920.9453	1823.8567	912.4320	1822.8727	911.9400	C	335.1496	168.0784	318.1231	159.5652	0	0	2
18							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 33055.

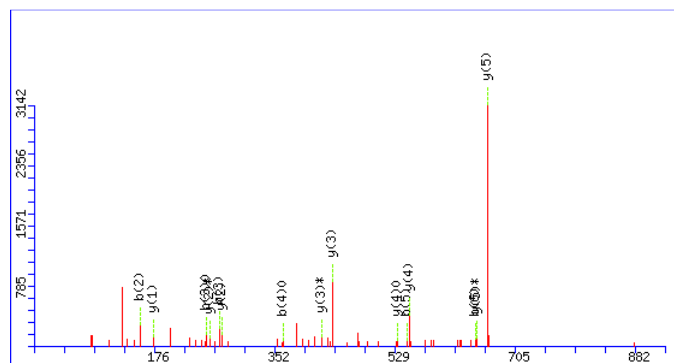
MS/MS Fragmentation of **GVDIYTR**:

Found in **IP100009268;IP100788719;IP100791053;IP100940464;IP100945211;IP100947447**

Title: 1.1.1.8618.2

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							7
2	157.0972	79.0522	0	0	0	0	V	766.4094	383.7083	749.3828	375.1951	748.3988	374.7030	6
3	272.1241	136.5657	0	0	254.1135	127.5604	D	667.3410	334.1741	650.3144	325.6608	649.3304	325.1688	5
4	385.2082	193.1077	0	0	367.1976	184.1024	I	552.3140	276.6606	535.2875	268.1474	534.3035	267.6554	4
5	548.2715	274.6394	0	0	530.2609	265.6341	Y	439.2300	220.1186	422.2034	211.6053	421.2194	211.1133	3
6	649.3192	325.1632	0	0	631.3086	316.1579	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
7							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 33133.

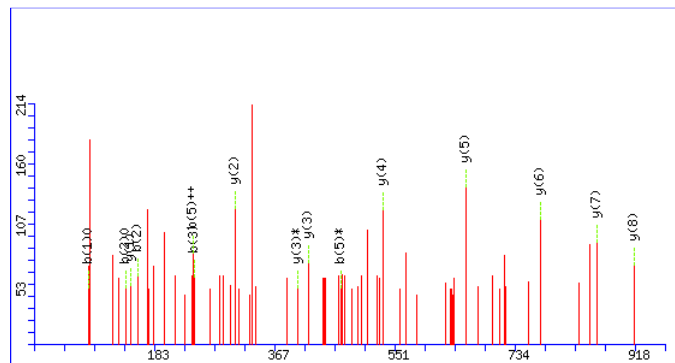
MS/MS Fragmentation of **TGSLQLICK: 57.021465@C:8**

Found in **IP100172474;IP100477661;IP100976838**

Title: 2.1.1.644.7

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							9
2	159.0764	80.0418	0	0	141.0659	71.0366	G	918.5077	459.7575	901.4812	451.2442	900.4972	450.7522	8
3	246.1084	123.5579	0	0	228.0979	114.5526	S	861.4863	431.2468	844.4597	422.7335	843.4757	422.2415	7
4	359.1925	180.0999	0	0	341.1819	171.0946	L	774.4542	387.7307	757.4277	379.2175	0	0	6
5	487.2511	244.1292	470.2245	235.6159	469.2405	235.1239	Q	661.3702	331.1887	644.3436	322.6754	0	0	5
6	600.3352	300.6712	583.3086	292.1579	582.3246	291.6659	L	533.3116	267.1594	516.2850	258.6462	0	0	4
7	713.4192	357.2132	696.3927	348.7000	695.4087	348.2080	I	420.2275	210.6174	403.2010	202.1041	0	0	3
8	873.4499	437.2286	856.4233	428.7153	855.4393	428.2233	C	307.1435	154.0754	290.1169	145.5621	0	0	2
9							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 33145.

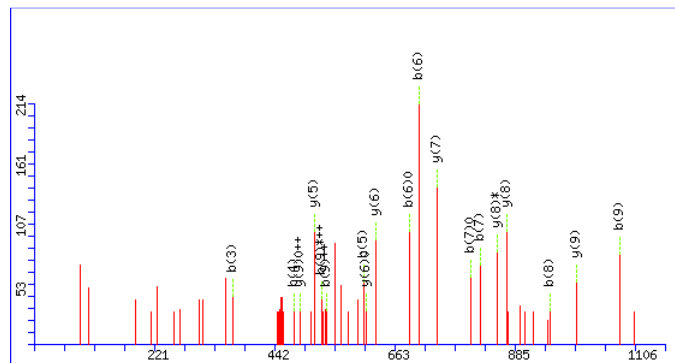
MS/MS Fragmentation of **IDHLETIQQLTAVVK**:

Found in **IP100008200**

Title: 4.1.1.1752.2

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120129ry¥120129ry_604A1-46_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							16
2	229.1183	115.0628	0	0	211.1077	106.0575	D	1707.9640	854.4856	1690.9374	845.9723	1689.9534	845.4803	15
3	366.1772	183.5922	0	0	348.1666	174.5870	H	1592.9370	796.9721	1575.9105	788.4589	1574.9265	787.9669	14
4	479.2613	240.1343	0	0	461.2507	231.1290	L	1455.8781	728.4427	1438.8516	719.9294	1437.8675	719.4374	13
5	608.3039	304.6556	0	0	590.2933	295.6503	E	1342.7940	671.9007	1325.7675	663.3874	1324.7835	662.8954	12
6	708.3515	355.1794	0	0	691.3410	346.1741	T	1213.7515	607.3794	1196.7249	598.8661	1195.7409	598.3741	11
7	822.4356	411.7214	0	0	804.4250	402.7162	I	1112.7038	556.8555	1095.6772	548.3422	1094.6932	547.8502	10
8	950.4942	475.7507	933.4676	467.2374	932.4836	466.7454	Q	999.6197	500.3135	982.5932	491.8002	981.6091	491.3082	9
9	1078.5528	539.7800	1061.5262	531.2667	1060.5422	530.7747	Q	871.5611	436.2842	854.5346	427.7709	853.5506	427.2789	8
10	1191.6368	596.3220	1174.6103	587.8088	1173.6263	587.3168	L	743.5026	372.2549	726.4760	363.7416	725.4920	363.2496	7
11	1304.7209	652.8641	1287.6943	644.3508	1286.7103	643.8588	L	630.4185	315.7129	613.3919	307.1996	612.4079	306.7076	6
12	1405.7686	703.3879	1388.7420	694.8746	1387.7580	694.3826	T	517.3344	259.1709	500.3079	250.6576	499.3239	250.1656	5
13	1476.8057	738.9065	1459.7791	730.3932	1458.7951	729.9012	A	416.2867	208.6470	399.2602	200.1337	0	0	4
14	1575.8741	788.4407	1558.8475	779.9274	1557.8635	779.4354	V	345.2496	173.1285	328.2231	164.6152	0	0	3
15	1674.9425	837.9749	1657.9160	829.4616	1656.9319	828.9696	V	246.1812	123.5942	229.1547	115.0810	0	0	2
16							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 33148.

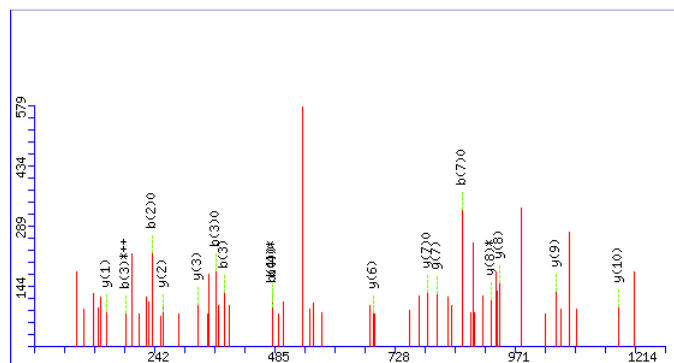
MS/MS Fragmentation of **EQQLQQELLALK**:

Found in **IP100010088;IP100217801;IP100328289;IP100556288;IP100892631;IP100892764**

Title: 3.1.1.931.7

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							12
2	258.1084	129.5579	241.0819	121.0446	240.0979	120.5526	Q	1311.7631	656.3852	1294.7365	647.8719	1293.7525	647.3799	11
3	386.1670	193.5872	369.1405	185.0739	368.1565	184.5819	Q	1183.7045	592.3559	1166.6780	583.8426	1165.6939	583.3506	10
4	499.2511	250.1292	482.2245	241.6159	481.2405	241.1239	L	1055.6459	528.3266	1038.6194	519.8133	1037.6354	519.3213	9
5	627.3097	314.1585	610.2831	305.6452	609.2991	305.1532	Q	942.5619	471.7846	925.5353	463.2713	924.5513	462.7793	8
6	755.3682	378.1878	738.3417	369.6745	737.3577	369.1825	Q	814.5033	407.7553	797.4767	399.2420	796.4927	398.7500	7
7	884.4108	442.7091	867.3843	434.1958	866.4003	433.7038	E	686.4447	343.7260	669.4182	335.2127	668.4341	334.7207	6
8	997.4949	499.2511	980.4684	490.7378	979.4843	490.2458	L	557.4021	279.2047	540.3756	270.6914	0	0	5
9	1110.5790	555.7931	1093.5524	547.2798	1092.5684	546.7878	L	444.3180	222.6627	427.2915	214.1494	0	0	4
10	1181.6161	591.3117	1164.5895	582.7984	1163.6055	582.3064	A	331.2340	166.1206	314.2074	157.6074	0	0	3
11	1294.7001	647.8537	1277.6736	639.3404	1276.6896	638.8484	L	260.1969	130.6021	243.1703	122.0888	0	0	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 33154.

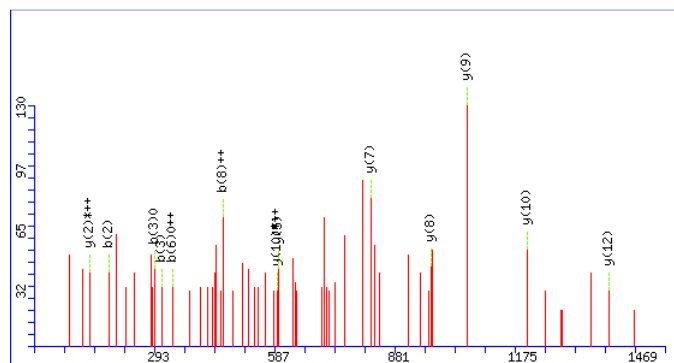
MS/MS Fragmentation of **IAEFSFDLLPVIR**:

Found in **IP100738216**

Title: 4.1.1.1492.10

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120118ry¥120118ry_201B7-32_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							13
2	185.1285	93.0679	0	0	0	0	A	1406.7678	703.8876	1389.7413	695.3743	1388.7573	694.8823	12
3	314.1710	157.5892	0	0	296.1605	148.5839	E	1335.7307	668.3690	1318.7042	659.8557	1317.7201	659.3637	11
4	461.2395	231.1234	0	0	443.2289	222.1181	F	1206.6881	603.8477	1189.6616	595.3344	1188.6776	594.8424	10
5	548.2715	274.6394	0	0	530.2609	265.6341	S	1059.6197	530.3135	1042.5932	521.8002	1041.6091	521.3082	9
6	695.3399	348.1736	0	0	677.3293	339.1683	F	972.5877	486.7975	955.5611	478.2842	954.5771	477.7922	8
7	810.3668	405.6871	0	0	792.3563	396.6818	D	825.5193	413.2633	808.4927	404.7500	807.5087	404.2580	7
8	923.4509	462.2291	0	0	905.4403	453.2238	L	710.4923	355.7498	693.4658	347.2365	0	0	6
9	1036.5350	518.7711	0	0	1018.5244	509.7658	L	597.4083	299.2078	580.3817	290.6945	0	0	5
10	1133.5877	567.2975	0	0	1115.5772	558.2922	P	484.3242	242.6657	467.2976	234.1525	0	0	4
11	1232.6562	616.8317	0	0	1214.6456	607.8264	V	387.2714	194.1394	370.2449	185.6261	0	0	3
12	1345.7402	673.3737	0	0	1327.7297	664.3685	I	288.2030	144.6051	271.1765	136.0919	0	0	2
13							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 33165.

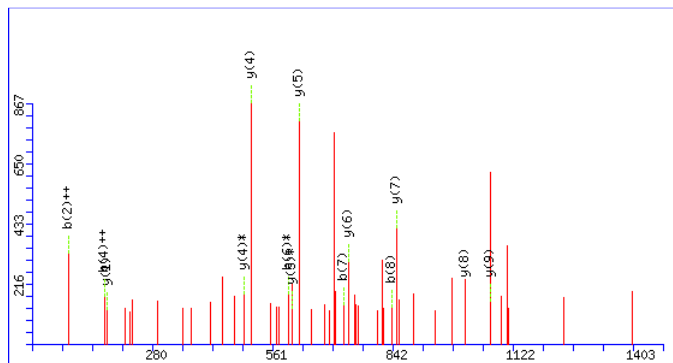
MS/MS Fragmentation of **GLLGCNIIPLQR: 57.021465@C:5**

Found in **IP100010860;IP100790782;IP101013039;IP101014410**

Title: 3.1.1.1304.7

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							12
2	171.1128	86.0600	0	0	0	0	L	1296.7457	648.8765	1279.7191	640.3632	0	0	11
3	284.1969	142.6021	0	0	0	0	L	1183.6616	592.3344	1166.6350	583.8212	0	0	10
4	341.2183	171.1128	0	0	0	0	G	1070.5775	535.7924	1053.5510	527.2791	0	0	9
5	501.2490	251.1281	0	0	0	0	C	1013.5561	507.2817	996.5295	498.7684	0	0	8
6	615.2919	308.1496	598.2654	299.6363	0	0	N	853.5254	427.2663	836.4989	418.7531	0	0	7
7	728.3760	364.6916	711.3494	356.1783	0	0	I	739.4825	370.2449	722.4559	361.7316	0	0	6
8	841.4600	421.2337	824.4335	412.7204	0	0	I	626.3984	313.7028	609.3719	305.1896	0	0	5
9	938.5128	469.7600	921.4863	461.2468	0	0	P	513.3144	257.1608	496.2878	248.6475	0	0	4
10	1051.5969	526.3021	1034.5703	517.7888	0	0	L	416.2616	208.6344	399.2350	200.1212	0	0	3
11	1179.6554	590.3314	1162.6289	581.8181	0	0	Q	303.1775	152.0924	286.1510	143.5791	0	0	2
12							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 33902.

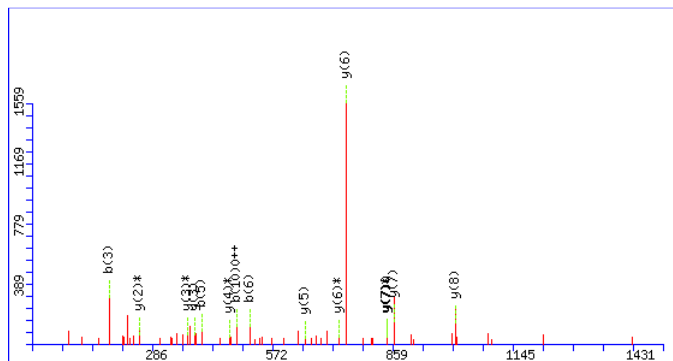
MS/MS Fragmentation of **AGGAFDPYTLVR**:

Found in **IP100013940;IP100178631;IP100796478;IP100878220;IP100879771**

Title: 3.1.1.560.9

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120212ry¥120212ry_aHDF1388-P9_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							12
2	129.0659	65.0366	0	0	0	0	G	1195.6106	598.3089	1178.5841	589.7957	1177.6000	589.3037	11
3	186.0873	93.5473	0	0	0	0	G	1138.5891	569.7982	1121.5626	561.2849	1120.5786	560.7929	10
4	257.1244	129.0659	0	0	0	0	A	1081.5677	541.2875	1064.5411	532.7742	1063.5571	532.2822	9
5	404.1928	202.6001	0	0	0	0	F	1010.5306	505.7689	993.5040	497.2556	992.5200	496.7636	8
6	519.2198	260.1135	0	0	501.2092	251.1083	D	863.4621	432.2347	846.4356	423.7214	845.4516	423.2294	7
7	616.2726	308.6399	0	0	598.2620	299.6346	P	748.4352	374.7212	731.4087	366.2080	730.4246	365.7160	6
8	779.3359	390.1716	0	0	761.3253	381.1663	Y	651.3824	326.1949	634.3559	317.6816	633.3719	317.1896	5
9	880.3836	440.6954	0	0	862.3730	431.6901	T	488.3191	244.6632	471.2926	236.1499	470.3085	235.6579	4
10	993.4676	497.2375	0	0	975.4571	488.2322	L	387.2714	194.1394	370.2449	185.6261	0	0	3
11	1092.5360	546.7717	0	0	1074.5255	537.7664	V	274.1874	137.5973	257.1608	129.0840	0	0	2
12							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 33942.

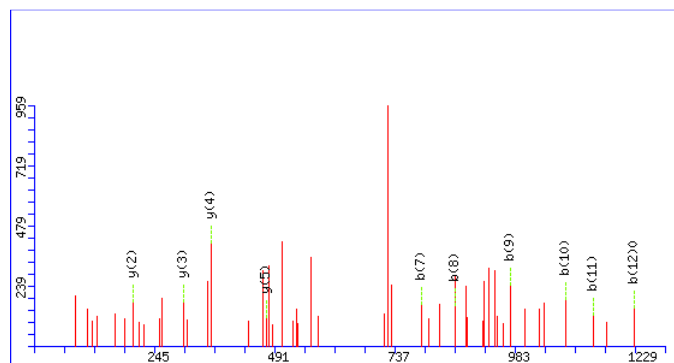
MS/MS Fragmentation of **GPKEEHNALIGTGK**:

Found in **IP100444146**

Title: 3.1.1.1974.10

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							14
2	155.0815	78.0444	0	0	0	0	P	1393.7434	697.3753	1376.7169	688.8621	1375.7328	688.3701	13
3	283.1765	142.0919	266.1499	133.5786	0	0	K	1296.6906	648.8490	1279.6641	640.3357	1278.6801	639.8437	12
4	412.2191	206.6132	395.1925	198.0999	394.2085	197.6079	E	1168.5957	584.8015	1151.5691	576.2882	1150.5851	575.7962	11
5	541.2617	271.1345	524.2351	262.6212	523.2511	262.1292	E	1039.5531	520.2802	1022.5265	511.7669	1021.5425	511.2749	10
6	678.3206	339.6639	661.2940	331.1506	660.3100	330.6586	H	910.5105	455.7589	893.4839	447.2456	892.4999	446.7536	9
7	792.3635	396.6854	775.3369	388.1721	774.3529	387.6801	N	773.4516	387.2294	756.4250	378.7162	755.4410	378.2241	8
8	863.4006	432.2039	846.3741	423.6907	845.3900	423.1987	A	659.4087	330.2080	642.3821	321.6947	641.3981	321.2027	7
9	976.4847	488.7460	959.4581	480.2327	958.4741	479.7407	L	588.3715	294.6894	571.3450	286.1761	570.3610	285.6841	6
10	1089.5687	545.2880	1072.5422	536.7747	1071.5582	536.2827	I	475.2875	238.1474	458.2609	229.6341	457.2769	229.1421	5
11	1146.5902	573.7987	1129.5636	565.2855	1128.5796	564.7935	G	362.2034	181.6053	345.1769	173.0921	344.1928	172.6001	4
12	1247.6379	624.3226	1230.6113	615.8093	1229.6273	615.3173	T	305.1819	153.0946	288.1554	144.5813	287.1714	144.0893	3
13	1304.6593	652.8333	1287.6328	644.3200	1286.6488	643.8280	G	204.1343	102.5708	187.1077	94.0575	0	0	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

2012/11/06

Peptide View

Peptide: **34102.**

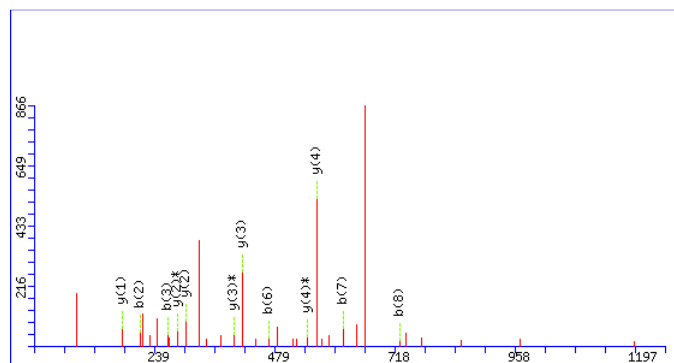
MS/MS Fragmentation of **LPGGGSFLQR**:

Found in **IP100555988**

Title: 4.1.1.1121.2

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120214ry¥120214ry_aHDF1419-P10_4.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							10
2	211.1441	106.0757	0	0	0	0	P	918.4792	459.7432	901.4526	451.2300	900.4686	450.7380	9
3	268.1656	134.5864	0	0	0	0	G	821.4264	411.2169	804.3999	402.7036	803.4159	402.2116	8
4	325.1870	163.0972	0	0	0	0	G	764.4050	382.7061	747.3784	374.1928	746.3944	373.7008	7
5	382.2085	191.6079	0	0	0	0	G	707.3835	354.1954	690.3570	345.6821	689.3729	345.1901	6
6	469.2405	235.1239	0	0	451.2300	226.1186	S	650.3620	325.6847	633.3355	317.1714	632.3515	316.6794	5
7	616.3089	308.6581	0	0	598.2984	299.6528	F	563.3300	282.1686	546.3035	273.6554	0	0	4
8	729.3930	365.2001	0	0	711.3824	356.1949	L	416.2616	208.6344	399.2350	200.1212	0	0	3
9	857.4516	429.2294	840.4250	420.7162	839.4410	420.2241	Q	303.1775	152.0924	286.1510	143.5791	0	0	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: **34369**.

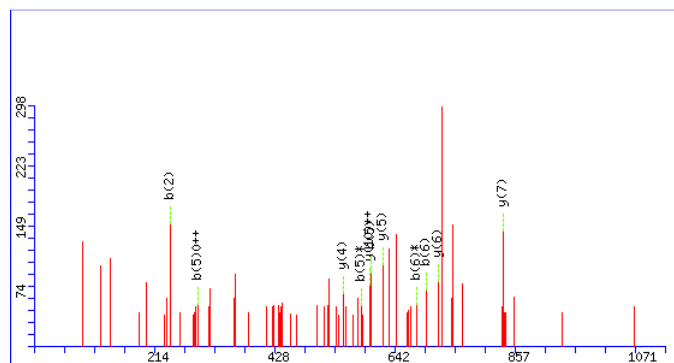
MS/MS Fragmentation of **DQVEEVTDVAQYIK**:

Found in **IP100414179**

Title: 3.1.1.4060.2

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							15
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	Q	1684.8428	842.9251	1667.8163	834.4118	1666.8323	833.9198	14
3	343.1612	172.0842	326.1347	163.5710	325.1506	163.0790	V	1556.7843	778.8958	1539.7577	770.3825	1538.7737	769.8905	13
4	472.2038	236.6055	455.1773	228.0923	454.1932	227.6003	E	1457.7159	729.3616	1440.6893	720.8483	1439.7053	720.3563	12
5	601.2464	301.1268	584.2198	292.6136	583.2358	292.1216	E	1328.6733	664.8403	1311.6467	656.3270	1310.6627	655.8350	11
6	700.3148	350.6610	683.2883	342.1478	682.3042	341.6558	V	1199.6307	600.3190	1182.6041	591.8057	1181.6201	591.3137	10
7	801.3625	401.1849	784.3359	392.6716	783.3519	392.1796	T	1100.5623	550.7848	1083.5357	542.2715	1082.5517	541.7795	9
8	964.4258	482.7165	947.3993	474.2033	946.4153	473.7113	Y	999.5146	500.2609	982.4880	491.7477	981.5040	491.2556	8
9	1079.4528	540.2300	1062.4262	531.7167	1061.4422	531.2247	D	836.4512	418.7293	819.4247	410.2160	818.4407	409.7240	7
10	1178.5212	589.7642	1161.4946	581.2510	1160.5106	580.7589	V	721.4243	361.2158	704.3978	352.7025	0	0	6
11	1249.5583	625.2828	1232.5317	616.7695	1231.5477	616.2775	A	622.3559	311.6816	605.3293	303.1683	0	0	5
12	1377.6169	689.3121	1360.5903	680.7988	1359.6063	680.3068	Q	551.3188	276.1630	534.2922	267.6498	0	0	4
13	1540.6802	770.8437	1523.6536	762.3305	1522.6696	761.8385	Y	423.2602	212.1337	406.2336	203.6205	0	0	3
14	1653.7643	827.3858	1636.7377	818.8725	1635.7537	818.3805	I	260.1969	130.6021	243.1703	122.0888	0	0	2
15							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 34471.

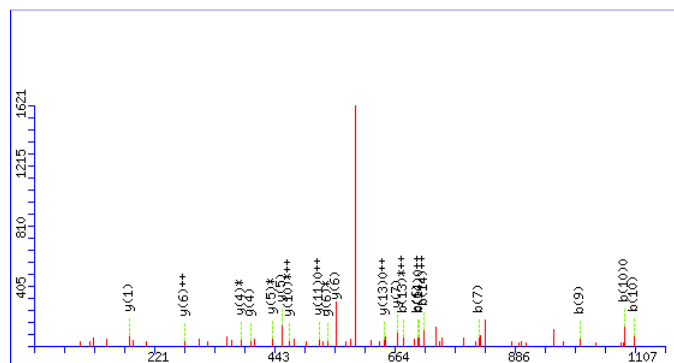
MS/MS Fragmentation of **INNEHVIDATLTGGPAR**:

Found in **IP100297859;IP100377245;IP100983407**

Title: 2.1.1.1918.7

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							17
2	228.1343	114.5708	211.1077	106.0575	0	0	N	1664.8351	832.9212	1647.8085	824.4079	1646.8245	823.9159	16
3	342.1772	171.5922	325.1506	163.0790	0	0	N	1550.7921	775.8997	1533.7656	767.3864	1532.7816	766.8944	15
4	471.2198	236.1135	454.1932	227.6003	453.2092	227.1082	E	1436.7492	718.8782	1419.7227	710.3650	1418.7387	709.8730	14
5	608.2787	304.6430	591.2521	296.1297	590.2681	295.6377	H	1307.7066	654.3570	1290.6801	645.8437	1289.6961	645.3517	13
6	707.3471	354.1772	690.3206	345.6639	689.3365	345.1719	V	1170.6477	585.8275	1153.6212	577.3142	1152.6372	576.8222	12
7	820.4312	410.7192	803.4046	402.2060	802.4206	401.7139	I	1071.5793	536.2933	1054.5528	527.7800	1053.5687	527.2880	11
8	935.4581	468.2327	918.4316	459.7194	917.4476	459.2274	D	958.4952	479.7513	941.4687	471.2380	940.4847	470.7460	10
9	1006.4952	503.7513	989.4687	495.2380	988.4847	494.7460	A	843.4683	422.2378	826.4417	413.7245	825.4577	413.2325	9
10	1107.5429	554.2751	1090.5164	545.7618	1089.5323	545.2698	T	772.4312	386.7192	755.4046	378.2060	754.4206	377.7139	8
11	1220.6270	610.8171	1203.6004	602.3039	1202.6164	601.8118	L	671.3835	336.1954	654.3570	327.6821	653.3729	327.1901	7
12	1321.6747	661.3410	1304.6481	652.8277	1303.6641	652.3357	T	558.2994	279.6534	541.2729	271.1401	540.2889	270.6481	6
13	1378.6961	689.8517	1361.6696	681.3384	1360.6856	680.8464	G	457.2518	229.1295	440.2252	220.6162	0	0	5
14	1435.7176	718.3624	1418.6910	709.8492	1417.7070	709.3571	G	400.2303	200.6188	383.2037	192.1055	0	0	4
15	1532.7703	766.8888	1515.7438	758.3755	1514.7598	757.8835	P	343.2088	172.1081	326.1823	163.5948	0	0	3
16	1603.8075	802.4074	1586.7809	793.8941	1585.7969	793.4021	A	246.1561	123.5817	229.1295	115.0684	0	0	2
17							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: **34625**.

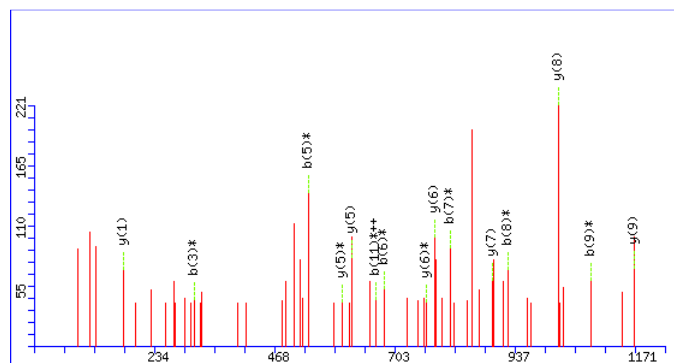
MS/MS Fragmentation of **QLSSHFGIYPFSLR: -17.026549@N-term(Q)**

Found in **IP100028338**

Title: 3.1.1.4258.9

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233	0	0	Q							14
2	242.1499	121.5786	225.1234	113.0653	0	0	L	1594.8376	797.9225	1577.8111	789.4092	1576.8271	788.9172	13
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	S	1481.7536	741.3804	1464.7270	732.8672	1463.7430	732.3751	12
4	416.2140	208.6106	399.1874	200.0974	398.2034	199.6053	S	1394.7215	697.8644	1377.6950	689.3511	1376.7110	688.8591	11
5	553.2729	277.1401	536.2463	268.6268	535.2623	268.1348	H	1307.6895	654.3484	1290.6630	645.8351	1289.6790	645.3431	10
6	700.3413	350.6743	683.3148	342.1610	682.3307	341.6690	F	1170.6306	585.8189	1153.6041	577.3057	1152.6200	576.8137	9
7	828.3999	414.7036	811.3733	406.1903	810.3893	405.6983	Q	1023.5622	512.2847	1006.5356	503.7715	1005.5516	503.2795	8
8	941.4839	471.2456	924.4574	462.7323	923.4734	462.2403	I	895.5036	448.2554	878.4771	439.7422	877.4931	439.2502	7
9	1104.5473	552.7773	1087.5207	544.2640	1086.5367	543.7720	Y	782.4196	391.7134	765.3930	383.2001	764.4090	382.7081	6
10	1201.6000	601.3037	1184.5735	592.7904	1183.5895	592.2984	P	619.3562	310.1817	602.3297	301.6685	601.3457	301.1765	5
11	1348.6684	674.8379	1331.6419	666.3246	1330.6579	665.8326	F	522.3035	261.6554	505.2769	253.1421	504.2929	252.6501	4
12	1435.7005	718.3539	1418.6739	709.8406	1417.6899	709.3486	S	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
13	1548.7845	774.8959	1531.7580	766.3826	1530.7740	765.8906	L	288.2030	144.6051	271.1765	136.0919	0	0	2
14							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 34702.

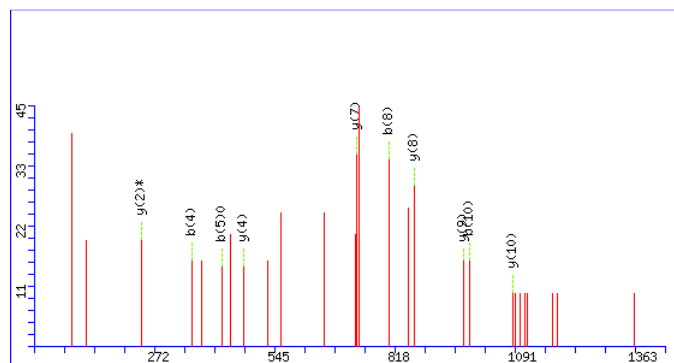
MS/MS Fragmentation of **SAAESMLDIALLMANASQLK**:

Found in **IP100295172**

Title: 4.1.1.4308.2

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							20
2	159.0764	80.0418	0	0	141.0659	71.0366	A	1990.0348	995.5210	1973.0082	987.0077	1972.0242	986.5157	19
3	230.1135	115.5604	0	0	212.1030	106.5551	A	1918.9976	960.0025	1901.9711	951.4892	1900.9871	950.9972	18
4	359.1561	180.0817	0	0	341.1456	171.0764	E	1847.9605	924.4839	1830.9340	915.9706	1829.9500	915.4786	17
5	446.1882	223.5977	0	0	428.1776	214.5924	S	1718.9179	859.9626	1701.8914	851.4493	1700.9074	850.9573	16
6	577.2286	289.1180	0	0	559.2181	280.1127	M	1631.8859	816.4466	1614.8594	807.9333	1613.8753	807.4413	15
7	690.3127	345.6600	0	0	672.3021	336.6547	L	1500.8454	750.9264	1483.8189	742.4131	1482.8349	741.9211	14
8	805.3396	403.1735	0	0	787.3291	394.1682	D	1387.7614	694.3843	1370.7348	685.8710	1369.7508	685.3790	13
9	918.4237	459.7155	0	0	900.4131	450.7102	I	1272.7344	636.8708	1255.7079	628.3576	1254.7239	627.8656	12
10	989.4608	495.2340	0	0	971.4503	486.2288	A	1159.6504	580.3288	1142.6238	571.8155	1141.6398	571.3235	11
11	1102.5449	551.7761	0	0	1084.5343	542.7708	L	1088.6132	544.8103	1071.5867	536.2970	1070.6027	535.8050	10
12	1215.6290	608.3181	0	0	1197.6184	599.3128	L	975.5292	488.2682	958.5026	479.7550	957.5186	479.2629	9
13	1346.6694	673.8384	0	0	1328.6589	664.8331	M	862.4451	431.7262	845.4186	423.2129	844.4345	422.7209	8
14	1417.7066	709.3569	0	0	1399.6960	700.3516	A	731.4046	366.2060	714.3781	357.6927	713.3941	357.2007	7
15	1531.7495	766.3784	1514.7229	757.8651	1513.7389	757.3731	N	660.3675	330.6874	643.3410	322.1741	642.3570	321.6821	6
16	1602.7866	801.8969	1585.7600	793.3837	1584.7760	792.8917	A	546.3246	273.6659	529.2980	265.1527	528.3140	264.6606	5
17	1689.8186	845.4129	1672.7921	836.8997	1671.8081	836.4077	S	475.2875	238.1474	458.2609	229.6341	457.2769	229.1421	4
18	1817.8772	909.4422	1800.8506	900.9290	1799.8666	900.4370	Q	388.2554	194.6314	371.2289	186.1181	0	0	3
19	1930.9613	965.9843	1913.9347	957.4710	1912.9507	956.9790	L	260.1969	130.6021	243.1703	122.0888	0	0	2
20							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 34711.

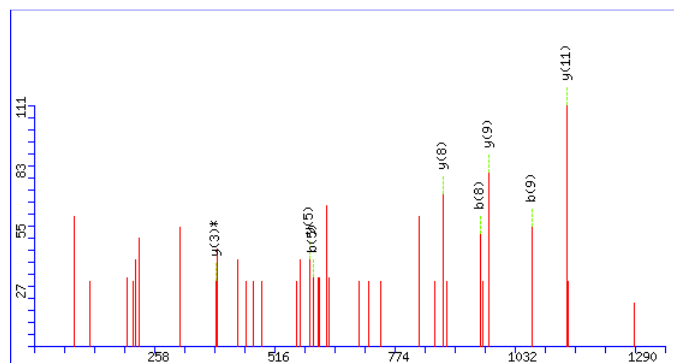
MS/MS Fragmentation of **LKPFIPDFIPAVGDIDAFK:**

Found in **IP100016335;IP100160349;IP100981053;IP100983826;IP100985061**

Title: 4.1.1.3698.4

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							20
2	242.1863	121.5968	225.1598	113.0835	0	0	K	2103.1525	1052.0799	2086.1259	1043.5666	2085.1419	1043.0746	19
3	339.2391	170.1232	322.2125	161.6099	0	0	P	1975.0575	988.0324	1958.0310	979.5191	1957.0470	979.0271	18
4	486.3075	243.6574	469.2809	235.1441	0	0	F	1878.0048	939.5060	1860.9782	930.9927	1859.9942	930.5007	17
5	599.3915	300.1994	582.3650	291.6861	0	0	I	1730.9364	865.9718	1713.9098	857.4585	1712.9258	856.9665	16
6	696.4443	348.7258	679.4178	340.2125	0	0	P	1617.8523	809.4298	1600.8257	800.9165	1599.8417	800.4245	15
7	811.4713	406.2393	794.4447	397.7260	793.4607	397.2340	D	1520.7995	760.9034	1503.7730	752.3901	1502.7890	751.8981	14
8	958.5397	479.7735	941.5131	471.2602	940.5291	470.7682	F	1405.7726	703.3899	1388.7460	694.8767	1387.7620	694.3846	13
9	1071.6237	536.3155	1054.5972	527.8022	1053.6132	527.3102	I	1258.7042	629.8557	1241.6776	621.3424	1240.6936	620.8504	12
10	1168.6765	584.8419	1151.6499	576.3286	1150.6659	575.8366	P	1145.6201	573.3137	1128.5936	564.8004	1127.6095	564.3084	11
11	1239.7136	620.3604	1222.6871	611.8472	1221.7030	611.3552	A	1048.5673	524.7873	1031.5408	516.2740	1030.5568	515.7820	10
12	1338.7820	669.8946	1321.7555	661.3814	1320.7715	660.8894	V	977.5302	489.2687	960.5037	480.7555	959.5197	480.2635	9
13	1395.8035	698.4054	1378.7769	689.8921	1377.7929	689.4001	G	878.4618	439.7345	861.4353	431.2213	860.4512	430.7293	8
14	1510.8304	755.9189	1493.8039	747.4056	1492.8199	746.9136	D	821.4403	411.2238	804.4138	402.7105	803.4298	402.2185	7
15	1623.9145	812.4609	1606.8879	803.9476	1605.9039	803.4556	I	706.4134	353.7103	689.3869	345.1971	688.4028	344.7051	6
16	1738.9414	869.9744	1721.9149	861.4611	1720.9309	860.9691	D	593.3293	297.1683	576.3028	288.6550	575.3188	288.1630	5
17	1809.9786	905.4929	1792.9520	896.9796	1791.9680	896.4876	A	478.3024	239.6548	461.2758	231.1416	0	0	4
18	1957.0470	979.0271	1940.0204	970.5138	1939.0364	970.0218	F	407.2653	204.1363	390.2387	195.6230	0	0	3
19	2070.1310	1035.5692	2053.1045	1027.0559	2052.1205	1026.5639	L	260.1969	130.6021	243.1703	122.0888	0	0	2
20							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 35307.

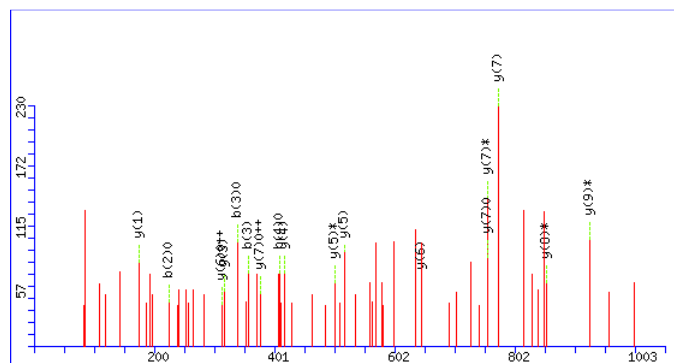
MS/MS Fragmentation of **ELDAEGLEAVQQTVGSR**:

Found in **IP100014472;IP100216586;IP100414362;IP100884002**

Title: 3.1.1.589.4

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120206ry¥120206ry_aHDF1419-P10_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							17
2	243.1339	122.0706	0	0	225.1234	113.0653	L	1672.8501	836.9287	1655.8235	828.4154	1654.8395	827.9234	16
3	358.1609	179.5841	0	0	340.1503	170.5788	D	1559.7660	780.3866	1542.7394	771.8734	1541.7554	771.3814	15
4	429.1980	215.1026	0	0	411.1874	206.0974	A	1444.7390	722.8732	1427.7125	714.3599	1426.7285	713.8679	14
5	558.2406	279.6239	0	0	540.2300	270.6186	E	1373.7019	687.3546	1356.6754	678.8413	1355.6914	678.3493	13
6	615.2620	308.1347	0	0	597.2515	299.1294	G	1244.6593	622.8333	1227.6328	614.3200	1226.6488	613.8280	12
7	728.3461	364.6767	0	0	710.3355	355.6714	L	1187.6379	594.3226	1170.6113	585.8093	1169.6273	585.3173	11
8	857.3887	429.1980	0	0	839.3781	420.1927	E	1074.5538	537.7805	1057.5273	529.2673	1056.5432	528.7753	10
9	928.4258	464.7165	0	0	910.4153	455.7113	A	945.5112	473.2592	928.4847	464.7460	927.5007	464.2540	9
10	1027.4942	514.2508	0	0	1009.4837	505.2455	V	874.4741	437.7407	857.4476	429.2274	856.4635	428.7354	8
11	1155.5528	578.2800	1138.5263	569.7668	1137.5422	569.2748	Q	775.4057	388.2065	758.3791	379.6932	757.3951	379.2012	7
12	1283.6114	642.3093	1266.5848	633.7961	1265.6008	633.3040	Q	647.3471	324.1772	630.3206	315.6639	629.3366	315.1719	6
13	1384.6591	692.8332	1367.6325	684.3199	1366.6485	683.8279	T	519.2885	260.1479	502.2620	251.6346	501.2780	251.1426	5
14	1483.7275	742.3674	1466.7009	733.8541	1465.7169	733.3621	V	418.2409	209.6241	401.2143	201.1108	400.2303	200.6188	4
15	1540.7489	770.8781	1523.7224	762.3648	1522.7384	761.8728	G	319.1724	160.0899	302.1459	151.5766	301.1619	151.0846	3
16	1627.7810	814.3941	1610.7544	805.8808	1609.7704	805.3888	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
17							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 35390.

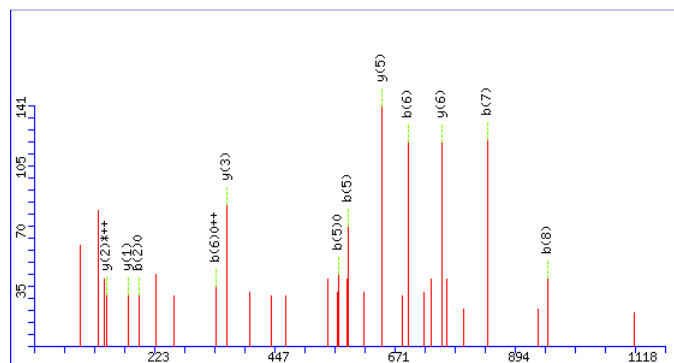
MS/MS Fragmentation of **DPQENIFLCQALR: 57.021465@C:9**

Found in **IP100030384;IP100964905**

Title: 3.1.1.1765.2

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							13
2	213.0870	107.0471	0	0	195.0764	98.0418	P	1488.7628	744.8850	1471.7362	736.3717	1470.7522	735.8797	12
3	341.1456	171.0764	324.1190	162.5631	323.1350	162.0711	Q	1391.7100	696.3586	1374.6834	687.8454	1373.6994	687.3534	11
4	470.1882	235.5977	453.1616	227.0844	452.1776	226.5924	E	1263.6514	632.3293	1246.6249	623.8161	1245.6409	623.3241	10
5	584.2311	292.6192	567.2045	284.1059	566.2205	283.6139	N	1134.6088	567.8081	1117.5823	559.2948	0	0	9
6	697.3151	349.1612	680.2886	340.6479	679.3046	340.1559	I	1020.5659	510.7866	1003.5394	502.2733	0	0	8
7	844.3836	422.6954	827.3570	414.1821	826.3730	413.6901	F	907.4818	454.2446	890.4553	445.7313	0	0	7
8	957.4676	479.2374	940.4411	470.7242	939.4571	470.2322	L	760.4134	380.7103	743.3869	372.1971	0	0	6
9	1117.4983	559.2528	1100.4717	550.7395	1099.4877	550.2475	C	647.3294	324.1683	630.3028	315.6550	0	0	5
10	1245.5569	623.2821	1228.5303	614.7688	1227.5463	614.2768	Q	487.2987	244.1530	470.2722	235.6397	0	0	4
11	1316.5940	658.8006	1299.5674	650.2873	1298.5834	649.7953	A	359.2401	180.1237	342.2136	171.6104	0	0	3
12	1429.6780	715.3427	1412.6515	706.8294	1411.6675	706.3374	L	288.2030	144.6051	271.1765	136.0919	0	0	2
13							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: **35464**.

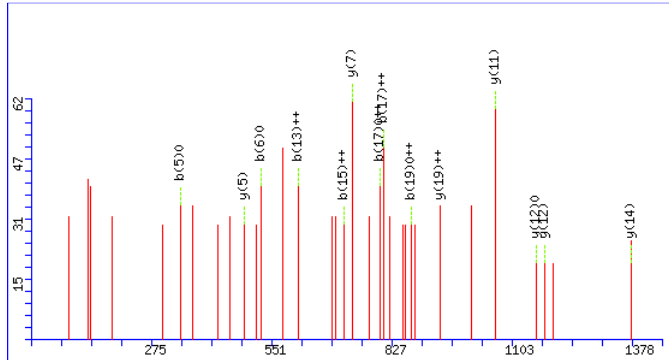
MS/MS Fragmentation of **SAGGSWLSLLAALAHAAAEK**:

Found in **IP100401195;IP100797825**

Title: 5.1.1.1063.2

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_2.5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							21
2	159.0764	80.0418	0	0	141.0659	71.0366	A	1950.0807	975.5440	1933.0542	967.0307	1932.0702	966.5387	20
3	216.0979	108.5526	0	0	198.0873	99.5473	G	1879.0436	940.0254	1862.0171	931.5122	1861.0330	931.0202	19
4	273.1193	137.0633	0	0	255.1088	128.0580	G	1822.0221	911.5147	1804.9956	903.0014	1804.0116	902.5094	18
5	360.1514	180.5793	0	0	342.1408	171.5740	S	1765.0007	883.0040	1747.9741	874.4907	1746.9901	873.9987	17
6	546.2307	273.6190	0	0	528.2201	264.6137	W	1677.9687	839.4880	1660.9421	830.9747	1659.9581	830.4827	16
7	659.3148	330.1610	0	0	641.3042	321.1557	L	1491.8893	746.4483	1474.8628	737.9350	1473.8788	737.4430	15
8	746.3468	373.6770	0	0	728.3362	364.6717	S	1378.8053	689.9063	1361.7787	681.3930	1360.7947	680.9010	14
9	859.4308	430.2191	0	0	841.4203	421.2138	L	1291.7732	646.3903	1274.7467	637.8770	1273.7627	637.3850	13
10	972.5149	486.7611	0	0	954.5043	477.7558	L	1178.6892	589.8482	1161.6626	581.3350	1160.6786	580.8429	12
11	1043.5520	522.2796	0	0	1025.5415	513.2744	A	1065.6051	533.3062	1048.5786	524.7929	1047.5946	524.3009	11
12	1114.5891	557.7982	0	0	1096.5786	548.7929	A	994.5680	497.7876	977.5415	489.2744	976.5574	488.7824	10
13	1227.6732	614.3402	0	0	1209.6626	605.3350	L	923.5309	462.2691	906.5043	453.7558	905.5203	453.2638	9
14	1298.7103	649.8588	0	0	1280.6997	640.8535	A	810.4468	405.7271	793.4203	397.2138	792.4363	396.7218	8
15	1435.7692	718.3883	0	0	1417.7587	709.3830	H	739.4097	370.2085	722.3832	361.6952	721.3992	361.2032	7
16	1548.8533	774.9303	0	0	1530.8427	765.9250	L	602.3508	301.6790	585.3243	293.1658	584.3402	292.6738	6
17	1619.8904	810.4488	0	0	1601.8798	801.4436	A	489.2667	245.1370	472.2402	236.6237	471.2562	236.1317	5
18	1690.9275	845.9674	0	0	1672.9170	836.9621	A	418.2296	209.6185	401.2031	201.1052	400.2191	200.6132	4
19	1761.9646	881.4860	0	0	1743.9541	872.4807	A	347.1925	174.0999	330.1660	165.5866	329.1819	165.0946	3
20	1891.0072	946.0073	0	0	1872.9967	937.0020	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
21							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 35524.

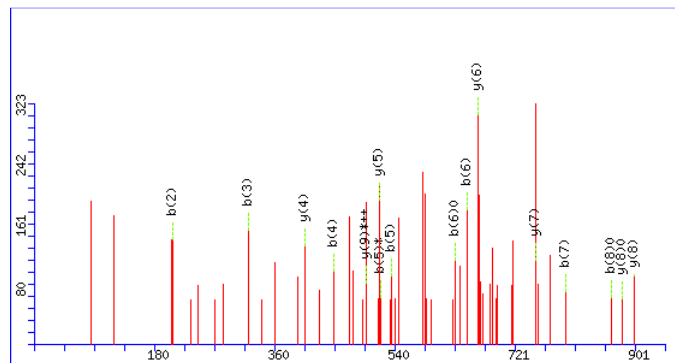
MS/MS Fragmentation of **AHIQSLFSFITGTK:**

Found in **IP100182106;IP100651636;IP100657785;IP100657966;IP100658093;IP100658169;IP101018128**

Title: 3.1.1.3861.3

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120210ry¥120210ry_585A1-55_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							14
2	209.1033	105.0553	0	0	0	0	H	1478.8002	739.9037	1461.7736	731.3905	1460.7896	730.8985	13
3	322.1874	161.5973	0	0	0	0	I	1341.7413	671.3743	1324.7147	662.8610	1323.7307	662.3690	12
4	450.2459	225.6266	433.2194	217.1133	0	0	Q	1228.6572	614.8322	1211.6307	606.3190	1210.6467	605.8270	11
5	537.2780	269.1426	520.2514	260.6293	519.2674	260.1373	S	1100.5986	550.8030	1083.5721	542.2897	1082.5881	541.7977	10
6	650.3620	325.6847	633.3355	317.1714	632.3515	316.6794	L	1013.5666	507.2869	996.5401	498.7737	995.5560	498.2817	9
7	797.4305	399.2189	780.4039	390.7056	779.4199	390.2136	F	900.4825	450.7449	883.4560	442.2316	882.4720	441.7396	8
8	884.4625	442.7349	867.4359	434.2216	866.4519	433.7296	S	753.4141	377.2107	736.3876	368.6974	735.4036	368.2054	7
9	1031.5309	516.2691	1014.5043	507.7558	1013.5203	507.2638	F	666.3821	333.6947	649.3556	325.1814	648.3715	324.6894	6
10	1144.6150	572.8111	1127.5884	564.2978	1126.6044	563.8058	I	519.3137	260.1605	502.2871	251.6472	501.3031	251.1552	5
11	1245.6626	623.3350	1228.6361	614.8217	1227.6521	614.3297	T	406.2296	203.6185	389.2031	195.1052	388.2191	194.6132	4
12	1302.6841	651.8457	1285.6575	643.3324	1284.6735	642.8404	G	305.1819	153.0946	288.1554	144.5813	287.1714	144.0893	3
13	1403.7318	702.3695	1386.7052	693.8563	1385.7212	693.3642	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

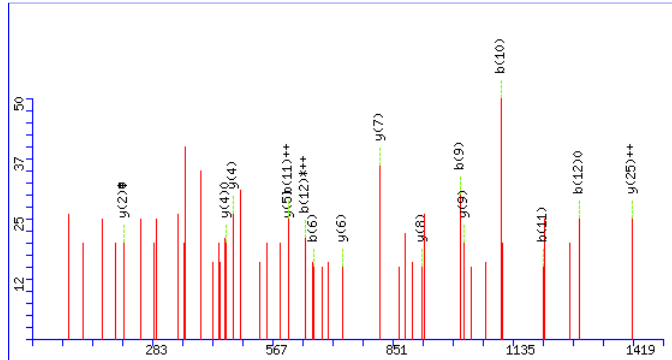
Peptide: 35803.

MS/MS Fragmentation of **SQHPSESSEVVTIEDLTQMLEEKDPVSQDSTVSQEENSK: 0.984016@Q:29**
Found in **IP100235842:IP100477250:IP101010334**

Title: 5.1.1.574.7

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_3.5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							40
2	216.0979	108.5526	199.0713	100.0393	198.0873	99.5473	Q	4416.0406	2208.5240	4399.0141	2200.0107	4398.0301	2199.5187	39
3	353.1568	177.0820	336.1302	168.5688	335.1462	168.0768	H	4287.9821	2144.4947	4270.9555	2135.9814	4269.9715	2135.4894	38
4	450.2096	225.6084	433.1830	217.0951	432.1990	216.6031	P	4150.9231	2075.9652	4133.8966	2067.4519	4132.9126	2066.9599	37
5	579.2522	290.1297	562.2256	281.6164	561.2416	281.1244	E	4053.8704	2027.4388	4036.8438	2018.9256	4035.8598	2018.4335	36
6	666.2842	333.6457	649.2576	325.1325	648.2736	324.6404	S	3924.8278	1962.9175	3907.8012	1954.4043	3906.8172	1953.9123	35
7	753.3162	377.1617	736.2897	368.6485	735.3056	368.1565	S	3837.7958	1919.4015	3820.7692	1910.8882	3819.7852	1910.3962	34
8	882.3588	441.6830	865.3323	433.1698	864.3482	432.6778	E	3750.7637	1875.8855	3733.7372	1867.3722	3732.7532	1866.8802	33
9	1011.4014	506.2043	994.3748	497.6911	993.3908	497.1991	E	3621.7211	1811.3642	3604.6946	1802.8509	3603.7106	1802.3589	32
10	1110.4698	555.7385	1093.4433	547.2253	1092.4592	546.7333	V	3492.6785	1746.8429	3475.6520	1738.3296	3474.6680	1737.8376	31
11	1209.5382	605.2727	1192.5117	596.7595	1191.5277	596.2675	V	3393.6101	1697.3087	3376.5836	1688.7954	3375.5996	1688.3034	30
12	1310.5859	655.7966	1293.5594	647.2833	1292.5753	646.7913	T	3294.5417	1647.7745	3277.5152	1639.2612	3276.5312	1638.7692	29
13	1423.6700	712.3386	1406.6434	703.8253	1405.6594	703.3333	L	3193.4940	1597.2507	3176.4675	1588.7374	3175.4835	1588.2454	28
14	1536.7540	768.8807	1519.7275	760.3674	1518.7435	759.8754	I	3080.4100	1540.7086	3063.3834	1532.1954	3062.3994	1531.7033	27
15	1665.7966	833.4019	1648.7701	824.8887	1647.7861	824.3967	E	2967.3259	1484.1666	2950.2994	1475.6533	2949.3153	1475.1613	26
16	1780.8236	890.9154	1763.7970	882.4021	1762.8130	881.9101	D	2838.2833	1419.6453	2821.2568	1411.1320	2820.2728	1410.6400	25
17	1893.9076	947.4575	1876.8811	938.9442	1875.8971	938.4522	L	2723.2564	1362.1318	2706.2298	1353.6186	2705.2458	1353.1265	24
18	1994.9553	997.9813	1977.9288	989.4680	1976.9447	988.9760	T	2610.1723	1305.5898	2593.1458	1297.0765	2592.1617	1296.5845	23
19	2123.0139	1062.0106	2105.9873	1053.4973	2105.0033	1053.0053	Q	2509.1246	1255.0660	2492.0981	1246.5527	2491.1141	1246.0607	22
20	2254.0544	1127.5308	2237.0278	1119.0175	2236.0438	1118.5255	M	2381.0661	1191.0367	2364.0395	1182.5234	2363.0555	1182.0314	21
21	2367.1384	1184.0729	2350.1119	1175.5596	2349.1279	1175.0676	L	2250.0256	1125.5164	2232.9990	1117.0031	2232.0150	1116.5111	20
22	2496.1810	1248.5942	2479.1545	1240.0809	2478.1705	1239.5889	E	2136.9415	1068.9744	2119.9150	1060.4611	2118.9309	1059.9691	19
23	2625.2236	1313.1154	2608.1971	1304.6022	2607.2131	1304.1102	E	2007.8989	1004.4531	1990.8724	995.9398	1989.8883	995.4478	18
24	2753.3186	1377.1629	2736.2920	1368.6497	2735.3080	1368.1576	K	1878.8563	939.9318	1861.8298	931.4185	1860.8458	930.9265	17
25	2868.3455	1434.6764	2851.3190	1426.1631	2850.3350	1425.6711	D	1750.7614	875.8843	1733.7348	867.3710	1732.7508	866.8790	16
26	2965.3983	1483.2028	2948.3717	1474.6895	2947.3877	1474.1975	P	1635.7344	818.3708	1618.7079	809.8576	1617.7239	809.3656	15
27	3064.4667	1532.7370	3047.4402	1524.2237	3046.4561	1523.7317	V	1538.6817	769.8445	1521.6551	761.3312	1520.6711	760.8392	14
28	3151.4987	1576.2530	3134.4722	1567.7397	3133.4882	1567.2477	S	1439.6132	720.3103	1422.5867	711.7970	1421.6027	711.3050	13
29	3280.5413	1640.7743	3263.5148	1632.2610	3262.5308	1631.7690	Q	1352.5812	676.7942	1335.5547	668.2810	1334.5706	667.7890	12
30	3395.5683	1698.2878	3378.5417	1689.7745	3377.5577	1689.2825	D	1223.5386	612.2729	1206.5121	603.7597	1205.5281	603.2677	11
31	3482.6003	1741.8038	3465.5737	1733.2905	3464.5897	1732.7985	S	1108.5117	554.7595	1091.4851	546.2462	1090.5011	545.7542	10
32	3583.6480	1792.3276	3566.6214	1783.8144	3565.6374	1783.3223	T	1021.4796	511.2435	1004.4531	502.7302	1003.4691	502.2382	9
33	3682.7164	1841.8618	3665.6898	1833.3486	3664.7058	1832.8566	V	920.4320	460.7196	903.4054	452.2063	902.4214	451.7143	8
34	3769.7484	1885.3778	3752.7219	1876.8646	3751.7379	1876.3726	S	821.3636	411.1854	804.3370	402.6721	803.3530	402.1801	7
35	3897.8070	1949.4071	3880.7804	1940.8939	3879.7964	1940.4019	Q	734.3315	367.6694	717.3050	359.1561	716.3210	358.6641	6
36	4026.8496	2013.9284	4009.8230	2005.4152	4008.8390	2004.9232	E	606.2729	303.6401	589.2464	295.1268	588.2624	294.6348	5
37	4155.8922	2078.4497	4138.8656	2069.9365	4137.8816	2069.4444	E	477.2304	239.1188	460.2038	230.6055	459.2198	230.1135	4
38	4269.9351	2135.4712	4252.9086	2126.9579	4251.9245	2126.4659	N	348.1878	174.5975	331.1612	166.0842	330.1772	165.5922	3
39	4356.9671	2178.9872	4339.9406	2170.4739	4338.9566	2169.9819	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
40							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 35839.

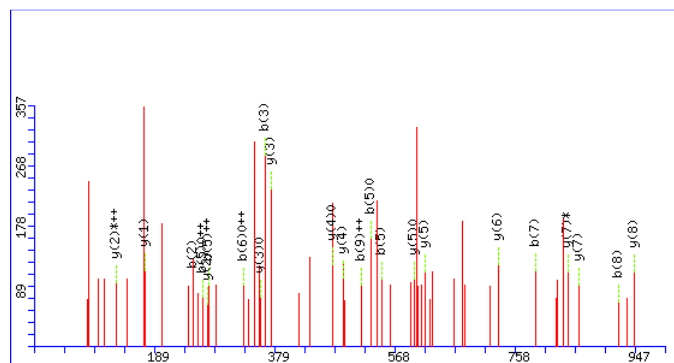
MS/MS Fragmentation of **HINPSQDELTVR**:

Found in **IP100024754,IP100337662,IP100409724,IP100409725,IP100409726,IP100409727,IP100409729,IP100478283,IP100815637,IP100871801**

Title: 1.1.1.8898.6

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	138.0662	69.5367	0	0	0	0	H							12
2	251.1503	126.0788	0	0	0	0	I	1271.6590	636.3331	1254.6325	627.8199	1253.6484	627.3279	11
3	365.1932	183.1002	348.1666	174.5870	0	0	N	1158.5749	579.7911	1141.5484	571.2778	1140.5644	570.7858	10
4	462.2459	231.6266	445.2194	223.1133	0	0	P	1044.5320	522.7696	1027.5055	514.2564	1026.5215	513.7644	9
5	549.2780	275.1426	532.2514	266.6293	531.2674	266.1373	S	947.4793	474.2433	930.4527	465.7300	929.4687	465.2380	8
6	677.3365	339.1719	660.3100	330.6586	659.3260	330.1666	Q	860.4472	430.7272	843.4207	422.2140	842.4367	421.7220	7
7	792.3635	396.6854	775.3369	388.1721	774.3529	387.6801	D	732.3886	366.6980	715.3621	358.1847	714.3781	357.6927	6
8	921.4061	461.2067	904.3795	452.6934	903.3955	452.2014	E	617.3617	309.1845	600.3352	300.6712	599.3511	300.1792	5
9	1034.4901	517.7487	1017.4636	509.2354	1016.4796	508.7434	L	488.3191	244.6632	471.2926	236.1499	470.3085	235.6579	4
10	1135.5378	568.2726	1118.5113	559.7593	1117.5273	559.2673	T	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
11	1234.6062	617.8068	1217.5797	609.2935	1216.5957	608.8015	V	274.1874	137.5973	257.1608	129.0840	0	0	2
12							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 35845.

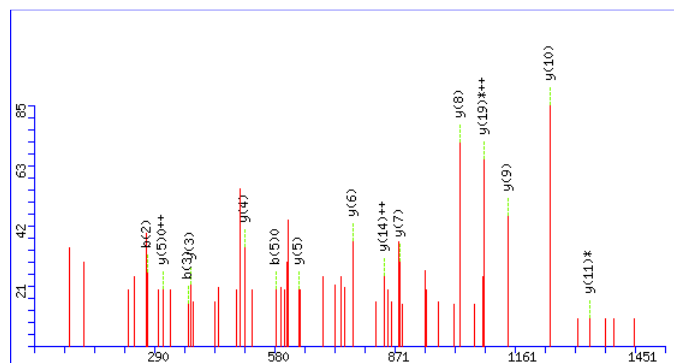
MS/MS Fragmentation of **NCVDIATSENLDFLMEMGFR: 57.021465@C:2**

Found in **IP100305986**

Title: 4.1.1.4493.4

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							21
2	275.0809	138.0441	258.0543	129.5308	0	0	C	2349.0560	1175.0316	2332.0294	1166.5183	2331.0454	1166.0263	20
3	374.1493	187.5783	357.1227	179.0650	0	0	V	2189.0253	1095.0163	2171.9988	1086.5030	2171.0148	1086.0110	19
4	489.1762	245.0917	472.1497	236.5785	471.1656	236.0865	D	2089.9569	1045.4821	2072.9304	1036.9688	2071.9463	1036.4768	18
5	602.2603	301.6338	585.2337	293.1205	584.2497	292.6285	I	1974.9300	987.9686	1957.9034	979.4553	1956.9194	978.9633	17
6	673.2974	337.1523	656.2708	328.6391	655.2868	328.1470	A	1861.8459	931.4266	1844.8193	922.9133	1843.8353	922.4213	16
7	774.3451	387.6762	757.3185	379.1629	756.3345	378.6709	T	1790.8088	895.9080	1773.7822	887.3948	1772.7982	886.9027	15
8	861.3771	431.1922	844.3505	422.6789	843.3665	422.1869	S	1689.7611	845.3842	1672.7346	836.8709	1671.7505	836.3789	14
9	990.4197	495.7135	973.3931	487.2002	972.4091	486.7082	E	1602.7291	801.8682	1585.7025	793.3549	1584.7185	792.8629	13
10	1104.4626	552.7349	1087.4361	544.2217	1086.4521	543.7297	N	1473.6865	737.3469	1456.6599	728.8336	1455.6759	728.3416	12
11	1217.5467	609.2770	1200.5201	600.7637	1199.5361	600.2717	L	1359.6436	680.3254	1342.6170	671.8121	1341.6330	671.3201	11
12	1318.5944	659.8008	1301.5678	651.2875	1300.5838	650.7955	T	1246.5595	623.7834	1229.5329	615.2701	1228.5489	614.7781	10
13	1433.6213	717.3143	1416.5948	708.8010	1415.6107	708.3090	D	1145.5118	573.2595	1128.4853	564.7463	1127.5012	564.2543	9
14	1580.6897	790.8485	1563.6632	782.3352	1562.6792	781.8432	F	1030.4849	515.7461	1013.4583	507.2328	1012.4743	506.7408	8
15	1693.7738	847.3905	1676.7472	838.8773	1675.7632	838.3852	L	883.4165	442.2119	866.3899	433.6986	865.4059	433.2066	7
16	1824.8143	912.9108	1807.7877	904.3975	1806.8037	903.9055	M	770.3324	385.6698	753.3058	377.1566	752.3218	376.6646	6
17	1953.8569	977.4321	1936.8303	968.9188	1935.8463	968.4268	E	639.2919	320.1496	622.2654	311.6363	621.2813	311.1443	5
18	2084.8973	1042.9523	2067.8708	1034.4390	2066.8868	1033.9470	M	510.2493	255.6283	493.2228	247.1150	0	0	4
19	2141.9188	1071.4630	2124.8923	1062.9498	2123.9082	1062.4578	G	379.2088	190.1081	362.1823	181.5948	0	0	3
20	2288.9872	1144.9972	2271.9607	1136.4840	2270.9767	1135.9920	F	322.1874	161.5973	305.1608	153.0840	0	0	2
21							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 36099.

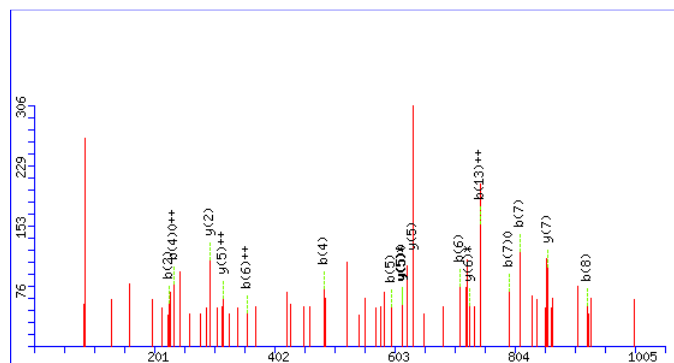
MS/MS Fragmentation of **ILEEIDTLILPENFK**:

Found in **IP100300531;IP100641336;IP100954014**

Title: 4.1.1.352.3

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							15
2	227.1754	114.0913	0	0	0	0	L	1673.8996	837.4535	1656.8731	828.9402	1655.8891	828.4482	14
3	356.2180	178.6126	0	0	338.2074	169.6074	E	1560.8156	780.9114	1543.7890	772.3981	1542.8050	771.9061	13
4	485.2606	243.1339	0	0	467.2500	234.1287	E	1431.7730	716.3901	1414.7464	707.8768	1413.7624	707.3848	12
5	598.3447	299.6760	0	0	580.3341	290.6707	I	1302.7304	651.8688	1285.7038	643.3556	1284.7198	642.8635	11
6	713.3716	357.1894	0	0	695.3610	348.1842	D	1189.6463	595.3268	1172.6198	586.8135	1171.6358	586.3215	10
7	814.4193	407.7133	0	0	796.4087	398.7080	T	1074.6194	537.8133	1057.5928	529.3000	1056.6088	528.8080	9
8	927.5033	464.2553	0	0	909.4928	455.2500	L	973.5717	487.2895	956.5451	478.7762	955.5611	478.2842	8
9	1040.5874	520.7973	0	0	1022.5768	511.7921	I	860.4876	430.7475	843.4611	422.2342	842.4771	421.7422	7
10	1153.6715	577.3394	0	0	1135.6609	568.3341	L	747.4036	374.2054	730.3770	365.6921	729.3930	365.2001	6
11	1250.7242	625.8658	0	0	1232.7137	616.8605	P	634.3195	317.6634	617.2930	309.1501	616.3089	308.6581	5
12	1379.7668	690.3871	0	0	1361.7563	681.3818	E	537.2667	269.1370	520.2402	260.6237	519.2562	260.1317	4
13	1493.8098	747.4085	1476.7832	738.8952	1475.7992	738.4032	N	408.2241	204.6157	391.1976	196.1024	0	0	3
14	1640.8782	820.9427	1623.8516	812.4294	1622.8676	811.9374	F	294.1812	147.5942	277.1547	139.0810	0	0	2
15							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 36140.

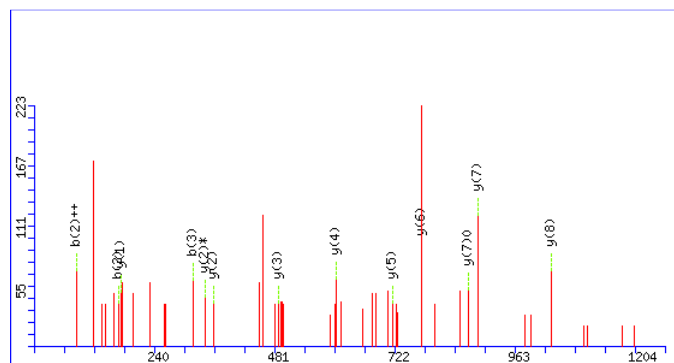
MS/MS Fragmentation of **GIFLGDEWR**:

Found in **IP100022184;IP100398749;IP100398750;IP100892704**

Title: 3.1.1.1110.7

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120126ry¥120126ry_585A1-55_1_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							10
2	171.1128	86.0600	0	0	0	0	I	1150.5527	575.7800	1133.5262	567.2667	1132.5422	566.7747	9
3	318.1812	159.5942	0	0	0	0	F	1037.4687	519.2380	1020.4421	510.7247	1019.4581	510.2327	8
4	431.2653	216.1363	0	0	0	0	L	890.4003	445.7038	873.3737	437.1905	872.3897	436.6985	7
5	488.2867	244.6470	0	0	0	0	G	777.3162	389.1617	760.2897	380.6485	759.3056	380.1565	6
6	603.3137	302.1605	0	0	585.3031	293.1552	D	720.2947	360.6510	703.2682	352.1377	702.2842	351.6457	5
7	718.3406	359.6740	0	0	700.3301	350.6687	D	605.2678	303.1375	588.2413	294.6243	587.2572	294.1323	4
8	847.3832	424.1953	0	0	829.3727	415.1900	E	490.2409	245.6241	473.2143	237.1108	472.2303	236.6188	3
9	1033.4625	517.2349	0	0	1015.4520	508.2296	W	361.1983	181.1028	344.1717	172.5895	0	0	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 36209.

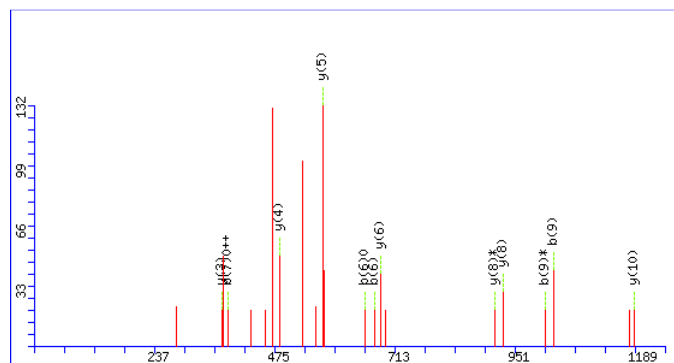
MS/MS Fragmentation of **ISVINFLDQLSLVVR**:

Found in **IP100032314**

Title: 5.1.1.945.2

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120208ry¥120208ry_Tig120slc-P8_1.5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							15
2	201.1234	101.0653	0	0	183.1128	92.0600	S	1602.9214	801.9643	1585.8948	793.4510	1584.9108	792.9590	14
3	300.1918	150.5995	0	0	282.1812	141.5942	V	1515.8893	758.4483	1498.8628	749.9350	1497.8788	749.4430	13
4	413.2758	207.1416	0	0	395.2653	198.1363	I	1416.8209	708.9141	1399.7944	700.4008	1398.8104	699.9088	12
5	527.3188	264.1630	510.2922	255.6497	509.3082	255.1577	N	1303.7369	652.3721	1286.7103	643.8588	1285.7263	643.3668	11
6	674.3872	337.6972	657.3606	329.1840	656.3766	328.6919	F	1189.6939	595.3506	1172.6674	586.8373	1171.6834	586.3453	10
7	787.4713	394.2393	770.4447	385.7260	769.4607	385.2340	L	1042.6255	521.8164	1025.5990	513.3031	1024.6150	512.8111	9
8	902.4982	451.7527	885.4716	443.2395	884.4876	442.7475	D	929.5415	465.2744	912.5149	456.7611	911.5309	456.2691	8
9	1030.5568	515.7820	1013.5302	507.2687	1012.5462	506.7767	Q	814.5145	407.7609	797.4880	399.2476	796.5039	398.7556	7
10	1143.6408	572.3241	1126.6143	563.8108	1125.6303	563.3188	L	686.4559	343.7316	669.4294	335.2183	668.4454	334.7263	6
11	1230.6729	615.8401	1213.6463	607.3268	1212.6623	606.8348	S	573.3719	287.1896	556.3453	278.6763	555.3613	278.1843	5
12	1343.7569	672.3821	1326.7304	663.8688	1325.7464	663.3768	L	486.3398	243.6736	469.3133	235.1603	0	0	4
13	1442.8253	721.9163	1425.7988	713.4030	1424.8148	712.9110	V	373.2558	187.1315	356.2292	178.6183	0	0	3
14	1541.8938	771.4505	1524.8672	762.9372	1523.8832	762.4452	V	274.1874	137.5973	257.1608	129.0840	0	0	2
15							R	175.1190	88.0631	158.0924	79.5498	0	0	1

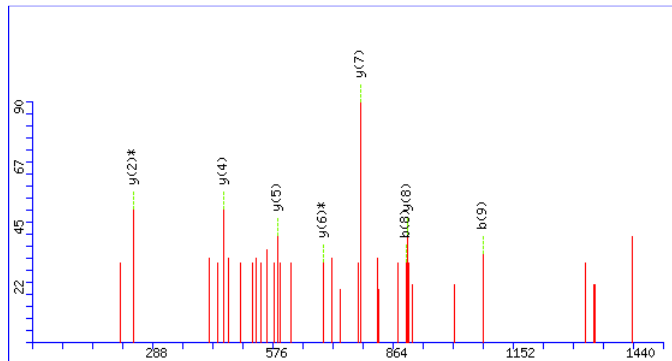
Peptide View

Peptide: 36551.

MS/MS Fragmentation of **DAEDSLHEWQDINLEELETLESNLLAQNSLK:**
Found in **IP100477535;IP100848102;IP100978010**

Title: 5.1.1.199.11

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4.5.mgf
ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							32
2	187.0713	94.0393	0	0	169.0608	85.0340	A	3609.7555	1805.3814	3592.7289	1796.8681	3591.7449	1796.3761	31
3	316.1139	158.5606	0	0	298.1034	149.5553	E	3538.7184	1769.8628	3521.6918	1761.3496	3520.7078	1760.8575	30
4	431.1409	216.0741	0	0	413.1303	207.0688	D	3409.6758	1705.3415	3392.6492	1696.8283	3391.6652	1696.3362	29
5	518.1729	259.5901	0	0	500.1623	250.5848	S	3294.6488	1647.8281	3277.6223	1639.3148	3276.6383	1638.8228	28
6	631.2570	316.1321	0	0	613.2464	307.1268	L	3207.6168	1604.3120	3190.5903	1595.7988	3189.6062	1595.3068	27
7	768.3159	384.6616	0	0	750.3053	375.6563	H	3094.5327	1547.7700	3077.5062	1539.2567	3076.5222	1538.7647	26
8	897.3585	449.1829	0	0	879.3479	440.1776	E	2957.4738	1479.2406	2940.4473	1470.7273	2939.4633	1470.2353	25
9	1083.4378	542.2225	0	0	1065.4272	533.2172	W	2828.4312	1414.7193	2811.4047	1406.2060	2810.4207	1405.7140	24
10	1211.4964	606.2518	1194.4698	597.7385	1193.4858	597.2465	Q	2642.3519	1321.6796	2625.3254	1313.1663	2624.3414	1312.6743	23
11	1326.5233	663.7653	1309.4968	655.2520	1308.5127	654.7600	D	2514.2934	1257.6503	2497.2668	1249.1370	2496.2828	1248.6450	22
12	1439.6074	720.3073	1422.5808	711.7940	1421.5968	711.3020	I	2399.2664	1200.1368	2382.2399	1191.6236	2381.2558	1191.1316	21
13	1553.6503	777.3288	1536.6237	768.8155	1535.6397	768.3235	N	2286.1823	1143.5948	2269.1558	1135.0815	2268.1718	1134.5895	20
14	1666.7344	833.8708	1649.7078	825.3575	1648.7238	824.8655	L	2172.1394	1086.5733	2155.1129	1078.0601	2154.1289	1077.5681	19
15	1795.7769	898.3921	1778.7504	889.8788	1777.7664	889.3868	E	2059.0554	1030.0313	2042.0288	1021.5180	2041.0448	1021.0260	18
16	1924.8195	962.9134	1907.7930	954.4001	1906.8090	953.9081	E	1930.0128	965.5100	1912.9862	956.9967	1912.0022	956.5047	17
17	2037.9036	1019.4554	2020.8771	1010.9422	2019.8930	1010.4502	L	1800.9702	900.9887	1783.9436	892.4754	1782.9596	891.9834	16
18	2166.9462	1083.9767	2149.9196	1075.4635	2148.9356	1074.9715	E	1687.8861	844.4467	1670.8596	835.9334	1669.8755	835.4414	15
19	2267.9939	1134.5006	2250.9673	1125.9873	2249.9833	1125.4953	T	1558.8435	779.9254	1541.8170	771.4121	1540.8329	770.9201	14
20	2381.0779	1191.0426	2364.0514	1182.5293	2363.0674	1182.0373	L	1457.7958	729.4016	1440.7693	720.8883	1439.7853	720.3963	13
21	2510.1205	1255.5639	2493.0940	1247.0506	2492.1100	1246.5586	E	1344.7118	672.8595	1327.6852	664.3462	1326.7012	663.8542	12
22	2597.1526	1299.0799	2580.1260	1290.5666	2579.1420	1290.0746	S	1215.6692	608.3382	1198.6426	599.8250	1197.6586	599.3329	11
23	2711.1955	1356.1014	2694.1689	1347.5881	2693.1849	1347.0961	N	1128.6371	564.8222	1111.6106	556.3089	1110.6266	555.8169	10
24	2824.2796	1412.6434	2807.2530	1404.1301	2806.2690	1403.6381	L	1014.5942	507.8007	997.5677	499.2875	996.5837	498.7955	9
25	2937.3636	1469.1854	2920.3371	1460.6722	2919.3531	1460.1802	L	901.5102	451.2587	884.4836	442.7454	883.4996	442.2534	8
26	3008.4007	1504.7040	2991.3742	1496.1907	2990.3902	1495.6987	A	788.4261	394.7167	771.3995	386.2034	770.4155	385.7114	7
27	3136.4593	1568.7333	3119.4328	1560.2200	3118.4487	1559.7280	Q	717.3890	359.1981	700.3624	350.6849	699.3784	350.1928	6
28	3264.5179	1632.7626	3247.4913	1624.2493	3246.5073	1623.7573	Q	589.3304	295.1688	572.3039	286.6556	571.3198	286.1636	5
29	3378.5608	1689.7840	3361.5343	1681.2708	3360.5502	1680.7788	N	461.2718	231.1395	444.2453	222.6263	443.2613	222.1343	4
30	3465.5928	1733.3001	3448.5663	1724.7868	3447.5823	1724.2948	S	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
31	3578.6769	1789.8421	3561.6504	1781.3288	3560.6663	1780.8368	L	260.1969	130.6021	243.1703	122.0888	0	0	2
32							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: **36620**.

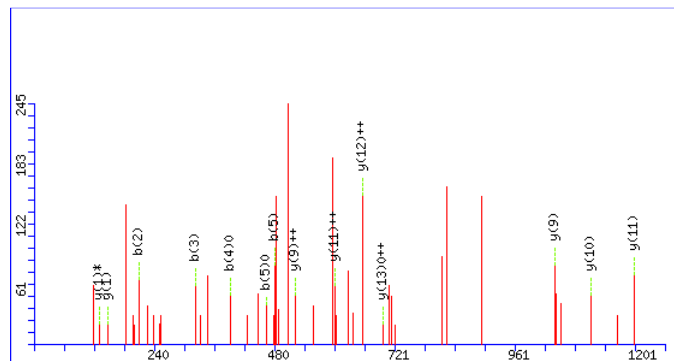
MS/MS Fragmentation of **IPLSAPRKNTNSVK**:

Found in **IP100295390**

Title: 4.1.1.2333.2

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							14
2	211.1441	106.0757	0	0	0	0	P	1411.8016	706.4044	1394.7750	697.8912	1393.7910	697.3991	13
3	324.2282	162.6177	0	0	0	0	L	1314.7488	657.8780	1297.7223	649.3648	1296.7383	648.8728	12
4	411.2602	206.1337	0	0	393.2496	197.1285	S	1201.6648	601.3360	1184.6382	592.8227	1183.6542	592.3307	11
5	482.2973	241.6523	0	0	464.2867	232.6470	A	1114.6327	557.8200	1097.6062	549.3067	1096.6222	548.8147	10
6	579.3501	290.1787	0	0	561.3395	281.1734	P	1043.5956	522.3014	1026.5691	513.7882	1025.5851	513.2962	9
7	735.4512	368.2292	718.4246	359.7160	717.4406	359.2239	R	946.5429	473.7751	929.5163	465.2618	928.5323	464.7698	8
8	863.5461	432.2767	846.5196	423.7634	845.5356	423.2714	K	790.4417	395.7245	773.4152	387.2112	772.4312	386.7192	7
9	977.5891	489.2982	960.5625	480.7849	959.5785	480.2929	N	662.3468	331.6770	645.3202	323.1638	644.3362	322.6717	6
10	1078.6368	539.8220	1061.6102	531.3087	1060.6262	530.8167	T	548.3039	274.6556	531.2773	266.1423	530.2933	265.6503	5
11	1192.6797	596.8435	1175.6531	588.3302	1174.6691	587.8382	N	447.2562	224.1317	430.2296	215.6184	429.2456	215.1264	4
12	1279.7117	640.3595	1262.6852	631.8462	1261.7011	631.3542	S	333.2132	167.1103	316.1867	158.5970	315.2027	158.1050	3
13	1378.7801	689.8937	1361.7536	681.3804	1360.7696	680.8884	V	246.1812	123.5942	229.1547	115.0810	0	0	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 36671.

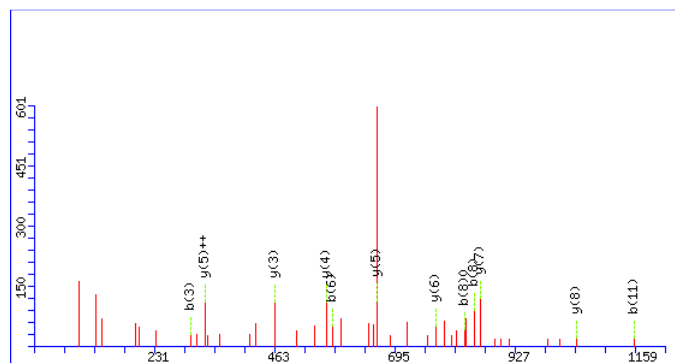
MS/MS Fragmentation of **MVAFAGWSLPVQYR**:

Found in **IP100299300;IP100790073;IP100793058;IP100903299;IP100910686**

Title: 3.1.1.4037.3

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	132.0478	66.5275	0	0	0	0	M							14
2	231.1162	116.0617	0	0	0	0	V	1493.7900	747.3986	1476.7634	738.8853	1475.7794	738.3933	13
3	302.1533	151.5803	0	0	0	0	A	1394.7215	697.8644	1377.6950	689.3511	1376.7110	688.8591	12
4	449.2217	225.1145	0	0	0	0	F	1323.6844	662.3459	1306.6579	653.8326	1305.6739	653.3406	11
5	520.2588	260.6330	0	0	0	0	A	1176.6160	588.8116	1159.5895	580.2984	1158.6055	579.8064	10
6	577.2803	289.1438	0	0	0	0	G	1105.5789	553.2931	1088.5524	544.7798	1087.5683	544.2878	9
7	763.3596	382.1834	0	0	0	0	W	1048.5574	524.7824	1031.5309	516.2691	1030.5469	515.7771	8
8	850.3916	425.6994	0	0	832.3811	416.6942	S	862.4781	431.7427	845.4516	423.2294	844.4676	422.7374	7
9	963.4757	482.2415	0	0	945.4651	473.2362	L	775.4461	388.2267	758.4196	379.7134	0	0	6
10	1060.5285	530.7679	0	0	1042.5179	521.7626	P	662.3620	331.6847	645.3355	323.1714	0	0	5
11	1159.5969	580.3021	0	0	1141.5863	571.2968	V	565.3093	283.1583	548.2827	274.6450	0	0	4
12	1287.6554	644.3314	1270.6289	635.8181	1269.6449	635.3261	Q	466.2409	233.6241	449.2143	225.1108	0	0	3
13	1450.7188	725.8630	1433.6922	717.3497	1432.7082	716.8577	Y	338.1823	169.5948	321.1557	161.0815	0	0	2
14							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 36685.

MS/MS Fragmentation of **EDHTLGNIHK**:

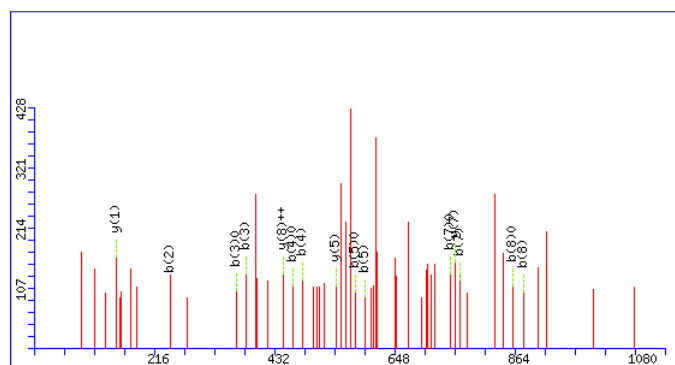
Found in

IP100003310;IP100016841;IP100556199;IP100854665;IP100879159;IP100884938;IP100935876;IP100939577;IP100941023;IP100966107;IP100966714;IP100967483;IP1009831

Title: 2.1.1.590.9

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120214ry¥120214ry_32R1-32_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							10
2	245.0768	123.0420	0	0	227.0662	114.0368	D	1010.5629	505.7851	993.5364	497.2718	992.5524	496.7798	9
3	382.1357	191.5715	0	0	364.1252	182.5662	H	895.5360	448.2716	878.5094	439.7584	877.5254	439.2663	8
4	483.1834	242.0953	0	0	465.1728	233.0901	T	758.4771	379.7422	741.4505	371.2289	740.4665	370.7369	7
5	596.2675	298.6374	0	0	578.2569	289.6321	L	657.4294	329.2183	640.4028	320.7051	0	0	6
6	653.2889	327.1481	0	0	635.2784	318.1428	G	544.3453	272.6763	527.3188	264.1630	0	0	5
7	767.3319	384.1696	750.3053	375.6563	749.3213	375.1643	N	487.3239	244.1656	470.2973	235.6523	0	0	4
8	880.4159	440.7116	863.3894	432.1983	862.4054	431.7063	I	373.2809	187.1441	356.2544	178.6308	0	0	3
9	993.5000	497.2536	976.4734	488.7404	975.4894	488.2483	I	260.1969	130.6021	243.1703	122.0888	0	0	2
10							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 36943.

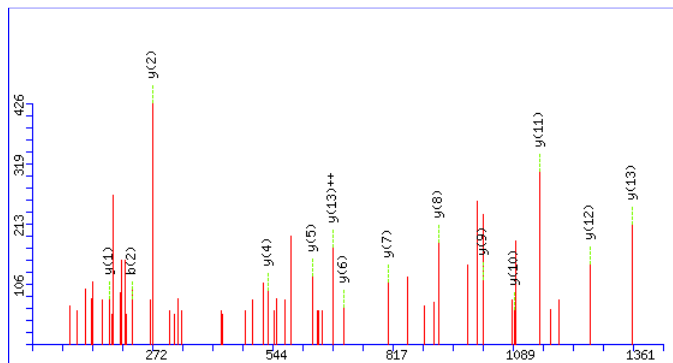
MS/MS Fragmentation of **LLPLGATDTAVFDVR**:

Found in **IP100744702;IP100787031;IP100788162;IP100979281;IP101009031**

Title: 3.1.1.2419.6

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120206ry¥120206ry_aHDF1419-P10_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							15
2	227.1754	114.0913	0	0	0	0	L	1474.7900	737.8986	1457.7635	729.3854	1456.7795	728.8934	14
3	324.2282	162.6177	0	0	0	0	P	1361.7060	681.3566	1344.6794	672.8433	1343.6954	672.3513	13
4	437.3122	219.1598	0	0	0	0	L	1264.6532	632.8302	1247.6266	624.3170	1246.6426	623.8250	12
5	494.3337	247.6705	0	0	0	0	G	1151.5691	576.2882	1134.5426	567.7749	1133.5586	567.2829	11
6	565.3708	283.1890	0	0	0	0	A	1094.5477	547.7775	1077.5211	539.2642	1076.5371	538.7722	10
7	666.4185	333.7129	0	0	648.4079	324.7076	T	1023.5106	512.2589	1006.4840	503.7456	1005.5000	503.2536	9
8	781.4454	391.2264	0	0	763.4349	382.2211	D	922.4629	461.7351	905.4363	453.2218	904.4523	452.7298	8
9	882.4931	441.7502	0	0	864.4825	432.7449	T	807.4359	404.2216	790.4094	395.7083	789.4254	395.2163	7
10	953.5302	477.2688	0	0	935.5197	468.2635	A	706.3883	353.6978	689.3617	345.1845	688.3777	344.6925	6
11	1052.5986	526.8030	0	0	1034.5881	517.7977	V	635.3511	318.1792	618.3246	309.6659	617.3406	309.1739	5
12	1199.6671	600.3372	0	0	1181.6565	591.3319	F	536.2827	268.6450	519.2562	260.1317	518.2722	259.6397	4
13	1314.6940	657.8506	0	0	1296.6834	648.8454	D	389.2143	195.1108	372.1878	186.5975	371.2037	186.1055	3
14	1413.7624	707.3848	0	0	1395.7518	698.3796	V	274.1874	137.5973	257.1608	129.0840	0	0	2
15							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 36993.

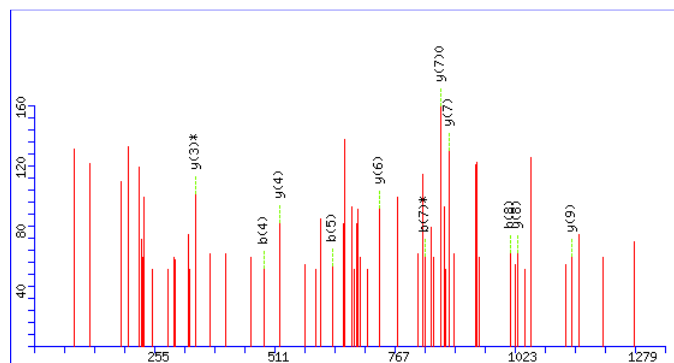
MS/MS Fragmentation of **VENFFTLNVK**:

Found in **IP100298870;IP100909633;IP101010016**

Title: 3.1.1.2356.7

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43.3.3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							11
2	229.1183	115.0628	0	0	211.1077	106.0575	E	1274.6416	637.8244	1257.6150	629.3111	1256.6310	628.8191	10
3	343.1612	172.0842	326.1347	163.5710	325.1506	163.0790	N	1145.5990	573.3031	1128.5724	564.7898	1127.5884	564.2978	9
4	490.2296	245.6185	473.2031	237.1052	472.2191	236.6132	F	1031.5560	516.2817	1014.5295	507.7684	1013.5455	507.2764	8
5	637.2980	319.1527	620.2715	310.6394	619.2875	310.1474	F	884.4876	442.7475	867.4611	434.2342	866.4771	433.7422	7
6	738.3457	369.6765	721.3192	361.1632	720.3352	360.6712	T	737.4192	369.2132	720.3927	360.7000	719.4087	360.2080	6
7	851.4298	426.2185	834.4032	417.7053	833.4192	417.2132	L	636.3715	318.6894	619.3450	310.1761	0	0	5
8	1014.4931	507.7502	997.4666	499.2369	996.4825	498.7449	Y	523.2875	262.1474	506.2609	253.6341	0	0	4
9	1128.5360	564.7717	1111.5095	556.2584	1110.5255	555.7664	N	360.2241	180.6157	343.1976	172.1024	0	0	3
10	1227.6045	614.3059	1210.5779	605.7926	1209.5939	605.3006	V	246.1812	123.5942	229.1547	115.0810	0	0	2
11							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 37070.

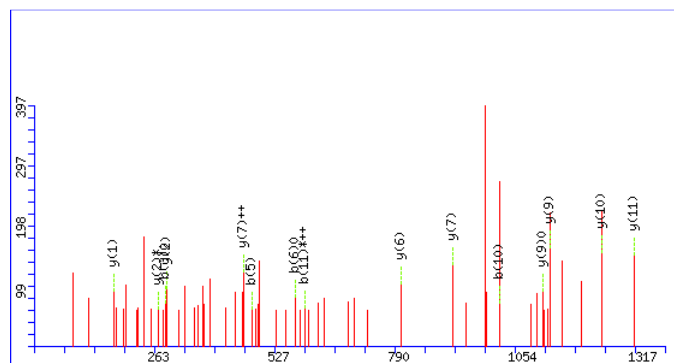
MS/MS Fragmentation of **GFTTAILTNTWLDDR**:

Found in **IP100104341;IP100974432;IP100977672;IP100978844;IP100984813**

Title: 3.1.1.3957.10

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120214ry¥120214ry_414C2-43_4_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							15
2	205.0972	103.0522	0	0	0	0	F	1666.8435	833.9254	1649.8170	825.4121	1648.8329	824.9201	14
3	306.1448	153.5761	0	0	288.1343	144.5708	T	1519.7751	760.3912	1502.7486	751.8779	1501.7645	751.3859	13
4	407.1925	204.0999	0	0	389.1819	195.0946	T	1418.7274	709.8673	1401.7009	701.3541	1400.7169	700.8621	12
5	478.2296	239.6185	0	0	460.2191	230.6132	A	1317.6797	659.3435	1300.6532	650.8302	1299.6692	650.3382	11
6	591.3137	296.1605	0	0	573.3031	287.1552	I	1246.6426	623.8250	1229.6161	615.3117	1228.6321	614.8197	10
7	704.3978	352.7025	0	0	686.3872	343.6972	L	1133.5586	567.2829	1116.5320	558.7696	1115.5480	558.2776	9
8	805.4454	403.2264	0	0	787.4349	394.2211	T	1020.4745	510.7409	1003.4480	502.2276	1002.4639	501.7356	8
9	919.4884	460.2478	902.4618	451.7345	901.4778	451.2425	N	919.4268	460.2170	902.4003	451.7038	901.4163	451.2118	7
10	1020.5360	510.7717	1003.5095	502.2584	1002.5255	501.7664	T	805.3839	403.1956	788.3573	394.6823	787.3733	394.1903	6
11	1206.6154	603.8113	1189.5888	595.2980	1188.6048	594.8060	W	704.3362	352.6717	687.3097	344.1585	686.3257	343.6665	5
12	1319.6994	660.3533	1302.6729	651.8401	1301.6889	651.3481	L	518.2569	259.6321	501.2304	251.1188	500.2463	250.6268	4
13	1434.7264	717.8668	1417.6998	709.3535	1416.7158	708.8615	D	405.1728	203.0901	388.1463	194.5768	387.1623	194.0848	3
14	1549.7533	775.3803	1532.7268	766.8670	1531.7427	766.3750	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
15							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 37197.

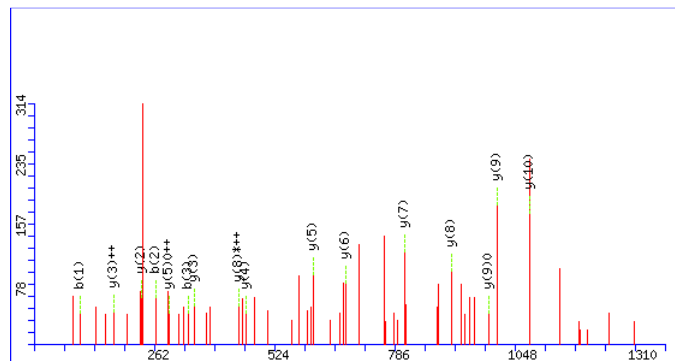
MS/MS Fragmentation of **TYATTEAFDSK**:

Found in **IP100298984;IP100373789;IP100913983**

Title: 2.1.1.2164.9

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120210ry¥120210ry_32R1-32_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							12
2	265.1183	133.0628	0	0	247.1077	124.0575	Y	1245.5998	623.3035	1228.5732	614.7902	1227.5892	614.2982	11
3	336.1554	168.5813	0	0	318.1448	159.5761	A	1082.5364	541.7719	1065.5099	533.2586	1064.5259	532.7666	10
4	437.2031	219.1052	0	0	419.1925	210.0999	T	1011.4993	506.2533	994.4728	497.7400	993.4888	497.2480	9
5	538.2508	269.6290	0	0	520.2402	260.6237	T	910.4516	455.7295	893.4251	447.2162	892.4411	446.7242	8
6	667.2933	334.1503	0	0	649.2828	325.1450	E	809.4040	405.2056	792.3774	396.6923	791.3934	396.2003	7
7	738.3305	369.6689	0	0	720.3199	360.6636	A	680.3614	340.6843	663.3348	332.1710	662.3508	331.6790	6
8	885.3989	443.2031	0	0	867.3883	434.1978	F	609.3243	305.1658	592.2977	296.6525	591.3137	296.1605	5
9	998.4829	499.7451	0	0	980.4724	490.7398	I	462.2558	231.6316	445.2293	223.1183	444.2453	222.6263	4
10	1113.5099	557.2586	0	0	1095.4993	548.2533	D	349.1718	175.0895	332.1452	166.5763	331.1612	166.0842	3
11	1200.5419	600.7746	0	0	1182.5313	591.7693	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 37418.

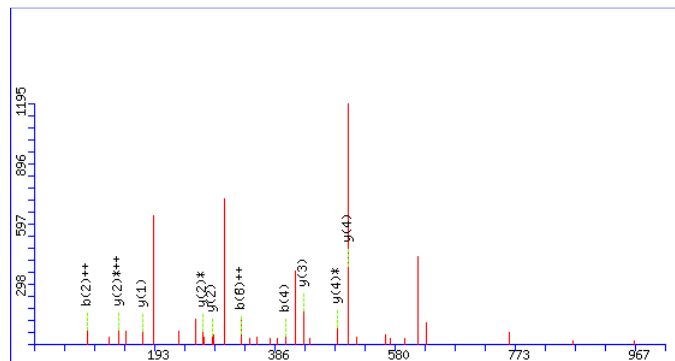
MS/MS Fragmentation of **VAYAFLR**:

Found in **IP100025442;IP100646992**

Title: 3.1.1.56.2

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							7
2	171.1128	86.0600	0	0	0	0	A	740.4090	370.7081	723.3824	362.1949	0	0	6
3	334.1761	167.5917	0	0	0	0	Y	669.3719	335.1896	652.3453	326.6763	0	0	5
4	405.2132	203.1103	0	0	0	0	A	506.3085	253.6579	489.2820	245.1446	0	0	4
5	552.2817	276.6445	0	0	0	0	F	435.2714	218.1394	418.2449	209.6261	0	0	3
6	665.3657	333.1865	0	0	0	0	L	288.2030	144.6051	271.1765	136.0919	0	0	2
7							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 37459.

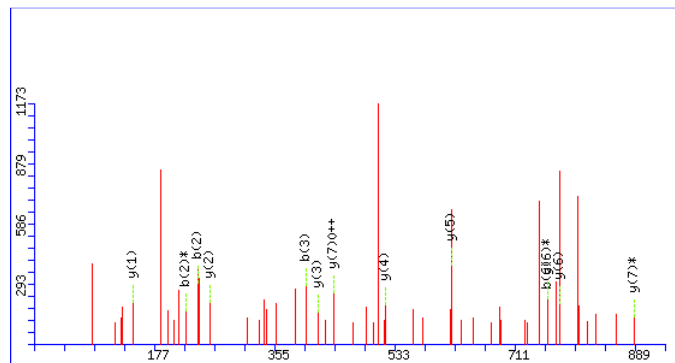
MS/MS Fragmentation of **LQCPTCIK: 57.021465@C:3.57.021465@C:6**

Found in **IP100022239;IP100965235;IP100967611;IP100967863**

Title: 1.1.1.7476.6

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							8
2	242.1499	121.5786	225.1234	113.0653	0	0	Q	906.4172	453.7122	889.3906	445.1990	888.4066	444.7070	7
3	402.1806	201.5939	385.1540	193.0806	0	0	C	778.3586	389.6829	761.3321	381.1697	760.3480	380.6777	6
4	499.2333	250.1203	482.2068	241.6070	0	0	P	618.3280	309.6676	601.3014	301.1543	600.3174	300.6623	5
5	600.2810	300.6441	583.2545	292.1309	582.2704	291.6389	T	521.2752	261.1412	504.2486	252.6280	503.2646	252.1360	4
6	760.3117	380.6595	743.2851	372.1462	742.3011	371.6542	C	420.2275	210.6174	403.2010	202.1041	0	0	3
7	873.3957	437.2015	856.3692	428.6882	855.3852	428.1962	I	260.1969	130.6021	243.1703	122.0888	0	0	2
8							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 37571.

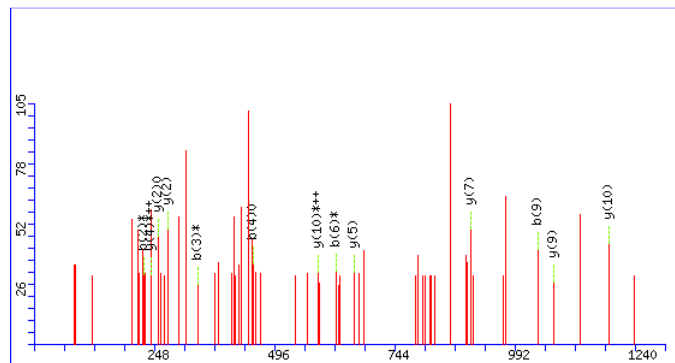
MS/MS Fragmentation of **NQLDAVLQC**LEK: 57.021465@C:9

Found in **IP100062869;IP100847479;IP100910063**

Title: 4.1.1.1516.4

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_2.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							13
2	243.1088	122.0580	226.0822	113.5448	0	0	Q	1429.7719	715.3896	1412.7454	706.8763	1411.7614	706.3843	12
3	356.1928	178.6001	339.1663	170.0868	0	0	L	1301.7134	651.3603	1284.6868	642.8470	1283.7028	642.3550	11
4	471.2198	236.1135	454.1932	227.6003	453.2092	227.1082	D	1188.6293	594.8183	1171.6027	586.3050	1170.6187	585.8130	10
5	542.2569	271.6321	525.2304	263.1188	524.2463	262.6268	A	1073.6023	537.3048	1056.5758	528.7915	1055.5918	528.2995	9
6	641.3253	321.1663	624.2988	312.6530	623.3148	312.1610	V	1002.5652	501.7863	985.5387	493.2730	984.5547	492.7810	8
7	754.4094	377.7083	737.3828	369.1951	736.3988	368.7030	L	903.4968	452.2520	886.4703	443.7388	885.4863	443.2468	7
8	882.4680	441.7376	865.4414	433.2243	864.4574	432.7323	Q	790.4128	395.7100	773.3862	387.1967	772.4022	386.7047	6
9	1042.4986	521.7529	1025.4721	513.2397	1024.4880	512.7477	C	662.3542	331.6807	645.3276	323.1675	644.3436	322.6754	5
10	1155.5827	578.2950	1138.5561	569.7817	1137.5721	569.2897	L	502.3235	251.6654	485.2970	243.1521	484.3130	242.6601	4
11	1268.6667	634.8370	1251.6402	626.3237	1250.6562	625.8317	L	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
12	1397.7093	699.3583	1380.6828	690.8450	1379.6988	690.3530	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 37578.

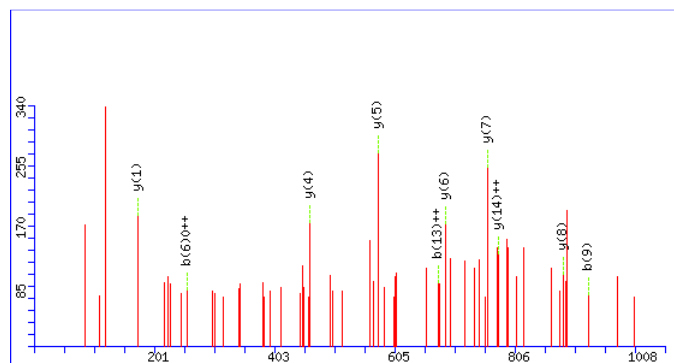
MS/MS Fragmentation of **DQSGTDHFQALDLSLR**:

Found in **IP100025695;IP100878645;IP100879106;IP100909930**

Title: 3.1.1.2958.2

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120124ry¥120124ry_414C2-43_1.3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							17
2	173.0557	87.0315	0	0	155.0451	78.0262	G	1703.8347	852.4210	1686.8082	843.9077	1685.8242	843.4157	16
3	260.0877	130.5475	0	0	242.0771	121.5422	S	1646.8133	823.9103	1629.7867	815.3970	1628.8027	814.9050	15
4	317.1092	159.0582	0	0	299.0986	150.0529	G	1559.7812	780.3943	1542.7547	771.8810	1541.7707	771.3890	14
5	418.1569	209.5821	0	0	400.1463	200.5768	T	1502.7598	751.8835	1485.7332	743.3703	1484.7492	742.8782	13
6	533.1838	267.0955	0	0	515.1732	258.0903	D	1401.7121	701.3597	1384.6856	692.8464	1383.7015	692.3544	12
7	670.2427	335.6250	0	0	652.2321	326.6197	H	1286.6852	643.8462	1269.6586	635.3329	1268.6746	634.8409	11
8	817.3111	409.1592	0	0	799.3006	400.1539	F	1149.6262	575.3168	1132.5997	566.8035	1131.6157	566.3115	10
9	930.3952	465.7012	0	0	912.3846	456.6959	I	1002.5578	501.7826	985.5313	493.2693	984.5473	492.7773	9
10	1058.4538	529.7305	1041.4272	521.2172	1040.4432	520.7252	Q	889.4738	445.2405	872.4472	436.7272	871.4632	436.2352	8
11	1129.4909	565.2491	1112.4643	556.7358	1111.4803	556.2438	A	761.4152	381.2112	744.3886	372.6980	743.4046	372.2060	7
12	1242.5749	621.7911	1225.5484	613.2778	1224.5644	612.7858	L	690.3781	345.6927	673.3515	337.1794	672.3675	336.6874	6
13	1357.6019	679.3046	1340.5753	670.7913	1339.5913	670.2993	D	577.2940	289.1506	560.2675	280.6374	559.2835	280.1454	5
14	1444.6339	722.8206	1427.6074	714.3073	1426.6233	713.8153	S	462.2671	231.6372	445.2405	223.1239	444.2565	222.6319	4
15	1557.7180	779.3626	1540.6914	770.8494	1539.7074	770.3573	L	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
16	1644.7500	822.8786	1627.7235	814.3654	1626.7394	813.8734	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
17							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 37594.

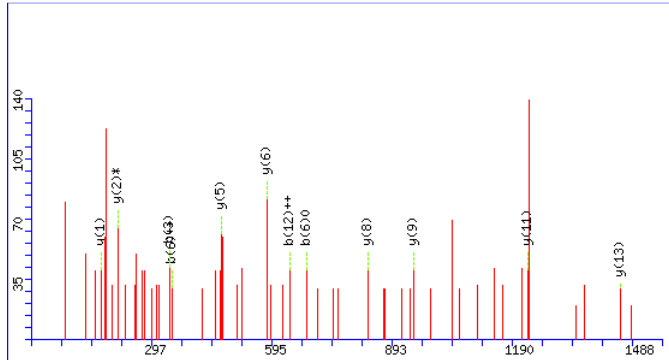
MS/MS Fragmentation of **TLEPYPLVIAGEHNIPWLLHLPQSGR**:

Found in **IP100900332**

Title: 4.1.1.2339.7

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	L							26
2	215.1390	108.0731	0	0	197.1285	99.0679	T	2778.5090	1389.7581	2761.4824	1381.2449	2760.4984	1380.7528	25
3	344.1816	172.5944	0	0	326.1710	163.5892	E	2665.4249	1333.2161	2648.3984	1324.7028	2647.4144	1324.2108	24
4	441.2344	221.1208	0	0	423.2238	212.1155	P	2536.3823	1268.6948	2519.3558	1260.1815	2518.3718	1259.6895	23
5	604.2977	302.6525	0	0	586.2871	293.6472	Y	2439.3296	1220.1684	2422.3030	1211.6551	2421.3190	1211.1631	22
6	701.3505	351.1789	0	0	683.3399	342.1736	P	2276.2662	1138.6368	2259.2397	1130.1235	2258.2557	1129.6315	21
7	814.4345	407.7209	0	0	796.4240	398.7156	L	2179.2135	1090.1104	2162.1869	1081.5971	2161.2029	1081.1051	20
8	913.5029	457.2551	0	0	895.4924	448.2498	V	2066.1294	1033.5683	2049.1029	1025.0551	2048.1188	1024.5631	19
9	1026.5870	513.7971	0	0	1008.5764	504.7919	I	1967.0610	984.0341	1950.0344	975.5209	1949.0504	975.0289	18
10	1097.6241	549.3157	0	0	1079.6136	540.3104	A	1853.9769	927.4921	1836.9504	918.9788	1835.9664	918.4868	17
11	1154.6456	577.8264	0	0	1136.6350	568.8212	G	1782.9398	891.9735	1765.9133	883.4603	1764.9292	882.9683	16
12	1283.6882	642.3477	0	0	1265.6776	633.3424	E	1725.9183	863.4628	1708.8918	854.9495	1707.9078	854.4575	15
13	1420.7471	710.8772	0	0	1402.7365	701.8719	H	1596.8758	798.9415	1579.8492	790.4282	1578.8652	789.9362	14
14	1534.7900	767.8986	1517.7635	759.3854	1516.7795	758.8934	N	1459.8168	730.4121	1442.7903	721.8988	1441.8063	721.4068	13
15	1647.8741	824.4407	1630.8475	815.9274	1629.8635	815.4354	I	1345.7739	673.3906	1328.7474	664.8773	1327.7634	664.3853	12
16	1744.9268	872.9671	1727.9003	864.4538	1726.9163	863.9618	P	1232.6899	616.8486	1215.6633	608.3353	1214.6793	607.8433	11
17	1931.0062	966.0067	1913.9796	957.4934	1912.9956	957.0014	W	1135.6371	568.3222	1118.6105	559.8089	1117.6265	559.3169	10
18	2044.0902	1022.5488	2027.0637	1014.0355	2026.0797	1013.5435	L	949.5578	475.2825	932.5312	466.7693	931.5472	466.2772	9
19	2157.1743	1079.0908	2140.1477	1070.5775	2139.1637	1070.0855	L	836.4737	418.7405	819.4472	410.2272	818.4631	409.7352	8
20	2294.2332	1147.6202	2277.2067	1139.1070	2276.2226	1138.6150	H	723.3896	362.1985	706.3631	353.6852	705.3791	353.1932	7
21	2407.3173	1204.1623	2390.2907	1195.6490	2389.3067	1195.1570	L	586.3307	293.6690	569.3042	285.1557	568.3202	284.6637	6
22	2504.3700	1252.6887	2487.3435	1244.1754	2486.3595	1243.6834	P	473.2467	237.1270	456.2201	228.6137	455.2361	228.1217	5
23	2561.3915	1281.1994	2544.3649	1272.6861	2543.3809	1272.1941	G	376.1939	188.6006	359.1674	180.0873	358.1833	179.5953	4
24	2648.4235	1324.7154	2631.3970	1316.2021	2630.4130	1315.7101	S	319.1724	160.0899	302.1459	151.5766	301.1619	151.0846	3
25	2705.4450	1353.2261	2688.4184	1344.7129	2687.4344	1344.2208	G	232.1404	116.5738	215.1139	108.0606	0	0	2
26							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 37702.

MS/MS Fragmentation of **DITEEIMSGAR**:

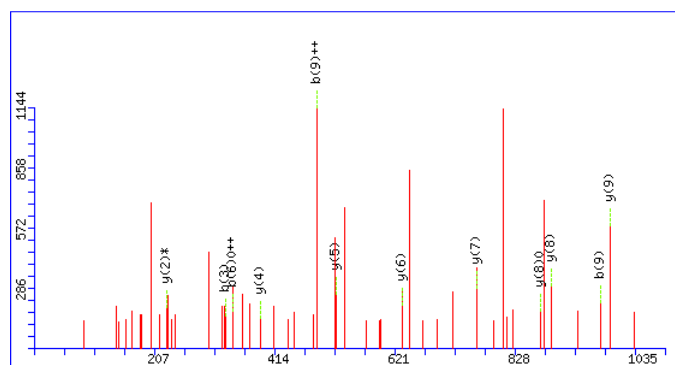
Found in

IP100479262;IP100552639;IP100759560;IP100798400;IP100924828;IP100925057;IP100925434;IP100926013;IP100926127;IP100926603;IP100926917;IP100927510;IP100927

Title: 3.1.1.271.5

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120214ry¥120214ry_aHDF1419-P10_4_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							11
2	229.1183	115.0628	0	0	211.1077	106.0575	I	1106.5510	553.7792	1089.5245	545.2659	1088.5405	544.7739	10
3	330.1660	165.5866	0	0	312.1554	156.5813	T	993.4670	497.2371	976.4404	488.7238	975.4564	488.2318	9
4	459.2086	230.1079	0	0	441.1980	221.1026	E	892.4193	446.7133	875.3927	438.2000	874.4087	437.7080	8
5	588.2511	294.6292	0	0	570.2406	285.6239	E	763.3767	382.1920	746.3502	373.6787	745.3661	373.1867	7
6	701.3352	351.1712	0	0	683.3246	342.1660	I	634.3341	317.6707	617.3076	309.1574	616.3235	308.6654	6
7	832.3757	416.6915	0	0	814.3651	407.6862	M	521.2500	261.1287	504.2235	252.6154	503.2395	252.1234	5
8	919.4077	460.2075	0	0	901.3972	451.2022	S	390.2096	195.6084	373.1830	187.0951	372.1990	186.6031	4
9	976.4292	488.7182	0	0	958.4186	479.7130	G	303.1775	152.0924	286.1510	143.5791	0	0	3
10	1047.4663	524.2368	0	0	1029.4557	515.2315	A	246.1561	123.5817	229.1295	115.0684	0	0	2
11							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 37767.

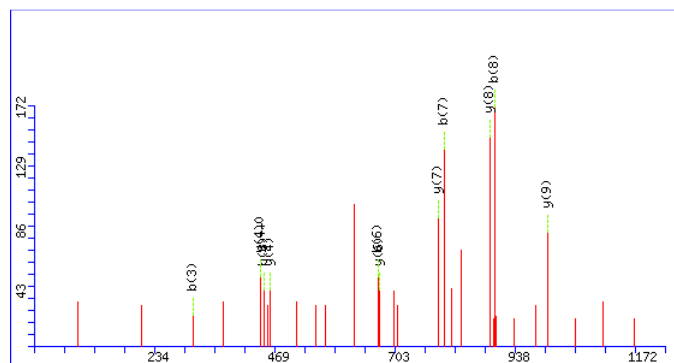
MS/MS Fragmentation of **TAHSFEQVLTDTTEAIK**:

Found in **IP100216744;IP100220076;IP100220077;IP100220078;IP100296360;IP100552471;IP100552604;IP100847840;IP100884053;IP100942030;IP100946204;IP100982341**

Title: 4.1.1.1889.3

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							17
2	173.0921	87.0497	0	0	155.0815	78.0444	A	1801.9331	901.4702	1784.9065	892.9569	1783.9225	892.4649	16
3	310.1510	155.5791	0	0	292.1404	146.5738	H	1730.8959	865.9516	1713.8694	857.4383	1712.8854	856.9463	15
4	397.1830	199.0951	0	0	379.1724	190.0899	S	1593.8370	797.4222	1576.8105	788.9089	1575.8265	788.4169	14
5	544.2514	272.6293	0	0	526.2409	263.6241	F	1506.8050	753.9061	1489.7785	745.3929	1488.7944	744.9009	13
6	673.2940	337.1506	0	0	655.2835	328.1454	E	1359.7366	680.3719	1342.7100	671.8587	1341.7260	671.3667	12
7	801.3528	401.1799	784.3260	392.6667	783.3420	392.1747	Q	1230.6940	615.8506	1213.6674	607.3374	1212.6834	606.8454	11
8	900.4210	450.7141	883.3945	442.2009	882.4104	441.7089	V	1102.6354	551.8213	1085.6089	543.3081	1084.6249	542.8161	10
9	1013.5051	507.2562	996.4785	498.7429	995.4945	498.2509	L	1003.5670	502.2871	986.5405	493.7739	985.5564	493.2819	9
10	1114.5528	557.7800	1097.5262	549.2667	1096.5422	548.7747	T	890.4829	445.7451	873.4564	437.2318	872.4724	436.7398	8
11	1229.5797	615.2935	1212.5531	606.7802	1211.5691	606.2882	D	789.4353	395.2213	772.4087	386.7080	771.4247	386.2160	7
12	1342.6638	671.8355	1325.6372	663.3222	1324.6532	662.8302	I	674.4083	337.7078	657.3818	329.1945	656.3978	328.7025	6
13	1443.7114	722.3594	1426.6849	713.8461	1425.7009	713.3541	T	561.3243	281.1658	544.2977	272.6525	543.3137	272.1605	5
14	1572.7540	786.8807	1555.7275	778.3674	1554.7435	777.8754	E	460.2766	230.6419	443.2500	222.1287	442.2660	221.6366	4
15	1643.7911	822.3992	1626.7646	813.8859	1625.7806	813.3939	A	331.2340	166.1206	314.2074	157.6074	0	0	3
16	1756.8752	878.9412	1739.8487	870.4280	1738.8646	869.9360	I	260.1969	130.6021	243.1703	122.0888	0	0	2
17							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: **37875**.

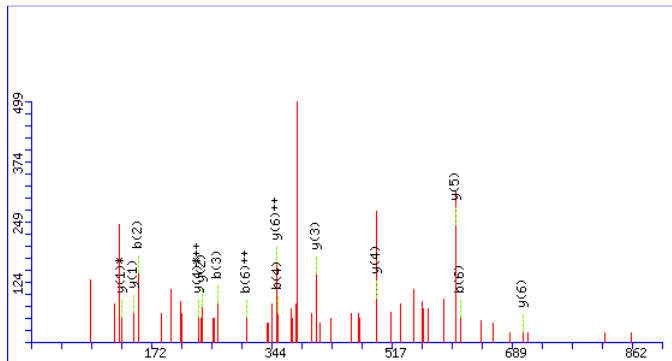
MS/MS Fragmentation of **GPLSYVK**:

Found in **IP100027181**

Title: 2.1.1.652.5

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							7
2	155.0815	78.0444	0	0	0	0	P	706.4134	353.7103	689.3869	345.1971	688.4028	344.7051	6
3	268.1656	134.5864	0	0	0	0	L	609.3606	305.1840	592.3341	296.6707	591.3501	296.1787	5
4	355.1976	178.1024	0	0	337.1870	169.0972	S	496.2766	248.6419	479.2500	240.1287	478.2660	239.6366	4
5	518.2609	259.6341	0	0	500.2504	250.6288	Y	409.2445	205.1259	392.2180	196.6126	0	0	3
6	617.3293	309.1683	0	0	599.3188	300.1630	V	246.1812	123.5942	229.1547	115.0810	0	0	2
7							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 38009.

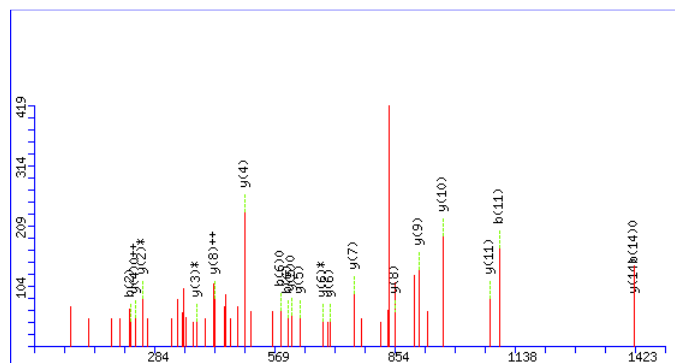
MS/MS Fragmentation of **VETGSEPGDTEPLELGGPGAEPQK**:

Found in **IP100000877;IP100922838;IP101010461;IP101012802**

Title: 2.1.1.2543.10

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_3.2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							25
2	229.1183	115.0628	0	0	211.1077	106.0575	E	2424.1049	1212.5561	2407.0783	1204.0428	2406.0943	1203.5508	24
3	330.1660	165.5866	0	0	312.1554	156.5813	T	2295.0623	1148.0348	2278.0357	1139.5215	2277.0517	1139.0295	23
4	387.1874	194.0974	0	0	369.1769	185.0921	G	2194.0146	1097.5109	2176.9881	1088.9977	2176.0041	1088.5057	22
5	474.2195	237.6134	0	0	456.2089	228.6081	S	2136.9932	1069.0002	2119.9666	1060.4869	2118.9826	1059.9949	21
6	603.2620	302.1347	0	0	585.2515	293.1294	E	2049.9611	1025.4842	2032.9346	1016.9709	2031.9506	1016.4789	20
7	700.3148	350.6610	0	0	682.3042	341.6558	P	1920.9185	960.9629	1903.8920	952.4496	1902.9080	951.9576	19
8	757.3363	379.1718	0	0	739.3257	370.1665	G	1823.8658	912.4365	1806.8392	903.9232	1805.8552	903.4312	18
9	872.3632	436.6852	0	0	854.3527	427.6800	D	1766.8443	883.9258	1749.8178	875.4125	1748.8337	874.9205	17
10	973.4109	487.2091	0	0	955.4003	478.2038	T	1651.8174	826.4123	1634.7908	817.8990	1633.8068	817.4070	16
11	1102.4535	551.7304	0	0	1084.4429	542.7251	E	1550.7697	775.8885	1533.7431	767.3752	1532.7591	766.8832	15
12	1199.5063	600.2568	0	0	1181.4957	591.2515	P	1421.7271	711.3672	1404.7005	702.8539	1403.7165	702.3619	14
13	1312.5903	656.7988	0	0	1294.5798	647.7935	L	1324.6743	662.8408	1307.6478	654.3275	1306.6638	653.8355	13
14	1441.6329	721.3201	0	0	1423.6223	712.3148	E	1211.5903	606.2988	1194.5637	597.7855	1193.5797	597.2935	12
15	1554.7170	777.8621	0	0	1536.7064	768.8568	L	1082.5477	541.7775	1065.5211	533.2642	1064.5371	532.7722	11
16	1611.7384	806.3729	0	0	1593.7279	797.3676	G	969.4636	485.2354	952.4371	476.7222	951.4530	476.2302	10
17	1668.7599	834.8836	0	0	1650.7493	825.8783	G	912.4421	456.7247	895.4156	448.2114	894.4316	447.7194	9
18	1765.8127	883.4100	0	0	1747.8021	874.4047	P	855.4207	428.2140	838.3941	419.7007	837.4101	419.2087	8
19	1822.8341	911.9207	0	0	1804.8236	902.9154	G	758.3679	379.6876	741.3414	371.1743	740.3573	370.6823	7
20	1893.8712	947.4393	0	0	1875.8607	938.4340	A	701.3464	351.1769	684.3199	342.6636	683.3359	342.1716	6
21	2022.9138	1011.9606	0	0	2004.9033	1002.9553	E	630.3093	315.6583	613.2828	307.1450	612.2988	306.6530	5
22	2119.9666	1060.4869	0	0	2101.9560	1051.4817	P	501.2667	251.1370	484.2402	242.6237	483.2562	242.1317	4
23	2249.0092	1125.0082	0	0	2230.9986	1116.0030	E	404.2140	202.6106	387.1874	194.0974	386.2034	193.6053	3
24	2377.0678	1189.0375	2360.0412	1180.5242	2359.0572	1180.0322	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
25							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: **38267**.

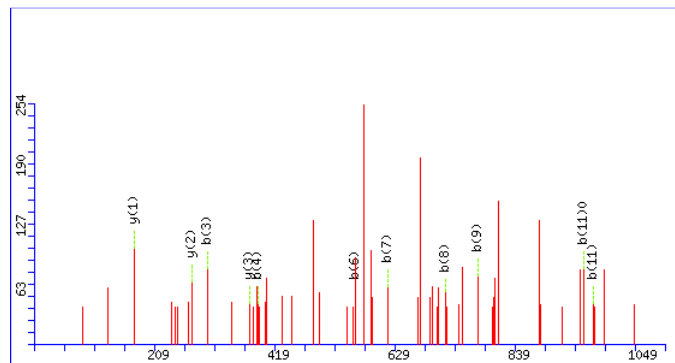
MS/MS Fragmentation of **TTTSLGGTGTTTR**:

Found in **IP100787305**

Title: 2.1.1.1154.7

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120208ry¥120208ry_Tig120slc-P8_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							12
2	203.1026	102.0550	0	0	185.0921	93.0497	T	1051.5378	526.2726	1034.5113	517.7593	1033.5273	517.2673	11
3	304.1503	152.5788	0	0	286.1397	143.5735	T	950.4902	475.7487	933.4636	467.2354	932.4796	466.7434	10
4	391.1823	196.0948	0	0	373.1718	187.0895	S	849.4425	425.2249	832.4159	416.7116	831.4319	416.2196	9
5	504.2664	252.6368	0	0	486.2558	243.6316	L	762.4104	381.7089	745.3839	373.1956	744.3999	372.7036	8
6	561.2879	281.1476	0	0	543.2773	272.1423	G	649.3264	325.1668	632.2998	316.6536	631.3158	316.1615	7
7	618.3093	309.6583	0	0	600.2988	300.6530	G	592.3049	296.6561	575.2784	288.1428	574.2944	287.6508	6
8	719.3570	360.1821	0	0	701.3464	351.1769	T	535.2835	268.1454	518.2569	259.6321	517.2729	259.1401	5
9	776.3785	388.6929	0	0	758.3679	379.6876	G	434.2358	217.6215	417.2092	209.1083	416.2252	208.6162	4
10	877.4262	439.2167	0	0	859.4156	430.2114	T	377.2143	189.1108	360.1878	180.5975	359.2037	180.1055	3
11	978.4738	489.7406	0	0	960.4633	480.7353	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
12							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: **38444**.

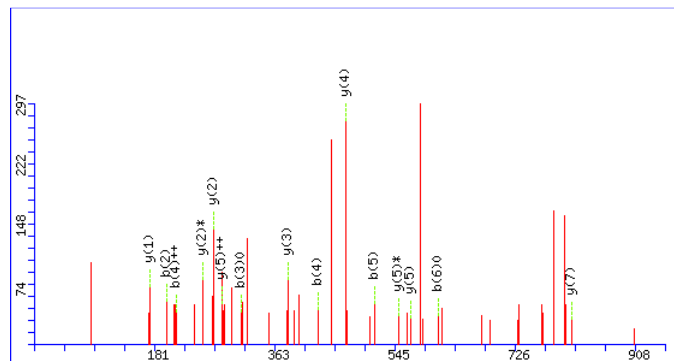
MS/MS Fragmentation of **SLMPSIPR**:

Found in **IP100479399**

Title: 3.1.1.10.2

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							8
2	201.1234	101.0653	0	0	183.1128	92.0600	L	813.4651	407.2362	796.4386	398.7229	795.4546	398.2309	7
3	332.1639	166.5856	0	0	314.1533	157.5803	M	700.3811	350.6942	683.3545	342.1809	682.3705	341.6889	6
4	429.2166	215.1119	0	0	411.2061	206.1067	P	569.3406	285.1739	552.3140	276.6606	551.3300	276.1686	5
5	516.2486	258.6280	0	0	498.2381	249.6227	S	472.2878	236.6475	455.2613	228.1343	454.2772	227.6423	4
6	629.3327	315.1700	0	0	611.3221	306.1647	I	385.2558	193.1315	368.2292	184.6183	0	0	3
7	726.3855	363.6964	0	0	708.3749	354.6911	P	272.1717	136.5895	255.1452	128.0762	0	0	2
8							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 38711.

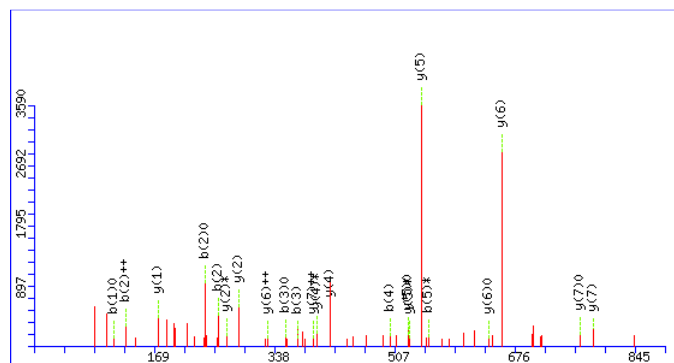
MS/MS Fragmentation of **EQLEAGIR: 0.984016@Q:2**

Found in **IP100867633;IP100910529;IP100945467**

Title: 2.1.1.2513.3

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							8
2	259.0925	130.0499	242.0659	121.5366	241.0819	121.0446	Q	787.4308	394.2191	770.4043	385.7058	769.4203	385.2138	7
3	372.1765	186.5919	355.1500	178.0786	354.1660	177.5866	L	658.3883	329.6978	641.3617	321.1845	640.3777	320.6925	6
4	501.2191	251.1132	484.1926	242.5999	483.2086	242.1079	E	545.3042	273.1557	528.2776	264.6425	527.2936	264.1504	5
5	572.2562	286.6318	555.2297	278.1185	554.2457	277.6265	A	416.2616	208.6344	399.2350	200.1212	0	0	4
6	629.2777	315.1425	612.2511	306.6292	611.2671	306.1372	G	345.2245	173.1159	328.1979	164.6026	0	0	3
7	742.3618	371.6845	725.3352	363.1712	724.3512	362.6792	I	288.2030	144.6051	271.1765	136.0919	0	0	2
8							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 38772.

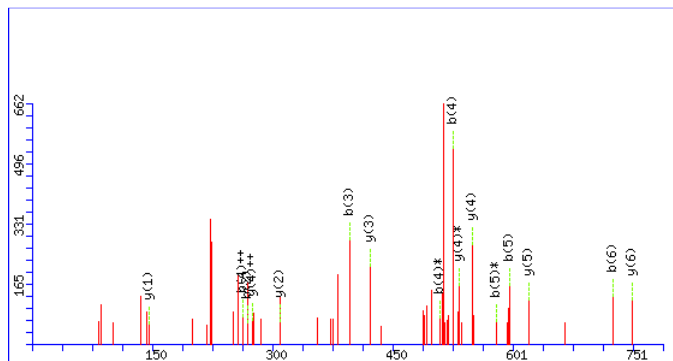
MS/MS Fragmentation of **RLGEAQLYK**:

Found in **IP100175096;IP100179408;IP100984886**

Title: 1.1.1.7351.3

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_3_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	157.1084	79.0578	140.0818	70.5446	0	0	R							9
2	270.1925	135.5999	253.1659	127.0866	0	0	L	992.5411	496.7742	975.5146	488.2609	974.5306	487.7689	8
3	398.2510	199.6292	381.2245	191.1159	0	0	Q	879.4571	440.2322	862.4305	431.7189	861.4465	431.2269	7
4	527.2936	264.1504	510.2671	255.6372	509.2831	255.1452	E	751.3985	376.2029	734.3719	367.6896	733.3879	367.1976	6
5	598.3307	299.6690	581.3042	291.1557	580.3202	290.6637	A	622.3559	311.6816	605.3293	303.1683	0	0	5
6	726.3893	363.6983	709.3628	355.1850	708.3787	354.6930	Q	551.3188	276.1630	534.2922	267.6498	0	0	4
7	839.4734	420.2403	822.4468	411.7271	821.4628	411.2350	L	423.2602	212.1337	406.2336	203.6205	0	0	3
8	1002.5367	501.7720	985.5102	493.2587	984.5261	492.7667	Y	310.1761	155.5917	293.1496	147.0784	0	0	2
9							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 38926.

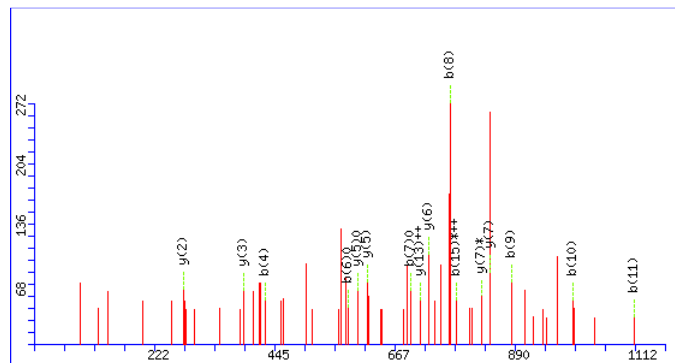
MS/MS Fragmentation of **QKLEDGGINLNDIEK**:

Found in **IP100011951;IP100604690;IP100902575**

Title: 2.1.1.3094.8

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							16
2	186.1237	93.5655	169.0972	85.0522	0	0	K	1672.8388	836.9230	1655.8123	828.4098	1654.8283	827.9178	15
3	299.2078	150.1075	282.1812	141.5942	0	0	L	1544.7439	772.8756	1527.7173	764.3623	1526.7333	763.8703	14
4	428.2504	214.6288	411.2238	206.1155	410.2398	205.6235	E	1431.6598	716.3335	1414.6332	707.8203	1413.6492	707.3283	13
5	543.2773	272.1423	526.2508	263.6290	525.2667	263.1370	D	1302.6172	651.8122	1285.5907	643.2990	1284.6066	642.8070	12
6	600.2988	300.6530	583.2722	292.1397	582.2882	291.6477	G	1187.5903	594.2988	1170.5637	585.7855	1169.5797	585.2935	11
7	715.3257	358.1665	698.2992	349.6532	697.3151	349.1612	D	1130.5688	565.7880	1113.5422	557.2748	1112.5582	556.7828	10
8	772.3472	386.6772	755.3206	378.1640	754.3366	377.6719	G	1015.5418	508.2746	998.5153	499.7613	997.5313	499.2693	9
9	885.4312	443.2193	868.4047	434.7060	867.4207	434.2140	I	958.5204	479.7638	941.4938	471.2506	940.5098	470.7585	8
10	999.4742	500.2407	982.4476	491.7274	981.4636	491.2354	N	845.4363	423.2218	828.4098	414.7085	827.4258	414.2165	7
11	1112.5582	556.7828	1095.5317	548.2695	1094.5477	547.7775	L	731.3934	366.2003	714.3668	357.6871	713.3828	357.1951	6
12	1226.6012	613.8042	1209.5746	605.2909	1208.5906	604.7989	N	618.3093	309.6583	601.2828	301.1450	600.2988	300.6530	5
13	1341.6281	671.3177	1324.6015	662.8044	1323.6175	662.3124	D	504.2664	252.6368	487.2399	244.1236	486.2558	243.6316	4
14	1454.7122	727.8597	1437.6856	719.3464	1436.7016	718.8544	I	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
15	1583.7548	792.3810	1566.7282	783.8677	1565.7442	783.3757	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
16							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 39299.

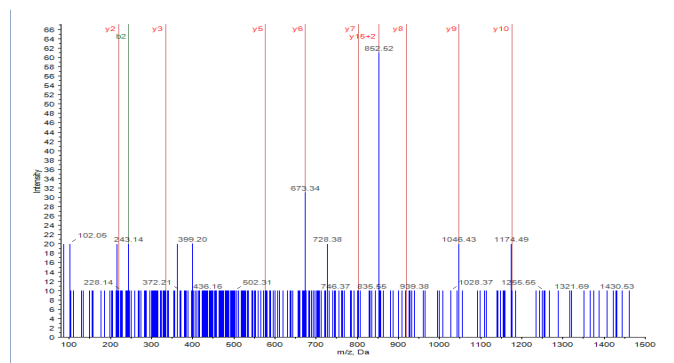
MS/MS Fragmentation of **IESSLQEDEPENDAK**:

Found in **IP100299387;IP100789388**

Title: 1.1.1.7757.10

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120129ry¥120129ry_604A1-46_3_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							15
2	243.1339	122.0706	0	0	225.1234	113.0653	E	1590.6766	795.8419	1573.6500	787.3286	1572.6660	786.8366	14
3	330.1660	165.5866	0	0	312.1554	156.5813	S	1461.6340	731.3206	1444.6074	722.8073	1443.6234	722.3153	13
4	417.1980	209.1026	0	0	399.1874	200.0974	S	1374.6019	687.8046	1357.5754	679.2913	1356.5914	678.7993	12
5	530.2821	265.6447	0	0	512.2715	256.6394	L	1287.5699	644.2886	1270.5434	635.7753	1269.5594	635.2833	11
6	658.3406	329.6740	641.3141	321.1607	640.3301	320.6687	Q	1174.4859	587.7466	1157.4593	579.2333	1156.4753	578.7413	10
7	787.3832	394.1953	770.3567	385.6820	769.3727	385.1900	E	1046.4273	523.7173	1029.4007	515.2040	1028.4167	514.7120	9
8	902.4102	451.7087	885.3836	443.1954	884.3996	442.7034	D	917.3847	459.1960	900.3581	450.6827	899.3741	450.1907	8
9	1031.4528	516.2300	1014.4262	507.7167	1013.4422	507.2247	E	802.3577	401.6825	785.3312	393.1692	784.3472	392.6772	7
10	1128.5055	564.7564	1111.4790	556.2431	1110.4950	555.7511	P	673.3151	337.1612	656.2886	328.6479	655.3046	328.1559	6
11	1257.5481	629.2777	1240.5216	620.7644	1239.5376	620.2724	E	576.2624	288.6348	559.2358	280.1216	558.2518	279.6295	5
12	1371.5910	686.2992	1354.5645	677.7859	1353.5805	677.2939	N	447.2198	224.1135	430.1932	215.6003	429.2092	215.1082	4
13	1486.6180	743.8126	1469.5914	735.2994	1468.6074	734.8073	D	333.1769	167.0921	316.1503	158.5788	315.1663	158.0868	3
14	1557.6551	779.3312	1540.6286	770.8179	1539.6445	770.3259	A	218.1499	109.5786	201.1234	101.0653	0	0	2
15							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 39345.

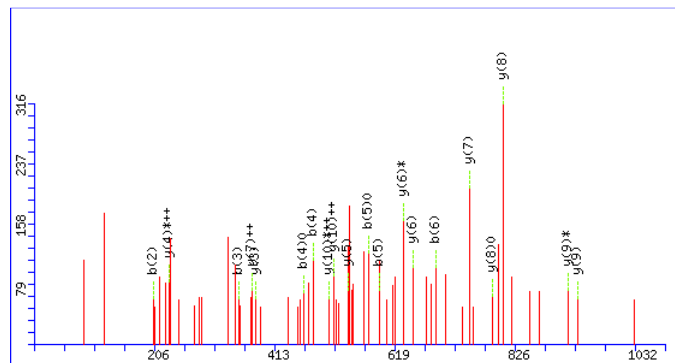
MS/MS Fragmentation of **FGFELPQGPLGTSFK**:

Found in **IP100007956;IP100514375**

Title: 3.1.1.3846.4

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120212ry¥120212ry_aHDF1388-P9_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							15
2	205.0972	103.0522	0	0	0	0	G	1477.7686	739.3879	1460.7420	730.8746	1459.7580	730.3826	14
3	352.1656	176.5864	0	0	0	0	F	1420.7471	710.8772	1403.7205	702.3639	1402.7365	701.8719	13
4	481.2082	241.1077	0	0	463.1976	232.1024	E	1273.6787	637.3430	1256.6521	628.8297	1255.6681	628.3377	12
5	594.2922	297.6498	0	0	576.2817	288.6445	L	1144.6361	572.8217	1127.6095	564.3084	1126.6255	563.8164	11
6	691.3450	346.1761	0	0	673.3344	337.1709	P	1031.5520	516.2796	1014.5255	507.7664	1013.5415	507.2744	10
7	819.4036	410.2054	802.3770	401.6921	801.3930	401.2001	Q	934.4993	467.7533	917.4727	459.2400	916.4887	458.7480	9
8	876.4250	438.7162	859.3985	430.2029	858.4145	429.7109	G	806.4407	403.7240	789.4141	395.2107	788.4301	394.7187	8
9	973.4778	487.2425	956.4512	478.7293	955.4672	478.2373	P	749.4192	375.2132	732.3927	366.7000	731.4087	366.2080	7
10	1086.5619	543.7846	1069.5353	535.2713	1068.5513	534.7793	L	652.3665	326.6869	635.3399	318.1736	634.3559	317.6816	6
11	1143.5833	572.2953	1126.5568	563.7820	1125.5728	563.2900	G	539.2824	270.1448	522.2558	261.6316	521.2718	261.1396	5
12	1244.6310	622.8191	1227.6045	614.3059	1226.6204	613.8139	T	482.2609	241.6341	465.2344	233.1208	464.2504	232.6288	4
13	1331.6630	666.3352	1314.6365	657.8219	1313.6525	657.3299	S	381.2132	191.1103	364.1867	182.5970	363.2027	182.1050	3
14	1478.7314	739.8694	1461.7049	731.3561	1460.7209	730.8641	F	294.1812	147.5942	277.1547	139.0810	0	0	2
15							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 39482.

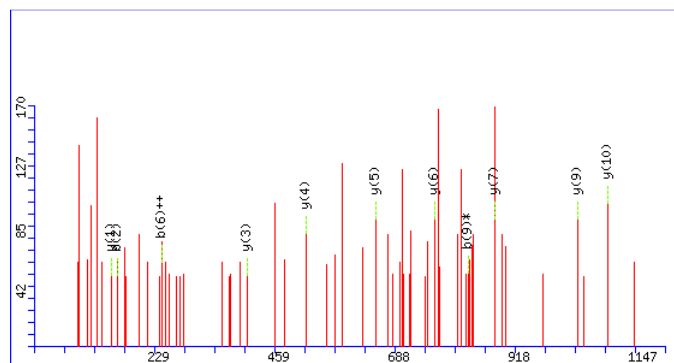
MS/MS Fragmentation of **GTGGTDLNFLK**:

Found in **IP100028096**

Title: 3.1.1.2373.6

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							12
2	159.0764	80.0418	0	0	141.0659	71.0366	T	1196.5980	598.8026	1179.5714	590.2894	1178.5874	589.7973	11
3	216.0979	108.5526	0	0	198.0873	99.5473	G	1095.5503	548.2788	1078.5238	539.7655	1077.5397	539.2735	10
4	273.1193	137.0633	0	0	255.1088	128.0580	G	1038.5288	519.7681	1021.5023	511.2548	1020.5183	510.7628	9
5	374.1670	187.5872	0	0	356.1565	178.5819	T	981.5074	491.2573	964.4808	482.7441	963.4968	482.2520	8
6	489.1940	245.1006	0	0	471.1834	236.0953	D	880.4597	440.7335	863.4332	432.2202	862.4491	431.7282	7
7	602.2780	301.6427	0	0	584.2675	292.6374	L	765.4328	383.2200	748.4062	374.7067	0	0	6
8	733.3185	367.1629	0	0	715.3080	358.1576	M	652.3487	326.6780	635.3221	318.1647	0	0	5
9	847.3614	424.1844	830.3349	415.6711	829.3509	415.1791	N	521.3082	261.1577	504.2817	252.6445	0	0	4
10	994.4299	497.7186	977.4033	489.2053	976.4193	488.7133	F	407.2653	204.1363	390.2387	195.6230	0	0	3
11	1107.5139	554.2606	1090.4874	545.7473	1089.5034	545.2553	L	260.1969	130.6021	243.1703	122.0888	0	0	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 39562.

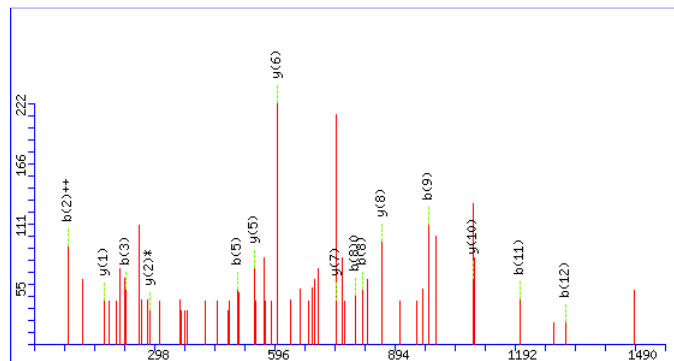
MS/MS Fragmentation of **GLGEFTPLYPMLFGGGQER**:

Found in **IP100101652;IP100556507;IP100884890;IP100909950;IP100910775;IP100915946;IP100916046;IP100917004**

Title: 4.1.1.1507.4

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120118ry¥120118ry_201B7-32_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							19
2	171.1128	86.0600	0	0	0	0	L	2011.9946	1006.5009	1994.9681	997.9877	1993.9840	997.4957	18
3	228.1343	114.5708	0	0	0	0	G	1898.9105	949.9589	1881.8840	941.4456	1880.9000	940.9536	17
4	357.1769	179.0921	0	0	339.1663	170.0868	E	1841.8891	921.4482	1824.8625	912.9349	1823.8785	912.4429	16
5	504.2453	252.6263	0	0	486.2347	243.6210	F	1712.8465	856.9269	1695.8199	848.4136	1694.8359	847.9216	15
6	605.2930	303.1501	0	0	587.2824	294.1448	T	1565.7781	783.3927	1548.7515	774.8794	1547.7675	774.3874	14
7	702.3457	351.6765	0	0	684.3352	342.6712	P	1464.7304	732.8688	1447.7038	724.3556	1446.7198	723.8636	13
8	815.4298	408.2185	0	0	797.4192	399.2132	L	1367.6776	684.3425	1350.6511	675.8292	1349.6671	675.3372	12
9	978.4931	489.7502	0	0	960.4825	480.7449	Y	1254.5936	627.8004	1237.5670	619.2871	1236.5830	618.7951	11
10	1075.5459	538.2766	0	0	1057.5353	529.2713	P	1091.5302	546.2688	1074.5037	537.7555	1073.5197	537.2635	10
11	1206.5864	603.7968	0	0	1188.5758	594.7915	M	994.4775	497.7424	977.4509	489.2291	976.4669	488.7371	9
12	1319.6704	660.3389	0	0	1301.6599	651.3336	L	863.4370	432.2221	846.4104	423.7089	845.4264	423.2169	8
13	1466.7388	733.8731	0	0	1448.7283	724.8678	F	750.3529	375.6801	733.3264	367.1668	732.3424	366.6748	7
14	1523.7603	762.3838	0	0	1505.7497	753.3785	G	603.2845	302.1459	586.2580	293.6326	585.2740	293.1406	6
15	1580.7818	790.8945	0	0	1562.7712	781.8892	G	546.2631	273.6352	529.2365	265.1219	528.2525	264.6299	5
16	1637.8032	819.4053	0	0	1619.7927	810.4000	G	489.2416	245.1244	472.2150	236.6112	471.2310	236.1191	4
17	1765.8618	883.4345	1748.8353	874.9213	1747.8512	874.4293	Q	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	3
18	1894.9044	947.9558	1877.8779	939.4426	1876.8938	938.9506	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
19							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 39820.

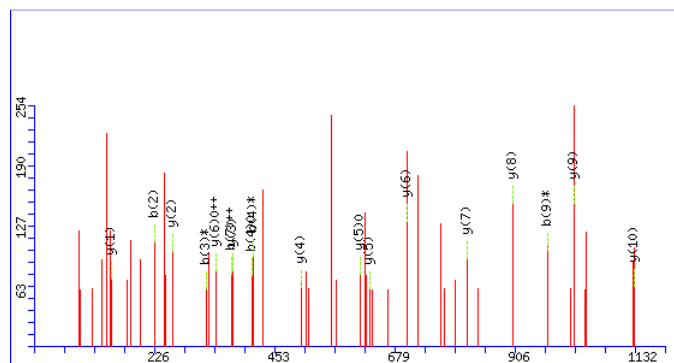
MS/MS Fragmentation of **LNDZIAEELNK**:

Found in **IP100215871;IP100289667;IP100442991;IP100604415;IP100877636;IP100877801;IP101020892**

Title: 2.1.1.1835.9

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120214ry¥120214ry_32R1-32_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							11
2	228.1343	114.5708	211.1077	106.0575	0	0	N	1132.5481	566.7777	1115.5215	558.2644	1114.5375	557.7724	10
3	343.1612	172.0842	326.1347	163.5710	325.1506	163.0790	D	1018.5051	509.7562	1001.4786	501.2429	1000.4946	500.7509	9
4	430.1932	215.6003	413.1667	207.0870	412.1827	206.5950	S	903.4782	452.2427	886.4516	443.7295	885.4676	443.2374	8
5	543.2773	272.1423	526.2508	263.6290	525.2667	263.1370	I	816.4462	408.7267	799.4196	400.2134	798.4356	399.7214	7
6	614.3144	307.6608	597.2879	299.1476	596.3039	298.6556	A	703.3621	352.1847	686.3355	343.6714	685.3515	343.1794	6
7	743.3570	372.1821	726.3305	363.6689	725.3464	363.1769	E	632.3250	316.6661	615.2984	308.1529	614.3144	307.6608	5
8	872.3996	436.7034	855.3731	428.1902	854.3890	427.6982	E	503.2824	252.1448	486.2558	243.6316	485.2718	243.1395	4
9	985.4837	493.2455	968.4571	484.7322	967.4731	484.2402	L	374.2398	187.6235	357.2132	179.1103	0	0	3
10	1099.5266	550.2669	1082.5000	541.7537	1081.5160	541.2617	N	261.1557	131.0815	244.1292	122.5682	0	0	2
11							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 39886.

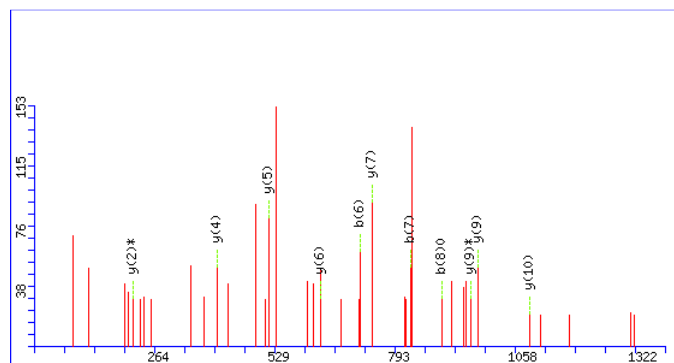
MS/MS Fragmentation of **IDPFEDLSFNLLAVSK:**

Found in **IP100012441;IP100658095;IP100945835**

Title: 4.1.1.2428.4

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							16
2	229.1183	115.0628	0	0	211.1077	106.0575	D	1694.8636	847.9354	1677.8370	839.4222	1676.8530	838.9301	15
3	326.1710	163.5892	0	0	308.1605	154.5839	P	1579.8366	790.4220	1562.8101	781.9087	1561.8261	781.4167	14
4	473.2395	237.1234	0	0	455.2289	228.1181	F	1482.7839	741.8956	1465.7573	733.3823	1464.7733	732.8903	13
5	602.2821	301.6447	0	0	584.2715	292.6394	E	1335.7155	668.3614	1318.6889	659.8481	1317.7049	659.3561	12
6	717.3090	359.1581	0	0	699.2984	350.1529	D	1206.6729	603.8401	1189.6463	595.3268	1188.6623	594.8348	11
7	830.3931	415.7002	0	0	812.3825	406.6949	L	1091.6459	546.3266	1074.6194	537.8133	1073.6354	537.3213	10
8	917.4251	459.2162	0	0	899.4145	450.2109	S	978.5619	489.7846	961.5353	481.2713	960.5513	480.7793	9
9	1064.4935	532.7504	0	0	1046.4829	523.7451	F	891.5298	446.2686	874.5033	437.7553	873.5193	437.2633	8
10	1178.5364	589.7719	1161.5099	581.2586	1160.5259	580.7666	N	744.4614	372.7343	727.4349	364.2211	726.4509	363.7291	7
11	1291.6205	646.3139	1274.5939	637.8006	1273.6099	637.3086	L	630.4185	315.7129	613.3919	307.1996	612.4079	306.7076	6
12	1404.7046	702.8559	1387.6780	694.3426	1386.6940	693.8506	L	517.3344	259.1708	500.3079	250.6576	499.3239	250.1656	5
13	1475.7417	738.3745	1458.7151	729.8612	1457.7311	729.3692	A	404.2504	202.6288	387.2238	194.1155	386.2398	193.6235	4
14	1574.8101	787.9087	1557.7835	779.3954	1556.7995	778.9034	V	333.2132	167.1103	316.1867	158.5970	315.2027	158.1050	3
15	1661.8421	831.4247	1644.8156	822.9114	1643.8315	822.4194	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
16							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 40170.

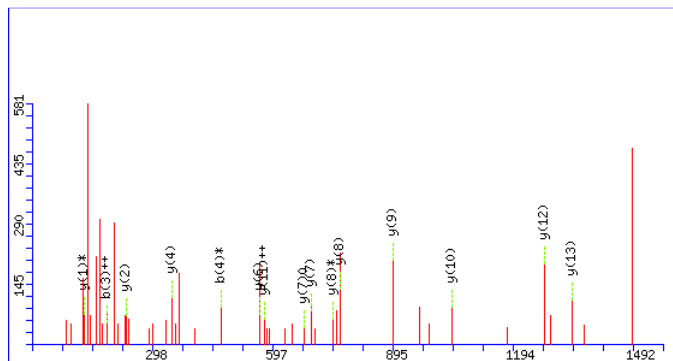
MS/MS Fragmentation of **WADNFMAEGCGGSK: 57.021465@C:10**

Found in **IP100550440:IP100892923**

Title: 2.1.1.2842.11

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120206ry¥120206ry_aHDF1419-P10_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	187.0866	94.0469	0	0	0	0	W							14
2	258.1237	129.5655	0	0	0	0	A	1343.5355	672.2714	1326.5089	663.7581	1325.5249	663.2661	13
3	373.1506	187.0790	0	0	355.1401	178.0737	D	1272.4983	636.7528	1255.4718	628.2395	1254.4878	627.7475	12
4	487.1936	244.1004	470.1670	235.5871	469.1830	235.0951	N	1157.4714	579.2393	1140.4449	570.7261	1139.4608	570.2341	11
5	634.2620	317.6346	617.2354	309.1214	616.2514	308.6293	F	1043.4285	522.2179	1026.4019	513.7046	1025.4179	513.2126	10
6	765.3025	383.1549	748.2759	374.6416	747.2919	374.1496	M	896.3601	448.6837	879.3335	440.1704	878.3495	439.6784	9
7	836.3396	418.6734	819.3130	410.1602	818.3290	409.6681	A	765.3196	383.1634	748.2930	374.6502	747.3090	374.1581	8
8	965.3822	483.1947	948.3556	474.6815	947.3716	474.1894	E	694.2825	347.6449	677.2559	339.1316	676.2719	338.6396	7
9	1022.4036	511.7055	1005.3771	503.1922	1004.3931	502.7002	G	565.2399	283.1236	548.2133	274.6103	547.2293	274.1183	6
10	1182.4343	591.7208	1165.4077	583.2075	1164.4237	582.7155	C	508.2184	254.6128	491.1919	246.0996	490.2078	245.6076	5
11	1239.4558	620.2315	1222.4292	611.7182	1221.4452	611.2262	G	348.1878	174.5975	331.1612	166.0842	330.1772	165.5922	4
12	1296.4772	648.7422	1279.4507	640.2290	1278.4667	639.7370	G	291.1663	146.0868	274.1397	137.5735	273.1557	137.0815	3
13	1383.5092	692.2583	1366.4827	683.7450	1365.4987	683.2530	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 40246.

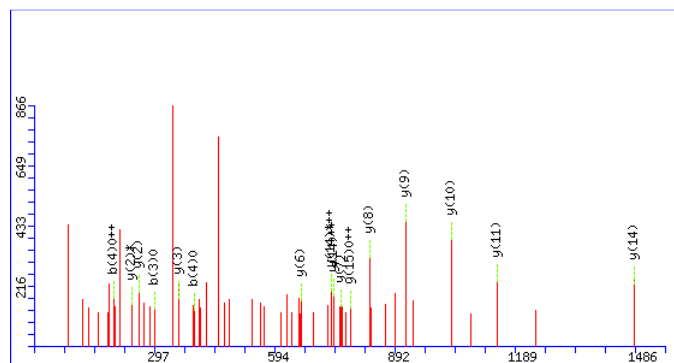
MS/MS Fragmentation of **DTTPDELLSAVMTAVLK**:

Found in **IP100011522;IP100012828;IP100303933;IP100789589;IP100924606;IP100927496**

Title: 5.1.1.1558.9

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120208ry¥120208ry_Tig120slc-P8_2.5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							17
2	217.0819	109.0446	0	0	199.0713	100.0393	T	1688.9139	844.9606	1671.8874	836.4473	1670.9033	835.9553	16
3	318.1296	159.5684	0	0	300.1190	150.5631	T	1587.8662	794.4367	1570.8397	785.9235	1569.8557	785.4315	15
4	415.1823	208.0948	0	0	397.1718	199.0895	P	1486.8185	743.9129	1469.7920	735.3996	1468.8080	734.9076	14
5	530.2093	265.6083	0	0	512.1987	256.6030	D	1389.7658	695.3865	1372.7392	686.8733	1371.7552	686.3812	13
6	659.2519	330.1296	0	0	641.2413	321.1243	E	1274.7388	637.8731	1257.7123	629.3598	1256.7283	628.8678	12
7	772.3359	386.6716	0	0	754.3254	377.6663	L	1145.6962	573.3518	1128.6697	564.8385	1127.6857	564.3465	11
8	885.4200	443.2136	0	0	867.4094	434.2084	L	1032.6122	516.8097	1015.5856	508.2965	1014.6016	507.8044	10
9	972.4520	486.7297	0	0	954.4415	477.7244	S	919.5281	460.2677	902.5016	451.7544	901.5176	451.2624	9
10	1043.4891	522.2482	0	0	1025.4786	513.2429	A	832.4961	416.7517	815.4695	408.2384	814.4855	407.7464	8
11	1142.5576	571.7824	0	0	1124.5470	562.7771	V	761.4590	381.2331	744.4324	372.7199	743.4484	372.2278	7
12	1273.5980	637.3027	0	0	1255.5875	628.2974	M	662.3906	331.6989	645.3640	323.1856	644.3800	322.6936	6
13	1374.6457	687.8265	0	0	1356.6352	678.8212	T	531.3501	266.1787	514.3235	257.6654	513.3395	257.1734	5
14	1445.6828	723.3451	0	0	1427.6723	714.3398	A	430.3024	215.6548	413.2758	207.1416	0	0	4
15	1544.7513	772.8793	0	0	1526.7407	763.8740	V	359.2653	180.1363	342.2387	171.6230	0	0	3
16	1657.8353	829.4213	0	0	1639.8248	820.4160	L	260.1969	130.6021	243.1703	122.0888	0	0	2
17							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 40454.

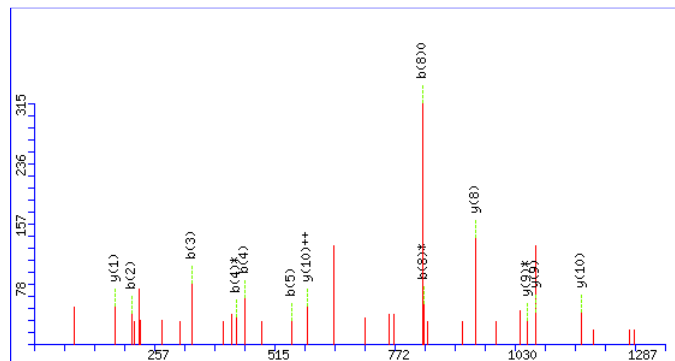
MS/MS Fragmentation of **LPQITEIGMKR**:

Found in **IP100015444;IP100167333**

Title: 3.1.1.1330.10

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							11
2	211.1441	106.0757	0	0	0	0	P	1172.6456	586.8264	1155.6191	578.3132	1154.6350	577.8212	10
3	339.2027	170.1050	322.1761	161.5917	0	0	Q	1075.5928	538.3001	1058.5663	529.7868	1057.5823	529.2948	9
4	452.2867	226.6470	435.2602	218.1337	0	0	I	947.5343	474.2708	930.5077	465.7575	929.5237	465.2655	8
5	553.3344	277.1709	536.3079	268.6576	535.3239	268.1656	T	834.4502	417.7287	817.4237	409.2155	816.4396	408.7235	7
6	682.3770	341.6921	665.3505	333.1789	664.3665	332.6869	E	733.4025	367.2049	716.3760	358.6916	715.3920	358.1996	6
7	795.4611	398.2342	778.4345	389.7209	777.4505	389.2289	I	604.3599	302.6836	587.3334	294.1703	0	0	5
8	852.4825	426.7449	835.4560	418.2316	834.4720	417.7396	G	491.2759	246.1416	474.2493	237.6283	0	0	4
9	983.5230	492.2652	966.4965	483.7519	965.5125	483.2599	M	434.2544	217.6308	417.2279	209.1176	0	0	3
10	1111.6180	556.3126	1094.5914	547.7994	1093.6074	547.3074	K	303.2139	152.1106	286.1874	143.5973	0	0	2
11							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 40544.

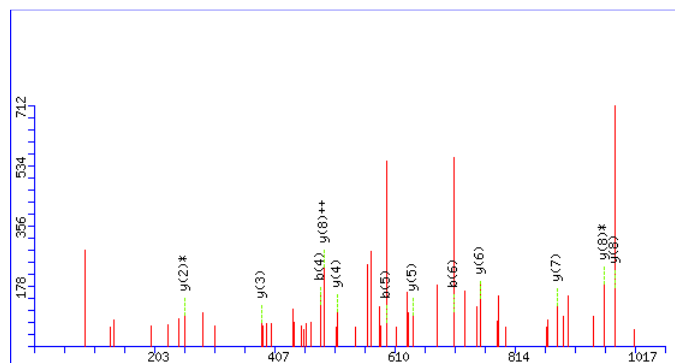
MS/MS Fragmentation of **ARPC11PENEEIPR: 57.021465@C:4**

Found in **IP100847665;IP100917369;IP100917648;IP100930460;IP101010460**

Title: 2.1.1.2048.9

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120212ry¥120212ry_aHDF1388-P9_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							14
2	228.1455	114.5764	211.1190	106.0631	0	0	R	1622.8319	811.9196	1605.8054	803.4063	1604.8213	802.9143	13
3	325.1983	163.1028	308.1717	154.5895	0	0	P	1466.7308	733.8690	1449.7042	725.3558	1448.7202	724.8638	12
4	485.2289	243.1181	468.2024	234.6048	0	0	C	1369.6780	685.3427	1352.6515	676.8294	1351.6675	676.3374	11
5	598.3130	299.6601	581.2864	291.1469	0	0	I	1209.6474	605.3273	1192.6208	596.8141	1191.6368	596.3220	10
6	711.3970	356.2022	694.3705	347.6889	0	0	I	1096.5633	548.7853	1079.5368	540.2720	1078.5527	539.7800	9
7	808.4498	404.7285	791.4233	396.2153	0	0	P	983.4792	492.2433	966.4527	483.7300	965.4687	483.2380	8
8	937.4924	469.2498	920.4659	460.7366	919.4818	460.2446	E	886.4265	443.7169	869.3999	435.2036	868.4159	434.7116	7
9	1051.5353	526.2713	1034.5088	517.7580	1033.5248	517.2660	N	757.3839	379.1956	740.3573	370.6823	739.3733	370.1903	6
10	1180.5779	590.7926	1163.5514	582.2793	1162.5674	581.7873	E	643.3410	322.1741	626.3144	313.6608	625.3304	313.1688	5
11	1309.6205	655.3139	1292.5940	646.8006	1291.6099	646.3086	E	514.2984	257.6528	497.2718	249.1395	496.2878	248.6475	4
12	1422.7046	711.8559	1405.6780	703.3427	1404.6940	702.8506	I	385.2558	193.1315	368.2292	184.6183	0	0	3
13	1519.7573	760.3823	1502.7308	751.8690	1501.7468	751.3770	P	272.1717	136.5895	255.1452	128.0762	0	0	2
14							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 40552.

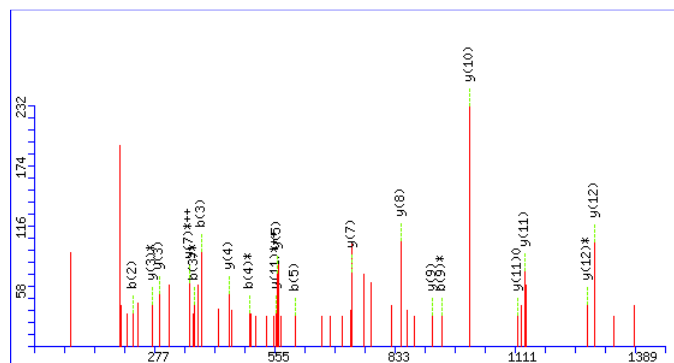
MS/MS Fragmentation of **NLCESADGILCSGK**: 57.021465@C:3,57.021465@C:11

Found in **IP100640865;IP100844069;IP100940202;IP101011309;IP101018875**

Title: 2.1.1.3127.11

Data file: Y:\TT5600(CiRA1)\2012-02\120201ry\120201ry_aHDF1388-P9_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							14
2	228.1343	114.5708	211.1077	106.0575	0	0	L	1409.6399	705.3236	1392.6134	696.8103	1391.6294	696.3183	13
3	388.1649	194.5861	371.1384	186.0728	0	0	C	1296.5559	648.7816	1279.5293	640.2683	1278.5453	639.7763	12
4	517.2075	259.1074	500.1810	250.5941	499.1969	250.1021	E	1136.5252	568.7662	1119.4987	560.2530	1118.5147	559.7610	11
5	604.2395	302.6234	587.2130	294.1101	586.2290	293.6181	S	1007.4826	504.2449	990.4561	495.7317	989.4721	495.2397	10
6	675.2767	338.1420	658.2501	329.6287	657.2661	329.1367	A	920.4506	460.7289	903.4240	452.2157	902.4400	451.7237	9
7	790.3036	395.6554	773.2770	387.1422	772.2930	386.6502	D	849.4135	425.2104	832.3869	416.6971	831.4029	416.2051	8
8	847.3251	424.1662	830.2985	415.6529	829.3145	415.1609	G	734.3865	367.6969	717.3600	359.1836	716.3760	358.6916	7
9	960.4091	480.7082	943.3826	472.1949	942.3986	471.7029	I	677.3651	339.1862	660.3385	330.6729	659.3545	330.1809	6
10	1073.4932	537.2502	1056.4666	528.7370	1055.4826	528.2449	L	564.2810	282.6441	547.2545	274.1309	546.2704	273.6389	5
11	1233.5238	617.2656	1216.4973	608.7523	1215.5133	608.2603	C	451.1969	226.1021	434.1704	217.5888	433.1864	217.0968	4
12	1320.5559	660.7816	1303.5293	652.2683	1302.5453	651.7763	S	291.1663	146.0868	274.1397	137.5735	273.1557	137.0815	3
13	1377.5773	689.2923	1360.5508	680.7790	1359.5668	680.2870	G	204.1343	102.5708	187.1077	94.0575	0	0	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 40659.

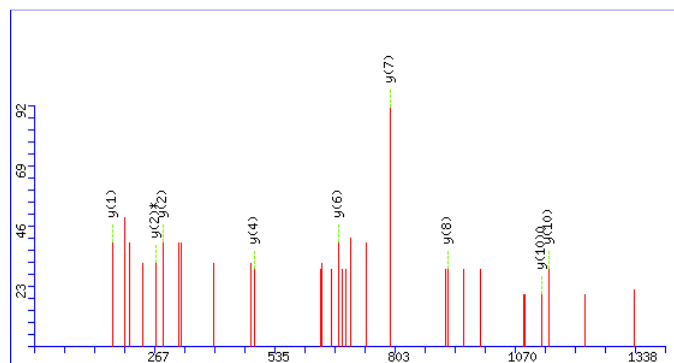
MS/MS Fragmentation of **FLDPDMYSLLEDSTDLR**:

Found in **IP100470580;IP100794828;IP100856080;IP101021137**

Title: 4.1.1.1132.6

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							18
2	261.1598	131.0835	0	0	0	0	L	1969.9059	985.4566	1952.8794	976.9433	1951.8953	976.4513	17
3	376.1867	188.5970	0	0	358.1761	179.5917	D	1856.8218	928.9146	1839.7953	920.4013	1838.8113	919.9093	16
4	473.2395	237.1234	0	0	455.2289	228.1181	P	1741.7949	871.4011	1724.7684	862.8878	1723.7843	862.3958	15
5	588.2664	294.6368	0	0	570.2558	285.6316	D	1644.7421	822.8747	1627.7156	814.3614	1626.7316	813.8694	14
6	719.3069	360.1571	0	0	701.2963	351.1518	M	1529.7152	765.3612	1512.6887	756.8480	1511.7046	756.3560	13
7	882.3702	441.6887	0	0	864.3597	432.6835	Y	1398.6747	699.8410	1381.6482	691.3277	1380.6642	690.8357	12
8	969.4022	485.2048	0	0	951.3917	476.1995	S	1235.6114	618.3093	1218.5848	609.7961	1217.6008	609.3040	11
9	1082.4863	541.7468	0	0	1064.4757	532.7415	L	1148.5794	574.7933	1131.5528	566.2800	1130.5688	565.7880	10
10	1195.5704	598.2888	0	0	1177.5598	589.2835	L	1035.4953	518.2513	1018.4687	509.7380	1017.4847	509.2460	9
11	1324.6130	662.8101	0	0	1306.6024	653.8048	E	922.4112	461.7093	905.3847	453.1960	904.4007	452.7040	8
12	1439.6399	720.3236	0	0	1421.6293	711.3183	D	793.3686	397.1880	776.3421	388.6747	775.3581	388.1827	7
13	1526.6719	763.8396	0	0	1508.6614	754.8343	S	678.3417	339.6745	661.3151	331.1612	660.3311	330.6692	6
14	1627.7196	814.3634	0	0	1609.7091	805.3582	T	591.3097	296.1585	574.2831	287.6452	573.2991	287.1532	5
15	1714.7516	857.8795	0	0	1696.7411	848.8742	S	490.2620	245.6346	473.2354	237.1214	472.2514	236.6293	4
16	1829.7786	915.3929	0	0	1811.7680	906.3876	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
17	1942.8627	971.9350	0	0	1924.8521	962.9297	L	288.2030	144.6051	271.1765	136.0919	0	0	2
18							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 40681.

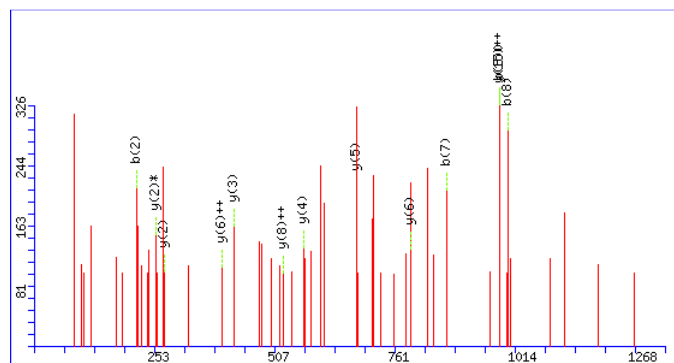
MS/MS Fragmentation of **SQMQHFLQQQIFFQK**:

Found in **IP100657938;IP100976895**

Title: 3.1.1.3466.6

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120206ry¥120206ry_aHDF1419-P10_2.3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							16
2	216.0979	108.5526	199.0713	100.0393	198.0873	99.5473	Q	1964.0211	982.5142	1946.9946	974.0009	0	0	15
3	347.1384	174.0728	330.1118	165.5595	329.1278	165.0675	M	1835.9625	918.4849	1818.9360	909.9716	0	0	14
4	475.1969	238.1021	458.1704	229.5888	457.1864	229.0968	Q	1704.9220	852.9647	1687.8955	844.4514	0	0	13
5	612.2559	306.6316	595.2293	298.1183	594.2453	297.6263	H	1576.8635	788.9354	1559.8369	780.4221	0	0	12
6	759.3243	380.1658	742.2977	371.6525	741.3137	371.1605	F	1439.8045	720.4059	1422.7780	711.8926	0	0	11
7	872.4083	436.7078	855.3818	428.1945	854.3978	427.7025	L	1292.7361	646.8717	1275.7096	638.3584	0	0	10
8	1000.4669	500.7371	983.4404	492.2238	982.4563	491.7318	Q	1179.6521	590.3297	1162.6255	581.8164	0	0	9
9	1128.5255	564.7664	1111.4989	556.2531	1110.5149	555.7611	Q	1051.5935	526.3004	1034.5669	517.7871	0	0	8
10	1256.5841	628.7957	1239.5575	620.2824	1238.5735	619.7904	Q	923.5349	462.2711	906.5084	453.7578	0	0	7
11	1369.6681	685.3377	1352.6416	676.8244	1351.6576	676.3324	I	795.4763	398.2418	778.4498	389.7285	0	0	6
12	1482.7522	741.8797	1465.7256	733.3665	1464.7416	732.8745	I	682.3923	341.6998	665.3657	333.1865	0	0	5
13	1629.8206	815.4139	1612.7941	806.9007	1611.8100	806.4087	F	569.3082	285.1577	552.2817	276.6445	0	0	4
14	1776.8890	888.9482	1759.8625	880.4349	1758.8785	879.9429	F	422.2398	211.6235	405.2132	203.1103	0	0	3
15	1904.9476	952.9774	1887.9211	944.4642	1886.9370	943.9722	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
16							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 40688.

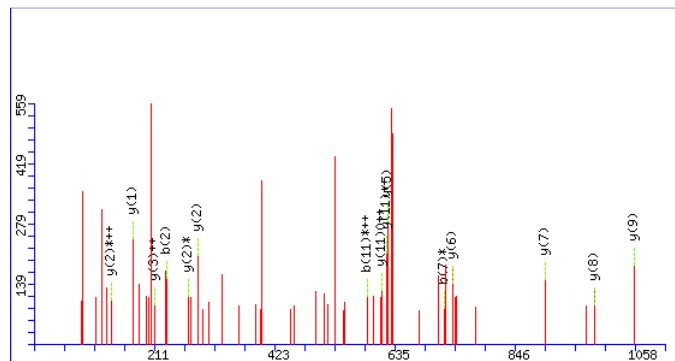
MS/MS Fragmentation of **SFANASYLAQHRLR**:

Found in **IP100292433**

Title: 2.1.1.3535.5

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							13
2	235.1077	118.0575	0	0	217.0972	109.0522	F	1390.7226	695.8649	1373.6961	687.3517	1372.7120	686.8597	12
3	306.1448	153.5761	0	0	288.1343	144.5708	A	1243.6542	622.3307	1226.6276	613.8175	1225.6436	613.3255	11
4	420.1878	210.5975	403.1612	202.0842	402.1772	201.5922	N	1172.6171	586.8122	1155.5905	578.2989	1154.6065	577.8069	10
5	491.2249	246.1161	474.1983	237.6028	473.2143	237.1108	A	1058.5742	529.7907	1041.5476	521.2774	1040.5636	520.7854	9
6	578.2569	289.6321	561.2304	281.1188	560.2463	280.6268	S	987.5370	494.2722	970.5105	485.7589	969.5265	485.2669	8
7	741.3202	371.1638	724.2937	362.6505	723.3097	362.1585	Y	900.5050	450.7561	883.4785	442.2429	0	0	7
8	854.4043	427.7058	837.3777	419.1925	836.3937	418.7005	L	737.4417	369.2245	720.4151	360.7112	0	0	6
9	925.4414	463.2243	908.4149	454.7111	907.4308	454.2191	A	624.3576	312.6824	607.3311	304.1692	0	0	5
10	1053.5000	527.2536	1036.4734	518.7404	1035.4894	518.2483	Q	553.3205	277.1639	536.2940	268.6506	0	0	4
11	1190.5589	595.7831	1173.5323	587.2698	1172.5483	586.7778	H	425.2619	213.1346	408.2354	204.6213	0	0	3
12	1303.6430	652.3251	1286.6164	643.8118	1285.6324	643.3198	L	288.2030	144.6051	271.1765	136.0919	0	0	2
13							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 40690.

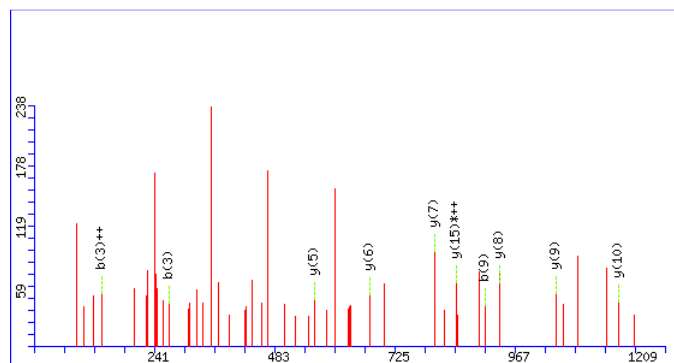
MS/MS Fragmentation of **AAQLPNDVVLQIMELCGATR: 57.021465@C:16**

Found in **IP100644155;IP100783030;IP100917829;IP100938352;IP100940373;IP100979219;IP101013778**

Title: 4.1.1.1509.2

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120212ry¥120212ry_414C2-43_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							20
2	143.0815	72.0444	0	0	0	0	A	2128.0889	1064.5481	2111.0624	1056.0348	2110.0784	1055.5428	19
3	271.1401	136.0737	254.1135	127.5604	0	0	Q	2057.0518	1029.0295	2040.0253	1020.5163	2039.0412	1020.0243	18
4	384.2241	192.6157	367.1976	184.1024	0	0	L	1928.9932	965.0003	1911.9667	956.4870	1910.9827	955.9950	17
5	481.2769	241.1421	464.2504	232.6288	0	0	P	1815.9092	908.4582	1798.8826	899.9449	1797.8986	899.4529	16
6	595.3198	298.1636	578.2933	289.6503	0	0	N	1718.8564	859.9318	1701.8299	851.4186	1700.8458	850.9266	15
7	710.3468	355.6770	693.3202	347.1638	692.3362	346.6717	D	1604.8135	802.9104	1587.7869	794.3971	1586.8029	793.9051	14
8	809.4152	405.2112	792.3886	396.6980	791.4046	396.2060	V	1489.7865	745.3969	1472.7600	736.8836	1471.7760	736.3916	13
9	908.4836	454.7454	891.4571	446.2322	890.4730	445.7402	V	1390.7181	695.8627	1373.6916	687.3494	1372.7076	686.8574	12
10	1021.5677	511.2875	1004.5411	502.7742	1003.5571	502.2822	L	1291.6497	646.3285	1274.6232	637.8152	1273.6391	637.3232	11
11	1149.6263	575.3168	1132.5997	566.8035	1131.6157	566.3115	Q	1178.5656	589.7865	1161.5391	581.2732	1160.5551	580.7812	10
12	1262.7103	631.8588	1245.6838	623.3455	1244.6997	622.8535	I	1050.5071	525.7572	1033.4805	517.2439	1032.4965	516.7519	9
13	1393.7508	697.3790	1376.7242	688.8658	1375.7402	688.3738	M	937.4230	469.2151	920.3965	460.7019	919.4124	460.2099	8
14	1522.7934	761.9003	1505.7668	753.3871	1504.7828	752.8951	E	806.3825	403.6949	789.3560	395.1816	788.3720	394.6896	7
15	1635.8775	818.4424	1618.8509	809.9291	1617.8669	809.4371	L	677.3399	339.1736	660.3134	330.6603	659.3294	330.1683	6
16	1795.9081	898.4577	1778.8816	889.9444	1777.8975	889.4524	C	564.2559	282.6316	547.2293	274.1183	546.2453	273.6263	5
17	1852.9296	926.9684	1835.9030	918.4551	1834.9190	917.9631	G	404.2252	202.6162	387.1987	194.1030	386.2146	193.6110	4
18	1923.9667	962.4870	1906.9401	953.9737	1905.9561	953.4817	A	347.2037	174.1055	330.1772	165.5922	329.1932	165.1002	3
19	2025.0144	1013.0108	2007.9878	1004.4975	2007.0038	1004.0055	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
20							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 40957.

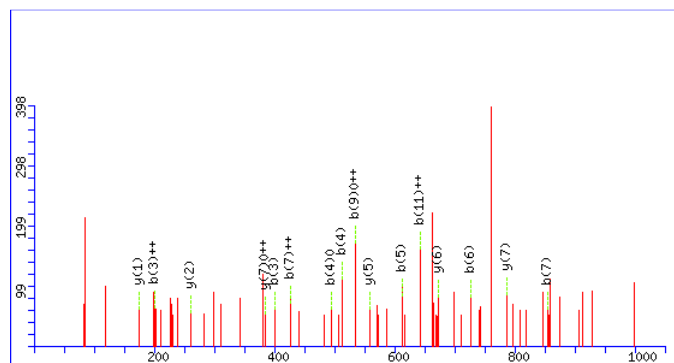
MS/MS Fragmentation of **REDIVNQMTACLNQSLDALLSR**: 57.021465@C:12

Found in **IP100021917:IP100554774**

Title: 4.1.1.1224.4

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120210ry¥120210ry_32R1-32_2.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	157.1084	79.0578	140.0818	70.5446	0	0	R							23
2	286.1510	143.5791	269.1244	135.0659	268.1404	134.5738	E	2520.2069	1260.6071	2503.1803	1252.0938	2502.1963	1251.6018	22
3	401.1779	201.0926	384.1514	192.5793	383.1674	192.0873	D	2391.1643	1196.0858	2374.1377	1187.5725	2373.1537	1187.0805	21
4	514.2620	257.6346	497.2354	249.1214	496.2514	248.6293	I	2276.1373	1138.5723	2259.1108	1130.0590	2258.1268	1129.5670	20
5	613.3304	307.1688	596.3039	298.6556	595.3198	298.1636	V	2163.0533	1082.0303	2146.0267	1073.5170	2145.0427	1073.0250	19
6	727.3733	364.1903	710.3468	355.6770	709.3628	355.1850	N	2063.9849	1032.4961	2046.9583	1023.9828	2045.9743	1023.4908	18
7	855.4319	428.2196	838.4054	419.7063	837.4213	419.2143	Q	1949.9419	975.4746	1932.9154	966.9613	1931.9314	966.4693	17
8	986.4724	493.7398	969.4458	485.2266	968.4618	484.7346	M	1821.8833	911.4453	1804.8568	902.9320	1803.8728	902.4400	16
9	1087.5201	544.2637	1070.4935	535.7504	1069.5095	535.2584	T	1690.8429	845.9251	1673.8163	837.4118	1672.8323	836.9198	15
10	1216.5627	608.7850	1199.5361	600.2717	1198.5521	599.7797	E	1589.7952	795.4012	1572.7686	786.8880	1571.7846	786.3959	14
11	1287.5998	644.3035	1270.5732	635.7903	1269.5892	635.2982	A	1460.7526	730.8799	1443.7260	722.3667	1442.7420	721.8747	13
12	1447.6304	724.3189	1430.6039	715.8056	1429.6199	715.3136	C	1389.7155	695.3614	1372.6889	686.8481	1371.7049	686.3561	12
13	1560.7145	780.8609	1543.6879	772.3476	1542.7039	771.8556	L	1229.6848	615.3461	1212.6583	606.8328	1211.6743	606.3408	11
14	1674.7574	837.8823	1657.7309	829.3691	1656.7469	828.8771	N	1116.6008	558.8040	1099.5742	550.2907	1098.5902	549.7987	10
15	1802.8160	901.9116	1785.7894	893.3984	1784.8054	892.9064	Q	1002.5578	501.7826	985.5313	493.2693	984.5473	492.7773	9
16	1889.8480	945.4277	1872.8215	936.9144	1871.8375	936.4224	S	874.4993	437.7533	857.4727	429.2400	856.4887	428.7480	8
17	2002.9321	1001.9697	1985.9055	993.4564	1984.9215	992.9644	L	787.4672	394.2373	770.4407	385.7240	769.4567	385.2320	7
18	2117.9590	1059.4832	2100.9325	1050.9699	2099.9485	1050.4779	D	674.3832	337.6952	657.3566	329.1819	656.3726	328.6899	6
19	2188.9961	1095.0017	2171.9696	1086.4884	2170.9856	1085.9964	A	559.3562	280.1817	542.3297	271.6685	541.3457	271.1765	5
20	2302.0802	1151.5437	2285.0537	1143.0305	2284.0696	1142.5385	L	488.3191	244.6632	471.2926	236.1499	470.3085	235.6579	4
21	2415.1643	1208.0858	2398.1377	1199.5725	2397.1537	1199.0805	L	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
22	2502.1963	1251.6018	2485.1698	1243.0885	2484.1857	1242.5965	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
23							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 40965.

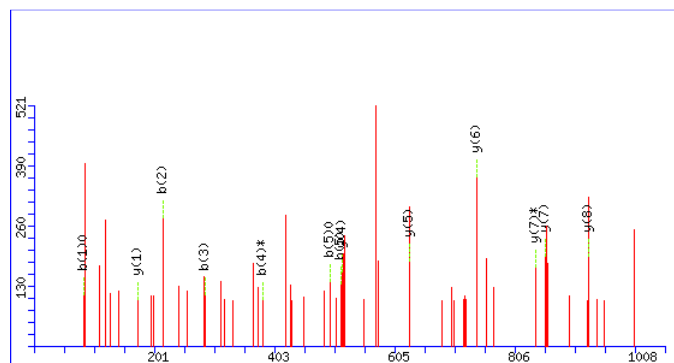
MS/MS Fragmentation of **TNADIIETLR**:

Found in **IP100000784;IP100216053;IP101011776**

Title: 2.1.1.2813.7

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							10
2	216.0979	108.5526	199.0713	100.0393	198.0873	99.5473	N	1044.5684	522.7878	1027.5419	514.2746	1026.5578	513.7826	9
3	287.1350	144.0711	270.1084	135.5579	269.1244	135.0659	A	930.5255	465.7664	913.4989	457.2531	912.5149	456.7611	8
4	402.1619	201.5846	385.1354	193.0713	384.1514	192.5793	D	859.4884	430.2478	842.4618	421.7345	841.4778	421.2425	7
5	515.2460	258.1266	498.2195	249.6134	497.2354	249.1214	I	744.4614	372.7343	727.4349	364.2211	726.4509	363.7291	6
6	628.3301	314.6687	611.3035	306.1554	610.3195	305.6634	I	631.3774	316.1923	614.3508	307.6790	613.3668	307.1870	5
7	757.3727	379.1900	740.3461	370.6767	739.3621	370.1847	E	518.2933	259.6503	501.2667	251.1370	500.2827	250.6450	4
8	858.4203	429.7138	841.3938	421.2005	840.4098	420.7085	T	389.2507	195.1290	372.2241	186.6157	371.2401	186.1237	3
9	971.5044	486.2558	954.4779	477.7426	953.4938	477.2506	L	288.2030	144.6051	271.1765	136.0919	0	0	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 41098.

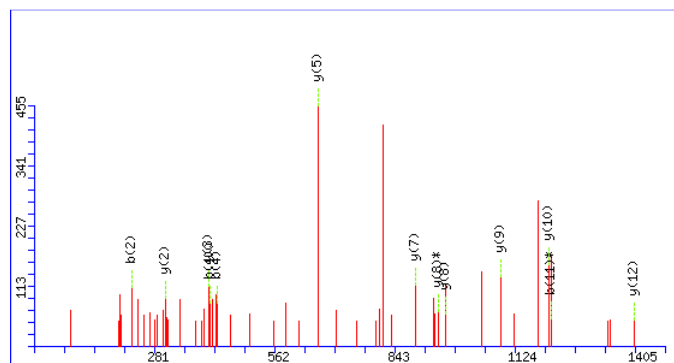
MS/MS Fragmentation of **EVALEANLPCTCK: 57.021465@C:11,57.021465@C:13**

Found in **IP100056432;IP100909362;IP100910610;IP100915920;IP100916053;IP100916680;IP100916820;IP100916946;IP100917130;IP100917266**

Title: 2.1.1.2523.10

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120214ry¥120214ry_32R1-32_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							14
2	229.1183	115.0628	0	0	211.1077	106.0575	V	1504.7134	752.8604	1487.6869	744.3471	1486.7029	743.8551	13
3	300.1554	150.5813	0	0	282.1448	141.5761	A	1405.6450	703.3261	1388.6185	694.8129	1387.6345	694.3209	12
4	429.1980	215.1026	0	0	411.1874	206.0974	E	1334.6079	667.8076	1317.5814	659.2943	1316.5973	658.8023	11
5	542.2821	271.6447	0	0	524.2715	262.6394	L	1205.5653	603.2863	1188.5388	594.7730	1187.5547	594.2810	10
6	671.3246	336.1660	0	0	653.3141	327.1607	E	1092.4812	546.7443	1075.4547	538.2310	1074.4707	537.7390	9
7	742.3618	371.6845	0	0	724.3512	362.6792	A	963.4387	482.2230	946.4121	473.7097	945.4281	473.2177	8
8	856.4047	428.7060	839.3781	420.1927	838.3941	419.7007	N	892.4015	446.7044	875.3750	438.1911	874.3910	437.6991	7
9	969.4888	485.2480	952.4622	476.7347	951.4782	476.2427	L	778.3586	389.6829	761.3321	381.1697	760.3480	380.6777	6
10	1066.5415	533.7744	1049.5150	525.2611	1048.5310	524.7691	P	665.2745	333.1409	648.2480	324.6276	647.2640	324.1356	5
11	1226.5722	613.7897	1209.5456	605.2764	1208.5616	604.7844	C	568.2218	284.6145	551.1952	276.1013	550.2112	275.6092	4
12	1327.6198	664.3136	1310.5933	655.8003	1309.6093	655.3083	T	408.1911	204.5992	391.1646	196.0859	390.1806	195.5939	3
13	1487.6505	744.3289	1470.6239	735.8156	1469.6399	735.3236	C	307.1435	154.0754	290.1169	145.5621	0	0	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 41152.

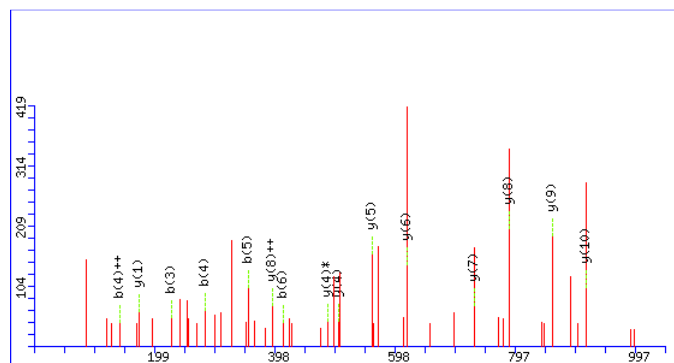
MS/MS Fragmentation of **GGIGAGLGGGLCR: 57.021465@C:12**

Found in **IP100004506**

Title: 2.1.1.1267.6

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120214ry¥120214ry_414C2-43_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							13
2	115.0502	58.0287	0	0	0	0	G	1087.5677	544.2875	1070.5411	535.7742	0	0	12
3	228.1343	114.5708	0	0	0	0	I	1030.5462	515.7768	1013.5197	507.2635	0	0	11
4	285.1557	143.0815	0	0	0	0	G	917.4622	459.2347	900.4356	450.7214	0	0	10
5	356.1928	178.6001	0	0	0	0	A	860.4407	430.7240	843.4142	422.2107	0	0	9
6	413.2143	207.1108	0	0	0	0	G	789.4036	395.2054	772.3770	386.6922	0	0	8
7	526.2984	263.6528	0	0	0	0	L	732.3821	366.6947	715.3556	358.1814	0	0	7
8	583.3198	292.1636	0	0	0	0	G	619.2981	310.1527	602.2715	301.6394	0	0	6
9	640.3413	320.6743	0	0	0	0	G	562.2766	281.6419	545.2500	273.1287	0	0	5
10	697.3628	349.1850	0	0	0	0	G	505.2551	253.1312	488.2286	244.6179	0	0	4
11	810.4468	405.7271	0	0	0	0	L	448.2337	224.6205	431.2071	216.1072	0	0	3
12	970.4775	485.7424	0	0	0	0	C	335.1496	168.0784	318.1231	159.5652	0	0	2
13							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 41444.

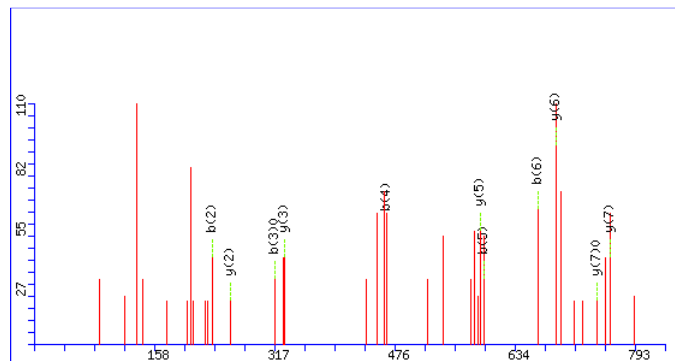
MS/MS Fragmentation of **YATEEALK**:

Found in **IP100020965;IP100946339;IP100947405;IP100982164**

Title: 1.1.1.6528.8

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_3_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	164.0706	82.5389	0	0	0	0	Y							8
2	235.1077	118.0575	0	0	0	0	A	761.4040	381.2056	744.3774	372.6923	743.3934	372.2003	7
3	336.1554	168.5813	0	0	318.1448	159.5761	T	690.3668	345.6871	673.3403	337.1738	672.3563	336.6818	6
4	465.1980	233.1026	0	0	447.1874	224.0974	E	589.3192	295.1632	572.2926	286.6499	571.3086	286.1579	5
5	594.2406	297.6239	0	0	576.2300	288.6186	E	460.2766	230.6419	443.2500	222.1287	442.2660	221.6366	4
6	665.2777	333.1425	0	0	647.2671	324.1372	A	331.2340	166.1206	314.2074	157.6074	0	0	3
7	778.3618	389.6845	0	0	760.3512	380.6792	L	260.1969	130.6021	243.1703	122.0888	0	0	2
8							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 41478.

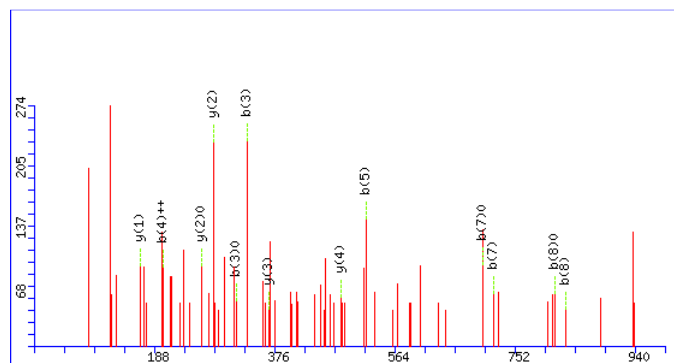
MS/MS Fragmentation of **ADFADISILSDF**:

Found in **IP100439924;IP100902748**

Title: 4.1.1.2531.3

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							12
2	187.0713	94.0393	0	0	169.0608	85.0340	D	1242.5889	621.7981	0	0	1224.5783	612.7928	11
3	334.1397	167.5735	0	0	316.1292	158.5682	F	1127.5619	564.2846	0	0	1109.5514	555.2793	10
4	405.1769	203.0921	0	0	387.1663	194.0868	A	980.4935	490.7504	0	0	962.4829	481.7451	9
5	520.2038	260.6055	0	0	502.1932	251.6003	D	909.4564	455.2318	0	0	891.4458	446.2266	8
6	633.2879	317.1476	0	0	615.2773	308.1423	I	794.4294	397.7184	0	0	776.4189	388.7131	7
7	720.3199	360.6636	0	0	702.3093	351.6583	S	681.3454	341.1763	0	0	663.3348	332.1710	6
8	833.4040	417.2056	0	0	815.3934	408.2003	I	594.3134	297.6603	0	0	576.3028	288.6550	5
9	946.4880	473.7477	0	0	928.4775	464.7424	L	481.2293	241.1183	0	0	463.2187	232.1130	4
10	1033.5201	517.2637	0	0	1015.5095	508.2584	S	368.1452	184.5763	0	0	350.1347	175.5710	3
11	1148.5470	574.7771	0	0	1130.5364	565.7719	D	281.1132	141.0602	0	0	263.1026	132.0550	2
12							F	166.0863	83.5468	0	0	0	0	1

Peptide View

Peptide: 41509.

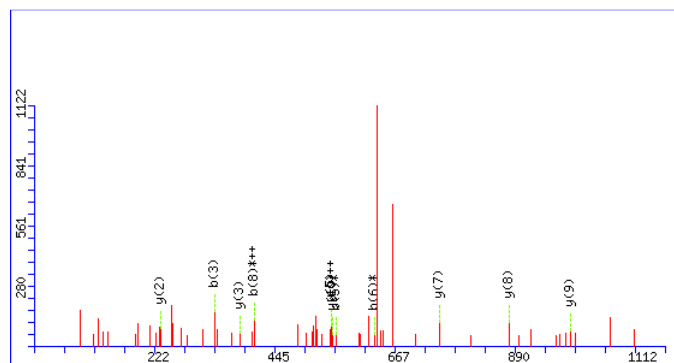
MS/MS Fragmentation of **GYNIEAQLFSK**:

Found in **IP100166976;IP100852896;IP100892797**

Title: 3.1.1.401.8

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							12
2	221.0921	111.0497	0	0	0	0	Y	1270.6314	635.8193	1253.6048	627.3061	1252.6208	626.8141	11
3	335.1350	168.0711	318.1084	159.5579	0	0	N	1107.5681	554.2877	1090.5415	545.7744	1089.5575	545.2824	10
4	448.2191	224.6132	431.1925	216.0999	0	0	I	993.5251	497.2662	976.4986	488.7529	975.5146	488.2609	9
5	577.2617	289.1345	560.2351	280.6212	559.2511	280.1292	E	880.4411	440.7242	863.4145	432.2109	862.4305	431.7189	8
6	648.2988	324.6530	631.2722	316.1397	630.2882	315.6477	A	751.3985	376.2029	734.3719	367.6896	733.3879	367.1976	7
7	777.3414	389.1743	760.3148	380.6610	759.3308	380.1690	E	680.3614	340.6843	663.3348	332.1710	662.3508	331.6790	6
8	834.3628	417.6851	817.3363	409.1718	816.3523	408.6798	G	551.3188	276.1630	534.2922	267.6498	533.3082	267.1577	5
9	947.4469	474.2271	930.4203	465.7138	929.4363	465.2218	L	494.2973	247.6523	477.2708	239.1390	476.2867	238.6470	4
10	1094.5153	547.7613	1077.4888	539.2480	1076.5047	538.7560	F	381.2132	191.1103	364.1867	182.5970	363.2027	182.1050	3
11	1181.5473	591.2773	1164.5208	582.7640	1163.5368	582.2720	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 41756.

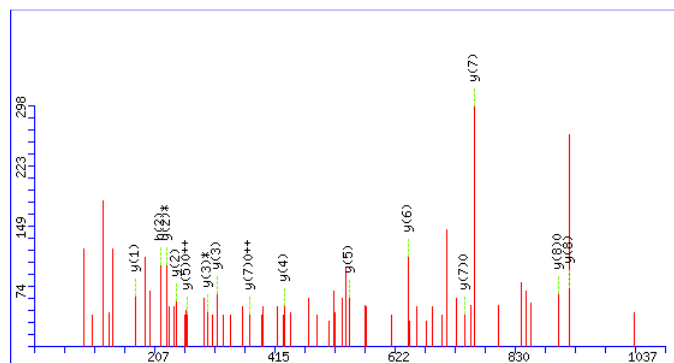
MS/MS Fragmentation of **AFYDTLDAAR**:

Found in **IP100064457;IP100792479;IP100977906;IP101015806**

Title: 2.1.1.3061.7

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120201ry¥120201ry_aHDF1388-P9_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							10
2	219.1128	110.0600	0	0	0	0	F	1071.5106	536.2589	1054.4840	527.7456	1053.5000	527.2536	9
3	382.1761	191.5917	0	0	0	0	Y	924.4421	462.7247	907.4156	454.2114	906.4316	453.7194	8
4	497.2031	249.1052	0	0	479.1925	240.0999	D	761.3788	381.1930	744.3523	372.6798	743.3682	372.1878	7
5	598.2508	299.6290	0	0	580.2402	290.6237	T	646.3519	323.6796	629.3253	315.1663	628.3413	314.6743	6
6	711.3348	356.1710	0	0	693.3243	347.1658	L	545.3042	273.1557	528.2776	264.6425	527.2936	264.1504	5
7	826.3618	413.6845	0	0	808.3512	404.6792	D	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	4
8	897.3989	449.2031	0	0	879.3883	440.1978	A	317.1932	159.1002	300.1666	150.5870	0	0	3
9	968.4360	484.7216	0	0	950.4254	475.7164	A	246.1561	123.5817	229.1295	115.0684	0	0	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 41916.

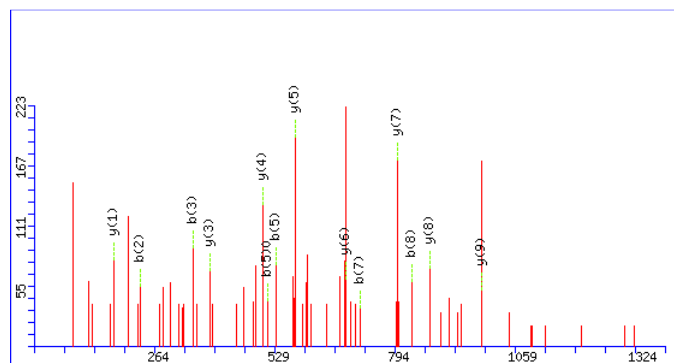
MS/MS Fragmentation of **SFDALLDLTR**:

Found in **IP100216744;IP100220076;IP100220077;IP100220078;IP100847840;IP100945328;IP100946204;IP100982341**

Title: 4.1.1.11.3

Data file: Y:\TT5600(CiRA1)\2012-01\120124ry\120124ry_414C2-43_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							11
2	235.1077	118.0575	0	0	217.0972	109.0522	F	1134.6154	567.8113	1117.5888	559.2980	1116.6048	558.8060	10
3	350.1347	175.5710	0	0	332.1241	166.5657	D	987.5469	494.2771	970.5204	485.7638	969.5364	485.2718	9
4	421.1718	211.0895	0	0	403.1612	202.0842	A	872.5200	436.7636	855.4934	428.2504	854.5094	427.7584	8
5	534.2558	267.6316	0	0	516.2453	258.6263	L	801.4829	401.2451	784.4563	392.7318	783.4723	392.2398	7
6	647.3399	324.1736	0	0	629.3293	315.1683	L	688.3988	344.7030	671.3723	336.1898	670.3883	335.6978	6
7	718.3770	359.6921	0	0	700.3665	350.6869	A	575.3148	288.1610	558.2882	279.6477	557.3042	279.1557	5
8	833.4040	417.2056	0	0	815.3934	408.2003	D	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	4
9	946.4880	473.7477	0	0	928.4775	464.7424	L	389.2507	195.1290	372.2241	186.6157	371.2401	186.1237	3
10	1047.5357	524.2715	0	0	1029.5251	515.2662	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
11							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 42216.

MS/MS Fragmentation of **WPLLDVQAGSLQSR**:

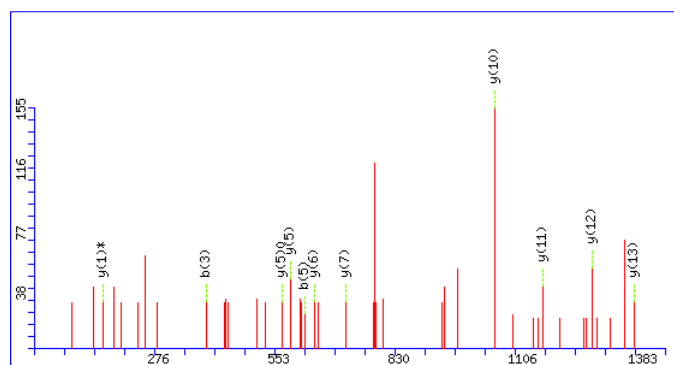
Found in

IP100164708;IP100221004;IP100221005;IP100221006;IP100221007;IP100221008;IP100221009;IP100221010;IP100221011;IP100335587;IP100479038;IP100479483;IP1006411

Title: 3.1.1.1908.9

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120210ry¥120210ry_585A1-55_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	187.0866	94.0469	0	0	0	0	W							14
2	284.1394	142.5733	0	0	0	0	P	1383.7591	692.3832	1366.7325	683.8699	1365.7485	683.3779	13
3	397.2234	199.1153	0	0	0	0	L	1286.7063	643.8568	1269.6797	635.3435	1268.6957	634.8515	12
4	510.3075	255.6574	0	0	0	0	L	1173.6222	587.3148	1156.5957	578.8015	1155.6117	578.3095	11
5	625.3344	313.1709	0	0	607.3239	304.1656	D	1060.5382	530.7727	1043.5116	522.2594	1042.5276	521.7674	10
6	724.4028	362.7051	0	0	706.3923	353.6998	V	945.5112	473.2592	928.4847	464.7460	927.5007	464.2540	9
7	852.4614	426.7343	835.4349	418.2211	834.4509	417.7291	Q	846.4428	423.7250	829.4163	415.2118	828.4322	414.7198	8
8	923.4985	462.2529	906.4720	453.7396	905.4880	453.2476	A	718.3842	359.6958	701.3577	351.1825	700.3737	350.6905	7
9	980.5200	490.7636	963.4934	482.2504	962.5094	481.7584	G	647.3471	324.1772	630.3206	315.6639	629.3365	315.1719	6
10	1067.5520	534.2796	1050.5255	525.7664	1049.5415	525.2744	S	590.3256	295.6665	573.2991	287.1532	572.3151	286.6612	5
11	1180.6361	590.8217	1163.6095	582.3084	1162.6255	581.8164	L	503.2936	252.1504	486.2671	243.6372	485.2831	243.1452	4
12	1308.6947	654.8510	1291.6681	646.3377	1290.6841	645.8457	Q	390.2096	195.6084	373.1830	187.0951	372.1990	186.6031	3
13	1395.7267	698.3670	1378.7001	689.8537	1377.7161	689.3617	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
14							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 42253.

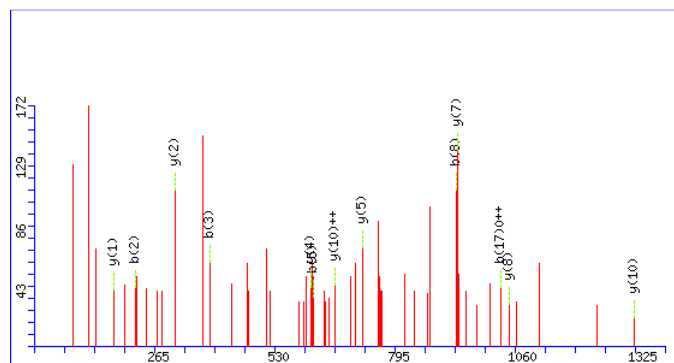
MS/MS Fragmentation of **SHYLDEADVFLNPLNLWLR**:

Found in **IP100145121;IP101011779**

Title: 4.1.1.2882.3

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_2.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							20
2	225.0982	113.0527	0	0	207.0877	104.0475	H	2415.1880	1208.0977	2398.1615	1199.5844	2397.1775	1199.0924	19
3	388.1615	194.5844	0	0	370.1510	185.5791	Y	2278.1291	1139.5682	2261.1026	1131.0549	2260.1186	1130.5629	18
4	501.2456	251.1264	0	0	483.2350	242.1212	L	2115.0658	1058.0365	2098.0393	1049.5233	2097.0552	1049.0313	17
5	616.2726	308.6399	0	0	598.2620	299.6346	D	2001.9817	1001.4945	1984.9552	992.9812	1983.9712	992.4892	16
6	745.3151	373.1612	0	0	727.3046	364.1559	E	1886.9548	943.9810	1869.9282	935.4678	1868.9442	934.9758	15
7	816.3523	408.6798	0	0	798.3417	399.6745	A	1757.9122	879.4597	1740.8857	870.9465	1739.9016	870.4545	14
8	931.3792	466.1932	0	0	913.3686	457.1880	D	1686.8751	843.9412	1669.8485	835.4279	1668.8645	834.9359	13
9	1030.4476	515.7274	0	0	1012.4371	506.7222	V	1571.8481	786.4277	1554.8216	777.9144	0	0	12
10	1177.5160	589.2617	0	0	1159.5055	580.2564	F	1472.7797	736.8935	1455.7532	728.3802	0	0	11
11	1340.5794	670.7933	0	0	1322.5688	661.7880	Y	1325.7113	663.3593	1308.6848	654.8460	0	0	10
12	1453.6634	727.3353	0	0	1435.6529	718.3301	L	1162.6480	581.8276	1145.6214	573.3144	0	0	9
13	1567.7064	784.3568	1550.6798	775.8435	1549.6958	775.3515	N	1049.5639	525.2856	1032.5374	516.7723	0	0	8
14	1664.7591	832.8832	1647.7326	824.3699	1646.7485	823.8779	P	935.5210	468.2641	918.4944	459.7509	0	0	7
15	1777.8432	889.4252	1760.8166	880.9120	1759.8326	880.4199	L	838.4682	419.7378	821.4417	411.2245	0	0	6
16	1891.8861	946.4467	1874.8596	937.9334	1873.8755	937.4414	N	725.3842	363.1957	708.3576	354.6824	0	0	5
17	2077.9654	1039.4863	2060.9389	1030.9731	2059.9549	1030.4811	W	611.3412	306.1743	594.3147	297.6610	0	0	4
18	2191.0495	1096.0284	2174.0229	1087.5151	2173.0389	1087.0231	L	425.2619	213.1346	408.2354	204.6213	0	0	3
19	2328.1084	1164.5578	2311.0818	1156.0446	2310.0978	1155.5526	H	312.1779	156.5926	295.1513	148.0793	0	0	2
20							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 42314.

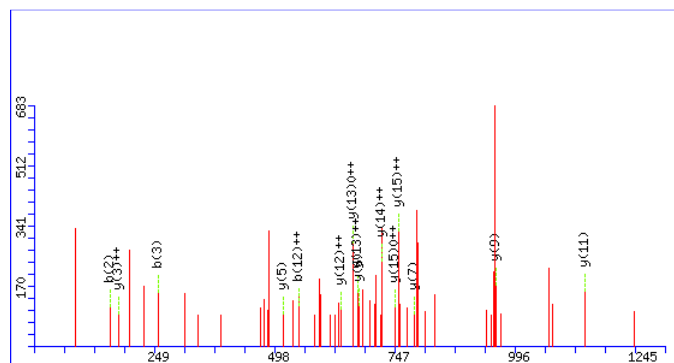
MS/MS Fragmentation of **SAVATAEALGLDRPASDK**:

Found in **IP100100291;IP100143877;IP100439548;IP100514505**

Title: 2.1.1.2410.5

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							18
2	159.0764	80.0418	0	0	141.0659	71.0366	A	1684.8864	842.9469	1667.8599	834.4336	1666.8759	833.9416	17
3	258.1448	129.5761	0	0	240.1343	120.5708	V	1613.8493	807.4283	1596.8228	798.9150	1595.8388	798.4230	16
4	329.1819	165.0946	0	0	311.1714	156.0893	A	1514.7809	757.8941	1497.7544	749.3808	1496.7703	748.8888	15
5	430.2296	215.6185	0	0	412.2191	206.6132	T	1443.7438	722.3755	1426.7172	713.8623	1425.7332	713.3703	14
6	501.2667	251.1370	0	0	483.2562	242.1317	A	1342.6961	671.8517	1325.6696	663.3384	1324.6856	662.8464	13
7	630.3093	315.6583	0	0	612.2988	306.6530	E	1271.6590	636.3331	1254.6325	627.8199	1253.6484	627.3279	12
8	701.3464	351.1769	0	0	683.3359	342.1716	A	1142.6164	571.8118	1125.5899	563.2986	1124.6058	562.8066	11
9	814.4305	407.7189	0	0	796.4199	398.7136	L	1071.5793	536.2933	1054.5527	527.7800	1053.5687	527.2880	10
10	871.4520	436.2296	0	0	853.4414	427.2243	G	958.4952	479.7513	941.4687	471.2380	940.4847	470.7460	9
11	984.5360	492.7717	0	0	966.5255	483.7664	L	901.4738	451.2405	884.4472	442.7272	883.4632	442.2352	8
12	1099.5630	550.2851	0	0	1081.5524	541.2798	D	788.3897	394.6985	771.3632	386.1852	770.3791	385.6932	7
13	1255.6641	628.3357	1238.6375	619.8224	1237.6535	619.3304	R	673.3628	337.1850	656.3362	328.6717	655.3522	328.1797	6
14	1352.7169	676.8621	1335.6903	668.3488	1334.7063	667.8568	P	517.2617	259.1345	500.2351	250.6212	499.2511	250.1292	5
15	1423.7540	712.3806	1406.7274	703.8673	1405.7434	703.3753	A	420.2089	210.6081	403.1823	202.0948	402.1983	201.6028	4
16	1510.7860	755.8966	1493.7594	747.3834	1492.7754	746.8914	S	349.1718	175.0895	332.1452	166.5763	331.1612	166.0842	3
17	1625.8129	813.4101	1608.7864	804.8968	1607.8024	804.4048	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
18							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 42336.

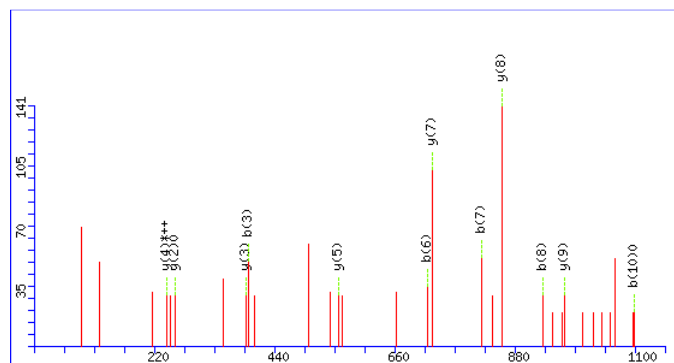
MS/MS Fragmentation of **YDITNVLEGIGLIEK**:

Found in **IP100292880**

Title: 4.1.1.3057.3

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							16
2	277.1547	139.0810	0	0	0	0	Y	1676.9105	838.9589	1659.8840	830.4456	1658.9000	829.9536	15
3	392.1816	196.5944	0	0	374.1710	187.5892	D	1513.8472	757.4272	1496.8207	748.9140	1495.8366	748.4220	14
4	505.2657	253.1365	0	0	487.2551	244.1312	I	1398.8203	699.9138	1381.7937	691.4005	1380.8097	690.9085	13
5	606.3134	303.6603	0	0	588.3028	294.6550	T	1285.7362	643.3717	1268.7096	634.8585	1267.7256	634.3665	12
6	720.3563	360.6818	703.3297	352.1685	702.3457	351.6765	N	1184.6885	592.8479	1167.6620	584.3346	1166.6780	583.8426	11
7	819.4247	410.2160	802.3981	401.7027	801.4141	401.2107	V	1070.6456	535.8264	1053.6190	527.3132	1052.6350	526.8211	10
8	932.5088	466.7580	915.4822	458.2447	914.4982	457.7527	L	971.5772	486.2922	954.5506	477.7790	953.5666	477.2869	9
9	1061.5514	531.2793	1044.5248	522.7660	1043.5408	522.2740	E	858.4931	429.7502	841.4666	421.2369	840.4825	420.7449	8
10	1118.5728	559.7900	1101.5463	551.2768	1100.5623	550.7848	G	729.4505	365.2289	712.4240	356.7156	711.4400	356.2236	7
11	1231.6569	616.3321	1214.6303	607.8188	1213.6463	607.3268	I	672.4291	336.7182	655.4025	328.2049	654.4185	327.7129	6
12	1288.6783	644.8428	1271.6518	636.3295	1270.6678	635.8375	G	559.3450	280.1761	542.3184	271.6629	541.3344	271.1709	5
13	1401.7624	701.3848	1384.7359	692.8716	1383.7518	692.3796	L	502.3235	251.6654	485.2970	243.1521	484.3130	242.6601	4
14	1514.8465	757.9269	1497.8199	749.4136	1496.8359	748.9216	I	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
15	1643.8891	822.4482	1626.8625	813.9349	1625.8785	813.4429	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
16							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 42644.

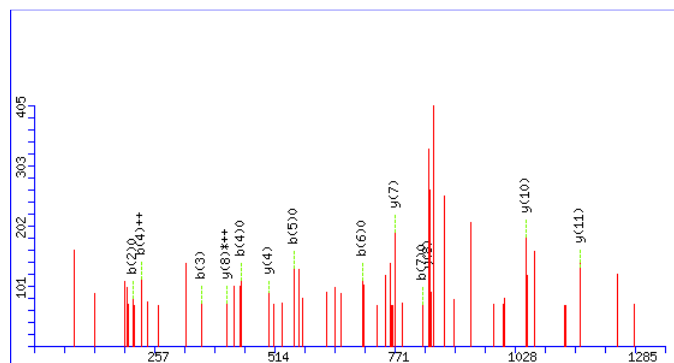
MS/MS Fragmentation of **TEETLFEIQGIDPIASAIQNLK**:

Found in **IP100299166;IP100893061;IP100894040;IP100917956**

Title: 4.1.1.2924.8

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120214ry¥120214ry_aHDF1419-P10_4.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							22
2	231.0975	116.0524	0	0	213.0870	107.0471	E	2329.2286	1165.1179	2312.2020	1156.6046	2311.2180	1156.1126	21
3	360.1401	180.5737	0	0	342.1296	171.5684	E	2200.1860	1100.5966	2183.1594	1092.0834	2182.1754	1091.5913	20
4	461.1878	231.0975	0	0	443.1773	222.0923	T	2071.1434	1036.0753	2054.1168	1027.5621	2053.1328	1027.0700	19
5	574.2719	287.6396	0	0	556.2613	278.6343	L	1970.0957	985.5515	1953.0692	977.0382	1952.0851	976.5462	18
6	721.3403	361.1738	0	0	703.3297	352.1685	F	1857.0116	929.0095	1839.9851	920.4962	1839.0011	920.0042	17
7	850.3829	425.6951	0	0	832.3723	416.6898	E	1709.9432	855.4753	1692.9167	846.9620	1691.9327	846.4700	16
8	963.4670	482.2371	0	0	945.4564	473.2318	I	1580.9006	790.9540	1563.8741	782.4407	1562.8901	781.9487	15
9	1091.5255	546.2664	1074.4990	537.7531	1073.5150	537.2611	Q	1467.8166	734.4119	1450.7900	725.8986	1449.8060	725.4066	14
10	1148.5470	574.7771	1131.5204	566.2639	1130.5364	565.7719	G	1339.7580	670.3826	1322.7314	661.8694	1321.7474	661.3774	13
11	1261.6311	631.3192	1244.6045	622.8059	1243.6205	622.3139	I	1282.7365	641.8719	1265.7100	633.3586	1264.7260	632.8666	12
12	1376.6580	688.8326	1359.6315	680.3194	1358.6474	679.8274	D	1169.6525	585.3299	1152.6259	576.8166	1151.6419	576.3246	11
13	1473.7108	737.3590	1456.6842	728.8457	1455.7002	728.3537	P	1054.6255	527.8164	1037.5990	519.3031	1036.6150	518.8111	10
14	1586.7948	793.9011	1569.7683	785.3878	1568.7843	784.8958	I	957.5728	479.2900	940.5462	470.7767	939.5622	470.2847	9
15	1657.8319	829.4196	1640.8054	820.9063	1639.8214	820.4143	A	844.4887	422.7480	827.4621	414.2347	826.4781	413.7427	8
16	1744.8640	872.9356	1727.8374	864.4224	1726.8534	863.9303	S	773.4516	387.2294	756.4250	378.7162	755.4410	378.2241	7
17	1815.9011	908.4542	1798.8745	899.9409	1797.8905	899.4489	A	686.4196	343.7134	669.3930	335.2001	0	0	6
18	1928.9852	964.9962	1911.9586	956.4829	1910.9746	955.9909	I	615.3824	308.1949	598.3559	299.6816	0	0	5
19	2057.0437	1029.0255	2040.0172	1020.5122	2039.0332	1020.0202	Q	502.2984	251.6528	485.2718	243.1395	0	0	4
20	2171.0867	1086.0470	2154.0601	1077.5337	2153.0761	1077.0417	N	374.2398	187.6235	357.2132	179.1103	0	0	3
21	2284.1707	1142.5890	2267.1442	1134.0757	2266.1602	1133.5837	L	260.1969	130.6021	243.1703	122.0888	0	0	2
22							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

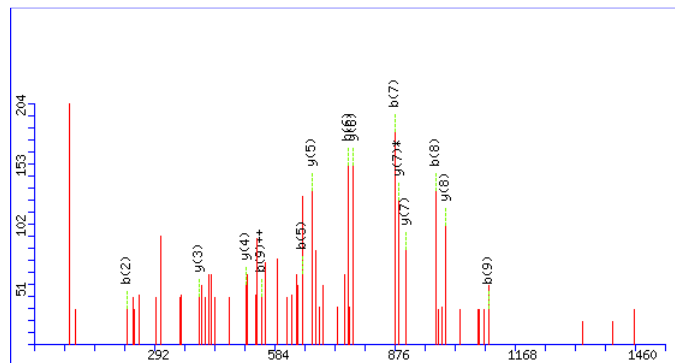
Peptide: 43036.

MS/MS Fragmentation of **ILCHQLLVQVCDLLR**: 57.021465@C:3,57.021465@C:11
Found in **IP100043622:IP100184707:IP101025960**

Title: 3.1.1.4517.3

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120208ry¥120208ry_Tig120slc-P8_1.3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							15
2	227.1754	114.0913	0	0	0	0	L	1766.9404	883.9738	1749.9139	875.4606	1748.9298	874.9686	14
3	387.2061	194.1067	0	0	0	0	C	1653.8563	827.4318	1636.8298	818.9185	1635.8458	818.4265	13
4	524.2650	262.6361	0	0	0	0	H	1493.8257	747.4165	1476.7991	738.9032	1475.8151	738.4112	12
5	652.3235	326.6654	635.2970	318.1521	0	0	Q	1356.7668	678.8870	1339.7402	670.3738	1338.7562	669.8817	11
6	765.4076	383.2074	748.3811	374.6942	0	0	L	1228.7082	614.8577	1211.6817	606.3445	1210.6976	605.8525	10
7	878.4917	439.7495	861.4651	431.2362	0	0	L	1115.6241	558.3157	1098.5976	549.8024	1097.6136	549.3104	9
8	977.5601	489.2837	960.5335	480.7704	0	0	V	1002.5401	501.7737	985.5135	493.2604	984.5295	492.7684	8
9	1105.6187	553.3130	1088.5921	544.7997	0	0	Q	903.4717	452.2395	886.4451	443.7262	885.4611	443.2342	7
10	1204.6871	602.8472	1187.6605	594.3339	0	0	V	775.4131	388.2102	758.3865	379.6969	757.4025	379.2049	6
11	1364.7177	682.8625	1347.6912	674.3492	0	0	C	676.3447	338.6760	659.3181	330.1627	658.3341	329.6707	5
12	1479.7447	740.3760	1462.7181	731.8627	1461.7341	731.3707	D	516.3140	258.6606	499.2875	250.1474	498.3035	249.6554	4
13	1592.8287	796.9180	1575.8022	788.4047	1574.8182	787.9127	L	401.2871	201.1472	384.2605	192.6339	0	0	3
14	1705.9128	853.4600	1688.8862	844.9468	1687.9022	844.4548	L	288.2030	144.6051	271.1765	136.0919	0	0	2
15							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 43105.

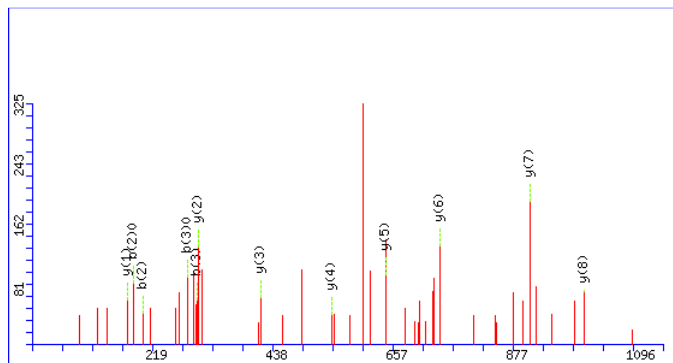
MS/MS Fragmentation of **TTVYVVEDQR**:

Found in **IP100382821**

Title: 1.1.1.9049.7

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							10
2	203.1028	102.0550	0	0	185.0921	93.0497	T	1108.5633	554.7853	1091.5368	546.2720	1090.5528	545.7800	9
3	302.1710	151.5892	0	0	284.1605	142.5839	V	1007.5156	504.2615	990.4891	495.7482	989.5051	495.2562	8
4	465.2344	233.1208	0	0	447.2238	224.1155	Y	908.4472	454.7272	891.4207	446.2140	890.4367	445.7220	7
5	564.3028	282.6550	0	0	546.2922	273.6498	V	745.3839	373.1956	728.3573	364.6823	727.3733	364.1903	6
6	663.3712	332.1892	0	0	645.3606	323.1840	V	646.3155	323.6614	629.2889	315.1481	628.3049	314.6561	5
7	792.4138	396.7105	0	0	774.4032	387.7053	E	547.2471	274.1272	530.2205	265.6139	529.2365	265.1219	4
8	907.4407	454.2240	0	0	889.4302	445.2187	D	418.2045	209.6059	401.1779	201.0926	400.1939	200.6006	3
9	1035.4993	518.2533	1018.4728	509.7400	1017.4888	509.2480	Q	303.1775	152.0924	286.1510	143.5791	0	0	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 43333.

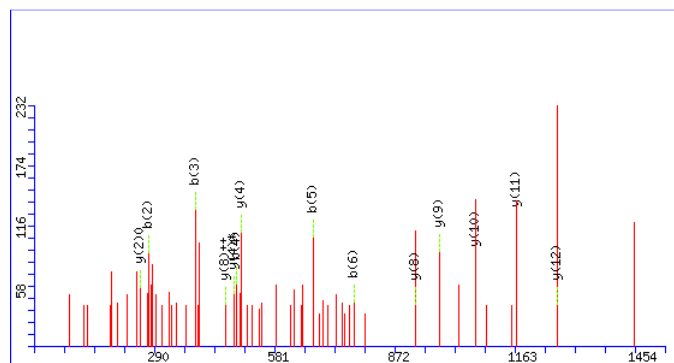
MS/MS Fragmentation of **FEDVWVVSQPLTLPGTR**:

Found in **IP100021106;IP100024713;IP100925869;IP100926574;IP101018335**

Title: 3.1.1.4157.10

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120212ry¥120212ry_aHDF1388-P9_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							17
2	277.1183	139.0628	0	0	259.1077	130.0575	E	1796.9541	898.9807	1779.9276	890.4674	1778.9436	889.9754	16
3	392.1452	196.5763	0	0	374.1347	187.5710	D	1667.9115	834.4594	1650.8850	825.9461	1649.9010	825.4541	15
4	491.2136	246.1105	0	0	473.2031	237.1052	V	1552.8846	776.9459	1535.8580	768.4327	1534.8740	767.9407	14
5	677.2930	339.1501	0	0	659.2824	330.1448	W	1453.8162	727.4117	1436.7896	718.8985	1435.8056	718.4064	13
6	776.3614	388.6843	0	0	758.3508	379.6790	V	1267.7369	634.3721	1250.7103	625.8588	1249.7263	625.3668	12
7	875.4298	438.2185	0	0	857.4192	429.2132	V	1168.6684	584.8379	1151.6419	576.3246	1150.6579	575.8326	11
8	962.4618	481.7345	0	0	944.4512	472.7293	S	1069.6000	535.3037	1052.5735	526.7904	1051.5895	526.2984	10
9	1019.4833	510.2453	0	0	1001.4727	501.2400	G	982.5680	491.7876	965.5415	483.2744	964.5574	482.7824	9
10	1116.5360	558.7717	0	0	1098.5255	549.7664	P	925.5465	463.2769	908.5200	454.7636	907.5360	454.2716	8
11	1229.6201	615.3137	0	0	1211.6095	606.3084	L	828.4938	414.7505	811.4672	406.2373	810.4832	405.7452	7
12	1330.6678	665.8375	0	0	1312.6572	656.8322	T	715.4097	358.2085	698.3832	349.6952	697.3992	349.2032	6
13	1443.7518	722.3796	0	0	1425.7413	713.3743	L	614.3620	307.6847	597.3355	299.1714	596.3515	298.6794	5
14	1540.8046	770.9059	0	0	1522.7940	761.9007	P	501.2780	251.1426	484.2514	242.6293	483.2674	242.1373	4
15	1668.8632	834.9352	1651.8366	826.4220	1650.8526	825.9299	Q	404.2252	202.6162	387.1987	194.1030	386.2146	193.6110	3
16	1769.9109	885.4591	1752.8843	876.9458	1751.9003	876.4538	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
17							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 43418.

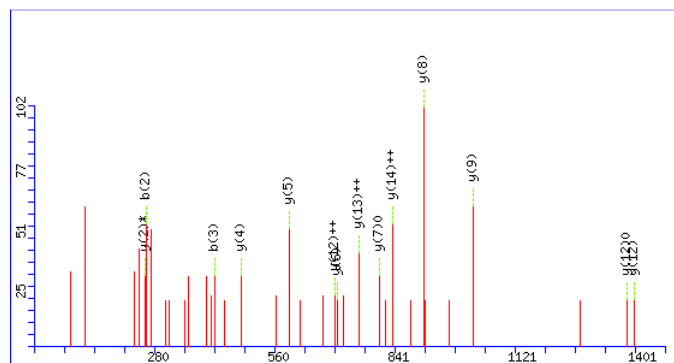
MS/MS Fragmentation of **LFCLETFLSDLIAHQK: 57.021465@C:3**

Found in **IP100024290:IP101012366**

Title: 4.1.1.4162.2

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							16
2	261.1598	131.0835	0	0	0	0	F	1821.9204	911.4638	1804.8938	902.9506	1803.9098	902.4585	15
3	421.1904	211.0988	0	0	0	0	C	1674.8520	837.9296	1657.8254	829.4163	1656.8414	828.9243	14
4	534.2745	267.6409	0	0	0	0	L	1514.8213	757.9143	1497.7948	749.4010	1496.8108	748.9090	13
5	663.3171	332.1622	0	0	645.3065	323.1569	E	1401.7373	701.3723	1384.7107	692.8590	1383.7267	692.3670	12
6	764.3647	382.6860	0	0	746.3542	373.6807	T	1272.6947	636.8510	1255.6681	628.3377	1254.6841	627.8457	11
7	911.4332	456.2202	0	0	893.4226	447.2149	F	1171.6470	586.3271	1154.6204	577.8139	1153.6364	577.3218	10
8	1024.5172	512.7622	0	0	1006.5067	503.7570	L	1024.5786	512.7929	1007.5520	504.2796	1006.5680	503.7876	9
9	1111.5492	556.2783	0	0	1093.5387	547.2730	S	911.4945	456.2509	894.4680	447.7376	893.4839	447.2456	8
10	1226.5762	613.7917	0	0	1208.5656	604.7865	D	824.4625	412.7349	807.4359	404.2216	806.4519	403.7296	7
11	1339.6603	670.3338	0	0	1321.6497	661.3285	L	709.4355	355.2214	692.4090	346.7081	0	0	6
12	1452.7443	726.8758	0	0	1434.7338	717.8705	I	596.3515	298.6794	579.3249	290.1661	0	0	5
13	1523.7814	762.3944	0	0	1505.7709	753.3891	A	483.2674	242.1373	466.2409	233.6241	0	0	4
14	1660.8403	830.9238	0	0	1642.8298	821.9185	H	412.2303	206.6188	395.2037	198.1055	0	0	3
15	1788.8989	894.9531	1771.8724	886.4398	1770.8884	885.9478	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
16							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

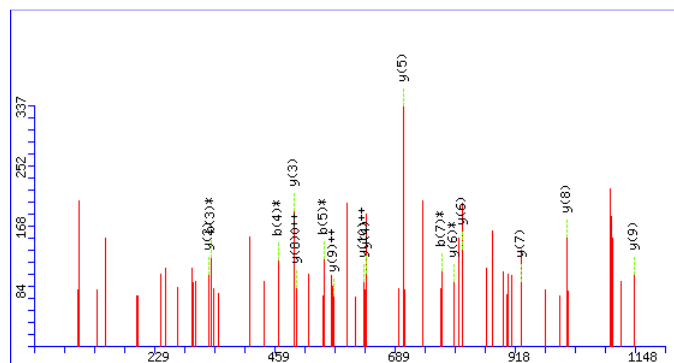
Peptide: 43431.

MS/MS Fragmentation of **QLLESLLAHYCR**: -17.026549@N-term(Q),57.021465@C:11
Found in **IP100242841;IP100644331;IP100646489**

Title: 4.1.1.1070.5

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233	0	0	Q							12
2	242.1499	121.5786	225.1234	113.0653	0	0	L	1374.7198	687.8636	1357.6933	679.3503	1356.7093	678.8583	11
3	355.2340	178.1206	338.2074	169.6074	0	0	L	1261.6358	631.3215	1244.6092	622.8082	1243.6252	622.3162	10
4	484.2766	242.6419	467.2500	234.1287	466.2660	233.6366	E	1148.5517	574.7795	1131.5252	566.2662	1130.5411	565.7742	9
5	571.3086	286.1579	554.2821	277.6447	553.2980	277.1527	S	1019.5091	510.2582	1002.4826	501.7449	1001.4985	501.2529	8
6	684.3927	342.7000	667.3661	334.1867	666.3821	333.6947	L	932.4771	466.7422	915.4505	458.2289	0	0	7
7	797.4767	399.2420	780.4502	390.7287	779.4662	390.2367	L	819.3930	410.2001	802.3665	401.6869	0	0	6
8	868.5138	434.7606	851.4873	426.2473	850.5033	425.7553	A	706.3090	353.6581	689.2824	345.1448	0	0	5
9	1005.5728	503.2900	988.5462	494.7767	987.5622	494.2847	H	635.2718	318.1396	618.2453	309.6263	0	0	4
10	1168.6361	584.8217	1151.6095	576.3084	1150.6255	575.8164	Y	498.2129	249.6101	481.1864	241.0968	0	0	3
11	1328.6667	664.8370	1311.6402	656.3237	1310.6562	655.8317	C	335.1496	168.0784	318.1231	159.5652	0	0	2
12							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 43488.

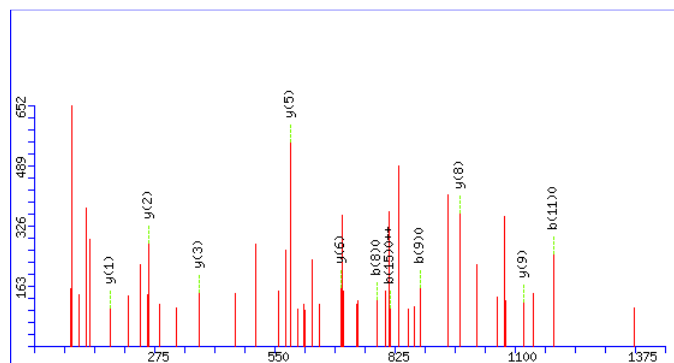
MS/MS Fragmentation of **MGLTLEGVFCLDPLDSR: 57.021465@C:11**

Found in **IP100790010;IP100910196;IP100916652**

Title: 4.1.1.1444.2

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	132.0478	66.5275	0	0	0	0	M							18
2	189.0692	95.0383	0	0	0	0	G	1892.9422	946.9748	1875.9157	938.4615	1874.9317	937.9695	17
3	302.1533	151.5803	0	0	0	0	L	1835.9208	918.4640	1818.8942	909.9508	1817.9102	909.4587	16
4	403.2010	202.1041	0	0	385.1904	193.0988	T	1722.8367	861.9220	1705.8102	853.4087	1704.8262	852.9167	15
5	516.2850	258.6462	0	0	498.2745	249.6409	L	1621.7890	811.3982	1604.7625	802.8849	1603.7785	802.3929	14
6	645.3276	323.1675	0	0	627.3171	314.1622	E	1508.7050	754.8561	1491.6784	746.3428	1490.6944	745.8508	13
7	702.3491	351.6782	0	0	684.3385	342.6729	G	1379.6624	690.3348	1362.6358	681.8216	1361.6518	681.3295	12
8	803.3968	402.2020	0	0	785.3862	393.1967	T	1322.6409	661.8241	1305.6144	653.3108	1304.6304	652.8188	11
9	902.4652	451.7362	0	0	884.4546	442.7309	V	1221.5932	611.3003	1204.5667	602.7870	1203.5827	602.2950	10
10	1049.5336	525.2704	0	0	1031.5230	516.2652	F	1122.5248	561.7660	1105.4983	553.2528	1104.5143	552.7608	9
11	1209.5642	605.2858	0	0	1191.5537	596.2805	C	975.4564	488.2318	958.4299	479.7186	957.4458	479.2266	8
12	1322.6483	661.8278	0	0	1304.6377	652.8225	L	815.4258	408.2165	798.3992	399.7032	797.4152	399.2112	7
13	1437.6753	719.3413	0	0	1419.6647	710.3360	D	702.3417	351.6745	685.3151	343.1612	684.3311	342.6692	6
14	1534.7280	767.8676	0	0	1516.7175	758.8624	P	587.3148	294.1610	570.2882	285.6477	569.3042	285.1557	5
15	1647.8121	824.4097	0	0	1629.8015	815.4044	L	490.2620	245.6346	473.2354	237.1214	472.2514	236.6293	4
16	1762.8390	881.9232	0	0	1744.8285	872.9179	D	377.1779	189.0926	360.1514	180.5793	359.1674	180.0873	3
17	1849.8711	925.4392	0	0	1831.8605	916.4339	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
18							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 43634.

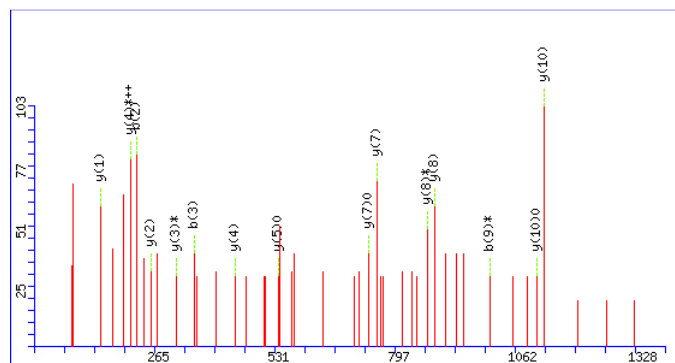
MS/MS Fragmentation of **LLEIQSLDAIK**:

Found in **IP100029227**

Title: 4.1.1.2105.7

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_3.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0								12
2	227.1754	114.0913	0	0	0	0	L	1242.7304	621.8688	1225.7038	613.3556	1224.7198	612.8635	11
3	356.2180	178.6126	0	0	338.2074	169.6074	E	1129.6463	565.3268	1112.6198	556.8135	1111.6358	556.3215	10
4	469.3021	235.1547	0	0	451.2915	226.1494	I	1000.6037	500.8055	983.5772	492.2922	982.5932	491.8002	9
5	597.3606	299.1840	580.3341	290.6707	579.3501	290.1787	Q	887.5197	444.2635	870.4931	435.7502	869.5091	435.2582	8
6	684.3927	342.7000	667.3661	334.1867	666.3821	333.6947	S	759.4611	380.2342	742.4345	371.7209	741.4505	371.2289	7
7	797.4767	399.2420	780.4502	390.7287	779.4662	390.2367	L	672.4291	336.7182	655.4025	328.2049	654.4185	327.7129	6
8	910.5608	455.7840	893.5342	447.2708	892.5502	446.7788	L	559.3450	280.1761	542.3184	271.6629	541.3344	271.1709	5
9	1025.5877	513.2975	1008.5612	504.7842	1007.5772	504.2922	D	446.2609	223.6341	429.2344	215.1208	428.2504	214.6288	4
10	1096.6249	548.8161	1079.5983	540.3028	1078.6143	539.8108	A	331.2340	166.1206	314.2074	157.6074	0	0	3
11	1209.7089	605.3581	1192.6824	596.8448	1191.6984	596.3528	I	260.1969	130.6021	243.1703	122.0888	0	0	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 43637.

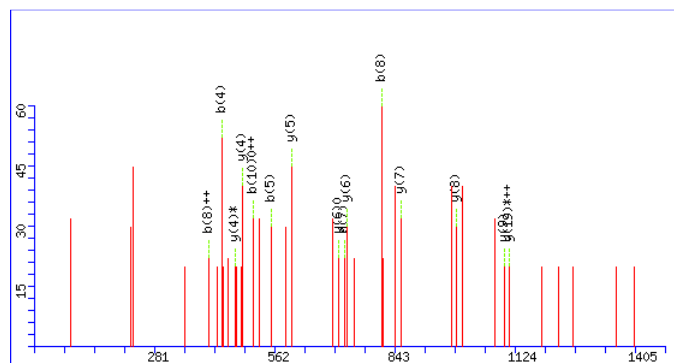
MS/MS Fragmentation of **RLNGLSSSVVEYNIMELEQELENVK:**

Found in **IP100168561;IP100385238;IP101012663**

Title: 4.1.1.3015.6

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_3.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	157.1084	79.0578	140.0818	70.5446	0	0	R							24
2	270.1925	135.5999	253.1659	127.0866	0	0	L	2638.2916	1319.6495	2621.2651	1311.1362	2620.2811	1310.6442	23
3	384.2354	192.6213	367.2088	184.1081	0	0	N	2525.2076	1263.1074	2508.1810	1254.5942	2507.1970	1254.1021	22
4	441.2568	221.1321	424.2303	212.6188	0	0	G	2411.1646	1206.0860	2394.1381	1197.5727	2393.1541	1197.0807	21
5	554.3409	277.6741	537.3144	269.1608	0	0	L	2354.1432	1177.5752	2337.1166	1169.0620	2336.1326	1168.5699	20
6	641.3729	321.1901	624.3464	312.6768	623.3624	312.1848	S	2241.0591	1121.0332	2224.0326	1112.5199	2223.0486	1112.0279	19
7	728.4050	364.7061	711.3784	356.1928	710.3944	355.7008	S	2154.0271	1077.5172	2137.0005	1069.0039	2136.0165	1068.5119	18
8	815.4370	408.2221	798.4104	399.7089	797.4264	399.2169	S	2066.9951	1034.0012	2049.9685	1025.4879	2048.9845	1024.9959	17
9	914.5054	457.7563	897.4789	449.2431	896.4948	448.7511	V	1979.9630	990.4852	1962.9365	981.9719	1961.9525	981.4799	16
10	1043.5480	522.2776	1026.5214	513.7644	1025.5374	513.2724	E	1880.8946	940.9509	1863.8681	932.4377	1862.8841	931.9457	15
11	1206.6113	603.8093	1189.5848	595.2960	1188.6008	594.8040	Y	1751.8520	876.4297	1734.8255	867.9164	1733.8415	867.4244	14
12	1320.6543	660.8308	1303.6277	652.3175	1302.6437	651.8255	N	1588.7887	794.8980	1571.7621	786.3847	1570.7781	785.8927	13
13	1433.7383	717.3728	1416.7118	708.8595	1415.7278	708.3675	I	1474.7458	737.8765	1457.7192	729.3632	1456.7352	728.8712	12
14	1564.7788	782.8930	1547.7523	774.3798	1546.7682	773.8878	M	1361.6617	681.3345	1344.6352	672.8212	1343.6511	672.3292	11
15	1693.8214	847.4143	1676.7948	838.9011	1675.8108	838.4091	E	1230.6212	615.8142	1213.5947	607.3010	1212.6107	606.8090	10
16	1806.9055	903.9564	1789.8789	895.4431	1788.8949	894.9511	L	1101.5786	551.2930	1084.5521	542.7797	1083.5681	542.2877	9
17	1935.9481	968.4777	1918.9215	959.9644	1917.9375	959.4724	E	988.4946	494.7509	971.4680	486.2376	970.4840	485.7456	8
18	2064.0066	1032.5070	2046.9801	1023.9937	2045.9961	1023.5017	Q	859.4520	430.2296	842.4254	421.7163	841.4414	421.2243	7
19	2193.0492	1097.0282	2176.0227	1088.5150	2175.0387	1088.0230	E	731.3934	366.2003	714.3668	357.6871	713.3828	357.1951	6
20	2306.1333	1153.5703	2289.1067	1145.0570	2288.1227	1144.5650	L	602.3508	301.6790	585.3243	293.1658	584.3402	292.6738	5
21	2435.1759	1218.0916	2418.1493	1209.5783	2417.1653	1209.0863	E	489.2667	245.1370	472.2402	236.6237	471.2562	236.1317	4
22	2549.2188	1275.1130	2532.1923	1266.5998	2531.2082	1266.1078	N	360.2241	180.6157	343.1976	172.1024	0	0	3
23	2648.2872	1324.6472	2631.2607	1316.1340	2630.2767	1315.6420	V	246.1812	123.5942	229.1547	115.0810	0	0	2
24							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 43869.

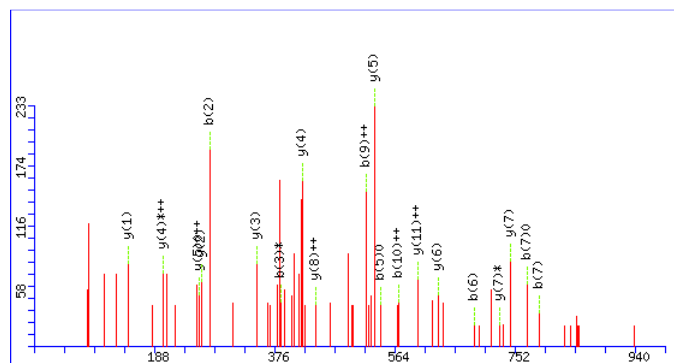
MS/MS Fragmentation of **HHQASETHNVIASDK**:

Found in **IP100020030;IP100549442;IP101025927**

Title: 1.1.1.6001.4

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	138.0662	69.5367	0	0	0	0	H							15
2	275.1251	138.0662	0	0	0	0	H	1536.7401	768.8737	1519.7136	760.3604	1518.7295	759.8684	14
3	403.1837	202.0955	386.1571	193.5822	0	0	Q	1399.6812	700.3442	1382.6546	691.8310	1381.6706	691.3390	13
4	474.2208	237.6140	457.1942	229.1008	0	0	A	1271.6226	636.3149	1254.5961	627.8017	1253.6121	627.3097	12
5	561.2528	281.1300	544.2263	272.6168	543.2423	272.1248	S	1200.5855	600.7964	1183.5590	592.2831	1182.5749	591.7911	11
6	690.2954	345.6513	673.2689	337.1381	672.2848	336.6461	E	1113.5535	557.2804	1096.5269	548.7671	1095.5429	548.2751	10
7	791.3431	396.1752	774.3165	387.6619	773.3325	387.1699	T	984.5109	492.7591	967.4843	484.2458	966.5003	483.7538	9
8	928.4020	464.7046	911.3755	456.1914	910.3914	455.6994	H	883.4632	442.2352	866.4367	433.7220	865.4526	433.2300	8
9	1042.4449	521.7261	1025.4184	513.2128	1024.4344	512.7208	N	746.4043	373.7058	729.3777	365.1925	728.3937	364.7005	7
10	1141.5133	571.2603	1124.4868	562.7470	1123.5028	562.2550	V	632.3614	316.6843	615.3348	308.1710	614.3508	307.6790	6
11	1254.5974	627.8023	1237.5709	619.2891	1236.5868	618.7971	I	533.2930	267.1501	516.2664	258.6368	515.2824	258.1448	5
12	1325.6345	663.3209	1308.6080	654.8076	1307.6240	654.3156	A	420.2089	210.6081	403.1823	202.0948	402.1983	201.6028	4
13	1412.6666	706.8369	1395.6400	698.3236	1394.6560	697.8316	S	349.1718	175.0895	332.1452	166.5763	331.1612	166.0842	3
14	1527.6935	764.3504	1510.6669	755.8371	1509.6829	755.3451	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
15							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

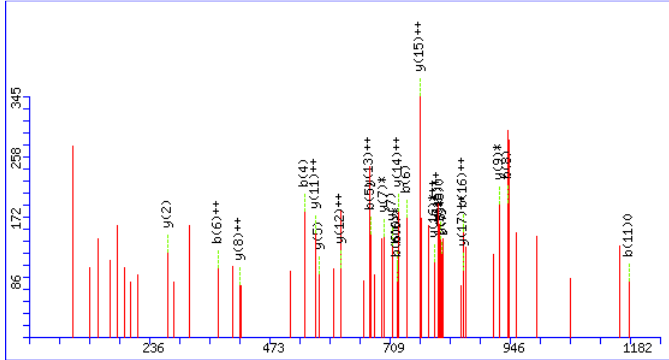
Peptide: 44057.

MS/MS Fragmentation of **EQREEAAEVASLDVANIISGSGRPR**:
Found in **IP100304875;IP100413871**

Title: 3.1.1.2340.4

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							25
2	258.1084	129.5579	241.0819	121.0446	240.0979	120.5526	Q	2525.3067	1263.1570	2508.2801	1254.6437	2507.2961	1254.1517	24
3	414.2096	207.6084	397.1830	199.0951	396.1990	198.6031	R	2397.2481	1199.1277	2380.2215	1190.6144	2379.2375	1190.1224	23
4	543.2522	272.1297	526.2256	263.6164	525.2416	263.1244	E	2241.1470	1121.0771	2224.1204	1112.5638	2223.1364	1112.0718	22
5	672.2947	336.6510	655.2682	328.1377	654.2842	327.6457	E	2112.1044	1056.5558	2095.0778	1048.0425	2094.0938	1047.5505	21
6	743.3319	372.1696	726.3053	363.6563	725.3213	363.1643	A	1983.0618	992.0345	1966.0352	983.5213	1965.0512	983.0292	20
7	814.3690	407.6881	797.3424	399.1748	796.3584	398.6828	A	1912.0247	956.5160	1894.9981	948.0027	1894.0141	947.5107	19
8	943.4116	472.2094	926.3850	463.6961	925.4010	463.2041	E	1840.9875	920.9974	1823.9610	912.4841	1822.9770	911.9921	18
9	1042.4800	521.7436	1025.4534	513.2304	1024.4694	512.7383	V	1711.9450	856.4761	1694.9184	847.9628	1693.9344	847.4708	17
10	1113.5171	557.2622	1096.4905	548.7489	1095.5065	548.2569	A	1612.8765	806.9419	1595.8500	798.4286	1594.8660	797.9366	16
11	1200.5491	600.7782	1183.5226	592.2649	1182.5386	591.7729	S	1541.8394	771.4234	1524.8129	762.9101	1523.8289	762.4181	15
12	1313.6332	657.3202	1296.6066	648.8070	1295.6226	648.3149	L	1454.8074	727.9073	1437.7809	719.3941	1436.7968	718.9021	14
13	1428.6601	714.8337	1411.6336	706.3204	1410.6496	705.8284	D	1341.7233	671.3653	1324.6968	662.8520	1323.7128	662.3600	13
14	1527.7285	764.3679	1510.7020	755.8546	1509.7180	755.3626	V	1226.6964	613.8518	1209.6698	605.3386	1208.6858	604.8466	12
15	1598.7657	799.8865	1581.7391	791.3732	1580.7551	790.8812	A	1127.6280	564.3176	1110.6014	555.8044	1109.6174	555.3123	11
16	1712.8086	856.9079	1695.7820	848.3947	1694.7980	847.9026	N	1056.5909	528.7991	1039.5643	520.2858	1038.5803	519.7938	10
17	1825.8926	913.4500	1808.8661	904.9367	1807.8821	904.4447	I	942.5479	471.7776	925.5214	463.2643	924.5374	462.7723	9
18	1938.9767	969.9920	1921.9502	961.4787	1920.9661	960.9867	I	829.4639	415.2356	812.4373	406.7223	811.4533	406.2303	8
19	2026.0087	1013.5080	2008.9822	1004.9947	2007.9982	1004.5027	S	716.3798	358.6935	699.3533	350.1803	698.3692	349.6883	7
20	2083.0302	1042.0187	2066.0037	1033.5055	2065.0196	1033.0135	G	629.3478	315.1775	612.3212	306.6643	611.3372	306.1722	6
21	2170.0622	1085.5348	2153.0357	1077.0215	2152.0517	1076.5295	S	572.3263	286.6668	555.2998	278.1535	554.3158	277.6615	5
22	2227.0837	1114.0455	2210.0571	1105.5322	2209.0731	1105.0402	G	485.2943	243.1508	468.2677	234.6375	0	0	4
23	2383.1848	1192.0960	2366.1583	1183.5828	2365.1742	1183.0908	R	428.2728	214.6401	411.2463	206.1268	0	0	3
24	2480.2376	1240.6224	2463.2110	1232.1091	2462.2270	1231.6171	P	272.1717	136.5895	255.1452	128.0762	0	0	2
25							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 44114.

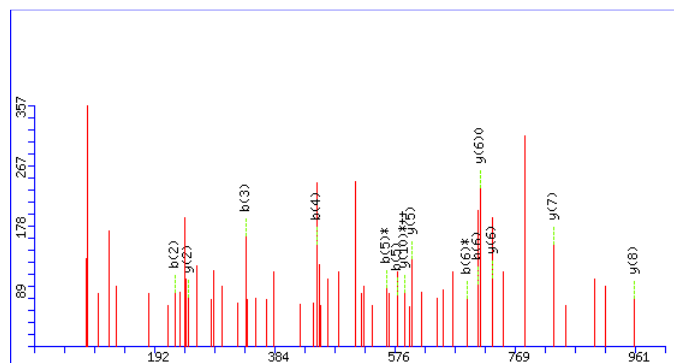
MS/MS Fragmentation of **HSDLQEVENEITK**:

Found in **IP100297263**

Title: 2.1.1.3153.6

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120201ry¥120201ry_aHDF1388-P9_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	138.0662	69.5367	0	0	0	0	H							13
2	225.0982	113.0527	0	0	207.0877	104.0475	S	1404.6853	702.8463	1387.6587	694.3330	1386.6747	693.8410	12
3	340.1252	170.5662	0	0	322.1146	161.5609	D	1317.6533	659.3303	1300.6267	650.8170	1299.6427	650.3250	11
4	453.2092	227.1082	0	0	435.1987	218.1030	L	1202.6263	601.8168	1185.5998	593.3035	1184.6157	592.8115	10
5	581.2678	291.1375	564.2413	282.6243	563.2572	282.1323	Q	1089.5422	545.2748	1072.5157	536.7615	1071.5317	536.2695	9
6	710.3104	355.6588	693.2838	347.1456	692.2998	346.6536	E	961.4837	481.2455	944.4571	472.7322	943.4731	472.2402	8
7	809.3788	405.1930	792.3523	396.6798	791.3682	396.1878	V	832.4411	416.7242	815.4145	408.2109	814.4305	407.7189	7
8	938.4214	469.7143	921.3949	461.2011	920.4108	460.7091	E	733.3727	367.1900	716.3461	358.6767	715.3621	358.1847	6
9	1052.4643	526.7358	1035.4378	518.2225	1034.4538	517.7305	N	604.3301	302.6687	587.3035	294.1554	586.3195	293.6634	5
10	1181.5069	591.2571	1164.4804	582.7438	1163.4964	582.2518	E	490.2871	245.6472	473.2606	237.1339	472.2766	236.6419	4
11	1294.5910	647.7991	1277.5644	639.2859	1276.5804	638.7938	I	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
12	1395.6387	698.3230	1378.6121	689.8097	1377.6281	689.3177	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 44174.

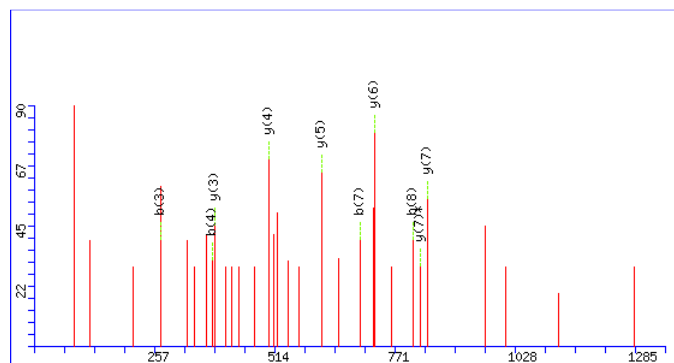
MS/MS Fragmentation of **APTISDLLNDQDLLDVIR**:

Found in **IP100103484;IP100152912**

Title: 4.1.1.2275.3

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							18
2	169.0972	85.0522	0	0	0	0	P	1940.0335	970.5204	1923.0069	962.0071	1922.0229	961.5151	17
3	270.1448	135.5761	0	0	252.1343	126.5708	T	1842.9807	921.9940	1825.9542	913.4807	1824.9702	912.9887	16
4	383.2289	192.1181	0	0	365.2183	183.1128	I	1741.9331	871.4702	1724.9065	862.9569	1723.9225	862.4649	15
5	470.2609	235.6341	0	0	452.2504	226.6288	S	1628.8490	814.9281	1611.8224	806.4149	1610.8384	805.9229	14
6	585.2879	293.1476	0	0	567.2773	284.1423	D	1541.8170	771.4121	1524.7904	762.8988	1523.8064	762.4068	13
7	698.3719	349.6896	0	0	680.3614	340.6843	L	1426.7900	713.8986	1409.7635	705.3854	1408.7795	704.8934	12
8	811.4560	406.2316	0	0	793.4454	397.2264	L	1313.7060	657.3566	1296.6794	648.8433	1295.6954	648.3513	11
9	925.4989	463.2531	908.4724	454.7398	907.4884	454.2478	N	1200.6219	600.8146	1183.5953	592.3013	1182.6113	591.8093	10
10	1040.5259	520.7666	1023.4993	512.2533	1022.5153	511.7613	D	1086.5790	543.7931	1069.5524	535.2798	1068.5684	534.7878	9
11	1168.5844	584.7959	1151.5579	576.2826	1150.5739	575.7906	Q	971.5520	486.2796	954.5255	477.7664	953.5415	477.2744	8
12	1283.6114	642.3093	1266.5848	633.7961	1265.6008	633.3040	D	843.4934	422.2504	826.4669	413.7371	825.4829	413.2451	7
13	1396.6955	698.8514	1379.6689	690.3381	1378.6849	689.8461	L	728.4665	364.7369	711.4400	356.2236	710.4559	355.7316	6
14	1509.7795	755.3934	1492.7530	746.8801	1491.7690	746.3881	L	615.3824	308.1949	598.3559	299.6816	597.3719	299.1896	5
15	1624.8065	812.9069	1607.7799	804.3936	1606.7959	803.9016	D	502.2984	251.6528	485.2718	243.1395	484.2878	242.6475	4
16	1723.8749	862.4411	1706.8483	853.9278	1705.8643	853.4358	V	387.2714	194.1394	370.2449	185.6261	0	0	3
17	1836.9589	918.9831	1819.9324	910.4698	1818.9484	909.9778	I	288.2030	144.6051	271.1765	136.0919	0	0	2
18							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 44467.

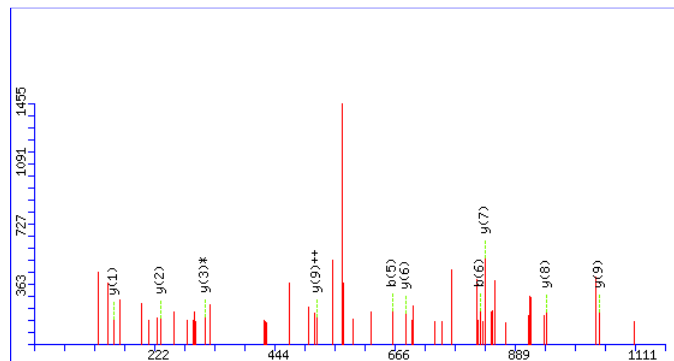
MS/MS Fragmentation of **LCQTCYPLFQQVVSK: 57.021465@C:2,57.021465@C:5**

Found in **IP100329054**

Title: 3.1.1.1146.4

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120208ry¥120208ry_Tig120slc-P8_2.3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							15
2	274.1220	137.5646	0	0	0	0	C	1757.8349	879.4211	1740.8084	870.9078	1739.8244	870.4158	14
3	402.1806	201.5939	385.1540	193.0806	0	0	Q	1597.8043	799.4058	1580.7777	790.8925	1579.7937	790.4005	13
4	503.2282	252.1178	486.2017	243.6045	485.2177	243.1125	T	1469.7457	735.3765	1452.7192	726.8632	1451.7352	726.3712	12
5	663.2589	332.1331	646.2323	323.6198	645.2483	323.1278	C	1368.6980	684.8527	1351.6715	676.3394	1350.6875	675.8474	11
6	826.3222	413.6648	809.2957	405.1515	808.3117	404.6595	Y	1208.6674	604.8373	1191.6408	596.3241	1190.6568	595.8320	10
7	923.3750	462.1911	906.3484	453.6779	905.3644	453.1859	P	1045.6041	523.3057	1028.5775	514.7924	1027.5935	514.3004	9
8	1036.4591	518.7332	1019.4325	510.2199	1018.4485	509.7279	L	948.5513	474.7793	931.5247	466.2660	930.5407	465.7740	8
9	1183.5275	592.2674	1166.5009	583.7541	1165.5169	583.2621	F	835.4672	418.2373	818.4407	409.7240	817.4567	409.2320	7
10	1311.5860	656.2967	1294.5595	647.7834	1293.5755	647.2914	Q	688.3988	344.7030	671.3723	336.1898	670.3883	335.6978	6
11	1439.6446	720.3260	1422.6181	711.8127	1421.6341	711.3207	Q	560.3402	280.6738	543.3137	272.1605	542.3297	271.6685	5
12	1538.7130	769.8602	1521.6865	761.3469	1520.7025	760.8549	V	432.2817	216.6445	415.2551	208.1312	414.2711	207.6392	4
13	1637.7815	819.3944	1620.7549	810.8811	1619.7709	810.3891	V	333.2132	167.1103	316.1867	158.5970	315.2027	158.1050	3
14	1724.8135	862.9104	1707.7869	854.3971	1706.8029	853.9051	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
15							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 44573.

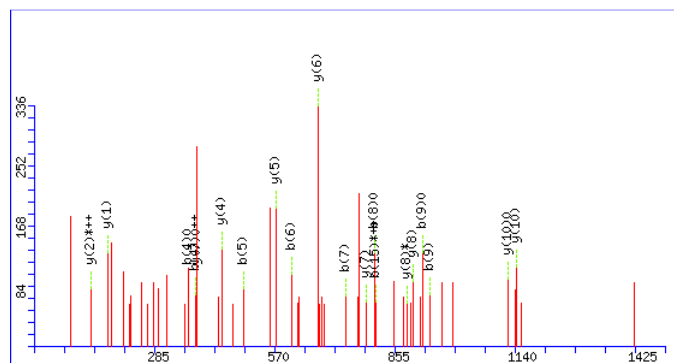
MS/MS Fragmentation of **GSHTDLESINENLVESALR**:

Found in **IP100465101;IP100943072;IP101020856**

Title: 3.1.1.2069.5

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_1_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							19
2	145.0608	73.0340	0	0	127.0502	64.0287	S	2027.0040	1014.0056	2009.9774	1005.4924	2008.9934	1005.0003	18
3	282.1197	141.5635	0	0	264.1091	132.5582	H	1939.9720	970.4896	1922.9454	961.9763	1921.9614	961.4843	17
4	383.1674	192.0873	0	0	365.1568	183.0820	T	1802.9130	901.9602	1785.8865	893.4469	1784.9025	892.9549	16
5	498.1943	249.6008	0	0	480.1837	240.5955	D	1701.8654	851.4363	1684.8388	842.9230	1683.8548	842.4310	15
6	611.2784	306.1428	0	0	593.2678	297.1375	L	1586.8384	793.9229	1569.8119	785.4096	1568.8279	784.9176	14
7	740.3210	370.6641	0	0	722.3104	361.6588	E	1473.7544	737.3808	1456.7278	728.8675	1455.7438	728.3755	13
8	827.3530	414.1801	0	0	809.3424	405.1748	S	1344.7118	672.8595	1327.6852	664.3462	1326.7012	663.8542	12
9	940.4371	470.7222	0	0	922.4265	461.7169	I	1257.6797	629.3435	1240.6532	620.8302	1239.6692	620.3382	11
10	1054.4800	527.7436	1037.4534	519.2304	1036.4694	518.7383	N	1144.5957	572.8015	1127.5691	564.2882	1126.5851	563.7962	10
11	1183.5226	592.2649	1166.4960	583.7516	1165.5120	583.2596	E	1030.5527	515.7800	1013.5262	507.2667	1012.5422	506.7747	9
12	1297.5655	649.2864	1280.5389	640.7731	1279.5549	640.2811	N	901.5102	451.2587	884.4836	442.7454	883.4996	442.2534	8
13	1410.6496	705.8284	1393.6230	697.3151	1392.6390	696.8231	L	787.4672	394.2373	770.4407	385.7240	769.4567	385.2320	7
14	1509.7180	755.3626	1492.6914	746.8494	1491.7074	746.3573	V	674.3832	337.6952	657.3566	329.1819	656.3726	328.6899	6
15	1638.7606	819.8839	1621.7340	811.3706	1620.7500	810.8786	E	575.3148	288.1610	558.2882	279.6477	557.3042	279.1557	5
16	1725.7926	863.3999	1708.7660	854.8867	1707.7820	854.3947	S	446.2722	223.6397	429.2456	215.1264	428.2616	214.6344	4
17	1796.8297	898.9185	1779.8032	890.4052	1778.8191	889.9132	A	359.2401	180.1237	342.2136	171.6104	0	0	3
18	1909.9138	955.4605	1892.8872	946.9473	1891.9032	946.4552	L	288.2030	144.6051	271.1765	136.0919	0	0	2
19							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: **44692**.

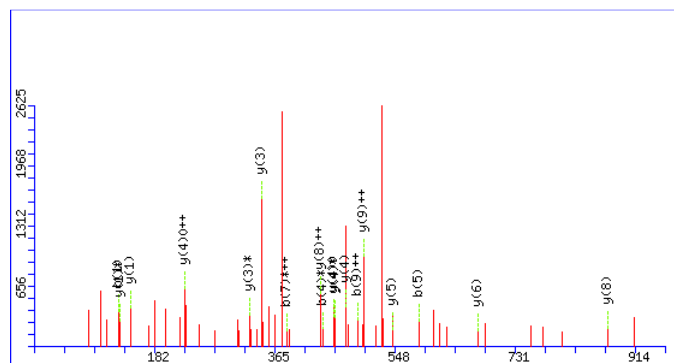
MS/MS Fragmentation of **QQKAEAEAQK: 0.984016@Q:2**

Found in **IP100166137;IP100790685;IP100980380;IP101013944**

Title: 1.1.1.5617.4

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_3_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233	0	0	Q							10
2	258.1084	129.5579	241.0819	121.0446	0	0	Q	1003.5055	502.2564	986.4789	493.7431	985.4949	493.2511	9
3	386.2034	193.6053	369.1769	185.0921	0	0	K	874.4629	437.7351	857.4363	429.2218	856.4523	428.7298	8
4	457.2405	229.1239	440.2140	220.6106	0	0	A	746.3679	373.6876	729.3414	365.1743	728.3573	364.6823	7
5	586.2831	293.6452	569.2566	285.1319	568.2726	284.6399	E	675.3308	338.1690	658.3042	329.6558	657.3202	329.1638	6
6	657.3202	329.1638	640.2937	320.6505	639.3097	320.1585	A	546.2882	273.6477	529.2617	265.1345	528.2776	264.6425	5
7	786.3628	393.6851	769.3363	385.1718	768.3523	384.6798	E	475.2511	238.1292	458.2245	229.6159	457.2405	229.1239	4
8	857.3999	429.2036	840.3734	420.6903	839.3894	420.1983	A	346.2085	173.6079	329.1819	165.0946	0	0	3
9	985.4585	493.2329	968.4320	484.7196	967.4480	484.2276	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
10							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 44711.

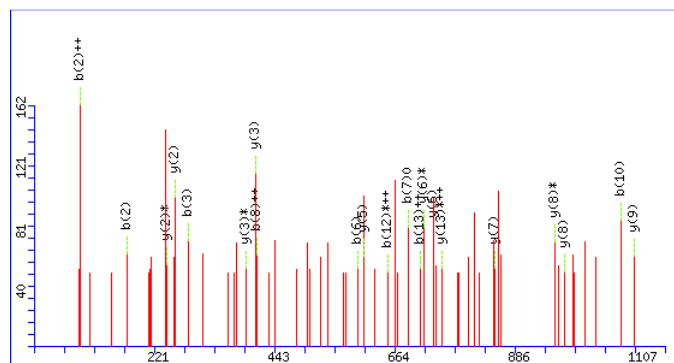
MS/MS Fragmentation of **AVLQPSINEEIQTVFNK**:

Found in **IP100057097;IP100513998;IP100514967;IP100640751;IP100642460**

Title: 3.1.1.3311.4

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							17
2	171.1128	86.0600	0	0	0	0	V	1858.9909	929.9991	1841.9644	921.4858	1840.9803	920.9938	16
3	284.1969	142.6021	0	0	0	0	L	1759.9225	880.4649	1742.8959	871.9516	1741.9119	871.4596	15
4	412.2554	206.6314	395.2289	198.1181	0	0	Q	1646.8384	823.9229	1629.8119	815.4096	1628.8279	814.9176	14
5	509.3082	255.1577	492.2817	246.6445	0	0	P	1518.7798	759.8936	1501.7533	751.3803	1500.7693	750.8883	13
6	596.3402	298.6738	579.3137	290.1605	578.3297	289.6685	S	1421.7271	711.3672	1404.7005	702.8539	1403.7165	702.3619	12
7	709.4243	355.2158	692.3978	346.7025	691.4137	346.2105	I	1334.6951	667.8512	1317.6685	659.3379	1316.6845	658.8459	11
8	823.4672	412.2373	806.4407	403.7240	805.4567	403.2320	N	1221.6110	611.3091	1204.5844	602.7959	1203.6004	602.3039	10
9	952.5098	476.7585	935.4833	468.2453	934.4993	467.7533	E	1107.5681	554.2877	1090.5415	545.7744	1089.5575	545.2824	9
10	1081.5524	541.2798	1064.5259	532.7666	1063.5419	532.2746	E	978.5255	489.7664	961.4989	481.2531	960.5149	480.7611	8
11	1194.6365	597.8219	1177.6099	589.3086	1176.6259	588.8166	I	849.4829	425.2451	832.4563	416.7318	831.4723	416.2398	7
12	1322.6951	661.8512	1305.6685	653.3379	1304.6845	652.8459	Q	736.3988	368.7030	719.3723	360.1898	718.3883	359.6978	6
13	1423.7427	712.3750	1406.7162	703.8617	1405.7322	703.3697	T	608.3402	304.6738	591.3137	296.1605	590.3297	295.6685	5
14	1522.8112	761.9092	1505.7846	753.3959	1504.8006	752.9039	V	507.2926	254.1499	490.2660	245.6366	0	0	4
15	1669.8796	835.4434	1652.8530	826.9301	1651.8690	826.4381	F	408.2241	204.6157	391.1976	196.1024	0	0	3
16	1783.9225	892.4649	1766.8959	883.9516	1765.9119	883.4596	N	261.1557	131.0815	244.1292	122.5682	0	0	2
17							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: **44924**.

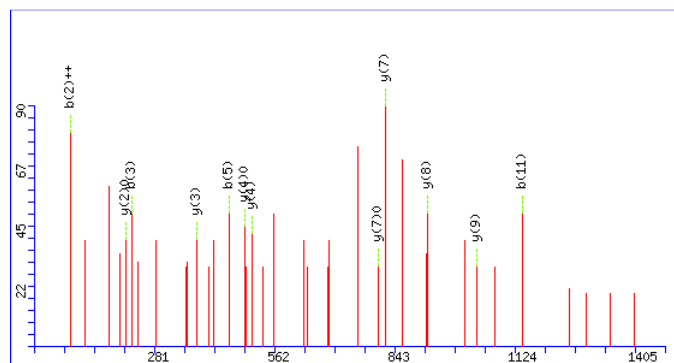
MS/MS Fragmentation of **LGGLDVLEAEFSK**:

Found in **IP100186145;IP100938269**

Title: 3.1.1.3728.5

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							13
2	171.1128	86.0600	0	0	0	0	G	1264.6420	632.8246	1247.6154	624.3113	1246.6314	623.8193	12
3	228.1343	114.5708	0	0	0	0	G	1207.6205	604.3139	1190.5939	595.8006	1189.6099	595.3086	11
4	341.2183	171.1128	0	0	0	0	L	1150.5990	575.8032	1133.5725	567.2899	1132.5885	566.7979	10
5	456.2453	228.6263	0	0	438.2347	219.6210	D	1037.5150	519.2611	1020.4884	510.7478	1019.5044	510.2558	9
6	555.3137	278.1605	0	0	537.3031	269.1552	V	922.4880	461.7476	905.4615	453.2344	904.4775	452.7424	8
7	668.3978	334.7025	0	0	650.3872	325.6972	L	823.4196	412.2134	806.3931	403.7002	805.4090	403.2082	7
8	797.4403	399.2238	0	0	779.4298	390.2185	E	710.3355	355.6714	693.3090	347.1581	692.3250	346.6661	6
9	868.4775	434.7424	0	0	850.4669	425.7371	A	581.2930	291.1501	564.2664	282.6368	563.2824	282.1448	5
10	997.5201	499.2637	0	0	979.5095	490.2584	E	510.2558	255.6316	493.2293	247.1183	492.2453	246.6263	4
11	1144.5885	572.7979	0	0	1126.5779	563.7926	F	381.2132	191.1103	364.1867	182.5970	363.2027	182.1050	3
12	1231.6205	616.3139	0	0	1213.6099	607.3086	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 45005.

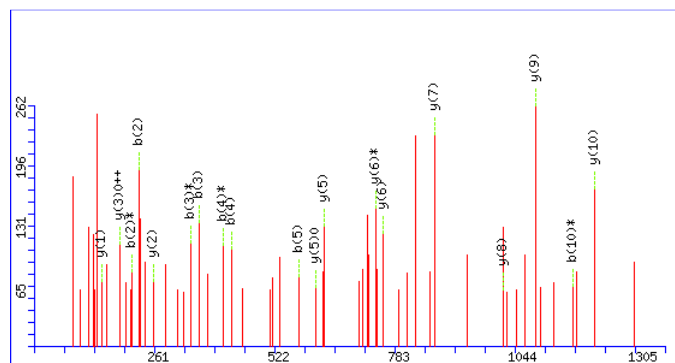
MS/MS Fragmentation of **NNEAFLQELELK**:

Found in **IP100011140**

Title: 3.1.1.2087.11

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							12
2	229.0931	115.0502	212.0666	106.5369	0	0	N	1333.6998	667.3535	1316.6733	658.8403	1315.6892	658.3483	11
3	358.1357	179.5715	341.1092	171.0582	340.1252	170.5662	E	1219.6569	610.3321	1202.6303	601.8188	1201.6463	601.3268	10
4	429.1728	215.0901	412.1463	206.5768	411.1623	206.0848	A	1090.6143	545.8108	1073.5877	537.2975	1072.6037	536.8055	9
5	576.2413	288.6243	559.2147	280.1110	558.2307	279.6190	F	1019.5772	510.2922	1002.5506	501.7790	1001.5666	501.2869	8
6	689.3253	345.1663	672.2988	336.6530	671.3148	336.1610	L	872.5088	436.7580	855.4822	428.2447	854.4982	427.7527	7
7	817.3839	409.1956	800.3573	400.6823	799.3733	400.1903	Q	759.4247	380.2160	742.3981	371.7027	741.4141	371.2107	6
8	946.4265	473.7169	929.3999	465.2036	928.4159	464.7116	E	631.3661	316.1867	614.3396	307.6734	613.3556	307.1814	5
9	1059.5106	530.2589	1042.4840	521.7456	1041.5000	521.2536	L	502.3235	251.6654	485.2970	243.1521	484.3130	242.6601	4
10	1188.5531	594.7802	1171.5266	586.2669	1170.5426	585.7749	E	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
11	1301.6372	651.3222	1284.6107	642.8090	1283.6266	642.3170	L	260.1969	130.6021	243.1703	122.0888	0	0	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 45224.

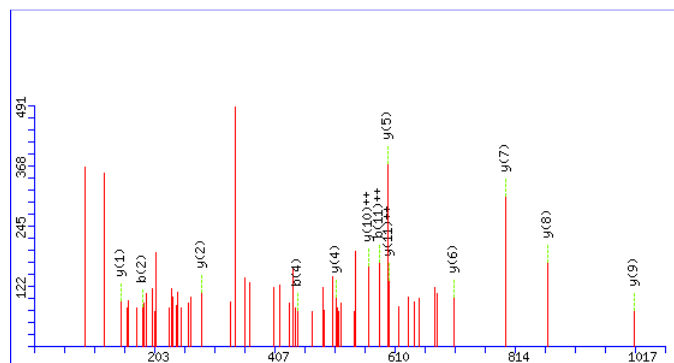
MS/MS Fragmentation of **LANFASLSDLHK**:

Found in **IP100869107**

Title: 2.1.1.3328.3

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_3.2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							12
2	185.1285	93.0679	0	0	0	0	A	1202.6164	601.8118	1185.5899	593.2986	1184.6058	592.8066	11
3	299.1714	150.0893	282.1448	141.5761	0	0	N	1131.5793	566.2933	1114.5527	557.7800	1113.5687	557.2880	10
4	446.2398	223.6235	429.2132	215.1103	0	0	F	1017.5364	509.2718	1000.5098	500.7585	999.5258	500.2665	9
5	517.2769	259.1421	500.2504	250.6288	0	0	A	870.4680	435.7376	853.4414	427.2243	852.4574	426.7323	8
6	604.3089	302.6581	587.2824	294.1448	586.2984	293.6528	S	799.4308	400.2191	782.4043	391.7058	781.4203	391.2138	7
7	717.3930	359.2001	700.3665	350.6869	699.3824	350.1949	L	712.3988	356.7030	695.3723	348.1898	694.3883	347.6978	6
8	804.4250	402.7162	787.3985	394.2029	786.4145	393.7109	S	599.3148	300.1610	582.2882	291.6477	581.3042	291.1557	5
9	919.4520	460.2296	902.4254	451.7163	901.4414	451.2243	D	512.2827	256.6450	495.2562	248.1317	494.2722	247.6397	4
10	1032.5360	516.7717	1015.5095	508.2584	1014.5255	507.7664	L	397.2558	199.1315	380.2292	190.6183	0	0	3
11	1169.5949	585.3011	1152.5684	576.7878	1151.5844	576.2958	H	284.1717	142.5895	267.1452	134.0762	0	0	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 45323.

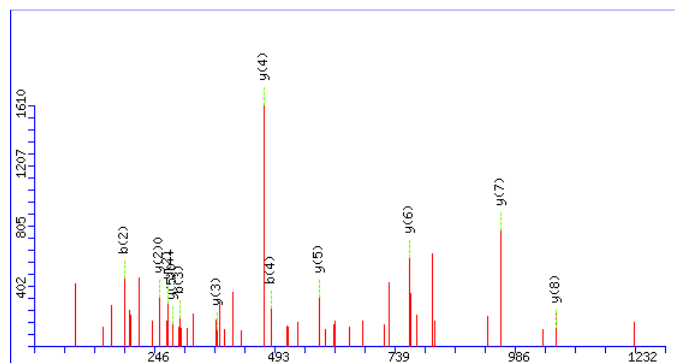
MS/MS Fragmentation of **SVLWWLPVEK**:

Found in **IP100334513;IP100334514;IP100783919;IP100910862;IP100926529;IP100926849;IP100927565;IP100972944**

Title: 4.1.1.400.4

Data file: Y:\TT5600(CiRA1)\2012-02\120201ry\120201ry_aHDF1388-P9_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							10
2	187.1077	94.0575	0	0	169.0972	85.0522	V	1169.6717	585.3395	1152.6452	576.8262	1151.6612	576.3342	9
3	300.1918	150.5995	0	0	282.1812	141.5942	L	1070.6033	535.8053	1053.5768	527.2920	1052.5928	526.8000	8
4	486.2711	243.6392	0	0	468.2605	234.6339	W	957.5193	479.2633	940.4927	470.7500	939.5087	470.2580	7
5	672.3504	336.6788	0	0	654.3398	327.6736	W	771.4400	386.2236	754.4134	377.7103	753.4294	377.2183	6
6	785.4345	393.2209	0	0	767.4239	384.2156	L	585.3606	293.1840	568.3341	284.6707	567.3501	284.1787	5
7	882.4872	441.7473	0	0	864.4767	432.7420	P	472.2766	236.6419	455.2500	228.1287	454.2660	227.6366	4
8	981.5557	491.2815	0	0	963.5451	482.2762	V	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
9	1110.5982	555.8028	0	0	1092.5877	546.7975	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
10							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 45661.

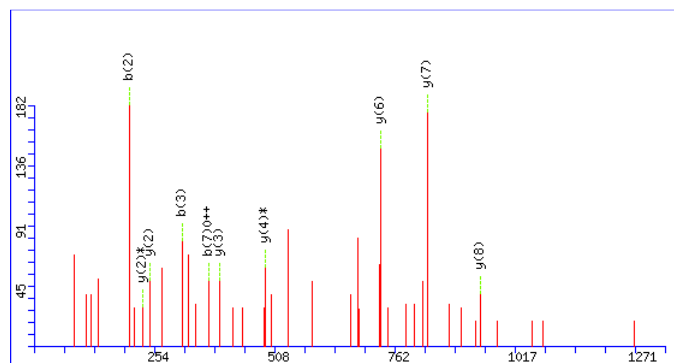
MS/MS Fragmentation of **SNIVDLLFVK**:

Found in **IP100006084;IP100396142;IP100401870;IP101019112**

Title: 3.1.1.4273.3

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							10
2	202.0822	101.5448	185.0557	93.0315	184.0717	92.5395	N	1060.6401	530.8237	1043.6136	522.3104	1042.6295	521.8184	9
3	315.1663	158.0868	298.1397	149.5735	297.1557	149.0815	I	946.5972	473.8022	929.5706	465.2890	928.5866	464.7969	8
4	414.2347	207.6210	397.2082	199.1077	396.2241	198.6157	V	833.5131	417.2602	816.4866	408.7469	815.5026	408.2549	7
5	529.2617	265.1345	512.2351	256.6212	511.2511	256.1292	D	734.4447	367.7260	717.4182	359.2127	716.4341	358.7207	6
6	642.3457	321.6765	625.3192	313.1632	624.3352	312.6712	L	619.4178	310.2125	602.3912	301.6992	0	0	5
7	755.4298	378.2185	738.4032	369.7053	737.4192	369.2132	L	506.3337	253.6705	489.3071	245.1572	0	0	4
8	902.4982	451.7527	885.4716	443.2395	884.4876	442.7475	F	393.2496	197.1285	376.2231	188.6152	0	0	3
9	1001.5666	501.2869	984.5401	492.7737	983.5560	492.2817	V	246.1812	123.5942	229.1547	115.0810	0	0	2
10							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 45785.

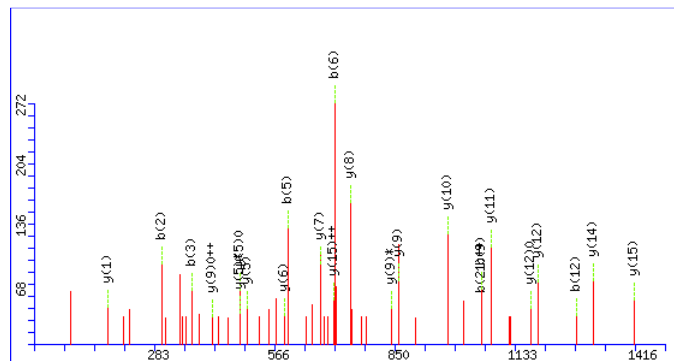
MS/MS Fragmentation of **YHALLIPSCPGALTDLASSGSLAR**: 57.021465@C:9

Found in **IP100168112;IP100719079;IP100976498;IP100983323;IP100985101;IP101008788;IP101012151**

Title: 3.1.1.2783.10

Data file: Y:\TT5600(CiRA1)\¥2012-01¥120129ry¥120129ry_604A1-46_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	164.0706	82.5389	0	0	0	0	Y							24
2	301.1295	151.0684	0	0	0	0	H	2307.2125	1154.1099	2290.1860	1145.5966	2289.2020	1145.1046	23
3	372.1666	186.5870	0	0	0	0	A	2170.1536	1085.5805	2153.1271	1077.0672	2152.1431	1076.5752	22
4	485.2507	243.1290	0	0	0	0	L	2099.1165	1050.0619	2082.0900	1041.5486	2081.1060	1041.0566	21
5	598.3348	299.6710	0	0	0	0	L	1986.0325	993.5199	1969.0059	985.0066	1968.0219	984.5146	20
6	711.4188	356.2130	0	0	0	0	I	1872.9484	936.9778	1855.9218	928.4646	1854.9378	927.9726	19
7	808.4716	404.7394	0	0	0	0	P	1759.8643	880.4358	1742.8378	871.9225	1741.8538	871.4305	18
8	895.5036	448.2554	0	0	877.4931	439.2502	S	1662.8116	831.9094	1645.7850	823.3961	1644.8010	822.9041	17
9	1055.5343	528.2708	0	0	1037.5237	519.2655	C	1575.7795	788.3934	1558.7530	779.8801	1557.7690	779.3881	16
10	1152.5870	576.7972	0	0	1134.5765	567.7919	P	1415.7489	708.3781	1398.7223	699.8648	1397.7383	699.3728	15
11	1209.6085	605.3079	0	0	1191.5979	596.3026	G	1318.6961	659.8517	1301.6696	651.3384	1300.6856	650.8464	14
12	1280.6456	640.8264	0	0	1262.6350	631.8212	A	1261.6747	631.3410	1244.6481	622.8277	1243.6641	622.3357	13
13	1393.7297	697.3685	0	0	1375.7191	688.3632	L	1190.6375	595.8224	1173.6110	587.3091	1172.6270	586.8171	12
14	1494.7774	747.8923	0	0	1476.7668	738.8870	T	1077.5535	539.2804	1060.5269	530.7671	1059.5429	530.2751	11
15	1609.8043	805.4058	0	0	1591.7937	796.4005	D	976.5058	488.7565	959.4792	480.2433	958.4952	479.7513	10
16	1722.8884	861.9478	0	0	1704.8778	852.9425	L	861.4789	431.2431	844.4523	422.7298	843.4683	422.2378	9
17	1793.9255	897.4664	0	0	1775.9149	888.4611	A	748.3948	374.7010	731.3682	366.1878	730.3842	365.6958	8
18	1880.9575	940.9824	0	0	1862.9469	931.9771	S	677.3577	339.1825	660.3311	330.6692	659.3471	330.1772	7
19	1967.9895	984.4984	0	0	1949.9790	975.4931	S	590.3256	295.6665	573.2991	287.1532	572.3151	286.6612	6
20	2025.0110	1013.0091	0	0	2007.0004	1004.0039	S	503.2936	252.1504	486.2671	243.6372	485.2831	243.1452	5
21	2112.0430	1056.5251	0	0	2094.0325	1047.5199	S	446.2722	223.6397	429.2456	215.1264	428.2616	214.6344	4
22	2225.1271	1113.0672	0	0	2207.1165	1104.0619	L	359.2401	180.1237	342.2136	171.6104	0	0	3
23	2296.1642	1148.5857	0	0	2278.1536	1139.5805	A	246.1561	123.5817	229.1295	115.0684	0	0	2
24							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 45846.

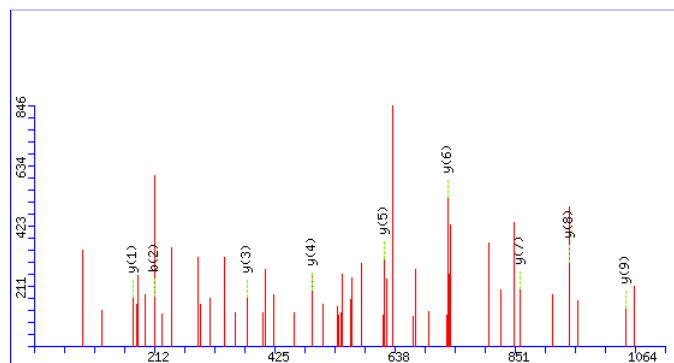
MS/MS Fragmentation of **LVSQIEDAMR**:

Found in **IP100107693;IP100220307;IP100554734;IP100879723;IP100879890**

Title: 2.1.1.2657.5

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							10
2	213.1598	107.0835	0	0	0	0	V	1048.5092	524.7582	1031.4826	516.2449	1030.4986	515.7529	9
3	300.1918	150.5995	0	0	282.1812	141.5942	S	949.4408	475.2240	932.4142	466.7107	931.4302	466.2187	8
4	428.2504	214.6288	411.2238	206.1155	410.2398	205.6235	Q	862.4087	431.7080	845.3822	423.1947	844.3982	422.7027	7
5	541.3344	271.1709	524.3079	262.6576	523.3239	262.1656	I	734.3502	367.6787	717.3236	359.1654	716.3396	358.6734	6
6	670.3770	335.6921	653.3505	327.1789	652.3665	326.6869	E	621.2661	311.1367	604.2395	302.6234	603.2555	302.1314	5
7	785.4040	393.2056	768.3774	384.6923	767.3934	384.2003	D	492.2235	246.6154	475.1969	238.1021	474.2129	237.6101	4
8	856.4411	428.7242	839.4145	420.2109	838.4305	419.7189	A	377.1966	189.1019	360.1700	180.5886	0	0	3
9	987.4816	494.2444	970.4550	485.7311	969.4710	485.2391	M	306.1594	153.5834	289.1329	145.0701	0	0	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 45997.

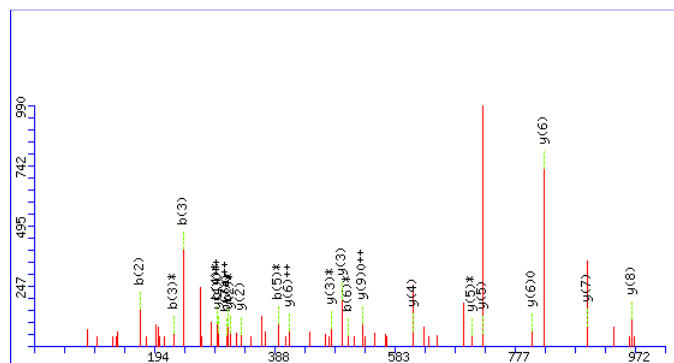
MS/MS Fragmentation of **GNAAVLDYCR: 57.021465@C:9**

Found in **IP100010427**

Title: 2.1.1.821.8

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							10
2	172.0717	86.5395	155.0451	78.0262	0	0	N	1081.5095	541.2584	1064.4830	532.7451	1063.4989	532.2531	9
3	243.1088	122.0580	226.0822	113.5448	0	0	A	967.4666	484.2369	950.4400	475.7237	949.4560	475.2316	8
4	314.1459	157.5766	297.1193	149.0633	0	0	A	896.4295	448.7184	879.4029	440.2051	878.4189	439.7131	7
5	413.2143	207.1108	396.1878	198.5975	0	0	V	825.3924	413.1998	808.3658	404.6865	807.3818	404.1945	6
6	526.2984	263.6528	509.2718	255.1395	0	0	L	726.3239	363.6656	709.2974	355.1523	708.3134	354.6603	5
7	641.3253	321.1663	624.2988	312.6530	623.3148	312.1610	D	613.2399	307.1236	596.2133	298.6103	595.2293	298.1183	4
8	804.3886	402.6980	787.3621	394.1847	786.3781	393.6927	Y	498.2129	249.6101	481.1864	241.0968	0	0	3
9	964.4193	482.7133	947.3927	474.2000	946.4087	473.7080	C	335.1496	168.0784	318.1231	159.5652	0	0	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: **46132.**

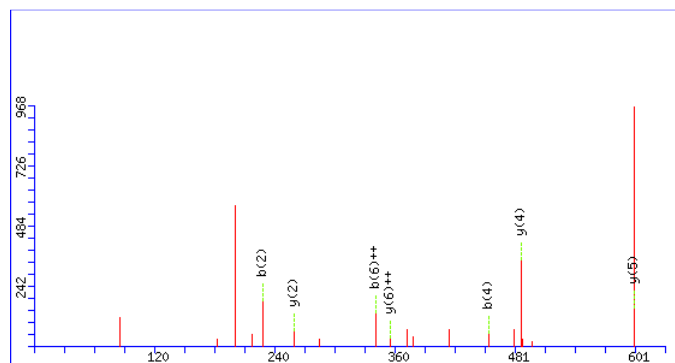
MS/MS Fragmentation of **DLLLDLK:**

Found in **IP100306457;IP100844416**

Title: 3.1.1.3270.2

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							7
2	229.1183	115.0628	0	0	211.1077	106.0575	L	714.4760	357.7416	697.4495	349.2284	696.4654	348.7364	6
3	342.2023	171.6048	0	0	324.1918	162.5995	L	601.3919	301.1996	584.3654	292.6863	583.3814	292.1943	5
4	455.2864	228.1468	0	0	437.2758	219.1416	L	488.3079	244.6576	471.2813	236.1443	470.2973	235.6523	4
5	570.3134	285.6603	0	0	552.3028	276.6550	D	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
6	683.3974	342.2023	0	0	665.3869	333.1971	L	260.1969	130.6021	243.1703	122.0888	0	0	2
7							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 46153.

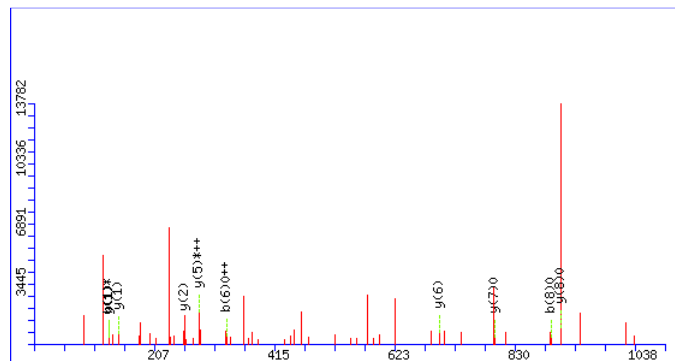
MS/MS Fragmentation of **QNNLLTVQLK: 0.984015@N:3**

Found in **IP100376439;IP100420061;IP100970801**

Title: 2.1.1.4014.7

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120206ry¥120206ry_aHDF1419-P10_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233	0	0	Q							10
2	243.1088	122.0580	226.0822	113.5448	0	0	N	1043.6095	522.3084	1026.5830	513.7951	1025.5990	513.3031	9
3	358.1357	179.5715	341.1092	171.0582	0	0	N	929.5666	465.2869	912.5401	456.7737	911.5560	456.2817	8
4	471.2198	236.1135	454.1932	227.6003	0	0	L	814.5397	407.7735	797.5131	399.2602	796.5291	398.7682	7
5	584.3039	292.6556	567.2773	284.1423	0	0	L	701.4556	351.2314	684.4291	342.7182	683.4450	342.2262	6
6	685.3515	343.1794	668.3250	334.6661	667.3410	334.1741	T	588.3715	294.6894	571.3450	286.1761	570.3610	285.6841	5
7	784.4199	392.7136	767.3934	384.2003	766.4094	383.7083	V	487.3239	244.1656	470.2973	235.6523	0	0	4
8	912.4785	456.7429	895.4520	448.2296	894.4680	447.7376	Q	388.2554	194.6314	371.2289	186.1181	0	0	3
9	1025.5626	513.2849	1008.5360	504.7717	1007.5520	504.2796	L	260.1969	130.6021	243.1703	122.0888	0	0	2
10							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 46276.

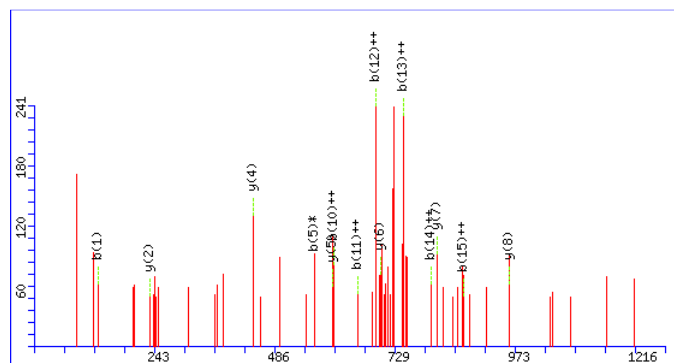
MS/MS Fragmentation of **KTEEP~~PR~~DFDPAL~~LE~~FLV~~C~~PLSK: 57.021465@C:19**

Found in **IP100063244**

Title: 4.1.1.1359.3

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120210ry¥120210ry_32R1-32_3.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	129.1022	65.0548	112.0757	56.5415	0	0	K							23
2	230.1499	115.5786	213.1234	107.0653	212.1394	106.5733	T	2573.2956	1287.1514	2556.2691	1278.6382	2555.2850	1278.1462	22
3	359.1925	180.0999	342.1660	171.5866	341.1819	171.0946	E	2472.2479	1236.6276	2455.2214	1228.1143	2454.2374	1227.6223	21
4	488.2351	244.6212	471.2086	236.1079	470.2245	235.6159	E	2343.2053	1172.1063	2326.1788	1163.5930	2325.1948	1163.1010	20
5	585.2879	293.1476	568.2613	284.6343	567.2773	284.1423	P	2214.1627	1107.5850	2197.1362	1099.0717	2196.1522	1098.5797	19
6	682.3406	341.6740	665.3141	333.1607	664.3301	332.6687	P	2117.1100	1059.0586	2100.0834	1050.5454	2099.0994	1050.0533	18
7	838.4417	419.7245	821.4152	411.2112	820.4312	410.7192	R	2020.0572	1010.5322	2003.0307	1002.0190	2002.0466	1001.5270	17
8	953.4687	477.2380	936.4421	468.7247	935.4581	468.2327	D	1863.9561	932.4817	1846.9296	923.9684	1845.9455	923.4764	16
9	1100.5371	550.7722	1083.5106	542.2589	1082.5265	541.7669	F	1748.9292	874.9682	1731.9026	866.4549	1730.9186	865.9629	15
10	1215.5640	608.2857	1198.5375	599.7724	1197.5535	599.2804	D	1601.8607	801.4340	1584.8342	792.9207	1583.8502	792.4287	14
11	1312.6168	656.8120	1295.5903	648.2988	1294.6062	647.8068	P	1486.8338	743.9205	1469.8073	735.4073	1468.8232	734.9153	13
12	1383.6539	692.3306	1366.6274	683.8173	1365.6434	683.3253	A	1389.7810	695.3942	1372.7545	686.8809	1371.7705	686.3889	12
13	1496.7380	748.8726	1479.7114	740.3594	1478.7274	739.8673	L	1318.7439	659.8756	1301.7174	651.3623	1300.7334	650.8703	11
14	1609.8220	805.4147	1592.7955	796.9014	1591.8115	796.4094	L	1205.6599	603.3336	1188.6333	594.8203	1187.6493	594.3283	10
15	1738.8646	869.9360	1721.8381	861.4227	1720.8541	860.9307	E	1092.5758	546.7915	1075.5492	538.2783	1074.5652	537.7863	9
16	1885.9331	943.4702	1868.9065	934.9569	1867.9225	934.4649	F	963.5332	482.2702	946.5067	473.7570	945.5226	473.2650	8
17	1999.0171	1000.0122	1981.9906	991.4989	1981.0066	991.0069	L	816.4648	408.7360	799.4382	400.2228	798.4542	399.7307	7
18	2098.0855	1049.5464	2081.0590	1041.0331	2080.0750	1040.5411	V	703.3807	352.1940	686.3542	343.6807	685.3702	343.1887	6
19	2258.1162	1129.5617	2241.0896	1121.0485	2240.1056	1120.5564	C	604.3123	302.6598	587.2858	294.1465	586.3017	293.6545	5
20	2355.1689	1178.0881	2338.1424	1169.5748	2337.1584	1169.0828	P	444.2817	222.6445	427.2551	214.1312	426.2711	213.6392	4
21	2468.2530	1234.6301	2451.2265	1226.1169	2450.2424	1225.6249	L	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
22	2555.2850	1278.1462	2538.2585	1269.6329	2537.2745	1269.1409	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
23							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 46345.

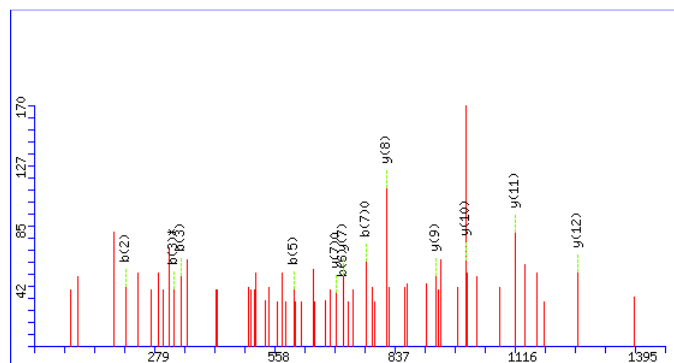
MS/MS Fragmentation of **NVEDFLALTGIESADK**:

Found in **IP100385712;IP100856089;IP101009207**

Title: 4.1.1.37.11

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							16
2	214.1188	107.5629	197.0921	99.0497	0	0	V	1607.8163	804.4118	1590.7897	795.8985	1589.8057	795.4065	15
3	343.1612	172.0842	326.1347	163.5710	325.1506	163.0790	E	1508.7479	754.8776	1491.7213	746.3643	1490.7373	745.8723	14
4	458.1882	229.5977	441.1616	221.0844	440.1776	220.5924	D	1379.7053	690.3563	1362.6787	681.8430	1361.6947	681.3510	13
5	605.2566	303.1319	588.2300	294.6186	587.2460	294.1266	F	1264.6783	632.8428	1247.6518	624.3295	1246.6678	623.8375	12
6	718.3406	359.6740	701.3141	351.1607	700.3301	350.6687	L	1117.6099	559.3086	1100.5834	550.7953	1099.5994	550.3033	11
7	789.3777	395.1925	772.3512	386.6792	771.3672	386.1872	A	1004.5259	502.7666	987.4993	494.2533	986.5153	493.7613	10
8	902.4618	451.7345	885.4353	443.2213	884.4512	442.7293	L	933.4888	467.2480	916.4622	458.7347	915.4782	458.2427	9
9	1003.5095	502.2584	986.4829	493.7451	985.4989	493.2531	T	820.4047	410.7060	803.3781	402.1927	802.3941	401.7007	8
10	1060.5310	530.7691	1043.5044	522.2558	1042.5204	521.7638	G	719.3570	360.1821	702.3305	351.6689	701.3464	351.1769	7
11	1173.6150	587.3111	1156.5885	578.7979	1155.6045	578.3059	I	662.3355	331.6714	645.3090	323.1581	644.3250	322.6661	6
12	1302.6576	651.8324	1285.6311	643.3192	1284.6470	642.8272	E	549.2515	275.1294	532.2249	266.6161	531.2409	266.1241	5
13	1389.6896	695.3485	1372.6631	686.8352	1371.6791	686.3432	S	420.2089	210.6081	403.1823	202.0948	402.1983	201.6028	4
14	1460.7268	730.8670	1443.7002	722.3537	1442.7162	721.8617	A	333.1769	167.0921	316.1503	158.5788	315.1663	158.0868	3
15	1575.7537	788.3805	1558.7271	779.8672	1557.7431	779.3752	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
16							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 46407.

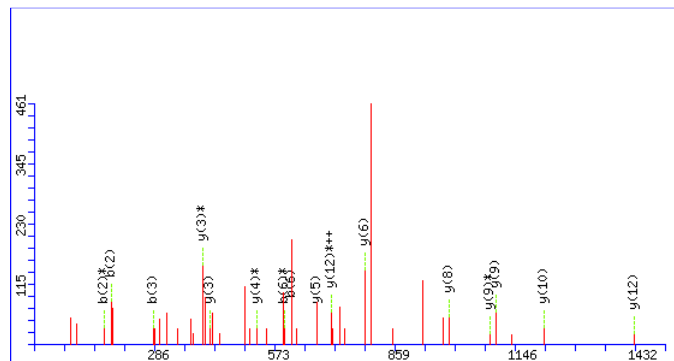
MS/MS Fragmentation of **ANVISELNSILQQMNR**:

Found in **IP100915354;IP100929746;IP100939371;IP100952742**

Title: 4.1.1.3577.2

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							16
2	186.0873	93.5473	169.0608	85.0340	0	0	N	1758.9167	879.9620	1741.8901	871.4487	1740.9061	870.9567	15
3	285.1557	143.0815	268.1292	134.5682	0	0	V	1644.8738	822.9405	1627.8472	814.4272	1626.8632	813.9352	14
4	398.2398	199.6235	381.2132	191.1103	0	0	I	1545.8054	773.4063	1528.7788	764.8930	1527.7948	764.4010	13
5	485.2718	243.1395	468.2453	234.6263	467.2613	234.1343	S	1432.7213	716.8643	1415.6947	708.3510	1414.7107	707.8590	12
6	614.3144	307.6608	597.2879	299.1476	596.3039	298.6556	E	1345.6893	673.3483	1328.6627	664.8350	1327.6787	664.3430	11
7	727.3985	364.2029	710.3719	355.6896	709.3879	355.1976	L	1216.6467	608.8270	1199.6201	600.3137	1198.6361	599.8217	10
8	841.4414	421.2243	824.4149	412.7111	823.4308	412.2191	N	1103.5626	552.2849	1086.5361	543.7717	1085.5520	543.2797	9
9	928.4734	464.7404	911.4469	456.2271	910.4629	455.7351	S	989.5197	495.2635	972.4931	486.7502	971.5091	486.2582	8
10	1041.5575	521.2824	1024.5309	512.7691	1023.5469	512.2771	I	902.4876	451.7475	885.4611	443.2342	0	0	7
11	1154.6416	577.8244	1137.6150	569.3111	1136.6310	568.8191	L	789.4036	395.2054	772.3770	386.6922	0	0	6
12	1282.7001	641.8537	1265.6736	633.3404	1264.6896	632.8484	Q	676.3195	338.6634	659.2930	330.1501	0	0	5
13	1410.7587	705.8830	1393.7322	697.3697	1392.7482	696.8777	Q	548.2609	274.6341	531.2344	266.1208	0	0	4
14	1541.7992	771.4032	1524.7727	762.8900	1523.7886	762.3980	M	420.2024	210.6048	403.1758	202.0915	0	0	3
15	1655.8421	828.4247	1638.8156	819.9114	1637.8316	819.4194	N	289.1619	145.0846	272.1353	136.5713	0	0	2
16							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 46962.

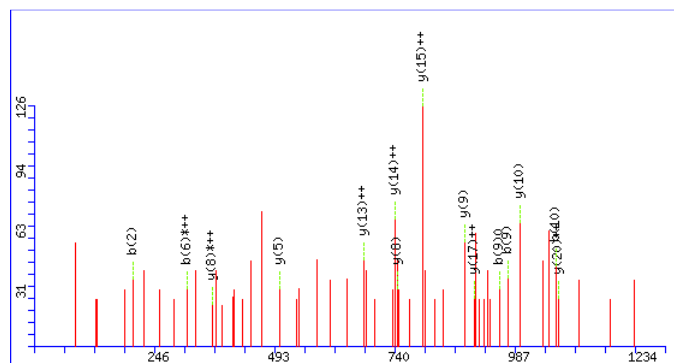
MS/MS Fragmentation of **AMSVEQLTDVLMNEILHGADGTSIK**:

Found in **IP100100933;IP100903152**

Title: 5.1.1.775.3

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3.5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							25
2	203.0849	102.0461	0	0	0	0	M	2601.2899	1301.1486	2584.2633	1292.6353	2583.2793	1292.1433	24
3	290.1169	145.5621	0	0	272.1063	136.5568	S	2470.2494	1235.6283	2453.2228	1227.1151	2452.2388	1226.6230	23
4	389.1853	195.0963	0	0	371.1748	186.0910	V	2383.2174	1192.1123	2366.1908	1183.5990	2365.2068	1183.1070	22
5	518.2279	259.6176	0	0	500.2173	250.6123	E	2284.1489	1142.5781	2267.1224	1134.0648	2266.1384	1133.5728	21
6	646.2865	323.6469	629.2599	315.1336	628.2759	314.6416	Q	2155.1063	1078.0568	2138.0798	1069.5435	2137.0958	1069.0515	20
7	759.3706	380.1889	742.3440	371.6756	741.3600	371.1836	L	2027.0478	1014.0275	2010.0212	1005.5142	2009.0372	1005.0222	19
8	860.4182	430.7128	843.3917	422.1995	842.4077	421.7075	T	1913.9637	957.4855	1896.9372	948.9722	1895.9531	948.4802	18
9	975.4452	488.2262	958.4186	479.7130	957.4346	479.2209	D	1812.9160	906.9617	1795.8895	898.4484	1794.9055	897.9564	17
10	1074.5138	537.7604	1057.4870	529.2472	1056.5030	528.7551	V	1697.8891	849.4482	1680.8625	840.9349	1679.8785	840.4429	16
11	1187.5977	594.3025	1170.5711	585.7892	1169.5871	585.2972	L	1598.8207	799.9140	1581.7941	791.4007	1580.8101	790.9087	15
12	1318.6381	659.8227	1301.6116	651.3094	1300.6276	650.8174	M	1485.7366	743.3719	1468.7101	734.8587	1467.7260	734.3667	14
13	1432.6811	716.8442	1415.6545	708.3309	1414.6705	707.8389	N	1354.6961	677.8517	1337.6696	669.3384	1336.6856	668.8464	13
14	1561.7237	781.3655	1544.6971	772.8522	1543.7131	772.3602	E	1240.6532	620.8302	1223.6266	612.3170	1222.6426	611.8250	12
15	1674.8077	837.9075	1657.7812	829.3942	1656.7972	828.9022	I	1111.6106	556.3089	1094.5841	547.7957	1093.6000	547.3037	11
16	1787.8918	894.4495	1770.8652	885.9363	1769.8812	885.4442	L	998.5265	499.7669	981.5000	491.2536	980.5160	490.7616	10
17	1924.9507	962.9790	1907.9241	954.4657	1906.9401	953.9737	H	885.4425	443.2249	868.4159	434.7116	867.4319	434.2196	9
18	1981.9722	991.4897	1964.9456	982.9764	1963.9616	982.4844	G	748.3836	374.6954	731.3570	366.1821	730.3730	365.6901	8
19	2053.0093	1027.0083	2035.9827	1018.4950	2034.9987	1018.0030	A	691.3621	346.1847	674.3355	337.6714	673.3515	337.1794	7
20	2168.0362	1084.5217	2151.0097	1076.0085	2150.0257	1075.5165	D	620.3250	310.6661	603.2984	302.1529	602.3144	301.6608	6
21	2225.0577	1113.0325	2208.0311	1104.5192	2207.0471	1104.0272	G	505.2980	253.1527	488.2715	244.6394	487.2875	244.1474	5
22	2326.1054	1163.5563	2309.0788	1155.0430	2308.0948	1154.5510	T	448.2766	224.6419	431.2500	216.1287	430.2660	215.6366	4
23	2413.1374	1207.0723	2396.1108	1198.5591	2395.1268	1198.0671	S	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
24	2526.2215	1263.6144	2509.1949	1255.1011	2508.2109	1254.6091	I	260.1969	130.6021	243.1703	122.0888	0	0	2
25							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 47153.

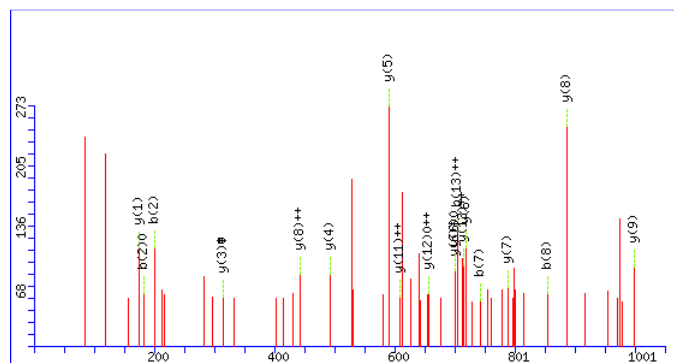
MS/MS Fragmentation of **VTLPDAFLPAQVCSAR**: 57.021465@C:13

Found in **IP100383396;IP100439694;IP100555659;IP100915836;IP100916010;IP100917201;IP100917317;IP100917846;IP100918016**

Title: 3.1.1.2073.2

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120208ry¥120208ry_Tig120slc-P8_3.3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							16
2	201.1234	101.0653	0	0	183.1128	92.0600	T	1645.8367	823.4220	1628.8101	814.9087	1627.8261	814.4167	15
3	314.2074	157.6074	0	0	296.1969	148.6021	L	1544.7890	772.8981	1527.7624	764.3849	1526.7784	763.8928	14
4	411.2602	206.1337	0	0	393.2496	197.1285	P	1431.7049	716.3561	1414.6784	707.8428	1413.6943	707.3508	13
5	526.2871	263.6472	0	0	508.2766	254.6419	D	1334.6521	667.8297	1317.6256	659.3164	1316.6416	658.8244	12
6	597.3243	299.1658	0	0	579.3137	290.1605	A	1219.6252	610.3162	1202.5987	601.8030	1201.6146	601.3110	11
7	744.3927	372.7000	0	0	726.3821	363.6947	F	1148.5881	574.7977	1131.5615	566.2844	1130.5775	565.7924	10
8	857.4767	429.2420	0	0	839.4662	420.2367	L	1001.5197	501.2635	984.4931	492.7502	983.5091	492.2582	9
9	954.5295	477.7684	0	0	936.5189	468.7631	P	888.4356	444.7214	871.4091	436.2082	870.4250	435.7162	8
10	1025.5666	513.2869	0	0	1007.5560	504.2817	A	791.3828	396.1951	774.3563	387.6818	773.3723	387.1898	7
11	1153.6252	577.3162	1136.5986	568.8030	1135.6146	568.3109	Q	720.3457	360.6765	703.3192	352.1632	702.3352	351.6712	6
12	1252.6936	626.8504	1235.6671	618.3372	1234.6830	617.8452	V	592.2872	296.6472	575.2606	288.1339	574.2766	287.6419	5
13	1412.7243	706.8658	1395.6977	698.3525	1394.7137	697.8605	C	493.2187	247.1130	476.1922	238.5997	475.2082	238.1077	4
14	1499.7563	750.3818	1482.7297	741.8685	1481.7457	741.3765	S	333.1881	167.0977	316.1615	158.5844	315.1775	158.0924	3
15	1570.7934	785.9003	1553.7668	777.3871	1552.7828	776.8951	A	246.1561	123.5817	229.1295	115.0684	0	0	2
16							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 47230.

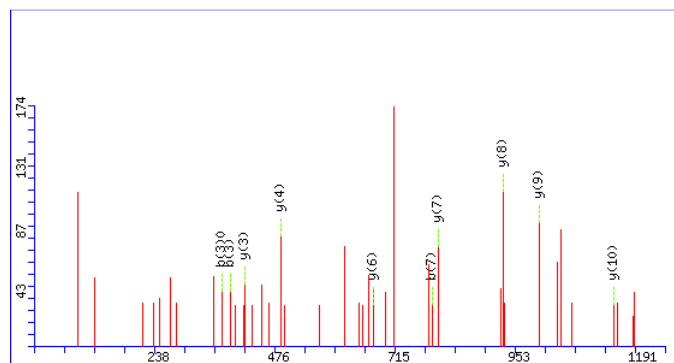
MS/MS Fragmentation of EIFAQEALAPFR:

Found in IP100168603

Title: 3.1.1.2461.8

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							12
2	243.1339	122.0706	0	0	225.1234	113.0653	I	1262.6892	631.8482	1245.6626	623.3350	1244.6786	622.8429	11
3	390.2023	195.6048	0	0	372.1918	186.5995	F	1149.6051	575.3062	1132.5786	566.7929	1131.5946	566.3009	10
4	461.2395	231.1234	0	0	443.2289	222.1181	A	1002.5367	501.7720	985.5102	493.2587	984.5261	492.7667	9
5	589.2980	295.1527	572.2715	286.6394	571.2875	286.1474	Q	931.4996	466.2534	914.4730	457.7402	913.4890	457.2482	8
6	718.3406	359.6740	701.3141	351.1607	700.3301	350.6687	E	803.4410	402.2241	786.4145	393.7109	785.4305	393.2189	7
7	789.3777	395.1925	772.3512	386.6792	771.3672	386.1872	A	674.3984	337.7028	657.3719	329.1896	0	0	6
8	902.4618	451.7345	885.4353	443.2213	884.4512	442.7293	L	603.3613	302.1843	586.3348	293.6710	0	0	5
9	973.4989	487.2531	956.4724	478.7398	955.4884	478.2478	A	490.2772	245.6423	473.2507	237.1290	0	0	4
10	1070.5517	535.7795	1053.5251	527.2662	1052.5411	526.7742	P	419.2401	210.1237	402.2136	201.6104	0	0	3
11	1217.6201	609.3137	1200.5936	600.8004	1199.6095	600.3084	F	322.1874	161.5973	305.1608	153.0840	0	0	2
12							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 47292.

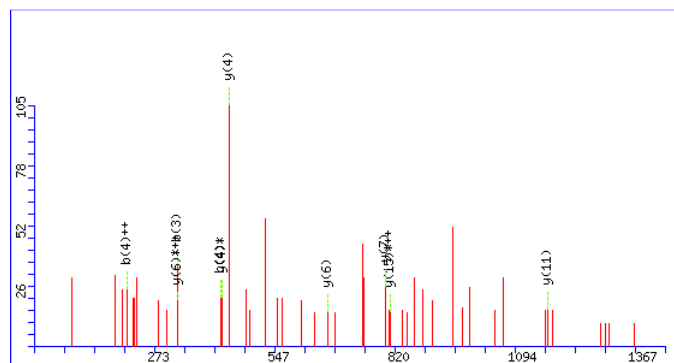
MS/MS Fragmentation of **VLLVSPELQAAVEEILPSLK**:

Found in **IP100024787;IP100447606**

Title: 5.1.1.496.3

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							20
2	213.1598	107.0835	0	0	0	0	L	2049.1842	1025.0957	2032.1576	1016.5825	2031.1736	1016.0904	19
3	326.2438	163.6255	0	0	0	0	L	1936.1001	968.5537	1919.0736	960.0404	1918.0896	959.5484	18
4	425.3122	213.1598	0	0	0	0	V	1823.0161	912.0117	1805.9895	903.4984	1805.0055	903.0064	17
5	512.3443	256.6758	0	0	494.3337	247.6705	S	1723.9476	862.4775	1706.9211	853.9642	1705.9371	853.4722	16
6	609.3970	305.2022	0	0	591.3865	296.1969	P	1636.9156	818.9614	1619.8891	810.4482	1618.9051	809.9562	15
7	738.4396	369.7234	0	0	720.4291	360.7182	E	1539.8629	770.4351	1522.8363	761.9218	1521.8523	761.4298	14
8	851.5237	426.2655	0	0	833.5131	417.2602	L	1410.8203	705.9138	1393.7937	697.4005	1392.8097	696.9085	13
9	979.5823	490.2948	962.5557	481.7815	961.5717	481.2895	Q	1297.7362	649.3717	1280.7096	640.8585	1279.7256	640.3665	12
10	1050.6194	525.8133	1033.5928	517.3000	1032.6088	516.8080	A	1169.6776	585.3424	1152.6511	576.8292	1151.6671	576.3372	11
11	1121.6565	561.3319	1104.6299	552.8186	1103.6459	552.3266	A	1098.6405	549.8239	1081.6140	541.3106	1080.6299	540.8186	10
12	1220.7249	610.8661	1203.6984	602.3528	1202.7143	601.8608	V	1027.6034	514.3053	1010.5768	505.7921	1009.5928	505.3000	9
13	1349.7675	675.3874	1332.7409	666.8741	1331.7569	666.3821	E	928.5350	464.7711	911.5084	456.2579	910.5244	455.7658	8
14	1478.8101	739.9087	1461.7835	731.3954	1460.7995	730.9034	E	799.4924	400.2498	782.4658	391.7366	781.4818	391.2445	7
15	1591.8942	796.4507	1574.8676	787.9374	1573.8836	787.4454	I	670.4498	335.7285	653.4232	327.2153	652.4392	326.7232	6
16	1704.9782	852.9927	1687.9517	844.4795	1686.9677	843.9875	L	557.3657	279.1865	540.3392	270.6732	539.3552	270.1812	5
17	1802.0310	901.5191	1785.0044	893.0059	1784.0204	892.5138	P	444.2817	222.6445	427.2551	214.1312	426.2711	213.6392	4
18	1889.0630	945.0351	1872.0365	936.5219	1871.0524	936.0299	S	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
19	2002.1471	1001.5772	1985.1205	993.0639	1984.1365	992.5719	L	260.1969	130.6021	243.1703	122.0888	0	0	2
20							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 47424.

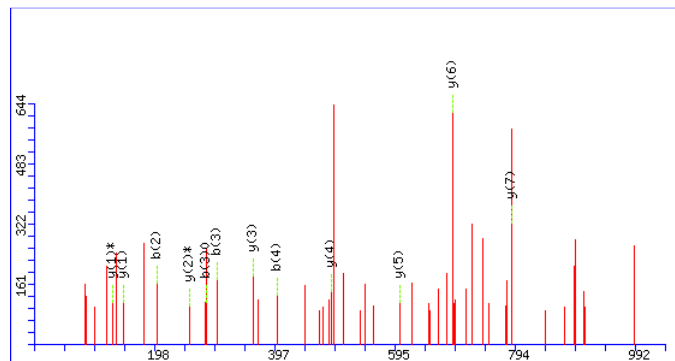
MS/MS Fragmentation of **DSVVSLESQK**:

Found in **IP100304493**

Title: 1.1.1.9353.9

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							10
2	203.0662	102.0368	0	0	185.0557	93.0315	S	976.5310	488.7691	959.5044	480.2558	958.5204	479.7638	9
3	302.1347	151.5710	0	0	284.1241	142.5657	V	889.4989	445.2531	872.4724	436.7398	871.4884	436.2478	8
4	401.2031	201.1052	0	0	383.1925	192.0999	V	790.4305	395.7189	773.4040	387.2056	772.4199	386.7136	7
5	488.2351	244.6212	0	0	470.2245	235.6159	S	691.3621	346.1847	674.3355	337.6714	673.3515	337.1794	6
6	601.3192	301.1632	0	0	583.3086	292.1579	L	604.3301	302.6687	587.3035	294.1554	586.3195	293.6634	5
7	730.3618	365.6845	0	0	712.3512	356.6792	E	491.2460	246.1266	474.2195	237.6134	473.2354	237.1214	4
8	817.3938	409.2005	0	0	799.3832	400.1952	S	362.2034	181.6053	345.1769	173.0921	344.1928	172.6001	3
9	945.4524	473.2298	928.4258	464.7165	927.4418	464.2245	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
10							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 47602.

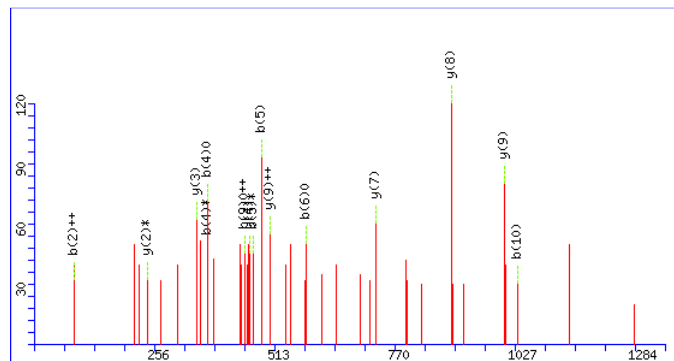
MS/MS Fragmentation of **DGTNVLYSALISLK**:

Found in **IP100016855;IP100642878;IP100871830;IP100913945;IP101013838**

Title: 4.1.1.730.3

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							14
2	173.0557	87.0315	0	0	155.0451	78.0262	G	1378.7940	689.9007	1361.7675	681.3874	1360.7835	680.8954	13
3	274.1034	137.5553	0	0	256.0928	128.5500	T	1321.7726	661.3899	1304.7460	652.8767	1303.7620	652.3846	12
4	388.1463	194.5768	371.1197	186.0635	370.1357	185.5715	N	1220.7249	610.8661	1203.6984	602.3528	1202.7143	601.8608	11
5	487.2147	244.1110	470.1882	235.5977	469.2041	235.1057	V	1106.6820	553.8446	1089.6554	545.3313	1088.6714	544.8393	10
6	600.2988	300.6530	583.2722	292.1397	582.2882	291.6477	L	1007.6136	504.3104	990.5870	495.7971	989.6030	495.3051	9
7	763.3621	382.1847	746.3355	373.6714	745.3515	373.1794	Y	894.5295	447.7684	877.5029	439.2551	876.5189	438.7631	8
8	850.3941	425.7007	833.3676	417.1874	832.3836	416.6954	S	731.4662	366.2367	714.4396	357.7234	713.4556	357.2314	7
9	921.4312	461.2193	904.4047	452.7060	903.4207	452.2140	A	644.4341	322.7207	627.4076	314.2074	626.4236	313.7154	6
10	1034.5153	517.7613	1017.4888	509.2480	1016.5047	508.7560	L	573.3970	287.2021	556.3705	278.6889	555.3865	278.1969	5
11	1147.5994	574.3033	1130.5728	565.7900	1129.5888	565.2980	I	460.3130	230.6601	443.2864	222.1468	442.3024	221.6548	4
12	1234.6314	617.8193	1217.6048	609.3061	1216.6208	608.8141	S	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
13	1347.7155	674.3614	1330.6889	665.8481	1329.7049	665.3561	L	260.1969	130.6021	243.1703	122.0888	0	0	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 47656.

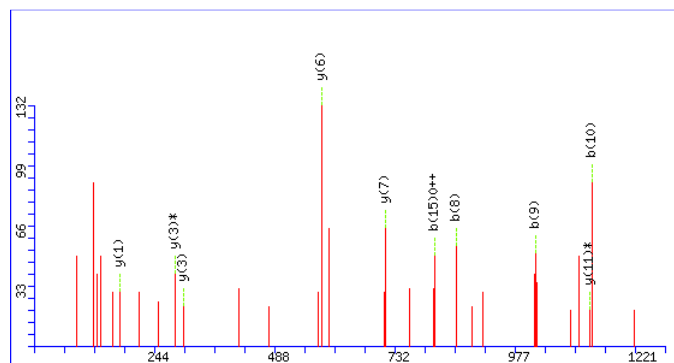
MS/MS Fragmentation of **LPDDCTVGIVYEGLLGAR: 57.021465@C:5**

Found in **IP100001793:IP101012125**

Title: 4.1.1.3549.2

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							18
2	211.1441	106.0757	0	0	0	0	P	1834.9004	917.9538	1817.8738	909.4406	1816.8898	908.9485	17
3	326.1710	163.5892	0	0	308.1605	154.5839	D	1737.8476	869.4274	1720.8211	860.9142	1719.8371	860.4222	16
4	441.1980	221.1026	0	0	423.1874	212.0974	D	1622.8207	811.9140	1605.7941	803.4007	1604.8101	802.9087	15
5	601.2286	301.1180	0	0	583.2181	292.1127	C	1507.7937	754.4005	1490.7672	745.8872	1489.7832	745.3952	14
6	702.2763	351.6418	0	0	684.2658	342.6365	T	1347.7631	674.3852	1330.7365	665.8719	1329.7525	665.3799	13
7	801.3447	401.1760	0	0	783.3342	392.1707	V	1246.7154	623.8613	1229.6889	615.3481	1228.7048	614.8561	12
8	858.3662	429.6867	0	0	840.3556	420.6815	G	1147.6470	574.3271	1130.6204	565.8139	1129.6364	565.3218	11
9	1021.4295	511.2184	0	0	1003.4190	502.2131	Y	1090.6255	545.8164	1073.5990	537.3031	1072.6150	536.8111	10
10	1134.5136	567.7604	0	0	1116.5030	558.7552	I	927.5622	464.2847	910.5356	455.7715	909.5516	455.2795	9
11	1233.5820	617.2946	0	0	1215.5714	608.2894	V	814.4781	407.7427	797.4516	399.2294	796.4676	398.7374	8
12	1362.6246	681.8159	0	0	1344.6140	672.8107	E	715.4097	358.2085	698.3832	349.6952	697.3992	349.2032	7
13	1419.6461	710.3267	0	0	1401.6355	701.3214	G	586.3671	293.6872	569.3406	285.1739	0	0	6
14	1532.7301	766.8687	0	0	1514.7196	757.8634	L	529.3457	265.1765	512.3191	256.6632	0	0	5
15	1645.8142	823.4107	0	0	1627.8036	814.4055	L	416.2616	208.6344	399.2350	200.1212	0	0	4
16	1702.8357	851.9215	0	0	1684.8251	842.9162	G	303.1775	152.0924	286.1510	143.5791	0	0	3
17	1773.8728	887.4400	0	0	1755.8622	878.4347	A	246.1561	123.5817	229.1295	115.0684	0	0	2
18							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 47740.

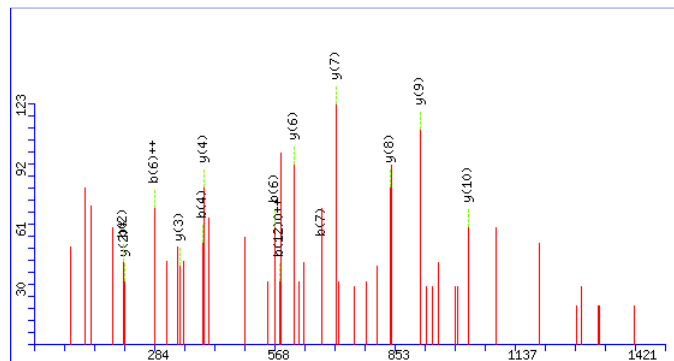
MS/MS Fragmentation of **VLGEAVLPFSPALAEVTLGIGR**:

Found in **IP100005277;IP101011920**

Title: 4.1.1.2911.6

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120212ry¥120212ry_414C2-43_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							22
2	213.1598	107.0835	0	0	0	0	L	2110.1907	1055.5990	2093.1641	1047.0857	2092.1801	1046.5937	21
3	270.1812	135.5942	0	0	0	0	G	1997.1066	999.0569	1980.0801	990.5437	1979.0960	990.0517	20
4	399.2238	200.1155	0	0	381.2132	191.1103	E	1940.0851	970.5462	1923.0586	962.0329	1922.0746	961.5409	19
5	470.2609	235.6341	0	0	452.2504	226.6288	A	1811.0425	906.0249	1794.0160	897.5116	1793.0320	897.0196	18
6	569.3293	285.1683	0	0	551.3188	276.1630	V	1740.0054	870.5064	1722.9789	861.9931	1721.9949	861.5011	17
7	682.4134	341.7103	0	0	664.4028	332.7051	L	1640.9370	820.9721	1623.9105	812.4589	1622.9265	811.9669	16
8	779.4662	390.2367	0	0	761.4556	381.2314	P	1527.8530	764.4301	1510.8264	755.9168	1509.8424	755.4248	15
9	926.5346	463.7709	0	0	908.5240	454.7656	F	1430.8002	715.9037	1413.7736	707.3905	1412.7896	706.8985	14
10	1013.5666	507.2869	0	0	995.5560	498.2817	S	1283.7318	642.3695	1266.7052	633.8563	1265.7212	633.3642	13
11	1110.6194	555.8133	0	0	1092.6088	546.8080	P	1196.6997	598.8535	1179.6732	590.3402	1178.6892	589.8482	12
12	1181.6565	591.3319	0	0	1163.6459	582.3266	A	1099.6470	550.3271	1082.6204	541.8139	1081.6364	541.3218	11
13	1294.7406	647.8739	0	0	1276.7300	638.8686	L	1028.6099	514.8086	1011.5833	506.2953	1010.5993	505.8033	10
14	1365.7777	683.3925	0	0	1347.7671	674.3872	A	915.5258	458.2665	898.4993	449.7533	897.5152	449.2613	9
15	1494.8203	747.9138	0	0	1476.8097	738.9085	E	844.4887	422.7480	827.4621	414.2347	826.4781	413.7427	8
16	1593.8887	797.4480	0	0	1575.8781	788.4427	V	715.4461	358.2267	698.4196	349.7134	697.4355	349.2214	7
17	1694.9364	847.9718	0	0	1676.9258	838.9665	T	616.3777	308.6925	599.3511	300.1792	598.3671	299.6872	6
18	1808.0204	904.5138	0	0	1790.0099	895.5086	L	515.3300	258.1686	498.3035	249.6554	0	0	5
19	1865.0419	933.0246	0	0	1847.0313	924.0193	G	402.2459	201.6266	385.2194	193.1133	0	0	4
20	1978.1259	989.5666	0	0	1960.1154	980.5613	I	345.2245	173.1159	328.1979	164.6026	0	0	3
21	2035.1474	1018.0773	0	0	2017.1368	1009.0721	G	232.1404	116.5738	215.1139	108.0606	0	0	2
22							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 48276.

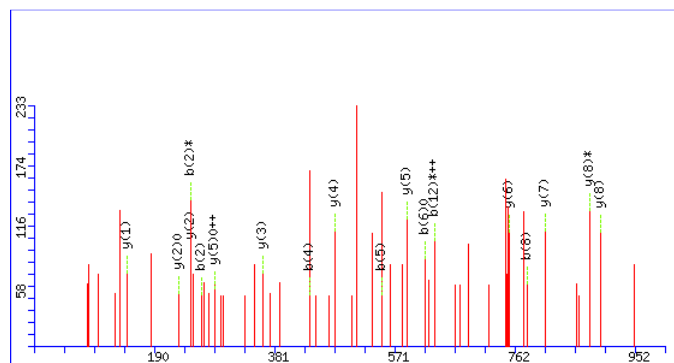
MS/MS Fragmentation of **HQGDLSGGYLDLDTK**:

Found in **IP100009146**

Title: 2.1.1.304.10

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	138.0662	69.5367	0	0	0	0	H							14
2	266.1248	133.5660	249.0982	125.0527	0	0	Q	1398.6383	699.8228	1381.6118	691.3095	1380.6278	690.8175	13
3	323.1462	162.0768	306.1197	153.5635	0	0	G	1270.5798	635.7935	1253.5532	627.2802	1252.5692	626.7882	12
4	438.1732	219.5902	421.1466	211.0769	420.1626	210.5849	D	1213.5583	607.2828	1196.5317	598.7695	1195.5477	598.2775	11
5	551.2572	276.1323	534.2307	267.6190	533.2467	267.1270	L	1098.5313	549.7693	1081.5048	541.2560	1080.5208	540.7640	10
6	638.2893	319.6483	621.2627	311.1350	620.2787	310.6430	S	985.4473	493.2273	968.4207	484.7140	967.4367	484.2220	9
7	725.3213	363.1643	708.2947	354.6510	707.3107	354.1590	S	898.4153	449.7113	881.3887	441.1980	880.4047	440.7060	8
8	782.3428	391.6750	765.3162	383.1617	764.3322	382.6697	G	811.3832	406.1953	794.3567	397.6820	793.3727	397.1900	7
9	945.4061	473.2067	928.3795	464.6934	927.3955	464.2014	Y	754.3618	377.6845	737.3352	369.1712	736.3512	368.6792	6
10	1058.4902	529.7487	1041.4636	521.2354	1040.4796	520.7434	L	591.2984	296.1529	574.2719	287.6396	573.2879	287.1476	5
11	1173.5171	587.2622	1156.4905	578.7489	1155.5065	578.2569	D	478.2144	239.6108	461.1878	231.0975	460.2038	230.6055	4
12	1288.5440	644.7757	1271.5175	636.2624	1270.5335	635.7704	D	363.1874	182.0974	346.1609	173.5841	345.1769	173.0921	3
13	1389.5917	695.2995	1372.5652	686.7862	1371.5812	686.2942	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 48542.

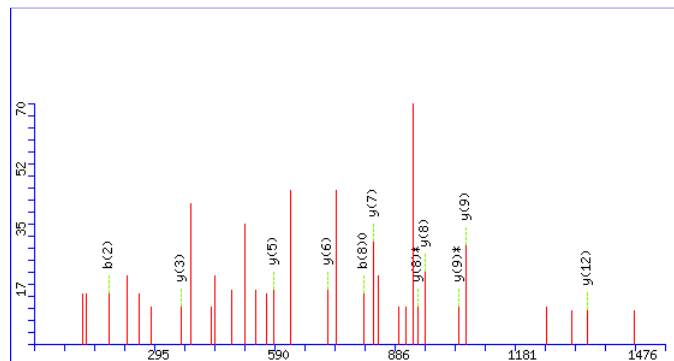
MS/MS Fragmentation of **QGTNEINALVQLMTQTLK**:

Found in **IP100021333;IP100440811;IP100946811**

Title: 4.1.1.4195.2

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120210ry¥120210ry_585A1-55_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							18
2	186.0873	93.5473	169.0608	85.0340	0	0	Q	1945.0423	973.0248	1928.0157	964.5115	1927.0317	964.0195	17
3	287.1350	144.0711	270.1084	135.5579	269.1244	135.0659	T	1816.9837	908.9955	1799.9572	900.4822	1798.9731	899.9902	16
4	401.1779	201.0926	384.1514	192.5793	383.1674	192.0873	N	1715.9360	858.4717	1698.9095	849.9584	1697.9255	849.4664	15
5	530.2205	265.6139	513.1940	257.1006	512.2100	256.6086	E	1601.8931	801.4502	1584.8666	792.9369	1583.8825	792.4449	14
6	643.3046	322.1559	626.2780	313.6427	625.2940	313.1506	I	1472.8505	736.9289	1455.8240	728.4156	1454.8399	727.9236	13
7	757.3475	379.1774	740.3210	370.6641	739.3369	370.1721	N	1359.7664	680.3869	1342.7399	671.8736	1341.7559	671.3816	12
8	828.3846	414.6959	811.3581	406.1827	810.3741	405.6907	A	1245.7235	623.3654	1228.6970	614.8521	1227.7130	614.3601	11
9	941.4687	471.2380	924.4421	462.7247	923.4581	462.2327	L	1174.6864	587.8468	1157.6599	579.3336	1156.6758	578.8416	10
10	1040.5371	520.7722	1023.5106	512.2589	1022.5265	511.7669	V	1061.6023	531.3048	1044.5758	522.7915	1043.5918	522.2995	9
11	1168.5957	584.8015	1151.5691	576.2882	1150.5851	575.7962	Q	962.5339	481.7706	945.5074	473.2573	944.5234	472.7653	8
12	1281.6797	641.3435	1264.6532	632.8302	1263.6692	632.3382	L	834.4754	417.7413	817.4488	409.2280	816.4648	408.7360	7
13	1412.7202	706.8638	1395.6937	698.3505	1394.7097	697.8585	M	721.3913	361.1993	704.3647	352.6860	703.3807	352.1940	6
14	1513.7679	757.3876	1496.7414	748.8743	1495.7573	748.3823	T	590.3508	295.6790	573.3243	287.1658	572.3402	286.6738	5
15	1641.8265	821.4169	1624.7999	812.9036	1623.8159	812.4116	Q	489.3031	245.1552	472.2766	236.6419	471.2926	236.1499	4
16	1742.8742	871.9407	1725.8476	863.4274	1724.8636	862.9354	T	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
17	1855.9582	928.4828	1838.9317	919.9695	1837.9477	919.4775	L	260.1969	130.6021	243.1703	122.0888	0	0	2
18							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 48614.

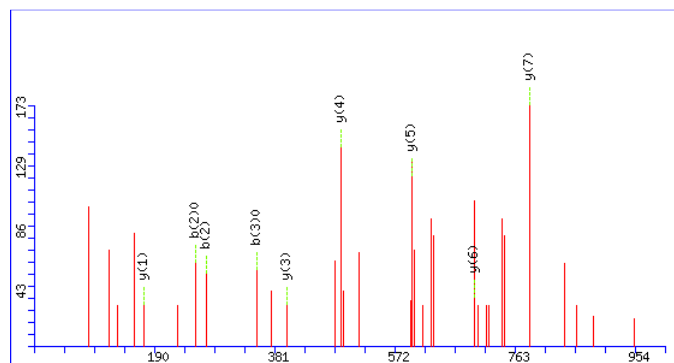
MS/MS Fragmentation of **WSVISLLR**:

Found in **IP100413289;IP100737059;IP100924837**

Title: 3.1.1.4108.2

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	187.0866	94.0469	0	0	0	0	W							8
2	274.1186	137.5629	0	0	256.1081	128.5577	S	787.5036	394.2554	770.4771	385.7422	769.4930	385.2502	7
3	373.1870	187.0972	0	0	355.1765	178.0919	V	700.4716	350.7394	683.4450	342.2262	682.4610	341.7341	6
4	486.2711	243.6392	0	0	468.2605	234.6339	I	601.4032	301.2052	584.3766	292.6919	583.3926	292.1999	5
5	573.3031	287.1552	0	0	555.2926	278.1499	S	488.3191	244.6632	471.2926	236.1499	470.3085	235.6579	4
6	686.3872	343.6972	0	0	668.3766	334.6919	L	401.2871	201.1472	384.2605	192.6339	0	0	3
7	799.4713	400.2393	0	0	781.4607	391.2340	L	288.2030	144.6051	271.1765	136.0919	0	0	2
8							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 48660.

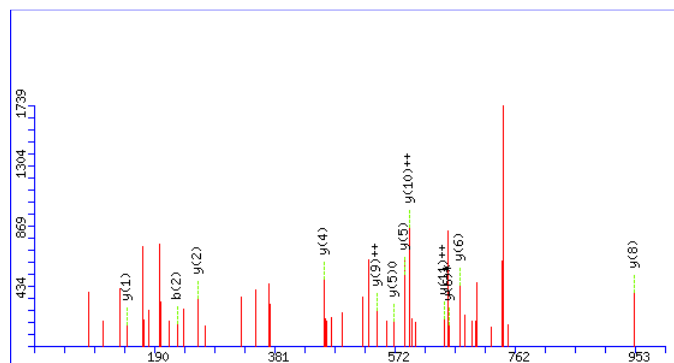
MS/MS Fragmentation of **NIVHNYSEAEIK**:

Found in **IP100027082;IP100300584;IP100386833;IP100397365;IP100647389;IP100910899;IP100966075;IP100966413;IP100968262;IP101012091**

Title: 2.1.1.394.5

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							12
2	228.1343	114.5708	211.1077	106.0575	0	0	I	1302.6688	651.8381	1285.6423	643.3248	1284.6583	642.8328	11
3	327.2027	164.1050	310.1761	155.5917	0	0	V	1189.5848	595.2960	1172.5582	586.7828	1171.5742	586.2907	10
4	464.2616	232.6344	447.2350	224.1212	0	0	H	1090.5164	545.7618	1073.4898	537.2485	1072.5058	536.7565	9
5	578.3045	289.6559	561.2780	281.1426	0	0	N	953.4575	477.2324	936.4309	468.7191	935.4469	468.2271	8
6	741.3678	371.1876	724.3413	362.6743	0	0	Y	839.4145	420.2109	822.3880	411.6976	821.4040	411.2056	7
7	828.3999	414.7036	811.3733	406.1903	810.3893	405.6983	S	676.3512	338.6792	659.3246	330.1660	658.3406	329.6740	6
8	957.4425	479.2249	940.4159	470.7116	939.4319	470.2196	E	589.3192	295.1632	572.2926	286.6499	571.3086	286.1579	5
9	1028.4796	514.7434	1011.4530	506.2302	1010.4690	505.7381	A	460.2766	230.6419	443.2500	222.1287	442.2660	221.6366	4
10	1157.5222	579.2647	1140.4956	570.7515	1139.5116	570.2594	E	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
11	1270.6062	635.8068	1253.5797	627.2935	1252.5957	626.8015	I	260.1969	130.6021	243.1703	122.0888	0	0	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 48974.

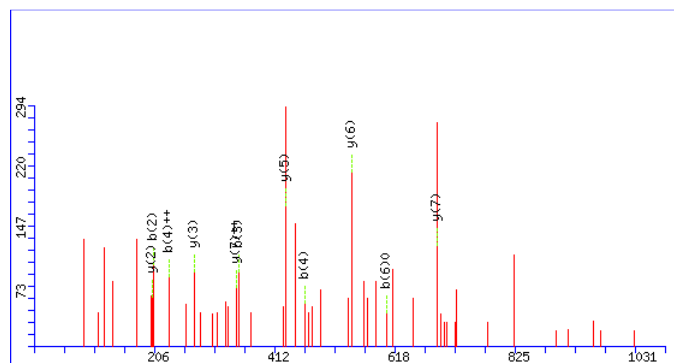
MS/MS Fragmentation of **GFFLSAAGK**:

Found in **IP100451941;IP100657943;IP100658061;IP100894217;IP100940410**

Title: 2.1.1.3211.3

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							9
2	205.0972	103.0522	0	0	0	0	F	840.4614	420.7343	823.4349	412.2211	822.4509	411.7291	8
3	352.1656	176.5864	0	0	0	0	F	693.3930	347.2001	676.3665	338.6869	675.3824	338.1949	7
4	465.2496	233.1285	0	0	0	0	L	546.3246	273.6659	529.2980	265.1527	528.3140	264.6606	6
5	552.2817	276.6445	0	0	534.2711	267.6392	S	433.2405	217.1239	416.2140	208.6106	415.2300	208.1186	5
6	623.3188	312.1630	0	0	605.3082	303.1577	A	346.2085	173.6079	329.1819	165.0946	0	0	4
7	694.3559	347.6816	0	0	676.3453	338.6763	A	275.1714	138.0893	258.1448	129.5761	0	0	3
8	751.3774	376.1923	0	0	733.3668	367.1870	G	204.1343	102.5708	187.1077	94.0575	0	0	2
9							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 49376.

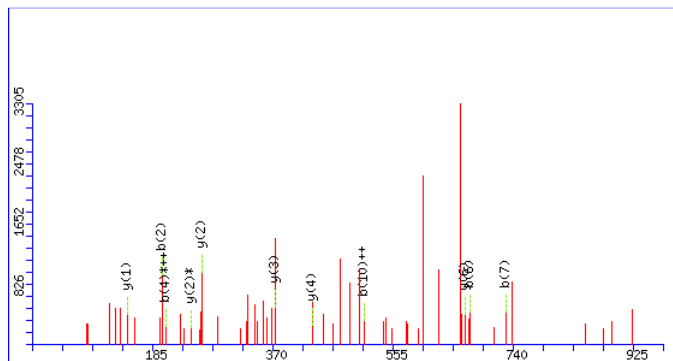
MS/MS Fragmentation of **LSQTMLGHVGLNK: 0.984015@N:12**

Found in **IP100217833;IP100219721**

Title: 3.1.1.267.3

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120212ry¥120212ry_aHDF1388-P9_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							13
2	201.1234	101.0653	0	0	183.1128	92.0600	S	1285.6569	643.3321	1268.6303	634.8188	1267.6463	634.3268	12
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	Q	1198.6249	599.8161	1181.5983	591.3028	1180.6143	590.8108	11
4	430.2296	215.6185	413.2031	207.1052	412.2191	206.6132	T	1070.5663	535.7868	1053.5397	527.2735	1052.5557	526.7815	10
5	561.2701	281.1387	544.2436	272.6254	543.2595	272.1334	M	969.5186	485.2629	952.4921	476.7497	0	0	9
6	674.3542	337.6807	657.3276	329.1675	656.3436	328.6754	L	838.4781	419.7427	821.4516	411.2294	0	0	8
7	731.3756	366.1915	714.3491	357.6782	713.3651	357.1862	G	725.3941	363.2007	708.3675	354.6874	0	0	7
8	868.4346	434.7209	851.4080	426.2076	850.4240	425.7156	H	668.3726	334.6899	651.3461	326.1767	0	0	6
9	967.5030	484.2551	950.4764	475.7418	949.4924	475.2498	V	531.3137	266.1605	514.2871	257.6472	0	0	5
10	1024.5244	512.7659	1007.4979	504.2526	1006.5139	503.7606	G	432.2453	216.6263	415.2187	208.1130	0	0	4
11	1137.6085	569.3079	1120.5819	560.7946	1119.5979	560.3026	L	375.2238	188.1155	358.1973	179.6023	0	0	3
12	1252.6354	626.8214	1235.6089	618.3081	1234.6249	617.8161	N	262.1397	131.5735	245.1132	123.0602	0	0	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 49422.

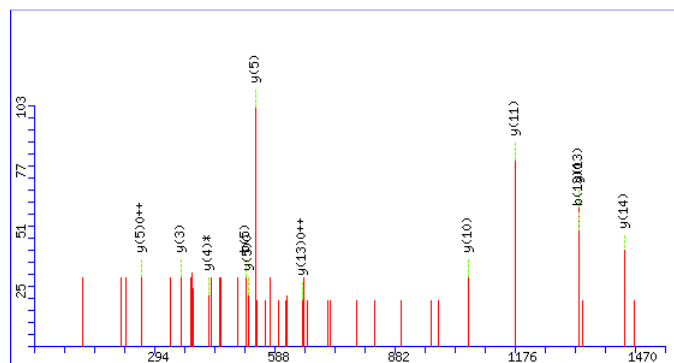
MS/MS Fragmentation of **GLSDFLGVISDTFAPSPDK**:

Found in **IPI00018026;IPI00414093;IPI00844452;IPI00844524;IPI00910328;IPI00941916;IPI00984538**

Title: 4.1.1.3446.11

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							19
2	171.1128	86.0600	0	0	0	0	L	1908.9589	954.9831	1891.9324	946.4698	1890.9484	945.9778	18
3	258.1448	129.5761	0	0	240.1343	120.5708	S	1795.8749	898.4411	1778.8483	889.9278	1777.8643	889.4358	17
4	373.1718	187.0895	0	0	355.1612	178.0842	D	1708.8428	854.9251	1691.8163	846.4118	1690.8323	845.9198	16
5	520.2402	260.6237	0	0	502.2296	251.6185	F	1593.8159	797.4116	1576.7894	788.8983	1575.8053	788.4063	15
6	633.3243	317.1658	0	0	615.3137	308.1605	L	1446.7475	723.8774	1429.7209	715.3641	1428.7369	714.8721	14
7	690.3457	345.6765	0	0	672.3352	336.6712	G	1333.6634	667.3353	1316.6369	658.8221	1315.6529	658.3301	13
8	789.4141	395.2107	0	0	771.4036	386.2054	V	1276.6420	638.8246	1259.6154	630.3113	1258.6314	629.8193	12
9	902.4982	451.7527	0	0	884.4876	442.7475	I	1177.5735	589.2904	1160.5470	580.7771	1159.5630	580.2851	11
10	989.5302	495.2687	0	0	971.5197	486.2635	S	1064.4895	532.7484	1047.4629	524.2351	1046.4789	523.7431	10
11	1104.5572	552.7822	0	0	1086.5466	543.7769	D	977.4575	489.2324	960.4309	480.7191	959.4469	480.2271	9
12	1205.6048	603.3061	0	0	1187.5943	594.3008	T	862.4305	431.7189	845.4040	423.2056	844.4199	422.7136	8
13	1352.6733	676.8403	0	0	1334.6627	667.8350	F	761.3828	381.1951	744.3563	372.6818	743.3723	372.1898	7
14	1423.7104	712.3588	0	0	1405.6998	703.3535	A	614.3144	307.6608	597.2879	299.1476	596.3039	298.6556	6
15	1520.7631	760.8852	0	0	1502.7526	751.8799	P	543.2773	272.1423	526.2508	263.6290	525.2667	263.1370	5
16	1607.7952	804.4012	0	0	1589.7846	795.3959	S	446.2245	223.6159	429.1980	215.1026	428.2140	214.6106	4
17	1704.8479	852.9276	0	0	1686.8374	843.9223	P	359.1925	180.0999	342.1660	171.5866	341.1819	171.0946	3
18	1819.8749	910.4411	0	0	1801.8643	901.4358	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
19							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 49620.

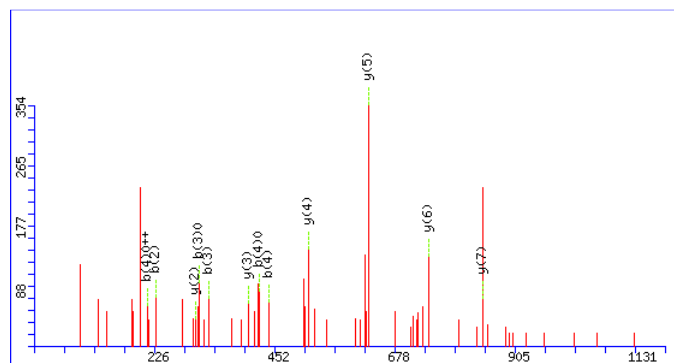
MS/MS Fragmentation of **DLTLILTER**:

Found in **IP100514190**

Title: 3.1.1.1360.3

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							9
2	229.1183	115.0628	0	0	211.1077	106.0575	L	958.5932	479.8002	941.5666	471.2869	940.5826	470.7949	8
3	330.1660	165.5866	0	0	312.1554	156.5813	T	845.5091	423.2582	828.4825	414.7449	827.4985	414.2529	7
4	443.2500	222.1287	0	0	425.2395	213.1234	L	744.4614	372.7343	727.4349	364.2211	726.4509	363.7291	6
5	556.3341	278.6707	0	0	538.3235	269.6654	L	631.3774	316.1923	614.3508	307.6790	613.3668	307.1870	5
6	669.4182	335.2127	0	0	651.4076	326.2074	I	518.2933	259.6503	501.2667	251.1370	500.2827	250.6450	4
7	770.4658	385.7366	0	0	752.4553	376.7313	T	405.2092	203.1082	388.1827	194.5950	387.1987	194.1030	3
8	899.5084	450.2579	0	0	881.4979	441.2526	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
9							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 49685.

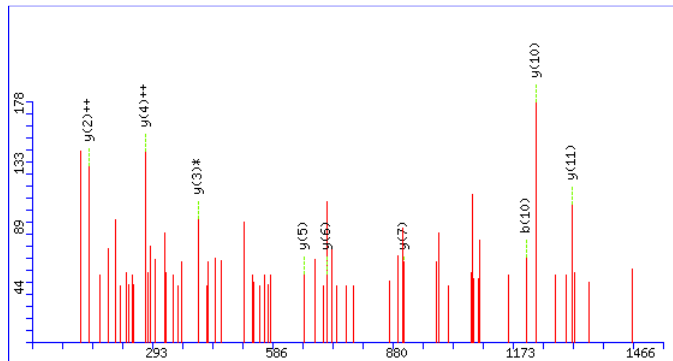
MS/MS Fragmentation of **FQEFSPNLWGLEFQK**:

Found in **IP100005126;IP100552558**

Title: 3.1.1.4460.9

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							15
2	276.1343	138.5708	259.1077	130.0575	0	0	Q	1722.8486	861.9279	1705.8220	853.4147	1704.8380	852.9227	14
3	405.1769	203.0921	388.1503	194.5788	387.1663	194.0868	E	1594.7900	797.8986	1577.7635	789.3854	1576.7795	788.8934	13
4	552.2453	276.6263	535.2187	268.1130	534.2347	267.6210	F	1465.7474	733.3774	1448.7209	724.8641	1447.7369	724.3721	12
5	639.2773	320.1423	622.2508	311.6290	621.2667	311.1370	S	1318.6790	659.8431	1301.6525	651.3299	1300.6684	650.8379	11
6	736.3301	368.6687	719.3035	360.1554	718.3195	359.6634	P	1231.6470	616.3271	1214.6204	607.8139	1213.6364	607.3218	10
7	850.3730	425.6901	833.3464	417.1769	832.3624	416.6849	N	1134.5942	567.8007	1117.5677	559.2875	1116.5837	558.7955	9
8	963.4571	482.2322	946.4305	473.7189	945.4465	473.2269	L	1020.5513	510.7793	1003.5247	502.2660	1002.5407	501.7740	8
9	1149.5364	575.2718	1132.5098	566.7585	1131.5258	566.2665	W	907.4672	454.2373	890.4407	445.7240	889.4567	445.2320	7
10	1206.5578	603.7826	1189.5313	595.2693	1188.5473	594.7773	G	721.3879	361.1976	704.3614	352.6843	703.3774	352.1923	6
11	1319.6419	660.3246	1302.6153	651.8113	1301.6313	651.3193	L	664.3665	332.6869	647.3399	324.1736	646.3559	323.6816	5
12	1448.6845	724.8459	1431.6579	716.3326	1430.6739	715.8406	E	551.2824	276.1448	534.2558	267.6316	533.2718	267.1396	4
13	1595.7529	798.3801	1578.7264	789.8668	1577.7423	789.3748	F	422.2398	211.6235	405.2132	203.1103	0	0	3
14	1723.8115	862.4094	1706.7849	853.8961	1705.8009	853.4041	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
15							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 49730.

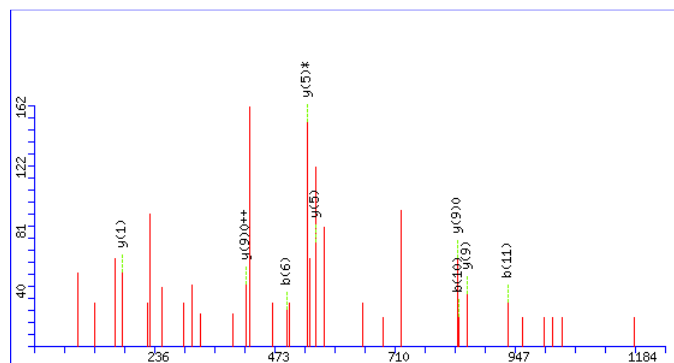
MS/MS Fragmentation of **QQAGLAGPGEPR**:

Found in **IP100060265**

Title: 4.1.1.1295.3

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120129ry¥120129ry_604A1-46_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							12
2	186.0873	93.5473	169.0608	85.0340	0	0	Q	1052.5483	526.7778	1035.5218	518.2645	1034.5378	517.7725	11
3	257.1244	129.0659	240.0979	120.5526	0	0	A	924.4898	462.7485	907.4632	454.2352	906.4792	453.7432	10
4	314.1459	157.5766	297.1193	149.0633	0	0	G	853.4526	427.2300	836.4261	418.7167	835.4421	418.2247	9
5	427.2300	214.1186	410.2034	205.6053	0	0	L	796.4312	398.7192	779.4046	390.2060	778.4206	389.7139	8
6	498.2671	249.6372	481.2405	241.1239	0	0	A	683.3471	342.1772	666.3206	333.6639	665.3366	333.1719	7
7	555.2885	278.1479	538.2620	269.6346	0	0	G	612.3100	306.6586	595.2835	298.1454	594.2994	297.6534	6
8	652.3413	326.6743	635.3148	318.1610	0	0	P	555.2885	278.1479	538.2620	269.6346	537.2780	269.1426	5
9	709.3628	355.1850	692.3362	346.6717	0	0	G	458.2358	229.6215	441.2092	221.1082	440.2252	220.6162	4
10	838.4054	419.7063	821.3788	411.1930	820.3948	410.7010	E	401.2143	201.1108	384.1878	192.5975	383.2037	192.1055	3
11	935.4581	468.2327	918.4316	459.7194	917.4476	459.2274	P	272.1717	136.5895	255.1452	128.0762	0	0	2
12							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 49739.

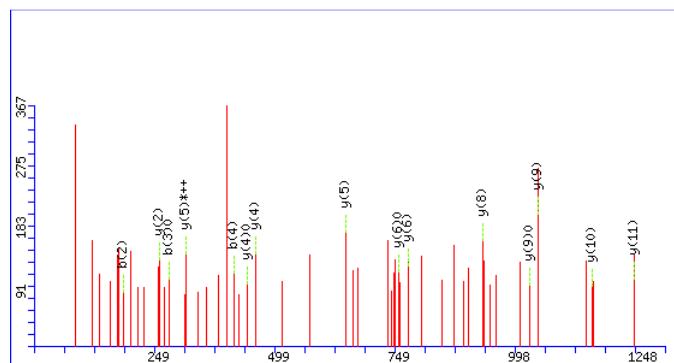
MS/MS Fragmentation of **VSIDGVEWSDIK**:

Found in **IP100376229;IP100975935;IP100976225;IP100977880;IP100984957**

Title: 3.1.1.1126.7

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							12
2	187.1077	94.0575	0	0	169.0972	85.0522	S	1248.6107	624.8090	1231.5841	616.2957	1230.6001	615.8037	11
3	300.1918	150.5995	0	0	282.1812	141.5942	I	1161.5786	581.2930	1144.5521	572.7797	1143.5681	572.2877	10
4	415.2187	208.1130	0	0	397.2082	199.1077	D	1048.4946	524.7509	1031.4680	516.2376	1030.4840	515.7456	9
5	472.2402	236.6237	0	0	454.2296	227.6185	G	933.4676	467.2374	916.4411	458.7242	915.4571	458.2322	8
6	571.3086	286.1579	0	0	553.2980	277.1527	V	876.4462	438.7267	859.4196	430.2134	858.4356	429.7214	7
7	700.3512	350.6792	0	0	682.3406	341.6740	E	777.3777	389.1925	760.3512	380.6792	759.3672	380.1872	6
8	886.4305	443.7189	0	0	868.4199	434.7136	W	648.3352	324.6712	631.3086	316.1579	630.3246	315.6659	5
9	973.4625	487.2349	0	0	955.4520	478.2296	S	462.2558	231.6316	445.2293	223.1183	444.2453	222.6263	4
10	1088.4895	544.7484	0	0	1070.4789	535.7431	D	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
11	1201.5735	601.2904	0	0	1183.5630	592.2851	I	260.1969	130.6021	243.1703	122.0888	0	0	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 49880.

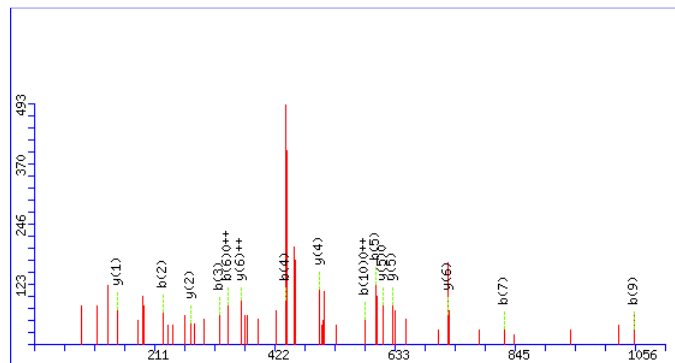
MS/MS Fragmentation of **RAVDCPENIKK: 57.021465@C:5**

Found in **IP100023664;IP100973081;IP100974222;IP100978454;IP100981751;IP101008883**

Title: 1.1.1.6934.7

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	157.1084	79.0578	140.0818	70.5446	0	0	R							11
2	228.1455	114.5764	211.1190	106.0631	0	0	A	1173.5932	587.3003	1156.5667	578.7870	1155.5827	578.2950	10
3	327.2139	164.1106	310.1874	155.5973	0	0	V	1102.5561	551.7817	1085.5296	543.2684	1084.5456	542.7764	9
4	442.2409	221.6241	425.2143	213.1108	424.2303	212.6188	D	1003.4877	502.2475	986.4612	493.7342	985.4771	493.2422	8
5	602.2715	301.6394	585.2450	293.1261	584.2609	292.6341	C	888.4608	444.7340	871.4342	436.2207	870.4502	435.7287	7
6	699.3243	350.1658	682.2977	341.6525	681.3137	341.1605	P	728.4301	364.7187	711.4036	356.2054	710.4196	355.7134	6
7	828.3669	414.6871	811.3403	406.1738	810.3563	405.6818	E	631.3774	316.1923	614.3508	307.6790	613.3668	307.1870	5
8	942.4098	471.7085	925.3832	463.1953	924.3992	462.7033	N	502.3348	251.6710	485.3082	243.1577	0	0	4
9	1055.4939	528.2506	1038.4673	519.7373	1037.4833	519.2453	I	388.2918	194.6496	371.2653	186.1363	0	0	3
10	1183.5888	592.2980	1166.5623	583.7848	1165.5783	583.2928	K	275.2078	138.1075	258.1812	129.5942	0	0	2
11							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 50011.

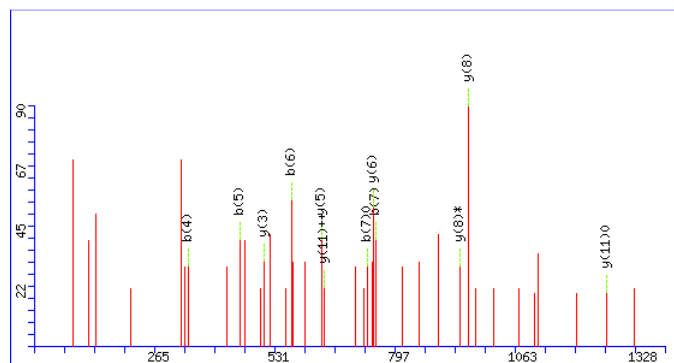
MS/MS Fragmentation of **DGPADIWPLDPLNGAWFR**:

Found in **IP100024083;IP100215844;IP100909751;IP100963955**

Title: 4.1.1.3990.7

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							18
2	173.0557	87.0315	0	0	155.0451	78.0262	G	1924.9704	962.9889	1907.9439	954.4756	1906.9599	953.9836	17
3	270.1084	135.5579	0	0	252.0979	126.5526	P	1867.9490	934.4781	1850.9224	925.9649	1849.9384	925.4728	16
4	341.1456	171.0764	0	0	323.1350	162.0711	A	1770.8962	885.9517	1753.8697	877.4385	1752.8857	876.9465	15
5	456.1725	228.5899	0	0	438.1619	219.5846	D	1699.8591	850.4332	1682.8326	841.9199	1681.8485	841.4279	14
6	569.2566	285.1319	0	0	551.2460	276.1266	I	1584.8322	792.9197	1567.8056	784.4064	1566.8216	783.9144	13
7	755.3359	378.1716	0	0	737.3253	369.1663	W	1471.7481	736.3777	1454.7215	727.8644	1453.7375	727.3724	12
8	852.3886	426.6980	0	0	834.3781	417.6927	P	1285.6688	643.3380	1268.6422	634.8248	1267.6582	634.3327	11
9	965.4727	483.2400	0	0	947.4621	474.2347	L	1188.6160	594.8116	1171.5895	586.2984	1170.6055	585.8064	10
10	1080.4997	540.7535	0	0	1062.4891	531.7482	D	1075.5320	538.2696	1058.5054	529.7563	1057.5214	529.2643	9
11	1177.5524	589.2798	0	0	1159.5419	580.2746	P	960.5050	480.7561	943.4785	472.2429	0	0	8
12	1290.6365	645.8219	0	0	1272.6259	636.8166	L	863.4522	432.2298	846.4257	423.7165	0	0	7
13	1404.6794	702.8433	1387.6529	694.3301	1386.6688	693.8381	N	750.3682	375.6877	733.3416	367.1745	0	0	6
14	1461.7009	731.3541	1444.6743	722.8408	1443.6903	722.3488	G	636.3253	318.6663	619.2987	310.1530	0	0	5
15	1532.7380	766.8726	1515.7114	758.3594	1514.7274	757.8673	A	579.3038	290.1555	562.2772	281.6423	0	0	4
16	1718.8173	859.9123	1701.7907	851.3990	1700.8067	850.9070	W	508.2667	254.6370	491.2401	246.1237	0	0	3
17	1865.8857	933.4465	1848.8592	924.9332	1847.8751	924.4412	F	322.1874	161.5973	305.1608	153.0840	0	0	2
18							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 50068.

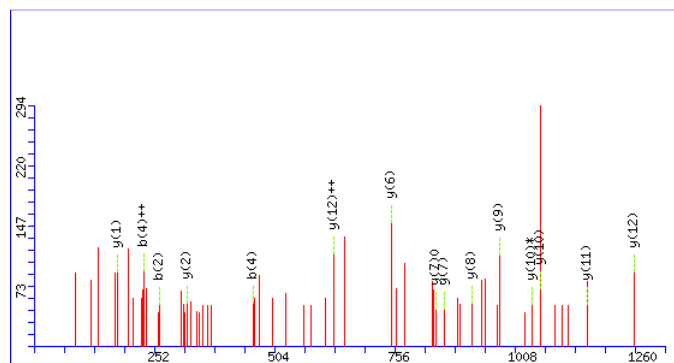
MS/MS Fragmentation of **VYPVSGQLSNLLFR**:

Found in **IP100031758**

Title: 3.1.1.3732.6

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							14
2	263.1390	132.0731	0	0	0	0	Y	1422.7740	711.8906	1405.7474	703.3774	1404.7634	702.8853	13
3	360.1918	180.5995	0	0	0	0	P	1259.7106	630.3590	1242.6841	621.8457	1241.7001	621.3537	12
4	459.2602	230.1337	0	0	0	0	V	1162.6579	581.8326	1145.6313	573.3193	1144.6473	572.8273	11
5	546.2922	273.6498	0	0	528.2817	264.6445	S	1063.5895	532.2984	1046.5629	523.7851	1045.5789	523.2931	10
6	603.3137	302.1605	0	0	585.3031	293.1552	G	976.5574	488.7824	959.5309	480.2691	958.5469	479.7771	9
7	660.3352	330.6712	0	0	642.3246	321.6659	G	919.5360	460.2716	902.5094	451.7584	901.5254	451.2663	8
8	773.4192	387.2132	0	0	755.4087	378.2080	L	862.5145	431.7609	845.4880	423.2476	844.5039	422.7556	7
9	860.4512	430.7293	0	0	842.4407	421.7240	S	749.4304	375.2189	732.4039	366.7056	731.4199	366.2136	6
10	974.4942	487.7507	957.4676	479.2374	956.4836	478.7454	N	662.3984	331.7028	645.3719	323.1896	0	0	5
11	1087.5782	544.2928	1070.5517	535.7795	1069.5677	535.2875	L	548.3555	274.6814	531.3289	266.1681	0	0	4
12	1200.6623	600.8348	1183.6358	592.3215	1182.6517	591.8295	L	435.2714	218.1394	418.2449	209.6261	0	0	3
13	1347.7307	674.3690	1330.7042	665.8557	1329.7201	665.3637	F	322.1874	161.5973	305.1608	153.0840	0	0	2
14							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 50149.

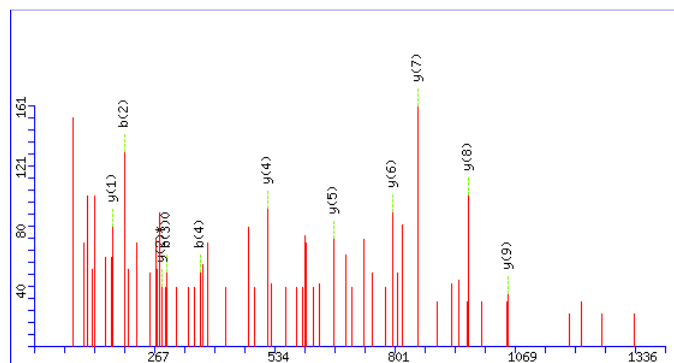
MS/MS Fragmentation of **LSLGEEFAQR**:

Found in **IP101012106**

Title: 3.1.1.2880.3

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							10
2	201.1234	101.0653	0	0	183.1128	92.0600	S	1054.5316	527.7694	1037.5051	519.2562	1036.5211	518.7642	9
3	314.2074	157.6074	0	0	296.1969	148.6021	L	967.4996	484.2534	950.4730	475.7402	949.4890	475.2482	8
4	371.2289	186.1181	0	0	353.2183	177.1128	G	854.4155	427.7114	837.3890	419.1981	836.4050	418.7061	7
5	500.2715	250.6394	0	0	482.2609	241.6341	E	797.3941	399.2007	780.3675	390.6874	779.3835	390.1954	6
6	647.3399	324.1736	0	0	629.3293	315.1683	F	668.3515	334.6794	651.3249	326.1661	0	0	5
7	794.4083	397.7078	0	0	776.3978	388.7025	F	521.2831	261.1452	504.2565	252.6319	0	0	4
8	865.4454	433.2264	0	0	847.4349	424.2211	A	374.2146	187.6110	357.1881	179.0977	0	0	3
9	993.5040	497.2556	976.4775	488.7424	975.4934	488.2504	Q	303.1775	152.0924	286.1510	143.5791	0	0	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 50216.

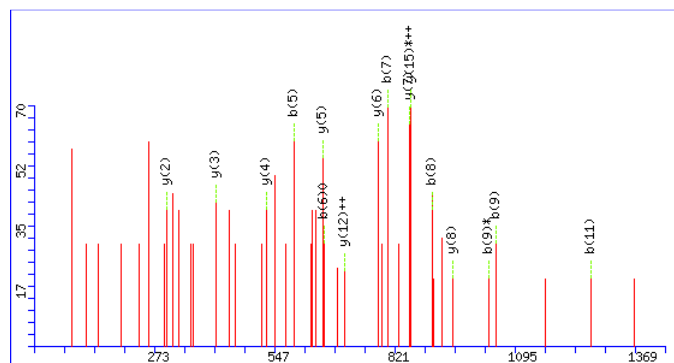
MS/MS Fragmentation of **LNHQVSEVFNTVAQELLQR**:

Found in **IP100007866;IP100917363**

Title: 4.1.1.1256.3

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							19
2	228.1343	114.5708	211.1077	106.0575	0	0	N	2112.0832	1056.5453	2095.0567	1048.0320	2094.0727	1047.5400	18
3	365.1932	183.1002	348.1666	174.5870	0	0	H	1998.0403	999.5238	1981.0138	991.0105	1980.0298	990.5185	17
4	493.2518	247.1295	476.2252	238.6162	0	0	Q	1860.9814	930.9943	1843.9549	922.4811	1842.9708	921.9891	16
5	592.3202	296.6637	575.2936	288.1504	0	0	V	1732.9228	866.9651	1715.8963	858.4518	1714.9123	857.9598	15
6	679.3522	340.1797	662.3256	331.6665	661.3416	331.1745	S	1633.8544	817.4308	1616.8279	808.9176	1615.8438	808.4256	14
7	808.3948	404.7010	791.3682	396.1878	790.3842	395.6958	E	1546.8224	773.9148	1529.7958	765.4016	1528.8118	764.9095	13
8	907.4632	454.2352	890.4367	445.7220	889.4526	445.2300	V	1417.7798	709.3935	1400.7532	700.8803	1399.7692	700.3883	12
9	1054.5316	527.7694	1037.5051	519.2562	1036.5211	518.7642	F	1318.7114	659.8593	1301.6848	651.3461	1300.7008	650.8540	11
10	1168.5745	584.7909	1151.5480	576.2776	1150.5640	575.7856	N	1171.6430	586.3251	1154.6164	577.8118	1153.6324	577.3198	10
11	1269.6222	635.3148	1252.5957	626.8015	1251.6117	626.3095	T	1057.6000	529.3037	1040.5735	520.7904	1039.5895	520.2984	9
12	1368.6906	684.8490	1351.6641	676.3357	1350.6801	675.8437	V	956.5524	478.7798	939.5258	470.2665	938.5418	469.7745	8
13	1439.7278	720.3675	1422.7012	711.8542	1421.7172	711.3622	A	857.4839	429.2456	840.4574	420.7323	839.4734	420.2403	7
14	1567.7863	784.3968	1550.7598	775.8835	1549.7758	775.3915	Q	786.4468	393.7271	769.4203	385.2138	768.4363	384.7218	6
15	1696.8289	848.9181	1679.8024	840.4048	1678.8184	839.9128	E	658.3883	329.6978	641.3617	321.1845	640.3777	320.6925	5
16	1809.9130	905.4601	1792.8864	896.9469	1791.9024	896.4549	L	529.3457	265.1765	512.3191	256.6632	0	0	4
17	1922.9971	962.0022	1905.9705	953.4889	1904.9865	952.9969	L	416.2616	208.6344	399.2350	200.1212	0	0	3
18	2051.0556	1026.0315	2034.0291	1017.5182	2033.0451	1017.0262	Q	303.1775	152.0924	286.1510	143.5791	0	0	2
19							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 50490.

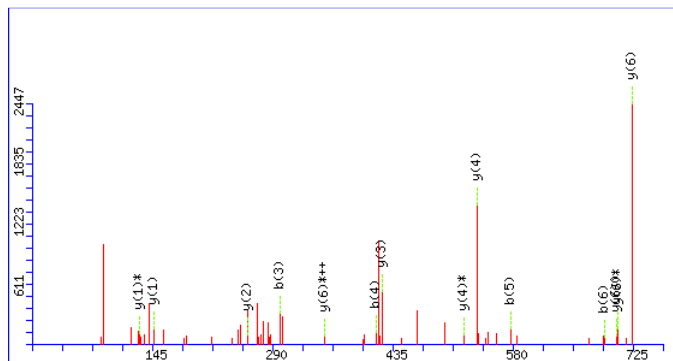
MS/MS Fragmentation of **LDADYIK**:

Found in **IP100021887,IP100883790,IP100921489**

Title: 2.1.1.3260.3

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							7
2	229.1183	115.0628	0	0	211.1077	106.0575	D	724.3512	362.6792	707.3246	354.1660	706.3406	353.6740	6
3	300.1554	150.5813	0	0	282.1448	141.5761	A	609.3243	305.1658	592.2977	296.6525	591.3137	296.1605	5
4	415.1823	208.0948	0	0	397.1718	199.0895	D	538.2871	269.6472	521.2606	261.1339	520.2766	260.6419	4
5	578.2457	289.6265	0	0	560.2351	280.6212	Y	423.2602	212.1337	406.2336	203.6205	0	0	3
6	691.3297	346.1685	0	0	673.3192	337.1632	I	260.1969	130.6021	243.1703	122.0888	0	0	2
7							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 50544.

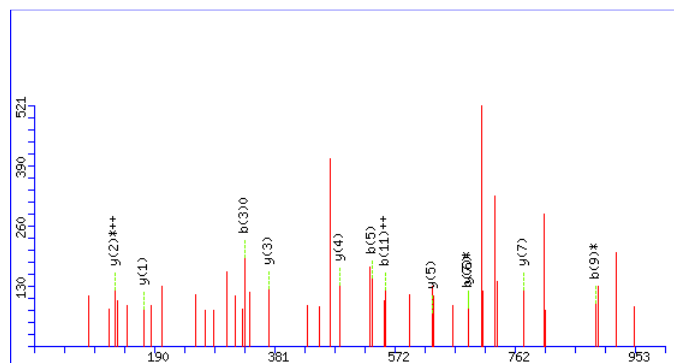
MS/MS Fragmentation of **LHTANLGDSGFLVVR**:

Found in **IP100169326**

Title: 2.1.1.4281.4

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							15
2	251.1503	126.0788	0	0	0	0	H	1485.7809	743.3941	1468.7543	734.8808	1467.7703	734.3888	14
3	352.1979	176.6026	0	0	334.1874	167.5973	T	1348.7219	674.8646	1331.6954	666.3513	1330.7114	665.8593	13
4	423.2350	212.1212	0	0	405.2245	203.1159	A	1247.6743	624.3408	1230.6477	615.8275	1229.6637	615.3355	12
5	537.2780	269.1426	520.2514	260.6293	519.2674	260.1373	N	1176.6371	588.8222	1159.6106	580.3089	1158.6266	579.8169	11
6	650.3620	325.6847	633.3355	317.1714	632.3515	316.6794	L	1062.5942	531.8007	1045.5677	523.2875	1044.5837	522.7955	10
7	707.3835	354.1954	690.3570	345.6821	689.3729	345.1901	G	949.5102	475.2587	932.4836	466.7454	931.4996	466.2534	9
8	822.4104	411.7089	805.3839	403.1956	804.3999	402.7036	D	892.4887	446.7480	875.4621	438.2347	874.4781	437.7427	8
9	909.4425	455.2249	892.4159	446.7116	891.4319	446.2196	S	777.4617	389.2345	760.4352	380.7212	759.4512	380.2292	7
10	966.4639	483.7356	949.4374	475.2223	948.4534	474.7303	G	690.4297	345.7185	673.4032	337.2052	0	0	6
11	1113.5323	557.2698	1096.5058	548.7565	1095.5218	548.2645	F	633.4083	317.2078	616.3817	308.6945	0	0	5
12	1226.6164	613.8118	1209.5899	605.2986	1208.6058	604.8066	L	486.3398	243.6736	469.3133	235.1603	0	0	4
13	1325.6848	663.3461	1308.6583	654.8328	1307.6743	654.3408	V	373.2558	187.1315	356.2292	178.6183	0	0	3
14	1424.7532	712.8803	1407.7267	704.3670	1406.7427	703.8750	V	274.1874	137.5973	257.1608	129.0840	0	0	2
15							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 50689.

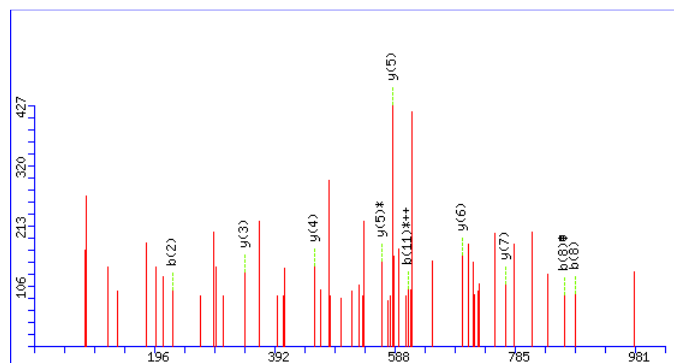
MS/MS Fragmentation of **ILNTPNCALQIVAR: 57.021465@C:7**

Found in **IP100413781;IP100651692;IP100719836;IP100848299;IP101011188**

Title: 2.1.1.4407.3

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							14
2	227.1754	114.0913	0	0	0	0	L	1469.7893	735.3983	1452.7628	726.8850	1451.7787	726.3930	13
3	341.2183	171.1128	324.1918	162.5995	0	0	N	1356.7052	678.8563	1339.6787	670.3430	1338.6947	669.8510	12
4	442.2660	221.6366	425.2395	213.1234	424.2554	212.6314	T	1242.6623	621.8348	1225.6358	613.3215	1224.6518	612.8295	11
5	539.3188	270.1630	522.2922	261.6498	521.3082	261.1577	P	1141.6146	571.3110	1124.5881	562.7977	0	0	10
6	653.3617	327.1845	636.3352	318.6712	635.3511	318.1792	N	1044.5619	522.7846	1027.5353	514.2713	0	0	9
7	813.3924	407.1998	796.3658	398.6865	795.3818	398.1945	C	930.5189	465.7631	913.4924	457.2498	0	0	8
8	884.4295	442.7184	867.4029	434.2051	866.4189	433.7131	A	770.4883	385.7478	753.4618	377.2345	0	0	7
9	997.5135	499.2604	980.4870	490.7471	979.5030	490.2551	L	699.4512	350.2292	682.4246	341.7160	0	0	6
10	1125.5721	563.2897	1108.5456	554.7764	1107.5615	554.2844	Q	586.3671	293.6872	569.3406	285.1739	0	0	5
11	1238.6562	619.8317	1221.6296	611.3184	1220.6456	610.8264	I	458.3085	229.6579	441.2820	221.1446	0	0	4
12	1337.7246	669.3659	1320.6980	660.8527	1319.7140	660.3606	V	345.2245	173.1159	328.1979	164.6026	0	0	3
13	1408.7617	704.8845	1391.7351	696.3712	1390.7511	695.8792	A	246.1561	123.5817	229.1295	115.0684	0	0	2
14							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 50902.

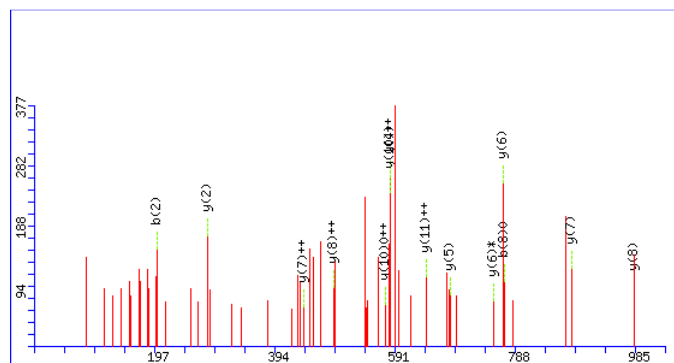
MS/MS Fragmentation of **SDSVTISVWNHK**:

Found in **IP100329664**

Title: 2.1.1.1782.4

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							12
2	203.0662	102.0368	0	0	185.0557	93.0315	D	1285.6535	643.3304	1268.6270	634.8171	1267.6430	634.3251	11
3	290.0983	145.5528	0	0	272.0877	136.5475	S	1170.6266	585.8169	1153.6000	577.3037	1152.6160	576.8116	10
4	389.1667	195.0870	0	0	371.1561	186.0817	V	1083.5946	542.3009	1066.5680	533.7876	1065.5840	533.2956	9
5	490.2144	245.6108	0	0	472.2038	236.6055	T	984.5261	492.7667	967.4996	484.2534	966.5156	483.7614	8
6	603.2984	302.1529	0	0	585.2879	293.1476	I	883.4785	442.2429	866.4519	433.7296	865.4679	433.2376	7
7	690.3305	345.6689	0	0	672.3199	336.6636	S	770.3944	385.7008	753.3678	377.1876	752.3838	376.6956	6
8	789.3989	395.2031	0	0	771.3883	386.1978	V	683.3624	342.1848	666.3358	333.6715	0	0	5
9	975.4782	488.2427	0	0	957.4676	479.2374	W	584.2940	292.6506	567.2674	284.1373	0	0	4
10	1089.5211	545.2642	1072.4946	536.7509	1071.5105	536.2589	N	398.2146	199.6110	381.1881	191.0977	0	0	3
11	1226.5800	613.7937	1209.5535	605.2804	1208.5695	604.7884	H	284.1717	142.5895	267.1452	134.0762	0	0	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

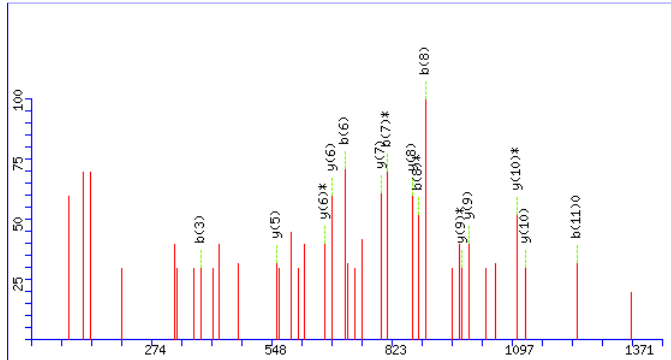
Peptide View

Peptide: 50947.

MS/MS Fragmentation of **NNCNVDLAFDTLDAIQQALQQGDIK: 57.021465@C:3**
Found in **IP100843865:IP100981312**

Title: 5.1.1.1392.5

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120206ry¥120206ry_aHDF1419-P10_2.5.mgf
ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							26
2	229.0931	115.0502	212.0666	106.5369	0	0	N	2761.3461	1381.1767	2744.3196	1372.6634	2743.3356	1372.1714	25
3	389.1238	195.0655	372.0972	186.5523	0	0	C	2647.3032	1324.1552	2630.2767	1315.6420	2629.2926	1315.1500	24
4	503.1667	252.0870	486.1402	243.5737	0	0	N	2487.2726	1244.1399	2470.2460	1235.6266	2469.2620	1235.1346	23
5	602.2351	301.6212	585.2086	293.1079	0	0	V	2373.2296	1187.1185	2356.2031	1178.6052	2355.2191	1178.1132	22
6	717.2621	359.1347	700.2355	350.6214	699.2515	350.1294	D	2274.1612	1137.5842	2257.1347	1129.0710	2256.1507	1128.5790	21
7	830.3461	415.6767	813.3196	407.1634	812.3356	406.6714	L	2159.1343	1080.0708	2142.1077	1071.5575	2141.1237	1071.0655	20
8	901.3832	451.1953	884.3567	442.6820	883.3727	442.1900	A	2046.0502	1023.5287	2029.0237	1015.0155	2028.0396	1014.5235	19
9	1048.4517	524.7295	1031.4251	516.2162	1030.4411	515.7242	F	1975.0131	988.0102	1957.9866	979.4969	1957.0025	979.0049	18
10	1163.4786	582.2429	1146.4520	573.7297	1145.4680	573.2377	D	1827.9447	914.4760	1810.9181	905.9627	1809.9341	905.4707	17
11	1264.5263	632.7668	1247.4997	624.2535	1246.5157	623.7615	T	1712.9177	856.9625	1695.8912	848.4492	1694.9072	847.9572	16
12	1377.6103	689.3088	1360.5838	680.7955	1359.5998	680.3035	L	1611.8701	806.4387	1594.8435	797.9254	1593.8595	797.4334	15
13	1448.6475	724.8274	1431.6209	716.3141	1430.6369	715.8221	A	1498.7860	749.8966	1481.7595	741.3834	1480.7754	740.8914	14
14	1563.6744	782.3408	1546.6478	773.8276	1545.6638	773.3356	D	1427.7489	714.3781	1410.7223	705.8648	1409.7383	705.3728	13
15	1634.7115	817.8594	1617.6850	809.3461	1616.7009	808.8541	A	1312.7219	656.8646	1295.6954	648.3513	1294.7114	647.8593	12
16	1747.7956	874.4014	1730.7690	865.8882	1729.7850	865.3961	I	1241.6848	621.3461	1224.6583	612.8328	1223.6743	612.3408	11
17	1875.8542	938.4307	1858.8276	929.9174	1857.8436	929.4254	Q	1128.6008	564.8040	1111.5742	556.2907	1110.5902	555.7987	10
18	2003.9127	1002.4600	1986.8862	993.9467	1985.9022	993.4547	Q	1000.5422	500.7747	983.5156	492.2615	982.5316	491.7694	9
19	2074.9498	1037.9786	2057.9233	1029.4653	2056.9393	1028.9733	A	872.4836	436.7454	855.4571	428.2322	854.4730	427.7402	8
20	2188.0339	1094.5206	2171.0074	1086.0073	2170.0233	1085.5153	L	801.4465	401.2269	784.4199	392.7136	783.4359	392.2216	7
21	2316.0925	1158.5499	2299.0659	1150.0366	2298.0819	1149.5446	Q	688.3624	344.6849	671.3359	336.1716	670.3519	335.6796	6
22	2444.1511	1222.5792	2427.1245	1214.0659	2426.1405	1213.5739	Q	560.3039	280.6556	543.2773	272.1423	542.2933	271.6503	5
23	2501.1725	1251.0899	2484.1460	1242.5766	2483.1620	1242.0846	G	432.2453	216.6263	415.2187	208.1130	414.2347	207.6210	4
24	2616.1995	1308.6034	2599.1729	1300.0901	2598.1889	1299.5981	D	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
25	2729.2835	1365.1454	2712.2570	1356.6321	2711.2730	1356.1401	I	260.1969	130.6021	243.1703	122.0888	0	0	2
26							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

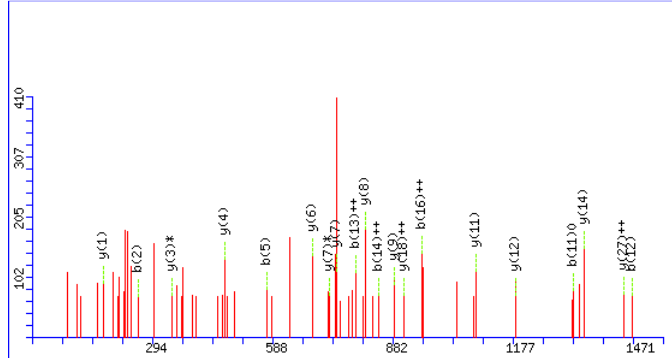
Peptide: 50980.

MS/MS Fragmentation of **FLSPEQHACSWQLLLPAPEAAAGSELALR**: 57.021465@C:9
Found in **IP100301201**

Title: 4.1.1.88.7

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							29
2	261.1598	131.0835	0	0	0	0	L	3015.5357	1508.2715	2998.5091	1499.7582	2997.5251	1499.2662	28
3	348.1918	174.5995	0	0	330.1812	165.5942	S	2902.4516	1451.7294	2885.4251	1443.2162	2884.4410	1442.7242	27
4	445.2445	223.1259	0	0	427.2340	214.1206	P	2815.4196	1408.2134	2798.3930	1399.7002	2797.4090	1399.2081	26
5	574.2871	287.6472	0	0	556.2766	278.6419	E	2718.3668	1359.6870	2701.3403	1351.1738	2700.3562	1350.6818	25
6	702.3457	351.6765	685.3192	343.1632	684.3352	342.6712	Q	2589.3242	1295.1657	2572.2977	1286.6525	2571.3137	1286.1605	24
7	839.4046	420.2060	822.3781	411.6927	821.3941	411.2007	H	2461.2656	1231.1365	2444.2391	1222.6232	2443.2551	1222.1312	23
8	910.4417	455.7245	893.4152	447.2112	892.4312	446.7192	A	2324.2067	1162.6070	2307.1802	1154.0937	2306.1962	1153.6017	22
9	1070.4724	535.7398	1053.4458	527.2266	1052.4618	526.7346	C	2253.1696	1127.0884	2236.1431	1118.5752	2235.1591	1118.0832	21
10	1157.5044	579.2558	1140.4779	570.7426	1139.4939	570.2506	S	2093.1390	1047.0731	2076.1124	1038.5598	2075.1284	1038.0678	20
11	1343.5837	672.2955	1326.5572	663.7822	1325.5732	663.2902	W	2006.1069	1003.5571	1989.0804	995.0438	1988.0964	994.5518	19
12	1471.6423	736.3248	1454.6158	727.8115	1453.6317	727.3195	Q	1820.0276	910.5175	1803.0011	902.0042	1802.0171	901.5122	18
13	1584.7264	792.8668	1567.6998	784.3536	1566.7158	783.8615	L	1691.9690	846.4882	1674.9425	837.9749	1673.9585	837.4829	17
14	1697.8104	849.4089	1680.7839	840.8956	1679.7999	840.4036	L	1578.8850	789.9461	1561.8584	781.4329	1560.8744	780.9408	16
15	1810.8945	905.9509	1793.8680	897.4376	1792.8839	896.9456	L	1465.8009	733.4041	1448.7744	724.8908	1447.7904	724.3988	15
16	1907.9473	954.4773	1890.9207	945.9640	1889.9367	945.4720	P	1352.7169	676.8621	1335.6903	668.3488	1334.7063	667.8568	14
17	1978.9844	989.9958	1961.9578	981.4826	1960.9738	980.9905	A	1255.6641	628.3357	1238.6375	619.8224	1237.6535	619.3304	13
18	2076.0371	1038.5222	2059.0106	1030.0089	2058.0266	1029.5169	P	1184.6270	592.8171	1167.6004	584.3039	1166.6164	583.8118	12
19	2205.0797	1103.0435	2188.0532	1094.5302	2187.0692	1094.0382	E	1087.5742	544.2907	1070.5477	535.7775	1069.5636	535.2855	11
20	2276.1169	1138.5621	2259.0903	1130.0488	2258.1063	1129.5568	A	958.5316	479.7694	941.5051	471.2562	940.5211	470.7642	10
21	2347.1540	1174.0806	2330.1274	1165.5673	2329.1434	1165.0753	A	887.4945	444.2509	870.4680	435.7376	869.4839	435.2456	9
22	2418.1911	1209.5992	2401.1645	1201.0859	2400.1805	1200.5939	A	816.4574	408.7323	799.4308	400.2191	798.4468	399.7271	8
23	2475.2125	1238.1099	2458.1860	1229.5966	2457.2020	1229.1046	G	745.4203	373.2138	728.3937	364.7005	727.4097	364.2085	7
24	2562.2446	1281.6259	2545.2180	1273.1126	2544.2340	1272.6206	S	688.3988	344.7030	671.3723	336.1898	670.3883	335.6978	6
25	2691.2872	1346.1472	2674.2606	1337.6339	2673.2766	1337.1419	E	601.3668	301.1870	584.3402	292.6738	583.3562	292.1817	5
26	2804.3712	1402.6893	2787.3447	1394.1760	2786.3607	1393.6840	L	472.3242	236.6657	455.2976	228.1525	0	0	4
27	2875.4083	1438.2078	2858.3818	1429.6945	2857.3978	1429.2025	A	359.2401	180.1237	342.2136	171.6104	0	0	3
28	2988.4924	1494.7498	2971.4659	1486.2366	2970.4818	1485.7446	L	288.2030	144.6051	271.1765	136.0919	0	0	2
29							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 51109.

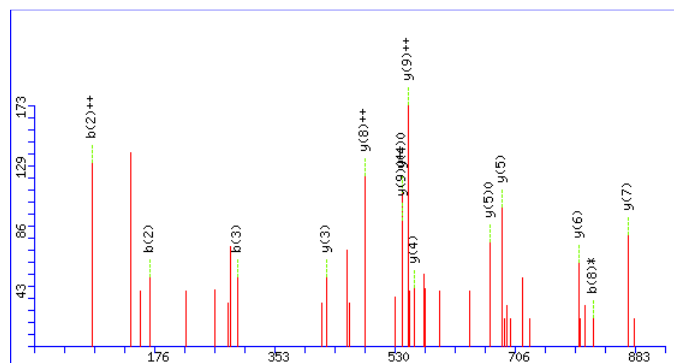
MS/MS Fragmentation of **GLQVALEEFHK**:

Found in **IP100019176;IP100945490**

Title: 2.1.1.3782.5

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							11
2	171.1128	86.0600	0	0	0	0	L	1213.6575	607.3324	1196.6310	598.8191	1195.6470	598.3271	10
3	299.1714	150.0893	282.1448	141.5761	0	0	Q	1100.5735	550.7904	1083.5469	542.2771	1082.5629	541.7851	9
4	398.2398	199.6235	381.2132	191.1103	0	0	V	972.5149	486.7611	955.4884	478.2478	954.5043	477.7558	8
5	469.2769	235.1421	452.2504	226.6288	0	0	A	873.4465	437.2269	856.4199	428.7136	855.4359	428.2216	7
6	582.3610	291.6841	565.3344	283.1709	0	0	L	802.4094	401.7083	785.3828	393.1951	784.3988	392.7030	6
7	711.4036	356.2054	694.3770	347.6921	693.3930	347.2001	E	689.3253	345.1663	672.2988	336.6530	671.3148	336.1610	5
8	840.4462	420.7267	823.4196	412.2134	822.4356	411.7214	E	560.2827	280.6450	543.2562	272.1317	542.2722	271.6397	4
9	987.5146	494.2609	970.4880	485.7477	969.5040	485.2556	F	431.2401	216.1237	414.2136	207.6104	0	0	3
10	1124.5735	562.7904	1107.5469	554.2771	1106.5629	553.7851	H	284.1717	142.5895	267.1452	134.0762	0	0	2
11							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 51143.

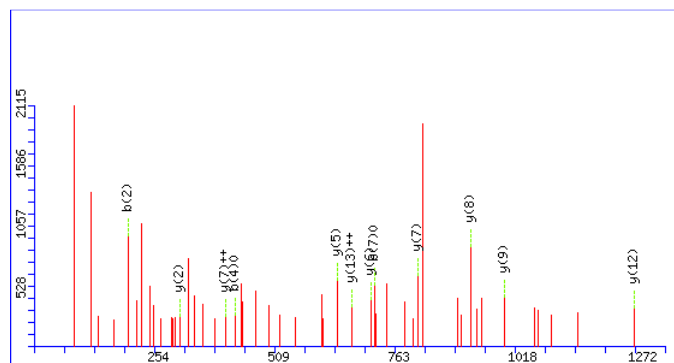
MS/MS Fragmentation of **EAPFVPVGIAGFAAIVAYGLYK**:

Found in **IP100295621;IP100856008;IP100926995;IP100927455**

Title: 5.1.1.1546.7

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120206ry¥120206ry_aHDF1419-P10_3.5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							22
2	201.0870	101.0471	0	0	183.0764	92.0418	A	2124.1892	1062.5982	2107.1627	1054.0850	0	0	21
3	298.1397	149.5735	0	0	280.1292	140.5682	P	2053.1521	1027.0797	2036.1256	1018.5664	0	0	20
4	445.2082	223.1077	0	0	427.1976	214.1024	F	1956.0993	978.5533	1939.0728	970.0400	0	0	19
5	544.2766	272.6419	0	0	526.2660	263.6366	V	1809.0309	905.0191	1792.0044	896.5058	0	0	18
6	641.3293	321.1683	0	0	623.3188	312.1630	P	1709.9625	855.4849	1692.9360	846.9716	0	0	17
7	740.3978	370.7025	0	0	722.3872	361.6972	V	1612.9097	806.9585	1595.8832	798.4452	0	0	16
8	797.4192	399.2132	0	0	779.4087	390.2080	G	1513.8413	757.4243	1496.8148	748.9110	0	0	15
9	910.5033	455.7553	0	0	892.4927	446.7500	I	1456.8199	728.9136	1439.7933	720.4003	0	0	14
10	981.5404	491.2738	0	0	963.5298	482.2686	A	1343.7358	672.3715	1326.7093	663.8583	0	0	13
11	1038.5619	519.7846	0	0	1020.5513	510.7793	G	1272.6987	636.8530	1255.6721	628.3397	0	0	12
12	1185.6303	593.3188	0	0	1167.6197	584.3135	F	1215.6772	608.3422	1198.6507	599.8290	0	0	11
13	1256.6674	628.8373	0	0	1238.6568	619.8320	A	1068.6088	534.8080	1051.5823	526.2948	0	0	10
14	1327.7045	664.3559	0	0	1309.6939	655.3506	A	997.5717	499.2895	980.5451	490.7762	0	0	9
15	1440.7886	720.8979	0	0	1422.7780	711.8926	I	926.5346	463.7709	909.5080	455.2577	0	0	8
16	1539.8570	770.4321	0	0	1521.8464	761.4268	V	813.4505	407.2289	796.4240	398.7156	0	0	7
17	1610.8941	805.9507	0	0	1592.8835	796.9454	A	714.3821	357.6947	697.3556	349.1814	0	0	6
18	1773.9574	887.4823	0	0	1755.9469	878.4771	Y	643.3450	322.1761	626.3184	313.6629	0	0	5
19	1830.9789	915.9931	0	0	1812.9683	906.9878	G	480.2817	240.6445	463.2551	232.1312	0	0	4
20	1944.0630	972.5351	0	0	1926.0524	963.5298	L	423.2602	212.1337	406.2336	203.6205	0	0	3
21	2107.1263	1054.0668	0	0	2089.1157	1045.0615	Y	310.1761	155.5917	293.1496	147.0784	0	0	2
22							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 51878.

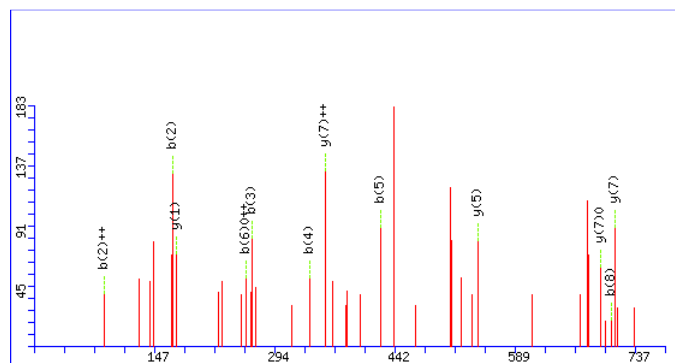
MS/MS Fragmentation of **GLPASLLGR**:

Found in **IP100856095;IP100954554**

Title: 1.1.1.6695.5

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_2_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							9
2	171.1128	86.0600	0	0	0	0	L	826.5145	413.7609	809.4880	405.2476	808.5039	404.7556	8
3	268.1656	134.5864	0	0	0	0	P	713.4304	357.2189	696.4039	348.7056	695.4199	348.2136	7
4	339.2027	170.1050	0	0	0	0	A	616.3777	308.6925	599.3511	300.1792	598.3671	299.6872	6
5	426.2347	213.6210	0	0	408.2241	204.6157	S	545.3406	273.1739	528.3140	264.6606	527.3300	264.1686	5
6	539.3188	270.1630	0	0	521.3082	261.1577	L	458.3085	229.6579	441.2820	221.1446	0	0	4
7	652.4028	326.7051	0	0	634.3923	317.6998	L	345.2245	173.1159	328.1979	164.6026	0	0	3
8	709.4243	355.2158	0	0	691.4137	346.2105	G	232.1404	116.5738	215.1139	108.0606	0	0	2
9							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 52035.

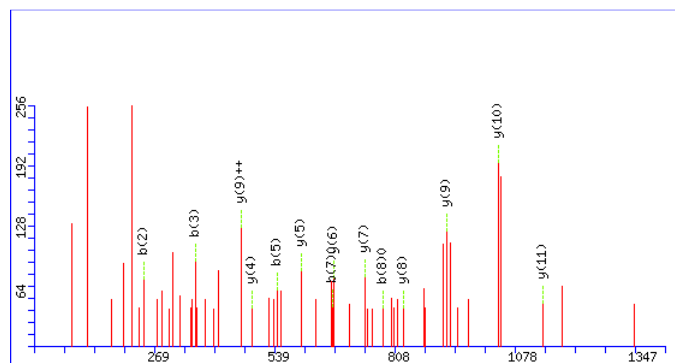
MS/MS Fragmentation of **FVDPSAALDLLK**:

Found in **IP100045496,IP100103951,IP101009333,IP101013069,IP101013105,IP101013469**

Title: 3.1.1.3776.3

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							12
2	247.1441	124.0757	0	0	0	0	V	1141.6463	571.3268	1124.6198	562.8135	1123.6358	562.3215	11
3	362.1710	181.5892	0	0	344.1605	172.5839	D	1042.5779	521.7926	1025.5514	513.2793	1024.5673	512.7873	10
4	459.2238	230.1155	0	0	441.2132	221.1103	P	927.5510	464.2791	910.5244	455.7658	909.5404	455.2738	9
5	546.2558	273.6316	0	0	528.2453	264.6263	S	830.4982	415.7527	813.4716	407.2395	812.4876	406.7475	8
6	617.2930	309.1501	0	0	599.2824	300.1448	A	743.4662	372.2367	726.4396	363.7234	725.4556	363.2314	7
7	688.3301	344.6687	0	0	670.3195	335.6634	A	672.4291	336.7182	655.4025	328.2049	654.4185	327.7129	6
8	801.4141	401.2107	0	0	783.4036	392.2054	L	601.3919	301.1996	584.3654	292.6863	583.3814	292.1943	5
9	916.4411	458.7242	0	0	898.4305	449.7189	D	488.3079	244.6576	471.2813	236.1443	470.2973	235.6523	4
10	1029.5251	515.2662	0	0	1011.5146	506.2609	L	373.2809	187.1441	356.2544	178.6308	0	0	3
11	1142.6092	571.8082	0	0	1124.5986	562.8030	L	260.1969	130.6021	243.1703	122.0888	0	0	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 52328.

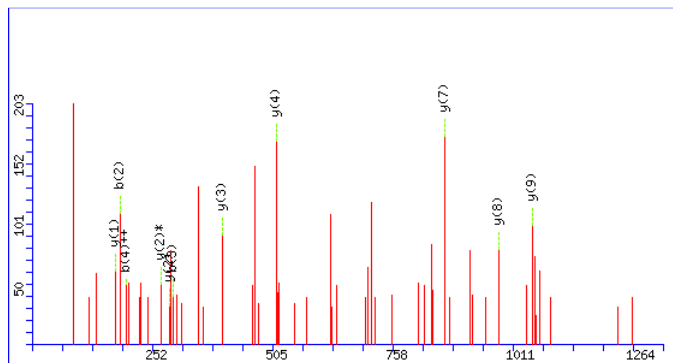
MS/MS Fragmentation of **LALPPCLLR: 57.021465@C:6**

Found in **IP100217781**

Title: 4.1.1.383.2

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_2.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							10
2	185.1285	93.0679	0	0	0	0	A	1053.5874	527.2973	1036.5608	518.7840	0	0	9
3	298.2125	149.6099	0	0	0	0	L	982.5502	491.7788	965.5237	483.2655	0	0	8
4	395.2653	198.1363	0	0	0	0	P	869.4662	435.2367	852.4396	426.7235	0	0	7
5	492.3180	246.6627	0	0	0	0	P	772.4134	386.7103	755.3869	378.1971	0	0	6
6	652.3487	326.6780	0	0	0	0	C	675.3607	338.1840	658.3341	329.6707	0	0	5
7	765.4328	383.2200	0	0	0	0	L	515.3300	258.1686	498.3035	249.6554	0	0	4
8	878.5168	439.7621	0	0	0	0	L	402.2459	201.6266	385.2194	193.1133	0	0	3
9	992.5598	496.7835	975.5332	488.2702	0	0	N	289.1619	145.0846	272.1353	136.5713	0	0	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 52344.

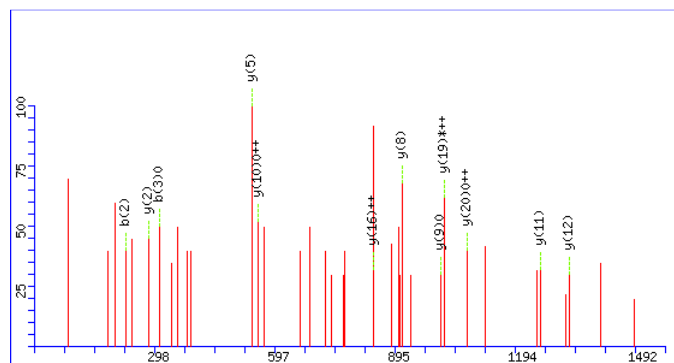
MS/MS Fragmentation of **DITCLELMPGSLAETICLVGTHK: 57.021465@C:4,57.021465@C:17**

Found in **IP100375879**

Title: 4.1.1.3633.9

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							24
2	229.1183	115.0628	0	0	211.1077	106.0575	I	2544.2870	1272.6472	2527.2605	1264.1339	2526.2765	1263.6419	23
3	330.1660	165.5866	0	0	312.1554	156.5813	T	2431.2030	1216.1051	2414.1764	1207.5918	2413.1924	1207.0998	22
4	490.1966	245.6019	0	0	472.1860	236.5967	C	2330.1553	1165.5813	2313.1287	1157.0680	2312.1447	1156.5760	21
5	603.2807	302.1440	0	0	585.2701	293.1387	L	2170.1246	1085.5660	2153.0981	1077.0527	2152.1141	1076.5607	20
6	732.3233	366.6653	0	0	714.3127	357.6600	E	2057.0406	1029.0239	2040.0140	1020.5107	2039.0300	1020.0186	19
7	845.4073	423.2073	0	0	827.3968	414.2020	L	1927.9980	964.5026	1910.9714	955.9894	1909.9874	955.4973	18
8	976.4478	488.7275	0	0	958.4373	479.7223	M	1814.9139	907.9606	1797.8874	899.4473	1796.9034	898.9553	17
9	1073.5006	537.2539	0	0	1055.4900	528.2486	P	1683.8734	842.4404	1666.8469	833.9271	1665.8629	833.4351	16
10	1130.5220	565.7647	0	0	1112.5115	556.7594	G	1586.8207	793.9140	1569.7941	785.4007	1568.8101	784.9087	15
11	1217.5541	609.2807	0	0	1199.5435	600.2754	S	1529.7992	765.4032	1512.7727	756.8900	1511.7886	756.3980	14
12	1330.6381	665.8227	0	0	1312.6276	656.8174	L	1442.7672	721.8872	1425.7406	713.3740	1424.7566	712.8819	13
13	1401.6753	701.3413	0	0	1383.6647	692.3360	A	1329.6831	665.3452	1312.6566	656.8319	1311.6726	656.3399	12
14	1530.7178	765.8626	0	0	1512.7073	756.8573	E	1258.6460	629.8266	1241.6195	621.3134	1240.6354	620.8214	11
15	1631.7655	816.3864	0	0	1613.7550	807.3811	T	1129.6034	565.3053	1112.5769	556.7921	1111.5928	556.3001	10
16	1744.8496	872.9284	0	0	1726.8390	863.9231	I	1028.5557	514.7815	1011.5292	506.2682	1010.5452	505.7762	9
17	1904.8802	952.9438	0	0	1886.8697	943.9385	C	915.4717	458.2395	898.4451	449.7262	897.4611	449.2342	8
18	2017.9643	1009.4858	0	0	1999.9537	1000.4805	L	755.4410	378.2241	738.4145	369.7109	737.4305	369.2189	7
19	2117.0327	1059.0200	0	0	2099.0222	1050.0147	V	642.3570	321.6821	625.3304	313.1688	624.3464	312.6768	6
20	2218.0804	1109.5438	0	0	2200.0698	1100.5386	T	543.2885	272.1479	526.2620	263.6346	525.2780	263.1426	5
21	2275.1019	1138.0546	0	0	2257.0913	1129.0493	G	442.2409	221.6241	425.2143	213.1108	424.2303	212.6188	4
22	2376.1495	1188.5784	0	0	2358.1390	1179.5731	T	385.2194	193.1133	368.1928	184.6001	367.2088	184.1081	3
23	2513.2085	1257.1079	0	0	2495.1979	1248.1026	H	284.1717	142.5895	267.1452	134.0762	0	0	2
24							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

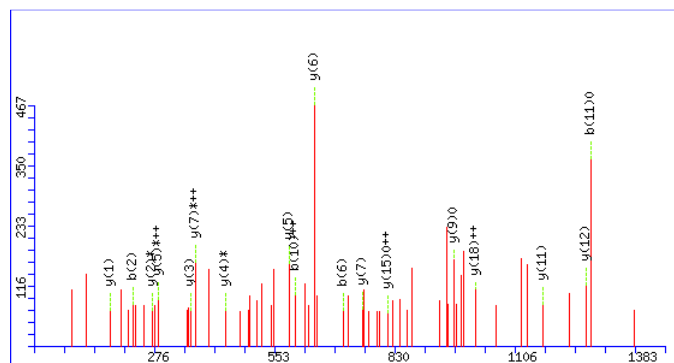
Peptide: 52780.

MS/MS Fragmentation of **DIPLDCCVLGTGEDILGEVANR**: 57.021465@C:6,57.021465@C:8
Found in **IP100737871:IP100854747**

Title: 4.1.1.494.8

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							22
2	229.1183	115.0628	0	0	211.1077	106.0575	I	2359.1268	1180.0671	2342.1003	1171.5538	2341.1163	1171.0618	21
3	326.1710	163.5892	0	0	308.1605	154.5839	P	2246.0428	1123.5250	2229.0162	1115.0117	2228.0322	1114.5197	20
4	439.2551	220.1312	0	0	421.2445	211.1259	L	2148.9900	1074.9986	2131.9634	1066.4854	2130.9794	1065.9934	19
5	554.2821	277.6447	0	0	536.2715	268.6394	D	2035.9059	1018.4566	2018.8794	1009.9433	2017.8954	1009.4513	18
6	714.3127	357.6600	0	0	696.3021	348.6547	C	1920.8790	960.9431	1903.8524	952.4299	1902.8684	951.9379	17
7	829.3396	415.1735	0	0	811.3291	406.1682	D	1760.8483	880.9278	1743.8218	872.4145	1742.8378	871.9225	16
8	989.3703	495.1888	0	0	971.3597	486.1835	C	1645.8214	823.4143	1628.7948	814.9011	1627.8108	814.4091	15
9	1088.4387	544.7230	0	0	1070.4281	535.7177	V	1485.7907	743.3990	1468.7642	734.8857	1467.7802	734.3937	14
10	1201.5228	601.2650	0	0	1183.5122	592.2597	L	1386.7223	693.8648	1369.6958	685.3515	1368.7118	684.8595	13
11	1302.5705	651.7889	0	0	1284.5599	642.7836	T	1273.6383	637.3228	1256.6117	628.8095	1255.6277	628.3175	12
12	1359.5919	680.2996	0	0	1341.5814	671.2943	G	1172.5906	586.7989	1155.5640	578.2857	1154.5800	577.7937	11
13	1488.6345	744.8209	0	0	1470.6239	735.8156	E	1115.5691	558.2882	1098.5426	549.7749	1097.5586	549.2829	10
14	1603.6615	802.3344	0	0	1585.6509	793.3291	D	986.5265	493.7669	969.5000	485.2536	968.5160	484.7616	9
15	1716.7455	858.8764	0	0	1698.7350	849.8711	I	871.4996	436.2534	854.4730	427.7402	853.4890	427.2482	8
16	1829.8296	915.4184	0	0	1811.8190	906.4131	L	758.4155	379.7114	741.3890	371.1981	740.4050	370.7061	7
17	1886.8510	943.9292	0	0	1868.8405	934.9239	G	645.3315	323.1694	628.3049	314.6561	627.3209	314.1641	6
18	2015.8936	1008.4505	0	0	1997.8831	999.4452	E	588.3100	294.6586	571.2835	286.1454	570.2994	285.6534	5
19	2114.9621	1057.9847	0	0	2096.9515	1048.9794	V	459.2674	230.1373	442.2409	221.6241	0	0	4
20	2185.9992	1093.5032	0	0	2167.9886	1084.4979	A	360.1990	180.6031	343.1724	172.0899	0	0	3
21	2300.0421	1150.5247	2283.0155	1142.0114	2282.0315	1141.5194	N	289.1619	145.0846	272.1353	136.5713	0	0	2
22							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 52880.

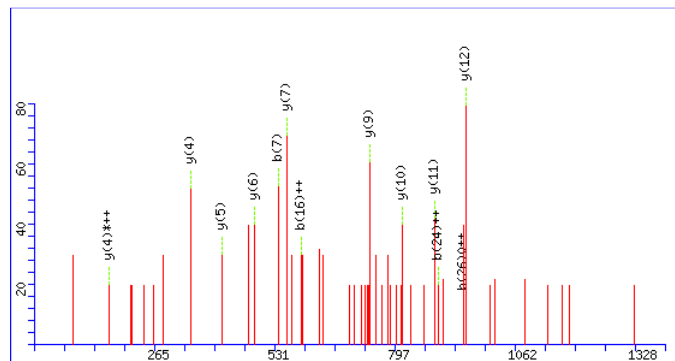
MS/MS Fragmentation of **ASAPAAAAAAAAAAAAAAAAALAAAGGGR**:

Found in **IP100297617**

Title: 4.1.1.3373.4

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							29
2	159.0764	80.0418	0	0	141.0659	71.0366	S	2135.1316	1068.0694	2118.1050	1059.5562	2117.1210	1059.0642	28
3	230.1135	115.5604	0	0	212.1030	106.5551	A	2048.0996	1024.5534	2031.0730	1016.0401	0	0	27
4	327.1663	164.0868	0	0	309.1557	155.0815	P	1977.0625	989.0349	1960.0359	980.5216	0	0	26
5	398.2034	199.6053	0	0	380.1928	190.6001	A	1880.0097	940.5085	1862.9831	931.9952	0	0	25
6	469.2405	235.1239	0	0	451.2300	226.1186	A	1808.9726	904.9899	1791.9460	896.4767	0	0	24
7	540.2776	270.6425	0	0	522.2671	261.6372	A	1737.9355	869.4714	1720.9089	860.9581	0	0	23
8	611.3148	306.1610	0	0	593.3042	297.1557	A	1666.8983	833.9528	1649.8718	825.4395	0	0	22
9	682.3519	341.6796	0	0	664.3413	332.6743	A	1595.8612	798.4343	1578.8347	789.9210	0	0	21
10	753.3890	377.1981	0	0	735.3784	368.1928	A	1524.8241	762.9157	1507.7976	754.4024	0	0	20
11	824.4261	412.7167	0	0	806.4155	403.7114	A	1453.7870	727.3971	1436.7605	718.8839	0	0	19
12	895.4632	448.2352	0	0	877.4526	439.2300	A	1382.7499	691.8786	1365.7233	683.3653	0	0	18
13	966.5003	483.7538	0	0	948.4898	474.7485	A	1311.7128	656.3600	1294.6862	647.8468	0	0	17
14	1037.5374	519.2724	0	0	1019.5269	510.2671	A	1240.6757	620.8415	1223.6491	612.3282	0	0	16
15	1108.5746	554.7909	0	0	1090.5640	545.7856	A	1169.6385	585.3229	1152.6120	576.8096	0	0	15
16	1179.6117	590.3095	0	0	1161.6011	581.3042	A	1098.6014	549.8044	1081.5749	541.2911	0	0	14
17	1250.6488	625.8280	0	0	1232.6382	616.8227	A	1027.5643	514.2858	1010.5378	505.7725	0	0	13
18	1321.6859	661.3466	0	0	1303.6753	652.3413	A	956.5272	478.7672	939.5007	470.2540	0	0	12
19	1392.7230	696.8651	0	0	1374.7124	687.8599	A	885.4901	443.2487	868.4635	434.7354	0	0	11
20	1463.7601	732.3837	0	0	1445.7496	723.3784	A	814.4530	407.7301	797.4264	399.2169	0	0	10
21	1576.8442	788.9257	0	0	1558.8336	779.9204	L	743.4159	372.2116	726.3893	363.6983	0	0	9
22	1647.8813	824.4443	0	0	1629.8707	815.4390	A	630.3318	315.6695	613.3053	307.1563	0	0	8
23	1718.9184	859.9628	0	0	1700.9078	850.9576	A	559.2947	280.1510	542.2681	271.6377	0	0	7
24	1789.9555	895.4814	0	0	1771.9450	886.4761	A	488.2576	244.6324	471.2310	236.1191	0	0	6
25	1860.9926	931.0000	0	0	1842.9821	921.9947	A	417.2205	209.1139	400.1939	200.6006	0	0	5
26	1918.0141	959.5107	0	0	1900.0035	950.5054	G	346.1833	173.5953	329.1568	165.0820	0	0	4
27	1975.0356	988.0214	0	0	1957.0250	979.0161	G	289.1619	145.0846	272.1353	136.5713	0	0	3
28	2032.0570	1016.5322	0	0	2014.0465	1007.5269	G	232.1404	116.5738	215.1139	108.0606	0	0	2
29							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 52897.

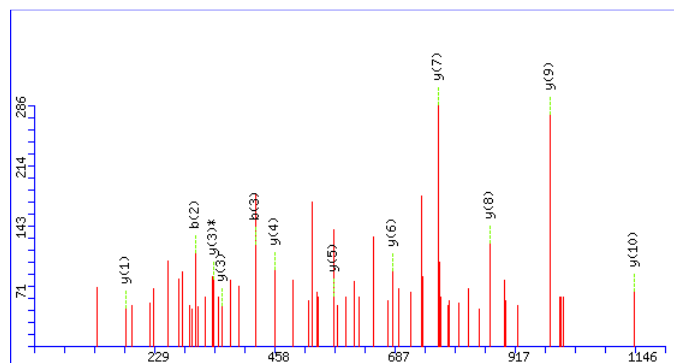
MS/MS Fragmentation of **FCDVSLLVQGR: 57.021465@C:2**

Found in **IP100060141**

Title: 2.1.1.4300.8

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							11
2	308.1063	154.5568	0	0	0	0	C	1146.5936	573.8004	1129.5670	565.2871	1128.5830	564.7951	10
3	423.1333	212.0703	0	0	405.1227	203.0650	D	986.5629	493.7851	969.5364	485.2718	968.5524	484.7798	9
4	522.2017	261.6045	0	0	504.1911	252.5992	V	871.5360	436.2716	854.5094	427.7584	853.5254	427.2663	8
5	609.2337	305.1205	0	0	591.2232	296.1152	S	772.4676	386.7374	755.4410	378.2241	754.4570	377.7321	7
6	722.3178	361.6625	0	0	704.3072	352.6573	L	685.4355	343.2214	668.4090	334.7081	0	0	6
7	835.4019	418.2046	0	0	817.3913	409.1993	L	572.3515	286.6794	555.3249	278.1661	0	0	5
8	934.4703	467.7388	0	0	916.4597	458.7335	V	459.2674	230.1373	442.2409	221.6241	0	0	4
9	1062.5288	531.7681	1045.5023	523.2548	1044.5183	522.7628	Q	360.1990	180.6031	343.1724	172.0899	0	0	3
10	1119.5503	560.2788	1102.5238	551.7655	1101.5397	551.2735	G	232.1404	116.5738	215.1139	108.0606	0	0	2
11							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 52920.

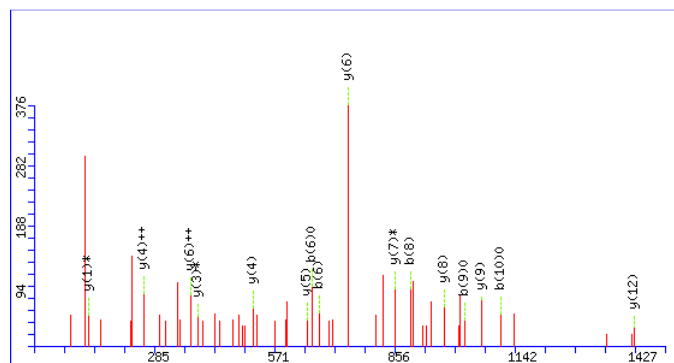
MS/MS Fragmentation of **FLSGSWSEFSTQPENFLK**:

Found in **IP100306087;IP100982224**

Title: 3.1.1.4041.7

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							18
2	261.1598	131.0835	0	0	0	0	L	1956.9338	978.9705	1939.9072	970.4573	1938.9232	969.9652	17
3	348.1918	174.5995	0	0	330.1812	165.5942	S	1843.8497	922.4285	1826.8232	913.9152	1825.8392	913.4232	16
4	405.2132	203.1103	0	0	387.2027	194.1050	G	1756.8177	878.9125	1739.7911	870.3992	1738.8071	869.9072	15
5	492.2453	246.6263	0	0	474.2347	237.6210	S	1699.7962	850.4018	1682.7697	841.8885	1681.7857	841.3965	14
6	678.3246	339.6659	0	0	660.3140	330.6606	W	1612.7642	806.8857	1595.7376	798.3725	1594.7536	797.8805	13
7	765.3566	383.1819	0	0	747.3461	374.1767	S	1426.6849	713.8461	1409.6583	705.3328	1408.6743	704.8408	12
8	894.3992	447.7032	0	0	876.3886	438.6980	E	1339.6529	670.3301	1322.6263	661.8168	1321.6423	661.3248	11
9	1041.4676	521.2374	0	0	1023.4571	512.2322	F	1210.6103	605.8088	1193.5837	597.2955	1192.5997	596.8035	10
10	1128.4997	564.7535	0	0	1110.4891	555.7482	S	1063.5419	532.2746	1046.5153	523.7613	1045.5313	523.2693	9
11	1229.5473	615.2773	0	0	1211.5368	606.2720	T	976.5098	488.7585	959.4833	480.2453	958.4993	479.7533	8
12	1357.6059	679.3066	1340.5794	670.7933	1339.5953	670.3013	Q	875.4621	438.2347	858.4356	429.7214	857.4516	429.2294	7
13	1454.6587	727.8330	1437.6321	719.3197	1436.6481	718.8277	P	747.4036	374.2054	730.3770	365.6921	729.3930	365.2001	6
14	1583.7013	792.3543	1566.6747	783.8410	1565.6907	783.3490	E	650.3508	325.6790	633.3243	317.1658	632.3402	316.6738	5
15	1697.7442	849.3757	1680.7176	840.8625	1679.7336	840.3705	N	521.3082	261.1577	504.2817	252.6445	0	0	4
16	1844.8126	922.9099	1827.7861	914.3967	1826.8020	913.9047	F	407.2653	204.1363	390.2387	195.6230	0	0	3
17	1957.8967	979.4520	1940.8701	970.9387	1939.8861	970.4467	L	260.1969	130.6021	243.1703	122.0888	0	0	2
18							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 52963.

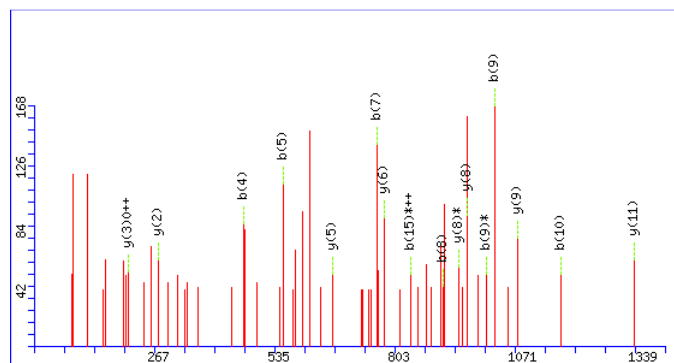
MS/MS Fragmentation of **RPTISPNNFLGQLLDYEK**:

Found in **IP100028428**

Title: 4.1.1.1446.6

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	157.1084	79.0578	140.0818	70.5446	0	0	R							19
2	254.1612	127.5842	237.1346	119.0709	0	0	P	2096.0699	1048.5386	2079.0433	1040.0253	2078.0593	1039.5333	18
3	355.2088	178.1081	338.1823	169.5948	337.1983	169.1028	T	1999.0171	1000.0122	1981.9906	991.4989	1981.0066	991.0069	17
4	468.2929	234.6501	451.2663	226.1368	450.2823	225.6448	I	1897.9694	949.4884	1880.9429	940.9751	1879.9589	940.4831	16
5	555.3249	278.1661	538.2984	269.6528	537.3144	269.1608	S	1784.8854	892.9463	1767.8588	884.4331	1766.8748	883.9410	15
6	652.3777	326.6925	635.3511	318.1792	634.3671	317.6872	P	1697.8533	849.4303	1680.8268	840.9170	1679.8428	840.4250	14
7	766.4206	383.7139	749.3941	375.2007	748.4100	374.7087	N	1600.8006	800.9039	1583.7740	792.3907	1582.7900	791.8986	13
8	913.4890	457.2482	896.4625	448.7349	895.4785	448.2429	F	1486.7577	743.8825	1469.7311	735.3692	1468.7471	734.8772	12
9	1027.5320	514.2696	1010.5054	505.7563	1009.5214	505.2643	N	1339.6892	670.3483	1322.6627	661.8350	1321.6787	661.3430	11
10	1174.6004	587.8038	1157.5738	579.2905	1156.5898	578.7985	F	1225.6463	613.3268	1208.6198	604.8135	1207.6358	604.3215	10
11	1287.6844	644.3459	1270.6579	635.8326	1269.6739	635.3406	L	1078.5779	539.7926	1061.5514	531.2793	1060.5673	530.7873	9
12	1344.7059	672.8566	1327.6793	664.3433	1326.6953	663.8513	G	965.4938	483.2506	948.4673	474.7373	947.4833	474.2453	8
13	1472.7645	736.8859	1455.7379	728.3726	1454.7539	727.8806	Q	908.4724	454.7398	891.4458	446.2266	890.4618	445.7345	7
14	1585.8485	793.4279	1568.8220	784.9146	1567.8380	784.4226	L	780.4138	390.7105	763.3872	382.1973	762.4032	381.7053	6
15	1698.9326	849.9699	1681.9061	841.4567	1680.9220	840.9647	L	667.3297	334.1685	650.3032	325.6552	649.3192	325.1632	5
16	1813.9595	907.4834	1796.9330	898.9701	1795.9490	898.4781	D	554.2457	277.6265	537.2191	269.1132	536.2351	268.6212	4
17	1977.0229	989.0151	1959.9963	980.5018	1959.0123	980.0098	Y	439.2187	220.1130	422.1922	211.5997	421.2082	211.1077	3
18	2106.0655	1053.5364	2089.0389	1045.0231	2088.0549	1044.5311	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
19							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 53012.

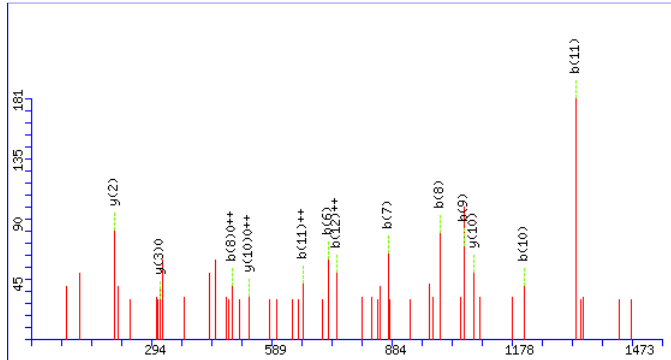
MS/MS Fragmentation of **RIDQSEFEGFEYINPLLLSTEEVS**:

Found in **IP100013749;IP100651700;IP100965675**

Title: 4.1.1.2845.8

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_3.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	157.1084	79.0578	140.0818	70.5446	0	0	R							24
2	270.1925	135.5999	253.1659	127.0866	0	0	I	2659.2661	1330.1367	2642.2396	1321.6234	2641.2556	1321.1314	23
3	385.2194	193.1133	368.1928	184.6001	367.2088	184.1081	D	2546.1821	1273.5947	2529.1555	1265.0814	2528.1715	1264.5894	22
4	513.2780	257.1426	496.2514	248.6293	495.2674	248.1373	Q	2431.1551	1216.0812	2414.1286	1207.5679	2413.1446	1207.0759	21
5	600.3100	300.6586	583.2835	292.1454	582.2994	291.6534	S	2303.0966	1152.0519	2286.0700	1143.5386	2285.0860	1143.0466	20
6	729.3526	365.1799	712.3260	356.6667	711.3420	356.1747	E	2216.0645	1108.5359	2199.0380	1100.0226	2198.0540	1099.5306	19
7	876.4210	438.7141	859.3945	430.2009	858.4104	429.7089	F	2087.0219	1044.0146	2069.9954	1035.5013	2069.0114	1035.0093	18
8	1005.4636	503.2354	988.4371	494.7222	987.4530	494.2302	E	1939.9535	970.4804	1922.9270	961.9671	1921.9430	961.4751	17
9	1062.4851	531.7462	1045.4585	523.2329	1044.4745	522.7409	G	1810.9109	905.9591	1793.8844	897.4458	1792.9004	896.9538	16
10	1209.5535	605.2804	1192.5269	596.7671	1191.5429	596.2751	F	1753.8895	877.4484	1736.8629	868.9351	1735.8789	868.4431	15
11	1338.5961	669.8017	1321.5695	661.2884	1320.5855	660.7964	E	1606.8210	803.9142	1589.7945	795.4009	1588.8105	794.9089	14
12	1501.6594	751.3333	1484.6329	742.8201	1483.6488	742.3281	Y	1477.7785	739.3929	1460.7519	730.8796	1459.7679	730.3876	13
13	1614.7435	807.8754	1597.7169	799.3621	1596.7329	798.8701	I	1314.7151	657.8612	1297.6886	649.3479	1296.7046	648.8559	12
14	1728.7864	864.8968	1711.7598	856.3836	1710.7758	855.8916	N	1201.6311	601.3192	1184.6045	592.8059	1183.6205	592.3139	11
15	1825.8392	913.4232	1808.8126	904.9099	1807.8286	904.4179	P	1087.5881	544.2977	0	0	1069.5776	535.2924	10
16	1938.9232	969.9652	1921.8967	961.4520	1920.9127	960.9600	L	990.5354	495.7713	0	0	972.5248	486.7660	9
17	2052.0073	1026.5073	2034.9807	1017.9940	2033.9967	1017.5020	L	877.4513	439.2293	0	0	859.4407	430.2240	8
18	2165.0913	1083.0493	2148.0648	1074.5360	2147.0808	1074.0440	L	764.3672	382.6873	0	0	746.3567	373.6820	7
19	2252.1234	1126.5653	2235.0968	1118.0521	2234.1128	1117.5600	S	651.2832	326.1452	0	0	633.2726	317.1399	6
20	2353.1711	1177.0892	2336.1445	1168.5759	2335.1605	1168.0839	T	564.2511	282.6292	0	0	546.2406	273.6239	5
21	2482.2136	1241.6105	2465.1871	1233.0972	2464.2031	1232.6052	E	463.2035	232.1054	0	0	445.1929	223.1001	4
22	2611.2562	1306.1318	2594.2297	1297.6185	2593.2457	1297.1265	E	334.1609	167.5841	0	0	316.1503	158.5788	3
23	2698.2883	1349.6478	2681.2617	1341.1345	2680.2777	1340.6425	S	205.1183	103.0628	0	0	187.1077	94.0575	2
24							V	118.0863	59.5468	0	0	0	0	1

Peptide View

Peptide: 53266.

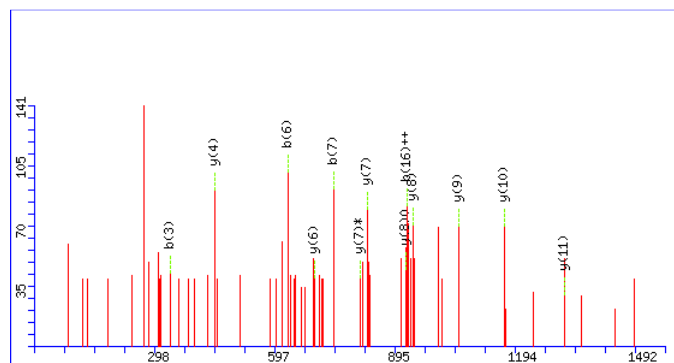
MS/MS Fragmentation of **ELPPPLELFDLDETFSSEK**:

Found in **IP100006535**

Title: 4.1.1.2209.7

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120214ry¥120214ry_414C2-43_4_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							20
2	243.1339	122.0706	0	0	225.1234	113.0653	L	2174.0903	1087.5488	2157.0638	1079.0355	2156.0798	1078.5435	19
3	340.1867	170.5970	0	0	322.1761	161.5917	P	2061.0063	1031.0068	2043.9797	1022.4935	2042.9957	1022.0015	18
4	437.2395	219.1234	0	0	419.2289	210.1181	P	1963.9535	982.4804	1946.9270	973.9671	1945.9430	973.4751	17
5	534.2922	267.6498	0	0	516.2817	258.6445	P	1866.9008	933.9540	1849.8742	925.4407	1848.8902	924.9487	16
6	631.3450	316.1761	0	0	613.3344	307.1709	P	1769.8480	885.4276	1752.8214	876.9144	1751.8374	876.4223	15
7	744.4291	372.7182	0	0	726.4185	363.7129	L	1672.7952	836.9012	1655.7687	828.3880	1654.7847	827.8960	14
8	873.4716	437.2395	0	0	855.4611	428.2342	E	1559.7112	780.3592	1542.6846	771.8459	1541.7006	771.3539	13
9	986.5557	493.7815	0	0	968.5451	484.7762	L	1430.6686	715.8379	1413.6420	707.3246	1412.6580	706.8326	12
10	1133.6241	567.3157	0	0	1115.6136	558.3104	F	1317.5845	659.2959	1300.5580	650.7826	1299.5739	650.2906	11
11	1248.6511	624.8292	0	0	1230.6405	615.8239	D	1170.5161	585.7617	1153.4895	577.2484	1152.5055	576.7564	10
12	1361.7351	681.3712	0	0	1343.7246	672.3659	L	1055.4891	528.2482	1038.4626	519.7349	1037.4786	519.2429	9
13	1476.7621	738.8847	0	0	1458.7515	729.8794	D	942.4051	471.7062	925.3785	463.1929	924.3945	462.7009	8
14	1605.8047	803.4060	0	0	1587.7941	794.4007	E	827.3781	414.1927	810.3516	405.6794	809.3676	405.1874	7
15	1706.8523	853.9298	0	0	1688.8418	844.9245	T	698.3355	349.6714	681.3090	341.1581	680.3250	340.6661	6
16	1853.9208	927.4640	0	0	1835.9102	918.4587	F	597.2879	299.1476	580.2613	290.6343	579.2773	290.1423	5
17	1940.9528	970.9800	0	0	1922.9422	961.9747	S	450.2195	225.6134	433.1929	217.1001	432.2089	216.6081	4
18	2027.9848	1014.4960	0	0	2009.9743	1005.4908	S	363.1874	182.0974	346.1609	173.5841	345.1769	173.0921	3
19	2157.0274	1079.0173	0	0	2139.0168	1070.0121	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
20							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 53308.

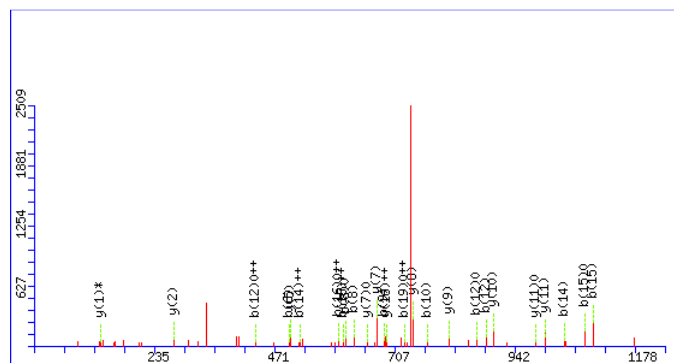
MS/MS Fragmentation of **PGTTGSGAGSGGPGGLTSAAPAGGDKK**:

Found in **IP100031812;IP100041601;IP100643807**

Title: 1.1.1.8494.11

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120210ry¥120210ry_32R1-32_3_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	98.0600	49.5337	0	0	0	0	P							27
2	155.0815	78.0444	0	0	0	0	G	2116.0265	1058.5169	2099.0000	1050.0036	2098.0160	1049.5116	26
3	256.1292	128.5682	0	0	238.1186	119.5629	T	2059.0051	1030.0062	2041.9785	1021.4929	2040.9945	1021.0009	25
4	357.1769	179.0921	0	0	339.1663	170.0868	T	1957.9574	979.4823	1940.9308	970.9691	1939.9468	970.4770	24
5	414.1983	207.6028	0	0	396.1878	198.5975	G	1856.9097	928.9585	1839.8831	920.4452	1838.8991	919.9532	23
6	501.2304	251.1188	0	0	483.2198	242.1135	S	1799.8882	900.4478	1782.8617	891.9345	1781.8777	891.4425	22
7	558.2518	279.6295	0	0	540.2413	270.6243	G	1712.8562	856.9317	1695.8297	848.4185	1694.8456	847.9265	21
8	629.2889	315.1481	0	0	611.2784	306.1428	A	1655.8347	828.4210	1638.8082	819.9077	1637.8242	819.4157	20
9	686.3104	343.6588	0	0	668.2998	334.6536	G	1584.7976	792.9025	1567.7711	784.3892	1566.7871	783.8972	19
10	773.3424	387.1749	0	0	755.3319	378.1696	S	1527.7762	764.3917	1510.7496	755.8784	1509.7656	755.3864	18
11	830.3639	415.6856	0	0	812.3533	406.6803	G	1440.7441	720.8757	1423.7176	712.3624	1422.7336	711.8704	17
12	887.3854	444.1963	0	0	869.3748	435.1910	G	1383.7227	692.3650	1366.6961	683.8517	1365.7121	683.3597	16
13	984.4381	492.7227	0	0	966.4276	483.7174	P	1326.7012	663.8542	1309.6747	655.3410	1308.6906	654.8490	15
14	1041.4596	521.2334	0	0	1023.4490	512.2281	G	1229.6484	615.3279	1212.6219	606.8146	1211.6379	606.3226	14
15	1098.4810	549.7442	0	0	1080.4705	540.7389	G	1172.6270	586.8171	1155.6004	578.3039	1154.6164	577.8118	13
16	1211.5651	606.2862	0	0	1193.5545	597.2809	L	1115.6055	558.3064	1098.5790	549.7931	1097.5950	549.3011	12
17	1312.6128	656.8100	0	0	1294.6022	647.8047	T	1002.5215	501.7644	985.4949	493.2511	984.5109	492.7591	11
18	1399.6448	700.3260	0	0	1381.6343	691.3208	S	901.4738	451.2405	884.4472	442.7272	883.4632	442.2352	10
19	1470.6819	735.8446	0	0	1452.6714	726.8393	A	814.4417	407.7245	797.4152	399.2112	796.4312	398.7192	9
20	1541.7190	771.3632	0	0	1523.7085	762.3579	A	743.4046	372.2060	726.3781	363.6927	725.3941	363.2007	8
21	1638.7718	819.8895	0	0	1620.7612	810.8843	P	672.3675	336.6874	655.3410	328.1741	654.3570	327.6821	7
22	1709.8089	855.4081	0	0	1691.7984	846.4028	A	575.3148	288.1610	558.2882	279.6477	557.3042	279.1557	6
23	1766.8304	883.9188	0	0	1748.8198	874.9135	G	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	5
24	1823.8518	912.4296	0	0	1805.8413	903.4243	G	447.2562	224.1317	430.2296	215.6185	429.2456	215.1264	4
25	1938.8788	969.9430	0	0	1920.8682	960.9378	D	390.2347	195.6210	373.2082	187.1077	372.2241	186.6157	3
26	2066.9738	1033.9905	2049.9472	1025.4772	2048.9632	1024.9852	K	275.2078	138.1075	258.1812	129.5942	0	0	2
27							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 53507.

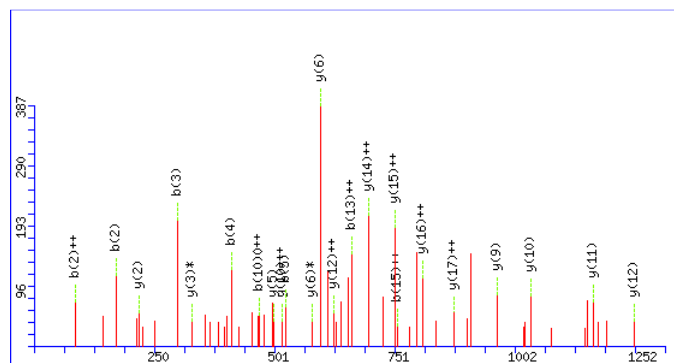
MS/MS Fragmentation of **GLELLAASEAPRPPGQAK**:

Found in **IP100219006;IP100880106**

Title: 2.1.1.2862.8

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120210ry¥120210ry_585A1-55_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							19
2	171.1128	86.0600	0	0	0	0	L	1862.9971	932.0022	1845.9705	923.4889	1844.9865	922.9969	18
3	300.1554	150.5813	0	0	282.1448	141.5761	E	1749.9130	875.4601	1732.8864	866.9469	1731.9024	866.4549	17
4	413.2395	207.1234	0	0	395.2289	198.1181	L	1620.8704	810.9388	1603.8438	802.4256	1602.8598	801.9336	16
5	526.3235	263.6654	0	0	508.3130	254.6601	L	1507.7863	754.3968	1490.7598	745.8835	1489.7758	745.3915	15
6	597.3606	299.1840	0	0	579.3501	290.1787	A	1394.7023	697.8548	1377.6757	689.3415	1376.6917	688.8495	14
7	668.3978	334.7025	0	0	650.3872	325.6972	A	1323.6652	662.3362	1306.6386	653.8229	1305.6546	653.3309	13
8	755.4298	378.2185	0	0	737.4192	369.2132	S	1252.6280	626.8177	1235.6015	618.3044	1234.6175	617.8124	12
9	884.4724	442.7398	0	0	866.4618	433.7345	E	1165.5960	583.3016	1148.5695	574.7884	1147.5854	574.2964	11
10	955.5095	478.2584	0	0	937.4989	469.2531	A	1036.5534	518.7803	1019.5269	510.2671	1018.5429	509.7751	10
11	1052.5623	526.7848	0	0	1034.5517	517.7795	P	965.5163	483.2618	948.4898	474.7485	947.5057	474.2565	9
12	1208.6634	604.8353	1191.6368	596.3220	1190.6528	595.8300	R	868.4635	434.7354	851.4370	426.2221	850.4530	425.7301	8
13	1323.6903	662.3488	1306.6638	653.8355	1305.6797	653.3435	D	712.3624	356.6849	695.3359	348.1716	694.3519	347.6796	7
14	1420.7431	710.8752	1403.7165	702.3619	1402.7325	701.8699	P	597.3355	299.1714	580.3089	290.6581	0	0	6
15	1517.7958	759.4016	1500.7693	750.8883	1499.7853	750.3963	P	500.2827	250.6450	483.2562	242.1317	0	0	5
16	1574.8173	787.9123	1557.7907	779.3990	1556.8067	778.9070	G	403.2300	202.1186	386.2034	193.6053	0	0	4
17	1702.8759	851.9416	1685.8493	843.4283	1684.8653	842.9363	Q	346.2085	173.6079	329.1819	165.0946	0	0	3
18	1773.9130	887.4601	1756.8864	878.9469	1755.9024	878.4549	A	218.1499	109.5786	201.1234	101.0653	0	0	2
19							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 53889.

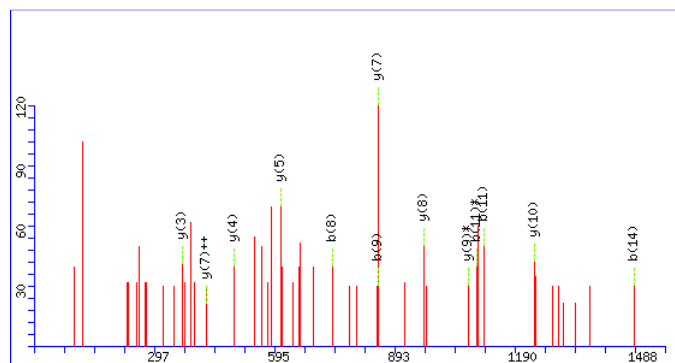
MS/MS Fragmentation of **GEPSSPGELNFPYLFQLLEDEGYK**:

Found in **IP100382748,IP100465271,IP100514542,IP100514834,IP100647220,IP100847938,IP100848045,IP100978535,IP100982934**

Title: 4.1.1.3872.11

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_2.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							24
2	187.0713	94.0393	0	0	169.0608	85.0340	E	2672.2766	1336.6420	2655.2501	1328.1287	2654.2661	1327.6367	23
3	284.1241	142.5657	0	0	266.1135	133.5604	P	2543.2340	1272.1207	2526.2075	1263.6074	2525.2235	1263.1154	22
4	371.1561	186.0817	0	0	353.1456	177.0764	S	2446.1813	1223.5943	2429.1547	1215.0810	2428.1707	1214.5890	21
5	458.1882	229.5977	0	0	440.1776	220.5924	S	2359.1493	1180.0783	2342.1227	1171.5650	2341.1387	1171.0730	20
6	555.2409	278.1241	0	0	537.2304	269.1188	P	2272.1172	1136.5623	2255.0907	1128.0490	2254.1067	1127.5570	19
7	612.2624	306.6348	0	0	594.2518	297.6295	G	2175.0645	1088.0359	2158.0379	1079.5226	2157.0539	1079.0306	18
8	741.3050	371.1561	0	0	723.2944	362.1508	E	2118.0430	1059.5251	2101.0165	1051.0119	2100.0324	1050.5199	17
9	854.3890	427.6982	0	0	836.3785	418.6929	L	1989.0004	995.0038	1971.9739	986.4906	1970.9898	985.9986	16
10	968.4320	484.7196	951.4054	476.2063	950.4214	475.7143	N	1875.9163	938.4618	1858.8898	929.9485	1857.9058	929.4565	15
11	1115.5004	558.2538	1098.4738	549.7406	1097.4898	549.2485	F	1761.8734	881.4403	1744.8469	872.9271	1743.8629	872.4351	14
12	1212.5531	606.7802	1195.5266	598.2669	1194.5426	597.7749	P	1614.8050	807.9061	1597.7785	799.3929	1596.7944	798.9009	13
13	1375.6165	688.3119	1358.5899	679.7986	1357.6059	679.3066	Y	1517.7522	759.3798	1500.7257	750.8665	1499.7417	750.3745	12
14	1488.7005	744.8539	1471.6740	736.3406	1470.6900	735.8486	L	1354.6889	677.8481	1337.6624	669.3348	1336.6783	668.8428	11
15	1635.7690	818.3881	1618.7424	809.8748	1617.7584	809.3828	F	1241.6048	621.3061	1224.5783	612.7928	1223.5943	612.3008	10
16	1763.8275	882.4174	1746.8010	873.9041	1745.8170	873.4121	Q	1094.5364	547.7719	1077.5099	539.2586	1076.5259	538.7666	9
17	1876.9116	938.9594	1859.8850	930.4462	1858.9010	929.9542	L	966.4779	483.7426	949.4513	475.2293	948.4673	474.7373	8
18	1989.9957	995.5015	1972.9691	986.9882	1971.9851	986.4962	L	853.3938	427.2005	836.3672	418.6873	835.3832	418.1953	7
19	2119.0382	1060.0228	2102.0117	1051.5095	2101.0277	1051.0175	E	740.3097	370.6585	723.2832	362.1452	722.2992	361.6532	6
20	2234.0652	1117.5362	2217.0386	1109.0230	2216.0546	1108.5310	D	611.2671	306.1372	594.2406	297.6239	593.2566	297.1319	5
21	2363.1078	1182.0575	2346.0812	1173.5443	2345.0972	1173.0522	E	496.2402	248.6237	479.2136	240.1105	478.2296	239.6185	4
22	2420.1292	1210.5683	2403.1027	1202.0550	2402.1187	1201.5630	G	367.1976	184.1024	350.1710	175.5892	0	0	3
23	2583.1926	1292.0999	2566.1660	1283.5867	2565.1820	1283.0946	Y	310.1761	155.5917	293.1496	147.0784	0	0	2
24							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 54013.

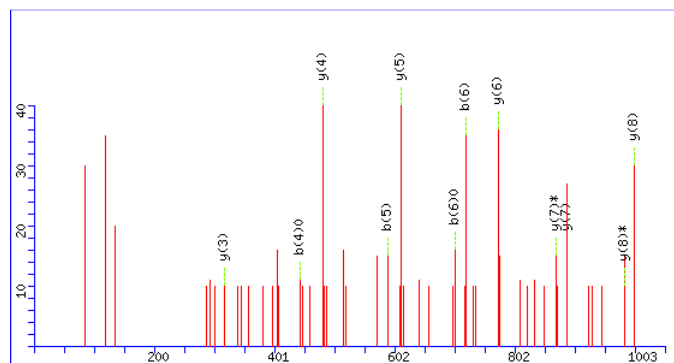
MS/MS Fragmentation of **SDIFEEVLNMYTAK**:

Found in **IP100307325**

Title: 4.1.1.4342.3

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							15
2	203.0662	102.0368	0	0	185.0557	93.0315	D	1735.8248	868.4160	1718.7982	859.9027	1717.8142	859.4107	14
3	316.1503	158.5788	0	0	298.1397	149.5735	I	1620.7978	810.9025	1603.7713	802.3893	1602.7872	801.8973	13
4	463.2187	232.1130	0	0	445.2082	223.1077	F	1507.7137	754.3605	1490.6872	745.8472	1489.7032	745.3552	12
5	592.2613	296.6343	0	0	574.2508	287.6290	E	1360.6453	680.8263	1343.6188	672.3130	1342.6348	671.8210	11
6	721.3039	361.1556	0	0	703.2933	352.1503	E	1231.6027	616.3050	1214.5762	607.7917	1213.5922	607.2997	10
7	820.3723	410.6898	0	0	802.3618	401.6845	V	1102.5601	551.7837	1085.5336	543.2704	1084.5496	542.7784	9
8	933.4564	467.2318	0	0	915.4458	458.2266	L	1003.4917	502.2495	986.4652	493.7362	985.4812	493.2442	8
9	1047.4993	524.2533	1030.4728	515.7400	1029.4888	515.2480	N	890.4077	445.7075	873.3811	437.1942	872.3971	436.7022	7
10	1210.5626	605.7850	1193.5361	597.2717	1192.5521	596.7797	Y	776.3647	388.6860	759.3382	380.1727	758.3542	379.6807	6
11	1341.6031	671.3052	1324.5766	662.7919	1323.5926	662.2999	M	613.3014	307.1543	596.2749	298.6411	595.2908	298.1491	5
12	1504.6665	752.8369	1487.6399	744.3236	1486.6559	743.8316	Y	482.2609	241.6341	465.2344	233.1208	464.2504	232.6288	4
13	1605.7141	803.3607	1588.6876	794.8474	1587.7036	794.3554	T	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	3
14	1676.7513	838.8793	1659.7247	830.3660	1658.7407	829.8740	A	218.1499	109.5786	201.1234	101.0653	0	0	2
15							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 54095.

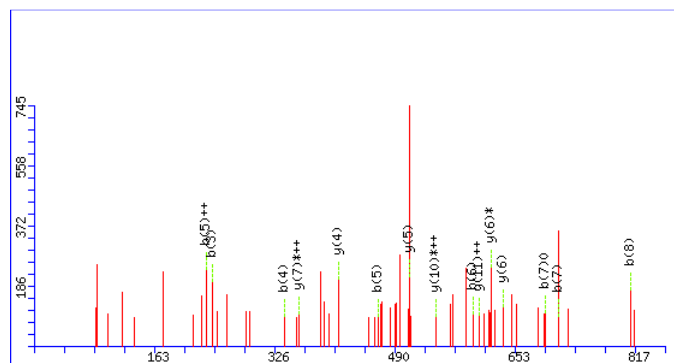
MS/MS Fragmentation of **AGIVQEDVQPPGLK**:

Found in **IP100397994;IP100942406;IP101018956**

Title: 2.1.1.2030.4

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							14
2	129.0659	65.0366	0	0	0	0	G	1379.7529	690.3801	1362.7264	681.8668	1361.7423	681.3748	13
3	242.1499	121.5786	0	0	0	0	I	1322.7314	661.8694	1305.7049	653.3561	1304.7209	652.8641	12
4	341.2183	171.1128	0	0	0	0	V	1209.6474	605.3273	1192.6208	596.8141	1191.6368	596.3220	11
5	469.2769	235.1421	452.2504	226.6288	0	0	Q	1110.5790	555.7931	1093.5524	547.2798	1092.5684	546.7878	10
6	598.3195	299.6634	581.2930	291.1501	580.3089	290.6581	E	982.5204	491.7638	965.4938	483.2506	964.5098	482.7585	9
7	713.3464	357.1769	696.3199	348.6636	695.3359	348.1716	D	853.4778	427.2425	836.4512	418.7293	835.4672	418.2373	8
8	812.4149	406.7111	795.3883	398.1978	794.4043	397.7058	V	738.4509	369.7291	721.4243	361.2158	0	0	7
9	940.4734	470.7404	923.4469	462.2271	922.4629	461.7351	Q	639.3824	320.1949	622.3559	311.6816	0	0	6
10	1037.5262	519.2667	1020.4997	510.7535	1019.5156	510.2615	P	511.3239	256.1656	494.2973	247.6523	0	0	5
11	1134.5790	567.7931	1117.5524	559.2798	1116.5684	558.7878	P	414.2711	207.6392	397.2445	199.1259	0	0	4
12	1191.6004	596.3039	1174.5739	587.7906	1173.5899	587.2986	G	317.2183	159.1128	300.1918	150.5995	0	0	3
13	1304.6845	652.8459	1287.6579	644.3326	1286.6739	643.8406	L	260.1969	130.6021	243.1703	122.0888	0	0	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 54158.

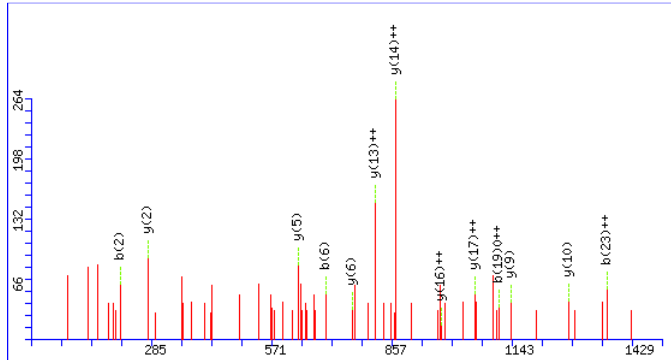
MS/MS Fragmentation of **VLMVEEPMNLEWLYGCPPPYHTFEFPVYMK: 57.021465@C:17**

Found in **IP100464968**

Title: 4.1.1.1782.10

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							31
2	213.1598	107.0835	0	0	0	0	L	3686.6714	1843.8394	3669.6449	1835.3261	3668.6609	1834.8341	30
3	344.2002	172.6038	0	0	0	0	M	3573.5874	1787.2973	3556.5608	1778.7841	3555.5768	1778.2920	29
4	443.2687	222.1380	0	0	0	0	V	3442.5469	1721.7771	3425.5203	1713.2638	3424.5363	1712.7718	28
5	572.3112	286.6593	0	0	554.3007	277.6540	E	3343.4785	1672.2429	3326.4519	1663.7296	3325.4679	1663.2376	27
6	701.3538	351.1806	0	0	683.3433	342.1753	E	3214.4359	1607.7216	3197.4093	1599.2083	3196.4253	1598.7163	26
7	798.4066	399.7069	0	0	780.3960	390.7017	P	3085.3933	1543.2003	3068.3667	1534.6870	3067.3827	1534.1950	25
8	885.4386	443.2230	0	0	867.4281	434.2177	S	2988.3405	1494.6739	2971.3140	1486.1606	2970.3300	1485.6686	24
9	1016.4791	508.7432	0	0	998.4686	499.7379	M	2901.3085	1451.1579	2884.2819	1442.6446	2883.2979	1442.1526	23
10	1130.5220	565.7647	1113.4955	557.2514	1112.5115	556.7594	N	2770.2680	1385.6376	2753.2415	1377.1244	2752.2574	1376.6324	22
11	1243.6061	622.3067	1226.5796	613.7934	1225.5955	613.3014	L	2656.2251	1328.6162	2639.1985	1320.1029	2638.2145	1319.6109	21
12	1372.6487	686.8280	1355.6222	678.3147	1354.6381	677.8227	E	2543.1410	1272.0741	2526.1145	1263.5609	2525.1305	1263.0689	20
13	1558.7280	779.8676	1541.7015	771.3544	1540.7174	770.8624	W	2414.0984	1207.5529	2397.0719	1199.0396	2396.0879	1198.5476	19
14	1671.8121	836.4097	1654.7855	827.8964	1653.8015	827.4044	L	2228.0191	1114.5132	2210.9926	1105.9999	2210.0086	1105.5079	18
15	1834.8754	917.9413	1817.8489	909.4281	1816.8648	908.9361	Y	2114.9351	1057.9712	2097.9085	1049.4579	2096.9245	1048.9659	17
16	1891.8969	946.4521	1874.8703	937.9388	1873.8863	937.4468	G	1951.8717	976.4395	1934.8452	967.9262	1933.8612	967.4342	16
17	2051.9275	1026.4674	2034.9010	1017.9541	2033.9170	1017.4621	C	1894.8503	947.9288	1877.8237	939.4155	1876.8397	938.9235	15
18	2148.9803	1074.9938	2131.9537	1066.4805	2130.9697	1065.9885	P	1734.8196	867.9134	1717.7931	859.4002	1716.8090	858.9082	14
19	2246.0330	1123.5202	2229.0065	1115.0069	2228.0225	1114.5149	P	1637.7668	819.3871	1620.7403	810.8738	1619.7563	810.3818	13
20	2343.0858	1172.0465	2326.0593	1163.5333	2325.0752	1163.0413	P	1540.7141	770.8607	1523.6875	762.3474	1522.7035	761.8554	12
21	2506.1491	1253.5782	2489.1226	1245.0649	2488.1386	1244.5729	Y	1443.6613	722.3343	1426.6348	713.8210	1425.6508	713.3290	11
22	2643.2081	1322.1077	2626.1815	1313.5944	2625.1975	1313.1024	H	1280.5980	640.8026	1263.5714	632.2894	1262.5874	631.7973	10
23	2744.2557	1372.6315	2727.2292	1364.1182	2726.2452	1363.6262	T	1143.5391	572.2732	1126.5125	563.7599	1125.5285	563.2679	9
24	2891.3241	1446.1657	2874.2976	1437.6524	2873.3136	1437.1604	F	1042.4914	521.7493	1025.4648	513.2361	1024.4808	512.7441	8
25	3020.3667	1510.6870	3003.3402	1502.1737	3002.3562	1501.6817	E	895.4230	448.2151	878.3964	439.7019	877.4124	439.2098	7
26	3149.4093	1575.2083	3132.3828	1566.6950	3131.3988	1566.2030	E	766.3804	383.6938	749.3538	375.1806	748.3698	374.6886	6
27	3246.4621	1623.7347	3229.4355	1615.2214	3228.4515	1614.7294	P	637.3378	319.1725	620.3112	310.6593	0	0	5
28	3345.5305	1673.2689	3328.5040	1664.7556	3327.5199	1664.2636	V	540.2850	270.6462	523.2585	262.1329	0	0	4
29	3508.5938	1754.8006	3491.5673	1746.2873	3490.5833	1745.7953	Y	441.2166	221.1119	424.1901	212.5987	0	0	3
30	3639.6343	1820.3208	3622.6078	1811.8075	3621.6238	1811.3155	M	278.1533	139.5803	261.1267	131.0670	0	0	2
31							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 54198.

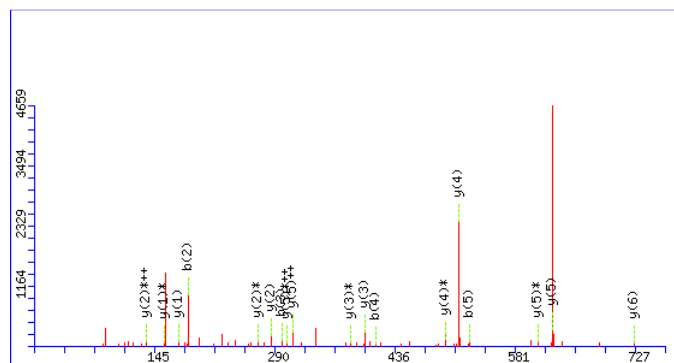
MS/MS Fragmentation of **SVINLLR**:

Found in **IP100185258;IP100335280;IP100373788;IP100910461;IP100924782;IP100927218;IP100939663;IP100983692**

Title: 2.1.1.3271.2

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4.2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							7
2	187.1077	94.0575	0	0	169.0972	85.0522	V	727.4825	364.2449	710.4559	355.7316	0	0	6
3	300.1918	150.5995	0	0	282.1812	141.5942	I	628.4141	314.7107	611.3875	306.1974	0	0	5
4	414.2347	207.6210	397.2082	199.1077	396.2241	198.6157	N	515.3300	258.1686	498.3035	249.6554	0	0	4
5	527.3188	264.1630	510.2922	255.6497	509.3082	255.1577	L	401.2871	201.1472	384.2605	192.6339	0	0	3
6	640.4028	320.7051	623.3763	312.1918	622.3923	311.6998	L	288.2030	144.6051	271.1765	136.0919	0	0	2
7							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 54304.

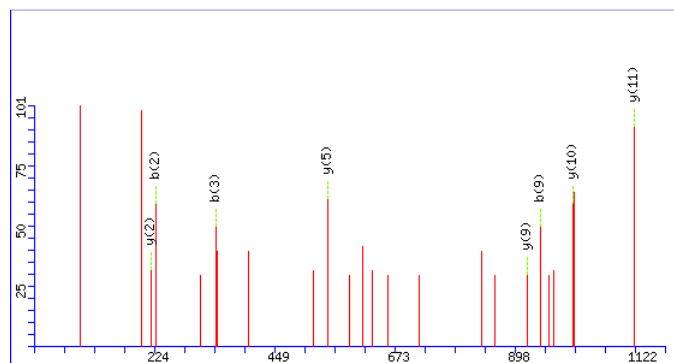
MS/MS Fragmentation of **NISSTALFLAAK**:

Found in **IP100030313;IP100217564;IP100925381;IP100927944**

Title: 3.1.1.3658.4

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							13
2	228.1343	114.5708	211.1077	106.0575	0	0	I	1234.7406	617.8739	1217.7140	609.3606	1216.7300	608.8686	12
3	341.2183	171.1128	324.1918	162.5995	0	0	I	1121.6565	561.3319	1104.6299	552.8186	1103.6459	552.3266	11
4	428.2504	214.6288	411.2238	206.1155	410.2398	205.6235	S	1008.5724	504.7898	991.5459	496.2766	990.5619	495.7846	10
5	515.2824	258.1448	498.2558	249.6316	497.2718	249.1395	S	921.5404	461.2738	904.5138	452.7606	903.5298	452.2686	9
6	616.3301	308.6687	599.3035	300.1554	598.3195	299.6634	T	834.5084	417.7578	817.4818	409.2445	816.4978	408.7525	8
7	687.3672	344.1872	670.3406	335.6740	669.3566	335.1819	A	733.4607	367.2340	716.4341	358.7207	0	0	7
8	800.4512	400.7293	783.4247	392.2160	782.4407	391.7240	L	662.4236	331.7154	645.3970	323.2022	0	0	6
9	947.5197	474.2635	930.4931	465.7502	929.5091	465.2582	F	549.3395	275.1734	532.3130	266.6601	0	0	5
10	1060.6037	530.8055	1043.5772	522.2922	1042.5932	521.8002	L	402.2711	201.6392	385.2445	193.1259	0	0	4
11	1131.6408	566.3241	1114.6143	557.8108	1113.6303	557.3188	A	289.1870	145.0972	272.1605	136.5839	0	0	3
12	1202.6780	601.8426	1185.6514	593.3293	1184.6674	592.8373	A	218.1499	109.5786	201.1234	101.0653	0	0	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 54379.

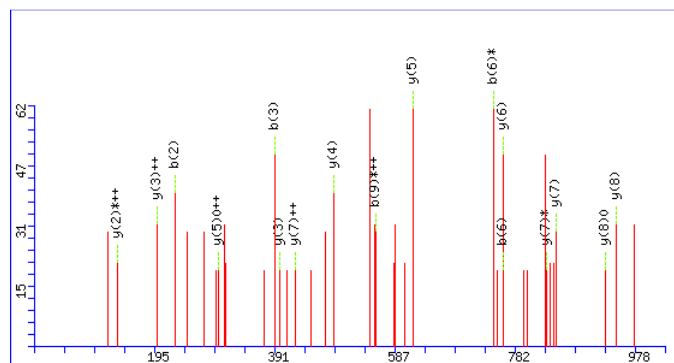
MS/MS Fragmentation of **LDYFQPSFESLIR: 0.984016@Q:5**

Found in **IP100032966;IP100556562;IP100955795;IP101014028**

Title: 3.1.1.4067.3

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_3_3.mgf

ProteinPilot Peptide Confidence > 99%

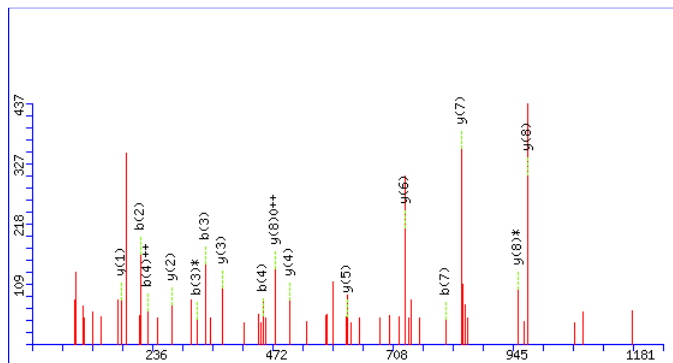


#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							13
2	229.1183	115.0628	0	0	211.1077	106.0575	D	1502.7162	751.8617	1485.6896	743.3485	1484.7056	742.8564	12
3	392.1816	196.5944	0	0	374.1710	187.5892	Y	1387.6892	694.3483	1370.6627	685.8350	1369.6787	685.3430	11
4	539.2500	270.1287	0	0	521.2395	261.1234	F	1224.6259	612.8166	1207.5994	604.3033	1206.6154	603.8113	10
5	668.2926	334.6499	651.2661	326.1367	650.2821	325.6447	Q	1077.5575	539.2824	1060.5310	530.7691	1059.5469	530.2771	9
6	765.3454	383.1763	748.3188	374.6631	747.3348	374.1710	P	948.5149	474.7611	931.4884	466.2478	930.5043	465.7558	8
7	852.3774	426.6923	835.3509	418.1791	834.3668	417.6871	S	851.4621	426.2347	834.4356	417.7214	833.4516	417.2294	7
8	999.4458	500.2266	982.4193	491.7133	981.4353	491.2213	F	764.4301	382.7187	747.4036	374.2054	746.4196	373.7134	6
9	1128.4884	564.7478	1111.4619	556.2346	1110.4779	555.7426	E	617.3617	309.1845	600.3352	300.6712	599.3511	300.1792	5
10	1215.5204	608.2639	1198.4939	599.7506	1197.5099	599.2586	S	488.3191	244.6632	471.2926	236.1499	470.3085	235.6579	4
11	1328.6045	664.8059	1311.5780	656.2926	1310.5939	655.8006	L	401.2871	201.1472	384.2605	192.6339	0	0	3
12	1441.6886	721.3479	1424.6620	712.8347	1423.6780	712.3426	I	288.2030	144.6051	271.1765	136.0919	0	0	2
13							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: **54753**.

MS/MS Fragmentation of **NVQILNMVTR**:
 Found in **IP100007309;IP100640747;IP100939500;IP100953449;IP100977435;IP101025371**
 Title: 2.1.1.4440.5
 Data file: Y:\TT5600(CiRA1)\¥2012-02¥120206ry¥120206ry_aHDF1419-P10_2_2.mgf
 ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							10
2	214.1186	107.5629	197.0921	99.0497	0	0	V	1073.6136	537.3104	1056.5870	528.7972	1055.6030	528.3051	9
3	342.1772	171.5922	325.1506	163.0790	0	0	Q	974.5452	487.7762	957.5186	479.2629	956.5346	478.7709	8
4	455.2613	228.1343	438.2347	219.6210	0	0	I	846.4866	423.7469	829.4600	415.2337	828.4760	414.7416	7
5	568.3453	284.6763	551.3188	276.1630	0	0	L	733.4025	367.2049	716.3760	358.6916	715.3920	358.1996	6
6	682.3883	341.6978	665.3617	333.1845	0	0	N	620.3185	310.6629	603.2919	302.1496	602.3079	301.6576	5
7	813.4287	407.2180	796.4022	398.7047	0	0	M	506.2755	253.6414	489.2490	245.1281	488.2650	244.6361	4
8	912.4971	456.7522	895.4706	448.2389	0	0	V	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
9	1013.5448	507.2761	996.5183	498.7628	995.5343	498.2708	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 54900.

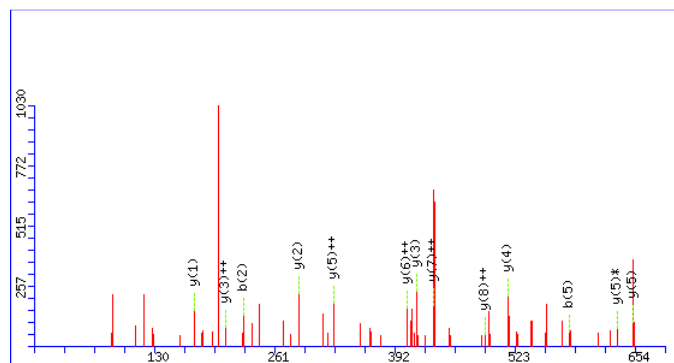
MS/MS Fragmentation of **DLGCHVELR: 57.021465@C:4**

Found in **IP100020196;IP100871811;IP101009398;IP101010733;IP101011916**

Title: 1.1.1.9664.2

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120210ry¥120210ry_585A1-55_3_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							9
2	229.1183	115.0628	0	0	211.1077	106.0575	L	983.5091	492.2582	966.4826	483.7449	965.4985	483.2529	8
3	286.1397	143.5735	0	0	268.1292	134.5682	G	870.4250	435.7162	853.3985	427.2029	852.4145	426.7109	7
4	446.1704	223.5888	0	0	428.1598	214.5836	C	813.4036	407.2054	796.3770	398.6922	795.3930	398.2001	6
5	583.2293	292.1183	0	0	565.2187	283.1130	H	653.3729	327.1901	636.3464	318.6768	635.3624	318.1848	5
6	682.2977	341.6525	0	0	664.2872	332.6472	V	516.3140	258.6606	499.2875	250.1474	498.3035	249.6554	4
7	811.3403	406.1738	0	0	793.3298	397.1685	E	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
8	924.4244	462.7158	0	0	906.4138	453.7105	L	288.2030	144.6051	271.1765	136.0919	0	0	2
9							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 54981.

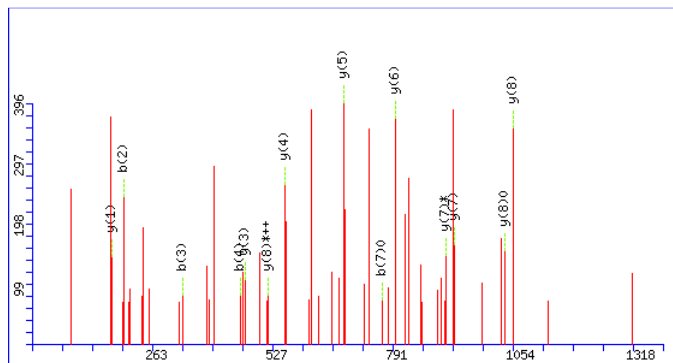
MS/MS Fragmentation of **SLEQIESFFR**:

Found in **IP100179969;IP100744602**

Title: 3.1.1.3941.5

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							10
2	201.1234	101.0653	0	0	183.1128	92.0600	L	1168.5997	584.8035	1151.5732	576.2902	1150.5891	575.7982	9
3	330.1660	165.5866	0	0	312.1554	156.5813	E	1055.5156	528.2615	1038.4891	519.7482	1037.5051	519.2562	8
4	458.2245	229.6159	441.1980	221.1026	440.2140	220.6106	Q	926.4730	463.7402	909.4465	455.2269	908.4625	454.7349	7
5	571.3086	286.1579	554.2821	277.6447	553.2980	277.1527	I	798.4145	399.7109	781.3879	391.1976	780.4039	390.7056	6
6	700.3512	350.6792	683.3246	342.1660	682.3406	341.6740	E	685.3304	343.1688	668.3039	334.6556	667.3198	334.1636	5
7	787.3832	394.1953	770.3567	385.6820	769.3727	385.1900	S	556.2878	278.6475	539.2613	270.1343	538.2772	269.6423	4
8	934.4516	467.7295	917.4251	459.2162	916.4411	458.7242	F	469.2558	235.1315	452.2292	226.6183	0	0	3
9	1081.5201	541.2637	1064.4935	532.7504	1063.5095	532.2584	F	322.1874	161.5973	305.1608	153.0840	0	0	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 55150.

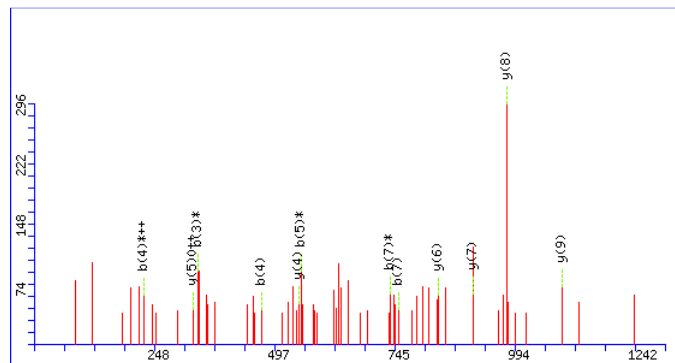
MS/MS Fragmentation of **QLLDTIAACEMLR: -17.026549@N-term(Q),57.021465@C:9**

Found in **IP100394805**

Title: 4.1.1.1114.8

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233	0	0	Q							14
2	242.1499	121.5786	225.1234	113.0653	0	0	L	1534.7604	767.8838	1517.7338	759.3706	1516.7498	758.8785	13
3	355.2340	178.1206	338.2074	169.6074	0	0	L	1421.6763	711.3418	1404.6498	702.8285	1403.6658	702.3365	12
4	470.2609	235.6341	453.2344	227.1208	452.2504	226.6288	D	1308.5923	654.7998	1291.5657	646.2865	1290.5817	645.7945	11
5	571.3086	286.1579	554.2821	277.6447	553.2980	277.1527	T	1193.5653	597.2863	1176.5388	588.7730	1175.5547	588.2810	10
6	684.3927	342.7000	667.3661	334.1867	666.3821	333.6947	I	1092.5176	546.7625	1075.4911	538.2492	1074.5071	537.7572	9
7	755.4298	378.2185	738.4032	369.7053	737.4192	369.2132	A	979.4336	490.2204	962.4070	481.7071	961.4230	481.2151	8
8	826.4669	413.7371	809.4403	405.2238	808.4563	404.7318	A	908.3965	454.7019	891.3699	446.1886	890.3859	445.6966	7
9	986.4975	493.7524	969.4710	485.2391	968.4870	484.7471	C	837.3593	419.1833	820.3328	410.6700	819.3488	410.1780	6
10	1115.5401	558.2737	1098.5136	549.7604	1097.5296	549.2684	E	677.3287	339.1680	660.3021	330.6547	659.3181	330.1627	5
11	1244.5827	622.7950	1227.5562	614.2817	1226.5722	613.7897	E	548.2861	274.6467	531.2595	266.1334	530.2755	265.6414	4
12	1375.6232	688.3152	1358.5967	679.8020	1357.6127	679.3100	M	419.2435	210.1254	402.2170	201.6121	0	0	3
13	1488.7073	744.8573	1471.6807	736.3440	1470.6967	735.8520	L	288.2030	144.6051	271.1765	136.0919	0	0	2
14							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 55153.

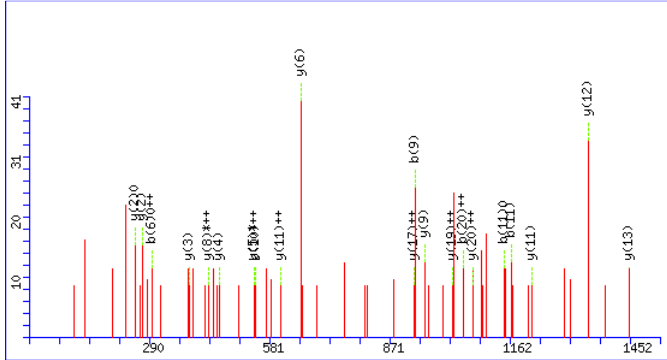
MS/MS Fragmentation of **VLDLTADFGYAVGEVEALVHEEA**EVPTALEK:

Found in **IPI00013621**

Title: 5.1.1.517.2

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							31
2	215.1026	108.0550	0	0	197.0921	99.0497	D	3217.5423	1609.2748	3200.5158	1600.7615	3199.5317	1600.2695	30
3	328.1867	164.5970	0	0	310.1761	155.5917	L	3102.5154	1551.7613	3085.4888	1543.2480	3084.5048	1542.7560	29
4	443.2136	222.1105	0	0	425.2031	213.1052	D	2989.4313	1495.2193	2972.4048	1486.7060	2971.4207	1486.2140	28
5	544.2613	272.6343	0	0	526.2508	263.6290	T	2874.4044	1437.7058	2857.3778	1429.1925	2856.3938	1428.7005	27
6	615.2984	308.1529	0	0	597.2879	299.1476	A	2773.3567	1387.1820	2756.3301	1378.6687	2755.3461	1378.1767	26
7	730.3254	365.6663	0	0	712.3148	356.6610	D	2702.3196	1351.6634	2685.2930	1343.1501	2684.3090	1342.6581	25
8	877.3938	439.2005	0	0	859.3832	430.1953	F	2587.2926	1294.1500	2570.2661	1285.6367	2569.2821	1285.1447	24
9	934.4153	467.7113	0	0	916.4047	458.7060	G	2440.2242	1220.6157	2423.1977	1212.1025	2422.2136	1211.6105	23
10	1097.4786	549.2429	0	0	1079.4680	540.2376	Y	2383.2027	1192.1050	2366.1762	1183.5917	2365.1922	1183.0997	22
11	1168.5157	584.7615	0	0	1150.5051	575.7562	A	2220.1394	1110.5733	2203.1129	1102.0601	2202.1289	1101.5681	21
12	1267.5841	634.2957	0	0	1249.5735	625.2904	V	2149.1023	1075.0548	2132.0758	1066.5415	2131.0917	1066.0495	20
13	1324.6056	662.8064	0	0	1306.5950	653.8011	G	2050.0339	1025.5206	2033.0073	1017.0073	2032.0233	1016.5153	19
14	1453.6482	727.3277	0	0	1435.6376	718.3224	E	1993.0124	997.0099	1975.9859	988.4966	1975.0019	988.0046	18
15	1552.7166	776.8619	0	0	1534.7060	767.8566	V	1863.9698	932.4886	1846.9433	923.9753	1845.9593	923.4833	17
16	1681.7592	841.3832	0	0	1663.7486	832.3779	E	1764.9014	882.9543	1747.8749	874.4411	1746.8909	873.9491	16
17	1752.7963	876.9018	0	0	1734.7857	867.8965	A	1635.8588	818.4331	1618.8323	809.9198	1617.8483	809.4278	15
18	1865.8804	933.4438	0	0	1847.8698	924.4385	L	1564.8217	782.9145	1547.7952	774.4012	1546.8112	773.9092	14
19	1964.9488	982.9780	0	0	1946.9382	973.9727	V	1451.7377	726.3725	1434.7111	717.8592	1433.7271	717.3672	13
20	2102.0077	1051.5075	0	0	2083.9931	1042.5022	H	1352.6692	676.8383	1335.6427	668.3250	1334.6587	667.8330	12
21	2231.0503	1116.0288	0	0	2213.0397	1107.0235	E	1215.6103	608.3088	1198.5838	599.7955	1197.5998	599.3035	11
22	2360.0929	1180.5501	0	0	2342.0823	1171.5448	E	1086.5677	543.7875	1069.5412	535.2742	1068.5572	534.7822	10
23	2431.1300	1216.0686	0	0	2413.1194	1207.0633	A	957.5251	479.2662	940.4986	470.7529	939.5146	470.2609	9
24	2560.1726	1280.5899	0	0	2542.1620	1271.5846	E	886.4880	443.7477	869.4615	435.2344	868.4775	434.7424	8
25	2659.2410	1330.1241	0	0	2641.2304	1321.1188	V	757.4454	379.2264	740.4189	370.7131	739.4349	370.2211	7
26	2756.2938	1378.6505	0	0	2738.2832	1369.6452	P	658.3770	329.6921	641.3505	321.1789	640.3665	320.6869	6
27	2857.3414	1429.1744	0	0	2839.3309	1420.1691	T	561.3243	281.1658	544.2977	272.6525	543.3137	272.1605	5
28	2928.3785	1464.6929	0	0	2910.3680	1455.6876	A	460.2766	230.6419	443.2500	222.1287	442.2660	221.6366	4
29	3041.4626	1521.2349	0	0	3023.4520	1512.2297	L	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
30	3170.5052	1585.7562	0	0	3152.4946	1576.7510	E	278.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
31							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 55404.

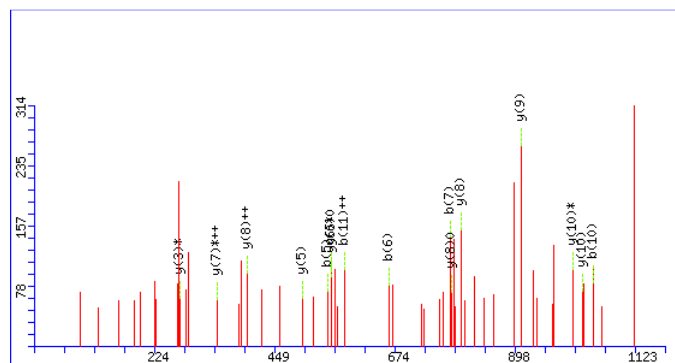
MS/MS Fragmentation of **HVSILDLPGNLIIPQATLGGR**:

Found in **IP100062050**

Title: 4.1.1.1244.5

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	138.0662	69.5367	0	0	0	0	H							22
2	237.1346	119.0709	0	0	0	0	V	2160.2751	1080.6412	2143.2485	1072.1279	2142.2645	1071.6359	21
3	324.1666	162.5870	0	0	306.1561	153.5817	S	2061.2067	1031.1070	2044.1801	1022.5937	2043.1961	1022.1017	20
4	437.2507	219.1290	0	0	419.2401	210.1237	I	1974.1746	987.5910	1957.1481	979.0777	1956.1641	978.5857	19
5	550.3348	275.6710	0	0	532.3242	266.6657	L	1861.0906	931.0489	1844.0640	922.5356	1843.0800	922.0436	18
6	665.3617	333.1845	0	0	647.3511	324.1792	D	1748.0065	874.5069	1730.9799	865.9936	1729.9959	865.5016	17
7	778.4458	389.7265	0	0	760.4352	380.7212	L	1632.9796	816.9934	1615.9530	808.4801	1614.9690	807.9881	16
8	875.4985	438.2529	0	0	857.4880	429.2476	P	1519.8955	760.4514	1502.8689	751.9381	1501.8849	751.4461	15
9	932.5200	466.7636	0	0	914.5094	457.7584	G	1422.8427	711.9250	1405.8162	703.4117	1404.8322	702.9197	14
10	1046.5629	523.7851	1029.5364	515.2718	1028.5524	514.7798	N	1365.8213	683.4143	1348.7947	674.9010	1347.8107	674.4090	13
11	1159.6470	580.3271	1142.6204	571.8139	1141.6364	571.3218	I	1251.7783	626.3928	1234.7518	617.8795	1233.7678	617.3875	12
12	1272.7310	636.8692	1255.7045	628.3559	1254.7205	627.8639	L	1138.6943	569.8508	1121.6677	561.3375	1120.6837	560.8455	11
13	1385.8151	693.4112	1368.7886	684.8979	1367.8045	684.4059	I	1025.6102	513.3087	1008.5837	504.7955	1007.5996	504.3035	10
14	1498.8992	749.9532	1481.8726	741.4400	1480.8886	740.9479	I	912.5261	456.7667	895.4996	448.2534	894.5156	447.7614	9
15	1595.9519	798.4796	1578.9254	789.9663	1577.9414	789.4743	P	799.4421	400.2247	782.4155	391.7114	781.4315	391.2194	8
16	1724.0105	862.5089	1706.9840	853.9956	1706.0000	853.5036	Q	702.3893	351.6983	685.3628	343.1850	684.3788	342.6930	7
17	1795.0476	898.0275	1778.0211	889.5142	1777.0371	889.0222	A	574.3307	287.6690	557.3042	279.1557	556.3202	278.6637	6
18	1896.0953	948.5513	1879.0688	940.0380	1878.0847	939.5460	T	503.2936	252.1504	486.2671	243.6372	485.2831	243.1452	5
19	2009.1794	1005.0933	1992.1528	996.5801	1991.1688	996.0880	L	402.2459	201.6266	385.2194	193.1133	0	0	4
20	2066.2008	1033.6041	2049.1743	1025.0908	2048.1903	1024.5988	G	289.1619	145.0846	272.1353	136.5713	0	0	3
21	2123.2223	1062.1148	2106.1958	1053.6015	2105.2117	1053.1095	G	232.1404	116.5738	215.1139	108.0606	0	0	2
22							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 55530.

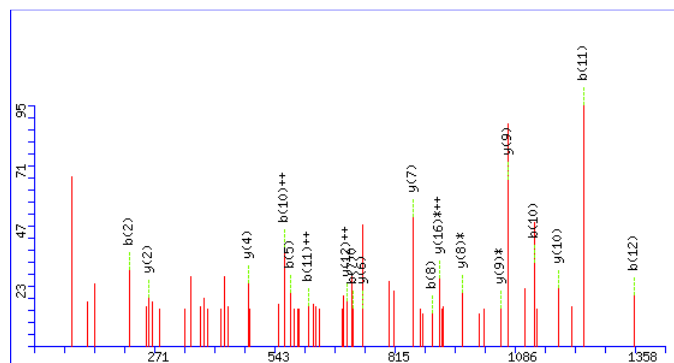
MS/MS Fragmentation of **SQLDHGTYNDLISQLEELIK**:

Found in **IP100010486;IP100219602;IP100980409**

Title: 5.1.1.892.3

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4.5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							21
2	216.0979	108.5526	199.0713	100.0393	198.0873	99.5473	Q	2342.2238	1171.6155	2325.1973	1163.1023	2324.2133	1162.6103	20
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	L	2214.1652	1107.5863	2197.1387	1099.0730	2196.1547	1098.5810	19
4	444.2089	222.6081	427.1823	214.0948	426.1983	213.6028	D	2101.0812	1051.0442	2084.0546	1042.5310	2083.0706	1042.0389	18
5	581.2678	291.1375	564.2413	282.6243	563.2572	282.1323	H	1986.0542	993.5308	1969.0277	985.0175	1968.0437	984.5255	17
6	638.2893	319.6483	621.2627	311.1350	620.2787	310.6430	G	1848.9953	925.0013	1831.9688	916.4880	1830.9848	915.9960	16
7	739.3369	370.1721	722.3104	361.6588	721.3264	361.1668	T	1791.9739	896.4906	1774.9473	887.9773	1773.9633	887.4853	15
8	902.4003	451.7038	885.3737	443.1905	884.3897	442.6985	Y	1690.9262	845.9667	1673.8996	837.4535	1672.9156	836.9614	14
9	1016.4432	508.7252	999.4167	500.2120	998.4326	499.7200	N	1527.8628	764.4351	1510.8363	755.9218	1509.8523	755.4298	13
10	1131.4701	566.2387	1114.4436	557.7254	1113.4596	557.2334	D	1413.8199	707.4136	1396.7934	698.9003	1395.8094	698.4083	12
11	1244.5542	622.7807	1227.5277	614.2675	1226.5436	613.7755	L	1298.7930	649.9001	1281.7664	641.3869	1280.7824	640.8948	11
12	1357.6383	679.3228	1340.6117	670.8095	1339.6277	670.3175	I	1185.7089	593.3581	1168.6824	584.8448	1167.6984	584.3528	10
13	1444.6703	722.8388	1427.6437	714.3255	1426.6597	713.8335	S	1072.6249	536.8161	1055.5983	528.3028	1054.6143	527.8108	9
14	1572.7289	786.8681	1555.7023	778.3548	1554.7183	777.8628	Q	985.5928	493.3000	968.5663	484.7868	967.5823	484.2948	8
15	1685.8129	843.4101	1668.7864	834.8968	1667.8024	834.4048	L	857.5342	429.2708	840.5077	420.7575	839.5237	420.2655	7
16	1814.8555	907.9314	1797.8290	899.4181	1796.8450	898.9261	E	744.4502	372.7287	727.4236	364.2155	726.4396	363.7234	6
17	1943.8981	972.4527	1926.8716	963.9394	1925.8876	963.4474	E	615.4076	308.2074	598.3810	299.6942	597.3970	299.2022	5
18	2056.9822	1028.9947	2039.9556	1020.4815	2038.9716	1019.9895	L	486.3650	243.6861	469.3384	235.1729	0	0	4
19	2170.0663	1085.5368	2153.0397	1077.0235	2152.0557	1076.5315	I	373.2809	187.1441	356.2544	178.6308	0	0	3
20	2283.1503	1142.0788	2266.1238	1133.5655	2265.1398	1133.0735	L	260.1969	130.6021	243.1703	122.0888	0	0	2
21							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 55970.

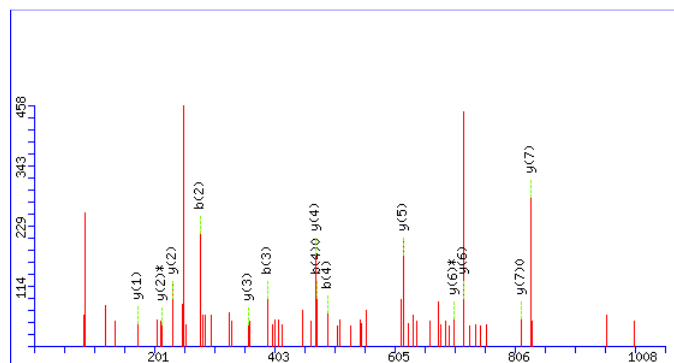
MS/MS Fragmentation of **DYITFIEGR**:

Found in **IP100419221;IP100945380**

Title: 3.1.1.1396.3

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							9
2	279.0975	140.0524	0	0	261.0870	131.0471	Y	998.5306	499.7689	981.5040	491.2556	980.5200	490.7636	8
3	392.1816	196.5944	0	0	374.1710	187.5892	I	835.4672	418.2373	818.4407	409.7240	817.4567	409.2320	7
4	493.2293	247.1183	0	0	475.2187	238.1130	T	722.3832	361.6952	705.3566	353.1819	704.3726	352.6899	6
5	640.2977	320.6525	0	0	622.2871	311.6472	F	621.3355	311.1714	604.3089	302.6581	603.3249	302.1661	5
6	753.3818	377.1945	0	0	735.3712	368.1892	I	474.2671	237.6372	457.2405	229.1239	456.2565	228.6319	4
7	882.4244	441.7158	0	0	864.4138	432.7105	E	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	3
8	939.4458	470.2266	0	0	921.4353	461.2213	G	232.1404	116.5738	215.1139	108.0606	0	0	2
9							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 56062.

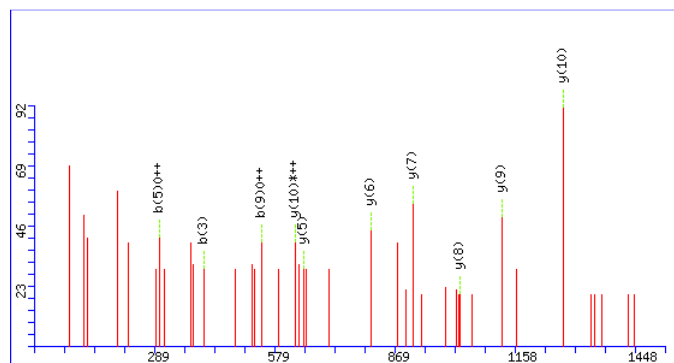
MS/MS Fragmentation of **NFFTDVVDLYIK**:

Found in **IP100005119,IP100940542,IP100979652**

Title: 4.1.1.3061.5

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							12
2	262.1186	131.5629	245.0921	123.0497	0	0	F	1423.7144	712.3608	1406.6878	703.8476	1405.7038	703.3556	11
3	409.1870	205.0972	392.1605	196.5839	0	0	F	1276.6460	638.8266	1259.6194	630.3134	1258.6354	629.8213	10
4	510.2347	255.6210	493.2082	247.1077	492.2241	246.6157	T	1129.5776	565.2924	1112.5510	556.7791	1111.5670	556.2871	9
5	625.2617	313.1345	608.2351	304.6212	607.2511	304.1292	D	1028.5299	514.7686	1011.5033	506.2553	1010.5193	505.7633	8
6	724.3301	362.6687	707.3035	354.1554	706.3195	353.6634	V	913.5029	457.2551	896.4764	448.7418	895.4924	448.2498	7
7	887.3934	444.2003	870.3668	435.6871	869.3828	435.1951	Y	814.4345	407.7209	797.4080	399.2076	796.4240	398.7156	6
8	1002.4203	501.7138	985.3938	493.2005	984.4098	492.7085	D	651.3712	326.1892	634.3447	317.6760	633.3606	317.1840	5
9	1115.5044	558.2558	1098.4779	549.7426	1097.4938	549.2506	L	536.3443	268.6758	519.3177	260.1625	0	0	4
10	1278.5677	639.7875	1261.5412	631.2742	1260.5572	630.7822	Y	423.2602	212.1337	406.2336	203.6205	0	0	3
11	1391.6518	696.3295	1374.6252	687.8163	1373.6412	687.3243	I	260.1969	130.6021	243.1703	122.0888	0	0	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 56212.

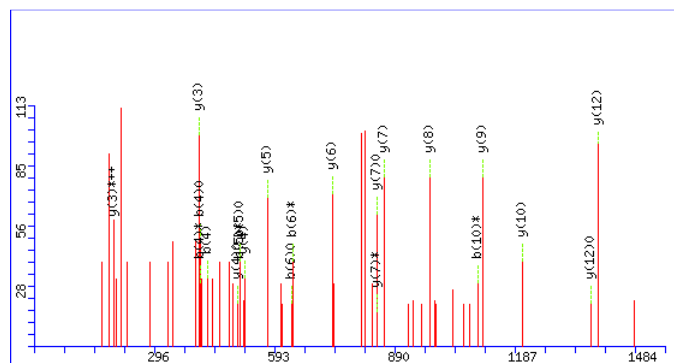
MS/MS Fragmentation of **QLGEVLQCGICTK: 57.021465@C:9,57.021465@C:12**

Found in **IP100328658;IP100328659;IP100333837;IP100974058**

Title: 2.1.1.2705.11

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233	0	0	Q							14
2	242.1499	121.5786	225.1234	113.0653	0	0	L	1506.7291	753.8682	1489.7025	745.3549	1488.7185	744.8629	13
3	299.1714	150.0893	282.1448	141.5761	0	0	G	1393.6450	697.3261	1376.6185	688.8129	1375.6345	688.3209	12
4	428.2140	214.6106	411.1874	206.0974	410.2034	205.6053	E	1336.6236	668.8154	1319.5970	660.3021	1318.6130	659.8101	11
5	527.2824	264.1448	510.2558	255.6316	509.2718	255.1396	V	1207.5810	604.2941	1190.5544	595.7808	1189.5704	595.2888	10
6	656.3250	328.6661	639.2984	320.1529	638.3144	319.6608	E	1108.5125	554.7599	1091.4860	546.2466	1090.5020	545.7546	9
7	769.4090	385.2082	752.3825	376.6949	751.3985	376.2029	L	979.4700	490.2386	962.4434	481.7253	961.4594	481.2333	8
8	897.4676	449.2375	880.4411	440.7242	879.4571	440.2322	Q	866.3859	433.6966	849.3593	425.1833	848.3753	424.6913	7
9	1057.4983	529.2528	1040.4717	520.7395	1039.4877	520.2475	C	738.3273	369.6673	721.3008	361.1540	720.3167	360.6620	6
10	1114.5197	557.7635	1097.4932	549.2502	1096.5092	548.7582	G	578.2967	289.6520	561.2701	281.1387	560.2861	280.6467	5
11	1227.6038	614.3055	1210.5773	605.7923	1209.5932	605.3003	I	521.2752	261.1412	504.2486	252.6280	503.2646	252.1360	4
12	1387.6345	694.3209	1370.6079	685.8076	1369.6239	685.3156	C	408.1911	204.5992	391.1646	196.0859	390.1806	195.5939	3
13	1488.6821	744.8447	1471.6556	736.3314	1470.6716	735.8394	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 56402.

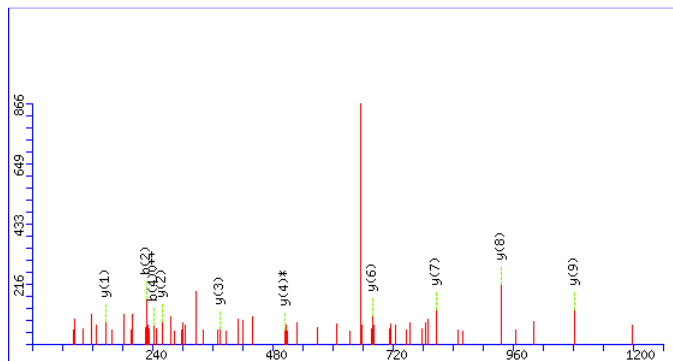
MS/MS Fragmentation of **EVFEETGFDIK**:

Found in **IP100292382;IP100440151**

Title: 2.1.1.4278.7

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							11
2	229.1183	115.0628	0	0	211.1077	106.0575	V	1184.5834	592.7953	1167.5568	584.2821	1166.5728	583.7900	10
3	376.1867	188.5970	0	0	358.1761	179.5917	F	1085.5150	543.2611	1068.4884	534.7478	1067.5044	534.2558	9
4	505.2293	253.1183	0	0	487.2187	244.1130	E	938.4466	469.7269	921.4200	461.2136	920.4360	460.7216	8
5	634.2719	317.6396	0	0	616.2613	308.6343	E	809.4040	405.2056	792.3774	396.6923	791.3934	396.2003	7
6	735.3196	368.1634	0	0	717.3090	359.1581	T	680.3614	340.6843	663.3348	332.1710	662.3508	331.6790	6
7	792.3410	396.6742	0	0	774.3305	387.6689	G	579.3137	290.1605	562.2871	281.6472	561.3031	281.1552	5
8	939.4094	470.2084	0	0	921.3989	461.2031	F	522.2922	261.6498	505.2657	253.1365	504.2817	252.6445	4
9	1054.4364	527.7218	0	0	1036.4258	518.7165	D	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
10	1167.5204	584.2639	0	0	1149.5099	575.2586	I	260.1969	130.6021	243.1703	122.0888	0	0	2
11							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 56589.

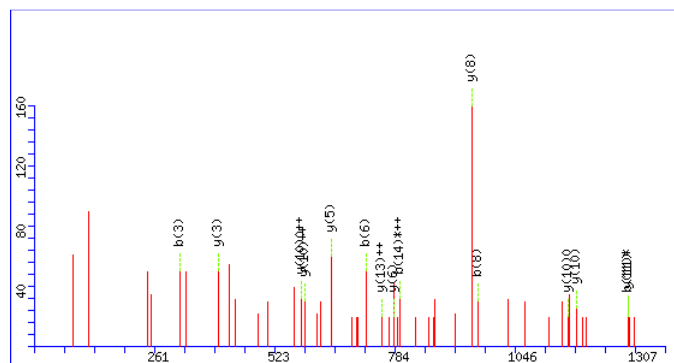
MS/MS Fragmentation of **FNGFQQQDSQELLAFLDGLHEDLNR**:

Found in **IP100185661;IP100423562;IP100423563;IP100423565**

Title: 5.1.1.415.4

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_3_5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							26
2	262.1186	131.5629	245.0921	123.0497	0	0	N	2900.4173	1450.7123	2883.3908	1442.1990	2882.4068	1441.7070	25
3	319.1401	160.0737	302.1135	151.5604	0	0	G	2786.3744	1393.6908	2769.3479	1385.1776	2768.3638	1384.6856	24
4	466.2085	233.6079	449.1819	225.0946	0	0	F	2729.3529	1365.1801	2712.3264	1356.6668	2711.3424	1356.1748	23
5	594.2671	297.6372	577.2405	289.1239	0	0	Q	2582.2845	1291.6459	2565.2580	1283.1326	2564.2740	1282.6406	22
6	722.3257	361.6665	705.2991	353.1532	0	0	Q	2454.2259	1227.6166	2437.1994	1219.1033	2436.2154	1218.6113	21
7	850.3842	425.6958	833.3577	417.1825	0	0	Q	2326.1674	1163.5873	2309.1408	1155.0740	2308.1568	1154.5820	20
8	965.4112	483.2092	948.3846	474.6959	947.4006	474.2039	D	2198.1088	1099.5580	2181.0822	1091.0448	2180.0982	1090.5527	19
9	1052.4432	526.7252	1035.4167	518.2120	1034.4326	517.7200	S	2083.0818	1042.0446	2066.0553	1033.5313	2065.0713	1033.0393	18
10	1180.5018	590.7545	1163.4752	582.2413	1162.4912	581.7492	Q	1996.0498	998.5285	1979.0233	990.0153	1978.0393	989.5233	17
11	1309.5444	655.2758	1292.5178	646.7625	1291.5338	646.2705	E	1867.9912	934.4993	1850.9647	925.9860	1849.9807	925.4940	16
12	1422.6284	711.8179	1405.6019	703.3046	1404.6179	702.8126	L	1738.9486	869.9780	1721.9221	861.4647	1720.9381	860.9727	15
13	1535.7125	768.3599	1518.6859	759.8466	1517.7019	759.3546	L	1625.8646	813.4359	1608.8380	804.9227	1607.8540	804.4306	14
14	1606.7496	803.8784	1589.7231	795.3652	1588.7390	794.8732	A	1512.7805	756.8939	1495.7540	748.3806	1494.7700	747.8886	13
15	1753.8180	877.4127	1736.7915	868.8994	1735.8075	868.4074	F	1441.7434	721.3753	1424.7169	712.8621	1423.7328	712.3701	12
16	1866.9021	933.9547	1849.8755	925.4414	1848.8915	924.9494	L	1294.6750	647.8411	1277.6484	639.3279	1276.6644	638.8359	11
17	1979.9862	990.4967	1962.9596	981.9834	1961.9756	981.4914	L	1181.5909	591.2991	1164.5644	582.7858	1163.5804	582.2938	10
18	2095.0131	1048.0102	2077.9865	1039.4969	2077.0025	1039.0049	D	1068.5069	534.7571	1051.4803	526.2438	1050.4963	525.7518	9
19	2152.0346	1076.5209	2135.0080	1068.0076	2134.0240	1067.5156	G	953.4799	477.2436	936.4534	468.7303	935.4694	468.2383	8
20	2265.1186	1133.0630	2248.0921	1124.5497	2247.1081	1124.0577	L	896.4585	448.7329	879.4319	440.2196	878.4479	439.7276	7
21	2402.1775	1201.5924	2385.1510	1193.0791	2384.1670	1192.5871	H	783.3744	392.1908	766.3478	383.6776	765.3638	383.1856	6
22	2531.2201	1266.1137	2514.1936	1257.6004	2513.2096	1257.1084	E	646.3155	323.6614	629.2889	315.1481	628.3049	314.6561	5
23	2646.2471	1323.6272	2629.2205	1315.1139	2628.2365	1314.6219	D	517.2729	259.1401	500.2463	250.6268	499.2623	250.1348	4
24	2759.3311	1380.1692	2742.3046	1371.6559	2741.3206	1371.1639	L	402.2459	201.6266	385.2194	193.1133	0	0	3
25	2873.3741	1437.1907	2856.3475	1428.6774	2855.3635	1428.1854	N	289.1619	145.0846	272.1353	136.5713	0	0	2
26							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 56647.

MS/MS Fragmentation of **FTDDYQLFEELGK**:

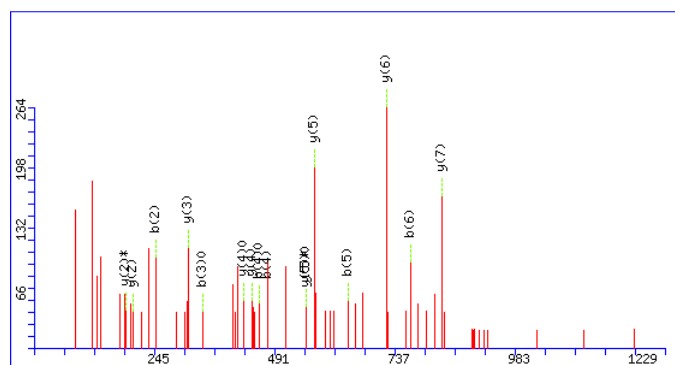
Found in

IP100172450;IP100216378;IP100296678;IP100334344;IP100336118;IP100556423;IP100646849;IP100908444;IP100910242;IP100915309;IP100915327;IP100915328

Title: 3.1.1.2907.2

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120201ry¥120201ry_aHDF1388-P9_1_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							13
2	249.1234	125.0653	0	0	231.1128	116.0600	T	1457.6795	729.3434	1440.6529	720.8301	1439.6689	720.3381	12
3	364.1503	182.5788	0	0	346.1397	173.5735	D	1356.6318	678.8195	1339.6052	670.3063	1338.6212	669.8143	11
4	479.1773	240.0923	0	0	461.1667	231.0870	D	1241.6048	621.3061	1224.5783	612.7928	1223.5943	612.3008	10
5	642.2406	321.6239	0	0	624.2300	312.6186	Y	1126.5779	563.7926	1109.5514	555.2793	1108.5673	554.7873	9
6	770.2992	385.6532	753.2726	377.1399	752.2886	376.6479	Q	963.5146	482.2609	946.4880	473.7477	945.5040	473.2556	8
7	883.3832	442.1953	866.3567	433.6820	865.3727	433.1900	L	835.4560	418.2316	818.4294	409.7184	817.4454	409.2264	7
8	1030.4516	515.7295	1013.4251	507.2162	1012.4411	506.7242	F	722.3719	361.6896	705.3454	353.1763	704.3614	352.6843	6
9	1159.4942	580.2508	1142.4677	571.7375	1141.4837	571.2455	E	575.3035	288.1554	558.2770	279.6421	557.2930	279.1501	5
10	1288.5368	644.7721	1271.5103	636.2588	1270.5263	635.7668	E	446.2609	223.6341	429.2344	215.1208	428.2504	214.6288	4
11	1401.6209	701.3141	1384.5943	692.8008	1383.6103	692.3088	L	317.2183	159.1128	300.1918	150.5995	0	0	3
12	1458.6424	729.8248	1441.6158	721.3115	1440.6318	720.8195	G	204.1343	102.5708	187.1077	94.0575	0	0	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 56881.

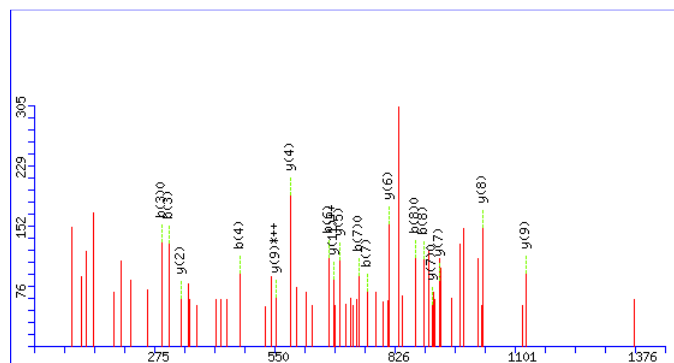
MS/MS Fragmentation of **DGHYGFSEPLTFCSSVVDLINHYR**: 57.021465@C:13

Found in **IP100011736;IP100796770;IP100929345**

Title: 4.1.1.3001.4

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_2.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							23
2	173.0557	87.0315	0	0	155.0451	78.0262	G	2611.2398	1306.1235	2594.2133	1297.6103	2593.2293	1297.1183	22
3	310.1146	155.5609	0	0	292.1040	146.5557	H	2554.2184	1277.6128	2537.1918	1269.0995	2536.2078	1268.6075	21
4	473.1779	237.0926	0	0	455.1674	228.0873	Y	2417.1594	1209.0834	2400.1329	1200.5701	2399.1489	1200.0781	20
5	530.1994	265.6033	0	0	512.1888	256.5980	G	2254.0961	1127.5517	2237.0696	1119.0384	2236.0856	1118.5464	19
6	677.2678	339.1375	0	0	659.2572	330.1323	F	2197.0747	1099.0410	2180.0481	1090.5277	2179.0641	1090.0357	18
7	764.2998	382.6536	0	0	746.2893	373.6483	S	2050.0062	1025.5068	2032.9797	1016.9935	2031.9957	1016.5015	17
8	893.3424	447.1748	0	0	875.3319	438.1696	E	1962.9742	981.9907	1945.9477	973.4775	1944.9636	972.9855	16
9	990.3952	495.7012	0	0	972.3846	486.6959	P	1833.9316	917.4694	1816.9051	908.9562	1815.9211	908.4642	15
10	1103.4793	552.2433	0	0	1085.4687	543.2380	L	1736.8789	868.9431	1719.8523	860.4298	1718.8683	859.9378	14
11	1204.5269	602.7671	0	0	1186.5164	593.7618	T	1623.7948	812.4010	1606.7682	803.8878	1605.7842	803.3958	13
12	1351.5953	676.3013	0	0	1333.5848	667.2960	F	1522.7471	761.8772	1505.7206	753.3639	1504.7365	752.8719	12
13	1511.6260	756.3166	0	0	1493.6154	747.3114	C	1375.6787	688.3430	1358.6521	679.8297	1357.6681	679.3377	11
14	1598.6580	799.8326	0	0	1580.6475	790.8274	S	1215.6480	608.3277	1198.6215	599.8144	1197.6375	599.3224	10
15	1697.7264	849.3669	0	0	1679.7159	840.3616	V	1128.6160	564.8116	1111.5895	556.2984	1110.6055	555.8064	9
16	1796.7949	898.9011	0	0	1778.7843	889.8958	V	1029.5476	515.2774	1012.5211	506.7642	1011.5370	506.2722	8
17	1911.8218	956.4145	0	0	1893.8112	947.4093	D	930.4792	465.7432	913.4526	457.2300	912.4686	456.7380	7
18	2024.9059	1012.9566	0	0	2006.8953	1003.9513	L	815.4522	408.2298	798.4257	399.7165	0	0	6
19	2137.9899	1069.4986	0	0	2119.9794	1060.4933	I	702.3682	351.6877	685.3416	343.1745	0	0	5
20	2252.0328	1126.5201	2235.0063	1118.0068	2234.0223	1117.5148	N	589.2841	295.1457	572.2576	286.6324	0	0	4
21	2389.0918	1195.0495	2372.0652	1186.5362	2371.0812	1186.0442	H	475.2412	238.1242	458.2146	229.6110	0	0	3
22	2552.1551	1276.5812	2535.1285	1268.0679	2534.1445	1267.5759	Y	338.1823	169.5948	321.1557	161.0815	0	0	2
23							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 57048.

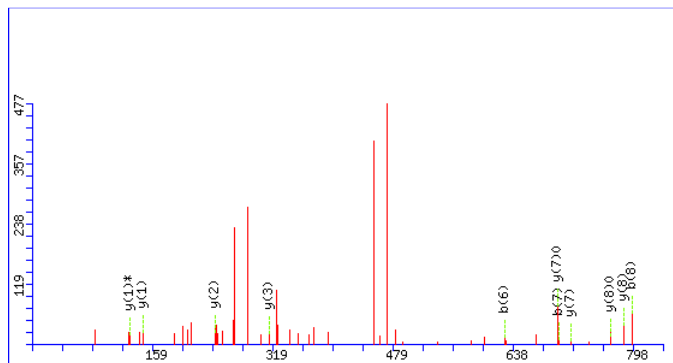
MS/MS Fragmentation of **RASSARAPK**:

Found in **IP100434629**

Title: 1.1.1.5793.4

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	157.1084	79.0578	140.0818	70.5446	0	0	R							9
2	228.1455	114.5764	211.1190	106.0631	0	0	A	787.4421	394.2247	770.4155	385.7114	769.4315	385.2194	8
3	315.1775	158.0924	298.1510	149.5791	297.1670	149.0871	S	716.4050	358.7061	699.3784	350.1928	698.3944	349.7008	7
4	402.2096	201.6084	385.1830	193.0951	384.1990	192.6031	S	629.3729	315.1901	612.3464	306.6768	611.3624	306.1848	6
5	473.2467	237.1270	456.2201	228.6137	455.2361	228.1217	A	542.3409	271.6741	525.3144	263.1608	0	0	5
6	629.3478	315.1775	612.3212	306.6643	611.3372	306.1722	R	471.3038	236.1555	454.2772	227.6423	0	0	4
7	700.3849	350.6961	683.3583	342.1828	682.3743	341.6908	A	315.2027	158.1050	298.1761	149.5917	0	0	3
8	797.4377	399.2225	780.4111	390.7092	779.4271	390.2172	P	244.1656	122.5864	227.1390	114.0731	0	0	2
9							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 57309.

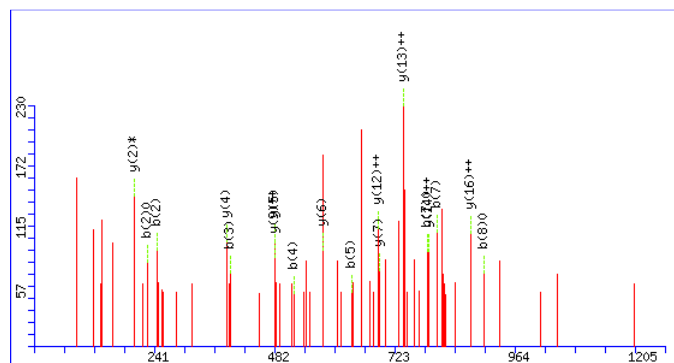
MS/MS Fragmentation of **MDFEDLGLVVDWDHLLPPAAK**:

Found in **IP100292354;IP100917561;IP100926363;IP100927050;IP100927509**

Title: 4.1.1.95.3

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	132.0478	66.5275	0	0	0	0	M							22
2	247.0747	124.0410	0	0	229.0641	115.0357	D	2371.1717	1186.0895	2354.1452	1177.5762	2353.1612	1177.0842	21
3	394.1431	197.5752	0	0	376.1326	188.5699	F	2256.1448	1128.5760	2239.1182	1120.0628	2238.1342	1119.5707	20
4	523.1857	262.0965	0	0	505.1751	253.0912	E	2109.0764	1055.0418	2092.0498	1046.5285	2091.0658	1046.0365	19
5	638.2127	319.6100	0	0	620.2021	310.6047	D	1980.0338	990.5205	1963.0072	982.0073	1962.0232	981.5152	18
6	751.2967	376.1520	0	0	733.2862	367.1467	L	1865.0068	933.0071	1847.9803	924.4938	1846.9963	924.0018	17
7	808.3182	404.6627	0	0	790.3076	395.6574	G	1751.9228	876.4650	1734.8962	867.9517	1733.9122	867.4597	16
8	921.4022	461.2048	0	0	903.3917	452.1995	L	1694.9013	847.9543	1677.8748	839.4410	1676.8907	838.9490	15
9	1020.4707	510.7390	0	0	1002.4601	501.7337	V	1581.8172	791.4123	1564.7907	782.8990	1563.8067	782.4070	14
10	1119.5391	560.2732	0	0	1101.5285	551.2679	V	1482.7488	741.8781	1465.7223	733.3648	1464.7383	732.8728	13
11	1234.5660	617.7866	0	0	1216.5555	608.7814	D	1383.6804	692.3438	1366.6539	683.8306	1365.6698	683.3386	12
12	1420.6453	710.8263	0	0	1402.6348	701.8210	W	1268.6535	634.8304	1251.6269	626.3171	1250.6429	625.8251	11
13	1535.6723	768.3398	0	0	1517.6617	759.3345	D	1082.5742	541.7907	1065.5476	533.2774	1064.5636	532.7854	10
14	1672.7312	836.8692	0	0	1654.7206	827.8639	H	967.5472	484.2772	950.5207	475.7640	0	0	9
15	1809.7901	905.3987	0	0	1791.7795	896.3934	H	830.4883	415.7478	813.4618	407.2345	0	0	8
16	1922.8742	961.9407	0	0	1904.8636	952.9354	L	693.4294	347.2183	676.4028	338.7051	0	0	7
17	2019.9269	1010.4671	0	0	2001.9164	1001.4618	P	580.3453	290.6763	563.3188	282.1630	0	0	6
18	2116.9797	1058.9935	0	0	2098.9691	1049.9882	P	483.2926	242.1499	466.2660	233.6366	0	0	5
19	2214.0325	1107.5199	0	0	2196.0219	1098.5146	P	386.2398	193.6235	369.2132	185.1103	0	0	4
20	2285.0696	1143.0384	0	0	2267.0590	1134.0331	A	289.1870	145.0972	272.1605	136.5839	0	0	3
21	2356.1067	1178.5570	0	0	2338.0961	1169.5517	A	218.1499	109.5786	201.1234	101.0653	0	0	2
22							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 57355.

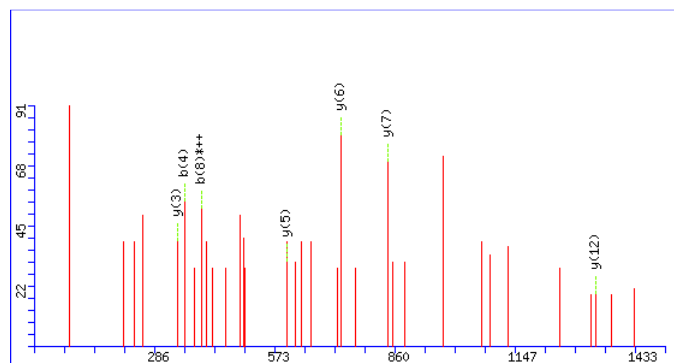
MS/MS Fragmentation of **GDADVFNVGNLLEFLAPR**:

Found in **IP100061520**

Title: 5.1.1.1418.2

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2.5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							19
2	173.0557	87.0315	0	0	155.0451	78.0262	D	1989.0440	995.0256	1972.0175	986.5124	1971.0334	986.0204	18
3	244.0928	122.5500	0	0	226.0822	113.5448	A	1874.0171	937.5122	1856.9905	928.9989	1856.0065	928.5069	17
4	359.1197	180.0635	0	0	341.1092	171.0582	D	1802.9799	901.9936	1785.9534	893.4803	1784.9694	892.9883	16
5	458.1882	229.5977	0	0	440.1776	220.5924	V	1687.9530	844.4801	1670.9265	835.9669	1669.9424	835.4749	15
6	605.2566	303.1319	0	0	587.2460	294.1266	F	1588.8846	794.9459	1571.8580	786.4327	1570.8740	785.9407	14
7	704.3250	352.6661	0	0	686.3144	343.6608	V	1441.8162	721.4117	1424.7896	712.8985	1423.8056	712.4064	13
8	818.3679	409.6876	801.3414	401.1743	800.3573	400.6823	N	1342.7478	671.8775	1325.7212	663.3642	1324.7372	662.8722	12
9	917.4363	459.2218	900.4098	450.7085	899.4258	450.2165	V	1228.7048	614.8561	1211.6783	606.3428	1210.6943	605.8508	11
10	974.4578	487.7325	957.4312	479.2193	956.4472	478.7272	G	1129.6364	565.3218	1112.6099	556.8086	1111.6259	556.3166	10
11	1088.5007	544.7540	1071.4742	536.2407	1070.4901	535.7487	N	1072.6150	536.8111	1055.5884	528.2978	1054.6044	527.8058	9
12	1201.5848	601.2960	1184.5582	592.7828	1183.5742	592.2907	L	958.5720	479.7897	941.5455	471.2764	940.5615	470.7844	8
13	1314.6688	657.8381	1297.6423	649.3248	1296.6583	648.8328	L	845.4880	423.2476	828.4614	414.7343	827.4774	414.2423	7
14	1443.7114	722.3594	1426.6849	713.8461	1425.7009	713.3541	E	732.4039	366.7056	715.3774	358.1923	714.3933	357.7003	6
15	1590.7798	795.8936	1573.7533	787.3803	1572.7693	786.8883	F	603.3613	302.1843	586.3348	293.6710	0	0	5
16	1703.8639	852.4356	1686.8374	843.9223	1685.8533	843.4303	L	456.2929	228.6501	439.2663	220.1368	0	0	4
17	1774.9010	887.9542	1757.8745	879.4409	1756.8905	878.9489	A	343.2088	172.1081	326.1823	163.5948	0	0	3
18	1871.9538	936.4805	1854.9272	927.9673	1853.9432	927.4753	P	272.1717	136.5895	255.1452	128.0762	0	0	2
19							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 57476.

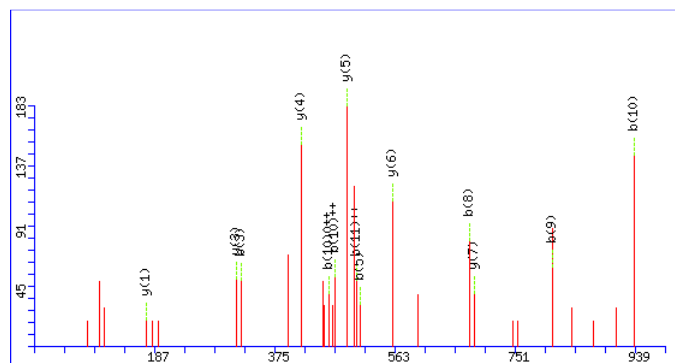
MS/MS Fragmentation of **VSHGEGGGEEAATAAR**:

Found in **IP100045801**

Title: 1.1.1.7163.6

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							16
2	187.1077	94.0575	0	0	169.0972	85.0522	S	1399.6197	700.3135	1382.5931	691.8002	1381.6091	691.3082	15
3	324.1666	162.5870	0	0	306.1561	153.5817	H	1312.5876	656.7975	1295.5611	648.2842	1294.5771	647.7922	14
4	381.1881	191.0977	0	0	363.1775	182.0924	G	1175.5287	588.2680	1158.5022	579.7547	1157.5182	579.2627	13
5	510.2307	255.6190	0	0	492.2201	246.6137	E	1118.5073	559.7573	1101.4807	551.2440	1100.4967	550.7520	12
6	567.2522	284.1297	0	0	549.2416	275.1244	G	989.4647	495.2360	972.4381	486.7227	971.4541	486.2307	11
7	624.2736	312.6404	0	0	606.2631	303.6352	G	932.4432	466.7252	915.4167	458.2120	914.4326	457.7200	10
8	681.2951	341.1512	0	0	663.2845	332.1459	G	875.4217	438.2145	858.3952	429.7012	857.4112	429.2092	9
9	810.3377	405.6725	0	0	792.3271	396.6672	E	818.4003	409.7038	801.3737	401.1905	800.3897	400.6985	8
10	939.3803	470.1938	0	0	921.3697	461.1885	E	689.3577	345.1825	672.3311	336.6692	671.3471	336.1772	7
11	1010.4174	505.7123	0	0	992.4068	496.7070	A	560.3151	280.6612	543.2885	272.1479	542.3045	271.6559	6
12	1081.4545	541.2309	0	0	1063.4439	532.2256	A	489.2780	245.1426	472.2514	236.6293	471.2674	236.1373	5
13	1182.5022	591.7547	0	0	1164.4916	582.7494	T	418.2409	209.6241	401.2143	201.1108	400.2303	200.6188	4
14	1253.5393	627.2733	0	0	1235.5287	618.2680	A	317.1932	159.1002	300.1666	150.5870	0	0	3
15	1324.5764	662.7918	0	0	1306.5658	653.7866	A	246.1561	123.5817	229.1295	115.0684	0	0	2
16							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 57514.

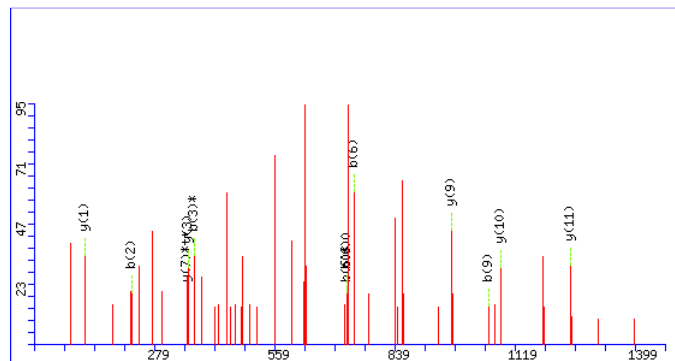
MS/MS Fragmentation of **NLYLEIKDAGLQT: 0.984015@N:1**

Found in **IP100925985**

Title: 5.1.1.957.2

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4.5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207	99.0077	50.0075	0	0	N							13
2	229.1183	115.0628	212.0917	106.5495	0	0	L	1363.7468	682.3770	1346.7202	673.8637	1345.7362	673.3717	12
3	392.1816	196.5944	375.1551	188.0812	0	0	Y	1250.6627	625.8350	1233.6361	617.3217	1232.6521	616.8297	11
4	505.2657	253.1365	488.2391	244.6232	0	0	L	1087.5994	544.3033	1070.5728	535.7900	1069.5888	535.2980	10
5	634.3083	317.6578	617.2817	309.1445	616.2977	308.6525	E	974.5153	487.7613	957.4888	479.2480	956.5047	478.7560	9
6	747.3923	374.1998	730.3658	365.6865	729.3818	365.1945	I	845.4727	423.2400	828.4462	414.7267	827.4621	414.2347	8
7	875.4873	438.2473	858.4607	429.7340	857.4767	429.2420	K	732.3886	366.6980	715.3621	358.1847	714.3781	357.6927	7
8	990.5142	495.7608	973.4877	487.2475	972.5037	486.7555	D	604.2937	302.6505	587.2671	294.1372	586.2831	293.6452	6
9	1061.5514	531.2793	1044.5248	522.7660	1043.5408	522.2740	A	489.2667	245.1370	472.2402	236.6237	471.2562	236.1317	5
10	1118.5728	559.7900	1101.5463	551.2768	1100.5623	550.7848	G	418.2296	209.6185	401.2031	201.1052	400.2191	200.6132	4
11	1231.6569	616.3321	1214.6303	607.8188	1213.6463	607.3268	L	361.2082	181.1077	344.1816	172.5944	343.1976	172.1024	3
12	1359.7155	680.3614	1342.6889	671.8481	1341.7049	671.3561	Q	248.1241	124.5657	231.0975	116.0524	230.1135	115.5604	2
13							T	120.0655	60.5364	0	0	102.0550	51.5311	1

Peptide View

Peptide: 57532.

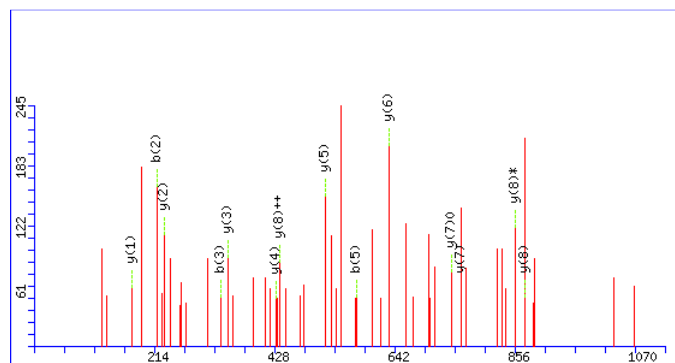
MS/MS Fragmentation of **AFNQNSSLGK**:

Found in **IP100419402;IP100847396**

Title: 1.1.1.8037.11

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_1.mgf

ProteinPilot Peptide Confidence > 99%



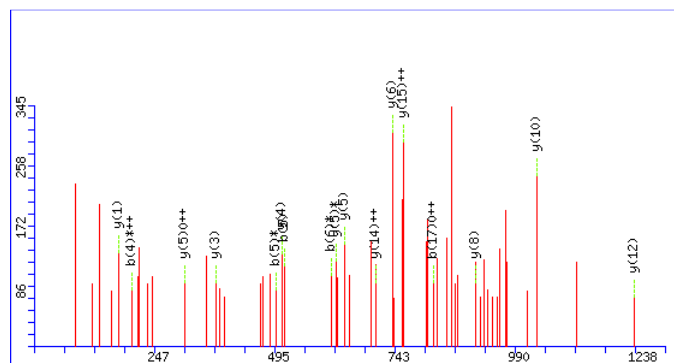
#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							10
2	219.1128	110.0600	0	0	0	0	F	1022.5014	511.7543	1005.4748	503.2411	1004.4908	502.7490	9
3	333.1557	167.0815	316.1292	158.5682	0	0	N	875.4330	438.2201	858.4064	429.7068	857.4224	429.2148	8
4	461.2143	231.1108	444.1878	222.5975	0	0	Q	761.3900	381.1987	744.3635	372.6854	743.3795	372.1934	7
5	575.2572	288.1323	558.2307	279.6190	0	0	N	633.3315	317.1694	616.3049	308.6561	615.3209	308.1641	6
6	662.2893	331.6483	645.2627	323.1350	644.2787	322.6430	S	519.2885	260.1479	502.2620	251.6346	501.2780	251.1426	5
7	749.3213	375.1643	732.2947	366.6510	731.3107	366.1590	S	432.2565	216.6319	415.2300	208.1186	414.2459	207.6266	4
8	862.4054	431.7063	845.3788	423.1930	844.3948	422.7010	L	345.2245	173.1159	328.1979	164.6026	0	0	3
9	919.4268	460.2170	902.4003	451.7038	901.4163	451.2118	G	232.1404	116.5738	215.1139	108.0606	0	0	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 57828.

MS/MS Fragmentation of **TTTNVLGDSLGAQIVEHLRS**:
Found in **IP100015473;IP100642894;IP100908330;IP100908777**
Title: 3.1.1.2464.6

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_3_3.mgf
ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							20
2	203.1026	102.0550	0	0	185.0921	93.0497	T	1939.0243	970.0158	1921.9978	961.5025	1921.0138	961.0105	19
3	304.1503	152.5788	0	0	286.1397	143.5735	T	1837.9767	919.4920	1820.9501	910.9787	1819.9661	910.4867	18
4	418.1932	209.6003	401.1667	201.0870	400.1827	200.5950	N	1736.9290	868.9681	1719.9024	860.4548	1718.9184	859.9628	17
5	517.2617	259.1345	500.2351	250.6212	499.2511	250.1292	V	1622.8860	811.9467	1605.8595	803.4334	1604.8755	802.9414	16
6	630.3457	315.6765	613.3192	307.1632	612.3352	306.6712	L	1523.8176	762.4125	1506.7911	753.8992	1505.8071	753.4072	15
7	687.3672	344.1872	670.3406	335.6740	669.3566	335.1819	G	1410.7336	705.8704	1393.7070	697.3571	1392.7230	696.8651	14
8	802.3941	401.7007	785.3676	393.1874	784.3836	392.6954	D	1353.7121	677.3597	1336.6856	668.8464	1335.7015	668.3544	13
9	889.4262	445.2167	872.3996	436.7034	871.4156	436.2114	S	1238.6852	619.8462	1221.6586	611.3329	1220.6746	610.8409	12
10	1002.5102	501.7587	985.4837	493.2455	984.4997	492.7535	L	1151.6531	576.3302	1134.6266	567.8169	1133.6426	567.3249	11
11	1059.5317	530.2695	1042.5051	521.7562	1041.5211	521.2642	G	1038.5691	519.7882	1021.5425	511.2749	1020.5585	510.7829	10
12	1130.5688	565.7880	1113.5422	557.2748	1112.5582	556.7828	A	981.5476	491.2774	964.5211	482.7642	963.5370	482.2722	9
13	1187.5903	594.2988	1170.5637	585.7855	1169.5797	585.2935	G	910.5105	455.7589	893.4839	447.2456	892.4999	446.7536	8
14	1300.6743	650.8408	1283.6478	642.3275	1282.6638	641.8355	I	853.4890	427.2482	836.4625	418.7349	835.4785	418.2429	7
15	1399.7427	700.3750	1382.7162	691.8617	1381.7322	691.3697	V	740.4050	370.7061	723.3784	362.1928	722.3944	361.7008	6
16	1528.7853	764.8963	1511.7588	756.3830	1510.7748	755.8910	E	641.3365	321.1719	624.3100	312.6586	623.3260	312.1666	5
17	1665.8442	833.4258	1648.8177	824.9125	1647.8337	824.4205	H	512.2940	256.6506	495.2674	248.1373	494.2834	247.6453	4
18	1778.9283	889.9678	1761.9018	881.4545	1760.9177	880.9625	L	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
19	1865.9603	933.4838	1848.9338	924.9705	1847.9498	924.4785	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
20							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 57849.

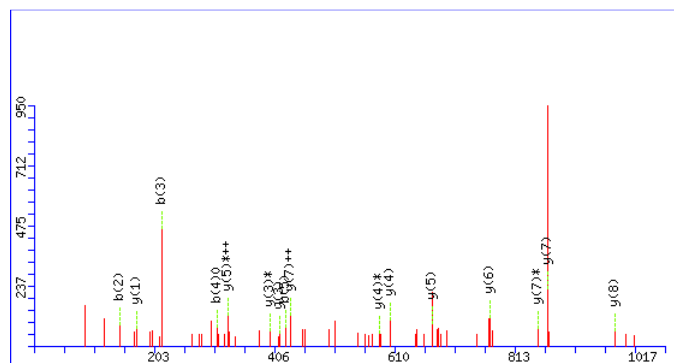
MS/MS Fragmentation of **SGALPVAWLER**:

Found in **IP100021594;IP100791388;IP100976100;IP100979149;IP100979924;IP101015615**

Title: 3.1.1.1494.7

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							11
2	145.0608	73.0340	0	0	127.0502	64.0287	G	1111.6259	556.3166	1094.5993	547.8033	1093.6153	547.3113	10
3	216.0979	108.5526	0	0	198.0873	99.5473	A	1054.6044	527.8058	1037.5778	519.2926	1036.5938	518.8006	9
4	329.1819	165.0946	0	0	311.1714	156.0893	L	983.5673	492.2873	966.5407	483.7740	965.5567	483.2820	8
5	426.2347	213.6210	0	0	408.2241	204.6157	P	870.4832	435.7452	853.4567	427.2320	852.4726	426.7400	7
6	525.3031	263.1552	0	0	507.2926	254.1499	V	773.4304	387.2189	756.4039	378.7056	755.4199	378.2136	6
7	596.3402	298.6738	0	0	578.3297	289.6685	A	674.3620	337.6847	657.3355	329.1714	656.3515	328.6794	5
8	782.4196	391.7134	0	0	764.4090	382.7081	W	603.3249	302.1661	586.2984	293.6528	585.3144	293.1608	4
9	895.5036	448.2554	0	0	877.4931	439.2502	L	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
10	1024.5462	512.7767	0	0	1006.5356	503.7715	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
11							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: **57972.**

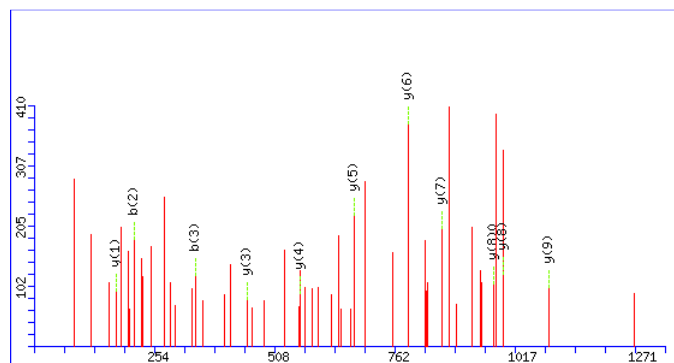
MS/MS Fragmentation of **LVEALDLFER**:

Found in **IP100171925;IP100903059;IP100926491**

Title: 3.1.1.2518.7

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120210ry¥120210ry_585A1-55_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							10
2	213.1598	107.0835	0	0	0	0	V	1091.5732	546.2902	1074.5466	537.7769	1073.5626	537.2849	9
3	342.2023	171.6048	0	0	324.1918	162.5995	E	992.5047	496.7560	975.4782	488.2427	974.4942	487.7507	8
4	413.2395	207.1234	0	0	395.2289	198.1181	A	863.4621	432.2347	846.4356	423.7214	845.4516	423.2294	7
5	526.3235	263.6654	0	0	508.3130	254.6601	L	792.4250	396.7162	775.3985	388.2029	774.4145	387.7109	6
6	641.3505	321.1789	0	0	623.3399	312.1736	D	679.3410	340.1741	662.3144	331.6608	661.3304	331.1688	5
7	754.4345	377.7209	0	0	736.4240	368.7156	L	564.3140	282.6606	547.2875	274.1474	546.3035	273.6554	4
8	901.5029	451.2551	0	0	883.4924	442.2498	F	451.2300	226.1186	434.2034	217.6053	433.2194	217.1133	3
9	1030.5455	515.7764	0	0	1012.5350	506.7711	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 58089.

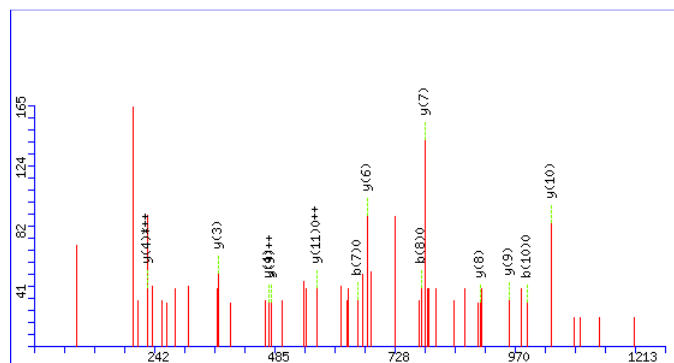
MS/MS Fragmentation of **DLSGLDAETLLK**:

Found in **IP100218604;IP100396552;IP100941721;IP101009534;IP101009928;IP101010249;IP101010823;IP101013529;IP101014461;IP101014929**

Title: 3.1.1.1591.6

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							12
2	229.1183	115.0628	0	0	211.1077	106.0575	L	1159.6569	580.3321	1142.6303	571.8188	1141.6463	571.3268	11
3	316.1503	158.5788	0	0	298.1397	149.5735	S	1046.5728	523.7900	1029.5463	515.2768	1028.5623	514.7848	10
4	373.1718	187.0895	0	0	355.1612	178.0842	G	959.5408	480.2740	942.5142	471.7608	941.5302	471.2688	9
5	486.2558	243.6316	0	0	468.2453	234.6263	L	902.5193	451.7633	885.4928	443.2500	884.5088	442.7580	8
6	601.2828	301.1450	0	0	583.2722	292.1397	D	789.4353	395.2213	772.4087	386.7080	771.4247	386.2160	7
7	672.3199	336.6636	0	0	654.3093	327.6583	A	674.4083	337.7078	657.3818	329.1945	656.3978	328.7025	6
8	801.3625	401.1849	0	0	783.3519	392.1796	E	603.3712	302.1892	586.3447	293.6760	585.3606	293.1840	5
9	902.4102	451.7087	0	0	884.3996	442.7034	T	474.3286	237.6679	457.3021	229.1547	456.3180	228.6627	4
10	1015.4942	508.2508	0	0	997.4837	499.2455	L	373.2809	187.1441	356.2544	178.6308	0	0	3
11	1128.5783	564.7928	0	0	1110.5677	555.7875	L	260.1969	130.6021	243.1703	122.0888	0	0	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 58113.

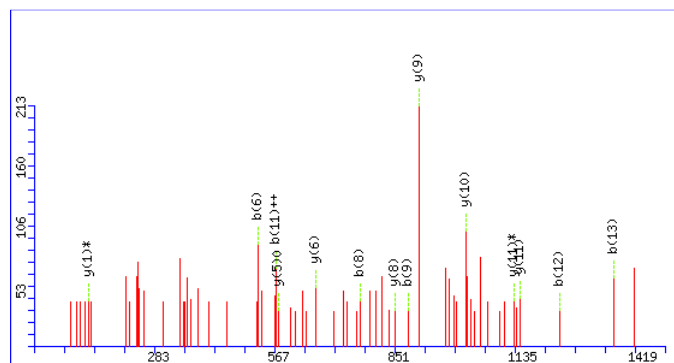
MS/MS Fragmentation of **SSGPTVDQLEELVQIGDAAFSLTK:**

Found in **IP100145726**

Title: 4.1.1.3649.9

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							25
2	175.0713	88.0393	0	0	157.0608	79.0340	S	2547.2825	1274.1449	2530.2559	1265.6316	2529.2719	1265.1396	24
3	232.0928	116.5500	0	0	214.0822	107.5448	G	2460.2504	1230.6289	2443.2239	1222.1156	2442.2399	1221.6236	23
4	329.1456	165.0764	0	0	311.1350	156.0711	P	2403.2290	1202.1181	2386.2024	1193.6048	2385.2184	1193.1128	22
5	430.1932	215.6003	0	0	412.1827	206.5950	T	2306.1762	1153.5917	2289.1497	1145.0785	2288.1656	1144.5865	21
6	529.2617	265.1345	0	0	511.2511	256.1292	V	2205.1285	1103.0679	2188.1020	1094.5546	2187.1180	1094.0626	20
7	644.2886	322.6479	0	0	626.2780	313.6427	D	2106.0601	1053.5337	2089.0336	1045.0204	2088.0495	1044.5284	19
8	772.3472	386.6772	755.3206	378.1640	754.3366	377.6719	Q	1991.0332	996.0202	1974.0066	987.5069	1973.0226	987.0149	18
9	885.4312	443.2193	868.4047	434.7060	867.4207	434.2140	L	1862.9746	931.9909	1845.9480	923.4777	1844.9640	922.9856	17
10	1014.4738	507.7406	997.4473	499.2273	996.4633	498.7353	E	1749.8905	875.4489	1732.8640	866.9356	1731.8800	866.4436	16
11	1143.5164	572.2619	1126.4899	563.7486	1125.5059	563.2566	E	1620.8479	810.9276	1603.8214	802.4143	1602.8374	801.9223	15
12	1242.5848	621.7961	1225.5583	613.2828	1224.5743	612.7908	V	1491.8053	746.4063	1474.7788	737.8930	1473.7948	737.4010	14
13	1371.6274	686.3174	1354.6009	677.8041	1353.6169	677.3121	E	1392.7369	696.8721	1375.7104	688.3588	1374.7264	687.8668	13
14	1484.7115	742.8594	1467.6849	734.3461	1466.7009	733.8541	L	1263.6943	632.3508	1246.6678	623.8375	1245.6838	623.3455	12
15	1612.7701	806.8887	1595.7435	798.3754	1594.7595	797.8834	Q	1150.6103	575.8088	1133.5837	567.2955	1132.5997	566.8035	11
16	1725.8541	863.4307	1708.8276	854.9174	1707.8436	854.4254	I	1022.5517	511.7795	1005.5251	503.2662	1004.5411	502.7742	10
17	1782.8756	891.9414	1765.8491	883.4282	1764.8650	882.9362	G	909.4676	455.2374	892.4411	446.7242	891.4571	446.2322	9
18	1897.9025	949.4549	1880.8760	940.9416	1879.8920	940.4496	D	852.4462	426.7267	835.4196	418.2134	834.4356	417.7214	8
19	1968.9397	984.9735	1951.9131	976.4602	1950.9291	975.9682	A	737.4192	369.2132	720.3927	360.7000	719.4087	360.2080	7
20	2039.9768	1020.4920	2022.9502	1011.9787	2021.9662	1011.4867	A	666.3821	333.6947	649.3556	325.1814	648.3715	324.6894	6
21	2187.0452	1094.0262	2170.0186	1085.5130	2169.0346	1085.0209	F	595.3450	298.1761	578.3184	289.6629	577.3344	289.1709	5
22	2274.0772	1137.5422	2257.0507	1129.0290	2256.0666	1128.5370	S	448.2766	224.6419	431.2500	216.1287	430.2660	215.6366	4
23	2387.1613	1194.0843	2370.1347	1185.5710	2369.1507	1185.0790	L	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
24	2488.2090	1244.6081	2471.1824	1236.0948	2470.1984	1235.6028	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
25							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 58172.

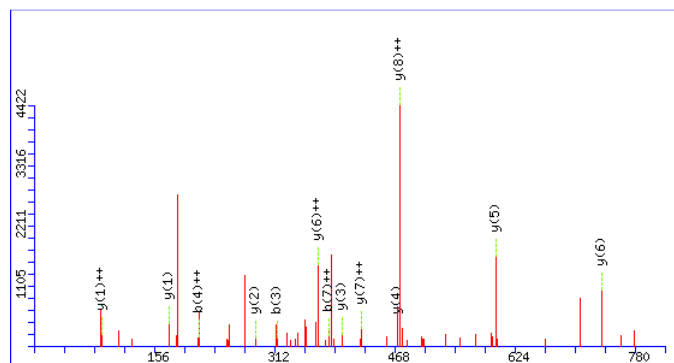
MS/MS Fragmentation of **DVTLHQALLR**:

Found in **IP100023552;IP100025081;IP100789985**

Title: 2.1.1.1292.3

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							10
2	215.1026	108.0550	0	0	197.0921	99.0497	V	1050.6418	525.8246	1033.6153	517.3113	1032.6313	516.8193	9
3	316.1503	158.5788	0	0	298.1397	149.5735	T	951.5734	476.2904	934.5469	467.7771	933.5629	467.2851	8
4	429.2344	215.1208	0	0	411.2238	206.1155	L	850.5257	425.7665	833.4992	417.2532	0	0	7
5	566.2933	283.6503	0	0	548.2827	274.6450	H	737.4417	369.2245	720.4151	360.7112	0	0	6
6	694.3519	347.6796	677.3253	339.1663	676.3413	338.6743	Q	600.3828	300.6950	583.3562	292.1817	0	0	5
7	765.3890	383.1981	748.3624	374.6849	747.3784	374.1928	A	472.3242	236.6657	455.2976	228.1525	0	0	4
8	878.4730	439.7402	861.4465	431.2269	860.4625	430.7349	L	401.2871	201.1472	384.2605	192.6339	0	0	3
9	991.5571	496.2822	974.5306	487.7689	973.5465	487.2769	L	288.2030	144.6051	271.1765	136.0919	0	0	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 58408.

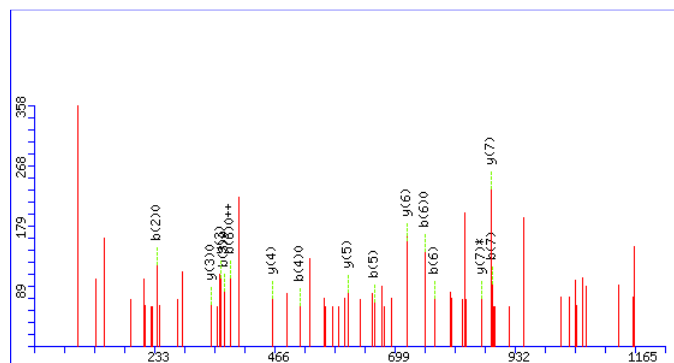
MS/MS Fragmentation of **EQEFQDIYNFVESK**:

Found in **IP100013215;IP100975911**

Title: 3.1.1.3583.5

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120210ry¥120210ry_585A1-55_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							14
2	258.1084	129.5579	241.0819	121.0446	240.0979	120.5526	Q	1646.7697	823.8885	1629.7431	815.3752	1628.7591	814.8832	13
3	387.1510	194.0792	370.1245	185.5659	369.1405	185.0739	E	1518.7111	759.8592	1501.6846	751.3459	1500.7005	750.8539	12
4	534.2195	267.6134	517.1929	259.1001	516.2089	258.6081	F	1389.6685	695.3379	1372.6420	686.8246	1371.6579	686.3326	11
5	662.2780	331.6427	645.2515	323.1294	644.2675	322.6374	Q	1242.6001	621.8037	1225.5735	613.2904	1224.5895	612.7984	10
6	777.3050	389.1561	760.2784	380.6429	759.2944	380.1508	D	1114.5415	557.7744	1097.5150	549.2611	1096.5310	548.7691	9
7	890.3890	445.6982	873.3625	437.1849	872.3785	436.6929	I	999.5146	500.2609	982.4880	491.7476	981.5040	491.2556	8
8	1053.4524	527.2298	1036.4258	518.7165	1035.4418	518.2245	Y	886.4305	443.7189	869.4040	435.2056	868.4199	434.7136	7
9	1167.4953	584.2513	1150.4687	575.7380	1149.4847	575.2460	N	723.3672	362.1872	706.3406	353.6740	705.3566	353.1819	6
10	1314.5637	657.7855	1297.5372	649.2722	1296.5531	648.7802	F	609.3243	305.1658	592.2977	296.6525	591.3137	296.1605	5
11	1413.6321	707.3197	1396.6056	698.8064	1395.6216	698.3144	V	462.2558	231.6316	445.2293	223.1183	444.2453	222.6263	4
12	1542.6747	771.8410	1525.6482	763.3277	1524.6642	762.8357	E	363.1874	182.0974	346.1609	173.5841	345.1769	173.0921	3
13	1629.7067	815.3570	1612.6802	806.8437	1611.6962	806.3517	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 58488.

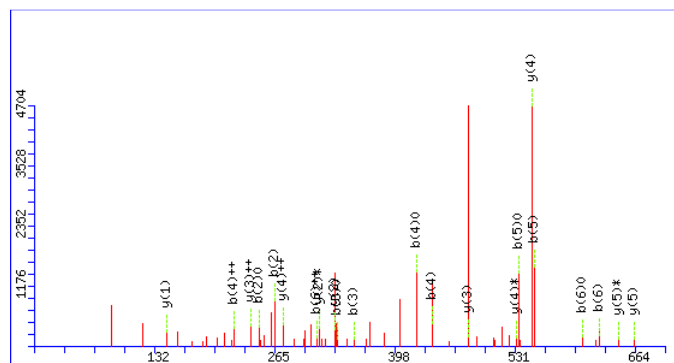
MS/MS Fragmentation of **EHSSLAFWK**:

Found in **IP100298828;IP100910625**

Title: 2.1.1.2850.2

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_2.2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							9
2	267.1088	134.0580	0	0	249.0982	125.0527	H	975.5047	488.2560	958.4781	479.7427	957.4941	479.2507	8
3	354.1408	177.5740	0	0	336.1302	168.5688	S	838.4458	419.7265	821.4192	411.2132	820.4352	410.7212	7
4	441.1728	221.0901	0	0	423.1623	212.0848	S	751.4137	376.2105	734.3872	367.6972	733.4032	367.2052	6
5	554.2569	277.6321	0	0	536.2463	268.6268	L	664.3817	332.6945	647.3552	324.1812	0	0	5
6	625.2940	313.1506	0	0	607.2835	304.1454	A	551.2976	276.1525	534.2711	267.6392	0	0	4
7	772.3624	386.6849	0	0	754.3519	377.6796	F	480.2605	240.6339	463.2340	232.1206	0	0	3
8	958.4417	479.7245	0	0	940.4312	470.7192	W	333.1921	167.0997	316.1656	158.5864	0	0	2
9							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 58632.

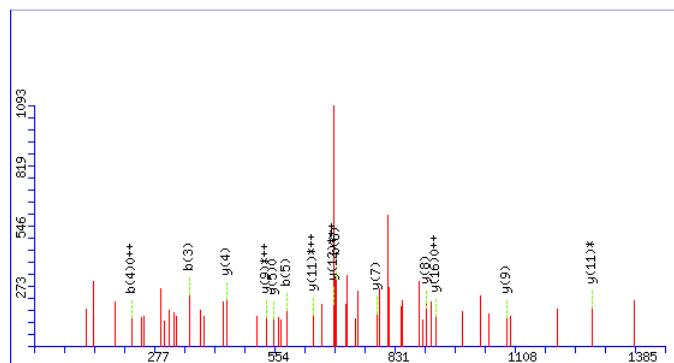
MS/MS Fragmentation of **TQQLNPVDWNFAQPEAK**:

Found in **IP100003926**

Title: 3.1.1.3000.8

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							18
2	230.1135	115.5604	213.0870	107.0471	212.1030	106.5551	Q	1998.0080	999.5076	1980.9814	990.9943	1979.9974	990.5023	17
3	358.1721	179.5897	341.1456	171.0764	340.1615	170.5844	Q	1869.9494	935.4783	1852.9228	926.9651	1851.9388	926.4730	16
4	471.2562	236.1317	454.2296	227.6185	453.2456	227.1264	L	1741.8908	871.4490	1724.8642	862.9358	1723.8802	862.4438	15
5	584.3402	292.6738	567.3137	284.1605	566.3297	283.6685	L	1628.8067	814.9070	1611.7802	806.3937	1610.7962	805.9017	14
6	698.3832	349.6952	681.3566	341.1819	680.3726	340.6899	N	1515.7227	758.3650	1498.6961	749.8517	1497.7121	749.3597	13
7	795.4359	398.2216	778.4094	389.7083	777.4254	389.2163	P	1401.6797	701.3435	1384.6532	692.8302	1383.6692	692.3382	12
8	894.5043	447.7558	877.4778	439.2425	876.4938	438.7505	V	1304.6270	652.8171	1287.6004	644.3039	1286.6164	643.8118	11
9	1009.5313	505.2693	992.5047	496.7560	991.5207	496.2640	D	1205.5586	603.2829	1188.5320	594.7696	1187.5480	594.2776	10
10	1195.6106	598.3089	1178.5841	589.7957	1177.6000	589.3037	W	1090.5316	545.7694	1073.5051	537.2562	1072.5211	536.7642	9
11	1309.6535	655.3304	1292.6270	646.8171	1291.6430	646.3251	N	904.4523	452.7298	887.4258	444.2165	886.4417	443.7245	8
12	1456.7219	728.8646	1439.6954	720.3513	1438.7114	719.8593	F	790.4094	395.7083	773.3828	387.1951	772.3988	386.7030	7
13	1527.7591	764.3832	1510.7325	755.8699	1509.7485	755.3779	A	643.3410	322.1741	626.3144	313.6608	625.3304	313.1688	6
14	1655.8176	828.4125	1638.7911	819.8992	1637.8071	819.4072	Q	572.3039	286.6556	555.2773	278.1423	554.2933	277.6503	5
15	1752.8704	876.9388	1735.8438	868.4256	1734.8598	867.9336	P	444.2453	222.6263	427.2187	214.1130	426.2347	213.6210	4
16	1881.9130	941.4601	1864.8864	932.9469	1863.9024	932.4549	E	347.1925	174.0999	330.1660	165.5866	329.1819	165.0946	3
17	1952.9501	976.9787	1935.9236	968.4654	1934.9395	967.9734	A	218.1499	109.5786	201.1234	101.0653	0	0	2
18							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 58675.

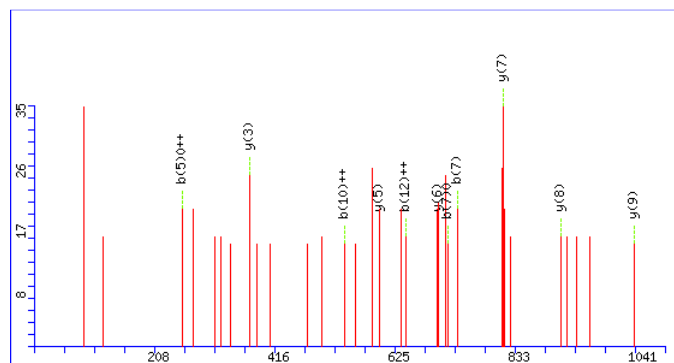
MS/MS Fragmentation of **VNSTMTTLQVLTLNKK**:

Found in **IP100386527;IP100556360;IP100644261;IP100760676**

Title: 4.1.1.3179.2

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							17
2	214.1186	107.5629	197.0921	99.0497	0	0	N	1790.0092	895.5082	1772.9826	886.9950	1771.9986	886.5030	16
3	301.1506	151.0790	284.1241	142.5657	283.1401	142.0737	S	1675.9663	838.4868	1658.9397	829.9735	1657.9557	829.4815	15
4	402.1983	201.6028	385.1718	193.0895	384.1878	192.5975	T	1588.9342	794.9708	1571.9077	786.4575	1570.9237	785.9655	14
5	533.2388	267.1230	516.2123	258.6098	515.2282	258.1178	M	1487.8866	744.4469	1470.8600	735.9336	1469.8760	735.4416	13
6	634.2865	317.6469	617.2599	309.1336	616.2759	308.6416	T	1356.8461	678.9267	1339.8195	670.4134	1338.8355	669.9214	12
7	735.3342	368.1707	718.3076	359.6574	717.3236	359.1654	T	1255.7984	628.4028	1238.7719	619.8896	1237.7878	619.3976	11
8	848.4182	424.7128	831.3917	416.1995	830.4077	415.7075	L	1154.7507	577.8790	1137.7242	569.3657	1136.7402	568.8737	10
9	976.4768	488.7420	959.4503	480.2288	958.4662	479.7368	Q	1041.6667	521.3370	1024.6401	512.8237	1023.6561	512.3317	9
10	1075.5452	538.2762	1058.5187	529.7630	1057.5347	529.2710	V	913.6081	457.3077	896.5815	448.7944	895.5975	448.3024	8
11	1188.6293	594.8183	1171.6027	586.3050	1170.6187	585.8130	L	814.5397	407.7735	797.5131	399.2602	796.5291	398.7682	7
12	1289.6770	645.3421	1272.6504	636.8288	1271.6664	636.3368	T	701.4556	351.2314	684.4291	342.7182	683.4450	342.2262	6
13	1402.7610	701.8842	1385.7345	693.3709	1384.7505	692.8789	L	600.4079	300.7076	583.3814	292.1943	0	0	5
14	1515.8451	758.4262	1498.8185	749.9129	1497.8345	749.4209	L	487.3239	244.1656	470.2973	235.6523	0	0	4
15	1628.9292	814.9682	1611.9026	806.4549	1610.9186	805.9629	L	374.2398	187.6235	357.2132	179.1103	0	0	3
16	1742.9721	871.9897	1725.9455	863.4764	1724.9615	862.9844	N	261.1557	131.0815	244.1292	122.5682	0	0	2
17							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 58838.

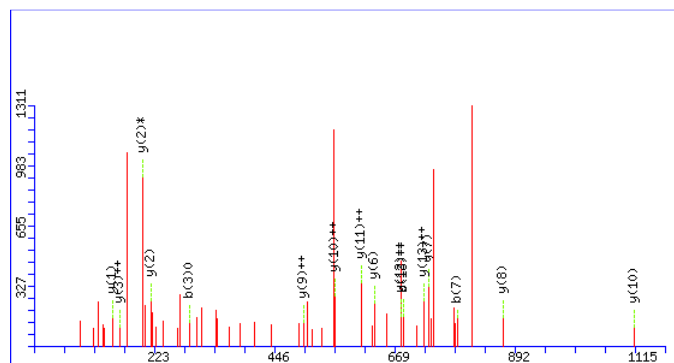
MS/MS Fragmentation of **ASFVDEHTVCGVAK: 57.021465@C:10**

Found in **IP100157820;IP100220566;IP100446645;IP100853011;IP100853628;IP100883598;IP101010380;IP101018202**

Title: 2.1.1.731.4

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120208ry¥120208ry_Tig120slc-P8_2.2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							14
2	159.0764	80.0418	0	0	141.0659	71.0366	S	1448.6838	724.8456	1431.6573	716.3323	1430.6733	715.8403	13
3	306.1448	153.5761	0	0	288.1343	144.5708	F	1361.6518	681.3295	1344.6253	672.8163	1343.6413	672.3243	12
4	405.2132	203.1103	0	0	387.2027	194.1050	V	1214.5834	607.7953	1197.5569	599.2821	1196.5728	598.7901	11
5	520.2402	260.6237	0	0	502.2296	251.6185	D	1115.5150	558.2611	1098.4884	549.7479	1097.5044	549.2558	10
6	649.2828	325.1450	0	0	631.2722	316.1397	E	1000.4880	500.7477	983.4615	492.2344	982.4775	491.7424	9
7	786.3417	393.6745	0	0	768.3311	384.6692	H	871.4455	436.2264	854.4189	427.7131	853.4349	427.2211	8
8	887.3894	444.1983	0	0	869.3788	435.1930	T	734.3865	367.6969	717.3600	359.1836	716.3760	358.6916	7
9	986.4578	493.7325	0	0	968.4472	484.7272	V	633.3389	317.1731	616.3123	308.6598	0	0	6
10	1146.4884	573.7479	0	0	1128.4779	564.7426	C	534.2704	267.6389	517.2439	259.1256	0	0	5
11	1203.5099	602.2586	0	0	1185.4993	593.2533	G	374.2398	187.6235	357.2132	179.1103	0	0	4
12	1302.5783	651.7928	0	0	1284.5678	642.7875	V	317.2183	159.1128	300.1918	150.5995	0	0	3
13	1373.6154	687.3114	0	0	1355.6049	678.3061	A	218.1499	109.5786	201.1234	101.0653	0	0	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 59103.

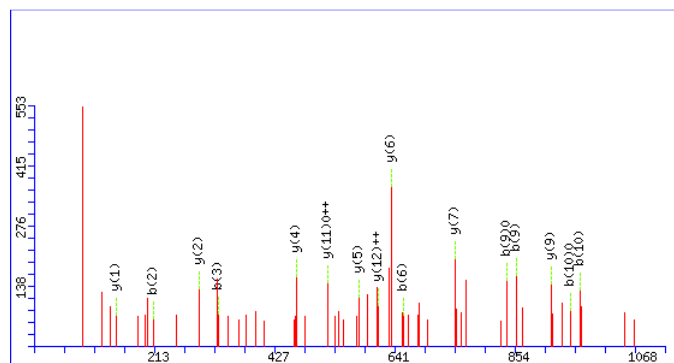
MS/MS Fragmentation of **VLDLGGSGLLGITAFK: 57.021465@C:6**

Found in **IP100009815**

Title: 3.1.1.4341.2

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120214ry¥120214ry_414C2-43_4_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							17
2	213.1598	107.0835	0	0	0	0	L	1621.8618	811.4345	1604.8353	802.9213	1603.8512	802.4293	16
3	328.1867	164.5970	0	0	310.1761	155.5917	D	1508.7777	754.8925	1491.7512	746.3792	1490.7672	745.8872	15
4	441.2708	221.1390	0	0	423.2602	212.1337	L	1393.7508	697.3790	1376.7243	688.8658	1375.7402	688.3738	14
5	498.2922	249.6498	0	0	480.2817	240.6445	G	1280.6667	640.8370	1263.6402	632.3237	1262.6562	631.8317	13
6	658.3229	329.6651	0	0	640.3123	320.6598	C	1223.6453	612.3263	1206.6187	603.8130	1205.6347	603.3210	12
7	715.3443	358.1758	0	0	697.3338	349.1705	G	1063.6146	532.3109	1046.5881	523.7977	1045.6041	523.3057	11
8	802.3764	401.6918	0	0	784.3658	392.6865	S	1006.5932	503.8002	989.5666	495.2869	988.5826	494.7949	10
9	859.3978	430.2026	0	0	841.3873	421.1973	G	919.5611	460.2842	902.5346	451.7709	901.5506	451.2789	9
10	972.4819	486.7446	0	0	954.4713	477.7393	L	862.5397	431.7735	845.5131	423.2602	844.5291	422.7682	8
11	1085.5660	543.2866	0	0	1067.5554	534.2813	L	749.4556	375.2314	732.4291	366.7182	731.4450	366.2262	7
12	1142.5874	571.7973	0	0	1124.5769	562.7921	G	636.3715	318.6894	619.3450	310.1761	618.3610	309.6841	6
13	1255.6715	628.3394	0	0	1237.6609	619.3341	I	579.3501	290.1787	562.3235	281.6654	561.3395	281.1734	5
14	1356.7192	678.8632	0	0	1338.7086	669.8579	T	466.2660	233.6366	449.2395	225.1234	448.2554	224.6314	4
15	1427.7563	714.3818	0	0	1409.7457	705.3765	A	365.2183	183.1128	348.1918	174.5995	0	0	3
16	1574.8247	787.9160	0	0	1556.8141	778.9107	F	294.1812	147.5942	277.1547	139.0810	0	0	2
17							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 59443.

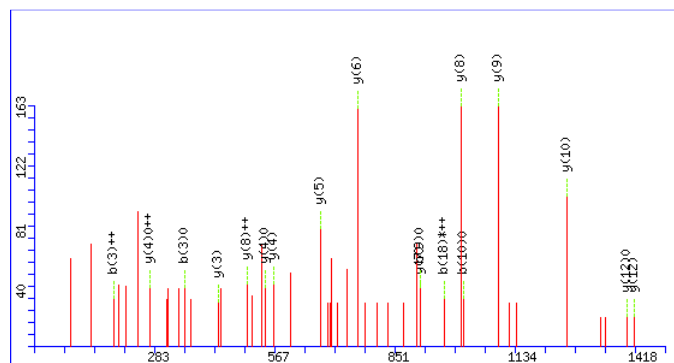
MS/MS Fragmentation of **CLTQSGINGTYSFPSLETQR**: 57.021465@C:1,57.021465@C:19

Found in **IP100004524;IP100925681;IP100926104;IP100927040;IP101018250**

Title: 3.1.1.1424.10

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120126ry¥120126ry_585A1-55_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	161.0379	81.0226	0	0	0	0	C							20
2	274.1220	137.5646	0	0	0	0	L	2131.0124	1066.0099	2113.9859	1057.4966	2113.0019	1057.0046	19
3	375.1697	188.0885	0	0	357.1591	179.0832	T	2017.9284	1009.4678	2000.9018	1000.9546	1999.9178	1000.4625	18
4	503.2282	252.1178	486.2017	243.6045	485.2177	243.1125	Q	1916.8807	958.9440	1899.8542	950.4307	1898.8701	949.9387	17
5	590.2603	295.6338	573.2337	287.1205	572.2497	286.6285	S	1788.8221	894.9147	1771.7956	886.4014	1770.8116	885.9094	16
6	647.2817	324.1445	630.2552	315.6312	629.2712	315.1392	G	1701.7901	851.3987	1684.7635	842.8854	1683.7795	842.3934	15
7	760.3658	380.6865	743.3393	372.1733	742.3552	371.6813	I	1644.7686	822.8880	1627.7421	814.3747	1626.7581	813.8827	14
8	874.4087	437.7080	857.3822	429.1947	856.3982	428.7027	N	1531.6846	766.3459	1514.6580	757.8326	1513.6740	757.3406	13
9	931.4302	466.2187	914.4036	457.7055	913.4196	457.2135	G	1417.6416	709.3245	1400.6151	700.8112	1399.6311	700.3192	12
10	1032.4779	516.7426	1015.4513	508.2293	1014.4673	507.7373	T	1360.6202	680.8137	1343.5936	672.3005	1342.6096	671.8084	11
11	1195.5412	598.2742	1178.5147	589.7610	1177.5306	589.2690	Y	1259.5725	630.2899	1242.5460	621.7766	1241.5619	621.2846	10
12	1282.5732	641.7903	1265.5467	633.2770	1264.5627	632.7850	S	1096.5092	548.7582	1079.4826	540.2449	1078.4986	539.7529	9
13	1379.6260	690.3166	1362.5994	681.8034	1361.6154	681.3114	P	1009.4771	505.2422	992.4506	496.7289	991.4666	496.2369	8
14	1526.6944	763.8508	1509.6679	755.3376	1508.6838	754.8456	F	912.4244	456.7158	895.3978	448.2026	894.4138	447.7105	7
15	1613.7264	807.3669	1596.6999	798.8536	1595.7159	798.3616	S	765.3560	383.1816	748.3294	374.6683	747.3454	374.1763	6
16	1726.8105	863.9089	1709.7840	855.3956	1708.7999	854.9036	L	678.3239	339.6656	661.2974	331.1523	660.3134	330.6603	5
17	1855.8531	928.4302	1838.8265	919.9169	1837.8425	919.4249	E	565.2399	283.1236	548.2133	274.6103	547.2293	274.1183	4
18	1956.9008	978.9540	1939.8742	970.4407	1938.8902	969.9487	T	436.1973	218.6023	419.1707	210.0890	418.1867	209.5970	3
19	2116.9314	1058.9693	2099.9049	1050.4561	2098.9209	1049.9641	C	335.1496	168.0784	318.1231	159.5652	0	0	2
20							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 59476.

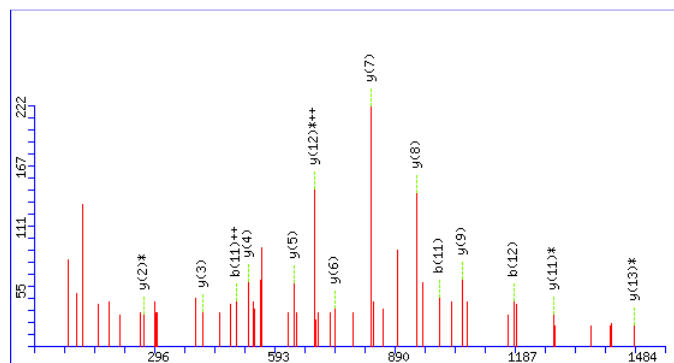
MS/MS Fragmentation of **ILACGGDGTGVWLSTLDQLR: 57.021465@C:4**

Found in **IP100013835;IP100300125;IP100398065;IP100556127;IP100867551;IP100976044;IP100977628;IP100983918**

Title: 5.1.1.446.4

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_2.5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							21
2	227.1754	114.0913	0	0	0	0	L	2132.0805	1066.5439	2115.0539	1058.0306	2114.0699	1057.5386	20
3	298.2125	149.6099	0	0	0	0	A	2018.9964	1010.0018	2001.9699	1001.4886	2000.9858	1000.9966	19
4	458.2432	229.6252	0	0	0	0	C	1947.9593	974.4833	1930.9327	965.9700	1929.9487	965.4780	18
5	515.2646	258.1360	0	0	0	0	G	1787.9286	894.4680	1770.9021	885.9547	1769.9181	885.4627	17
6	572.2861	286.6467	0	0	0	0	G	1730.9072	865.9572	1713.8806	857.4440	1712.8966	856.9519	16
7	687.3130	344.1602	0	0	669.3025	335.1549	D	1673.8857	837.4465	1656.8592	828.9332	1655.8751	828.4412	15
8	744.3345	372.6709	0	0	726.3239	363.6656	G	1558.8588	779.9330	1541.8322	771.4197	1540.8482	770.9277	14
9	845.3822	423.1947	0	0	827.3716	414.1894	T	1501.8373	751.4223	1484.8108	742.9090	1483.8267	742.4170	13
10	944.4506	472.7289	0	0	926.4400	463.7237	V	1400.7896	700.8985	1383.7631	692.3852	1382.7791	691.8932	12
11	1001.4721	501.2397	0	0	983.4615	492.2344	G	1301.7212	651.3642	1284.6947	642.8510	1283.7106	642.3590	11
12	1187.5514	594.2793	0	0	1169.5408	585.2740	W	1244.6997	622.8535	1227.6732	614.3402	1226.6892	613.8482	10
13	1300.6354	650.8214	0	0	1282.6249	641.8161	I	1058.6204	529.8139	1041.5939	521.3006	1040.6099	520.8086	9
14	1413.7195	707.3634	0	0	1395.7089	698.3581	L	945.5364	473.2718	928.5098	464.7585	927.5258	464.2665	8
15	1500.7515	750.8794	0	0	1482.7410	741.8741	S	832.4523	416.7298	815.4258	408.2165	814.4417	407.7245	7
16	1601.7992	801.4032	0	0	1583.7886	792.3980	T	745.4203	373.2138	728.3937	364.7005	727.4097	364.2085	6
17	1714.8833	857.9453	0	0	1696.8727	848.9400	L	644.3726	322.6899	627.3461	314.1767	626.3620	313.6847	5
18	1829.9102	915.4587	0	0	1811.8997	906.4535	D	531.2885	266.1479	514.2620	257.6346	513.2780	257.1426	4
19	1957.9688	979.4880	1940.9422	970.9748	1939.9582	970.4828	Q	416.2616	208.6344	399.2350	200.1212	0	0	3
20	2071.0529	1036.0301	2054.0263	1027.5168	2053.0423	1027.0248	L	288.2030	144.6051	271.1765	136.0919	0	0	2
21							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 59629.

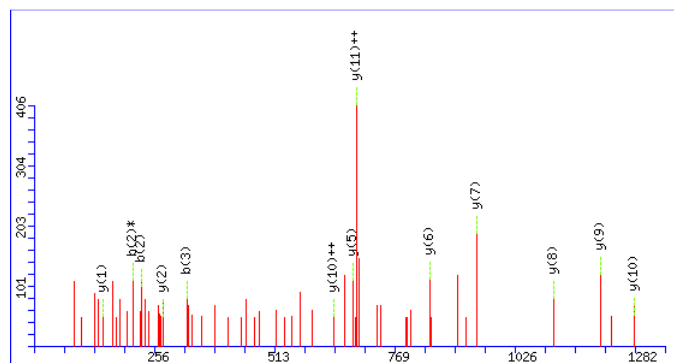
MS/MS Fragmentation of **NNVPATYTYDEYKK**:

Found in **IP100152756;IP100979798**

Title: 2.1.1.676.7

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							14
2	229.0931	115.0502	212.0666	106.5369	0	0	N	1591.7639	796.3856	1574.7373	787.8723	1573.7533	787.3803	13
3	328.1615	164.5844	311.1350	156.0711	0	0	V	1477.7209	739.3641	1460.6944	730.8508	1459.7104	730.3588	12
4	425.2143	213.1108	408.1878	204.5975	0	0	P	1378.6525	689.8299	1361.6260	681.3166	1360.6420	680.8246	11
5	496.2514	248.6293	479.2249	240.1161	0	0	A	1281.5998	641.3035	1264.5732	632.7902	1263.5892	632.2982	10
6	597.2991	299.1532	580.2726	290.6399	579.2885	290.1479	T	1210.5626	605.7850	1193.5361	597.2717	1192.5521	596.7797	9
7	760.3624	380.6849	743.3359	372.1716	742.3519	371.6796	Y	1109.5150	555.2611	1092.4884	546.7478	1091.5044	546.2558	8
8	861.4101	431.2087	844.3836	422.6954	843.3995	422.2034	T	946.4516	473.7295	929.4251	465.2162	928.4411	464.7242	7
9	1024.4734	512.7404	1007.4469	504.2271	1006.4629	503.7351	Y	845.4040	423.2056	828.3774	414.6923	827.3934	414.2003	6
10	1139.5004	570.2538	1122.4738	561.7406	1121.4898	561.2485	D	682.3406	341.6740	665.3141	333.1607	664.3301	332.6687	5
11	1268.5430	634.7751	1251.5164	626.2619	1250.5324	625.7698	E	567.3137	284.1605	550.2871	275.6472	549.3031	275.1552	4
12	1431.6063	716.3068	1414.5798	707.7935	1413.5957	707.3015	Y	438.2711	219.6392	421.2445	211.1259	0	0	3
13	1559.7013	780.3543	1542.6747	771.8410	1541.6907	771.3490	K	275.2078	138.1075	258.1812	129.5942	0	0	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 59755.

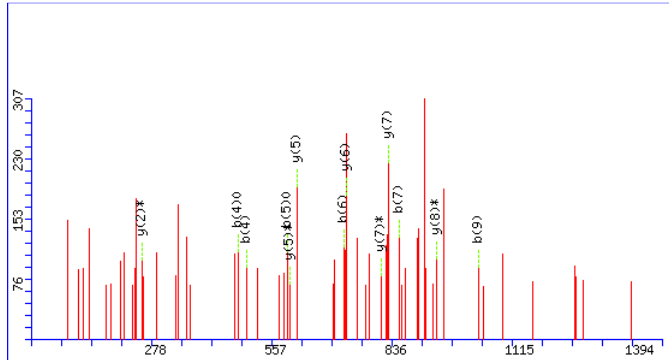
MS/MS Fragmentation of **EIEQLIELANYQVLSQQQK**:

Found in **IP100028450;IP100216107;IP100216108;IP100216109;IP100878240;IP100893158;IP101010475**

Title: 4.1.1.363.8

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							19
2	243.1339	122.0706	0	0	225.1234	113.0653	I	2145.1550	1073.0811	2128.1285	1064.5679	2127.1444	1064.0759	18
3	372.1765	186.5919	0	0	354.1660	177.5866	E	2032.0709	1016.5391	2015.0444	1008.0258	2014.0604	1007.5338	17
4	500.2351	250.6212	483.2086	242.1079	482.2245	241.6159	Q	1903.0284	952.0178	1886.0018	943.5045	1885.0178	943.0125	16
5	613.3192	307.1632	596.2926	298.6499	595.3086	298.1579	L	1774.9698	887.9885	1757.9432	879.4753	1756.9592	878.9832	15
6	726.4032	363.7053	709.3767	355.1920	708.3927	354.7000	I	1661.8857	831.4465	1644.8592	822.9332	1643.8751	822.4412	14
7	855.4458	428.2266	838.4193	419.7133	837.4353	419.2213	E	1548.8016	774.9045	1531.7751	766.3912	1530.7911	765.8992	13
8	968.5299	484.7686	951.5033	476.2553	950.5193	475.7633	L	1419.7591	710.3832	1402.7325	701.8699	1401.7485	701.3779	12
9	1039.5670	520.2871	1022.5405	511.7739	1021.5564	511.2819	A	1306.6750	653.8411	1289.6484	645.3279	1288.6644	644.8359	11
10	1153.6099	577.3086	1136.5834	568.7953	1135.5994	568.3033	N	1235.6379	618.3226	1218.6113	609.8093	1217.6273	609.3173	10
11	1316.6733	658.8403	1299.6467	650.3270	1298.6627	649.8350	Y	1121.5950	561.3011	1104.5684	552.7878	1103.5844	552.2958	9
12	1444.7318	722.8696	1427.7053	714.3563	1426.7213	713.8643	Q	958.5316	479.7694	941.5051	471.2562	940.5211	470.7642	8
13	1543.8003	772.4038	1526.7737	763.8905	1525.7897	763.3985	V	830.4730	415.7402	813.4465	407.2269	812.4625	406.7349	7
14	1656.8843	828.9458	1639.8578	820.4325	1638.8738	819.9405	L	731.4046	366.2060	714.3781	357.6927	713.3941	357.2007	6
15	1743.9163	872.4618	1726.8898	863.9485	1725.9058	863.4565	S	618.3206	309.6639	601.2940	301.1506	600.3100	300.6586	5
16	1871.9749	936.4911	1854.9484	927.9778	1853.9644	927.4858	Q	531.2885	266.1479	514.2620	257.6346	0	0	4
17	2000.0335	1000.5204	1983.0069	992.0071	1982.0229	991.5151	Q	403.2300	202.1186	386.2034	193.6053	0	0	3
18	2128.0921	1064.5497	2111.0655	1056.0364	2110.0815	1055.5444	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
19							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 59864.

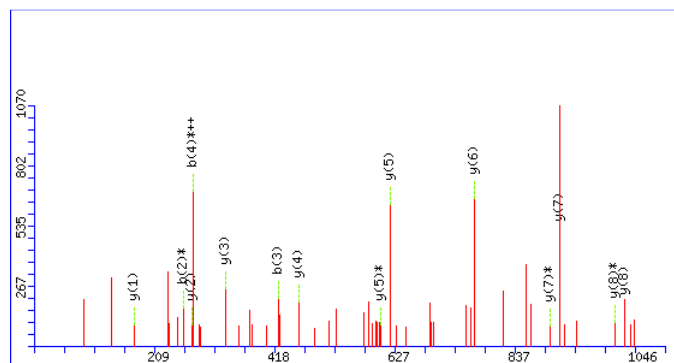
MS/MS Fragmentation of **YNFFCQGTR: 57.021465@C:5**

Found in **IP100328307,IP100910962,IP101009951**

Title: 2.1.1.3065.7

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	164.0706	82.5389	0	0	0	0	Y							9
2	278.1135	139.5604	261.0870	131.0471	0	0	N	1029.4571	515.2322	1012.4305	506.7189	1011.4465	506.2269	8
3	425.1819	213.0946	408.1554	204.5813	0	0	F	915.4142	458.2107	898.3876	449.6974	897.4036	449.2054	7
4	572.2504	286.6288	555.2238	278.1155	0	0	F	768.3457	384.6765	751.3192	376.1632	750.3352	375.6712	6
5	732.2810	366.6441	715.2545	358.1309	0	0	C	621.2773	311.1423	604.2508	302.6290	603.2668	302.1370	5
6	860.3396	430.6734	843.3130	422.1602	0	0	Q	461.2467	231.1270	444.2201	222.6137	443.2361	222.1217	4
7	917.3611	459.1842	900.3345	450.6709	0	0	G	333.1881	167.0977	316.1615	158.5844	315.1775	158.0924	3
8	1018.4087	509.7080	1001.3822	501.1947	1000.3982	500.7027	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
9							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 60025.

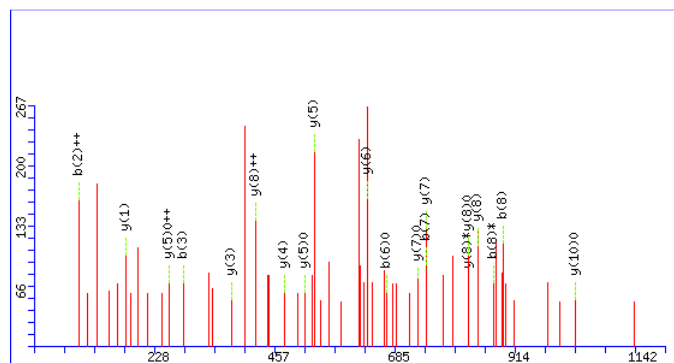
MS/MS Fragmentation of **AVLEQFGFPLTGTEAR**:

Found in **IP100021106;IP100925148;IP100925869;IP100927095**

Title: 3.1.1.2905.4

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4.3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							16
2	171.1128	86.0600	0	0	0	0	V	1664.8642	832.9358	1647.8377	824.4225	1646.8537	823.9305	15
3	284.1969	142.6021	0	0	0	0	L	1565.7958	783.4016	1548.7693	774.8883	1547.7853	774.3963	14
4	413.2395	207.1234	0	0	395.2289	198.1181	E	1452.7118	726.8595	1435.6852	718.3462	1434.7012	717.8542	13
5	541.2980	271.1527	524.2715	262.6394	523.2875	262.1474	Q	1323.6692	662.3382	1306.6426	653.8250	1305.6586	653.3329	12
6	688.3665	344.6869	671.3399	336.1736	670.3559	335.6816	F	1195.6106	598.3089	1178.5841	589.7957	1177.6000	589.3037	11
7	745.3879	373.1976	728.3614	364.6843	727.3774	364.1923	G	1048.5422	524.7747	1031.5156	516.2615	1030.5316	515.7694	10
8	892.4563	446.7318	875.4298	438.2185	874.4458	437.7265	F	991.5207	496.2640	974.4942	487.7507	973.5102	487.2587	9
9	989.5091	495.2582	972.4825	486.7449	971.4985	486.2529	P	844.4523	422.7298	827.4258	414.2165	826.4417	413.7245	8
10	1102.5932	551.8002	1085.5666	543.2869	1084.5826	542.7949	L	747.3995	374.2034	730.3730	365.6901	729.3890	365.1981	7
11	1203.6408	602.3241	1186.6143	593.8108	1185.6303	593.3188	T	634.3155	317.6614	617.2889	309.1481	616.3049	308.6561	6
12	1260.6623	630.8348	1243.6358	622.3215	1242.6517	621.8295	G	533.2678	267.1375	516.2413	258.6243	515.2572	258.1323	5
13	1361.7100	681.3586	1344.6834	672.8454	1343.6994	672.3533	T	476.2463	238.6268	459.2198	230.1135	458.2358	229.6215	4
14	1490.7526	745.8799	1473.7260	737.3667	1472.7420	736.8746	E	375.1987	188.1030	358.1721	179.5897	357.1881	179.0977	3
15	1561.7897	781.3985	1544.7631	772.8852	1543.7791	772.3932	A	246.1561	123.5817	229.1295	115.0684	0	0	2
16							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 60111.

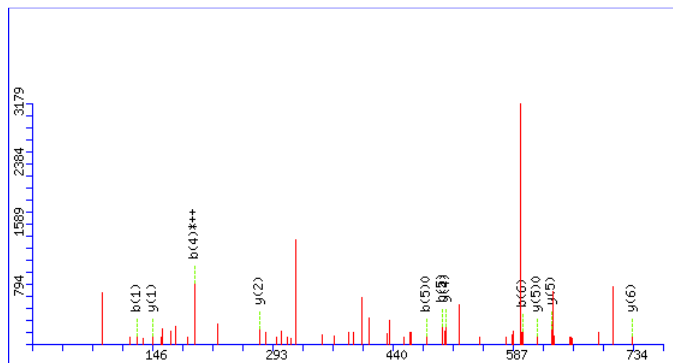
MS/MS Fragmentation of **KGDLSVEEVMK**:

Found in **IP100410618**

Title: 2.1.1.1142.2

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	129.1022	65.0548	112.0757	56.5415	0	0	K							11
2	186.1237	93.5655	169.0972	85.0522	0	0	G	1106.5398	553.7735	1089.5133	545.2603	1088.5292	544.7683	10
3	301.1506	151.0790	284.1241	142.5657	283.1401	142.0737	D	1049.5183	525.2628	1032.4918	516.7495	1031.5078	516.2575	9
4	414.2347	207.6210	397.2082	199.1077	396.2241	198.6157	L	934.4914	467.7493	917.4648	459.2361	916.4808	458.7441	8
5	501.2667	251.1370	484.2402	242.6237	483.2562	242.1317	S	821.4073	411.2073	804.3808	402.6940	803.3968	402.2020	7
6	600.3352	300.6712	583.3086	292.1579	582.3246	291.6659	V	734.3753	367.6913	717.3488	359.1780	716.3647	358.6860	6
7	729.3777	365.1925	712.3512	356.6792	711.3672	356.1872	E	635.3069	318.1571	618.2803	309.6438	617.2963	309.1518	5
8	858.4203	429.7138	841.3938	421.2005	840.4098	420.7085	E	506.2643	253.6358	489.2377	245.1225	488.2537	244.6305	4
9	957.4888	479.2480	940.4622	470.7347	939.4782	470.2427	V	377.2217	189.1145	360.1952	180.6012	0	0	3
10	1088.5292	544.7683	1071.5027	536.2550	1070.5187	535.7630	M	278.1533	139.5803	261.1267	131.0670	0	0	2
11							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 60230.

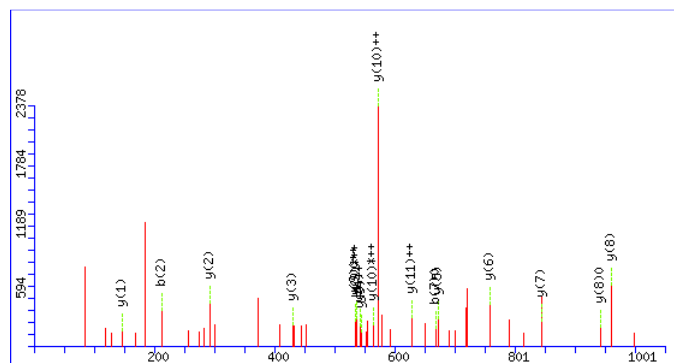
MS/MS Fragmentation of **VIGQDSSEIHF**K:

Found in **IP100303105;IP100418254;IP100917683;IP100917832;IP100917981**

Title: 2.1.1.688.4

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2.2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							12
2	213.1598	107.0835	0	0	0	0	I	1260.6219	630.8146	1243.5953	622.3013	1242.6113	621.8093	11
3	270.1812	135.5942	0	0	0	0	G	1147.5378	574.2726	1130.5113	565.7593	1129.5273	565.2673	10
4	398.2398	199.6235	381.2132	191.1103	0	0	Q	1090.5164	545.7618	1073.4898	537.2485	1072.5058	536.7565	9
5	513.2667	257.1370	496.2402	248.6237	495.2562	248.1317	D	962.4578	481.7325	945.4312	473.2193	944.4472	472.7272	8
6	600.2988	300.6530	583.2722	292.1397	582.2882	291.6477	S	847.4308	424.2191	830.4043	415.7058	829.4203	415.2138	7
7	687.3308	344.1690	670.3042	335.6558	669.3202	335.1638	S	760.3988	380.7030	743.3723	372.1898	742.3883	371.6978	6
8	816.3734	408.6903	799.3468	400.1771	798.3628	399.6850	E	673.3668	337.1870	656.3402	328.6738	655.3562	328.1817	5
9	929.4575	465.2324	912.4309	456.7191	911.4469	456.2271	I	544.3242	272.6657	527.2976	264.1525	0	0	4
10	1066.5164	533.7618	1049.4898	525.2485	1048.5058	524.7565	H	431.2401	216.1237	414.2136	207.6104	0	0	3
11	1213.5848	607.2960	1196.5582	598.7828	1195.5742	598.2907	F	294.1812	147.5942	277.1547	139.0810	0	0	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 60845.

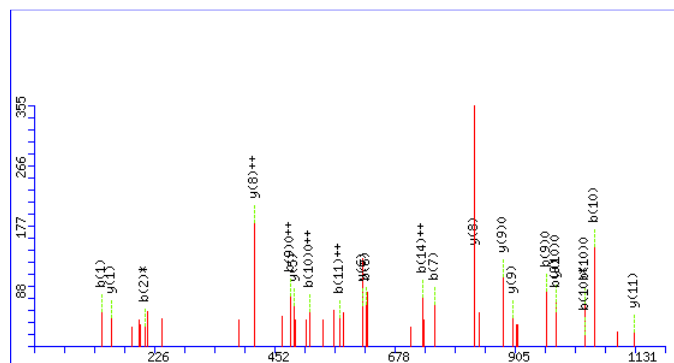
MS/MS Fragmentation of **KPAEQAEETAPIEATATK**:

Found in **IP100177428;IP100748354**

Title: 1.1.1.8000.11

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_3_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	129.1022	65.0548	112.0757	56.5415	0	0	K							18
2	226.1550	113.5811	209.1285	105.0679	0	0	P	1756.8600	878.9336	1739.8334	870.4203	1738.8494	869.9283	17
3	297.1921	149.0997	280.1656	140.5864	0	0	A	1659.8072	830.4072	1642.7806	821.8940	1641.7966	821.4020	16
4	426.2347	213.6210	409.2082	205.1077	408.2241	204.6157	E	1588.7701	794.8887	1571.7435	786.3754	1570.7595	785.8834	15
5	554.2933	277.6503	537.2667	269.1370	536.2827	268.6450	Q	1459.7275	730.3674	1442.7009	721.8541	1441.7169	721.3621	14
6	625.3304	313.1688	608.3039	304.6556	607.3198	304.1636	A	1331.6689	666.3381	1314.6424	657.8248	1313.6583	657.3328	13
7	754.3730	377.6901	737.3464	369.1769	736.3624	368.6849	E	1260.6318	630.8195	1243.6052	622.3063	1242.6212	621.8143	12
8	883.4156	442.2114	866.3890	433.6982	865.4050	433.2061	E	1131.5892	566.2982	1114.5626	557.7850	1113.5786	557.2930	11
9	984.4633	492.7353	967.4367	484.2220	966.4527	483.7300	T	1002.5466	501.7769	985.5201	493.2637	984.5360	492.7717	10
10	1055.5004	528.2538	1038.4738	519.7406	1037.4898	519.2485	A	901.4989	451.2531	884.4724	442.7398	883.4884	442.2478	9
11	1152.5531	576.7802	1135.5266	568.2669	1134.5426	567.7749	P	830.4618	415.7345	813.4353	407.2213	812.4512	406.7293	8
12	1265.6372	633.3222	1248.6107	624.8090	1247.6266	624.3170	I	733.4090	367.2082	716.3825	358.6949	715.3985	358.2029	7
13	1394.6798	697.8435	1377.6533	689.3303	1376.6692	688.8383	E	620.3250	310.6661	603.2984	302.1529	602.3144	301.6608	6
14	1465.7169	733.3621	1448.6904	724.8488	1447.7064	724.3568	A	491.2824	246.1448	474.2558	237.6316	473.2718	237.1396	5
15	1566.7646	783.8859	1549.7380	775.3727	1548.7540	774.8807	T	420.2453	210.6263	403.2187	202.1130	402.2347	201.6210	4
16	1637.8017	819.4045	1620.7752	810.8912	1619.7911	810.3992	A	319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	3
17	1738.8494	869.9283	1721.8228	861.4151	1720.8388	860.9230	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
18							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 60895.

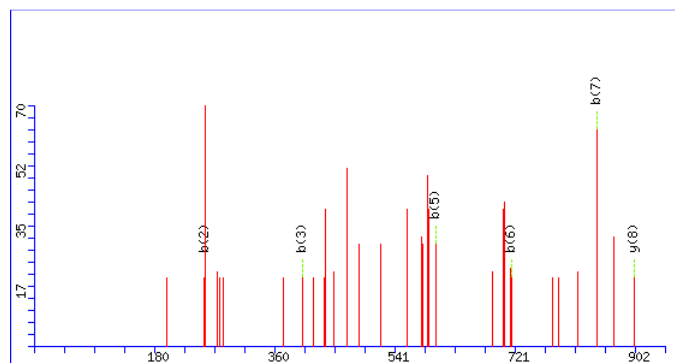
MS/MS Fragmentation of **QQFLSLEQANK**:

Found in **IP100217121**

Title: 4.1.1.4156.3

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233	0	0	Q							11
2	257.1244	129.0659	240.0979	120.5526	0	0	Q	1177.6212	589.3142	1160.5946	580.8009	1159.6106	580.3089	10
3	404.1928	202.6001	387.1663	194.0868	0	0	F	1049.5626	525.2849	1032.5360	516.7717	1031.5520	516.2796	9
4	517.2769	259.1421	500.2504	250.6288	0	0	L	902.4942	451.7507	885.4676	443.2374	884.4836	442.7454	8
5	604.3089	302.6581	587.2824	294.1448	586.2984	293.6528	S	789.4101	395.2087	772.3836	386.6954	771.3995	386.2034	7
6	717.3930	359.2001	700.3665	350.6869	699.3824	350.1949	L	702.3781	351.6927	685.3515	343.1794	684.3675	342.6874	6
7	846.4356	423.7214	829.4090	415.2082	828.4250	414.7162	E	589.2940	295.1506	572.2675	286.6374	571.2835	286.1454	5
8	974.4942	487.7507	957.4676	479.2374	956.4836	478.7454	Q	460.2514	230.6293	443.2249	222.1161	0	0	4
9	1045.5313	523.2693	1028.5047	514.7560	1027.5207	514.2640	A	332.1928	166.6001	315.1663	158.0868	0	0	3
10	1159.5742	580.2907	1142.5477	571.7775	1141.5636	571.2855	N	261.1557	131.0815	244.1292	122.5682	0	0	2
11							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 61163.

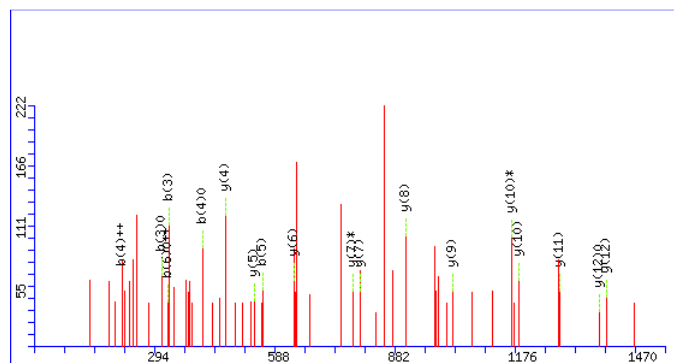
MS/MS Fragmentation of **PFSVEDTYLLOPAPILK**: 57.021465@C:11

Found in **IP100030431,IP100071177,IP100816778,IP100871735,IP100979310**

Title: 3.1.1.4021.11

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120208ry¥120208ry_Tig120slc-P8_1.3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	98.0600	49.5337	0	0	0	0	P							17
2	245.1285	123.0679	0	0	0	0	F	1865.9718	933.4895	1848.9452	924.9762	1847.9612	924.4842	16
3	332.1605	166.5839	0	0	314.1499	157.5786	S	1718.9033	859.9553	1701.8768	851.4420	1700.8928	850.9500	15
4	431.2289	216.1181	0	0	413.2183	207.1128	V	1631.8713	816.4393	1614.8448	807.9260	1613.8607	807.4340	14
5	560.2715	280.6394	0	0	542.2609	271.6341	E	1532.8029	766.9051	1515.7763	758.3918	1514.7923	757.8998	13
6	675.2984	338.1529	0	0	657.2879	329.1476	D	1403.7603	702.3838	1386.7338	693.8705	1385.7497	693.3785	12
7	776.3461	388.6767	0	0	758.3355	379.6714	T	1288.7334	644.8703	1271.7068	636.3570	1270.7228	635.8650	11
8	939.4094	470.2084	0	0	921.3989	461.2031	Y	1187.6857	594.3465	1170.6591	585.8332	0	0	10
9	1052.4935	526.7504	0	0	1034.4829	517.7451	L	1024.6224	512.8148	1007.5958	504.3015	0	0	9
10	1165.5776	583.2924	0	0	1147.5670	574.2871	L	911.5383	456.2728	894.5117	447.7595	0	0	8
11	1325.6082	663.3077	0	0	1307.5977	654.3025	C	798.4542	399.7307	781.4277	391.2175	0	0	7
12	1422.6610	711.8341	0	0	1404.6504	702.8288	P	638.4236	319.7154	621.3970	311.2022	0	0	6
13	1493.6981	747.3527	0	0	1475.6875	738.3474	A	541.3708	271.1890	524.3443	262.6758	0	0	5
14	1590.7509	795.8791	0	0	1572.7403	786.8738	P	470.3337	235.6705	453.3071	227.1572	0	0	4
15	1703.8349	852.4211	0	0	1685.8244	843.4158	I	373.2809	187.1441	356.2544	178.6308	0	0	3
16	1816.9190	908.9631	0	0	1798.9084	899.9578	L	260.1969	130.6021	243.1703	122.0888	0	0	2
17							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 61285.

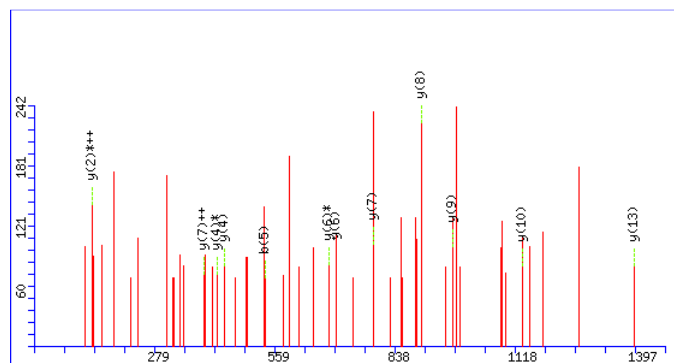
MS/MS Fragmentation of **IGGFYALSPYPGLR**:

Found in **IP100218784;IP100296461;IP100385421;IP100385801**

Title: 3.1.1.2330.7

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							14
2	171.1128	86.0600	0	0	0	0	G	1397.7212	699.3642	1380.6947	690.8510	1379.7106	690.3590	13
3	228.1343	114.5708	0	0	0	0	G	1340.6997	670.8535	1323.6732	662.3402	1322.6892	661.8482	12
4	375.2027	188.1050	0	0	0	0	F	1283.6783	642.3428	1266.6517	633.8295	1265.6677	633.3375	11
5	538.2660	269.6366	0	0	0	0	Y	1136.6099	568.8086	1119.5833	560.2953	1118.5993	559.8033	10
6	609.3031	305.1552	0	0	0	0	A	973.5465	487.2769	956.5200	478.7636	955.5360	478.2716	9
7	722.3872	361.6972	0	0	0	0	L	902.5094	451.7584	885.4829	443.2451	884.4989	442.7531	8
8	809.4192	405.2132	0	0	791.4087	396.2080	S	789.4254	395.2163	772.3988	386.7030	771.4148	386.2110	7
9	906.4720	453.7396	0	0	888.4614	444.7343	P	702.3933	351.7003	685.3668	343.1870	0	0	6
10	1069.5353	535.2713	0	0	1051.5247	526.2660	Y	605.3406	303.1739	588.3140	294.6606	0	0	5
11	1166.5881	583.7977	0	0	1148.5775	574.7924	P	442.2772	221.6423	425.2507	213.1290	0	0	4
12	1223.6095	612.3084	0	0	1205.5990	603.3031	G	345.2245	173.1159	328.1979	164.6026	0	0	3
13	1336.6936	668.8504	0	0	1318.6830	659.8452	L	288.2030	144.6051	271.1765	136.0919	0	0	2
14							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 61321.

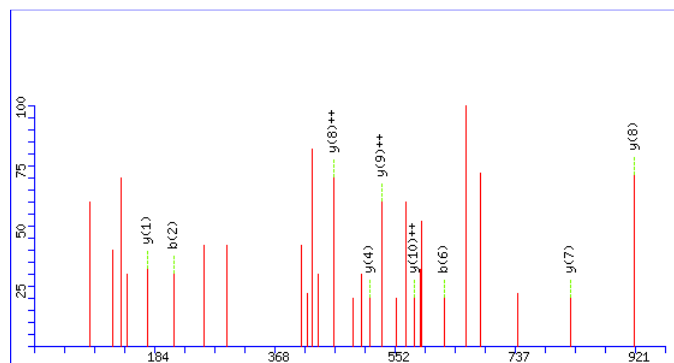
MS/MS Fragmentation of **ITFPGLHELVR**:

Found in **IP100394952;IP100411413;IP100515097;IP100940423;IP100981557**

Title: 3.1.1.989.2

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120129ry¥120129ry_604A1-46_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							11
2	215.1390	108.0731	0	0	197.1285	99.0679	T	1168.6473	584.8273	1151.6208	576.3140	1150.6368	575.8220	10
3	362.2074	181.6074	0	0	344.1969	172.6021	F	1067.5996	534.3035	1050.5731	525.7902	1049.5891	525.2982	9
4	459.2602	230.1337	0	0	441.2496	221.1285	P	920.5312	460.7693	903.5047	452.2560	902.5207	451.7640	8
5	516.2817	258.6445	0	0	498.2711	249.6392	G	823.4785	412.2429	806.4519	403.7296	805.4679	403.2376	7
6	629.3657	315.1865	0	0	611.3552	306.1812	L	766.4570	383.7321	749.4304	375.2189	748.4464	374.7269	6
7	766.4246	383.7160	0	0	748.4141	374.7107	H	653.3729	327.1901	636.3464	318.6768	635.3624	318.1848	5
8	895.4672	448.2373	0	0	877.4567	439.2320	E	516.3140	258.6606	499.2875	250.1474	498.3035	249.6554	4
9	1008.5513	504.7793	0	0	990.5407	495.7740	L	387.2714	194.1394	370.2449	185.6261	0	0	3
10	1107.6197	554.3135	0	0	1089.6091	545.3082	V	274.1874	137.5973	257.1608	129.0840	0	0	2
11							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 61341.

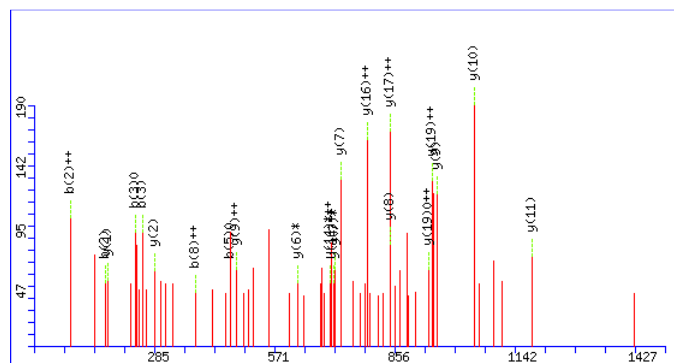
MS/MS Fragmentation of **VASLIGVEGGHSIDSSLGVLR**:

Found in **IP100059476**

Title: 3.1.1.1431.7

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120129ry¥120129ry_604A1-46_1_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							21
2	171.1128	86.0600	0	0	0	0	A	1967.0556	984.0315	1950.0291	975.5182	1949.0451	975.0262	20
3	258.1448	129.5761	0	0	240.1343	120.5708	S	1896.0185	948.5129	1878.9920	939.9996	1878.0080	939.5076	19
4	371.2289	186.1181	0	0	353.2183	177.1128	L	1808.9865	904.9969	1791.9599	896.4836	1790.9759	895.9916	18
5	484.3130	242.6601	0	0	466.3024	233.6548	I	1695.9024	848.4548	1678.8759	839.9416	1677.8919	839.4496	17
6	541.3344	271.1709	0	0	523.3239	262.1656	G	1582.8184	791.9128	1565.7918	783.3995	1564.8078	782.9075	16
7	640.4028	320.7051	0	0	622.3923	311.6998	V	1525.7969	763.4021	1508.7703	754.8888	1507.7863	754.3968	15
8	769.4454	385.2264	0	0	751.4349	376.2211	E	1426.7285	713.8679	1409.7019	705.3546	1408.7179	704.8626	14
9	826.4669	413.7371	0	0	808.4563	404.7318	G	1297.6859	649.3466	1280.6593	640.8333	1279.6753	640.3413	13
10	883.4884	442.2478	0	0	865.4778	433.2425	G	1240.6644	620.8359	1223.6379	612.3226	1222.6539	611.8306	12
11	1020.5473	510.7773	0	0	1002.5367	501.7720	H	1183.6430	592.3251	1166.6164	583.8118	1165.6324	583.3198	11
12	1107.5793	554.2933	0	0	1089.5687	545.2880	S	1046.5840	523.7957	1029.5575	515.2824	1028.5735	514.7904	10
13	1220.6634	610.8353	0	0	1202.6528	601.8300	I	959.5520	480.2796	942.5255	471.7664	941.5415	471.2744	9
14	1335.6903	668.3488	0	0	1317.6797	659.3435	D	846.4680	423.7376	829.4414	415.2243	828.4574	414.7323	8
15	1422.7223	711.8648	0	0	1404.7118	702.8595	S	731.4410	366.2241	714.4145	357.7109	713.4304	357.2189	7
16	1509.7544	755.3808	0	0	1491.7438	746.3755	S	644.4090	322.7081	627.3824	314.1949	626.3984	313.7028	6
17	1622.8384	811.9229	0	0	1604.8279	802.9176	L	557.3770	279.1921	540.3504	270.6788	0	0	5
18	1679.8599	840.4336	0	0	1661.8493	831.4283	G	444.2929	222.6501	427.2663	214.1368	0	0	4
19	1778.9283	889.9678	0	0	1760.9177	880.9625	V	387.2714	194.1394	370.2449	185.6261	0	0	3
20	1892.0124	946.5098	0	0	1874.0018	937.5045	L	288.2030	144.6051	271.1765	136.0919	0	0	2
21							R	175.1190	88.0631	158.0924	79.5498	0	0	

Peptide View

Peptide: 61422.

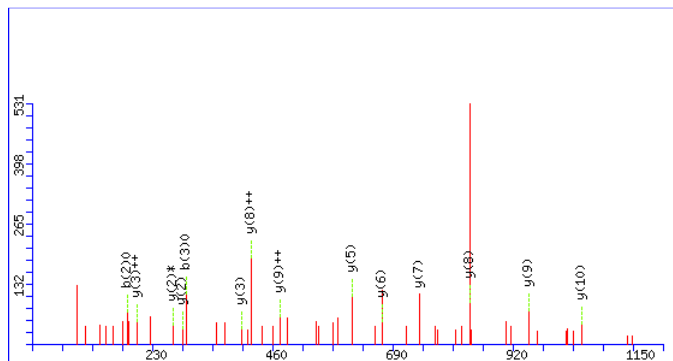
MS/MS Fragmentation of **VTLPAGPDILR**:

Found in **IP100056414**

Title: 2.1.1.4225.6

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							11
2	201.1234	101.0653	0	0	183.1128	92.0600	T	1052.6099	526.8086	1035.5833	518.2953	1034.5993	517.8033	10
3	314.2074	157.6074	0	0	296.1969	148.6021	L	951.5622	476.2847	934.5356	467.7715	933.5516	467.2795	9
4	411.2602	206.1337	0	0	393.2496	197.1285	P	838.4781	419.7427	821.4516	411.2294	820.4676	410.7374	8
5	482.2973	241.6523	0	0	464.2867	232.6470	A	741.4254	371.2163	724.3988	362.7030	723.4148	362.2110	7
6	539.3188	270.1630	0	0	521.3082	261.1577	G	670.3883	335.6978	653.3617	327.1845	652.3777	326.6925	6
7	636.3715	318.6894	0	0	618.3610	309.6841	P	613.3668	307.1870	596.3402	298.6738	595.3562	298.1817	5
8	751.3985	376.2029	0	0	733.3879	367.1976	D	516.3140	258.6606	499.2875	250.1474	498.3035	249.6554	4
9	864.4825	432.7449	0	0	846.4720	423.7396	I	401.2871	201.1472	384.2605	192.6339	0	0	3
10	977.5666	489.2869	0	0	959.5560	480.2817	L	288.2030	144.6051	271.1765	136.0919	0	0	2
11							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 61787.

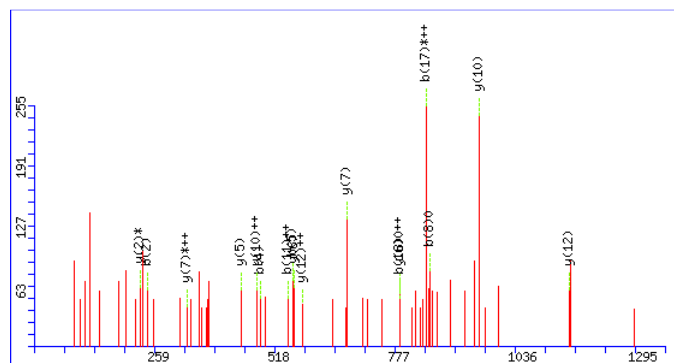
MS/MS Fragmentation of **IMDQAITVGAPVIGLNDSGGAR:**

Found in **IP100007247;IP100387103;IP100792361;IP100921904;IP100945117;IP100946553;IP100946876;IP100947051;IP100947150;IP100947502;IP100985361**

Title: 3.1.1.1495.8

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120210ry¥120210ry_32R1-32_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							22
2	245.1318	123.0696	0	0	0	0	M	2042.0335	1021.5204	2025.0070	1013.0071	2024.0230	1012.5151	21
3	360.1588	180.5830	0	0	342.1482	171.5777	D	1910.9930	956.0002	1893.9665	947.4869	1892.9825	946.9949	20
4	488.2173	244.6123	471.1908	236.0990	470.2068	235.6070	Q	1795.9661	898.4867	1778.9395	889.9734	1777.9555	889.4814	19
5	559.2545	280.1309	542.2279	271.6176	541.2439	271.1256	A	1667.9075	834.4574	1650.8810	825.9441	1649.8969	825.4521	18
6	672.3385	336.6729	655.3120	328.1596	654.3280	327.6676	I	1596.8704	798.9388	1579.8438	790.4256	1578.8598	789.9336	17
7	773.3862	387.1967	756.3597	378.6835	755.3756	378.1915	T	1483.7863	742.3968	1466.7598	733.8835	1465.7758	733.3915	16
8	872.4546	436.7309	855.4281	428.2177	854.4441	427.7257	V	1382.7387	691.8730	1365.7121	683.3597	1364.7281	682.8677	15
9	929.4761	465.2417	912.4495	456.7284	911.4655	456.2364	G	1283.6702	642.3388	1266.6437	633.8255	1265.6597	633.3335	14
10	1000.5132	500.7602	983.4866	492.2470	982.5026	491.7550	A	1226.6488	613.8280	1209.6222	605.3148	1208.6382	604.8227	13
11	1097.5660	549.2866	1080.5394	540.7733	1079.5554	540.2813	P	1155.6117	578.3095	1138.5851	569.7962	1137.6011	569.3042	12
12	1196.6344	598.8208	1179.6078	590.3075	1178.6238	589.8155	V	1058.5589	529.7831	1041.5323	521.2698	1040.5483	520.7778	11
13	1309.7184	655.3629	1292.6919	646.8496	1291.7079	646.3576	I	959.4905	480.2489	942.4639	471.7356	941.4799	471.2436	10
14	1366.7399	683.8736	1349.7134	675.3603	1348.7293	674.8683	G	846.4064	423.7068	829.3799	415.1936	828.3959	414.7016	9
15	1479.8240	740.4156	1462.7974	731.9023	1461.8134	731.4103	L	789.3850	395.1961	772.3584	386.6828	771.3744	386.1908	8
16	1593.8669	797.4371	1576.8403	788.9238	1575.8563	788.4318	N	676.3009	338.6541	659.2743	330.1408	658.2903	329.6488	7
17	1708.8938	854.9506	1691.8673	846.4373	1690.8833	845.9453	D	562.2580	281.6326	545.2314	273.1193	544.2474	272.6273	6
18	1795.9259	898.4666	1778.8993	889.9533	1777.9153	889.4613	S	447.2310	224.1191	430.2045	215.6059	429.2205	215.1139	5
19	1852.9473	926.9773	1835.9208	918.4640	1834.9368	917.9720	G	360.1990	180.6031	343.1724	172.0899	0	0	4
20	1909.9688	955.4880	1892.9422	946.9748	1891.9582	946.4828	G	303.1775	152.0924	286.1510	143.5791	0	0	3
21	1981.0059	991.0066	1963.9794	982.4933	1962.9953	982.0013	A	246.1561	123.5817	229.1295	115.0684	0	0	2
22							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 62073.

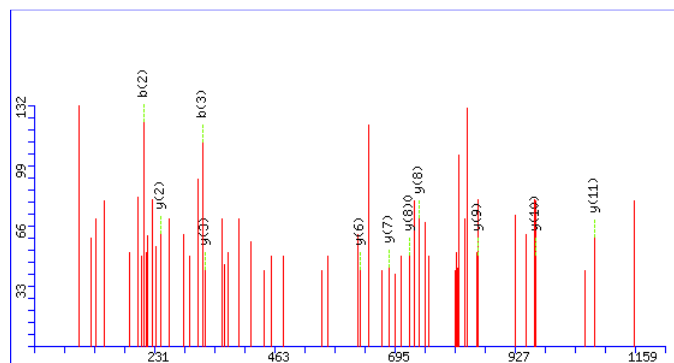
MS/MS Fragmentation of **VLILLGGNALSPK**:

Found in **IP100014173;IP100455983**

Title: 3.1.1.1684.4

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							13
2	213.1598	107.0835	0	0	0	0	L	1195.7409	598.3741	1178.7143	589.8608	1177.7303	589.3688	12
3	326.2438	163.6255	0	0	0	0	I	1082.6568	541.8320	1065.6303	533.3188	1064.6463	532.8268	11
4	439.3279	220.1676	0	0	0	0	L	969.5728	485.2900	952.5462	476.7767	951.5622	476.2847	10
5	552.4119	276.7096	0	0	0	0	L	856.4887	428.7480	839.4621	420.2347	838.4781	419.7427	9
6	609.4334	305.2203	0	0	0	0	G	743.4046	372.2060	726.3781	363.6927	725.3941	363.2007	8
7	666.4549	333.7311	0	0	0	0	G	686.3832	343.6952	669.3566	335.1819	668.3726	334.6899	7
8	780.4978	390.7525	763.4713	382.2393	0	0	N	629.3617	315.1845	612.3352	306.6712	611.3511	306.1792	6
9	851.5349	426.2711	834.5084	417.7578	0	0	A	515.3188	258.1630	498.2922	249.6498	497.3082	249.1577	5
10	964.6190	482.8131	947.5924	474.2999	0	0	L	444.2817	222.6445	427.2551	214.1312	426.2711	213.6392	4
11	1051.6510	526.3291	1034.6245	517.8159	1033.6404	517.3239	S	331.1976	166.1024	314.1710	157.5892	313.1870	157.0972	3
12	1148.7038	574.8555	1131.6772	566.3422	1130.6932	565.8502	P	244.1656	122.5864	227.1390	114.0731	0	0	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 62295.

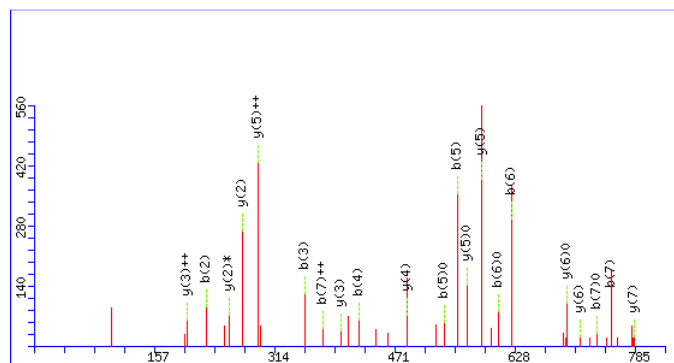
MS/MS Fragmentation of **SHEAEAPSEPR**:

Found in **IP100004988**

Title: 1.1.1.6887.6

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							12
2	225.0982	113.0527	0	0	207.0877	104.0475	H	1251.5600	626.2836	1234.5335	617.7704	1233.5495	617.2784	11
3	354.1408	177.5740	0	0	336.1302	168.5688	E	1114.5011	557.7542	1097.4746	549.2409	1096.4905	548.7489	10
4	425.1779	213.0926	0	0	407.1674	204.0873	A	985.4585	493.2329	968.4320	484.7196	967.4480	484.2276	9
5	554.2205	277.6139	0	0	536.2100	268.6086	E	914.4214	457.7143	897.3949	449.2011	896.4108	448.7091	8
6	625.2576	313.1325	0	0	607.2471	304.1272	A	785.3788	393.1930	768.3523	384.6798	767.3682	384.1878	7
7	754.3002	377.6537	0	0	736.2897	368.6485	E	714.3417	357.6745	697.3151	349.1612	696.3311	348.6692	6
8	851.3530	426.1801	0	0	833.3424	417.1748	P	585.2991	293.1532	568.2726	284.6399	567.2885	284.1479	5
9	938.3850	469.6961	0	0	920.3745	460.6909	S	488.2463	244.6268	471.2198	236.1135	470.2358	235.6215	4
10	1067.4276	534.2174	0	0	1049.4170	525.2122	E	401.2143	201.1108	384.1878	192.5975	383.2037	192.1055	3
11	1164.4804	582.7438	0	0	1146.4698	573.7385	P	272.1717	136.5895	255.1452	128.0762	0	0	2
12							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 62594.

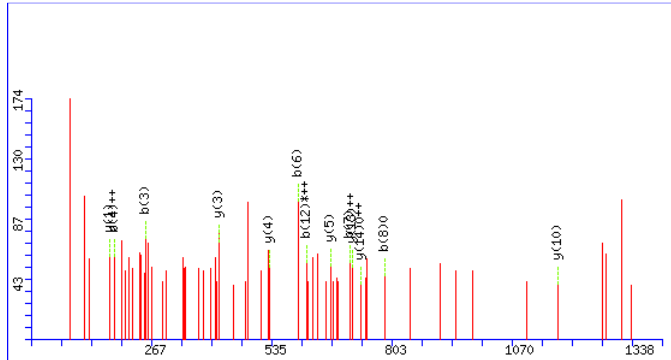
MS/MS Fragmentation of **IAALLDLPIQPTTEVLGFGLGSSTSTQHL**PFR: 0.984016@Q:27

Found in **IP100169441;IP100916141;IP100916269;IP100916890;IP100917061**

Title: 4.1.1.2418.8

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							32
2	185.1285	93.0679	0	0	0	0	A	3267.7260	1634.3666	3250.6994	1625.8534	3249.7154	1625.3613	31
3	256.1656	128.5864	0	0	0	0	A	3196.6889	1598.8481	3179.6623	1590.3348	3178.6783	1589.8428	30
4	369.2496	185.1285	0	0	0	0	L	3125.6517	1563.3295	3108.6252	1554.8162	3107.6412	1554.3242	29
5	482.3337	241.6705	0	0	0	0	L	3012.5677	1506.7875	2995.5411	1498.2742	2994.5571	1497.7822	28
6	597.3606	299.1840	0	0	579.3501	290.1787	D	2899.4836	1450.2454	2882.4571	1441.7322	2881.4731	1441.2402	27
7	710.4447	355.7260	0	0	692.4341	346.7207	L	2784.4567	1392.7320	2767.4301	1384.2187	2766.4461	1383.7267	26
8	807.4975	404.2524	0	0	789.4869	395.2471	P	2671.3726	1336.1899	2654.3461	1327.6767	2653.3620	1327.1847	25
9	920.5815	460.7944	0	0	902.5710	451.7891	I	2574.3198	1287.6636	2557.2933	1279.1503	2556.3093	1278.6583	24
10	1048.6401	524.8237	1031.6136	516.3104	1030.6295	515.8184	Q	2461.2358	1231.1215	2444.2092	1222.6083	2443.2252	1222.1162	23
11	1145.6929	573.3501	1128.6663	564.8368	1127.6823	564.3448	P	2333.1772	1167.0922	2316.1507	1158.5790	2315.1666	1158.0870	22
12	1246.7406	623.8739	1229.7140	615.3606	1228.7300	614.8686	T	2236.1244	1118.5659	2219.0979	1110.0526	2218.1139	1109.5606	21
13	1347.7882	674.3978	1330.7617	665.8845	1329.7777	665.3925	T	2135.0768	1068.0420	2118.0502	1059.5287	2117.0662	1059.0367	20
14	1476.8308	738.9191	1459.8043	730.4058	1458.8203	729.9138	E	2034.0291	1017.5182	2017.0025	1009.0049	2016.0185	1008.5129	19
15	1575.8992	788.4533	1558.8727	779.9400	1557.8887	779.4480	V	1904.9865	952.9969	1887.9599	944.4836	1886.9759	943.9916	18
16	1688.9833	844.9953	1671.9568	836.4820	1670.9727	835.9900	L	1805.9181	903.4627	1788.8915	894.9494	1787.9075	894.4574	17
17	1746.0048	873.5060	1728.9782	864.9927	1727.9942	864.5007	G	1692.8340	846.9206	1675.8075	838.4074	1674.8234	837.9154	16
18	1893.0732	947.0402	1876.0466	938.5270	1875.0626	938.0349	F	1635.8125	818.4099	1618.7860	809.8966	1617.8020	809.4046	15
19	1950.0946	975.5510	1933.0681	967.0377	1932.0841	966.5457	G	1488.7441	744.8757	1471.7176	736.3624	1470.7336	735.8704	14
20	2063.1787	1032.0930	2046.1522	1023.5797	2045.1681	1023.0877	L	1431.7227	716.3650	1414.6961	707.8517	1413.7121	707.3597	13
21	2120.2002	1060.6037	2103.1736	1052.0904	2102.1896	1051.5984	G	1318.6386	659.8229	1301.6121	651.3097	1300.6280	650.8177	12
22	2207.2322	1104.1197	2190.2057	1095.6065	2189.2216	1095.1145	S	1261.6171	631.3122	1244.5906	622.7989	1243.6066	622.3069	11
23	2294.2642	1147.6358	2277.2377	1139.1225	2276.2537	1138.6305	S	1174.5851	587.7962	1157.5586	579.2829	1156.5745	578.7909	10
24	2395.3119	1198.1596	2378.2854	1189.6463	2377.3013	1189.1543	T	1087.5531	544.2802	1070.5265	535.7669	1069.5425	535.2749	9
25	2482.3439	1241.6756	2465.3174	1233.1623	2464.3334	1232.6703	S	986.5054	493.7563	969.4789	485.2431	968.4948	484.7511	8
26	2583.3916	1292.1994	2566.3651	1283.6862	2565.3810	1283.1942	T	899.4734	450.2403	882.4468	441.7271	881.4628	441.2350	7
27	2712.4342	1356.7207	2695.4077	1348.2075	2694.4236	1347.7155	Q	798.4257	399.7165	781.3992	391.2032	0	0	6
28	2849.4931	1425.2502	2832.4666	1416.7369	2831.4826	1416.2449	H	669.3831	335.1952	652.3566	326.6819	0	0	5
29	2962.5772	1481.7922	2945.5506	1473.2790	2944.5666	1472.7869	L	532.3242	266.6657	515.2976	258.1525	0	0	4
30	3059.6299	1530.3186	3042.6034	1521.8053	3041.6194	1521.3133	P	419.2401	210.1237	402.2136	201.6104	0	0	3
31	3206.6984	1603.8528	3189.6718	1595.3395	3188.6878	1594.8475	F	322.1874	161.5973	305.1608	153.0840	0	0	2
32							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 62667.

MS/MS Fragmentation of **VWGLELILFNSPEYQR**:

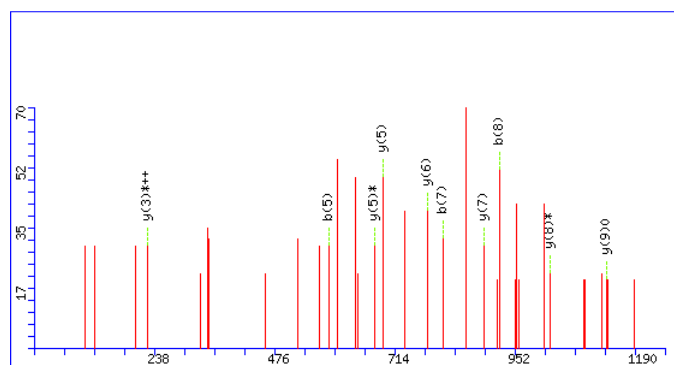
Found in

IP100219863;IP100219864;IP100607670;IP100895831;IP100944500;IP100944590;IP100944599;IP100956382;IP100956438;IP100956439;IP100956457;IP100956738;IP100979

Title: 4.1.1.2965.4

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120214ry¥120214ry_aHDF1419-P10_4_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							16
2	286.1550	143.5811	0	0	0	0	W	1864.9592	932.9832	1847.9327	924.4700	1846.9486	923.9780	15
3	343.1765	172.0919	0	0	0	0	G	1678.8799	839.9436	1661.8533	831.4303	1660.8693	830.9383	14
4	456.2605	228.6339	0	0	0	0	L	1621.8584	811.4329	1604.8319	802.9196	1603.8479	802.4276	13
5	585.3031	293.1552	0	0	567.2926	284.1499	E	1508.7744	754.8908	1491.7478	746.3775	1490.7638	745.8855	12
6	698.3872	349.6972	0	0	680.3766	340.6919	L	1379.7318	690.3695	1362.7052	681.8563	1361.7212	681.3642	11
7	811.4713	406.2393	0	0	793.4607	397.2340	I	1266.6477	633.8275	1249.6212	625.3142	1248.6371	624.8222	10
8	924.5553	462.7813	0	0	906.5448	453.7760	L	1153.5636	577.2855	1136.5371	568.7722	1135.5531	568.2802	9
9	1071.6237	536.3155	0	0	1053.6132	527.3102	F	1040.4796	520.7434	1023.4530	512.2302	1022.4690	511.7381	8
10	1185.6667	593.3370	1168.6401	584.8237	1167.6561	584.3317	N	893.4112	447.2092	876.3846	438.6959	875.4006	438.2039	7
11	1272.6987	636.8530	1255.6721	628.3397	1254.6881	627.8477	S	779.3682	390.1878	762.3417	381.6745	761.3577	381.1825	6
12	1369.7514	685.3794	1352.7249	676.8661	1351.7409	676.3741	P	692.3362	346.6717	675.3097	338.1585	674.3257	337.6665	5
13	1498.7940	749.9007	1481.7675	741.3874	1480.7835	740.8954	E	595.2835	298.1454	578.2569	289.6321	577.2729	289.1401	4
14	1661.8574	831.4323	1644.8308	822.9190	1643.8468	822.4270	Y	466.2409	233.6241	449.2143	225.1108	0	0	3
15	1789.9159	895.4616	1772.8894	886.9483	1771.9054	886.4563	Q	303.1775	152.0924	286.1510	143.5791	0	0	2
16							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 62782.

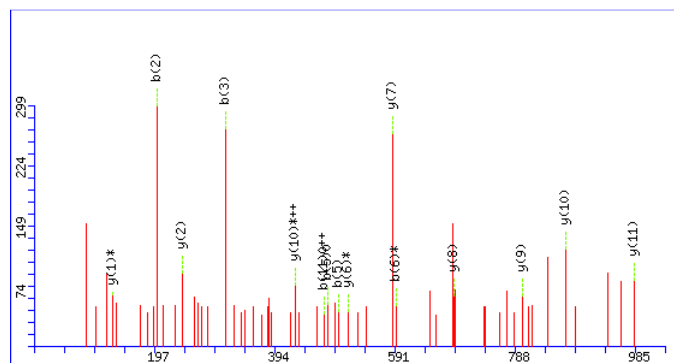
MS/MS Fragmentation of **SNLLALVGGGSSPK**:

Found in **IP100026634;IP100642108;IP100642665;IP100647947;IP100944955;IP100945407;IP100945413;IP100947041;IP101008744;IP101012561;IP101015746**

Title: 3.1.1.448.5

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120212ry¥120212ry_aHDF1388-P9_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							14
2	202.0822	101.5448	185.0557	93.0315	184.0717	92.5395	N	1212.6947	606.8510	1195.6681	598.3377	1194.6841	597.8457	13
3	315.1663	158.0868	298.1397	149.5735	297.1557	149.0815	L	1098.6517	549.8295	1081.6252	541.3162	1080.6412	540.8242	12
4	428.2504	214.6288	411.2238	206.1155	410.2398	205.6235	L	985.5677	493.2875	968.5411	484.7742	967.5571	484.2822	11
5	499.2875	250.1474	482.2609	241.6341	481.2769	241.1421	A	872.4836	436.7454	855.4571	428.2322	854.4730	427.7402	10
6	612.3715	306.6894	595.3450	298.1761	594.3610	297.6841	L	801.4465	401.2269	784.4199	392.7136	783.4359	392.2216	9
7	711.4400	356.2236	694.4134	347.7103	693.4294	347.2183	V	688.3624	344.6849	671.3359	336.1716	670.3519	335.6796	8
8	768.4614	384.7343	751.4349	376.2211	750.4509	375.7291	G	589.2940	295.1506	572.2675	286.6374	571.2835	286.1454	7
9	825.4829	413.2451	808.4563	404.7318	807.4723	404.2398	G	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	6
10	882.5043	441.7558	865.4778	433.2425	864.4938	432.7505	G	475.2511	238.1292	458.2245	229.6159	457.2405	229.1239	5
11	969.5364	485.2718	952.5098	476.7585	951.5258	476.2665	S	418.2296	209.6184	401.2031	201.1052	400.2191	200.6132	4
12	1056.5684	528.7878	1039.5418	520.2746	1038.5578	519.7826	S	331.1976	166.1024	314.1710	157.5892	313.1870	157.0972	3
13	1153.6212	577.3142	1136.5946	568.8009	1135.6106	568.3089	P	244.1656	122.5864	227.1390	114.0731	0	0	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 62932.

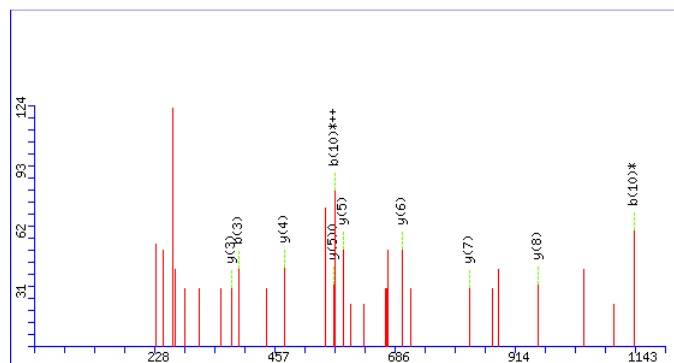
MS/MS Fragmentation of **EYPSEQIVTEK**:

Found in **IP100031563**

Title: 2.1.1.1911.11

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							12
2	293.1132	147.0602	0	0	275.1026	138.0550	Y	1306.6889	653.8481	1289.6624	645.3348	1288.6783	644.8428	11
3	390.1660	195.5866	0	0	372.1554	186.5813	P	1143.6256	572.3164	1126.5990	563.8032	1125.6150	563.3111	10
4	477.1980	239.1026	0	0	459.1874	230.0974	S	1046.5728	523.7900	1029.5463	515.2768	1028.5623	514.7848	9
5	606.2406	303.6239	0	0	588.2300	294.6186	E	959.5408	480.2740	942.5142	471.7608	941.5302	471.2688	8
6	734.2992	367.6532	717.2726	359.1399	716.2886	358.6479	Q	830.4982	415.7527	813.4716	407.2395	812.4876	406.7475	7
7	847.3832	424.1953	830.3567	415.6820	829.3727	415.1900	I	702.4396	351.7234	685.4131	343.2102	684.4291	342.7182	6
8	960.4673	480.7373	943.4407	472.2240	942.4567	471.7320	I	589.3556	295.1814	572.3290	286.6681	571.3450	286.1761	5
9	1059.5357	530.2715	1042.5092	521.7582	1041.5251	521.2662	V	476.2715	238.6394	459.2449	230.1261	458.2609	229.6341	4
10	1160.5834	580.7953	1143.5568	572.2821	1142.5728	571.7900	T	377.2031	189.1052	360.1765	180.5919	359.1925	180.0999	3
11	1289.6260	645.3166	1272.5994	636.8034	1271.6154	636.3113	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 62997.

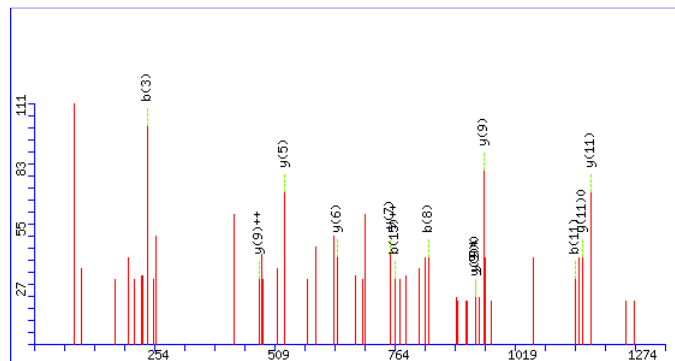
MS/MS Fragmentation of **AGLLPCPEPTIISALK: 57.021465@C:6**

Found in **IP100238469;IP100383439;IP100910764**

Title: 4.1.1.1227.2

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120210ry¥120210ry_585A1-55_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							17
2	129.0659	65.0366	0	0	0	0	G	1721.9870	861.4971	1704.9605	852.9839	1703.9764	852.4919	16
3	242.1499	121.5786	0	0	0	0	L	1664.9655	832.9864	1647.9390	824.4731	1646.9550	823.9811	15
4	355.2340	178.1206	0	0	0	0	L	1551.8815	776.4444	1534.8549	767.9311	1533.8709	767.4391	14
5	452.2867	226.6470	0	0	0	0	P	1438.7974	719.9023	1421.7709	711.3891	1420.7869	710.8971	13
6	612.3174	306.6623	0	0	0	0	C	1341.7447	671.3760	1324.7181	662.8627	1323.7341	662.3707	12
7	709.3702	355.1887	0	0	0	0	P	1181.7140	591.3606	1164.6875	582.8474	1163.7034	582.3554	11
8	838.4128	419.7100	0	0	820.4022	410.7047	E	1084.6612	542.8343	1067.6347	534.3210	1066.6507	533.8290	10
9	935.4655	468.2364	0	0	917.4550	459.2311	P	955.6186	478.3130	938.5921	469.7997	937.6081	469.3077	9
10	1036.5132	518.7602	0	0	1018.5026	509.7550	T	858.5659	429.7866	841.5393	421.2733	840.5553	420.7813	8
11	1149.5973	575.3023	0	0	1131.5867	566.2970	I	757.5182	379.2627	740.4917	370.7495	739.5076	370.2575	7
12	1262.6813	631.8443	0	0	1244.6708	622.8390	I	644.4341	322.7207	627.4076	314.2074	626.4236	313.7154	6
13	1349.7134	675.3603	0	0	1331.7028	666.3550	S	531.3501	266.1787	514.3235	257.6654	513.3395	257.1734	5
14	1420.7505	710.8789	0	0	1402.7399	701.8736	A	444.3180	222.6627	427.2915	214.1494	0	0	4
15	1533.8345	767.4209	0	0	1515.8240	758.4156	I	373.2809	187.1441	356.2544	178.6308	0	0	3
16	1646.9186	823.9629	0	0	1628.9080	814.9577	L	260.1969	130.6021	243.1703	122.0888	0	0	2
17							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 63128.

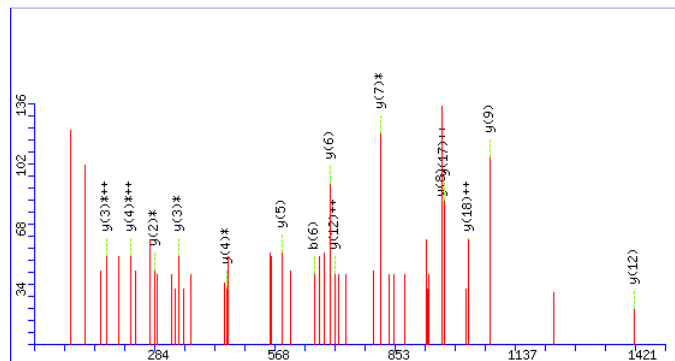
MS/MS Fragmentation of **GNFWSADILSTIGYDNIQLNNGRK**:

Found in **IP100016620:IP100170554**

Title: 4.1.1.2109.5

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_2.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							26
2	172.0717	86.5395	155.0451	78.0262	0	0	N	2889.4642	1445.2357	2872.4377	1436.7225	2871.4537	1436.2305	25
3	319.1401	160.0737	302.1135	151.5604	0	0	F	2775.4213	1388.2143	2758.3947	1379.7010	2757.4107	1379.2090	24
4	505.2194	253.1133	488.1928	244.6001	0	0	W	2628.3529	1314.6801	2611.3263	1306.1668	2610.3423	1305.6748	23
5	592.2514	296.6293	575.2249	288.1161	574.2409	287.6241	S	2442.2736	1221.6404	2425.2470	1213.1271	2424.2630	1212.6351	22
6	663.2885	332.1479	646.2620	323.6346	645.2780	323.1426	A	2355.2415	1178.1244	2338.2150	1169.6111	2337.2310	1169.1191	21
7	778.3155	389.6614	761.2889	381.1481	760.3049	380.6561	D	2284.2044	1142.6058	2267.1779	1134.0926	2266.1939	1133.6006	20
8	891.3995	446.2034	874.3730	437.6901	873.3890	437.1981	I	2169.1775	1085.0924	2152.1509	1076.5791	2151.1669	1076.0871	19
9	1004.4836	502.7454	987.4571	494.2322	986.4730	493.7402	L	2056.0934	1028.5503	2039.0669	1020.0371	2038.0828	1019.5451	18
10	1091.5156	546.2615	1074.4891	537.7482	1073.5051	537.2562	S	1943.0093	972.0083	1925.9828	963.4950	1924.9988	963.0030	17
11	1192.5633	596.7853	1175.5368	588.2720	1174.5527	587.7800	T	1855.9773	928.4923	1838.9508	919.9790	1837.9668	919.4870	16
12	1305.6474	653.3273	1288.6208	644.8141	1287.6368	644.3220	I	1754.9296	877.9685	1737.9031	869.4552	1736.9191	868.9632	15
13	1362.6688	681.8381	1345.6423	673.3248	1344.6583	672.8328	G	1641.8456	821.4264	1624.8190	812.9132	1623.8350	812.4211	14
14	1525.7322	763.3697	1508.7056	754.8564	1507.7216	754.3644	Y	1584.8241	792.9157	1567.7976	784.4024	1566.8135	783.9104	13
15	1640.7591	820.8832	1623.7326	812.3699	1622.7485	811.8779	D	1421.7608	711.3840	1404.7342	702.8708	1403.7502	702.3787	12
16	1754.8020	877.9047	1737.7755	869.3914	1736.7915	868.8994	N	1306.7338	653.8706	1289.7073	645.3573	0	0	11
17	1867.8861	934.4467	1850.8596	925.9334	1849.8755	925.4414	I	1192.6909	596.8491	1175.6644	588.3358	0	0	10
18	1980.9702	990.9887	1963.9436	982.4754	1962.9596	981.9834	I	1079.6069	540.3071	1062.5803	531.7938	0	0	9
19	2109.0287	1055.0180	2092.0022	1046.5047	2091.0182	1046.0127	Q	966.5228	483.7650	949.4962	475.2518	0	0	8
20	2246.0877	1123.5475	2229.0611	1115.0342	2228.0771	1114.5422	H	838.4642	419.7357	821.4377	411.2225	0	0	7
21	2359.1717	1180.0895	2342.1452	1171.5762	2341.1612	1171.0842	L	701.4053	351.2063	684.3787	342.6930	0	0	6
22	2473.2147	1237.1110	2456.1881	1228.5977	2455.2041	1228.1057	N	588.3212	294.6643	571.2947	286.1510	0	0	5
23	2587.2576	1294.1324	2570.2310	1285.6192	2569.2470	1285.1271	N	474.2783	237.6428	457.2518	229.1295	0	0	4
24	2644.2790	1322.6432	2627.2525	1314.1299	2626.2685	1313.6379	G	360.2354	180.6213	343.2088	172.1081	0	0	3
25	2800.3802	1400.6937	2783.3536	1392.1804	2782.3696	1391.6884	R	303.2139	152.1106	286.1874	143.5973	0	0	2
26							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 63152.

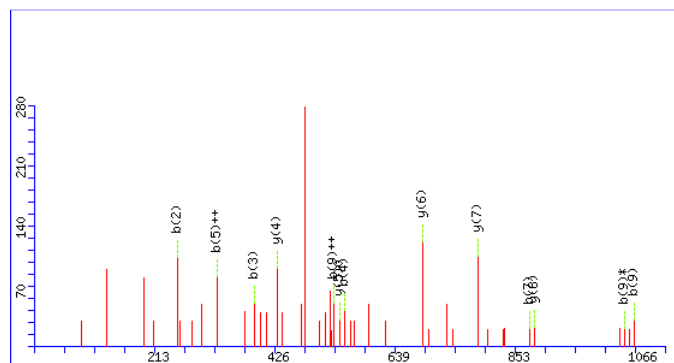
MS/MS Fragmentation of **RPHCTVEEGVQK: 57.021465@C:4**

Found in **IP100307683;IP100924932;IP100939143;IP101009718**

Title: 1.1.1.7023.7

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120214ry¥120214ry_414C2-43_4_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	157.1084	79.0578	140.0818	70.5446	0	0	R							12
2	254.1612	127.5842	237.1346	119.0709	0	0	P	1283.6049	642.3061	1266.5783	633.7928	1265.5943	633.3008	11
3	391.2201	196.1137	374.1935	187.6004	0	0	H	1186.5521	593.7797	1169.5256	585.2664	1168.5415	584.7744	10
4	551.2507	276.1290	534.2242	267.6157	0	0	C	1049.4932	525.2502	1032.4666	516.7370	1031.4826	516.2450	9
5	652.2984	326.6528	635.2718	318.1396	634.2878	317.6476	T	889.4625	445.2349	872.4360	436.7216	871.4520	436.2296	8
6	751.3668	376.1870	734.3403	367.6738	733.3562	367.1818	V	788.4149	394.7111	771.3883	386.1978	770.4043	385.7058	7
7	880.4094	440.7083	863.3828	432.1951	862.3988	431.7031	E	689.3464	345.1769	672.3199	336.6636	671.3359	336.1716	6
8	1009.4520	505.2296	992.4254	496.7164	991.4414	496.2244	E	560.3039	280.6556	543.2773	272.1423	542.2933	271.6503	5
9	1066.4735	533.7404	1049.4469	525.2271	1048.4629	524.7351	G	431.2613	216.1343	414.2347	207.6210	0	0	4
10	1165.5419	583.2746	1148.5153	574.7613	1147.5313	574.2693	V	374.2398	187.6235	357.2132	179.1103	0	0	3
11	1293.6004	647.3039	1276.5739	638.7906	1275.5899	638.2986	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 63155.

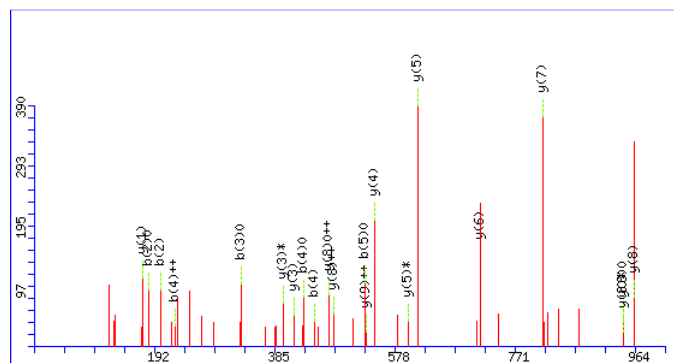
MS/MS Fragmentation of **TTFTVAQNER**:

Found in **IP100030730;IP100300026;IP100300027;IP100640414;IP100654711;IP100895850**

Title: 1.1.1.8606.11

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120214ry¥120214ry_414C2-43_4_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							10
2	203.1026	102.0550	0	0	185.0921	93.0497	T	1065.5323	533.2698	1048.5058	524.7565	1047.5218	524.2645	9
3	350.1710	175.5892	0	0	332.1605	166.5839	F	964.4847	482.7460	947.4581	474.2327	946.4741	473.7407	8
4	451.2187	226.1130	0	0	433.2082	217.1077	T	817.4163	409.2118	800.3897	400.6985	799.4057	400.2065	7
5	550.2871	275.6472	0	0	532.2766	266.6419	V	716.3686	358.6879	699.3420	350.1747	698.3580	349.6826	6
6	621.3243	311.1658	0	0	603.3137	302.1605	A	617.3002	309.1537	600.2736	300.6404	599.2896	300.1484	5
7	749.3828	375.1951	732.3563	366.6818	731.3723	366.1898	Q	546.2630	273.6352	529.2365	265.1219	528.2525	264.6299	4
8	863.4258	432.2165	846.3992	423.7032	845.4152	423.2112	N	418.2045	209.6059	401.1779	201.0926	400.1939	200.6006	3
9	992.4684	496.7378	975.4418	488.2245	974.4578	487.7325	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

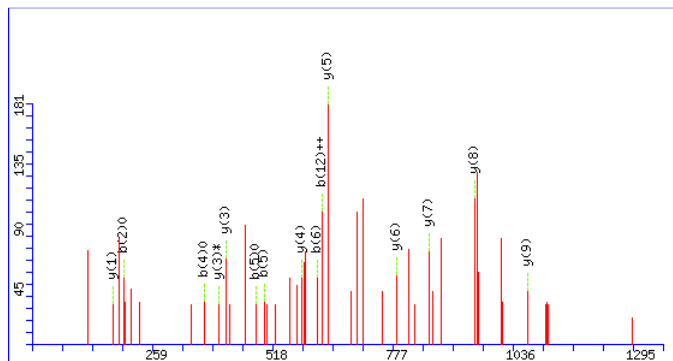
Peptide: 63183.

MS/MS Fragmentation of **DVSSIIVAFGYPR**:
Found in **IP100418582;IP100477131;IP100910352**

Title: 4.1.1.2695.4

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_3.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							14
2	215.1026	108.0550	0	0	197.0921	99.0497	V	1455.7995	728.4034	1438.7729	719.8901	1437.7889	719.3981	13
3	302.1347	151.5710	0	0	284.1241	142.5657	S	1356.7310	678.8692	1339.7045	670.3559	1338.7205	669.8639	12
4	389.1667	195.0870	0	0	371.1561	186.0817	S	1269.6990	635.3531	1252.6725	626.8399	1251.6885	626.3479	11
5	502.2508	251.6290	0	0	484.2402	242.6237	I	1182.6670	591.8371	1165.6404	583.3239	0	0	10
6	615.3348	308.1710	0	0	597.3243	299.1658	I	1069.5829	535.2951	1052.5564	526.7818	0	0	9
7	714.4032	357.7053	0	0	696.3927	348.7000	V	956.4989	478.7531	939.4723	470.2398	0	0	8
8	785.4403	393.2238	0	0	767.4298	384.2185	A	857.4305	429.2189	840.4039	420.7056	0	0	7
9	932.5088	466.7580	0	0	914.4982	457.7527	F	786.3933	393.7003	769.3668	385.1870	0	0	6
10	989.5302	495.2687	0	0	971.5197	486.2635	G	639.3249	320.1661	622.2984	311.6528	0	0	5
11	1152.5936	576.8004	0	0	1134.5830	567.7951	Y	582.3035	291.6554	565.2769	283.1421	0	0	4
12	1249.6463	625.3268	0	0	1231.6358	616.3215	P	419.2401	210.1237	402.2136	201.6104	0	0	3
13	1396.7147	698.8610	0	0	1378.7042	689.8557	F	322.1874	161.5973	305.1608	153.0840	0	0	2
14							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 63571.

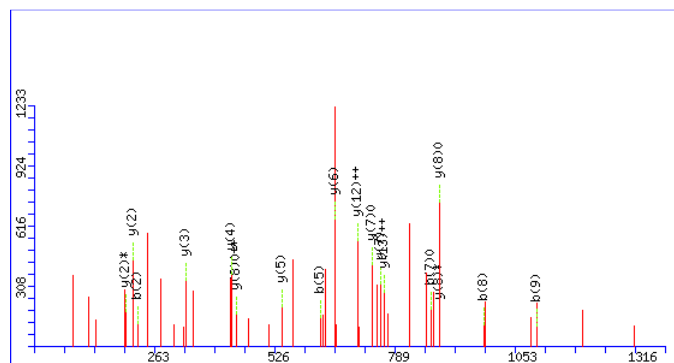
MS/MS Fragmentation of **LIDRENFVDIVDAK**:

Found in **IP100414548;IP100924471;IP100924993**

Title: 3.1.1.229.4

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120210ry¥120210ry_585A1-55_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							14
2	227.1754	114.0913	0	0	0	0	I	1533.7907	767.3990	1516.7642	758.8857	1515.7802	758.3937	13
3	342.2023	171.6048	0	0	324.1918	162.5995	D	1420.7067	710.8570	1403.6801	702.3437	1402.6961	701.8517	12
4	498.3035	249.6554	481.2769	241.1421	480.2929	240.6501	R	1305.6797	653.3435	1288.6532	644.8302	1287.6692	644.3382	11
5	627.3461	314.1767	610.3195	305.6634	609.3355	305.1714	E	1149.5786	575.2930	1132.5521	566.7797	1131.5681	566.2877	10
6	741.3890	371.1981	724.3624	362.6849	723.3784	362.1928	N	1020.5360	510.7717	1003.5095	502.2584	1002.5255	501.7664	9
7	888.4574	444.7323	871.4308	436.2191	870.4468	435.7271	F	906.4931	453.7502	889.4666	445.2369	888.4825	444.7449	8
8	987.5258	494.2665	970.4993	485.7533	969.5152	485.2613	V	759.4247	380.2160	742.3981	371.7027	741.4141	371.2107	7
9	1102.5527	551.7800	1085.5262	543.2667	1084.5422	542.7747	D	660.3563	330.6818	643.3297	322.1685	642.3457	321.6765	6
10	1215.6368	608.3220	1198.6103	599.8088	1197.6262	599.3168	I	545.3293	273.1683	528.3028	264.6550	527.3188	264.1630	5
11	1314.7052	657.8563	1297.6787	649.3430	1296.6947	648.8510	V	432.2453	216.6263	415.2187	208.1130	414.2347	207.6210	4
12	1429.7322	715.3697	1412.7056	706.8564	1411.7216	706.3644	D	333.1769	167.0921	316.1503	158.5788	315.1663	158.0868	3
13	1500.7693	750.8883	1483.7427	742.3750	1482.7587	741.8830	A	218.1499	109.5786	201.1234	101.0653	0	0	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 63809.

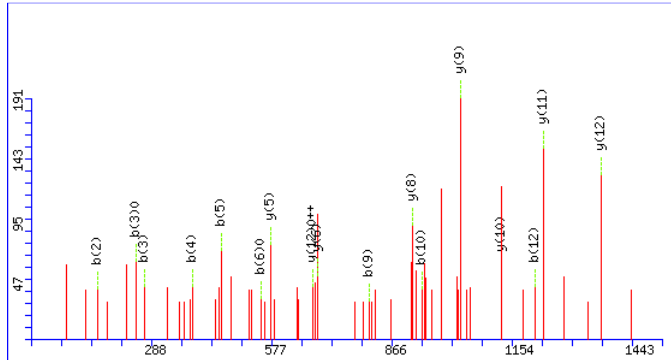
MS/MS Fragmentation of **GTLDALLAGERDPWTVSSEGVHTVDQVLSEVSR**:

Found in **IP100472106**

Title: 4.1.1.3182.9

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							33
2	159.0764	80.0418	0	0	141.0659	71.0366	T	3466.7449	1733.8761	3449.7183	1725.3628	3448.7343	1724.8708	32
3	272.1605	136.5839	0	0	254.1499	127.5786	L	3365.6972	1683.3522	3348.6706	1674.8390	3347.6866	1674.3470	31
4	387.1874	194.0974	0	0	369.1769	185.0921	D	3252.6131	1626.8102	3235.5866	1618.2969	3234.6026	1617.8049	30
5	458.2245	229.6159	0	0	440.2140	220.6106	A	3137.5862	1569.2967	3120.5596	1560.7835	3119.5756	1560.2914	29
6	571.3086	286.1579	0	0	553.2980	277.1527	L	3066.5491	1533.7782	3049.5225	1525.2649	3048.5385	1524.7729	28
7	684.3927	342.7000	0	0	666.3821	333.6947	L	2953.4650	1477.2361	2936.4385	1468.7229	2935.4544	1468.2309	27
8	755.4298	378.2185	0	0	737.4192	369.2132	A	2840.3809	1420.6941	2823.3544	1412.1808	2822.3704	1411.6888	26
9	812.4512	406.7293	0	0	794.4407	397.7240	G	2769.3438	1385.1756	2752.3173	1376.6623	2751.3333	1376.1703	25
10	941.4938	471.2506	0	0	923.4833	462.2453	E	2712.3224	1356.6648	2695.2958	1348.1515	2694.3118	1347.6595	24
11	1097.5950	549.3011	1080.5684	540.7878	1079.5844	540.2958	R	2583.2798	1292.1435	2566.2532	1283.6302	2565.2692	1283.1382	23
12	1212.6219	606.8146	1195.5953	598.3013	1194.6113	597.8093	D	2427.1787	1214.0930	2410.1521	1205.5797	2409.1681	1205.0877	22
13	1309.6747	655.3410	1292.6481	646.8277	1291.6641	646.3357	P	2312.1517	1156.5795	2295.1252	1148.0662	2294.1412	1147.5742	21
14	1495.7540	748.3806	1478.7274	739.8673	1477.7434	739.3753	W	2215.0990	1108.0531	2198.0724	1099.5398	2197.0884	1099.0478	20
15	1596.8016	798.9045	1579.7751	790.3912	1578.7911	789.8992	T	2029.0196	1015.0135	2011.9931	1006.5002	2011.0091	1006.0082	19
16	1695.8701	848.4387	1678.8435	839.9254	1677.8595	839.4334	V	1927.9720	964.4896	1910.9454	955.9763	1909.9614	955.4843	18
17	1782.9021	891.9547	1765.8755	883.4414	1764.8915	882.9494	S	1828.9035	914.9554	1811.8770	906.4421	1810.8930	905.9501	17
18	1869.9341	935.4707	1852.9076	926.9574	1851.9236	926.4654	S	1741.8715	871.4394	1724.8450	862.9261	1723.8610	862.4341	16
19	1998.9767	999.9920	1981.9502	991.4787	1980.9661	990.9867	E	1654.8395	827.9234	1637.8129	819.4101	1636.8289	818.9181	15
20	2055.9982	1028.5027	2038.9716	1019.9895	2037.9876	1019.4974	G	1525.7969	763.4021	1508.7703	754.8888	1507.7863	754.3968	14
21	2155.0666	1078.0369	2138.0400	1069.5237	2137.0560	1069.0317	V	1468.7754	734.8914	1451.7489	726.3781	1450.7649	725.8861	13
22	2292.1255	1146.5664	2275.0990	1138.0531	2274.1149	1137.5611	H	1369.7070	685.3571	1352.6805	676.8439	1351.6965	676.3519	12
23	2393.1732	1197.0902	2376.1466	1188.5770	2375.1626	1188.0849	T	1232.6481	616.8277	1215.6216	608.3144	1214.6375	607.8224	11
24	2492.2416	1246.6244	2475.2150	1238.1112	2474.2310	1237.6192	V	1131.6004	566.3039	1114.5739	557.7906	1113.5899	557.2986	10
25	2607.2685	1304.1379	2590.2420	1295.6246	2589.2580	1295.1326	D	1032.5320	516.7696	1015.5055	508.2564	1014.5214	507.7644	9
26	2735.3271	1368.1672	2718.3006	1359.6539	2717.3166	1359.1619	Q	917.5051	459.2562	900.4785	450.7429	899.4945	450.2509	8
27	2834.3955	1417.7014	2817.3690	1409.1881	2816.3850	1408.6961	V	789.4465	395.2269	772.4199	386.7136	771.4359	386.2216	7
28	2947.4796	1474.2434	2930.4530	1465.7302	2929.4690	1465.2382	L	690.3781	345.6927	673.3515	337.1794	672.3675	336.6874	6
29	3034.5116	1517.7594	3017.4851	1509.2462	3016.5011	1508.7542	S	577.2940	289.1506	560.2675	280.6374	559.2835	280.1454	5
30	3163.5542	1582.2807	3146.5277	1573.7675	3145.5437	1573.2755	E	490.2620	245.6346	473.2354	237.1214	472.2514	236.6293	4
31	3262.6226	1631.8150	3245.5961	1623.3017	3244.6121	1622.8097	V	361.2194	181.1133	344.1928	172.6001	343.2088	172.1081	3
32	3349.6547	1675.3310	3332.6281	1666.8177	3331.6441	1666.3257	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
33							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 63840.

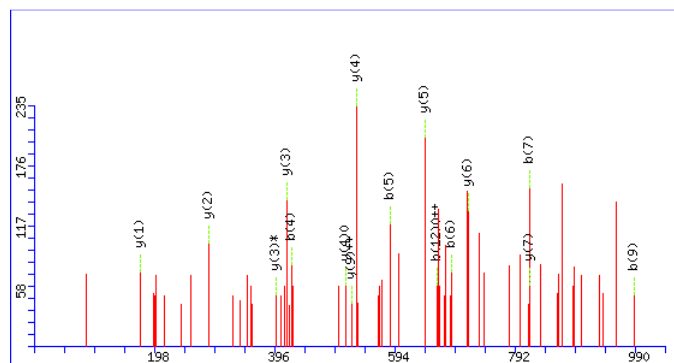
MS/MS Fragmentation of **SAEHYTETALDEIR**:

Found in **IP100290439;IP100412344;IP100966190;IP100968125**

Title: 2.1.1.2723.6

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4.2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							14
2	159.0764	80.0418	0	0	141.0659	71.0366	A	1547.7336	774.3705	1530.7071	765.8572	1529.7231	765.3652	13
3	288.1190	144.5631	0	0	270.1084	135.5579	E	1476.6965	738.8519	1459.6700	730.3386	1458.6860	729.8466	12
4	425.1779	213.0926	0	0	407.1674	204.0873	H	1347.6539	674.3306	1330.6274	665.8173	1329.6434	665.3253	11
5	588.2413	294.6243	0	0	570.2307	285.6190	Y	1210.5950	605.8011	1193.5685	597.2879	1192.5844	596.7959	10
6	689.2889	345.1481	0	0	671.2784	336.1428	T	1047.5317	524.2695	1030.5051	515.7562	1029.5211	515.2642	9
7	818.3315	409.6694	0	0	800.3210	400.6641	E	946.4840	473.7456	929.4575	465.2324	928.4734	464.7404	8
8	919.3792	460.1932	0	0	901.3686	451.1880	T	817.4414	409.2243	800.4149	400.7111	799.4308	400.2191	7
9	990.4163	495.7118	0	0	972.4058	486.7065	A	716.3937	358.7005	699.3672	350.1872	698.3832	349.6952	6
10	1103.5004	552.2538	0	0	1085.4898	543.2485	L	645.3566	323.1819	628.3301	314.6687	627.3461	314.1767	5
11	1218.5273	609.7673	0	0	1200.5168	600.7620	D	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
12	1347.5699	674.2886	0	0	1329.5594	665.2833	E	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
13	1460.6540	730.8306	0	0	1442.6434	721.8253	I	288.2030	144.6051	271.1765	136.0919	0	0	2
14							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: **63853**.

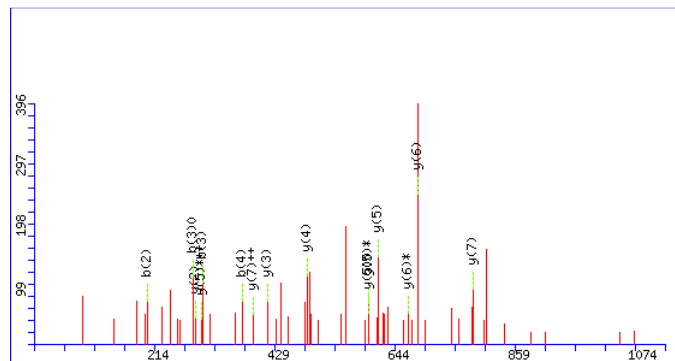
MS/MS Fragmentation of **DSVAQAELR**:

Found in **IP100014239**

Title: 1.1.1.8327.8

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							9
2	203.0662	102.0368	0	0	185.0557	93.0315	S	873.4789	437.2431	856.4523	428.7298	855.4683	428.2378	8
3	302.1347	151.5710	0	0	284.1241	142.5657	V	786.4468	393.7271	769.4203	385.2138	768.4363	384.7218	7
4	373.1718	187.0895	0	0	355.1612	178.0842	A	687.3784	344.1928	670.3519	335.6796	669.3679	335.1876	6
5	501.2304	251.1188	484.2038	242.6055	483.2198	242.1135	Q	616.3413	308.6743	599.3148	300.1610	598.3307	299.6690	5
6	572.2675	286.6374	555.2409	278.1241	554.2569	277.6321	A	488.2827	244.6450	471.2562	236.1317	470.2722	235.6397	4
7	701.3101	351.1587	684.2835	342.6454	683.2995	342.1534	E	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
8	814.3941	407.7007	797.3676	399.1874	796.3836	398.6954	L	288.2030	144.6051	271.1765	136.0919	0	0	2
9							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: **64097.**

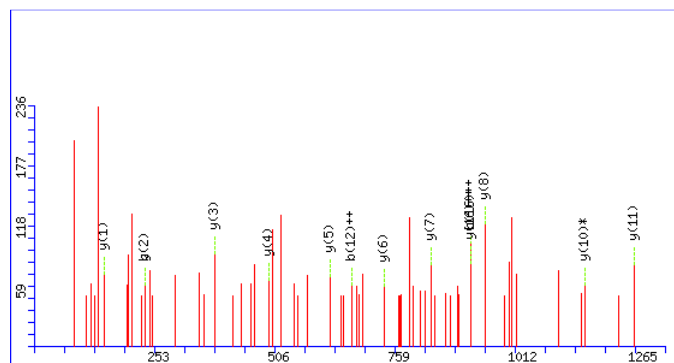
MS/MS Fragmentation of **AYPDNHLSQVDVNELFSK:**

Found in **IP100016387;IP100984750**

Title: 3.1.1.1418.8

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							18
2	235.1077	118.0575	0	0	0	0	Y	2004.9661	1002.9867	1987.9396	994.4734	1986.9556	993.9814	17
3	332.1605	166.5839	0	0	0	0	P	1841.9028	921.4550	1824.8763	912.9418	1823.8923	912.4498	16
4	447.1874	224.0974	0	0	429.1769	215.0921	D	1744.8501	872.9287	1727.8235	864.4154	1726.8395	863.9234	15
5	561.2304	281.1188	544.2038	272.6055	543.2198	272.1135	N	1629.8231	815.4152	1612.7966	806.9019	1611.8125	806.4099	14
6	698.2893	349.6483	681.2627	341.1350	680.2787	340.6430	H	1515.7802	758.3937	1498.7536	749.8805	1497.7696	749.3884	13
7	811.3733	406.1903	794.3468	397.6770	793.3628	397.1850	L	1378.7213	689.8643	1361.6947	681.3510	1360.7107	680.8590	12
8	898.4054	449.7063	881.3788	441.1930	880.3948	440.7010	S	1265.6372	633.3222	1248.6107	624.8090	1247.6266	624.3170	11
9	1026.4639	513.7356	1009.4374	505.2223	1008.4534	504.7303	Q	1178.6052	589.8062	1161.5786	581.2930	1160.5946	580.8009	10
10	1125.5323	563.2698	1108.5058	554.7565	1107.5218	554.2645	V	1050.5466	525.7769	1033.5201	517.2637	1032.5360	516.7717	9
11	1240.5593	620.7833	1223.5327	612.2700	1222.5487	611.7780	D	951.4782	476.2427	934.4516	467.7295	933.4676	467.2374	8
12	1339.6277	670.3175	1322.6012	661.8042	1321.6171	661.3122	V	836.4512	418.7293	819.4247	410.2160	818.4407	409.7240	7
13	1453.6706	727.3390	1436.6441	718.8257	1435.6601	718.3337	N	737.3828	369.1951	720.3563	360.6818	719.3723	360.1898	6
14	1582.7132	791.8603	1565.6867	783.3470	1564.7027	782.8550	E	623.3399	312.1736	606.3134	303.6603	605.3293	303.1683	5
15	1695.7973	848.4023	1678.7707	839.8890	1677.7867	839.3970	L	494.2973	247.6523	477.2708	239.1390	476.2867	238.6470	4
16	1842.8657	921.9365	1825.8392	913.4232	1824.8551	912.9312	F	381.2132	191.1103	364.1867	182.5970	363.2027	182.1050	3
17	1929.8977	965.4525	1912.8712	956.9392	1911.8872	956.4472	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
18							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: **64133**.

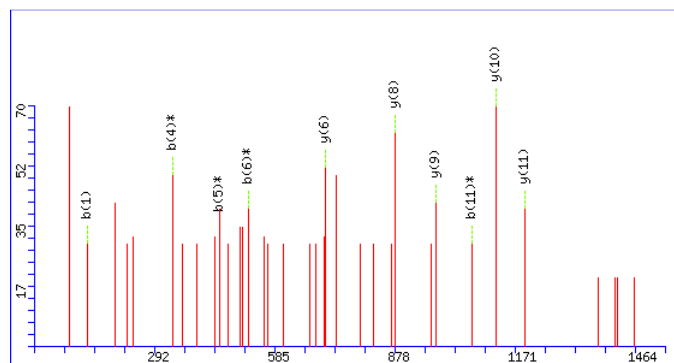
MS/MS Fragmentation of **QGVALAFVGLQVPVLR: -17.026549@N-term(Q)**

Found in **IP100410334**

Title: 4.1.1.3022.7

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233	0	0	Q							16
2	186.0873	93.5473	169.0608	85.0340	0	0	G	1538.9417	769.9745	1521.9152	761.4612	0	0	15
3	285.1557	143.0815	268.1292	134.5682	0	0	V	1481.9202	741.4638	1464.8937	732.9505	0	0	14
4	356.1928	178.6001	339.1663	170.0868	0	0	A	1382.8518	691.9296	1365.8253	683.4163	0	0	13
5	469.2769	235.1421	452.2504	226.6288	0	0	L	1311.8147	656.4110	1294.7882	647.8977	0	0	12
6	540.3140	270.6607	523.2875	262.1474	0	0	A	1198.7307	599.8690	1181.7041	591.3557	0	0	11
7	687.3824	344.1949	670.3559	335.6816	0	0	F	1127.6935	564.3504	1110.6670	555.8371	0	0	10
8	786.4509	393.7291	769.4243	385.2158	0	0	V	980.6251	490.8162	963.5986	482.3029	0	0	9
9	843.4723	422.2398	826.4458	413.7265	0	0	G	881.5567	441.2820	864.5302	432.7687	0	0	8
10	956.5564	478.7818	939.5298	470.2686	0	0	L	824.5352	412.7713	807.5087	404.2580	0	0	7
11	1084.6150	542.8111	1067.5884	534.2978	0	0	Q	711.4512	356.2292	694.4246	347.7160	0	0	6
12	1183.6834	592.3453	1166.6568	583.8320	0	0	V	583.3926	292.1999	566.3661	283.6867	0	0	5
13	1280.7361	640.8717	1263.7096	632.3584	0	0	P	484.3242	242.6657	467.2976	234.1525	0	0	4
14	1379.8046	690.4059	1362.7780	681.8926	0	0	V	387.2714	194.1394	370.2449	185.6261	0	0	3
15	1492.8886	746.9479	1475.8621	738.4347	0	0	L	288.2030	144.6051	271.1765	136.0919	0	0	2
16							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 64156.

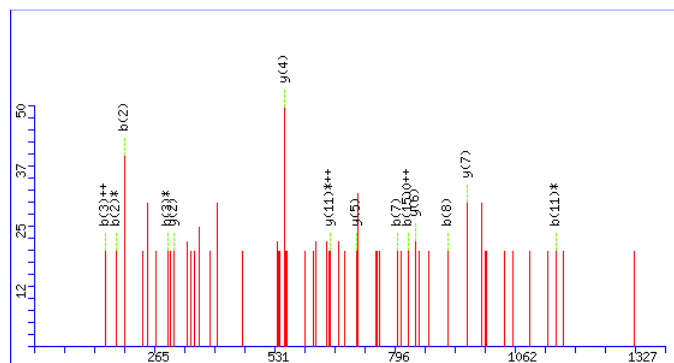
MS/MS Fragmentation of **AQLTQLFLASVLECPFYK: 57.021465@C:14**

Found in **IP100031696,IP100292255,IP100964536**

Title: 4.1.1.3384.3

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							18
2	200.1030	100.5551	183.0764	92.0418	0	0	Q	2057.0776	1029.0424	2040.0511	1020.5292	2039.0671	1020.0372	17
3	313.1870	157.0972	296.1605	148.5839	0	0	L	1929.0190	965.0132	1911.9925	956.4999	1911.0085	956.0079	16
4	414.2347	207.6210	397.2082	199.1077	396.2241	198.6157	T	1815.9350	908.4711	1798.9084	899.9578	1797.9244	899.4658	15
5	542.2933	271.6503	525.2667	263.1370	524.2827	262.6450	Q	1714.8873	857.9473	1697.8607	849.4340	1696.8767	848.9420	14
6	655.3774	328.1923	638.3508	319.6790	637.3668	319.1870	L	1586.8287	793.9180	1569.8022	785.4047	1568.8182	784.9127	13
7	802.4458	401.7265	785.4192	393.2132	784.4352	392.7212	F	1473.7447	737.3760	1456.7181	728.8627	1455.7341	728.3707	12
8	915.5298	458.2686	898.5033	449.7553	897.5193	449.2633	L	1326.6762	663.8418	1309.6497	655.3285	1308.6657	654.8365	11
9	986.5669	493.7871	969.5404	485.2738	968.5564	484.7818	A	1213.5922	607.2997	1196.5656	598.7865	1195.5816	598.2944	10
10	1073.5990	537.3031	1056.5724	528.7898	1055.5884	528.2978	S	1142.5551	571.7812	1125.5285	563.2679	1124.5445	562.7759	9
11	1172.6674	586.8373	1155.6408	578.3241	1154.6568	577.8320	V	1055.5230	528.2652	1038.4965	519.7519	1037.5125	519.2599	8
12	1285.7515	643.3794	1268.7249	634.8661	1267.7409	634.3741	L	956.4546	478.7309	939.4281	470.2177	938.4441	469.7257	7
13	1414.7940	707.9007	1397.7675	699.3874	1396.7835	698.8954	E	843.3706	422.1889	826.3440	413.6756	825.3600	413.1836	6
14	1574.8247	787.9160	1557.7981	779.4027	1556.8141	778.9107	C	714.3280	357.6676	697.3014	349.1543	0	0	5
15	1671.8775	836.4424	1654.8509	827.9291	1653.8669	827.4371	P	554.2973	277.6523	537.2708	269.1390	0	0	4
16	1818.9459	909.9766	1801.9193	901.4633	1800.9353	900.9713	F	457.2445	229.1259	440.2180	220.6126	0	0	3
17	1982.0092	991.5082	1964.9827	982.9950	1963.9986	982.5030	Y	310.1761	155.5917	293.1496	147.0784	0	0	2
18							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: **64212**.

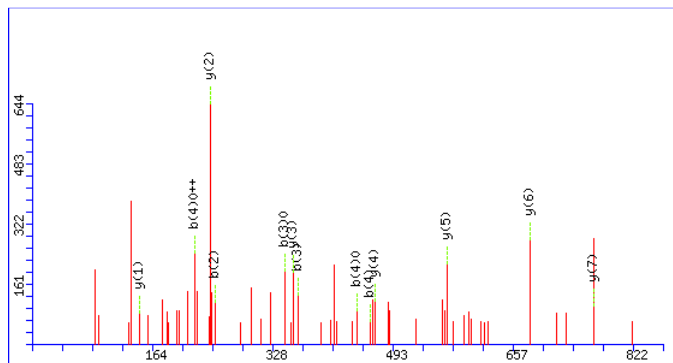
MS/MS Fragmentation of **YSLVIPP**K:

Found in **IP100022832;IP100640179**

Title: 2.1.1.3943.3

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	164.0706	82.5389	0	0	0	0	Y							8
2	251.1026	126.0550	0	0	233.0921	117.0497	S	769.5182	385.2627	752.4917	376.7495	751.5076	376.2575	7
3	364.1867	182.5970	0	0	346.1761	173.5917	L	682.4862	341.7467	665.4596	333.2335	0	0	6
4	463.2551	232.1312	0	0	445.2445	223.1259	V	569.4021	285.2047	552.3756	276.6914	0	0	5
5	576.3392	288.6732	0	0	558.3286	279.6679	I	470.3337	235.6705	453.3071	227.1572	0	0	4
6	689.4232	345.2153	0	0	671.4127	336.2100	I	357.2496	179.1285	340.2231	170.6152	0	0	3
7	786.4760	393.7416	0	0	768.4654	384.7364	P	244.1656	122.5864	227.1390	114.0731	0	0	2
8							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 64217.

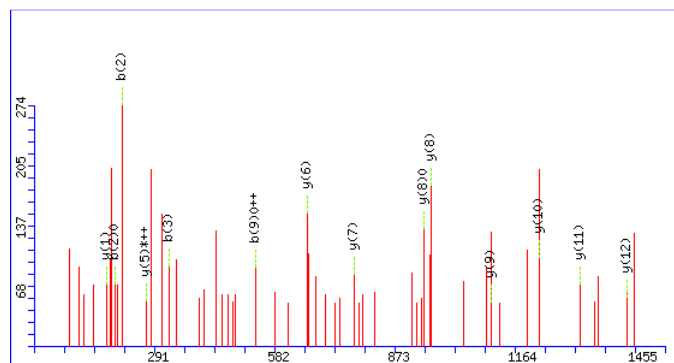
MS/MS Fragmentation of **TILVDFWDTAGQER**:

Found in **IP100002644;IP100009415;IP100220774;IP100221207;IP100853111;IP100853263;IP100853329;IP100916376;IP100916620;IP100917072**

Title: 3.1.1.3842.5

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120208ry¥120208ry_Tig120slc-P8_2.3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							14
2	215.1390	108.0731	0	0	197.1285	99.0679	I	1549.7645	775.3859	1532.7380	766.8726	1531.7540	766.3806	13
3	328.2231	164.6152	0	0	310.2125	155.6099	L	1436.6805	718.8439	1419.6539	710.3306	1418.6699	709.8386	12
4	427.2915	214.1494	0	0	409.2809	205.1441	V	1323.5964	662.3018	1306.5699	653.7886	1305.5858	653.2966	11
5	542.3184	271.6629	0	0	524.3079	262.6576	D	1224.5280	612.7676	1207.5014	604.2544	1206.5174	603.7624	10
6	689.3869	345.1971	0	0	671.3763	336.1918	F	1109.5010	555.2542	1092.4745	546.7409	1091.4905	546.2489	9
7	875.4662	438.2367	0	0	857.4556	429.2314	W	962.4326	481.7200	945.4061	473.2067	944.4221	472.7147	8
8	990.4931	495.7502	0	0	972.4825	486.7449	D	776.3533	388.6803	759.3268	380.1670	758.3428	379.6750	7
9	1091.5408	546.2740	0	0	1073.5302	537.2688	T	661.3264	331.1668	644.2998	322.6536	643.3158	322.1615	6
10	1162.5779	581.7926	0	0	1144.5673	572.7873	A	560.2787	280.6430	543.2522	272.1297	542.2681	271.6377	5
11	1219.5994	610.3033	0	0	1201.5888	601.2980	G	489.2416	245.1244	472.2150	236.6112	471.2310	236.1191	4
12	1347.6579	674.3326	1330.6314	665.8193	1329.6474	665.3273	Q	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	3
13	1476.7005	738.8539	1459.6740	730.3406	1458.6900	729.8486	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
14							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: **64360**.

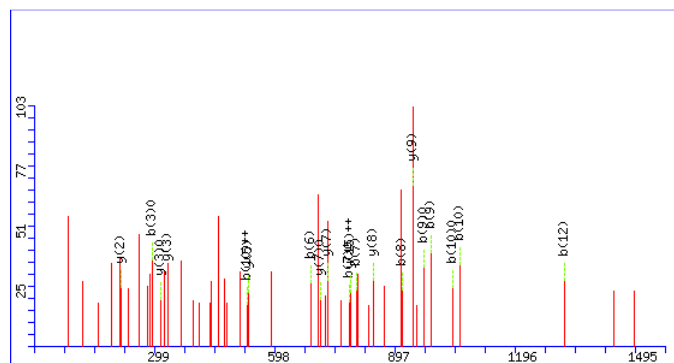
MS/MS Fragmentation of **TPDFDDLLAAFDPDPTSLDAK**:

Found in **IP100022460**

Title: 5.1.1.277.4

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120210ry¥120210ry_585A1-55_3_5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							22
2	199.1077	100.0575	0	0	181.0972	91.0522	P	2276.0969	1138.5521	2259.0703	1130.0388	2258.0863	1129.5468	21
3	314.1347	157.5710	0	0	296.1241	148.5657	D	2179.0441	1090.0257	2162.0176	1081.5124	2161.0336	1081.0204	20
4	461.2031	231.1052	0	0	443.1925	222.0999	F	2064.0172	1032.5122	2046.9906	1023.9990	2046.0066	1023.5069	19
5	576.2300	288.6186	0	0	558.2195	279.6134	D	1916.9488	958.9780	1899.9222	950.4647	1898.9382	949.9727	18
6	691.2570	346.1321	0	0	673.2464	337.1268	D	1801.9218	901.4645	1784.8953	892.9513	1783.9113	892.4593	17
7	804.3410	402.6742	0	0	786.3305	393.6689	L	1686.8949	843.9511	1669.8683	835.4378	1668.8843	834.9458	16
8	917.4251	459.2162	0	0	899.4145	450.2109	L	1573.8108	787.4090	1556.7843	778.8958	1555.8003	778.4038	15
9	988.4622	494.7347	0	0	970.4516	485.7295	A	1460.7268	730.8670	1443.7002	722.3537	1442.7162	721.8617	14
10	1059.4993	530.2533	0	0	1041.4888	521.2480	A	1389.6896	695.3485	1372.6631	686.8352	1371.6791	686.3432	13
11	1206.5677	603.7875	0	0	1188.5572	594.7822	F	1318.6525	659.8299	1301.6260	651.3166	1300.6420	650.8246	12
12	1321.5947	661.3010	0	0	1303.5841	652.2957	D	1171.5841	586.2957	1154.5576	577.7824	1153.5735	577.2904	11
13	1434.6787	717.8430	0	0	1416.6682	708.8377	I	1056.5572	528.7822	1039.5306	520.2689	1038.5466	519.7769	10
14	1531.7315	766.3694	0	0	1513.7209	757.3641	P	943.4731	472.2402	926.4466	463.7269	925.4625	463.2349	9
15	1646.7584	823.8829	0	0	1628.7479	814.8776	D	846.4203	423.7138	829.3938	415.2005	828.4098	414.7085	8
16	1743.8112	872.4092	0	0	1725.8006	863.4040	P	731.3934	366.2003	714.3668	357.6871	713.3828	357.1951	7
17	1844.8589	922.9331	0	0	1826.8483	913.9278	T	634.3406	317.6740	617.3141	309.1607	616.3301	308.6687	6
18	1931.8909	966.4491	0	0	1913.8804	957.4438	S	533.2930	267.1501	516.2664	258.6368	515.2824	258.1448	5
19	2044.9750	1022.9911	0	0	2026.9644	1013.9858	L	446.2609	223.6341	429.2344	215.1208	428.2504	214.6288	4
20	2160.0019	1080.5046	0	0	2141.9914	1071.4993	D	333.1769	167.0921	316.1503	158.5788	315.1663	158.0868	3
21	2231.0390	1116.0232	0	0	2213.0285	1107.0179	A	218.1499	109.5786	201.1234	101.0653	0	0	2
22							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: **64365**.

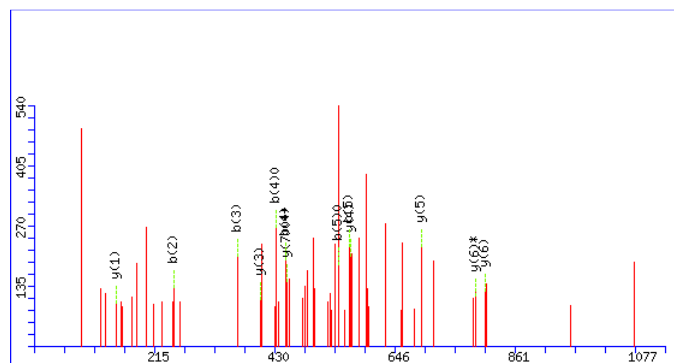
MS/MS Fragmentation of **HNLSLNECFIK: 57.021465@C:8**

Found in **IP100010550;IP100030319;IP100871189;IP101014622**

Title: 2.1.1.2780.3

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	138.0662	69.5367	0	0	0	0	H							11
2	252.1091	126.5582	235.0826	118.0449	0	0	N	1237.6245	619.3159	1220.5980	610.8026	1219.6140	610.3106	10
3	365.1932	183.1002	348.1666	174.5870	0	0	L	1123.5816	562.2944	1106.5551	553.7812	1105.5710	553.2892	9
4	452.2252	226.6162	435.1987	218.1030	434.2146	217.6110	S	1010.4975	505.7524	993.4710	497.2391	992.4870	496.7471	8
5	565.3093	283.1583	548.2827	274.6450	547.2987	274.1530	L	923.4655	462.2364	906.4390	453.7231	905.4550	453.2311	7
6	679.3522	340.1797	662.3256	331.6665	661.3416	331.1745	N	810.3815	405.6944	793.3549	397.1811	792.3709	396.6891	6
7	808.3948	404.7010	791.3682	396.1878	790.3842	395.6958	E	696.3385	348.6729	679.3120	340.1596	678.3280	339.6676	5
8	968.4254	484.7164	951.3989	476.2031	950.4149	475.7111	C	567.2959	284.1516	550.2694	275.6383	0	0	4
9	1115.4939	558.2506	1098.4673	549.7373	1097.4833	549.2453	F	407.2653	204.1363	390.2387	195.6230	0	0	3
10	1228.5779	614.7926	1211.5514	606.2793	1210.5674	605.7873	I	260.1969	130.6021	243.1703	122.0888	0	0	2
11							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: **64531**.

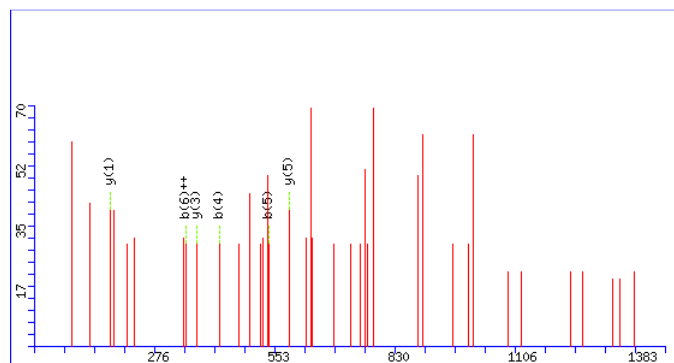
MS/MS Fragmentation of **LQQQLCDVSIR: 0.984016@Q:4.57.021465@C:6**

Found in **IP100289476;IP100642147;IP100795614**

Title: 4.1.1.2863.3

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120124ry¥120124ry_414C2-43_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							11
2	242.1499	121.5786	225.1234	113.0653	0	0	Q	1176.5678	588.7875	1159.5412	580.2742	1158.5572	579.7822	10
3	299.1714	150.0893	282.1448	141.5761	0	0	G	1048.5092	524.7582	1031.4826	516.2449	1030.4986	515.7529	9
4	428.2140	214.6106	411.1874	206.0974	0	0	Q	991.4877	496.2475	974.4612	487.7342	973.4771	487.2422	8
5	541.2980	271.1527	524.2715	262.6394	0	0	L	862.4451	431.7262	845.4186	423.2129	844.4346	422.7209	7
6	701.3287	351.1680	684.3021	342.6547	0	0	C	749.3611	375.1842	732.3345	366.6709	731.3505	366.1789	6
7	816.3556	408.6815	799.3291	400.1682	798.3451	399.6762	D	589.3304	295.1688	572.3039	286.6556	571.3198	286.1636	5
8	915.4240	458.2157	898.3975	449.7024	897.4135	449.2104	V	474.3035	237.6554	457.2769	229.1421	456.2929	228.6501	4
9	1002.4561	501.7317	985.4295	493.2184	984.4455	492.7264	S	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
10	1115.5401	558.2737	1098.5136	549.7604	1097.5296	549.2684	I	288.2030	144.6051	271.1765	136.0919	0	0	2
11							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: **64537**.

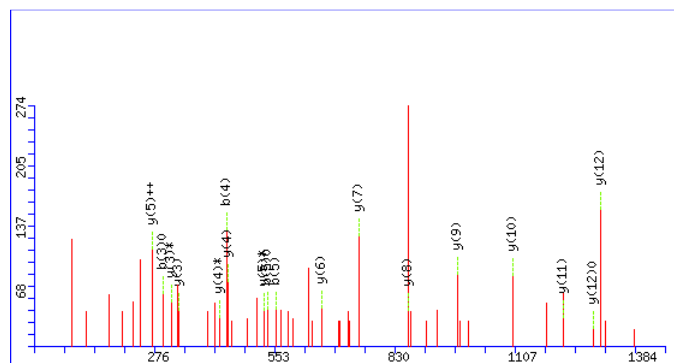
MS/MS Fragmentation of **ISDEILSDTIGEK**:

Found in **IP100019373**

Title: 2.1.1.4188.10

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							13
2	201.1234	101.0653	0	0	183.1128	92.0600	S	1306.6373	653.8223	1289.6107	645.3090	1288.6267	644.8170	12
3	316.1503	158.5788	0	0	298.1397	149.5735	D	1219.6052	610.3063	1202.5787	601.7930	1201.5947	601.3010	11
4	445.1929	223.1001	0	0	427.1823	214.0948	E	1104.5783	552.7928	1087.5517	544.2795	1086.5677	543.7875	10
5	558.2770	279.6421	0	0	540.2664	270.6368	I	975.5357	488.2715	958.5092	479.7582	957.5251	479.2662	9
6	671.3610	336.1842	0	0	653.3505	327.1789	L	862.4516	431.7295	845.4251	423.2162	844.4411	422.7242	8
7	758.3931	379.7002	0	0	740.3825	370.6949	S	749.3676	375.1874	732.3410	366.6742	731.3570	366.1821	7
8	873.4200	437.2136	0	0	855.4094	428.2084	D	662.3355	331.6714	645.3090	323.1581	644.3250	322.6661	6
9	974.4677	487.7375	0	0	956.4571	478.7322	T	547.3086	274.1579	530.2821	265.6447	529.2980	265.1527	5
10	1087.5517	544.2795	0	0	1069.5412	535.2742	I	446.2609	223.6341	429.2344	215.1208	428.2504	214.6288	4
11	1144.5732	572.7902	0	0	1126.5626	563.7850	G	333.1769	167.0921	316.1503	158.5788	315.1663	158.0868	3
12	1273.6158	637.3115	0	0	1255.6052	628.3063	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: **64822**.

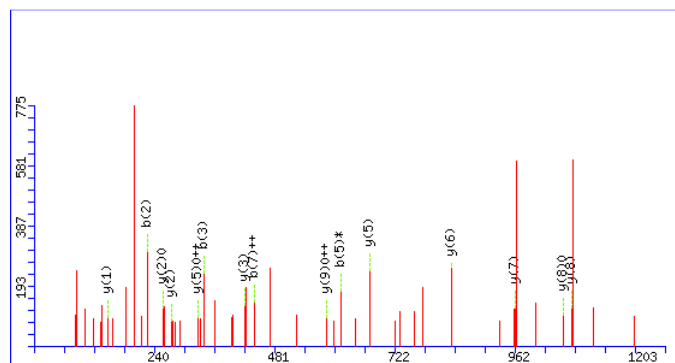
MS/MS Fragmentation of **NLLEYSYFEK**:

Found in **IP100168606,IP100794596**

Title: 3.1.1.1004.4

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							10
2	228.1343	114.5708	211.1077	106.0575	0	0	L	1191.5932	596.3002	1174.5667	587.7870	1173.5827	587.2950	9
3	341.2183	171.1128	324.1918	162.5995	0	0	L	1078.5092	539.7582	1061.4826	531.2449	1060.4986	530.7529	8
4	470.2609	235.6341	453.2344	227.1208	452.2504	226.6288	E	965.4251	483.2162	948.3985	474.7029	947.4145	474.2109	7
5	633.3243	317.1658	616.2977	308.6525	615.3137	308.1605	Y	836.3825	418.6949	819.3559	410.1816	818.3719	409.6896	6
6	720.3563	360.6818	703.3297	352.1685	702.3457	351.6765	S	673.3192	337.1632	656.2926	328.6499	655.3086	328.1579	5
7	883.4196	442.2134	866.3931	433.7002	865.4090	433.2082	Y	586.2871	293.6472	569.2606	285.1339	568.2766	284.6419	4
8	1030.4880	515.7477	1013.4615	507.2344	1012.4775	506.7424	F	423.2238	212.1155	406.1973	203.6023	405.2132	203.1103	3
9	1159.5306	580.2689	1142.5041	571.7557	1141.5201	571.2637	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
10							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 64951.

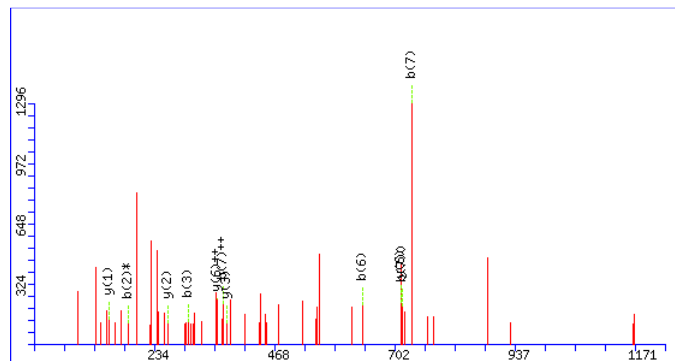
MS/MS Fragmentation of **NSVPQNPNNK: 0.984015@N:8**

Found in **IP100020903;IP100178914;IP100221389;IP100221390;IP100929187;IP100954787**

Title: 2.1.1.2224.5

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							10
2	202.0822	101.5448	185.0557	93.0315	184.0717	92.5395	S	998.4901	499.7487	981.4636	491.2354	980.4796	490.7434	9
3	301.1506	151.0790	284.1241	142.5657	283.1401	142.0737	V	911.4581	456.2327	894.4316	447.7194	0	0	8
4	398.2034	199.6053	381.1769	191.0921	380.1928	190.6001	P	812.3897	406.6985	795.3632	398.1852	0	0	7
5	526.2620	263.6346	509.2354	255.1214	508.2514	254.6293	Q	715.3369	358.1721	698.3104	349.6588	0	0	6
6	640.3049	320.6561	623.2784	312.1428	622.2943	311.6508	N	587.2784	294.1428	570.2518	285.6295	0	0	5
7	737.3577	369.1825	720.3311	360.6692	719.3471	360.1772	P	473.2354	237.1214	456.2089	228.6081	0	0	4
8	852.3846	426.6959	835.3581	418.1827	834.3741	417.6907	N	376.1827	188.5950	359.1561	180.0817	0	0	3
9	966.4275	483.7174	949.4010	475.2041	948.4170	474.7121	N	261.1557	131.0815	244.1292	122.5682	0	0	2
10							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

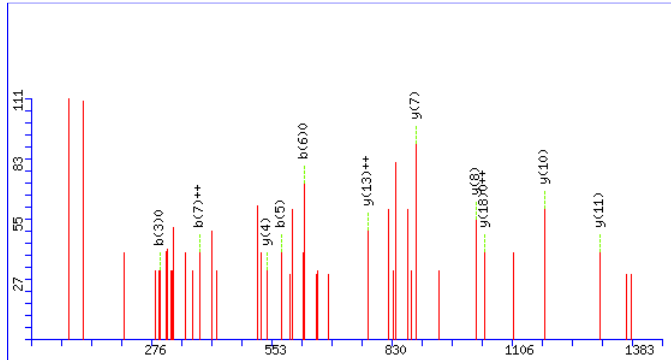
Peptide: 65231.

MS/MS Fragmentation of **EADFLAQEAQLLEELEASHITEQQLR**
Found in **IP100160622:IP100292871**

Title: 4.1.1.2658.6

Data file: Y:\TT5600(CiRA1)\2012-02\120201ry\120201ry_aHDF1388-P9_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							26
2	201.0870	101.0471	0	0	183.0764	92.0418	A	2882.4530	1441.7302	2865.4265	1433.2169	2864.4425	1432.7249	25
3	316.1139	158.5606	0	0	298.1034	149.5553	D	2811.4159	1406.2116	2794.3894	1397.6983	2793.4054	1397.2063	24
4	463.1823	232.0948	0	0	445.1718	223.0895	F	2696.3890	1348.6981	2679.3624	1340.1849	2678.3784	1339.6928	23
5	578.2664	288.6368	0	0	558.2558	279.6316	L	2549.3206	1275.1639	2532.2940	1266.6507	2531.3100	1266.1586	22
6	647.3035	324.1554	0	0	629.2930	315.1501	A	2436.2365	1218.6219	2419.2100	1210.1086	2418.2259	1209.6166	21
7	775.3621	388.1847	758.3355	379.6714	757.3515	379.1794	Q	2365.1994	1183.1033	2348.1728	1174.5901	2347.1888	1174.0981	20
8	904.4047	452.7060	887.3781	444.1927	886.3941	443.7007	E	2237.1408	1119.0740	2220.1143	1110.5608	2219.1303	1110.0688	19
9	975.4418	488.2245	958.4153	479.7113	957.4312	479.2193	A	2108.0982	1054.5528	2091.0717	1046.0395	2090.0877	1045.5475	18
10	1103.5004	552.2538	1086.4738	543.7406	1085.4898	543.2485	Q	2037.0611	1019.0342	2020.0346	1010.5209	2019.0505	1010.0289	17
11	1216.5844	608.7959	1199.5579	600.2826	1198.5739	599.7906	L	1909.0025	955.0049	1891.9760	946.4916	1890.9920	945.9996	16
12	1329.6685	665.3379	1312.6420	656.8246	1311.6579	656.3326	L	1795.9185	898.4629	1778.8919	889.9496	1777.9079	889.4576	15
13	1458.7111	729.8592	1441.6846	721.3459	1440.7005	720.8539	E	1682.8344	841.9208	1665.8079	833.4076	1664.8238	832.9156	14
14	1587.7537	794.3805	1570.7271	785.8672	1569.7431	785.3752	E	1553.7918	777.3995	1536.7653	768.8863	1535.7812	768.3943	13
15	1700.8378	850.9225	1683.8112	842.4092	1682.8272	841.9172	L	1424.7492	712.8782	1407.7227	704.3650	1406.7387	703.8730	12
16	1829.8804	915.4438	1812.8538	906.9305	1811.8698	906.4385	E	1311.6652	656.3362	1294.6386	647.8229	1293.6546	647.3309	11
17	1900.9175	950.9624	1883.8909	942.4491	1882.9069	941.9571	A	1182.6226	591.8149	1165.5960	583.3016	1164.6120	582.8096	10
18	1987.9495	994.4784	1970.9229	985.9651	1969.9389	985.4731	S	1111.5854	556.2964	1094.5589	547.7831	1093.5749	547.2911	9
19	2125.0084	1063.0078	2107.9819	1054.4946	2106.9978	1054.0026	H	1024.5534	512.7803	1007.5269	504.2671	1006.5429	503.7751	8
20	2238.0925	1119.5499	2221.0659	1111.0366	2220.0819	1110.5446	I	887.4945	444.2509	870.4680	435.7376	869.4839	435.2456	7
21	2339.1401	1170.0737	2322.1136	1161.5604	2321.1296	1161.0684	T	774.4104	387.7089	757.3839	379.1956	756.3999	378.7036	6
22	2468.1827	1234.5950	2451.1562	1226.0817	2450.1722	1225.5897	E	673.3628	337.1850	656.3362	328.6717	655.3522	328.1797	5
23	2596.2413	1298.6243	2579.2148	1290.1110	2578.2308	1289.6190	Q	544.3202	272.6637	527.2936	264.1504	0	0	4
24	2724.2999	1362.6536	2707.2733	1354.1403	2706.2893	1353.6483	Q	416.2616	208.6344	399.2350	200.1212	0	0	3
25	2837.3840	1419.1956	2820.3574	1410.6823	2819.3734	1410.1903	L	288.2030	144.6051	271.1765	136.0919	0	0	2
26							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: **65262.**

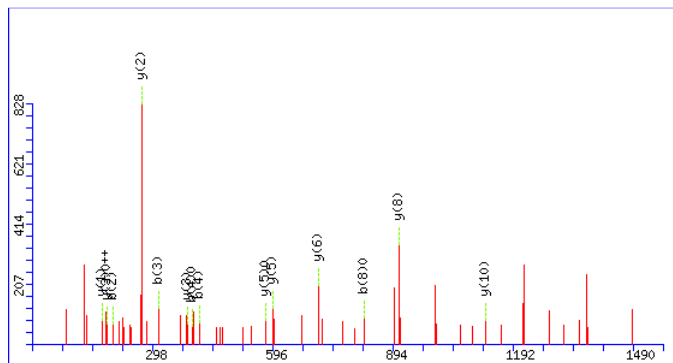
MS/MS Fragmentation of **AEDTISILPDDPR:**

Found in **IP100102920;IP100797096;IP101021016;IP101022341**

Title: 2.1.1.3654.8

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120208ry¥120208ry_Tig120slc-P8_2.2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							13
2	201.0870	101.0471	0	0	183.0764	92.0418	E	1370.6798	685.8435	1353.6533	677.3303	1352.6692	676.8383	12
3	316.1139	158.5606	0	0	298.1034	149.5553	D	1241.6372	621.3222	1224.6107	612.8090	1223.6266	612.3170	11
4	417.1616	209.0844	0	0	399.1510	200.0792	T	1126.6103	563.8088	1109.5837	555.2955	1108.5997	554.8035	10
5	530.2457	265.6265	0	0	512.2351	256.6212	I	1025.5626	513.2849	1008.5360	504.7717	1007.5520	504.2796	9
6	617.2777	309.1425	0	0	599.2671	300.1372	S	912.4785	456.7429	895.4520	448.2296	894.4680	447.7376	8
7	730.3618	365.6845	0	0	712.3512	356.6792	I	825.4465	413.2269	808.4199	404.7136	807.4359	404.2216	7
8	843.4458	422.2266	0	0	825.4353	413.2213	L	712.3624	356.6849	695.3359	348.1716	694.3519	347.6796	6
9	940.4986	470.7529	0	0	922.4880	461.7477	P	599.2784	300.1428	582.2518	291.6295	581.2678	291.1375	5
10	1055.5255	528.2664	0	0	1037.5150	519.2611	D	502.2256	251.6164	485.1991	243.1032	484.2150	242.6112	4
11	1170.5525	585.7799	0	0	1152.5419	576.7746	D	387.1987	194.1030	370.1721	185.5897	369.1881	185.0977	3
12	1267.6052	634.3063	0	0	1249.5947	625.3010	P	272.1717	136.5895	255.1452	128.0762	0	0	2
13							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 65369.

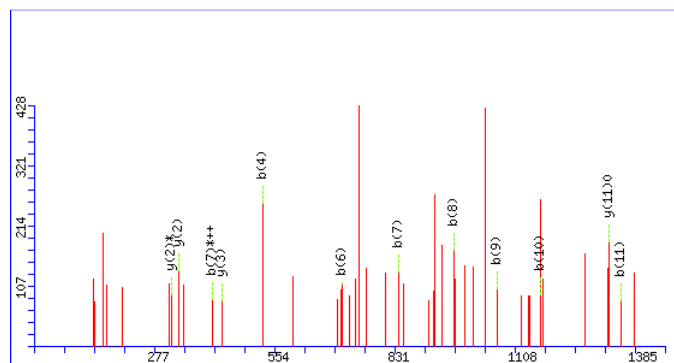
MS/MS Fragmentation of **RELQPSEEVTK**:

Found in **IP100025725;IP100943798**

Title: 2.1.1.948.11

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120208ry¥120208ry_Tig120slc-P8_2.2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	157.1084	79.0578	140.0818	70.5446	0	0	R							12
2	286.1510	143.5791	269.1244	135.0659	268.1404	134.5738	E	1345.6634	673.3353	1328.6369	664.8221	1327.6529	664.3301	11
3	399.2350	200.1212	382.2085	191.6079	381.2245	191.1159	L	1216.6208	608.8141	1199.5943	600.3008	1198.6103	599.8088	10
4	527.2936	264.1504	510.2671	255.6372	509.2831	255.1452	Q	1103.5368	552.2720	1086.5102	543.7587	1085.5262	543.2667	9
5	624.3464	312.6768	607.3198	304.1636	606.3358	303.6715	P	975.4782	488.2427	958.4516	479.7295	957.4676	479.2374	8
6	711.3784	356.1928	694.3519	347.6796	693.3678	347.1876	S	878.4254	439.7163	861.3989	431.2031	860.4149	430.7111	7
7	840.4210	420.7141	823.3945	412.2009	822.4104	411.7089	E	791.3934	396.2003	774.3668	387.6871	773.3828	387.1951	6
8	969.4636	485.2354	952.4371	476.7222	951.4530	476.2302	E	662.3508	331.6790	645.3243	323.1658	644.3402	322.6738	5
9	1068.5320	534.7696	1051.5055	526.2564	1050.5214	525.7644	V	533.3082	267.1577	516.2817	258.6445	515.2976	258.1525	4
10	1169.5797	585.2935	1152.5531	576.7802	1151.5691	576.2882	T	434.2398	217.6235	417.2132	209.1103	416.2292	208.6183	3
11	1355.6590	678.3331	1338.6325	669.8199	1337.6484	669.3279	W	333.1921	167.0997	316.1656	158.5864	0	0	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 65652.

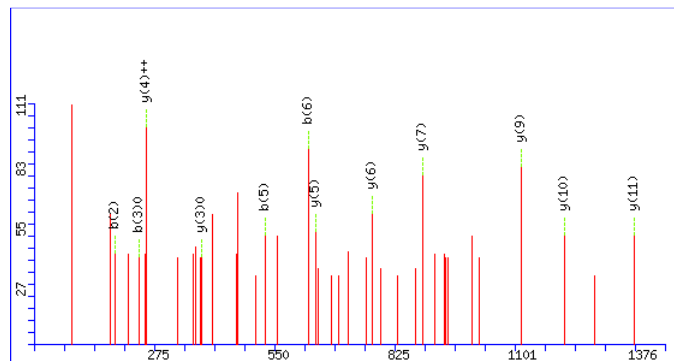
MS/MS Fragmentation of **DAALCVLIDEMNERP**: 57.021465@C:5

Found in **IP100003562**

Title: 4.1.1.245.10

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							15
2	187.0713	94.0393	0	0	169.0608	85.0340	A	1630.7927	815.9000	1613.7662	807.3867	1612.7822	806.8947	14
3	258.1084	129.5579	0	0	240.0979	120.5526	A	1559.7556	780.3815	1542.7291	771.8682	1541.7451	771.3762	13
4	371.1925	186.0999	0	0	353.1819	177.0946	L	1488.7185	744.8629	1471.6920	736.3496	1470.7079	735.8576	12
5	531.2232	266.1152	0	0	513.2126	257.1099	C	1375.6344	688.3209	1358.6079	679.8076	1357.6239	679.3156	11
6	630.2916	315.6494	0	0	612.2810	306.6441	V	1215.6038	608.3055	1198.5772	599.7923	1197.5932	599.3003	10
7	743.3756	372.1915	0	0	725.3651	363.1862	L	1116.5354	558.7713	1099.5088	550.2581	1098.5248	549.7660	9
8	856.4597	428.7335	0	0	838.4491	419.7282	I	1003.4513	502.2293	986.4248	493.7160	985.4408	493.2240	8
9	971.4866	486.2470	0	0	953.4761	477.2417	D	890.3673	445.6873	873.3407	437.1740	872.3567	436.6820	7
10	1100.5292	550.7683	0	0	1082.5187	541.7630	E	775.3403	388.1738	758.3138	379.6605	757.3297	379.1685	6
11	1231.5697	616.2885	0	0	1213.5592	607.2832	M	646.2977	323.6525	629.2712	315.1392	628.2872	314.6472	5
12	1345.6127	673.3100	1328.5861	664.7967	1327.6021	664.3047	N	515.2572	258.1323	498.2307	249.6190	497.2467	249.1270	4
13	1474.6552	737.8313	1457.6287	729.3180	1456.6447	728.8260	E	401.2143	201.1108	384.1878	192.5975	383.2037	192.1055	3
14	1630.7564	815.8818	1613.7298	807.3685	1612.7458	806.8765	R	272.1717	136.5895	255.1452	128.0762	0	0	2
15							P	116.0706	58.5389	0	0	0	0	1

Peptide View

Peptide: **65658.**

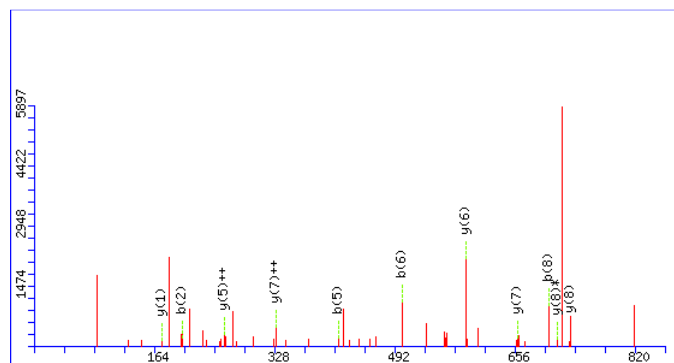
MS/MS Fragmentation of **MAAAASVTGR**:

Found in **IP100169261;IP100915343**

Title: 1.1.1.8319.8

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	132.0478	66.5275	0	0	0	0	M							10
2	203.0849	102.0461	0	0	0	0	A	803.4370	402.2221	786.4104	393.7089	785.4264	393.2169	9
3	274.1220	137.5646	0	0	0	0	A	732.3999	366.7036	715.3733	358.1903	714.3893	357.6983	8
4	345.1591	173.0832	0	0	0	0	A	661.3628	331.1850	644.3362	322.6717	643.3522	322.1797	7
5	416.1962	208.6017	0	0	0	0	A	590.3257	295.6665	573.2991	287.1532	572.3151	286.6612	6
6	503.2282	252.1178	0	0	485.2177	243.1125	S	519.2885	260.1479	502.2620	251.6346	501.2780	251.1426	5
7	602.2967	301.6520	0	0	584.2861	292.6467	V	432.2565	216.6319	415.2300	208.1186	414.2459	207.6266	4
8	703.3443	352.1758	0	0	685.3338	343.1705	T	333.1881	167.0977	316.1615	158.5844	315.1775	158.0924	3
9	760.3658	380.6865	0	0	742.3552	371.6813	G	232.1404	116.5738	215.1139	108.0606	0	0	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 65937.

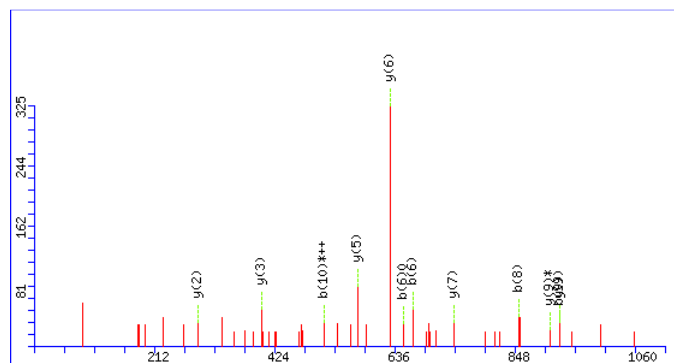
MS/MS Fragmentation of **LLNSELADLGGLNR**:

Found in **IP100062839;IP100911041**

Title: 4.1.1.1548.2

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120210ry¥120210ry_585A1-55_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0								16
2	227.1754	114.0913	0	0	0	0	L	1555.8438	778.4256	1538.8173	769.9123	1537.8333	769.4203	15
3	341.2183	171.1128	324.1918	162.5995	0	0	N	1442.7598	721.8835	1425.7332	713.3703	1424.7492	712.8782	14
4	428.2504	214.6288	411.2238	206.1155	410.2398	205.6235	S	1328.7169	664.8621	1311.6903	656.3488	1310.7063	655.8568	13
5	557.2930	279.1501	540.2664	270.6368	539.2824	270.1448	E	1241.6848	621.3461	1224.6583	612.8328	1223.6743	612.3408	12
6	670.3770	335.6921	653.3505	327.1789	652.3665	326.6869	L	1112.6422	556.8248	1095.6157	548.3115	1094.6317	547.8195	11
7	741.4141	371.2107	724.3876	362.6974	723.4036	362.2054	A	999.5582	500.2827	982.5316	491.7694	981.5476	491.2774	10
8	856.4411	428.7242	839.4145	420.2109	838.4305	419.7189	D	928.5211	464.7642	911.4945	456.2509	910.5105	455.7589	9
9	927.4782	464.2427	910.4516	455.7295	909.4676	455.2374	A	813.4941	407.2507	796.4676	398.7374	0	0	8
10	1040.5623	520.7848	1023.5357	512.2715	1022.5517	511.7795	L	742.4570	371.7321	725.4304	363.2189	0	0	7
11	1097.5837	549.2955	1080.5572	540.7822	1079.5732	540.2902	G	629.3729	315.1901	612.3464	306.6768	0	0	6
12	1154.6052	577.8062	1137.5786	569.2930	1136.5946	568.8009	G	572.3515	286.6794	555.3249	278.1661	0	0	5
13	1267.6892	634.3483	1250.6627	625.8350	1249.6787	625.3430	L	515.3300	258.1686	498.3035	249.6554	0	0	4
14	1380.7733	690.8903	1363.7468	682.3770	1362.7627	681.8850	L	402.2459	201.6266	385.2194	193.1133	0	0	3
15	1494.8162	747.9118	1477.7897	739.3985	1476.8057	738.9065	N	289.1619	145.0846	272.1353	136.5713	0	0	2
16							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 65993.

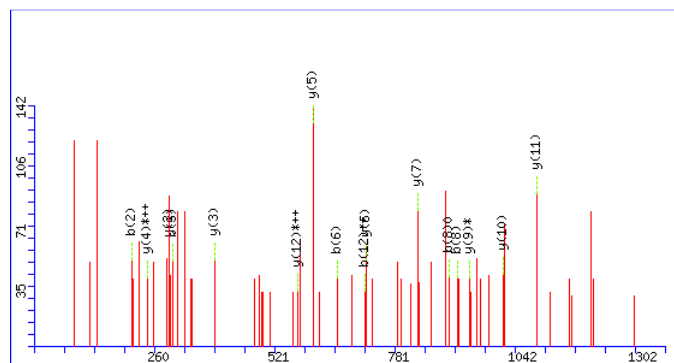
MS/MS Fragmentation of **VLSTEEMELYELAQAGGAIDPDVFK:**

Found in **IP100410094;IP100916581;IP100917656**

Title: 4.1.1.3761.4

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							26
2	213.1598	107.0835	0	0	0	0	L	2697.2964	1349.1518	2680.2698	1340.6386	2679.2858	1340.1466	25
3	300.1918	150.5995	0	0	282.1812	141.5942	S	2584.2123	1292.6098	2567.1858	1284.0965	2566.2018	1283.6045	24
4	401.2395	201.1234	0	0	383.2289	192.1181	T	2497.1803	1249.0938	2480.1538	1240.5805	2479.1697	1240.0885	23
5	530.2821	265.6447	0	0	512.2715	256.6394	E	2396.1326	1198.5699	2379.1061	1190.0567	2378.1221	1189.5647	22
6	659.3246	330.1660	0	0	641.3141	321.1607	E	2267.0900	1134.0487	2250.0635	1125.5354	2249.0795	1125.0434	21
7	790.3651	395.6862	0	0	772.3546	386.6809	M	2138.0474	1069.5274	2121.0209	1061.0141	2120.0369	1060.5221	20
8	919.4077	460.2075	0	0	901.3972	451.2022	E	2007.0070	1004.0071	1989.9804	995.4938	1988.9964	995.0018	19
9	1032.4918	516.7495	0	0	1014.4812	507.7443	L	1877.9644	939.4858	1860.9378	930.9725	1859.9538	930.4805	18
10	1195.5551	598.2812	0	0	1177.5446	589.2759	Y	1764.8803	882.9438	1747.8537	874.4305	1746.8697	873.9385	17
11	1324.5977	662.8025	0	0	1306.5871	653.7972	E	1601.8170	801.4121	1584.7904	792.8988	1583.8064	792.4068	16
12	1437.6818	719.3445	0	0	1419.6712	710.3392	L	1472.7744	736.8908	1455.7478	728.3775	1454.7638	727.8855	15
13	1508.7189	754.8631	0	0	1490.7083	745.8578	A	1359.6903	680.3488	1342.6638	671.8355	1341.6797	671.3435	14
14	1636.7775	818.8924	1619.7509	810.3791	1618.7669	809.8871	Q	1288.6532	644.8302	1271.6266	636.3170	1270.6426	635.8250	13
15	1707.8146	854.4109	1690.7880	845.8977	1689.8040	845.4056	A	1160.5946	580.8009	1143.5681	572.2877	1142.5841	571.7957	12
16	1778.8517	889.9295	1761.8251	881.4162	1760.8411	880.9242	A	1089.5575	545.2824	1072.5310	536.7691	1071.5469	536.2771	11
17	1835.8732	918.4402	1818.8466	909.9269	1817.8626	909.4349	G	1018.5204	509.7638	1001.4938	501.2506	1000.5098	500.7585	10
18	1892.8946	946.9509	1875.8681	938.4377	1874.8841	937.9457	G	961.4989	481.2531	944.4724	472.7398	943.4884	472.2478	9
19	1963.9317	982.4695	1946.9052	973.9562	1945.9212	973.4642	A	904.4775	452.7424	887.4509	444.2291	886.4669	443.7371	8
20	2077.0158	1039.0115	2059.9893	1030.4983	2059.0052	1030.0063	I	833.4403	417.2238	816.4138	408.7105	815.4298	408.2185	7
21	2192.0427	1096.5250	2175.0162	1088.0117	2174.0322	1087.5197	D	720.3563	360.6818	703.3297	352.1685	702.3457	351.6765	6
22	2289.0955	1145.0514	2272.0690	1136.5381	2271.0849	1136.0461	P	605.3293	303.1683	588.3028	294.6550	587.3188	294.1630	5
23	2404.1225	1202.5649	2387.0959	1194.0516	2386.1119	1193.5596	D	508.2766	254.6419	491.2500	246.1287	490.2660	245.6366	4
24	2503.1909	1252.0991	2486.1643	1243.5858	2485.1803	1243.0938	V	393.2496	197.1285	376.2231	188.6152	0	0	3
25	2650.2593	1325.6333	2633.2327	1317.1200	2632.2487	1316.6280	F	294.1812	147.5942	277.1547	139.0810	0	0	2
26							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 66016.

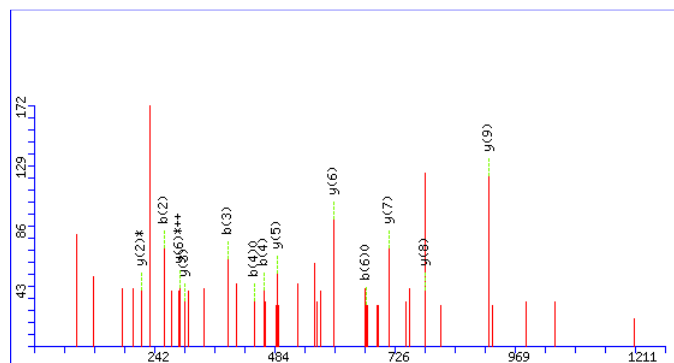
MS/MS Fragmentation of **DFEALLADASK**:

Found in **IP100297151;IP100794653**

Title: 3.1.1.2339.3

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_1_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							11
2	263.1026	132.0550	0	0	245.0921	123.0497	F	1064.5623	532.7848	1047.5357	524.2715	1046.5517	523.7795	10
3	392.1452	196.5763	0	0	374.1347	187.5710	E	917.4938	459.2506	900.4673	450.7373	899.4833	450.2453	9
4	463.1823	232.0948	0	0	445.1718	223.0895	A	788.4512	394.7293	771.4247	386.2160	770.4407	385.7240	8
5	576.2664	288.6368	0	0	558.2558	279.6316	L	717.4141	359.2107	700.3876	350.6974	699.4036	350.2054	7
6	689.3505	345.1789	0	0	671.3399	336.1736	L	604.3301	302.6687	587.3035	294.1554	586.3195	293.6634	6
7	760.3876	380.6974	0	0	742.3770	371.6921	A	491.2460	246.1266	474.2195	237.6134	473.2354	237.1214	5
8	875.4145	438.2109	0	0	857.4040	429.2056	D	420.2089	210.6081	403.1823	202.0948	402.1983	201.6028	4
9	946.4516	473.7295	0	0	928.4411	464.7242	A	305.1819	153.0946	288.1554	144.5813	287.1714	144.0893	3
10	1033.4837	517.2455	0	0	1015.4731	508.2402	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
11							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 66345.

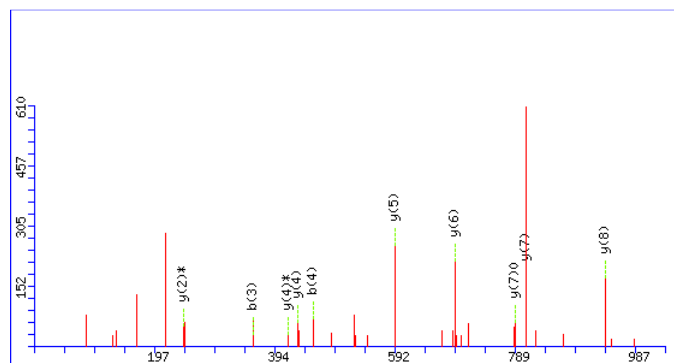
MS/MS Fragmentation of **LMDVCATSR: 57.021465@C:5**

Found in **IP100007811,IP100059926,IP101021327,IP101021794,IP101022249,IP101022897**

Title: 1.1.1.8452.10

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120201ry¥120201ry_aHDF1388-P9_1_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							9
2	245.1318	123.0696	0	0	0	0	M	939.4023	470.2048	922.3757	461.6915	921.3917	461.1995	8
3	360.1588	180.5830	0	0	342.1482	171.5777	D	808.3618	404.6845	791.3352	396.1713	790.3512	395.6792	7
4	459.2272	230.1172	0	0	441.2166	221.1119	V	693.3348	347.1711	676.3083	338.6578	675.3243	338.1658	6
5	619.2578	310.1326	0	0	601.2473	301.1273	C	594.2664	297.6368	577.2399	289.1236	576.2559	288.6316	5
6	690.2949	345.6511	0	0	672.2844	336.6458	A	434.2358	217.6215	417.2092	209.1082	416.2252	208.6162	4
7	791.3426	396.1750	0	0	773.3321	387.1697	T	363.1987	182.1030	346.1721	173.5897	345.1881	173.0977	3
8	878.3747	439.6910	0	0	860.3641	430.6857	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
9							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 66873.

MS/MS Fragmentation of **GPQELGAPGTVALVAAR**:

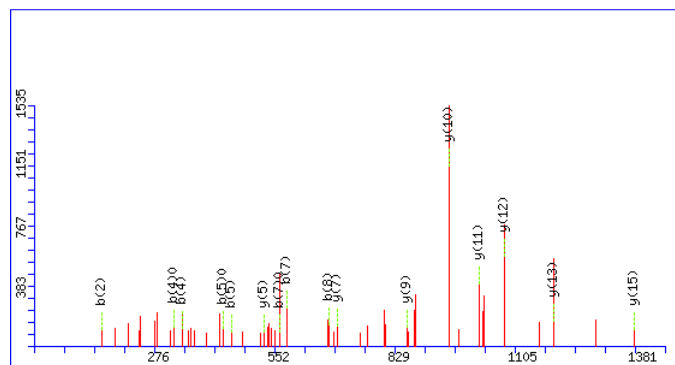
Found in

IP100093977;IP100299472;IP100375408;IP100375410;IP100375412;IP100375413;IP100375414;IP100375417;IP100377036;IP100383356;IP100844070;IP100872337;IP1009090

Title: 2.1.1.3727.10

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120208ry¥120208ry_Tig120slc-P8_2.2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							17
2	155.0815	78.0444	0	0	0	0	P	1478.8326	739.9199	1461.8060	731.4066	1460.8220	730.9146	16
3	212.1030	106.5551	0	0	0	0	G	1381.7798	691.3935	1364.7532	682.8803	1363.7692	682.3883	15
4	341.1456	171.0764	0	0	323.1350	162.0711	E	1324.7583	662.8828	1307.7318	654.3695	1306.7478	653.8775	14
5	454.2296	227.6185	0	0	436.2191	218.6132	L	1195.7157	598.3615	1178.6892	589.8482	1177.7052	589.3562	13
6	511.2511	256.1292	0	0	493.2405	247.1239	G	1082.6317	541.8195	1065.6051	533.3062	1064.6211	532.8142	12
7	582.2882	291.6477	0	0	564.2776	282.6425	A	1025.6102	513.3087	1008.5837	504.7955	1007.5996	504.3035	11
8	679.3410	340.1741	0	0	661.3304	331.1688	P	954.5731	477.7902	937.5465	469.2769	936.5625	468.7849	10
9	736.3624	368.6849	0	0	718.3519	359.6796	G	857.5203	429.2638	840.4938	420.7505	839.5098	420.2585	9
10	837.4101	419.2087	0	0	819.3995	410.2034	T	800.4989	400.7531	783.4723	392.2398	782.4883	391.7478	8
11	936.4785	468.7429	0	0	918.4680	459.7376	V	699.4512	350.2292	682.4246	341.7160	0	0	7
12	1007.5156	504.2615	0	0	989.5051	495.2562	A	600.3828	300.6950	583.3562	292.1817	0	0	6
13	1120.5997	560.8035	0	0	1102.5891	551.7982	L	529.3457	265.1765	512.3191	256.6632	0	0	5
14	1219.6681	610.3377	0	0	1201.6576	601.3324	V	416.2616	208.6344	399.2350	200.1212	0	0	4
15	1290.7052	645.8563	0	0	1272.6947	636.8510	A	317.1932	159.1002	300.1666	150.5870	0	0	3
16	1361.7423	681.3748	0	0	1343.7318	672.3695	A	246.1561	123.5817	229.1295	115.0684	0	0	2
17							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 66976.

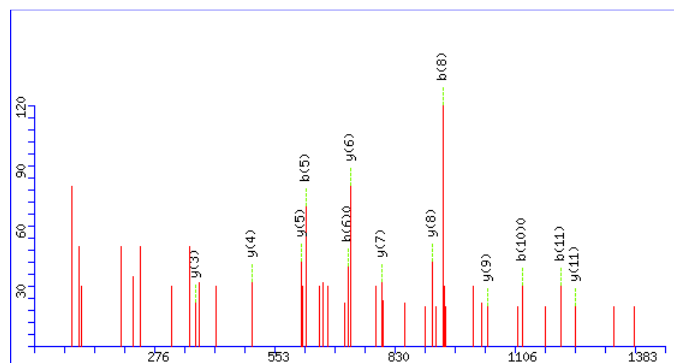
MS/MS Fragmentation of **KLQEELSDLSAMEDALDELIK**:

Found in **IP100289560;IP100414333;IP101011061**

Title: 4.1.1.3740.2

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120214ry¥120214ry_32R1-32_4.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	129.1022	65.0548	112.0757	56.5415	0	0	K							21
2	242.1863	121.5968	225.1598	113.0835	0	0	L	2262.1057	1131.5565	2245.0792	1123.0432	2244.0952	1122.5512	20
3	370.2449	185.6261	353.2183	177.1128	0	0	Q	2149.0217	1075.0145	2131.9951	1066.5012	2131.0111	1066.0092	19
4	499.2875	250.1474	482.2609	241.6341	481.2769	241.1421	E	2020.9631	1010.9852	2003.9365	1002.4719	2002.9525	1001.9799	18
5	628.3301	314.6687	611.3035	306.1554	610.3195	305.6634	E	1891.9205	946.4639	1874.8940	937.9506	1873.9099	937.4586	17
6	741.4141	371.2107	724.3876	362.6974	723.4036	362.2054	L	1762.8779	881.9426	1745.8514	873.4293	1744.8673	872.9373	16
7	828.4462	414.7267	811.4196	406.2134	810.4356	405.7214	S	1649.7938	825.4006	1632.7673	816.8873	1631.7833	816.3953	15
8	943.4731	472.2402	926.4466	463.7269	925.4625	463.2349	D	1562.7618	781.8845	1545.7353	773.3713	1544.7513	772.8793	14
9	1056.5572	528.7822	1039.5306	520.2689	1038.5466	519.7769	L	1447.7349	724.3711	1430.7083	715.8578	1429.7243	715.3658	13
10	1143.5892	572.2982	1126.5626	563.7850	1125.5786	563.2930	S	1334.6508	667.8290	1317.6243	659.3158	1316.6402	658.8238	12
11	1214.6263	607.8168	1197.5998	599.3035	1196.6157	598.8115	A	1247.6188	624.3130	1230.5922	615.7998	1229.6082	615.3077	11
12	1345.6668	673.3370	1328.6402	664.8238	1327.6562	664.3318	M	1176.5817	588.7945	1159.5551	580.2812	1158.5711	579.7892	10
13	1474.7094	737.8583	1457.6828	729.3451	1456.6988	728.8530	E	1045.5412	523.2742	1028.5146	514.7610	1027.5306	514.2689	9
14	1589.7363	795.3718	1572.7098	786.8585	1571.7258	786.3665	D	916.4986	458.7529	899.4720	450.2397	898.4880	449.7477	8
15	1660.7734	830.8904	1643.7469	822.3771	1642.7629	821.8851	A	801.4716	401.2395	784.4451	392.7262	783.4611	392.2342	7
16	1773.8575	887.4324	1756.8310	878.9191	1755.8469	878.4271	L	730.4345	365.7209	713.4080	357.2076	712.4240	356.7156	6
17	1888.8845	944.9459	1871.8579	936.4326	1870.8739	935.9406	D	617.3505	309.1789	600.3239	300.6656	599.3399	300.1736	5
18	2017.9270	1009.4672	2000.9005	1000.9539	1999.9165	1000.4619	E	502.3235	251.6654	485.2970	243.1521	484.3130	242.6601	4
19	2131.0111	1066.0092	2113.9846	1057.4959	2113.0005	1057.0039	L	373.2809	187.1441	356.2544	178.6308	0	0	3
20	2244.0952	1122.5512	2227.0686	1114.0379	2226.0846	1113.5459	I	260.1969	130.6021	243.1703	122.0888	0	0	2
21							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 67096.

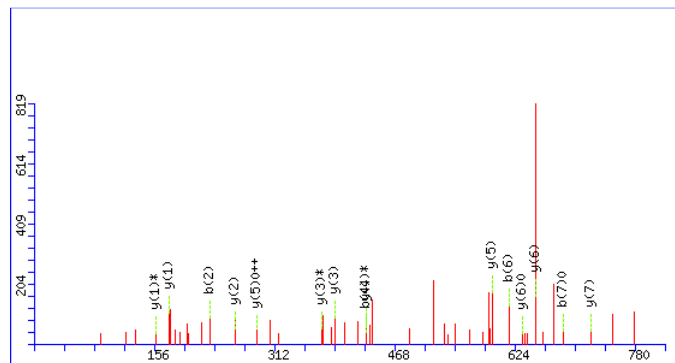
MS/MS Fragmentation of **RAGFGESR**:

Found in **IP100152637**

Title: 1.1.1.7393.3

Data file: Y:\TT5600(CiRA1)\2012-02\120201ry\120201ry_aHDF1388-P9_1_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	157.1084	79.0578	140.0818	70.5446	0	0	R							8
2	228.1455	114.5764	211.1190	106.0631	0	0	A	723.3420	362.1747	706.3155	353.6614	705.3315	353.1694	7
3	285.1670	143.0871	268.1404	134.5738	0	0	G	652.3049	326.6561	635.2784	318.1428	634.2944	317.6508	6
4	432.2354	216.6213	415.2088	208.1081	0	0	F	595.2835	298.1454	578.2569	289.6321	577.2729	289.1401	5
5	489.2568	245.1321	472.2303	236.6188	0	0	G	448.2150	224.6112	431.1885	216.0979	430.2045	215.6059	4
6	618.2994	309.6534	601.2729	301.1401	600.2889	300.6481	E	391.1936	196.1004	374.1670	187.5871	373.1830	187.0951	3
7	705.3315	353.1694	688.3049	344.6561	687.3209	344.1641	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
8							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 67265.

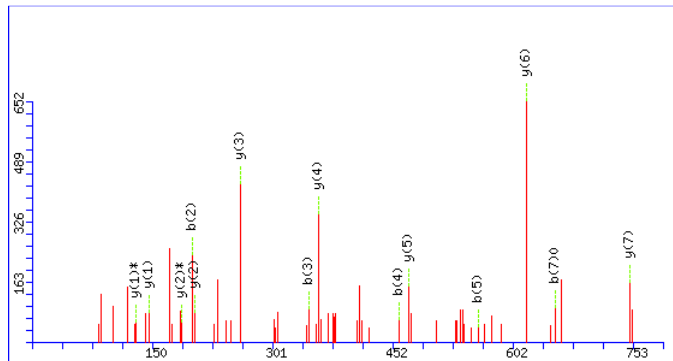
MS/MS Fragmentation of **AEFIVGGK**:

Found in **IP100183400;IP100448798;IP100965679;IP100966927;IP100976381**

Title: 2.1.1.366.5

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120208ry¥120208ry_Tig120slc-P8_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							8
2	201.0870	101.0471	0	0	183.0764	92.0418	E	749.4192	375.2132	732.3927	366.7000	731.4087	366.2080	7
3	348.1554	174.5813	0	0	330.1448	165.5761	F	620.3766	310.6919	603.3501	302.1787	0	0	6
4	461.2395	231.1234	0	0	443.2289	222.1181	I	473.3082	237.1577	456.2817	228.6445	0	0	5
5	560.3079	280.6576	0	0	542.2973	271.6523	V	360.2241	180.6157	343.1976	172.1024	0	0	4
6	617.3293	309.1683	0	0	599.3188	300.1630	G	261.1557	131.0815	244.1292	122.5682	0	0	3
7	674.3508	337.6790	0	0	656.3402	328.6738	G	204.1343	102.5708	187.1077	94.0575	0	0	2
8							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 67299.

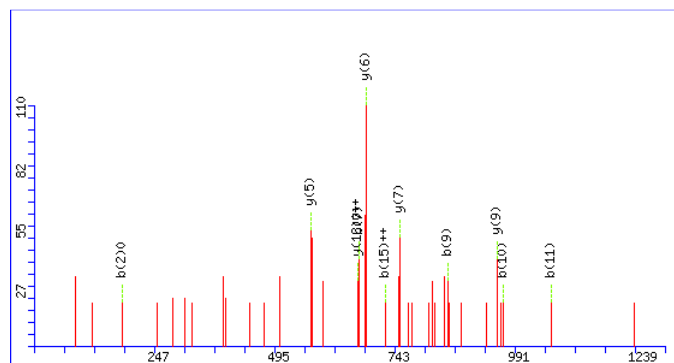
MS/MS Fragmentation of **ISLAGVEPSLVQAALGQLVR**:

Found in **IP100445654;IP100795260;IP100887374;IP100937971;IP100938081;IP101025703**

Title: 4.1.1.3277.5

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							20
2	201.1234	101.0653	0	0	183.1128	92.0600	S	1908.0913	954.5493	1891.0647	946.0360	1890.0807	945.5440	19
3	314.2074	157.6074	0	0	296.1969	148.6021	L	1821.0593	911.0333	1804.0327	902.5200	1803.0487	902.0280	18
4	385.2445	193.1259	0	0	367.2340	184.1206	A	1707.9752	854.4912	1690.9486	845.9780	1689.9646	845.4860	17
5	442.2660	221.6366	0	0	424.2554	212.6314	G	1636.9381	818.9727	1619.9115	810.4594	1618.9275	809.9674	16
6	541.3344	271.1709	0	0	523.3239	262.1656	V	1579.9166	790.4619	1562.8901	781.9487	1561.9061	781.4567	15
7	670.3770	335.6921	0	0	652.3665	326.6869	E	1480.8482	740.9277	1463.8217	732.4145	1462.8376	731.9225	14
8	767.4298	384.2185	0	0	749.4192	375.2132	P	1351.8056	676.4064	1334.7791	667.8932	1333.7950	667.4012	13
9	854.4618	427.7345	0	0	836.4512	418.7293	S	1254.7528	627.8801	1237.7263	619.3668	1236.7423	618.8748	12
10	967.5459	484.2766	0	0	949.5353	475.2713	L	1167.7208	584.3640	1150.6943	575.8508	0	0	11
11	1066.6143	533.8108	0	0	1048.6037	524.8055	V	1054.6368	527.8220	1037.6102	519.3087	0	0	10
12	1194.6729	597.8401	1177.6463	589.3268	1176.6623	588.8348	Q	955.5683	478.2878	938.5418	469.7745	0	0	9
13	1265.7100	633.3586	1248.6834	624.8454	1247.6994	624.3533	A	827.5098	414.2585	810.4832	405.7452	0	0	8
14	1336.7471	668.8772	1319.7205	660.3639	1318.7365	659.8719	A	756.4726	378.7400	739.4461	370.2267	0	0	7
15	1449.8312	725.4192	1432.8046	716.9059	1431.8206	716.4139	L	685.4355	343.2214	668.4090	334.7081	0	0	6
16	1506.8526	753.9299	1489.8261	745.4167	1488.8421	744.9247	G	572.3515	286.6794	555.3249	278.1661	0	0	5
17	1634.9112	817.9592	1617.8846	809.4460	1616.9006	808.9540	Q	515.3300	258.1686	498.3035	249.6554	0	0	4
18	1747.9953	874.5013	1730.9687	865.9880	1729.9847	865.4960	L	387.2714	194.1394	370.2449	185.6261	0	0	3
19	1847.0637	924.0355	1830.0371	915.5222	1829.0531	915.0302	V	274.1874	137.5973	257.1608	129.0840	0	0	2
20							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 67678.

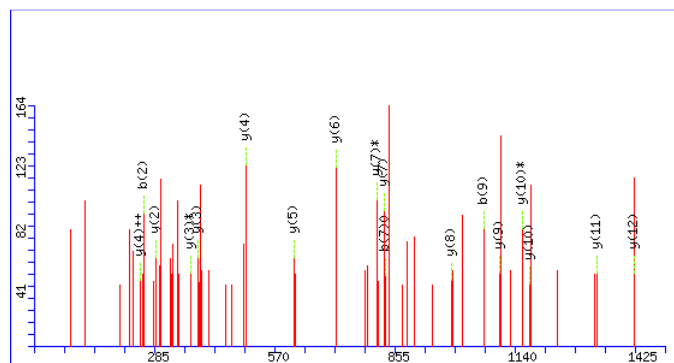
MS/MS Fragmentation of **LFSCANCDTILTNR: 57.021465@C:4,57.021465@C:7**

Found in **IP100429538**

Title: 2.1.1.3287.10

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							14
2	261.1598	131.0835	0	0	0	0	F	1571.6941	786.3507	1554.6675	777.8374	1553.6835	777.3454	13
3	348.1918	174.5995	0	0	330.1812	165.5942	S	1424.6257	712.8165	1407.5991	704.3032	1406.6151	703.8112	12
4	508.2224	254.6149	0	0	490.2119	245.6096	C	1337.5936	669.3005	1320.5671	660.7872	1319.5831	660.2952	11
5	579.2595	290.1334	0	0	561.2490	281.1281	A	1177.5630	589.2851	1160.5364	580.7719	1159.5524	580.2799	10
6	693.3025	347.1549	676.2759	338.6416	675.2919	338.1496	N	1106.5259	553.7666	1089.4993	545.2533	1088.5153	544.7613	9
7	853.3331	427.1702	836.3066	418.6569	835.3226	418.1649	C	992.4830	496.7451	975.4564	488.2318	974.4724	487.7398	8
8	968.3601	484.6837	951.3335	476.1704	950.3495	475.6784	D	832.4523	416.7298	815.4258	408.2165	814.4417	407.7245	7
9	1069.4077	535.2075	1052.3812	526.6942	1051.3972	526.2022	T	717.4254	359.2163	700.3988	350.7030	699.4148	350.2110	6
10	1182.4918	591.7495	1165.4653	583.2363	1164.4812	582.7443	I	616.3777	308.6925	599.3511	300.1792	598.3671	299.6872	5
11	1295.5759	648.2916	1278.5493	639.7783	1277.5653	639.2863	L	503.2936	252.1504	486.2671	243.6372	485.2831	243.1452	4
12	1396.6236	698.8154	1379.5970	690.3021	1378.6130	689.8101	T	390.2096	195.6084	373.1830	187.0951	372.1990	186.6031	3
13	1510.6665	755.8369	1493.6399	747.3236	1492.6559	746.8316	N	289.1619	145.0846	272.1353	136.5713	0	0	2
14							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 67867.

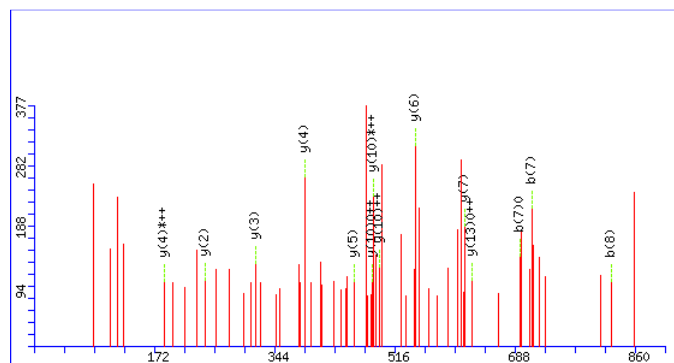
MS/MS Fragmentation of **ATLLGEELASAAAAR**:

Found in **IP100011232;IP100384901;IP100788619;IP100792755;IP100794512;IP100902761;IP101020723**

Title: 3.1.1.1544.2

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2.3.mgf

ProteinPilot Peptide Confidence > 99%



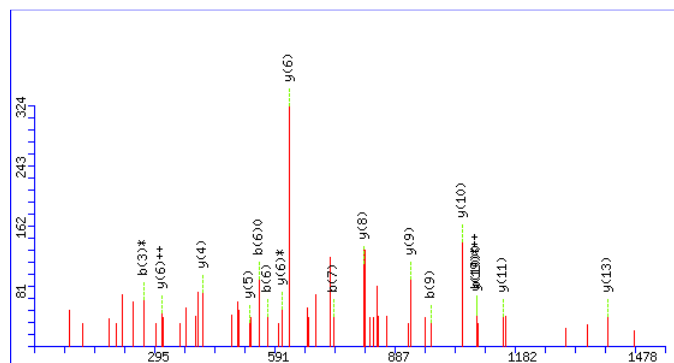
#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							15
2	173.0921	87.0497	0	0	155.0815	78.0444	T	1372.7431	686.8752	1355.7165	678.3619	1354.7325	677.8699	14
3	286.1761	143.5917	0	0	268.1656	134.5864	L	1271.6954	636.3513	1254.6688	627.8381	1253.6848	627.3461	13
4	399.2602	200.1337	0	0	381.2496	191.1285	L	1158.6113	579.8093	1141.5848	571.2960	1140.6008	570.8040	12
5	456.2817	228.6445	0	0	438.2711	219.6392	G	1045.5273	523.2673	1028.5007	514.7540	1027.5167	514.2620	11
6	585.3243	293.1658	0	0	567.3137	284.1605	E	988.5058	494.7565	971.4793	486.2433	970.4952	485.7513	10
7	714.3668	357.6871	0	0	696.3563	348.6818	E	859.4632	430.2352	842.4367	421.7220	841.4526	421.2300	9
8	827.4509	414.2291	0	0	809.4403	405.2238	L	730.4206	365.7139	713.3941	357.2007	712.4100	356.7087	8
9	898.4880	449.7477	0	0	880.4775	440.7424	A	617.3365	309.1719	600.3100	300.6586	599.3260	300.1666	7
10	985.5201	493.2637	0	0	967.5095	484.2584	S	546.2994	273.6534	529.2729	265.1401	528.2889	264.6481	6
11	1056.5572	528.7822	0	0	1038.5466	519.7769	A	459.2674	230.1373	442.2409	221.6241	0	0	5
12	1127.5943	564.3008	0	0	1109.5837	555.2955	A	388.2303	194.6188	371.2037	186.1055	0	0	4
13	1198.6314	599.8193	0	0	1180.6208	590.8141	A	317.1932	159.1002	300.1666	150.5870	0	0	3
14	1269.6685	635.3379	0	0	1251.6579	626.3326	A	246.1561	123.5817	229.1295	115.0684	0	0	2
15							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 67970.

MS/MS Fragmentation of **ASQTSVYLQEWDPFEQVELGEPIGQGR**:
Found in **IP100013384;IP100217124;IP101015914;IP101018676;IP101026015**
Title: 4.1.1.1578.6

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_3.4.mgf
ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							28
2	159.0764	80.0418	0	0	141.0659	71.0366	S	3105.5164	1553.2618	3088.4898	1544.7486	3087.5058	1544.2565	27
3	287.1350	144.0711	270.1084	135.5579	269.1244	135.0659	Q	3018.4843	1509.7458	3001.4578	1501.2325	3000.4738	1500.7405	26
4	388.1827	194.5950	371.1561	186.0817	370.1721	185.5897	T	2890.4258	1445.7165	2873.3992	1437.2032	2872.4152	1436.7112	25
5	475.2147	238.1110	458.1882	229.5977	457.2041	229.1057	S	2789.3781	1395.1927	2772.3515	1386.6794	2771.3675	1386.1874	24
6	574.2831	287.6452	557.2566	279.1319	556.2726	278.6399	V	2702.3461	1351.6767	2685.3195	1343.1634	2684.3355	1342.6714	23
7	737.3464	369.1769	720.3199	360.6636	719.3359	360.1716	Y	2603.2776	1302.1425	2586.2511	1293.6292	2585.2671	1293.1372	22
8	850.4305	425.7189	833.4040	417.2056	832.4199	416.7136	L	2440.2143	1220.6108	2423.1878	1212.0975	2422.2038	1211.6055	21
9	978.4891	489.7482	961.4625	481.2349	960.4785	480.7429	Q	2327.1303	1164.0688	2310.1037	1155.5555	2309.1197	1155.0635	20
10	1107.5317	554.2695	1090.5051	545.7562	1089.5211	545.2642	E	2199.0717	1100.0395	2182.0451	1091.5262	2181.0611	1091.0342	19
11	1293.6110	647.3091	1276.5844	638.7959	1275.6004	638.3039	W	2070.0291	1035.5182	2053.0025	1027.0049	2052.0185	1026.5129	18
12	1408.6379	704.8226	1391.6114	696.3093	1390.6274	695.8173	D	1883.9498	942.4785	1866.9232	933.9652	1865.9392	933.4732	17
13	1521.7220	761.3646	1504.6955	752.8514	1503.7114	752.3594	I	1768.9228	884.9651	1751.8963	876.4518	1750.9123	875.9598	16
14	1618.7748	809.8910	1601.7482	801.3777	1600.7642	800.8857	P	1655.8388	828.4230	1638.8122	819.9097	1637.8282	819.4177	15
15	1765.8432	883.4252	1748.8166	874.9120	1747.8326	874.4199	F	1558.7860	779.8966	1541.7594	771.3834	1540.7754	770.8914	14
16	1894.8858	947.9465	1877.8592	939.4332	1876.8752	938.9412	E	1411.7176	706.3624	1394.6910	697.8492	1393.7070	697.3571	13
17	2022.9444	1011.9758	2005.9178	1003.4625	2004.9338	1002.9705	Q	1282.6750	641.8411	1265.6484	633.3279	1264.6644	632.8359	12
18	2122.0128	1061.5100	2104.9862	1052.9967	2104.0022	1052.5047	V	1154.6164	577.8118	1137.5899	569.2986	1136.6058	568.8066	11
19	2251.0554	1126.0313	2234.0288	1117.5180	2233.0448	1117.0260	E	1055.5480	528.2776	1038.5215	519.7644	1037.5374	519.2724	10
20	2364.1394	1182.5733	2347.1129	1174.0601	2346.1289	1173.5681	L	928.5054	463.7563	909.4789	455.2431	908.4948	454.7511	9
21	2421.1609	1211.0841	2404.1343	1202.5708	2403.1503	1202.0788	G	813.4213	407.2143	796.3948	398.7010	795.4108	398.2090	8
22	2550.2035	1275.6054	2533.1769	1267.0921	2532.1929	1266.6001	E	756.3999	378.7036	739.3733	370.1903	738.3893	369.6983	7
23	2647.2562	1324.1318	2630.2297	1315.6185	2629.2457	1315.1265	P	627.3573	314.1823	610.3307	305.6690	0	0	6
24	2760.3403	1380.6738	2743.3138	1372.1605	2742.3297	1371.6685	I	530.3045	265.6559	513.2780	257.1426	0	0	5
25	2817.3618	1409.1845	2800.3352	1400.6712	2799.3512	1400.1792	G	417.2205	209.1139	400.1939	200.6006	0	0	4
26	2945.4203	1473.2138	2928.3938	1464.7005	2927.4098	1464.2085	Q	360.1990	180.6031	343.1724	172.0899	0	0	3
27	3002.4418	1501.7245	2985.4153	1493.2113	2984.4312	1492.7193	G	232.1404	116.5738	215.1139	108.0606	0	0	2
28							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 68209.

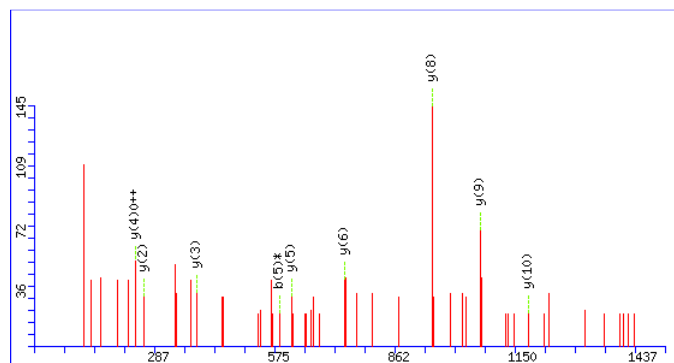
MS/MS Fragmentation of **QTFIDPLQLLQDK: -17.026549@N-term(Q)**

Found in **IP100019172;IP100216201;IP100216202;IP100216203;IP100924807**

Title: 4.1.1.2701.7

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233	0	0	Q							13
2	230.1135	115.5604	213.0870	107.0471	212.1030	106.5551	T	1430.7890	715.8981	1413.7624	707.3848	1412.7784	706.8928	12
3	377.1819	189.0946	360.1554	180.5813	359.1714	180.0893	F	1329.7413	665.3743	1312.7147	656.8610	1311.7307	656.3690	11
4	490.2660	245.6366	473.2395	237.1234	472.2554	236.6314	I	1182.6729	591.8401	1165.6463	583.3268	1164.6623	582.8348	10
5	605.2930	303.1501	588.2664	294.6368	587.2824	294.1448	D	1069.5888	535.2980	1052.5623	526.7848	1051.5782	526.2928	9
6	702.3457	351.6765	685.3192	343.1632	684.3352	342.6712	P	954.5619	477.7846	937.5353	469.2713	936.5513	468.7793	8
7	815.4298	408.2185	798.4032	399.7053	797.4192	399.2132	L	857.5091	429.2582	840.4825	420.7449	839.4985	420.2529	7
8	943.4884	472.2478	926.4618	463.7345	925.4778	463.2425	Q	744.4250	372.7162	727.3985	364.2029	726.4145	363.7109	6
9	1056.5724	528.7899	1039.5459	520.2766	1038.5619	519.7846	L	616.3665	308.6869	599.3399	300.1736	598.3559	299.6816	5
10	1169.6565	585.3319	1152.6299	576.8186	1151.6459	576.3266	L	503.2824	252.1448	486.2558	243.6316	485.2718	243.1396	4
11	1297.7151	649.3612	1280.6885	640.8479	1279.7045	640.3559	Q	390.1983	195.6028	373.1718	187.0895	372.1878	186.5975	3
12	1412.7420	706.8746	1395.7155	698.3614	1394.7314	697.8694	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: **68263**.

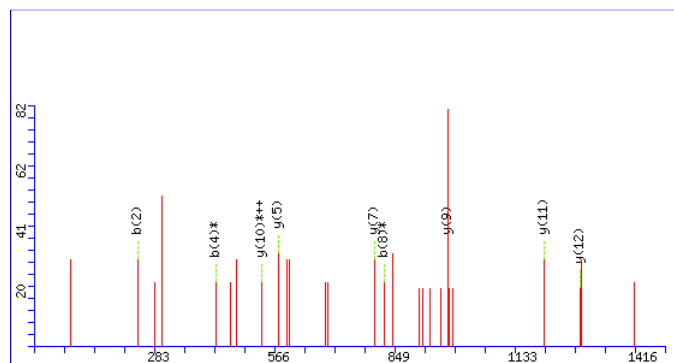
MS/MS Fragmentation of **NESNLGDLLLGFLK**:

Found in **IP100167560;IP100895778;IP100965928**

Title: 4.1.1.3562.5

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							14
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	E	1418.7890	709.8981	1401.7624	701.3848	1400.7784	700.8928	13
3	331.1248	166.0661	314.0983	157.5528	313.1143	157.0608	S	1289.7464	645.3768	1272.7198	636.8635	1271.7358	636.3715	12
4	445.1678	223.0875	428.1412	214.5742	427.1572	214.0822	N	1202.7143	601.8608	1185.6878	593.3475	1184.7038	592.8555	11
5	558.2518	279.6295	541.2253	271.1163	540.2413	270.6243	L	1088.6714	544.8393	1071.6449	536.3261	1070.6608	535.8341	10
6	615.2733	308.1403	598.2467	299.6270	597.2627	299.1350	G	975.5873	488.2973	958.5608	479.7840	957.5768	479.2920	9
7	730.3002	365.6537	713.2737	357.1405	712.2897	356.6485	D	918.5659	459.7866	901.5393	451.2733	900.5553	450.7813	8
8	843.3843	422.1958	826.3577	413.6825	825.3737	413.1905	L	803.5389	402.2731	786.5124	393.7598	0	0	7
9	956.4684	478.7378	939.4418	470.2245	938.4578	469.7325	L	690.4549	345.7311	673.4283	337.2178	0	0	6
10	1069.5524	535.2798	1052.5259	526.7666	1051.5418	526.2746	L	577.3708	289.1890	560.3443	280.6758	0	0	5
11	1126.5739	563.7906	1109.5473	555.2773	1108.5633	554.7853	G	464.2867	232.6470	447.2602	224.1337	0	0	4
12	1273.6423	637.3248	1256.6157	628.8115	1255.6317	628.3195	F	407.2653	204.1363	390.2387	195.6230	0	0	3
13	1386.7264	693.8668	1369.6998	685.3535	1368.7158	684.8615	L	260.1969	130.6021	243.1703	122.0888	0	0	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: **68282**.

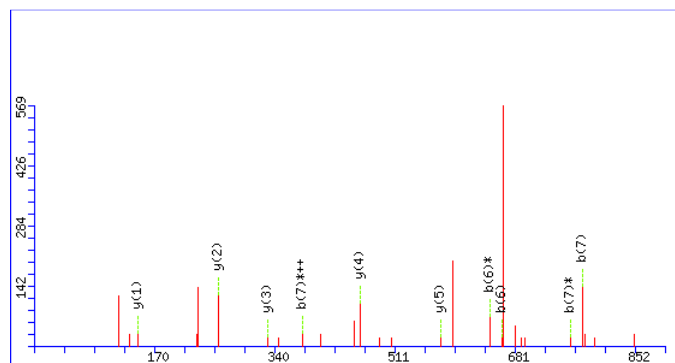
MS/MS Fragmentation of **SIFNMANK**:

Found in **IP100187159;IP100873629;IP100952618**

Title: 1.1.1.6501.11

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120212ry¥120212ry_aHDF1388-P9_3_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							8
2	201.1234	101.0653	0	0	183.1128	92.0600	I	837.4287	419.2180	820.4022	410.7047	0	0	7
3	348.1918	174.5995	0	0	330.1812	165.5942	F	724.3447	362.6760	707.3181	354.1627	0	0	6
4	462.2347	231.6210	445.2082	223.1077	444.2241	222.6157	N	577.2763	289.1418	560.2497	280.6285	0	0	5
5	593.2752	297.1412	576.2486	288.6280	575.2646	288.1360	M	463.2333	232.1203	446.2068	223.6070	0	0	4
6	664.3123	332.6598	647.2858	324.1465	646.3017	323.6545	A	332.1928	166.6001	315.1663	158.0868	0	0	3
7	778.3552	389.6813	761.3287	381.1680	760.3447	380.6760	N	261.1557	131.0815	244.1292	122.5682	0	0	2
8							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 68317.

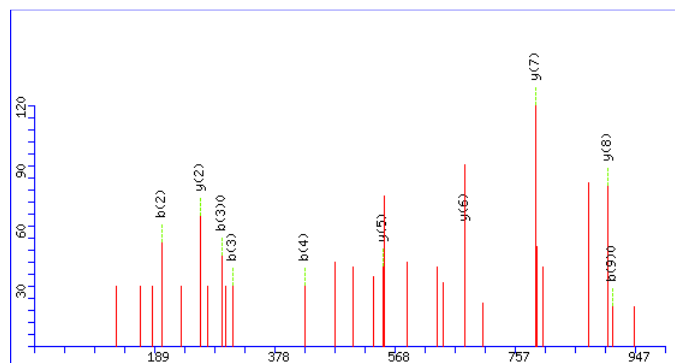
MS/MS Fragmentation of **VTLQSSDSR**:

Found in **IP100183425;IP100220051;IP100329602;IP100386740;IP100551026;IP100647476;IP100921819;IP101013233;IP101014151**

Title: 1.1.1.7954.10

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120126ry¥120126ry_585A1-55_1_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							10
2	201.1234	101.0653	0	0	183.1128	92.0600	T	1006.5164	503.7618	989.4898	495.2485	988.5058	494.7565	9
3	314.2074	157.6074	0	0	296.1969	148.6021	I	905.4687	453.2380	888.4421	444.7247	887.4581	444.2327	8
4	427.2915	214.1494	0	0	409.2809	205.1441	L	792.3846	396.6959	775.3581	388.1827	774.3741	387.6907	7
5	555.3501	278.1787	538.3235	269.6654	537.3395	269.1734	Q	679.3006	340.1539	662.2740	331.6406	661.2900	331.1486	6
6	642.3821	321.6947	625.3556	313.1814	624.3715	312.6894	S	551.2420	276.1246	534.2154	267.6114	533.2314	267.1193	5
7	729.4141	365.2107	712.3876	356.6974	711.4036	356.2054	S	464.2100	232.6086	447.1834	224.0953	446.1994	223.6033	4
8	844.4411	422.7242	827.4145	414.2109	826.4305	413.7189	D	377.1779	189.0926	360.1514	180.5793	359.1674	180.0873	3
9	931.4731	466.2402	914.4466	457.7269	913.4625	457.2349	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 68530.

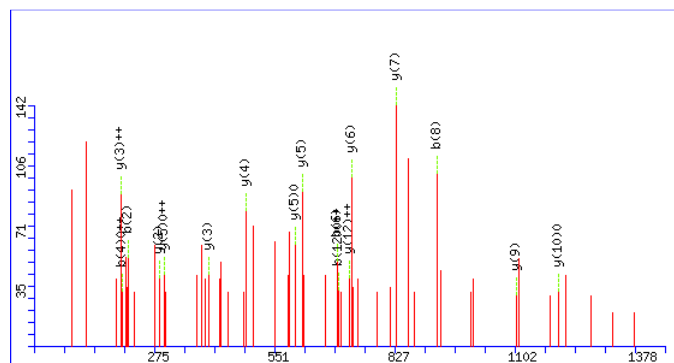
MS/MS Fragmentation of **SEGFCDDIDFQTLESILR: 57.021465@C:5**

Found in **IP100007300:IP100375386**

Title: 4.1.1.2624.4

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120212ry¥120212ry_414C2-43_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							17
2	217.0819	109.0446	0	0	199.0713	100.0393	E	1942.9215	971.9644	1925.8950	963.4511	1924.9109	962.9591	16
3	274.1034	137.5553	0	0	256.0928	128.5500	G	1813.8789	907.4431	1796.8524	898.9298	1795.8683	898.4378	15
4	421.1718	211.0895	0	0	403.1612	202.0842	F	1756.8574	878.9324	1739.8309	870.4191	1738.8469	869.9271	14
5	581.2024	291.1049	0	0	563.1919	282.0996	C	1609.7890	805.3982	1592.7625	796.8849	1591.7785	796.3929	13
6	696.2294	348.6183	0	0	678.2188	339.6130	D	1449.7584	725.3828	1432.7318	716.8696	1431.7478	716.3775	12
7	809.3134	405.1604	0	0	791.3029	396.1551	I	1334.7314	667.8694	1317.7049	659.3561	1316.7209	658.8641	11
8	924.3404	462.6738	0	0	906.3298	453.6685	D	1221.6474	611.3273	1204.6208	602.8141	1203.6368	602.3220	10
9	1071.4088	536.2080	0	0	1053.3982	527.2028	F	1106.6204	553.8139	1089.5939	545.3006	1088.6099	544.8086	9
10	1199.4674	600.2373	1182.4408	591.7240	1181.4568	591.2320	Q	959.5520	480.2796	942.5255	471.7664	941.5415	471.2744	8
11	1300.5150	650.7612	1283.4885	642.2479	1282.5045	641.7559	T	831.4934	416.2504	814.4669	407.7371	813.4829	407.2451	7
12	1413.5991	707.3032	1396.5726	698.7899	1395.5885	698.2979	L	730.4458	365.7265	713.4192	357.2132	712.4352	356.7212	6
13	1542.6417	771.8245	1525.6152	763.3112	1524.6311	762.8192	E	617.3617	309.1845	600.3352	300.6712	599.3511	300.1792	5
14	1629.6737	815.3405	1612.6472	806.8272	1611.6632	806.3352	S	488.3191	244.6632	471.2926	236.1499	470.3085	235.6579	4
15	1742.7578	871.8825	1725.7312	863.3693	1724.7472	862.8773	I	401.2871	201.1472	384.2605	192.6339	0	0	3
16	1855.8419	928.4246	1838.8153	919.9113	1837.8313	919.4193	L	288.2030	144.6051	271.1765	136.0919	0	0	2
17							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: **68746**.

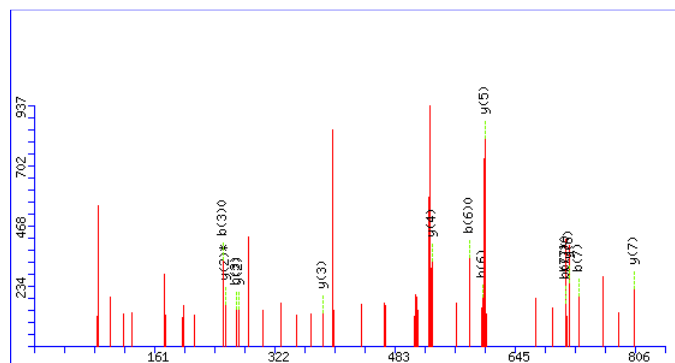
MS/MS Fragmentation of **ASLAFLQK**:

Found in **IP100011588**

Title: 2.1.1.2468.4

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2.2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							8
2	159.0764	80.0418	0	0	141.0659	71.0366	S	806.4771	403.7422	789.4505	395.2289	788.4665	394.7369	7
3	272.1605	136.5839	0	0	254.1499	127.5786	L	719.4450	360.2262	702.4185	351.7129	0	0	6
4	343.1976	172.1024	0	0	325.1870	163.0972	A	606.3610	303.6841	589.3344	295.1709	0	0	5
5	490.2660	245.6366	0	0	472.2554	236.6314	F	535.3239	268.1656	518.2973	259.6523	0	0	4
6	603.3501	302.1787	0	0	585.3395	293.1734	L	388.2554	194.6314	371.2289	186.1181	0	0	3
7	731.4087	366.2080	714.3821	357.6947	713.3981	357.2027	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
8							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 68886.

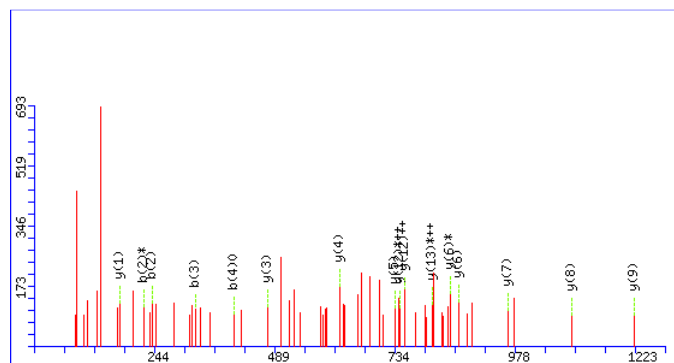
MS/MS Fragmentation of **IQSPTEETEIFYHR**:

Found in **IP100412741;IP100607781;IP100743741**

Title: 2.1.1.3176.7

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							14
2	242.1499	121.5786	225.1234	113.0653	0	0	Q	1636.7602	818.8837	1619.7336	810.3705	1618.7496	809.8784	13
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	S	1508.7016	754.8544	1491.6751	746.3412	1490.6910	745.8492	12
4	426.2347	213.6210	409.2082	205.1077	408.2241	204.6157	P	1421.6696	711.3384	1404.6430	702.8251	1403.6590	702.3331	11
5	527.2824	264.1448	510.2558	255.6316	509.2718	255.1396	T	1324.6168	662.8120	1307.5903	654.2988	1306.6062	653.8068	10
6	656.3250	328.6661	639.2984	320.1529	638.3144	319.6608	E	1223.5691	612.2882	1206.5426	603.7749	1205.5586	603.2829	9
7	785.3676	393.1874	768.3410	384.6742	767.3570	384.1821	E	1094.5265	547.7669	1077.5000	539.2536	1076.5160	538.7616	8
8	886.4153	443.7113	869.3887	435.1980	868.4047	434.7060	T	965.4839	483.2456	948.4574	474.7323	947.4734	474.2403	7
9	1015.4578	508.2326	998.4313	499.7193	997.4473	499.2273	E	864.4363	432.7218	847.4097	424.2085	846.4257	423.7165	6
10	1128.5419	564.7746	1111.5154	556.2613	1110.5313	555.7693	I	735.3937	368.2005	718.3671	359.6872	0	0	5
11	1275.6103	638.3088	1258.5838	629.7955	1257.5998	629.3035	F	622.3096	311.6584	605.2831	303.1452	0	0	4
12	1438.6737	719.8405	1421.6471	711.3272	1420.6631	710.8352	Y	475.2412	238.1242	458.2146	229.6110	0	0	3
13	1575.7326	788.3699	1558.7060	779.8566	1557.7220	779.3646	H	312.1779	156.5926	295.1513	148.0793	0	0	2
14							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 69067.

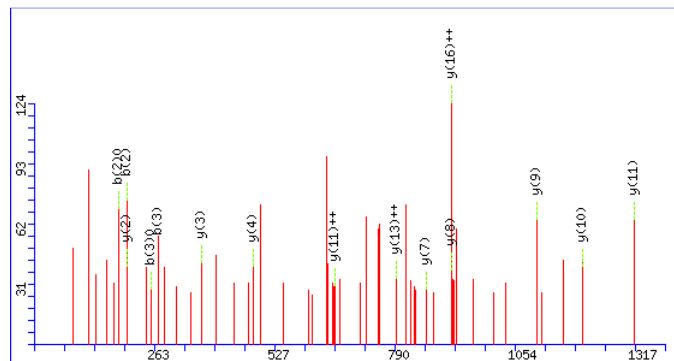
MS/MS Fragmentation of **TTAGLCLLTWGGHWLYGK: 57.021465@C:6**

Found in **IP100019353;IP100553233;IP100945593;IP100945912**

Title: 4.1.1.1238.3

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							18
2	203.1028	102.0550	0	0	185.0921	93.0497	T	1932.9789	966.9931	1915.9524	958.4798	1914.9683	957.9878	17
3	274.1397	137.5735	0	0	256.1292	128.5682	A	1831.9312	916.4693	1814.9047	907.9560	1813.9207	907.4640	16
4	331.1612	166.0842	0	0	313.1506	157.0790	G	1760.8941	880.9507	1743.8676	872.4374	1742.8835	871.9454	15
5	444.2453	222.6263	0	0	426.2347	213.6210	L	1703.8726	852.4400	1686.8461	843.9267	1685.8621	843.4347	14
6	604.2759	302.6416	0	0	586.2654	293.6363	C	1590.7886	795.8979	1573.7620	787.3847	1572.7780	786.8926	13
7	717.3600	359.1836	0	0	699.3494	350.1784	L	1430.7579	715.8826	1413.7314	707.3693	1412.7474	706.8773	12
8	830.4441	415.7257	0	0	812.4335	406.7204	L	1317.6739	659.3406	1300.6473	650.8273	1299.6633	650.3353	11
9	931.4917	466.2495	0	0	913.4812	457.2442	T	1204.5898	602.7985	1187.5633	594.2853	1186.5792	593.7933	10
10	1117.5710	559.2892	0	0	1099.5605	550.2839	W	1103.5421	552.2747	1086.5156	543.7614	0	0	9
11	1174.5925	587.7999	0	0	1156.5819	578.7946	G	917.4628	459.2350	900.4363	450.7218	0	0	8
12	1231.6140	616.3106	0	0	1213.6034	607.3053	G	860.4413	430.7243	843.4148	422.2110	0	0	7
13	1368.6729	684.8401	0	0	1350.6623	675.8348	H	803.4199	402.2136	786.3933	393.7003	0	0	6
14	1554.7522	777.8797	0	0	1536.7416	768.8745	W	666.3610	333.6841	649.3344	325.1709	0	0	5
15	1667.8363	834.4218	0	0	1649.8257	825.4165	L	480.2817	240.6445	463.2551	232.1312	0	0	4
16	1830.8996	915.9534	0	0	1812.8890	906.9482	Y	367.1976	184.1024	350.1710	175.5892	0	0	3
17	1887.9211	944.4642	0	0	1869.9105	935.4589	G	204.1343	102.5708	187.1077	94.0575	0	0	2
18							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 69158.

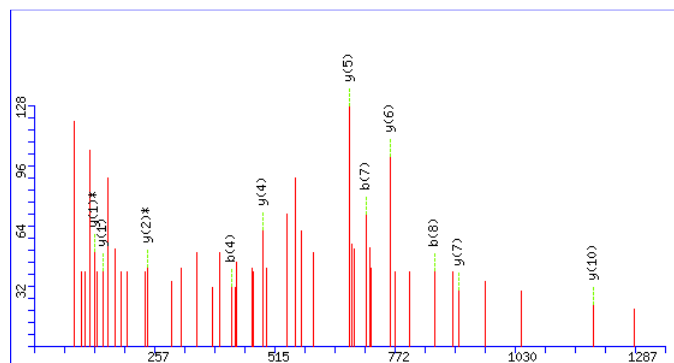
MS/MS Fragmentation of **ITAHSSDFSWTELK**:

Found in **IP100102275;IP100902522;IP100911110;IP100954842**

Title: 2.1.1.4246.6

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120126ry¥120126ry_585A1-55_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							14
2	215.1390	108.0731	0	0	197.1285	99.0679	T	1508.7016	754.8544	1491.6750	746.3412	1490.6910	745.8492	13
3	286.1761	143.5917	0	0	268.1656	134.5864	A	1407.6539	704.3306	1390.6274	695.8173	1389.6434	695.3253	12
4	423.2350	212.1212	0	0	405.2245	203.1159	H	1336.6168	668.8120	1319.5903	660.2988	1318.6062	659.8068	11
5	510.2671	255.6372	0	0	492.2565	246.6319	S	1199.5579	600.2826	1182.5313	591.7693	1181.5473	591.2773	10
6	597.2991	299.1532	0	0	579.2885	290.1479	S	1112.5259	556.7666	1095.4993	548.2533	1094.5153	547.7613	9
7	712.3260	356.6667	0	0	694.3155	347.6614	D	1025.4938	513.2506	1008.4673	504.7373	1007.4833	504.2453	8
8	859.3945	430.2009	0	0	841.3839	421.1956	F	910.4669	455.7371	893.4403	447.2238	892.4563	446.7318	7
9	946.4265	473.7169	0	0	928.4159	464.7116	S	763.3965	382.2029	746.3719	373.6896	745.3879	373.1976	6
10	1132.5058	566.7565	0	0	1114.4952	557.7513	W	676.3665	338.6869	659.3399	330.1736	658.3559	329.6816	5
11	1233.5535	617.2804	0	0	1215.5429	608.2751	T	490.2871	245.6472	473.2606	237.1339	472.2766	236.6419	4
12	1362.5961	681.8017	0	0	1344.5855	672.7964	E	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
13	1475.6801	738.3437	0	0	1457.6696	729.3384	L	260.1969	130.6021	243.1703	122.0888	0	0	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 69259.

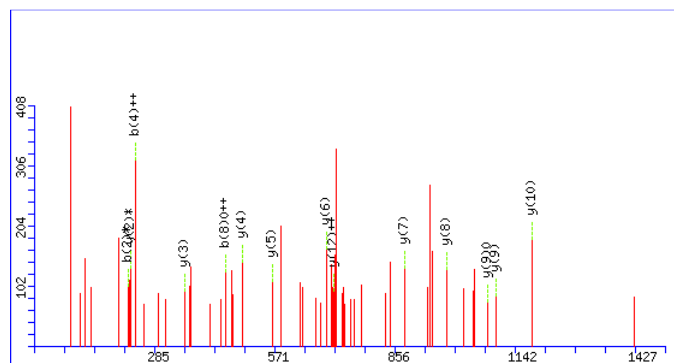
MS/MS Fragmentation of **LQLQELSDTWQAHLAR**:

Found in **IP100060473;IP100930364**

Title: 3.1.1.2058.6

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120212ry¥120212ry_aHDF1388-P9_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							16
2	242.1499	121.5786	225.1234	113.0653	0	0	Q	1795.9086	898.4579	1778.8820	889.9447	1777.8980	889.4526	15
3	355.2340	178.1206	338.2074	169.6074	0	0	L	1667.8500	834.4286	1650.8234	825.9154	1649.8394	825.4234	14
4	483.2926	242.1499	466.2660	233.6366	0	0	Q	1554.7659	777.8866	1537.7394	769.3733	1536.7554	768.8813	13
5	612.3352	306.6712	595.3086	298.1579	594.3246	297.6659	E	1426.7074	713.8573	1409.6808	705.3440	1408.6968	704.8520	12
6	725.4192	363.2132	708.3927	354.7000	707.4087	354.2080	L	1297.6648	649.3360	1280.6382	640.8227	1279.6542	640.3307	11
7	812.4512	406.7293	795.4247	398.2160	794.4407	397.7240	S	1184.5807	592.7940	1167.5541	584.2807	1166.5701	583.7887	10
8	927.4782	464.2427	910.4516	455.7295	909.4676	455.2374	D	1097.5487	549.2780	1080.5221	540.7647	1079.5381	540.2727	9
9	1028.5259	514.7666	1011.4993	506.2533	1010.5153	505.7613	T	982.5217	491.7645	965.4952	483.2512	964.5112	482.7592	8
10	1214.6052	607.8062	1197.5786	599.2930	1196.5946	598.8009	W	881.4740	441.2407	864.4475	432.7274	0	0	7
11	1342.6638	671.8355	1325.6372	663.3222	1324.6532	662.8302	Q	695.3947	348.2010	678.3682	339.6877	0	0	6
12	1413.7009	707.3541	1396.6743	698.8408	1395.6903	698.3488	A	567.3362	284.1717	550.3096	275.6584	0	0	5
13	1550.7598	775.8835	1533.7332	767.3703	1532.7492	766.8782	H	496.2990	248.6532	479.2725	240.1399	0	0	4
14	1663.8438	832.4256	1646.8173	823.9123	1645.8333	823.4203	L	359.2401	180.1237	342.2136	171.6104	0	0	3
15	1734.8810	867.9441	1717.8544	859.4308	1716.8704	858.9388	A	246.1561	123.5817	229.1295	115.0684	0	0	2
16							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 69348.

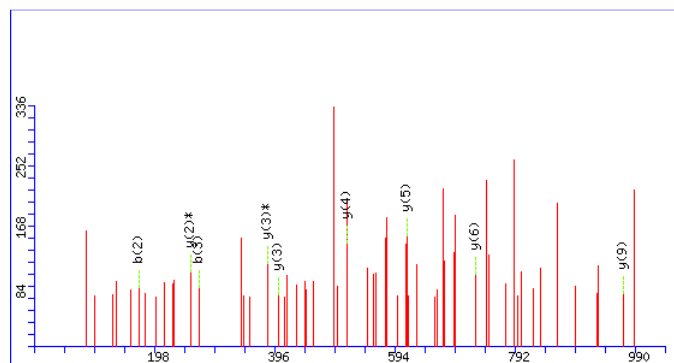
MS/MS Fragmentation of **TAVWEEGPGGELVIQK**:

Found in **IP100026512**

Title: 3.1.1.463.7

Data file: Y:\TT5600(CiRA1)\2012-01\120124ry\120124ry_414C2-43_1_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							17
2	173.0921	87.0497	0	0	155.0815	78.0444	A	1739.8963	870.4518	1722.8697	861.9385	1721.8857	861.4465	16
3	272.1605	136.5839	0	0	254.1499	127.5786	V	1668.8592	834.9332	1651.8326	826.4199	1650.8486	825.9279	15
4	458.2398	229.6235	0	0	440.2292	220.6183	W	1569.7907	785.3990	1552.7642	776.8857	1551.7802	776.3937	14
5	587.2824	294.1448	0	0	569.2718	285.1396	E	1383.7114	692.3594	1366.6849	683.8461	1365.7009	683.3541	13
6	716.3250	358.6661	0	0	698.3144	349.6608	E	1254.6688	627.8381	1237.6423	619.3248	1236.6583	618.8328	12
7	773.3464	387.1769	0	0	755.3359	378.1716	G	1125.6263	563.3168	1108.5997	554.8035	1107.6157	554.3115	11
8	870.3992	435.7032	0	0	852.3886	426.6980	P	1068.6048	534.8060	1051.5782	526.2928	1050.5942	525.8007	10
9	927.4207	464.2140	0	0	909.4101	455.2087	G	971.5520	486.2796	954.5255	477.7664	953.5415	477.2744	9
10	984.4421	492.7247	0	0	966.4316	483.7194	G	914.5306	457.7689	897.5040	449.2556	896.5200	448.7636	8
11	1113.4847	557.2460	0	0	1095.4742	548.2407	E	857.5091	429.2582	840.4825	420.7449	839.4985	420.2529	7
12	1226.5688	613.7880	0	0	1208.5582	604.7828	L	728.4665	364.7369	711.4400	356.2236	0	0	6
13	1325.6372	663.3222	0	0	1307.6266	654.3170	V	615.3824	308.1949	598.3559	299.6816	0	0	5
14	1438.7213	719.8643	0	0	1420.7107	710.8590	I	516.3140	258.6606	499.2875	250.1474	0	0	4
15	1566.7799	783.8936	1549.7533	775.3803	1548.7693	774.8883	Q	403.2300	202.1186	386.2034	193.6053	0	0	3
16	1694.8384	847.9229	1677.8119	839.4096	1676.8279	838.9176	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
17							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 69419.

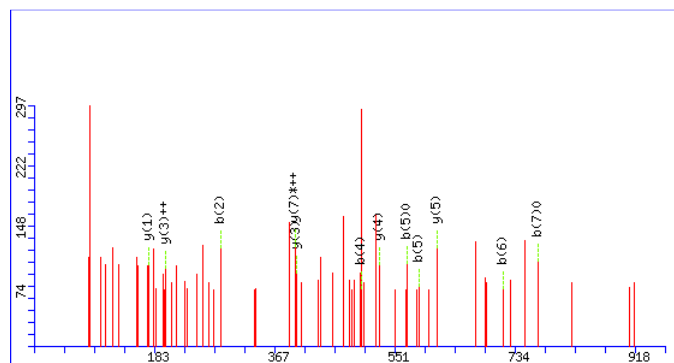
MS/MS Fragmentation of **HFSESEASQILR**:

Found in **IP100022536;IP100479926;IP100982822**

Title: 2.1.1.1483.2

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120206ry¥120206ry_aHDF1419-P10_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	138.0662	69.5367	0	0	0	0	H							12
2	285.1346	143.0709	0	0	0	0	F	1266.6325	633.8199	1249.6059	625.3066	1248.6219	624.8146	11
3	372.1666	186.5870	0	0	354.1561	177.5817	S	1119.5640	560.2857	1102.5375	551.7724	1101.5535	551.2804	10
4	501.2092	251.1082	0	0	483.1987	242.1030	E	1032.5320	516.7696	1015.5055	508.2564	1014.5214	507.7644	9
5	588.2413	294.6243	0	0	570.2307	285.6190	S	903.4894	452.2483	886.4629	443.7351	885.4789	443.2431	8
6	717.2838	359.1456	0	0	699.2733	350.1403	E	816.4574	408.7323	799.4308	400.2191	798.4468	399.7271	7
7	788.3210	394.6641	0	0	770.3104	385.6588	A	687.4148	344.2110	670.3883	335.6978	669.4042	335.2058	6
8	875.3530	438.1801	0	0	857.3424	429.1748	S	616.3777	308.6925	599.3511	300.1792	598.3671	299.6872	5
9	1003.4116	502.2094	986.3850	493.6961	985.4010	493.2041	Q	529.3457	265.1765	512.3191	256.6632	0	0	4
10	1116.4956	558.7515	1099.4691	550.2382	1098.4851	549.7462	I	401.2871	201.1472	384.2605	192.6339	0	0	3
11	1229.5797	615.2935	1212.5531	606.7802	1211.5691	606.2882	L	288.2030	144.6051	271.1765	136.0919	0	0	2
12							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 69447.

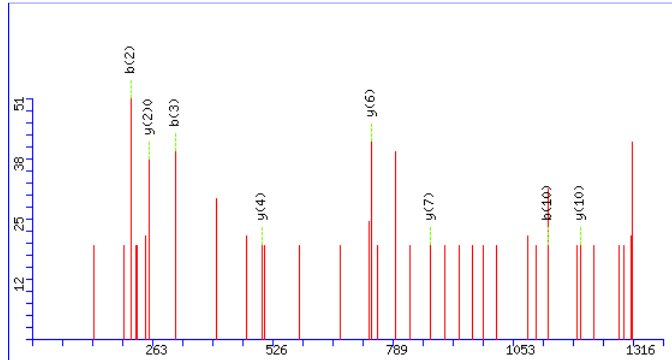
MS/MS Fragmentation of **TNVLADFEQLRDILDWEESNELQNLEK**:

Found in **IP100394971;IP100394972;IP100394973;IP100394974;IP100394975;IP100658075;IP100873422;IP100879744;IP101012489**

Title: 5.1.1.238.3

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_3_5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							27
2	216.0979	108.5526	199.0713	100.0393	198.0873	99.5473	N	3160.5433	1580.7753	3143.5168	1572.2620	3142.5327	1571.7700	26
3	315.1663	158.0868	298.1397	149.5735	297.1557	149.0815	V	3046.5004	1523.7538	3029.4738	1515.2406	3028.4898	1514.7485	25
4	428.2504	214.6288	411.2238	206.1155	410.2398	205.6235	L	2947.4320	1474.2196	2930.4054	1465.7063	2929.4214	1465.2143	24
5	499.2875	250.1474	482.2609	241.6341	481.2769	241.1421	A	2834.3479	1417.6776	2817.3214	1409.1643	2816.3373	1408.6723	23
6	614.3144	307.6608	597.2879	299.1476	596.3039	298.6556	D	2763.3108	1382.1590	2746.2842	1373.6458	2745.3002	1373.1538	22
7	761.3828	381.1951	744.3563	372.6818	743.3723	372.1898	F	2648.2839	1324.6456	2631.2573	1316.1323	2630.2733	1315.6403	21
8	890.4254	445.7164	873.3989	437.2031	872.4149	436.7111	E	2501.2154	1251.1114	2484.1889	1242.5981	2483.2049	1242.1061	20
9	1018.4840	509.7456	1001.4575	501.2324	1000.4734	500.7404	Q	2372.1728	1186.5901	2355.1463	1178.0768	2354.1623	1177.5848	19
10	1131.5681	566.2877	1114.5415	557.7744	1113.5575	557.2824	L	2244.1143	1122.5608	2227.0877	1114.0475	2226.1037	1113.5555	18
11	1287.6692	644.3382	1270.6426	635.8250	1269.6586	635.3329	R	2131.0302	1066.0187	2114.0037	1057.5055	2113.0196	1057.0135	17
12	1402.6961	701.8517	1385.6696	693.3384	1384.6856	692.8464	D	1974.9291	987.9682	1957.9025	979.4549	1956.9185	978.9629	16
13	1515.7802	758.3937	1498.7536	749.8805	1497.7696	749.3884	I	1859.9021	930.4547	1842.8756	921.9414	1841.8916	921.4494	15
14	1628.8642	814.9358	1611.8377	806.4225	1610.8537	805.9305	L	1746.8181	873.9127	1729.7915	865.3994	1728.8075	864.9074	14
15	1743.8912	872.4492	1726.8646	863.9360	1725.8806	863.4440	D	1633.7340	817.3706	1616.7075	808.8574	1615.7235	808.3654	13
16	1929.9705	965.4889	1912.9440	956.9756	1911.9599	956.4836	W	1518.7071	759.8572	1501.6805	751.3439	1500.6965	750.8519	12
17	2059.0131	1030.0102	2041.9865	1021.4969	2041.0025	1021.0049	E	1332.6278	666.8175	1315.6012	658.3042	1314.6172	657.8122	11
18	2188.0557	1094.5315	2171.0291	1086.0182	2170.0451	1085.5262	E	1203.5852	602.2962	1186.5586	593.7829	1185.5746	593.2909	10
19	2275.0877	1138.0475	2258.0612	1129.5342	2257.0772	1129.0422	S	1074.5426	537.7749	1057.5160	529.2617	1056.5320	528.7696	9
20	2389.1306	1195.0690	2372.1041	1186.5557	2371.1201	1186.0637	N	987.5105	494.2589	970.4840	485.7456	969.5000	485.2536	8
21	2518.1732	1259.5903	2501.1467	1251.0770	2500.1627	1250.5850	E	873.4676	437.2374	856.4411	428.7242	855.4571	428.2322	7
22	2631.2573	1316.1323	2614.2308	1307.6190	2613.2467	1307.1270	L	744.4250	372.7162	727.3985	364.2029	726.4145	363.7109	6
23	2759.3159	1380.1616	2742.2893	1371.6483	2741.3053	1371.1563	Q	631.3410	316.1741	614.3144	307.6608	613.3304	307.1688	5
24	2873.3588	1437.1830	2856.3323	1428.6698	2855.3482	1428.1778	N	503.2824	252.1448	486.2558	243.6316	485.2718	243.1395	4
25	2986.4429	1493.7251	2969.4163	1485.2118	2968.4323	1484.7198	L	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
26	3115.4855	1558.2464	3098.4589	1549.7331	3097.4749	1549.2411	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
27							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 69455.

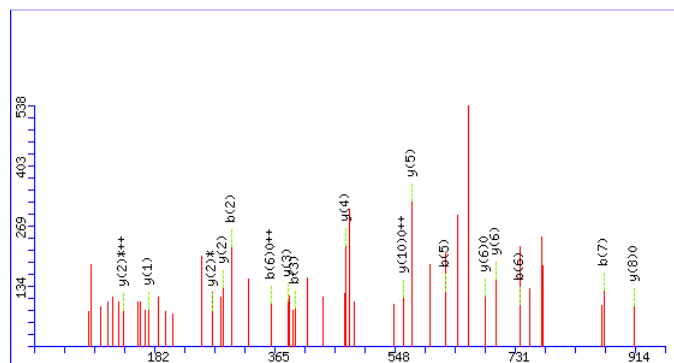
MS/MS Fragmentation of **YHPIDIETSVIR**:

Found in **IP100032087;IP100654865;IP100941011;IP101009642;IP101014516**

Title: 2.1.1.3159.2

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	164.0706	82.5389	0	0	0	0	Y							12
2	301.1295	151.0684	0	0	0	0	H	1279.7005	640.3539	1262.6739	631.8406	1261.6899	631.3486	11
3	398.1823	199.5948	0	0	0	0	P	1142.6416	571.8244	1125.6150	563.3111	1124.6310	562.8191	10
4	511.2663	256.1368	0	0	0	0	I	1045.5888	523.2980	1028.5623	514.7848	1027.5782	514.2928	9
5	626.2933	313.6503	0	0	608.2827	304.6450	D	932.5047	466.7560	915.4782	458.2427	914.4942	457.7507	8
6	739.3774	370.1923	0	0	721.3668	361.1870	I	817.4778	409.2425	800.4512	400.7293	799.4672	400.2373	7
7	868.4199	434.7136	0	0	850.4094	425.7083	E	704.3937	352.7005	687.3672	344.1872	686.3832	343.6952	6
8	969.4676	485.2375	0	0	951.4571	476.2322	T	575.3511	288.1792	558.3246	279.6659	557.3406	279.1739	5
9	1056.4997	528.7535	0	0	1038.4891	519.7482	S	474.3035	237.6554	457.2769	229.1421	456.2929	228.6501	4
10	1155.5681	578.2877	0	0	1137.5575	569.2824	V	387.2714	194.1394	370.2449	185.6261	0	0	3
11	1268.6521	634.8297	0	0	1250.6416	625.8244	I	288.2030	144.6051	271.1765	136.0919	0	0	2
12							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 69710.

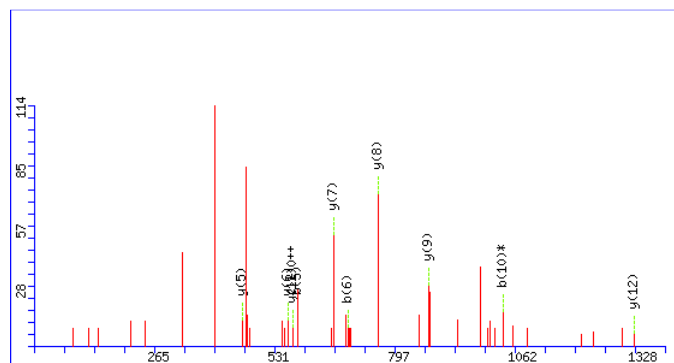
MS/MS Fragmentation of **GAYYKLVTTGSPIS**:

Found in **IP100184848**

Title: 5.1.1.1040.4

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4.5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							14
2	129.0659	65.0366	0	0	0	0	A	1399.7468	700.3770	1382.7202	691.8637	1381.7362	691.3717	13
3	292.1292	146.5682	0	0	0	0	Y	1328.7096	664.8585	1311.6831	656.3452	1310.6991	655.8532	12
4	455.1925	228.0999	0	0	0	0	Y	1165.6463	583.3268	1148.6198	574.8135	1147.6358	574.3215	11
5	583.2875	292.1474	566.2609	283.6341	0	0	K	1002.5830	501.7951	985.5564	493.2819	984.5724	492.7898	10
6	696.3715	348.6894	679.3450	340.1761	0	0	L	874.4880	437.7477	0	0	856.4775	428.7424	9
7	795.4400	398.2236	778.4134	389.7103	0	0	V	761.4040	381.2056	0	0	743.3934	372.2003	8
8	896.4876	448.7475	879.4611	440.2342	878.4771	439.7422	T	662.3355	331.6714	0	0	644.3250	322.6661	7
9	997.5353	499.2713	980.5088	490.7580	979.5247	490.2660	T	561.2879	281.1476	0	0	543.2773	272.1423	6
10	1054.5568	527.7820	1037.5302	519.2688	1036.5462	518.7767	G	460.2402	230.6237	0	0	442.2296	221.6185	5
11	1141.5888	571.2980	1124.5623	562.7848	1123.5782	562.2928	S	403.2187	202.1130	0	0	385.2082	193.1077	4
12	1238.6416	619.8244	1221.6150	611.3111	1220.6310	610.8191	P	316.1867	158.5970	0	0	298.1761	149.5917	3
13	1351.7256	676.3665	1334.6991	667.8532	1333.7151	667.3612	I	219.1339	110.0706	0	0	201.1234	101.0653	2
14							S	106.0499	53.5286	0	0	88.0393	44.5233	1

Peptide View

Peptide: 69915.

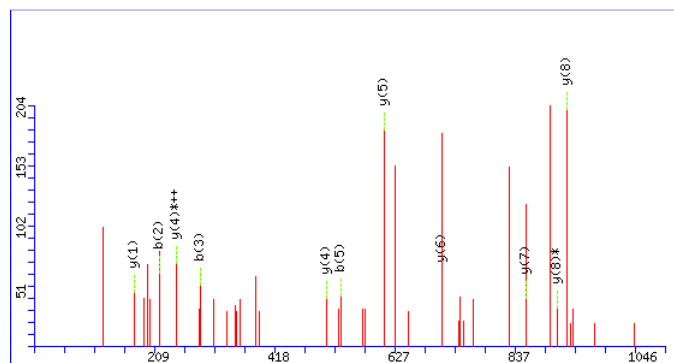
MS/MS Fragmentation of **GCAFVTFSTR: 57.021485@C:2**

Found in **IP100410277;IP100607544;IP100845479;IP100845480;IP100853320;IP101011300**

Title: 2.1.1.2949.8

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							10
2	218.0594	109.5333	0	0	0	0	C	1088.5193	544.7633	1071.4928	536.2500	1070.5088	535.7580	9
3	289.0965	145.0519	0	0	0	0	A	928.4887	464.7480	911.4621	456.2347	910.4781	455.7427	8
4	436.1649	218.5861	0	0	0	0	F	857.4516	429.2294	840.4250	420.7162	839.4410	420.2241	7
5	535.2333	268.1203	0	0	0	0	V	710.3832	355.6952	693.3566	347.1819	692.3726	346.6899	6
6	636.2810	318.6441	0	0	618.2704	309.6389	T	611.3148	306.1610	594.2882	297.6477	593.3042	297.1557	5
7	783.3494	392.1784	0	0	765.3389	383.1731	F	510.2671	255.6372	493.2405	247.1239	492.2565	246.6319	4
8	870.3815	435.6944	0	0	852.3709	426.6891	S	363.1987	182.1030	346.1721	173.5897	345.1881	173.0977	3
9	971.4291	486.2182	0	0	953.4186	477.2129	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 70129.

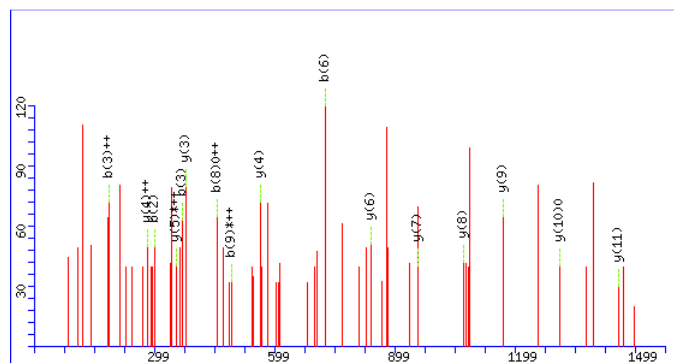
MS/MS Fragmentation of **LWALQDGFANLECVNDNYWFGR**: 57.021465@C:13.0.984015@N:15

Found in **IP100014072;IP100030746;IP100423149;IP100607619;IP100607680;IP100607739;IP100607753;IP100607851;IP100871524;IP100877689;IP100877980;IP100982188**

Title: 4.1.1.2902.10

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							22
2	300.1707	150.5890	0	0	0	0	W	2576.1299	1288.5686	2559.1034	1280.0553	2558.1194	1279.5633	21
3	371.2078	186.1075	0	0	0	0	A	2390.0506	1195.5289	2373.0241	1187.0157	2372.0401	1186.5237	20
4	484.2918	242.6496	0	0	0	0	L	2319.0135	1160.0104	2301.9870	1151.4971	2301.0029	1151.0051	19
5	612.3504	306.6788	595.3239	298.1656	0	0	Q	2205.9294	1103.4684	2188.9029	1094.9551	2187.9189	1094.4631	18
6	727.3774	364.1923	710.3508	355.6790	709.3668	355.1870	D	2077.8709	1039.4391	2060.8443	1030.9258	2059.8603	1030.4338	17
7	784.3988	392.7030	767.3723	384.1898	766.3883	383.6978	G	1962.8439	981.9256	1945.8174	973.4123	1944.8334	972.9203	16
8	931.4672	466.2373	914.4407	457.7240	913.4567	457.2320	F	1905.8225	953.4149	1888.7959	944.9016	1887.8119	944.4096	15
9	1002.5043	501.7558	985.4778	493.2425	984.4938	492.7505	A	1758.7540	879.8807	1741.7275	871.3674	1740.7435	870.8754	14
10	1116.5473	558.7773	1099.5207	550.2640	1098.5367	549.7720	N	1687.7169	844.3621	1670.6904	835.8488	1669.7064	835.3568	13
11	1229.6313	615.3193	1212.6048	606.8060	1211.6208	606.3140	L	1573.6740	787.3406	1556.6475	778.8274	1555.6634	778.3354	12
12	1358.6739	679.8406	1341.6474	671.3273	1340.6634	670.8353	E	1460.5899	730.7986	1443.5634	722.2853	1442.5794	721.7933	11
13	1518.7046	759.8559	1501.6780	751.3427	1500.6940	750.8506	C	1331.5473	666.2773	1314.5208	657.7640	1313.5368	657.2720	10
14	1617.7730	809.3901	1600.7464	800.8769	1599.7624	800.3849	V	1171.5167	586.2620	1154.4901	577.7487	1153.5061	577.2567	9
15	1732.7999	866.9036	1715.7734	858.3903	1714.7894	857.8983	N	1072.4483	536.7278	1055.4217	528.2145	1054.4377	527.7225	8
16	1847.8269	924.4171	1830.8003	915.9038	1829.8163	915.4118	D	957.4213	479.2143	940.3948	470.7010	939.4108	470.2090	7
17	1961.8698	981.4385	1944.8433	972.9253	1943.8592	972.4333	N	842.3944	421.7008	825.3678	413.1876	0	0	6
18	2124.9331	1062.9702	2107.9066	1054.4569	2106.9226	1053.9649	Y	728.3515	364.6794	711.3249	356.1661	0	0	5
19	2311.0124	1156.0099	2293.9859	1147.4966	2293.0019	1147.0046	W	565.2881	283.1477	548.2616	274.6344	0	0	4
20	2458.0809	1229.5441	2441.0543	1221.0308	2440.0703	1220.5388	F	379.2088	190.1081	362.1823	181.5948	0	0	3
21	2515.1023	1258.0548	2498.0758	1249.5415	2497.0918	1249.0495	G	232.1404	116.5738	215.1139	108.0606	0	0	2
22							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

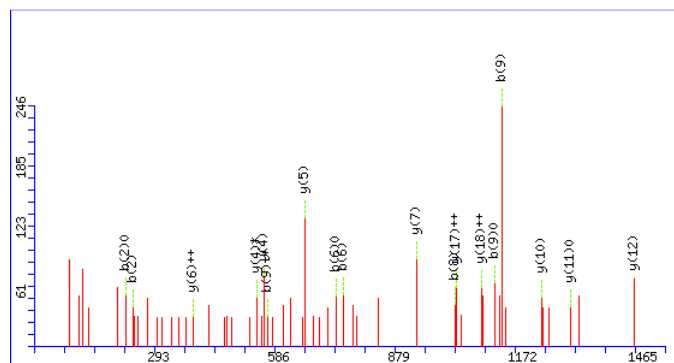
Peptide: 70267.

MS/MS Fragmentation of **ELLCHTLCDILESACCDHSGSYCLVSWLR**: 57.021465@C:4,57.021465@C:8,57.021465@C:15,57.021465@C:16,57.021465@C:23
Found in **IP100549993:IP100885206**

Title: 4.1.1.3216.9

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							29
2	243.1339	122.0706	0	0	225.1234	113.0653	L	3425.5204	1713.2638	3408.4938	1704.7506	3407.5098	1704.2585	28
3	356.2180	178.6126	0	0	338.2074	169.6074	L	3312.4363	1656.7218	3295.4098	1648.2085	3294.4257	1647.7165	27
4	516.2486	258.6280	0	0	498.2381	249.6227	C	3199.3522	1600.1798	3182.3257	1591.6665	3181.3417	1591.1745	26
5	653.3076	327.1574	0	0	635.2970	318.1521	H	3039.3216	1520.1644	3022.2951	1511.6512	3021.3110	1511.1592	25
6	754.3552	377.6813	0	0	736.3447	368.6760	T	2902.2627	1451.6350	2885.2361	1443.1217	2884.2521	1442.6297	24
7	867.4393	434.2233	0	0	849.4287	425.2180	L	2801.2150	1401.1111	2784.1885	1392.5979	2783.2044	1392.1059	23
8	1027.4700	514.2386	0	0	1009.4594	505.2333	C	2688.1309	1344.5691	2671.1044	1336.0558	2670.1204	1335.5638	22
9	1142.4969	571.7521	0	0	1124.4863	562.7468	D	2528.1003	1264.5538	2511.0737	1256.0405	2510.0897	1255.5485	21
10	1255.5810	628.2941	0	0	1237.5704	619.2888	I	2413.0734	1207.0403	2396.0468	1198.5270	2395.0628	1198.0350	20
11	1368.6650	684.8361	0	0	1350.6545	675.8309	L	2299.9893	1150.4983	2282.9627	1141.9850	2281.9787	1141.4930	19
12	1497.7076	749.3574	0	0	1479.6971	740.3522	E	2186.9052	1093.9562	2169.8787	1085.4430	2168.8947	1084.9510	18
13	1584.7396	792.8735	0	0	1566.7291	783.8682	S	2057.8626	1029.4350	2040.8361	1020.9217	2039.8521	1020.4297	17
14	1655.7768	828.3920	0	0	1637.7662	819.3867	A	1970.8306	985.9189	1953.8041	977.4057	1952.8200	976.9137	16
15	1815.8074	908.4073	0	0	1797.7968	899.4021	C	1899.7935	950.4004	1882.7669	941.8871	1881.7829	941.3951	15
16	1975.8381	988.4227	0	0	1957.8275	979.4174	C	1739.7628	870.3851	1722.7363	861.8718	1721.7523	861.3798	14
17	2090.8650	1045.9361	0	0	2072.8544	1036.9309	D	1579.7322	790.3697	1562.7056	781.8565	1561.7216	781.3645	13
18	2227.9239	1114.4656	0	0	2209.9133	1105.4603	H	1464.7052	732.8563	1447.6787	724.3430	1446.6947	723.8510	12
19	2314.9559	1157.9816	0	0	2296.9454	1148.9763	S	1327.6463	664.3268	1310.6198	655.8135	1309.6358	655.3215	11
20	2371.9774	1186.4923	0	0	2353.9668	1177.4871	G	1240.6143	620.8108	1223.5878	612.2975	1222.6037	611.8055	10
21	2459.0094	1230.0084	0	0	2440.9989	1221.0031	S	1183.5928	592.3001	1166.5663	583.7868	1165.5823	583.2948	9
22	2622.0728	1311.5400	0	0	2604.0622	1302.5347	Y	1096.5608	548.7840	1079.5343	540.2708	1078.5502	539.7788	8
23	2782.1034	1391.5553	0	0	2764.0928	1382.5501	C	933.4975	467.2524	916.4709	458.7391	915.4869	458.2471	7
24	2895.1875	1448.0974	0	0	2877.1769	1439.0921	L	773.4668	387.2371	756.4403	378.7238	755.4563	378.2318	6
25	2994.2559	1497.6316	0	0	2976.2453	1488.6263	V	660.3828	330.6950	643.3562	322.1817	642.3722	321.6897	5
26	3081.2879	1541.1476	0	0	3063.2774	1532.1423	S	561.3144	281.1608	544.2878	272.6475	543.3038	272.1555	4
27	3267.3672	1634.1873	0	0	3249.3567	1625.1820	W	474.2823	237.6448	457.2558	229.1315	0	0	3
28	3380.4513	1690.7293	0	0	3362.4407	1681.7240	L	288.2030	144.6051	271.1765	136.0919	0	0	2
29							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 70365.

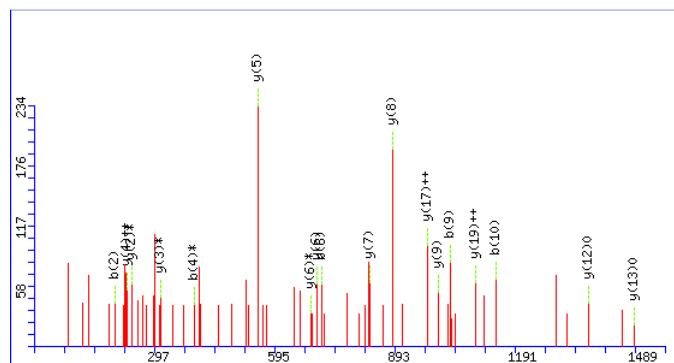
MS/MS Fragmentation of **SLSQHCDFGLDNLETDLNYYNNLGEFPQA**IK: 57.021465@C:6

Found in **IP100217954;IP100798136**

Title: 4.1.1.664.9

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							31
2	201.1234	101.0653	0	0	183.1128	92.0600	L	3478.6584	1739.8328	3461.6318	1731.3195	3460.6478	1730.8275	30
3	288.1554	144.5813	0	0	270.1448	135.5761	S	3365.5743	1683.2908	3348.5477	1674.7775	3347.5637	1674.2855	29
4	416.2140	208.6106	399.1874	200.0974	398.2034	199.6053	Q	3278.5423	1639.7748	3261.5157	1631.2615	3260.5317	1630.7695	28
5	553.2729	277.1401	536.2463	268.6268	535.2623	268.1348	H	3150.4837	1575.7455	3133.4571	1567.2322	3132.4731	1566.7402	27
6	713.3035	357.1554	696.2770	348.6421	695.2930	348.1501	C	3013.4248	1507.2160	2996.3982	1498.7028	2995.4142	1498.2107	26
7	860.3720	430.6896	843.3454	422.1763	842.3614	421.6843	F	2853.3941	1427.2007	2836.3676	1418.6874	2835.3836	1418.1954	25
8	975.3989	488.2031	958.3723	479.6898	957.3883	479.1978	D	2706.3257	1353.6665	2689.2992	1345.1532	2688.3152	1344.6612	24
9	1032.4204	516.7138	1015.3938	508.2005	1014.4098	507.7085	G	2591.2988	1296.1530	2574.2722	1287.6398	2573.2882	1287.1477	23
10	1145.5044	573.2558	1128.4779	564.7426	1127.4939	564.2506	L	2534.2773	1267.6423	2517.2508	1259.1290	2516.2667	1258.6370	22
11	1260.5314	630.7693	1243.5048	622.2560	1242.5208	621.7640	D	2421.1932	1211.1003	2404.1667	1202.5870	2403.1827	1202.0950	21
12	1374.5743	687.7908	1357.5477	679.2775	1356.5637	678.7855	N	2306.1663	1153.5868	2289.1398	1145.0735	2288.1557	1144.5815	20
13	1487.6584	744.3328	1470.6318	735.8195	1469.6478	735.3275	L	2192.1234	1096.5653	2175.0968	1088.0521	2174.1128	1087.5600	19
14	1616.7009	808.8541	1599.6744	800.3408	1598.6904	799.8488	E	2079.0393	1040.0233	2062.0128	1031.5100	2061.0287	1031.0180	18
15	1717.7486	859.3780	1700.7221	850.8647	1699.7381	850.3727	T	1949.9967	975.5020	1932.9702	966.9887	1931.9862	966.4967	17
16	1830.8327	915.9200	1813.8061	907.4067	1812.8221	906.9147	L	1848.9490	924.9782	1831.9225	916.4649	1830.9385	915.9729	16
17	1945.8596	973.4335	1928.8331	964.9202	1927.8491	964.4282	D	1735.8650	868.4361	1718.8384	859.9229	1717.8544	859.4308	15
18	2058.9437	1029.9755	2041.9171	1021.4622	2040.9331	1020.9702	L	1620.8380	810.9227	1603.8115	802.4094	1602.8275	801.9174	14
19	2172.9866	1086.9970	2155.9601	1078.4837	2154.9761	1077.9917	N	1507.7540	754.3806	1490.7274	745.8673	1489.7434	745.3753	13
20	2336.0500	1168.5286	2319.0234	1160.0153	2318.0394	1159.5233	Y	1393.7110	697.3592	1376.6845	688.8459	1375.7005	688.3539	12
21	2450.0929	1225.5501	2433.0663	1217.0368	2432.0823	1216.5448	N	1230.6477	615.8275	1213.6212	607.3142	1212.6371	606.8222	11
22	2564.1358	1282.5715	2547.1093	1274.0583	2546.1252	1273.5663	N	1116.6048	558.8060	1099.5782	550.2928	1098.5942	549.8007	10
23	2677.2199	1339.1136	2660.1933	1330.6003	2659.2093	1330.1083	L	1002.5619	501.7846	985.5353	493.2713	984.5513	492.7793	9
24	2734.2413	1367.6243	2717.2148	1359.1110	2716.2308	1358.6190	G	889.4778	445.2425	872.4512	436.7293	871.4672	436.2373	8
25	2863.2839	1432.1456	2846.2574	1423.6323	2845.2734	1423.1403	E	832.4563	416.7318	815.4298	408.2185	814.4458	407.7265	7
26	3010.3523	1505.6798	2993.3258	1497.1665	2992.3418	1496.6745	F	703.4137	352.2105	686.3872	343.6972	0	0	6
27	3107.4051	1554.2062	3090.3786	1545.6929	3089.3945	1545.2009	P	556.3453	278.6763	539.3188	270.1630	0	0	5
28	3235.4637	1618.2355	3218.4371	1609.7222	3217.4531	1609.2302	Q	459.2926	230.1499	442.2660	221.6366	0	0	4
29	3306.5008	1653.7540	3289.4742	1645.2408	3288.4902	1644.7488	A	331.2340	166.1206	314.2074	157.6074	0	0	3
30	3419.5849	1710.2961	3402.5583	1701.7828	3401.5743	1701.2908	I	260.1969	130.6021	243.1703	122.0888	0	0	2
31							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 70590.

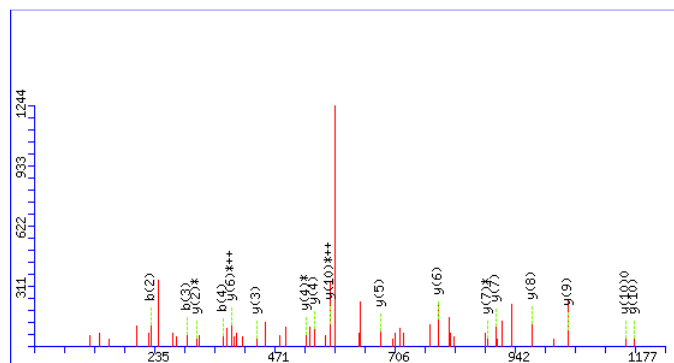
MS/MS Fragmentation of **VEAALNENTCR: 57.021465@C:10**

Found in **IP100023586;IP100747900;IP100941249;IP100966088;IP100967649;IP101010921**

Title: 1.1.1.7625.10

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120214ry¥120214ry_32R1-32_4_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							11
2	229.1183	115.0628	0	0	211.1077	106.0575	E	1177.5266	589.2669	1160.5001	580.7537	1159.5160	580.2617	10
3	300.1554	150.5813	0	0	282.1448	141.5761	A	1048.4840	524.7456	1031.4575	516.2324	1030.4735	515.7404	9
4	371.1925	186.0999	0	0	353.1819	177.0946	A	977.4469	489.2271	960.4204	480.7138	959.4363	480.2218	8
5	484.2766	242.6419	0	0	466.2660	233.6366	L	906.4098	453.7085	889.3832	445.1953	888.3992	444.7033	7
6	598.3195	299.6634	581.2930	291.1501	580.3089	290.6581	N	793.3257	397.1665	776.2992	388.6532	775.3152	388.1612	6
7	727.3621	364.1847	710.3355	355.6714	709.3515	355.1794	E	679.2828	340.1450	662.2563	331.6318	661.2722	331.1398	5
8	841.4050	421.2061	824.3785	412.6929	823.3945	412.2009	N	550.2402	275.6237	533.2137	267.1105	532.2296	266.6185	4
9	942.4527	471.7300	925.4262	463.2167	924.4421	462.7247	T	436.1973	218.6023	419.1707	210.0890	418.1867	209.5970	3
10	1102.4834	551.7453	1085.4568	543.2320	1084.4728	542.7400	C	335.1496	168.0784	318.1231	159.5652	0	0	2
11							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 70741.

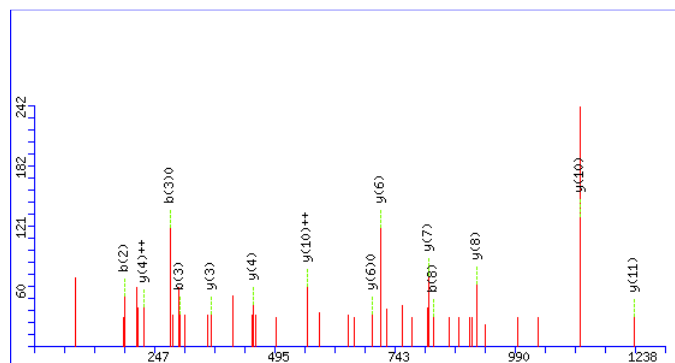
MS/MS Fragmentation of **VSILPDVVFDSP**LH:

Found in **IP100099179**

Title: 3.1.1.4286.6

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							14
2	187.1077	94.0575	0	0	169.0972	85.0522	S	1438.7577	719.8825	0	0	1420.7471	710.8772	13
3	300.1918	150.5995	0	0	282.1812	141.5942	I	1351.7256	676.3665	0	0	1333.7151	667.3612	12
4	413.2758	207.1416	0	0	395.2653	198.1363	L	1238.6416	619.8244	0	0	1220.6310	610.8191	11
5	510.3286	255.6679	0	0	492.3180	246.6627	P	1125.5575	563.2824	0	0	1107.5469	554.2771	10
6	625.3556	313.1814	0	0	607.3450	304.1761	D	1028.5047	514.7560	0	0	1010.4942	505.7507	9
7	724.4240	362.7156	0	0	706.4134	353.7103	V	913.4778	457.2425	0	0	895.4672	448.2373	8
8	823.4924	412.2498	0	0	805.4818	403.2445	V	814.4094	407.7083	0	0	796.3988	398.7030	7
9	970.5608	485.7840	0	0	952.5502	476.7788	F	715.3410	358.1741	0	0	697.3304	349.1688	6
10	1085.5877	543.2975	0	0	1067.5772	534.2922	D	568.2726	284.6399	0	0	550.2620	275.6346	5
11	1172.6198	586.8135	0	0	1154.6092	577.8082	S	453.2456	227.1264	0	0	435.2350	218.1212	4
12	1269.6725	635.3399	0	0	1251.6620	626.3346	P	366.2136	183.6104	0	0	0	0	3
13	1382.7566	691.8819	0	0	1364.7460	682.8767	L	269.1608	135.0840	0	0	0	0	2
14							H	156.0768	78.5420	0	0	0	0	1

Peptide View

Peptide: 70751.

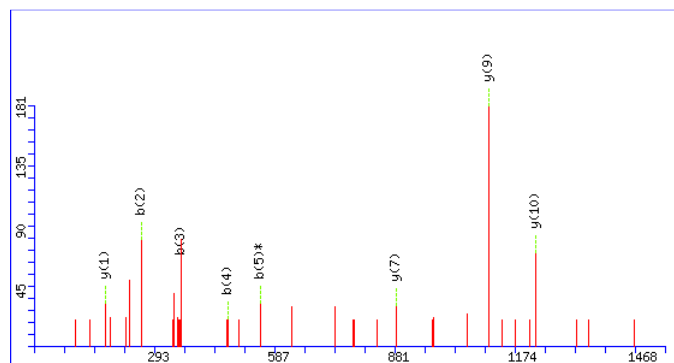
MS/MS Fragmentation of **NFVLPEEIQEV**R:

Found in **IP100019451**

Title: 3.1.1.4224.7

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							13
2	262.1186	131.5629	245.0921	123.0497	0	0	F	1471.8155	736.4114	1454.7890	727.8981	1453.8049	727.4061	12
3	361.1870	181.0972	344.1605	172.5839	0	0	V	1324.7471	662.8772	1307.7205	654.3639	1306.7365	653.8719	11
4	474.2711	237.6392	457.2445	229.1259	0	0	L	1225.6787	613.3430	1208.6521	604.8297	1207.6681	604.3377	10
5	571.3239	286.1656	554.2973	277.6523	0	0	P	1112.5946	556.8009	1095.5681	548.2877	1094.5841	547.7957	9
6	700.3665	350.6869	683.3399	342.1736	682.3559	341.6816	E	1015.5419	508.2746	998.5153	499.7613	997.5313	499.2693	8
7	829.4090	415.2082	812.3825	406.6949	811.3985	406.2029	E	886.4993	443.7533	869.4727	435.2400	868.4887	434.7480	7
8	942.4931	471.7502	925.4666	463.2369	924.4825	462.7449	I	757.4567	379.2320	740.4301	370.7187	739.4461	370.2267	6
9	1055.5772	528.2922	1038.5506	519.7789	1037.5666	519.2869	I	644.3726	322.6899	627.3461	314.1767	626.3620	313.6847	5
10	1183.6358	592.3215	1166.6092	583.8082	1165.6252	583.3162	Q	531.2885	266.1479	514.2620	257.6346	513.2780	257.1426	4
11	1312.6783	656.8428	1295.6518	648.3295	1294.6678	647.8375	E	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
12	1411.7468	706.3770	1394.7202	697.8637	1393.7362	697.3717	V	274.1874	137.5973	257.1608	129.0840	0	0	2
13							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

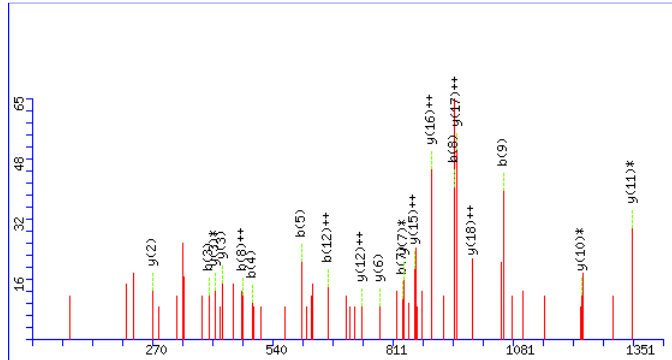
Peptide: 70760.

MS/MS Fragmentation of **LQRPLPEDLAELASGVLCQLANQLRPR**: 57.021465@C:20
Found in **IP100000173;IP100945006;IP100945129**

Title: 5.1.1.361.5

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_2.5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							29
2	242.1499	121.5786	225.1234	113.0653	0	0	Q	3128.6997	1564.8535	3111.6732	1556.3402	3110.6892	1555.8482	28
3	398.2510	199.6292	381.2245	191.1159	0	0	R	3000.6411	1500.8242	2983.6146	1492.3109	2982.6306	1491.8189	27
4	495.3038	248.1555	478.2772	239.6423	0	0	P	2844.5400	1422.7737	2827.5135	1414.2604	2826.5295	1413.7684	26
5	608.3879	304.6976	591.3613	296.1843	0	0	L	2747.4873	1374.2473	2730.4607	1365.7340	2729.4767	1365.2420	25
6	705.4406	353.2239	688.4141	344.7107	0	0	P	2634.4032	1317.7052	2617.3766	1309.1920	2616.3926	1308.7000	24
7	834.4832	417.7452	817.4567	409.2320	816.4726	408.7400	E	2537.3504	1269.1789	2520.3239	1260.6656	2519.3399	1260.1736	23
8	949.5102	475.2587	932.4836	466.7454	931.4996	466.2534	D	2408.3078	1204.6576	2391.2813	1196.1443	2390.2973	1195.6523	22
9	1062.5942	531.8007	1045.5677	523.2875	1044.5837	522.7955	L	2293.2809	1147.1441	2276.2543	1138.6308	2275.2703	1138.1388	21
10	1133.6313	567.3193	1116.6048	558.8060	1115.6208	558.3140	A	2180.1968	1090.6021	2163.1703	1082.0888	2162.1863	1081.5968	20
11	1262.6739	631.8406	1245.6474	623.3273	1244.6634	622.8353	E	2109.1597	1055.0835	2092.1332	1046.5702	2091.1492	1046.0782	19
12	1333.7110	667.3592	1316.6845	658.8459	1315.7005	658.3539	A	1980.1171	990.5622	1963.0906	982.0489	1962.1066	981.5569	18
13	1446.7951	723.9012	1429.7686	715.3879	1428.7845	714.8959	L	1909.0800	955.0436	1892.0535	946.5304	1891.0694	946.0384	17
14	1517.8322	759.4197	1500.8057	750.9065	1499.8217	750.4145	A	1795.9959	898.5016	1778.9694	889.9883	1777.9854	889.4963	16
15	1604.8642	802.9358	1587.8377	794.4225	1586.8537	793.9305	S	1724.9588	862.9831	1707.9323	854.4698	1706.9483	853.9778	15
16	1661.8857	831.4465	1644.8592	822.9332	1643.8751	822.4412	G	1637.9268	819.4670	1620.9003	810.9538	0	0	14
17	1760.9541	880.9807	1743.9276	872.4674	1742.9436	871.9754	V	1580.9053	790.9563	1563.8788	782.4430	0	0	13
18	1874.0382	937.5227	1857.0116	929.0095	1856.0276	928.5175	I	1481.8369	741.4221	1464.8104	732.9088	0	0	12
19	1987.1223	994.0648	1970.0957	985.5515	1969.1117	985.0595	L	1368.7529	684.8801	1351.7263	676.3668	0	0	11
20	2147.1529	1074.0801	2130.1264	1065.5668	2129.1423	1065.0748	C	1255.6688	628.3380	1238.6423	619.8248	0	0	10
21	2275.2115	1138.1094	2258.1849	1129.5961	2257.2009	1129.1041	Q	1095.6382	548.3227	1078.6116	539.8094	0	0	9
22	2388.2955	1194.6514	2371.2690	1186.1381	2370.2850	1185.6461	L	967.5796	484.2934	950.5530	475.7802	0	0	8
23	2459.3327	1230.1700	2442.3061	1221.6567	2441.3221	1221.1647	A	854.4955	427.7514	837.4690	419.2381	0	0	7
24	2573.3756	1287.1914	2556.3490	1278.6782	2555.3650	1278.1861	N	783.4584	392.2328	766.4318	383.7196	0	0	6
25	2701.4342	1351.2207	2684.4076	1342.7074	2683.4236	1342.2154	Q	669.4155	335.2114	652.3889	326.6981	0	0	5
26	2814.5182	1407.7628	2797.4917	1399.2495	2796.5077	1398.7575	L	541.3569	271.1821	524.3303	262.6688	0	0	4
27	2970.6193	1485.8133	2953.5928	1477.3000	2952.6088	1476.8080	R	428.2728	214.6401	411.2463	206.1268	0	0	3
28	3067.6721	1534.3397	3050.6456	1525.8264	3049.6615	1525.3344	P	272.1717	136.5895	255.1452	128.0762	0	0	2
29							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 70763.

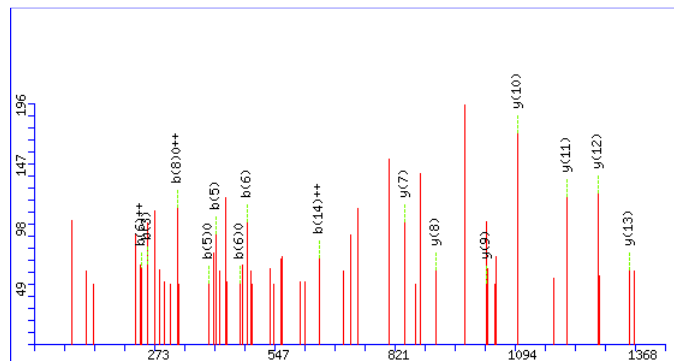
MS/MS Fragmentation of **DAASAALADAAEELLDR**:

Found in **IP100329142;IP100974015;IP100976517;IP100985273;IP101015058**

Title: 4.1.1.1925.9

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							17
2	187.0713	94.0393	0	0	169.0608	85.0340	A	1586.8020	793.9047	1569.7755	785.3914	1568.7915	784.8994	16
3	258.1084	129.5579	0	0	240.0979	120.5526	A	1515.7649	758.3861	1498.7384	749.8728	1497.7544	749.3808	15
4	345.1405	173.0739	0	0	327.1299	164.0686	S	1444.7278	722.8675	1427.7013	714.3543	1426.7172	713.8623	14
5	418.1776	208.5924	0	0	398.1670	199.5872	A	1357.6958	679.3515	1340.6692	670.8383	1339.6852	670.3462	13
6	487.2147	244.1110	0	0	469.2041	235.1057	A	1286.6587	643.8330	1269.6321	635.3197	1268.6481	634.8277	12
7	600.2988	300.6530	0	0	582.2882	291.6477	L	1215.6216	608.3144	1198.5950	599.8011	1197.6110	599.3091	11
8	671.3359	336.1716	0	0	653.3253	327.1663	A	1102.5375	551.7724	1085.5109	543.2591	1084.5269	542.7671	10
9	786.3628	393.6851	0	0	768.3523	384.6798	D	1031.5004	516.2538	1014.4738	507.7406	1013.4898	507.2485	9
10	857.3999	429.2036	0	0	839.3894	420.1983	A	916.4734	458.7404	899.4469	450.2271	898.4629	449.7351	8
11	928.4371	464.7222	0	0	910.4265	455.7169	A	845.4363	423.2218	828.4098	414.7085	827.4258	414.2165	7
12	1057.4796	529.2435	0	0	1039.4691	520.2382	E	774.3992	387.7032	757.3727	379.1900	756.3886	378.6980	6
13	1186.5222	593.7648	0	0	1168.5117	584.7595	E	645.3566	323.1819	628.3301	314.6687	627.3461	314.1767	5
14	1299.6063	650.3068	0	0	1281.5957	641.3015	L	516.3140	258.6606	499.2875	250.1474	498.3035	249.6554	4
15	1412.6904	706.8488	0	0	1394.6798	697.8435	L	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
16	1527.7173	764.3623	0	0	1509.7067	755.3570	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
17							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 71223.

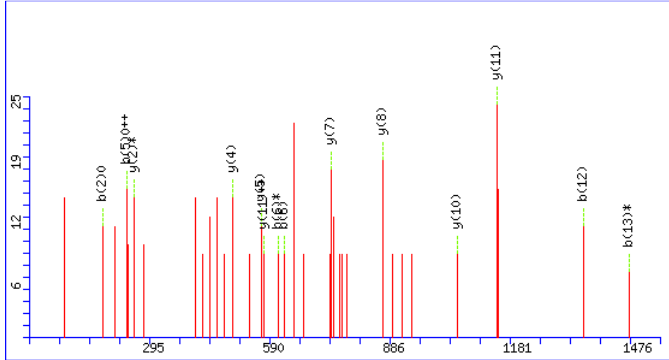
MS/MS Fragmentation of **SLGNEQWEFTLGMP LAQAVAILQK:**

Found in **IPI00013779**

Title: 5.1.1.295.3

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_1_5.mgf

ProteinPilot Peptide Confidence > 99%

[illegible]

Peptide View

Peptide: 71366.

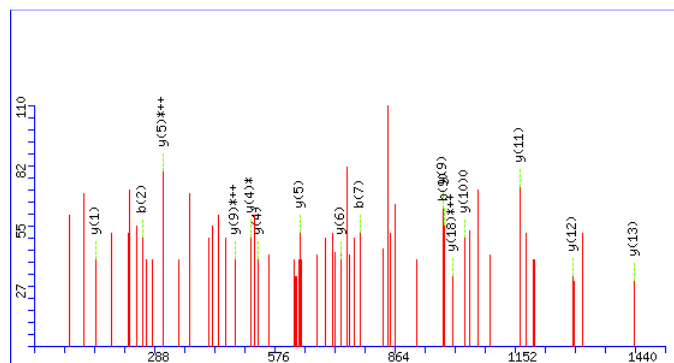
MS/MS Fragmentation of **VCQQPGLSLWVPFQNAATAVTNLYK: 57.021465@C:2**

Found in **IP100374163**

Title: 4.1.1.3725.10

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4.4.mgf

ProteinPilot Peptide Confidence > 99%



Peptide View

Peptide: 71495.

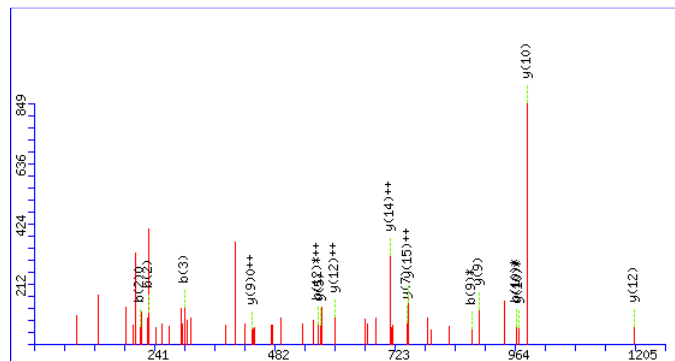
MS/MS Fragmentation of **TEAPESKPGSSSSLSLR**:

Found in **IP100012448;IP100028312;IP100186092;IP100217835;IP100217836;IP100217837;IP100383566;IP100383568;IP100384849;IP100639963;IP100640605;IP100642284**

Title: 1.1.1.7892.6

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							17
2	231.0975	116.0524	0	0	213.0870	107.0471	E	1631.8235	816.4154	1614.7970	807.9021	1613.8129	807.4101	16
3	302.1347	151.5710	0	0	284.1241	142.5657	A	1502.7809	751.8941	1485.7544	743.3808	1484.7703	742.8888	15
4	399.1874	200.0974	0	0	381.1769	191.0921	P	1431.7438	716.3755	1414.7172	707.8623	1413.7332	707.3703	14
5	528.2300	264.6186	0	0	510.2195	255.6134	E	1334.6910	667.8492	1317.6645	659.3359	1316.6805	658.8439	13
6	615.2620	308.1347	0	0	597.2515	299.1294	S	1205.6484	603.3279	1188.6219	594.8146	1187.6379	594.3226	12
7	743.3570	372.1821	726.3305	363.6689	725.3464	363.1769	K	1118.6164	559.8118	1101.5899	551.2986	1100.6058	550.8066	11
8	840.4098	420.7085	823.3832	412.1953	822.3992	411.7032	P	990.5214	495.7644	973.4949	487.2511	972.5109	486.7591	10
9	897.4312	449.2193	880.4047	440.7060	879.4207	440.2140	G	893.4687	447.2380	876.4421	438.7247	875.4581	438.2327	9
10	984.4633	492.7353	967.4367	484.2220	966.4527	483.7300	S	836.4472	418.7272	819.4207	410.2140	818.4367	409.7220	8
11	1071.4953	536.2513	1054.4687	527.7380	1053.4847	527.2460	S	749.4152	375.2112	732.3886	366.6980	731.4046	366.2060	7
12	1158.5273	579.7673	1141.5008	571.2540	1140.5168	570.7620	S	662.3832	331.6952	645.3566	323.1819	644.3726	322.6899	6
13	1245.5594	623.2833	1228.5328	614.7700	1227.5488	614.2780	S	575.3511	288.1792	558.3246	279.6659	557.3406	279.1739	5
14	1358.6434	679.8253	1341.6169	671.3121	1340.6328	670.8201	L	488.3191	244.6632	471.2926	236.1499	470.3085	235.6579	4
15	1445.6754	723.3414	1428.6489	714.8281	1427.6649	714.3361	S	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
16	1558.7595	779.8834	1541.7330	771.3701	1540.7489	770.8781	L	288.2030	144.6051	271.1765	136.0919	0	0	2
17							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 71562.

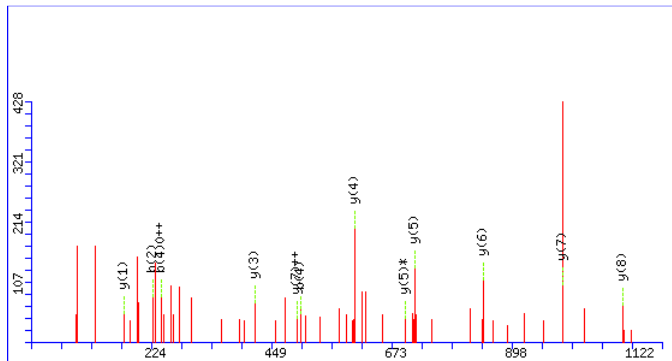
MS/MS Fragmentation of **LIFELWQDR**:

Found in **IP100152681;IP100792585;IP100965512;IP100967147**

Title: 3.1.1.3641.3

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							9
2	227.1754	114.0913	0	0	0	0	I	1106.5629	553.7851	1089.5364	545.2718	1088.5524	544.7798	8
3	374.2438	187.6255	0	0	0	0	F	993.4789	497.2431	976.4523	488.7298	975.4683	488.2378	7
4	503.2864	252.1468	0	0	485.2758	243.1416	E	846.4104	423.7089	829.3839	415.1956	828.3999	414.7036	6
5	616.3705	308.6889	0	0	598.3599	299.6836	L	717.3678	359.1876	700.3413	350.6743	699.3573	350.1823	5
6	802.4498	401.7285	0	0	784.4392	392.7232	W	604.2838	302.6455	587.2572	294.1323	586.2732	293.6402	4
7	930.5084	465.7578	913.4818	457.2445	912.4978	456.7525	Q	418.2045	209.6059	401.1779	201.0926	400.1939	200.6006	3
8	1045.5353	523.2713	1028.5088	514.7580	1027.5247	514.2660	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
9							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 71587.

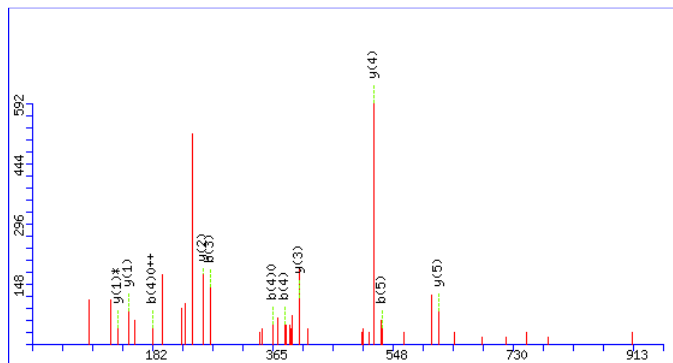
MS/MS Fragmentation of **DGVFLK**:

Found in **IP100020406**

Title: 2.1.1.4346.2

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							7
2	173.0557	87.0315	0	0	155.0451	78.0262	G	676.4392	338.7232	659.4127	330.2100	0	0	6
3	272.1241	136.5657	0	0	254.1135	127.5604	V	619.4178	310.2125	602.3912	301.6992	0	0	5
4	385.2082	193.1077	0	0	367.1976	184.1024	L	520.3493	260.6783	503.3228	252.1650	0	0	4
5	532.2766	266.6419	0	0	514.2660	257.6366	F	407.2653	204.1363	390.2387	195.6230	0	0	3
6	645.3606	323.1840	0	0	627.3501	314.1787	L	260.1969	130.6021	243.1703	122.0888	0	0	2
7							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 71634.

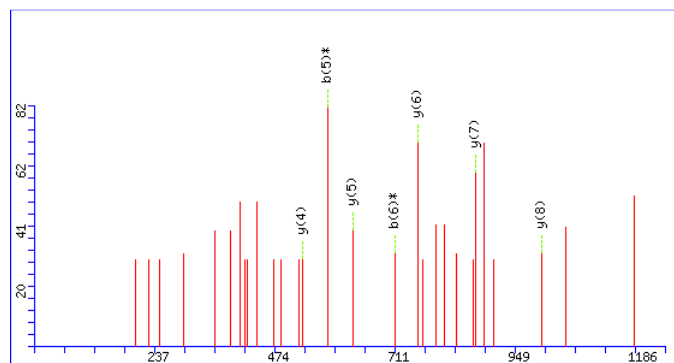
MS/MS Fragmentation of **QILNEMLEVVEQR: -17.026549@N-term(Q)**

Found in **IP100177937**

Title: 4.1.1.3905.5

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233	0	0	Q							13
2	242.1499	121.5786	225.1234	113.0653	0	0	I	1472.7777	736.8925	1455.7512	728.3792	1454.7672	727.8872	12
3	355.2340	178.1206	338.2074	169.6074	0	0	L	1359.6937	680.3505	1342.6671	671.8372	1341.6831	671.3452	11
4	469.2769	235.1421	452.2504	226.6288	0	0	N	1246.6096	623.8084	1229.5831	615.2952	1228.5990	614.8032	10
5	598.3195	299.6634	581.2930	291.1501	580.3089	290.6581	E	1132.5667	566.7870	1115.5401	558.2737	1114.5561	557.7817	9
6	729.3600	365.1836	712.3334	356.6704	711.3494	356.1783	M	1003.5241	502.2657	986.4975	493.7524	985.5135	493.2604	8
7	842.4441	421.7257	825.4175	413.2124	824.4335	412.7204	L	872.4836	436.7454	855.4571	428.2322	854.4730	427.7402	7
8	971.4866	486.2470	954.4601	477.7337	953.4761	477.2417	E	759.3995	380.2034	742.3730	371.6901	741.3890	371.1981	6
9	1070.5551	535.7812	1053.5285	527.2679	1052.5445	526.7759	V	630.3570	315.6821	613.3304	307.1688	612.3464	306.6768	5
10	1169.6235	585.3154	1152.5969	576.8021	1151.6129	576.3101	V	531.2885	266.1479	514.2620	257.6346	513.2780	257.1426	4
11	1298.6661	649.8367	1281.6395	641.3234	1280.6555	640.8314	E	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	3
12	1426.7246	713.8660	1409.6981	705.3527	1408.7141	704.8607	Q	303.1775	152.0924	286.1510	143.5791	0	0	2
13							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 71760.

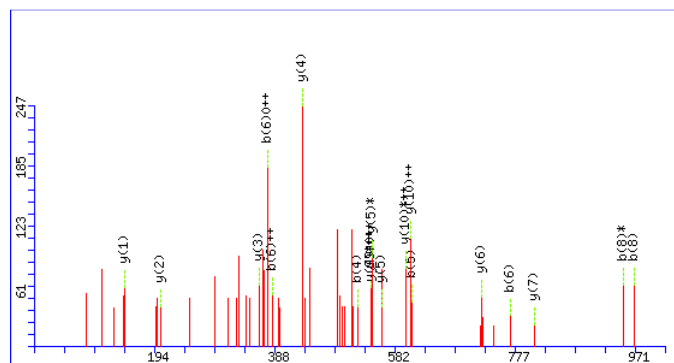
MS/MS Fragmentation of **ILHCSCQACGK: 57.021465@C:4,57.021465@C:6,57.021465@C:9**

Found in **IP100013299;IP100844060;IP100852617;IP100852703;IP100853585;IP100985199**

Title: 1.1.1.6876.6

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_2_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							11
2	227.1754	114.0913	0	0	0	0	L	1220.4969	610.7521	1203.4704	602.2388	1202.4863	601.7468	10
3	364.2343	182.6208	0	0	0	0	H	1107.4128	554.2101	1090.3863	545.6968	1089.4023	545.2048	9
4	524.2650	262.6361	0	0	0	0	C	970.3539	485.6806	953.3274	477.1673	952.3434	476.6753	8
5	611.2970	306.1521	0	0	593.2864	297.1469	S	810.3233	405.6653	793.2967	397.1520	792.3127	396.6600	7
6	771.3276	386.1675	0	0	753.3171	377.1622	C	723.2913	362.1493	706.2647	353.6360	0	0	6
7	899.3862	450.1967	882.3597	441.6835	881.3757	441.1915	Q	563.2806	282.1339	546.2341	273.6207	0	0	5
8	970.4233	485.7153	953.3968	477.2020	952.4128	476.7100	A	435.2020	218.1047	418.1755	209.5914	0	0	4
9	1130.4540	565.7306	1113.4274	557.2174	1112.4434	556.7253	C	364.1649	182.5861	347.1384	174.0728	0	0	3
10	1187.4755	594.2414	1170.4489	585.7281	1169.4649	585.2361	G	204.1343	102.5708	187.1077	94.0575	0	0	2
11							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 72155.

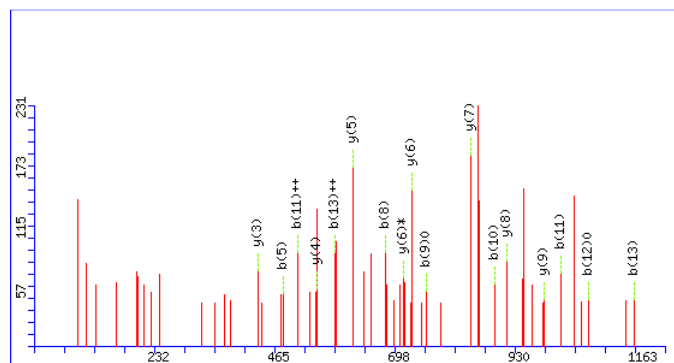
MS/MS Fragmentation of **VPEGVAGAPNEAALLALMER**:

Found in **IP100005042;IP100169342;IP100964984;IP100965625;IP100965724;IP100965845;IP100966779;IP100967035;IP100967966;IP100968211**

Title: 3.1.1.4050.7

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_1_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							20
2	197.1285	99.0679	0	0	0	0	P	1908.9848	954.9960	1891.9582	946.4828	1890.9742	945.9907	19
3	326.1710	163.5892	0	0	308.1605	154.5839	E	1811.9320	906.4696	1794.9055	897.9564	1793.9214	897.4644	18
4	383.1925	192.0999	0	0	365.1819	183.0946	G	1682.8894	841.9483	1665.8629	833.4351	1664.8789	832.9431	17
5	482.2609	241.6341	0	0	464.2504	232.6288	V	1625.8680	813.4376	1608.8414	804.9243	1607.8574	804.4323	16
6	553.2980	277.1527	0	0	535.2875	268.1474	A	1526.7995	763.9034	1509.7730	755.3901	1508.7890	754.8981	15
7	610.3195	305.6634	0	0	592.3089	296.6581	G	1455.7624	728.3849	1438.7359	719.8716	1437.7519	719.3796	14
8	681.3566	341.1819	0	0	663.3461	332.1767	A	1398.7410	699.8741	1381.7144	691.3608	1380.7304	690.8688	13
9	778.4094	389.7083	0	0	760.3988	380.7030	P	1327.7038	664.3556	1310.6773	655.8423	1309.6933	655.3503	12
10	892.4523	446.7298	875.4258	438.2165	874.4417	437.7245	N	1230.6511	615.8292	1213.6245	607.3159	1212.6405	606.8239	11
11	1021.4949	511.2511	1004.4684	502.7378	1003.4843	502.2458	E	1116.6082	558.8077	1099.5816	550.2944	1098.5976	549.8024	10
12	1092.5320	546.7696	1075.5055	538.2564	1074.5215	537.7644	A	987.5656	494.2864	970.5390	485.7731	969.5550	485.2811	9
13	1163.5691	582.2882	1146.5426	573.7749	1145.5586	573.2829	A	916.5284	458.7679	899.5019	450.2546	898.5179	449.7626	8
14	1276.6532	638.8302	1259.6266	630.3170	1258.6426	629.8250	L	845.4913	423.2493	828.4648	414.7360	827.4808	414.2440	7
15	1389.7373	695.3723	1372.7107	686.8590	1371.7267	686.3670	L	732.4073	366.7073	715.3807	358.1940	714.3967	357.7020	6
16	1460.7744	730.8908	1443.7478	722.3775	1442.7638	721.8855	A	619.3232	310.1652	602.2967	301.6520	601.3126	301.1600	5
17	1573.8584	787.4329	1556.8319	778.9196	1555.8479	778.4276	L	548.2861	274.6467	531.2595	266.1334	530.2755	265.6414	4
18	1704.8989	852.9531	1687.8724	844.4398	1686.8884	843.9478	M	435.2020	218.1047	418.1755	209.5914	417.1915	209.0994	3
19	1833.9415	917.4744	1816.9150	908.9611	1815.9309	908.4691	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
20							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 72192.

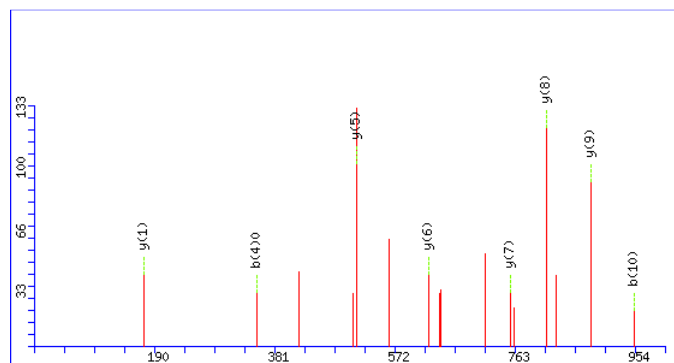
MS/MS Fragmentation of **ENAGEDPGLAR**:

Found in **IP100027547;IP100847793**

Title: 1.1.1.6478.9

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_1_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							11
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	N	999.4854	500.2463	982.4588	491.7331	981.4748	491.2411	10
3	315.1299	158.0686	298.1034	149.5553	297.1193	149.0633	A	885.4425	443.2249	868.4159	434.7116	867.4319	434.2196	9
4	372.1514	186.5793	355.1248	178.0661	354.1408	177.5740	G	814.4054	407.7063	797.3788	399.1930	796.3948	398.7010	8
5	501.1940	251.1006	484.1674	242.5873	483.1834	242.0953	E	757.3839	379.1956	740.3573	370.6823	739.3733	370.1903	7
6	616.2209	308.6141	599.1944	300.1008	598.2103	299.6088	D	628.3413	314.6743	611.3148	306.1610	610.3307	305.6690	6
7	713.2737	357.1405	696.2471	348.6272	695.2631	348.1352	P	513.3144	257.1608	496.2878	248.6475	0	0	5
8	770.2951	385.6512	753.2686	377.1379	752.2846	376.6459	G	416.2616	208.6344	399.2350	200.1212	0	0	4
9	883.3792	442.1932	866.3527	433.6800	865.3686	433.1880	L	359.2401	180.1237	342.2136	171.6104	0	0	3
10	954.4163	477.7118	937.3898	469.1985	936.4058	468.7065	A	246.1561	123.5817	229.1295	115.0684	0	0	2
11							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 72199.

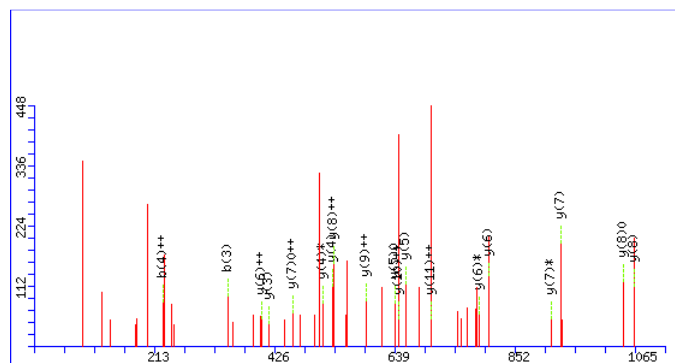
MS/MS Fragmentation of **LDDIEEFENIRK**:

Found in **IP100169387;IP100921214**

Title: 2.1.1.4059.4

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							12
2	229.1183	115.0628	0	0	211.1077	106.0575	D	1407.6750	704.3412	1390.6485	695.8279	1389.6645	695.3359	11
3	344.1452	172.5763	0	0	326.1347	163.5710	D	1292.6481	646.8277	1275.6216	638.3144	1274.6375	637.8224	10
4	457.2293	229.1183	0	0	439.2187	220.1130	I	1177.6212	589.3142	1160.5946	580.8009	1159.6106	580.3089	9
5	586.2719	293.6396	0	0	568.2613	284.6343	E	1064.5371	532.7722	1047.5105	524.2589	1046.5265	523.7669	8
6	715.3145	358.1609	0	0	697.3039	349.1556	E	935.4945	468.2509	918.4680	459.7376	917.4839	459.2456	7
7	862.3829	431.6951	0	0	844.3723	422.6898	F	806.4519	403.7296	789.4254	395.2163	788.4413	394.7243	6
8	991.4255	496.2164	0	0	973.4149	487.2111	E	659.3835	330.1954	642.3569	321.6821	641.3729	321.1901	5
9	1105.4684	553.2378	1088.4419	544.7246	1087.4578	544.2326	N	530.3409	265.6741	513.3144	257.1608	0	0	4
10	1218.5525	609.7799	1201.5259	601.2666	1200.5419	600.7746	I	416.2980	208.6526	399.2714	200.1394	0	0	3
11	1374.6536	687.8304	1357.6270	679.3172	1356.6430	678.8251	R	303.2139	152.1106	286.1874	143.5973	0	0	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 72224.

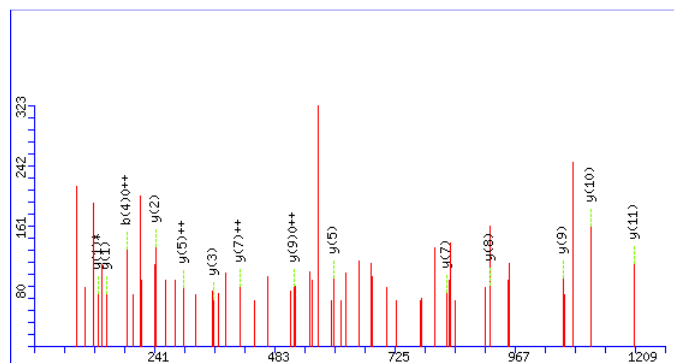
MS/MS Fragmentation of **VSGFSDLIEDVK**:

Found in **IPI00013488,IPI00221041,IPI00910824,IPI00916084,IPI00916361,IPI00916484,IPI00916715,IPI00917444**

Title: 3.1.1.1551.8

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120214ry¥120214ry_32R1-32_4_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							12
2	187.1077	94.0575	0	0	169.0972	85.0522	S	1209.5998	605.3035	1192.5732	596.7902	1191.5892	596.2982	11
3	244.1292	122.5682	0	0	226.1186	113.5629	G	1122.5677	561.7875	1105.5412	553.2742	1104.5572	552.7822	10
4	391.1976	196.1024	0	0	373.1870	187.0972	F	1065.5483	533.2768	1048.5197	524.7635	1047.5357	524.2715	9
5	478.2296	239.6185	0	0	460.2191	230.6132	S	918.4779	459.7426	901.4513	451.2293	900.4673	450.7373	8
6	593.2566	297.1319	0	0	575.2460	288.1266	D	831.4458	416.2266	814.4193	407.7133	813.4353	407.2213	7
7	706.3406	353.6740	0	0	688.3301	344.6687	L	716.4189	358.7131	699.3923	350.1998	698.4083	349.7078	6
8	819.4247	410.2160	0	0	801.4141	401.2107	I	603.3348	302.1710	586.3083	293.6578	585.3243	293.1658	5
9	948.4673	474.7373	0	0	930.4567	465.7320	E	490.2508	245.6290	473.2242	237.1157	472.2402	236.6237	4
10	1063.4942	532.2508	0	0	1045.4837	523.2455	D	361.2082	181.1077	344.1816	172.5944	343.1976	172.1024	3
11	1162.5626	581.7850	0	0	1144.5521	572.7797	V	246.1812	123.5942	229.1547	115.0810	0	0	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 72380.

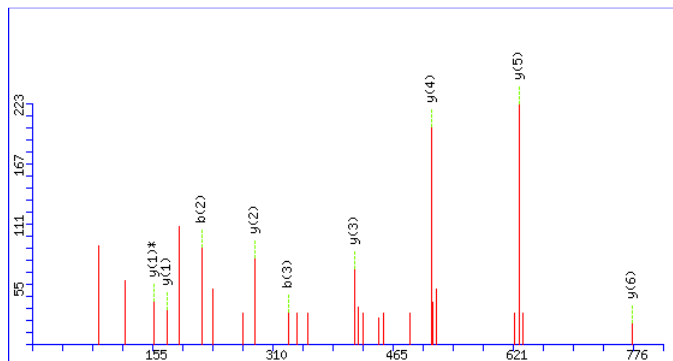
MS/MS Fragmentation of **AFIVELR**:

Found in **IP100218566;IP100218567;IP100241935;IP100295738;IP100909160**

Title: 2.1.1.3809.2

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							7
2	219.1128	110.0600	0	0	0	0	F	776.4665	388.7369	759.4400	380.2236	758.4559	379.7316	6
3	332.1969	166.6021	0	0	0	0	I	629.3981	315.2027	612.3715	306.6894	611.3875	306.1974	5
4	431.2653	216.1363	0	0	0	0	V	516.3140	258.6606	499.2875	250.1474	498.3035	249.6554	4
5	560.3079	280.6576	0	0	542.2973	271.6523	E	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
6	673.3919	337.1996	0	0	655.3814	328.1943	L	288.2030	144.6051	271.1765	136.0919	0	0	2
7							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 72409.

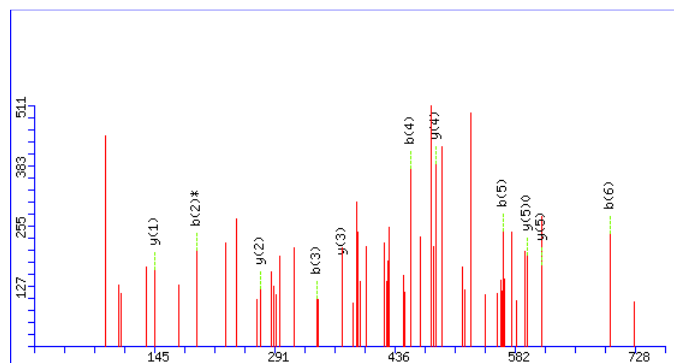
MS/MS Fragmentation of **GREILELVQK**:

Found in **IP100175092;IP100917006**

Title: 2.1.1.2031.3

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2.2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							10
2	214.1299	107.5686	197.1033	99.0553	0	0	R	1127.6783	564.3428	1110.6517	555.8295	1109.6677	555.3375	9
3	343.1724	172.0899	326.1459	163.5766	325.1619	163.0846	E	971.5772	486.2922	954.5506	477.7790	953.5666	477.2869	8
4	456.2565	228.6319	439.2300	220.1186	438.2459	219.6266	I	842.5346	421.7709	825.5080	413.2577	824.5240	412.7656	7
5	569.3406	285.1739	552.3140	276.6606	551.3300	276.1686	L	729.4505	365.2289	712.4240	356.7156	711.4400	356.2236	6
6	698.3832	349.6952	681.3566	341.1819	680.3726	340.6899	E	616.3665	308.6869	599.3399	300.1736	598.3559	299.6816	5
7	811.4672	406.2373	794.4407	397.7240	793.4567	397.2320	L	487.3239	244.1656	470.2973	235.6523	0	0	4
8	910.5356	455.7715	893.5091	447.2582	892.5251	446.7662	V	374.2398	187.6235	357.2132	179.1103	0	0	3
9	1038.5942	519.8007	1021.5677	511.2875	1020.5837	510.7955	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
10							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 72497.

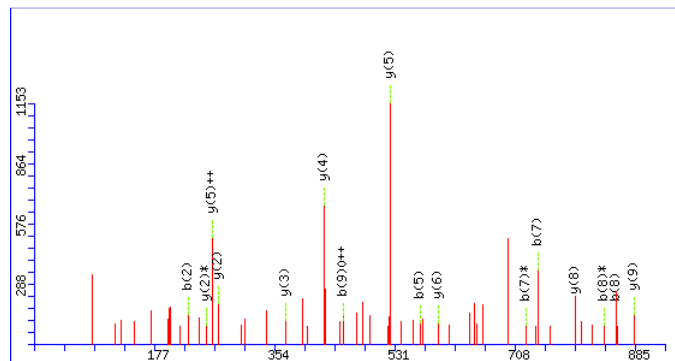
MS/MS Fragmentation of **ILNDLSSDAPGVPR**:

Found in **IP100027713;IP100218334;IP100433048;IP100922143;IP100924733;IP100925815;IP100927413;IP100927840;IP101011288**

Title: 2.1.1.2617.3

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120118ry¥120118ry_201B7-32_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							14
2	227.1754	114.0913	0	0	0	0	L	1340.6805	670.8439	1323.6539	662.3306	1322.6699	661.8386	13
3	341.2183	171.1128	324.1918	162.5995	0	0	N	1227.5964	614.3018	1210.5699	605.7886	1209.5858	605.2966	12
4	456.2453	228.6263	439.2187	220.1130	438.2347	219.6210	D	1113.5535	557.2804	1096.5269	548.7671	1095.5429	548.2751	11
5	569.3293	285.1683	552.3028	276.6550	551.3188	276.1630	L	998.5265	499.7669	981.5000	491.2536	980.5160	490.7616	10
6	656.3614	328.6843	639.3348	320.1710	638.3508	319.6790	S	885.4425	443.2249	868.4159	434.7116	867.4319	434.2196	9
7	743.3934	372.2003	726.3668	363.6871	725.3828	363.1951	S	798.4104	399.7089	781.3839	391.1956	780.3999	390.7036	8
8	858.4203	429.7138	841.3938	421.2005	840.4098	420.7085	D	711.3784	356.1928	694.3519	347.6796	693.3679	347.1876	7
9	929.4575	465.2324	912.4309	456.7191	911.4469	456.2271	A	596.3515	298.6794	579.3249	290.1661	0	0	6
10	1026.5102	513.7587	1009.4837	505.2455	1008.4997	504.7535	P	525.3144	263.1608	508.2878	254.6475	0	0	5
11	1083.5317	542.2695	1066.5051	533.7562	1065.5211	533.2642	G	428.2616	214.6344	411.2350	206.1212	0	0	4
12	1182.6001	591.8037	1165.5735	583.2904	1164.5895	582.7984	V	371.2401	186.1237	354.2136	177.6104	0	0	3
13	1279.6529	640.3301	1262.6263	631.8168	1261.6423	631.3248	P	272.1717	136.5895	255.1452	128.0762	0	0	2
14							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 72575.

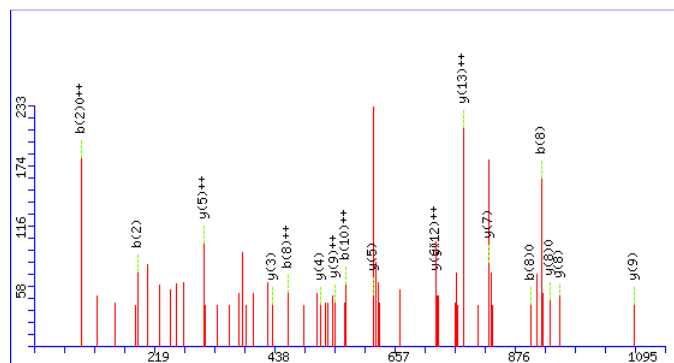
MS/MS Fragmentation of **STVEELHEPIPSLFR**:

Found in **IP100410487;IP100830092**

Title: 3.1.1.1281.5

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							15
2	189.0870	95.0471	0	0	171.0764	86.0418	T	1666.8799	833.9436	1649.8533	825.4303	1648.8693	824.9383	14
3	288.1554	144.5813	0	0	270.1448	135.5761	V	1565.8322	783.4197	1548.8057	774.9065	1547.8217	774.4145	13
4	417.1980	209.1026	0	0	399.1874	200.0974	E	1466.7638	733.8855	1449.7373	725.3723	1448.7532	724.8803	12
5	546.2406	273.6239	0	0	528.2300	264.6186	E	1337.7212	669.3642	1320.6947	660.8510	1319.7106	660.3590	11
6	659.3246	330.1660	0	0	641.3141	321.1607	L	1208.6786	604.8429	1191.6521	596.3297	1190.6681	595.8377	10
7	796.3836	398.6954	0	0	778.3730	389.6901	H	1095.5946	548.3009	1078.5680	539.7876	1077.5840	539.2956	9
8	925.4262	463.2167	0	0	907.4156	454.2114	E	958.5356	479.7715	941.5091	471.2582	940.5251	470.7662	8
9	1022.4789	511.7431	0	0	1004.4684	502.7378	P	829.4930	415.2502	812.4665	406.7369	811.4825	406.2449	7
10	1135.5630	568.2851	0	0	1117.5524	559.2798	I	732.4403	366.7238	715.4137	358.2105	714.4297	357.7185	6
11	1232.6157	616.8115	0	0	1214.6052	607.8062	P	619.3562	310.1817	602.3297	301.6685	601.3457	301.1765	5
12	1319.6478	660.3275	0	0	1301.6372	651.3222	S	522.3035	261.6554	505.2769	253.1421	504.2929	252.6501	4
13	1432.7318	716.8696	0	0	1414.7213	707.8643	L	435.2714	218.1394	418.2449	209.6261	0	0	3
14	1579.8003	790.4038	0	0	1561.7897	781.3985	F	322.1874	161.5973	305.1608	153.0840	0	0	2
15							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 72826.

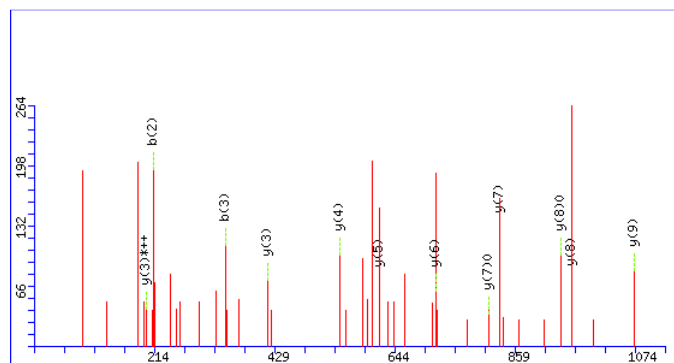
MS/MS Fragmentation of **VLELTAENER**:

Found in **IP100289773;IP100977352**

Title: 2.1.1.759.7

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							10
2	213.1598	107.0835	0	0	0	0	L	1074.5426	537.7749	1057.5160	529.2617	1056.5320	528.7696	9
3	342.2023	171.6048	0	0	324.1918	162.5995	E	961.4585	481.2329	944.4320	472.7196	943.4480	472.2276	8
4	455.2864	228.1468	0	0	437.2758	219.1416	L	832.4159	416.7116	815.3894	408.1983	814.4054	407.7063	7
5	556.3341	278.6707	0	0	538.3235	269.6654	T	719.3319	360.1696	702.3053	351.6563	701.3213	351.1643	6
6	627.3712	314.1892	0	0	609.3606	305.1840	A	618.2842	309.6457	601.2576	301.1325	600.2736	300.6404	5
7	756.4138	378.7105	0	0	738.4032	369.7053	E	547.2471	274.1272	530.2205	265.6139	529.2365	265.1219	4
8	870.4567	435.7320	853.4302	427.2187	852.4462	426.7267	N	418.2045	209.6059	401.1779	201.0926	400.1939	200.6006	3
9	999.4993	500.2533	982.4728	491.7400	981.4888	491.2480	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 73023.

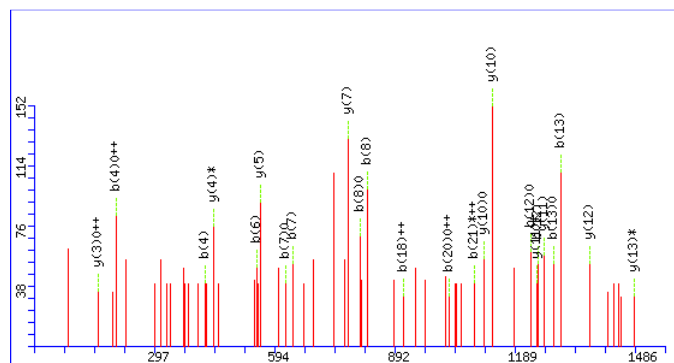
MS/MS Fragmentation of **EASHAGSWYTASGPQLNAQLEGWLSQVQSTK:**

Found in **IP100032426;IP100893200;IP100893861;IP101015226**

Title: 4.1.1.912.9

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2_4.mgf

ProteinPilot Peptide Confidence > 99%

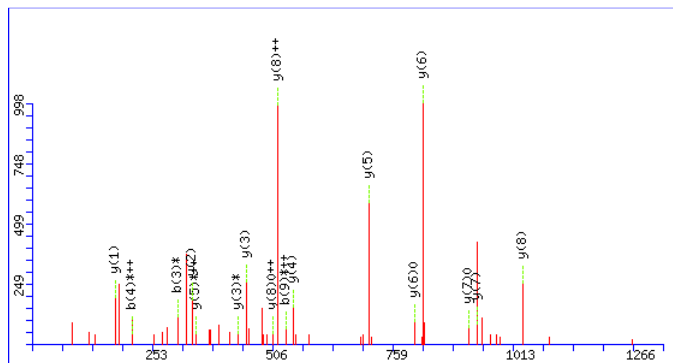


#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							31
2	201.0870	101.0471	0	0	183.0764	92.0418	A	3202.5552	1601.7812	3185.5287	1593.2680	3184.5447	1592.7760	30
3	288.1190	144.5631	0	0	270.1084	135.5579	S	3131.5181	1566.2627	3114.4916	1557.7494	3113.5075	1557.2574	29
4	425.1779	213.0926	0	0	407.1674	204.0873	H	3044.4861	1522.7467	3027.4595	1514.2334	3026.4755	1513.7414	28
5	496.2150	248.6112	0	0	478.2045	239.6059	A	2907.4272	1454.2172	2890.4006	1445.7039	2889.4166	1445.2119	27
6	553.2365	277.1219	0	0	535.2259	268.1166	G	2836.3901	1418.6987	2819.3635	1410.1854	2818.3795	1409.6934	26
7	640.2685	320.6379	0	0	622.2580	311.6326	S	2779.3686	1390.1879	2762.3420	1381.6747	2761.3580	1381.1826	25
8	826.3478	413.6776	0	0	808.3373	404.6723	W	2692.3366	1346.6719	2675.3100	1338.1586	2674.3260	1337.6666	24
9	989.4112	495.2092	0	0	971.4006	486.2039	Y	2506.2572	1253.6323	2489.2307	1245.1190	2488.2467	1244.6270	23
10	1090.4589	545.7331	0	0	1072.4483	536.7278	T	2343.1939	1172.1006	2326.1674	1163.5873	2325.1834	1163.0953	22
11	1161.4960	581.2516	0	0	1143.4854	572.2463	A	2242.1462	1121.5768	2225.1197	1113.0635	2224.1357	1112.5715	21
12	1248.5280	624.7676	0	0	1230.5174	615.7624	S	2171.1091	1086.0582	2154.0826	1077.5449	2153.0986	1077.0529	20
13	1305.5495	653.2784	0	0	1287.5389	644.2731	G	2084.0771	1042.5422	2067.0505	1034.0289	2066.0665	1033.5369	19
14	1402.6022	701.8047	0	0	1384.5917	692.7995	P	2027.0556	1014.0315	2010.0291	1005.5182	2009.0451	1005.0262	18
15	1530.6608	765.8340	1513.6342	757.3208	1512.6502	756.8288	Q	1930.0029	965.5051	1912.9763	956.9918	1911.9923	956.4998	17
16	1643.7449	822.3761	1626.7183	813.8628	1625.7343	813.3708	L	1801.9443	901.4758	1784.9177	892.9625	1783.9337	892.4705	16
17	1757.7878	879.3975	1740.7612	870.8843	1739.7772	870.3923	N	1688.8602	844.9338	1671.8337	836.4205	1670.8497	835.9285	15
18	1828.8249	914.9161	1811.7984	906.4028	1810.8143	905.9108	A	1574.8173	787.9123	1557.7907	779.3990	1556.8067	778.9070	14
19	1956.8835	978.9454	1939.8569	970.4321	1938.8729	969.9401	Q	1503.7802	752.3937	1486.7536	743.8805	1485.7696	743.3884	13
20	2069.9675	1035.4874	2052.9410	1026.9741	2051.9570	1026.4821	L	1375.7216	688.3644	1358.6951	679.8512	1357.7110	679.3592	12
21	2199.0101	1100.0087	2181.9836	1091.4954	2180.9996	1091.0034	E	1262.6375	631.8224	1245.6110	623.3091	1244.6270	622.8171	11
22	2256.0316	1128.5194	2239.0051	1120.0062	2238.0210	1119.5142	G	1133.5949	567.3011	1116.5684	558.7878	1115.5844	558.2958	10
23	2442.1109	1221.5591	2425.0844	1213.0458	2424.1004	1212.5538	W	1076.5735	538.7904	1059.5469	530.2771	1058.5629	529.7851	9
24	2555.1950	1278.1011	2538.1684	1269.5879	2537.1844	1269.0958	L	890.4942	445.7507	873.4676	437.2374	872.4836	436.7454	8
25	2642.2270	1321.6171	2625.2005	1313.1039	2624.2164	1312.6119	S	777.4101	389.2087	760.3836	380.6954	759.3995	380.2034	7
26	2770.2856	1385.6464	2753.2590	1377.1332	2752.2750	1376.6411	Q	690.3781	345.6927	673.3515	337.1794	672.3675	336.6874	6
27	2869.3540	1435.1806	2852.3274	1426.6674	2851.3434	1426.1754	V	562.3195	281.6634	545.2930	273.1501	544.3089	272.6581	5
28	2997.4126	1499.2099	2980.3860	1490.6967	2979.4020	1490.2046	Q	463.2511	232.1292	446.2245	223.6159	445.2405	223.1239	4
29	3084.4446	1542.7259	3067.4181	1534.2127	3066.4340	1533.7207	S	335.1925	168.0999	318.1660	159.5866	317.1819	159.0946	3
30	3185.4923	1593.2498	3168.4657	1584.7365	3167.4817	1584.2445	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
31							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 73486.

MS/MS Fragmentation of **QVPLDCVLYR**: -17.026549@N-term(Q),57.021465@C:6
 Found in **IP100031630;IP100795159;IP100797732;IP100952617;IP100952781;IP101021588;IP101022799**
 Title: 3.1.1.2513.7
 Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_2_3.mgf
 ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233	0	0	Q							10
2	228.1343	114.5708	211.1077	106.0575	0	0	V	1134.5976	567.8024	1117.5710	559.2892	1116.5870	558.7972	9
3	325.1870	163.0972	308.1605	154.5839	0	0	P	1035.5292	518.2682	1018.5026	509.7550	1017.5186	509.2629	8
4	438.2711	219.6392	421.2445	211.1259	0	0	L	938.4764	469.7418	921.4499	461.2286	920.4659	460.7366	7
5	553.2980	277.1527	536.2715	268.6394	535.2875	268.1474	D	825.3924	413.1998	808.3658	404.6865	807.3818	404.1945	6
6	713.3287	357.1680	696.3021	348.6547	695.3181	348.1627	C	710.3654	355.6863	693.3389	347.1731	0	0	5
7	812.3971	406.7022	795.3706	398.1889	794.3865	397.6969	V	550.3348	275.6710	533.3082	267.1577	0	0	4
8	925.4812	463.2442	908.4546	454.7309	907.4706	454.2389	L	451.2663	226.1368	434.2398	217.6235	0	0	3
9	1088.5445	544.7759	1071.5179	536.2626	1070.5339	535.7706	Y	338.1823	169.5948	321.1557	161.0815	0	0	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 73555.

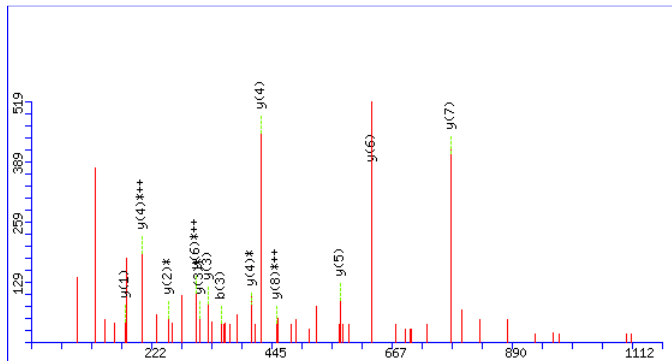
MS/MS Fragmentation of **GFFGFPGPR**:

Found in **IP100010440;IP100479876;IP100604587;IP100641973;IP100878396;IP100954523**

Title: 3.1.1.1632.3

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120210ry¥120210ry_585A1-55_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							9
2	205.0972	103.0522	0	0	0	0	F	924.4726	462.7400	907.4461	454.2267	0	0	8
3	352.1656	176.5864	0	0	0	0	F	777.4042	389.2058	760.3777	380.6925	0	0	7
4	409.1870	205.0972	0	0	0	0	G	630.3358	315.6715	613.3093	307.1583	0	0	6
5	556.2554	278.6314	0	0	0	0	F	573.3144	287.1608	556.2878	278.6475	0	0	5
6	653.3082	327.1577	0	0	0	0	P	426.2459	213.6266	409.2194	205.1133	0	0	4
7	710.3297	355.6685	0	0	0	0	G	329.1932	165.1002	312.1666	156.5870	0	0	3
8	807.3824	404.1949	0	0	0	0	P	272.1717	136.5895	255.1452	128.0762	0	0	2
9							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 73637.

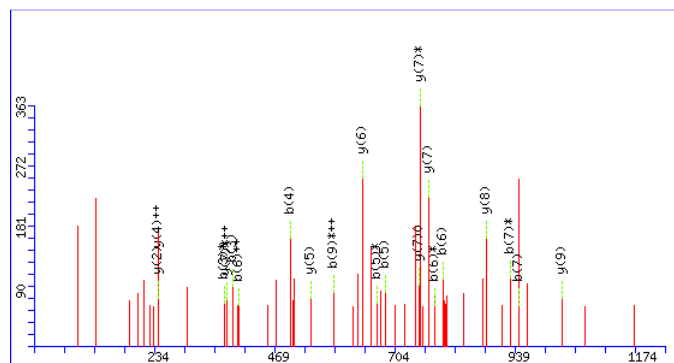
MS/MS Fragmentation of **CNNLWLFLETGQLPK: 57.021465@C:1**

Found in **IP100063300**

Title: 4.1.1.1229.3

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	161.0379	81.0226	0	0	0	0	C							15
2	275.0809	138.0441	258.0543	129.5308	0	0	N	1672.9057	836.9565	1655.8792	828.4432	1654.8952	827.9512	14
3	389.1238	195.0655	372.0972	186.5523	0	0	N	1558.8628	779.9350	1541.8362	771.4218	1540.8522	770.9298	13
4	502.2078	251.6076	485.1813	243.0943	0	0	L	1444.8199	722.9136	1427.7933	714.4003	1426.8093	713.9083	12
5	688.2872	344.6472	671.2606	336.1339	0	0	W	1331.7358	666.3715	1314.7093	657.8583	1313.7252	657.3663	11
6	801.3712	401.1892	784.3447	392.6760	0	0	L	1145.6565	573.3319	1128.6299	564.8186	1127.6459	564.3266	10
7	948.4396	474.7235	931.4131	466.2102	0	0	F	1032.5724	516.7898	1015.5459	508.2766	1014.5619	507.7846	9
8	1061.5237	531.2655	1044.4971	522.7522	0	0	L	885.5040	443.2556	868.4775	434.7424	867.4934	434.2504	8
9	1190.5663	595.7868	1173.5397	587.2735	1172.5557	586.7815	E	772.4199	386.7136	755.3934	378.2003	754.4094	377.7083	7
10	1291.6140	646.3106	1274.5874	637.7973	1273.6034	637.3053	T	643.3774	322.1923	626.3508	313.6790	625.3668	313.1870	6
11	1348.6354	674.8214	1331.6089	666.3081	1330.6249	665.8161	G	542.3297	271.6685	525.3031	263.1552	0	0	5
12	1476.6940	738.8506	1459.6675	730.3374	1458.6834	729.8454	Q	485.3082	243.1577	468.2817	234.6445	0	0	4
13	1589.7781	795.3927	1572.7515	786.8794	1571.7675	786.3874	L	357.2496	179.1285	340.2231	170.6152	0	0	3
14	1686.8308	843.9191	1669.8043	835.4058	1668.8203	834.9138	P	244.1656	122.5864	227.1390	114.0731	0	0	2
15							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 73714.

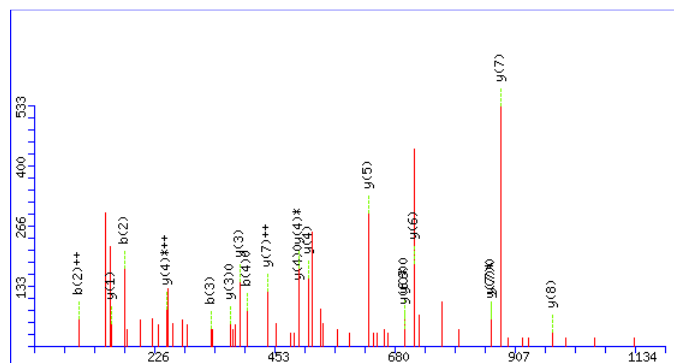
MS/MS Fragmentation of **AVYSIQNEK**:

Found in **IP100016776;IP100794048;IP100945326;IP100946225**

Title: 1.1.1.7579.10

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							9
2	171.1128	86.0600	0	0	0	0	V	980.5047	490.7560	963.4782	482.2427	962.4942	481.7507	8
3	334.1761	167.5917	0	0	0	0	Y	881.4363	441.2218	864.4098	432.7085	863.4258	432.2165	7
4	421.2082	211.1077	0	0	403.1976	202.1024	S	718.3730	359.6901	701.3464	351.1769	700.3624	350.6849	6
5	534.2922	267.6498	0	0	516.2817	258.6445	I	631.3410	316.1741	614.3144	307.6608	613.3304	307.1688	5
6	662.3508	331.6790	645.3243	323.1658	644.3402	322.6738	Q	518.2569	259.6321	501.2304	251.1188	500.2463	250.6268	4
7	776.3937	388.7005	759.3672	380.1872	758.3832	379.6952	N	390.1983	195.6028	373.1718	187.0895	372.1878	186.5975	3
8	905.4363	453.2218	888.4098	444.7085	887.4258	444.2165	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
9							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 73718.

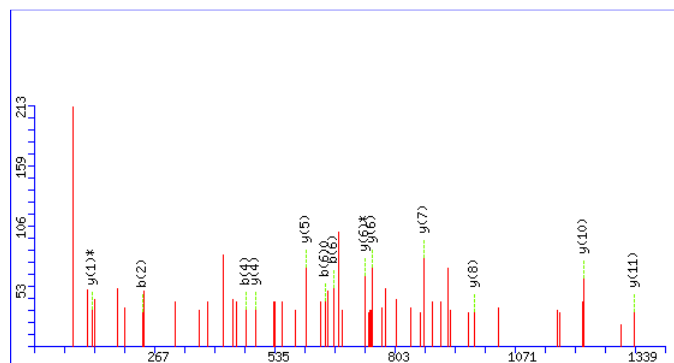
MS/MS Fragmentation of **NQDNPVIDEIDFLEAFK**:

Found in **IP100031608;IP100890778;IP101012737**

Title: 4.1.1.3564.3

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							17
2	243.1088	122.0580	226.0822	113.5448	0	0	Q	1892.9276	946.9675	1875.9011	938.4542	1874.9171	937.9622	16
3	358.1357	179.5715	341.1092	171.0582	340.1252	170.5662	D	1764.8691	882.9382	1747.8425	874.4249	1746.8585	873.9329	15
4	472.1787	236.5930	455.1521	228.0797	454.1681	227.5877	N	1649.8421	825.4247	1632.8156	816.9114	1631.8316	816.4194	14
5	569.2314	285.1193	552.2049	276.6061	551.2209	276.1141	P	1535.7992	768.4032	1518.7726	759.8900	1517.7886	759.3979	13
6	668.2998	334.6536	651.2733	326.1403	650.2893	325.6483	V	1438.7464	719.8768	1421.7199	711.3636	1420.7359	710.8716	12
7	781.3839	391.1956	764.3573	382.6823	763.3733	382.1903	I	1339.6780	670.3426	1322.6515	661.8294	1321.6674	661.3374	11
8	896.4108	448.7091	879.3843	440.1958	878.4003	439.7038	D	1226.5939	613.8006	1209.5674	605.2873	1208.5834	604.7953	10
9	1025.4534	513.2304	1008.4269	504.7171	1007.4429	504.2251	E	1111.5670	556.2871	1094.5405	547.7739	1093.5564	547.2819	9
10	1138.5375	569.7724	1121.5109	561.2591	1120.5269	560.7671	I	982.5244	491.7658	965.4979	483.2526	964.5138	482.7606	8
11	1253.5644	627.2859	1236.5379	618.7726	1235.5539	618.2806	D	869.4403	435.2238	852.4138	426.7105	851.4298	426.2185	7
12	1400.6329	700.8201	1383.6063	692.3068	1382.6223	691.8148	F	754.4134	377.7103	737.3869	369.1971	736.4028	368.7051	6
13	1513.7169	757.3621	1496.6904	748.8488	1495.7063	748.3568	L	607.3450	304.1761	590.3184	295.6629	589.3344	295.1709	5
14	1642.7595	821.8834	1625.7330	813.3701	1624.7489	812.8781	E	494.2609	247.6341	477.2344	239.1208	476.2504	238.6288	4
15	1713.7966	857.4019	1696.7701	848.8887	1695.7861	848.3967	A	365.2183	183.1128	348.1918	174.5995	0	0	3
16	1860.8650	930.9362	1843.8385	922.4229	1842.8545	921.9309	F	294.1812	147.5942	277.1547	139.0810	0	0	2
17							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 73767.

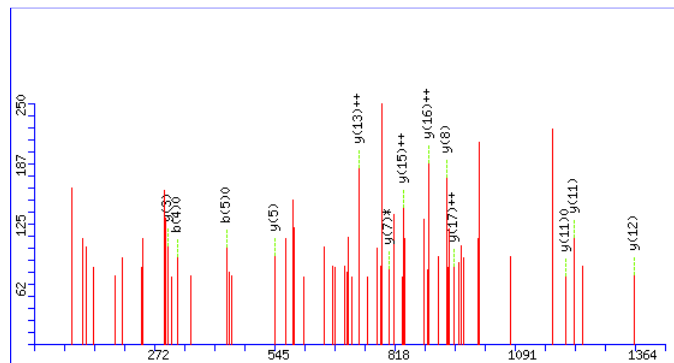
MS/MS Fragmentation of **AGTLIMALHDSSDYLLSAK**:

Found in **IP100305304;IP100472101;IP100642378**

Title: 3.1.1.4007.5

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							20
2	129.0659	65.0366	0	0	0	0	G	2064.0318	1032.5195	2047.0052	1024.0063	2046.0212	1023.5142	19
3	230.1135	115.5604	0	0	212.1030	106.5551	T	2007.0103	1004.0088	1989.9838	995.4955	1988.9998	995.0035	18
4	343.1976	172.1024	0	0	325.1870	163.0972	L	1905.9626	953.4850	1888.9361	944.9717	1887.9521	944.4797	17
5	456.2817	228.6445	0	0	438.2711	219.6392	I	1792.8786	896.9429	1775.8520	888.4297	1774.8680	887.9376	16
6	587.3221	294.1647	0	0	569.3116	285.1594	M	1679.7945	840.4009	1662.7680	831.8876	1661.7839	831.3956	15
7	658.3593	329.6833	0	0	640.3487	320.6780	A	1548.7540	774.8807	1531.7275	766.3674	1530.7435	765.8754	14
8	771.4433	386.2253	0	0	753.4328	377.2200	L	1477.7169	739.3621	1460.6904	730.8488	1459.7063	730.3568	13
9	908.5022	454.7548	0	0	890.4917	445.7495	H	1364.6328	682.8201	1347.6063	674.3068	1346.6223	673.8148	12
10	1023.5292	512.2682	0	0	1005.5186	503.2629	D	1227.5739	614.2906	1210.5474	605.7773	1209.5634	605.2853	11
11	1110.5612	555.7842	0	0	1092.5506	546.7790	S	1112.5470	556.7771	1095.5204	548.2639	1094.5364	547.7719	10
12	1197.5932	599.3003	0	0	1179.5827	590.2950	S	1025.5150	513.2611	1008.4884	504.7478	1007.5044	504.2558	9
13	1312.6202	656.8137	0	0	1294.6096	647.8084	D	938.4829	469.7451	921.4564	461.2318	920.4724	460.7398	8
14	1475.6835	738.3454	0	0	1457.6729	729.3401	Y	823.4560	412.2316	806.4294	403.7184	805.4454	403.2264	7
15	1588.7676	794.8874	0	0	1570.7570	785.8821	L	660.3927	330.7000	643.3661	322.1867	642.3821	321.6947	6
16	1701.8516	851.4295	0	0	1683.8411	842.4242	L	547.3086	274.1579	530.2821	265.6447	529.2980	265.1527	5
17	1830.8942	915.9508	0	0	1812.8837	906.9455	E	434.2245	217.6159	417.1980	209.1026	416.2140	208.6106	4
18	1917.9263	959.4668	0	0	1899.9157	950.4615	S	305.1819	153.0946	288.1554	144.5813	287.1714	144.0893	3
19	1988.9634	994.9853	0	0	1970.9528	985.9800	A	218.1499	109.5786	201.1234	101.0653	0	0	2
20							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 73882.

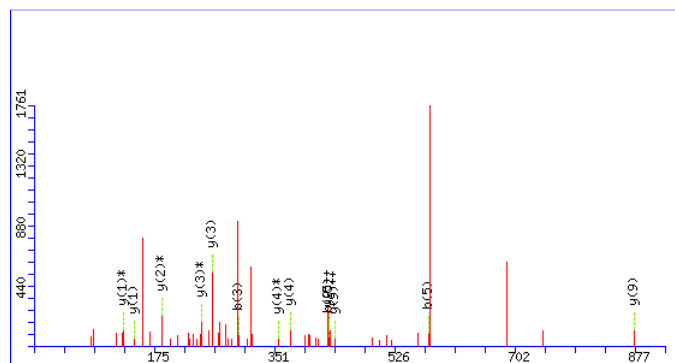
MS/MS Fragmentation of **EGYLGGLGQK**:

Found in **IP100982629**

Title: 4.1.1.397.2

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							10
2	187.0713	94.0393	0	0	169.0608	85.0340	G	877.5142	439.2607	860.4876	430.7475	0	0	9
3	300.1554	150.5813	0	0	282.1448	141.5761	I	820.4927	410.7500	803.4662	402.2367	0	0	8
4	463.2187	232.1130	0	0	445.2082	223.1077	Y	707.4087	354.2080	690.3821	345.6947	0	0	7
5	576.3028	288.6550	0	0	558.2922	279.6498	L	544.3453	272.6763	527.3188	264.1630	0	0	6
6	633.3243	317.1658	0	0	615.3137	308.1605	G	431.2613	216.1343	414.2347	207.6210	0	0	5
7	746.4083	373.7078	0	0	728.3978	364.7025	L	374.2398	187.6235	357.2132	179.1103	0	0	4
8	803.4298	402.2185	0	0	785.4192	393.2132	G	261.1557	131.0815	244.1292	122.5682	0	0	3
9	860.4512	430.7293	0	0	842.4407	421.7240	G	204.1343	102.5708	187.1077	94.0575	0	0	2
10							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 74043.

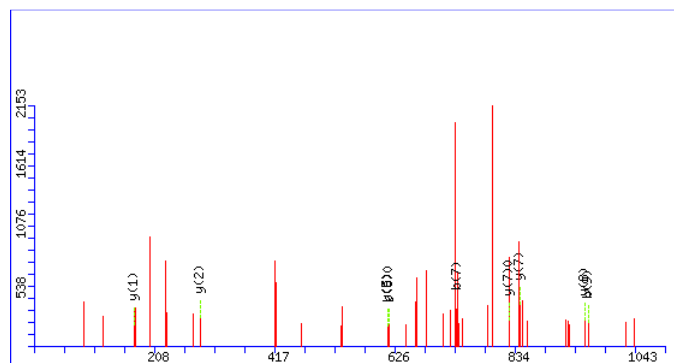
MS/MS Fragmentation of **ALSQHPNLDDLPNR: 0.984015@N:9**

Found in **IP100215760;IP100921588**

Title: 2.1.1.3446.5

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_3.2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							15
2	185.1285	93.0679	0	0	0	0	L	1620.7976	810.9024	1603.7711	802.3892	1602.7871	801.8972	14
3	272.1605	136.5839	0	0	254.1499	127.5786	S	1507.7136	754.3604	1490.6870	745.8471	1489.7030	745.3551	13
4	400.2191	200.6132	383.1925	192.0999	382.2085	191.6079	Q	1420.6815	710.8444	1403.6550	702.3311	1402.6710	701.8391	12
5	537.2780	269.1426	520.2514	260.6293	519.2674	260.1373	H	1292.6230	646.8151	1275.5964	638.3018	1274.6124	637.8098	11
6	634.3307	317.6690	617.3042	309.1557	616.3202	308.6637	P	1155.5640	578.2857	1138.5375	569.7724	1137.5535	569.2804	10
7	735.3784	368.1928	718.3519	359.6796	717.3679	359.1876	T	1058.5113	529.7593	1041.4847	521.2460	1040.5007	520.7540	9
8	848.4625	424.7349	831.4359	416.2216	830.4519	415.7296	L	957.4636	479.2354	940.4370	470.7222	939.4530	470.2302	8
9	963.4894	482.2483	946.4629	473.7351	945.4789	473.2431	N	844.3795	422.6934	827.3530	414.1801	826.3690	413.6881	7
10	1078.5164	539.7618	1061.4898	531.2485	1060.5058	530.7565	D	729.3526	365.1799	712.3260	356.6667	711.3420	356.1747	6
11	1193.5433	597.2753	1176.5168	588.7620	1175.5327	588.2700	D	614.3256	307.6665	597.2991	299.1532	596.3151	298.6612	5
12	1306.6274	653.8173	1289.6008	645.3040	1288.6168	644.8120	L	499.2987	250.1530	482.2722	241.6397	0	0	4
13	1403.6801	702.3437	1386.6536	693.8304	1385.6696	693.3384	P	386.2146	193.6110	369.1881	185.0977	0	0	3
14	1517.7231	759.3652	1500.6965	750.8519	1499.7125	750.3599	N	289.1619	145.0846	272.1353	136.5713	0	0	2
15							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 74347.

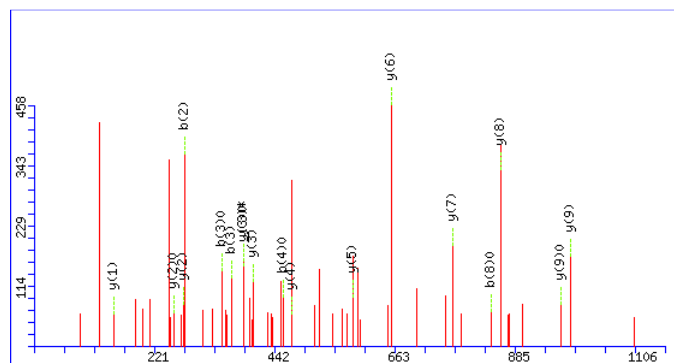
MS/MS Fragmentation of **FESIAIAQEK**:

Found in **IP100375577**

Title: 2.1.1.1357.7

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							10
2	277.1183	139.0628	0	0	259.1077	130.0575	E	988.5310	494.7691	971.5044	486.2558	970.5204	485.7638	9
3	364.1503	182.5788	0	0	346.1397	173.5735	S	859.4884	430.2478	842.4618	421.7345	841.4778	421.2425	8
4	477.2344	239.1208	0	0	459.2238	230.1155	I	772.4563	386.7318	755.4298	378.2185	754.4458	377.7265	7
5	548.2715	274.6394	0	0	530.2609	265.6341	A	659.3723	330.1898	642.3457	321.6765	641.3617	321.1845	6
6	661.3556	331.1814	0	0	643.3450	322.1761	I	588.3352	294.6712	571.3086	286.1579	570.3246	285.6659	5
7	732.3927	366.7000	0	0	714.3821	357.6947	A	475.2511	238.1292	458.2245	229.6159	457.2405	229.1239	4
8	860.4512	430.7293	843.4247	422.2160	842.4407	421.7240	Q	404.2140	202.6106	387.1874	194.0974	386.2034	193.6053	3
9	989.4938	495.2506	972.4673	486.7373	971.4833	486.2453	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
10							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 74484.

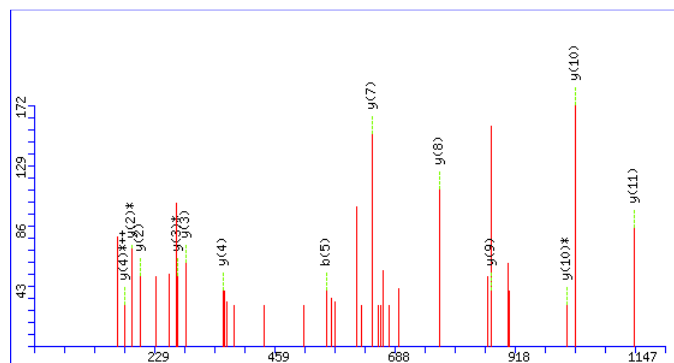
MS/MS Fragmentation of **SVICVEGNIASGK: 57.021465@C:4**

Found in **IP100215650;IP100337439;IP100939299**

Title: 2.1.1.1403.9

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120201ry¥120201ry_aHDF1388-P9_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							13
2	187.1077	94.0575	0	0	169.0972	85.0522	V	1246.6460	623.8266	1229.6195	615.3134	1228.6354	614.8214	12
3	300.1918	150.5995	0	0	282.1812	141.5942	I	1147.5776	574.2924	1130.5510	565.7792	1129.5670	565.2871	11
4	460.2224	230.6149	0	0	442.2119	221.6096	C	1034.4935	517.7504	1017.4670	509.2371	1016.4830	508.7451	10
5	559.2908	280.1491	0	0	541.2803	271.1438	V	874.4629	437.7351	857.4363	429.2218	856.4523	428.7298	9
6	688.3334	344.6704	0	0	670.3229	335.6651	E	775.3945	388.2009	758.3679	379.6876	757.3839	379.1956	8
7	745.3549	373.1811	0	0	727.3443	364.1758	G	646.3519	323.6796	629.3253	315.1663	628.3413	314.6743	7
8	859.3978	430.2026	842.3713	421.6893	841.3873	421.1973	N	589.3304	295.1688	572.3039	286.6556	571.3198	286.1636	6
9	972.4819	486.7446	955.4553	478.2313	954.4713	477.7393	I	475.2875	238.1474	458.2609	229.6341	457.2769	229.1421	5
10	1043.5190	522.2631	1026.4925	513.7499	1025.5084	513.2579	A	362.2034	181.6053	345.1769	173.0921	344.1928	172.6001	4
11	1130.5510	565.7792	1113.5245	557.2659	1112.5405	556.7739	S	291.1663	146.0868	274.1397	137.5735	273.1557	137.0815	3
12	1187.5725	594.2899	1170.5460	585.7766	1169.5619	585.2846	G	204.1343	102.5708	187.1077	94.0575	0	0	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 74531.

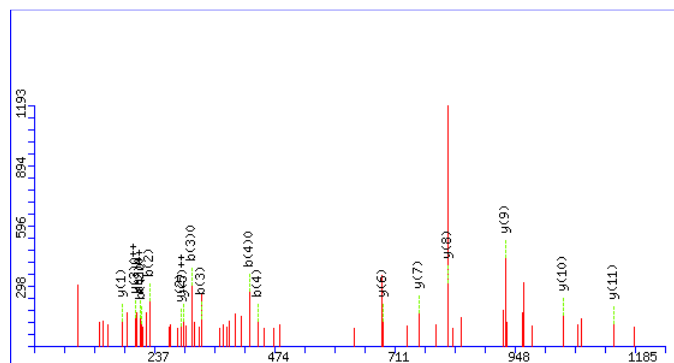
MS/MS Fragmentation of **DLTLLGATAVEDR**:

Found in **IP100255653;IP100456983;IP100470412;IP100848250**

Title: 3.1.1.643.8

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							13
2	229.1183	115.0628	0	0	211.1077	106.0575	L	1258.7001	629.8537	1241.6736	621.3404	1240.6896	620.8484	12
3	330.1660	165.5866	0	0	312.1554	156.5813	T	1145.6161	573.3117	1128.5895	564.7984	1127.6055	564.3064	11
4	443.2500	222.1287	0	0	425.2395	213.1234	L	1044.5684	522.7878	1027.5419	514.2746	1026.5578	513.7826	10
5	556.3341	278.6707	0	0	538.3235	269.6654	L	931.4843	466.2458	914.4578	457.7325	913.4738	457.2405	9
6	613.3556	307.1814	0	0	595.3450	298.1761	G	818.4003	409.7038	801.3737	401.1905	800.3897	400.6985	8
7	684.3927	342.7000	0	0	666.3821	333.6947	A	761.3788	381.1930	744.3523	372.6798	743.3682	372.1878	7
8	785.4403	393.2238	0	0	767.4298	384.2185	T	690.3417	345.6745	673.3151	337.1612	672.3311	336.6692	6
9	856.4775	428.7424	0	0	838.4669	419.7371	A	589.2940	295.1506	572.2675	286.6374	571.2835	286.1454	5
10	955.5459	478.2766	0	0	937.5353	469.2713	V	518.2569	259.6321	501.2304	251.1188	500.2463	250.6268	4
11	1084.5885	542.7979	0	0	1066.5779	533.7926	E	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	3
12	1199.6154	600.3113	0	0	1181.6048	591.3061	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
13							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 74631.

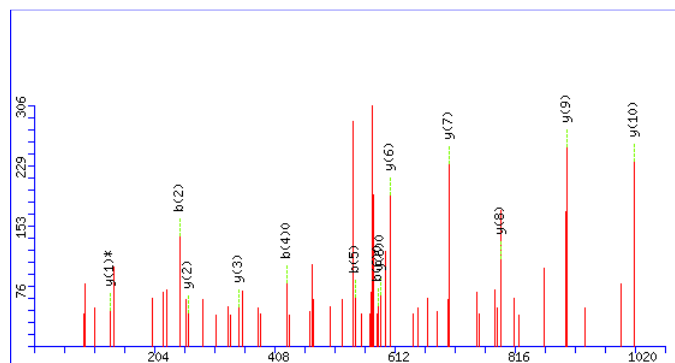
MS/MS Fragmentation of **MDLSVGSLSDK**:

Found in **IP100152296;IP100385511;IP100940033**

Title: 2.1.1.2727.5

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	132.0478	66.5275	0	0	0	0	M							11
2	247.0747	124.0410	0	0	229.0641	115.0357	D	1020.5208	510.7640	1003.4942	502.2508	1002.5102	501.7587	10
3	360.1588	180.5830	0	0	342.1482	171.5777	L	905.4938	453.2506	888.4673	444.7373	887.4833	444.2453	9
4	447.1908	224.0990	0	0	429.1802	215.0938	S	792.4098	396.7085	775.3832	388.1952	774.3992	387.7032	8
5	546.2592	273.6332	0	0	528.2486	264.6280	V	705.3777	353.1925	688.3512	344.6792	687.3672	344.1872	7
6	603.2807	302.1440	0	0	585.2701	293.1387	G	606.3093	303.6583	589.2828	295.1450	588.2988	294.6530	6
7	690.3127	345.6600	0	0	672.3021	336.6547	S	549.2879	275.1476	532.2613	266.6343	531.2773	266.1423	5
8	803.3968	402.2020	0	0	785.3862	393.1967	L	462.2558	231.6316	445.2293	223.1183	444.2453	222.6263	4
9	890.4288	445.7180	0	0	872.4182	436.7128	S	349.1718	175.0895	332.1452	166.5763	331.1612	166.0842	3
10	1005.4557	503.2315	0	0	987.4452	494.2262	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
11							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 74800.

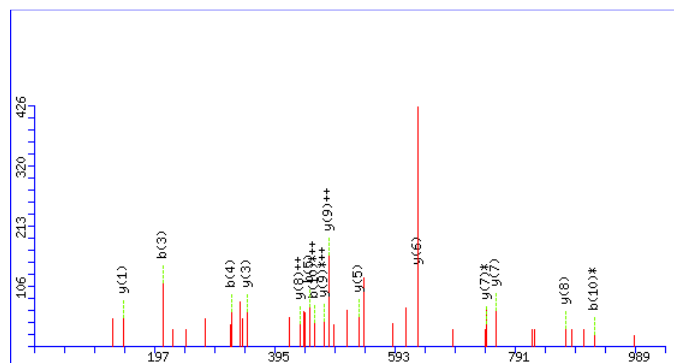
MS/MS Fragmentation of **GGPNQPGQGFK**:

Found in **IP100217810**

Title: 1.1.1.7138.10

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							11
2	115.0502	58.0287	0	0	0	0	G	1029.5112	515.2592	1012.4847	506.7460	0	0	10
3	212.1030	106.5551	0	0	0	0	P	972.4898	486.7485	955.4632	478.2352	0	0	9
4	326.1459	163.5766	309.1193	155.0633	0	0	N	875.4370	438.2221	858.4104	429.7089	0	0	8
5	454.2045	227.6059	437.1779	219.0926	0	0	Q	761.3941	381.2007	744.3675	372.6874	0	0	7
6	551.2572	276.1323	534.2307	267.6190	0	0	P	633.3355	317.1714	616.3089	308.6581	0	0	6
7	608.2787	304.6430	591.2522	296.1297	0	0	G	536.2827	268.6450	519.2562	260.1317	0	0	5
8	736.3373	368.6723	719.3107	360.1590	0	0	Q	479.2613	240.1343	462.2347	231.6210	0	0	4
9	793.3587	397.1830	776.3322	388.6697	0	0	G	351.2027	176.1050	334.1761	167.5917	0	0	3
10	940.4272	470.7172	923.4006	462.2039	0	0	F	294.1812	147.5942	277.1547	139.0810	0	0	2
11							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 75080.

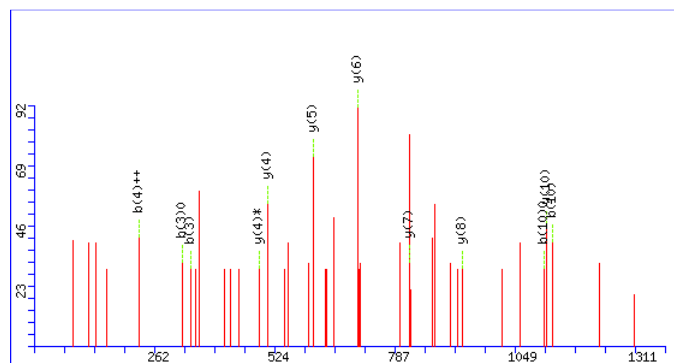
MS/MS Fragmentation of **LLDDEVFPDSPLLVVYATR**:

Found in **IP100010486;IP100219602;IP101015693**

Title: 4.1.1.1914.5

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							19
2	227.1754	114.0913	0	0	0	0	L	2049.0539	1025.0306	2032.0274	1016.5173	2031.0433	1016.0253	18
3	342.2023	171.6048	0	0	324.1918	162.5995	D	1935.9698	968.4886	1918.9433	959.9753	1917.9593	959.4833	17
4	457.2293	229.1183	0	0	439.2187	220.1130	D	1820.9429	910.9751	1803.9163	902.4618	1802.9323	901.9698	16
5	586.2719	293.6396	0	0	568.2613	284.6343	E	1705.9159	853.4616	1688.8894	844.9483	1687.9054	844.4563	15
6	685.3403	343.1738	0	0	667.3297	334.1685	V	1576.8734	788.9403	1559.8468	780.4270	1558.8628	779.9350	14
7	782.3931	391.7002	0	0	764.3825	382.6949	P	1477.8049	739.4061	1460.7784	730.8928	1459.7944	730.4008	13
8	929.4615	465.2344	0	0	911.4509	456.2291	F	1380.7522	690.8797	1363.7256	682.3665	1362.7416	681.8744	12
9	1044.4884	522.7478	0	0	1026.4779	513.7426	D	1233.6838	617.3455	1216.6572	608.8322	1215.6732	608.3402	11
10	1131.5204	566.2639	0	0	1113.5099	557.2586	S	1118.6568	559.8320	1101.6303	551.3188	1100.6463	550.8268	10
11	1228.5732	614.7902	0	0	1210.5626	605.7850	P	1031.6248	516.3160	1014.5982	507.8028	1013.6142	507.3108	9
12	1341.6573	671.3323	0	0	1323.6467	662.3270	L	934.5720	467.7897	917.5455	459.2764	916.5615	458.7844	8
13	1454.7413	727.8743	0	0	1436.7308	718.8690	L	821.4880	411.2476	804.4614	402.7343	803.4774	402.2423	7
14	1553.8098	777.4085	0	0	1535.7992	768.4032	V	708.4039	354.7056	691.3774	346.1923	690.3933	345.7003	6
15	1652.8782	826.9427	0	0	1634.8676	817.9374	V	609.3355	305.1714	592.3089	296.6581	591.3249	296.1661	5
16	1815.9415	908.4744	0	0	1797.9309	899.4691	Y	510.2671	255.6372	493.2405	247.1239	492.2565	246.6319	4
17	1886.9786	943.9929	0	0	1868.9680	934.9877	A	347.2037	174.1055	330.1772	165.5922	329.1932	165.1002	3
18	1988.0263	994.5168	0	0	1970.0157	985.5115	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
19							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 75155.

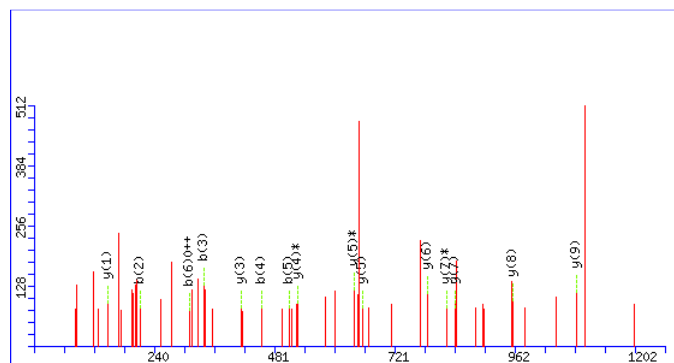
MS/MS Fragmentation of **LVKNGENQLRK**:

Found in **IP100470455;IP100470456;IP100947448;IP100967759;IP100968001;IP100973509**

Title: 3.1.1.1283.8

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_1_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							11
2	213.1598	107.0835	0	0	0	0	V	1185.6698	593.3386	1168.6433	584.8253	1167.6593	584.3333	10
3	341.2547	171.1310	324.2282	162.6177	0	0	K	1086.6014	543.8044	1069.5749	535.2911	1068.5909	534.7991	9
4	455.2976	228.1525	438.2711	219.6392	0	0	N	958.5065	479.7569	941.4799	471.2436	940.4959	470.7516	8
5	512.3191	256.6632	495.2926	248.1499	0	0	G	844.4635	422.7354	827.4370	414.2221	826.4530	413.7301	7
6	641.3617	321.1845	624.3352	312.6712	623.3511	312.1792	E	787.4421	394.2247	770.4155	385.7114	769.4315	385.2194	6
7	755.4046	378.2060	738.3781	369.6927	737.3941	369.2007	N	658.3995	329.7034	641.3729	321.1901	0	0	5
8	883.4632	442.2352	866.4367	433.7220	865.4526	433.2300	Q	544.3566	272.6819	527.3300	264.1686	0	0	4
9	996.5473	498.7773	979.5207	490.2640	978.5367	489.7720	L	416.2980	208.6526	399.2714	200.1394	0	0	3
10	1152.6484	576.8278	1135.6218	568.3146	1134.6378	567.8225	R	303.2139	152.1106	286.1874	143.5973	0	0	2
11							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: **75269.**

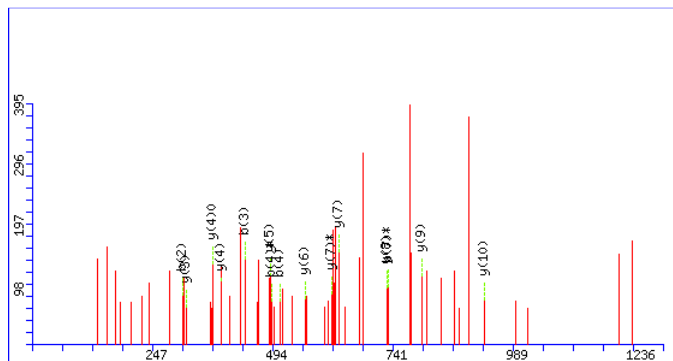
MS/MS Fragmentation of **FYQAVAATAGKD:**

Found in **IP100016726**

Title: 1.1.1.8381.10

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							12
2	311.1390	156.0731	0	0	0	0	Y	1094.5477	547.7775	1077.5211	539.2642	1076.5371	538.7722	11
3	439.1976	220.1024	422.1710	211.5892	0	0	Q	931.4843	466.2458	914.4578	457.7325	913.4738	457.2405	10
4	510.2347	255.6210	493.2082	247.1077	0	0	A	803.4258	402.2165	786.3992	393.7032	785.4152	393.2112	9
5	609.3031	305.1552	592.2766	296.6419	0	0	V	732.3886	366.6980	715.3621	358.1847	714.3781	357.6927	8
6	680.3402	340.6738	663.3137	332.1605	0	0	A	633.3202	317.1638	616.2937	308.6505	615.3097	308.1585	7
7	751.3774	376.1923	734.3508	367.6790	0	0	A	562.2831	281.6452	545.2566	273.1319	544.2726	272.6399	6
8	852.4250	426.7162	835.3985	418.2029	834.4145	417.7109	T	491.2460	246.1266	474.2195	237.6134	473.2354	237.1214	5
9	923.4621	462.2347	906.4356	453.7214	905.4516	453.2294	A	390.1983	195.6028	373.1718	187.0895	372.1878	186.5975	4
10	980.4836	490.7454	963.4571	482.2322	962.4730	481.7402	G	319.1612	160.0842	302.1347	151.5710	301.1506	151.0790	3
11	1108.5786	554.7929	1091.5520	546.2796	1090.5680	545.7876	K	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
12							D	134.0448	67.5260	0	0	116.0342	58.5207	1

Peptide View

Peptide: 75485.

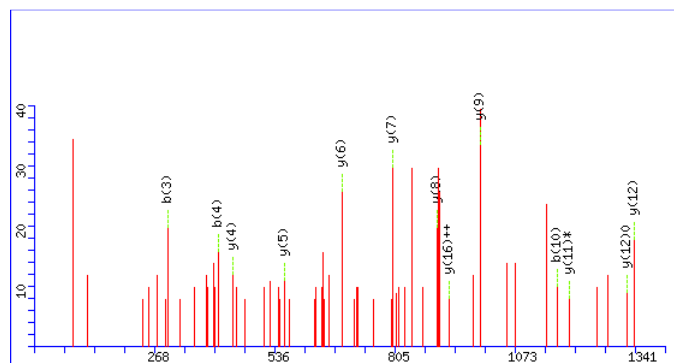
MS/MS Fragmentation of **GEILLQCLLENTPVLEDVLGR: 57.021465@C:7**

Found in **IP100554739;IP100556642**

Title: 5.1.1.1390.2

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							21
2	187.0713	94.0393	0	0	169.0608	85.0340	E	2324.2530	1162.6301	2307.2265	1154.1169	2306.2424	1153.6249	20
3	300.1554	150.5813	0	0	282.1448	141.5761	I	2195.2104	1098.1088	2178.1839	1089.5956	2177.1999	1089.1036	19
4	413.2395	207.1234	0	0	395.2289	198.1181	L	2082.1264	1041.5668	2065.0998	1033.0535	2064.1158	1032.5615	18
5	526.3235	263.6654	0	0	508.3130	254.6601	L	1969.0423	985.0248	1952.0157	976.5115	1951.0317	976.0195	17
6	654.3821	327.6947	637.3556	319.1814	636.3715	318.6894	Q	1855.9582	928.4828	1838.9317	919.9695	1837.9477	919.4775	16
7	814.4128	407.7100	797.3862	399.1967	796.4022	398.7047	C	1727.8996	864.4535	1710.8731	855.9402	1709.8891	855.4482	15
8	927.4968	464.2520	910.4703	455.7388	909.4863	455.2468	L	1567.8690	784.4381	1550.8424	775.9249	1549.8584	775.4329	14
9	1040.5809	520.7941	1023.5543	512.2808	1022.5703	511.7888	L	1454.7849	727.8961	1437.7584	719.3828	1436.7744	718.8908	13
10	1169.6235	585.3154	1152.5969	576.8021	1151.6129	576.3101	E	1341.7009	671.3541	1324.6743	662.8408	1323.6903	662.3488	12
11	1283.6664	642.3368	1266.6399	633.8236	1265.6558	633.3316	N	1212.6583	606.8328	1195.6317	598.3195	1194.6477	597.8275	11
12	1384.7141	692.8607	1367.6875	684.3474	1366.7035	683.8554	T	1098.6154	549.8113	1081.5888	541.2980	1080.6048	540.8060	10
13	1481.7668	741.3871	1464.7403	732.8738	1463.7563	732.3818	P	997.5677	499.2875	980.5411	490.7742	979.5571	490.2822	9
14	1580.8353	790.9213	1563.8087	782.4080	1562.8247	781.9160	V	900.5149	450.7611	883.4884	442.2478	882.5043	441.7558	8
15	1693.9193	847.4633	1676.8928	838.9500	1675.9088	838.4580	L	801.4465	401.2269	784.4199	392.7136	783.4359	392.2216	7
16	1822.9619	911.9846	1805.9354	903.4713	1804.9514	902.9793	E	688.3624	344.6849	671.3359	336.1716	670.3519	335.6796	6
17	1937.9889	969.4981	1920.9623	960.9848	1919.9783	960.4928	D	559.3198	280.1636	542.2933	271.6503	541.3093	271.1583	5
18	2037.0573	1019.0323	2020.0307	1010.5190	2019.0467	1010.0270	V	444.2929	222.6501	427.2663	214.1368	0	0	4
19	2150.1413	1075.5743	2133.1148	1067.0610	2132.1308	1066.5690	L	345.2245	173.1159	328.1979	164.6026	0	0	3
20	2207.1628	1104.0850	2190.1363	1095.5718	2189.1522	1095.0798	G	232.1404	116.5738	215.1139	108.0606	0	0	2
21							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 75688.

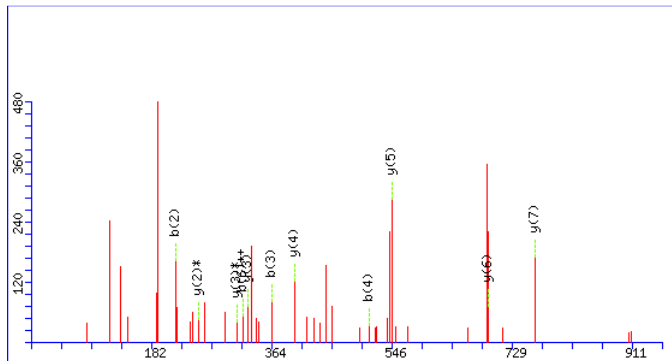
MS/MS Fragmentation of **FAFFAGPR**:

Found in **IP100412988;IP100412989;IP100477903;IP100478407;IP100478746;IP100479203;IP100552926;IP100745200;IP101012396;IP101012862**

Title: 3.1.1.167.5

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120206ry¥120206ry_aHDF1419-P10_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							8
2	219.1128	110.0600	0	0	0	0	A	765.4042	383.2058	748.3777	374.6925	0	0	7
3	366.1812	183.5942	0	0	0	0	F	694.3671	347.6872	677.3406	339.1739	0	0	6
4	513.2496	257.1285	0	0	0	0	F	547.2987	274.1530	530.2722	265.6397	0	0	5
5	584.2867	292.6470	0	0	0	0	A	400.2303	200.6188	383.2037	192.1055	0	0	4
6	641.3082	321.1577	0	0	0	0	G	329.1932	165.1002	312.1666	156.5870	0	0	3
7	738.3610	369.6841	0	0	0	0	P	272.1717	136.5895	255.1452	128.0762	0	0	2
8							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 75704.

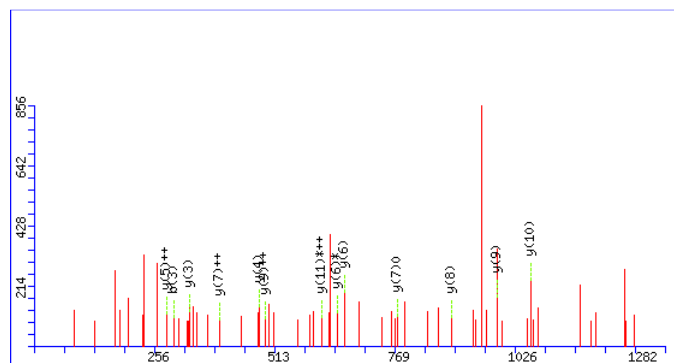
MS/MS Fragmentation of **ILAWAPVEPSFSAR**:

Found in **IP100306260**

Title: 3.1.1.1954.10

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							14
2	227.1754	114.0913	0	0	0	0	L	1430.7427	715.8750	1413.7161	707.3617	1412.7321	706.8697	13
3	298.2125	149.6099	0	0	0	0	A	1317.6586	659.3329	1300.6321	650.8197	1299.6480	650.3277	12
4	484.2918	242.6496	0	0	0	0	W	1246.6215	623.8144	1229.5949	615.3011	1228.6109	614.8091	11
5	555.3289	278.1681	0	0	0	0	A	1060.5422	530.7747	1043.5156	522.2615	1042.5316	521.7694	10
6	652.3817	326.6945	0	0	0	0	P	989.5051	495.2562	972.4785	486.7429	971.4945	486.2509	9
7	751.4501	376.2287	0	0	0	0	V	892.4523	446.7298	875.4258	438.2165	874.4417	437.7245	8
8	880.4927	440.7500	0	0	862.4822	431.7447	E	793.3839	397.1956	776.3573	388.6823	775.3733	388.1903	7
9	977.5455	489.2764	0	0	959.5349	480.2711	P	664.3413	332.6743	647.3148	324.1610	646.3307	323.6690	6
10	1064.5775	532.7924	0	0	1046.5669	523.7871	S	567.2885	284.1479	550.2620	275.6346	549.2780	275.1426	5
11	1211.6459	606.3266	0	0	1193.6354	597.3213	F	480.2565	240.6319	463.2300	232.1186	462.2459	231.6266	4
12	1298.6780	649.8426	0	0	1280.6674	640.8373	S	333.1881	167.0977	316.1615	158.5844	315.1775	158.0924	3
13	1369.7151	685.3612	0	0	1351.7045	676.3559	A	246.1561	123.5817	229.1295	115.0684	0	0	2
14							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: **75744**.

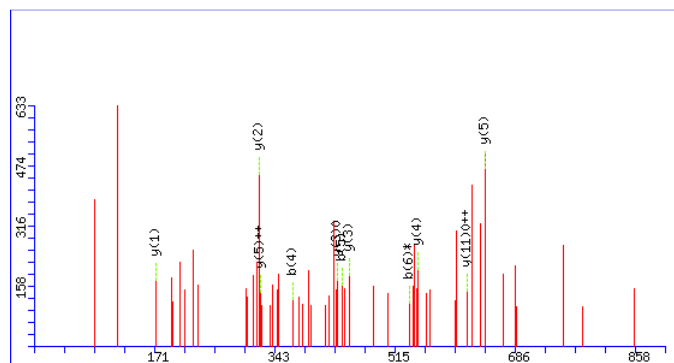
MS/MS Fragmentation of **AALNALQPPEFR**:

Found in **IP100146447**

Title: 2.1.1.4364.4

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							12
2	143.0815	72.0444	0	0	0	0	A	1255.6793	628.3433	1238.6528	619.8300	1237.6688	619.3380	11
3	256.1656	128.5864	0	0	0	0	L	1184.6422	592.8248	1167.6157	584.3115	1166.6317	583.8195	10
4	370.2085	185.6079	353.1819	177.0946	0	0	N	1071.5582	536.2827	1054.5316	527.7694	1053.5476	527.2774	9
5	441.2456	221.1264	424.2191	212.6132	0	0	A	957.5152	479.2613	940.4887	470.7480	939.5047	470.2560	8
6	554.3297	277.6685	537.3031	269.1552	0	0	L	886.4781	443.7427	869.4516	435.2294	868.4676	434.7374	7
7	682.3883	341.6978	665.3617	333.1845	0	0	Q	773.3941	387.2007	756.3675	378.6874	755.3835	378.1954	6
8	779.4410	390.2241	762.4145	381.7109	0	0	P	645.3355	323.1714	628.3089	314.6581	627.3249	314.1661	5
9	876.4938	438.7505	859.4672	430.2373	0	0	P	548.2827	274.6450	531.2562	266.1317	530.2722	265.6397	4
10	1005.5364	503.2718	988.5098	494.7585	987.5258	494.2665	E	451.2300	226.1186	434.2034	217.6053	433.2194	217.1133	3
11	1152.6048	576.8060	1135.5782	568.2928	1134.5942	567.8007	F	322.1874	161.5973	305.1608	153.0840	0	0	2
12							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 75777.

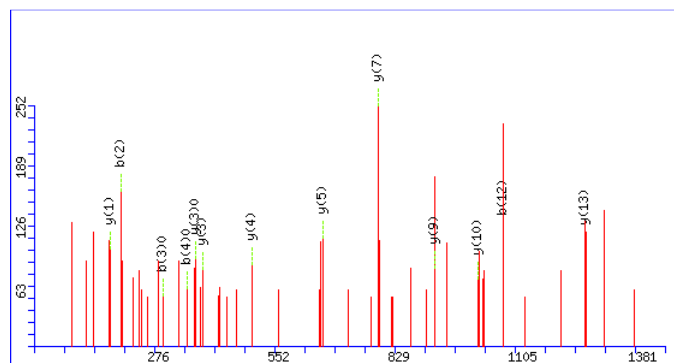
MS/MS Fragmentation of **SIIGMTGAGAYILTR**:

Found in **IP100022078;IP100974351;IP100977187;IP100978066;IP100979312;IP100981993;IP100982468;IP101011666;IP101019118**

Title: 3.1.1.1932.9

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120212ry¥120212ry_aHDF1388-P9_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							16
2	201.1234	101.0653	0	0	183.1128	92.0600	I	1493.8145	747.4109	1476.7879	738.8976	1475.8039	738.4056	15
3	314.2074	157.6074	0	0	296.1969	148.6021	I	1380.7304	690.8688	1363.7039	682.3556	1362.7198	681.8636	14
4	371.2289	186.1181	0	0	353.2183	177.1128	G	1267.6463	634.3268	1250.6198	625.8135	1249.6358	625.3215	13
5	502.2694	251.6383	0	0	484.2588	242.6330	M	1210.6249	605.8161	1193.5983	597.3028	1192.6143	596.8108	12
6	559.2908	280.1491	0	0	541.2803	271.1438	G	1079.5844	540.2958	1062.5578	531.7826	1061.5738	531.2905	11
7	660.3385	330.6729	0	0	642.3280	321.6676	T	1022.5629	511.7851	1005.5364	503.2718	1004.5524	502.7798	10
8	717.3600	359.1836	0	0	699.3494	350.1783	G	921.5152	461.2613	904.4887	452.7480	903.5047	452.2560	9
9	788.3971	394.7022	0	0	770.3865	385.6969	A	864.4938	432.7505	847.4672	424.2373	846.4832	423.7452	8
10	845.4186	423.2129	0	0	827.4080	414.2076	G	793.4567	397.2320	776.4301	388.7187	775.4461	388.2267	7
11	916.4557	458.7315	0	0	898.4451	449.7262	A	736.4352	368.7212	719.4087	360.2080	718.4246	359.7160	6
12	1079.5190	540.2631	0	0	1061.5084	531.2579	Y	665.3981	333.2027	648.3715	324.6894	647.3875	324.1974	5
13	1192.6031	596.8052	0	0	1174.5925	587.7999	I	502.3348	251.6710	485.3082	243.1577	484.3242	242.6657	4
14	1305.6871	653.3472	0	0	1287.6766	644.3419	L	389.2507	195.1290	372.2241	186.6157	371.2401	186.1237	3
15	1406.7348	703.8710	0	0	1388.7243	694.8658	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
16							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 75805.

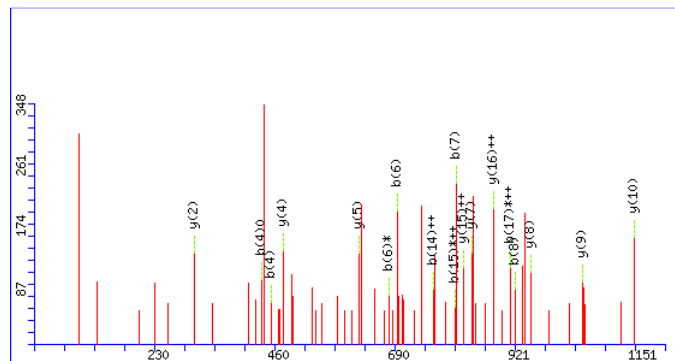
MS/MS Fragmentation of **DLKPENILLDSVGHVVLTDGLCK: 57.021465@C:23**

Found in **IP100335929:IP100655852**

Title: 4.1.1.4557.2

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							24
2	229.1183	115.0628	0	0	211.1077	106.0575	L	2567.3902	1284.1987	2550.3636	1275.6855	2549.3796	1275.1934	23
3	357.2132	179.1103	340.1867	170.5970	339.2027	170.1050	K	2454.3061	1227.6567	2437.2796	1219.1434	2436.2955	1218.6514	22
4	454.2680	227.6366	437.2395	219.1234	436.2554	218.6314	P	2326.2111	1163.6092	2309.1846	1155.0959	2308.2006	1154.6039	21
5	583.3086	292.1579	566.2821	283.6447	565.2980	283.1527	E	2229.1584	1115.0828	2212.1318	1106.5696	2211.1478	1106.0775	20
6	697.3515	349.1794	680.3250	340.6661	679.3410	340.1741	N	2100.1158	1050.5615	2083.0892	1042.0483	2082.1052	1041.5563	19
7	810.4356	405.7214	793.4090	397.2082	792.4250	396.7162	I	1986.0729	993.5401	1969.0463	985.0268	1968.0623	984.5348	18
8	923.5197	462.2635	906.4931	453.7502	905.5091	453.2582	L	1872.9888	936.9980	1855.9622	928.4848	1854.9782	927.9928	17
9	1036.6037	518.8055	1019.5772	510.2922	1018.5932	509.8002	L	1759.9047	880.4560	1742.8782	871.9427	1741.8942	871.4507	16
10	1151.6307	576.3190	1134.6041	567.8057	1133.6201	567.3137	D	1646.8207	823.9140	1629.7941	815.4007	1628.8101	814.9087	15
11	1238.6627	619.8350	1221.6361	611.3217	1220.6521	610.8297	S	1531.7937	766.4005	1514.7672	757.8872	1513.7832	757.3952	14
12	1337.7311	669.3692	1320.7046	660.8559	1319.7205	660.3639	V	1444.7617	722.8845	1427.7352	714.3712	1426.7511	713.8792	13
13	1394.7526	697.8799	1377.7260	689.3666	1376.7420	688.8746	G	1345.6933	673.3503	1328.6667	664.8370	1327.6827	664.3450	12
14	1531.8115	766.4094	1514.7849	757.8961	1513.8009	757.4041	H	1288.6718	644.8395	1271.6453	636.3263	1270.6613	635.8343	11
15	1630.8799	815.9436	1613.8533	807.4303	1612.8693	806.9383	V	1151.6129	576.3101	1134.5864	567.7968	1133.6023	567.3048	10
16	1729.9483	865.4778	1712.9218	856.9645	1711.9377	856.4725	V	1052.5445	526.7759	1035.5179	518.2626	1034.5339	517.7706	9
17	1843.0324	922.0198	1826.0058	913.5066	1825.0218	913.0145	L	953.4761	477.2417	936.4495	468.7284	935.4655	468.2364	8
18	1944.0801	972.5437	1927.0535	964.0304	1926.0695	963.5384	T	840.3920	420.6996	823.3655	412.1864	822.3815	411.6944	7
19	2059.1070	1030.0571	2042.0804	1021.5439	2041.0964	1021.0519	D	739.3443	370.1758	722.3178	361.6625	721.3338	361.1705	6
20	2206.1754	1103.5913	2189.1489	1095.0781	2188.1648	1094.5861	F	624.3174	312.6623	607.2908	304.1491	0	0	5
21	2263.1969	1132.1021	2246.1703	1123.5888	2245.1863	1123.0968	G	477.2490	239.1281	460.2224	230.6149	0	0	4
22	2376.2809	1188.6441	2359.2544	1180.1308	2358.2704	1179.6388	L	420.2275	210.6174	403.2010	202.1041	0	0	3
23	2536.3116	1268.6594	2519.2850	1260.1462	2518.3010	1259.6542	C	307.1435	154.0754	290.1169	145.5621	0	0	2
24							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 75820.

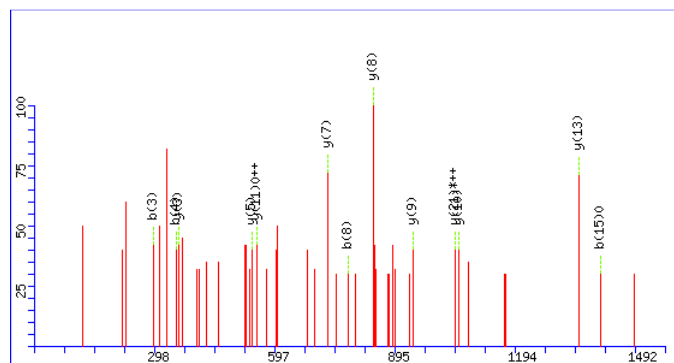
MS/MS Fragmentation of **EAPGSLLLCSAPSAEALVDSVIAPSR: 57.021465@C:9**

Found in **IP100033770**

Title: 4.1.1.1269.11

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							28
2	201.0870	101.0471	0	0	183.0764	92.0418	A	2649.3916	1325.1995	2632.3651	1316.6862	2631.3811	1316.1942	27
3	298.1397	149.5735	0	0	280.1292	140.5682	P	2578.3545	1289.6809	2561.3280	1281.1676	2560.3440	1280.6756	26
4	355.1612	178.0842	0	0	337.1506	169.0790	G	2481.3018	1241.1545	2464.2752	1232.6412	2463.2912	1232.1492	25
5	442.1932	221.6003	0	0	424.1827	212.5950	S	2424.2803	1212.6438	2407.2537	1204.1305	2406.2697	1203.6385	24
6	555.2773	278.1423	0	0	537.2667	269.1370	L	2337.2483	1169.1278	2320.2217	1160.6145	2319.2377	1160.1225	23
7	668.3614	334.6843	0	0	650.3508	325.6790	L	2224.1642	1112.5857	2207.1376	1104.0725	2206.1536	1103.5805	22
8	781.4454	391.2264	0	0	763.4349	382.2211	L	2111.0801	1056.0437	2094.0536	1047.5304	2093.0696	1047.0384	21
9	941.4761	471.2417	0	0	923.4655	462.2364	C	1997.9961	999.5017	1980.9695	990.9884	1979.9855	990.4964	20
10	1028.5081	514.7577	0	0	1010.4975	505.7524	S	1837.9654	919.4863	1820.9389	910.9731	1819.9549	910.4811	19
11	1099.5452	550.2762	0	0	1081.5347	541.2710	A	1750.9334	875.9703	1733.9068	867.4571	1732.9228	866.9651	18
12	1196.5980	598.8026	0	0	1178.5874	589.7973	P	1679.8963	840.4518	1662.8697	831.9385	1661.8857	831.4465	17
13	1283.6300	642.3186	0	0	1265.6195	633.3134	S	1582.8435	791.9254	1565.8170	783.4121	1564.8329	782.9201	16
14	1354.6671	677.8372	0	0	1336.6566	668.8319	A	1495.8115	748.4094	1478.7849	739.8961	1477.8009	739.4041	15
15	1425.7042	713.3558	0	0	1407.6937	704.3505	A	1424.7744	712.8908	1407.7478	704.3775	1406.7638	703.8855	14
16	1522.7570	761.8821	0	0	1504.7464	752.8769	P	1353.7373	677.3723	1336.7107	668.8590	1335.7267	668.3670	13
17	1651.7996	826.4034	0	0	1633.7890	817.3982	E	1256.6845	628.8459	1239.6579	620.3326	1238.6739	619.8406	12
18	1722.8367	861.9220	0	0	1704.8261	852.9167	A	1127.6419	564.3246	1110.6153	555.8113	1109.6313	555.3193	11
19	1835.9208	918.4640	0	0	1817.9102	909.4587	L	1056.6048	528.8060	1039.5782	520.2928	1038.5942	519.8007	10
20	1934.9892	967.9982	0	0	1916.9786	958.9930	V	943.5207	472.2640	926.4942	463.7507	925.5102	463.2587	9
21	2050.0161	1025.5117	0	0	2032.0056	1016.5064	D	844.4523	422.7298	827.4258	414.2165	826.4417	413.7245	8
22	2137.0482	1069.0277	0	0	2119.0376	1060.0224	S	729.4254	365.2163	712.3988	356.7030	711.4148	356.2110	7
23	2236.1166	1118.5619	0	0	2218.1060	1109.5566	V	642.3933	321.7003	625.3668	313.1870	624.3828	312.6950	6
24	2349.2006	1175.1040	0	0	2331.1901	1166.0987	I	543.3249	272.1661	526.2984	263.6528	525.3144	263.1608	5
25	2420.2378	1210.6225	0	0	2402.2272	1201.6172	A	430.2409	215.6241	413.2143	207.1108	412.2303	206.6188	4
26	2517.2905	1259.1489	0	0	2499.2800	1250.1436	P	359.2037	180.1055	342.1772	171.5922	341.1932	171.1002	3
27	2604.3225	1302.6649	0	0	2586.3120	1293.6596	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
28							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 75911.

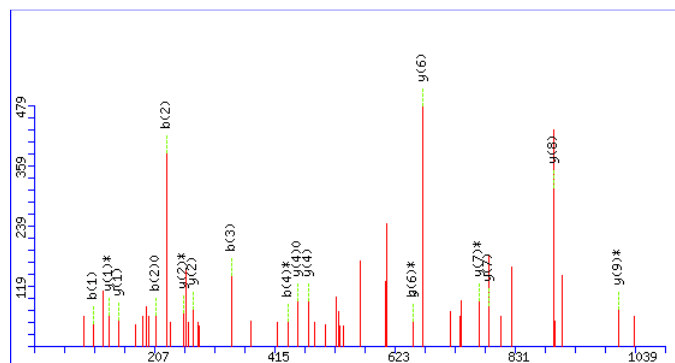
MS/MS Fragmentation of **TQLNPTSLQK**:

Found in **IP100183118,IP100185037,IP100220505,IP100220506,IP100220507,IP100220508,IP100220509,IP100292809,IP100827718**

Title: 1.1.1.8720.11

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							10
2	230.1135	115.5604	213.0870	107.0471	212.1030	106.5551	Q	1028.5735	514.7904	1011.5469	506.2771	1010.5629	505.7851	9
3	343.1976	172.1024	326.1710	163.5892	325.1870	163.0972	L	900.5149	450.7611	883.4884	442.2478	882.5043	441.7558	8
4	457.2405	229.1239	440.2140	220.6106	439.2300	220.1186	N	787.4308	394.2191	770.4043	385.7058	769.4203	385.2138	7
5	554.2933	277.6503	537.2667	269.1370	536.2827	268.6450	P	673.3879	337.1976	656.3614	328.6843	655.3774	328.1923	6
6	655.3410	328.1741	638.3144	319.6608	637.3304	319.1688	T	576.3352	288.6712	559.3086	280.1579	558.3246	279.6659	5
7	742.3730	371.6901	725.3464	363.1769	724.3624	362.6849	S	475.2875	238.1474	458.2609	229.6341	457.2769	229.1421	4
8	855.4571	428.2322	838.4305	419.7189	837.4465	419.2269	L	388.2554	194.6314	371.2289	186.1181	0	0	3
9	983.5156	492.2615	966.4891	483.7482	965.5051	483.2562	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
10							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 76060.

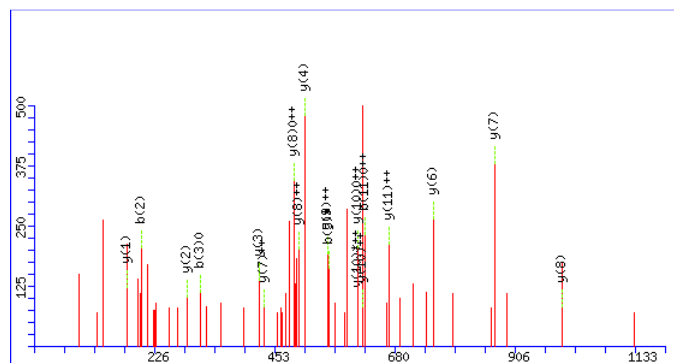
MS/MS Fragmentation of **TTELQDELSHLR**:

Found in **IP100071826;IP100470480;IP100645882;IP100975799;IP100975933;IP100978829;IP100981915;IP100983754;IP101013869**

Title: 2.1.1.4398.3

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120212ry¥120212ry_aHDF1388-P9_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							12
2	203.1028	102.0550	0	0	185.0921	93.0497	T	1340.6805	670.8439	1323.6539	662.3306	1322.6699	661.8386	11
3	332.1452	166.5763	0	0	314.1347	157.5710	E	1239.6328	620.3200	1222.6062	611.8068	1221.6222	611.3148	10
4	445.2293	223.1183	0	0	427.2187	214.1130	L	1110.5902	555.7987	1093.5636	547.2855	1092.5796	546.7935	9
5	573.2879	287.1476	556.2613	278.6343	555.2773	278.1423	Q	997.5061	499.2567	980.4796	490.7434	979.4956	490.2514	8
6	688.3148	344.6610	671.2883	336.1478	670.3042	335.6558	D	869.4476	435.2274	852.4210	426.7141	851.4370	426.2221	7
7	817.3574	409.1823	800.3309	400.6691	799.3468	400.1771	E	754.4206	377.7139	737.3941	369.2007	736.4100	368.7087	6
8	930.4415	465.7244	913.4149	457.2111	912.4309	456.7191	L	625.3780	313.1926	608.3515	304.6794	607.3675	304.1874	5
9	1017.4735	509.2404	1000.4469	500.7271	999.4629	500.2351	S	512.2940	256.6506	495.2674	248.1373	494.2834	247.6453	4
10	1154.5324	577.7698	1137.5059	569.2566	1136.5218	568.7646	H	425.2619	213.1346	408.2354	204.6213	0	0	3
11	1267.6165	634.3119	1250.5899	625.7986	1249.6059	625.3066	L	288.2030	144.6051	271.1765	136.0919	0	0	2
12							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 76193.

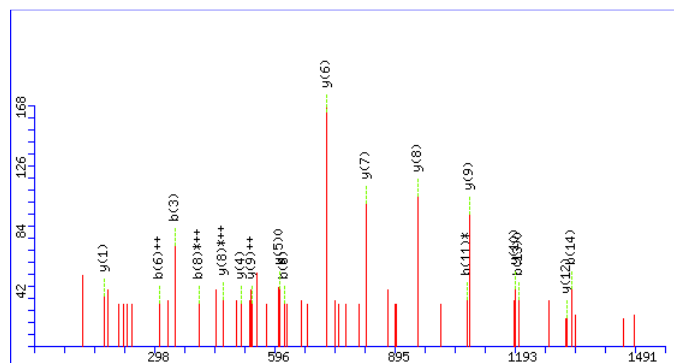
MS/MS Fragmentation of **FGFIVGSQGAEGALEEVPLEVL**R:

Found in **IP100011167**

Title: 4.1.1.2145.9

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							23
2	205.0972	103.0522	0	0	0	0	G	2270.2027	1135.6050	2253.1761	1127.0917	2252.1921	1126.5997	22
3	352.1656	176.5864	0	0	0	0	F	2213.1812	1107.0943	2196.1547	1098.5810	2195.1707	1098.0890	21
4	465.2496	233.1285	0	0	0	0	I	2066.1128	1033.5600	2049.0863	1025.0468	2048.1022	1024.5548	20
5	564.3180	282.6627	0	0	0	0	V	1953.0287	977.0180	1936.0022	968.5047	1935.0182	968.0127	19
6	621.3395	311.1734	0	0	0	0	G	1853.9603	927.4838	1836.9338	918.9705	1835.9498	918.4785	18
7	708.3715	354.6894	0	0	690.3610	345.6841	S	1796.9389	898.9731	1779.9123	890.4598	1778.9283	889.9678	17
8	836.4301	418.7187	819.4036	410.2054	818.4196	409.7134	Q	1709.9068	855.4571	1692.8803	846.9438	1691.8963	846.4518	16
9	893.4516	447.2294	876.4250	438.7162	875.4410	438.2241	G	1581.8483	791.4278	1564.8217	782.9145	1563.8377	782.4225	15
10	964.4887	482.7480	947.4621	474.2347	946.4781	473.7427	A	1524.8268	762.9170	1507.8003	754.4038	1506.8162	753.9118	14
11	1093.5313	547.2693	1076.5047	538.7560	1075.5207	538.2640	E	1453.7897	727.3985	1436.7631	718.8852	1435.7791	718.3932	13
12	1150.5528	575.7800	1133.5262	567.2667	1132.5422	566.7747	G	1324.7471	662.8772	1307.7205	654.3639	1306.7365	653.8719	12
13	1221.5899	611.2986	1204.5633	602.7853	1203.5793	602.2933	A	1267.7256	634.3665	1250.6991	625.8532	1249.7151	625.3612	11
14	1334.6739	667.8406	1317.6474	659.3273	1316.6634	658.8353	L	1196.6885	598.8479	1179.6620	590.3346	1178.6780	589.8426	10
15	1463.7165	732.3619	1446.6900	723.8486	1445.7060	723.3566	E	1083.6045	542.3059	1066.5779	533.7926	1065.5939	533.3006	9
16	1592.7591	796.8832	1575.7326	788.3699	1574.7486	787.8779	E	954.5619	477.7846	937.5353	469.2713	936.5513	468.7793	8
17	1691.8275	846.4174	1674.8010	837.9041	1673.8170	837.4121	V	825.5193	413.2633	808.4927	404.7500	807.5087	404.2580	7
18	1788.8803	894.9438	1771.8537	886.4305	1770.8697	885.9385	P	726.4509	363.7291	709.4243	355.2158	708.4403	354.7238	6
19	1901.9644	951.4858	1884.9378	942.9725	1883.9538	942.4805	L	629.3981	315.2027	612.3715	306.6894	611.3875	306.1974	5
20	2031.0070	1016.0071	2013.9804	1007.4938	2012.9964	1007.0018	E	516.3140	258.6606	499.2875	250.1474	498.3035	249.6554	4
21	2130.0754	1065.5413	2113.0488	1057.0280	2112.0648	1056.5360	V	387.2714	194.1394	370.2449	185.6261	0	0	3
22	2243.1594	1122.0834	2226.1329	1113.5701	2225.1489	1113.0781	L	288.2030	144.6051	271.1765	136.0919	0	0	2
23							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 76365.

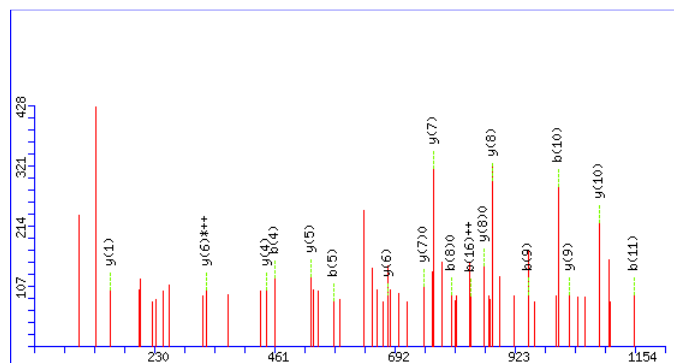
MS/MS Fragmentation of **IPDHLTSQEGFDSFSSLVK:**

Found in **IP100296858:IP100479789**

Title: 3.1.1.1734.5

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							19
2	211.1441	106.0757	0	0	0	0	P	1922.9130	961.9602	1905.8865	953.4469	1904.9025	952.9549	18
3	326.1710	163.5892	0	0	308.1605	154.5839	D	1825.8603	913.4338	1808.8337	904.9205	1807.8497	904.4285	17
4	463.2300	232.1186	0	0	445.2194	223.1133	H	1710.8333	855.9203	1693.8068	847.4070	1692.8228	846.9150	16
5	578.3140	288.6606	0	0	558.3035	279.6554	L	1573.7744	787.3909	1556.7479	778.8776	1555.7639	778.3856	15
6	677.3617	339.1845	0	0	659.3511	330.1792	T	1460.6904	730.8488	1443.6638	722.3355	1442.6798	721.8435	14
7	764.3937	382.7005	0	0	746.3832	373.6952	S	1359.6427	680.3250	1342.6161	671.8117	1341.6321	671.3197	13
8	821.4152	411.2112	0	0	803.4046	402.2060	G	1272.6107	636.8090	1255.5841	628.2957	1254.6001	627.8037	12
9	950.4578	475.7325	0	0	932.4472	466.7272	E	1215.5892	608.2982	1198.5626	599.7850	1197.5786	599.2930	11
10	1007.4793	504.2433	0	0	989.4687	495.2380	G	1086.5466	543.7769	1069.5201	535.2637	1068.5360	534.7717	10
11	1154.5477	577.7775	0	0	1136.5371	568.7722	F	1029.5251	515.2662	1012.4986	506.7529	1011.5146	506.2609	9
12	1269.5746	635.2909	0	0	1251.5640	626.2857	D	882.4567	441.7320	865.4302	433.2187	864.4462	432.7267	8
13	1356.6066	678.8070	0	0	1338.5961	669.8017	S	767.4298	384.2185	750.4032	375.7053	749.4192	375.2132	7
14	1503.6751	752.3412	0	0	1485.6645	743.3359	F	680.3978	340.7025	663.3712	332.1892	662.3872	331.6972	6
15	1590.7071	795.8572	0	0	1572.6965	786.8519	S	533.3293	267.1683	516.3028	258.6550	515.3188	258.1630	5
16	1677.7391	839.3732	0	0	1659.7285	830.3679	S	446.2973	223.6523	429.2708	215.1390	428.2867	214.6470	4
17	1790.8232	895.9152	0	0	1772.8126	886.9099	L	359.2653	180.1363	342.2387	171.6230	0	0	3
18	1889.8916	945.4494	0	0	1871.8810	936.4441	V	246.1812	123.5942	229.1547	115.0810	0	0	2
19							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 76482.

MS/MS Fragmentation of **NLFEQLVR**:

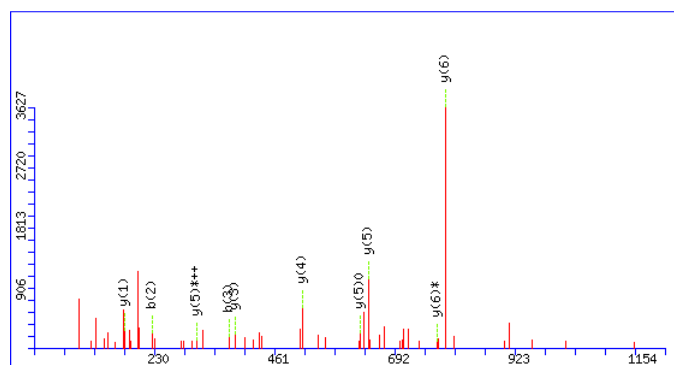
Found in

IP100012480;IP100152946;IP101021045;IP101021341;IP101021379;IP101021461;IP101021671;IP101021887;IP101021983;IP101022025;IP101022191;IP101022330;IP1010224

Title: 3.1.1.1485.3

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120214ry¥120214ry_32R1-32_4_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							8
2	228.1343	114.5708	211.1077	106.0575	0	0	L	904.5251	452.7662	887.4985	444.2529	886.5145	443.7609	7
3	375.2027	188.1050	358.1761	179.5917	0	0	F	791.4410	396.2241	774.4145	387.7109	773.4305	387.2189	6
4	504.2453	252.6263	487.2187	244.1130	486.2347	243.6210	E	644.3726	322.6899	627.3461	314.1767	626.3620	313.6847	5
5	632.3039	316.6556	615.2773	308.1423	614.2933	307.6503	Q	515.3300	258.1686	498.3035	249.6554	0	0	4
6	745.3879	373.1976	728.3614	364.6843	727.3774	364.1923	L	387.2714	194.1394	370.2449	185.6261	0	0	3
7	844.4563	422.7318	827.4298	414.2185	826.4458	413.7265	V	274.1874	137.5973	257.1608	129.0840	0	0	2
8							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 76580.

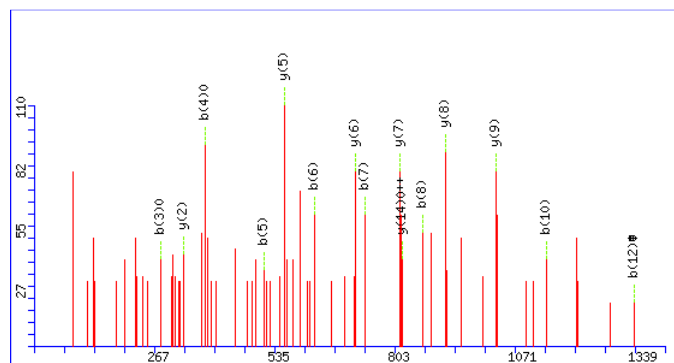
MS/MS Fragmentation of **EGDPLILQYLLTVCPGAWK: 57.021465@C:14**

Found in **IP100418468;IP100552205;IP100553055**

Title: 4.1.1.3803.5

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							19
2	187.0713	94.0393	0	0	169.0608	85.0340	G	2044.0936	1022.5504	2027.0671	1014.0372	2026.0830	1013.5452	18
3	302.0983	151.5528	0	0	284.0877	142.5475	D	1987.0721	994.0397	1970.0456	985.5264	1969.0616	985.0344	17
4	399.1510	200.0792	0	0	381.1405	191.0739	P	1872.0452	936.5262	1855.0186	928.0130	1854.0346	927.5210	16
5	512.2351	256.6212	0	0	494.2245	247.6159	L	1774.9924	887.9999	1757.9659	879.4866	1756.9819	878.9946	15
6	625.3192	313.1632	0	0	607.3086	304.1579	I	1661.9084	831.4578	1644.8818	822.9445	1643.8978	822.4525	14
7	738.4032	369.7053	0	0	720.3927	360.7000	L	1548.8243	774.9158	1531.7978	766.4025	1530.8137	765.9105	13
8	866.4618	433.7345	849.4353	425.2213	848.4512	424.7293	Q	1435.7402	718.3738	1418.7137	709.8605	1417.7297	709.3685	12
9	1029.5251	515.2662	1012.4986	506.7529	1011.5146	506.2609	Y	1307.6817	654.3445	1290.6551	645.8312	1289.6711	645.3392	11
10	1142.6092	571.8082	1125.5827	563.2950	1124.5986	562.8030	L	1144.6183	572.8128	1127.5918	564.2995	1126.6078	563.8075	10
11	1255.6933	628.3503	1238.6667	619.8370	1237.6827	619.3450	L	1031.5343	516.2708	1014.5077	507.7575	1013.5237	507.2655	9
12	1356.7409	678.8741	1339.7144	670.3608	1338.7304	669.8688	T	918.4502	459.7287	901.4237	451.2155	900.4396	450.7235	8
13	1455.8094	728.4083	1438.7828	719.8950	1437.7988	719.4030	V	817.4025	409.2049	800.3760	400.6916	0	0	7
14	1615.8400	808.4236	1598.8135	799.9104	1597.8294	799.4184	C	718.3341	359.6707	701.3076	351.1574	0	0	6
15	1712.8928	856.9500	1695.8662	848.4368	1694.8822	847.9447	P	558.3035	279.6554	541.2769	271.1421	0	0	5
16	1769.9142	885.4608	1752.8877	876.9475	1751.9037	876.4555	G	461.2507	231.1290	444.2241	222.6157	0	0	4
17	1840.9514	920.9793	1823.9248	912.4660	1822.9408	911.9740	A	404.2292	202.6183	387.2027	194.1050	0	0	3
18	2027.0307	1014.0190	2010.0041	1005.5057	2009.0201	1005.0137	W	333.1921	167.0997	316.1656	158.5864	0	0	2
19							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 76706.

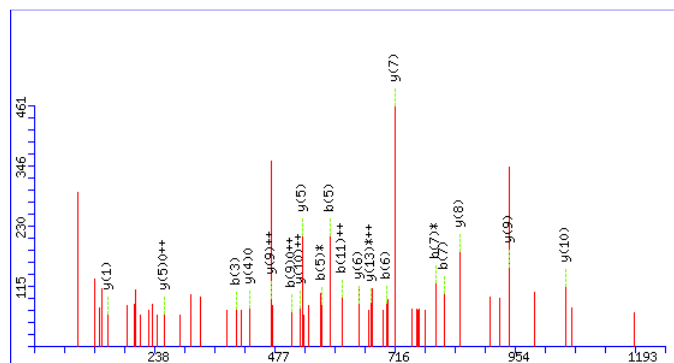
MS/MS Fragmentation of **LCEQGINPEALSSVIK: 57.021465@C:2**

Found in **IP100456981**

Title: 3.1.1.1250.4

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							16
2	274.1220	137.5646	0	0	0	0	C	1644.8261	822.9167	1627.7996	814.4034	1626.8156	813.9114	15
3	403.1646	202.0859	0	0	385.1540	193.0806	E	1484.7955	742.9014	1467.7689	734.3881	1466.7849	733.8961	14
4	531.2232	266.1152	514.1966	257.6019	513.2126	257.1099	Q	1355.7529	678.3801	1338.7264	669.8668	1337.7423	669.3748	13
5	588.2446	294.6260	571.2181	286.1127	570.2341	285.6207	G	1227.6943	614.3508	1210.6678	605.8375	1209.6838	605.3455	12
6	701.3287	351.1680	684.3021	342.6547	683.3181	342.1627	I	1170.6729	585.8401	1153.6463	577.3268	1152.6623	576.8348	11
7	815.3716	408.1894	798.3451	399.6762	797.3611	399.1842	N	1057.5888	529.2980	1040.5623	520.7848	1039.5782	520.2928	10
8	912.4244	456.7158	895.3978	448.2026	894.4138	447.7105	P	943.5459	472.2766	926.5193	463.7633	925.5353	463.2713	9
9	1041.4670	521.2371	1024.4404	512.7238	1023.4564	512.2318	E	846.4931	423.7502	829.4666	415.2369	828.4825	414.7449	8
10	1112.5041	556.7557	1095.4775	548.2424	1094.4935	547.7504	A	717.4505	359.2289	700.4240	350.7156	699.4400	350.2236	7
11	1225.5882	613.2977	1208.5616	604.7844	1207.5776	604.2924	L	646.4134	323.7103	629.3869	315.1971	628.4028	314.7051	6
12	1312.6202	656.8137	1295.5936	648.3005	1294.6096	647.8084	S	533.3293	267.1683	516.3028	258.6550	515.3188	258.1630	5
13	1399.6522	700.3297	1382.6257	691.8165	1381.6416	691.3245	S	446.2973	223.6523	429.2708	215.1390	428.2867	214.6470	4
14	1498.7206	749.8639	1481.6941	741.3507	1480.7101	740.8587	V	359.2653	180.1363	342.2387	171.6230	0	0	3
15	1611.8047	806.4060	1594.7781	797.8927	1593.7941	797.4007	I	260.1969	130.6021	243.1703	122.0888	0	0	2
16							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 76731.

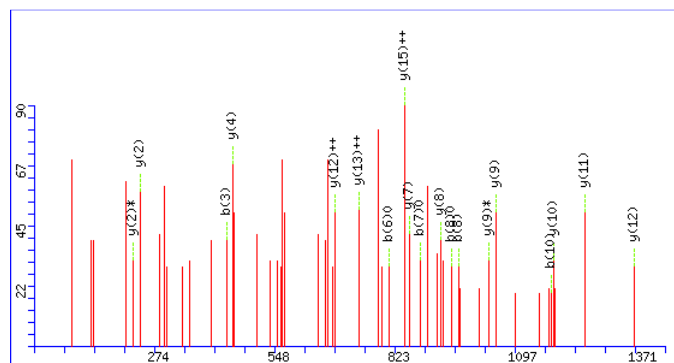
MS/MS Fragmentation of **YYNWTTAAPLLAMQAFQKPLPK:**

Found in **IP100788867,IP100788897,IP100790250,IP101009658**

Title: 4.1.1.3857.3

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	164.0706	82.5389	0	0	0	0	Y							23
2	327.1339	164.0706	0	0	0	0	Y	2502.3578	1251.6825	2485.3312	1243.1692	2484.3472	1242.6772	22
3	441.1769	221.0921	424.1503	212.5788	0	0	N	2339.2944	1170.1508	2322.2679	1161.6376	2321.2839	1161.1456	21
4	627.2562	314.1317	610.2296	305.6185	0	0	W	2225.2515	1113.1294	2208.2249	1104.6161	2207.2409	1104.1241	20
5	728.3039	364.6556	711.2773	356.1423	710.2933	355.6503	T	2039.1722	1020.0897	2022.1456	1011.5765	2021.1616	1011.0844	19
6	829.3515	415.1794	812.3250	406.6661	811.3410	406.1741	T	1938.1245	969.5659	1921.0980	961.0526	1920.1139	960.5606	18
7	900.3886	450.6980	883.3621	442.1847	882.3781	441.6927	A	1837.0768	919.0421	1820.0503	910.5288	0	0	17
8	971.4258	486.2165	954.3992	477.7032	953.4152	477.2112	A	1766.0397	883.5235	1749.0132	875.0102	0	0	16
9	1068.4785	534.7429	1051.4520	526.2296	1050.4680	525.7376	P	1695.0026	848.0049	1677.9760	839.4917	0	0	15
10	1181.5626	591.2849	1164.5360	582.7717	1163.5520	582.2796	L	1597.9498	799.4786	1580.9233	790.9653	0	0	14
11	1294.6467	647.8270	1277.6201	639.3137	1276.6361	638.8217	L	1484.8658	742.9365	1467.8392	734.4232	0	0	13
12	1407.7307	704.3690	1390.7042	695.8557	1389.7202	695.3637	L	1371.7817	686.3945	1354.7552	677.8812	0	0	12
13	1478.7678	739.8876	1461.7413	731.3743	1460.7573	730.8823	A	1258.6976	629.8525	1241.6711	621.3392	0	0	11
14	1609.8083	805.4078	1592.7818	796.8945	1591.7978	796.4025	M	1187.6605	594.3339	1170.6340	585.8206	0	0	10
15	1737.8669	869.4371	1720.8403	860.9238	1719.8563	860.4318	Q	1056.6200	528.8137	1039.5935	520.3004	0	0	9
16	1808.9040	904.9556	1791.8775	896.4424	1790.8934	895.9504	A	928.5615	464.7844	911.5349	456.2711	0	0	8
17	1955.9724	978.4898	1938.9459	969.9766	1937.9619	969.4846	F	857.5244	429.2658	840.4978	420.7525	0	0	7
18	2084.0310	1042.5191	2067.0044	1034.0059	2066.0204	1033.5139	Q	710.4559	355.7316	693.4294	347.2183	0	0	6
19	2212.1260	1106.5666	2195.0994	1098.0533	2194.1154	1097.5613	K	582.3974	291.7023	565.3708	283.1890	0	0	5
20	2309.1787	1155.0930	2292.1522	1146.5797	2291.1682	1146.0877	P	454.3024	227.6548	437.2758	219.1416	0	0	4
21	2422.2628	1211.6350	2405.2362	1203.1218	2404.2522	1202.6298	L	357.2496	179.1285	340.2231	170.6152	0	0	3
22	2519.3156	1260.1614	2502.2890	1251.6481	2501.3050	1251.1561	P	244.1656	122.5864	227.1390	114.0731	0	0	2
23							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 77165.

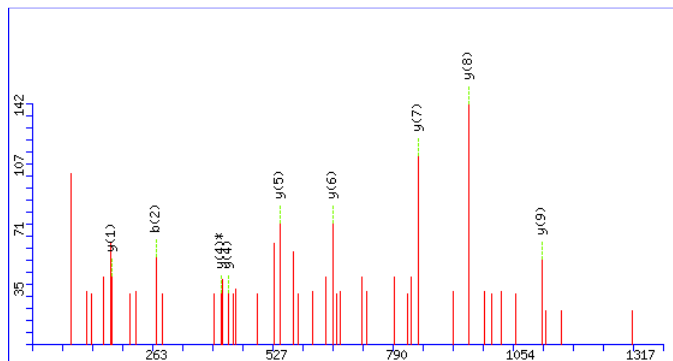
MS/MS Fragmentation of **LCLWDLAEGR: 57.021485@C:2**

Found in **IP100107339;IP100218734;IP100879333**

Title: 3.1.1.2826.5

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							10
2	274.1220	137.5646	0	0	0	0	C	1119.5252	560.2662	1102.4986	551.7529	1101.5146	551.2609	9
3	387.2061	194.1067	0	0	0	0	L	959.4945	480.2509	942.4680	471.7376	941.4839	471.2456	8
4	573.2854	287.1463	0	0	0	0	W	846.4104	423.7089	829.3839	415.1956	828.3999	414.7036	7
5	688.3123	344.6598	0	0	670.3017	335.6545	D	660.3311	330.6692	643.3046	322.1559	642.3206	321.6639	6
6	801.3964	401.2018	0	0	783.3858	392.1965	L	545.3042	273.1557	528.2776	264.6425	527.2936	264.1504	5
7	872.4335	436.7204	0	0	854.4229	427.7151	A	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	4
8	1001.4761	501.2417	0	0	983.4655	492.2364	E	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	3
9	1058.4975	529.7524	0	0	1040.4870	520.7471	G	232.1404	116.5738	215.1139	108.0606	0	0	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 77203.

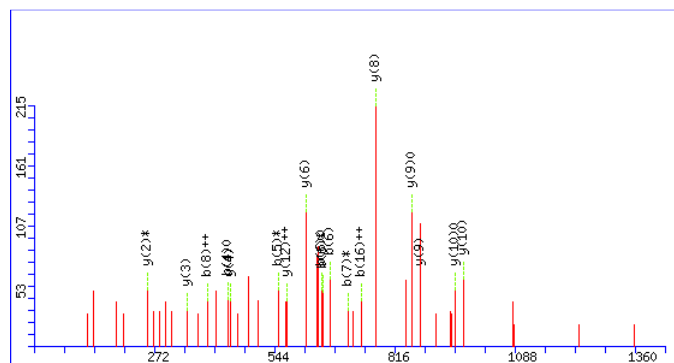
MS/MS Fragmentation of **EQVTNVGGAVVTGVTAVAQK**:

Found in **IP100024107;IP100218467;IP100218468;IP100965305**

Title: 3.1.1.177.7

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120129ry¥120129ry_604A1-46_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							20
2	258.1084	129.5579	241.0819	121.0446	240.0979	120.5526	Q	1799.0021	900.0047	1781.9756	891.4914	1780.9916	890.9994	19
3	357.1769	179.0921	340.1503	170.5788	339.1663	170.0868	V	1670.9436	835.9754	1653.9170	827.4621	1652.9330	826.9701	18
4	458.2245	229.6159	441.1980	221.1026	440.2140	220.6106	T	1571.8751	786.4412	1554.8486	777.9279	1553.8646	777.4359	17
5	572.2675	286.6374	555.2409	278.1241	554.2569	277.6321	N	1470.8275	735.9174	1453.8009	727.4041	1452.8169	726.9121	16
6	671.3359	336.1716	654.3093	327.6583	653.3253	327.1663	V	1356.7845	678.8959	1339.7580	670.3826	1338.7740	669.8906	15
7	728.3573	364.6823	711.3308	356.1690	710.3468	355.6770	G	1257.7161	629.3617	1240.6896	620.8484	1239.7056	620.3564	14
8	785.3788	393.1930	768.3523	384.6798	767.3682	384.1878	G	1200.6947	600.8510	1183.6681	592.3377	1182.6841	591.8457	13
9	856.4159	428.7116	839.3894	420.1983	838.4054	419.7063	A	1143.6732	572.3402	1126.6467	563.8270	1125.6626	563.3350	12
10	955.4843	478.2458	938.4578	469.7325	937.4738	469.2405	V	1072.6361	536.8217	1055.6095	528.3084	1054.6255	527.8164	11
11	1054.5528	527.7800	1037.5262	519.2667	1036.5422	518.7747	V	973.5677	487.2875	956.5411	478.7742	955.5571	478.2822	10
12	1155.6004	578.3039	1138.5739	569.7906	1137.5899	569.2986	T	874.4993	437.7533	857.4727	429.2400	856.4887	428.7480	9
13	1212.6219	606.8146	1195.5953	598.3013	1194.6113	597.8093	G	773.4516	387.2294	756.4250	378.7162	755.4410	378.2241	8
14	1311.6903	656.3488	1294.6638	647.8355	1293.6797	647.3435	V	716.4301	358.7187	699.4036	350.2054	698.4196	349.7134	7
15	1412.7380	706.8726	1395.7114	698.3594	1394.7274	697.8673	T	617.3617	309.1845	600.3352	300.6712	599.3511	300.1792	6
16	1483.7751	742.3912	1466.7486	733.8779	1465.7645	733.3859	A	516.3140	258.6606	499.2875	250.1474	0	0	5
17	1582.8435	791.9254	1565.8170	783.4121	1564.8330	782.9201	V	445.2769	223.1421	428.2504	214.6288	0	0	4
18	1653.8806	827.4440	1636.8541	818.9307	1635.8701	818.4387	A	346.2085	173.6079	329.1819	165.0946	0	0	3
19	1781.9392	891.4732	1764.9127	882.9600	1763.9286	882.4680	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
20							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 77289.

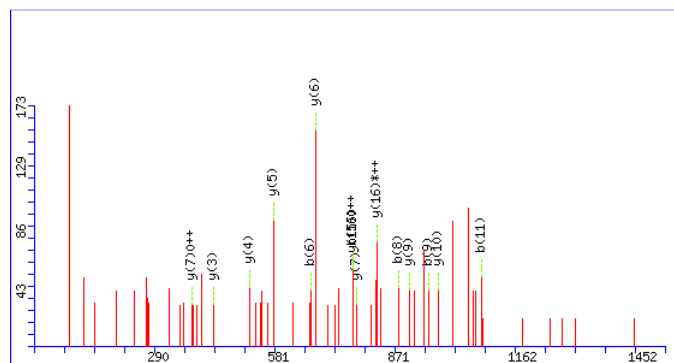
MS/MS Fragmentation of **DALSHFVIAGAVTGSLFR**:

Found in **IP100299387;IP100945609**

Title: 4.1.1.785.3

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							18
2	187.0713	94.0393	0	0	169.0608	85.0340	A	1745.9697	873.4885	1728.9432	864.9752	1727.9592	864.4832	17
3	300.1554	150.5813	0	0	282.1448	141.5761	L	1674.9326	837.9699	1657.9061	829.4567	1656.9220	828.9647	16
4	387.1874	194.0974	0	0	369.1769	185.0921	S	1561.8485	781.4279	1544.8220	772.9146	1543.8380	772.4226	15
5	524.2463	262.6268	0	0	506.2358	253.6215	H	1474.8165	737.9119	1457.7900	729.3986	1456.8059	728.9066	14
6	671.3148	336.1610	0	0	653.3042	327.1557	F	1337.7576	669.3824	1320.7310	660.8692	1319.7470	660.3772	13
7	770.3832	385.6952	0	0	752.3726	376.6899	V	1190.6892	595.8482	1173.6626	587.3350	1172.6786	586.8429	12
8	883.4672	442.2373	0	0	865.4567	433.2320	I	1091.6208	546.3140	1074.5942	537.8007	1073.6102	537.3087	11
9	954.5043	477.7558	0	0	936.4938	468.7505	A	978.5367	489.7720	961.5102	481.2587	960.5261	480.7667	10
10	1011.5258	506.2665	0	0	993.5152	497.2613	G	907.4996	454.2534	890.4730	445.7402	889.4890	445.2482	9
11	1082.5629	541.7851	0	0	1064.5524	532.7798	A	850.4781	425.7427	833.4516	417.2294	832.4676	416.7374	8
12	1181.6313	591.3193	0	0	1163.6208	582.3140	V	779.4410	390.2241	762.4145	381.7109	761.4305	381.2189	7
13	1282.6790	641.8431	0	0	1264.6684	632.8379	T	680.3726	340.6899	663.3461	332.1767	662.3620	331.6847	6
14	1339.7005	670.3539	0	0	1321.6899	661.3486	G	579.3249	290.1661	562.2984	281.6528	561.3144	281.1608	5
15	1426.7325	713.8699	0	0	1408.7219	704.8646	S	522.3035	261.6554	505.2769	253.1421	504.2929	252.6501	4
16	1539.8166	770.4119	0	0	1521.8060	761.4066	L	435.2714	218.1394	418.2449	209.6261	0	0	3
17	1686.8850	843.9461	0	0	1668.8744	834.9408	F	322.1874	161.5973	305.1608	153.0840	0	0	2
18							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 77483.

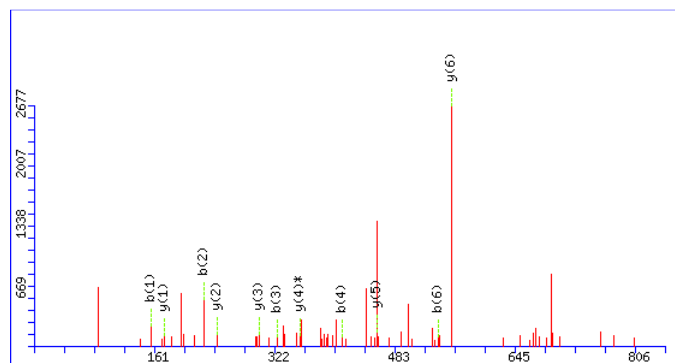
MS/MS Fragmentation of **RAVSAGAR**:

Found in **IP100883929**

Title: 1.1.1.7662.3

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120214ry¥120214ry_414C2-43_4_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	157.1084	79.0578	140.0818	70.5446	0	0	R							8
2	228.1455	114.5764	211.1190	106.0631	0	0	A	631.3522	316.1797	614.3257	307.6665	613.3416	307.1745	7
3	327.2139	164.1106	310.1874	155.5973	0	0	V	560.3151	280.6612	543.2885	272.1479	542.3045	271.6559	6
4	414.2459	207.6266	397.2194	199.1133	396.2354	198.6213	S	461.2467	231.1270	444.2201	222.6137	443.2361	222.1217	5
5	485.2831	243.1452	468.2565	234.6319	467.2725	234.1399	A	374.2146	187.6110	357.1881	179.0977	0	0	4
6	542.3045	271.6559	525.2780	263.1426	524.2940	262.6506	G	303.1775	152.0924	286.1510	143.5791	0	0	3
7	613.3416	307.1745	596.3151	298.6612	595.3311	298.1692	A	246.1561	123.5817	229.1295	115.0684	0	0	2
8							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 77769.

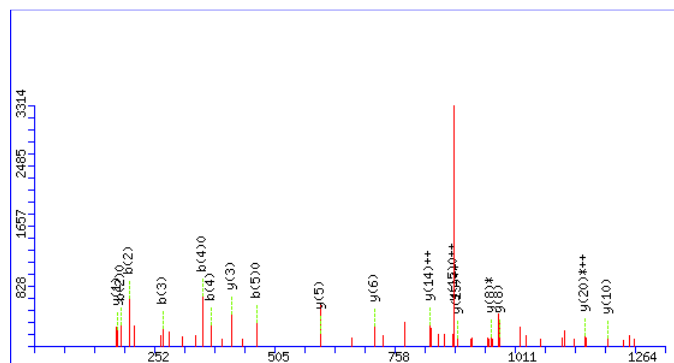
MS/MS Fragmentation of **AEATPLVGRDEDFVGRDDFDADQLR**:

Found in **IP100012235**

Title: 3.1.1.1624.8

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							28
2	201.0870	101.0471	0	0	183.0764	92.0418	E	3061.4497	1531.2285	3044.4232	1522.7152	3043.4392	1522.2232	27
3	272.1241	136.5657	0	0	254.1135	127.5604	A	2932.4072	1466.7072	2915.3806	1458.1939	2914.3966	1457.7019	26
4	373.1718	187.0895	0	0	355.1612	178.0842	T	2861.3700	1431.1887	2844.3435	1422.6754	2843.3595	1422.1834	25
5	486.2558	243.6316	0	0	468.2453	234.6263	I	2760.3224	1380.6648	2743.2958	1372.1515	2742.3118	1371.6595	24
6	583.3086	292.1579	0	0	565.2980	283.1527	P	2647.2383	1324.1228	2630.2118	1315.6095	2629.2277	1315.1175	23
7	696.3927	348.7000	0	0	678.3821	339.6947	L	2550.1855	1275.5964	2533.1590	1267.0831	2532.1750	1266.5911	22
8	795.4611	398.2342	0	0	777.4505	389.2289	V	2437.1015	1219.0544	2420.0749	1210.5411	2419.0909	1210.0491	21
9	892.5138	446.7606	0	0	874.5033	437.7553	P	2338.0331	1169.5202	2321.0065	1161.0069	2320.0225	1160.5149	20
10	949.5353	475.2713	0	0	931.5247	466.2660	G	2240.9803	1120.9938	2223.9537	1112.4805	2222.9697	1111.9885	19
11	1105.6364	553.3218	1088.6099	544.8086	1087.6259	544.3166	R	2183.9588	1092.4831	2166.9323	1083.9698	2165.9483	1083.4778	18
12	1220.6634	610.8353	1203.6368	602.3220	1202.6528	601.8300	D	2027.8577	1014.4325	2010.8312	1005.9192	2009.8472	1005.4272	17
13	1349.7060	675.3566	1332.6794	666.8433	1331.6954	666.3513	E	1912.8308	956.9190	1895.8042	948.4058	1894.8202	947.9137	16
14	1464.7329	732.8701	1447.7064	724.3568	1446.7223	723.8648	D	1783.7882	892.3977	1766.7616	883.8845	1765.7776	883.3924	15
15	1611.8013	806.4043	1594.7748	797.8910	1593.7907	797.3990	F	1668.7612	834.8843	1651.7347	826.3710	1650.7507	825.8790	14
16	1710.8697	855.9385	1693.8432	847.4252	1692.8592	846.9332	V	1521.6928	761.3501	1504.6663	752.8368	1503.6823	752.3448	13
17	1767.8912	884.4492	1750.8646	875.9360	1749.8806	875.4440	G	1422.6244	711.8158	1405.5979	703.3026	1404.6138	702.8106	12
18	1923.9923	962.4998	1906.9658	953.9865	1905.9817	953.4945	R	1365.6029	683.3051	1348.5764	674.7918	1347.5924	674.2998	11
19	2039.0192	1020.0133	2021.9927	1011.5000	2021.0087	1011.0080	D	1209.5018	605.2546	1192.4753	596.7413	1191.4913	596.2493	10
20	2154.0462	1077.5267	2137.0196	1069.0135	2136.0356	1068.5215	D	1094.4749	547.7411	1077.4483	539.2278	1076.4643	538.7358	9
21	2301.1146	1151.0609	2284.0881	1142.5477	2283.1040	1142.0557	F	979.4480	490.2276	962.4214	481.7143	961.4374	481.2223	8
22	2416.1415	1208.5744	2399.1150	1200.0611	2398.1310	1199.5691	D	832.3795	416.6934	815.3530	408.1801	814.3690	407.6881	7
23	2531.1685	1266.0879	2514.1419	1257.5746	2513.1579	1257.0826	D	717.3526	359.1799	700.3260	350.6667	699.3420	350.1747	6
24	2602.2056	1301.6064	2585.1791	1293.0932	2584.1950	1292.6012	A	602.3257	301.6665	585.2991	293.1532	584.3151	292.6612	5
25	2717.2325	1359.1199	2700.2060	1350.6066	2699.2220	1350.1146	D	531.2885	266.1479	514.2620	257.6346	513.2780	257.1426	4
26	2845.2911	1423.1492	2828.2646	1414.6359	2827.2806	1414.1439	Q	416.2616	208.6344	399.2350	200.1212	0	0	3
27	2958.3752	1479.6912	2941.3486	1471.1780	2940.3646	1470.6859	L	288.2030	144.6051	271.1765	136.0919	0	0	2
28							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 77772.

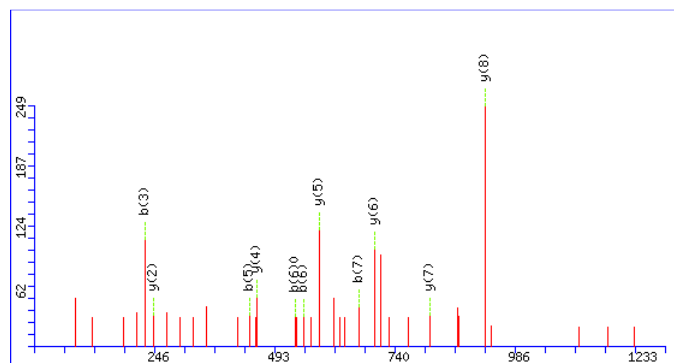
MS/MS Fragmentation of **GGLVDLLQVLAR**:

Found in **IP100386243**

Title: 4.1.1.2517.3

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							12
2	115.0502	58.0287	0	0	0	0	G	1196.7361	598.8717	1179.7096	590.3584	1178.7256	589.8664	11
3	228.1343	114.5708	0	0	0	0	L	1139.7147	570.3610	1122.6881	561.8477	1121.7041	561.3557	10
4	327.2027	164.1050	0	0	0	0	V	1026.6306	513.8189	1009.6041	505.3057	1008.6200	504.8137	9
5	442.2296	221.6185	0	0	424.2191	212.6132	D	927.5622	464.2847	910.5356	455.7715	909.5516	455.2795	8
6	555.3137	278.1605	0	0	537.3031	269.1552	L	812.5352	406.7713	795.5087	398.2580	0	0	7
7	668.3978	334.7025	0	0	650.3872	325.6972	L	699.4512	350.2292	682.4246	341.7160	0	0	6
8	796.4563	398.7318	779.4298	390.2185	778.4458	389.7265	Q	586.3671	293.6872	569.3406	285.1739	0	0	5
9	895.5247	448.2660	878.4982	439.7527	877.5142	439.2607	V	458.3085	229.6579	441.2820	221.1446	0	0	4
10	1008.6088	504.8080	991.5823	496.2948	990.5982	495.8028	L	359.2401	180.1237	342.2136	171.6104	0	0	3
11	1079.6459	540.3266	1062.6194	531.8133	1061.6354	531.3213	A	246.1561	123.5817	229.1295	115.0684	0	0	2
12							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 77934.

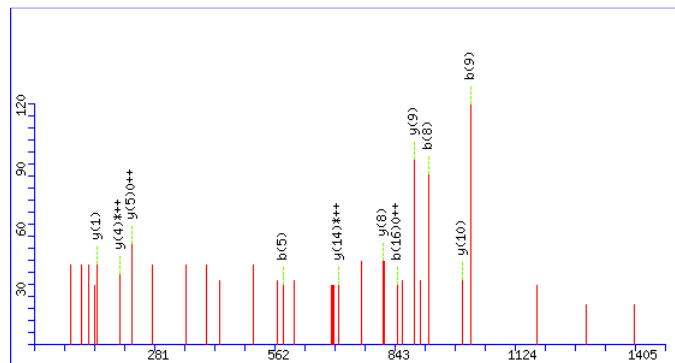
MS/MS Fragmentation of **TDVHELLDVIIADLDGGTIK**:

Found in **IP100654703;IP100719299**

Title: 5.1.1.1461.2

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2.5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							20
2	217.0819	109.0446	0	0	199.0713	100.0393	D	2036.0910	1018.5491	2019.0645	1010.0359	2018.0804	1009.5439	19
3	316.1503	158.5788	0	0	298.1397	149.5735	V	1921.0641	961.0357	1904.0375	952.5224	1903.0535	952.0304	18
4	453.2092	227.1083	0	0	435.1987	218.1030	H	1821.9957	911.5015	1804.9691	902.9882	1803.9851	902.4962	17
5	582.2518	291.6295	0	0	564.2413	282.6243	E	1684.9367	842.9720	1667.9102	834.4587	1666.9262	833.9667	16
6	695.3359	348.1716	0	0	677.3253	339.1663	L	1555.8942	778.4507	1538.8676	769.9374	1537.8836	769.4454	15
7	808.4199	404.7136	0	0	790.4094	395.7083	L	1442.8101	721.9087	1425.7835	713.3954	1424.7995	712.9034	14
8	923.4469	462.2271	0	0	905.4363	453.2218	D	1329.7260	665.3666	1312.6995	656.8534	1311.7155	656.3614	13
9	1022.5153	511.7613	0	0	1004.5047	502.7560	V	1214.6991	607.8532	1197.6725	599.3399	1196.6885	598.8479	12
10	1135.5994	568.3033	0	0	1117.5888	559.2980	I	1115.6307	558.3190	1098.6041	549.8057	1097.6201	549.3137	11
11	1248.6834	624.8454	0	0	1230.6729	615.8401	I	1002.5466	501.7769	985.5201	493.2637	984.5360	492.7717	10
12	1319.7205	660.3639	0	0	1301.7100	651.3586	A	889.4625	445.2349	872.4360	436.7216	871.4520	436.2296	9
13	1434.7475	717.8774	0	0	1416.7369	708.8721	D	818.4254	409.7164	801.3989	401.2031	800.4149	400.7111	8
14	1547.8316	774.4194	0	0	1529.8210	765.4141	L	703.3985	352.2029	686.3719	343.6896	685.3879	343.1976	7
15	1662.8585	831.9329	0	0	1644.8479	822.9276	D	590.3144	295.6608	573.2879	287.1476	572.3039	286.6556	6
16	1719.8800	860.4436	0	0	1701.8694	851.4383	G	475.2875	238.1474	458.2609	229.6341	457.2769	229.1421	5
17	1776.9014	888.9543	0	0	1758.8909	879.9491	G	418.2660	209.6366	401.2395	201.1234	400.2554	200.6314	4
18	1877.9491	939.4782	0	0	1859.9385	930.4729	T	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
19	1991.0332	996.0202	0	0	1973.0226	987.0149	I	260.1969	130.6021	243.1703	122.0888	0	0	2
20							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 78068.

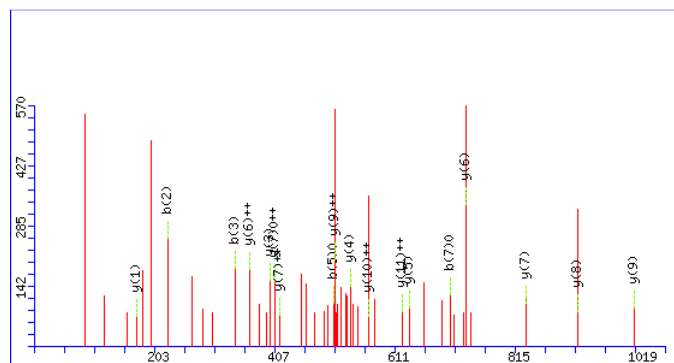
MS/MS Fragmentation of **LLDPSTPVHILR**:

Found in **IP100015809**

Title: 2.1.1.3174.3

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							12
2	227.1754	114.0913	0	0	0	0	L	1247.7106	624.3590	1230.6841	615.8457	1229.7001	615.3537	11
3	342.2023	171.6048	0	0	324.1918	162.5995	D	1134.6266	567.8169	1117.6000	559.3037	1116.6160	558.8116	10
4	439.2551	220.1312	0	0	421.2445	211.1259	P	1019.5996	510.3035	1002.5731	501.7902	1001.5891	501.2982	9
5	526.2871	263.6472	0	0	508.2766	254.6419	S	922.5469	461.7771	905.5203	453.2638	904.5363	452.7718	8
6	627.3348	314.1710	0	0	609.3243	305.1658	T	835.5148	418.2611	818.4883	409.7478	817.5043	409.2558	7
7	724.3876	362.6974	0	0	706.3770	353.6921	P	734.4672	367.7372	717.4406	359.2239	0	0	6
8	823.4560	412.2316	0	0	805.4454	403.2264	V	637.4144	319.2108	620.3879	310.6976	0	0	5
9	960.5149	480.7611	0	0	942.5043	471.7558	H	538.3460	269.6766	521.3194	261.1634	0	0	4
10	1073.5990	537.3031	0	0	1055.5884	528.2978	I	401.2871	201.1472	384.2605	192.6339	0	0	3
11	1186.6830	593.8452	0	0	1168.6725	584.8399	L	288.2030	144.6051	271.1765	136.0919	0	0	2
12							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 78154.

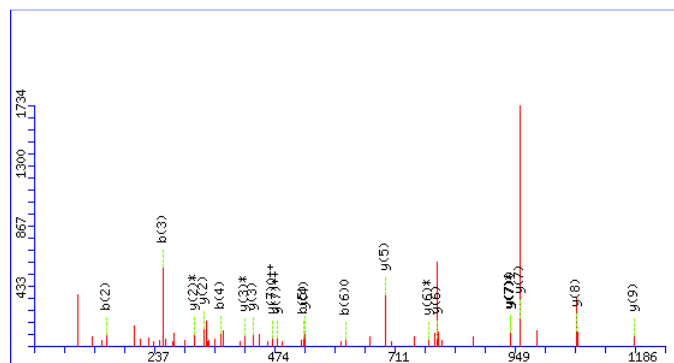
MS/MS Fragmentation of **AALIYTCVCR**: 57.021465@C:7,57.021465@C:10

Found in **IP100183657;IP100976387;IP100979126;IP100984953**

Title: 2.1.1.1279.9

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120214ry¥120214ry_414C2-43_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							11
2	143.0815	72.0444	0	0	0	0	A	1256.6126	628.8099	1239.5860	620.2967	1238.6020	619.8047	10
3	256.1656	128.5864	0	0	0	0	L	1185.5755	593.2914	1168.5489	584.7781	1167.5649	584.2861	9
4	369.2496	185.1285	0	0	0	0	I	1072.4914	536.7493	1055.4649	528.2361	1054.4809	527.7441	8
5	532.3130	266.6601	0	0	0	0	Y	959.4074	480.2073	942.3808	471.6940	941.3968	471.2020	7
6	633.3606	317.1840	0	0	615.3501	308.1787	T	796.3440	398.6756	779.3175	390.1624	778.3335	389.6704	6
7	793.3913	397.1993	0	0	775.3807	388.1940	C	695.2963	348.1518	678.2698	339.6385	677.2858	339.1465	5
8	894.4390	447.7231	0	0	876.4284	438.7178	T	535.2657	268.1365	518.2391	259.6232	517.2551	259.1312	4
9	993.5074	497.2573	0	0	975.4968	488.2520	V	434.2180	217.6126	417.1915	209.0994	0	0	3
10	1153.5380	577.2727	0	0	1135.5275	568.2674	C	335.1496	168.0784	318.1231	159.5652	0	0	2
11							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 78608.

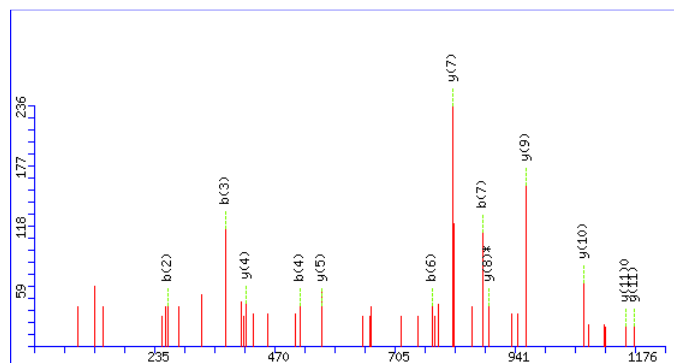
MS/MS Fragmentation of **FNLPCVLGSPCFIAGR**: 57.021465@C:8,57.021465@C:12

Found in **IP100426252;IP100892663;IP100892915;IP100894328;IP101012273**

Title: 4.1.1.1121.3

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							17
2	262.1186	131.5629	245.0921	123.0497	0	0	N	1807.8982	904.4527	1790.8717	895.9395	1789.8876	895.4475	16
3	375.2027	188.1050	358.1761	179.5917	0	0	L	1693.8553	847.4313	1676.8287	838.9180	1675.8447	838.4260	15
4	522.2711	261.6392	505.2445	253.1259	0	0	F	1580.7712	790.8892	1563.7447	782.3760	1562.7607	781.8840	14
5	619.3239	310.1656	602.2973	301.6523	0	0	P	1433.7028	717.3550	1416.6763	708.8418	1415.6922	708.3498	13
6	779.3545	390.1809	762.3280	381.6676	0	0	C	1336.6500	668.8287	1319.6235	660.3154	1318.6395	659.8234	12
7	878.4229	439.7151	861.3964	431.2018	0	0	V	1176.6194	588.8133	1159.5928	580.3001	1158.6088	579.8081	11
8	991.5070	496.2571	974.4804	487.7439	0	0	L	1077.5510	539.2791	1060.5244	530.7659	1059.5404	530.2738	10
9	1048.5285	524.7679	1031.5019	516.2546	0	0	G	964.4669	482.7371	947.4404	474.2238	946.4563	473.7318	9
10	1135.5605	568.2839	1118.5339	559.7706	1117.5499	559.2786	S	907.4454	454.2264	890.4189	445.7131	889.4349	445.2211	8
11	1232.6132	616.8103	1215.5867	608.2970	1214.6027	607.8050	P	820.4134	410.7103	803.3869	402.1971	0	0	7
12	1392.6439	696.8256	1375.6173	688.3123	1374.6333	687.8203	C	723.3607	362.1840	706.3341	353.6707	0	0	6
13	1539.7123	770.3598	1522.6858	761.8465	1521.7017	761.3545	F	563.3300	282.1686	546.3035	273.6554	0	0	5
14	1652.7964	826.9018	1635.7698	818.3885	1634.7858	817.8965	I	416.2616	208.6344	399.2350	200.1212	0	0	4
15	1723.8335	862.4204	1706.8069	853.9071	1705.8229	853.4151	A	303.1775	152.0924	286.1510	143.5791	0	0	3
16	1780.8549	890.9311	1763.8284	882.4178	1762.8444	881.9258	G	232.1404	116.5738	215.1139	108.0606	0	0	2
17							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 78852.

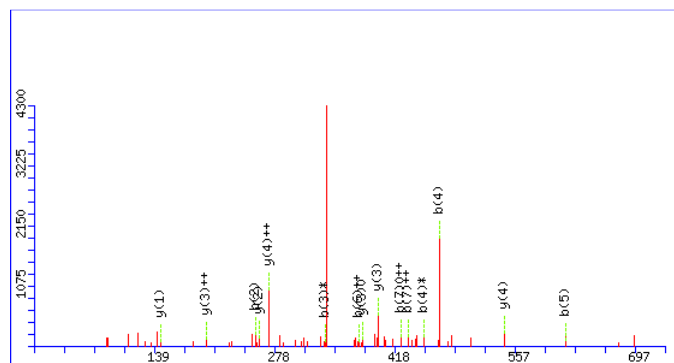
MS/MS Fragmentation of **RTPDFHDK**:

Found in **IP100028003**

Title: 1.1.1.7103.4

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	157.1084	79.0578	140.0818	70.5446	0	0	R							8
2	258.1561	129.5817	241.1295	121.0684	240.1455	120.5764	T	859.3945	430.2009	842.3679	421.6876	841.3839	421.1956	7
3	355.2088	178.1081	338.1823	169.5948	337.1983	169.1028	P	758.3468	379.6770	741.3202	371.1638	740.3362	370.6717	6
4	470.2358	235.6215	453.2092	227.1082	452.2252	226.6162	D	661.2940	331.1506	644.2675	322.6374	643.2835	322.1454	5
5	617.3042	309.1557	600.2776	300.6425	599.2936	300.1504	F	546.2671	273.6372	529.2405	265.1239	528.2565	264.6319	4
6	754.3631	377.6852	737.3365	369.1719	736.3525	368.6799	H	399.1987	200.1030	382.1721	191.5897	381.1881	191.0977	3
7	869.3900	435.1987	852.3635	426.6854	851.3795	426.1934	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
8							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 78928.

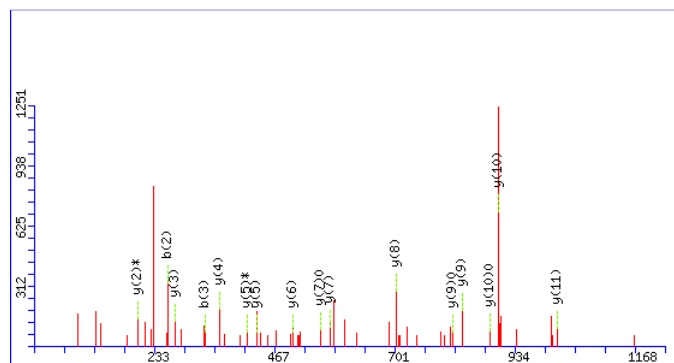
MS/MS Fragmentation of **FIAEEAAASGAK**:

Found in **IP100023635;IP100555726**

Title: 1.1.1.8685.11

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							12
2	261.1598	131.0835	0	0	0	0	I	1017.5211	509.2642	1000.4946	500.7509	999.5106	500.2589	11
3	332.1969	166.6021	0	0	0	0	A	904.4371	452.7222	887.4105	444.2089	886.4265	443.7169	10
4	461.2395	231.1234	0	0	443.2289	222.1181	E	833.3999	417.2036	816.3734	408.6903	815.3894	408.1983	9
5	590.2821	295.6447	0	0	572.2715	286.6394	E	704.3573	352.6823	687.3308	344.1690	686.3468	343.6770	8
6	661.3192	331.1632	0	0	643.3086	322.1579	A	575.3148	288.1610	558.2882	279.6477	557.3042	279.1557	7
7	732.3563	366.6818	0	0	714.3457	357.6765	A	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	6
8	803.3934	402.2003	0	0	785.3828	393.1951	A	433.2405	217.1239	416.2140	208.6106	415.2300	208.1186	5
9	890.4254	445.7164	0	0	872.4149	436.7111	S	362.2034	181.6053	345.1769	173.0921	344.1928	172.6001	4
10	947.4469	474.2271	0	0	929.4363	465.2218	G	275.1714	138.0893	258.1448	129.5761	0	0	3
11	1018.4840	509.7456	0	0	1000.4734	500.7404	A	218.1499	109.5786	201.1234	101.0653	0	0	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

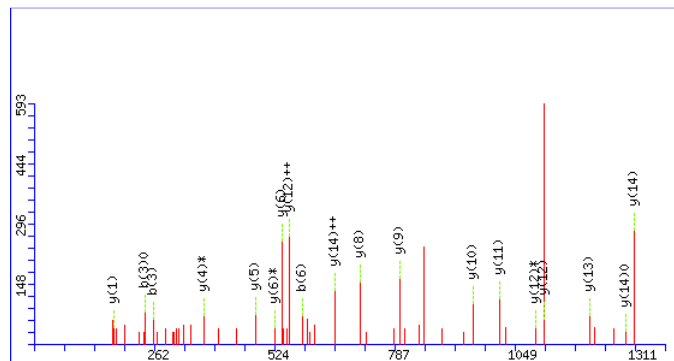
Peptide: 79032.

MS/MS Fragmentation of **GDSEPTPGCSQLPGGVR: 57.021465@C:9**
 Found in **IP100450071;IP100642943;IP100828179;IP100978645;IP100980533**

Title: 1.1.1.9459.11

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							18
2	173.0557	87.0315	0	0	155.0451	78.0262	D	1642.7490	821.8781	1625.7224	813.3648	1624.7384	812.8728	17
3	260.0877	130.5475	0	0	242.0771	121.5422	S	1527.7220	764.3646	1510.6955	755.8514	1509.7115	755.3594	16
4	389.1303	195.0688	0	0	371.1197	186.0635	E	1440.6900	720.8486	1423.6634	712.3354	1422.6794	711.8434	15
5	486.1831	243.5952	0	0	468.1725	234.5899	P	1311.6474	656.3273	1294.6208	647.8141	1293.6368	647.3221	14
6	587.2307	294.1190	0	0	569.2202	285.1137	T	1214.5946	607.8010	1197.5681	599.2877	1196.5841	598.7957	13
7	684.2835	342.6454	0	0	666.2729	333.6401	P	1113.5470	557.2771	1096.5204	548.7638	1095.5364	548.2718	12
8	741.3050	371.1561	0	0	723.2944	362.1508	G	1016.4942	508.7507	999.4676	500.2375	998.4836	499.7455	11
9	901.3356	451.1715	0	0	883.3251	442.1662	C	959.4727	480.2400	942.4462	471.7267	941.4622	471.2347	10
10	988.3677	494.6875	0	0	970.3571	485.6822	S	799.4421	400.2247	782.4155	391.7114	781.4315	391.2194	9
11	1045.3891	523.1982	0	0	1027.3786	514.1929	G	712.4100	356.7087	695.3835	348.1954	0	0	8
12	1158.4732	579.7402	0	0	1140.4626	570.7349	L	655.3886	328.1979	638.3620	319.6847	0	0	7
13	1215.4946	608.2510	0	0	1197.4841	599.2457	G	542.3045	271.6559	525.2780	263.1426	0	0	6
14	1312.5474	656.7773	0	0	1294.5368	647.7721	P	485.2831	243.1452	468.2565	234.6319	0	0	5
15	1369.5689	685.2881	0	0	1351.5583	676.2828	G	388.2303	194.6188	371.2037	186.1055	0	0	4
16	1426.5903	713.7988	0	0	1408.5798	704.7935	G	331.2088	166.1081	314.1823	157.5948	0	0	3
17	1525.6588	763.3330	0	0	1507.6482	754.3277	V	274.1874	137.5973	257.1608	129.0840	0	0	2
18							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 79266.

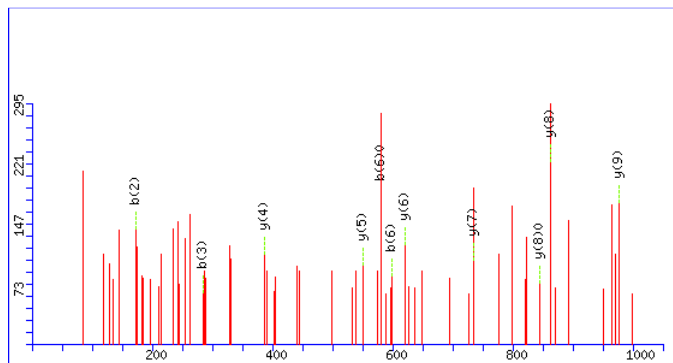
MS/MS Fragmentation of **TAIELAYLGAK**:

Found in **IP100183018;IP100414591;IP100552407;IP100922235;IP100976400;IP100979386;IP101009917**

Title: 2.1.1.4289.5

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							11
2	173.0921	87.0497	0	0	155.0815	78.0444	A	1048.6037	524.8055	1031.5772	516.2922	1030.5932	515.8002	10
3	286.1761	143.5917	0	0	268.1656	134.5864	I	977.5666	489.2869	960.5401	480.7737	959.5560	480.2817	9
4	415.2187	208.1130	0	0	397.2082	199.1077	E	864.4825	432.7449	847.4560	424.2316	846.4720	423.7396	8
5	528.3028	264.6550	0	0	510.2922	255.6498	L	735.4400	368.2236	718.4134	359.7103	0	0	7
6	599.3399	300.1736	0	0	581.3293	291.1683	A	622.3559	311.6816	605.3293	303.1683	0	0	6
7	762.4032	381.7053	0	0	744.3927	372.7000	Y	551.3188	276.1630	534.2922	267.6498	0	0	5
8	875.4873	438.2473	0	0	857.4767	429.2420	L	388.2554	194.6314	371.2289	186.1181	0	0	4
9	932.5088	466.7580	0	0	914.4982	457.7527	G	275.1714	138.0893	258.1448	129.5761	0	0	3
10	1003.5459	502.2766	0	0	985.5353	493.2713	A	218.1499	109.5786	201.1234	101.0653	0	0	2
11							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 79685.

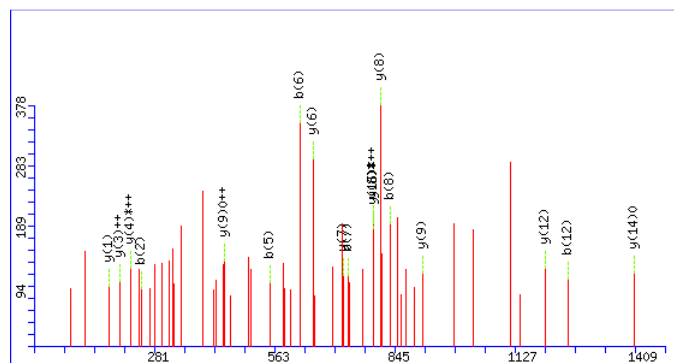
MS/MS Fragmentation of **DHTSLALVQNGDVSAPSAILR: 0.984015@N:10**

Found in **IP100061168**

Title: 3.1.1.650.8

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							21
2	253.0931	127.0502	0	0	235.0826	118.0449	H	2050.0927	1025.5500	2033.0662	1017.0367	2032.0822	1016.5447	20
3	354.1408	177.5740	0	0	336.1302	168.5688	T	1913.0338	957.0206	1896.0073	948.5073	1895.0233	948.0153	19
4	441.1728	221.0901	0	0	423.1623	212.0848	S	1811.9862	906.4967	1794.9596	897.9834	1793.9756	897.4914	18
5	554.2569	277.6321	0	0	536.2463	268.6268	L	1724.9541	862.9807	1707.9276	854.4674	1706.9436	853.9754	17
6	625.2940	313.1506	0	0	607.2835	304.1454	A	1611.8701	806.4387	1594.8435	797.9254	1593.8595	797.4334	16
7	738.3781	369.6927	0	0	720.3675	360.6874	L	1540.8329	770.9201	1523.8064	762.4068	1522.8224	761.9148	15
8	837.4465	419.2269	0	0	819.4359	410.2216	V	1427.7489	714.3781	1410.7223	705.8648	1409.7383	705.3728	14
9	965.5051	483.2562	948.4785	474.7429	947.4945	474.2509	Q	1328.6805	664.8439	1311.6539	656.3306	1310.6699	655.8386	13
10	1080.5320	540.7696	1063.5055	532.2564	1062.5214	531.7644	N	1200.6219	600.8146	1183.5953	592.3013	1182.6113	591.8093	12
11	1137.5535	569.2804	1120.5269	560.7671	1119.5429	560.2751	G	1085.5949	543.3011	1068.5684	534.7878	1067.5844	534.2958	11
12	1252.5804	626.7938	1235.5539	618.2806	1234.5699	617.7886	D	1028.5735	514.7904	1011.5469	506.2771	1010.5629	505.7851	10
13	1351.6488	676.3281	1334.6223	667.8148	1333.6383	667.3228	V	913.5465	457.2769	896.5200	448.7636	895.5360	448.2716	9
14	1438.6809	719.8441	1421.6543	711.3308	1420.6703	710.8388	S	814.4781	407.7427	797.4516	399.2294	796.4676	398.7374	8
15	1509.7180	755.3626	1492.6914	746.8494	1491.7074	746.3573	A	727.4461	364.2267	710.4196	355.7134	709.4355	355.2214	7
16	1606.7707	803.8890	1589.7442	795.3757	1588.7602	794.8837	P	656.4090	328.7081	639.3824	320.1949	638.3984	319.7028	6
17	1693.8028	847.4050	1676.7762	838.8917	1675.7922	838.3997	S	559.3562	280.1817	542.3297	271.6685	541.3457	271.1765	5
18	1764.8399	882.9236	1747.8133	874.4103	1746.8293	873.9183	A	472.3242	236.6657	455.2976	228.1525	0	0	4
19	1877.9239	939.4656	1860.8974	930.9523	1859.9134	930.4603	I	401.2871	201.1472	384.2605	192.6339	0	0	3
20	1991.0080	996.0076	1973.9815	987.4944	1972.9974	987.0024	L	288.2030	144.6051	271.1765	136.0919	0	0	2
21							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 79989.

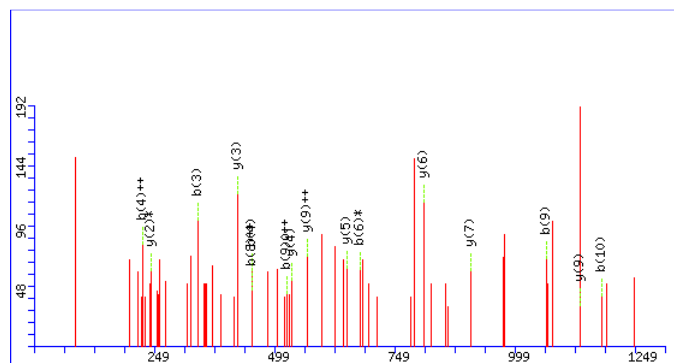
MS/MS Fragmentation of **ILLQNDPCLLPEVCLLYNK**: 57.021465@C:9,57.021465@C:15

Found in **IP100062866**

Title: 4.1.1.1874.5

Data file: Y:\TT5600(CiRA1)\2012-02\120201ry\120201ry_aHDF1388-P9_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							20
2	227.1754	114.0913	0	0	0	0	L	2315.2138	1158.1105	2298.1872	1149.5973	2297.2032	1149.1053	19
3	340.2595	170.6334	0	0	0	0	L	2202.1297	1101.5685	2185.1032	1093.0552	2184.1192	1092.5632	18
4	453.3435	227.1754	0	0	0	0	L	2089.0457	1045.0265	2072.0191	1036.5132	2071.0351	1036.0212	17
5	581.4021	291.2047	564.3756	282.6914	0	0	Q	1975.9616	988.4844	1958.9350	979.9712	1957.9510	979.4792	16
6	695.4450	348.2262	678.4185	339.7129	0	0	N	1847.9030	924.4551	1830.8765	915.9419	1829.8925	915.4499	15
7	810.4720	405.7396	793.4454	397.2264	792.4614	396.7343	D	1733.8601	867.4337	1716.8335	858.9204	1715.8495	858.4284	14
8	907.5247	454.2660	890.4982	445.7527	889.5142	445.2607	P	1618.8332	809.9202	1601.8066	801.4069	1600.8226	800.9149	13
9	1067.5554	534.2813	1050.5288	525.7681	1049.5448	525.2761	C	1521.7804	761.3938	1504.7538	752.8806	1503.7698	752.3885	12
10	1180.6395	590.8234	1163.6129	582.3101	1162.6289	581.8181	L	1361.7497	681.3785	1344.7232	672.8652	1343.7392	672.3732	11
11	1293.7235	647.3654	1276.6970	638.8521	1275.7130	638.3601	L	1248.6657	624.8365	1231.6391	616.3232	1230.6551	615.8312	10
12	1390.7763	695.8918	1373.7497	687.3785	1372.7657	686.8865	P	1135.5816	568.2944	1118.5551	559.7812	1117.5710	559.2892	9
13	1519.8189	760.4131	1502.7923	751.8998	1501.8083	751.4078	E	1038.5288	519.7681	1021.5023	511.2548	1020.5183	510.7628	8
14	1618.8873	809.9473	1601.8607	801.4340	1600.8767	800.9420	V	909.4863	455.2468	892.4597	446.7335	0	0	7
15	1778.9179	889.9626	1761.8914	881.4493	1760.9074	880.9573	C	810.4178	405.7126	793.3913	397.1993	0	0	6
16	1892.0020	946.5046	1874.9755	937.9914	1873.9914	937.4994	L	650.3872	325.6972	633.3606	317.1840	0	0	5
17	2005.0861	1003.0467	1988.0595	994.5334	1987.0755	994.0414	L	537.3031	269.1552	520.2766	260.6419	0	0	4
18	2168.1494	1084.5783	2151.1229	1076.0651	2150.1388	1075.5731	Y	424.2191	212.6132	407.1925	204.0999	0	0	3
19	2282.1923	1141.5998	2265.1658	1133.0865	2264.1818	1132.5945	N	261.1557	131.0815	244.1292	122.5682	0	0	2
20							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 80127.

MS/MS Fragmentation of **DAWVQAIESQILASLQSCSSK: 57.021465@C:18**

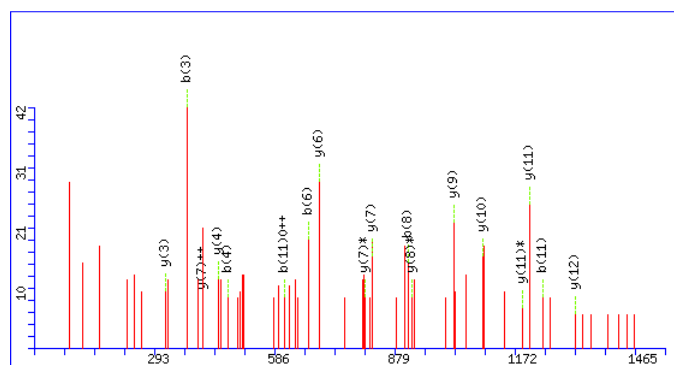
Found in

IP100159901;IP100398893;IP100413998;IP100454973;IP100456242;IP100456244;IP100456856;IP100645616;IP100883586;IP100884922;IP100903295;IP100913910;IP100916;

Title: 5.1.1.104.4

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120210ry¥120210ry_32R1-32_3_5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							22
2	187.0713	94.0393	0	0	169.0608	85.0340	A	2335.1598	1168.0836	2318.1333	1159.5703	2317.1493	1159.0783	21
3	373.1506	187.0790	0	0	355.1401	178.0737	W	2264.1227	1132.5650	2247.0962	1124.0517	2246.1122	1123.5597	20
4	472.2191	236.6132	0	0	454.2085	227.6079	V	2078.0434	1039.5253	2061.0169	1031.0121	2060.0328	1030.5201	19
5	600.2776	300.6425	583.2511	292.1292	582.2671	291.6372	Q	1978.9750	989.9911	1961.9484	981.4779	1960.9644	980.9859	18
6	671.3148	336.1610	654.2882	327.6477	653.3042	327.1557	A	1850.9164	925.9618	1833.8899	917.4486	1832.9059	916.9566	17
7	784.3988	392.7030	767.3723	384.1898	766.3883	383.6978	I	1779.8793	890.4433	1762.8528	881.9300	1761.8687	881.4380	16
8	913.4414	457.2243	896.4149	448.7111	895.4308	448.2191	E	1666.7952	833.9013	1649.7687	825.3880	1648.7847	824.8960	15
9	1000.4734	500.7404	983.4469	492.2271	982.4629	491.7351	S	1537.7526	769.3800	1520.7261	760.8667	1519.7421	760.3747	14
10	1128.5320	564.7696	1111.5055	556.2564	1110.5215	555.7644	Q	1450.7206	725.8639	1433.6941	717.3507	1432.7101	716.8587	13
11	1241.6161	621.3117	1224.5895	612.7984	1223.6055	612.3064	I	1322.6620	661.8347	1305.6355	653.3214	1304.6515	652.8294	12
12	1354.7001	677.8537	1337.6736	669.3404	1336.6896	668.8484	L	1209.5780	605.2926	1192.5514	596.7794	1191.5674	596.2873	11
13	1425.7373	713.3723	1408.7107	704.8590	1407.7267	704.3670	A	1096.4939	548.7506	1079.4674	540.2373	1078.4834	539.7453	10
14	1512.7693	756.8883	1495.7427	748.3750	1494.7587	747.8830	S	1025.4568	513.2320	1008.4303	504.7188	1007.4462	504.2268	9
15	1625.8533	813.4303	1608.8268	804.9170	1607.8428	804.4250	L	938.4248	469.7160	921.3982	461.2027	920.4142	460.7107	8
16	1753.9119	877.4596	1736.8854	868.9463	1735.9014	868.4543	Q	825.3407	413.1740	808.3142	404.6607	807.3301	404.1687	7
17	1840.9440	920.9756	1823.9174	912.4623	1822.9334	911.9703	S	697.2821	349.1447	680.2556	340.6314	679.2716	340.1394	6
18	2000.9746	1000.9909	1983.9481	992.4777	1982.9640	991.9857	C	610.2501	305.6287	593.2236	297.1154	592.2395	296.6234	5
19	2130.0172	1065.5122	2112.9906	1056.9990	2112.0066	1056.5070	E	450.2195	225.6134	433.1929	217.1001	432.2089	216.6081	4
20	2217.0492	1109.0283	2200.0227	1100.5150	2199.0387	1100.0230	S	321.1769	161.0921	304.1503	152.5788	303.1663	152.0868	3
21	2304.0813	1152.5443	2287.0547	1144.0310	2286.0707	1143.5390	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
22							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 80229.

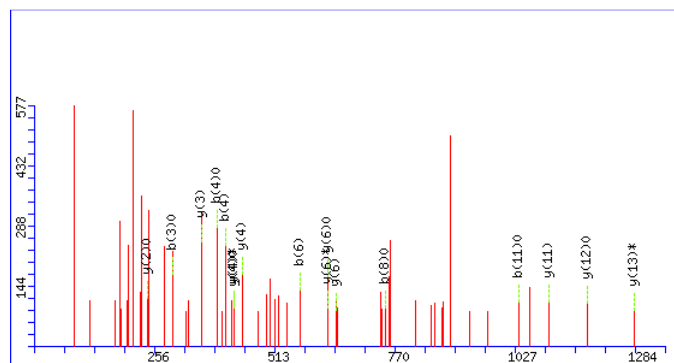
MS/MS Fragmentation of **LTVPTGLSVTSPDK**:

Found in **IP100011159;IP100383471;IP100401785;IP100473049;IP100478422**

Title: 4.1.1.2414.6

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							14
2	215.1390	108.0731	0	0	197.1285	99.0679	T	1301.6947	651.3510	1284.6682	642.8377	1283.6842	642.3457	13
3	314.2074	157.6074	0	0	296.1969	148.6021	V	1200.6470	600.8272	1183.6205	592.3139	1182.6365	591.8219	12
4	411.2602	206.1337	0	0	393.2496	197.1285	P	1101.5786	551.2930	1084.5521	542.7797	1083.5681	542.2877	11
5	512.3079	256.6576	0	0	494.2973	247.6523	T	1004.5259	502.7666	987.4993	494.2533	986.5153	493.7613	10
6	569.3293	285.1683	0	0	551.3188	276.1630	G	903.4782	452.2427	886.4516	443.7295	885.4676	443.2374	9
7	682.4134	341.7103	0	0	664.4028	332.7051	L	846.4567	423.7320	829.4302	415.2187	828.4462	414.7267	8
8	769.4454	385.2264	0	0	751.4349	376.2211	S	733.3727	367.1900	716.3461	358.6767	715.3621	358.1847	7
9	868.5138	434.7606	0	0	850.5033	425.7553	V	646.3406	323.6740	629.3141	315.1607	628.3301	314.6687	6
10	969.5615	485.2844	0	0	951.5510	476.2791	T	547.2722	274.1397	530.2457	265.6265	529.2617	265.1345	5
11	1056.5936	528.8004	0	0	1038.5830	519.7951	S	446.2245	223.6159	429.1980	215.1026	428.2140	214.6106	4
12	1153.6463	577.3268	0	0	1135.6358	568.3215	P	359.1925	180.0999	342.1660	171.5866	341.1819	171.0946	3
13	1268.6733	634.8403	0	0	1250.6627	625.8350	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 80398.

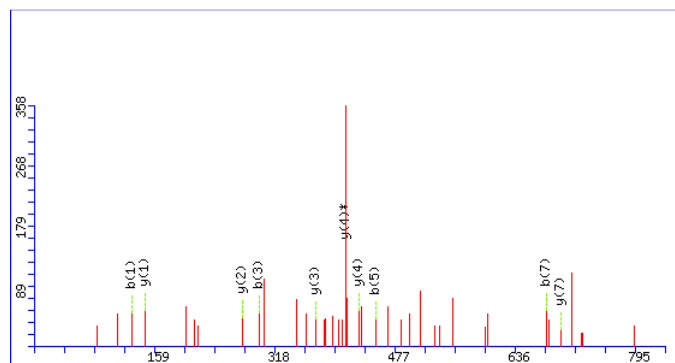
MS/MS Fragmentation of **QGLPGPEK**:

Found in **IP100019794;IP100847618**

Title: 1.1.1.6926.5

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120212ry¥120212ry_aHDF1388-P9_2_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233	0	0	Q							8
2	186.0873	93.5473	169.0608	85.0340	0	0	G	697.3879	349.1976	680.3614	340.6843	679.3774	340.1923	7
3	299.1714	150.0893	282.1448	141.5761	0	0	L	640.3665	320.6869	623.3399	312.1736	622.3559	311.6816	6
4	396.2241	198.6157	379.1976	190.1024	0	0	P	527.2824	264.1448	510.2558	255.6316	509.2718	255.1396	5
5	453.2456	227.1264	436.2191	218.6132	0	0	G	430.2296	215.6185	413.2031	207.1052	412.2191	206.6132	4
6	550.2984	275.6528	533.2718	267.1396	0	0	P	373.2082	187.1077	356.1816	178.5944	355.1976	178.1024	3
7	679.3410	340.1741	662.3144	331.6608	661.3304	331.1688	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
8							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 80427.

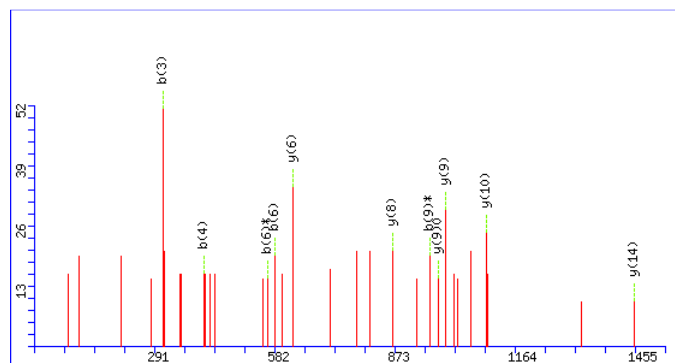
MS/MS Fragmentation of **NAQVAVTQYQVLSSTLSSALVELQPITGIK**:

Found in **IP100304069**

Title: 5.1.1.853.6

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_3_5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							30
2	186.0873	93.5473	169.0608	85.0340	0	0	A	3044.6878	1522.8475	3027.6612	1514.3343	3026.6772	1513.8423	29
3	314.1459	157.5766	297.1193	149.0633	0	0	Q	2973.6507	1487.3290	2956.6241	1478.8157	2955.6401	1478.3237	28
4	413.2143	207.1108	396.1878	198.5975	0	0	V	2845.5921	1423.2997	2828.5656	1414.7864	2827.5815	1414.2944	27
5	484.2514	242.6293	467.2249	234.1161	0	0	A	2746.5237	1373.7655	2729.4971	1365.2522	2728.5131	1364.7602	26
6	583.3198	292.1636	566.2933	283.6503	0	0	V	2675.4866	1338.2469	2658.4600	1329.7337	2657.4760	1329.2416	25
7	684.3675	342.6874	667.3410	334.1741	666.3570	333.6821	T	2576.4182	1288.7127	2559.3916	1280.1994	2558.4076	1279.7074	24
8	812.4261	406.7167	795.3995	398.2034	794.4155	397.7114	Q	2475.3705	1238.1889	2458.3439	1229.6756	2457.3599	1229.1836	23
9	975.4894	488.2483	958.4629	479.7351	957.4789	479.2431	Y	2347.3119	1174.1596	2330.2854	1165.6463	2329.3013	1165.1543	22
10	1103.5480	552.2776	1086.5215	543.7644	1085.5374	543.2724	Q	2184.2486	1092.6279	2167.2220	1084.1147	2166.2380	1083.6226	21
11	1202.6164	601.8118	1185.5899	593.2986	1184.6059	592.8066	V	2056.1900	1028.5986	2039.1634	1020.0854	2038.1794	1019.5934	20
12	1315.7005	658.3539	1298.6739	649.8406	1297.6899	649.3486	L	1957.1216	979.0644	1940.0950	970.5512	1939.1110	970.0591	19
13	1402.7325	701.8699	1385.7060	693.3566	1384.7219	692.8646	S	1844.0375	922.5224	1827.0110	914.0091	1826.0270	913.5171	18
14	1489.7645	745.3859	1472.7380	736.8726	1471.7540	736.3806	S	1757.0055	879.0064	1739.9789	870.4931	1738.9949	870.0011	17
15	1590.8122	795.9097	1573.7857	787.3965	1572.8016	786.9045	T	1669.9735	835.4904	1652.9469	826.9771	1651.9629	826.4851	16
16	1703.8963	852.4518	1686.8697	843.9385	1685.8857	843.4465	L	1568.9258	784.9665	1551.8992	776.4533	1550.9152	775.9612	15
17	1790.9283	895.9678	1773.9018	887.4545	1772.9177	886.9625	S	1455.8417	728.4245	1438.8152	719.9112	1437.8312	719.4192	14
18	1877.9603	939.4838	1860.9338	930.9705	1859.9498	930.4785	S	1368.8097	684.9085	1351.7831	676.3952	1350.7991	675.9032	13
19	1948.9974	975.0024	1931.9709	966.4891	1930.9869	965.9971	A	1281.7777	641.3925	1264.7511	632.8792	1263.7671	632.3872	12
20	2062.0815	1031.5444	2045.0550	1023.0311	2044.0709	1022.5391	L	1210.7406	605.8739	1193.7140	597.3606	1192.7300	596.8686	11
21	2161.1499	1081.0786	2144.1234	1072.5653	2143.1394	1072.0733	V	1097.6565	549.3319	1080.6299	540.8186	1079.6459	540.3266	10
22	2290.1925	1145.5999	2273.1660	1137.0866	2272.1820	1136.5946	E	998.5881	499.7977	981.5615	491.2844	980.5775	490.7924	9
23	2403.2766	1202.1419	2386.2500	1193.6287	2385.2660	1193.1366	L	869.5455	435.2764	852.5189	426.7631	851.5349	426.2711	8
24	2531.3352	1266.1712	2514.3086	1257.6579	2513.3246	1257.1659	Q	756.4614	378.7343	739.4349	370.2211	738.4509	369.7291	7
25	2628.3879	1314.6976	2611.3614	1306.1843	2610.3774	1305.6923	P	628.4028	314.7051	611.3763	306.1918	610.3923	305.6998	6
26	2741.4720	1371.2396	2724.4454	1362.7264	2723.4614	1362.2344	I	531.3501	266.1787	514.3235	257.6654	513.3395	257.1734	5
27	2842.5197	1421.7635	2825.4931	1413.2502	2824.5091	1412.7582	T	418.2660	209.6366	401.2395	201.1234	400.2554	200.6314	4
28	2899.5411	1450.2742	2882.5146	1441.7609	2881.5306	1441.2689	G	317.2183	159.1128	300.1918	150.5995	0	0	3
29	3012.6252	1506.8162	2995.5986	1498.3030	2994.6146	1497.8110	I	260.1969	130.6021	243.1703	122.0888	0	0	2
30							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 80470.

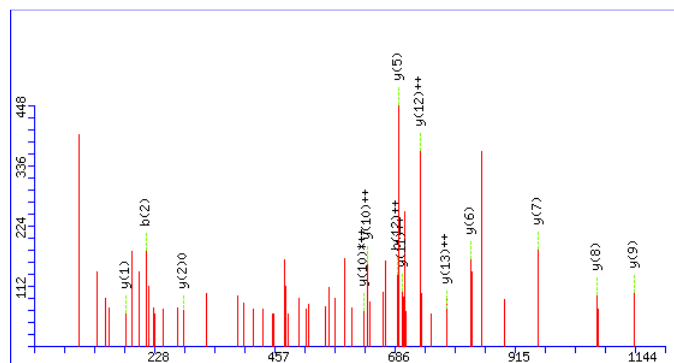
MS/MS Fragmentation of **LTAEQALQHPFFER**:

Found in **IP100012891;IP100956068**

Title: 3.1.1.517.4

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							14
2	215.1390	108.0731	0	0	197.1285	99.0679	T	1573.7758	787.3915	1556.7492	778.8782	1555.7652	778.3862	13
3	286.1761	143.5917	0	0	268.1656	134.5864	A	1472.7281	736.8677	1455.7015	728.3544	1454.7175	727.8624	12
4	415.2187	208.1130	0	0	397.2082	199.1077	E	1401.6910	701.3491	1384.6644	692.8359	1383.6804	692.3438	11
5	543.2773	272.1423	526.2508	263.6290	525.2667	263.1370	Q	1272.6484	636.8278	1255.6218	628.3146	1254.6378	627.8225	10
6	614.3144	307.6608	597.2879	299.1476	596.3039	298.6556	A	1144.5898	572.7985	1127.5633	564.2853	1126.5792	563.7933	9
7	727.3985	364.2029	710.3719	355.6896	709.3879	355.1976	L	1073.5527	537.2800	1056.5261	528.7667	1055.5421	528.2747	8
8	855.4571	428.2322	838.4305	419.7189	837.4465	419.2269	Q	960.4686	480.7380	943.4421	472.2247	942.4581	471.7327	7
9	992.5160	496.7616	975.4894	488.2483	974.5054	487.7563	H	832.4100	416.7087	815.3835	408.1954	814.3995	407.7034	6
10	1089.5687	545.2880	1072.5422	536.7747	1071.5582	536.2827	P	695.3511	348.1792	678.3246	339.6659	677.3406	339.1739	5
11	1236.6372	618.8222	1219.6106	610.3089	1218.6266	609.8169	F	598.2984	299.6528	581.2718	291.1395	580.2878	290.6475	4
12	1383.7056	692.3564	1366.6790	683.8431	1365.6950	683.3511	F	451.2300	226.1186	434.2034	217.6053	433.2194	217.1133	3
13	1512.7482	756.8777	1495.7216	748.3644	1494.7376	747.8724	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
14							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 80791.

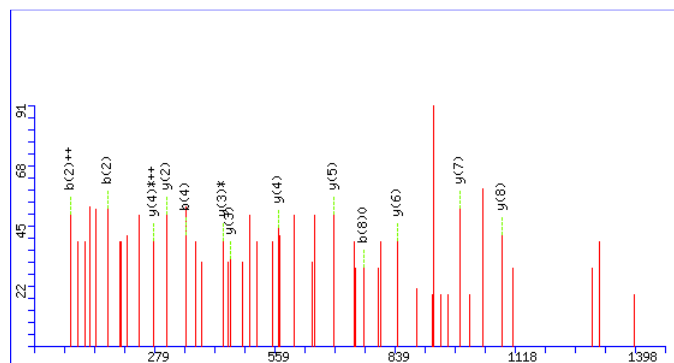
MS/MS Fragmentation of **AVLASCSPPFFQLFYK: 57.021465@C:6**

Found in **IP100165014;IP100985099**

Title: 4.1.1.1309.3

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							15
2	171.1128	86.0600	0	0	0	0	V	1706.8611	853.9342	1689.8345	845.4209	1688.8505	844.9289	14
3	284.1969	142.6021	0	0	0	0	L	1607.7927	804.4000	1590.7661	795.8867	1589.7821	795.3947	13
4	355.2340	178.1206	0	0	0	0	A	1494.7086	747.8579	1477.6821	739.3447	1476.6980	738.8527	12
5	442.2660	221.6366	0	0	424.2554	212.6314	S	1423.6715	712.3394	1406.6449	703.8261	1405.6609	703.3341	11
6	602.2967	301.6520	0	0	584.2861	292.6467	C	1336.6395	668.8234	1319.6129	660.3101	1318.6289	659.8181	10
7	689.3287	345.1680	0	0	671.3181	336.1627	S	1176.6088	588.8080	1159.5823	580.2948	1158.5982	579.8028	9
8	786.3815	393.6944	0	0	768.3709	384.6891	P	1089.5768	545.2920	1072.5502	536.7788	0	0	8
9	933.4499	467.2286	0	0	915.4393	458.2233	F	992.5240	496.7656	975.4975	488.2524	0	0	7
10	1080.5183	540.7628	0	0	1062.5077	531.7575	F	845.4556	423.2314	828.4291	414.7182	0	0	6
11	1208.5769	604.7921	1191.5503	596.2788	1190.5663	595.7868	Q	698.3872	349.6972	681.3606	341.1840	0	0	5
12	1321.6609	661.3341	1304.6344	652.8208	1303.6504	652.3288	L	570.3286	285.6679	553.3021	277.1547	0	0	4
13	1468.7293	734.8683	1451.7028	726.3550	1450.7188	725.8630	F	457.2445	229.1259	440.2180	220.6126	0	0	3
14	1631.7927	816.4000	1614.7661	807.8867	1613.7821	807.3947	Y	310.1761	155.5917	293.1496	147.0784	0	0	2
15							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 80815.

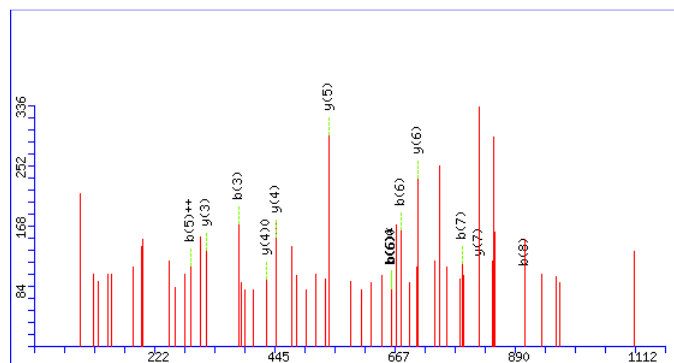
MS/MS Fragmentation of **IQLSTIDYVEDGK**:

Found in **IP100011090;IP100168371;IP100910386**

Title: 2.1.1.1586.8

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120206ry¥120206ry_aHDF1419-P10_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							14
2	242.1499	121.5786	225.1234	113.0653	0	0	Q	1504.7278	752.8675	1487.7013	744.3543	1486.7173	743.8623	13
3	379.2088	190.1081	362.1823	181.5948	0	0	H	1376.6692	688.8383	1359.6427	680.3250	1358.6587	679.8330	12
4	492.2929	246.6501	475.2663	238.1368	0	0	L	1239.6103	620.3088	1222.5838	611.7955	1221.5998	611.3035	11
5	579.3249	290.1661	562.2984	281.6528	561.3144	281.1608	S	1126.5263	563.7668	1109.4997	555.2535	1108.5157	554.7615	10
6	680.3726	340.6899	663.3461	332.1767	662.3620	331.6847	T	1039.4942	520.2508	1022.4677	511.7375	1021.4837	511.2455	9
7	793.4567	397.2320	776.4301	388.7187	775.4461	388.2267	I	938.4466	469.7269	921.4200	461.2136	920.4360	460.7216	8
8	908.4836	454.7454	891.4571	446.2322	890.4730	445.7402	D	825.3625	413.1849	808.3359	404.6716	807.3519	404.1796	7
9	1071.5469	536.2771	1054.5204	527.7638	1053.5364	527.2718	Y	710.3355	355.6714	693.3090	347.1581	692.3250	346.6661	6
10	1170.6154	585.8113	1153.5888	577.2980	1152.6048	576.8060	V	547.2722	274.1397	530.2457	265.6265	529.2617	265.1345	5
11	1299.6579	650.3326	1282.6314	641.8193	1281.6474	641.3273	E	448.2038	224.6055	431.1773	216.0923	430.1932	215.6003	4
12	1414.6849	707.8461	1397.6583	699.3328	1396.6743	698.8408	D	319.1612	160.0842	302.1347	151.5710	301.1506	151.0790	3
13	1471.7064	736.3568	1454.6798	727.8435	1453.6958	727.3515	G	204.1343	102.5708	187.1077	94.0575	0	0	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 80957.

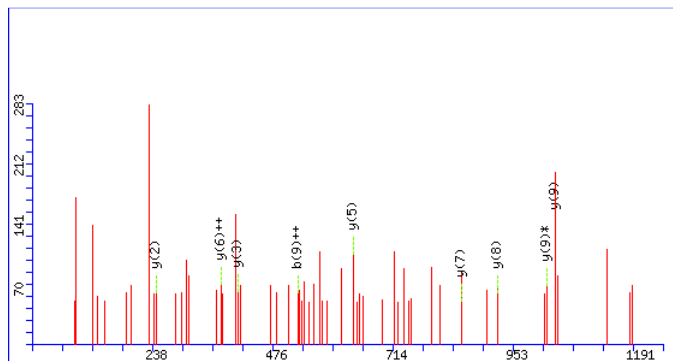
MS/MS Fragmentation of **LFDATLTQYVK**:

Found in **IP100550644;IP100880058;IP100910722**

Title: 3.1.1.791.3

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							11
2	261.1598	131.0835	0	0	0	0	F	1185.6150	593.3111	1168.5885	584.7979	1167.6045	584.3059	10
3	376.1867	188.5970	0	0	358.1761	179.5917	D	1038.5466	519.7769	1021.5201	511.2637	1020.5360	510.7717	9
4	447.2238	224.1155	0	0	429.2132	215.1103	A	923.5197	462.2635	906.4931	453.7502	905.5091	453.2582	8
5	548.2715	274.6394	0	0	530.2609	265.6341	T	852.4825	426.7449	835.4560	418.2316	834.4720	417.7396	7
6	661.3556	331.1814	0	0	643.3450	322.1761	L	751.4349	376.2211	734.4083	367.7078	733.4243	367.2158	6
7	762.4032	381.7053	0	0	744.3927	372.7000	T	638.3508	319.6790	621.3243	311.1658	620.3402	310.6738	5
8	890.4618	445.7345	873.4353	437.2213	872.4512	436.7293	Q	537.3031	269.1552	520.2766	260.6419	0	0	4
9	1053.5251	527.2662	1036.4986	518.7529	1035.5146	518.2609	Y	409.2445	205.1259	392.2180	196.6126	0	0	3
10	1152.5936	576.8004	1135.5670	568.2871	1134.5830	567.7951	V	246.1812	123.5942	229.1547	115.0810	0	0	2
11							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 81130.

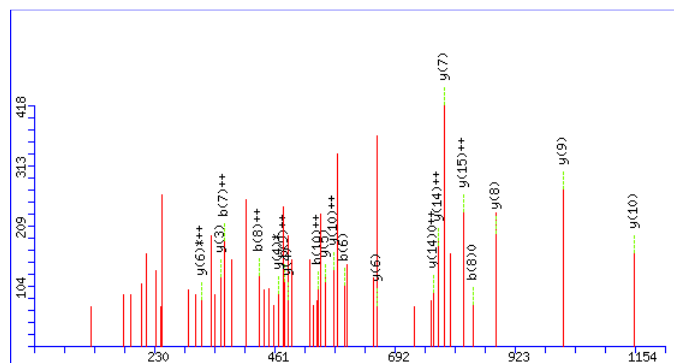
MS/MS Fragmentation of **TPGNLHEVETAQQQR**:

Found in **IP100298618;IP100976744;IP100978664;IP100980832;IP100981348;IP100984067**

Title: 1.1.1.8162.9

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							16
2	199.1077	100.0575	0	0	181.0972	91.0522	P	1649.7990	825.4031	1632.7725	816.8899	1631.7885	816.3979	15
3	256.1292	128.5682	0	0	238.1186	119.5629	G	1552.7463	776.8768	1535.7197	768.3635	1534.7357	767.8715	14
4	370.1721	185.5897	353.1456	177.0764	352.1615	176.5844	N	1495.7248	748.3660	1478.6982	739.8528	1477.7142	739.3608	13
5	484.2150	242.6112	467.1885	234.0979	466.2045	233.6059	N	1381.6819	691.3446	1364.6553	682.8313	1363.6713	682.3393	12
6	597.2991	299.1532	580.2726	290.6399	579.2885	290.1479	L	1267.6389	634.3231	1250.6124	625.8098	1249.6284	625.3178	11
7	734.3580	367.6826	717.3315	359.1694	716.3474	358.6774	H	1154.5549	577.7811	1137.5283	569.2678	1136.5443	568.7758	10
8	863.4006	432.2039	846.3741	423.6907	845.3900	423.1987	E	1017.4960	509.2516	1000.4694	500.7383	999.4854	500.2463	9
9	962.4690	481.7381	945.4425	473.2249	944.4585	472.7329	V	888.4534	444.7303	871.4268	436.2170	870.4428	435.7250	8
10	1091.5116	546.2594	1074.4851	537.7462	1073.5010	537.2542	E	789.3850	395.1961	772.3584	386.6828	771.3744	386.1908	7
11	1192.5593	596.7833	1175.5327	588.2700	1174.5487	587.7780	T	660.3424	330.6748	643.3158	322.1615	642.3318	321.6695	6
12	1263.5964	632.3018	1246.5699	623.7886	1245.5858	623.2966	A	559.2947	280.1510	542.2681	271.6377	0	0	5
13	1391.6550	696.3311	1374.6284	687.8179	1373.6444	687.3258	Q	488.2576	244.6324	471.2310	236.1191	0	0	4
14	1448.6764	724.8419	1431.6499	716.3286	1430.6659	715.8366	G	360.1990	180.6031	343.1724	172.0899	0	0	3
15	1576.7350	788.8712	1559.7085	780.3579	1558.7245	779.8659	Q	303.1775	152.0924	286.1510	143.5791	0	0	2
16							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 81135.

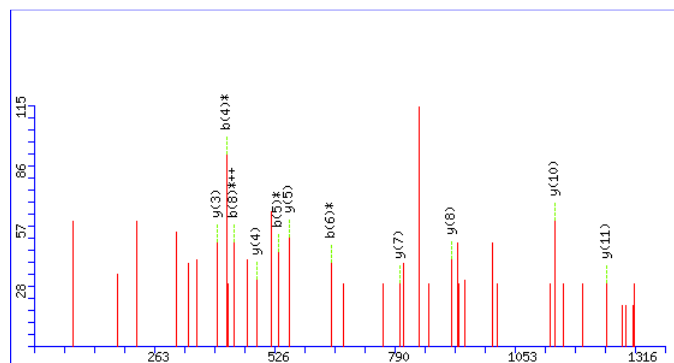
MS/MS Fragmentation of **QTPLIDLLEASPER: -17.026549@N-term(Q)**

Found in **IP100218052:IP100760714**

Title: 5.1.1.201.8

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233	0	0	Q							15
2	230.1135	115.5604	213.0870	107.0471	212.1030	106.5551	T	1566.8737	783.9405	1549.8472	775.4272	1548.8632	774.9352	14
3	327.1663	164.0868	310.1397	155.5735	309.1557	155.0815	P	1465.8261	733.4167	1448.7995	724.9034	1447.8155	724.4114	13
4	440.2504	220.6288	423.2238	212.1155	422.2398	211.6235	L	1368.7733	684.8903	1351.7468	676.3770	1350.7627	675.8850	12
5	553.3344	277.1709	536.3079	268.6576	535.3239	268.1656	I	1255.6892	628.3483	1238.6627	619.8350	1237.6787	619.3430	11
6	668.3614	334.6843	651.3348	326.1710	650.3508	325.6790	D	1142.6052	571.8062	1125.5786	563.2930	1124.5946	562.8009	10
7	781.4454	391.2264	764.4189	382.7131	763.4349	382.2211	L	1027.5782	514.2928	1010.5517	505.7795	1009.5677	505.2875	9
8	894.5295	447.7684	877.5029	439.2551	876.5189	438.7631	L	914.4942	457.7507	897.4676	449.2374	896.4836	448.7454	8
9	1007.6136	504.3104	990.5870	495.7971	989.6030	495.3051	L	801.4101	401.2087	784.3836	392.6954	783.3995	392.2034	7
10	1136.6562	568.8317	1119.6296	560.3184	1118.6456	559.8264	E	688.3260	344.6667	671.2995	336.1534	670.3155	335.6614	6
11	1207.6933	604.3503	1190.6667	595.8370	1189.6827	595.3450	A	559.2835	280.1454	542.2569	271.6321	541.2729	271.1401	5
12	1294.7253	647.8663	1277.6987	639.3530	1276.7147	638.8610	S	488.2463	244.6268	471.2198	236.1135	470.2358	235.6215	4
13	1391.7781	696.3927	1374.7515	687.8794	1373.7675	687.3874	P	401.2143	201.1108	384.1878	192.5975	383.2037	192.1055	3
14	1520.8207	760.9140	1503.7941	752.4007	1502.8101	751.9087	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
15							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 81236.

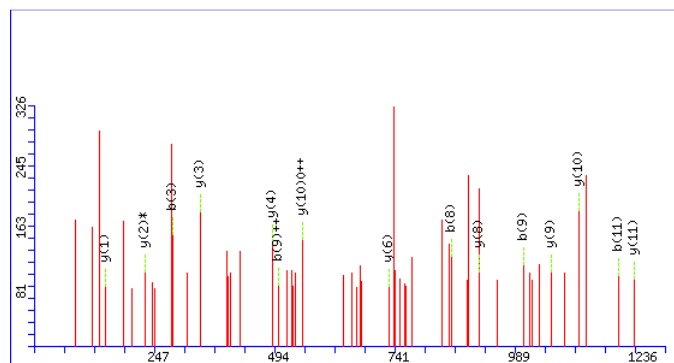
MS/MS Fragmentation of **LDGFGQEIFPVK**:

Found in **IP100018914**

Title: 3.1.1.1411.6

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							12
2	229.1183	115.0628	0	0	211.1077	106.0575	D	1236.6259	618.8166	1219.5994	610.3033	1218.6154	609.8113	11
3	286.1397	143.5735	0	0	268.1292	134.5682	G	1121.5990	561.3031	1104.5724	552.7898	1103.5884	552.2978	10
4	433.2082	217.1077	0	0	415.1976	208.1024	F	1064.5775	532.7924	1047.5510	524.2791	1046.5669	523.7871	9
5	490.2296	245.6185	0	0	472.2191	236.6132	G	917.5091	459.2582	900.4825	450.7449	899.4985	450.2529	8
6	618.2882	309.6477	601.2617	301.1345	600.2776	300.6425	Q	860.4876	430.7475	843.4611	422.2342	842.4771	421.7422	7
7	747.3308	374.1690	730.3042	365.6558	729.3202	365.1638	E	732.4291	366.7182	715.4025	358.2049	714.4185	357.7129	6
8	860.4149	430.7111	843.3883	422.1978	842.4043	421.7058	I	603.3865	302.1969	586.3599	293.6836	0	0	5
9	1007.4833	504.2453	990.4567	495.7320	989.4727	495.2400	F	490.3024	245.6548	473.2758	237.1416	0	0	4
10	1104.5360	552.7717	1087.5095	544.2584	1086.5255	543.7664	P	343.2340	172.1206	326.2074	163.6074	0	0	3
11	1203.6045	602.3059	1186.5779	593.7926	1185.5939	593.3006	V	246.1812	123.5942	229.1547	115.0810	0	0	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 81326.

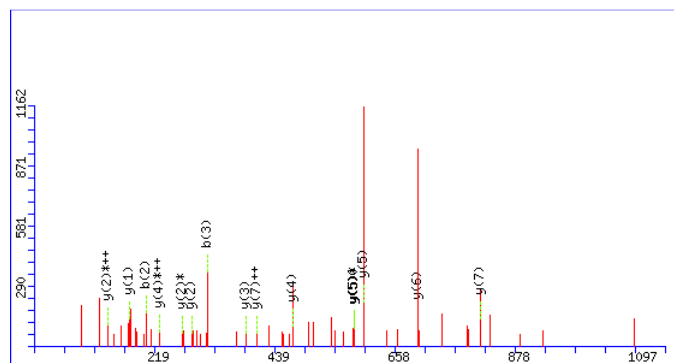
MS/MS Fragmentation of **GFIVESVLK**:

Found in **IP100300073;IP100419995;IP100939162**

Title: 3.1.1.425.3

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120214ry¥120214ry_32R1-32_4_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							9
2	205.0972	103.0522	0	0	0	0	F	962.5669	481.7871	945.5404	473.2738	944.5564	472.7818	8
3	318.1812	159.5942	0	0	0	0	I	815.4985	408.2529	798.4720	399.7396	797.4880	399.2476	7
4	417.2496	209.1285	0	0	0	0	V	702.4145	351.7109	685.3879	343.1976	684.4039	342.7056	6
5	546.2922	273.6498	0	0	528.2817	264.6445	E	603.3461	302.1767	586.3195	293.6634	585.3355	293.1714	5
6	633.3243	317.1658	0	0	615.3137	308.1605	S	474.3035	237.6554	457.2769	229.1421	456.2929	228.6501	4
7	732.3927	366.7000	0	0	714.3821	357.6947	V	387.2714	194.1394	370.2449	185.6261	0	0	3
8	845.4767	423.2420	0	0	827.4662	414.2367	L	288.2030	144.6051	271.1765	136.0919	0	0	2
9							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 81343.

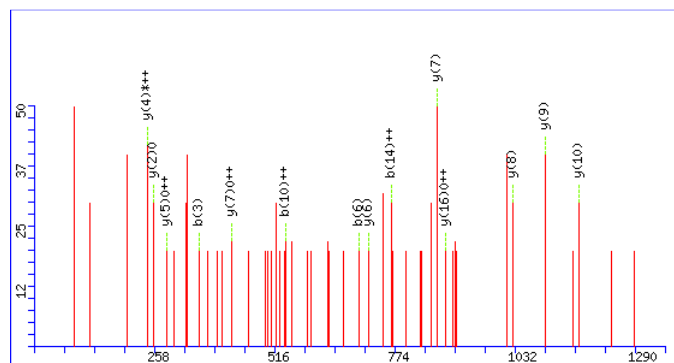
MS/MS Fragmentation of **EQPDNIPFAAAAYFESLLEK**:

Found in **IP100017966**

Title: 5.1.1.529.5

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							20
2	258.1084	129.5579	241.0819	121.0446	240.0979	120.5526	Q	2124.0648	1062.5360	2107.0382	1054.0228	2106.0542	1053.5308	19
3	355.1612	178.0842	338.1347	169.5710	337.1506	169.0790	P	1996.0062	998.5067	1978.9797	989.9935	1977.9957	989.5015	18
4	470.1882	235.5977	453.1616	227.0844	452.1776	226.5924	D	1898.9535	949.9804	1881.9269	941.4671	1880.9429	940.9751	17
5	584.2311	292.6192	567.2045	284.1059	566.2205	283.6139	N	1783.9265	892.4669	1766.9000	883.9536	1765.9159	883.4616	16
6	697.3151	349.1612	680.2886	340.6479	679.3046	340.1559	I	1669.8836	835.4454	1652.8570	826.9322	1651.8730	826.4401	15
7	794.3679	397.6876	777.3414	389.1743	776.3573	388.6823	P	1556.7995	778.9034	1539.7730	770.3901	1538.7890	769.8981	14
8	865.4050	433.2061	848.3785	424.6929	847.3945	424.2009	A	1459.7468	730.3770	1442.7202	721.8637	1441.7362	721.3717	13
9	1012.4734	506.7404	995.4469	498.2271	994.4629	497.7351	F	1388.7096	694.8585	1371.6831	686.3452	1370.6991	685.8532	12
10	1083.5106	542.2589	1066.4840	533.7456	1065.5000	533.2536	A	1241.6412	621.3243	1224.6147	612.8110	1223.6307	612.3190	11
11	1154.5477	577.7775	1137.5211	569.2642	1136.5371	568.7722	A	1170.6041	585.8057	1153.5776	577.2924	1152.5936	576.8004	10
12	1225.5848	613.2960	1208.5582	604.7828	1207.5742	604.2907	A	1099.5670	550.2871	1082.5405	541.7739	1081.5564	541.2819	9
13	1388.6481	694.8277	1371.6216	686.3144	1370.6375	685.8224	Y	1028.5299	514.7686	1011.5033	506.2553	1010.5193	505.7633	8
14	1535.7165	768.3619	1518.6900	759.8486	1517.7060	759.3566	F	865.4666	433.2369	848.4400	424.7236	847.4560	424.2316	7
15	1664.7591	832.8832	1647.7326	824.3699	1646.7486	823.8779	E	718.3981	359.7027	701.3716	351.1894	700.3876	350.6974	6
16	1751.7911	876.3992	1734.7646	867.8859	1733.7806	867.3939	S	589.3556	295.1814	572.3290	286.6681	571.3450	286.1761	5
17	1864.8752	932.9412	1847.8487	924.4280	1846.8646	923.9360	L	502.3235	251.6654	485.2970	243.1521	484.3130	242.6601	4
18	1977.9593	989.4833	1960.9327	980.9700	1959.9487	980.4780	L	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
19	2107.0019	1054.0046	2089.9753	1045.4913	2088.9913	1044.9993	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
20							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 81355.

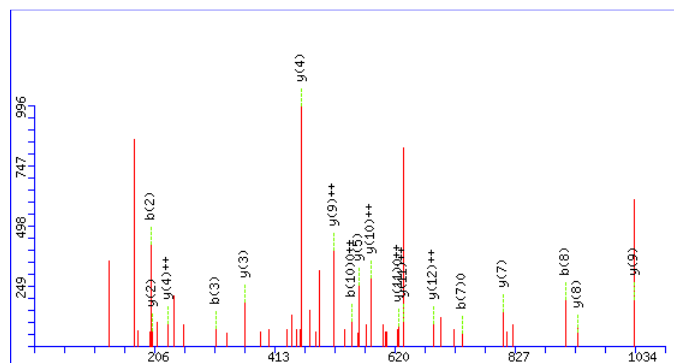
MS/MS Fragmentation of **TVIKPESCVPGK: 57.021465@C:8,57.021465@C:11**

Found in **IP100152946;IP1021484**

Title: 1.1.1.8708.8

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120210ry¥120210ry_585A1-55_3_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							13
2	201.1234	101.0653	0	0	183.1128	92.0600	V	1373.6916	687.3494	1356.6650	678.8361	1355.6810	678.3441	12
3	314.2074	157.6074	0	0	296.1969	148.6021	I	1274.6232	637.8152	1257.5966	629.3019	1256.6126	628.8099	11
4	442.3024	221.6548	425.2758	213.1416	424.2918	212.6496	K	1161.5391	581.2732	1144.5125	572.7599	1143.5285	572.2679	10
5	539.3552	270.1812	522.3286	261.6679	521.3446	261.1759	P	1033.4441	517.2257	1016.4176	508.7124	1015.4336	508.2204	9
6	668.3978	334.7025	651.3712	326.1892	650.3872	325.6972	E	936.3914	468.6993	919.3648	460.1860	918.3808	459.6940	8
7	755.4298	378.2185	738.4032	369.7053	737.4192	369.2132	S	807.3488	404.1780	790.3222	395.6648	789.3382	395.1727	7
8	915.4604	458.2339	898.4339	449.7206	897.4499	449.2286	C	720.3167	360.6620	703.2902	352.1487	0	0	6
9	1014.5288	507.7681	997.5023	499.2548	996.5183	498.7628	V	560.2861	280.6467	543.2595	272.1334	0	0	5
10	1111.5816	556.2944	1094.5551	547.7812	1093.5710	547.2892	P	461.2177	231.1125	444.1911	222.5992	0	0	4
11	1271.6123	636.3098	1254.5857	627.7965	1253.6017	627.3045	C	364.1649	182.5861	347.1384	174.0728	0	0	3
12	1328.6337	664.8205	1311.6072	656.3072	1310.6232	655.8152	G	204.1343	102.5708	187.1077	94.0575	0	0	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 81439.

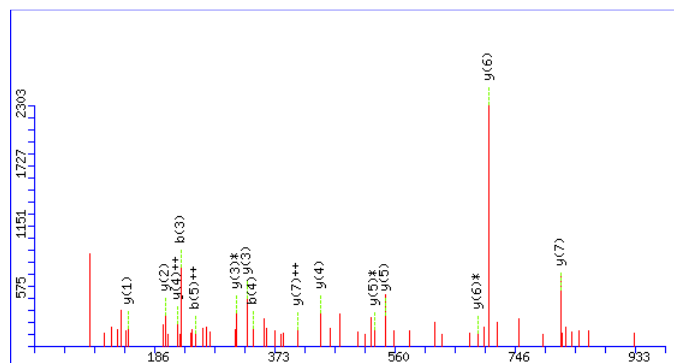
MS/MS Fragmentation of **GLLCTLQGK: 57.021465@C:5**

Found in **IP100021594;IP100400944;IP100789883;IP100978533;IP100979149**

Title: 2.1.1.2818.4

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							10
2	115.0502	58.0287	0	0	0	0	G	989.5448	495.2761	972.5183	486.7628	971.5343	486.2708	9
3	228.1343	114.5708	0	0	0	0	L	932.5234	466.7653	915.4968	458.2520	914.5128	457.7600	8
4	341.2183	171.1128	0	0	0	0	L	819.4393	410.2233	802.4128	401.7100	801.4287	401.2180	7
5	501.2490	251.1281	0	0	0	0	C	706.3552	353.6813	689.3287	345.1680	688.3447	344.6760	6
6	602.2967	301.6520	0	0	584.2861	292.6467	T	546.3246	273.6659	529.2980	265.1527	528.3140	264.6607	5
7	715.3807	358.1940	0	0	697.3702	349.1887	L	445.2769	223.1421	428.2504	214.6288	0	0	4
8	843.4393	422.2233	826.4128	413.7100	825.4287	413.2180	Q	332.1928	166.6001	315.1663	158.0868	0	0	3
9	900.4608	450.7340	883.4342	442.2207	882.4502	441.7287	G	204.1343	102.5708	187.1077	94.0575	0	0	2
10							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 81549.

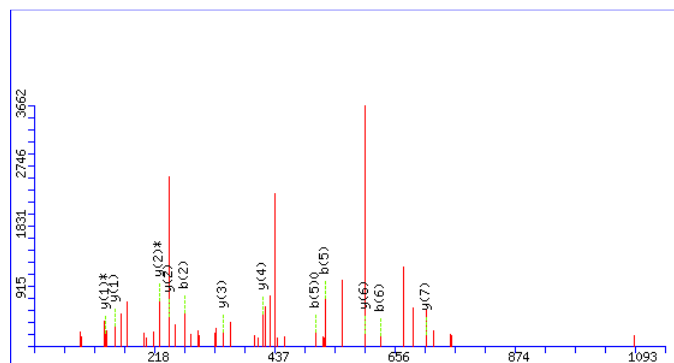
MS/MS Fragmentation of **GLADAVVK: 57.021465@C:1**

Found in **IP100062298;IP100816419;IP100977644;IP100978529**

Title: 1.1.1.8996.4

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	161.0379	81.0226	0	0	0	0	C							8
2	274.1220	137.5646	0	0	0	0	L	715.4349	358.2211	698.4083	349.7078	697.4243	349.2158	7
3	345.1591	173.0832	0	0	0	0	A	602.3508	301.6790	585.3243	293.1658	584.3402	292.6738	6
4	460.1860	230.5967	0	0	442.1755	221.5914	D	531.3137	266.1605	514.2871	257.6472	513.3031	257.1552	5
5	531.2232	266.1152	0	0	513.2126	257.1099	A	416.2867	208.6470	399.2602	200.1337	0	0	4
6	630.2916	315.6494	0	0	612.2810	306.6441	V	345.2496	173.1285	328.2231	164.6152	0	0	3
7	729.3600	365.1836	0	0	711.3494	356.1784	V	246.1812	123.5942	229.1547	115.0810	0	0	2
8							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 81586.

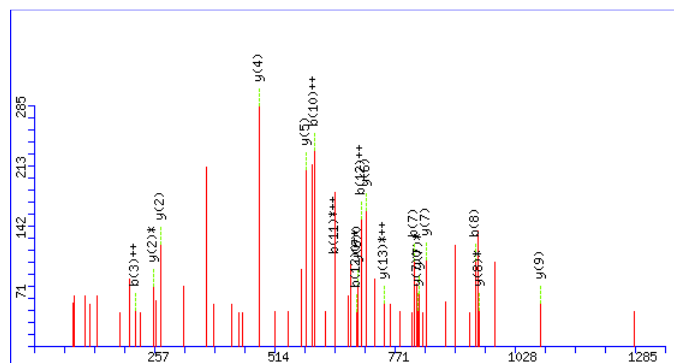
MS/MS Fragmentation of **RLYPVDEQETPLPR**:

Found in **IP100465275;IP100513912**

Title: 2.1.1.2233.9

Data file: Y:\TT5600(CiRA1)\2012-02\120201ry\120201ry_aHDF1388-P9_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	157.1084	79.0578	140.0818	70.5446	0	0	R							15
2	270.1925	135.5999	253.1659	127.0866	0	0	L	1627.8326	814.4199	1610.8061	805.9067	1609.8221	805.4147	14
3	433.2558	217.1315	416.2292	208.6183	0	0	Y	1514.7486	757.8779	1497.7220	749.3646	1496.7380	748.8726	13
4	530.3085	265.6579	513.2820	257.1446	0	0	P	1351.6852	676.3462	1334.6587	667.8330	1333.6747	667.3410	12
5	601.3457	301.1765	584.3191	292.6632	0	0	A	1254.6325	627.8199	1237.6059	619.3066	1236.6219	618.8146	11
6	700.4141	350.7107	683.3875	342.1974	0	0	V	1183.5953	592.3013	1166.5688	583.7880	1165.5848	583.2960	10
7	815.4410	408.2241	798.4145	399.7109	797.4305	399.2189	D	1084.5269	542.7671	1067.5004	534.2538	1066.5164	533.7618	9
8	944.4836	472.7454	927.4571	464.2322	926.4730	463.7402	E	969.5000	485.2536	952.4734	476.7404	951.4894	476.2483	8
9	1072.5422	536.7747	1055.5156	528.2615	1054.5316	527.7694	Q	840.4574	420.7323	823.4308	412.2191	822.4468	411.7271	7
10	1201.5848	601.2960	1184.5582	592.7828	1183.5742	592.2907	E	712.3988	356.7030	695.3723	348.1898	694.3883	347.6978	6
11	1302.6325	651.8199	1285.6059	643.3066	1284.6219	642.8146	T	583.3562	292.1817	566.3297	283.6685	565.3457	283.1765	5
12	1399.6852	700.3462	1382.6587	691.8330	1381.6747	691.3410	P	482.3085	241.6579	465.2820	233.1446	0	0	4
13	1512.7693	756.8883	1495.7427	748.3750	1494.7587	747.8830	L	385.2558	193.1315	368.2292	184.6183	0	0	3
14	1609.8221	805.4147	1592.7955	796.9014	1591.8115	796.4094	P	272.1717	136.5895	255.1452	128.0762	0	0	2
15							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 81798.

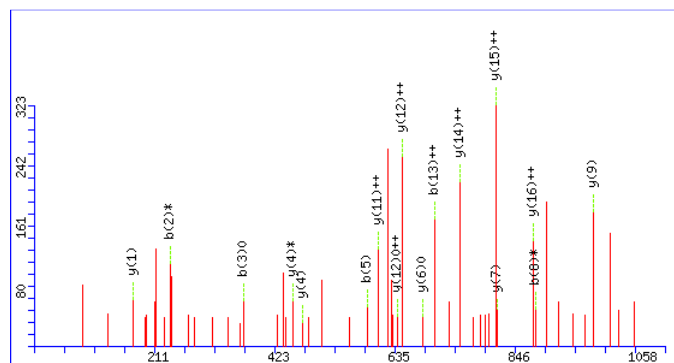
MS/MS Fragmentation of **QEESLSARPALETEGLR**:

Found in **IP100020468**

Title: 2.1.1.1702.9

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233	0	0	Q							17
2	258.1084	129.5579	241.0819	121.0446	240.0979	120.5526	E	1757.9028	879.4550	1740.8763	870.9418	1739.8923	870.4498	16
3	387.1510	194.0792	370.1245	185.5659	369.1405	185.0739	E	1628.8602	814.9338	1611.8337	806.4205	1610.8497	805.9285	15
4	474.1831	237.5952	457.1565	229.0819	456.1725	228.5899	S	1499.8176	750.4125	1482.7911	741.8992	1481.8071	741.4072	14
5	587.2671	294.1372	570.2406	285.6239	569.2566	285.1319	L	1412.7856	706.8964	1395.7591	698.3832	1394.7750	697.8912	13
6	674.2992	337.6532	657.2726	329.1399	656.2886	328.6479	S	1299.7015	650.3544	1282.6750	641.8411	1281.6910	641.3491	12
7	745.3363	373.1718	728.3097	364.6585	727.3257	364.1665	A	1212.6695	606.8384	1195.6430	598.3251	1194.6589	597.8331	11
8	901.4374	451.2223	884.4108	442.7091	883.4268	442.2170	R	1141.6324	571.3198	1124.6058	562.8066	1123.6218	562.3146	10
9	998.4901	499.7487	981.4636	491.2354	980.4796	490.7434	P	985.5313	493.2693	968.5047	484.7560	967.5207	484.2640	9
10	1069.5273	535.2673	1052.5007	526.7540	1051.5167	526.2620	A	888.4785	444.7429	871.4520	436.2296	870.4680	435.7376	8
11	1182.6113	591.8093	1165.5848	583.2960	1164.6008	582.8040	L	817.4414	409.2243	800.4149	400.7111	799.4308	400.2191	7
12	1311.6539	656.3306	1294.6274	647.8173	1293.6434	647.3253	E	704.3573	352.6823	687.3308	344.1690	686.3468	343.6770	6
13	1412.7016	706.8544	1395.6750	698.3412	1394.6910	697.8492	T	575.3148	288.1610	558.2882	279.6477	557.3042	279.1557	5
14	1541.7442	771.3757	1524.7176	762.8625	1523.7336	762.3705	E	474.2671	237.6372	457.2405	229.1239	456.2565	228.6319	4
15	1598.7657	799.8865	1581.7391	791.3732	1580.7551	790.8812	G	345.2245	173.1159	328.1979	164.6026	0	0	3
16	1711.8497	856.4285	1694.8232	847.9152	1693.8392	847.4232	L	288.2030	144.6051	271.1765	136.0919	0	0	2
17							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 81850.

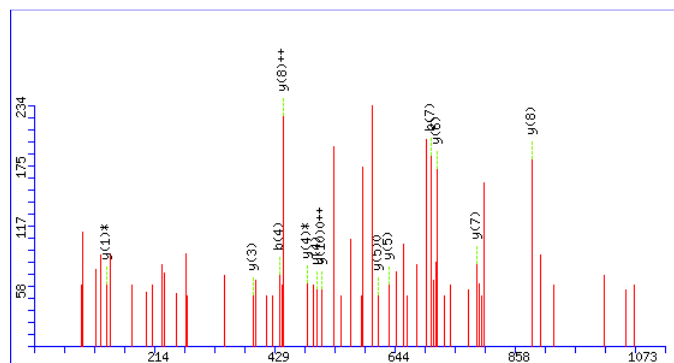
MS/MS Fragmentation of **NDPLLGVPASENPFK**:

Found in **IP100028509**

Title: 3.1.1.2078.4

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_1_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							16
2	230.0771	115.5422	213.0506	107.0289	212.0666	106.5369	D	1582.8475	791.9274	1565.8210	783.4141	1564.8370	782.9221	15
3	327.1299	164.0686	310.1034	155.5553	309.1193	155.0633	P	1467.8206	734.4139	1450.7940	725.9007	1449.8100	725.4087	14
4	440.2140	220.6106	423.1874	212.0974	422.2034	211.6053	L	1370.7678	685.8876	1353.7413	677.3743	1352.7573	676.8823	13
5	553.2980	277.1527	536.2715	268.6394	535.2875	268.1474	L	1257.6838	629.3455	1240.6572	620.8322	1239.6732	620.3402	12
6	652.3665	326.6869	635.3399	318.1736	634.3559	317.6816	V	1144.5997	572.8035	1127.5732	564.2902	1126.5891	563.7982	11
7	709.3879	355.1976	692.3614	346.6843	691.3774	346.1923	G	1045.5313	523.2693	1028.5047	514.7560	1027.5207	514.2640	10
8	808.4563	404.7318	791.4298	396.2185	790.4458	395.7265	V	988.5098	494.7585	971.4833	486.2453	970.4993	485.7533	9
9	905.5091	453.2582	888.4825	444.7449	887.4985	444.2529	P	889.4414	445.2243	872.4149	436.7111	871.4308	436.2191	8
10	976.5462	488.7767	959.5197	480.2635	958.5356	479.7715	A	792.3886	396.6980	775.3621	388.1847	774.3781	387.6927	7
11	1063.5782	532.2928	1046.5517	523.7795	1045.5677	523.2875	S	721.3515	361.1794	704.3250	352.6661	703.3410	352.1741	6
12	1192.6208	596.8141	1175.5943	588.3008	1174.6103	587.8088	E	634.3195	317.6634	617.2930	309.1501	616.3089	308.6581	5
13	1306.6638	653.8355	1289.6372	645.3222	1288.6532	644.8302	N	505.2769	253.1421	488.2504	244.6288	0	0	4
14	1403.7165	702.3619	1386.6900	693.8486	1385.7060	693.3566	P	391.2340	196.1206	374.2074	187.6074	0	0	3
15	1550.7849	775.8961	1533.7584	767.3828	1532.7744	766.8908	F	294.1812	147.5942	277.1547	139.0810	0	0	2
16							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 82074.

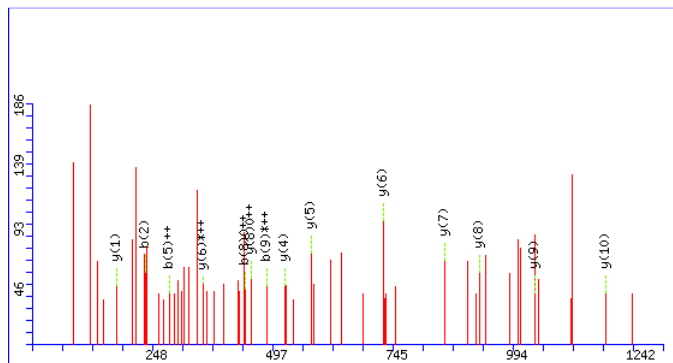
MS/MS Fragmentation of **SFFNAQFGSLFR**:

Found in **IP100465170;IP100927948**

Title: 4.1.1.100.2

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_2.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							12
2	235.1077	118.0575	0	0	217.0972	109.0522	F	1333.6688	667.3380	1316.6422	658.8248	1315.6582	658.3327	11
3	382.1761	191.5917	0	0	364.1656	182.5864	F	1186.6004	593.8038	1169.5738	585.2905	1168.5898	584.7985	10
4	496.2191	248.6132	479.1925	240.0999	478.2085	239.6079	N	1039.5320	520.2696	1022.5054	511.7563	1021.5214	511.2643	9
5	567.2562	284.1317	550.2296	275.6184	549.2456	275.1264	A	925.4890	463.2482	908.4625	454.7349	907.4785	454.2429	8
6	695.3148	348.1610	678.2882	339.6477	677.3042	339.1557	Q	854.4519	427.7296	837.4254	419.2163	836.4413	418.7243	7
7	842.3832	421.6952	825.3566	413.1819	824.3726	412.6899	F	726.3933	363.7003	709.3668	355.1870	708.3828	354.6950	6
8	899.4046	450.2060	882.3781	441.6927	881.3941	441.2007	G	579.3249	290.1661	562.2984	281.6528	561.3144	281.1608	5
9	986.4367	493.7220	969.4101	485.2087	968.4261	484.7167	S	522.3035	261.6554	505.2769	253.1421	504.2929	252.6501	4
10	1099.5207	550.2640	1082.4942	541.7507	1081.5102	541.2587	L	435.2714	218.1394	418.2449	209.6261	0	0	3
11	1246.5891	623.7982	1229.5626	615.2849	1228.5786	614.7929	F	322.1874	161.5973	305.1608	153.0840	0	0	2
12							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 82265.

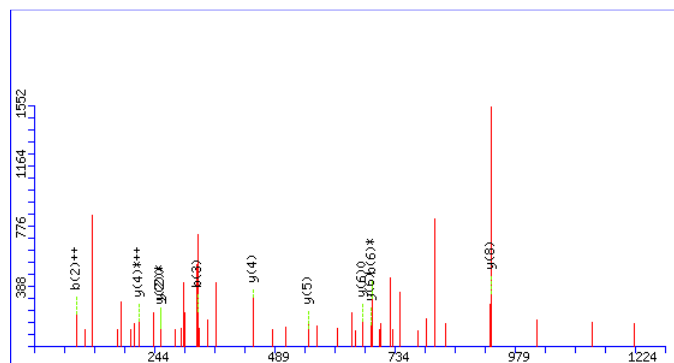
MS/MS Fragmentation of **AVYENELVATR**:

Found in **IP100009612**

Title: 4.1.1.3598.2

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							11
2	171.1128	86.0600	0	0	0	0	V	1193.6161	597.3117	1176.5895	588.7984	1175.6055	588.3064	10
3	334.1761	167.5917	0	0	0	0	Y	1094.5477	547.7775	1077.5211	539.2642	1076.5371	538.7722	9
4	463.2187	232.1130	0	0	445.2082	223.1077	E	931.4843	466.2458	914.4578	457.7325	913.4738	457.2405	8
5	577.2617	289.1345	560.2351	280.6212	559.2511	280.1292	N	802.4417	401.7245	785.4152	393.2112	784.4312	392.7192	7
6	706.3042	353.6558	689.2777	345.1425	688.2937	344.6505	E	688.3988	344.7030	671.3723	336.1898	670.3883	335.6978	6
7	819.3883	410.1978	802.3618	401.6845	801.3777	401.1925	L	559.3562	280.1817	542.3297	271.6685	541.3457	271.1765	5
8	918.4567	459.7320	901.4302	451.2187	900.4462	450.7267	V	446.2722	223.6397	429.2456	215.1264	428.2616	214.6344	4
9	989.4938	495.2506	972.4673	486.7373	971.4833	486.2453	A	347.2037	174.1055	330.1772	165.5922	329.1932	165.1002	3
10	1090.5415	545.7744	1073.5150	537.2611	1072.5310	536.7691	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
11							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 82480.

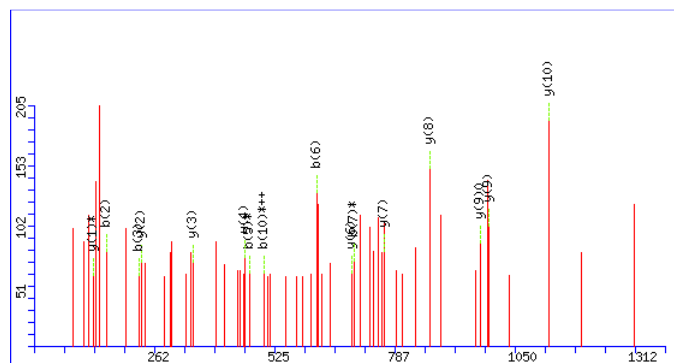
MS/MS Fragmentation of **SAAQMEVASFLLSK**:

Found in **IP100329526;IP100382768;IP100909999**

Title: 3.1.1.3030.7

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							14
2	159.0764	80.0418	0	0	141.0659	71.0366	A	1394.7348	697.8710	1377.7083	689.3578	1376.7242	688.8658	13
3	230.1135	115.5604	0	0	212.1030	106.5551	A	1323.6977	662.3525	1306.6712	653.8392	1305.6871	653.3472	12
4	358.1721	179.5897	341.1456	171.0764	340.1615	170.5844	Q	1252.6606	626.8339	1235.6340	618.3207	1234.6500	617.8286	11
5	489.2126	245.1099	472.1860	236.5967	471.2020	236.1047	M	1124.6020	562.8046	1107.5755	554.2914	1106.5914	553.7994	10
6	618.2552	309.6312	601.2286	301.1180	600.2446	300.6259	E	993.5615	497.2844	976.5350	488.7711	975.5510	488.2791	9
7	717.3236	359.1654	700.2971	350.6522	699.3130	350.1602	V	864.5189	432.7631	847.4924	424.2498	846.5084	423.7578	8
8	788.3607	394.6840	771.3342	386.1707	770.3502	385.6787	A	765.4505	383.2289	748.4240	374.7156	747.4400	374.2236	7
9	875.3927	438.2000	858.3662	429.6867	857.3822	429.1947	S	694.4134	347.7103	677.3869	339.1971	676.4028	338.7051	6
10	1022.4612	511.7342	1005.4346	503.2209	1004.4506	502.7289	F	607.3814	304.1943	590.3548	295.6811	589.3708	295.1890	5
11	1135.5452	568.2762	1118.5187	559.7630	1117.5347	559.2710	L	460.3130	230.6601	443.2864	222.1468	442.3024	221.6548	4
12	1248.6293	624.8183	1231.6027	616.3050	1230.6187	615.8130	L	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
13	1335.6613	668.3343	1318.6348	659.8210	1317.6507	659.3290	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 82517.

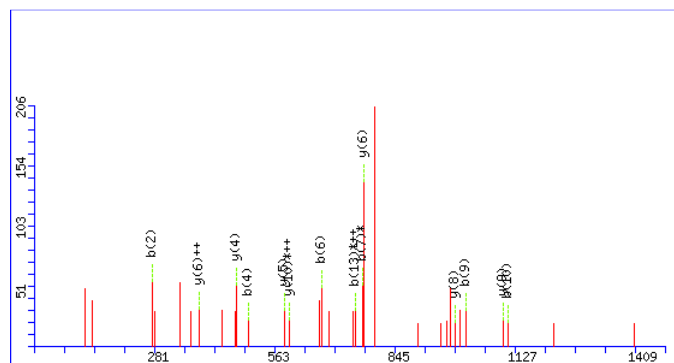
MS/MS Fragmentation of **YNPEGLLNLVWLNNTK**:

Found in **IP100514013**

Title: 4.1.1.1491.7

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	164.0706	82.5389	0	0	0	0	Y							16
2	278.1135	139.5604	261.0870	131.0471	0	0	N	1724.9330	862.9701	1707.9064	854.4569	1706.9224	853.9649	15
3	375.1663	188.0868	358.1397	179.5735	0	0	P	1610.8901	805.9487	1593.8635	797.4354	1592.8795	796.9434	14
4	504.2089	252.6081	487.1823	244.0948	486.1983	243.6028	E	1513.8373	757.4223	1496.8108	748.9090	1495.8267	748.4170	13
5	561.2304	281.1188	544.2038	272.6055	543.2198	272.1135	G	1384.7947	692.9010	1367.7682	684.3877	1366.7841	683.8957	12
6	674.3144	337.6608	657.2879	329.1476	656.3039	328.6556	L	1327.7732	664.3903	1310.7467	655.8770	1309.7627	655.3850	11
7	787.3985	394.2029	770.3719	385.6896	769.3879	385.1976	L	1214.6892	607.8482	1197.6626	599.3350	1196.6786	598.8429	10
8	901.4414	451.2243	884.4149	442.7111	883.4308	442.2191	N	1101.6051	551.3062	1084.5786	542.7929	1083.5946	542.3009	9
9	1014.5255	507.7664	997.4989	499.2531	996.5149	498.7611	L	987.5622	494.2847	970.5356	485.7715	969.5516	485.2795	8
10	1113.5939	557.3006	1096.5673	548.7873	1095.5833	548.2953	V	874.4781	437.7427	857.4516	429.2294	856.4676	428.7374	7
11	1299.6732	650.3402	1282.6466	641.8270	1281.6626	641.3350	W	775.4097	388.2085	758.3832	379.6952	757.3991	379.2032	6
12	1412.7573	706.8823	1395.7307	698.3690	1394.7467	697.8770	L	589.3304	295.1688	572.3039	286.6556	571.3198	286.1636	5
13	1526.8002	763.9037	1509.7736	755.3905	1508.7896	754.8985	N	476.2463	238.6268	459.2198	230.1135	458.2358	229.6215	4
14	1640.8431	820.9252	1623.8166	812.4119	1622.8326	811.9199	N	362.2034	181.6053	345.1769	173.0921	344.1928	172.6001	3
15	1741.8908	871.4490	1724.8642	862.9358	1723.8802	862.4438	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
16							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 82746.

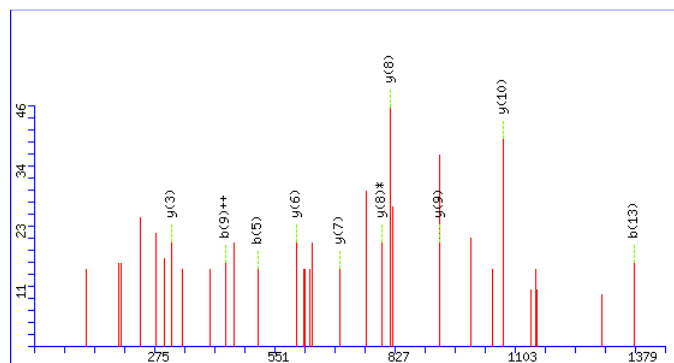
MS/MS Fragmentation of **AVLACAAGYFQNLFNTGLDAAR: 57.021465@C:5**

Found in **IP100006589**

Title: 4.1.1.3408.6

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							23
2	171.1128	86.0600	0	0	0	0	V	2385.2020	1193.1046	2368.1754	1184.5914	2367.1914	1184.0993	22
3	284.1969	142.6021	0	0	0	0	L	2286.1336	1143.5704	2269.1070	1135.0571	2268.1230	1134.5651	21
4	355.2340	178.1206	0	0	0	0	A	2173.0495	1087.0284	2156.0230	1078.5151	2155.0389	1078.0231	20
5	515.2646	258.1360	0	0	0	0	C	2102.0124	1051.5098	2084.9858	1042.9966	2084.0018	1042.5046	19
6	586.3017	293.6545	0	0	0	0	A	1941.9817	971.4945	1924.9552	962.9812	1923.9712	962.4892	18
7	657.3389	329.1731	0	0	0	0	A	1870.9446	935.9760	1853.9181	927.4627	1852.9341	926.9707	17
8	714.3603	357.6838	0	0	0	0	G	1799.9075	900.4574	1782.8810	891.9441	1781.8969	891.4521	16
9	877.4237	439.2155	0	0	0	0	Y	1742.8860	871.9467	1725.8595	863.4334	1724.8755	862.9414	15
10	1024.4921	512.7497	0	0	0	0	F	1579.8227	790.4150	1562.7962	781.9017	1561.8122	781.4097	14
11	1152.5506	576.7790	1135.5241	568.2657	0	0	Q	1432.7543	716.8808	1415.7278	708.3675	1414.7437	707.8755	13
12	1266.5936	633.8004	1249.5670	625.2871	0	0	N	1304.6957	652.8515	1287.6692	644.3382	1286.6852	643.8462	12
13	1379.6776	690.3425	1362.6511	681.8292	0	0	L	1190.6528	595.8300	1173.6262	587.3168	1172.6422	586.8248	11
14	1526.7461	763.8767	1509.7195	755.3634	0	0	F	1077.5687	539.2880	1060.5422	530.7747	1059.5582	530.2827	10
15	1639.8301	820.4187	1622.8036	811.9054	0	0	L	930.5003	465.7538	913.4738	457.2405	912.4898	456.7485	9
16	1753.8730	877.4402	1736.8465	868.9269	0	0	N	817.4163	409.2118	800.3897	400.6985	799.4057	400.2065	8
17	1854.9207	927.9640	1837.8942	919.4507	1836.9102	918.9587	T	703.3733	352.1903	686.3468	343.6770	685.3628	343.1850	7
18	1911.9422	956.4747	1894.9156	947.9615	1893.9316	947.4694	G	602.3257	301.6665	585.2991	293.1532	584.3151	292.6612	6
19	2025.0262	1013.0168	2007.9997	1004.5035	2007.0157	1004.0115	L	545.3042	273.1557	528.2776	264.6425	527.2936	264.1504	5
20	2140.0532	1070.5302	2123.0266	1062.0170	2122.0426	1061.5250	D	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	4
21	2211.0903	1106.0488	2194.0638	1097.5355	2193.0797	1097.0435	A	317.1932	159.1002	300.1666	150.5870	0	0	3
22	2282.1274	1141.5673	2265.1009	1133.0541	2264.1169	1132.5621	A	246.1561	123.5817	229.1295	115.0684	0	0	2
23							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 83016.

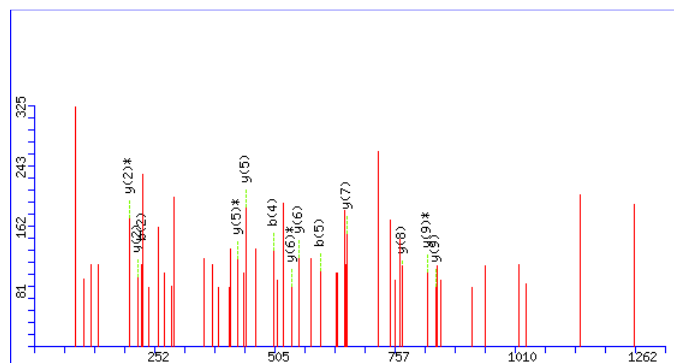
MS/MS Fragmentation of **DLNCVPEIADTLGAVAK**: 57.021465@C:4

Found in **IP1004411473;IP100794580;IP101024830;IP101025348;IP101025770;IP101025850;IP101026356;IP101026489**

Title: 3.1.1.3317.5

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							17
2	229.1183	115.0628	0	0	211.1077	106.0575	L	1670.8782	835.9427	1653.8516	827.4295	1652.8676	826.9374	16
3	343.1612	172.0842	326.1347	163.5710	325.1506	163.0790	N	1557.7941	779.4007	1540.7676	770.8874	1539.7836	770.3954	15
4	503.1919	252.0996	486.1653	243.5863	485.1813	243.0943	C	1443.7512	722.3792	1426.7246	713.8660	1425.7406	713.3740	14
5	602.2603	301.6338	585.2337	293.1205	584.2497	292.6285	V	1283.7205	642.3639	1266.6940	633.8506	1265.7100	633.3586	13
6	699.3130	350.1602	682.2865	341.6469	681.3025	341.1549	P	1184.6521	592.8297	1167.6256	584.3164	1166.6416	583.8244	12
7	828.3556	414.6815	811.3291	406.1682	810.3451	405.6762	E	1087.5994	544.3033	1070.5728	535.7900	1069.5888	535.2980	11
8	941.4397	471.2235	924.4131	462.7102	923.4291	462.2182	I	958.5568	479.7820	941.5302	471.2688	940.5462	470.7767	10
9	1012.4768	506.7420	995.4503	498.2288	994.4662	497.7368	A	845.4727	423.2400	828.4462	414.7267	827.4621	414.2347	9
10	1127.5038	564.2555	1110.4772	555.7422	1109.4932	555.2502	D	774.4356	387.7214	757.4090	379.2082	756.4250	378.7162	8
11	1228.5514	614.7794	1211.5249	606.2661	1210.5409	605.7741	T	659.4087	330.2080	642.3821	321.6947	641.3981	321.2027	7
12	1341.6355	671.3214	1324.6089	662.8081	1323.6249	662.3161	L	558.3610	279.6841	541.3344	271.1709	0	0	6
13	1398.6570	699.8321	1381.6304	691.3188	1380.6464	690.8268	G	445.2769	223.1421	428.2504	214.6288	0	0	5
14	1469.6941	735.3507	1452.6675	726.8374	1451.6835	726.3454	A	388.2554	194.6314	371.2289	186.1181	0	0	4
15	1568.7625	784.8849	1551.7359	776.3716	1550.7519	775.8796	V	317.2183	159.1128	300.1918	150.5995	0	0	3
16	1639.7996	820.4034	1622.7731	811.8902	1621.7890	811.3982	A	218.1499	109.5786	201.1234	101.0653	0	0	2
17							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

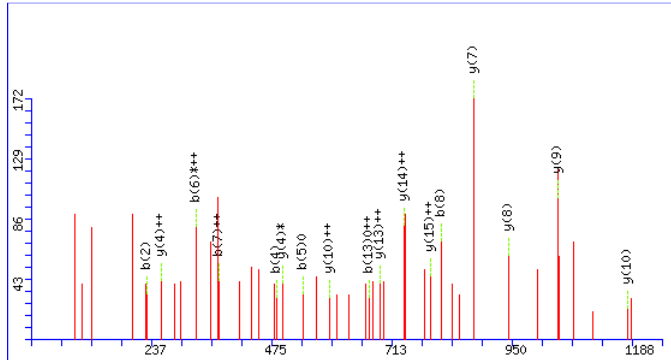
Peptide: 83164.

MS/MS Fragmentation of **DLEQALAAFLSTPGGSHPALCSLNR: 57.021465@C:21**
Found in **IP100166767:IP100377163**

Title: 4.1.1.3615.3

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							26
2	229.1183	115.0628	0	0	211.1077	106.0575	L	2623.3661	1312.1867	2606.3395	1303.6734	2605.3555	1303.1814	25
3	358.1609	179.5841	0	0	340.1503	170.5788	E	2510.2820	1255.6446	2493.2555	1247.1314	2492.2715	1246.6394	24
4	486.2195	243.6134	469.1929	235.1001	468.2089	234.6081	Q	2381.2394	1191.1234	2364.2129	1182.6101	2363.2289	1182.1181	23
5	557.2566	279.1319	540.2300	270.6186	539.2460	270.1266	A	2253.1808	1127.0941	2236.1543	1118.5808	2235.1703	1118.0888	22
6	670.3406	335.6740	653.3141	327.1607	652.3301	326.6687	L	2182.1437	1091.5755	2165.1172	1083.0622	2164.1332	1082.5702	21
7	741.3777	371.1925	724.3512	362.6792	723.3672	362.1872	A	2069.0597	1035.0335	2052.0331	1026.5202	2051.0491	1026.0282	20
8	812.4149	406.7111	795.3883	398.1978	794.4043	397.7058	A	1998.0226	999.5149	1980.9960	991.0016	1980.0120	990.5096	19
9	959.4833	480.2453	942.4567	471.7320	941.4727	471.2400	F	1926.9854	963.9964	1909.9589	955.4831	1908.9749	954.9911	18
10	1072.5673	536.7873	1055.5408	528.2740	1054.5568	527.7820	L	1779.9170	890.4622	1762.8905	881.9489	1761.9065	881.4569	17
11	1159.5994	580.3033	1142.5728	571.7900	1141.5888	571.2980	S	1666.8330	833.9201	1649.8064	825.4068	1648.8224	824.9148	16
12	1260.6470	630.8272	1243.6205	622.3139	1242.6365	621.8219	T	1579.8009	790.4041	1562.7744	781.8908	1561.7904	781.3988	15
13	1357.6998	679.3535	1340.6733	670.8403	1339.6892	670.3483	P	1478.7533	739.8803	1461.7267	731.3670	1460.7427	730.8750	14
14	1414.7213	707.8643	1397.6947	699.3510	1396.7107	698.8590	G	1381.7005	691.3539	1364.6739	682.8406	1363.6899	682.3486	13
15	1471.7427	736.3750	1454.7162	727.8617	1453.7322	727.3697	G	1324.6790	662.8432	1307.6525	654.3299	1306.6685	653.8379	12
16	1558.7748	779.8910	1541.7482	771.3777	1540.7642	770.8857	S	1267.6576	634.3324	1250.6310	625.8191	1249.6470	625.3271	11
17	1695.8337	848.4205	1678.8071	839.9072	1677.8231	839.4152	H	1180.6255	590.8164	1163.5990	582.3031	1162.6150	581.8111	10
18	1792.8864	896.9469	1775.8599	888.4336	1774.8759	887.9416	P	1043.5666	522.2870	1026.5401	513.7737	1025.5561	513.2817	9
19	1863.9236	932.4654	1846.8970	923.9521	1845.9130	923.4601	A	946.5139	473.7606	929.4873	465.2473	928.5033	464.7553	8
20	1977.0076	989.0074	1959.9811	980.4942	1958.9971	980.0022	L	875.4767	438.2420	858.4502	429.7287	857.4662	429.2367	7
21	2137.0383	1069.0228	2120.0117	1060.5095	2119.0277	1060.0175	C	762.3927	381.7000	745.3661	373.1867	744.3821	372.6947	6
22	2224.0703	1112.5388	2207.0437	1104.0255	2206.0597	1103.5335	S	602.3620	301.6847	585.3355	293.1714	584.3515	292.6794	5
23	2337.1544	1169.0808	2320.1278	1160.5675	2319.1438	1160.0755	L	515.3300	258.1686	498.3035	249.6554	0	0	4
24	2451.1973	1226.1023	2434.1707	1217.5890	2433.1867	1217.0970	N	402.2459	201.6266	385.2194	193.1133	0	0	3
25	2564.2814	1282.6443	2547.2548	1274.1310	2546.2708	1273.6390	L	288.2030	144.6051	271.1765	136.0919	0	0	2
26							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 83293.

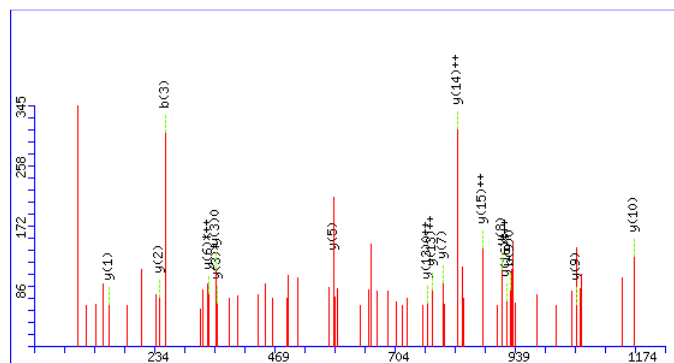
MS/MS Fragmentation of **SGLVVEDHLFDLPLEVK**:

Found in **IP100018213**

Title: 3.1.1.3910.4

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_3.mgf

ProteinPilot Peptide Confidence > 99%



Peptide View

Peptide: 83296.

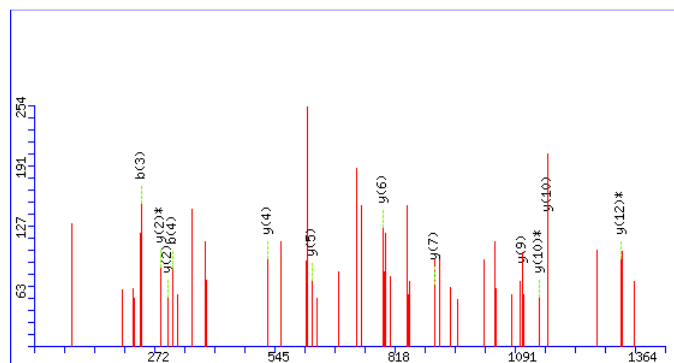
MS/MS Fragmentation of **GEGAIGSLDYTPPEER**:

Found in **IP100006937;IP101011831**

Title: 2.1.1.2466.11

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							15
2	187.0713	94.0393	0	0	169.0608	85.0340	E	1536.7176	768.8625	1519.6911	760.3492	1518.7071	759.8572	14
3	244.0928	122.5500	0	0	226.0822	113.5448	G	1407.6751	704.3412	1390.6485	695.8279	1389.6645	695.3359	13
4	315.1299	158.0686	0	0	297.1193	149.0633	A	1350.6536	675.8304	1333.6270	667.3172	1332.6430	666.8251	12
5	428.2140	214.6106	0	0	410.2034	205.6053	I	1279.6165	640.3119	1262.5899	631.7986	1261.6059	631.3066	11
6	485.2354	243.1214	0	0	467.2249	234.1161	G	1166.5324	583.7698	1149.5059	575.2566	1148.5218	574.7646	10
7	572.2675	286.6374	0	0	554.2569	277.6321	S	1109.5109	555.2591	1092.4844	546.7458	1091.5004	546.2538	9
8	685.3515	343.1794	0	0	667.3410	334.1741	L	1022.4789	511.7431	1005.4524	503.2298	1004.4684	502.7378	8
9	800.3785	400.6929	0	0	782.3679	391.6876	D	909.3949	455.2011	892.3683	446.6878	891.3843	446.1958	7
10	963.4418	482.2245	0	0	945.4312	473.2193	Y	794.3679	397.6876	777.3414	389.1743	776.3573	388.6823	6
11	1064.4895	532.7484	0	0	1046.4789	523.7431	T	631.3046	316.1559	614.2780	307.6427	613.2940	307.1506	5
12	1161.5422	581.2748	0	0	1143.5317	572.2695	P	530.2569	265.6321	513.2304	257.1188	512.2463	256.6268	4
13	1290.5848	645.7961	0	0	1272.5743	636.7908	E	433.2041	217.1057	416.1776	208.5924	415.1936	208.1004	3
14	1419.6274	710.3174	0	0	1401.6169	701.3121	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
15							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 83308.

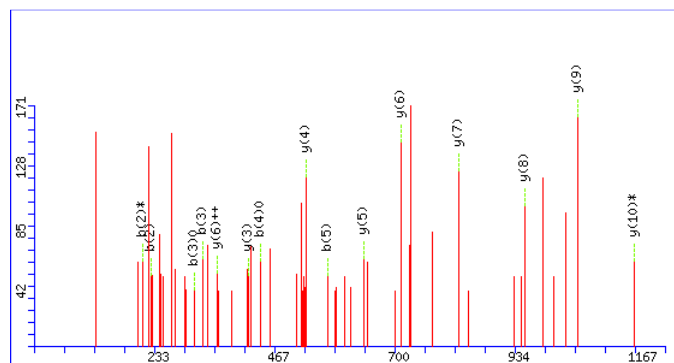
MS/MS Fragmentation of **VQTEIALLQR**:

Found in **IP100218566;IP100295738;IP100641808**

Title: 3.1.1.1715.5

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							11
2	228.1343	114.5708	211.1077	106.0575	0	0	Q	1184.6997	592.8535	1167.6732	584.3402	1166.6892	583.8482	10
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	T	1056.6412	528.8242	1039.6146	520.3109	1038.6306	519.8189	9
4	458.2245	229.6159	441.1980	221.1026	440.2140	220.6106	E	955.5935	478.3004	938.5669	469.7871	937.5829	469.2951	8
5	571.3086	286.1579	554.2821	277.6447	553.2980	277.1527	I	826.5509	413.7791	809.5244	405.2658	0	0	7
6	642.3457	321.6765	625.3192	313.1632	624.3352	312.6712	A	713.4668	357.2371	696.4403	348.7238	0	0	6
7	755.4298	378.2185	738.4032	369.7053	737.4192	369.2132	L	642.4297	321.7185	625.4032	313.2052	0	0	5
8	868.5138	434.7606	851.4873	426.2473	850.5033	425.7553	L	529.3457	265.1765	512.3191	256.6632	0	0	4
9	981.5979	491.3026	964.5714	482.7893	963.5873	482.2973	L	416.2616	208.6344	399.2350	200.1212	0	0	3
10	1109.6565	555.3319	1092.6299	546.8186	1091.6459	546.3266	Q	303.1775	152.0924	286.1510	143.5791	0	0	2
11							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 83353.

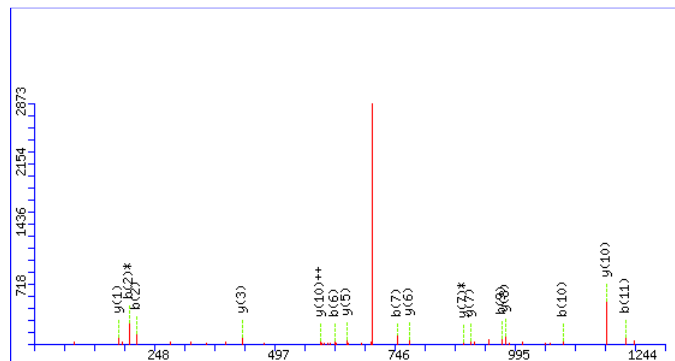
MS/MS Fragmentation of **GRPLAESEQER**:

Found in **IP100550440;IP100908962;IP100909361**

Title: 1.1.1.7154.10

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120214ry¥120214ry_aHDF1419-P10_4_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							12
2	214.1299	107.5686	197.1033	99.0553	0	0	R	1343.6550	672.3311	1326.6284	663.8179	1325.6444	663.3258	11
3	311.1826	156.0949	294.1561	147.5817	0	0	P	1187.5539	594.2806	1170.5273	585.7673	1169.5433	585.2753	10
4	424.2667	212.6370	407.2401	204.1237	0	0	L	1090.5011	545.7542	1073.4746	537.2409	1072.4905	536.7489	9
5	495.3038	248.1555	478.2772	239.6423	0	0	A	977.4170	489.2122	960.3905	480.6989	959.4065	480.2069	8
6	624.3464	312.6768	607.3198	304.1636	606.3358	303.6715	E	906.3799	453.6936	889.3534	445.1803	888.3694	444.6883	7
7	753.3890	377.1981	736.3624	368.6849	735.3784	368.1928	E	777.3373	389.1723	760.3108	380.6590	759.3268	380.1670	6
8	840.4210	420.7141	823.3945	412.2009	822.4104	411.7089	S	648.2947	324.6510	631.2682	316.1377	630.2842	315.6457	5
9	969.4636	485.2354	952.4371	476.7222	951.4530	476.2302	E	561.2627	281.1350	544.2362	272.6217	543.2522	272.1297	4
10	1097.5222	549.2647	1080.4956	540.7515	1079.5116	540.2594	Q	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	3
11	1226.5648	613.7860	1209.5382	605.2727	1208.5542	604.7807	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
12							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 83624.

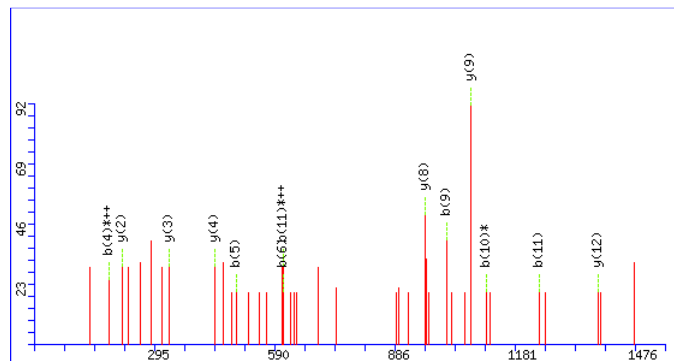
MS/MS Fragmentation of **PSSNLLEQFILLAK**:

Found in **IP100009301;IP100445209;IP100916095;IP100916369;IP100916504;IP100916690;IP100917012;IP100917140;IP100917467;IP100917481**

Title: 4.1.1.2764.6

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	98.0600	49.5337	0	0	0	0	P							14
2	185.0921	93.0497	0	0	167.0815	84.0444	S	1475.8468	738.4270	1458.8203	729.9138	1457.8362	729.4218	13
3	272.1241	136.5657	0	0	254.1135	127.5604	S	1388.8148	694.9110	1371.7882	686.3978	1370.8042	685.9057	12
4	386.1670	193.5871	369.1405	185.0739	368.1565	184.5819	N	1301.7827	651.3950	1284.7562	642.8817	1283.7722	642.3897	11
5	499.2511	250.1292	482.2245	241.6159	481.2405	241.1239	L	1187.7398	594.3735	1170.7133	585.8603	1169.7293	585.3683	10
6	612.3352	306.6712	595.3086	298.1579	594.3246	297.6659	L	1074.6558	537.8315	1057.6292	529.3182	1056.6452	528.8262	9
7	741.3777	371.1925	724.3512	362.6792	723.3672	362.1872	E	961.5717	481.2895	944.5451	472.7762	943.5611	472.2842	8
8	869.4363	435.2218	852.4098	426.7085	851.4258	426.2165	Q	832.5291	416.7682	815.5026	408.2549	0	0	7
9	1016.5047	508.7560	999.4782	500.2427	998.4942	499.7507	F	704.4705	352.7389	687.4440	344.2256	0	0	6
10	1129.5888	565.2980	1112.5623	556.7848	1111.5782	556.2928	I	557.4021	279.2047	540.3756	270.6914	0	0	5
11	1242.6729	621.8401	1225.6463	613.3268	1224.6623	612.8348	L	444.3180	222.6627	427.2915	214.1494	0	0	4
12	1355.7569	678.3821	1338.7304	669.8688	1337.7464	669.3768	L	331.2340	166.1206	314.2074	157.6074	0	0	3
13	1426.7940	713.9007	1409.7675	705.3874	1408.7835	704.8954	A	218.1499	109.5786	201.1234	101.0653	0	0	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 83848.

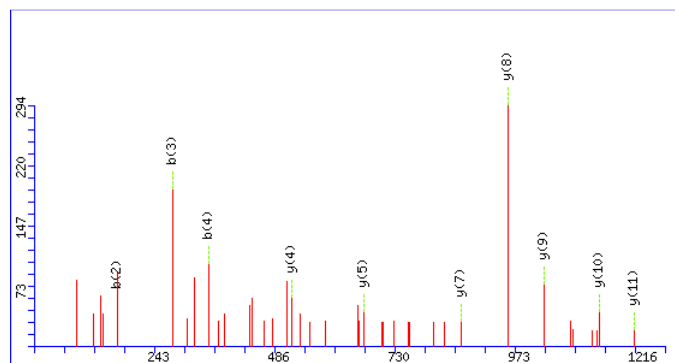
MS/MS Fragmentation of **PAIAPPVVFVQK**:

Found in **IP100026337;IP100179121;IP100456728;IP100456729;IP100874033;IP100922347**

Title: 3.1.1.1791.7

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	98.0600	49.5337	0	0	0	0	P							12
2	169.0972	85.0522	0	0	0	0	A	1216.7089	608.8581	1199.6823	600.3448	0	0	11
3	282.1812	141.5942	0	0	0	0	I	1145.6717	573.3395	1128.6452	564.8262	0	0	10
4	353.2183	177.1128	0	0	0	0	A	1032.5877	516.7975	1015.5611	508.2842	0	0	9
5	450.2711	225.6392	0	0	0	0	P	961.5506	481.2789	944.5240	472.7656	0	0	8
6	547.3239	274.1656	0	0	0	0	P	864.4978	432.7525	847.4713	424.2393	0	0	7
7	646.3923	323.6998	0	0	0	0	V	767.4450	384.2262	750.4185	375.7129	0	0	6
8	793.4607	397.2340	0	0	0	0	F	668.3766	334.6919	651.3501	326.1787	0	0	5
9	892.5291	446.7682	0	0	0	0	V	521.3082	261.1577	504.2817	252.6445	0	0	4
10	1039.5975	520.3024	0	0	0	0	F	422.2398	211.6235	405.2132	203.1103	0	0	3
11	1167.6561	584.3317	1150.6295	575.8184	0	0	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 84322.

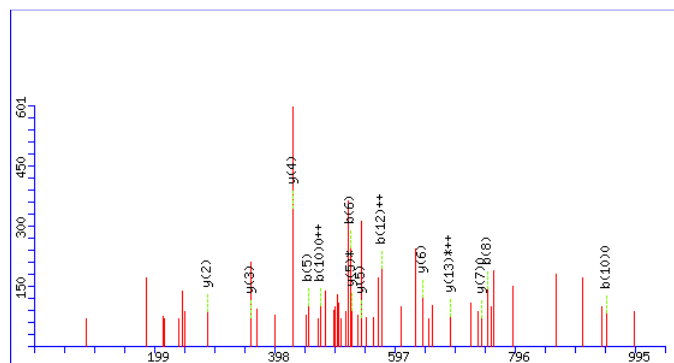
MS/MS Fragmentation of **GGSHDAPENTLAAIR: 0.984015@N:9**

Found in **IP100010279**

Title: 2.1.1.572.7

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							15
2	115.0502	58.0287	0	0	0	0	G	1452.7077	726.8575	1435.6812	718.3442	1434.6972	717.8522	14
3	202.0822	101.5448	0	0	184.0717	92.5395	S	1395.6863	698.3468	1378.6597	689.8335	1377.6757	689.3415	13
4	339.1411	170.0742	0	0	321.1306	161.0689	H	1308.6543	654.8308	1291.6277	646.3175	1290.6437	645.8255	12
5	454.1681	227.5877	0	0	436.1575	218.5824	D	1171.5953	586.3013	1154.5688	577.7880	1153.5848	577.2960	11
6	525.2052	263.1062	0	0	507.1946	254.1010	A	1056.5684	528.7878	1039.5419	520.2746	1038.5578	519.7826	10
7	622.2580	311.6326	0	0	604.2474	302.6273	P	985.5313	493.2693	968.5047	484.7560	967.5207	484.2640	9
8	751.3006	376.1539	0	0	733.2900	367.1486	E	888.4785	444.7429	871.4520	436.2296	870.4680	435.7376	8
9	866.3275	433.6674	849.3010	425.1541	848.3169	424.6621	N	759.4359	380.2216	742.4094	371.7083	741.4254	371.2163	7
10	967.3752	484.1912	950.3486	475.6780	949.3646	475.1859	T	644.4090	322.7081	627.3824	314.1949	626.3984	313.7028	6
11	1080.4592	540.7333	1063.4327	532.2200	1062.4487	531.7280	L	543.3613	272.1843	526.3348	263.6710	0	0	5
12	1151.4964	576.2518	1134.4698	567.7385	1133.4858	567.2465	A	430.2772	215.6423	413.2507	207.1290	0	0	4
13	1222.5335	611.7704	1205.5069	603.2571	1204.5229	602.7651	A	359.2401	180.1237	342.2136	171.6104	0	0	3
14	1335.6175	668.3124	1318.5910	659.7991	1317.6070	659.3071	I	288.2030	144.6051	271.1765	136.0919	0	0	2
15							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 84483.

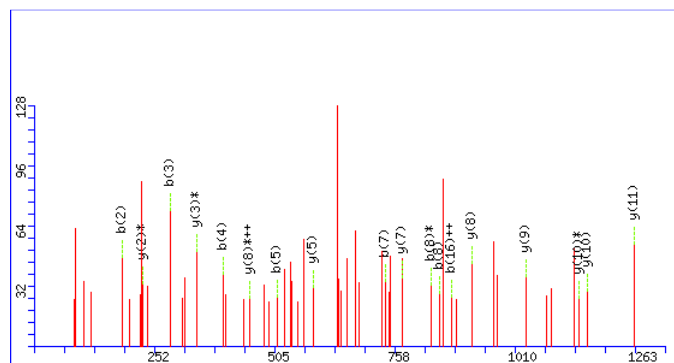
MS/MS Fragmentation of **DAVLLNNIVQNFQMLDLVK:**

Found in **IP100159770:IP100645960**

Title: 5.1.1.90.4

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_3.5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							19
2	187.0713	94.0393	0	0	169.0608	85.0340	A	2001.1201	1001.0637	1984.0936	992.5504	1983.1096	992.0584	18
3	286.1397	143.5735	0	0	268.1292	134.5682	V	1930.0830	965.5452	1913.0565	957.0319	1912.0725	956.5399	17
4	399.2238	200.1155	0	0	381.2132	191.1103	L	1831.0146	916.0109	1813.9881	907.4977	1813.0041	907.0057	16
5	512.3079	256.6576	0	0	494.2973	247.6523	L	1717.9306	859.4689	1700.9040	850.9556	1699.9200	850.4636	15
6	626.3508	313.6790	609.3243	305.1658	608.3402	304.6738	N	1604.8465	802.9269	1587.8199	794.4136	1586.8359	793.9216	14
7	740.3937	370.7005	723.3672	362.1872	722.3832	361.6952	N	1490.8036	745.9054	1473.7770	737.3921	1472.7930	736.9001	13
8	853.4778	427.2425	836.4512	418.7293	835.4672	418.2373	I	1376.7606	688.8840	1359.7341	680.3707	1358.7501	679.8787	12
9	952.5462	476.7767	935.5197	468.2635	934.5356	467.7715	V	1263.6766	632.3419	1246.6500	623.8286	1245.6660	623.3366	11
10	1080.6048	540.8060	1063.5782	532.2928	1062.5942	531.8007	Q	1164.6082	582.8077	1147.5816	574.2944	1146.5976	573.8024	10
11	1194.6477	597.8275	1177.6212	589.3142	1176.6371	588.8222	N	1036.5496	518.7784	1019.5230	510.2652	1018.5390	509.7731	9
12	1341.7161	671.3617	1324.6896	662.8484	1323.7056	662.3564	F	922.5067	461.7570	905.4801	453.2437	904.4961	452.7517	8
13	1398.7376	699.8724	1381.7110	691.3592	1380.7270	690.8672	G	775.4382	388.2228	758.4117	379.7095	757.4277	379.2175	7
14	1529.7781	765.3927	1512.7515	756.8794	1511.7675	756.3874	M	718.4168	359.7120	701.3902	351.1988	700.4062	350.7067	6
15	1642.8621	821.9347	1625.8356	813.4214	1624.8516	812.9294	L	587.3763	294.1918	570.3497	285.6785	569.3657	285.1865	5
16	1757.8891	879.4482	1740.8625	870.9349	1739.8785	870.4429	D	474.2922	237.6498	457.2657	229.1365	456.2817	228.6445	4
17	1870.9731	935.9902	1853.9466	927.4769	1852.9626	926.9849	L	359.2653	180.1363	342.2387	171.6230	0	0	3
18	1970.0416	985.5244	1953.0150	977.0111	1952.0310	976.5191	V	246.1812	123.5942	229.1547	115.0810	0	0	2
19							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 84529.

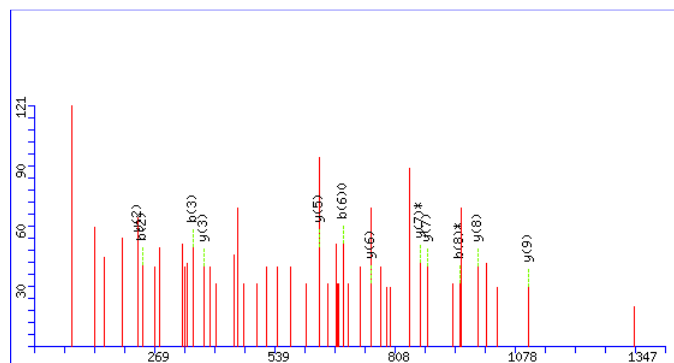
MS/MS Fragmentation of **EDLLQNPYFSK**:

Found in **IP100302658;IP100328634;IP100333633;IP101025426;IP101025678;IP101025702;IP101025870;IP101026066**

Title: 3.1.1.398.7

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							11
2	245.0768	123.0420	0	0	227.0662	114.0368	D	1224.6259	612.8166	1207.5994	604.3033	1206.6154	603.8113	10
3	358.1609	179.5841	0	0	340.1503	170.5788	L	1109.5990	555.3031	1092.5724	546.7898	1091.5884	546.2978	9
4	471.2449	236.1261	0	0	453.2344	227.1208	L	996.5149	498.7611	979.4884	490.2478	978.5043	489.7558	8
5	599.3035	300.1554	582.2770	291.6421	581.2930	291.1501	Q	883.4308	442.2191	866.4043	433.7058	865.4203	433.2138	7
6	713.3464	357.1769	696.3199	348.6636	695.3359	348.1716	N	755.3723	378.1898	738.3457	369.6765	737.3617	369.1845	6
7	810.3992	405.7032	793.3727	397.1900	792.3886	396.6980	P	641.3293	321.1683	624.3028	312.6550	623.3188	312.1630	5
8	973.4625	487.2349	956.4360	478.7216	955.4520	478.2296	Y	544.2766	272.6419	527.2500	264.1287	526.2660	263.6366	4
9	1120.5310	560.7691	1103.5044	552.2558	1102.5204	551.7638	F	381.2132	191.1103	364.1867	182.5970	363.2027	182.1050	3
10	1207.5630	604.2851	1190.5364	595.7719	1189.5524	595.2798	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
11							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 84536.

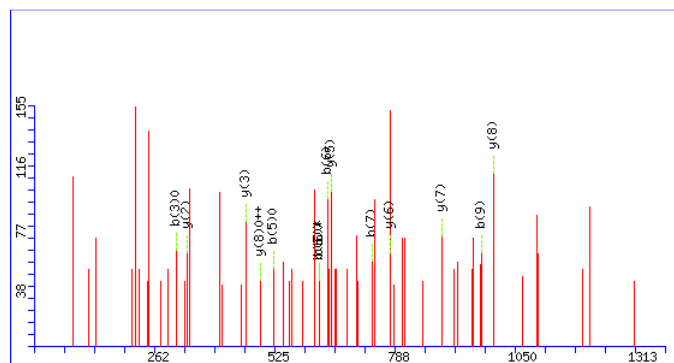
MS/MS Fragmentation of **ESLVNVPLQLIESVEGR: 57.021465@C:16**

Found in **IP100171273;IP100171274;IP100185018;IP100892979**

Title: 4.1.1.2740.4

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							17
2	217.0819	109.0446	0	0	199.0713	100.0393	S	1855.9946	928.5009	1838.9681	919.9877	1837.9840	919.4957	16
3	330.1660	165.5866	0	0	312.1554	156.5813	L	1768.9626	884.9849	1751.9360	876.4717	1750.9520	875.9796	15
4	429.2344	215.1208	0	0	411.2238	206.1155	V	1655.8785	828.4429	1638.8520	819.9296	1637.8680	819.4376	14
5	543.2773	272.1423	526.2508	263.6290	525.2667	263.1370	N	1556.8101	778.9087	1539.7836	770.3954	1538.7995	769.9034	13
6	642.3457	321.6765	625.3192	313.1632	624.3352	312.6712	V	1442.7672	721.8872	1425.7406	713.3740	1424.7566	712.8819	12
7	739.3985	370.2029	722.3719	361.6896	721.3879	361.1976	P	1343.6988	672.3530	1326.6722	663.8397	1325.6882	663.3477	11
8	852.4825	426.7449	835.4560	418.2316	834.4720	417.7396	L	1246.6460	623.8266	1229.6195	615.3134	1228.6354	614.8214	10
9	980.5411	490.7742	963.5146	482.2609	962.5306	481.7689	Q	1133.5619	567.2846	1116.5354	558.7713	1115.5514	558.2793	9
10	1093.6252	547.3162	1076.5986	538.8030	1075.6146	538.3109	L	1005.5034	503.2553	988.4768	494.7420	987.4928	494.2500	8
11	1206.7093	603.8583	1189.6827	595.3450	1188.6987	594.8530	I	892.4193	446.7133	875.3927	438.2000	874.4087	437.7080	7
12	1335.7518	668.3796	1318.7253	659.8663	1317.7413	659.3743	E	779.3352	390.1713	762.3087	381.6580	761.3247	381.1660	6
13	1422.7839	711.8956	1405.7573	703.3823	1404.7733	702.8903	S	650.2926	325.6500	633.2661	317.1367	632.2821	316.6447	5
14	1521.8523	761.4298	1504.8257	752.9165	1503.8417	752.4245	V	563.2606	282.1339	546.2341	273.6207	545.2500	273.1287	4
15	1650.8949	825.9511	1633.8683	817.4378	1632.8843	816.9458	E	464.1922	232.5997	447.1656	224.0865	446.1816	223.5945	3
16	1810.9255	905.9664	1793.8990	897.4531	1792.9150	896.9611	C	335.1496	168.0784	318.1231	159.5652	0	0	2
17							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 84620.

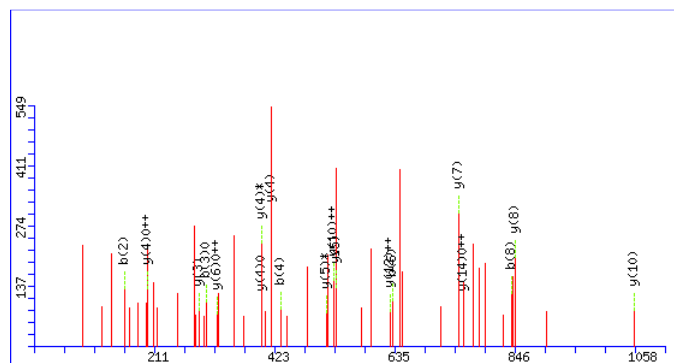
MS/MS Fragmentation of **GTYPVPVIVSELQSGK:**

Found in **IP100297550;IP100642188;IP100855773**

Title: 3.1.1.2877.3

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2.3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							16
2	159.0764	80.0418	0	0	141.0659	71.0366	T	1630.9051	815.9562	1613.8785	807.4429	1612.8945	806.9509	15
3	322.1397	161.5735	0	0	304.1292	152.5682	Y	1529.8574	765.4323	1512.8308	756.9190	1511.8468	756.4270	14
4	435.2238	218.1155	0	0	417.2132	209.1103	I	1366.7940	683.9007	1349.7675	675.3874	1348.7835	674.8954	13
5	532.2766	266.6419	0	0	514.2660	257.6366	P	1253.7100	627.3586	1236.6834	618.8454	1235.6994	618.3533	12
6	631.3450	316.1761	0	0	613.3344	307.1709	V	1156.6572	578.8322	1139.6307	570.3190	1138.6467	569.8270	11
7	728.3978	364.7025	0	0	710.3872	355.6972	P	1057.5888	529.2980	1040.5623	520.7848	1039.5782	520.2928	10
8	841.4818	421.2445	0	0	823.4713	412.2393	I	960.5360	480.7717	943.5095	472.2584	942.5255	471.7664	9
9	940.5502	470.7788	0	0	922.5397	461.7735	V	847.4520	424.2296	830.4254	415.7163	829.4414	415.2243	8
10	1027.5823	514.2948	0	0	1009.5717	505.2895	S	748.3836	374.6954	731.3570	366.1821	730.3730	365.6901	7
11	1156.6249	578.8161	0	0	1138.6143	569.8108	E	661.3515	331.1794	644.3250	322.6661	643.3410	322.1741	6
12	1269.7089	635.3581	0	0	1251.6984	626.3528	L	532.3089	266.6581	515.2824	258.1448	514.2984	257.6528	5
13	1397.7675	699.3874	1380.7409	690.8741	1379.7569	690.3821	Q	419.2249	210.1161	402.1983	201.6028	401.2143	201.1108	4
14	1484.7995	742.9034	1467.7730	734.3901	1466.7890	733.8981	S	291.1663	146.0868	274.1397	137.5735	273.1557	137.0815	3
15	1541.8210	771.4141	1524.7944	762.9009	1523.8104	762.4088	G	204.1343	102.5708	187.1077	94.0575	0	0	2
16							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 84912.

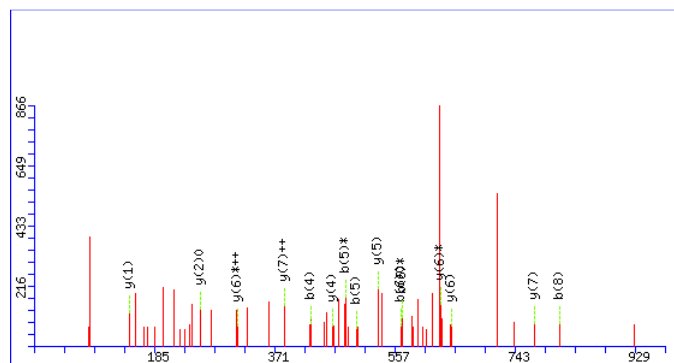
MS/MS Fragmentation of **ANELASVEK**:

Found in **IP100152863;IP100845255;IP100978760**

Title: 1.1.1.8011.11

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							9
2	186.0873	93.5473	169.0608	85.0340	0	0	N	889.4625	445.2349	872.4360	436.7216	871.4520	436.2296	8
3	315.1299	158.0686	298.1034	149.5553	297.1193	149.0633	E	775.4196	388.2134	758.3931	379.7002	757.4090	379.2082	7
4	428.2140	214.6106	411.1874	206.0974	410.2034	205.6053	L	646.3770	323.6921	629.3505	315.1789	628.3665	314.6869	6
5	499.2511	250.1292	482.2245	241.6159	481.2405	241.1239	A	533.2930	267.1501	516.2664	258.6368	515.2824	258.1448	5
6	586.2831	293.6452	569.2566	285.1319	568.2726	284.6399	S	462.2558	231.6316	445.2293	223.1183	444.2453	222.6263	4
7	685.3515	343.1794	668.3250	334.6661	667.3410	334.1741	V	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
8	814.3941	407.7007	797.3676	399.1874	796.3836	398.6954	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
9							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 84923.

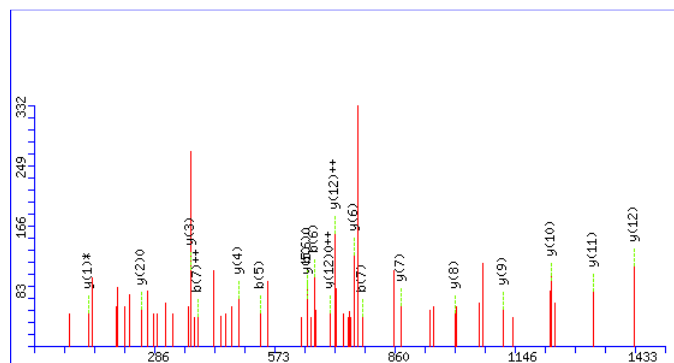
MS/MS Fragmentation of **IPTNDELLYDPEK**:

Found in **IP100306299;IP101024895**

Title: 2.1.1.3255.10

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							13
2	211.1441	106.0757	0	0	0	0	P	1433.6795	717.3434	1416.6529	708.8301	1415.6689	708.3381	12
3	312.1918	156.5995	0	0	294.1812	147.5942	T	1336.6267	668.8170	1319.6002	660.3037	1318.6161	659.8117	11
4	426.2347	213.6210	409.2082	205.1077	408.2241	204.6157	N	1235.5790	618.2931	1218.5525	609.7799	1217.5685	609.2879	10
5	541.2617	271.1345	524.2351	262.6212	523.2511	262.1292	D	1121.5361	561.2717	1104.5095	552.7584	1103.5255	552.2664	9
6	670.3042	335.6558	653.2777	327.1425	652.2937	326.6505	E	1006.5092	503.7582	989.4826	495.2449	988.4986	494.7529	8
7	783.3883	392.1978	766.3618	383.6845	765.3777	383.1925	L	877.4666	439.2369	860.4400	430.7236	859.4560	430.2316	7
8	896.4724	448.7398	879.4458	440.2266	878.4618	439.7345	L	764.3825	382.6949	747.3559	374.1816	746.3719	373.6896	6
9	1059.5357	530.2715	1042.5092	521.7582	1041.5251	521.2662	Y	651.2984	326.1529	634.2719	317.6396	633.2879	317.1476	5
10	1174.5626	587.7850	1157.5361	579.2717	1156.5521	578.7797	D	488.2351	244.6212	471.2086	236.1079	470.2245	235.6159	4
11	1271.6154	636.3113	1254.5889	627.7981	1253.6048	627.3061	P	373.2082	187.1077	356.1816	178.5944	355.1976	178.1024	3
12	1400.6580	700.8326	1383.6315	692.3194	1382.6474	691.8274	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: **84996**.

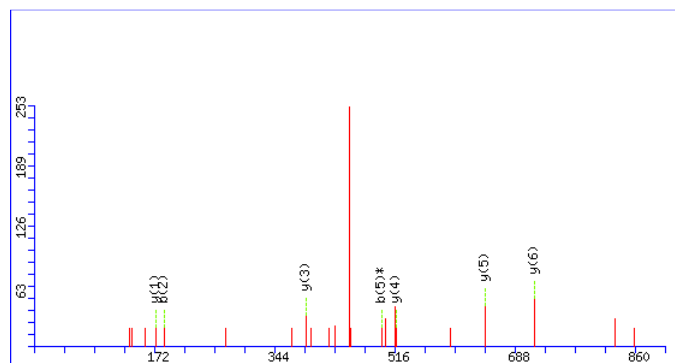
MS/MS Fragmentation of **GEAKELTR**:

Found in **IP100011245**

Title: 1.1.1.5582.8

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120208ry¥120208ry_Tig120slc-P8_1_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							8
2	187.0713	94.0393	0	0	169.0608	85.0340	E	846.4680	423.7376	829.4414	415.2243	828.4574	414.7323	7
3	258.1084	129.5579	0	0	240.0979	120.5526	A	717.4254	359.2163	700.3988	350.7030	699.4148	350.2110	6
4	386.2034	193.6053	369.1769	185.0921	368.1928	184.6001	K	646.3883	323.6978	629.3617	315.1845	628.3777	314.6925	5
5	515.2460	258.1266	498.2195	249.6134	497.2354	249.1214	E	518.2933	259.6503	501.2667	251.1370	500.2827	250.6450	4
6	628.3301	314.6687	611.3035	306.1554	610.3195	305.6634	L	389.2507	195.1290	372.2241	186.6157	371.2401	186.1237	3
7	729.3777	365.1925	712.3512	356.6792	711.3672	356.1872	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
8							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 85124.

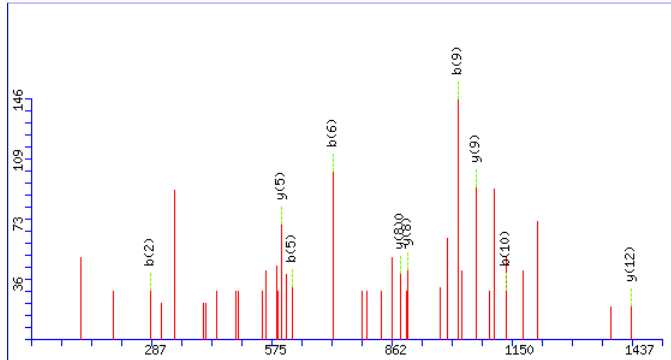
MS/MS Fragmentation of **RQPELVEGNLPVVFPTTELIFYADDQSTHK:**

Found in **IP100164251;IP100553204;IP100604569;IP100910930**

Title: 4.1.1.3381.8

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	157.1084	79.0578	140.0818	70.5446	0	0	R							30
2	285.1670	143.0871	268.1404	134.5738	0	0	Q	3333.6678	1667.3375	3316.6412	1658.8243	3315.6572	1658.3323	29
3	382.2197	191.6135	365.1932	183.1002	0	0	P	3205.6092	1603.3082	3188.5827	1594.7950	3187.5986	1594.3030	28
4	511.2623	256.1348	494.2358	247.6215	493.2518	247.1295	E	3108.5564	1554.7819	3091.5299	1546.2686	3090.5459	1545.7766	27
5	624.3464	312.6768	607.3198	304.1636	606.3358	303.6715	L	2979.5139	1490.2606	2962.4873	1481.7473	2961.5033	1481.2553	26
6	723.4148	362.2110	706.3883	353.6978	705.4042	353.2058	V	2866.4298	1433.7185	2849.4032	1425.2053	2848.4192	1424.7133	25
7	852.4574	426.7323	835.4308	418.2191	834.4468	417.7271	E	2767.3614	1384.1843	2750.3348	1375.6711	2749.3508	1375.1790	24
8	909.4789	455.2431	892.4523	446.7298	891.4683	446.2378	G	2638.3188	1319.6630	2621.2922	1311.1498	2620.3082	1310.6577	23
9	1023.5218	512.2645	1006.4952	503.7513	1005.5112	503.2592	N	2581.2973	1291.1523	2564.2708	1282.6390	2563.2868	1282.1470	22
10	1136.6058	568.8066	1119.5793	560.2933	1118.5953	559.8013	L	2467.2544	1234.1308	2450.2278	1225.6176	2449.2438	1225.1256	21
11	1233.6586	617.3329	1216.6321	608.8197	1215.6480	608.3277	P	2354.1703	1177.5888	2337.1438	1169.0755	2336.1598	1168.5835	20
12	1332.7270	666.8672	1315.7005	658.3539	1314.7165	657.8619	V	2257.1176	1129.0624	2240.0910	1120.5491	2239.1070	1120.0571	19
13	1479.7954	740.4014	1462.7689	731.8881	1461.7849	731.3961	F	2158.0491	1079.5282	2141.0226	1071.0149	2140.0386	1070.5229	18
14	1578.8639	789.9356	1561.8373	781.4223	1560.8533	780.9303	V	2010.9807	1005.9940	1993.9542	997.4807	1992.9702	996.9887	17
15	1725.9323	863.4698	1708.9057	854.9565	1707.9217	854.4645	F	1911.9123	956.4598	1894.8858	947.9465	1893.9018	947.4545	16
16	1822.9850	911.9962	1805.9585	903.4829	1804.9745	902.9909	P	1764.8439	882.9256	1747.8174	874.4123	1746.8333	873.9203	15
17	1924.0327	962.5200	1907.0062	954.0067	1906.0221	953.5147	T	1667.7911	834.3992	1650.7646	825.8859	1649.7806	825.3939	14
18	2053.0753	1027.0413	2036.0488	1018.5280	2035.0647	1018.0360	E	1566.7435	783.8754	1549.7169	775.3621	1548.7329	774.8701	13
19	2166.1594	1083.5833	2149.1328	1075.0700	2148.1488	1074.5780	L	1437.7009	719.3541	1420.6743	710.8408	1419.6903	710.3488	12
20	2279.2434	1140.1254	2262.2169	1131.6121	2261.2329	1131.1201	I	1324.6168	662.8120	1307.5903	654.2988	1306.6062	653.8068	11
21	2426.3118	1213.6596	2409.2853	1205.1463	2408.3013	1204.6543	F	1211.5327	606.2700	1194.5062	597.7567	1193.5222	597.2647	10
22	2589.3752	1295.1912	2572.3486	1286.6780	2571.3646	1286.1859	Y	1064.4643	532.7358	1047.4378	524.2225	1046.4538	523.7305	9
23	2660.4123	1330.7098	2643.3857	1322.1965	2642.4017	1321.7045	A	901.4010	451.2041	884.3745	442.6909	883.3904	442.1989	8
24	2775.4392	1388.2233	2758.4127	1379.7100	2757.4287	1379.2180	D	830.3639	415.6856	813.3373	407.1723	812.3533	406.6803	7
25	2890.4662	1445.7367	2873.4396	1437.2235	2872.4556	1436.7314	D	715.3369	358.1721	698.3104	349.6588	697.3264	349.1668	6
26	3018.5248	1509.7660	3001.4982	1501.2527	3000.5142	1500.7607	Q	600.3100	300.6586	583.2835	292.1454	582.2994	291.6534	5
27	3105.5568	1553.2820	3088.5302	1544.7688	3087.5462	1544.2767	S	472.2514	236.6293	455.2249	228.1161	454.2409	227.6241	4
28	3206.6045	1603.8059	3189.5779	1595.2926	3188.5939	1594.8006	T	385.2194	193.1133	368.1928	184.6001	367.2088	184.1081	3
29	3343.6634	1672.3353	3326.6368	1663.8220	3325.6528	1663.3300	H	284.1717	142.5895	267.1452	134.0762	0	0	2
30							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 85292.

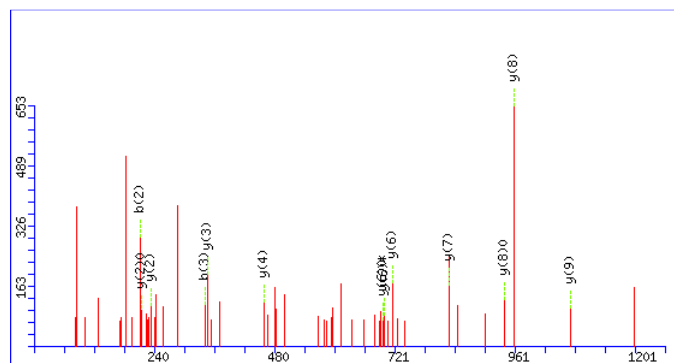
MS/MS Fragmentation of **VIELQEIIISK**:

Found in **IP100163496;IP100219754;IP100977583;IP100978294**

Title: 3.1.1.682.6

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2.3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							10
2	213.1598	107.0835	0	0	0	0	I	1072.6249	536.8161	1055.5983	528.3028	1054.6143	527.8108	9
3	342.2023	171.6048	0	0	324.1918	162.5995	E	959.5408	480.2740	942.5142	471.7608	941.5302	471.2687	8
4	455.2864	228.1468	0	0	437.2758	219.1416	L	830.4982	415.7527	813.4716	407.2395	812.4876	406.7475	7
5	583.3450	292.1761	566.3184	283.6629	565.3344	283.1709	Q	717.4141	359.2107	700.3876	350.6974	699.4036	350.2054	6
6	712.3876	356.6974	695.3610	348.1842	694.3770	347.6921	E	589.3556	295.1814	572.3290	286.6681	571.3450	286.1761	5
7	825.4716	413.2395	808.4451	404.7262	807.4611	404.2342	I	460.3130	230.6601	443.2864	222.1468	442.3024	221.6548	4
8	938.5557	469.7815	921.5292	461.2682	920.5451	460.7762	I	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
9	1025.5877	513.2975	1008.5612	504.7842	1007.5772	504.2922	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
10							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 85493.

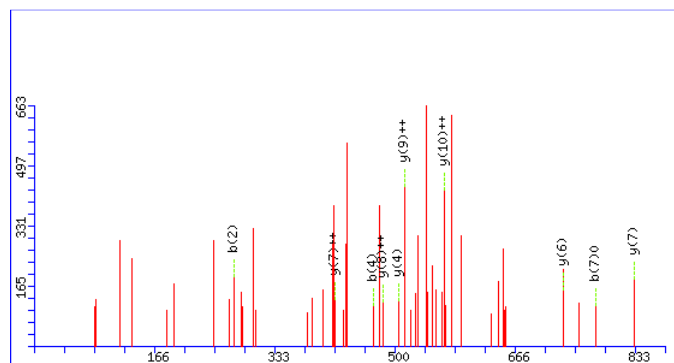
MS/MS Fragmentation of **YLGHVEVDESR**:

Found in **IP100028059;IP100180634;IP100180920;IP100216241;IP101015175;IP101025077;IP101025201;IP101025423;IP101025649;IP101026302;IP101026389**

Title: 1.1.1.7848.3

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120124ry¥120124ry_414C2-43_1_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	164.0706	82.5389	0	0	0	0	Y							11
2	277.1547	139.0810	0	0	0	0	L	1140.5644	570.7858	1123.5378	562.2726	1122.5538	561.7805	10
3	334.1761	167.5917	0	0	0	0	G	1027.4803	514.2438	1010.4538	505.7305	1009.4697	505.2385	9
4	471.2350	236.1212	0	0	0	0	H	970.4588	485.7331	953.4323	477.2198	952.4483	476.7278	8
5	570.3035	285.6554	0	0	0	0	V	833.3999	417.2036	816.3734	408.6903	815.3894	408.1983	7
6	699.3461	350.1767	0	0	681.3355	341.1714	E	734.3315	367.6694	717.3050	359.1561	716.3210	358.6641	6
7	798.4145	399.7109	0	0	780.4039	390.7056	V	605.2889	303.1481	588.2624	294.6348	587.2784	294.1428	5
8	913.4414	457.2243	0	0	895.4308	448.2191	D	506.2205	253.6139	489.1940	245.1006	488.2100	244.6086	4
9	1042.4840	521.7456	0	0	1024.4734	512.7404	E	391.1936	196.1004	374.1670	187.5871	373.1830	187.0951	3
10	1129.5160	565.2617	0	0	1111.5055	556.2564	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
11							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 85668.

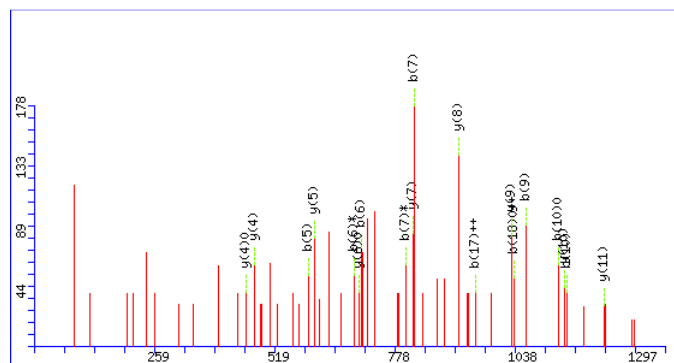
MS/MS Fragmentation of **LHTLENLLESIDPTLESWGK**:

Found in **IP100470896;IP100796956;IP100879253;IP100985431**

Title: 4.1.1.3045.5

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							20
2	251.1503	126.0788	0	0	0	0	H	2182.1026	1091.5550	2165.0761	1083.0417	2164.0921	1082.5497	19
3	352.1979	176.6026	0	0	334.1874	167.5973	T	2045.0437	1023.0255	2028.0172	1014.5122	2027.0332	1014.0202	18
4	465.2820	233.1446	0	0	447.2714	224.1394	L	1943.9960	972.5017	1926.9695	963.9884	1925.9855	963.4964	17
5	594.3246	297.6659	0	0	576.3140	288.6606	E	1830.9120	915.9596	1813.8854	907.4464	1812.9014	906.9543	16
6	708.3675	354.6874	691.3410	346.1741	690.3570	345.6821	N	1701.8694	851.4383	1684.8428	842.9251	1683.8588	842.4331	15
7	821.4516	411.2294	804.4250	402.7162	803.4410	402.2241	L	1587.8265	794.4169	1570.7999	785.9036	1569.8159	785.4116	14
8	934.5356	467.7715	917.5091	459.2582	916.5251	458.7662	L	1474.7424	737.8748	1457.7159	729.3616	1456.7318	728.8696	13
9	1063.5782	532.2928	1046.5517	523.7795	1045.5677	523.2875	E	1361.6583	681.3328	1344.6318	672.8195	1343.6478	672.3275	12
10	1150.6103	575.8088	1133.5837	567.2955	1132.5997	566.8035	S	1232.6157	616.8115	1215.5892	608.2982	1214.6052	607.8062	11
11	1263.6943	632.3508	1246.6678	623.8375	1245.6838	623.3455	I	1145.5837	573.2955	1128.5572	564.7822	1127.5732	564.2902	10
12	1378.7213	689.8643	1361.6947	681.3510	1360.7107	680.8590	D	1032.4997	516.7535	1015.4731	508.2402	1014.4891	507.7482	9
13	1475.7740	738.3907	1458.7475	729.8774	1457.7635	729.3854	P	917.4727	459.2400	900.4462	450.7267	899.4621	450.2347	8
14	1576.8217	788.9145	1559.7952	780.4012	1558.8111	779.9092	T	820.4199	410.7136	803.3934	402.2003	802.4094	401.7083	7
15	1689.9058	845.4565	1672.8792	836.9433	1671.8952	836.4512	L	719.3723	360.1898	702.3457	351.6765	701.3617	351.1845	6
16	1818.9484	909.9778	1801.9218	901.4645	1800.9378	900.9725	E	606.2882	303.6477	589.2617	295.1345	588.2776	294.6425	5
17	1905.9804	953.4938	1888.9538	944.9806	1887.9698	944.4886	S	477.2456	239.1264	460.2191	230.6132	459.2350	230.1212	4
18	2092.0597	1046.5335	2075.0332	1038.0202	2074.0491	1037.5282	W	390.2136	195.6104	373.1870	187.0972	0	0	3
19	2149.0812	1075.0442	2132.0546	1066.5310	2131.0706	1066.0389	G	204.1343	102.5708	187.1077	94.0575	0	0	2
20							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 85817.

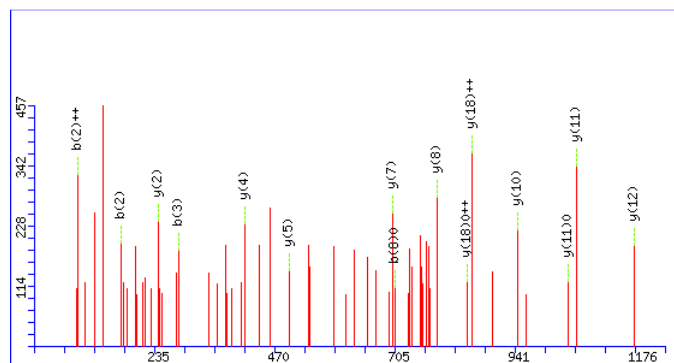
MS/MS Fragmentation of **GLLPGGTQVLDTSGFSPAPK:**

Found in **IP100066458;IP100787908;IP100909844**

Title: 3.1.1.1261.8

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							21
2	171.1128	86.0600	0	0	0	0	L	1942.0280	971.5176	1925.0015	963.0044	1924.0175	962.5124	20
3	284.1969	142.6021	0	0	0	0	L	1828.9440	914.9756	1811.9174	906.4623	1810.9334	905.9703	19
4	381.2496	191.1285	0	0	0	0	P	1715.8599	858.4336	1698.8333	849.9203	1697.8493	849.4283	18
5	438.2711	219.6392	0	0	0	0	G	1618.8071	809.9072	1601.7806	801.3939	1600.7966	800.9019	17
6	495.2926	248.1499	0	0	0	0	G	1561.7857	781.3965	1544.7591	772.8832	1543.7751	772.3912	16
7	596.3402	298.6738	0	0	578.3297	289.6685	T	1504.7642	752.8857	1487.7377	744.3725	1486.7536	743.8805	15
8	724.3988	362.7030	707.3723	354.1898	706.3883	353.6978	Q	1403.7165	702.3619	1386.6900	693.8486	1385.7060	693.3566	14
9	823.4672	412.2373	806.4407	403.7240	805.4567	403.2320	V	1275.6579	638.3326	1258.6314	629.8193	1257.6474	629.3273	13
10	936.5513	468.7793	919.5247	460.2660	918.5407	459.7740	L	1176.5895	588.7984	1159.5630	580.2851	1158.5790	579.7931	12
11	1051.5782	526.2928	1034.5517	517.7795	1033.5677	517.2875	D	1063.5055	532.2564	1046.4789	523.7431	1045.4949	523.2511	11
12	1108.5997	554.8035	1091.5732	546.2902	1090.5891	545.7982	G	948.4785	474.7429	931.4520	466.2296	930.4680	465.7376	10
13	1209.6474	605.3273	1192.6208	596.8141	1191.6368	596.3220	T	891.4571	446.2322	874.4305	437.7189	873.4465	437.2269	9
14	1296.6794	648.8433	1279.6529	640.3301	1278.6688	639.8381	S	790.4094	395.7083	773.3828	387.1951	772.3988	386.7030	8
15	1353.7009	677.3541	1336.6743	668.8408	1335.6903	668.3488	G	703.3774	352.1923	686.3508	343.6790	685.3668	343.1870	7
16	1500.7693	750.8883	1483.7427	742.3750	1482.7587	741.8830	F	646.3559	323.6816	629.3293	315.1683	628.3453	314.6763	6
17	1587.8013	794.4043	1570.7748	785.8910	1569.7908	785.3990	S	499.2875	250.1474	482.2609	241.6341	481.2769	241.1421	5
18	1684.8541	842.9307	1667.8275	834.4174	1666.8435	833.9254	P	412.2554	206.6314	395.2289	198.1181	0	0	4
19	1755.8912	878.4492	1738.8646	869.9360	1737.8806	869.4440	A	315.2027	158.1050	298.1761	149.5917	0	0	3
20	1852.9440	926.9756	1835.9174	918.4623	1834.9334	917.9703	P	244.1656	122.5864	227.1390	114.0731	0	0	2
21							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 85894.

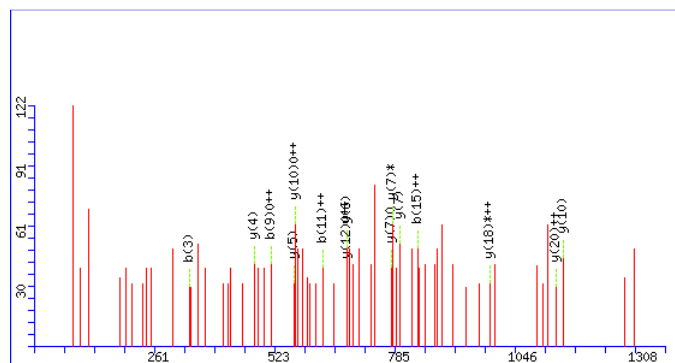
MS/MS Fragmentation of **DHSVEPLRDPNPSSDLENLDDSVFSK**:

Found in **IP100784883;IP100787950;IP100953625**

Title: 4.1.1.418.5

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							26
2	253.0931	127.0502	0	0	235.0826	118.0449	H	2823.3795	1412.1934	2806.3530	1403.6801	2805.3690	1403.1881	25
3	340.1252	170.5662	0	0	322.1146	161.5609	S	2686.3206	1343.6640	2669.2941	1335.1507	2668.3101	1334.6587	24
4	439.1936	220.1004	0	0	421.1830	211.0951	V	2599.2886	1300.1479	2582.2621	1291.6347	2581.2780	1291.1427	23
5	568.2382	284.6217	0	0	550.2256	275.6164	E	2500.2202	1250.6137	2483.1936	1242.1005	2482.2096	1241.6084	22
6	665.2889	333.1481	0	0	647.2784	324.1428	P	2371.1776	1186.0924	2354.1510	1177.5792	2353.1670	1177.0872	21
7	778.3730	389.6901	0	0	760.3624	380.6849	L	2274.1248	1137.5661	2257.0983	1129.0528	2256.1143	1128.5608	20
8	934.4741	467.7407	917.4476	459.2274	916.4635	458.7354	R	2161.0408	1081.0240	2144.0142	1072.5107	2143.0302	1072.0187	19
9	1049.5010	525.2542	1032.4745	516.7409	1031.4905	516.2489	D	2004.9397	1002.9735	1987.9131	994.4602	1986.9291	993.9682	18
10	1146.5538	573.7805	1129.5273	565.2673	1128.5432	564.7753	P	1889.9127	945.4600	1872.8862	936.9467	1871.9021	936.4547	17
11	1260.5967	630.8020	1243.5702	622.2887	1242.5862	621.7967	N	1792.8599	896.9336	1775.8334	888.4203	1774.8494	887.9283	16
12	1357.6495	679.3284	1340.6230	670.8151	1339.6389	670.3231	P	1678.8170	839.9121	1661.7905	831.3989	1660.8065	830.9069	15
13	1444.6815	722.8444	1427.6550	714.3311	1426.6710	713.8391	S	1581.7643	791.3858	1564.7377	782.8725	1563.7537	782.3805	14
14	1559.7085	780.3579	1542.6819	771.8446	1541.6979	771.3526	D	1494.7322	747.8698	1477.7057	739.3565	1476.7217	738.8645	13
15	1672.7925	836.8999	1655.7660	828.3866	1654.7820	827.8946	L	1379.7053	690.3563	1362.6787	681.8430	1361.6947	681.3510	12
16	1785.8766	893.4419	1768.8501	884.9287	1767.8660	884.4367	L	1266.6212	633.8142	1249.5947	625.3010	1248.6107	624.8090	11
17	1914.9192	957.9632	1897.8926	949.4500	1896.9086	948.9580	E	1153.5372	577.2722	1136.5106	568.7589	1135.5266	568.2669	10
18	2028.9621	1014.9847	2011.9356	1006.4714	2010.9516	1005.9794	N	1024.4946	512.7509	1007.4680	504.2376	1006.4840	503.7456	9
19	2142.0462	1071.5267	2125.0196	1063.0135	2124.0356	1062.5214	L	910.4516	455.7295	893.4251	447.2162	892.4411	446.7242	8
20	2257.0731	1129.0402	2240.0466	1120.5269	2239.0626	1120.0349	D	797.3676	399.1874	780.3410	390.6742	779.3570	390.1821	7
21	2372.1001	1186.5537	2355.0735	1178.0404	2354.0895	1177.5484	D	682.3406	341.6740	665.3141	333.1607	664.3301	332.6687	6
22	2459.1321	1230.0697	2442.1056	1221.5564	2441.1215	1221.0644	S	567.3137	284.1605	550.2871	275.6472	549.3031	275.1552	5
23	2558.2005	1279.6039	2541.1740	1271.0906	2540.1899	1270.5986	V	480.2817	240.6445	463.2551	232.1312	462.2711	231.6392	4
24	2705.2689	1353.1381	2688.2424	1344.6248	2687.2584	1344.1328	F	381.2132	191.1103	364.1867	182.5970	363.2027	182.1050	3
25	2792.3010	1396.6541	2775.2744	1388.1408	2774.2904	1387.6488	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
26							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 85983.

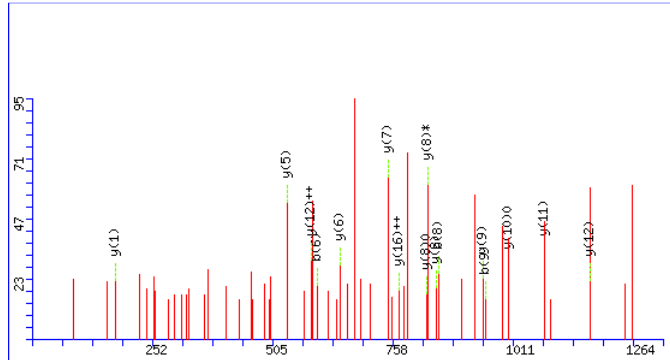
MS/MS Fragmentation of **SDVDALQVVEEAVGQALPGATVTLTGGR**:
 5. b₁ **1022000005** y₁ **1022001000**

Found in **IPI00002325;IPI00924893**

Title: 5.1.1.1099.3

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_414C2-43_3_5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							30
2	203.0662	102.0368	0	0	185.0557	93.0315	D	2941.5265	1471.2669	2924.5000	1462.7536	2923.5160	1462.2616	29
3	302.1347	151.5710	0	0	284.1241	142.5657	V	2826.4996	1413.7534	2809.4731	1405.2402	2808.4890	1404.7482	28
4	417.1616	209.0844	0	0	399.1510	200.0792	D	2727.4312	1364.2192	2710.4046	1355.7060	2709.4206	1355.2140	27
5	488.1987	244.6030	0	0	470.1882	235.5977	A	2612.4042	1306.7058	2595.3777	1298.1925	2594.3937	1297.7005	26
6	601.2828	301.1450	0	0	583.2722	292.1397	L	2541.3671	1271.1872	2524.3406	1262.6739	2523.3566	1262.1819	25
7	729.3414	365.1743	712.3148	356.6610	711.3308	356.1690	Q	2428.2831	1214.6452	2411.2565	1206.1319	2410.2725	1205.6399	24
8	857.3999	429.2036	840.3734	420.6903	839.3894	420.1983	Q	2300.2245	1150.6159	2283.1979	1142.1026	2282.2139	1141.6106	23
9	956.4684	478.7378	939.4418	470.2245	938.4578	469.7325	V	2172.1659	1086.5866	2155.1394	1078.0733	2154.1553	1077.5813	22
10	1055.5368	528.2720	1038.5102	519.7587	1037.5262	519.2667	V	2073.0975	1037.0524	2056.0709	1028.5391	2055.0869	1028.0471	21
11	1184.5794	592.7933	1167.5528	584.2800	1166.5688	583.7880	E	1974.0291	987.5182	1957.0025	979.0049	1956.0185	978.5129	20
12	1313.6220	657.3146	1296.5954	648.8013	1295.6114	648.3093	E	1844.9865	922.9969	1827.9599	914.4836	1826.9759	913.9916	19
13	1384.6591	692.8332	1367.6325	684.3199	1366.6485	683.8279	A	1715.9439	858.4756	1698.9173	849.9623	1697.9333	849.4703	18
14	1483.7275	742.3674	1466.7009	733.8541	1465.7169	733.3621	V	1644.9068	822.9570	1627.8802	814.4438	1626.8962	813.9517	17
15	1540.7489	770.8781	1523.7224	762.3648	1522.7384	761.8728	G	1545.8384	773.4228	1528.8118	764.9095	1527.8278	764.4175	16
16	1668.8075	834.9074	1651.7810	826.3941	1650.7970	825.9021	Q	1488.8169	744.9121	1471.7904	736.3988	1470.8063	735.9068	15
17	1739.8446	870.4260	1722.8181	861.9127	1721.8341	861.4207	A	1360.7583	680.8828	1343.7318	672.3695	1342.7478	671.8775	14
18	1852.9287	926.9680	1835.9022	918.4547	1834.9181	917.9627	L	1289.7212	645.3642	1272.6947	636.8510	1271.7107	636.3590	13
19	1949.9815	975.4944	1932.9549	966.9811	1931.9709	966.4891	P	1176.6372	588.8222	1159.6106	580.3089	1158.6266	579.8169	12
20	2007.0029	1004.0051	1989.9764	995.4918	1988.9924	994.9998	G	1079.5844	540.2958	1062.5578	531.7826	1061.5738	531.2905	11
21	2078.0400	1039.5237	2061.0135	1031.0104	2060.0295	1030.5184	A	1022.5629	511.7851	1005.5364	503.2718	1004.5524	502.7798	10
22	2179.0877	1090.0475	2162.0612	1081.5342	2161.0772	1081.0422	T	951.5258	476.2665	934.4993	467.7533	933.5152	467.2613	9
23	2278.1561	1139.5817	2261.1296	1131.0684	2260.1456	1130.5764	V	850.4781	425.7427	833.4516	417.2294	832.4676	416.7374	8
24	2379.2038	1190.1055	2362.1773	1181.5923	2361.1932	1181.1003	T	751.4097	376.2085	734.3832	367.6952	733.3992	367.2032	7
25	2492.2879	1246.6476	2475.2613	1238.1343	2474.2773	1237.6423	L	650.3620	325.6847	633.3355	317.1714	632.3515	316.6794	6
26	2593.3356	1297.1714	2576.3090	1288.6581	2575.3250	1288.1661	T	537.2780	269.1426	520.2514	260.6293	519.2674	260.1373	5
27	2650.3570	1325.6821	2633.3305	1317.1689	2632.3465	1316.6769	G	436.2303	218.6188	419.2037	210.1055	0	0	4
28	2707.3785	1354.1929	2690.3519	1345.6796	2689.3679	1345.1876	G	379.2088	190.1081	362.1823	181.5948	0	0	3
29	2854.4469	1427.7271	2837.4203	1419.2138	2836.4363	1418.7218	F	322.1874	161.5973	305.1608	153.0840	0	0	2
30							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 86050.

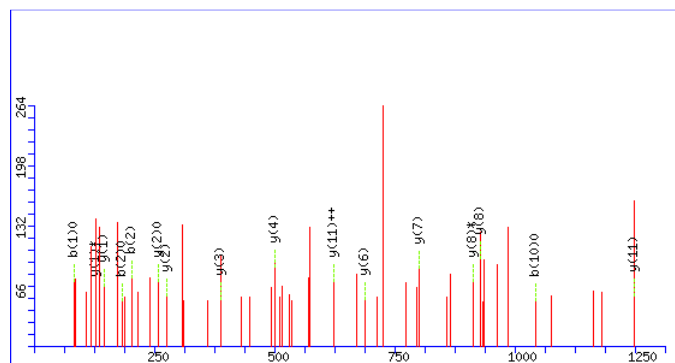
MS/MS Fragmentation of **TTDGFQNSVILEK**:

Found in **IP100011174**

Title: 2.1.1.2248.6

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120214ry¥120214ry_414C2-43_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							13
2	203.1028	102.0550	0	0	185.0921	93.0497	T	1350.6900	675.8486	1333.6634	667.3353	1332.6794	666.8433	12
3	318.1296	159.5684	0	0	300.1190	150.5631	D	1249.6423	625.3248	1232.6157	616.8115	1231.6317	616.3195	11
4	375.1510	188.0792	0	0	357.1405	179.0739	G	1134.6153	567.8113	1117.5888	559.2980	1116.6048	558.8060	10
5	522.2195	261.6134	0	0	504.2089	252.6081	F	1077.5939	539.3006	1060.5673	530.7873	1059.5833	530.2953	9
6	650.2780	325.6427	633.2515	317.1294	632.2675	316.6374	Q	930.5255	465.7664	913.4989	457.2531	912.5149	456.7611	8
7	764.3210	382.6641	747.2944	374.1508	746.3104	373.6588	N	802.4669	401.7371	785.4403	393.2238	784.4563	392.7318	7
8	851.3530	426.1801	834.3264	417.6669	833.3424	417.1748	S	688.4240	344.7156	671.3974	336.2023	670.4134	335.7103	6
9	950.4214	475.7143	933.3949	467.2011	932.4108	466.7091	V	601.3919	301.1996	584.3654	292.6863	583.3814	292.1943	5
10	1063.5055	532.2564	1046.4789	523.7431	1045.4949	523.2511	I	502.3235	251.6654	485.2970	243.1521	484.3130	242.6601	4
11	1176.5895	588.7984	1159.5630	580.2851	1158.5790	579.7931	L	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
12	1305.6321	653.3197	1288.6056	644.8064	1287.6216	644.3144	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 86118.

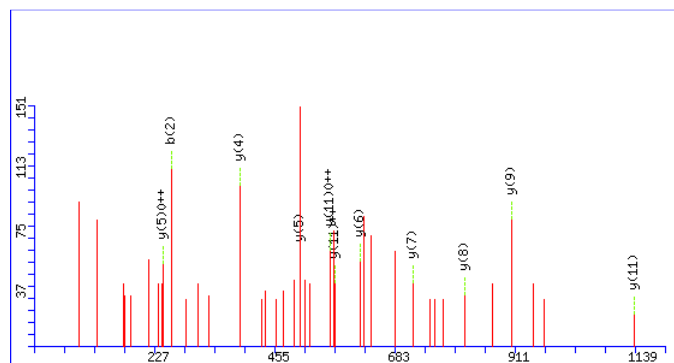
MS/MS Fragmentation of **FNIPHSVTLDAGR**:

Found in **IP100552937;IP100556271;IP100946232**

Title: 2.1.1.3177.6

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							14
2	262.1186	131.5629	245.0921	123.0497	0	0	N	1366.7074	683.8573	1349.6808	675.3440	1348.6968	674.8520	13
3	375.2027	188.1050	358.1761	179.5917	0	0	I	1252.6644	626.8359	1235.6379	618.3226	1234.6539	617.8306	12
4	472.2554	236.6314	455.2289	228.1181	0	0	P	1139.5804	570.2938	1122.5538	561.7805	1121.5698	561.2885	11
5	609.3144	305.1608	592.2878	296.6475	0	0	H	1042.5276	521.7674	1025.5010	513.2542	1024.5170	512.7622	10
6	696.3464	348.6768	679.3198	340.1636	678.3358	339.6715	S	905.4687	453.2380	888.4421	444.7247	887.4581	444.2327	9
7	795.4148	398.2110	778.3882	389.6978	777.4042	389.2058	V	818.4367	409.7220	801.4101	401.2087	800.4261	400.7167	8
8	896.4625	448.7349	879.4359	440.2216	878.4519	439.7296	T	719.3682	360.1878	702.3417	351.6745	701.3577	351.1825	7
9	1009.5465	505.2769	992.5200	496.7636	991.5360	496.2716	L	618.3206	309.6639	601.2940	301.1506	600.3100	300.6586	6
10	1124.5735	562.7904	1107.5469	554.2771	1106.5629	553.7851	D	505.2365	253.1219	488.2100	244.6086	487.2259	244.1166	5
11	1211.6055	606.3064	1194.5790	597.7931	1193.5949	597.3011	S	390.2096	195.6084	373.1830	187.0951	372.1990	186.6031	4
12	1282.6426	641.8250	1265.6161	633.3117	1264.6321	632.8197	A	303.1775	152.0924	286.1510	143.5791	0	0	3
13	1339.6641	670.3357	1322.6375	661.8224	1321.6535	661.3304	G	232.1404	116.5738	215.1139	108.0606	0	0	2
14							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 86180.

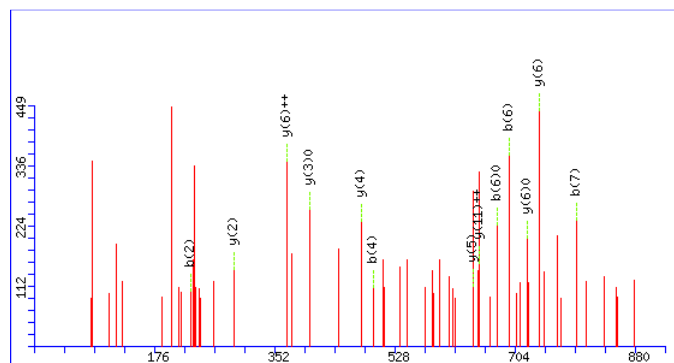
MS/MS Fragmentation of **DILRPTVPYGEFK**:

Found in **IP100219601;IP100376860;IP100426283;IP100910923**

Title: 2.1.1.4447.3

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120208ry¥120208ry_Tig120slc-P8_2.2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							13
2	229.1183	115.0628	0	0	211.1077	106.0575	I	1419.7995	710.4034	1402.7729	701.8901	1401.7889	701.3981	12
3	342.2023	171.6048	0	0	324.1918	162.5995	L	1306.7154	653.8613	1289.6889	645.3481	1288.7048	644.8561	11
4	498.3035	249.6554	481.2769	241.1421	480.2929	240.6501	R	1193.6313	597.3193	1176.6048	588.8060	1175.6208	588.3140	10
5	595.3562	298.1817	578.3297	289.6685	577.3457	289.1765	P	1037.5302	519.2688	1020.5037	510.7555	1019.5197	510.2635	9
6	696.4039	348.7056	679.3774	340.1923	678.3933	339.7003	T	940.4775	470.7424	923.4509	462.2291	922.4669	461.7371	8
7	795.4723	398.2398	778.4458	389.7265	777.4618	389.2345	V	839.4298	420.2185	822.4032	411.7053	821.4192	411.2132	7
8	892.5251	446.7662	875.4985	438.2529	874.5145	437.7609	P	740.3614	370.6843	723.3348	362.1710	722.3508	361.6790	6
9	1055.5884	528.2978	1038.5619	519.7846	1037.5778	519.2926	Y	643.3086	322.1579	626.2821	313.6447	625.2980	313.1527	5
10	1112.6099	556.8086	1095.5833	548.2953	1094.5993	547.8033	G	480.2453	240.6263	463.2187	232.1130	462.2347	231.6210	4
11	1241.6525	621.3299	1224.6259	612.8166	1223.6419	612.3246	E	423.2238	212.1155	406.1973	203.6023	405.2132	203.1103	3
12	1388.7209	694.8641	1371.6943	686.3508	1370.7103	685.8588	F	294.1812	147.5942	277.1547	139.0810	0	0	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 86374.

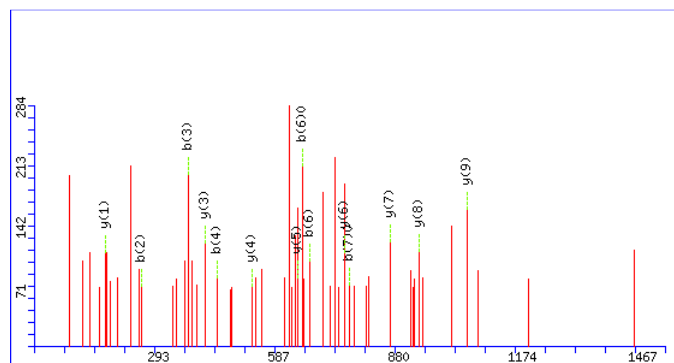
MS/MS Fragmentation of **DFDALILDLER**:

Found in **IP100005621;IP100171137;IP100793111**

Title: 4.1.1.1432.4

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120212ry¥120212ry_aHDF1388-P9_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							11
2	263.1026	132.0550	0	0	245.0921	123.0497	F	1204.6572	602.8322	1187.6307	594.3190	1186.6467	593.8270	10
3	378.1296	189.5684	0	0	360.1190	180.5631	D	1057.5888	529.2980	1040.5623	520.7848	1039.5782	520.2928	9
4	449.1667	225.0870	0	0	431.1561	216.0817	A	942.5619	471.7846	925.5353	463.2713	924.5513	462.7793	8
5	562.2508	281.6290	0	0	544.2402	272.6237	L	871.5247	436.2660	854.4982	427.7527	853.5142	427.2607	7
6	675.3348	338.1710	0	0	657.3243	329.1658	I	758.4407	379.7240	741.4141	371.2107	740.4301	370.7187	6
7	788.4189	394.7131	0	0	770.4083	385.7078	L	645.3566	323.1819	628.3301	314.6687	627.3461	314.1767	5
8	903.4458	452.2266	0	0	885.4353	443.2213	D	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
9	1016.5299	508.7686	0	0	998.5193	499.7633	L	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
10	1145.5725	573.2899	0	0	1127.5619	564.2846	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
11							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 86647.

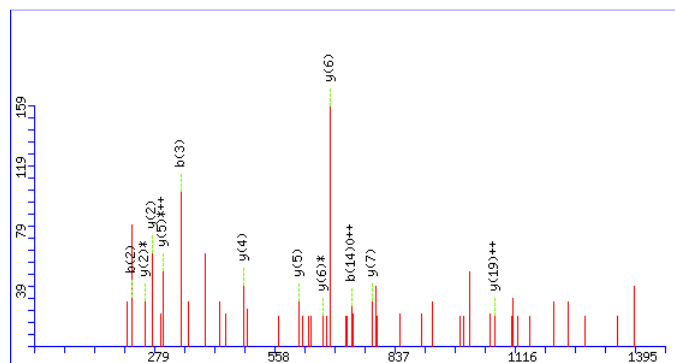
MS/MS Fragmentation of **LLNLGLITESQAHTLEDEVAEVLQK:**

Found in **IP100292071**

Title: 4.1.1.4424.2

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120118ry¥120118ry_201B7-32_3.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							25
2	227.1754	114.0913	0	0	0	0	L	2650.3934	1325.7003	2633.3669	1317.1871	2632.3828	1316.6951	24
3	341.2183	171.1128	324.1918	162.5995	0	0	N	2537.3093	1269.1583	2520.2828	1260.6450	2519.2988	1260.1530	23
4	454.3024	227.6548	437.2758	219.1416	0	0	L	2423.2664	1212.1368	2406.2399	1203.6236	2405.2558	1203.1316	22
5	511.3239	256.1656	494.2973	247.6523	0	0	G	2310.1823	1155.5948	2293.1558	1147.0815	2292.1718	1146.5895	21
6	624.4079	312.7076	607.3814	304.1943	0	0	L	2253.1609	1127.0841	2236.1343	1118.5708	2235.1503	1118.0788	20
7	737.4920	369.2496	720.4654	360.7364	0	0	I	2140.0768	1070.5420	2123.0503	1062.0288	2122.0663	1061.5368	19
8	838.5397	419.7735	821.5131	411.2602	820.5291	410.7682	T	2026.9928	1014.0000	2009.9662	1005.4867	2008.9822	1004.9947	18
9	967.5823	484.2948	950.5557	475.7815	949.5717	475.2895	E	1925.9451	963.4762	1908.9185	954.9629	1907.9345	954.4709	17
10	1054.6143	527.8108	1037.5877	519.2975	1036.6037	518.8055	S	1796.9025	898.9549	1779.8759	890.4416	1778.8919	889.9496	16
11	1182.6729	591.8401	1165.6463	583.3268	1164.6623	582.8348	Q	1709.8705	855.4389	1692.8439	846.9256	1691.8599	846.4336	15
12	1253.7100	627.3586	1236.6834	618.8454	1235.6994	618.3533	A	1581.8119	791.4096	1564.7853	782.8963	1563.8013	782.4043	14
13	1390.7689	695.8881	1373.7423	687.3748	1372.7583	686.8828	H	1510.7748	755.8910	1493.7482	747.3777	1492.7642	746.8857	13
14	1491.8166	746.4119	1474.7900	737.8986	1473.8060	737.4066	T	1373.7159	687.3616	1356.6893	678.8483	1355.7053	678.3563	12
15	1604.9006	802.9540	1587.8741	794.4407	1586.8901	793.9487	L	1272.6682	636.8377	1255.6416	628.3245	1254.6576	627.8324	11
16	1733.9432	867.4753	1716.9167	858.9620	1715.9327	858.4700	E	1159.5841	580.2957	1142.5576	571.7824	1141.5735	571.2904	10
17	1848.9702	924.9887	1831.9436	916.4754	1830.9596	915.9834	D	1030.5415	515.7744	1013.5150	507.2611	1012.5310	506.7691	9
18	1978.0128	989.5100	1960.9862	980.9967	1960.0022	980.5047	E	915.5146	458.2609	898.4880	449.7477	897.5040	449.2556	8
19	2077.0812	1039.0442	2060.0546	1030.5310	2059.0706	1030.0389	V	786.4720	393.7396	769.4454	385.2264	768.4614	384.7343	7
20	2148.1183	1074.5628	2131.0917	1066.0495	2130.1077	1065.5575	A	687.4036	344.2054	670.3770	335.6921	669.3930	335.2001	6
21	2277.1609	1139.0841	2260.1343	1130.5708	2259.1503	1130.0788	E	616.3665	308.6869	599.3399	300.1736	598.3559	299.6816	5
22	2376.2293	1188.6183	2359.2027	1180.1050	2358.2187	1179.6130	V	487.3239	244.1656	470.2973	235.6523	0	0	4
23	2489.3134	1245.1603	2472.2868	1236.6470	2471.3028	1236.1550	L	388.2554	194.6314	371.2289	186.1181	0	0	3
24	2617.3719	1309.1896	2600.3454	1300.6763	2599.3614	1300.1843	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
25							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 86767.

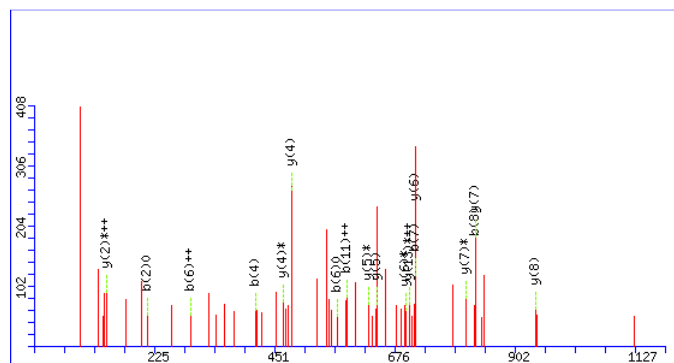
MS/MS Fragmentation of **TEDAGLELLACPVL**R: 57.021465@C:11

Found in **IP100644486;IP100791699;IP101015930**

Title: 3.1.1.3171.3

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							15
2	231.0975	116.0524	0	0	213.0870	107.0471	E	1555.8149	778.4111	1538.7883	769.8978	1537.8043	769.4058	14
3	346.1245	173.5659	0	0	328.1139	164.5606	D	1426.7723	713.8898	1409.7457	705.3765	1408.7617	704.8845	13
4	417.1616	209.0844	0	0	399.1510	200.0792	A	1311.7453	656.3763	1294.7188	647.8630	1293.7348	647.3710	12
5	474.1831	237.5952	0	0	456.1725	228.5899	G	1240.7082	620.8577	1223.6817	612.3445	1222.6976	611.8525	11
6	587.2671	294.1372	0	0	569.2566	285.1319	L	1183.6867	592.3470	1166.6602	583.8337	1165.6762	583.3417	10
7	716.3097	358.6585	0	0	698.2992	349.6532	E	1070.6027	535.8050	1053.5761	527.2917	1052.5921	526.7997	9
8	829.3938	415.2005	0	0	811.3832	406.1953	L	941.5601	471.2837	924.5335	462.7704	0	0	8
9	942.4779	471.7426	0	0	924.4673	462.7373	L	828.4760	414.7416	811.4495	406.2284	0	0	7
10	1013.5150	507.2611	0	0	995.5044	498.2558	A	715.3920	358.1996	698.3654	349.6863	0	0	6
11	1173.5456	587.2764	0	0	1155.5351	578.2712	C	644.3548	322.6811	627.3283	314.1678	0	0	5
12	1270.5984	635.8028	0	0	1252.5878	626.7975	P	484.3242	242.6657	467.2976	234.1525	0	0	4
13	1369.6668	685.3370	0	0	1351.6562	676.3318	V	387.2714	194.1394	370.2449	185.6261	0	0	3
14	1482.7509	741.8791	0	0	1464.7403	732.8738	L	288.2030	144.6051	271.1765	136.0919	0	0	2
15							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 86989.

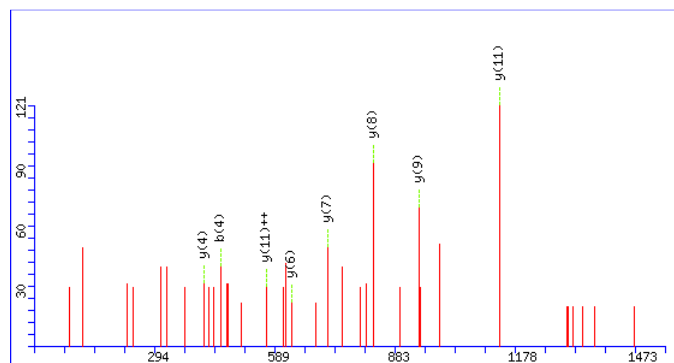
MS/MS Fragmentation of **DVLETPVDLAGFPVLLSDTAGLR**:

Found in **IP100464994;IP100644024;IP100783945;IP100982192**

Title: 4.1.1.3339.3

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							23
2	215.1026	108.0550	0	0	197.0921	99.0497	V	2283.2595	1142.1334	2266.2329	1133.6201	2265.2489	1133.1281	22
3	328.1867	164.5970	0	0	310.1761	155.5917	L	2184.1911	1092.5992	2167.1645	1084.0859	2166.1805	1083.5939	21
4	457.2293	229.1183	0	0	439.2187	220.1130	E	2071.1070	1036.0571	2054.0804	1027.5439	2053.0964	1027.0519	20
5	558.2770	279.6421	0	0	540.2664	270.6368	T	1942.0644	971.5358	1925.0379	963.0226	1924.0538	962.5306	19
6	655.3297	328.1685	0	0	637.3192	319.1632	P	1841.0167	921.0120	1823.9902	912.4987	1823.0062	912.0067	18
7	754.3981	377.7027	0	0	736.3876	368.6974	V	1743.9640	872.4856	1726.9374	863.9723	1725.9534	863.4803	17
8	869.4251	435.2162	0	0	851.4145	426.2109	D	1644.8955	822.9514	1627.8690	814.4381	1626.8850	813.9461	16
9	982.5092	491.7582	0	0	964.4986	482.7529	L	1529.8686	765.4379	1512.8421	756.9247	1511.8580	756.4327	15
10	1053.5463	527.2768	0	0	1035.5357	518.2715	A	1416.7845	708.8959	1399.7580	700.3826	1398.7740	699.8906	14
11	1110.5677	555.7875	0	0	1092.5572	546.7822	G	1345.7474	673.3774	1328.7209	664.8641	1327.7369	664.3721	13
12	1257.6361	629.3217	0	0	1239.6256	620.3164	F	1288.7260	644.8666	1271.6994	636.3533	1270.7154	635.8613	12
13	1354.6889	677.8481	0	0	1336.6783	668.8428	P	1141.6575	571.3324	1124.6310	562.8191	1123.6470	562.3271	11
14	1453.7573	727.3823	0	0	1435.7468	718.3770	V	1044.6048	522.8060	1027.5782	514.2928	1026.5942	513.8007	10
15	1566.8414	783.9243	0	0	1548.8308	774.9190	L	945.5364	473.2718	928.5098	464.7585	927.5258	464.2665	9
16	1679.9255	840.4664	0	0	1661.9149	831.4611	L	832.4523	416.7298	815.4258	408.2165	814.4417	407.7245	8
17	1766.9575	883.9824	0	0	1748.9469	874.9771	S	719.3682	360.1878	702.3417	351.6745	701.3577	351.1825	7
18	1881.9844	941.4958	0	0	1863.9739	932.4906	D	632.3362	316.6717	615.3097	308.1585	614.3257	307.6665	6
19	1983.0321	992.0197	0	0	1965.0215	983.0144	T	517.3093	259.1583	500.2827	250.6450	499.2987	250.1530	5
20	2054.0692	1027.5382	0	0	2036.0587	1018.5330	A	416.2616	208.6344	399.2350	200.1212	0	0	4
21	2111.0907	1056.0490	0	0	2093.0801	1047.0437	G	345.2245	173.1159	328.1979	164.6026	0	0	3
22	2224.1747	1112.5910	0	0	2206.1642	1103.5857	L	288.2030	144.6051	271.1765	136.0919	0	0	2
23							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 87140.

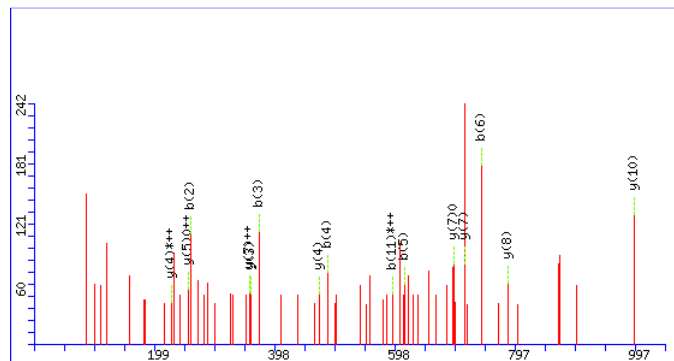
MS/MS Fragmentation of **LFLQQPLAPSQLTK:**

Found in **IP100010255;IP100184433;IP100925356**

Title: 3.1.1.4119.6

Data file: Y:\TT5600(CiRA1)\2012-02\120201ry\120201ry_aHDF1388-P9_1_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							16
2	261.1598	131.0835	0	0	0	0	F	1625.9625	813.4849	1608.9360	804.9716	1607.9519	804.4796	15
3	374.2438	187.6255	0	0	0	0	L	1478.8941	739.9507	1461.8675	731.4374	1460.8835	730.9454	14
4	487.3279	244.1676	0	0	0	0	L	1365.8100	683.4087	1348.7835	674.8954	1347.7995	674.4034	13
5	615.3865	308.1969	598.3599	299.6836	0	0	Q	1252.7260	626.8666	1235.6994	618.3533	1234.7154	617.8613	12
6	743.4450	372.2262	726.4185	363.7129	0	0	Q	1124.6674	562.8373	1107.6408	554.3241	1106.6568	553.8320	11
7	840.4978	420.7525	823.4713	412.2393	0	0	P	996.6088	498.8080	979.5823	490.2948	978.5982	489.8028	10
8	953.5819	477.2946	936.5553	468.7813	0	0	L	899.5560	450.2817	882.5295	441.7684	881.5455	441.2764	9
9	1024.6190	512.8131	1007.5924	504.2999	0	0	A	786.4720	393.7396	769.4454	385.2264	768.4614	384.7343	8
10	1121.6717	561.3395	1104.6452	552.8262	0	0	P	715.4349	358.2211	698.4083	349.7078	697.4243	349.2158	7
11	1208.7038	604.8555	1191.6772	596.3422	1190.6932	595.8502	S	618.3821	309.6947	601.3556	301.1814	600.3715	300.6894	6
12	1265.7252	633.3663	1248.6987	624.8530	1247.7147	624.3610	G	531.3501	266.1787	514.3235	257.6654	513.3395	257.1734	5
13	1378.8093	689.9083	1361.7828	681.3950	1360.7987	680.9030	L	474.3286	237.6679	457.3021	229.1547	456.3180	228.6627	4
14	1479.8570	740.4321	1462.8304	731.9189	1461.8464	731.4268	T	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
15	1592.9410	796.9742	1575.9145	788.4609	1574.9305	787.9689	L	260.1969	130.6021	243.1703	122.0888	0	0	2
16							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 87464.

MS/MS Fragmentation of **NQVDVEIK**:

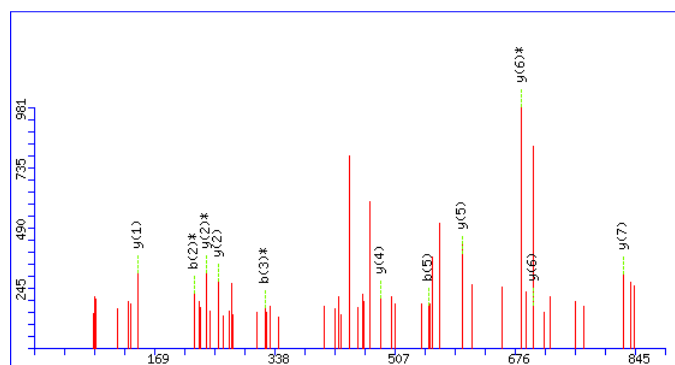
Found in

IP100152946;IP101020716;IP101021045;IP101021379;IP101021461;IP101021671;IP101021697;IP101021887;IP101021983;IP101022025;IP101022118;IP101022330;IP1010224

Title: 1.1.1.8484.6

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120214ry¥120214ry_32R1-32_4_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							8
2	243.1088	122.0580	226.0822	113.5448	0	0	Q	830.4618	415.7345	813.4353	407.2213	812.4512	406.7293	7
3	342.1772	171.5922	325.1506	163.0790	0	0	V	702.4032	351.7053	685.3767	343.1920	684.3927	342.7000	6
4	457.2041	229.1057	440.1776	220.5924	439.1936	220.1004	D	603.3348	302.1710	586.3083	293.6578	585.3243	293.1658	5
5	556.2726	278.6399	539.2460	270.1266	538.2620	269.6346	V	488.3079	244.6576	471.2813	236.1443	470.2973	235.6523	4
6	685.3151	343.1612	668.2886	334.6479	667.3046	334.1559	E	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
7	798.3992	399.7032	781.3727	391.1900	780.3886	390.6980	I	260.1969	130.6021	243.1703	122.0888	0	0	2
8							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 87504.

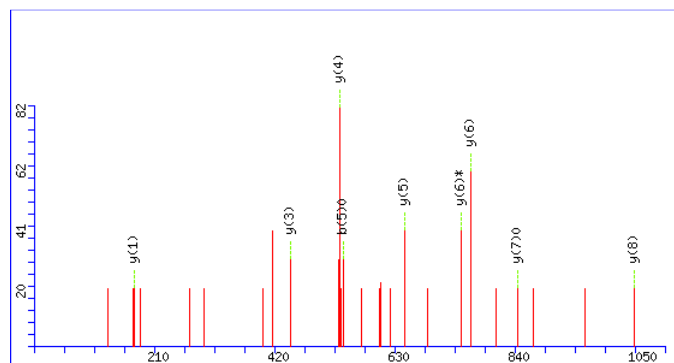
MS/MS Fragmentation of **LLGFEWTLSSWR**:

Found in **IP100305698,IP100917475**

Title: 4.1.1.1906.3

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							13
2	227.1754	114.0913	0	0	0	0	L	1496.7169	748.8621	1479.6903	740.3488	1478.7063	739.8568	12
3	284.1969	142.6021	0	0	0	0	G	1383.6328	692.3200	1366.6062	683.8068	1365.6222	683.3148	11
4	431.2653	216.1363	0	0	0	0	F	1326.6113	663.8093	1309.5848	655.2960	1308.6008	654.8040	10
5	560.3079	280.6576	0	0	542.2973	271.6523	E	1179.5429	590.2751	1162.5164	581.7618	1161.5323	581.2698	9
6	746.3872	373.6972	0	0	728.3766	364.6919	W	1050.5003	525.7538	1033.4738	517.2405	1032.4898	516.7485	8
7	847.4349	424.2211	0	0	829.4243	415.2158	T	864.4210	432.7141	847.3945	424.2009	846.4104	423.7089	7
8	962.4618	481.7345	0	0	944.4512	472.7293	D	763.3733	382.1903	746.3468	373.6770	745.3628	373.1850	6
9	1075.5459	538.2766	0	0	1057.5353	529.2713	L	648.3464	324.6768	631.3198	316.1636	630.3358	315.6715	5
10	1162.5779	581.7926	0	0	1144.5673	572.7873	S	535.2623	268.1348	518.2358	259.6215	517.2518	259.1295	4
11	1249.6099	625.3086	0	0	1231.5994	616.3033	S	448.2303	224.6188	431.2037	216.1055	430.2197	215.6135	3
12	1435.6892	718.3483	0	0	1417.6787	709.3430	W	361.1983	181.1028	344.1717	172.5895	0	0	2
13							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 87578.

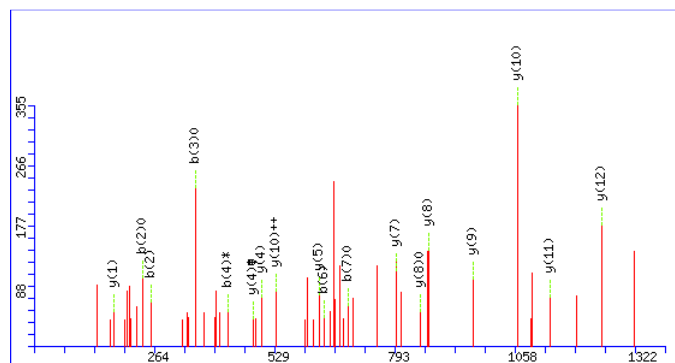
MS/MS Fragmentation of **EQDAPVAGLQPVER**:

Found in **IP100292150;IP101025308;IP101025396**

Title: 2.1.1.910.8

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							14
2	258.1084	129.5579	241.0819	121.0446	240.0979	120.5526	Q	1379.7278	690.3675	1362.7012	681.8542	1361.7172	681.3622	13
3	373.1354	187.0713	356.1088	178.5581	355.1248	178.0661	D	1251.6692	626.3382	1234.6426	617.8250	1233.6586	617.3329	12
4	444.1725	222.5899	427.1460	214.0766	426.1619	213.5846	A	1136.6422	568.8248	1119.6157	560.3115	1118.6317	559.8195	11
5	541.2253	271.1163	524.1987	262.6030	523.2147	262.1110	P	1065.6051	533.3062	1048.5786	524.7929	1047.5946	524.3009	10
6	640.2937	320.6505	623.2671	312.1372	622.2831	311.6452	V	968.5524	484.7798	951.5258	476.2665	950.5418	475.7745	9
7	711.3308	356.1690	694.3042	347.6558	693.3202	347.1638	A	869.4839	435.2456	852.4574	426.7323	851.4734	426.2403	8
8	768.3523	384.6798	751.3257	376.1665	750.3417	375.6745	G	798.4468	399.7271	781.4203	391.2138	780.4363	390.7218	7
9	881.4363	441.2218	864.4098	432.7085	863.4258	432.2165	L	741.4254	371.2163	724.3988	362.7030	723.4148	362.2110	6
10	1009.4949	505.2511	992.4684	496.7378	991.4843	496.2458	Q	628.3413	314.6743	611.3148	306.1610	610.3307	305.6690	5
11	1106.5477	553.7775	1089.5211	545.2642	1088.5371	544.7722	P	500.2827	250.6450	483.2562	242.1317	482.2722	241.6397	4
12	1205.6161	603.3117	1188.5895	594.7984	1187.6055	594.3064	V	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
13	1334.6587	667.8330	1317.6321	659.3197	1316.6481	658.8277	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
14							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

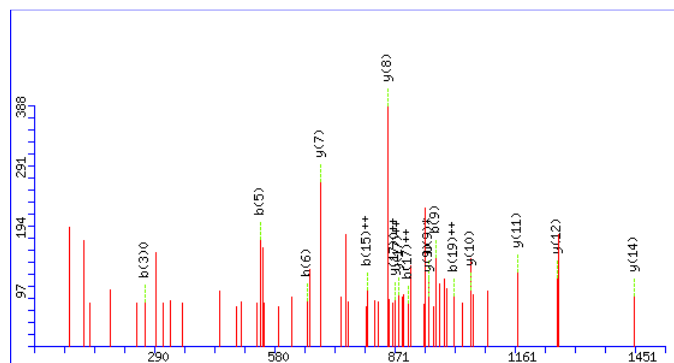
Peptide: 87597.

MS/MS Fragmentation of **VVSNFILQALQGEPLTVYGGSGSQR**:
 Found in **IP100410544;IP100657807;IP100658111;IP100910001;IP100916638**

Title: 4.1.1.1649.9

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120212ry¥120212ry_aHDF1388-P9_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							25
2	199.1441	100.0757	0	0	0	0	V	2565.3307	1283.1690	2548.3042	1274.6557	2547.3202	1274.1637	24
3	286.1761	143.5917	0	0	268.1656	134.5864	S	2466.2623	1233.6348	2449.2358	1225.1215	2448.2518	1224.6295	23
4	400.2191	200.6132	383.1925	192.0999	382.2085	191.6079	N	2379.2303	1190.1188	2362.2038	1181.6055	2361.2197	1181.1135	22
5	547.2875	274.1474	530.2609	265.6341	529.2769	265.1421	F	2265.1874	1133.0973	2248.1608	1124.5841	2247.1768	1124.0920	21
6	660.3715	330.6894	643.3450	322.1761	642.3610	321.6841	I	2118.1190	1059.5631	2101.0924	1051.0498	2100.1084	1050.5578	20
7	773.4556	387.2314	756.4291	378.7182	755.4450	378.2262	L	2005.0349	1003.0211	1988.0083	994.5078	1987.0243	994.0158	19
8	901.5142	451.2607	884.4876	442.7475	883.5036	442.2554	Q	1891.9508	946.4791	1874.9243	937.9658	1873.9403	937.4738	18
9	972.5513	486.7793	955.5247	478.2660	954.5407	477.7740	A	1763.8923	882.4498	1746.8657	873.9365	1745.8817	873.4445	17
10	1085.6354	543.3213	1068.6088	534.8080	1067.6248	534.3160	L	1692.8551	846.9312	1675.8286	838.4179	1674.8446	837.9259	16
11	1213.6939	607.3506	1196.6674	598.8373	1195.6834	598.3453	Q	1579.7711	790.3892	1562.7445	781.8759	1561.7605	781.3839	15
12	1270.7154	635.8613	1253.6888	627.3481	1252.7048	626.8561	G	1451.7125	726.3599	1434.6860	717.8466	1433.7019	717.3546	14
13	1399.7580	700.3826	1382.7314	691.8694	1381.7474	691.3774	E	1394.6910	697.8492	1377.6645	689.3359	1376.6805	688.8439	13
14	1496.8108	748.9090	1479.7842	740.3957	1478.8002	739.9037	P	1265.6484	633.3279	1248.6219	624.8146	1247.6379	624.3226	12
15	1609.8948	805.4510	1592.8683	796.9378	1591.8843	796.4458	L	1168.5957	584.8015	1151.5691	576.2882	1150.5851	575.7962	11
16	1710.9425	855.9749	1693.9159	847.4616	1692.9319	846.9696	T	1055.5116	528.2594	1038.4851	519.7462	1037.5011	519.2542	10
17	1810.0109	905.5091	1792.9844	896.9958	1792.0003	896.5038	V	954.4639	477.7356	937.4374	469.2223	936.4534	468.7303	9
18	1973.0742	987.0408	1956.0477	978.5275	1955.0637	978.0355	Y	855.3955	428.2014	838.3690	419.6881	837.3850	419.1961	8
19	2030.0957	1015.5515	2013.0692	1007.0382	2012.0851	1006.5462	G	692.3322	346.6697	675.3056	338.1565	674.3216	337.6645	7
20	2117.1277	1059.0675	2100.1012	1050.5542	2099.1172	1050.0622	S	635.3107	318.1590	618.2842	309.6457	617.3002	309.1537	6
21	2174.1492	1087.5782	2157.1226	1079.0650	2156.1386	1078.5730	G	548.2787	274.6430	531.2522	266.1297	530.2681	265.6377	5
22	2261.1812	1131.0943	2244.1547	1122.5810	2243.1707	1122.0890	S	491.2572	246.1323	474.2307	237.6190	473.2467	237.1270	4
23	2389.2398	1195.1235	2372.2133	1186.6103	2371.2292	1186.1183	Q	404.2252	202.6162	387.1987	194.1030	386.2146	193.6110	3
24	2490.2875	1245.6474	2473.2609	1237.1341	2472.2769	1236.6421	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
25							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 87783.

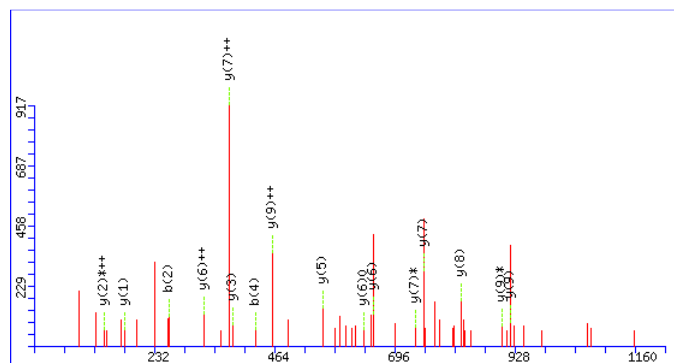
MS/MS Fragmentation of **FIPAPPSSPLR**:

Found in **IP100791933;IP100878368;IP100924836;IP101014565;IP101015949**

Title: 2.1.1.2519.7

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							11
2	261.1598	131.0835	0	0	0	0	I	1034.5993	517.8033	1017.5728	509.2900	1016.5887	508.7980	10
3	358.2125	179.6099	0	0	0	0	P	921.5152	461.2613	904.4887	452.7480	903.5047	452.2560	9
4	429.2496	215.1285	0	0	0	0	A	824.4625	412.7349	807.4359	404.2216	806.4519	403.7296	8
5	526.3024	263.6548	0	0	0	0	P	753.4254	377.2163	736.3988	368.7030	735.4148	368.2110	7
6	623.3552	312.1812	0	0	0	0	P	656.3726	328.6899	639.3461	320.1767	638.3620	319.6847	6
7	710.3872	355.6972	0	0	692.3766	346.6919	S	559.3198	280.1636	542.2933	271.6503	541.3093	271.1583	5
8	797.4192	399.2132	0	0	779.4087	390.2080	S	472.2878	236.6475	455.2613	228.1343	454.2772	227.6423	4
9	894.4720	447.7396	0	0	876.4614	438.7343	P	385.2558	193.1315	368.2292	184.6183	0	0	3
10	1007.5560	504.2817	0	0	989.5455	495.2764	L	288.2030	144.6051	271.1765	136.0919	0	0	2
11							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

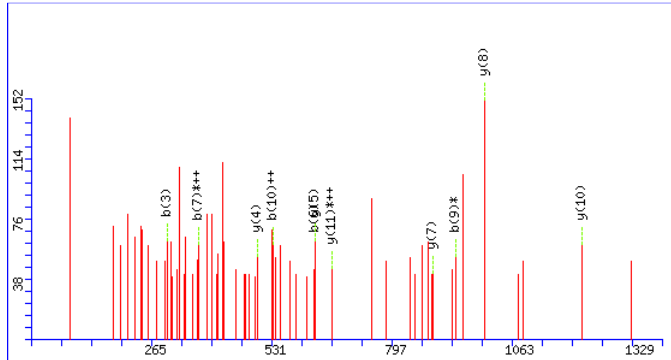
Peptide: 87989.

MS/MS Fragmentation of **DQGSQLEALEPDPLLTALESQDCVEQLLK: 0.984016@Q:7.57.021465@C:24**
Found in **IP100375638;IP100414872;IP100853587;IP100939295;IP100942736**

Title: 4.1.1.3838.8

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							30
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	Q	3253.6144	1627.3109	3236.5879	1618.7976	3235.6039	1618.3056	29
3	301.1143	151.0608	284.0877	142.5475	283.1037	142.0555	G	3125.5559	1563.2816	3108.5293	1554.7683	3107.5453	1554.2763	28
4	388.1463	194.5768	371.1197	186.0635	370.1357	185.5715	S	3068.5344	1534.7708	3051.5078	1526.2576	3050.5238	1525.7656	27
5	516.2049	258.6061	499.1783	250.0928	498.1943	249.6008	Q	2981.5024	1491.2548	2964.4758	1482.7415	2963.4918	1482.2495	26
6	629.2889	315.1481	612.2624	306.6348	611.2784	306.1428	L	2853.4438	1427.2255	2836.4172	1418.7123	2835.4332	1418.2202	25
7	758.3315	379.6694	741.3050	371.1561	740.3210	370.6641	Q	2740.3597	1370.6835	2723.3332	1362.1702	2722.3492	1361.6782	24
8	887.3741	444.1907	870.3476	435.6774	869.3636	435.1854	E	2611.3171	1306.1622	2594.2906	1297.6489	2593.3066	1297.1569	23
9	958.4112	479.7093	941.3847	471.1960	940.4007	470.7040	A	2482.2745	1241.6409	2465.2480	1233.1276	2464.2640	1232.6356	22
10	1071.4953	536.2513	1054.4687	527.7380	1053.4847	527.2460	L	2411.2374	1206.1223	2394.2109	1197.6091	2393.2269	1197.1171	21
11	1200.5379	600.7726	1183.5113	592.2593	1182.5273	591.7673	E	2298.1534	1149.5803	2281.1268	1141.0670	2280.1428	1140.5750	20
12	1297.5907	649.2990	1280.5641	640.7857	1279.5801	640.2937	P	2169.1108	1085.0590	2152.0842	1076.5457	2151.1002	1076.0537	19
13	1412.6176	706.8124	1395.5910	698.2992	1394.6070	697.8072	D	2072.0580	1036.5326	2055.0315	1028.0194	2054.0474	1027.5274	18
14	1509.6704	755.3388	1492.6438	746.8255	1491.6598	746.3335	P	1957.0311	979.0192	1940.0045	970.5059	1939.0205	970.0139	17
15	1622.7544	811.8809	1605.7279	803.3676	1604.7439	802.8756	L	1859.9783	930.4928	1842.9517	921.9795	1841.9677	921.4875	16
16	1735.8385	868.4229	1718.8119	859.9096	1717.8279	859.4176	L	1746.8942	873.9508	1729.8677	865.4375	1728.8837	864.9455	15
17	1836.8862	918.9467	1819.8596	910.4334	1818.8756	909.9414	T	1633.8102	817.4087	1616.7836	808.8954	1615.7996	808.4034	14
18	1907.9233	954.4653	1890.8967	945.9520	1889.9127	945.4600	A	1532.7625	766.8849	1515.7359	758.3716	1514.7519	757.8796	13
19	2021.0073	1011.0073	2003.9808	1002.4940	2002.9968	1002.0020	L	1461.7254	731.3663	1444.6988	722.8530	1443.7148	722.3610	12
20	2150.0499	1075.5286	2133.0234	1067.0153	2132.0394	1066.5233	E	1348.6413	674.8243	1331.6148	666.3110	1330.6307	665.8190	11
21	2237.0820	1119.0446	2220.0554	1110.5313	2219.0714	1110.0393	S	1219.5987	610.3030	1202.5722	601.7897	1201.5882	601.2977	10
22	2365.1405	1183.0739	2348.1140	1174.5606	2347.1300	1174.0686	Q	1132.5667	566.7870	1115.5401	558.2737	1114.5561	557.7817	9
23	2480.1675	1240.5874	2463.1409	1232.0741	2462.1569	1231.5821	D	1004.5081	502.7577	987.4816	494.2444	986.4975	493.7524	8
24	2640.1981	1320.6027	2623.1716	1312.0894	2622.1876	1311.5974	C	889.4812	445.2442	872.4546	436.7309	871.4706	436.2389	7
25	2739.2666	1370.1369	2722.2400	1361.6236	2721.2560	1361.1316	V	729.4505	365.2289	712.4240	356.7156	711.4400	356.2236	6
26	2868.3091	1434.6582	2851.2826	1426.1449	2850.2986	1425.6529	E	630.3821	315.6947	613.3556	307.1814	612.3715	306.6894	5
27	2996.3677	1498.6875	2979.3412	1490.1742	2978.3572	1489.6822	Q	501.3395	251.1734	484.3130	242.6601	0	0	4
28	3109.4518	1555.2295	3092.4252	1546.7163	3091.4412	1546.2242	L	373.2809	187.1441	356.2544	178.6308	0	0	3
29	3222.5359	1611.7716	3205.5093	1603.2583	3204.5253	1602.7663	L	260.1969	130.6021	243.1703	122.0888	0	0	2
30							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 88178.

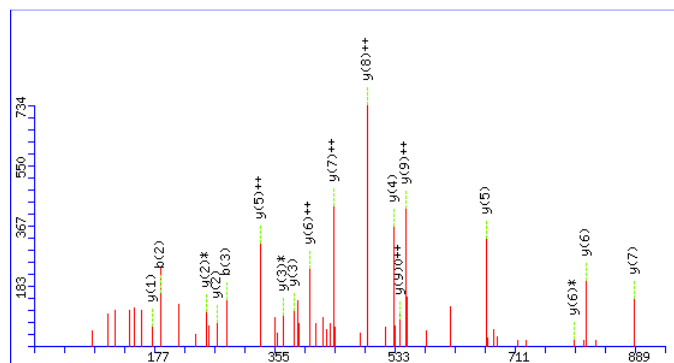
MS/MS Fragmentation of **ADVAFHFNPR**:

Found in **IP100010844;IP100165587;IP100382683;IP100479062;IP100644218;IP100646437;IP100874257;IP100974239;IP100983338**

Title: 2.1.1.1925.2

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120206ry¥120206ry_aHDF1419-P10_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							10
2	187.0713	94.0393	0	0	169.0608	85.0340	D	1102.5429	551.7751	1085.5163	543.2618	1084.5323	542.7698	9
3	286.1397	143.5735	0	0	268.1292	134.5682	V	987.5159	494.2616	970.4894	485.7483	0	0	8
4	357.1769	179.0921	0	0	339.1663	170.0868	A	888.4475	444.7274	871.4209	436.2141	0	0	7
5	504.2453	252.6263	0	0	486.2347	243.6210	F	817.4104	409.2088	800.3838	400.6956	0	0	6
6	641.3042	321.1557	0	0	623.2936	312.1504	H	670.3420	335.6746	653.3154	327.1613	0	0	5
7	788.3726	394.6899	0	0	770.3620	385.6847	F	533.2831	267.1452	516.2565	258.6319	0	0	4
8	902.4155	451.7114	885.3890	443.1981	884.4050	442.7061	N	386.2146	193.6110	369.1881	185.0977	0	0	3
9	999.4683	500.2378	982.4417	491.7245	981.4577	491.2325	P	272.1717	136.5895	255.1452	128.0762	0	0	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 88219.

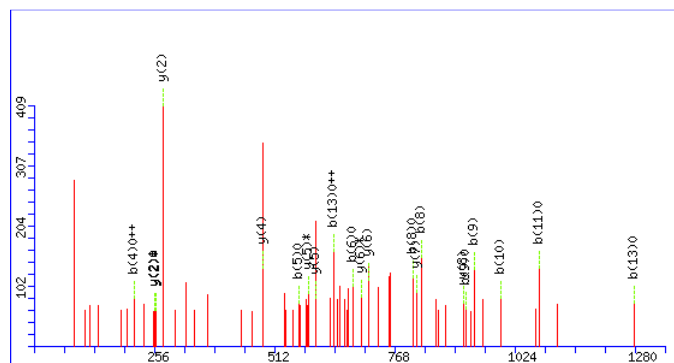
MS/MS Fragmentation of **EGFLHLGALGTTLLPDTR**:

Found in **IP100168921**

Title: 3.1.1.3444.4

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120212ry¥120212ry_414C2-43_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							19
2	187.0713	94.0393	0	0	169.0608	85.0340	G	1883.0385	942.0229	1866.0120	933.5096	1865.0280	933.0176	18
3	334.1397	167.5735	0	0	316.1292	158.5682	F	1826.0171	913.5122	1808.9905	904.9989	1808.0065	904.5069	17
4	447.2238	224.1155	0	0	429.2132	215.1103	L	1678.9486	839.9780	1661.9221	831.4647	1660.9381	830.9727	16
5	584.2827	292.6450	0	0	566.2722	283.6397	H	1565.8646	783.4359	1548.8380	774.9227	1547.8540	774.4306	15
6	697.3668	349.1870	0	0	679.3562	340.1817	L	1428.8057	714.9065	1411.7791	706.3932	1410.7951	705.9012	14
7	754.3883	377.6978	0	0	736.3777	368.6925	G	1315.7216	658.3644	1298.6951	649.8512	1297.7110	649.3592	13
8	825.4254	413.2163	0	0	807.4148	404.2110	A	1258.7001	629.8537	1241.6736	621.3404	1240.6896	620.8484	12
9	938.5094	469.7584	0	0	920.4989	460.7531	L	1187.6630	594.3352	1170.6365	585.8219	1169.6525	585.3299	11
10	995.5309	498.2691	0	0	977.5203	489.2638	G	1074.5790	537.7931	1057.5524	529.2798	1056.5684	528.7878	10
11	1096.5786	548.7929	0	0	1078.5680	539.7876	T	1017.5575	509.2824	1000.5310	500.7691	999.5469	500.2771	9
12	1197.6263	599.3168	0	0	1179.6157	590.3115	T	916.5098	458.7585	899.4833	450.2453	898.4993	449.7533	8
13	1298.6739	649.8406	0	0	1280.6634	640.8353	T	815.4621	408.2347	798.4356	399.7214	797.4516	399.2294	7
14	1411.7580	706.3826	0	0	1393.7474	697.3774	L	714.4145	357.7109	697.3879	349.1976	696.4039	348.7056	6
15	1524.8421	762.9247	0	0	1506.8315	753.9194	L	601.3304	301.1688	584.3039	292.6556	583.3198	292.1636	5
16	1621.8948	811.4510	0	0	1603.8843	802.4458	P	488.2463	244.6268	471.2198	236.1135	470.2358	235.6215	4
17	1736.9218	868.9645	0	0	1718.9112	859.9592	D	391.1936	196.1004	374.1670	187.5872	373.1830	187.0951	3
18	1837.9694	919.4884	0	0	1819.9589	910.4831	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
19							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 88299.

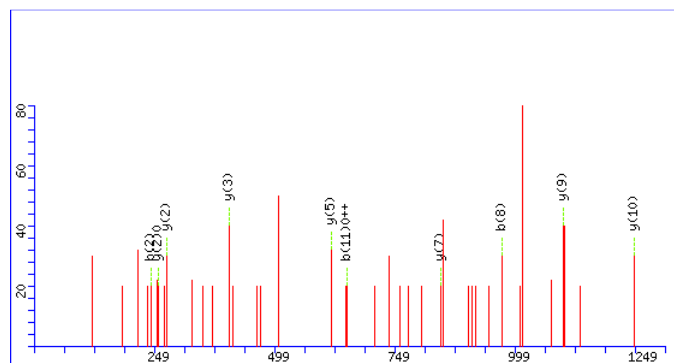
MS/MS Fragmentation of **ELFQELLLETR**:

Found in **IP100002919**

Title: 4.1.1.848.7

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							12
2	243.1339	122.0706	0	0	225.1234	113.0653	L	1362.7627	681.8850	1345.7362	673.3717	1344.7522	672.8797	11
3	390.2023	195.6048	0	0	372.1918	186.5995	F	1249.6787	625.3430	1232.6521	616.8297	1231.6681	616.3377	10
4	518.2609	259.6341	501.2344	251.1208	500.2504	250.6288	Q	1102.6103	551.8088	1085.5837	543.2955	1084.5997	542.8035	9
5	647.3035	324.1554	630.2770	315.6421	629.2930	315.1501	E	974.5517	487.7795	957.5251	479.2662	956.5411	478.7742	8
6	760.3876	380.6974	743.3610	372.1842	742.3770	371.6921	L	845.5091	423.2582	828.4825	414.7449	827.4985	414.2529	7
7	873.4716	437.2395	856.4451	428.7262	855.4611	428.2342	L	732.4250	366.7162	715.3985	358.2029	714.4145	357.7109	6
8	974.5193	487.7633	957.4928	479.2500	956.5088	478.7580	T	619.3410	310.1741	602.3144	301.6608	601.3304	301.1688	5
9	1087.6034	544.3053	1070.5768	535.7921	1069.5928	535.3001	L	518.2933	259.6503	501.2667	251.1370	500.2827	250.6450	4
10	1216.6460	608.8266	1199.6194	600.3134	1198.6354	599.8213	E	405.2092	203.1082	388.1827	194.5950	387.1987	194.1030	3
11	1317.6937	659.3505	1300.6671	650.8372	1299.6831	650.3452	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
12							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 88625.

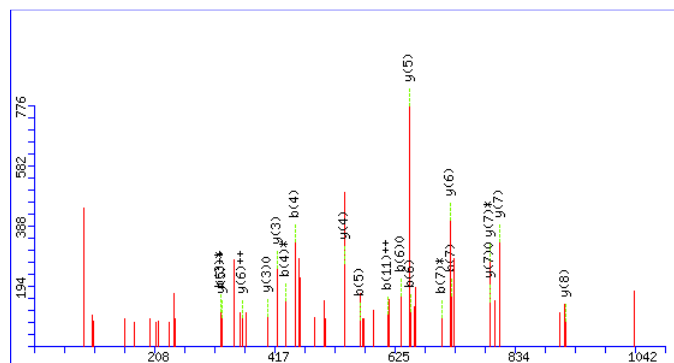
MS/MS Fragmentation of **DKPLLSALDFEK**:

Found in **IP100335437;IP100916154;IP100916826**

Title: 3.1.1.1076.2

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							12
2	244.1292	122.5682	227.1026	114.0550	226.1186	113.5629	K	1260.7198	630.8635	1243.6933	622.3503	1242.7093	621.8583	11
3	341.1819	171.0946	324.1554	162.5813	323.1714	162.0893	P	1132.6249	566.8161	1115.5983	558.3028	1114.6143	557.8108	10
4	454.2660	227.6366	437.2395	219.1234	436.2554	218.6314	L	1035.5721	518.2897	1018.5455	509.7764	1017.5615	509.2844	9
5	567.3501	284.1787	550.3235	275.6654	549.3395	275.1734	L	922.4880	461.7476	905.4615	453.2344	904.4775	452.7424	8
6	654.3821	327.6947	637.3556	319.1814	636.3715	318.6894	S	809.4040	405.2056	792.3774	396.6923	791.3934	396.2003	7
7	725.4192	363.2132	708.3927	354.7000	707.4087	354.2080	A	722.3719	361.6896	705.3454	353.1763	704.3614	352.6843	6
8	838.5033	419.7553	821.4767	411.2420	820.4927	410.7500	L	651.3348	326.1710	634.3083	317.6578	633.3243	317.1658	5
9	953.5302	477.2687	936.5037	468.7555	935.5197	468.2635	D	538.2508	269.6290	521.2242	261.1157	520.2402	260.6237	4
10	1100.5986	550.8030	1083.5721	542.2897	1082.5881	541.7977	F	423.2238	212.1155	406.1973	203.6023	405.2132	203.1103	3
11	1229.6412	615.3243	1212.6147	606.8110	1211.6307	606.3190	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
12							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 88679.

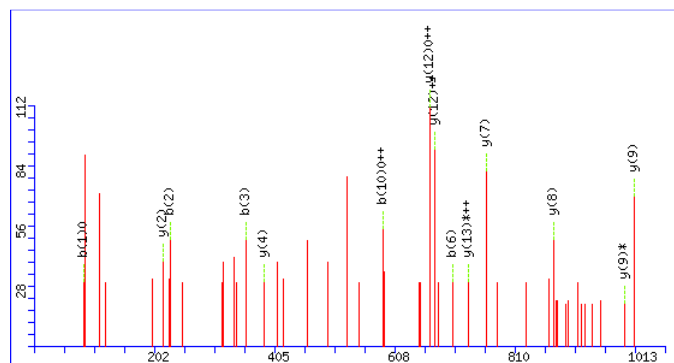
MS/MS Fragmentation of **TQQVIHIDFGLAK**:

Found in **IP100181294;IP100218437;IP100410228;IP100788259;IP100941996;IP100964868;IP100965975**

Title: 3.1.1.1546.2

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							14
2	230.1135	115.5604	213.0870	107.0471	212.1030	106.5551	Q	1481.8475	741.4274	1464.8209	732.9141	1463.8369	732.4221	13
3	358.1721	179.5897	341.1456	171.0764	340.1615	170.5844	Q	1353.7889	677.3981	1336.7623	668.8848	1335.7783	668.3928	12
4	457.2405	229.1239	440.2140	220.6106	439.2300	220.1186	V	1225.7303	613.3688	1208.7038	604.8555	1207.7198	604.3635	11
5	570.3246	285.6659	553.2980	277.1527	552.3140	276.6607	I	1126.6619	563.8346	1109.6354	555.3213	1108.6513	554.8293	10
6	707.3835	354.1954	690.3570	345.6821	689.3729	345.1901	H	1013.5778	507.2926	996.5513	498.7793	995.5673	498.2873	9
7	820.4676	410.7374	803.4410	402.2241	802.4570	401.7321	I	876.5189	438.7631	859.4924	430.2498	858.5084	429.7578	8
8	933.5516	467.2795	916.5251	458.7662	915.5411	458.2742	I	763.4349	382.2211	746.4083	373.7078	745.4243	373.2158	7
9	1048.5786	524.7929	1031.5520	516.2796	1030.5680	515.7876	D	650.3508	325.6790	633.3243	317.1658	632.3402	316.6738	6
10	1195.6470	598.3271	1178.6204	589.8139	1177.6364	589.3218	F	535.3239	268.1656	518.2973	259.6523	0	0	5
11	1252.6685	626.8379	1235.6419	618.3246	1234.6579	617.8326	G	388.2554	194.6314	371.2289	186.1181	0	0	4
12	1365.7525	683.3799	1348.7260	674.8666	1347.7419	674.3746	L	331.2340	166.1206	314.2074	157.6074	0	0	3
13	1436.7896	718.8985	1419.7631	710.3852	1418.7791	709.8932	A	218.1499	109.5786	201.1234	101.0653	0	0	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 88744.

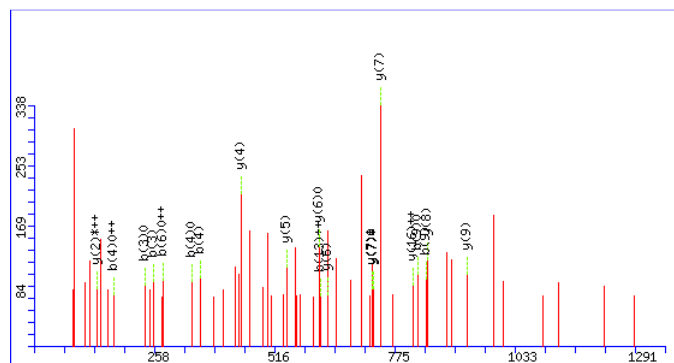
MS/MS Fragmentation of **SGLTTLVATSVNSVTGIR**:

Found in **IP100007959;IP100383612;IP100744200;IP100828024;IP100966629;IP100967001**

Title: 3.1.1.4426.4

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_3.mgf

ProteinPilot Peptide Confidence > 99%

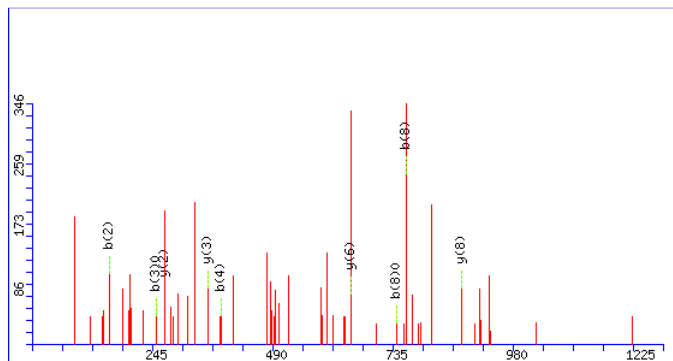


#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							18
2	145.0608	73.0340	0	0	127.0502	64.0287	G	1688.9541	844.9807	1671.9276	836.4674	1670.9436	835.9754	17
3	258.1448	129.5761	0	0	240.1343	120.5708	L	1631.9327	816.4700	1614.9061	807.9567	1613.9221	807.4647	16
4	359.1925	180.0999	0	0	341.1819	171.0946	T	1518.8486	759.9279	1501.8220	751.4147	1500.8380	750.9227	15
5	460.2402	230.6237	0	0	442.2296	221.6185	T	1417.8009	709.4041	1400.7744	700.8908	1399.7904	700.3988	14
6	573.3243	287.1658	0	0	555.3137	278.1605	L	1316.7532	658.8803	1299.7267	650.3670	1298.7427	649.8750	13
7	672.3927	336.7000	0	0	654.3821	327.6947	V	1203.6692	602.3382	1186.6426	593.8250	1185.6586	593.3329	12
8	743.4298	372.2185	0	0	725.4192	363.2132	A	1104.6008	552.8040	1087.5742	544.2907	1086.5902	543.7987	11
9	844.4775	422.7424	0	0	826.4669	413.7371	T	1033.5636	517.2855	1016.5371	508.7722	1015.5531	508.2802	10
10	931.5095	466.2584	0	0	913.4989	457.2531	S	932.5160	466.7616	915.4894	458.2483	914.5054	457.7563	9
11	1030.5779	515.7926	0	0	1012.5673	506.7873	V	845.4839	423.2456	828.4574	414.7323	827.4734	414.2403	8
12	1144.6208	572.8141	1127.5943	564.3008	1126.6103	563.8088	N	746.4155	373.7114	729.3890	365.1981	728.4050	364.7061	7
13	1231.6529	616.3301	1214.6263	607.8168	1213.6423	607.3248	S	632.3726	316.6899	615.3461	308.1767	614.3620	307.6847	6
14	1330.7213	665.8643	1313.6947	657.3510	1312.7107	656.8590	V	545.3406	273.1739	528.3140	264.6606	527.3300	264.1686	5
15	1431.7690	716.3881	1414.7424	707.8748	1413.7584	707.3828	T	446.2722	223.6397	429.2456	215.1264	428.2616	214.6344	4
16	1488.7904	744.8988	1471.7639	736.3856	1470.7799	735.8936	G	345.2245	173.1159	328.1979	164.6026	0	0	3
17	1601.8745	801.4409	1584.8479	792.9276	1583.8639	792.4356	I	288.2030	144.6051	271.1765	136.0919	0	0	2
18							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 88886.

MS/MS Fragmentation of **SALLPPSPR**:
 Found in **IP100658112;IP100658151;IP100852805;IP100869082;IP100892669;IP100915314**
 Title: 4.1.1.98.3
 Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_3_4.mgf
 ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							10
2	159.0764	80.0418	0	0	141.0659	71.0366	A	947.5673	474.2873	930.5407	465.7740	929.5567	465.2820	9
3	272.1605	136.5839	0	0	254.1499	127.5786	L	876.5302	438.7687	859.5036	430.2554	858.5196	429.7634	8
4	385.2445	193.1259	0	0	367.2340	184.1206	L	763.4461	382.2267	746.4196	373.7134	745.4355	373.2214	7
5	482.2973	241.6523	0	0	464.2867	232.6470	P	650.3620	325.6847	633.3355	317.1714	632.3515	316.6794	6
6	579.3501	290.1787	0	0	561.3395	281.1734	P	553.3093	277.1583	536.2827	268.6450	535.2987	268.1530	5
7	676.4028	338.7051	0	0	658.3923	329.6998	P	456.2565	228.6319	439.2300	220.1186	438.2459	219.6266	4
8	763.4349	382.2211	0	0	745.4243	373.2158	S	359.2037	180.1055	342.1772	171.5922	341.1932	171.1002	3
9	860.4876	430.7475	0	0	842.4771	421.7422	P	272.1717	136.5895	255.1452	128.0762	0	0	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 89045.

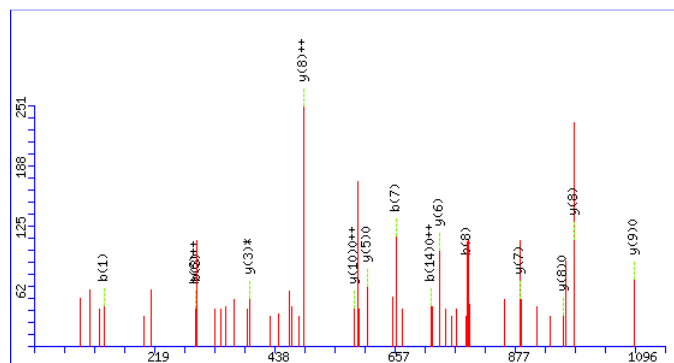
MS/MS Fragmentation of **KPAPVPAEPFDNTTYK**:

Found in **IP100008214;IP100916085**

Title: 2.1.1.1192.9

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120129ry¥120129ry_604A1-46_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	129.1022	65.0548	112.0757	56.5415	0	0	K							16
2	226.1550	113.5811	209.1285	105.0679	0	0	P	1646.8061	823.9067	1629.7795	815.3934	1628.7955	814.9014	15
3	297.1921	149.0997	280.1656	140.5864	0	0	A	1549.7533	775.3803	1532.7268	766.8670	1531.7427	766.3750	14
4	394.2449	197.6261	377.2183	189.1128	0	0	P	1478.7162	739.8617	1461.6896	731.3485	1460.7056	730.8564	13
5	493.3133	247.1603	476.2867	238.6470	0	0	V	1381.6634	691.3353	1364.6369	682.8221	1363.6529	682.3301	12
6	590.3661	295.6867	573.3395	287.1734	0	0	P	1282.5950	641.8011	1265.5685	633.2879	1264.5844	632.7959	11
7	661.4032	331.2052	644.3766	322.6919	0	0	A	1185.5422	593.2748	1168.5157	584.7615	1167.5317	584.2695	10
8	790.4458	395.7265	773.4192	387.2132	772.4352	386.7212	E	1114.5051	557.7562	1097.4786	549.2429	1096.4946	548.7509	9
9	887.4985	444.2529	870.4720	435.7396	869.4880	435.2476	P	985.4625	493.2349	968.4360	484.7216	967.4520	484.2296	8
10	1034.5669	517.7871	1017.5404	509.2738	1016.5564	508.7818	F	888.4098	444.7085	871.3832	436.1953	870.3992	435.7032	7
11	1149.5939	575.3006	1132.5673	566.7873	1131.5833	566.2953	D	741.3414	371.1743	724.3148	362.6610	723.3308	362.1690	6
12	1263.6368	632.3220	1246.6103	623.8088	1245.6262	623.3168	N	626.3144	313.6608	609.2879	305.1476	608.3039	304.6556	5
13	1364.6845	682.8459	1347.6579	674.3326	1346.6739	673.8406	T	512.2715	256.6394	495.2449	248.1261	494.2609	247.6341	4
14	1465.7322	733.3697	1448.7056	724.8564	1447.7216	724.3644	T	411.2238	206.1155	394.1973	197.6023	393.2132	197.1103	3
15	1628.7955	814.9014	1611.7690	806.3881	1610.7849	805.8961	Y	310.1761	155.5917	293.1496	147.0784	0	0	2
16							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 89313.

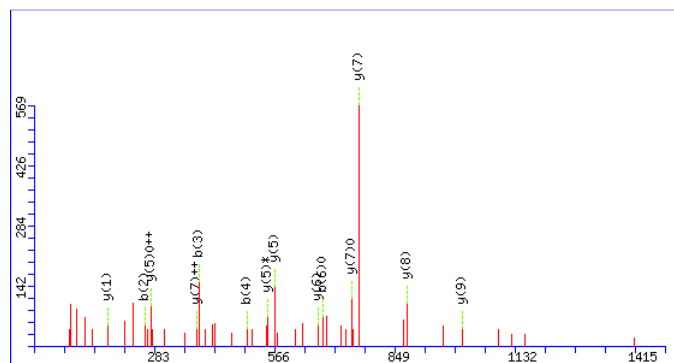
MS/MS Fragmentation of **LFQLTPPLSR**:

Found in **IP100005775**

Title: 3.1.1.1562.7

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							11
2	261.1598	131.0835	0	0	0	0	F	1155.6521	578.3297	1138.6255	569.8164	1137.6415	569.3244	10
3	389.2183	195.1128	372.1918	186.5995	0	0	Q	1008.5837	504.7955	991.5571	496.2822	990.5731	495.7902	9
4	502.3024	251.6548	485.2758	243.1416	0	0	L	880.5251	440.7662	863.4985	432.2529	862.5145	431.7609	8
5	599.3552	300.1812	582.3286	291.6679	0	0	P	767.4410	384.2241	750.4145	375.7109	749.4305	375.2189	7
6	700.4028	350.7051	683.3763	342.1918	682.3923	341.6998	T	670.3883	335.6978	653.3617	327.1845	652.3777	326.6925	6
7	797.4556	399.2314	780.4291	390.7182	779.4450	390.2262	P	569.3406	285.1739	552.3140	276.6606	551.3300	276.1686	5
8	894.5084	447.7578	877.4818	439.2445	876.4978	438.7525	P	472.2878	236.6475	455.2613	228.1343	454.2772	227.6423	4
9	1007.5924	504.2999	990.5659	495.7866	989.5819	495.2946	L	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
10	1094.6245	547.8159	1077.5979	539.3026	1076.6139	538.8106	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
11							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 89352.

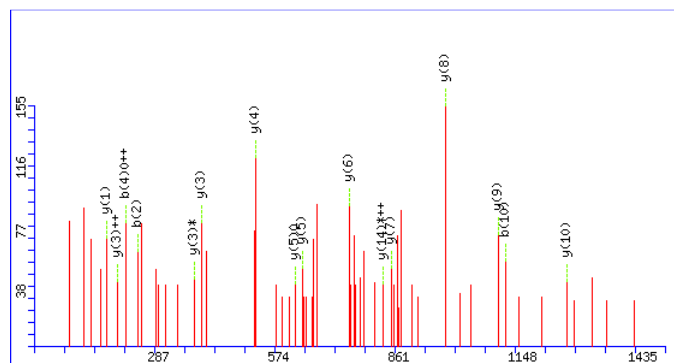
MS/MS Fragmentation of **TFLPCPAELVYQEVLQPER: 57.021465@C:5**

Found in **IP100000865:IP100791237:IP100797338**

Title: 4.1.1.2149.5

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							20
2	249.1234	125.0653	0	0	231.1128	116.0600	F	2301.1948	1151.1010	2284.1682	1142.5877	2283.1842	1142.0957	19
3	362.2074	181.6074	0	0	344.1969	172.6021	L	2154.1264	1077.5668	2137.0998	1069.0535	2136.1158	1068.5615	18
4	459.2602	230.1337	0	0	441.2496	221.1285	P	2041.0423	1021.0248	2024.0157	1012.5115	2023.0317	1012.0195	17
5	619.2908	310.1491	0	0	601.2803	301.1438	C	1943.9895	972.4984	1926.9630	963.9851	1925.9790	963.4931	16
6	716.3436	358.6754	0	0	698.3330	349.6702	P	1783.9589	892.4831	1766.9323	883.9698	1765.9483	883.4778	15
7	787.3807	394.1940	0	0	769.3702	385.1887	A	1686.9061	843.9567	1669.8796	835.4434	1668.8955	834.9514	14
8	916.4233	458.7153	0	0	898.4128	449.7100	E	1615.8690	808.4381	1598.8425	799.9249	1597.8584	799.4329	13
9	1029.5074	515.2573	0	0	1011.4968	506.2520	L	1486.8264	743.9168	1469.7999	735.4036	1468.8158	734.9116	12
10	1128.5758	564.7915	0	0	1110.5652	555.7863	V	1373.7423	687.3748	1356.7158	678.8615	1355.7318	678.3695	11
11	1291.6391	646.3232	0	0	1273.6286	637.3179	Y	1274.6739	637.8406	1257.6474	629.3273	1256.6634	628.8353	10
12	1419.6977	710.3525	1402.6712	701.8392	1401.6871	701.3472	Q	1111.6106	556.3089	1094.5841	547.7957	1093.6000	547.3037	9
13	1548.7403	774.8738	1531.7137	766.3605	1530.7297	765.8685	E	983.5520	492.2796	966.5255	483.7664	965.5415	483.2744	8
14	1647.8087	824.4080	1630.7822	815.8947	1629.7981	815.4027	V	854.5094	427.7584	837.4829	419.2451	836.4989	418.7531	7
15	1760.8928	880.9500	1743.8662	872.4368	1742.8822	871.9447	I	755.4410	378.2241	738.4145	369.7109	737.4305	369.2189	6
16	1873.9768	937.4921	1856.9503	928.9788	1855.9663	928.4868	L	642.3570	321.6821	625.3304	313.1688	624.3464	312.6768	5
17	2002.0354	1001.5213	1985.0089	993.0081	1984.0249	992.5161	Q	529.2729	265.1401	512.2463	256.6268	511.2623	256.1348	4
18	2099.0882	1050.0477	2082.0616	1041.5345	2081.0776	1041.0424	P	401.2143	201.1108	384.1878	192.5975	383.2037	192.1055	3
19	2228.1308	1114.5690	2211.1042	1106.0557	2210.1202	1105.5637	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
20							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 89463.

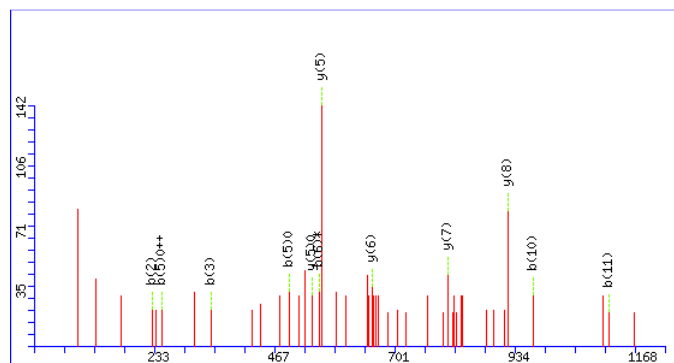
MS/MS Fragmentation of **DDNGIGTAIDFVLSNAR**:

Found in **IP100300223;IP100396121;IP100465336;IP100878714**

Title: 4.1.1.2488.2

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							17
2	231.0612	116.0342	0	0	213.0506	107.0289	D	1662.8446	831.9259	1645.8180	823.4127	1644.8340	822.9206	16
3	345.1041	173.0557	328.0775	164.5424	327.0935	164.0504	N	1547.8176	774.4125	1530.7911	765.8992	1529.8071	765.4072	15
4	402.1256	201.5664	385.0990	193.0531	384.1150	192.5611	G	1433.7747	717.3910	1416.7482	708.8777	1415.7641	708.3857	14
5	515.2096	258.1084	498.1831	249.5952	497.1991	249.1032	I	1376.7532	688.8803	1359.7267	680.3670	1358.7427	679.8750	13
6	572.2311	286.6192	555.2045	278.1059	554.2205	277.6139	G	1263.6692	632.3382	1246.6426	623.8250	1245.6586	623.3329	12
7	673.2788	337.1430	656.2522	328.6297	655.2682	328.1377	T	1206.6477	603.8275	1189.6212	595.3142	1188.6371	594.8222	11
8	744.3159	372.6616	727.2893	364.1483	726.3053	363.6563	A	1105.6000	553.3037	1088.5735	544.7904	1087.5895	544.2984	10
9	857.3999	429.2036	840.3734	420.6903	839.3894	420.1983	I	1034.5629	517.7851	1017.5364	509.2718	1016.5524	508.7798	9
10	972.4269	486.7171	955.4003	478.2038	954.4163	477.7118	D	921.4789	461.2431	904.4523	452.7298	903.4683	452.2378	8
11	1119.4953	560.2513	1102.4687	551.7380	1101.4847	551.2460	F	806.4519	403.7296	789.4254	395.2163	788.4413	394.7243	7
12	1218.5637	609.7855	1201.5372	601.2722	1200.5531	600.7802	V	659.3835	330.1954	642.3569	321.6821	641.3729	321.1901	6
13	1331.6478	666.3275	1314.6212	657.8142	1313.6372	657.3222	L	560.3151	280.6612	543.2885	272.1479	542.3045	271.6559	5
14	1418.6798	709.8435	1401.6533	701.3303	1400.6692	700.8383	S	447.2310	224.1191	430.2045	215.6059	429.2205	215.1139	4
15	1532.7227	766.8650	1515.6962	758.3517	1514.7122	757.8597	N	360.1990	180.6031	343.1724	172.0899	0	0	3
16	1603.7598	802.3836	1586.7333	793.8703	1585.7493	793.3783	A	246.1561	123.5817	229.1295	115.0684	0	0	2
17							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 89851.

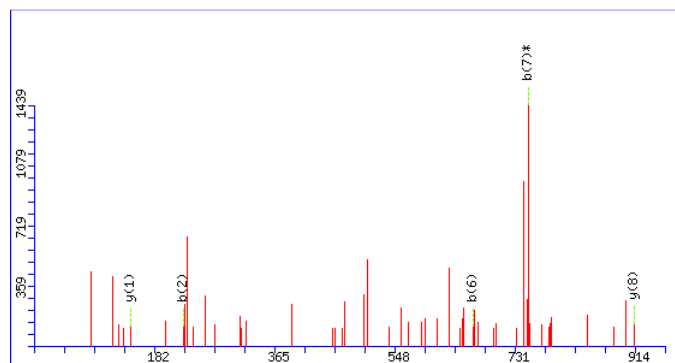
MS/MS Fragmentation of **VQSKEPTPK**:

Found in **IP100002221;IP100896471;IP100970827**

Title: 2.1.1.3896.5

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							9
2	228.1343	114.5708	211.1077	106.0575	0	0	Q	914.4942	457.7507	897.4676	449.2374	896.4836	448.7454	8
3	315.1663	158.0868	298.1397	149.5735	297.1557	149.0815	S	786.4356	393.7214	769.4090	385.2082	768.4250	384.7162	7
4	443.2613	222.1343	426.2347	213.6210	425.2507	213.1290	K	699.4036	350.2054	682.3770	341.6921	681.3930	341.2001	6
5	572.3039	286.6556	555.2773	278.1423	554.2933	277.6503	E	571.3086	286.1579	554.2821	277.6447	553.2980	277.1527	5
6	669.3566	335.1819	652.3301	326.6687	651.3461	326.1767	P	442.2660	221.6366	425.2395	213.1234	424.2554	212.6314	4
7	770.4043	385.7058	753.3777	377.1925	752.3937	376.7005	T	345.2132	173.1103	328.1867	164.5970	327.2027	164.1050	3
8	867.4571	434.2322	850.4305	425.7189	849.4465	425.2269	P	244.1656	122.5864	227.1390	114.0731	0	0	2
9							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 89986.

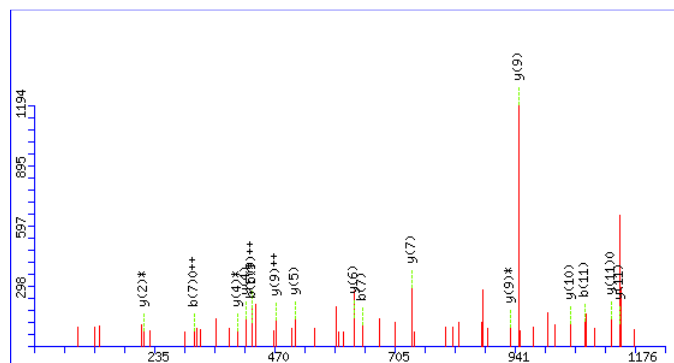
MS/MS Fragmentation of **EGSGNPTPLINPLAGR**:

Found in **IP100005011,IP100410621,IP100410623,IP101021364,IP101022323,IP101022977,IP101023019,IP101025434,IP101025585**

Title: 2.1.1.3880.10

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120212ry¥120212ry_414C2-43_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							16
2	187.0713	94.0393	0	0	169.0608	85.0340	G	1463.7965	732.4019	1446.7700	723.8886	1445.7859	723.3966	15
3	274.1034	137.5553	0	0	256.0928	128.5500	S	1406.7750	703.8912	1389.7485	695.3779	1388.7645	694.8859	14
4	331.1248	166.0661	0	0	313.1143	157.0608	G	1319.7430	660.3751	1302.7165	651.8619	1301.7324	651.3699	13
5	445.1678	223.0875	428.1412	214.5742	427.1572	214.0822	N	1262.7215	631.8644	1245.6950	623.3511	1244.7110	622.8591	12
6	542.2205	271.6139	525.1940	263.1006	524.2100	262.6086	P	1148.6786	574.8429	1131.6521	566.3297	1130.6681	565.8377	11
7	643.2682	322.1377	626.2416	313.6245	625.2576	313.1325	T	1051.6259	526.3166	1034.5993	517.8033	1033.6153	517.3113	10
8	740.3210	370.6641	723.2944	362.1508	722.3104	361.6588	P	950.5782	475.7927	933.5516	467.2795	0	0	9
9	853.4050	427.2061	836.3785	418.6929	835.3945	418.2009	L	853.5254	427.2663	836.4989	418.7531	0	0	8
10	966.4891	483.7482	949.4625	475.2349	948.4785	474.7429	I	740.4413	370.7243	723.4148	362.2110	0	0	7
11	1080.5320	540.7696	1063.5055	532.2564	1062.5214	531.7644	N	627.3573	314.1823	610.3307	305.6690	0	0	6
12	1177.5848	589.2960	1160.5582	580.7828	1159.5742	580.2907	P	513.3144	257.1608	496.2878	248.6475	0	0	5
13	1290.6688	645.8381	1273.6423	637.3248	1272.6583	636.8328	L	416.2616	208.6344	399.2350	200.1212	0	0	4
14	1361.7060	681.3566	1344.6794	672.8433	1343.6954	672.3513	A	303.1775	152.0924	286.1510	143.5791	0	0	3
15	1418.7274	709.8673	1401.7009	701.3541	1400.7169	700.8621	G	232.1404	116.5738	215.1139	108.0606	0	0	2
16							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 90080.

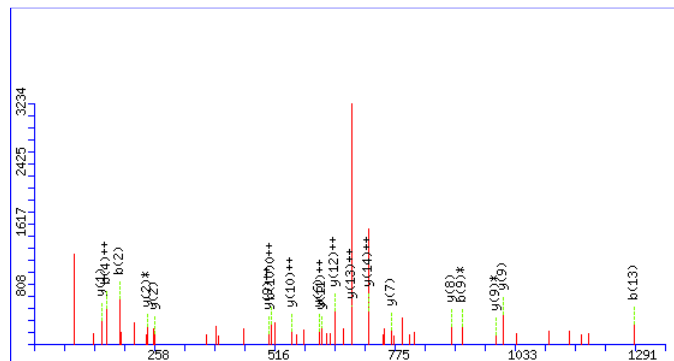
MS/MS Fragmentation of **IAAGEVIQRPANAIK**:

Found in **IP100029754;IP100783152;IP100795011;IP100927918**

Title: 2.1.1.471.5

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120214ry¥120214ry_414C2-43_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							15
2	185.1285	93.0679	0	0	0	0	A	1437.8172	719.4123	1420.7907	710.8990	1419.8067	710.4070	14
3	256.1656	128.5864	0	0	0	0	A	1366.7801	683.8937	1349.7536	675.3804	1348.7696	674.8884	13
4	313.1870	157.0972	0	0	0	0	G	1295.7430	648.3751	1278.7165	639.8619	1277.7324	639.3699	12
5	442.2296	221.6185	0	0	424.2191	212.6132	E	1238.7215	619.8644	1221.6950	611.3511	1220.7110	610.8591	11
6	541.2980	271.1527	0	0	523.2875	262.1474	V	1109.6790	555.3431	1092.6524	546.8298	0	0	10
7	654.3821	327.6947	0	0	636.3715	318.6894	I	1010.6105	505.8089	993.5840	497.2956	0	0	9
8	782.4407	391.7240	765.4141	383.2107	764.4301	382.7187	Q	897.5265	449.2669	880.4999	440.7536	0	0	8
9	938.5418	469.7745	921.5152	461.2613	920.5312	460.7693	R	769.4679	385.2376	752.4413	376.7243	0	0	7
10	1035.5946	518.3009	1018.5680	509.7876	1017.5840	509.2956	P	613.3668	307.1870	596.3402	298.6738	0	0	6
11	1106.6317	553.8195	1089.6051	545.3062	1088.6211	544.8142	A	516.3140	258.6606	499.2875	250.1474	0	0	5
12	1220.6746	610.8409	1203.6480	602.3277	1202.6640	601.8357	N	445.2769	223.1421	428.2504	214.6288	0	0	4
13	1291.7117	646.3595	1274.6852	637.8462	1273.7011	637.3542	A	331.2340	166.1206	314.2074	157.6074	0	0	3
14	1404.7958	702.9015	1387.7692	694.3883	1386.7852	693.8962	I	260.1969	130.6021	243.1703	122.0888	0	0	2
15							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 90151.

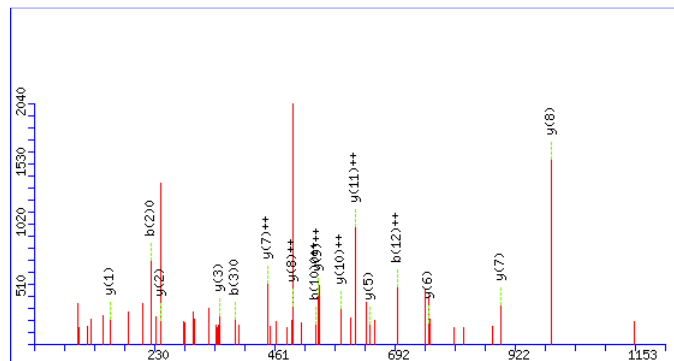
MS/MS Fragmentation of **ENCGSVPHDTWLPK: 57.021465@C:3**

Found in **IP100008499;IP100020964;IP100956535**

Title: 2.1.1.1628.10

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							14
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	N	1510.7107	755.8590	1493.6842	747.3457	1492.7002	746.8537	13
3	404.1234	202.5654	387.0969	194.0521	386.1129	193.5601	C	1396.6678	698.8375	1379.6412	690.3243	1378.6572	689.8323	12
4	461.1449	231.0761	444.1184	222.5628	443.1343	222.0708	G	1236.6371	618.8222	1219.6106	610.3089	1218.6266	609.8169	11
5	548.1769	274.5921	531.1504	266.0788	530.1664	265.5868	S	1179.6157	590.3115	1162.5891	581.7982	1161.6051	581.3062	10
6	647.2454	324.1263	630.2188	315.6130	629.2348	315.1210	V	1092.5837	546.7955	1075.5571	538.2822	1074.5731	537.7902	9
7	744.2981	372.6527	727.2716	364.1394	726.2876	363.6474	P	993.5152	497.2613	976.4887	488.7480	975.5047	488.2560	8
8	881.3570	441.1822	864.3305	432.6689	863.3465	432.1769	H	896.4625	448.7349	879.4359	440.2216	878.4519	439.7296	7
9	996.3840	498.6956	979.3574	490.1823	978.3734	489.6903	D	759.4036	380.2054	742.3770	371.6921	741.3930	371.2001	6
10	1097.4317	549.2195	1080.4051	540.7062	1079.4211	540.2142	T	644.3766	322.6919	627.3501	314.1787	626.3661	313.6867	5
11	1283.5110	642.2591	1266.4844	633.7458	1265.5004	633.2538	W	543.3289	272.1681	526.3024	263.6548	0	0	4
12	1396.5950	698.8012	1379.5685	690.2879	1378.5845	689.7959	L	357.2496	179.1285	340.2231	170.6152	0	0	3
13	1493.6478	747.3275	1476.6212	738.8143	1475.6372	738.3223	P	244.1656	122.5864	227.1390	114.0731	0	0	2
14							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 90449.

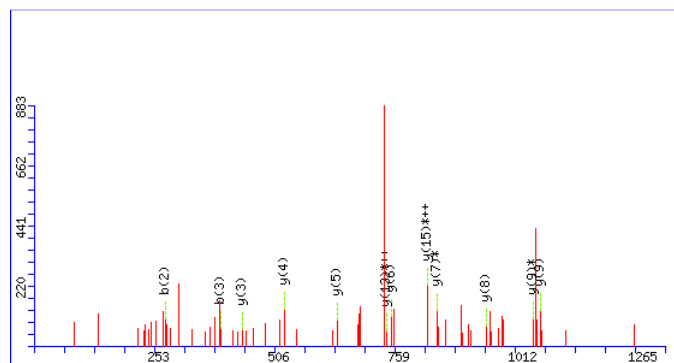
MS/MS Fragmentation of **YNDFGNSFTVNSNLISHQR**: 0.984015@N:6

Found in **IP100642617:IP100784071**

Title: 3.1.1.42.10

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	164.0706	82.5389	0	0	0	0	Y							19
2	278.1135	139.5604	261.0870	131.0471	0	0	N	2050.9577	1025.9825	2033.9312	1017.4692	2032.9471	1016.9772	18
3	393.1405	197.0739	376.1139	188.5606	375.1299	188.0686	D	1936.9148	968.9610	1919.8882	960.4478	1918.9042	959.9557	17
4	540.2089	270.6081	523.1823	262.0948	522.1983	261.6028	F	1821.8878	911.4476	1804.8613	902.9343	1803.8773	902.4423	16
5	597.2304	299.1188	580.2038	290.6055	579.2198	290.1135	G	1674.8194	837.9133	1657.7929	829.4001	1656.8089	828.9081	15
6	712.2573	356.6323	695.2307	348.1190	694.2467	347.6270	N	1617.7980	809.4026	1600.7714	800.8893	1599.7874	800.3973	14
7	799.2893	400.1483	782.2628	391.6350	781.2788	391.1430	S	1502.7710	751.8891	1485.7445	743.3759	1484.7605	742.8839	13
8	946.3577	473.6825	929.3312	465.1692	928.3472	464.6772	F	1415.7390	708.3731	1398.7124	699.8599	1397.7284	699.3678	12
9	1047.4054	524.2063	1030.3789	515.6931	1029.3949	515.2011	T	1268.6706	634.8389	1251.6440	626.3256	1250.6600	625.8336	11
10	1146.4738	573.7406	1129.4473	565.2273	1128.4633	564.7353	V	1167.6229	584.3151	1150.5963	575.8018	1149.6123	575.3098	10
11	1260.5168	630.7620	1243.4902	622.2487	1242.5062	621.7567	N	1068.5545	534.7809	1051.5279	526.2676	1050.5439	525.7756	9
12	1347.5488	674.2780	1330.5222	665.7648	1329.5382	665.2727	S	954.5116	477.7594	937.4850	469.2461	936.5010	468.7541	8
13	1461.5917	731.2995	1444.5652	722.7862	1443.5811	722.2942	N	867.4795	434.2434	850.4530	425.7301	849.4690	425.2381	7
14	1574.6758	787.8415	1557.6492	779.3283	1556.6652	778.8362	L	753.4366	377.2219	736.4100	368.7087	735.4260	368.2167	6
15	1687.7598	844.3836	1670.7333	835.8703	1669.7493	835.3783	I	640.3525	320.6799	623.3260	312.1666	622.3420	311.6746	5
16	1774.7919	887.8996	1757.7653	879.3863	1756.7813	878.8943	S	527.2685	264.1379	510.2419	255.6246	509.2579	255.1326	4
17	1911.8508	956.4290	1894.8242	947.9158	1893.8402	947.4237	H	440.2364	220.6219	423.2099	212.1086	0	0	3
18	2039.9094	1020.4583	2022.8828	1011.9450	2021.8988	1011.4530	Q	303.1775	152.0924	286.1510	143.5791	0	0	2
19							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 90587.

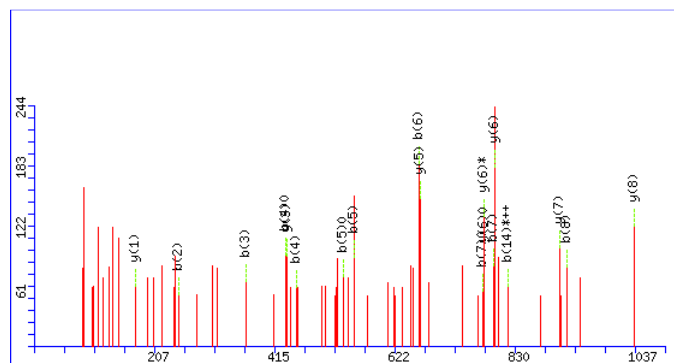
MS/MS Fragmentation of **HLDSVLQQLQTEVYR**:

Found in **IP100029235;IP101022800**

Title: 3.1.1.2365.6

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120201ry¥120201ry_aHDF1388-P9_1_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	138.0662	69.5367	0	0	0	0	H							15
2	251.1503	126.0788	0	0	0	0	L	1691.8963	846.4518	1674.8697	837.9385	1673.8857	837.4465	14
3	366.1772	183.5922	0	0	348.1666	174.5870	D	1578.8122	789.9097	1561.7857	781.3965	1560.8016	780.9045	13
4	453.2092	227.1082	0	0	435.1987	218.1030	S	1463.7853	732.3963	1446.7587	723.8830	1445.7747	723.3910	12
5	552.2776	276.6425	0	0	534.2671	267.6372	V	1376.7532	688.8803	1359.7267	680.3670	1358.7427	679.8750	11
6	665.3617	333.1845	0	0	647.3511	324.1792	L	1277.6848	639.3461	1260.6583	630.8328	1259.6743	630.3408	10
7	793.4203	397.2138	776.3937	388.7005	775.4097	388.2085	Q	1164.6008	582.8040	1147.5742	574.2907	1146.5902	573.7987	9
8	921.4789	461.2431	904.4523	452.7298	903.4683	452.2378	Q	1036.5422	518.7747	1019.5156	510.2615	1018.5316	509.7694	8
9	1034.5629	517.7851	1017.5364	509.2718	1016.5524	508.7798	L	908.4836	454.7454	891.4571	446.2322	890.4730	445.7402	7
10	1162.6215	581.8144	1145.5949	573.3011	1144.6109	572.8091	Q	795.3995	398.2034	778.3730	389.6901	777.3890	389.1981	6
11	1263.6692	632.3382	1246.6426	623.8250	1245.6586	623.3329	T	667.3410	334.1741	650.3144	325.6608	649.3304	325.1688	5
12	1392.7118	696.8595	1375.6852	688.3462	1374.7012	687.8542	E	566.2933	283.6503	549.2667	275.1370	548.2827	274.6450	4
13	1491.7802	746.3937	1474.7536	737.8805	1473.7696	737.3884	V	437.2507	219.1290	420.2241	210.6157	0	0	3
14	1654.8435	827.9254	1637.8170	819.4121	1636.8329	818.9201	Y	338.1823	169.5948	321.1557	161.0815	0	0	2
15							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 90902.

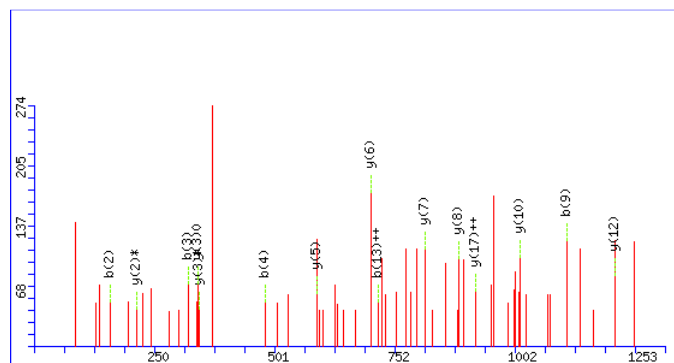
MS/MS Fragmentation of **SAYCPYSHFPVGAALLTQEGR: 57.021465@C:4**

Found in **IP100027983**

Title: 3.1.1.1555.10

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120210ry¥120210ry_32R1-32_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							21
2	159.0764	80.0418	0	0	141.0659	71.0366	A	2237.0808	1119.0440	2220.0543	1110.5308	2219.0702	1110.0388	20
3	322.1397	161.5735	0	0	304.1292	152.5682	Y	2166.0437	1083.5255	2149.0171	1075.0122	2148.0331	1074.5202	19
4	482.1704	241.5888	0	0	464.1598	232.5836	C	2002.9804	1001.9938	1985.9538	993.4805	1984.9698	992.9885	18
5	579.2232	290.1152	0	0	561.2126	281.1099	P	1842.9497	921.9785	1825.9232	913.4652	1824.9391	912.9732	17
6	742.2865	371.6469	0	0	724.2759	362.6416	Y	1745.8969	873.4521	1728.8704	864.9388	1727.8864	864.4468	16
7	829.3185	415.1629	0	0	811.3080	406.1576	S	1582.8336	791.9204	1565.8071	783.4072	1564.8231	782.9152	15
8	966.3774	483.6924	0	0	948.3669	474.6871	H	1495.8016	748.4044	1478.7750	739.8912	1477.7910	739.3992	14
9	1113.4458	557.2266	0	0	1095.4353	548.2213	F	1358.7427	679.8750	1341.7161	671.3617	1340.7321	670.8697	13
10	1210.4986	605.7529	0	0	1192.4880	596.7477	P	1211.6743	606.3408	1194.6477	597.8275	1193.6637	597.3355	12
11	1309.5670	655.2871	0	0	1291.5565	646.2819	V	1114.6215	557.8144	1097.5950	549.3011	1096.6109	548.8091	11
12	1366.5885	683.7979	0	0	1348.5779	674.7926	G	1015.5531	508.2802	998.5265	499.7669	997.5425	499.2749	10
13	1437.6256	719.3164	0	0	1419.6150	710.3112	A	958.5316	479.7694	941.5051	471.2562	940.5211	470.7642	9
14	1508.6627	754.8350	0	0	1490.6521	745.8297	A	887.4945	444.2509	870.4680	435.7376	869.4839	435.2456	8
15	1621.7468	811.3770	0	0	1603.7362	802.3717	L	818.4574	408.7323	799.4308	400.2191	798.4468	399.7271	7
16	1734.8308	867.9191	0	0	1716.8203	858.9138	L	703.3733	352.1903	686.3468	343.6770	685.3628	343.1850	6
17	1835.8785	918.4429	0	0	1817.8680	909.4376	T	590.2893	295.6483	573.2627	287.1350	572.2787	286.6430	5
18	1963.9371	982.4722	1946.9105	973.9589	1945.9265	973.4669	Q	489.2416	245.1244	472.2150	236.6112	471.2310	236.1191	4
19	2092.9797	1046.9935	2075.9531	1038.4802	2074.9691	1037.9882	E	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	3
20	2150.0012	1075.5042	2132.9746	1066.9909	2131.9906	1066.4989	G	232.1404	116.5738	215.1139	108.0606	0	0	2
21							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 91363.

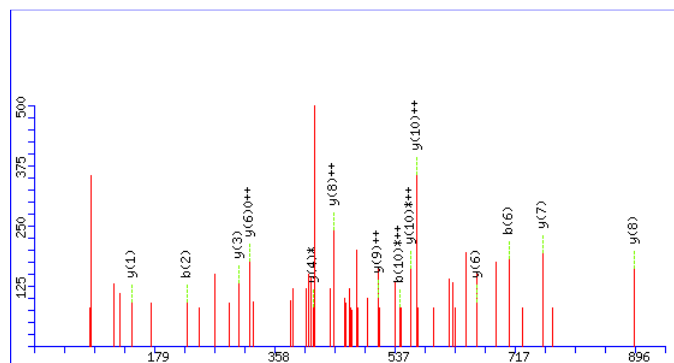
MS/MS Fragmentation of **LNMHVNIQTGK**:

Found in **IP100031030;IP100220977;IP100220978;IP100334946;IP100884988;IP100973038;IP100973819;IP100975666;IP100978328;IP100983004;IP100983691**

Title: 2.1.1.489.3

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4.2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							11
2	228.1343	114.5708	211.1077	106.0575	0	0	N	1141.5783	571.2928	1124.5517	562.7795	1123.5677	562.2875	10
3	359.1748	180.0910	342.1482	171.5777	0	0	M	1027.5353	514.2713	1010.5088	505.7580	1009.5248	505.2660	9
4	496.2337	248.6205	479.2071	240.1072	0	0	H	896.4948	448.7511	879.4683	440.2378	878.4843	439.7458	8
5	595.3021	298.1547	578.2755	289.6414	0	0	V	759.4359	380.2216	742.4094	371.7083	741.4254	371.2163	7
6	708.3450	355.1761	692.3185	346.6629	0	0	N	660.3675	330.6874	643.3410	322.1741	642.3570	321.6821	6
7	822.4291	411.7182	805.4025	403.2049	0	0	I	546.3246	273.6659	529.2980	265.1527	528.3140	264.6607	5
8	950.4876	475.7475	933.4611	467.2342	0	0	Q	433.2405	217.1239	416.2140	208.6106	415.2300	208.1186	4
9	1051.5353	526.2713	1034.5088	517.7580	1033.5248	517.2660	T	305.1819	153.0946	288.1554	144.5813	287.1714	144.0893	3
10	1108.5568	554.7820	1091.5302	546.2688	1090.5462	545.7768	G	204.1343	102.5708	187.1077	94.0575	0	0	2
11							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

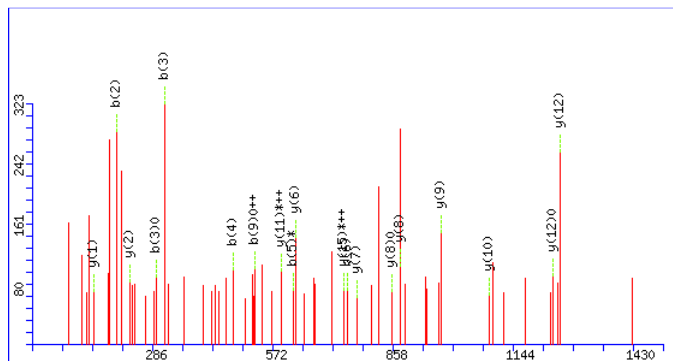
Peptide: 91424.

MS/MS Fragmentation of **SNLYCLKPTICSDQDNYCVTVSASAGIGNLVTFGHSLSK**: 57.021465@C:5,57.021465@C:11,57.021465@C:18
Found in **IP100002899;IP100979994**

Title: 3.1.1.4450.8

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							39
2	202.0822	101.5448	185.0557	93.0315	184.0717	92.5395	N	4189.9991	2095.5032	4172.9726	2086.9899	4171.9886	2086.4979	38
3	315.1663	158.0868	298.1397	149.5735	297.1557	149.0815	L	4075.9562	2038.4817	4058.9297	2029.9685	4057.9456	2029.4765	37
4	478.2296	239.6185	461.2031	231.1052	460.2191	230.6132	Y	3962.8721	1981.9397	3945.8456	1973.4264	3944.8616	1972.9344	36
5	638.2603	319.6338	621.2337	311.1205	620.2497	310.6285	C	3799.8088	1900.4080	3782.7823	1891.8948	3781.7982	1891.4028	35
6	751.3443	376.1758	734.3178	367.6625	733.3338	367.1705	L	3639.7782	1820.3927	3622.7516	1811.8794	3621.7676	1811.3874	34
7	879.4393	440.2233	862.4128	431.7100	861.4287	431.2180	K	3526.6941	1763.8507	3509.6675	1755.3374	3508.6835	1754.8454	33
8	976.4921	488.7497	959.4655	480.2364	958.4815	479.7444	P	3398.5991	1699.8032	3381.5726	1691.2899	3380.5886	1690.7979	32
9	1077.5397	539.2735	1060.5132	530.7602	1059.5292	530.2682	T	3301.5464	1651.2768	3284.5198	1642.7635	3283.5358	1642.2715	31
10	1190.6238	595.8155	1173.5973	587.3023	1172.6132	586.8103	I	3200.4987	1600.7530	3183.4721	1592.2397	3182.4881	1591.7477	30
11	1350.6545	675.8309	1333.6279	667.3176	1332.6439	666.8256	C	3087.4146	1544.2110	3070.3881	1535.6977	3069.4041	1535.2057	29
12	1437.6865	719.3469	1420.6599	710.8336	1419.6759	710.3416	S	2927.3840	1464.1956	2910.3574	1455.6824	2909.3734	1455.1903	28
13	1552.7134	776.8604	1535.6869	768.3471	1534.7029	767.8551	D	2840.3520	1420.6796	2823.3254	1412.1663	2822.3414	1411.6743	27
14	1680.7720	840.8896	1663.7455	832.3764	1662.7614	831.8844	Q	2725.3250	1363.1661	2708.2985	1354.6529	2707.3144	1354.1609	26
15	1795.7990	898.4031	1778.7724	889.8898	1777.7884	889.3978	D	2597.2664	1299.1369	2580.2399	1290.6236	2579.2559	1290.1316	25
16	1909.8419	955.4246	1892.8153	946.9113	1891.8313	946.4193	N	2482.2395	1241.6234	2465.2129	1233.1101	2464.2289	1232.6181	24
17	2072.9052	1036.9562	2055.8787	1028.4430	2054.8946	1027.9510	Y	2368.1966	1184.6019	2351.1700	1176.0886	2350.1860	1175.5966	23
18	2232.9359	1116.9716	2215.9093	1108.4583	2214.9253	1107.9663	C	2205.1332	1103.0703	2188.1067	1094.5570	2187.1227	1094.0650	22
19	2332.0043	1166.5058	2314.9777	1157.9925	2313.9937	1157.5005	V	2045.1026	1023.0549	2028.0760	1014.5417	2027.0920	1014.0496	21
20	2433.0519	1217.0296	2416.0254	1208.5163	2415.0414	1208.0243	T	1946.0342	973.5207	1929.0076	965.0074	1928.0236	964.5154	20
21	2532.1204	1266.5638	2515.0938	1258.0505	2514.1098	1257.5585	V	1844.9865	922.9969	1827.9599	914.4836	1826.9759	913.9916	19
22	2619.1524	1310.0798	2602.1258	1301.5666	2601.1418	1301.0746	S	1745.9181	873.4627	1728.8915	864.9494	1727.9075	864.4574	18
23	2690.1895	1345.5984	2673.1630	1337.0851	2672.1789	1336.5931	A	1658.8860	829.9467	1641.8595	821.4334	1640.8755	820.9414	17
24	2777.2215	1389.1144	2760.1950	1380.6011	2759.2110	1380.1091	S	1587.8489	794.4281	1570.8224	785.9148	1569.8384	785.4228	16
25	2848.2586	1424.6330	2831.2321	1416.1197	2830.2481	1415.6277	A	1500.8169	750.9121	1483.7904	742.3988	1482.8063	741.9068	15
26	2905.2801	1453.1437	2888.2536	1444.6304	2887.2695	1444.1384	G	1429.7798	715.3935	1412.7532	706.8803	1411.7692	706.3883	14
27	3018.3642	1509.6857	3001.3376	1501.1725	3000.3536	1500.6804	I	1372.7583	686.8828	1355.7318	678.3695	1354.7478	677.8775	13
28	3075.3856	1538.1965	3058.3591	1529.6832	3057.3751	1529.1912	G	1259.6743	630.3408	1242.6477	621.8275	1241.6637	621.3355	12
29	3189.4286	1595.2179	3172.4020	1586.7046	3171.4180	1586.2126	N	1202.6528	601.8300	1185.6262	593.3168	1184.6422	592.8248	11
30	3302.5126	1651.7600	3285.4861	1643.2467	3284.5021	1642.7547	L	1088.6099	544.8086	1071.5833	536.2953	1070.5993	535.8033	10
31	3401.5810	1701.2942	3384.5545	1692.7809	3383.5705	1692.2889	V	975.5258	488.2665	958.4993	479.7533	957.5152	479.2613	9
32	3502.6287	1751.8180	3485.6022	1743.3047	3484.6182	1742.8127	T	876.4574	438.7323	859.4308	430.2191	858.4468	429.7271	8
33	3649.6971	1825.3522	3632.6706	1816.8389	3631.6866	1816.3469	F	775.4097	388.2085	758.3832	379.6952	757.3991	379.2032	7
34	3706.7186	1853.8629	3689.6921	1845.3497	3688.7080	1844.8577	G	628.3413	314.6743	611.3148	306.1610	610.3307	305.6690	6
35	3843.7775	1922.3924	3826.7510	1913.8791	3825.7669	1913.3871	H	571.3198	286.1636	554.2933	277.6503	553.3093	277.1583	5
36	3930.8095	1965.9084	3913.7830	1957.3951	3912.7990	1956.9031	S	434.2609	217.6341	417.2344	209.1208	416.2504	208.6288	4
37	4043.8936	2022.4504	4026.8671	2013.9372	4025.8830	2013.4452	L	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
38	4130.9256	2065.9665	4113.8991	2057.4532	4112.9151	2056.9612	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
39							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 91526.

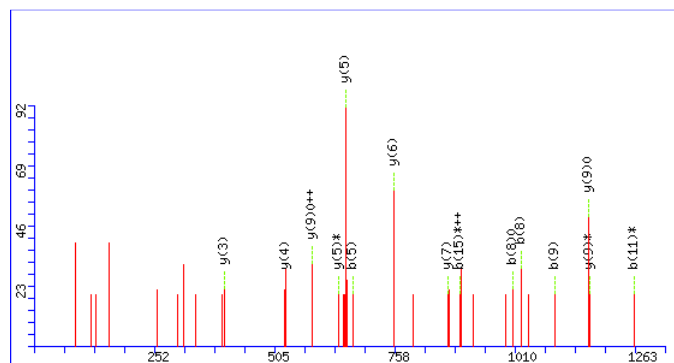
MS/MS Fragmentation of **ECEHDLQAALQWLTTQPER: 57.021465@C:2**

Found in **IP100166852:IP100296724**

Title: 4.1.1.4262.3

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							20
2	290.0805	145.5439	0	0	272.0700	136.5386	C	2336.1452	1168.5762	2319.1186	1160.0630	2318.1346	1159.5710	19
3	419.1231	210.0652	0	0	401.1125	201.0599	E	2176.1145	1088.5609	2159.0880	1080.0476	2158.1040	1079.5556	18
4	556.1820	278.5947	0	0	538.1715	269.5894	H	2047.0720	1024.0396	2030.0454	1015.5263	2029.0614	1015.0343	17
5	671.2090	336.1081	0	0	653.1984	327.1028	D	1910.0130	955.5102	1892.9865	946.9969	1892.0025	946.5049	16
6	784.2930	392.6502	0	0	766.2825	383.6449	L	1794.9861	897.9967	1777.9595	889.4834	1776.9755	888.9914	15
7	897.3771	449.1922	0	0	879.3665	440.1869	L	1681.9020	841.4547	1664.8755	832.9414	1663.8915	832.4494	14
8	1025.4357	513.2215	1008.4091	504.7082	1007.4251	504.2162	Q	1568.8180	784.9126	1551.7914	776.3993	1550.8074	775.9073	13
9	1096.4728	548.7400	1079.4462	540.2268	1078.4622	539.7347	A	1440.7594	720.8833	1423.7328	712.3701	1422.7488	711.8781	12
10	1167.5099	584.2586	1150.4834	575.7453	1149.4993	575.2533	A	1369.7223	685.3648	1352.6957	676.8515	1351.7117	676.3595	11
11	1280.5940	640.8006	1263.5674	632.2873	1262.5834	631.7953	L	1298.6852	649.8462	1281.6586	641.3329	1280.6746	640.8409	10
12	1408.6525	704.8299	1391.6260	696.3166	1390.6420	695.8246	Q	1185.6011	593.3042	1168.5745	584.7909	1167.5905	584.2989	9
13	1594.7319	797.8696	1577.7053	789.3563	1576.7213	788.8643	W	1057.5425	529.2749	1040.5160	520.7616	1039.5320	520.2696	8
14	1707.8159	854.4116	1690.7894	845.8983	1689.8054	845.4063	L	871.4632	436.2352	854.4367	427.7220	853.4526	427.2300	7
15	1808.8636	904.9354	1791.8370	896.4222	1790.8530	895.9302	T	758.3791	379.6932	741.3526	371.1799	740.3686	370.6879	6
16	1936.9222	968.9647	1919.8956	960.4515	1918.9116	959.9594	Q	657.3315	329.1694	640.3049	320.6561	639.3209	320.1641	5
17	2064.9808	1032.9940	2047.9542	1024.4807	2046.9702	1023.9887	Q	529.2729	265.1401	512.2463	256.6268	511.2623	256.1348	4
18	2162.0335	1081.5204	2145.0070	1073.0071	2144.0230	1072.5151	P	401.2143	201.1108	384.1878	192.5975	383.2037	192.1055	3
19	2291.0761	1146.0417	2274.0496	1137.5284	2273.0655	1137.0364	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
20							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 91603.

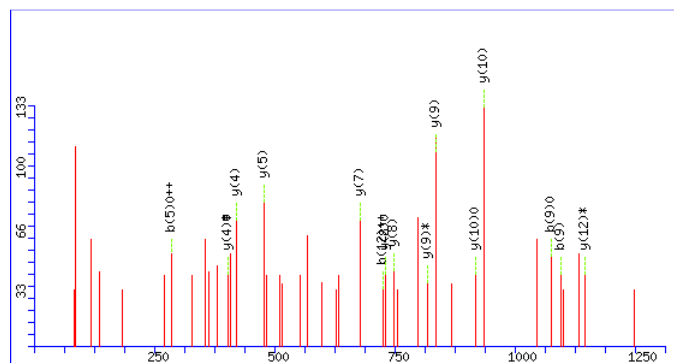
MS/MS Fragmentation of **QLYPSCSFIGNLVASLQSTSK: 57.021465@C:6**

Found in **IP100013418;IP100977511;IP100980653;IP100984201;IP100984575**

Title: 4.1.1.2412.8

Data file: Y:\TT5600(CiRA1)\2012-01\120124ry\120124ry_414C2-43_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233	0	0	Q							22
2	242.1499	121.5786	225.1234	113.0653	0	0	L	2259.1326	1130.0699	2242.1060	1121.5566	2241.1220	1121.0646	21
3	405.2132	203.1103	388.1867	194.5970	0	0	Y	2146.0485	1073.5279	2129.0219	1065.0146	2128.0379	1064.5226	20
4	502.2660	251.6366	485.2395	243.1234	0	0	P	1982.9852	991.9962	1965.9586	983.4829	1964.9746	982.9909	19
5	589.2980	295.1527	572.2715	286.6394	571.2875	286.1474	S	1885.9324	943.4698	1868.9059	934.9566	1867.9218	934.4646	18
6	749.3287	375.1680	732.3021	366.6547	731.3181	366.1627	C	1798.9004	899.9538	1781.8738	891.4406	1780.8898	890.9485	17
7	836.3607	418.6840	819.3342	410.1707	818.3502	409.6787	S	1638.8697	819.9385	1621.8432	811.4252	1620.8592	810.9332	16
8	983.4291	492.2182	966.4026	483.7049	965.4186	483.2129	F	1551.8377	776.4225	1534.8111	767.9092	1533.8271	767.4172	15
9	1096.5132	548.7602	1079.4866	540.2470	1078.5026	539.7550	I	1404.7693	702.8883	1387.7427	694.3750	1386.7587	693.8830	14
10	1224.5718	612.7895	1207.5452	604.2762	1206.5612	603.7842	Q	1291.6852	646.3462	1274.6587	637.8330	1273.6747	637.3410	13
11	1338.6147	669.8110	1321.5882	661.2977	1320.6041	660.8057	N	1163.6266	582.3170	1146.6001	573.8037	1145.6161	573.3117	12
12	1451.6988	726.3530	1434.6722	717.8397	1433.6882	717.3477	L	1049.5837	525.2955	1032.5572	516.7822	1031.5732	516.2902	11
13	1550.7672	775.8872	1533.7406	767.3740	1532.7566	766.8819	V	936.4997	468.7535	919.4731	460.2402	918.4891	459.7482	10
14	1637.7992	819.4032	1620.7727	810.8900	1619.7886	810.3980	S	837.4312	419.2193	820.4047	410.7060	819.4207	410.2140	9
15	1708.8363	854.9218	1691.8098	846.4085	1690.8258	845.9165	A	750.3992	375.7032	733.3727	367.1900	732.3886	366.6980	8
16	1795.8683	898.4378	1778.8418	889.9245	1777.8578	889.4325	S	679.3621	340.1847	662.3355	331.6714	661.3515	331.1794	7
17	1908.9524	954.9798	1891.9259	946.4666	1890.9418	945.9746	L	592.3301	296.6687	575.3035	288.1554	574.3195	287.6634	6
18	1965.9739	983.4906	1948.9473	974.9773	1947.9633	974.4853	G	479.2460	240.1266	462.2195	231.6134	461.2354	231.1214	5
19	2053.0059	1027.0066	2035.9794	1018.4933	2034.9953	1018.0013	S	422.2245	211.6159	405.1980	203.1026	404.2140	202.6106	4
20	2154.0536	1077.5304	2137.0270	1069.0172	2136.0430	1068.5251	T	335.1925	168.0999	318.1660	159.5866	317.1819	159.0946	3
21	2241.0856	1121.0464	2224.0591	1112.5332	2223.0750	1112.0412	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
22							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 91612.

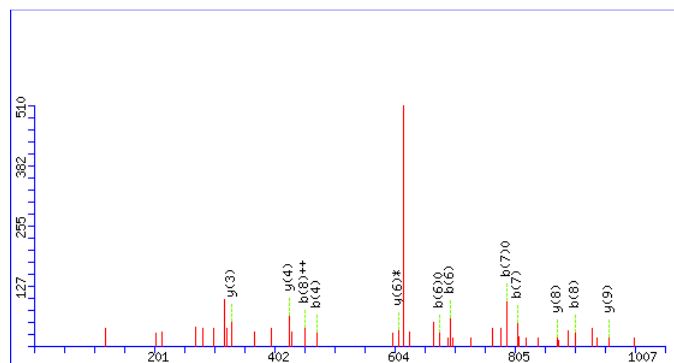
MS/MS Fragmentation of **ICSLHSLPPQS: 57.021465@C:2**

Found in **IP100008528;IP101021823;IP101022807;IP101022929**

Title: 2.1.1.195.10

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							11
2	274.1220	137.5646	0	0	0	0	C	1125.5357	563.2715	1108.5092	554.7582	1107.5252	554.2662	10
3	361.1540	181.0806	0	0	343.1435	172.0754	S	965.5051	483.2562	948.4785	474.7429	947.4945	474.2509	9
4	474.2381	237.6227	0	0	456.2275	228.6174	L	878.4730	439.7402	861.4465	431.2269	860.4625	430.7349	8
5	611.2970	306.1521	0	0	593.2864	297.1469	H	765.3890	383.1981	748.3624	374.6849	747.3784	374.1928	7
6	698.3290	349.6681	0	0	680.3185	340.6629	S	628.3301	314.6687	611.3035	306.1554	610.3195	305.6634	6
7	811.4131	406.2102	0	0	793.4025	397.2049	L	541.2980	271.1527	524.2715	262.6394	523.2875	262.1474	5
8	908.4659	454.7366	0	0	890.4553	445.7313	P	428.2140	214.6106	411.1874	206.0974	410.2034	205.6053	4
9	1005.5186	503.2629	0	0	987.5080	494.2577	P	331.1612	166.0842	314.1347	157.5710	313.1506	157.0790	3
10	1133.5772	567.2922	1116.5506	558.7790	1115.5666	558.2870	Q	234.1084	117.5579	217.0819	109.0446	216.0979	108.5526	2
11							S	106.0499	53.5286	0	0	88.0393	44.5233	1

Peptide View

Peptide: 91873.

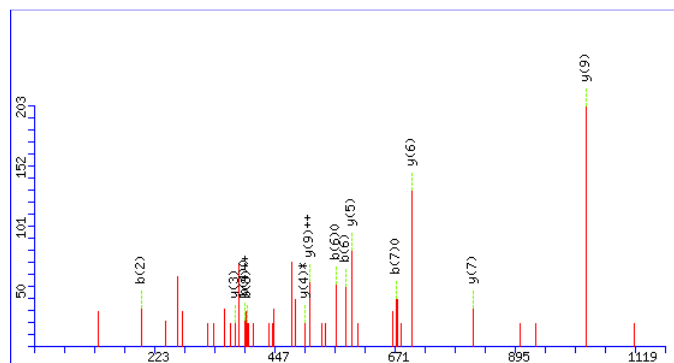
MS/MS Fragmentation of **VTIPGILVPDLIAFNLK**:

Found in **IP100018786;IP100855958**

Title: 4.1.1.3492.4

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							17
2	201.1234	101.0653	0	0	183.1128	92.0600	T	1724.0357	862.5215	1707.0091	854.0082	1706.0251	853.5162	16
3	314.2074	157.6074	0	0	296.1969	148.6021	I	1622.9880	811.9976	1605.9614	803.4844	1604.9774	802.9924	15
4	411.2602	206.1337	0	0	393.2496	197.1285	P	1509.9039	755.4556	1492.8774	746.9423	1491.8934	746.4503	14
5	468.2817	234.6445	0	0	450.2711	225.6392	G	1412.8512	706.9292	1395.8246	698.4159	1394.8406	697.9239	13
6	581.3657	291.1865	0	0	563.3552	282.1812	I	1355.8297	678.4185	1338.8032	669.9052	1337.8191	669.4132	12
7	694.4498	347.7285	0	0	676.4392	338.7233	L	1242.7456	621.8765	1225.7191	613.3632	1224.7351	612.8712	11
8	793.5182	397.2627	0	0	775.5076	388.2575	V	1129.6616	565.3344	1112.6350	556.8211	1111.6510	556.3291	10
9	890.5710	445.7891	0	0	872.5604	436.7838	P	1030.5932	515.8002	1013.5666	507.2869	1012.5826	506.7949	9
10	1005.5979	503.3026	0	0	987.5873	494.2973	D	933.5404	467.2738	916.5138	458.7606	915.5298	458.2686	8
11	1118.6820	559.8446	0	0	1100.6714	550.8393	L	818.5135	409.7604	801.4869	401.2471	0	0	7
12	1231.7660	616.3867	0	0	1213.7555	607.3814	I	705.4294	353.2183	688.4028	344.7051	0	0	6
13	1302.8032	651.9052	0	0	1284.7926	642.8999	A	592.3453	296.6763	575.3188	288.1630	0	0	5
14	1449.8716	725.4394	0	0	1431.8610	716.4341	F	521.3082	261.1577	504.2817	252.6445	0	0	4
15	1563.9145	782.4609	1546.8879	773.9476	1545.9039	773.4556	N	374.2398	187.6235	357.2132	179.1103	0	0	3
16	1676.9986	839.0029	1659.9720	830.4896	1658.9880	829.9976	L	260.1969	130.6021	243.1703	122.0888	0	0	2
17							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 91924.

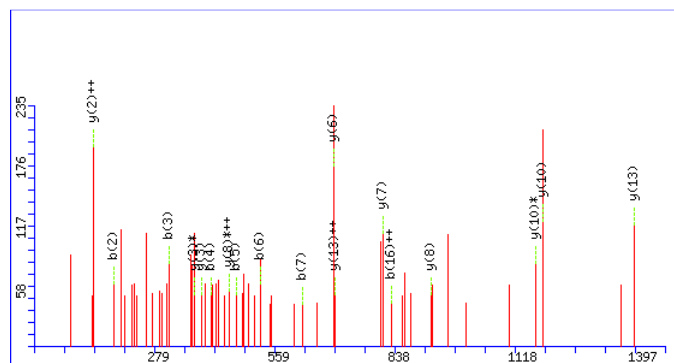
MS/MS Fragmentation of **IAEVGGVPYLLPLVNQK**:

Found in **IP100061507;IP100072044;IP100761072;IP100975776;IP100977111;IP100977701;IP100979593;IP100981758;IP100984827;IP100985388**

Title: 3.1.1.3803.8

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120208ry¥120208ry_Tig120slc-P8_2_3.mgf

ProteinPilot Peptide Confidence > 99%

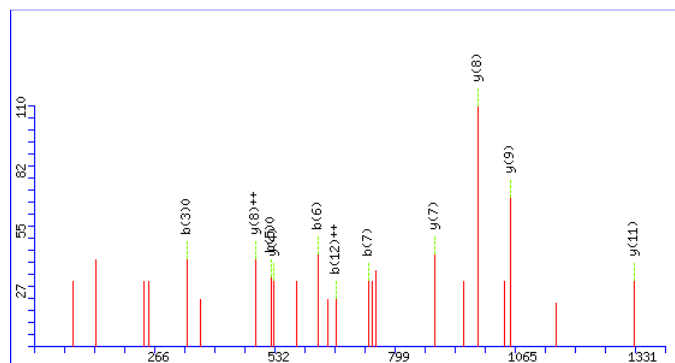


#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							17
2	185.1285	93.0679	0	0	0	0	A	1696.9632	848.9853	1679.9367	840.4720	1678.9527	839.9800	16
3	314.1710	157.5892	0	0	296.1605	148.5839	E	1625.9261	813.4667	1608.8996	804.9534	1607.9156	804.4614	15
4	413.2395	207.1234	0	0	395.2289	198.1181	V	1496.8835	748.9454	1479.8570	740.4321	0	0	14
5	470.2609	235.6341	0	0	452.2504	226.6288	G	1397.8151	699.4112	1380.7886	690.8979	0	0	13
6	527.2824	264.1448	0	0	509.2718	255.1396	G	1340.7936	670.9005	1323.7671	662.3872	0	0	12
7	626.3508	313.6790	0	0	608.3402	304.6738	V	1283.7722	642.3897	1266.7456	633.8765	0	0	11
8	723.4036	362.2054	0	0	705.3930	353.2001	P	1184.7038	592.8555	1167.6772	584.3422	0	0	10
9	886.4669	443.7371	0	0	868.4563	434.7318	Y	1087.6510	544.3291	1070.6245	535.8159	0	0	9
10	999.5510	500.2791	0	0	981.5404	491.2738	L	924.5877	462.7975	907.5611	454.2842	0	0	8
11	1112.6350	556.8212	0	0	1094.6245	547.8159	L	811.5036	406.2554	794.4771	397.7422	0	0	7
12	1209.6878	605.3475	0	0	1191.6772	596.3422	P	698.4196	349.7134	681.3930	341.2001	0	0	6
13	1322.7719	661.8896	0	0	1304.7613	652.8843	L	601.3668	301.1870	584.3402	292.6738	0	0	5
14	1421.8403	711.4238	0	0	1403.8297	702.4185	V	488.2827	244.6450	471.2562	236.1317	0	0	4
15	1535.8832	768.4452	1518.8566	759.9320	1517.8726	759.4400	N	389.2143	195.1108	372.1878	186.5975	0	0	3
16	1663.9418	832.4745	1646.9152	823.9612	1645.9312	823.4692	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
17							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 91996.

MS/MS Fragmentation of **ELDQGSLOTSFVGTQLQYLAPELLEQQK: 57.021465@C:8**
 Found in **IP100024709;IP100556516;IP100656051;IP100798101;IP100977664;IP100982033;IP101010552;IP101022343**
 Title: 4.1.1.3931.6
 Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_3_4.mgf
 ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							27
2	243.1339	122.0706	0	0	225.1234	113.0653	L	2938.4867	1469.7470	2921.4601	1461.2337	2920.4761	1460.7417	26
3	358.1609	179.5841	0	0	340.1503	170.5788	D	2825.4026	1413.2049	2808.3760	1404.6917	2807.3920	1404.1997	25
4	486.2195	243.6134	469.1929	235.1001	468.2089	234.6081	Q	2710.3756	1355.6915	2693.3491	1347.1782	2692.3651	1346.6862	24
5	543.2409	272.1241	526.2144	263.6108	525.2304	263.1188	G	2582.3171	1291.6622	2565.2905	1283.1489	2564.3065	1282.6569	23
6	630.2729	315.6401	613.2464	307.1268	612.2624	306.6348	S	2525.2956	1263.1514	2508.2691	1254.6382	2507.2850	1254.1462	22
7	743.3570	372.1821	726.3305	363.6689	725.3464	363.1769	L	2438.2636	1219.6354	2421.2370	1211.1222	2420.2530	1210.6301	21
8	903.3877	452.1975	886.3611	443.6842	885.3771	443.1922	C	2325.1795	1163.0934	2308.1530	1154.5801	2307.1690	1154.0881	20
9	1004.4353	502.7213	987.4088	494.2080	986.4248	493.7160	T	2165.1489	1083.0781	2148.1223	1074.5648	2147.1383	1074.0728	19
10	1091.4674	546.2373	1074.4408	537.7240	1073.4568	537.2320	S	2064.1012	1032.5542	2047.0746	1024.0410	2046.0906	1023.5489	18
11	1238.5358	619.7715	1221.5092	611.2583	1220.5252	610.7662	F	1977.0692	989.0382	1960.0426	980.5249	1959.0586	980.0329	17
12	1337.6042	669.3057	1320.5776	660.7925	1319.5936	660.3005	V	1830.0007	915.5040	1812.9742	906.9907	1811.9902	906.4987	16
13	1394.6257	697.8165	1377.5991	689.3032	1376.6151	688.8112	G	1730.9323	865.9698	1713.9058	857.4565	1712.9218	856.9645	15
14	1495.6733	748.3403	1478.6468	739.8270	1477.6628	739.3350	T	1673.9109	837.4591	1656.8843	828.9458	1655.9003	828.4538	14
15	1608.7574	804.8823	1591.7309	796.3691	1590.7468	795.8771	L	1572.8632	786.9352	1555.8366	778.4220	1554.8526	777.9299	13
16	1736.8160	868.9116	1719.7894	860.3984	1718.8054	859.9063	Q	1459.7791	730.3932	1442.7526	721.8799	1441.7686	721.3879	12
17	1899.8793	950.4433	1882.8528	941.9300	1881.8687	941.4380	Y	1331.7205	666.3639	1314.6940	657.8506	1313.7100	657.3586	11
18	2012.9634	1006.9853	1995.9368	998.4720	1994.9528	997.9800	L	1168.6572	584.8322	1151.6307	576.3190	1150.6467	575.8270	10
19	2084.0005	1042.5039	2066.9739	1033.9906	2065.9899	1033.4986	A	1055.5732	528.2902	1038.5466	519.7769	1037.5626	519.2849	9
20	2181.0533	1091.0303	2164.0267	1082.5170	2163.0427	1082.0250	P	984.5360	492.7717	967.5095	484.2584	966.5255	483.7664	8
21	2310.0958	1155.5516	2293.0693	1147.0383	2292.0853	1146.5463	E	887.4833	444.2453	870.4567	435.7320	869.4727	435.2400	7
22	2423.1799	1212.0936	2406.1534	1203.5803	2405.1693	1203.0883	L	758.4407	379.7240	741.4141	371.2107	740.4301	370.7187	6
23	2536.2640	1268.6356	2519.2374	1260.1223	2518.2534	1259.6303	L	645.3566	323.1819	628.3301	314.6687	627.3461	314.1767	5
24	2665.3066	1333.1569	2648.2800	1324.6436	2647.2960	1324.1516	E	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
25	2793.3651	1397.1862	2776.3386	1388.6729	2775.3546	1388.1809	Q	403.2300	202.1186	386.2034	193.6053	0	0	3
26	2921.4237	1461.2155	2904.3972	1452.7022	2903.4132	1452.2102	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
27							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 92011.

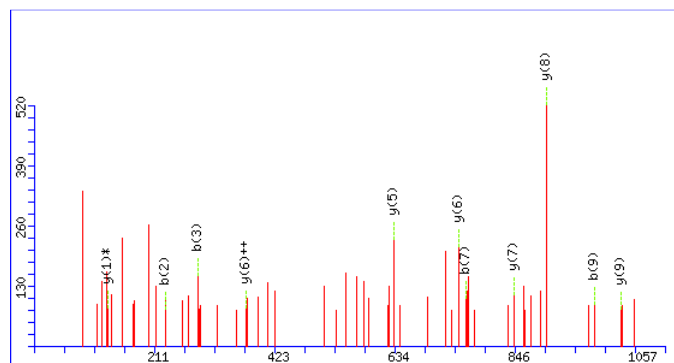
MS/MS Fragmentation of **VMGVNPLYLK**:

Found in **IP100219890;IP100396970;IP100513896;IP100514207;IP100748809;IP100844050;IP101009393;IP101009633**

Title: 2.1.1.3803.5

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							10
2	231.1162	116.0617	0	0	0	0	M	1034.5703	517.7888	1017.5438	509.2755	0	0	9
3	288.1376	144.5725	0	0	0	0	G	903.5298	452.2686	886.5033	443.7553	0	0	8
4	387.2061	194.1067	0	0	0	0	V	846.5084	423.7578	829.4818	415.2445	0	0	7
5	501.2490	251.1281	484.2224	242.6149	0	0	N	747.4400	374.2236	730.4134	365.7103	0	0	6
6	598.3017	299.6545	581.2752	291.1412	0	0	P	633.3970	317.2022	616.3705	308.6889	0	0	5
7	761.3651	381.1862	744.3385	372.6729	0	0	Y	536.3443	268.6758	519.3177	260.1625	0	0	4
8	874.4491	437.7282	857.4226	429.2149	0	0	I	373.2809	187.1441	356.2544	178.6308	0	0	3
9	987.5332	494.2702	970.5067	485.7570	0	0	L	260.1969	130.6021	243.1703	122.0888	0	0	2
10							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 92027.

MS/MS Fragmentation of **LIGEELAQLK**:

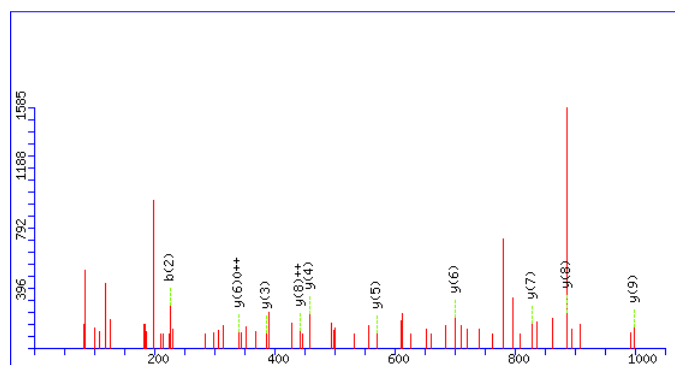
Found in

IP100219863,IP100219864,IP100607670,IP100816562,IP100895820,IP100895831,IP100944576,IP100944590,IP100944599,IP100956202,IP100956438,IP100956439,IP1009564

Title: 2.1.1.4210.6

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120210ry¥120210ry_32R1-32_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							10
2	227.1754	114.0913	0	0	0	0	I	1000.5673	500.7873	983.5408	492.2740	982.5568	491.7820	9
3	284.1969	142.6021	0	0	0	0	G	887.4833	444.2453	870.4567	435.7320	869.4727	435.2400	8
4	413.2395	207.1234	0	0	395.2289	198.1181	E	830.4618	415.7345	813.4353	407.2213	812.4512	406.7293	7
5	542.2821	271.6447	0	0	524.2715	262.6394	E	701.4192	351.2132	684.3927	342.7000	683.4087	342.2080	6
6	655.3661	328.1867	0	0	637.3556	319.1814	L	572.3766	286.6919	555.3501	278.1787	0	0	5
7	726.4032	363.7053	0	0	708.3927	354.7000	A	459.2926	230.1499	442.2660	221.6366	0	0	4
8	854.4618	427.7345	837.4353	419.2213	836.4512	418.7293	Q	388.2554	194.6314	371.2289	186.1181	0	0	3
9	967.5459	484.2766	950.5193	475.7633	949.5353	475.2713	L	260.1969	130.6021	243.1703	122.0888	0	0	2
10							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 92199.

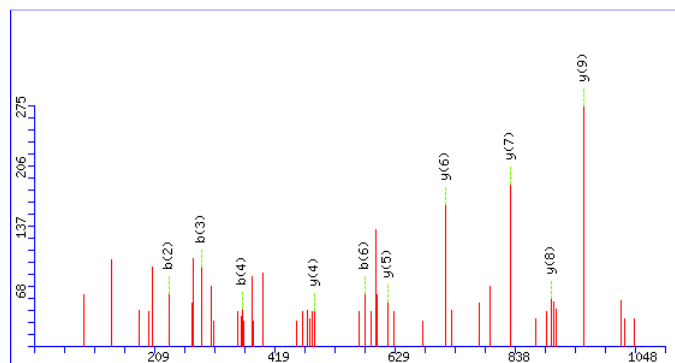
MS/MS Fragmentation of **AYGALTENVTR**:

Found in **IP100513803**

Title: 2.1.1.475.11

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							11
2	235.1077	118.0575	0	0	0	0	Y	1123.5742	562.2907	1106.5477	553.7775	1105.5637	553.2855	10
3	292.1292	146.5682	0	0	0	0	G	960.5109	480.7591	943.4843	472.2458	942.5003	471.7538	9
4	363.1663	182.0868	0	0	0	0	A	903.4894	452.2483	886.4629	443.7351	885.4789	443.2431	8
5	476.2504	238.6288	0	0	0	0	L	832.4523	416.7298	815.4258	408.2165	814.4417	407.7245	7
6	577.2980	289.1527	0	0	559.2875	280.1474	T	719.3682	360.1878	702.3417	351.6745	701.3577	351.1825	6
7	706.3406	353.6740	0	0	688.3301	344.6687	E	618.3206	309.6639	601.2940	301.1506	600.3100	300.6586	5
8	820.3836	410.6954	803.3570	402.1821	802.3730	401.6901	N	489.2780	245.1426	472.2514	236.6293	471.2674	236.1373	4
9	919.4520	460.2296	902.4254	451.7164	901.4414	451.2243	V	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
10	1020.4997	510.7535	1003.4731	502.2402	1002.4891	501.7482	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
11							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 92646.

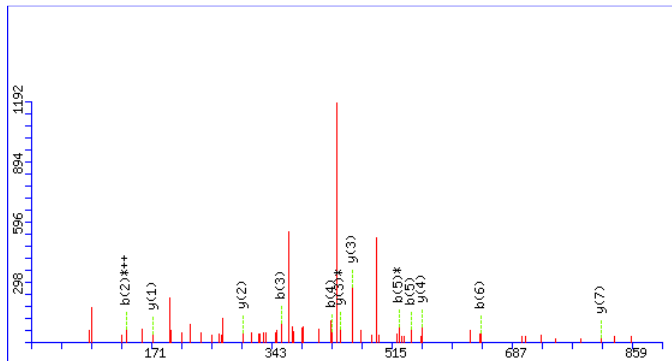
MS/MS Fragmentation of **RMAANVRER**:

Found in **IP100394927**

Title: 1.1.1.6125.2

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_1_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	157.1084	79.0578	140.0818	70.5446	0	0	R							9
2	288.1489	144.5781	271.1223	136.0648	0	0	M	946.4887	473.7480	929.4622	465.2347	928.4781	464.7427	8
3	359.1860	180.0966	342.1594	171.5834	0	0	A	815.4482	408.2278	798.4217	399.7145	797.4377	399.2225	7
4	430.2231	215.6152	413.1966	207.1019	0	0	A	744.4111	372.7092	727.3846	364.1959	726.4005	363.7039	6
5	544.2660	272.6367	527.2395	264.1234	0	0	N	673.3740	337.1906	656.3474	328.6774	655.3634	328.1854	5
6	643.3344	322.1709	626.3079	313.6576	0	0	V	559.3311	280.1692	542.3045	271.6559	541.3205	271.1639	4
7	799.4356	400.2214	782.4090	391.7081	0	0	R	460.2627	230.6350	443.2361	222.1217	442.2521	221.6297	3
8	928.4781	464.7427	911.4516	456.2294	910.4676	455.7374	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
9							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 92649.

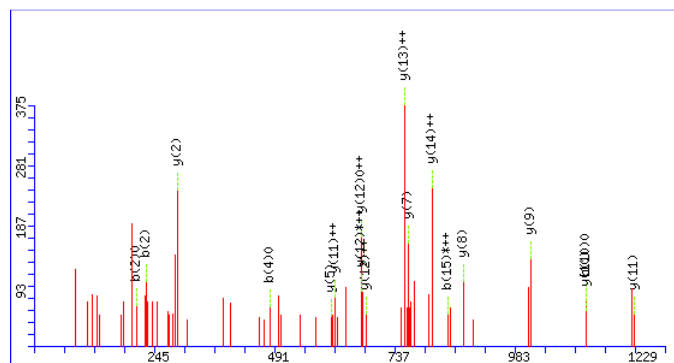
MS/MS Fragmentation of **EVICQVLHLGTVTDFK**: 57.021465@C:4

Found in **IP100013162;IP100465447;IP100946319;IP100971173**

Title: 3.1.1.2641.5

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							16
2	229.1183	115.0628	0	0	211.1077	106.0575	V	1729.9306	865.4689	1712.9040	856.9556	1711.9200	856.4636	15
3	342.2023	171.6048	0	0	324.1918	162.5995	I	1630.8621	815.9347	1613.8356	807.4214	1612.8516	806.9294	14
4	502.2330	251.6201	0	0	484.2224	242.6149	C	1517.7781	759.3927	1500.7515	750.8794	1499.7675	750.3874	13
5	630.2916	315.6494	613.2650	307.1362	612.2810	306.6441	Q	1357.7474	679.3774	1340.7209	670.8641	1339.7369	670.3721	12
6	729.3600	365.1836	712.3334	356.6704	711.3494	356.1784	V	1229.6889	615.3481	1212.6623	606.8348	1211.6783	606.3428	11
7	842.4441	421.7257	825.4175	413.2124	824.4335	412.7204	L	1130.6204	565.8139	1113.5939	557.3006	1112.6099	556.8086	10
8	979.5030	490.2551	962.4764	481.7418	961.4924	481.2498	H	1017.5364	509.2718	1000.5098	500.7585	999.5258	500.2665	9
9	1092.5870	546.7972	1075.5605	538.2839	1074.5765	537.7919	L	880.4775	440.7424	863.4509	432.2291	862.4669	431.7371	8
10	1149.6085	575.3079	1132.5819	566.7946	1131.5979	566.3026	G	767.3934	384.2003	750.3668	375.6871	749.3828	375.1951	7
11	1250.6562	625.8317	1233.6296	617.3184	1232.6456	616.8264	T	710.3719	355.6896	693.3454	347.1763	692.3614	346.6843	6
12	1349.7246	675.3659	1332.6980	666.8527	1331.7140	666.3606	V	609.3243	305.1658	592.2977	296.6525	591.3137	296.1605	5
13	1450.7723	725.8898	1433.7457	717.3765	1432.7617	716.8845	T	510.2558	255.6316	493.2293	247.1183	492.2453	246.6263	4
14	1565.7992	783.4032	1548.7727	774.8900	1547.7886	774.3980	D	409.2082	205.1077	392.1816	196.5944	391.1976	196.1024	3
15	1712.8676	856.9374	1695.8411	848.4242	1694.8571	847.9322	F	294.1812	147.5942	277.1547	139.0810	0	0	2
16							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

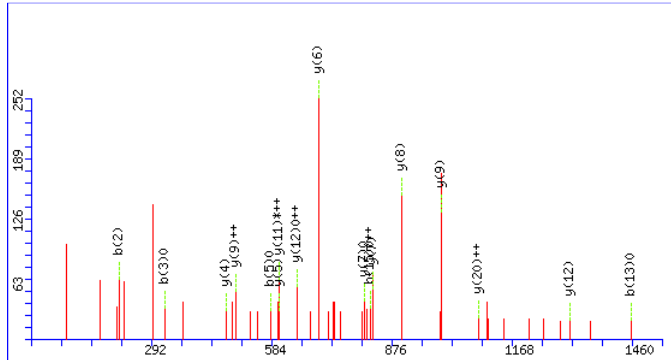
Peptide: 93042.

MS/MS Fragmentation of **LTEEQIEALLHTVTSILPAEPEAEQK: 0.984016@Q:5**
Found in **IP100004477;IP100335708;IP100759701;IP100927312**

Title: 4.1.1.4122.5

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							26
2	215.1390	108.0731	0	0	197.1285	99.0679	T	2777.4091	1389.2082	2760.3826	1380.6949	2759.3986	1380.2029	25
3	344.1816	172.5944	0	0	326.1710	163.5892	E	2676.3614	1338.6844	2659.3349	1330.1711	2658.3509	1329.6791	24
4	473.2242	237.1157	0	0	455.2136	228.1105	E	2547.3188	1274.1631	2530.2923	1265.6498	2529.3083	1265.1578	23
5	602.2668	301.6370	585.2402	293.1238	584.2562	292.6318	Q	2418.2762	1209.6418	2401.2497	1201.1285	2400.2657	1200.6365	22
6	715.3509	358.1791	698.3243	349.6658	697.3403	349.1738	I	2289.2337	1145.1205	2272.2071	1136.6072	2271.2231	1136.1152	21
7	844.3935	422.7004	827.3669	414.1871	826.3829	413.6951	E	2176.1496	1088.5784	2159.1230	1080.0652	2158.1390	1079.5732	20
8	915.4306	458.2189	898.4040	449.7056	897.4200	449.2136	A	2047.1070	1024.0571	2030.0804	1015.5439	2029.0964	1015.0519	19
9	1028.5146	514.7610	1011.4881	506.2477	1010.5041	505.7557	L	1976.0699	988.5386	1959.0433	980.0253	1958.0593	979.5333	18
10	1141.5987	571.3030	1124.5721	562.7897	1123.5881	562.2977	L	1862.9858	931.9965	1845.9593	923.4833	1844.9753	922.9913	17
11	1278.6576	639.8324	1261.6311	631.3192	1260.6470	630.8272	H	1749.9018	875.4545	1732.8752	866.9412	1731.8912	866.4492	16
12	1379.7053	690.3563	1362.6787	681.8430	1361.6947	681.3510	T	1612.8428	806.9251	1595.8163	798.4118	1594.8323	797.9198	15
13	1478.7737	739.8905	1461.7472	731.3772	1460.7631	730.8852	V	1511.7952	756.4012	1494.7686	747.8879	1493.7846	747.3959	14
14	1579.8214	790.4143	1562.7948	781.9011	1561.8108	781.4090	T	1412.7268	706.8670	1395.7002	698.3537	1394.7162	697.8617	13
15	1666.8534	833.9303	1649.8269	825.4171	1648.8428	824.9251	S	1311.6791	656.3432	1294.6525	647.8299	1293.6685	647.3379	12
16	1779.9375	890.4724	1762.9109	881.9591	1761.9269	881.4671	I	1224.6470	612.8272	1207.6205	604.3139	1206.6365	603.8219	11
17	1893.0215	947.0144	1875.9950	938.5011	1875.0110	938.0091	L	1111.5630	556.2851	1094.5364	547.7719	1093.5524	547.2798	10
18	1990.0743	995.5408	1973.0478	987.0275	1972.0637	986.5355	P	998.4789	499.7431	981.4524	491.2298	980.4684	490.7378	9
19	2061.1114	1031.0593	2044.0849	1022.5461	2043.1009	1022.0541	A	901.4262	451.2167	884.3996	442.7034	883.4156	442.2114	8
20	2190.1540	1095.5806	2173.1275	1087.0674	2172.1434	1086.5754	E	830.3890	415.6982	813.3625	407.1849	812.3785	406.6929	7
21	2287.2068	1144.1070	2270.1802	1135.5937	2269.1962	1135.1017	P	701.3464	351.1769	684.3199	342.6636	683.3359	342.1716	6
22	2416.2494	1208.6283	2399.2228	1200.1150	2398.2388	1199.6230	E	604.2937	302.6505	587.2671	294.1372	586.2831	293.6452	5
23	2487.2865	1244.1469	2470.2599	1235.6336	2469.2759	1235.1416	A	475.2511	238.1292	458.2245	229.6159	457.2405	229.1239	4
24	2616.3291	1308.6682	2599.3025	1300.1549	2598.3185	1299.6629	E	404.2140	202.6106	387.1874	194.0974	386.2034	193.6053	3
25	2744.3877	1372.6975	2727.3611	1364.1842	2726.3771	1363.6922	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
26							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 93128.

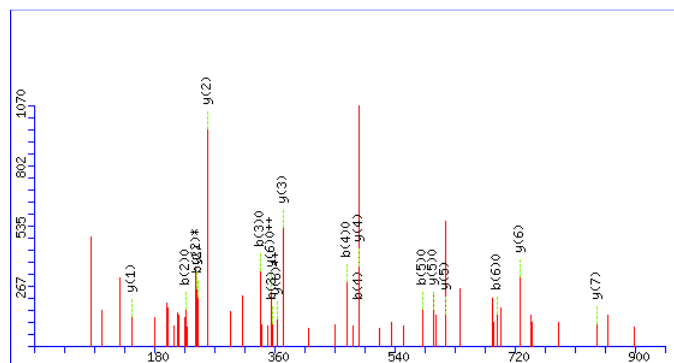
MS/MS Fragmentation of **EDLELINK:**

Found in **IP100010717;IP101010641;IP101014999**

Title: 2.1.1.1305.6

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120208ry¥120208ry_Tig120slc-P8_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							8
2	245.0768	123.0420	0	0	227.0662	114.0368	D	844.4775	422.7424	827.4509	414.2291	826.4669	413.7371	7
3	358.1609	179.5841	0	0	340.1503	170.5788	L	729.4505	365.2289	712.4240	356.7156	711.4400	356.2236	6
4	487.2035	244.1054	0	0	469.1929	235.1001	E	616.3665	308.6869	599.3399	300.1736	598.3559	299.6816	5
5	600.2875	300.6474	0	0	582.2770	291.6421	L	487.3239	244.1656	470.2973	235.6523	0	0	4
6	713.3716	357.1894	0	0	695.3610	348.1842	I	374.2398	187.6235	357.2132	179.1103	0	0	3
7	827.4145	414.2109	810.3880	405.6976	809.4040	405.2056	N	261.1557	131.0815	244.1292	122.5682	0	0	2
8							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 93169.

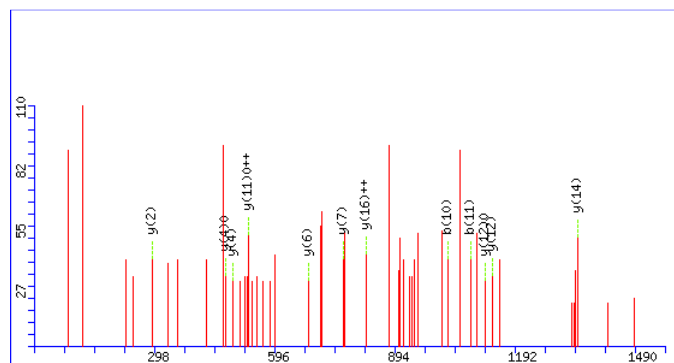
MS/MS Fragmentation of **DDSSGGWLPLGGSQLSSVTVFK**:

Found in **IP100166291**

Title: 4.1.1.622.5

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							22
2	231.0612	116.0342	0	0	213.0506	107.0289	D	2051.0444	1026.0258	2034.0178	1017.5126	2033.0338	1017.0206	21
3	318.0932	159.5502	0	0	300.0826	150.5450	S	1936.0175	968.5124	1918.9909	959.9991	1918.0069	959.5071	20
4	405.1252	203.0662	0	0	387.1147	194.0610	S	1848.9854	924.9964	1831.9589	916.4831	1830.9749	915.9911	19
5	462.1467	231.5770	0	0	444.1361	222.5717	G	1761.9534	881.4803	1744.9268	872.9671	1743.9428	872.4751	18
6	519.1681	260.0877	0	0	501.1576	251.0824	G	1704.9319	852.9696	1687.9054	844.4563	1686.9214	843.9643	17
7	705.2475	353.1274	0	0	687.2369	344.1221	W	1647.9105	824.4589	1630.8839	815.9456	1629.8999	815.4536	16
8	818.3315	409.6694	0	0	800.3210	400.6641	L	1461.8312	731.4192	1444.8046	722.9059	1443.8206	722.4139	15
9	915.3843	458.1958	0	0	897.3737	449.1905	P	1348.7471	674.8772	1331.7205	666.3639	1330.7365	665.8719	14
10	1028.4684	514.7378	0	0	1010.4578	505.7325	L	1251.6943	626.3508	1234.6678	617.8375	1233.6838	617.3455	13
11	1085.4898	543.2485	0	0	1067.4793	534.2433	G	1138.6103	569.8088	1121.5837	561.2955	1120.5997	560.8035	12
12	1142.5113	571.7593	0	0	1124.5007	562.7540	G	1081.5888	541.2980	1064.5623	532.7848	1063.5782	532.2928	11
13	1229.5433	615.2753	0	0	1211.5327	606.2700	S	1024.5673	512.7873	1007.5408	504.2740	1006.5568	503.7820	10
14	1286.5648	643.7860	0	0	1268.5542	634.7807	G	937.5353	469.2713	920.5088	460.7580	919.5247	460.2660	9
15	1399.6488	700.3281	0	0	1381.6383	691.3228	L	880.5138	440.7606	863.4873	432.2473	862.5033	431.7553	8
16	1486.6809	743.8441	0	0	1468.6703	734.8388	S	767.4298	384.2185	750.4032	375.7053	749.4192	375.2132	7
17	1573.7129	787.3601	0	0	1555.7023	778.3548	S	680.3978	340.7025	663.3712	332.1892	662.3872	331.6972	6
18	1672.7813	836.8943	0	0	1654.7707	827.8890	V	593.3657	297.1865	576.3392	288.6732	575.3552	288.1812	5
19	1773.8290	887.4181	0	0	1755.8184	878.4128	T	494.2973	247.6523	477.2708	239.1390	476.2867	238.6470	4
20	1872.8974	936.9523	0	0	1854.8868	927.9471	V	393.2496	197.1285	376.2231	188.6152	0	0	3
21	2019.9658	1010.4865	0	0	2001.9552	1001.4813	F	294.1812	147.5942	277.1547	139.0810	0	0	2
22							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 93199.

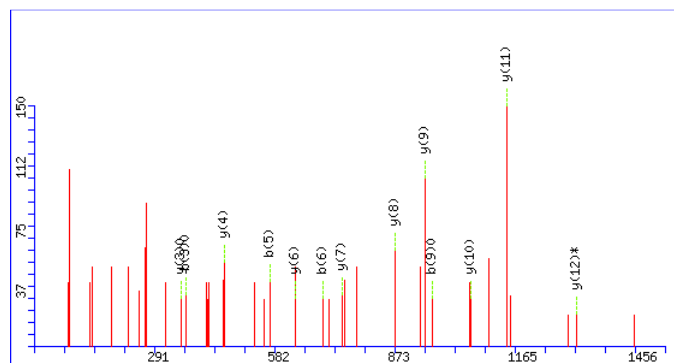
MS/MS Fragmentation of **LWSLAEIATSDLK**:

Found in **IP100395326**

Title: 3.1.1.4155.7

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							13
2	300.1707	150.5890	0	0	0	0	W	1333.6998	667.3535	1316.6733	658.8403	1315.6892	658.3483	12
3	387.2027	194.1050	0	0	369.1921	185.0997	S	1147.6205	574.3139	1130.5939	565.8006	1129.6099	565.3086	11
4	500.2867	250.6470	0	0	482.2762	241.6417	L	1060.5885	530.7979	1043.5619	522.2846	1042.5779	521.7926	10
5	571.3239	286.1656	0	0	553.3133	277.1603	A	947.5044	474.2558	930.4779	465.7426	929.4938	465.2506	9
6	700.3665	350.6869	0	0	682.3559	341.6816	E	876.4673	438.7373	859.4407	430.2240	858.4567	429.7320	8
7	813.4505	407.2289	0	0	795.4400	398.2236	I	747.4247	374.2160	730.3981	365.7027	729.4141	365.2107	7
8	884.4876	442.7475	0	0	866.4771	433.7422	A	634.3406	317.6740	617.3141	309.1607	616.3301	308.6687	6
9	985.5353	493.2713	0	0	967.5247	484.2660	T	563.3035	282.1554	546.2770	273.6421	545.2930	273.1501	5
10	1072.5673	536.7873	0	0	1054.5568	527.7820	S	462.2558	231.6316	445.2293	223.1183	444.2453	222.6263	4
11	1187.5943	594.3008	0	0	1169.5837	585.2955	D	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
12	1300.6783	650.8428	0	0	1282.6678	641.8375	L	260.1969	130.6021	243.1703	122.0888	0	0	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

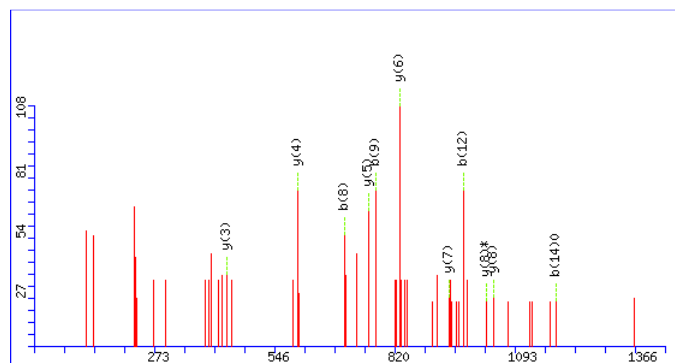
Peptide: 93558.

MS/MS Fragmentation of **GATGHLLGAAGAVEAAFTTLACYQK: 57.021465@C:22**
Found in **IP100016637;IP100922369**

Title: 4.1.1.3399.2

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120208ry¥120208ry_Tig120slc-P8_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							26
2	129.0659	65.0366	0	0	0	0	A	2584.2864	1292.6469	2567.2599	1284.1336	2566.2759	1283.6416	25
3	230.1135	115.5604	0	0	212.1030	106.5551	T	2513.2493	1257.1283	2496.2228	1248.6150	2495.2388	1248.1230	24
4	287.1350	144.0711	0	0	269.1244	135.0659	G	2412.2016	1206.6045	2395.1751	1198.0912	2394.1911	1197.5992	23
5	424.1939	212.6006	0	0	406.1833	203.5953	H	2355.1802	1178.0937	2338.1536	1169.5805	2337.1696	1169.0884	22
6	537.2780	269.1426	0	0	519.2674	260.1373	L	2218.1213	1109.5643	2201.0947	1101.0510	2200.1107	1100.5590	21
7	650.3620	325.6847	0	0	632.3515	316.6794	L	2105.0372	1053.0222	2088.0107	1044.5090	2087.0266	1044.0170	20
8	707.3835	354.1954	0	0	689.3729	345.1901	G	1991.9531	996.4802	1974.9266	987.9669	1973.9426	987.4749	19
9	778.4206	389.7139	0	0	760.4101	380.7087	A	1934.9317	967.9695	1917.9051	959.4562	1916.9211	958.9642	18
10	849.4577	425.2325	0	0	831.4472	416.2272	A	1863.8946	932.4509	1846.8680	923.9376	1845.8840	923.4456	17
11	906.4792	453.7432	0	0	888.4686	444.7380	G	1792.8575	896.9324	1775.8309	888.4191	1774.8469	887.9271	16
12	977.5163	489.2618	0	0	959.5057	480.2565	A	1735.8360	868.4216	1718.8094	859.9084	1717.8254	859.4164	15
13	1076.5847	538.7960	0	0	1058.5742	529.7907	V	1664.7989	832.9031	1647.7723	824.3898	1646.7883	823.8978	14
14	1205.6273	603.3173	0	0	1187.6167	594.3120	E	1565.7305	783.3689	1548.7039	774.8556	1547.7199	774.3636	13
15	1276.6644	638.8359	0	0	1258.6539	629.8306	A	1436.6879	718.8476	1419.6613	710.3343	1418.6773	709.8423	12
16	1347.7015	674.3544	0	0	1329.6910	665.3491	A	1365.6508	683.3290	1348.6242	674.8157	1347.6402	674.3237	11
17	1494.7700	747.8886	0	0	1476.7594	738.8833	F	1294.6136	647.8105	1277.5871	639.2972	1276.6031	638.8052	10
18	1595.8176	798.4125	0	0	1577.8071	789.4072	T	1147.5452	574.2763	1130.5187	565.7630	1129.5347	565.2710	9
19	1696.8653	848.9363	0	0	1678.8547	839.9310	T	1046.4975	523.7524	1029.4710	515.2391	1028.4870	514.7471	8
20	1809.9494	905.4783	0	0	1791.9388	896.4730	L	945.4499	473.2286	928.4233	464.7153	0	0	7
21	1880.9865	940.9969	0	0	1862.9759	931.9916	A	832.3658	416.6865	815.3393	408.1733	0	0	6
22	2041.0171	1021.0122	0	0	2023.0066	1012.0069	C	761.3287	381.1680	744.3021	372.6547	0	0	5
23	2204.0805	1102.5439	0	0	2186.0699	1093.5386	Y	601.2980	301.1527	584.2715	292.6394	0	0	4
24	2367.1438	1184.0755	0	0	2349.1332	1175.0703	Y	438.2347	219.6210	421.2082	211.1077	0	0	3
25	2495.2024	1248.1048	2478.1758	1239.5916	2477.1918	1239.0995	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
26							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 93595.

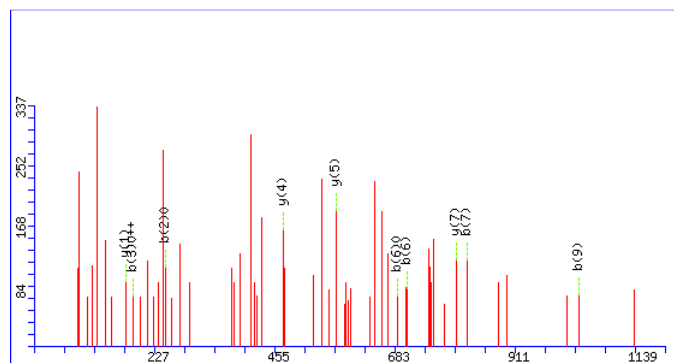
MS/MS Fragmentation of **EHQALQDLVDLAR**:

Found in **IP100291796;IP100412364**

Title: 3.1.1.1390.3

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286	0	0	112.0393	56.5233	E							13
2	267.1088	134.0580	0	0	249.0982	125.0527	H	1378.7437	689.8755	1361.7172	681.3622	1360.7332	680.8702	12
3	395.1674	198.0873	378.1408	189.5740	377.1568	189.0820	Q	1241.6848	621.3461	1224.6583	612.8328	1223.6743	612.3408	11
4	466.2045	233.6059	449.1779	225.0926	448.1939	224.6006	A	1113.6262	557.3168	1096.5997	548.8035	1095.6157	548.3115	10
5	579.2885	290.1479	562.2620	281.6346	561.2780	281.1426	L	1042.5891	521.7982	1025.5626	513.2849	1024.5786	512.7929	9
6	707.3471	354.1772	690.3206	345.6639	689.3366	345.1719	Q	929.5051	465.2562	912.4785	456.7429	911.4945	456.2509	8
7	822.3741	411.6907	805.3475	403.1774	804.3635	402.6854	D	801.4465	401.2269	784.4199	392.7136	783.4359	392.2216	7
8	935.4581	468.2327	918.4316	459.7194	917.4476	459.2274	L	686.4196	343.7134	669.3930	335.2001	668.4090	334.7081	6
9	1034.5265	517.7669	1017.5000	509.2536	1016.5160	508.7616	V	573.3355	287.1714	556.3089	278.6581	555.3249	278.1661	5
10	1149.5535	575.2804	1132.5269	566.7671	1131.5429	566.2751	D	474.2671	237.6372	457.2405	229.1239	456.2565	228.6319	4
11	1262.6375	631.8224	1245.6110	623.3091	1244.6270	622.8171	L	359.2401	180.1237	342.2136	171.6104	0	0	3
12	1333.6747	667.3410	1316.6481	658.8277	1315.6641	658.3357	A	246.1561	123.5817	229.1295	115.0684	0	0	2
13							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 94118.

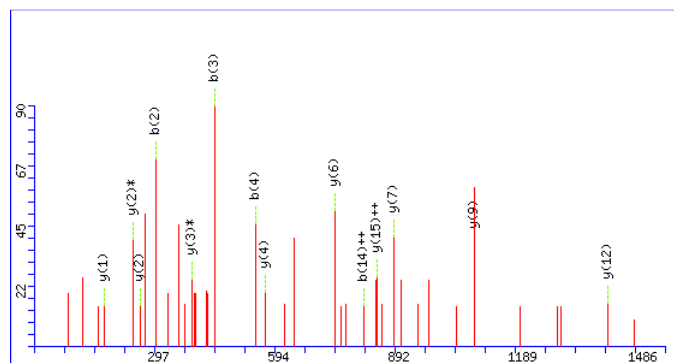
MS/MS Fragmentation of **DWFLPFLPSPDTNPTFATYFSR**:

Found in **IP100302965;IP100477281;IP100879760;IP100924918**

Title: 5.1.1.1021.6

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							23
2	302.1135	151.5604	0	0	284.1030	142.5551	W	2603.2969	1302.1521	2586.2704	1293.6388	2585.2864	1293.1468	22
3	449.1819	225.0946	0	0	431.1714	216.0893	F	2417.2176	1209.1124	2400.1911	1200.5992	2399.2070	1200.1072	21
4	548.2504	274.6288	0	0	530.2398	265.6235	V	2270.1492	1135.5782	2253.1226	1127.0650	2252.1386	1126.5730	20
5	661.3344	331.1709	0	0	643.3239	322.1656	L	2171.0808	1086.0440	2154.0542	1077.5308	2153.0702	1077.0387	19
6	758.3872	379.6972	0	0	740.3766	370.6919	P	2057.9967	1029.5020	2040.9702	1020.9887	2039.9862	1020.4967	18
7	905.4556	453.2314	0	0	887.4450	444.2262	F	1960.9440	980.9756	1943.9174	972.4623	1942.9334	971.9703	17
8	1018.5397	509.7735	0	0	1000.5291	500.7682	L	1813.8755	907.4414	1796.8490	898.9281	1795.8650	898.4361	16
9	1115.5924	558.2999	0	0	1097.5819	549.2946	P	1700.7915	850.8994	1683.7649	842.3861	1682.7809	841.8941	15
10	1202.6245	601.8159	0	0	1184.6139	592.8106	S	1603.7387	802.3730	1586.7122	793.8597	1585.7281	793.3677	14
11	1299.6772	650.3422	0	0	1281.6667	641.3370	P	1516.7067	758.8570	1499.6801	750.3437	1498.6961	749.8517	13
12	1414.7042	707.8557	0	0	1396.6936	698.8504	D	1419.6539	710.3306	1402.6274	701.8173	1401.6434	701.3253	12
13	1515.7518	758.3796	0	0	1497.7413	749.3743	T	1304.6270	652.8171	1287.6004	644.3039	1286.6164	643.8118	11
14	1629.7948	815.4010	1612.7682	806.8877	1611.7842	806.3957	N	1203.5793	602.2933	1186.5528	593.7800	1185.5687	593.2880	10
15	1726.8475	863.9274	1709.8210	855.4141	1708.8370	854.9221	P	1089.5364	545.2718	1072.5098	536.7585	1071.5258	536.2665	9
16	1827.8952	914.4512	1810.8687	905.9380	1809.8846	905.4460	T	992.4836	496.7454	975.4571	488.2322	974.4730	487.7402	8
17	1974.9636	987.9855	1957.9371	979.4722	1956.9531	978.9802	F	891.4359	446.2216	874.4094	437.7083	873.4254	437.2163	7
18	2046.0007	1023.5040	2028.9742	1014.9907	2027.9902	1014.4987	A	744.3675	372.6874	727.3410	364.1741	726.3570	363.6821	6
19	2147.0484	1074.0278	2130.0219	1065.5146	2129.0379	1065.0226	T	673.3304	337.1688	656.3039	328.6556	655.3198	328.1636	5
20	2310.1118	1155.5595	2293.0852	1147.0462	2292.1012	1146.5542	Y	572.2827	286.6450	555.2562	278.1317	554.2722	277.6397	4
21	2457.1802	1229.0937	2440.1536	1220.5804	2439.1696	1220.0884	F	409.2194	205.1133	392.1928	196.6001	391.2088	196.1081	3
22	2544.2122	1272.6097	2527.1856	1264.0965	2526.2016	1263.6045	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
23							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 94418.

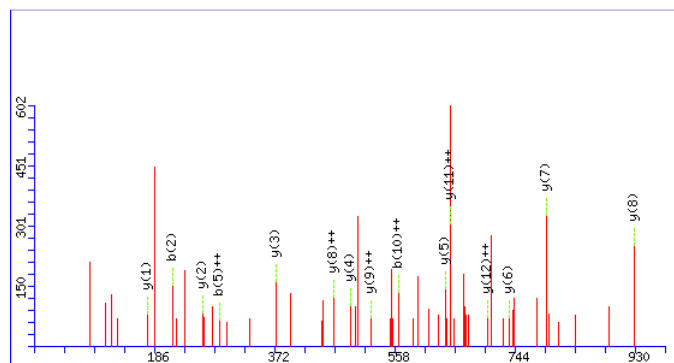
MS/MS Fragmentation of **TLCSLHGVFDLSR: 57.021465@C:3**

Found in **IP100025276;IP100644296;IP100892681;IP100895929;IP100941929;IP100942649;IP100946340**

Title: 3.1.1.318.2

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120212ry¥120212ry_aHDF1388-P9_2_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							13
2	215.1390	108.0731	0	0	197.1285	99.0679	L	1403.7100	702.3586	1386.6834	693.8454	1385.6994	693.3534	12
3	375.1697	188.0885	0	0	357.1591	179.0832	C	1290.6259	645.8166	1273.5994	637.3033	1272.6154	636.8113	11
4	462.2017	231.6045	0	0	444.1911	222.5992	S	1130.5953	565.8013	1113.5687	557.2880	1112.5847	556.7960	10
5	575.2858	288.1465	0	0	557.2752	279.1412	L	1043.5633	522.2853	1026.5367	513.7720	1025.5527	513.2800	9
6	712.3447	356.6760	0	0	694.3341	347.6707	H	930.4792	465.7432	913.4526	457.2300	912.4686	456.7380	8
7	769.3661	385.1867	0	0	751.3556	376.1814	G	793.4203	397.2138	776.3937	388.7005	775.4097	388.2085	7
8	868.4346	434.7209	0	0	850.4240	425.7156	V	736.3988	368.7030	719.3723	360.1898	718.3883	359.6978	6
9	1015.5030	508.2551	0	0	997.4924	499.2498	F	637.3304	319.1688	620.3039	310.6556	619.3198	310.1636	5
10	1130.5299	565.7686	0	0	1112.5193	556.7633	D	490.2620	245.6346	473.2354	237.1214	472.2514	236.6293	4
11	1243.6140	622.3106	0	0	1225.6034	613.3053	L	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
12	1330.6460	665.8266	0	0	1312.6354	656.8214	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
13							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: **94638**.

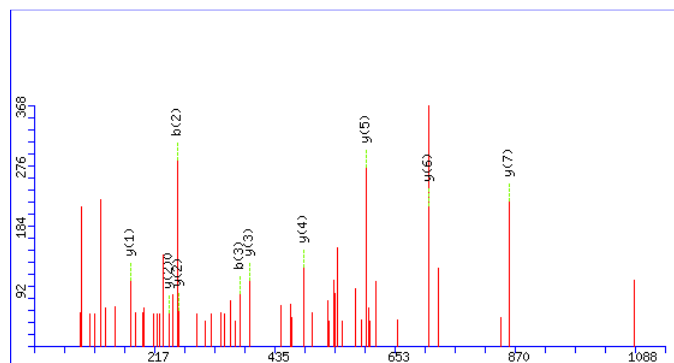
MS/MS Fragmentation of **IFLLVQSR**:

Found in **IP100550571,IP100908756**

Title: 2.1.1.4363.2

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							8
2	261.1598	131.0835	0	0	0	0	F	862.5145	431.7609	845.4880	423.2476	844.5039	422.7556	7
3	374.2438	187.6255	0	0	0	0	L	715.4461	358.2267	698.4196	349.7134	697.4355	349.2214	6
4	487.3279	244.1676	0	0	0	0	L	602.3620	301.6847	585.3355	293.1714	584.3515	292.6794	5
5	586.3963	293.7018	0	0	0	0	V	489.2780	245.1426	472.2514	236.6293	471.2674	236.1373	4
6	714.4549	357.7311	697.4283	349.2178	0	0	Q	390.2096	195.6084	373.1830	187.0951	372.1990	186.6031	3
7	801.4869	401.2471	784.4604	392.7338	783.4763	392.2418	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
8							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: **94777**.

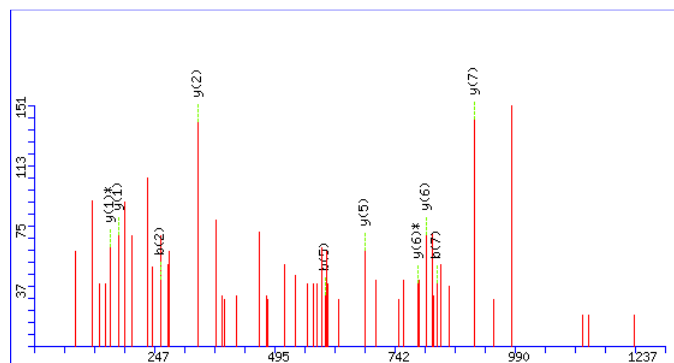
MS/MS Fragmentation of **FLVLDDYR**:

Found in **IP100306934;IP100908844;IP100963917;IP100964312;IP100964489;IP100965187;IP100965692;IP100967163;IP100967568;IP100967808**

Title: 3.1.1.364.4

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120129ry¥120129ry_604A1-46_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	148.0757	74.5415	0	0	0	0	F							9
2	261.1598	131.0835	0	0	0	0	L	1021.5313	511.2693	1004.5047	502.7560	1003.5207	502.2640	8
3	360.2282	180.6177	0	0	0	0	V	908.4472	454.7272	891.4207	446.2140	890.4367	445.7220	7
4	488.2867	244.6470	471.2602	236.1337	0	0	Q	809.3788	405.1930	792.3523	396.6798	791.3682	396.1878	6
5	601.3708	301.1890	584.3443	292.6758	0	0	L	681.3202	341.1638	664.2937	332.6505	663.3097	332.1585	5
6	716.3978	358.7025	699.3712	350.1892	698.3872	349.6972	D	568.2362	284.6217	551.2096	276.1084	550.2256	275.6164	4
7	831.4247	416.2160	814.3981	407.7027	813.4141	407.2107	D	453.2092	227.1082	436.1827	218.5950	435.1987	218.1030	3
8	994.4880	497.7477	977.4615	489.2344	976.4775	488.7424	Y	338.1823	169.5948	321.1557	161.0815	0	0	2
9							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 94801.

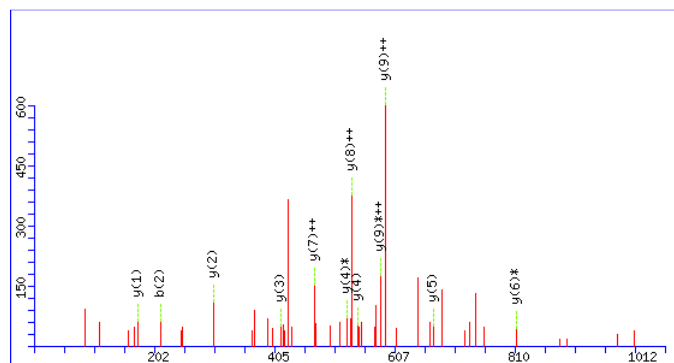
MS/MS Fragmentation of **VNELREELQR**:

Found in **IP100013070,IP100167147,IP100258093,IP100402391**

Title: 1.1.1.9238.6

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_2_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							10
2	214.1188	107.5629	197.0921	99.0497	0	0	N	1186.6175	593.8124	1169.5909	585.2991	1168.6069	584.8071	9
3	343.1612	172.0842	326.1347	163.5710	325.1506	163.0790	E	1072.5745	536.7909	1055.5480	528.2776	1054.5640	527.7856	8
4	456.2453	228.6263	439.2187	220.1130	438.2347	219.6210	L	943.5320	472.2696	926.5054	463.7563	925.5214	463.2643	7
5	612.3464	306.6768	595.3198	298.1636	594.3358	297.6715	R	830.4479	415.7276	813.4213	407.2143	812.4373	406.7223	6
6	741.3890	371.1981	724.3624	362.6849	723.3784	362.1928	E	674.3468	337.6770	657.3202	329.1638	656.3362	328.6717	5
7	870.4316	435.7194	853.4050	427.2061	852.4210	426.7141	E	545.3042	273.1557	528.2776	264.6425	527.2936	264.1504	4
8	983.5156	492.2615	966.4891	483.7482	965.5051	483.2562	L	416.2616	208.6344	399.2350	200.1212	0	0	3
9	1111.5742	556.2907	1094.5477	547.7775	1093.5636	547.2855	Q	303.1775	152.0924	286.1510	143.5791	0	0	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 95313.

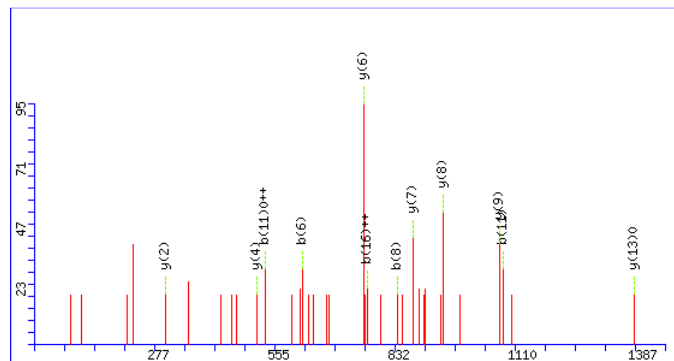
MS/MS Fragmentation of **HVSAPEFATSGVAAVLAGTTEAIFTPLER**:

Found in **IP100009807**

Title: 4.1.1.4606.7

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	138.0662	69.5367	0	0	0	0	H							29
2	237.1346	119.0709	0	0	0	0	V	2805.4669	1403.2371	2788.4404	1394.7238	2787.4563	1394.2318	28
3	324.1666	162.5870	0	0	306.1561	153.5817	S	2706.3985	1353.7029	2689.3719	1345.1896	2688.3879	1344.6976	27
4	395.2037	198.1055	0	0	377.1932	189.1002	A	2619.3665	1310.1869	2602.3399	1301.6736	2601.3559	1301.1816	26
5	492.2565	246.6319	0	0	474.2459	237.6266	P	2548.3293	1274.6683	2531.3028	1266.1550	2530.3188	1265.6630	25
6	621.2991	311.1532	0	0	603.2885	302.1479	E	2451.2766	1226.1419	2434.2500	1217.6287	2433.2660	1217.1366	24
7	768.3675	384.6874	0	0	750.3570	375.6821	F	2322.2340	1161.6206	2305.2074	1153.1074	2304.2234	1152.6154	23
8	839.4046	420.2060	0	0	821.3941	411.2007	A	2175.1656	1088.0864	2158.1390	1079.5732	2157.1550	1079.0811	22
9	940.4523	470.7298	0	0	922.4417	461.7245	T	2104.1285	1052.5679	2087.1019	1044.0546	2086.1179	1043.5626	21
10	1027.4843	514.2458	0	0	1009.4738	505.2405	S	2003.0808	1002.0440	1986.0542	993.5308	1985.0702	993.0387	20
11	1084.5058	542.7565	0	0	1066.4952	533.7513	G	1916.0488	958.5280	1899.0222	950.0147	1898.0382	949.5227	19
12	1183.5742	592.2907	0	0	1165.5636	583.2855	V	1859.0273	930.0173	1842.0007	921.5040	1841.0167	921.0120	18
13	1254.6113	627.8093	0	0	1236.6008	618.8040	A	1759.9589	880.4831	1742.9323	871.9698	1741.9483	871.4778	17
14	1325.6484	663.3279	0	0	1307.6379	654.3226	A	1688.9218	844.9645	1671.8952	836.4512	1670.9112	835.9592	16
15	1424.7169	712.8621	0	0	1406.7063	703.8568	V	1617.8847	809.4460	1600.8581	800.9327	1599.8741	800.4407	15
16	1537.8009	769.4041	0	0	1519.7904	760.3988	L	1518.8162	759.9118	1501.7897	751.3985	1500.8057	750.9065	14
17	1608.8380	804.9227	0	0	1590.8275	795.9174	A	1405.7322	703.3697	1388.7056	694.8564	1387.7216	694.3644	13
18	1665.8595	833.4334	0	0	1647.8489	824.4281	G	1334.6951	667.8512	1317.6685	659.3379	1316.6845	658.8459	12
19	1766.9072	883.9572	0	0	1748.8966	874.9519	T	1277.6736	639.3404	1260.6470	630.8272	1259.6630	630.3352	11
20	1867.9549	934.4811	0	0	1849.9443	925.4758	T	1176.6259	588.8166	1159.5994	580.3033	1158.6154	579.8113	10
21	1996.9974	999.0024	0	0	1978.9869	989.9971	E	1075.5782	538.2928	1058.5517	529.7795	1057.5677	529.2875	9
22	2068.0346	1034.5209	0	0	2050.0240	1025.5156	A	946.5356	473.7715	929.5091	465.2582	928.5251	464.7662	8
23	2181.1186	1091.0630	0	0	2163.1081	1082.0577	I	875.4985	438.2529	858.4720	429.7396	857.4880	429.2476	7
24	2328.1870	1164.5972	0	0	2310.1765	1155.5919	F	762.4145	381.7109	745.3879	373.1976	744.4039	372.7056	6
25	2429.2347	1215.1210	0	0	2411.2242	1206.1157	T	615.3461	308.1767	598.3195	299.6634	597.3355	299.1714	5
26	2526.2875	1263.6474	0	0	2508.2769	1254.6421	P	514.2984	257.6528	497.2718	249.1395	496.2878	248.6475	4
27	2639.3715	1320.1894	0	0	2621.3610	1311.1841	L	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
28	2768.4141	1384.7107	0	0	2750.4036	1375.7054	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
29							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 95398.

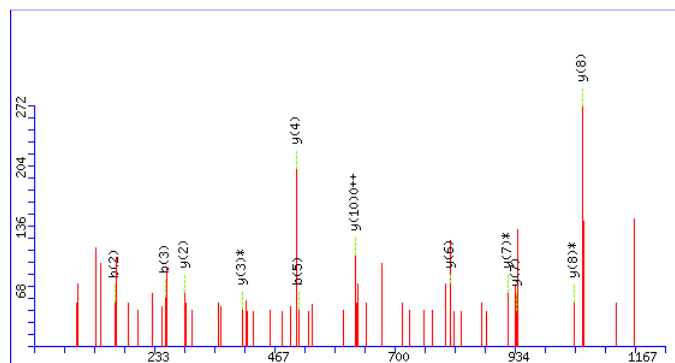
MS/MS Fragmentation of **GVVEWLSEFK**:

Found in **IP100102291;IP100910812;IP100915994;IP100917287**

Title: 4.1.1.1251.3

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120212ry¥120212ry_aHDF1388-P9_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							11
2	157.0972	79.0522	0	0	0	0	V	1265.6412	633.3243	1248.6147	624.8110	1247.6307	624.3190	10
3	256.1656	128.5864	0	0	0	0	V	1166.5728	583.7900	1149.5463	575.2768	1148.5623	574.7848	9
4	385.2082	193.1077	0	0	367.1976	184.1024	E	1067.5044	534.2558	1050.4779	525.7426	1049.4938	525.2506	8
5	514.2508	257.6290	0	0	496.2402	248.6237	E	938.4618	469.7345	921.4353	461.2213	920.4512	460.7293	7
6	700.3301	350.6687	0	0	682.3195	341.6634	W	809.4192	405.2132	792.3927	396.7000	791.4087	396.2080	6
7	813.4141	407.2107	0	0	795.4036	398.2054	L	623.3399	312.1736	606.3134	303.6603	605.3293	303.1683	5
8	900.4462	450.7267	0	0	882.4356	441.7214	S	510.2558	255.6316	493.2293	247.1183	492.2453	246.6263	4
9	1029.4888	515.2480	0	0	1011.4782	506.2427	E	423.2238	212.1155	406.1973	203.6023	405.2132	203.1103	3
10	1176.5572	588.7822	0	0	1158.5466	579.7769	F	294.1812	147.5942	277.1547	139.0810	0	0	2
11							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 95571.

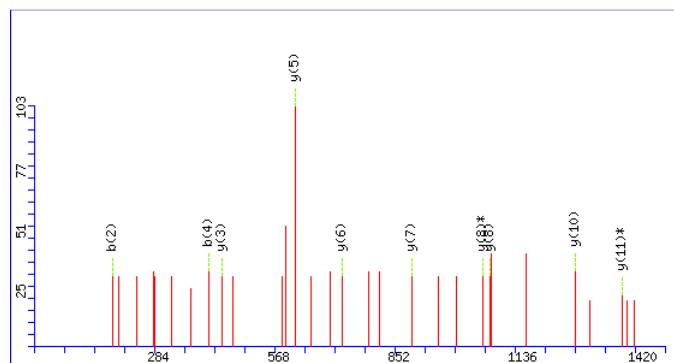
MS/MS Fragmentation of **GQQVLGLVENQSDWYLGNLWK:**

Found in **IP100029050;IP100607752;IP100880187;IP100889585**

Title: 4.1.1.1979.8

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							21
2	186.0873	93.5473	169.0608	85.0340	0	0	Q	2390.2139	1195.6106	2373.1874	1187.0973	2372.2034	1186.6053	20
3	314.1459	157.5766	297.1193	149.0633	0	0	Q	2262.1553	1131.5813	2245.1288	1123.0680	2244.1448	1122.5760	19
4	413.2143	207.1108	396.1878	198.5975	0	0	V	2134.0968	1067.5520	2117.0702	1059.0387	2116.0862	1058.5467	18
5	526.2984	263.6528	509.2718	255.1396	0	0	L	2035.0284	1018.0178	2018.0018	1009.5045	2017.0178	1009.0125	17
6	583.3198	292.1636	566.2933	283.6503	0	0	G	1921.9443	961.4758	1904.9177	952.9625	1903.9337	952.4705	16
7	696.4039	348.7056	679.3774	340.1923	0	0	L	1864.9228	932.9651	1847.8963	924.4518	1846.9123	923.9598	15
8	795.4723	398.2398	778.4458	389.7265	0	0	V	1751.8388	876.4230	1734.8122	867.9097	1733.8282	867.4177	14
9	924.5149	462.7611	907.4884	454.2478	906.5043	453.7558	E	1652.7703	826.8888	1635.7438	818.3755	1634.7598	817.8835	13
10	1038.5578	519.7826	1021.5313	511.2693	1020.5473	510.7773	N	1523.7278	762.3675	1506.7012	753.8542	1505.7172	753.3622	12
11	1166.6164	583.8118	1149.5899	575.2986	1148.6058	574.8066	Q	1409.6848	705.3461	1392.6583	696.8328	1391.6743	696.3408	11
12	1253.6484	627.3279	1236.6219	618.8146	1235.6379	618.3226	S	1281.6262	641.3168	1264.5997	632.8035	1263.6157	632.3115	10
13	1368.6754	684.8413	1351.6488	676.3281	1350.6648	675.8360	D	1194.5942	597.8007	1177.5677	589.2875	1176.5837	588.7955	9
14	1554.7547	777.8810	1537.7281	769.3677	1536.7441	768.8757	W	1079.5673	540.2873	1062.5407	531.7740	0	0	8
15	1717.8180	859.4127	1700.7915	850.8994	1699.8075	850.4074	Y	893.4880	447.2476	876.4614	438.7343	0	0	7
16	1830.9021	915.9547	1813.8755	907.4414	1812.8915	906.9494	L	730.4246	365.7160	713.3981	357.2027	0	0	6
17	1887.9236	944.4654	1870.8970	935.9521	1869.9130	935.4601	G	617.3406	309.1739	600.3140	300.6606	0	0	5
18	2001.9665	1001.4869	1984.9399	992.9736	1983.9559	992.4816	N	560.3191	280.6632	543.2926	272.1499	0	0	4
19	2115.0505	1058.0289	2098.0240	1049.5156	2097.0400	1049.0236	L	446.2762	223.6417	429.2496	215.1285	0	0	3
20	2301.1299	1151.0686	2284.1033	1142.5553	2283.1193	1142.0633	W	333.1921	167.0997	316.1656	158.5864	0	0	2
21							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 95619.

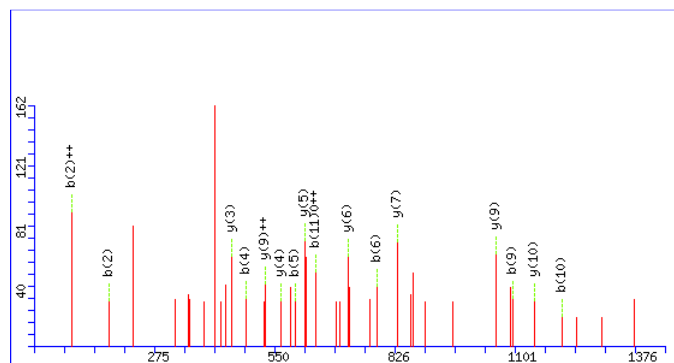
MS/MS Fragmentation of **GLEWLSPQIVGLYNR**:

Found in **IP100026952**

Title: 4.1.1.2349.4

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							16
2	171.1128	86.0600	0	0	0	0	L	1873.9959	937.5016	1856.9694	928.9883	1855.9854	928.4963	15
3	300.1554	150.5813	0	0	282.1448	141.5761	E	1760.9119	880.9596	1743.8853	872.4463	1742.9013	871.9543	14
4	486.2347	243.6210	0	0	468.2241	234.6157	W	1631.8693	816.4383	1614.8427	807.9250	1613.8587	807.4330	13
5	599.3188	300.1630	0	0	581.3082	291.1577	L	1445.7900	723.3986	1428.7634	714.8853	1427.7794	714.3933	12
6	785.3981	393.2027	0	0	767.3875	384.1974	W	1332.7059	666.8566	1315.6793	658.3433	1314.6953	657.8513	11
7	872.4301	436.7187	0	0	854.4196	427.7134	S	1146.6266	573.8169	1129.6000	565.3037	1128.6160	564.8116	10
8	969.4829	485.2451	0	0	951.4723	476.2398	P	1059.5946	530.3009	1042.5680	521.7876	0	0	9
9	1097.5415	549.2744	1080.5149	540.7611	1079.5309	540.2691	Q	962.5418	481.7745	945.5152	473.2613	0	0	8
10	1210.6255	605.8164	1193.5990	597.3031	1192.6150	596.8111	I	834.4832	417.7452	817.4567	409.2320	0	0	7
11	1309.6939	655.3506	1292.6674	646.8373	1291.6834	646.3453	V	721.3991	361.2032	704.3726	352.6899	0	0	6
12	1366.7154	683.8613	1349.6888	675.3481	1348.7048	674.8561	G	622.3307	311.6690	605.3042	303.1557	0	0	5
13	1479.7995	740.4034	1462.7729	731.8901	1461.7889	731.3981	L	565.3093	283.1583	548.2827	274.6450	0	0	4
14	1642.8628	821.9350	1625.8362	813.4218	1624.8522	812.9298	Y	452.2252	226.6162	435.1987	218.1030	0	0	3
15	1756.9057	878.9565	1739.8792	870.4432	1738.8952	869.9512	N	289.1619	145.0846	272.1353	136.5713	0	0	2
16							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 95901.

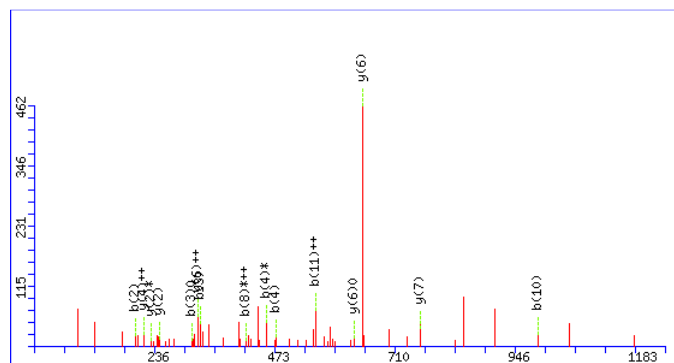
MS/MS Fragmentation of **SIKMEASSSGITNGKTK: 15.994915@M:4**

Found in **IP100921990**

Title: 5.1.1.3109.2

Data file: Y:\TT5600(CiRA1)\2012-01\120126ry\120126ry_585A1-55_1_5.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							17
2	201.1234	101.0653	0	0	183.1128	92.0600	I	1667.8633	834.4353	1650.8367	825.9220	1649.8527	825.4300	16
3	329.2183	165.1128	312.1918	156.5995	311.2078	156.1075	K	1554.7792	777.8932	1537.7526	769.3800	1536.7686	768.8880	15
4	476.2537	238.6305	459.2272	230.1172	458.2432	229.6252	M	1426.6842	713.8458	1409.6577	705.3325	1408.6737	704.8405	14
5	605.2963	303.1518	588.2698	294.6385	587.2858	294.1465	E	1279.6488	640.3281	1262.6223	631.8148	1261.6383	631.3228	13
6	676.3334	338.6704	659.3069	330.1571	658.3229	329.6651	A	1150.6062	575.8068	1133.5797	567.2935	1132.5957	566.8015	12
7	763.3655	382.1864	746.3389	373.6731	745.3549	373.1811	S	1079.5691	540.2882	1062.5426	531.7749	1061.5586	531.2829	11
8	850.3975	425.7024	833.3709	417.1891	832.3869	416.6971	S	992.5371	496.7722	975.5106	488.2589	974.5265	487.7669	10
9	937.4295	469.2184	920.4030	460.7051	919.4190	460.2131	S	905.5051	453.2562	888.4785	444.7429	887.4945	444.2509	9
10	994.4510	497.7291	977.4244	489.2159	976.4404	488.7238	G	818.4730	409.7402	801.4465	401.2269	800.4625	400.7349	8
11	1107.5351	554.2712	1090.5085	545.7579	1089.5245	545.2659	I	761.4516	381.2294	744.4250	372.7162	743.4410	372.2241	7
12	1208.5827	604.7950	1191.5562	596.2817	1190.5722	595.7897	T	648.3675	324.6874	631.3410	316.1741	630.3570	315.6821	6
13	1322.6257	661.8165	1305.5991	653.3032	1304.6151	652.8112	N	547.3198	274.1636	530.2933	265.6503	529.3093	265.1583	5
14	1379.6471	690.3272	1362.6206	681.8139	1361.6366	681.3219	G	433.2769	217.1421	416.2504	208.6288	415.2663	208.1368	4
15	1507.7421	754.3747	1490.7155	745.8614	1489.7315	745.3694	K	376.2554	188.6314	359.2289	180.1181	358.2449	179.6261	3
16	1608.7898	804.8985	1591.7632	796.3852	1590.7792	795.8932	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
17							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 96527.

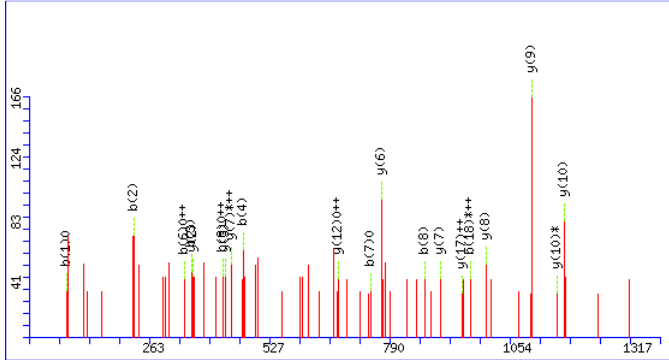
MS/MS Fragmentation of **TQQLLLATLQEAATTQENVAWR**:

Found in **IPI00978059**

Title: 4.1.1.1217.7

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_3_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							22
2	230.1135	115.5604	213.0870	107.0471	212.1030	106.5551	Q	2384.2569	1192.6321	2367.2303	1184.1188	2366.2463	1183.6268	21
3	358.1721	179.5897	341.1456	171.0764	340.1615	170.5844	Q	2256.1983	1128.6028	2239.1717	1120.0895	2238.1877	1119.5975	20
4	471.2562	236.1317	454.2296	227.6185	453.2456	227.1264	L	2128.1397	1064.5735	2111.1131	1056.0602	2110.1291	1055.5682	19
5	584.3402	292.6738	567.3137	284.1605	566.3297	283.6685	L	2015.0556	1008.0315	1998.0291	999.5182	1997.0451	999.0262	18
6	697.4243	349.2158	680.3978	340.7025	679.4137	340.2105	L	1901.9716	951.4894	1884.9450	942.9761	1883.9610	942.4841	17
7	768.4614	384.7343	751.4349	376.2211	750.4509	375.7291	A	1788.8875	894.9474	1771.8610	886.4341	1770.8769	885.9421	16
8	869.5091	435.2582	852.4825	426.7449	851.4985	426.2529	T	1717.8504	859.4288	1700.8238	850.9156	1699.8398	850.4236	15
9	982.5932	491.8002	965.5666	483.2869	964.5826	482.7949	L	1616.8027	808.9050	1599.7762	800.3917	1598.7921	799.8997	14
10	1110.6517	555.8295	1093.6252	547.3162	1092.6412	546.8242	Q	1503.7186	752.3630	1486.6921	743.8497	1485.7081	743.3577	13
11	1239.6943	620.3508	1222.6678	611.8375	1221.6838	611.3455	E	1375.6601	688.3337	1358.6335	679.8204	1357.6495	679.3284	12
12	1310.7314	655.8694	1293.7049	647.3561	1292.7209	646.8641	A	1246.6175	623.8124	1229.5909	615.2991	1228.6069	614.8071	11
13	1381.7686	691.3879	1364.7420	682.8746	1363.7580	682.3826	A	1175.5804	588.2938	1158.5538	579.7805	1157.5698	579.2885	10
14	1482.8162	741.9118	1465.7897	733.3985	1464.8057	732.9065	T	1104.5432	552.7753	1087.5167	544.2620	1086.5327	543.7700	9
15	1583.8639	792.4356	1566.8374	783.9223	1565.8534	783.4303	T	1003.4956	502.2514	986.4690	493.7381	985.4850	493.2461	8
16	1711.9225	856.4649	1694.8959	847.9516	1693.9119	847.4596	Q	902.4479	451.7276	885.4213	443.2143	884.4373	442.7223	7
17	1840.9651	920.9862	1823.9385	912.4729	1822.9545	911.9809	E	774.3893	387.6983	757.3628	379.1850	756.3787	378.6930	6
18	1955.0080	978.0076	1937.9815	969.4944	1936.9975	969.0024	N	645.3467	323.1770	628.3202	314.6637	0	0	5
19	2054.0764	1027.5419	2037.0499	1019.5286	2036.0659	1018.5366	V	531.3038	266.1555	514.2772	257.6423	0	0	4
20	2125.1135	1063.0604	2108.0870	1054.5471	2107.1030	1054.0551	A	432.2354	216.6213	415.2088	208.1081	0	0	3
21	2311.1929	1156.1001	2294.1663	1147.5868	2293.1823	1147.0948	W	361.1983	181.1028	344.1717	172.5895	0	0	2
22							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: **96582**.

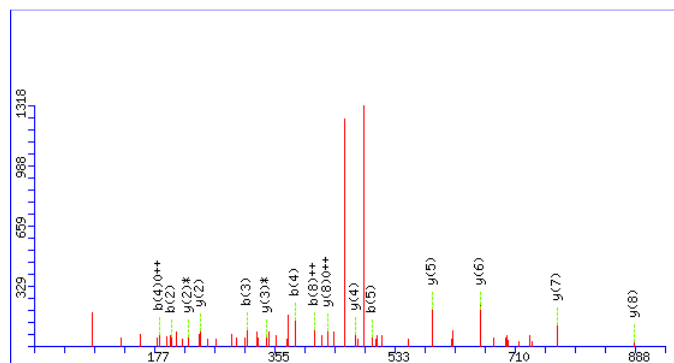
MS/MS Fragmentation of **SDIAIDVVK**:

Found in **IP100183750;IP100410484**

Title: 1.1.1.9509.7

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_2_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							9
2	203.0662	102.0368	0	0	185.0557	93.0315	D	888.4673	444.7373	871.4407	436.2240	870.4567	435.7320	8
3	316.1503	158.5788	0	0	298.1397	149.5735	I	773.4403	387.2238	756.4138	378.7105	755.4298	378.2185	7
4	387.1874	194.0974	0	0	369.1769	185.0921	A	660.3563	330.6818	643.3297	322.1685	642.3457	321.6765	6
5	500.2715	250.6394	0	0	482.2609	241.6341	I	589.3192	295.1632	572.2926	286.6499	571.3086	286.1579	5
6	615.2984	308.1529	0	0	597.2879	299.1476	D	476.2351	238.6212	459.2086	230.1079	458.2245	229.6159	4
7	730.3254	365.6663	0	0	712.3148	356.6610	D	361.2082	181.1077	344.1816	172.5944	343.1976	172.1024	3
8	829.3938	415.2005	0	0	811.3832	406.1953	V	246.1812	123.5942	229.1547	115.0810	0	0	2
9							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 96606.

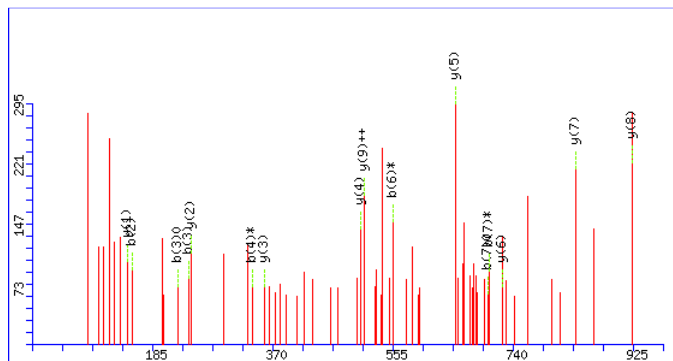
MS/MS Fragmentation of **GPSNAFFLVK**:

Found in **IP100216204;IP100410573;IP100410574**

Title: 2.1.1.4211.4

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							10
2	155.0815	78.0444	0	0	0	0	P	1022.5669	511.7871	1005.5404	503.2738	1004.5564	502.7818	9
3	242.1135	121.5604	0	0	224.1030	112.5551	S	925.5142	463.2607	908.4876	454.7475	907.5036	454.2554	8
4	356.1565	178.5819	339.1299	170.0686	338.1459	169.5766	N	838.4822	419.7447	821.4556	411.2314	0	0	7
5	427.1936	214.1004	410.1670	205.5871	409.1830	205.0951	A	724.4392	362.7232	707.4127	354.2100	0	0	6
6	574.2620	287.6346	557.2354	279.1214	556.2514	278.6293	F	653.4021	327.2047	636.3756	318.6914	0	0	5
7	721.3304	361.1688	704.3039	352.6556	703.3198	352.1636	F	506.3337	253.6705	489.3071	245.1572	0	0	4
8	834.4145	417.7109	817.3879	409.1976	816.4039	408.7056	L	359.2653	180.1363	342.2387	171.6230	0	0	3
9	933.4829	467.2451	916.4563	458.7318	915.4723	458.2398	V	246.1812	123.5942	229.1547	115.0810	0	0	2
10							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 96685.

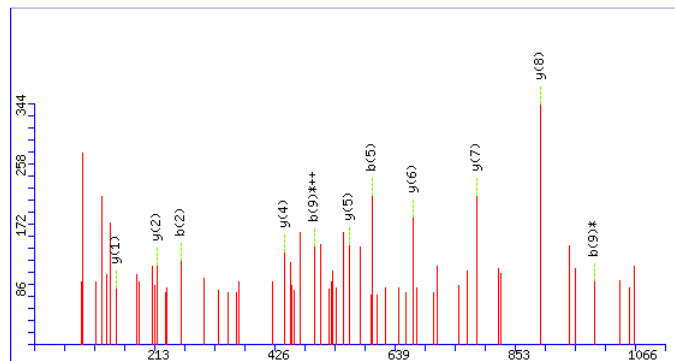
MS/MS Fragmentation of **YPLLLDNIAK**:

Found in **IP100022164,IP100339353**

Title: 3.1.1.1133.4

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_2.3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	164.0706	82.5389	0	0	0	0	Y							10
2	261.1234	131.0653	0	0	0	0	P	996.6088	498.8080	979.5823	490.2948	978.5982	489.8028	9
3	374.2074	187.6074	0	0	0	0	L	899.5560	450.2817	882.5295	441.7684	881.5455	441.2764	8
4	487.2915	244.1494	0	0	0	0	L	786.4720	393.7396	769.4454	385.2264	768.4614	384.7343	7
5	600.3756	300.6914	0	0	0	0	L	673.3879	337.1976	656.3614	328.6843	655.3774	328.1923	6
6	715.4025	358.2049	0	0	697.3919	349.1996	D	560.3039	280.6556	543.2773	272.1423	542.2933	271.6503	5
7	829.4454	415.2264	812.4189	406.7131	811.4349	406.2211	N	445.2769	223.1421	428.2504	214.6288	0	0	4
8	942.5295	471.7684	925.5029	463.2551	924.5189	462.7631	I	331.2340	166.1206	314.2074	157.6074	0	0	3
9	1013.5666	507.2869	996.5401	498.7737	995.5560	498.2817	A	218.1499	109.5786	201.1234	101.0653	0	0	2
10							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 96837.

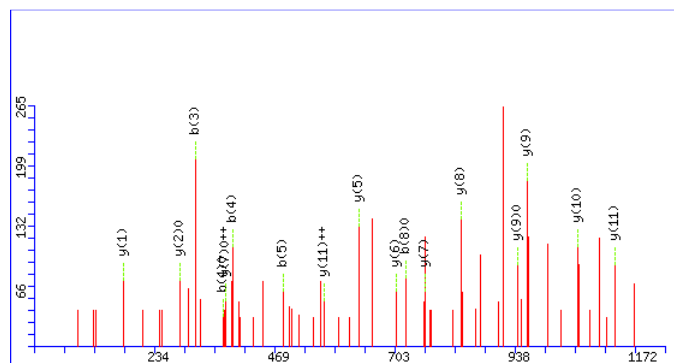
MS/MS Fragmentation of **SDLAVEAGAPYAER**:

Found in **IP100056478;IP100186736;IP100386204**

Title: 2.1.1.1442.11

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							14
2	203.0662	102.0368	0	0	185.0557	93.0315	D	1361.6696	681.3384	1344.6430	672.8251	1343.6590	672.3331	13
3	316.1503	158.5788	0	0	298.1397	149.5735	L	1246.6426	623.8250	1229.6161	615.3117	1228.6321	614.8197	12
4	387.1874	194.0974	0	0	369.1769	185.0921	A	1133.5586	567.2829	1116.5320	558.7696	1115.5480	558.2776	11
5	486.2558	243.6316	0	0	468.2453	234.6263	V	1062.5215	531.7644	1045.4949	523.2511	1044.5109	522.7591	10
6	615.2984	308.1529	0	0	597.2879	299.1476	E	963.4530	482.2302	946.4265	473.7169	945.4425	473.2249	9
7	686.3355	343.6714	0	0	668.3250	334.6661	A	834.4104	417.7089	817.3839	409.1956	816.3999	408.7036	8
8	743.3570	372.1821	0	0	725.3464	363.1769	G	763.3733	382.1903	746.3468	373.6770	745.3628	373.1850	7
9	814.3941	407.7007	0	0	796.3836	398.6954	A	706.3519	353.6796	689.3253	345.1663	688.3413	344.6743	6
10	911.4469	456.2271	0	0	893.4363	447.2218	P	635.3148	318.1610	618.2882	309.6477	617.3042	309.1557	5
11	1074.5102	537.7587	0	0	1056.4997	528.7535	Y	538.2620	269.6346	521.2354	261.1214	520.2514	260.6293	4
12	1145.5473	573.2773	0	0	1127.5368	564.2720	A	375.1987	188.1030	358.1721	179.5897	357.1881	179.0977	3
13	1274.5899	637.7986	0	0	1256.5794	628.7933	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
14							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 96926.

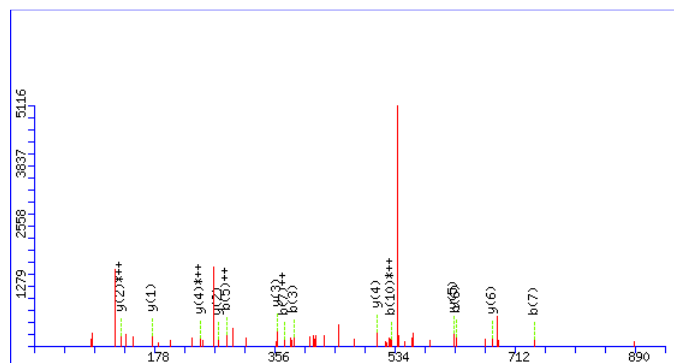
MS/MS Fragmentation of **LRDPSGDFSVR**:

Found in **IP100061111**

Title: 2.1.1.780.3

Data file: Y:\TT5600(CiRA1)\2012-01\120124ry\120124ry_414C2-43_1_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							11
2	270.1925	135.5999	253.1659	127.0866	0	0	R	1135.5491	568.2782	1118.5225	559.7649	1117.5385	559.2729	10
3	385.2194	193.1133	368.1928	184.6001	367.2088	184.1081	D	979.4479	490.2276	962.4214	481.7143	961.4374	481.2223	9
4	482.2722	241.6397	465.2456	233.1264	464.2616	232.6344	P	864.4210	432.7141	847.3945	424.2009	846.4104	423.7089	8
5	569.3042	285.1557	552.2776	276.6425	551.2936	276.1504	S	767.3682	384.1878	750.3417	375.6745	749.3577	375.1825	7
6	626.3257	313.6665	609.2991	305.1532	608.3151	304.6612	G	680.3362	340.6717	663.3097	332.1585	662.3257	331.6665	6
7	741.3526	371.1799	724.3260	362.6667	723.3420	362.1747	D	623.3148	312.1610	606.2882	303.6477	605.3042	303.1557	5
8	888.4210	444.7141	871.3945	436.2009	870.4104	435.7089	F	508.2878	254.6475	491.2613	246.1343	490.2772	245.6423	4
9	975.4530	488.2302	958.4265	479.7169	957.4425	479.2249	S	361.2194	181.1133	344.1928	172.6001	343.2088	172.1081	3
10	1074.5214	537.7644	1057.4949	529.2511	1056.5109	528.7591	V	274.1874	137.5973	257.1608	129.0840	0	0	2
11							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 96958.

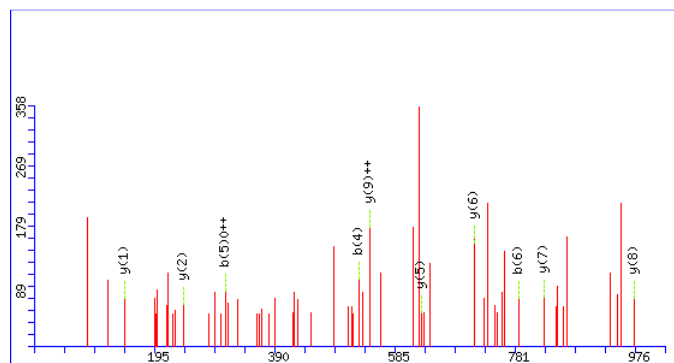
MS/MS Fragmentation of **VLEWLFISQEQPK**:

Found in **IP100031595;IP100795749;IP100945548;IP100946634;IP100985295;IP101008717;IP101008774**

Title: 3.1.1.3997.5

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	100.0757	50.5415	0	0	0	0	V							13
2	213.1598	107.0835	0	0	0	0	L	1517.7999	759.4036	1500.7733	750.8903	1499.7893	750.3983	12
3	342.2023	171.6048	0	0	324.1918	162.5995	E	1404.7158	702.8615	1387.6892	694.3483	1386.7052	693.8563	11
4	528.2817	264.6445	0	0	510.2711	255.6392	W	1275.6732	638.3402	1258.6467	629.8270	1257.6626	629.3350	10
5	641.3657	321.1865	0	0	623.3552	312.1812	L	1089.5939	545.3006	1072.5673	536.7873	1071.5833	536.2953	9
6	788.4341	394.7207	0	0	770.4236	385.7154	F	976.5098	488.7585	959.4833	480.2453	958.4993	479.7533	8
7	901.5182	451.2627	0	0	883.5076	442.2575	I	829.4414	415.2243	812.4149	406.7111	811.4308	406.2191	7
8	988.5502	494.7788	0	0	970.5397	485.7735	S	716.3573	358.6823	699.3308	350.1690	698.3468	349.6770	6
9	1116.6088	558.8080	1099.5823	550.2948	1098.5982	549.8028	Q	629.3253	315.1663	612.2988	306.6530	611.3148	306.1610	5
10	1245.6514	623.3293	1228.6249	614.8161	1227.6408	614.3241	E	501.2667	251.1370	484.2402	242.6237	483.2562	242.1317	4
11	1373.7100	687.3586	1356.6834	678.8454	1355.6994	678.3533	Q	372.2241	186.6157	355.1976	178.1024	0	0	3
12	1470.7627	735.8850	1453.7362	727.3717	1452.7522	726.8797	P	244.1656	122.5864	227.1390	114.0731	0	0	2
13							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 97090.

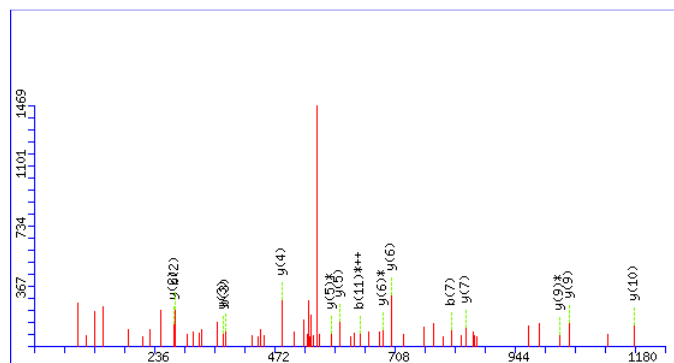
MS/MS Fragmentation of **YIVLESDFTNVVVR**:

Found in **IP100001597;IP101012092**

Title: 3.1.1.1441.5

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_aHDF1419-P10_4.3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	164.0706	82.5389	0	0	0	0	Y							14
2	277.1547	139.0810	0	0	0	0	I	1505.7958	753.4016	1488.7693	744.8883	1487.7853	744.3963	13
3	376.2231	188.6152	0	0	0	0	V	1392.7118	696.8595	1375.6852	688.3462	1374.7012	687.8542	12
4	489.3071	245.1572	0	0	0	0	L	1293.6434	647.3253	1276.6168	638.8120	1275.6328	638.3200	11
5	618.3497	309.6785	0	0	600.3392	300.6732	E	1180.5593	590.7833	1163.5327	582.2700	1162.5487	581.7780	10
6	705.3818	353.1945	0	0	687.3712	344.1892	S	1051.5167	526.2620	1034.4901	517.7487	1033.5061	517.2567	9
7	820.4087	410.7080	0	0	802.3981	401.7027	D	964.4847	482.7460	947.4581	474.2327	946.4741	473.7407	8
8	967.4771	484.2422	0	0	949.4666	475.2369	F	849.4577	425.2325	832.4312	416.7192	831.4472	416.2272	7
9	1068.5248	534.7660	0	0	1050.5142	525.7608	T	702.3893	351.6983	685.3628	343.1850	684.3787	342.6930	6
10	1182.5677	591.7875	1165.5412	583.2742	1164.5572	582.7822	N	601.3416	301.1745	584.3151	292.6612	0	0	5
11	1296.6107	648.8090	1279.5841	640.2957	1278.6001	639.8037	N	487.2987	244.1530	470.2722	235.6397	0	0	4
12	1395.6791	698.3432	1378.6525	689.8299	1377.6685	689.3379	V	373.2558	187.1315	356.2292	178.6183	0	0	3
13	1494.7475	747.8774	1477.7209	739.3641	1476.7369	738.8721	V	274.1874	137.5973	257.1608	129.0840	0	0	2
14							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 97121.

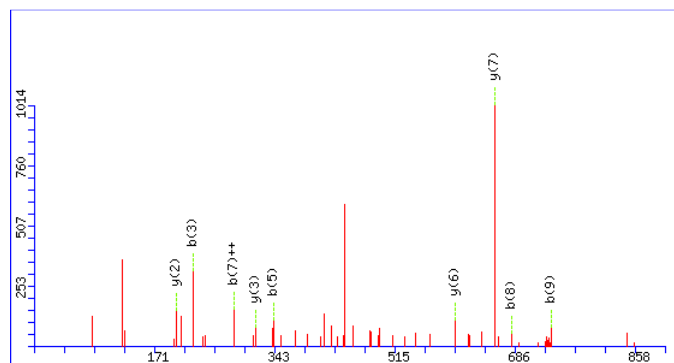
MS/MS Fragmentation of **IGGGGVQLGK**:

Found in **IP100025846;IP100220146;IP100941287;IP101009989**

Title: 1.1.1.6234.4

Data file: Y:¥TT5600(CiRA1)¥2012-01¥120129ry¥120129ry_604A1-46_3_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	I							10
2	171.1128	86.0600	0	0	0	0	G	772.4312	386.7192	755.4046	378.2060	0	0	9
3	228.1343	114.5708	0	0	0	0	G	715.4097	358.2085	698.3832	349.6952	0	0	8
4	285.1557	143.0815	0	0	0	0	G	658.3883	329.6978	641.3617	321.1845	0	0	7
5	342.1772	171.5922	0	0	0	0	G	601.3668	301.1870	584.3402	292.6738	0	0	6
6	441.2456	221.1264	0	0	0	0	V	544.3453	272.6763	527.3188	264.1630	0	0	5
7	569.3042	285.1557	552.2776	276.6425	0	0	Q	445.2769	223.1421	428.2504	214.6288	0	0	4
8	682.3883	341.6978	665.3617	333.1845	0	0	L	317.2183	159.1128	300.1918	150.5995	0	0	3
9	739.4097	370.2085	722.3832	361.6952	0	0	G	204.1343	102.5708	187.1077	94.0575	0	0	2
10							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 97324.

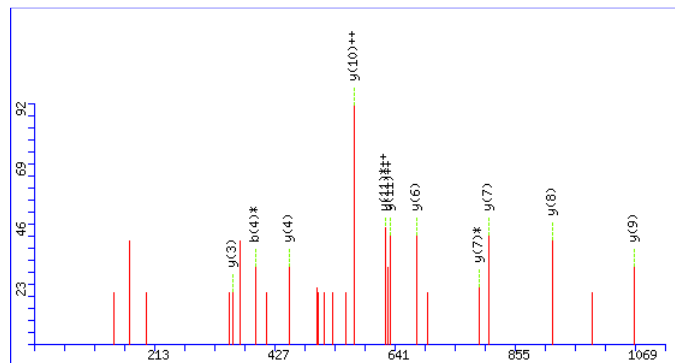
MS/MS Fragmentation of **QLQLQAFLQNLVAHK: -17.026549@N-term(Q)**

Found in **IP100170730;IP100171077;IP100974153;IP100982627**

Title: 4.1.1.3761.2

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120212ry¥120212ry_aHDF1388-P9_3_4.mgf

ProteinPilot Peptide Confidence > 99%

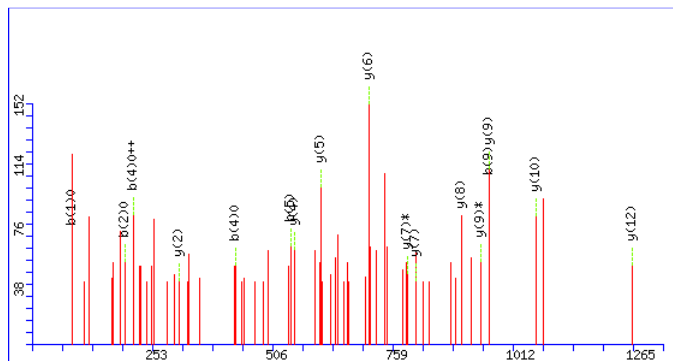


#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233	0	0	Q							15
2	242.1499	121.5786	225.1234	113.0653	0	0	L	1551.9006	776.4539	1534.8740	767.9407	0	0	14
3	299.1714	150.0893	282.1448	141.5761	0	0	G	1438.8165	719.9119	1421.7900	711.3986	0	0	13
4	412.2554	206.6314	395.2289	198.1181	0	0	L	1381.7950	691.4012	1364.7685	682.8879	0	0	12
5	540.3140	270.6607	523.2875	262.1474	0	0	Q	1268.7110	634.8591	1251.6844	626.3459	0	0	11
6	611.3511	306.1792	594.3246	297.6659	0	0	A	1140.6524	570.8298	1123.6259	562.3166	0	0	10
7	758.4196	379.7134	741.3930	371.2001	0	0	F	1069.6153	535.3113	1052.5887	526.7980	0	0	9
8	871.5036	436.2554	854.4771	427.7422	0	0	L	922.5469	461.7771	905.5203	453.2638	0	0	8
9	999.5622	500.2847	982.5356	491.7715	0	0	Q	809.4628	405.2350	792.4363	396.7218	0	0	7
10	1113.6051	557.3062	1096.5786	548.7929	0	0	N	681.4042	341.2058	664.3777	332.6925	0	0	6
11	1226.6892	613.8482	1209.6626	605.3350	0	0	L	567.3613	284.1843	550.3348	275.6710	0	0	5
12	1325.7576	663.3824	1308.7310	654.8692	0	0	V	454.2772	227.6423	437.2507	219.1290	0	0	4
13	1396.7947	698.9010	1379.7682	690.3877	0	0	A	355.2088	178.1081	338.1823	169.5948	0	0	3
14	1533.8536	767.4305	1516.8271	758.9172	0	0	H	284.1717	142.5895	267.1452	134.0762	0	0	2
15							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 97395.

MS/MS Fragmentation of **TLTMVSLGCGFVGPVVGWYK: 57.021465@C:9**
 Found in **IP100023958;IP100892687;IP100892971;IP100893014;IP100893772;IP100893905**
 Title: 4.1.1.1276.9
 Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2_4.mgf
 ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	102.0550	51.5311	0	0	84.0444	42.5258	T							21
2	215.1390	108.0731	0	0	197.1285	99.0679	L	2127.0766	1064.0419	2110.0500	1055.5286	2109.0660	1055.0366	20
3	316.1867	158.5970	0	0	298.1761	149.5917	T	2013.9925	1007.4999	1996.9660	998.9866	1995.9819	998.4946	19
4	447.2272	224.1172	0	0	429.2166	215.1119	M	1912.9448	956.9761	1895.9183	948.4628	1894.9343	947.9708	18
5	546.2956	273.6514	0	0	528.2850	264.6462	V	1781.9043	891.4558	1764.8778	882.9425	1763.8938	882.4505	17
6	633.3276	317.1675	0	0	615.3171	308.1622	S	1682.8359	841.9216	1665.8094	833.4083	1664.8254	832.9163	16
7	746.4117	373.7095	0	0	728.4011	364.7042	L	1595.8039	798.4056	1578.7774	789.8923	0	0	15
8	803.4332	402.2202	0	0	785.4226	393.2149	G	1482.7198	741.8636	1465.6933	733.3503	0	0	14
9	963.4638	482.2355	0	0	945.4532	473.2303	C	1425.6984	713.3528	1408.6718	704.8395	0	0	13
10	1020.4853	510.7463	0	0	1002.4747	501.7410	G	1265.6677	633.3375	1248.6412	624.8242	0	0	12
11	1167.5537	584.2805	0	0	1149.5431	575.2752	F	1208.6463	604.8268	1191.6197	596.3135	0	0	11
12	1266.6221	633.8147	0	0	1248.6115	624.8094	V	1061.5778	531.2926	1044.5513	522.7793	0	0	10
13	1323.6436	662.3254	0	0	1305.6330	653.3201	G	962.5094	481.7584	945.4829	473.2451	0	0	9
14	1420.6963	710.8518	0	0	1402.6858	701.8465	P	905.4880	453.2476	888.4614	444.7343	0	0	8
15	1519.7647	760.3860	0	0	1501.7542	751.3807	V	808.4352	404.7212	791.4087	396.2080	0	0	7
16	1618.8332	809.9202	0	0	1600.8226	800.9149	V	709.3668	355.1870	692.3402	346.6738	0	0	6
17	1675.8546	838.4309	0	0	1657.8441	829.4257	G	610.2984	305.6528	593.2718	297.1396	0	0	5
18	1732.8761	866.9417	0	0	1714.8655	857.9364	G	553.2769	277.1421	536.2504	268.6288	0	0	4
19	1918.9554	959.9813	0	0	1900.9448	950.9761	W	496.2554	248.6314	479.2289	240.1181	0	0	3
20	2082.0187	1041.5130	0	0	2064.0082	1032.5077	Y	310.1761	155.5917	293.1496	147.0784	0	0	2
21							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 97448.

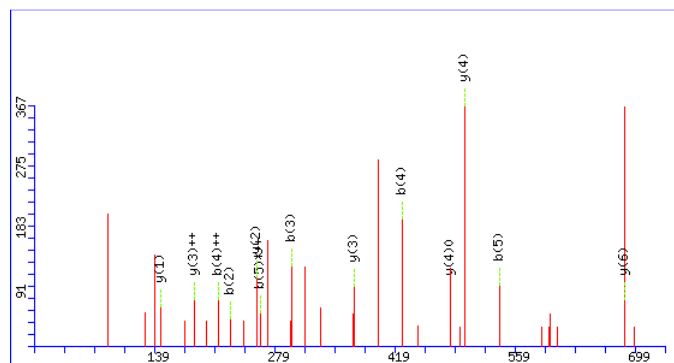
MS/MS Fragmentation of **LNAELLK: 0.984015@N:2**

Found in **IP100020265,IP100478457,IP100478693,IP100552956,IP100644106,IP100889596,IP100930540**

Title: 3.1.1.124.2

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120212ry¥120212ry_aHDF1388-P9_3_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	114.0913	57.5493	0	0	0	0	L							7
2	229.1183	115.0628	212.0917	106.5495	0	0	N	688.3876	344.6974	671.3610	336.1842	670.3770	335.6921	6
3	300.1554	150.5813	283.1288	142.0681	0	0	A	573.3606	287.1840	556.3341	278.6707	555.3501	278.1787	5
4	429.1980	215.1026	412.1714	206.5894	411.1874	206.0974	E	502.3235	251.6654	485.2970	243.1521	484.3130	242.6601	4
5	542.2821	271.6447	525.2555	263.1314	524.2715	262.6394	L	373.2809	187.1441	356.2544	178.6308	0	0	3
6	655.3661	328.1867	638.3396	319.6734	637.3556	319.1814	L	260.1969	130.6021	243.1703	122.0888	0	0	2
7							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: **97641.**

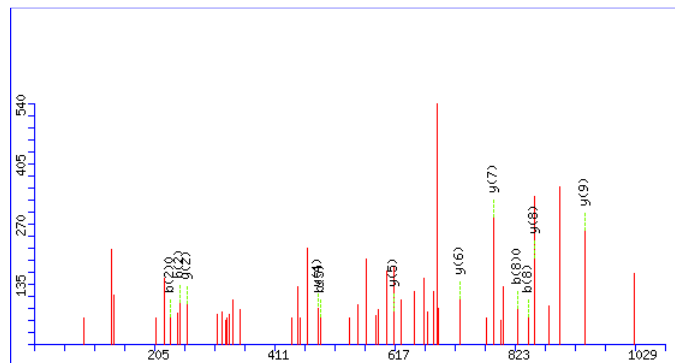
MS/MS Fragmentation of **YSAGLELLSR:**

Found in **IP100328918;IP100394984;IP100479571;IP101011214**

Title: 2.1.1.3937.8

Data file: Y:\TT5600(CiRA1)\2012-02\120212ry\120212ry_aHDF1388-P9_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	164.0706	82.5389	0	0	0	0	Y							10
2	251.1026	126.0550	0	0	233.0921	117.0497	S	945.5364	473.2718	928.5098	464.7585	927.5258	464.2665	9
3	322.1397	161.5735	0	0	304.1292	152.5682	A	858.5043	429.7558	841.4778	421.2425	840.4938	420.7505	8
4	379.1612	190.0842	0	0	361.1506	181.0790	G	787.4672	394.2373	770.4407	385.7240	769.4567	385.2320	7
5	492.2453	246.6263	0	0	474.2347	237.6210	L	730.4458	365.7265	713.4192	357.2132	712.4352	356.7212	6
6	621.2879	311.1476	0	0	603.2773	302.1423	E	617.3617	309.1845	600.3352	300.6712	599.3511	300.1792	5
7	734.3719	367.6896	0	0	716.3614	358.6843	L	488.3191	244.6632	471.2926	236.1499	470.3085	235.6579	4
8	847.4560	424.2316	0	0	829.4454	415.2264	L	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
9	934.4880	467.7477	0	0	916.4775	458.7424	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
10							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 97717.

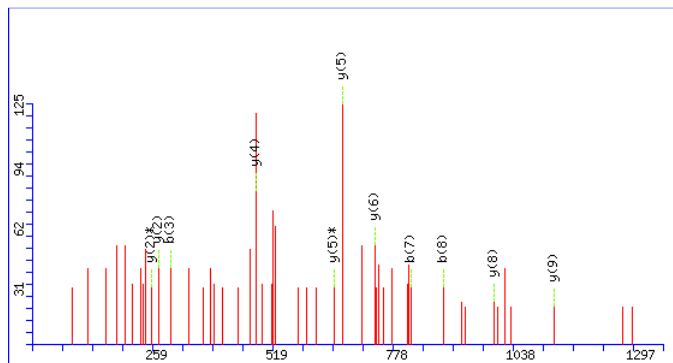
MS/MS Fragmentation of **NLAPFFEAWAWPIQK**:

Found in **IP100006050;IP100885016;IP100978701;IP101019099**

Title: 4.1.1.2981.3

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_1_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							15
2	228.1343	114.5708	211.1077	106.0575	0	0	L	1703.8944	852.4509	1686.8679	843.9376	1685.8839	843.4456	14
3	299.1714	150.0893	282.1448	141.5761	0	0	A	1590.8104	795.9088	1573.7838	787.3955	1572.7998	786.9035	13
4	396.2241	198.6157	379.1976	190.1024	0	0	P	1519.7732	760.3903	1502.7467	751.8770	1501.7627	751.3850	12
5	543.2926	272.1499	526.2660	263.6366	0	0	F	1422.7205	711.8639	1405.6939	703.3506	1404.7099	702.8586	11
6	690.3610	345.6841	673.3344	337.1708	0	0	F	1275.6521	638.3297	1258.6255	629.8164	1257.6415	629.3244	10
7	819.4036	410.2054	802.3770	401.6921	801.3930	401.2001	E	1128.5837	564.7955	1111.5571	556.2822	1110.5731	555.7902	9
8	890.4407	445.7240	873.4141	437.2107	872.4301	436.7187	A	999.5411	500.2742	982.5145	491.7609	0	0	8
9	1076.5200	538.7636	1059.4934	530.2504	1058.5094	529.7584	W	928.5039	464.7556	911.4774	456.2423	0	0	7
10	1147.5571	574.2822	1130.5306	565.7689	1129.5465	565.2769	A	742.4246	371.7160	725.3981	363.2027	0	0	6
11	1333.6364	667.3218	1316.6099	658.8086	1315.6259	658.3166	W	671.3875	336.1974	654.3610	327.6841	0	0	5
12	1430.6892	715.8482	1413.6626	707.3350	1412.6786	706.8429	P	485.3082	243.1577	468.2817	234.6445	0	0	4
13	1543.7732	772.3903	1526.7467	763.8770	1525.7627	763.3850	I	388.2554	194.6314	371.2289	186.1181	0	0	3
14	1671.8318	836.4196	1654.8053	827.9063	1653.8213	827.4143	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
15							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 98080.

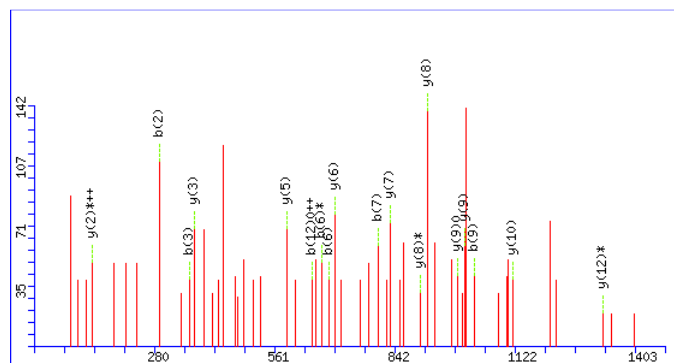
MS/MS Fragmentation of **YQAPDIDVQLSSELTDSLR**:

Found in **IP100024567;IP100383200;IP100386308;IP100412788;IP100909733;IP100910443**

Title: 3.1.1.3662.7

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_414C2-43_4_3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	164.0706	82.5389	0	0	0	0	Y							19
2	292.1292	146.5682	275.1026	138.0550	0	0	Q	1986.9978	994.0026	1969.9713	985.4893	1968.9873	984.9973	18
3	363.1663	182.0868	346.1397	173.5735	0	0	A	1858.9393	929.9733	1841.9127	921.4600	1840.9287	920.9680	17
4	460.2191	230.6132	443.1925	222.0999	0	0	P	1787.9021	894.4547	1770.8756	885.9414	1769.8916	885.4494	16
5	575.2460	288.1266	558.2195	279.6134	557.2354	279.1214	D	1690.8494	845.9283	1673.8228	837.4151	1672.8388	836.9230	15
6	688.3301	344.6687	671.3035	336.1554	670.3195	335.6634	I	1575.8224	788.4149	1558.7959	779.9016	1557.8119	779.4096	14
7	803.3570	402.1821	786.3305	393.6689	785.3464	393.1769	D	1462.7384	731.8728	1445.7118	723.3596	1444.7278	722.8675	13
8	902.4254	451.7164	885.3989	443.2031	884.4149	442.7111	V	1347.7114	674.3594	1330.6849	665.8461	1329.7009	665.3541	12
9	1030.4840	515.7456	1013.4575	507.2324	1012.4734	506.7404	Q	1248.6430	624.8251	1231.6165	616.3119	1230.6325	615.8199	11
10	1143.5681	572.2877	1126.5415	563.7744	1125.5575	563.2824	L	1120.5844	560.7959	1103.5579	552.2826	1102.5739	551.7906	10
11	1230.6001	615.8037	1213.5735	607.2904	1212.5895	606.7984	S	1007.5004	504.2538	990.4738	495.7406	989.4898	495.2485	9
12	1317.6321	659.3197	1300.6056	650.8064	1299.6216	650.3144	S	920.4684	460.7378	903.4418	452.2245	902.4578	451.7325	8
13	1446.6747	723.8410	1429.6482	715.3277	1428.6642	714.8357	E	833.4363	417.2218	816.4098	408.7085	815.4258	408.2165	7
14	1559.7588	780.3830	1542.7322	771.8698	1541.7482	771.3777	L	704.3937	352.7005	687.3672	344.1872	686.3832	343.6952	6
15	1660.8065	830.9069	1643.7799	822.3936	1642.7959	821.9016	T	591.3097	296.1585	574.2831	287.6452	573.2991	287.1532	5
16	1775.8334	888.4203	1758.8069	879.9071	1757.8228	879.4151	D	490.2620	245.6346	473.2354	237.1214	472.2514	236.6293	4
17	1862.8654	931.9364	1845.8389	923.4231	1844.8549	922.9311	S	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
18	1975.9495	988.4784	1958.9229	979.9651	1957.9389	979.4731	L	288.2030	144.6051	271.1765	136.0919	0	0	2
19							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 98092.

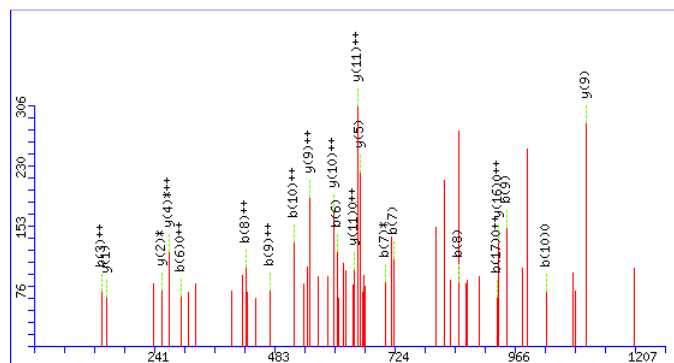
MS/MS Fragmentation of **GGRPNEIEPPPPPEMPWQK**:

Found in **IP100174442,IP100760837,IP100872161,IP100894178,IP101009687**

Title: 2.1.1.3855.11

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_32R1-32_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							19
2	115.0502	58.0287	0	0	0	0	G	2099.0379	1050.0226	2082.0113	1041.5093	2081.0273	1041.0173	18
3	271.1513	136.0793	254.1248	127.5660	0	0	R	2042.0164	1021.5118	2024.9899	1012.9986	2024.0058	1012.5066	17
4	368.2041	184.6057	351.1775	176.0924	0	0	P	1885.9153	943.4613	1868.8887	934.9480	1867.9047	934.4560	16
5	482.2470	241.6271	465.2205	233.1139	0	0	N	1788.8625	894.9349	1771.8360	886.4216	1770.8520	885.9296	15
6	611.2896	306.1484	594.2630	297.6352	593.2790	297.1432	E	1674.8196	837.9134	1657.7931	829.4002	1656.8090	828.9082	14
7	724.3737	362.6905	707.3471	354.1772	706.3631	353.6852	I	1545.7770	773.3921	1528.7505	764.8789	1527.7664	764.3869	13
8	853.4163	427.2118	836.3897	418.6985	835.4057	418.2065	E	1432.6929	716.8501	1415.6664	708.3368	1414.6824	707.8448	12
9	950.4690	475.7381	933.4425	467.2249	932.4585	466.7329	P	1303.6504	652.3288	1286.6238	643.8155	1285.6398	643.3235	11
10	1047.5218	524.2645	1030.4952	515.7513	1029.5112	515.2592	P	1206.5976	603.8024	1189.5710	595.2892	1188.5870	594.7972	10
11	1144.5745	572.7909	1127.5480	564.2776	1126.5640	563.7856	P	1109.5448	555.2761	1092.5183	546.7628	1091.5343	546.2708	9
12	1241.6273	621.3173	1224.6008	612.8040	1223.6167	612.3120	P	1012.4921	506.7497	995.4655	498.2364	994.4815	497.7444	8
13	1370.6699	685.8386	1353.6434	677.3253	1352.6593	676.8333	E	915.4393	458.2233	898.4128	449.7100	897.4287	449.2180	7
14	1501.7104	751.3588	1484.6838	742.8456	1483.6998	742.3536	M	786.3967	393.7020	769.3702	385.1887	0	0	6
15	1598.7632	799.8852	1581.7366	791.3719	1580.7526	790.8799	P	655.3562	328.1817	638.3297	319.6685	0	0	5
16	1695.8159	848.4116	1678.7894	839.8983	1677.8054	839.4063	P	558.3035	279.6554	541.2769	271.1421	0	0	4
17	1881.8952	941.4513	1864.8687	932.9380	1863.8847	932.4460	W	461.2507	231.1290	444.2241	222.6157	0	0	3
18	2009.9538	1005.4805	1992.9273	996.9673	1991.9432	996.4753	Q	275.1714	138.0893	258.1448	129.5761	0	0	2
19							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 98160.

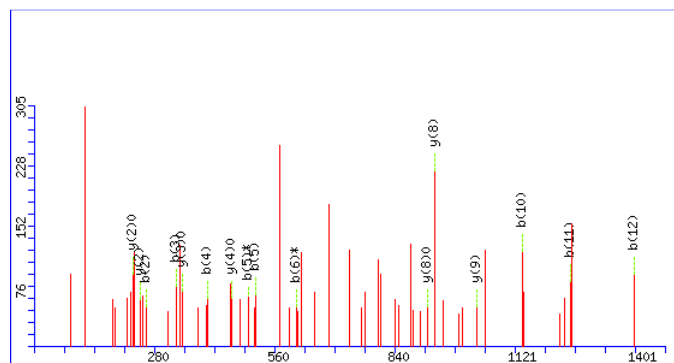
MS/MS Fragmentation of **NFAALLEEHDFVPEDDDDDD**:

Found in **IP100154512**

Title: 4.1.1.907.7

Data file: Y:\TT5600(CiRA1)\2012-01\120118ry\120118ry_201B7-32_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							21
2	262.1186	131.5629	245.0921	123.0497	0	0	F	2319.9776	1160.4924	0	0	2301.9670	1151.4871	20
3	333.1557	167.0815	316.1292	158.5682	0	0	A	2172.9091	1086.9582	0	0	2154.8986	1077.9529	19
4	404.1928	202.6001	387.1663	194.0868	0	0	A	2101.8720	1051.4397	0	0	2083.8615	1042.4344	18
5	517.2789	259.1421	500.2504	250.6288	0	0	L	2030.8349	1015.9211	0	0	2012.8244	1006.9158	17
6	630.3610	315.6841	613.3344	307.1708	0	0	L	1917.7509	959.3791	0	0	1899.7403	950.3738	16
7	759.4036	380.2054	742.3770	371.6921	741.3930	371.2001	E	1804.6668	902.8370	0	0	1786.6562	893.8318	15
8	888.4462	444.7267	871.4196	436.2134	870.4356	435.7214	E	1675.6242	838.3157	0	0	1657.6136	829.3105	14
9	1025.5051	513.2562	1008.4785	504.7429	1007.4945	504.2509	H	1546.5816	773.7944	0	0	1528.5710	764.7892	13
10	1140.5320	570.7696	1123.5055	562.2564	1122.5214	561.7644	D	1409.5227	705.2650	0	0	1391.5121	696.2597	12
11	1253.6161	627.3117	1236.5895	618.7984	1235.6055	618.3064	I	1294.4957	647.7515	0	0	1276.4852	638.7462	11
12	1400.6845	700.8459	1383.6579	692.3326	1382.6739	691.8406	F	1181.4117	591.2095	0	0	1163.4011	582.2042	10
13	1499.7529	750.3801	1482.7264	741.8668	1481.7423	741.3748	V	1034.3433	517.6753	0	0	1016.3327	508.6700	9
14	1596.8057	798.9065	1579.7791	790.3932	1578.7951	789.9012	P	935.2749	468.1411	0	0	917.2643	459.1358	8
15	1725.8483	863.4278	1708.8217	854.9145	1707.8377	854.4225	E	838.2221	419.6147	0	0	820.2115	410.6094	7
16	1840.8752	920.9412	1823.8487	912.4280	1822.8646	911.9360	D	709.1795	355.0934	0	0	691.1689	346.0881	6
17	1955.9021	978.4547	1938.8756	969.9414	1937.8916	969.4494	D	594.1526	297.5799	0	0	576.1420	288.5746	5
18	2070.9291	1035.9682	2053.9025	1027.4549	2052.9185	1026.9629	D	479.1256	240.0664	0	0	461.1150	231.0612	4
19	2185.9560	1093.4817	2168.9295	1084.9684	2167.9455	1084.4764	D	364.0987	182.5530	0	0	346.0881	173.5477	3
20	2300.9830	1150.9951	2283.9564	1142.4819	2282.9724	1141.9898	D	249.0717	125.0395	0	0	231.0612	116.0342	2
21							D	134.0448	67.5260	0	0	116.0342	58.5207	1

Peptide View

Peptide: 98207.

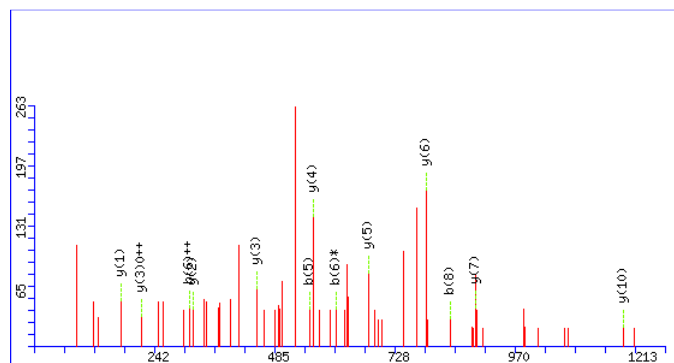
MS/MS Fragmentation of **NVLNDAVDLLEFR**:

Found in **IP100175647;IP100792392;IP100946083**

Title: 4.1.1.1922.2

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_2.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b*++	b0	b0++	SEQ	y	y++	y*	y*++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							13
2	214.1186	107.5629	197.0921	99.0497	0	0	V	1403.7529	702.3801	1386.7264	693.8668	1385.7423	693.3748	12
3	327.2027	164.1050	310.1761	155.5917	0	0	L	1304.6845	652.8459	1287.6579	644.3326	1286.6739	643.8406	11
4	441.2456	221.1264	424.2191	212.6132	0	0	N	1191.6004	596.3039	1174.5739	587.7906	1173.5899	587.2986	10
5	556.2726	278.6399	539.2460	270.1266	538.2620	269.6346	D	1077.5575	539.2824	1060.5310	530.7691	1059.5469	530.2771	9
6	627.3097	314.1585	610.2831	305.6452	609.2991	305.1532	A	962.5306	481.7689	945.5040	473.2556	944.5200	472.7636	8
7	726.3781	363.6927	709.3515	355.1794	708.3675	354.6874	V	891.4934	446.2504	874.4669	437.7371	873.4829	437.2451	7
8	841.4050	421.2061	824.3785	412.6929	823.3945	412.2009	D	792.4250	396.7162	775.3985	388.2029	774.4145	387.7109	6
9	954.4891	477.7482	937.4625	469.2349	936.4785	468.7429	L	677.3981	339.2027	660.3715	330.6894	659.3875	330.1974	5
10	1067.5732	534.2902	1050.5466	525.7769	1049.5626	525.2849	L	564.3140	282.6606	547.2875	274.1474	546.3035	273.6554	4
11	1196.6157	598.8115	1179.5892	590.2982	1178.6052	589.8062	E	451.2300	226.1186	434.2034	217.6053	433.2194	217.1133	3
12	1343.6842	672.3457	1326.6576	663.8324	1325.6736	663.3404	F	322.1874	161.5973	305.1608	153.0840	0	0	2
13							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: **98262**.

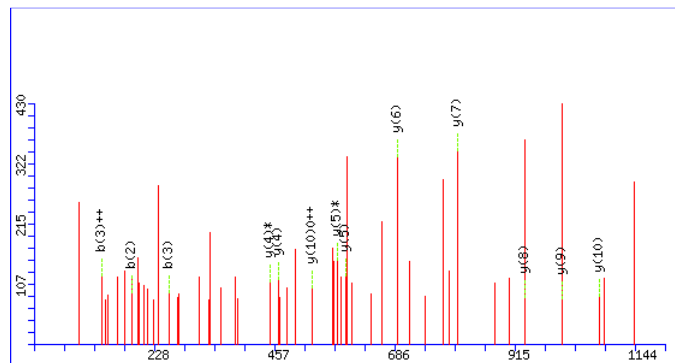
MS/MS Fragmentation of **NAAEIVQYGVK**:

Found in **IP100019209;IP101014918**

Title: 2.1.1.1062.7

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120212ry¥120212ry_aHDF1388-P9_2_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	115.0502	58.0287	98.0237	49.5155	0	0	N							11
2	186.0873	93.5473	169.0608	85.0340	0	0	A	1077.5939	539.3006	1060.5673	530.7873	1059.5833	530.2953	10
3	257.1244	129.0659	240.0979	120.5526	0	0	A	1006.5568	503.7820	989.5302	495.2688	988.5462	494.7767	9
4	386.1670	193.5872	369.1405	185.0739	368.1565	184.5819	E	935.5197	468.2635	918.4931	459.7502	917.5091	459.2582	8
5	499.2511	250.1292	482.2245	241.6159	481.2405	241.1239	I	806.4771	403.7422	789.4505	395.2289	0	0	7
6	598.3195	299.6634	581.2930	291.1501	580.3089	290.6581	V	693.3930	347.2001	676.3665	338.6869	0	0	6
7	726.3781	363.6927	709.3515	355.1794	708.3675	354.6874	Q	594.3246	297.6659	577.2980	289.1527	0	0	5
8	889.4414	445.2243	872.4149	436.7111	871.4308	436.2191	Y	466.2660	233.6366	449.2395	225.1234	0	0	4
9	946.4629	473.7351	929.4363	465.2218	928.4523	464.7298	G	303.2027	152.1050	286.1761	143.5917	0	0	3
10	1045.5313	523.2693	1028.5047	514.7560	1027.5207	514.2640	V	246.1812	123.5942	229.1547	115.0810	0	0	2
11							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 98358.

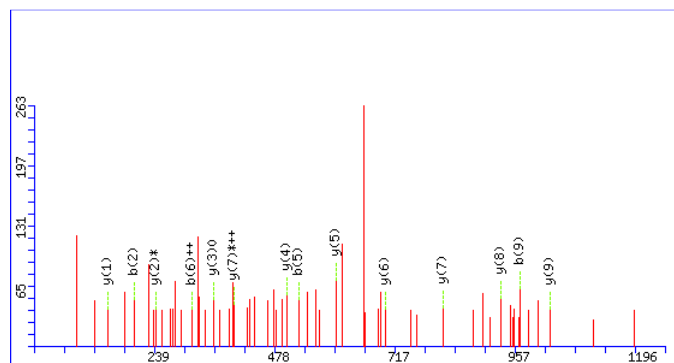
MS/MS Fragmentation of **AEVDLVVQDLK**:

Found in **IP100101652;IP100909950;IP100910431;IP100910775**

Title: 2.1.1.4349.10

Data file: Y:\TT5600(CiRA1)\2012-02\120208ry\120208ry_Tig120slc-P8_2.2.mgf

ProteinPilot Peptide Confidence > 99%



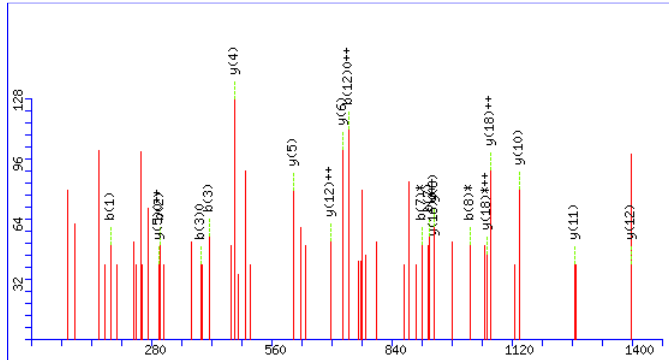
#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							11
2	201.0870	101.0471	0	0	183.0764	92.0418	E	1157.6412	579.3243	1140.6147	570.8110	1139.6307	570.3190	10
3	300.1554	150.5813	0	0	282.1448	141.5761	V	1028.5986	514.8030	1011.5721	506.2897	1010.5881	505.7977	9
4	415.1823	208.0948	0	0	397.1718	199.0895	D	929.5302	465.2687	912.5037	456.7555	911.5197	456.2635	8
5	528.2664	264.6368	0	0	510.2558	255.6316	L	814.5033	407.7553	797.4767	399.2420	796.4927	398.7500	7
6	627.3348	314.1710	0	0	609.3243	305.1658	V	701.4192	351.2132	684.3927	342.7000	683.4087	342.2080	6
7	726.4032	363.7053	0	0	708.3927	354.7000	V	602.3508	301.6790	585.3243	293.1658	584.3402	292.6738	5
8	854.4618	427.7345	837.4353	419.2213	836.4512	418.7293	Q	503.2824	252.1448	486.2558	243.6316	485.2718	243.1396	4
9	969.4888	485.2480	952.4622	476.7347	951.4782	476.2427	D	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
10	1082.5728	541.7900	1065.5463	533.2768	1064.5623	532.7848	L	260.1969	130.6021	243.1703	122.0888	0	0	2
11							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 98360.

MS/MS Fragmentation of **WLDEQQIMESLNVLHSELK**:
Found in **IP100074020;IP100966445;IP100967498;IP100967904**
Title: 4.1.1.1417.9

Data file: Y:\TT5600(CiRA1)\2012-02\120210ry\120210ry_585A1-55_3_4.mgf
ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	187.0866	94.0469	0	0	0	0	W							20
2	300.1707	150.5890	0	0	0	0	L	2254.1384	1127.5728	2237.1118	1119.0596	2236.1278	1118.5675	19
3	415.1976	208.1024	0	0	397.1870	199.0972	D	2141.0543	1071.0308	2124.0278	1062.5175	2123.0437	1062.0255	18
4	544.2402	272.6237	0	0	526.2296	263.6185	E	2026.0274	1013.5173	2009.0008	1005.0040	2008.0168	1004.5120	17
5	672.2988	336.6530	655.2722	328.1397	654.2882	327.6477	Q	1896.9848	948.9960	1879.9582	940.4828	1878.9742	939.9907	16
6	800.3573	400.6823	783.3308	392.1690	782.3468	391.6770	Q	1768.9262	884.9667	1751.8996	876.4535	1750.9156	875.9615	15
7	928.4159	464.7116	911.3894	456.1983	910.4054	455.7063	Q	1640.8676	820.9374	1623.8411	812.4242	1622.8571	811.9322	14
8	1041.5000	521.2536	1024.4734	512.7404	1023.4894	512.2483	I	1512.8090	756.9082	1495.7825	748.3949	1494.7985	747.9029	13
9	1172.5405	586.7739	1155.5139	578.2606	1154.5299	577.7686	M	1399.7250	700.3661	1382.6984	691.8529	1381.7144	691.3608	12
10	1301.5831	651.2952	1284.5565	642.7819	1283.5725	642.2899	E	1268.6845	634.8459	1251.6579	626.3326	1250.6739	625.8406	11
11	1388.6151	694.8112	1371.5885	686.2979	1370.6045	685.8059	S	1139.6419	570.3246	1122.6153	561.8113	1121.6313	561.3193	10
12	1501.6992	751.3532	1484.6726	742.8399	1483.6886	742.3479	L	1052.6099	526.8086	1035.5833	518.2953	1034.5993	517.8033	9
13	1615.7421	808.3747	1598.7155	799.8614	1597.7315	799.3694	N	939.5258	470.2665	922.4993	461.7533	921.5152	461.2613	8
14	1714.8105	857.9089	1697.7839	849.3956	1696.7999	848.9036	V	825.4829	413.2451	808.4563	404.7318	807.4723	404.2398	7
15	1827.8946	914.4509	1810.8680	905.9376	1809.8840	905.4456	L	728.4145	363.7109	709.3879	355.1976	708.4039	354.7056	6
16	1964.9535	982.9804	1947.9269	974.4671	1946.9429	973.9751	H	613.3304	307.1688	596.3039	298.6556	595.3198	298.1636	5
17	2051.9855	1026.4964	2034.9590	1017.9831	2033.9749	1017.4911	S	476.2715	238.6394	459.2449	230.1261	458.2609	229.6341	4
18	2181.0281	1091.0177	2164.0015	1082.5044	2163.0175	1082.0124	E	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
19	2294.1122	1147.5597	2277.0856	1139.0464	2276.1016	1138.5544	L	260.1969	130.6021	243.1703	122.0888	0	0	2
20							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 98389.

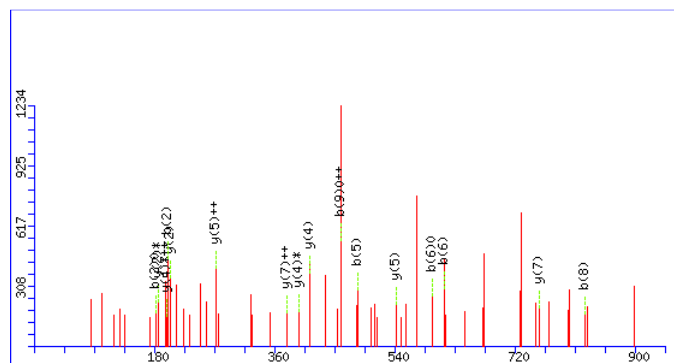
MS/MS Fragmentation of **AEALTEPLNA:**

Found in **IP100015801**

Title: 2.1.1.1731.5

Data file: Y:¥TT5600(CiRA1)¥2012-02¥120210ry¥120210ry_585A1-55_3_2.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	72.0444	36.5258	0	0	0	0	A							10
2	201.0870	101.0471	0	0	183.0764	92.0418	E	957.4888	479.2480	940.4622	470.7347	939.4782	470.2427	9
3	272.1241	136.5657	0	0	254.1135	127.5604	A	828.4462	414.7267	811.4196	406.2134	810.4356	405.7214	8
4	385.2082	193.1077	0	0	367.1976	184.1024	L	757.4090	379.2082	740.3825	370.6949	739.3985	370.2029	7
5	486.2558	243.6316	0	0	468.2453	234.6263	T	644.3250	322.6661	627.2984	314.1529	626.3144	313.6608	6
6	615.2984	308.1529	0	0	597.2879	299.1476	E	543.2773	272.1423	526.2508	263.6290	525.2667	263.1370	5
7	712.3512	356.6792	0	0	694.3406	347.6740	P	414.2347	207.6210	397.2082	199.1077	0	0	4
8	825.4353	413.2213	0	0	807.4247	404.2160	L	317.1819	159.0946	300.1554	150.5813	0	0	3
9	939.4782	470.2427	922.4516	461.7295	921.4676	461.2374	N	204.0979	102.5526	187.0713	94.0393	0	0	2
10							A	90.0550	45.5311	0	0	0	0	1

Peptide View

Peptide: 98435.

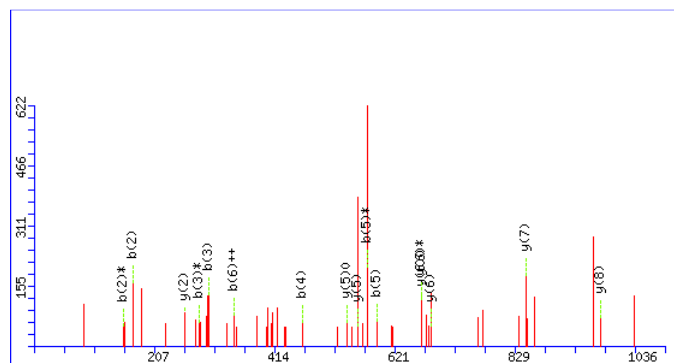
MS/MS Fragmentation of **GNEYQPSNIK**:

Found in **IP100028390**

Title: 1.1.1.7787.11

Data file: Y:\TT5600(CiRA1)\2012-02\120214ry\120214ry_32R1-32_4_1.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	58.0287	29.5180	0	0	0	0	G							10
2	172.0717	86.5395	155.0451	78.0262	0	0	N	1092.5320	546.7696	1075.5055	538.2564	1074.5214	537.7644	9
3	301.1143	151.0608	284.0877	142.5475	283.1037	142.0555	E	978.4891	489.7482	961.4625	481.2349	960.4785	480.7429	8
4	464.1776	232.5924	447.1510	224.0792	446.1670	223.5872	Y	849.4465	425.2269	832.4199	416.7136	831.4359	416.2216	7
5	592.2362	296.6217	575.2096	288.1084	574.2256	287.6164	Q	686.3832	343.6952	669.3566	335.1819	668.3726	334.6899	6
6	689.2889	345.1481	672.2624	336.6348	671.2784	336.1428	P	558.3246	279.6659	541.2980	271.1527	540.3140	270.6606	5
7	776.3210	388.6641	759.2944	380.1508	758.3104	379.6588	S	461.2718	231.1395	444.2453	222.6263	443.2613	222.1343	4
8	890.3639	445.6856	873.3373	437.1723	872.3533	436.6803	N	374.2398	187.6235	357.2132	179.1103	0	0	3
9	1003.4480	502.2276	986.4214	493.7143	985.4374	493.2223	I	260.1969	130.6021	243.1703	122.0888	0	0	2
10							K	147.1128	74.0600	130.0863	65.5468	0	0	1

Peptide View

Peptide: 98791.

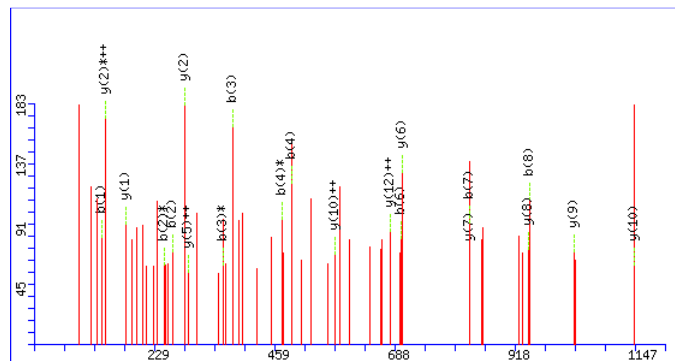
MS/MS Fragmentation of **QHIIPLENVTIDSIKDEGDLR: 0.984015@N:8**

Found in **IP100002424**

Title: 3.1.1.1596.5

Data file: Y:\TT5600(CiRA1)\¥2012-02¥120206ry¥120206ry_aHDF1419-P10_2.3.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b+++	b0	b0++	SEQ	y	y++	y*	y+++	y0	y0++	#
1	129.0659	65.0366	112.0393	56.5233	0	0	Q							21
2	266.1248	133.5660	249.0982	125.0527	0	0	H	2278.1925	1139.5999	2261.1660	1131.0866	2260.1820	1130.5946	20
3	379.2088	190.1081	362.1823	181.5948	0	0	I	2141.1336	1071.0704	2124.1071	1062.5572	2123.1230	1062.0652	19
4	492.2929	246.6501	475.2663	238.1368	0	0	I	2028.0495	1014.5284	2011.0230	1006.0151	2010.0390	1005.5231	18
5	589.3457	295.1765	572.3191	286.6632	0	0	P	1914.9655	957.9864	1897.9389	949.4731	1896.9549	948.9811	17
6	702.4297	351.7185	685.4032	343.2052	0	0	L	1817.9127	909.4600	1800.8862	900.9467	1799.9021	900.4547	16
7	831.4723	416.2398	814.4458	407.7265	813.4618	407.2345	E	1704.8286	852.9180	1687.8021	844.4047	1686.8181	843.9127	15
8	946.4993	473.7533	929.4727	465.2400	928.4887	464.7480	N	1575.7861	788.3967	1558.7595	779.8834	1557.7755	779.3914	14
9	1045.5677	523.2875	1028.5411	514.7742	1027.5571	514.2822	V	1460.7591	730.8832	1443.7326	722.3699	1442.7485	721.8779	13
10	1146.6154	573.8113	1129.5888	565.2980	1128.6048	564.8060	T	1361.6907	681.3490	1344.6642	672.8357	1343.6801	672.3437	12
11	1259.6994	630.3533	1242.6729	621.8401	1241.6888	621.3481	I	1260.6430	630.8251	1243.6165	622.3119	1242.6325	621.8199	11
12	1374.7264	687.8668	1357.6998	679.3535	1356.7158	678.8615	D	1147.5590	574.2831	1130.5324	565.7698	1129.5484	565.2778	10
13	1461.7584	731.3828	1444.7318	722.8696	1443.7478	722.3775	S	1032.5320	516.7696	1015.5055	508.2564	1014.5214	507.7644	9
14	1574.8424	787.9249	1557.8159	779.4116	1556.8319	778.9196	I	945.5000	473.2536	928.4734	464.7404	927.4894	464.2483	8
15	1702.9374	851.9723	1685.9109	843.4591	1684.9268	842.9671	K	832.4159	416.7116	815.3894	408.1983	814.4054	407.7063	7
16	1817.9644	909.4858	1800.9378	900.9725	1799.9538	900.4805	D	704.3210	352.6641	687.2944	344.1508	686.3104	343.6588	6
17	1947.0069	974.0071	1929.9804	965.4938	1928.9964	965.0018	E	589.2940	295.1506	572.2675	286.6374	571.2835	286.1454	5
18	2004.0284	1002.5178	1987.0019	994.0046	1986.0178	993.5126	G	460.2514	230.6293	443.2249	222.1161	442.2409	221.6241	4
19	2119.0554	1060.0313	2102.0288	1051.5180	2101.0448	1051.0260	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
20	2232.1394	1116.5733	2215.1129	1108.0601	2214.1289	1107.5681	L	288.2030	144.6051	271.1765	136.0919	0	0	2
21							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 99115.

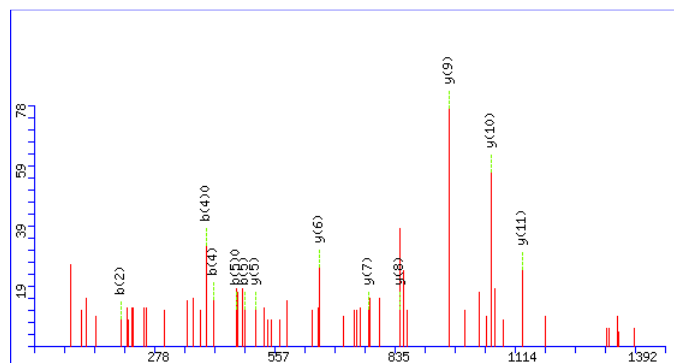
MS/MS Fragmentation of **SDLTAVLADFLAVR**:

Found in **IP100437565**

Title: 4.1.1.3226.4

Data file: Y:\TT5600(CiRA1)\2012-01\120129ry\120129ry_604A1-46_2_4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	88.0393	44.5233	0	0	70.0287	35.5180	S							15
2	203.0662	102.0368	0	0	185.0557	93.0315	D	1460.8108	730.9090	1443.7842	722.3957	1442.8002	721.9037	14
3	316.1503	158.5788	0	0	298.1397	149.5735	L	1345.7838	673.3955	1328.7573	664.8823	1327.7732	664.3903	13
4	417.1980	209.1026	0	0	399.1874	200.0974	T	1232.6997	616.8535	1215.6732	608.3402	1214.6892	607.8482	12
5	488.2351	244.6212	0	0	470.2245	235.6159	A	1131.6521	566.3297	1114.6255	557.8164	1113.6415	557.3244	11
6	587.3035	294.1554	0	0	569.2930	285.1501	V	1060.6150	530.8111	1043.5884	522.2978	1042.6044	521.8058	10
7	700.3876	350.6974	0	0	682.3770	341.6921	L	961.5465	481.2769	944.5200	472.7636	943.5360	472.2716	9
8	771.4247	386.2160	0	0	753.4141	377.2107	A	848.4625	424.7349	831.4359	416.2216	830.4519	415.7296	8
9	886.4516	443.7295	0	0	868.4411	434.7242	D	777.4254	389.2163	760.3988	380.7030	759.4148	380.2110	7
10	1033.5201	517.2637	0	0	1015.5095	508.2584	F	662.3984	331.7028	645.3719	323.1896	0	0	6
11	1090.5415	545.7744	0	0	1072.5310	536.7691	G	515.3300	258.1686	498.3035	249.6554	0	0	5
12	1203.6256	602.3164	0	0	1185.6150	593.3111	L	458.3085	229.6579	441.2820	221.1446	0	0	4
13	1274.6627	637.8350	0	0	1256.6521	628.8297	A	345.2245	173.1159	328.1979	164.6026	0	0	3
14	1373.7311	687.3692	0	0	1355.7205	678.3639	V	274.1874	137.5973	257.1608	129.0840	0	0	2
15							R	175.1190	88.0631	158.0924	79.5498	0	0	1

Peptide View

Peptide: 99620.

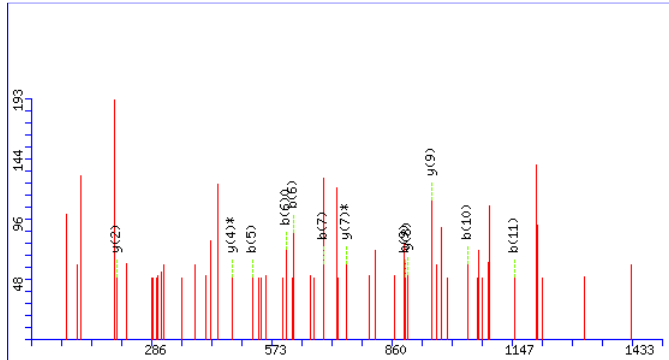
MS/MS Fragmentation of **DPDVTVAPVFLGESSVEYGK**:

Found in **IP100028040;IP100556443;IP100922814;IP100978189;IP100978788;IP100980633;IP100982107**

Title: 4.1.1.366.6

Data file: Y:\TT5600(CiRA1)\2012-02\120206ry\120206ry_aHDF1419-P10_2.4.mgf

ProteinPilot Peptide Confidence > 99%



#	b	b++	b*	b***	b0	b0++	SEQ	y	y++	y*	y***	y0	y0++	#
1	116.0342	58.5207	0	0	98.0237	49.5155	D							21
2	213.0870	107.0471	0	0	195.0764	98.0418	P	2107.0958	1054.0515	2090.0692	1045.5382	2089.0852	1045.0462	20
3	328.1139	164.5606	0	0	310.1034	155.5553	D	2010.0430	1005.5251	1993.0165	997.0119	1992.0324	996.5199	19
4	427.1823	214.0948	0	0	409.1718	205.0895	V	1895.0161	948.0117	1877.9895	939.4984	1877.0055	939.0064	18
5	528.2300	264.6186	0	0	510.2195	255.6134	T	1795.9476	898.4775	1778.9211	889.9642	1777.9371	889.4722	17
6	627.2984	314.1529	0	0	609.2879	305.1476	V	1694.9000	847.9536	1677.8734	839.4403	1676.8894	838.9483	16
7	698.3355	349.6714	0	0	680.3250	340.6661	A	1595.8316	798.4194	1578.8050	789.9061	1577.8210	789.4141	15
8	795.3883	398.1978	0	0	777.3777	389.1925	P	1524.7944	762.9009	1507.7679	754.3876	1506.7839	753.8956	14
9	894.4567	447.7320	0	0	876.4462	438.7267	V	1427.7417	714.3745	1410.7151	705.8612	1409.7311	705.3692	13
10	1041.5251	521.2662	0	0	1023.5146	512.2609	F	1328.6733	664.8403	1311.6467	656.3270	1310.6627	655.8350	12
11	1154.6092	577.8082	0	0	1136.5986	568.8030	L	1181.6048	591.3061	1164.5783	582.7928	1163.5943	582.3008	11
12	1267.6933	634.3503	0	0	1249.6827	625.3450	L	1068.5208	534.7640	1051.4942	526.2508	1050.5102	525.7587	10
13	1324.7147	662.8610	0	0	1306.7042	653.8557	G	955.4367	478.2220	938.4102	469.7087	937.4262	469.2167	9
14	1453.7573	727.3823	0	0	1435.7468	718.3770	E	898.4153	449.7113	881.3887	441.1980	880.4047	440.7060	8
15	1540.7894	770.8983	0	0	1522.7788	761.8930	S	769.3727	385.1900	752.3461	376.6767	751.3621	376.1847	7
16	1627.8214	814.4143	0	0	1609.8108	805.4090	S	682.3406	341.6740	665.3141	333.1607	664.3301	332.6687	6
17	1726.8898	863.9485	0	0	1708.8792	854.9433	V	595.3086	298.1579	578.2821	289.6447	577.2980	289.1527	5
18	1855.9324	928.4698	0	0	1837.9218	919.4645	E	496.2402	248.6237	479.2136	240.1105	478.2296	239.6185	4
19	2018.9957	1010.0015	0	0	2000.9852	1000.9962	Y	367.1976	184.1024	350.1710	175.5892	0	0	3
20	2076.0172	1038.5122	0	0	2058.0066	1029.5069	G	204.1343	102.5708	187.1077	94.0575	0	0	2
21							K	147.1128	74.0600	130.0863	65.5468	0	0	1