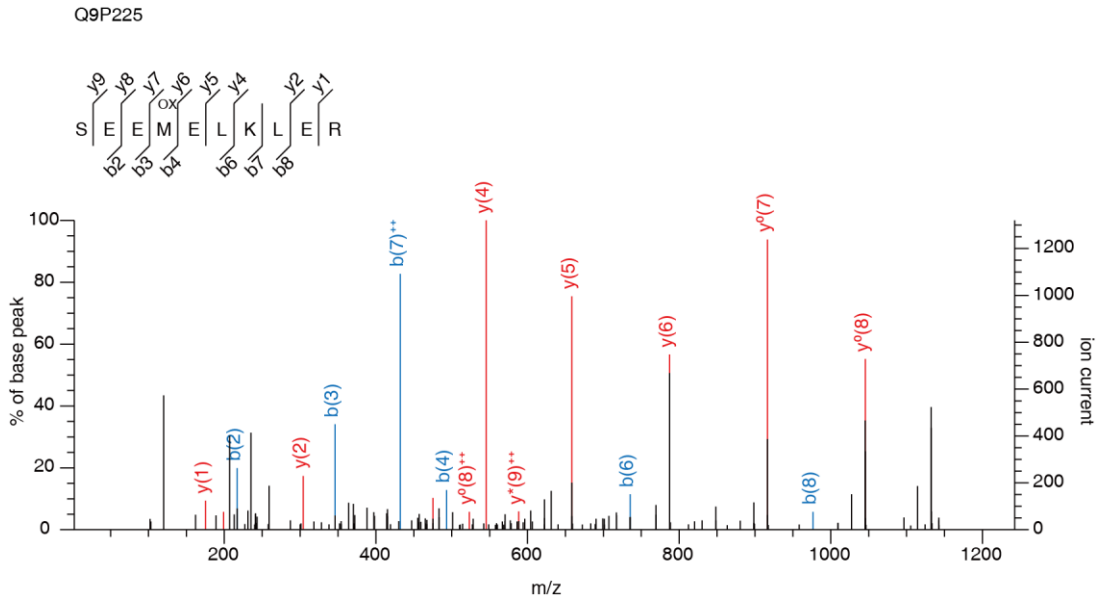
No. 1: **Q9P225**, Dynein heavy chain 2, axonemal OS=Homo sapiens GN=DNAH2 **PE=2** SV=3.

Unique peptide: MS/MS Fragmentation of **SEEMELKLER**.

Spectrum: Found in **Q9P225** in **MHCC97H-TSA** cell line (Ion Score cut-off=28).



Monoisotopic mass of neutral peptide Mr (calc): 1278.6125

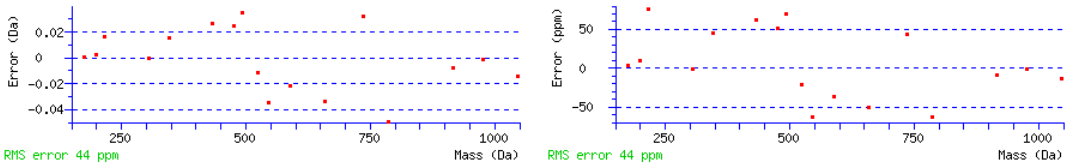
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

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

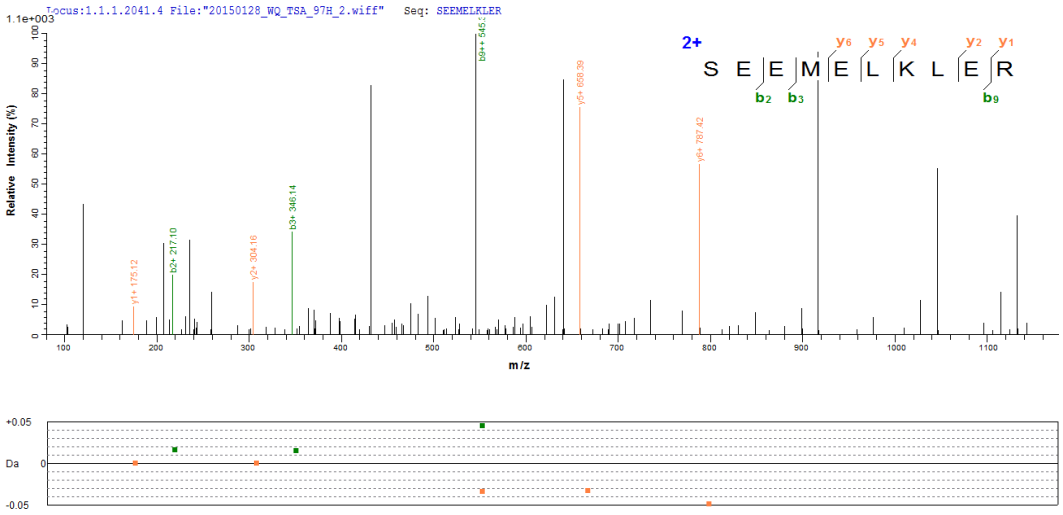
Ions Score: 36 **Expect:** 0.005

Matches: 17/142 fragment ions using 33 most intense peaks

#	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	*217.0819*	109.0446			199.0713	100.0393	E	1192.5878	596.7975	1175.5613	588.2843	1174.5773	587.7923	9
3	*346.1245*	173.5659			328.1139	164.5606	E	1063.5452	532.2762	1046.5187	523.7630	1045.5347	523.2710	8
4	*493.1599*	247.0836			475.1493	238.0783	M	934.5026	467.7550	917.4761	459.2417	916.4921	458.7497	7
5	622.2025	311.6049			604.1919	302.5996	E	*787.4672*	394.2373	770.4407	385.7240	769.4567	385.2320	6
6	*735.2865*	368.1469			717.2760	359.1416	L	*658.4246*	329.7160	641.3981	321.2027	640.4141	320.7107	5
7	863.3815	**432.1944**	846.3550	423.6811	845.3709	423.1891	K	*545.3406*	273.1739	528.3140	264.6606	527.3300	264.1686	4
8	*976.4656*	488.7364	959.4390	480.2232	958.4550	479.7311	L	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
9	1105.5082	553.2577	1088.4816	544.7444	1087.4976	544.2524	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



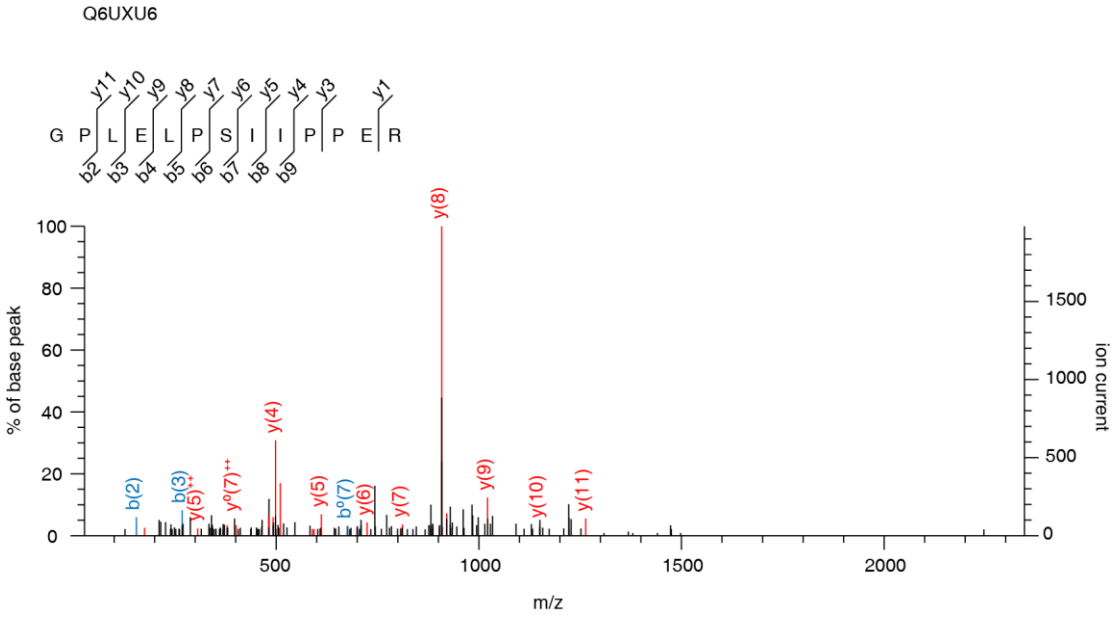
pLabel re-inspection:



No. 2: **Q6UXU6**, Transmembrane protein 92 OS=Homo sapiens GN=TMEM92 **PE=2** SV=1

Unique peptide 1: MS/MS Fragmentation of **GPLELPSIIPPER**.

Spectrum 1: Found in **Q6UXU6** in **A549-S2101** cell line (Ion Score cut-off=29).



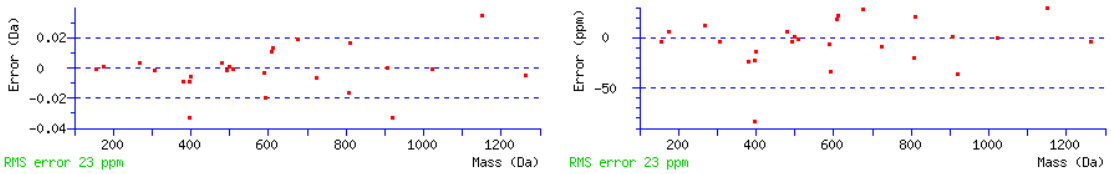
Monoisotopic mass of neutral peptide Mr(calc): 1416.7976

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

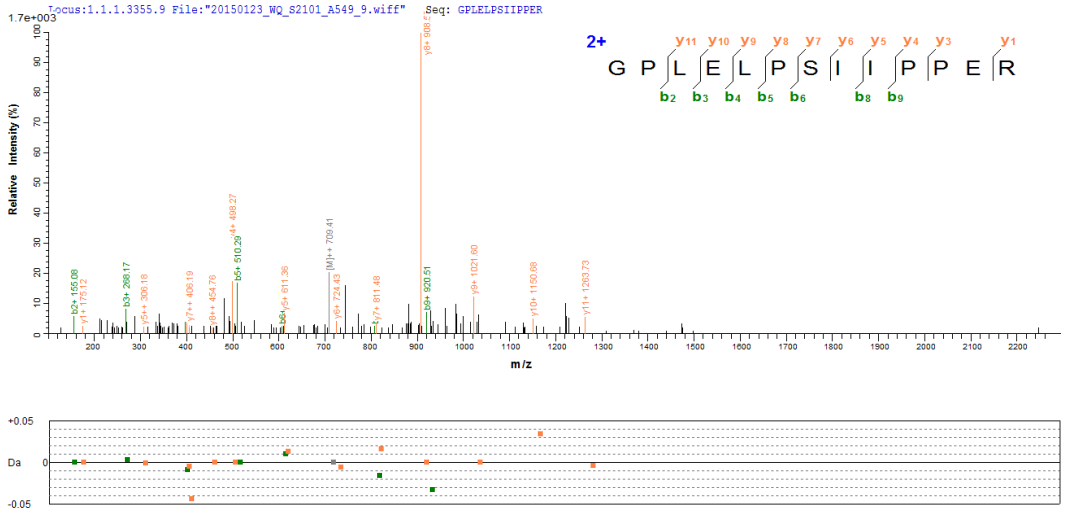
Ions Score: 43 **Expect:** 9e-005

Matches : 25/112 fragment ions using 95 most intense peaks

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180			G							13
2	155.0815	78.0444			P	1360.7835	680.8954	1343.7569	672.3821	1342.7729	671.8901	12
3	268.1656	134.5864			L	*1263.7307*	632.3690	1246.7042	623.8557	1245.7201	623.3637	11
4	397.2082	199.1077	379.1976	190.1024	E	*1150.6466*	575.8270	1133.6201	567.3137	1132.6361	566.8217	10
5	510.2922	255.6498	492.2817	246.6445	L	*1021.6041*	511.3057	1004.5775	502.7924	1003.5935	502.3004	9
6	607.3450	304.1761	589.3344	295.1709	P	*908.5200*	454.7636	891.4934	446.2504	890.5094	445.7584	8
7	694.3770	347.6921	676.3665	338.6869	S	*811.4672*	406.2373	794.4407	397.7240	793.4567	397.2320	7
8	807.4611	404.2342	789.4505	395.2289	I	*724.4352*	362.7212	707.4087	354.2080	706.4246	353.7160	6
9	920.5451	460.7762	902.5346	451.7709	I	*611.3511*	306.1792	594.3246	297.6659	593.3406	297.1739	5
10	1017.5979	509.3026	999.5873	500.2973	P	*498.2671*	249.6372	481.2405	241.1239	480.2565	240.6319	4
11	1114.6507	557.8290	1096.6401	548.8237	P	*401.2143*	201.1108	384.1878	192.5975	383.2037	192.1055	3
12	1243.6933	622.3503	1225.6827	613.3450	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



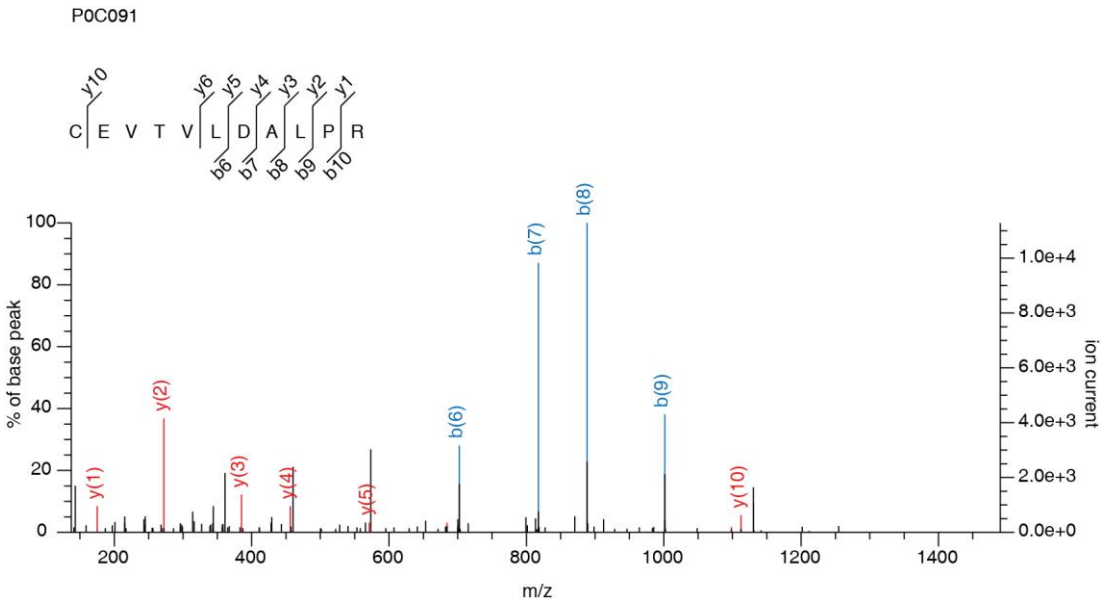
pLabel re-inspection:



No. 3: P0C091, FRAS1-related extracellular matrix protein 3 OS=Homo sapiens GN=FREM3 **PE=2** SV=2.

Unique peptide: MS/MS Fragmentation of **CEVTVLDALPR**.

Spectrum: Found in **P0C091** in **MHCC97H-S2101** cell line (Ion Score cut-off=28).



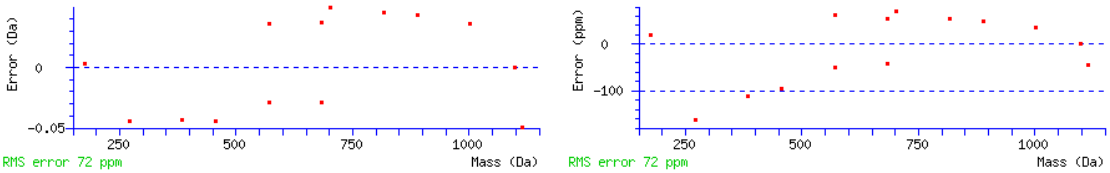
Monoisotopic mass of neutral peptide Mr (calc): 1271.6544

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

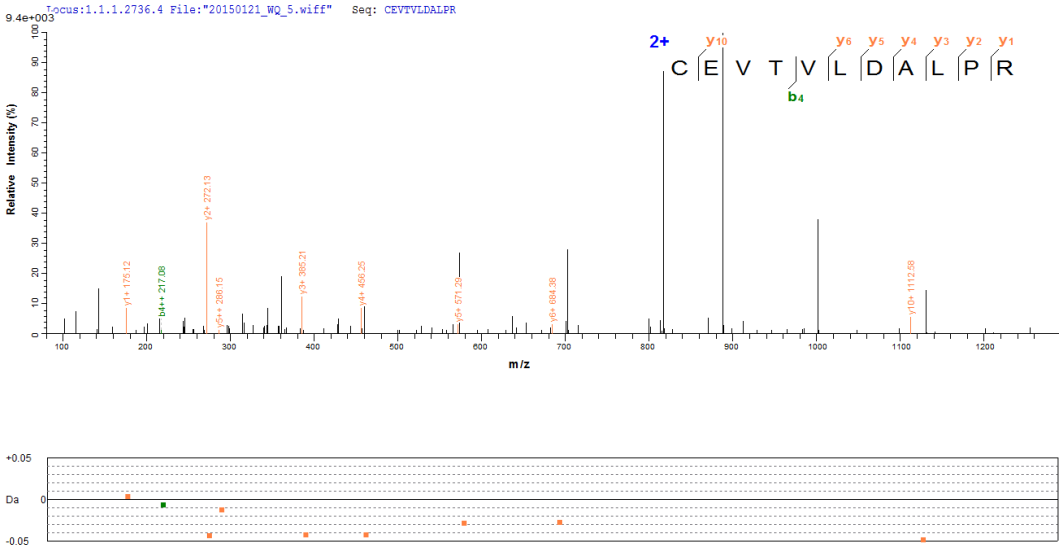
Ions Score: 33 **Expect:** 0.015

Matches: 14/90 fragment ions using 35 most intense peaks

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	161.0379	81.0226			C							11
2	290.0805	145.5439	272.0700	136.5386	E	*1112.6310*	556.8191	1095.6045	548.3059	1094.6204	547.8139	10
3	389.1489	195.0781	371.1384	186.0728	V	983.5884	492.2978	966.5619	483.7846	965.5778	483.2926	9
4	490.1966	245.6019	472.1860	236.5967	T	884.5200	442.7636	867.4934	434.2504	866.5094	433.7584	8
5	589.2650	295.1362	571.2545	286.1309	V	783.4723	392.2398	766.4458	383.7265	765.4617	383.2345	7
6	702.3491	351.6782	684.3385	342.6729	L	*684.4039*	342.7056	667.3774	334.1923	666.3933	333.7003	6
7	817.3760	409.1917	799.3655	400.1864	D	*571.3198*	286.1636	554.2933	277.6503	553.3093	277.1583	5
8	888.4131	444.7102	870.4026	435.7049	A	*456.2929*	228.6501	439.2663	220.1368			4
9	1001.4972	501.2522	983.4866	492.2470	L	*385.2558*	193.1315	368.2292	184.6183			3
10	1098.5500	549.7786	1080.5394	540.7733	P	*272.1717*	136.5895	255.1452	128.0762			2
11					R	*175.1190*	88.0631	158.0924	79.5498			1



pLabel re-inspection:

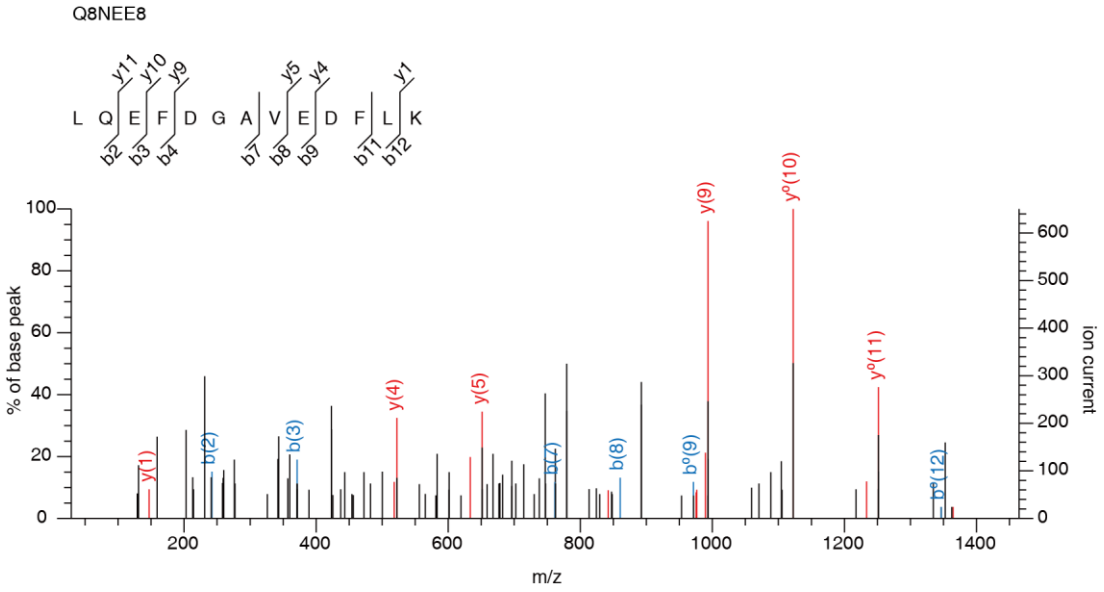


No. 4: **Q8NEE8**, Tetratricopeptide repeat protein 16 OS=Homo sapiens GN=TTC16 **PE=2**

SV=2.

Unique peptide: MS/MS Fragmentation of **LQEFDGAVEDFLK**.

Spectrum: Found in **Q8NEE8** in **MHCC97H-S2101** cell line (Ion Score cut-off=28).



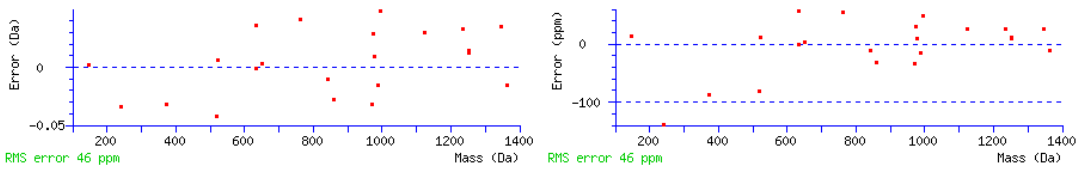
Monoisotopic mass of neutral peptide Mr (calc): 1509.7351

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

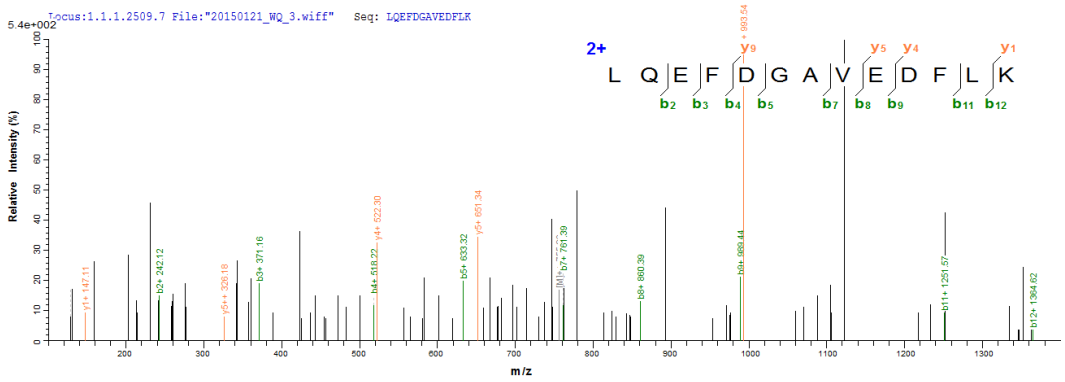
Ions Score: 30 **Expect:** 0.0031

Matches: 22/132 fragment ions using 90 most intense peaks

#	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	*242.1499*	121.5786	225.1234	113.0653			Q	1397.6583	699.3328	1380.6318	690.8195	1379.6478	690.3275	12
3	*371.1925*	186.0999	354.1660	177.5866	353.1819	177.0946	E	1269.5998	635.3035	1252.5732	626.7902	1251.5892	626.2982	11
4	*518.2609*	259.6341	501.2344	251.1208	500.2504	250.6288	F	1140.5572	570.7822	1123.5306	562.2689	1122.5466	561.7769	10
5	*633.2879*	317.1476	616.2613	308.6343	615.2773	308.1423	D	**993.4888**	497.2480	976.4622	488.7347	975.4782	488.2427	9
6	690.3093	345.6583	673.2828	337.1450	672.2988	336.6530	G	878.4618	439.7345	861.4353	431.2213	860.4512	430.7293	8
7	*761.3464*	381.1769	744.3199	372.6636	743.3359	372.1716	A	821.4403	411.2238	804.4138	402.7105	803.4298	402.2185	7
8	*860.4149*	430.7111	843.3883	422.1978	842.4043	421.7058	V	750.4032	375.7053	733.3767	367.1920	732.3927	366.7000	6
9	*989.4575*	495.2324	972.4309	486.7191	971.4469	486.2271	E	**651.3348**	326.1710	634.3083	317.6578	633.3243	317.1658	5
10	1104.4844	552.7458	1087.4578	544.2326	1086.4738	543.7406	D	**522.2922**	261.6498	505.2657	253.1365	504.2817	252.6445	4
11	*1251.5528*	626.2800	1234.5263	617.7668	1233.5422	617.2748	F	407.2653	204.1363	390.2387	195.6230			3
12	*1364.6369*	682.8221	1347.6103	674.3088	1346.6263	673.8168	L	260.1969	130.6021	243.1703	122.0888			2
13							K	**147.1128**	74.0600	130.0863	65.5468			1



pLabel re-inspection:

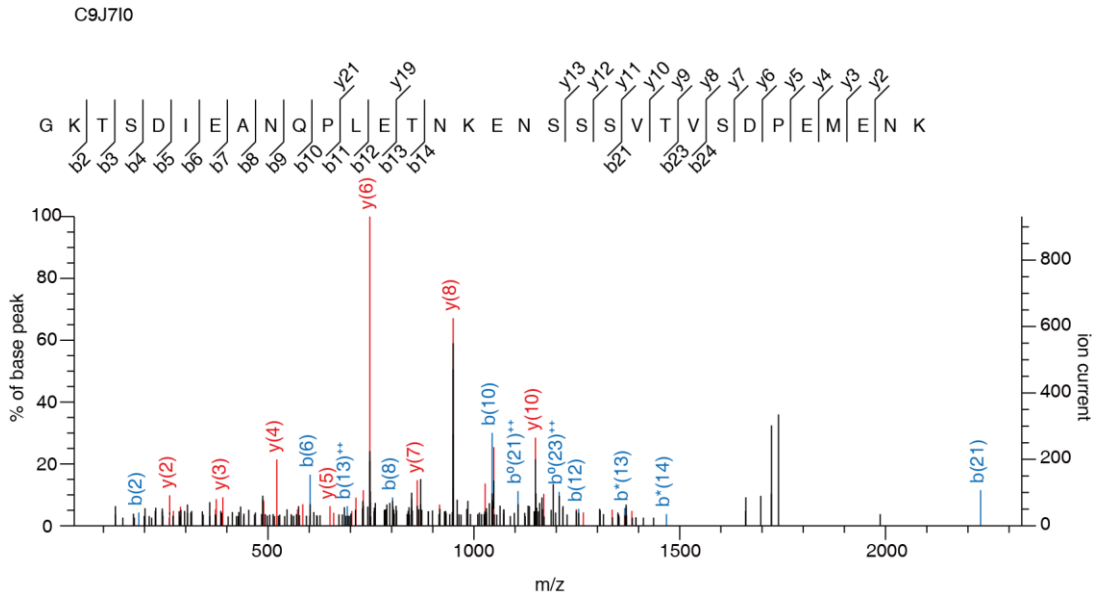


No. 5: **C9J7I0**, UBAP1-MVB12-associated (UMA)-domain containing protein 1 OS=Homo sapiens GN=UMAD1 **PE=3** SV=1.

Unique peptide 1: MS/MS Fragmentation of

GKTSDIEANQPLETNKENSSSVTVSDPEMENK.

Spectrum 1: Found in **C9J7I0** in **MHCC97H-GSK126** cell line (Ion Score cut-off=26).



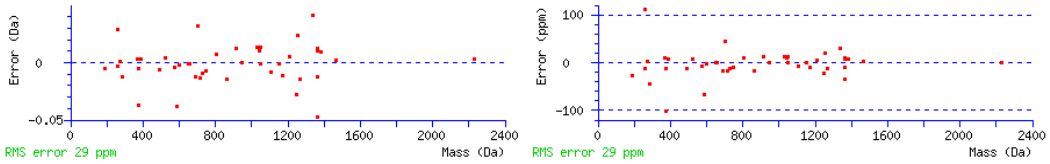
Monoisotopic mass of neutral peptide Mr (calc): 3477.6053

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

Ions Score: 68 **Expect:** 4.2e-007

Matches: 44/362 fragment ions using 101 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							32
2	*186.1237*	93.5655	169.0972	85.0522			K	3421.5911	1711.2992	3404.5646	1702.7859	3403.5806	1702.2939	31
3	*287.1714*	144.0893	270.1448	135.5761	269.1608	135.0840	T	3293.4962	1647.2517	3276.4696	1638.7384	3275.4856	1638.2464	30
4	*374.2034*	187.6053	357.1769	179.0921	356.1928	178.6001	S	3192.4485	1596.7279	3175.4219	1588.2146	3174.4379	1587.7226	29
5	*489.2304*	245.1188	472.2038	236.6055	471.2198	236.1135	D	3105.4165	1553.2119	3088.3899	1544.6986	3087.4059	1544.2066	28
6	*602.3144*	301.6608	585.2879	293.1476	584.3039	292.6556	I	2990.3895	1495.6984	2973.3630	1487.1851	2972.3789	1486.6931	27
7	*731.3570*	366.1821	714.3305	357.6689	713.3464	357.1769	E	2877.3054	1439.1564	2860.2789	1430.6431	2859.2949	1430.1511	26
8	*802.3941*	401.7007	785.3676	393.1874	784.3836	392.6954	A	2748.2629	1374.6351	2731.2363	1366.1218	2730.2523	1365.6298	25
9	*916.4371*	458.7222	899.4105	450.2089	898.4265	449.7169	N	2677.2257	1339.1165	2660.1992	1330.6032	2659.2152	1330.1112	24
10	*1044.4956*	522.7515	1027.4691	514.2382	1026.4851	513.7462	Q	2563.1828	1282.0950	2546.1563	1273.5818	2545.1723	1273.0898	23
11	1141.5484	**571.2778**	1124.5218	562.7646	1123.5378	562.2726	P	2435.1242	1218.0658	2418.0977	1209.5525	2417.1137	1209.0605	22
12	*1254.6325*	627.8199	1237.6059	619.3066	1236.6219	618.8146	L	2338.0715	**1169.5394**	2321.0449	1161.0261	2320.0609	1160.5341	21
13	*1383.6751*	**692.3412**	1366.6485	683.8279	1365.6645	683.3359	E	2224.9874	1112.9973	2207.9609	1104.4841	2206.9768	1103.9921	20
14	1484.7227	742.8650	1467.6962	734.3517	1466.7122	733.8597	T	2095.9448	**1048.4760**	2078.9183	1039.9628	2077.9343	1039.4708	19
15	1598.7657	799.8865	1581.7391	791.3732	1580.7551	790.8812	N	1994.8971	997.9522	1977.8706	989.4389	1976.8866	988.9469	18
16	1726.8606	863.9339	1709.8341	855.4207	1708.8501	854.9287	K	1880.8542	940.9307	1863.8277	932.4175	1862.8436	931.9255	17
17	1855.9032	928.4552	1838.8767	919.9420	1837.8926	919.4500	E	1752.7592	876.8833	1735.7327	868.3700	1734.7487	867.8780	16
18	1969.9461	985.4767	1952.9196	976.9634	1951.9356	976.4714	N	1623.7167	812.3620	1606.6901	803.8487	1605.7061	803.3567	15
19	2056.9782	1028.9927	2039.9516	1020.4794	2038.9676	1019.9874	S	1509.6737	755.3405	1492.6472	746.8272	1491.6632	746.3352	14
20	2144.0102	1072.5087	2126.9836	1063.9955	2125.9996	1063.5035	S	1422.6417	711.8245	1405.6152	703.3112	1404.6311	702.8192	13
21	*2231.0422*	1116.0247	2214.0157	1107.5115	2213.0317	1107.0195	S	*1335.6097*	668.3085	1318.5831	659.7952	1317.5991	659.3032	12
22	2330.1106	1165.5590	2313.0841	1157.0457	2312.1001	1156.5537	V	*1248.5776*	624.7925	1231.5511	616.2792	1230.5671	615.7872	11
23	2431.1583	1216.0828	2414.1318	1207.5695	2413.1478	1207.0775	T	*1149.5092*	575.2583	1132.4827	566.7450	1131.4987	566.2530	10
24	2530.2267	**1265.6170**	2513.2002	1257.1037	2512.2162	1256.6117	V	*1048.4616*	524.7344	1031.4350	516.2211	1030.4510	515.7291	9
25	2617.2588	1309.1330	2600.2322	1300.6197	2599.2482	1300.1277	S	*949.3931*	475.2002	932.3666	466.6869	931.3826	466.1949	8
26	2732.2857	**1366.6465**	2715.2592	1358.1332	2714.2751	1357.6412	D	*862.3611*	431.6842	845.3346	423.1709	844.3505	422.6789	7
27	2829.3385	1415.1729	2812.3119	1406.6596	2811.3279	1406.1676	P	*747.3342*	**374.1707**	730.3076	365.6574	729.3236	365.1654	6
28	2958.3811	1479.6942	2941.3545	1471.1809	2940.3705	1470.6889	E	*650.2814*	325.6443	633.2549	317.1311	632.2708	316.6391	5
29	3089.4215	1545.2144	3072.3950	1536.7011	3071.4110	1536.2091	M	*521.2388*	**261.1230**	504.2123	252.6098	503.2282	252.1178	4
30	3218.4641	1609.7357	3201.4376	1601.2224	3200.4536	1600.7304	E	*390.1983*	195.6028	373.1718	187.0895	372.1878	186.5975	3
31	3332.5071	1666.7572	3315.4805	1658.2439	3314.4965	1657.7519	N	*261.1557*	131.0815	244.1292	122.5682			2
32							K	147.1128	74.0600	130.0863	65.5468			1



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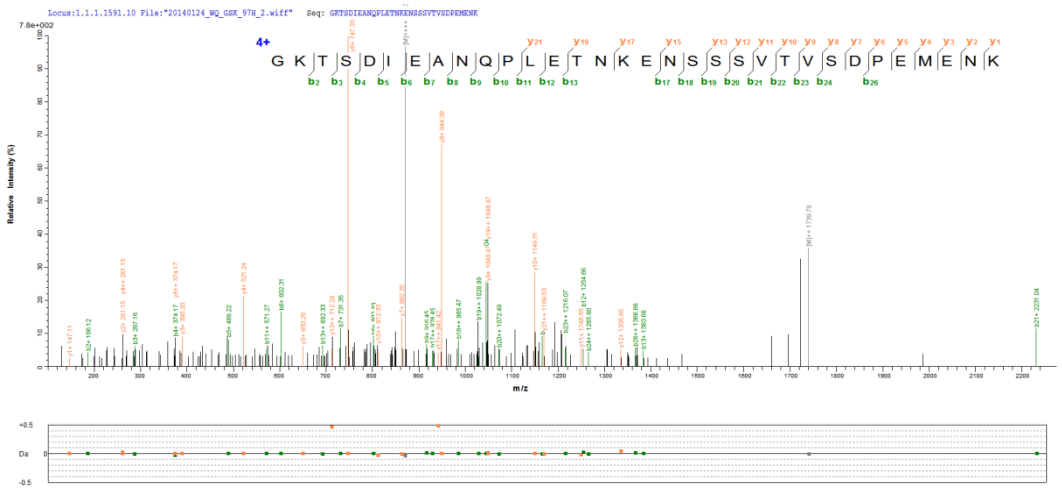
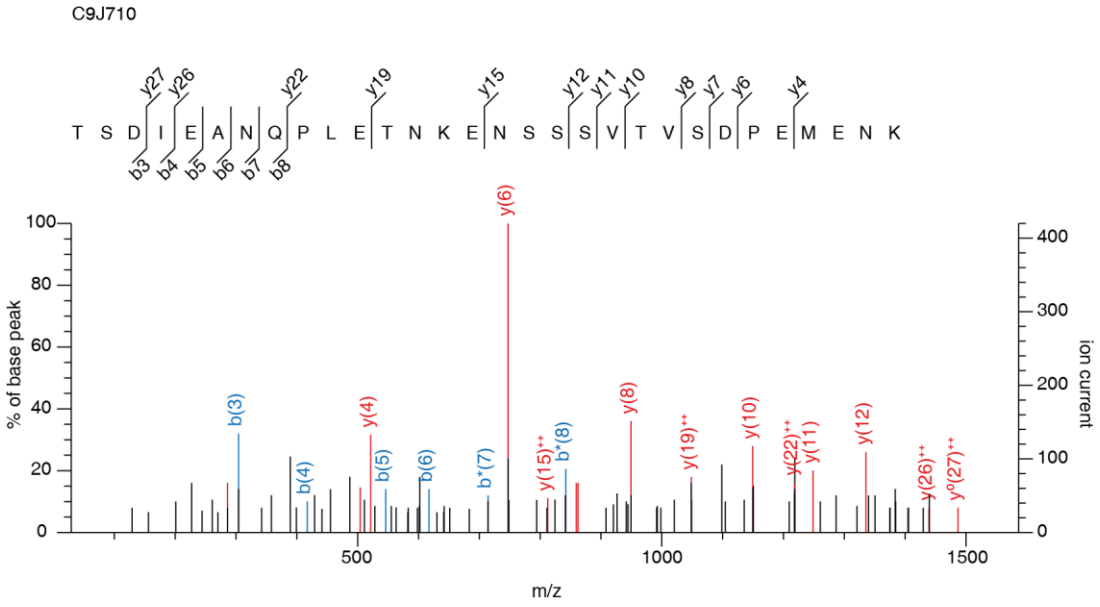


Unique peptide 2: MS/MS Fragmentation of

TSDIEANQPLETNKENSSSVTVSDPEMENK.

Spectrum 2: Found in **C9J7I0** in **MHCC97H-GSK126** cell line (Ion Score cut-off=26).



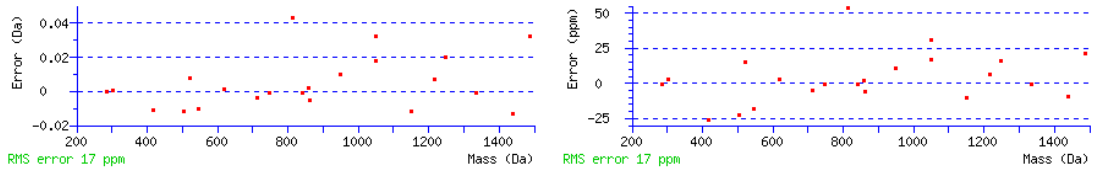
Monoisotopic mass of neutral peptide Mr (calc): 3292.4888

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

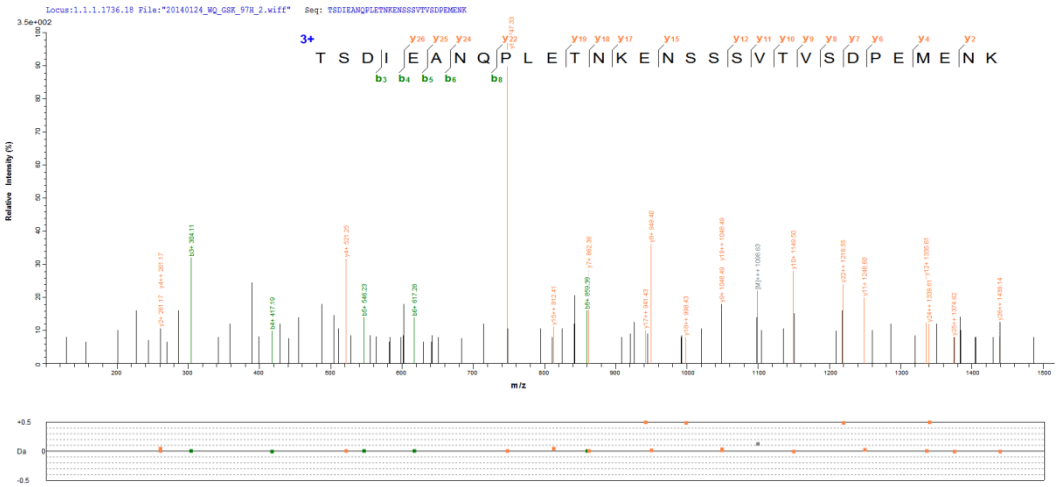
Ions Score: 44 **Expect:** 8e-005

Matches: 22/332 fragment ions using 42 most intense peaks

#	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							30
2	189.0870	95.0471			171.0764	86.0418	S	3192.4485	1596.7279	3175.4219	1588.2146	3174.4379	1587.7226	29
3	***304.1139***	152.5606			286.1034	143.5553	D	3105.4165	1553.2119	3088.3899	1544.6986	3087.4059	1544.2066	28
4	***417.1980***	209.1026			399.1874	200.0974	I	2990.3895	1495.6984	2973.3630	1487.1851	2972.3789	1486.6931	27
5	***546.2406***	273.6239			528.2300	264.6186	E	2877.3054	**1439.1564**	2860.2789	1430.6431	2859.2949	1430.1511	26
6	***617.2777***	309.1425			599.2671	300.1372	A	2748.2629	1374.6351	2731.2363	1366.1218	2730.2523	1365.6298	25
7	731.3206	366.1640	714.2941	357.6507	713.3101	357.1587	N	2677.2257	1339.1165	2660.1992	1330.6032	2659.2152	1330.1112	24
8	***859.3792***	430.1932	842.3527	421.6800	841.3686	421.1880	Q	2563.1828	1282.0950	2546.1563	1273.5818	2545.1723	1273.0898	23
9	956.4320	478.7196	939.4054	470.2063	938.4214	469.7143	P	2435.1242	**1218.0658**	2418.0977	1209.5525	2417.1137	1209.0605	22
10	1069.5160	535.2617	1052.4895	526.7484	1051.5055	526.2564	L	2338.0715	1169.5394	2321.0449	1161.0261	2320.0609	1160.5341	21
11	1198.5586	599.7829	1181.5321	591.2697	1180.5481	590.7777	E	2224.9874	1112.9973	2207.9609	1104.4841	2206.9768	1103.9921	20
12	1299.6063	650.3068	1282.5798	641.7935	1281.5957	641.3015	T	2095.9448	**1048.4760**	2078.9183	1039.9628	2077.9343	1039.4708	19
13	1413.6492	707.3283	1396.6227	698.8150	1395.6387	698.3230	N	1994.8971	997.9522	1977.8706	989.4389	1976.8866	988.9469	18
14	1541.7442	771.3757	1524.7176	762.8625	1523.7336	762.3705	K	1880.8542	940.9307	1863.8277	932.4175	1862.8436	931.9255	17
15	1670.7868	835.8970	1653.7602	827.3838	1652.7762	826.8917	E	1752.7592	876.8833	1735.7327	868.3700	1734.7487	867.8780	16
16	1784.8297	892.9185	1767.8032	884.4052	1766.8191	883.9132	N	1623.7167	**812.3620**	1606.6901	803.8487	1605.7061	803.3567	15
17	1871.8617	936.4345	1854.8352	927.9212	1853.8512	927.4292	S	1509.6737	755.3405	1492.6472	746.8272	1491.6632	746.3352	14
18	1958.8938	979.9505	1941.8672	971.4372	1940.8832	970.9452	S	1422.6417	711.8245	1405.6152	703.3112	1404.6311	702.8192	13
19	2045.9258	1023.4665	2028.8992	1014.9533	2027.9152	1014.4613	S	***1335.6097***	668.3085	1318.5831	659.7952	1317.5991	659.3032	12
20	2144.9942	1073.0007	2127.9677	1064.4875	2126.9836	1063.9955	V	***1248.5776***	624.7925	1231.5511	616.2792	1230.5671	615.7872	11
21	2246.0419	1123.5246	2229.0153	1115.0113	2228.0313	1114.5193	T	***1149.5092***	575.2583	1132.4827	566.7450	1131.4987	566.2530	10
22	2345.1103	1173.0588	2328.0838	1164.5455	2327.0997	1164.0535	V	***1048.4616***	524.7344	1031.4350	516.2211	1030.4510	515.7291	9
23	2432.1423	1216.5748	2415.1158	1208.0615	2414.1318	1207.5695	S	***949.3931***	475.2002	932.3666	466.6869	931.3826	466.1949	8
24	2547.1693	1274.0883	2530.1427	1265.5750	2529.1587	1265.0830	D	***862.3611***	431.6842	845.3346	423.1709	844.3505	422.6789	7
25	2644.2220	1322.6147	2627.1955	1314.1014	2626.2115	1313.6094	P	***747.3342***	374.1707	730.3076	365.6574	729.3236	365.1654	6
26	2773.2646	1387.1360	2756.2381	1378.6227	2755.2541	1378.1307	E	650.2814	325.6443	633.2549	317.1311	632.2708	316.6391	5
27	2904.3051	1452.6562	2887.2786	1444.1429	2886.2946	1443.6509	M	***521.2388***	261.1230	504.2123	252.6098	503.2282	252.1178	4
28	3033.3477	1517.1775	3016.3212	1508.6642	3015.3371	1508.1722	E	390.1983	195.6028	373.1718	187.0895	372.1878	186.5975	3
29	3147.3906	1574.1990	3130.3641	1565.6857	3129.3801	1565.1937	N	261.1557	131.0815	244.1292	122.5682			2
30							K	147.1128	74.0600	130.0863	65.5468			1

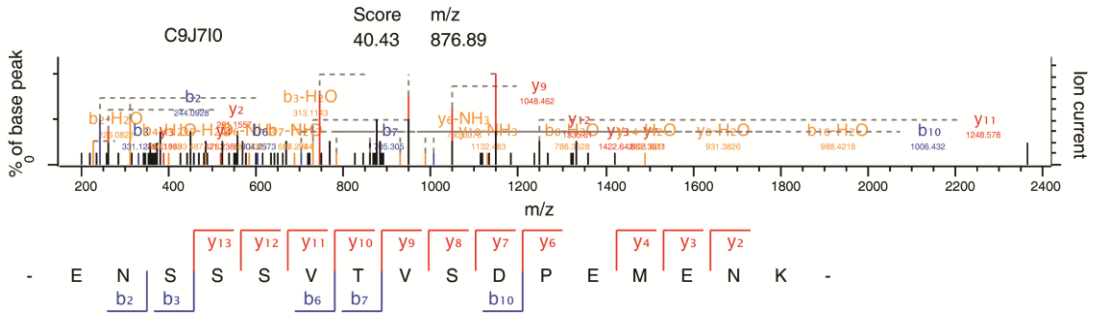


pLabel re-inspection:



Unique peptide 3: MS/MS Fragmentation of **ENSSSVTVSDPEMENK**

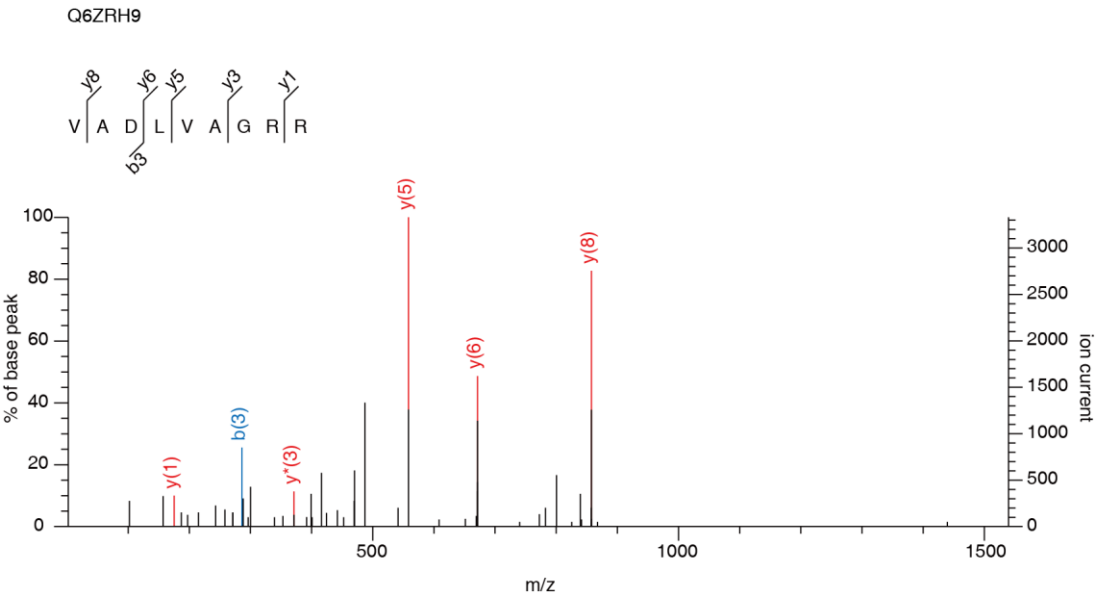
Spectrum: Found in **C9J7I0**, in **MHCC97H-S2101** cell line (Ion Score cut-off=26).



No. 6: **Q6ZRH9**, Uncharacterized protein FLJ46347 OS=Homo sapiens **PE=2** SV=1.

Unique peptide: MS/MS Fragmentation of **VADLVAGRR**.

Spectrum: Found in **Q6ZRH9** in **MHCC97H-S2101** cell line (Ion Score cut-off=28).



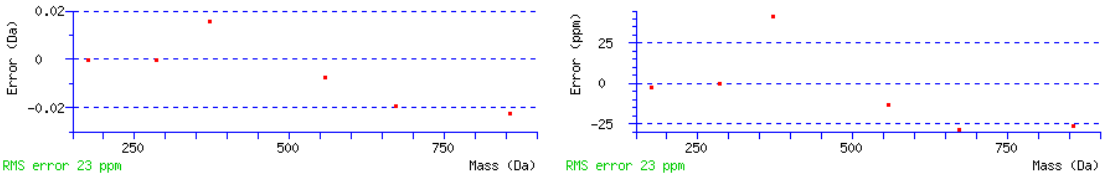
Monoisotopic mass of neutral peptide Mr (calc): 955.5563

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

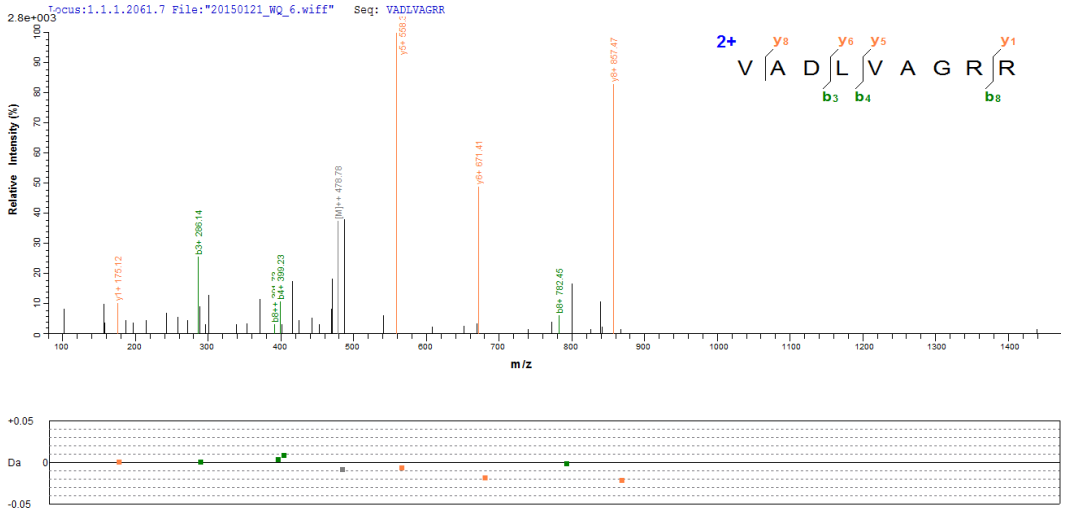
Ions Score: 30 **Expect:** 0.023

Matches: 6/66 fragment ions using 8 most intense peaks

#	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	171.1128	86.0600					A	***857.4952***	429.2512	840.4686	420.7380	839.4846	420.2459	8
3	**286.1397**	143.5735			268.1292	134.5682	D	786.4581	393.7327	769.4315	385.2194	768.4475	384.7274	7
4	399.2238	200.1155			381.2132	191.1103	L	***671.4311***	336.2192	654.4046	327.7059			6
5	498.2922	249.6498			480.2817	240.6445	V	***558.3471***	279.6772	541.3205	271.1639			5
6	569.3293	285.1683			551.3188	276.1630	A	459.2786	230.1430	442.2521	221.6297			4
7	626.3508	313.6790			608.3402	304.6738	G	388.2415	194.6244	371.2150	186.1111			3
8	782.4519	391.7296	765.4254	383.2163	764.4413	382.7243	R	331.2201	166.1137	314.1935	157.6004			2
9							R	***175.1190***	88.0631	158.0924	79.5498			1



pLabel re-inspection:

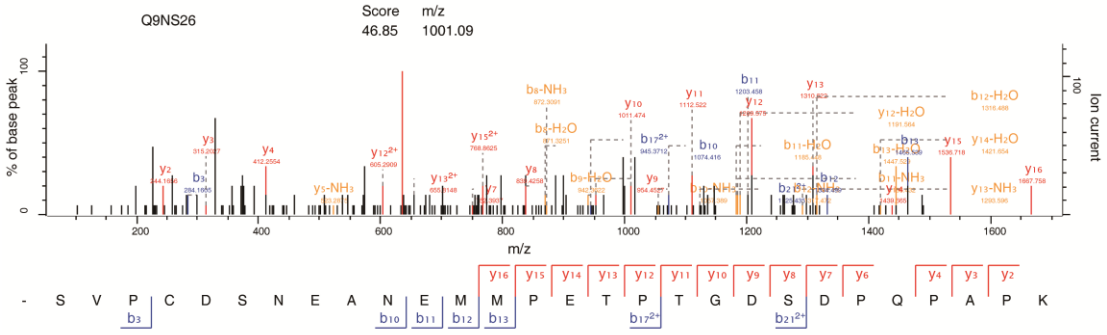


No. 7 Q9NS26, Sperm protein associated with the nucleus on the X chromosome A

OS=Homo sapiens GN=SPANXA1 **PE=2** SV=1

Unique peptide: MS/MS Fragmentation of **SVPCDSNEANEMMPETPTGDSDPQPAPK.**

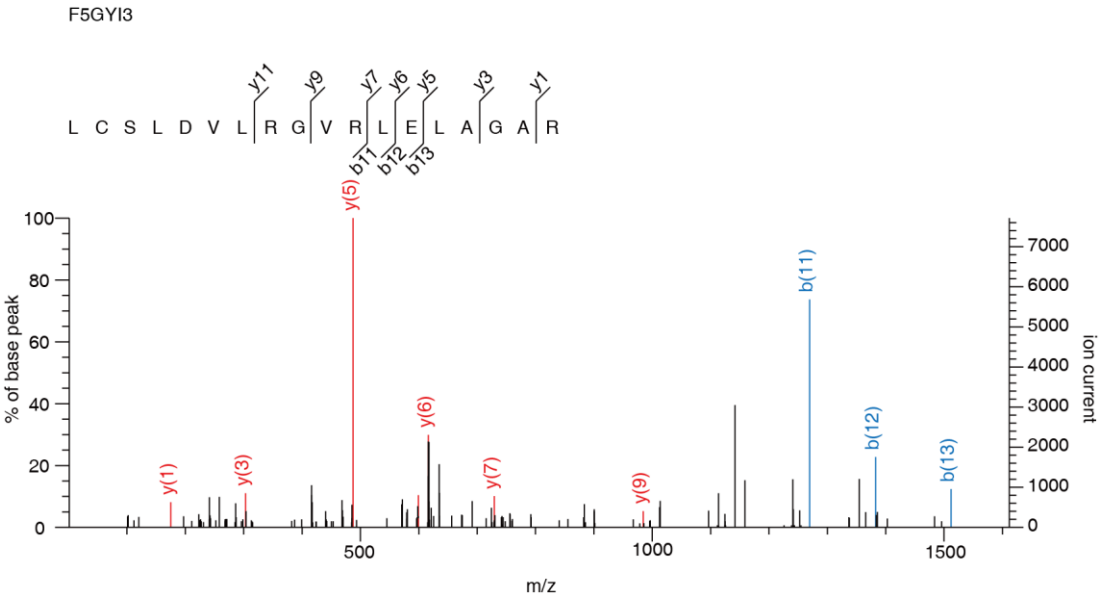
Spectrum: Found in **Q9NS26** in **MHCC97H-GSK126** cell line (Ion Score cut-off=26).



No.8: F5GYI3, Ubiquitin-associated protein 1-like OS=Homo sapiens GN=UBAP1L **PE=2** SV=1.

Unique peptide: MS/MS Fragmentation of **LCSLDVLRGVRLELAGAR**.

Spectrum: Found in **F5GYI3** in **MHCC97H-GSK126** cell line (Ion Score cut-off=26).



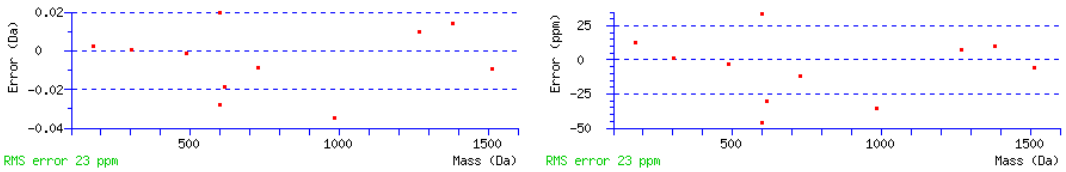
Monoisotopic mass of neutral peptide Mr (calc): 1997.1204

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

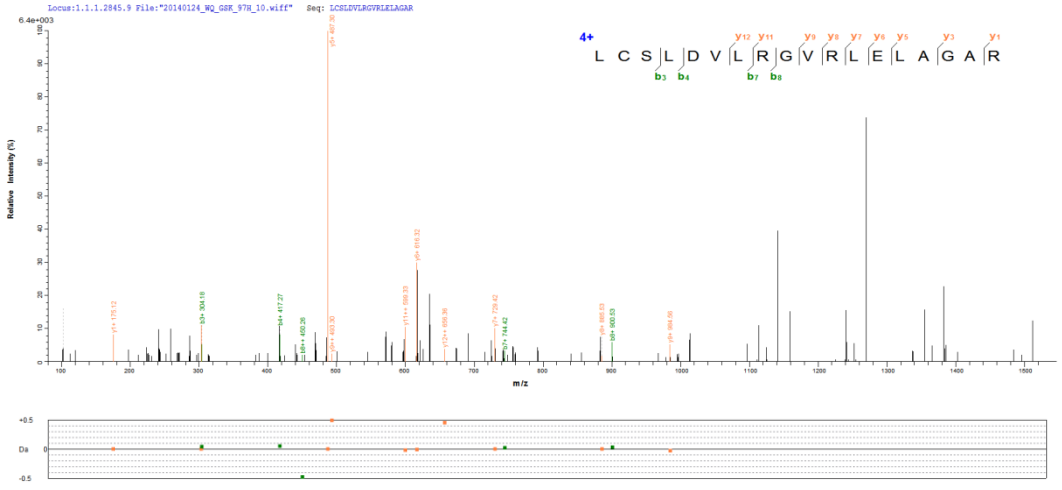
Ions Score: 36 **Expect:** 0.0024

Matches: 11/176 fragment ions using 15 most intense peaks

#	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	274.1220	137.5646					C	1885.0436	943.0255	1868.0171	934.5122	1867.0331	934.0202	17
3	361.1540	181.0806			343.1435	172.0754	S	1725.0130	863.0101	1707.9864	854.4969	1707.0024	854.0048	16
4	474.2381	237.6227			456.2275	228.6174	L	1637.9809	819.4941	1620.9544	810.9808	1619.9704	810.4888	15
5	589.2650	295.1362			571.2545	286.1309	D	1524.8969	762.9521	1507.8703	754.4388	1506.8863	753.9468	14
6	688.3334	344.6704			670.3229	335.6651	V	1409.8699	705.4386	1392.8434	696.9253	1391.8594	696.4333	13
7	801.4175	401.2124			783.4069	392.2071	L	1310.8015	655.9044	1293.7750	647.3911	1292.7910	646.8991	12
8	957.5186	479.2629	940.4921	470.7497	939.5080	470.2577	R	1197.7175	**599.3624**	1180.6909	590.8491	1179.7069	590.3571	11
9	1014.5401	507.7737	997.5135	499.2604	996.5295	498.7684	G	1041.6164	521.3118	1024.5898	512.7985	1023.6058	512.3065	10
10	1113.6085	557.3079	1096.5819	548.7946	1095.5979	548.3026	V	***984.5949***	492.8011	967.5683	484.2878	966.5843	483.7958	9
11	**1269.7096**	635.3584	1252.6831	626.8452	1251.6990	626.3532	R	885.5265	443.2669	868.4999	434.7536	867.5159	434.2616	8
12	**1382.7937**	691.9005	1365.7671	683.3872	1364.7831	682.8952	L	***729.4254***	365.2163	712.3988	356.7030	711.4148	356.2110	7
13	**1511.8363**	756.4218	1494.8097	747.9085	1493.8257	747.4165	E	***616.3413***	308.6743	599.3148	300.1610	598.3307	299.6690	6
14	1624.9203	812.9638	1607.8938	804.4505	1606.9098	803.9585	L	***487.2987***	244.1530	470.2722	235.6397			5
15	1695.9574	848.4824	1678.9309	839.9691	1677.9469	839.4771	A	374.2146	187.6110	357.1881	179.0977			4
16	1752.9789	876.9931	1735.9524	868.4798	1734.9683	867.9878	G	***303.1775***	152.0924	286.1510	143.5791			3
17	1824.0160	912.5116	1806.9895	903.9984	1806.0054	903.5064	A	246.1561	123.5817	229.1295	115.0684			2
18							R	***175.1190***	88.0631	158.0924	79.5498			1



pLabel re-inspection:

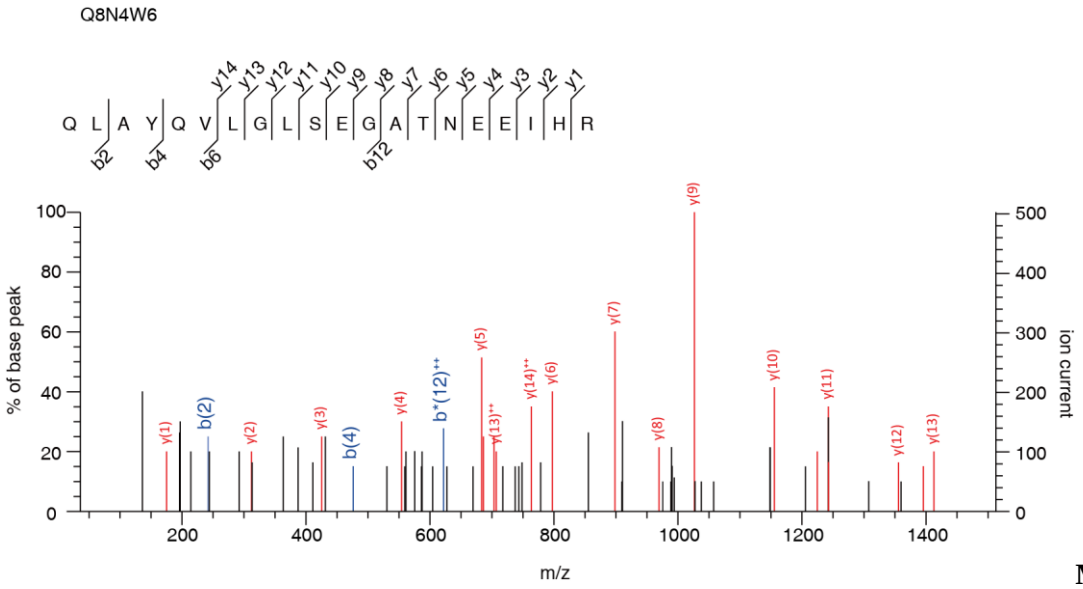


No. 9: **Q8N4W6**, DnaJ homolog subfamily C member 22 OS=Homo sapiens GN=DNAJC22

PE=2 SV=1.

Unique peptide: MS/MS Fragmentation of **QLAYQVLGLSEGATNEEIHR**.

Spectrum: Found in **Q8N4W6** in **MHCC97H** cell line (Ion Score cut-off=29).



M

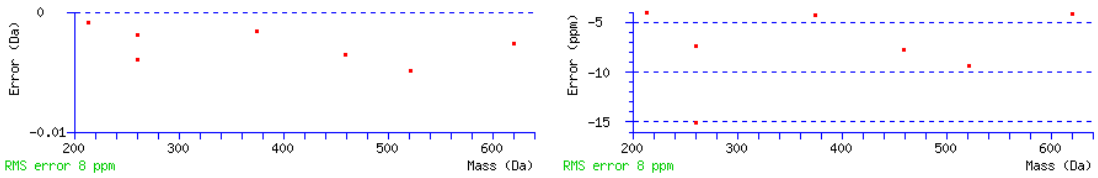
onoisotopic mass of neutral peptide Mr (calc): 2227.1233

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

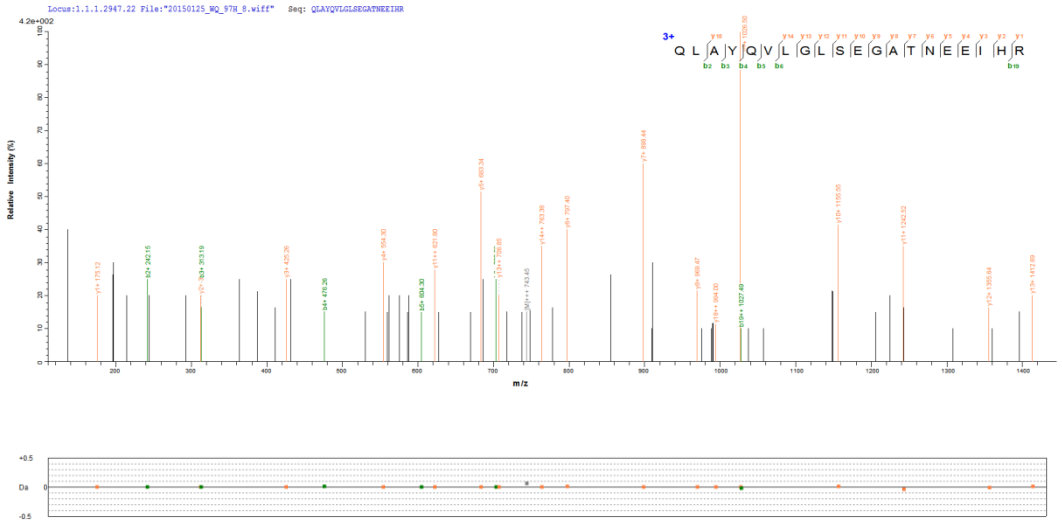
Ions Score: 77 **Expect:** 6.3e-008

Matches: 25/204 fragment ions using 48 most intense peaks

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	100.0757	50.5415			V					7
2	**213.1598**	107.0835			I	733.4607	367.2340	716.4341	358.7207	6
3	312.2282	156.6177			V	***620.3766***	310.6919	603.3501	302.1787	5
4	**459.2966**	230.1519			F	***521.3082***	**261.1577**	504.2817	252.6445	4
5	572.3806	286.6940			L	***374.2398***	187.6235	357.2132	179.1103	3
6	686.4236	343.7154	669.3970	335.2022	N	***261.1557***	131.0815	244.1292	122.5682	2
7					K	147.1128	74.0600	130.0863	65.5468	1



pLabel re-inspection:

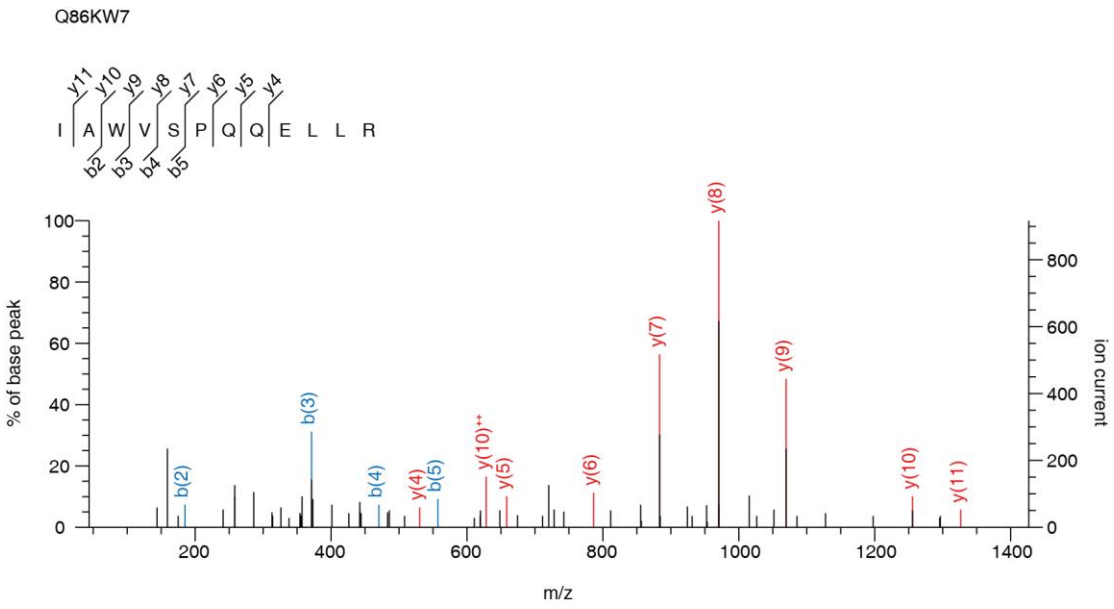


No. 10: **Q86WK7**, Amphoterin-induced protein 3 OS=Homo sapiens GN=AMIGO3 **PE=2**

SV=1

Unique peptide 1:MS/MS Fragmentation of **IAWVSPQQELLR**

Spectrum 1: Found in **Q86WK7** in **HCT116-TSA** cell line (Ion Score cut-off=27)



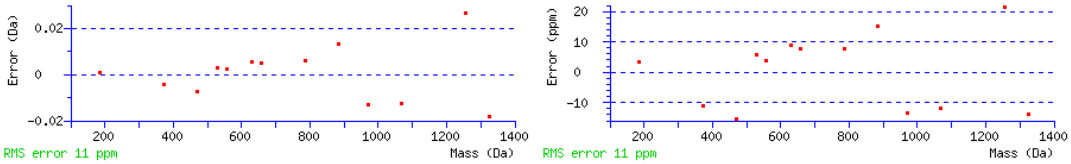
Monoisotopic mass of neutral peptide Mr(calc): 1438.7932

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

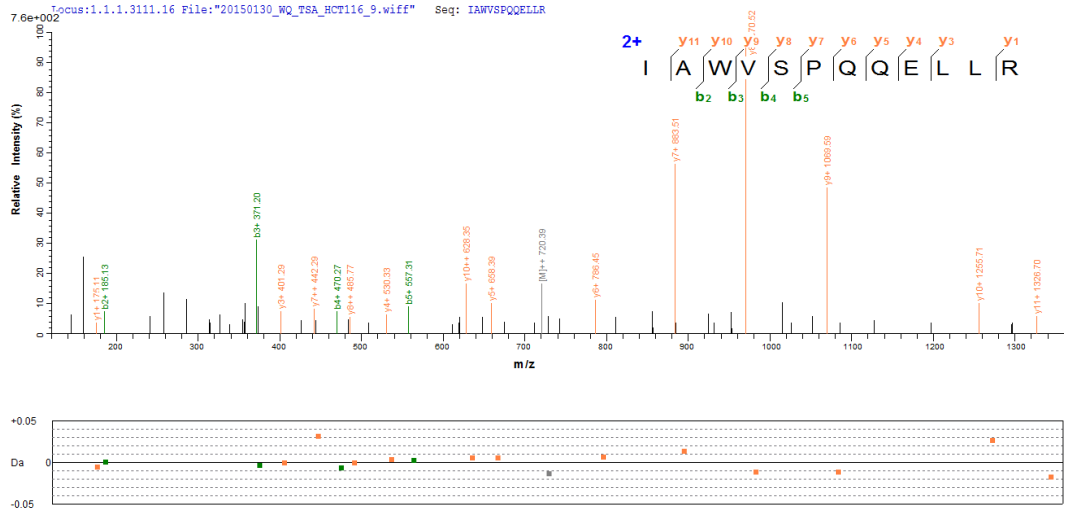
Ions Score: 65 **Expect:** 1.6e-006

Matches : 13/106 fragment ions using 23 most intense peaks

#	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	185.1285	93.0679					A	*1326.7165*	663.8619	1309.6899	655.3486	1308.7059	654.8566	11
3	371.2078	186.1075					W	*1255.6793*	628.3433	1238.6528	619.8300	1237.6688	619.3380	10
4	470.2762	235.6417					V	*1069.6000*	535.3037	1052.5735	526.7904	1051.5895	526.2984	9
5	557.3082	279.1577			539.2976	270.1525	S	*970.5316*	485.7694	953.5051	477.2562	952.5211	476.7642	8
6	654.3610	327.6841			636.3504	318.6788	P	*883.4996*	442.2534	866.4730	433.7402	865.4890	433.2482	7
7	782.4196	391.7134	765.3930	383.2001	764.4090	382.7081	Q	*786.4468*	393.7271	769.4203	385.2138	768.4363	384.7218	6
8	910.4781	455.7427	893.4516	447.2294	892.4676	446.7374	Q	*658.3883*	329.6978	641.3617	321.1845	640.3777	320.6925	5
9	1039.5207	520.2640	1022.4942	511.7507	1021.5102	511.2587	E	*530.3297*	265.6685	513.3031	257.1552	512.3191	256.6632	4
10	1152.6048	576.8060	1135.5782	568.2928	1134.5942	567.8007	L	401.2871	201.1472	384.2605	192.6339			3
11	1265.6888	633.3481	1248.6623	624.8348	1247.6783	624.3428	L	288.2030	144.6051	271.1765	136.0919			2
12							R	175.1190	88.0631	158.0924	79.5498			1

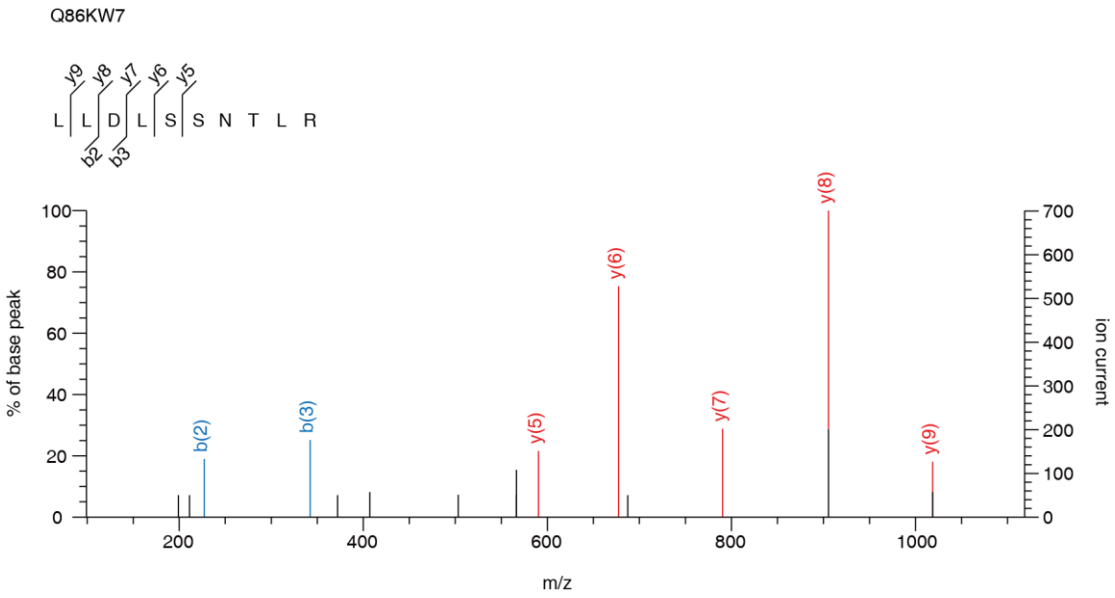


pLabel re-inspection:



Unique peptide 2:MS/MS Fragmentation of **LLDLSSNTLR**

Spectrum 1: Found in **Q86WK7** in **HCT116-TSA** cell line (Ion Score cut-off=27).



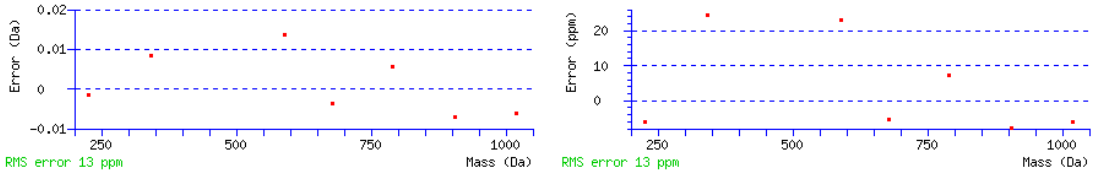
Monoisotopic mass of neutral peptide Mr(calc): 1130.6295

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

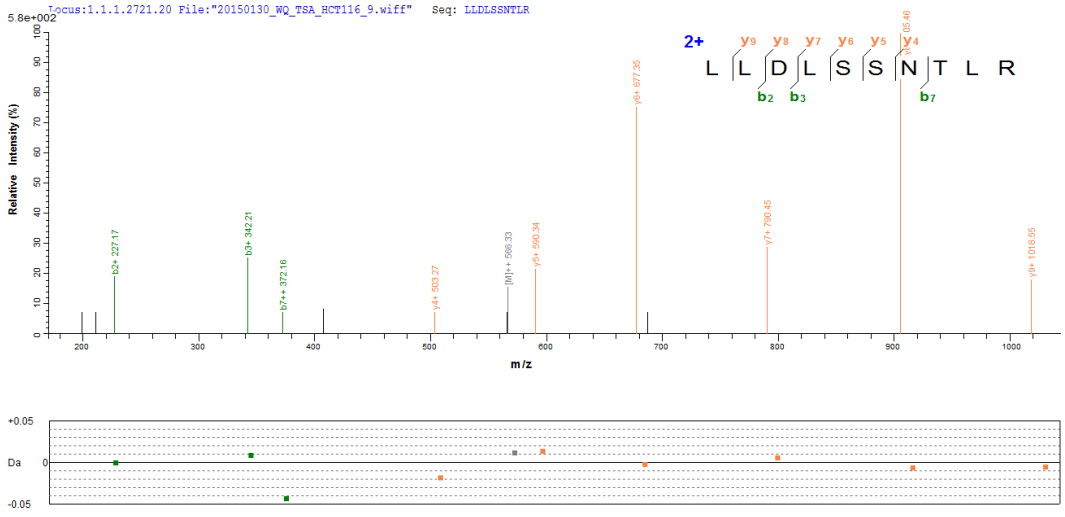
Ions Score: 46 **Expect:** 0.00091

Matches : 7/88 fragment ions using 8 most intense peaks

#	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	*1018.5527*	509.7800	1001.5262	501.2667	1000.5422	500.7747	9
3	342.2023	171.6048			324.1918	162.5995	D	*905.4687*	453.2380	888.4421	444.7247	887.4581	444.2327	8
4	455.2864	228.1468			437.2758	219.1416	L	*790.4417*	395.7245	773.4152	387.2112	772.4312	386.7192	7
5	542.3184	271.6629			524.3079	262.6576	S	*677.3577*	339.1825	660.3311	330.6692	659.3471	330.1772	6
6	629.3505	315.1789			611.3399	306.1736	S	*590.3257*	295.6665	573.2991	287.1532	572.3151	286.6612	5
7	743.3934	372.2003	726.3668	363.6871	725.3828	363.1951	N	503.2936	252.1504	486.2671	243.6372	485.2831	243.1452	4
8	844.4411	422.7242	827.4145	414.2109	826.4305	413.7189	T	389.2507	195.1290	372.2241	186.6157	371.2401	186.1237	3
9	957.5251	479.2662	940.4986	470.7529	939.5146	470.2609	L	288.2030	144.6051	271.1765	136.0919			2
10							R	175.1190	88.0631	158.0924	79.5498			1



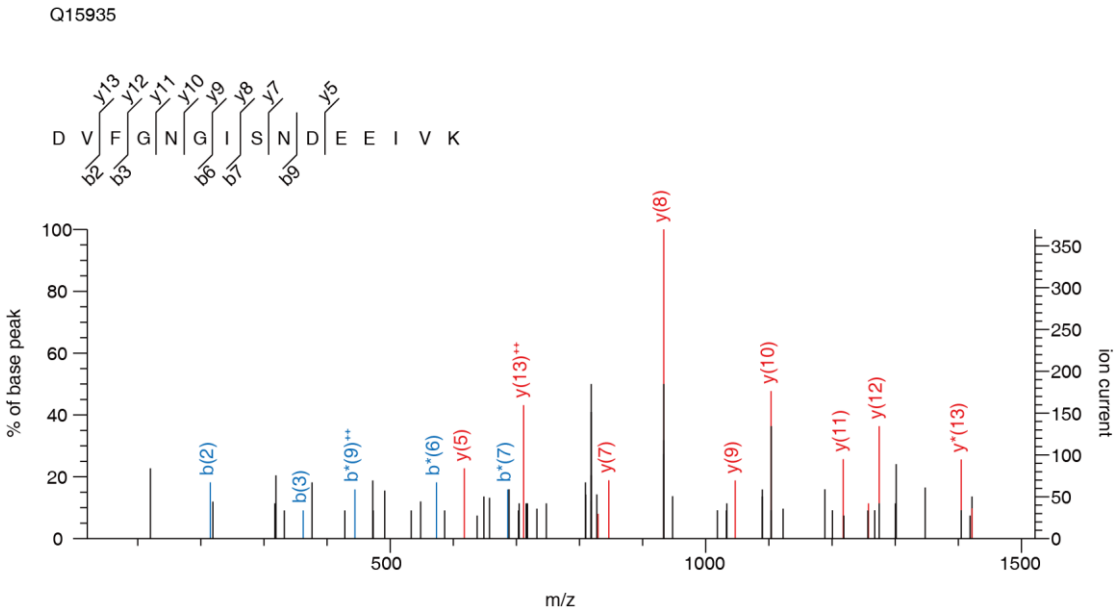
pLabel re-inspection:



No. 11: **Q15935**, Zinc finger protein 77 OS=Homo sapiens GN=ZNF77 **PE=2** SV=2

Unique peptide 1:MS/MS Fragmentation of **DVFGNGISNDEEIVK**

Spectrum 1: Found in **Q15935** in **HCT116-TSA** cell line (Ion Score cut-off=27).



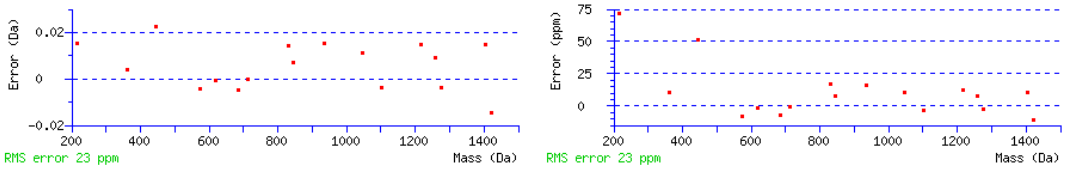
Monoisotopic mass of neutral peptide Mr(calc): 1634.7788

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

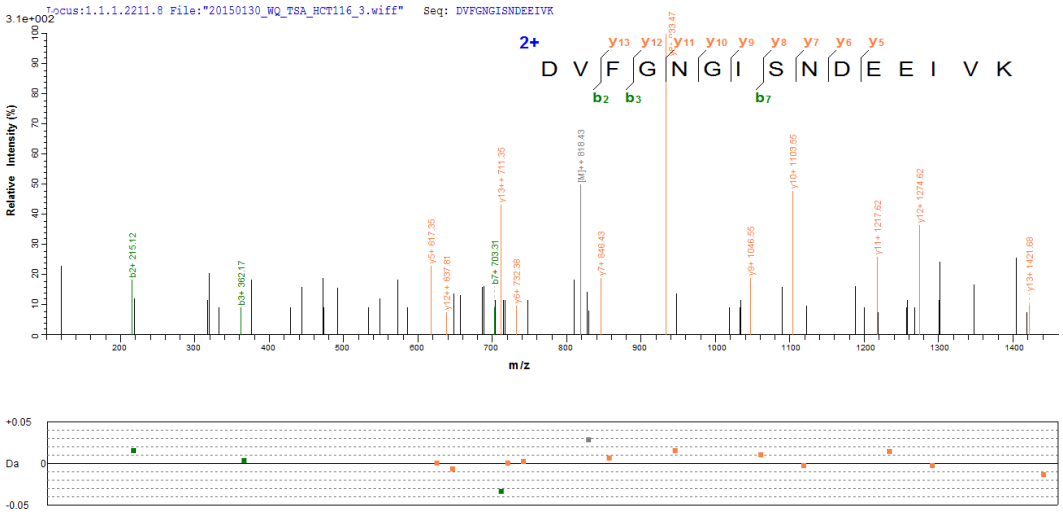
Ions Score: 47 **Expect:** 0.00026

Matches : 17/154 fragment ions using 40 most intense peaks

#	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	1520.7591	760.8832	1503.7326	752.3699	1502.7485	751.8779	14
3	362.1710	181.5892			344.1605	172.5839	F	*1421.6907*	711.3490	1404.6642	702.8357	1403.6801	702.3437	13
4	419.1925	210.0999			401.1819	201.0946	G	*1274.6223*	637.8148	1257.5957	629.3015	1256.6117	628.8095	12
5	533.2354	267.1214	516.2089	258.6081	515.2249	258.1161	N	*1217.6008*	609.3040	1200.5743	600.7908	1199.5903	600.2988	11
6	590.2569	295.6321	573.2304	287.1188	572.2463	286.6268	G	*1103.5579*	552.2826	1086.5313	543.7693	1085.5473	543.2773	10
7	703.3410	352.1741	686.3144	343.6608	685.3304	343.1688	I	*1046.5364*	523.7719	1029.5099	515.2586	1028.5259	514.7666	9
8	790.3730	395.6901	773.3464	387.1769	772.3624	386.6849	S	*933.4524*	467.2298	916.4258	458.7165	915.4418	458.2245	8
9	904.4159	452.7116	887.3894	444.1983	886.4054	443.7063	N	*846.4203*	423.7138	829.3938	415.2005	828.4098	414.7085	7
10	1019.4429	510.2251	1002.4163	501.7118	1001.4323	501.2198	D	732.3774	366.6923	715.3509	358.1791	714.3668	357.6871	6
11	1148.4855	574.7464	1131.4589	566.2331	1130.4749	565.7411	E	*617.3505*	309.1789	600.3239	300.6656	599.3399	300.1736	5
12	1277.5281	639.2677	1260.5015	630.7544	1259.5175	630.2624	E	488.3079	244.6576	471.2813	236.1443	470.2973	235.6523	4
13	1390.6121	695.8097	1373.5856	687.2964	1372.6015	686.8044	I	359.2653	180.1363	342.2387	171.6230			3
14	1489.6805	745.3439	1472.6540	736.8306	1471.6700	736.3386	V	246.1812	123.5942	229.1547	115.0810			2
15							K	147.1128	74.0600	130.0863	65.5468			1



pLabel re-inspection:

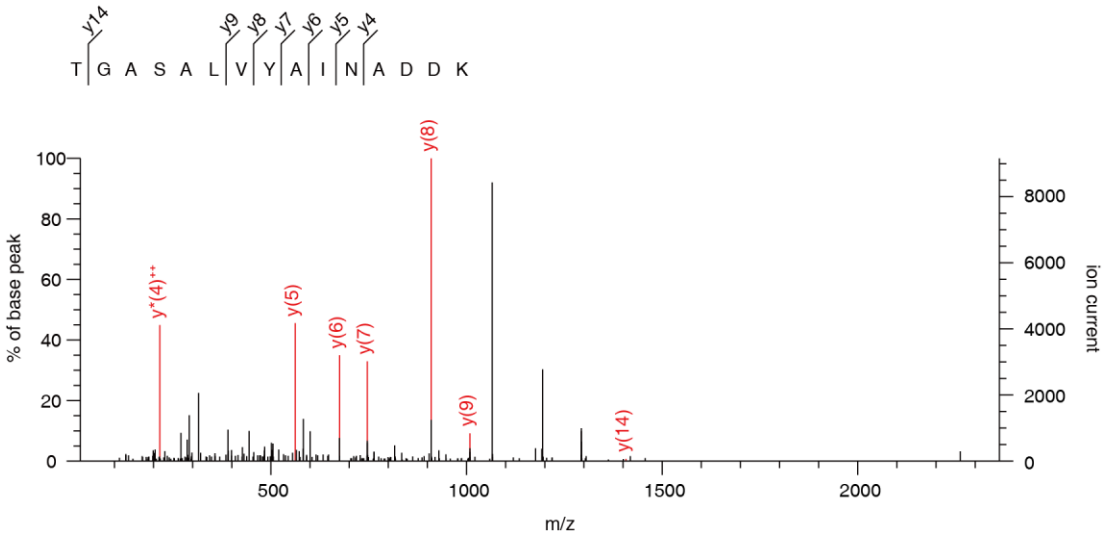


No. 12: P0C6C1, Ankyrin repeat domain-containing protein 34C OS=Homo sapiens GN=ANKRD34C **PE=2** SV=2.

Unique peptide: MS/MS Fragmentation of **TGASALVYAINADDK**.

Spectrum: Found in **P0C6C1** in **MHCC97H** cell line (Ion Score cut-off=29).

P0C6C1



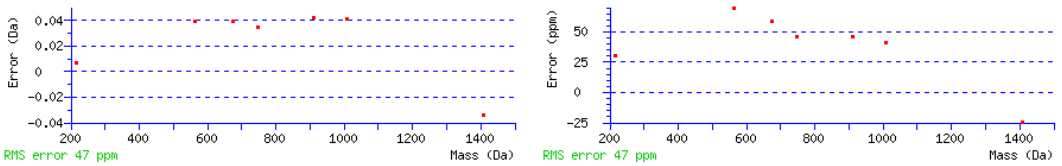
Monoisotopic mass of neutral peptide Mr (calc): 1507.7518

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

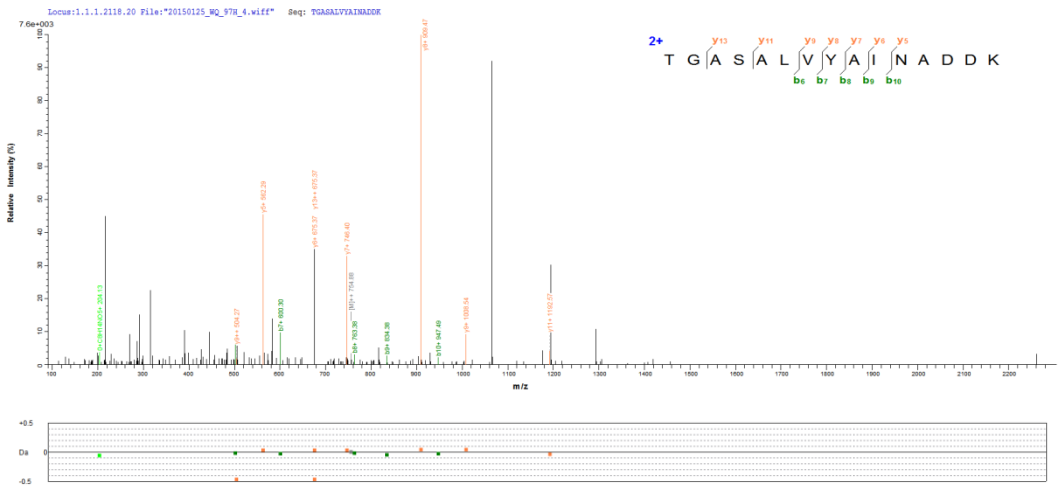
Ions Score: 32 **Expect:** 0.0059

Matches: 7/146 fragment ions using 14 most intense peaks

#	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							15
2	159.0764	80.0418			141.0659	71.0366	G	*1407.7114*	704.3594	1390.6849	695.8461	1389.7009	695.3541	14
3	230.1135	115.5604			212.1030	106.5551	A	1350.6900	675.8486	1333.6634	667.3353	1332.6794	666.8433	13
4	317.1456	159.0764			299.1350	150.0711	S	1279.6529	640.3301	1262.6263	631.8168	1261.6423	631.3248	12
5	388.1827	194.5950			370.1721	185.5897	A	1192.6208	596.8141	1175.5943	588.3008	1174.6103	587.8088	11
6	501.2667	251.1370			483.2562	242.1317	L	1121.5837	561.2955	1104.5572	552.7822	1103.5732	552.2902	10
7	600.3352	300.6712			582.3246	291.6659	V	*1008.4997*	504.7535	991.4731	496.2402	990.4891	495.7482	9
8	763.3985	382.2029			745.3879	373.1976	Y	*909.4312*	455.2193	892.4047	446.7060	891.4207	446.2140	8
9	834.4356	417.7214			816.4250	408.7162	A	*746.3679*	373.6876	729.3414	365.1743	728.3573	364.6823	7
10	947.5197	474.2635			929.5091	465.2582	I	*675.3308*	338.1690	658.3042	329.6558	657.3202	329.1638	6
11	1061.5626	531.2849	1044.5360	522.7717	1043.5520	522.2796	N	*562.2467*	281.6270	545.2202	273.1137	544.2362	272.6217	5
12	1132.5997	566.8035	1115.5732	558.2902	1114.5891	557.7982	A	448.2038	224.6055	431.1773	216.0923	430.1932	215.6003	4
13	1247.6266	624.3170	1230.6001	615.8037	1229.6161	615.3117	D	377.1667	189.0870	360.1401	180.5737	359.1561	180.0817	3
14	1362.6536	681.8304	1345.6270	673.3172	1344.6430	672.8251	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
15							K	147.1128	74.0600	130.0863	65.5468			1



pLabel re-inspection:

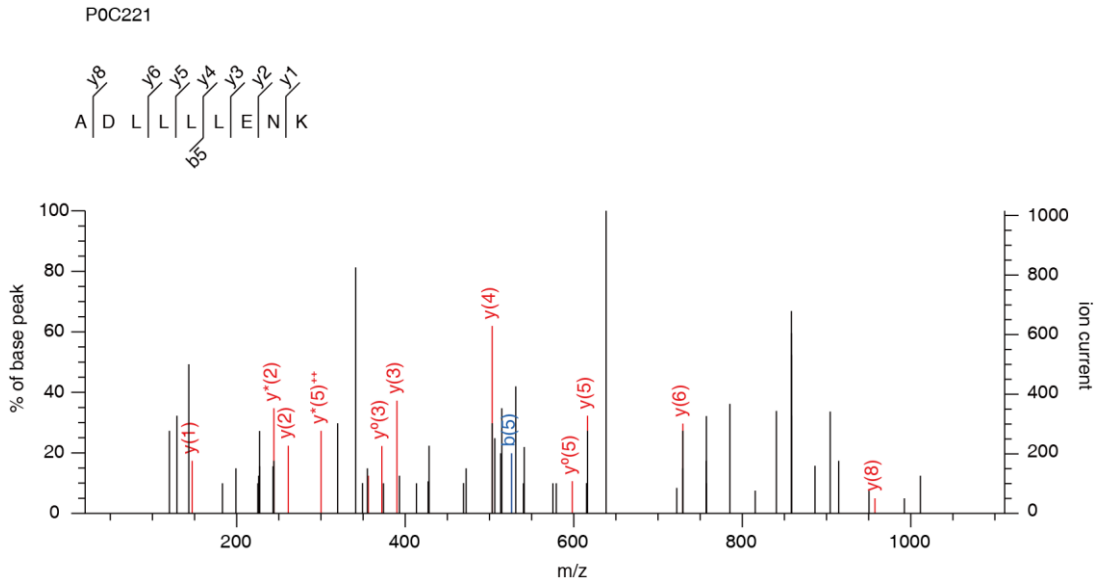


No. 13: P0C221, Coiled-coil domain-containing protein 175 OS=Homo sapiens

GN=CCDC175 **PE=2** SV=2.

Unique peptide: MS/MS Fragmentation of **ADLLLLENK**.

Spectrum: Found in **P0C221** in **MHCC97H** cell line (Ion Score cut-off=29).



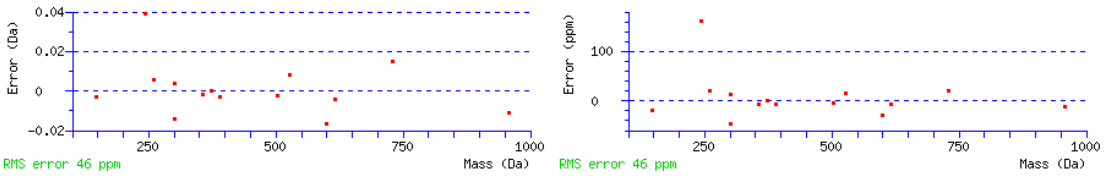
Monoisotopic mass of neutral peptide Mr (calc): 1027.5913

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

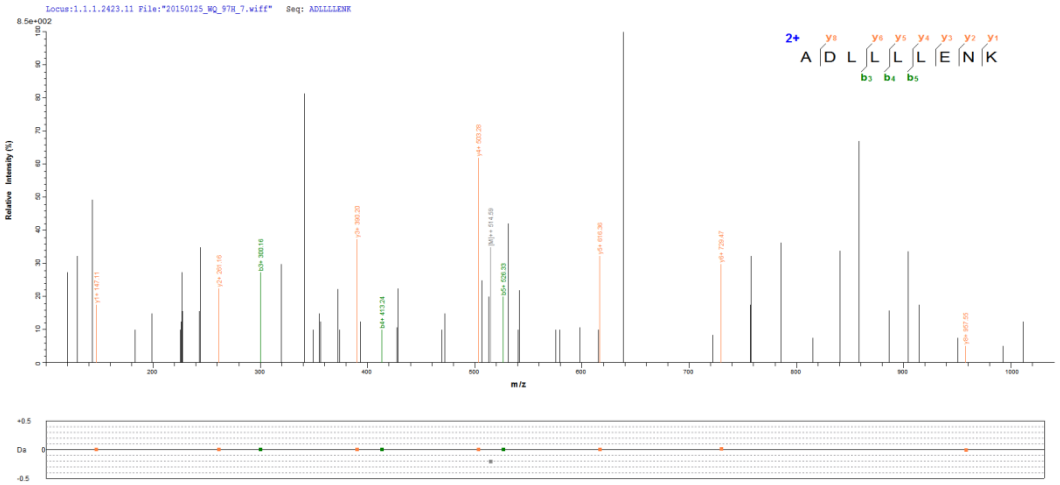
Ions Score: 32 **Expect:** 0.0041

Matches: 14/76 fragment ions using 48 most intense peaks

#	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	187.0713	94.0393			169.0608	85.0340	D	***957.5615***	479.2844	940.5350	470.7711	939.5510	470.2791	8
3	**300.1554**	150.5813			282.1448	141.5761	L	842.5346	421.7709	825.5080	413.2577	824.5240	412.7656	7
4	413.2395	207.1234			395.2289	198.1181	L	***729.4505***	365.2289	712.4240	356.7156	711.4400	356.2236	6
5	**526.3235**	263.6654			508.3130	254.6601	L	***616.3665***	308.6869	599.3399	300.1736	598.3559	299.6816	5
6	639.4076	320.2074			621.3970	311.2022	L	***503.2824***	252.1448	486.2558	243.6316	485.2718	243.1395	4
7	768.4502	384.7287			750.4396	375.7234	E	***390.1983***	195.6028	373.1718	187.0895	372.1878	186.5975	3
8	882.4931	441.7502	865.4666	433.2369	864.4825	432.7449	N	***261.1557***	131.0815	244.1292	122.5682			2
9							K	***147.1128***	74.0600	130.0863	65.5468			1



pLabel re-inspection:

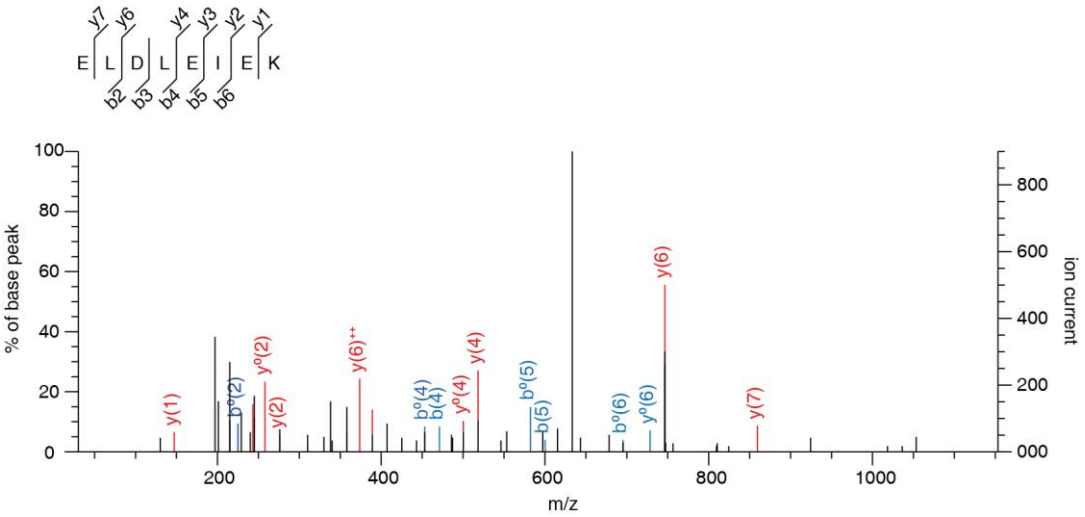


No. 14: **O75901**, Ras association domain-containing protein 9 OS=Homo sapiens GN=RASSF9 **PE=2** SV=2.

Unique peptide: MS/MS Fragmentation of **ELDLEIEK**.

Spectrum: Found in **O75901** in **MHCC97H** cell line (Ion Score cut-off=29).

O75901



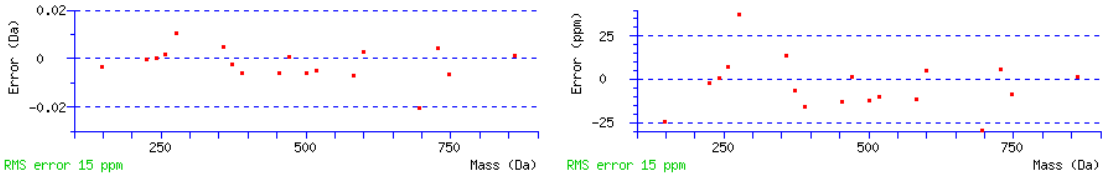
Monoisotopic mass of neutral peptide Mr (calc): 987.5124

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

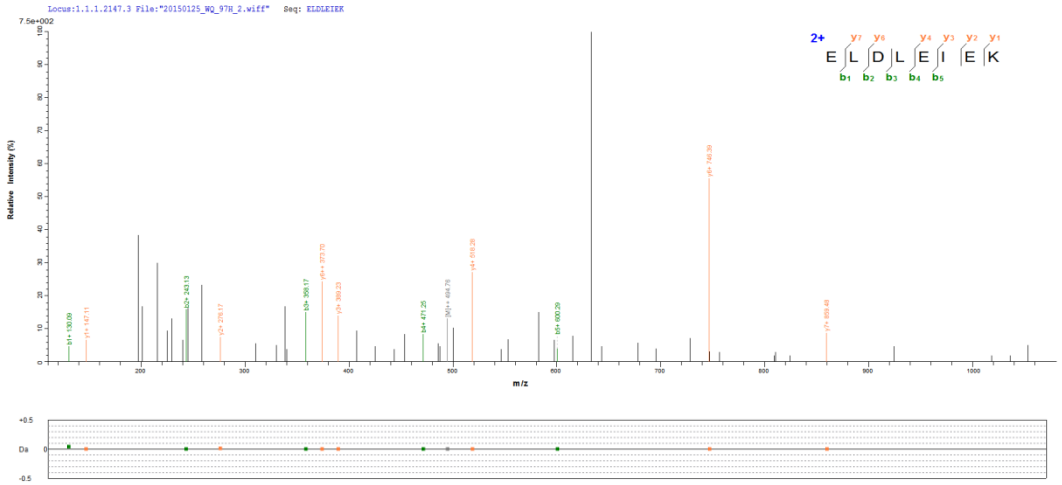
Ions Score: 31 **Expect:** 0.026

Matches: 18/68 fragment ions using 51 most intense peaks

#	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	**243.1339**	122.0706	225.1234	113.0653	L	***859.4771***	430.2422	842.4506	421.7289	841.4666	421.2369	7
3	**358.1609**	179.5841	340.1503	170.5788	D	***746.3931***	**373.7002**	729.3665	365.1869	728.3825	364.6949	6
4	**471.2449**	236.1261	453.2344	227.1208	L	631.3661	316.1867	614.3396	307.6734	613.3556	307.1814	5
5	**600.2875**	300.6474	582.2770	291.6421	E	***518.2821***	259.6447	501.2555	251.1314	500.2715	250.6394	4
6	713.3716	357.1894	695.3610	348.1842	I	***389.2395***	195.1234	372.2129	186.6101	371.2289	186.1181	3
7	842.4142	421.7107	824.4036	412.7055	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



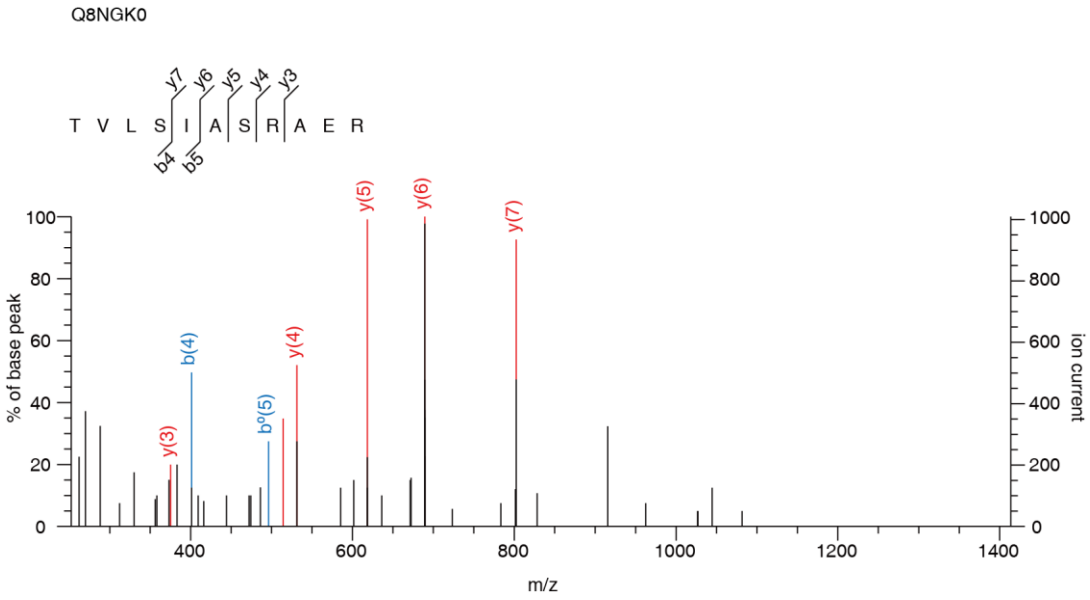
pLabel re-inspection:



No. 15: **Q8NGK0**, Olfactory receptor 51G2 OS=Homo sapiens GN=OR51G2 **PE=2** SV=1.

Unique peptide: MS/MS Fragmentation of **TVLSIASRAER**.

Spectrum: Found in **Q8NGK0** in **MHCC97H-GSK126** cell line (Ion Score cut-off=26).



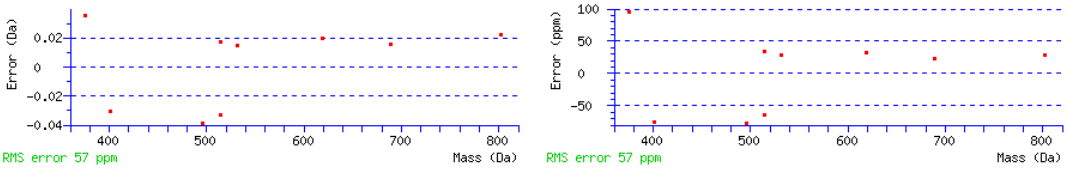
Monoisotopic mass of neutral peptide Mr (calc): 1201.6779

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

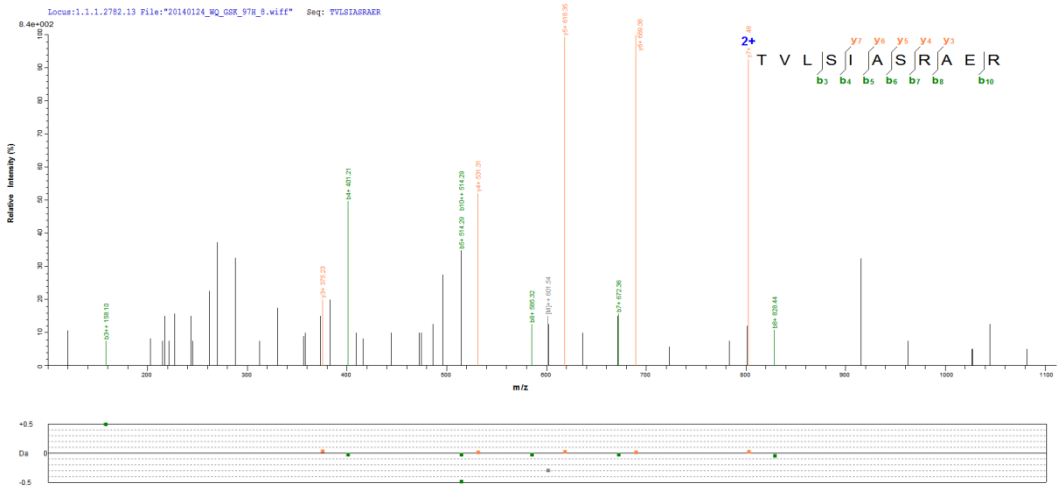
Ions Score: 27 **Expect:** 0.033

Matches: 9/104 fragment ions using 19 most intense peaks

#	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	201.1234	101.0653			183.1128	92.0600	V	1101.6375	551.3224	1084.6109	542.8091	1083.6269	542.3171	10
3	314.2074	157.6074			296.1969	148.6021	L	1002.5691	501.7882	985.5425	493.2749	984.5585	492.7829	9
4	**401.2395**	201.1234			383.2289	192.1181	S	889.4850	445.2461	872.4585	436.7329	871.4744	436.2409	8
5	**514.3235**	257.6654			496.3130	248.6601	I	***802.4530***	401.7301	785.4264	393.2169	784.4424	392.7248	7
6	585.3606	293.1840			567.3501	284.1787	A	***689.3689***	345.1881	672.3424	336.6748	671.3583	336.1828	6
7	672.3927	336.7000			654.3821	327.6947	S	***618.3318***	309.6695	601.3052	301.1563	600.3212	300.6643	5
8	828.4938	414.7505	811.4672	406.2373	810.4832	405.7452	R	***531.2998***	266.1535	514.2732	257.6402	513.2892	257.1482	4
9	899.5309	450.2691	882.5043	441.7558	881.5203	441.2638	A	***375.1987***	188.1030	358.1721	179.5897	357.1881	179.0977	3
10	1028.5735	514.7904	1011.5469	506.2771	1010.5629	505.7851	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



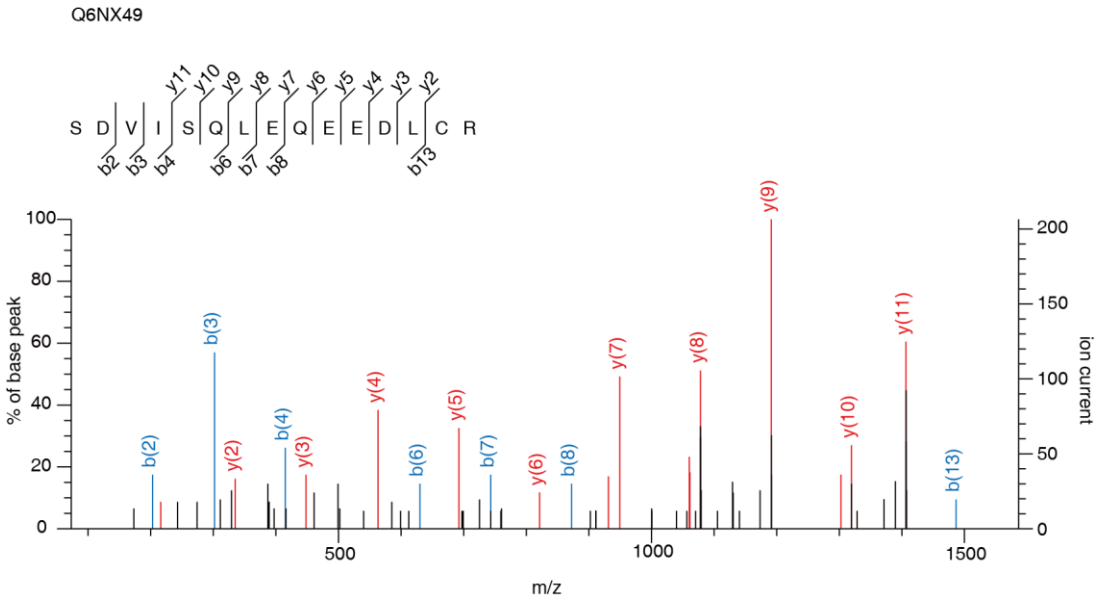
pLabel re-inspection:



No. 16: **Q6NX49**, Zinc finger protein 544 OS=Homo sapiens GN=ZNF544 **PE=2** SV=1.

Unique peptide: MS/MS Fragmentation of **SDVISQLEQEEDLCR**.

Spectrum: Found in **Q6NX49** in **MHCC97H-GSK126** cell line (Ion Score cut-off=26).



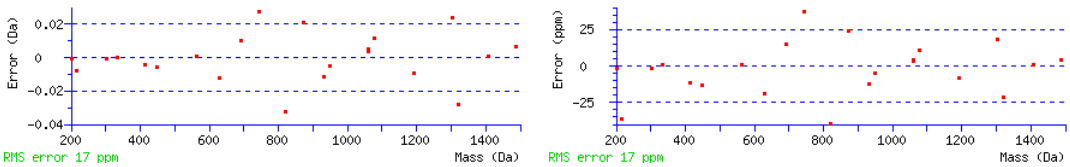
Monoisotopic mass of neutral peptide Mr (calc): 1819.8258

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

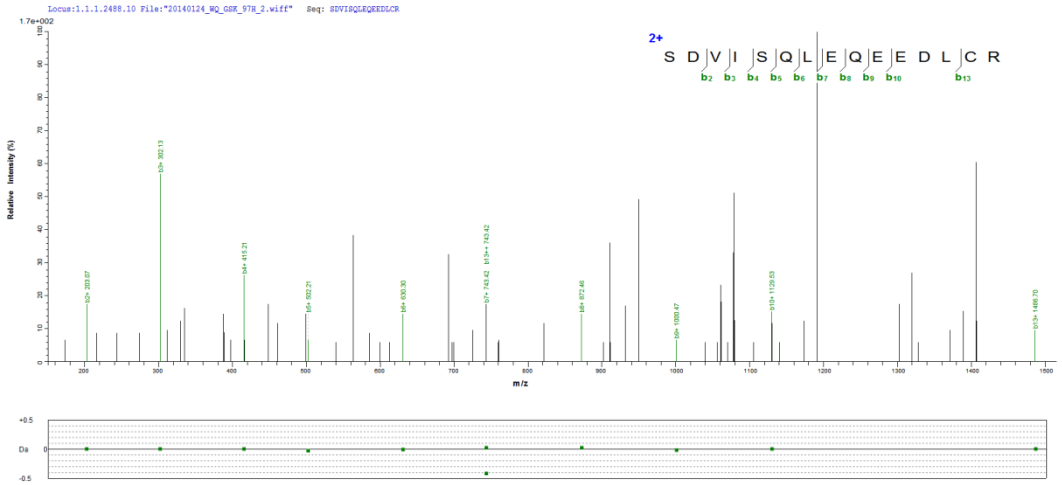
Ions Score: 99 **Expect:** 4.9e-010

Matches: 22/152 fragment ions using 27 most intense peaks

#	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	*203.0662*	102.0368			185.0557	93.0315	D	1733.8011	867.4042	1716.7745	858.8909	1715.7905	858.3989	14
3	*302.1347*	151.5710			284.1241	142.5657	V	1618.7741	809.8907	1601.7476	801.3774	1600.7635	800.8854	13
4	*415.2187*	208.1130			397.2082	199.1077	I	1519.7057	760.3565	1502.6792	751.8432	1501.6951	751.3512	12
5	502.2508	251.6290			484.2402	242.6237	S	*1406.6216*	703.8145	1389.5951	695.3012	1388.6111	694.8092	11
6	*630.3093*	315.6583	613.2828	307.1450	612.2988	306.6530	Q	*1319.5896*	660.2984	1302.5631	651.7852	1301.5790	651.2932	10
7	*743.3934*	372.2003	726.3668	363.6871	725.3828	363.1951	L	*1191.5310*	596.2692	1174.5045	587.7559	1173.5205	587.2639	9
8	*872.4360*	436.7216	855.4094	428.2084	854.4254	427.7163	E	*1078.4470*	539.7271	1061.4204	531.2138	1060.4364	530.7218	8
9	1000.4946	500.7509	983.4680	492.2376	982.4840	491.7456	Q	*949.4044*	475.2058	932.3778	466.6925	931.3938	466.2005	7
10	1129.5372	565.2722	1112.5106	556.7589	1111.5266	556.2669	E	*821.3458*	411.1765	804.3192	402.6633	803.3352	402.1713	6
11	1258.5798	629.7935	1241.5532	621.2802	1240.5692	620.7882	E	*692.3032*	346.6552	675.2767	338.1420	674.2926	337.6500	5
12	1373.6067	687.3070	1356.5801	678.7937	1355.5961	678.3017	D	*563.2606*	282.1339	546.2341	273.6207	545.2500	273.1287	4
13	*1486.6908*	743.8490	1469.6642	735.3357	1468.6802	734.8437	L	*448.2337*	224.6205	431.2071	216.1072			3
14	1646.7214	823.8643	1629.6949	815.3511	1628.7108	814.8591	C	*335.1496*	168.0784	318.1231	159.5652			2
15							R	175.1190	88.0631	158.0924	79.5498			1



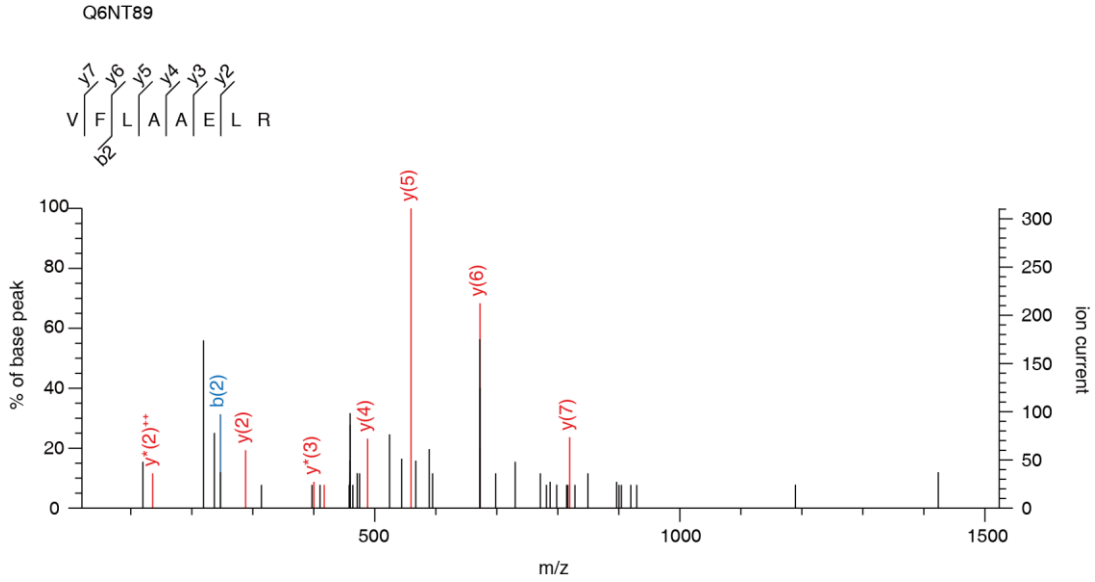
pLabel re-inspection:



No. 17: **Q6NT89**, TMF-regulated nuclear protein 1 OS=Homo sapiens GN=TRNP1 **PE=2** SV=2.

Unique peptide: MS/MS Fragmentation of **VFLAAELR**.

Spectrum: Found in **Q6NT89** in **MHCC97H** cell line (Ion Score cut-off=29).



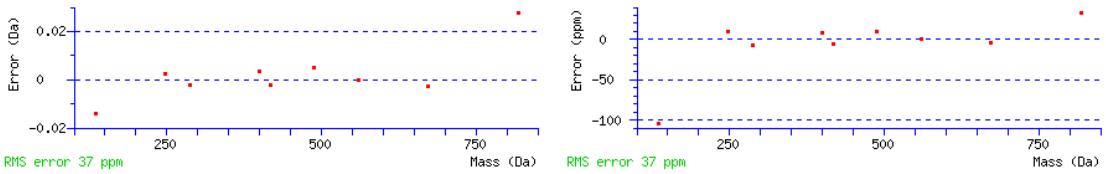
Monoisotopic mass of neutral peptide Mr (calc): 917.5334

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

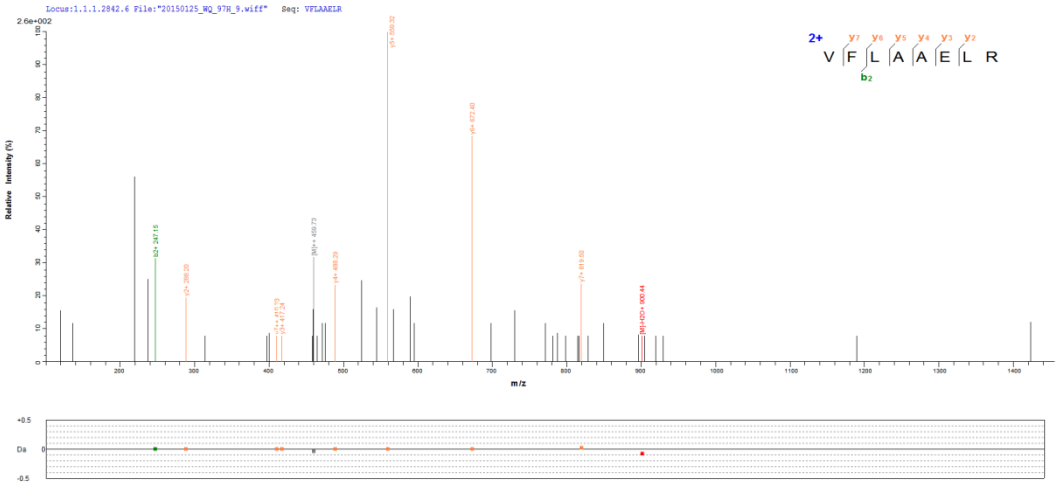
Ions Score: 35 **Expect:** 0.0074

Matches: 9/56 fragment ions using 24 most intense peaks

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415			V							8
2	247.1441	124.0757			F	*819.4723*	410.2398	802.4458	401.7265	801.4618	401.2345	7
3	360.2282	180.6177			L	*672.4039*	336.7056	655.3774	328.1923	654.3933	327.7003	6
4	431.2653	216.1363			A	*559.3198*	280.1636	542.2933	271.6503	541.3093	271.1583	5
5	502.3024	251.6548			A	*488.2827*	244.6450	471.2562	236.1317	470.2722	235.6397	4
6	631.3450	316.1761	613.3344	307.1709	E	*417.2456*	209.1264	400.2191	200.6132	399.2350	200.1212	3
7	744.4291	372.7182	726.4185	363.7129	L	*288.2030*	144.6051	271.1765	136.0919			2
8					R	175.1190	88.0631	158.0924	79.5498			1



pLabel re-inspection:



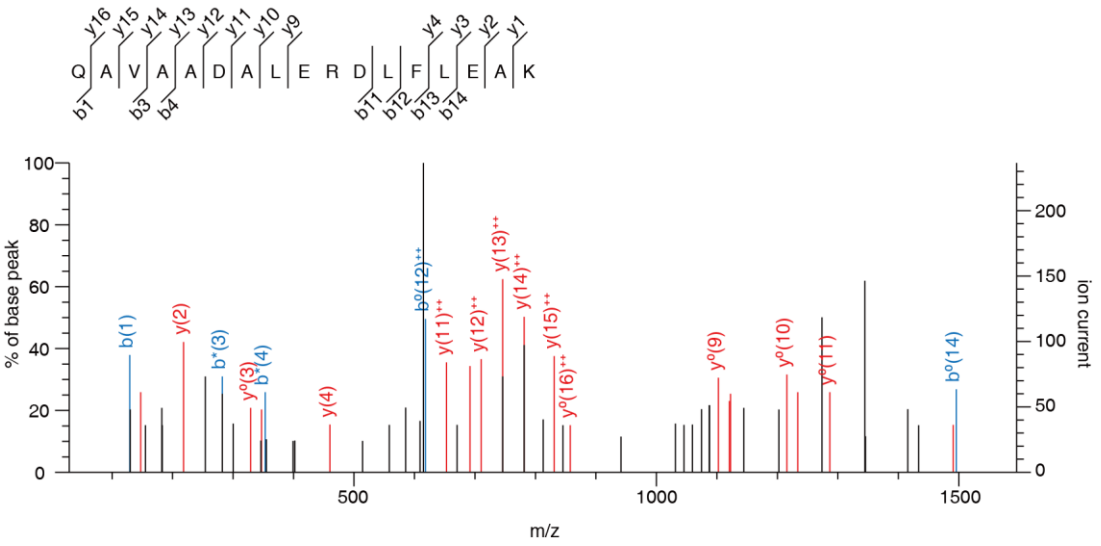
No. 18: **O15375**, Monocarboxylate transporter 6 OS=Homo sapiens GN=SLC16A5 **PE=2**

SV=1.

Unique peptide: MS/MS Fragmentation of **QAVAADALERDLFLEAK**.

Spectrum: Found in **O15375** in **MHCC97H-GSK126** cell line (Ion Score cut-off=26).

O15375



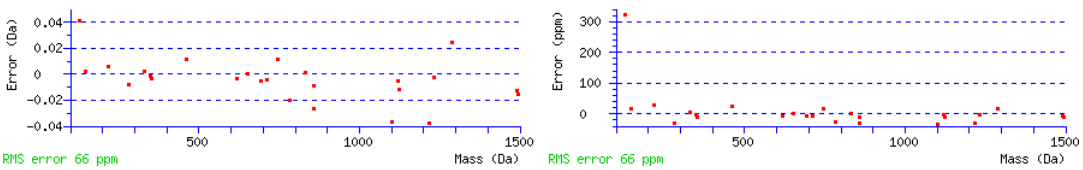
Monoisotopic mass of neutral peptide Mr (calc): 1858.9788

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

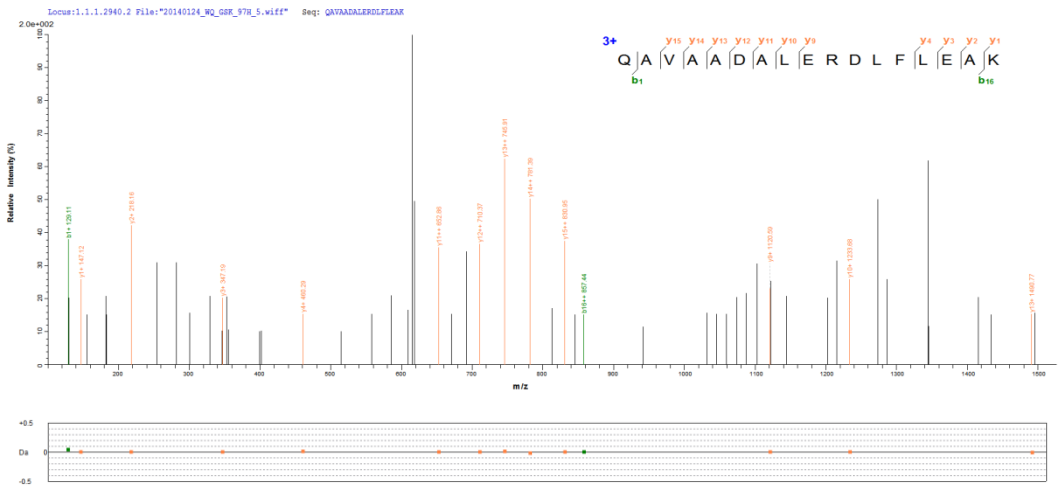
Ions Score: 50 **Expect:** 2e-005

Matches: 25/178 fragment ions using 39 most intense peaks

#	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	1731.9276	866.4674	1714.9010	857.9542	1713.9170	857.4621	16
3	299.1714	150.0893	282.1448	141.5761			V	1660.8905	*830.9489*	1643.8639	822.4356	1642.8799	821.9436	15
4	370.2085	185.6079	353.1819	177.0946			A	1561.8220	*781.4147*	1544.7955	772.9014	1543.8115	772.4094	14
5	441.2456	221.1264	424.2191	212.6132			A	*1490.7849*	*745.8961*	1473.7584	737.3828	1472.7744	736.8908	13
6	556.2726	278.6399	539.2460	270.1266	538.2620	269.6346	D	1419.7478	*710.3775*	1402.7213	701.8643	1401.7373	701.3723	12
7	627.3097	314.1585	610.2831	305.6452	609.2991	305.1532	A	1304.7209	*652.8641*	1287.6943	644.3508	1286.7103	643.8588	11
8	740.3937	370.7005	723.3672	362.1872	722.3832	361.6952	L	*1233.6838*	617.3455	1216.6572	608.8322	1215.6732	608.3402	10
9	869.4363	435.2218	852.4098	426.7085	851.4258	426.2165	E	*1120.5997*	560.8035	1103.5732	552.2902	1102.5891	551.7982	9
10	1025.5374	513.2724	1008.5109	504.7591	1007.5269	504.2671	R	991.5571	496.2822	974.5306	487.7689	973.5465	487.2769	8
11	1140.5644	570.7858	1123.5378	562.2726	1122.5538	561.7805	D	835.4560	418.2316	818.4294	409.7184	817.4454	409.2264	7
12	1253.6484	627.3279	1236.6219	618.8146	1235.6379	618.3226	L	720.4291	360.7182	703.4025	352.2049	702.4185	351.7129	6
13	1400.7169	700.8621	1383.6903	692.3488	1382.7063	691.8568	F	607.3450	304.1761	590.3184	295.6629	589.3344	295.1709	5
14	1513.8009	757.4041	1496.7744	748.8908	1495.7904	748.3988	L	*460.2766*	230.6419	443.2500	222.1287	442.2660	221.6366	4
15	1642.8435	821.9254	1625.8170	813.4121	1624.8329	812.9201	E	*347.1925*	174.0999	330.1660	165.5866	329.1819	165.0946	3
16	1713.8806	857.4440	1696.8541	848.9307	1695.8701	848.4387	A	*218.1499*	109.5786	201.1234	101.0653			2
17							K	*147.1128*	74.0600	130.0863	65.5468			1



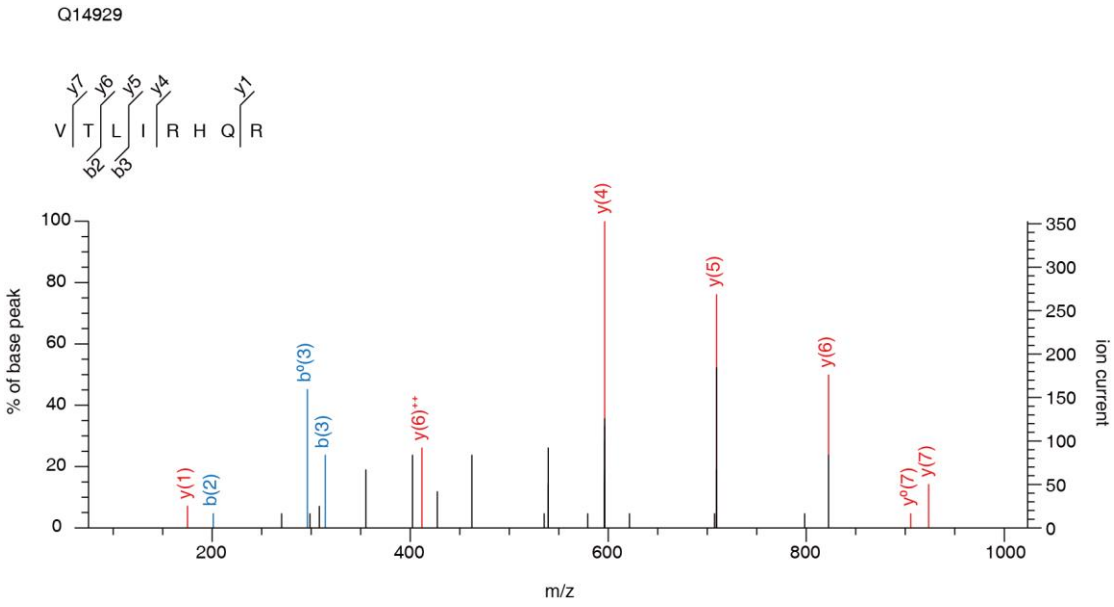
pLabel re-inspection:



No. 19: **Q14929**, Zinc finger protein 169 OS=Homo sapiens GN=ZNF169 **PE=2** SV=3

Unique peptide 1:MS/MS Fragmentation of **VTLIRHQR**

Spectrum 1: Found in **Q14929** in **HCT116-S2101** cell line (Ion Score cut-off=27).



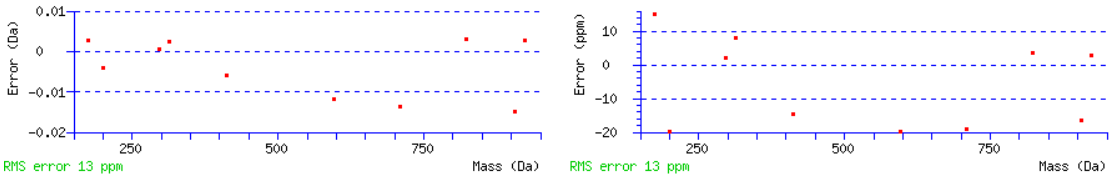
Monoisotopic mass of neutral peptide Mr(calc): 1021.6145

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

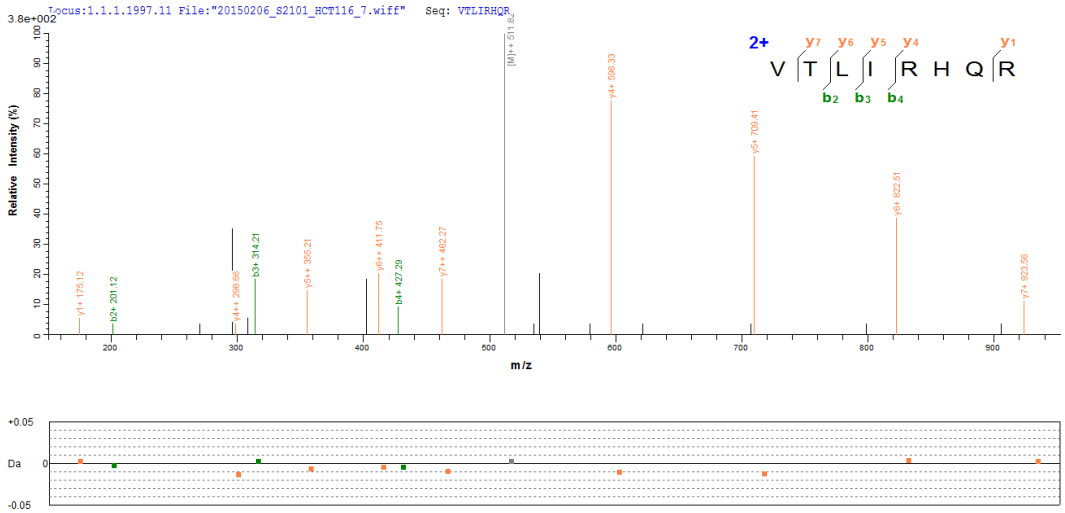
Ions Score: 41 **Expect:** 0.0011

Matches : 10/62 fragment ions using 16 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							8
2	**201.1234**	101.0653			183.1128	92.0600	T	***923.5534***	462.2803	906.5268	453.7670	905.5428	453.2750	7
3	**314.2074**	157.6074			296.1969	148.6021	L	***822.5057***	**411.7565**	805.4791	403.2432			6
4	427.2915	214.1494			409.2809	205.1441	I	***709.4216***	355.2144	692.3951	346.7012			5
5	583.3926	292.1999	566.3661	283.6867	565.3820	283.1947	R	***596.3376***	298.6724	579.3110	290.1591			4
6	720.4515	360.7294	703.4250	352.2161	702.4410	351.7241	H	440.2364	220.6219	423.2099	212.1086			3
7	848.5101	424.7587	831.4835	416.2454	830.4995	415.7534	Q	303.1775	152.0924	286.1510	143.5791			2
8							R	***175.1190***	88.0631	158.0924	79.5498			1



pLabel re-inspection:



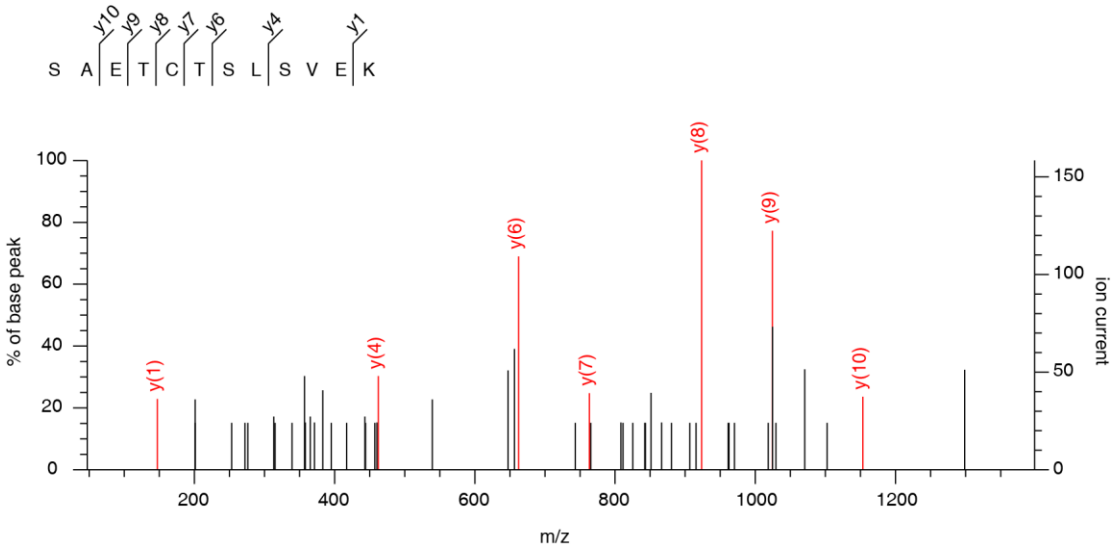
No. 20: Q8IZF3, Probable G-protein coupled receptor 115 OS=Homo sapiens GN=GPR115

PE=2 SV=3

Unique peptide 1: MS/MS Fragmentation of **SAETCTSLSVEK**.

Spectrum 1: Found in **Q8IZF3** in **A549** cell line (Ion Score cut-off=28).

Q8IZF3



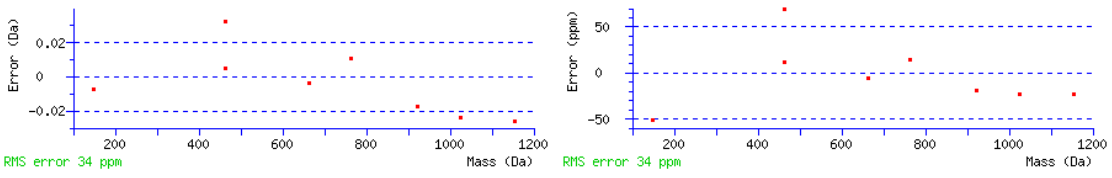
Monoisotopic mass of neutral peptide Mr(calc): 1310.6024

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

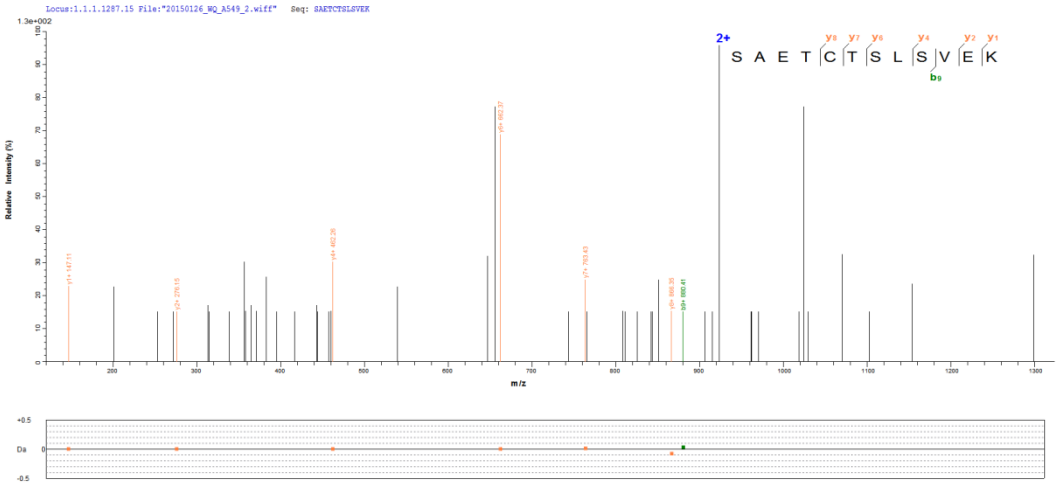
Ions Score: 53 **Expect:** 1.3e-005

Matches : 8/108 fragment ions using 11 most intense peaks

#	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	1224.5776	612.7925	1207.5511	604.2792	1206.5671	603.7872	11
3	288.1190	144.5631	270.1084	135.5579	E	***1153.5405***	577.2739	1136.5140	568.7606	1135.5300	568.2686	10
4	389.1667	195.0870	371.1561	186.0817	T	***1024.4979***	512.7526	1007.4714	504.2393	1006.4874	503.7473	9
5	549.1973	275.1023	531.1868	266.0970	C	***923.4503***	**462.2288**	906.4237	453.7155	905.4397	453.2235	8
6	650.2450	325.6261	632.2345	316.6209	T	***763.4196***	382.2134	746.3931	373.7002	745.4090	373.2082	7
7	737.2770	369.1422	719.2665	360.1369	S	***662.3719***	331.6896	645.3454	323.1763	644.3614	322.6843	6
8	850.3611	425.6842	832.3505	416.6789	L	575.3399	288.1736	558.3134	279.6603	557.3293	279.1683	5
9	937.3931	469.2002	919.3826	460.1949	S	***462.2558***	231.6316	445.2293	223.1183	444.2453	222.6263	4
10	1036.4616	518.7344	1018.4510	509.7291	V	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
11	1165.5041	583.2557	1147.4936	574.2504	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



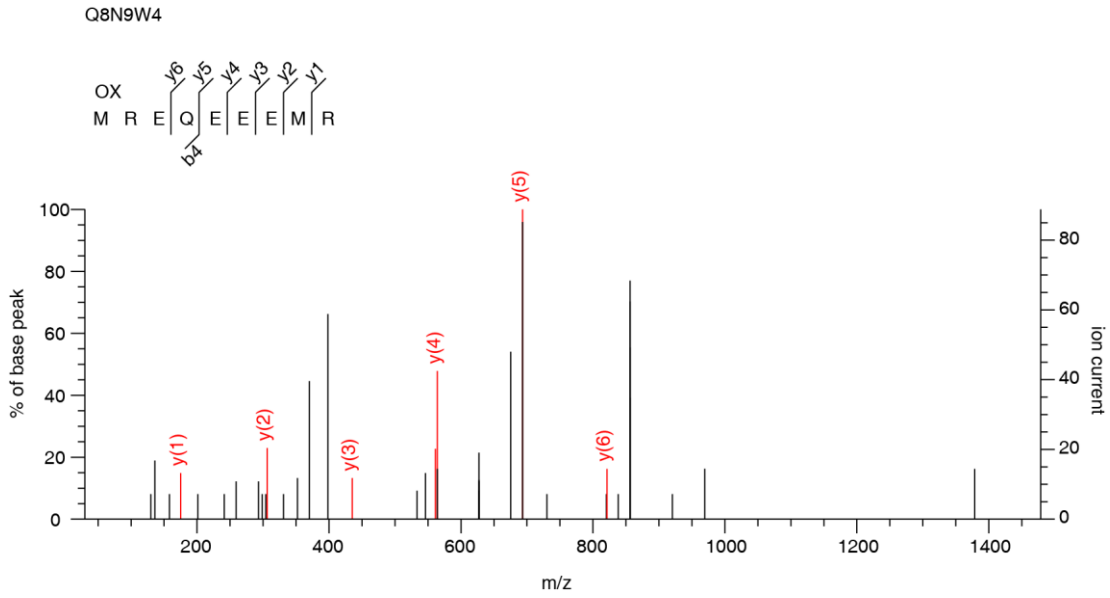
pLabel re-inspection:



No. 21: Q8N9W4, Golgin subfamily A member 6-like protein 2 OS=Homo sapiens GN=GOLGA6L2 **PE=2** SV=2

Unique peptide 1: MS/MS Fragmentation of **MREQEEEMR**.

Spectrum 1: Found in **Q8N9W4** in **A549** cell line (Ion Score cut-off=28).



Monoisotopic mass of neutral peptide Mr(calc): 1252.5176

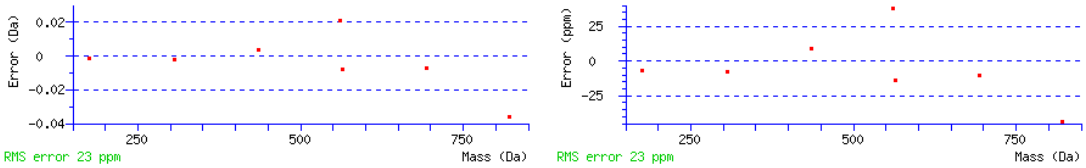
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

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

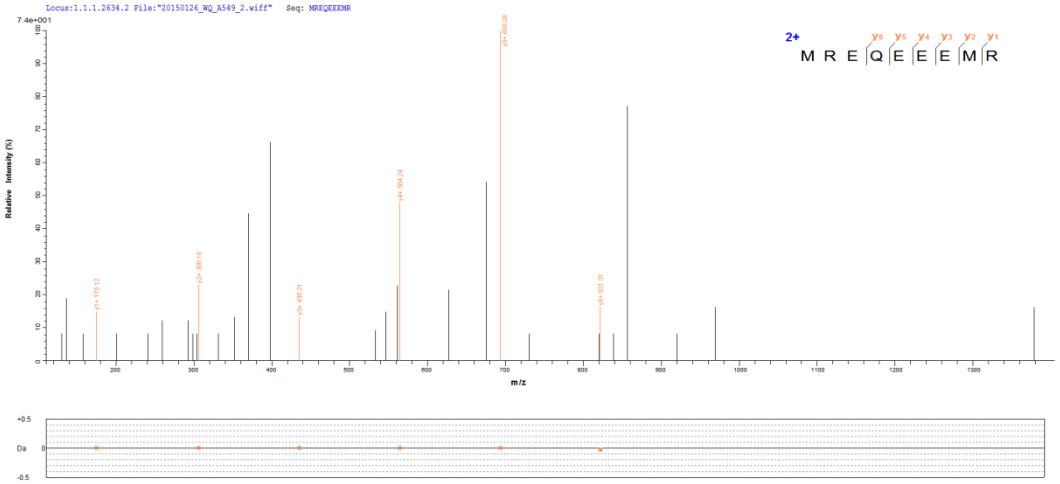
Ions Score: 34 **Expect:** 0.0014

Matches : 7/128 fragment ions using 16 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.0427	74.5250					M							9
2	304.1438	152.5755	287.1172	144.0623			R	1106.4895	553.7484	1089.4629	545.2351	1088.4789	544.7431	8
3	433.1864	217.0968	416.1598	208.5836	415.1758	208.0915	E	950.3884	475.6978	933.3618	467.1846	932.3778	466.6925	7
4	561.2450	281.1261	544.2184	272.6128	543.2344	272.1208	Q	821.3458	411.1765	804.3192	402.6633	803.3352	402.1713	6
5	690.2876	345.6474	673.2610	337.1341	672.2770	336.6421	E	693.2872	347.1472	676.2607	338.6340	675.2767	338.1420	5
6	819.3301	410.1687	802.3036	401.6554	801.3196	401.1634	E	564.2446	282.6259	547.2181	274.1127	546.2341	273.6207	4
7	948.3727	474.6900	931.3462	466.1767	930.3622	465.6847	E	435.2020	218.1047	418.1755	209.5914	417.1915	209.0994	3
8	1079.4132	540.2102	1062.3867	531.6970	1061.4027	531.2050	M	306.1594	153.5834	289.1329	145.0701			2
9							R	175.1190	88.0631	158.0924	79.5498			1



pLabel re-inspection:

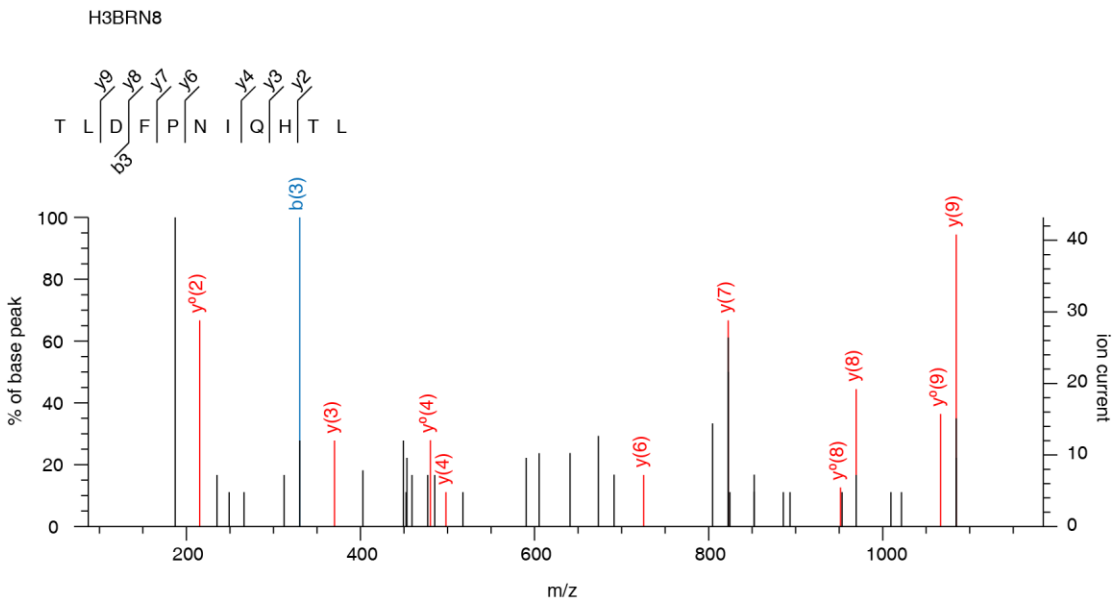


No. 22: H3BRN8, Uncharacterized protein C15orf65 OS=Homo sapiens GN=C15orf65

PE=2 SV=1

Unique peptide 1: MS/MS Fragmentation of **TLDFPNIQHTL**.

Spectrum 1: Found in **H3BRN8** in **A549-GSK126** cell line (Ion Score cut-off=28).



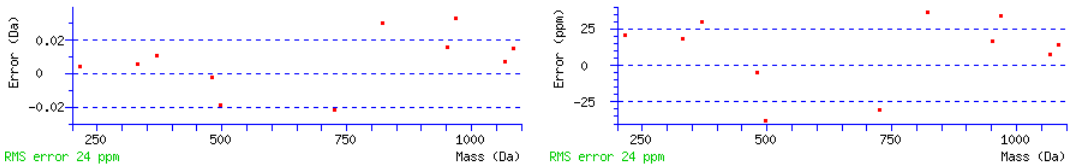
Monoisotopic mass of neutral peptide Mr(calc): 1297.6667

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

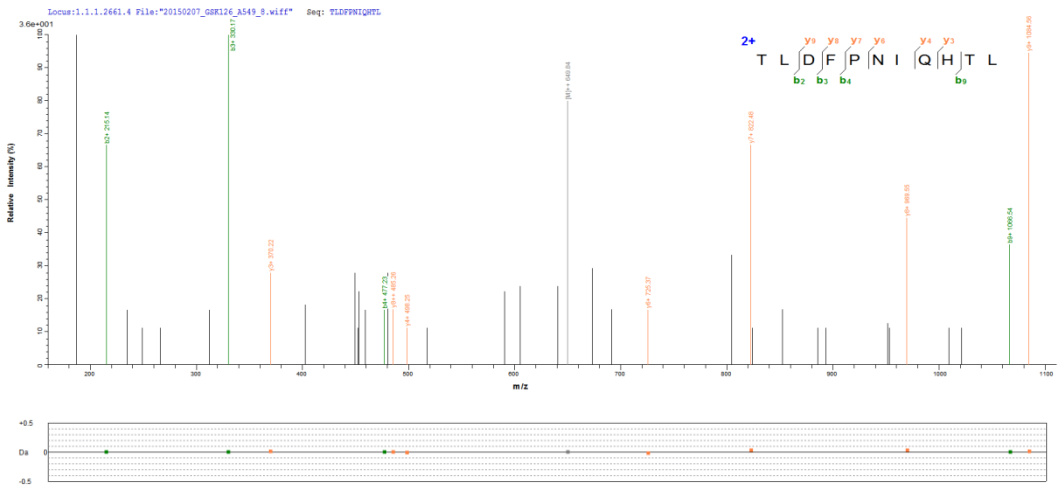
Ions Score: 40 **Expect:** 0.00023

Matches : 13/102 fragment ions using 25 most intense peaks

#	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	1197.6263	599.3168	1180.5997	590.8035	1179.6157	590.3115	10
3	**330.1660**	165.5866			312.1554	156.5813	D	***1084.5422***	542.7747	1067.5156	534.2615	1066.5316	533.7694	9
4	477.2344	239.1208			459.2238	230.1155	F	***969.5152***	485.2613	952.4887	476.7480	951.5047	476.2560	8
5	574.2871	287.6472			556.2766	278.6419	P	***822.4468***	411.7271	805.4203	403.2138	804.4363	402.7218	7
6	688.3301	344.6687	671.3035	336.1554	670.3195	335.6634	N	***725.3941***	363.2007	708.3675	354.6874	707.3835	354.1954	6
7	801.4141	401.2107	784.3876	392.6974	783.4036	392.2054	I	611.3511	306.1792	594.3246	297.6659	593.3406	297.1739	5
8	929.4727	465.2400	912.4462	456.7267	911.4621	456.2347	Q	***498.2671***	249.6372	481.2405	241.1239	480.2565	240.6319	4
9	**1066.5316**	533.7694	1049.5051	525.2562	1048.5211	524.7642	H	***370.2085***	185.6079			352.1979	176.6026	3
10	1167.5793	584.2933	1150.5528	575.7800	1149.5687	575.2880	T	233.1496	117.0784			215.1390	108.0731	2
11							L	132.1019	66.5546					1



pLabel re-inspection:

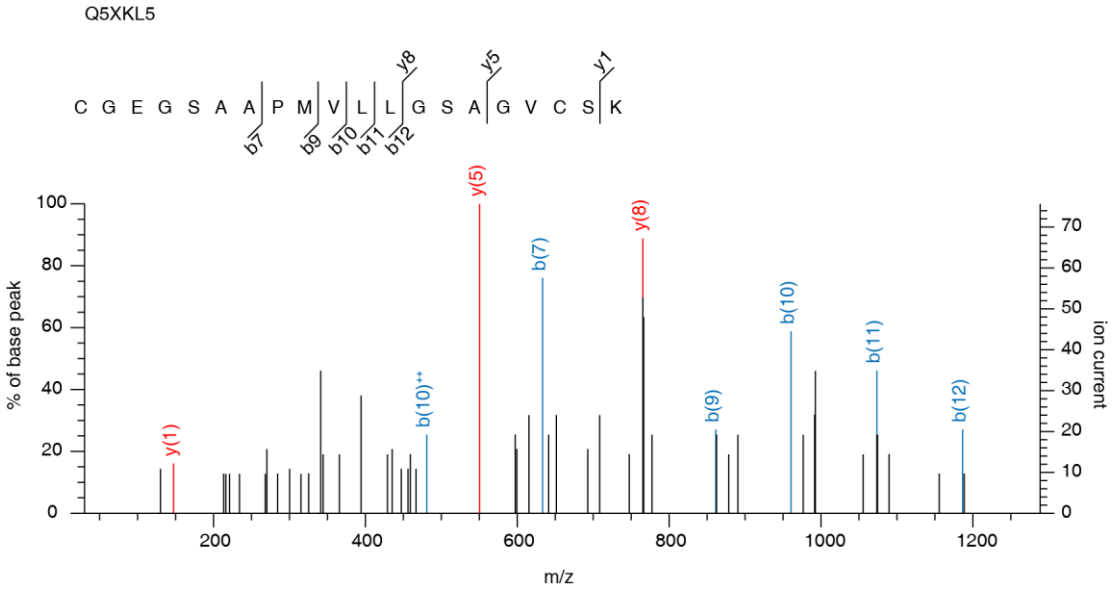


No. 23: **Q5XKL5**, BTB/POZ domain-containing protein 8 OS=Homo sapiens GN=BTBD8

PE=2 SV=2

Unique peptide 1: MS/MS Fragmentation of **CGEGSAAPMVLLGSAGVCSK**.

Spectrum 1: Found in **Q5XKL5** in **A549-GSK126** cell line (Ion Score cut-off=28)



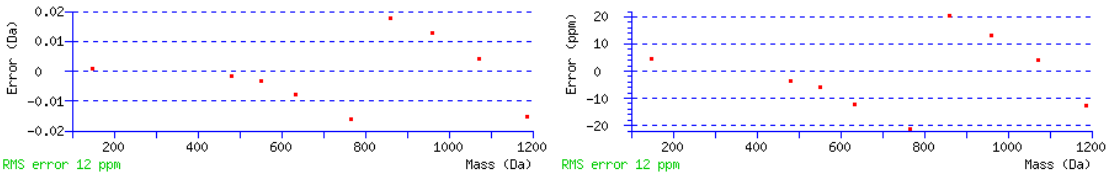
Monoisotopic mass of neutral peptide Mr(calc): 1949.9009

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

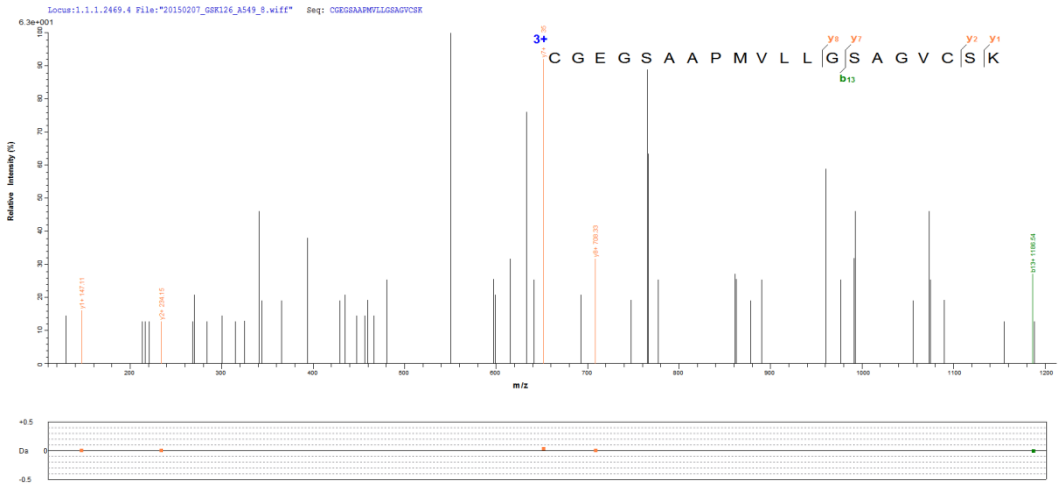
Ions Score: 35 **Expect:** 0.00048

Matches : 9/184 fragment ions using 11 most intense peaks

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	161.0379	81.0226			C							20
2	218.0594	109.5333			G	1790.8775	895.9424	1773.8510	887.4291	1772.8670	886.9371	19
3	347.1020	174.0546	329.0914	165.0493	E	1733.8561	867.4317	1716.8295	858.9184	1715.8455	858.4264	18
4	404.1234	202.5654	386.1129	193.5601	G	1604.8135	802.9104	1587.7869	794.3971	1586.8029	793.9051	17
5	491.1555	246.0814	473.1449	237.0761	S	1547.7920	774.3996	1530.7655	765.8864	1529.7814	765.3944	16
6	562.1926	281.5999	544.1820	272.5946	A	1460.7600	730.8836	1443.7334	722.3704	1442.7494	721.8783	15
7	*633.2297*	317.1185	615.2191	308.1132	A	1389.7229	695.3651	1372.6963	686.8518	1371.7123	686.3598	14
8	730.2825	365.6449	712.2719	356.6396	P	1318.6858	659.8465	1301.6592	651.3332	1300.6752	650.8412	13
9	*861.3230*	431.1651	843.3124	422.1598	M	1221.6330	611.3201	1204.6064	602.8069	1203.6224	602.3149	12
10	*960.3914*	**480.6993**	942.3808	471.6940	V	1090.5925	545.7999	1073.5660	537.2866	1072.5819	536.7946	11
11	*1073.4754*	537.2414	1055.4649	528.2361	L	991.5241	496.2657	974.4975	487.7524	973.5135	487.2604	10
12	*1186.5595*	593.7834	1168.5489	584.7781	L	878.4400	439.7237	861.4135	431.2104	860.4295	430.7184	9
13	1243.5810	622.2941	1225.5704	613.2888	G	*765.3560*	383.1816	748.3294	374.6683	747.3454	374.1763	8
14	1330.6130	665.8101	1312.6024	656.8048	S	708.3345	354.6709	691.3080	346.1576	690.3239	345.6656	7
15	1401.6501	701.3287	1383.6395	692.3234	A	621.3025	311.1549	604.2759	302.6416	603.2919	302.1496	6
16	1458.6716	729.8394	1440.6610	720.8341	G	*550.2654*	275.6363	533.2388	267.1230	532.2548	266.6310	5
17	1557.7400	779.3736	1539.7294	770.3683	V	493.2439	247.1256	476.2173	238.6123	475.2333	238.1203	4
18	1717.7706	859.3890	1699.7601	850.3837	C	394.1755	197.5914	377.1489	189.0781	376.1649	188.5861	3
19	1804.8027	902.9050	1786.7921	893.8997	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
20					K	*147.1128*	74.0600	130.0863	65.5468			1



pLabel re-inspection:

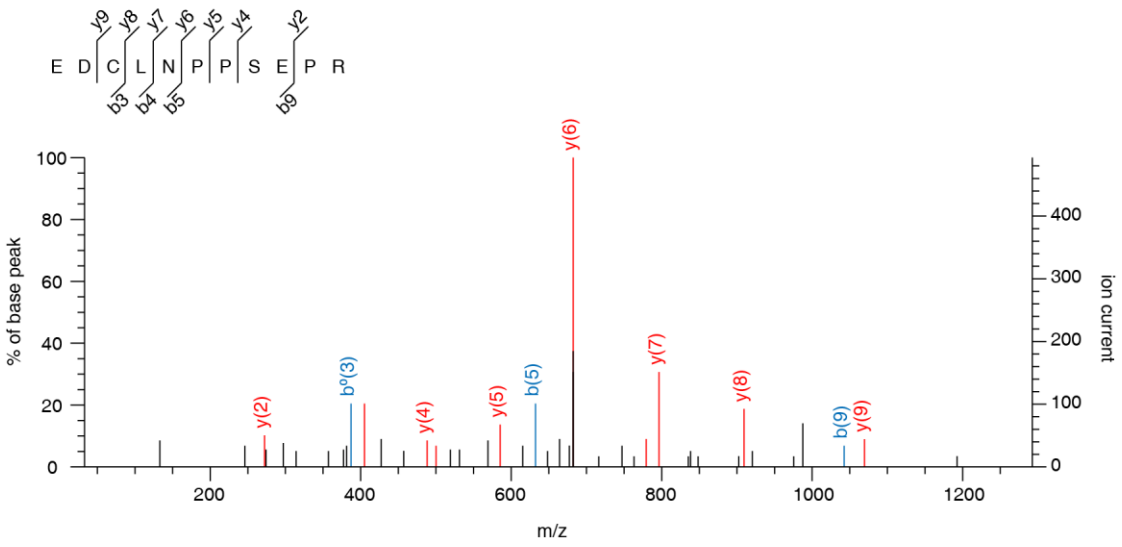


No. 24: **Q9UN75**, Protocadherin alpha-12 OS=Homo sapiens GN=PCDHA12 **PE=2** SV=1

Unique peptide 1: MS/MS Fragmentation of **EDCLNPPSEPR**.

Spectrum 1: Found in **Q9UN75** in **A549-S2101** cell line (Ion Score cut-off=29).

Q9UN75



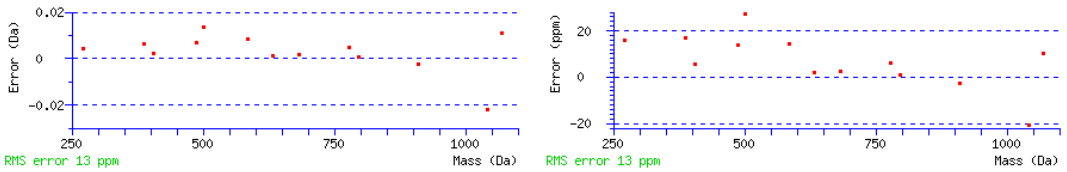
Monoisotopic mass of neutral peptide Mr(calc): 1312.5717

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

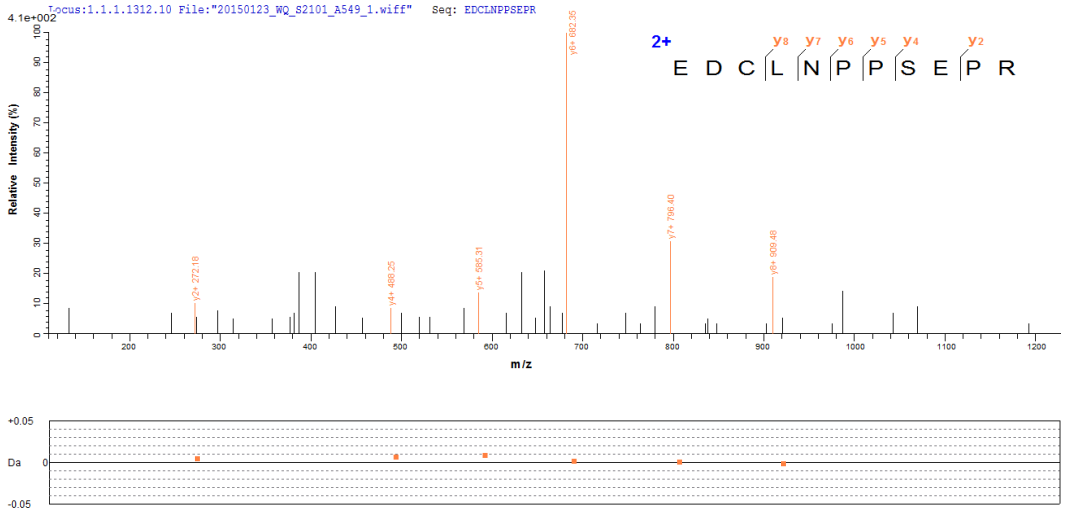
Ions Score: 54 **Expect:** 8.1e-006

Matches : 13/108 fragment ions using 20 most intense peaks

#	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	245.0768	123.0420			227.0662	114.0368	D	1184.5364	592.7719	1167.5099	584.2586	1166.5259	583.7666	10
3	**405.1075**	203.0574			387.0969	194.0521	C	***1069.5095***	535.2584	1052.4830	526.7451	1051.4989	526.2531	9
4	518.1915	259.5994			500.1810	250.5941	L	***909.4789***	455.2431	892.4523	446.7298	891.4683	446.2378	8
5	**632.2345**	316.6209	615.2079	308.1076	614.2239	307.6156	N	***796.3948***	398.7010	779.3682	390.1878	778.3842	389.6958	7
6	729.2872	365.1472	712.2607	356.6340	711.2767	356.1420	P	***682.3519***	341.6796	665.3253	333.1663	664.3413	332.6743	6
7	826.3400	413.6736	809.3134	405.1604	808.3294	404.6683	P	***585.2991***	293.1532	568.2726	284.6399	567.2885	284.1479	5
8	913.3720	457.1896	896.3455	448.6764	895.3614	448.1844	S	***488.2463***	244.6268	471.2198	236.1135	470.2358	235.6215	4
9	**1042.4146**	521.7109	1025.3881	513.1977	1024.4040	512.7057	E	401.2143	201.1108	384.1878	192.5975	383.2037	192.1055	3
10	1139.4674	570.2373	1122.4408	561.7240	1121.4568	561.2320	P	***272.1717***	136.5895	255.1452	128.0762			2
11							R	175.1190	88.0631	158.0924	79.5498			1



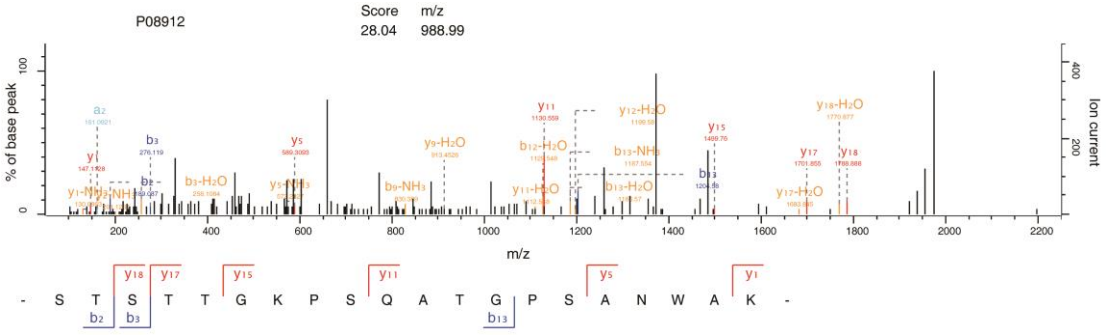
pLabel re-inspection:



No. 25: **P08912**, Muscarinic acetylcholine receptor M5 OS=Homo sapiens GN=CHRM5 **PE=2** SV=2

Unique peptide: MS/MS Fragmentation of **STSTTGKPSQATGPSANWAK.**

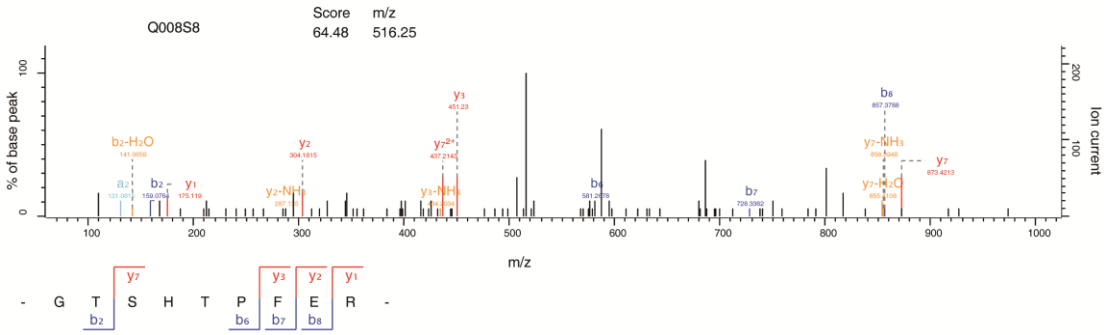
Spectrum: Found in **P08912** in **MHCC97H-GSK126** cell line (Ion Score cut-off=26).



No. 26: **Q008S8**, Epithelial cell-transforming sequence 2 oncogene-like OS=Homo sapiens GN=ECT2L **PE=2** SV=2

Unique peptide: MS/MS Fragmentation of **GTSHTPFER.**

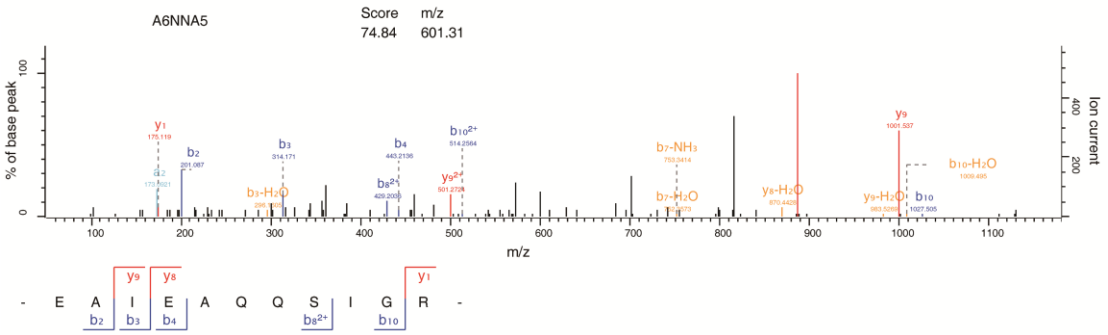
Spectrum: Found in **Q008S8** in **MHCC97H** cell line (Ion Score cut-off=29).



No. 27: **A6NNA5**, Dorsal root ganglia homeobox protein OS=Homo sapiens GN=DRGX **PE=2** SV=1

Unique peptide: MS/MS Fragmentation of **EAIEAQQSIGR.**

Spectrum: Found in **A6NNA5** in **MHCC97H-GSK126** cell line (Ion Score cut-off=29).

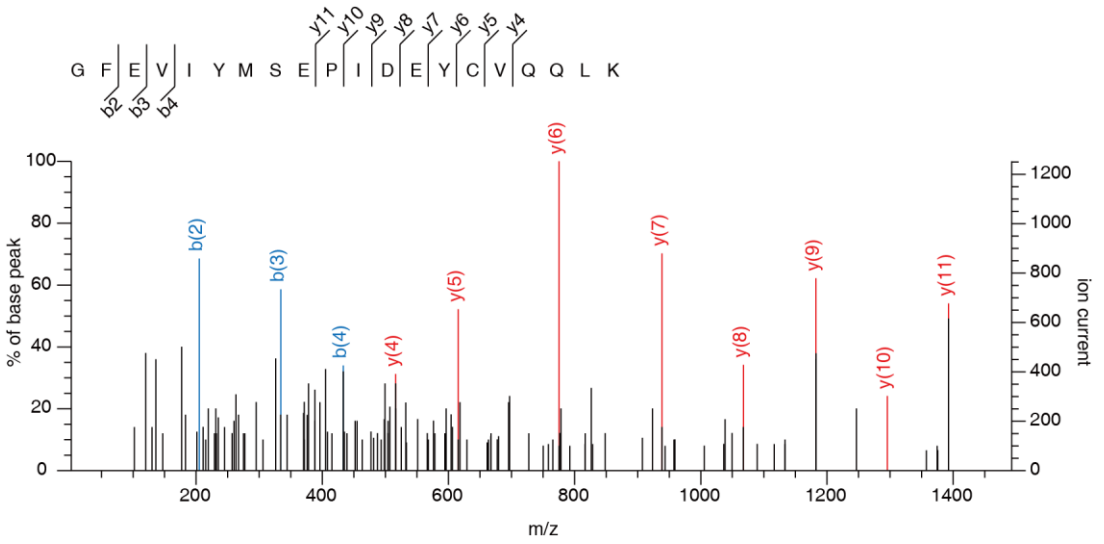


No. 28: **Q58FF6**, Putative heat shock protein HSP 90-beta 4 OS=Homo sapiens GN=HSP90AB4P **PE=5** SV=1.

Unique peptide 1: MS/MS Fragmentation of **GFEVIYMSEPIDEYCVQQLK**.

Spectrum 1: Found in **Q58FF6** in **MHCC97H-TSA** cell line (on Score cut-off=28).

Q58FF6



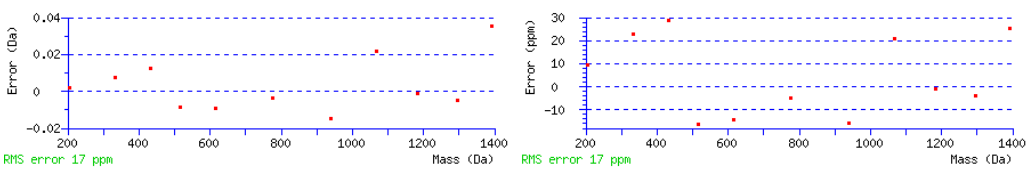
Monoisotopic mass of neutral peptide Mr (calc): 2447.1389

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

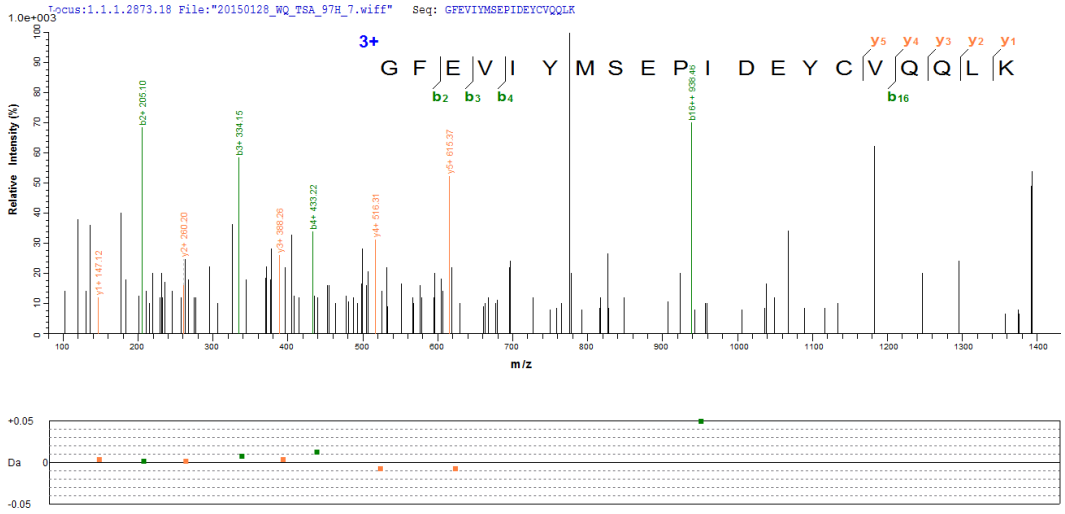
Ions Score: 61 **Expect:** 1.6e-005

Matches: 11/178 fragment ions using 13 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							20
2	205.0972	103.0522					F	2391.1247	1196.0660	2374.0982	1187.5527	2373.1141	1187.0607	19
3	334.1397	167.5735			316.1292	158.5682	E	2244.0563	1122.5318	2227.0297	1114.0185	2226.0457	1113.5265	18
4	433.2082	217.1077			415.1976	208.1024	V	2115.0137	1058.0105	2097.9871	1049.4972	2097.0031	1049.0052	17
5	546.2922	273.6498			528.2817	264.6445	I	2015.9453	1008.4763	1998.9187	999.9630	1997.9347	999.4710	16
6	709.3556	355.1814			691.3450	346.1761	Y	1902.8612	951.9342	1885.8347	943.4210	1884.8507	942.9290	15
7	840.3960	420.7017			822.3855	411.6964	M	1739.7979	870.4026	1722.7713	861.8893	1721.7873	861.3973	14
8	927.4281	464.2177			909.4175	455.2124	S	1608.7574	804.8823	1591.7309	796.3691	1590.7468	795.8771	13
9	1056.4707	528.7390			1038.4601	519.7337	E	1521.7254	761.3663	1504.6988	752.8531	1503.7148	752.3610	12
10	1153.5234	577.2654			1135.5129	568.2601	P	*1392.6828*	696.8450	1375.6562	688.3318	1374.6722	687.8397	11
11	1266.6075	633.8074			1248.5969	624.8021	I	*1295.6300*	648.3186	1278.6035	639.8054	1277.6195	639.3134	10
12	1381.6344	691.3209			1363.6239	682.3156	D	*1182.5460*	591.7766	1165.5194	583.2633	1164.5354	582.7713	9
13	1510.6770	755.8421			1492.6665	746.8369	E	*1067.5190*	534.2631	1050.4925	525.7499	1049.5084	525.2579	8
14	1673.7404	837.3738			1655.7298	828.3685	Y	*938.4764*	469.7418	921.4499	461.2286			7
15	1833.7710	917.3891			1815.7604	908.3839	C	*775.4131*	388.2102	758.3865	379.6969			6
16	1932.8394	966.9233			1914.8289	957.9181	V	*615.3824*	308.1949	598.3559	299.6816			5
17	2060.8980	1030.9526	2043.8714	1022.4394	2042.8874	1021.9474	Q	*516.3140*	258.6607	499.2875	250.1474			4
18	2188.9566	1094.9819	2171.9300	1086.4686	2170.9460	1085.9766	Q	388.2554	194.6314	371.2289	186.1181			3
19	2302.0406	1151.5240	2285.0141	1143.0107	2284.0301	1142.5187	L	260.1969	130.6021	243.1703	122.0888			2
20							K	147.1128	74.0600	130.0863	65.5468			1

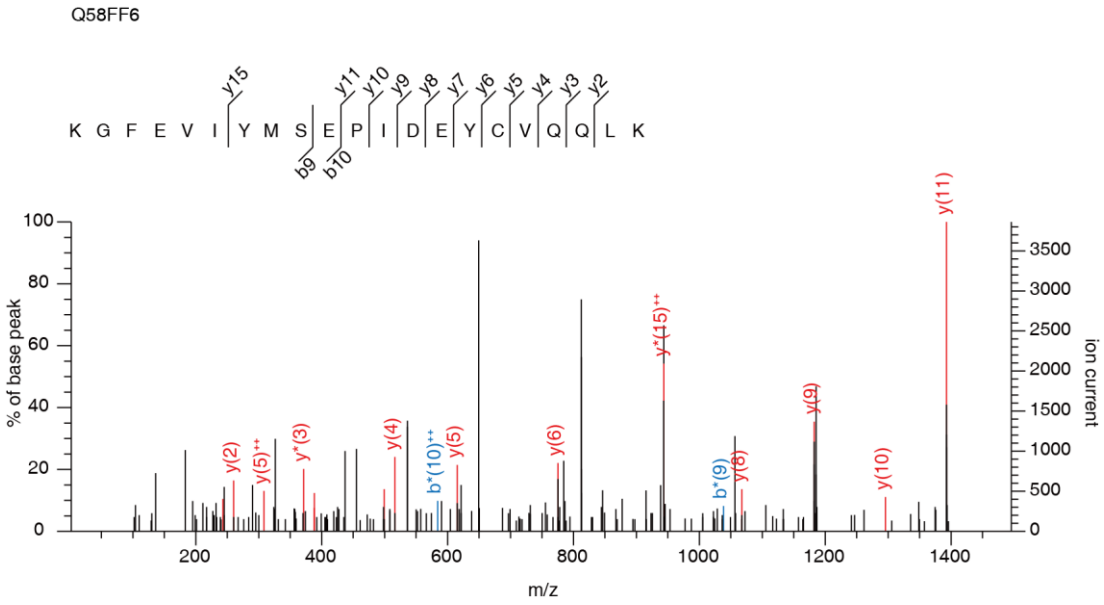


pLabel re-inspection:



Unique peptide 2: MS/MS Fragmentation of **KGFEVIYMSEPIDEYCVQQLK**.

Spectrum 2: Found in **Q58FF6** in **MHCC97H-TSA** cell line (Ion Score cut-off=28).



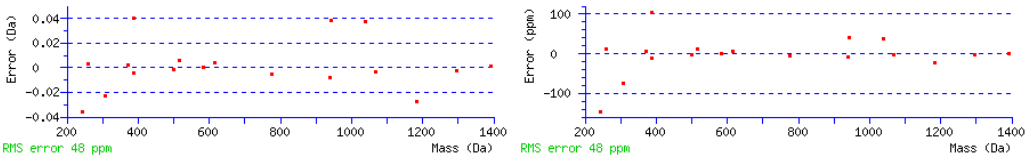
Monoisotopic mass of neutral peptide Mr (calc): 2575.2338

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

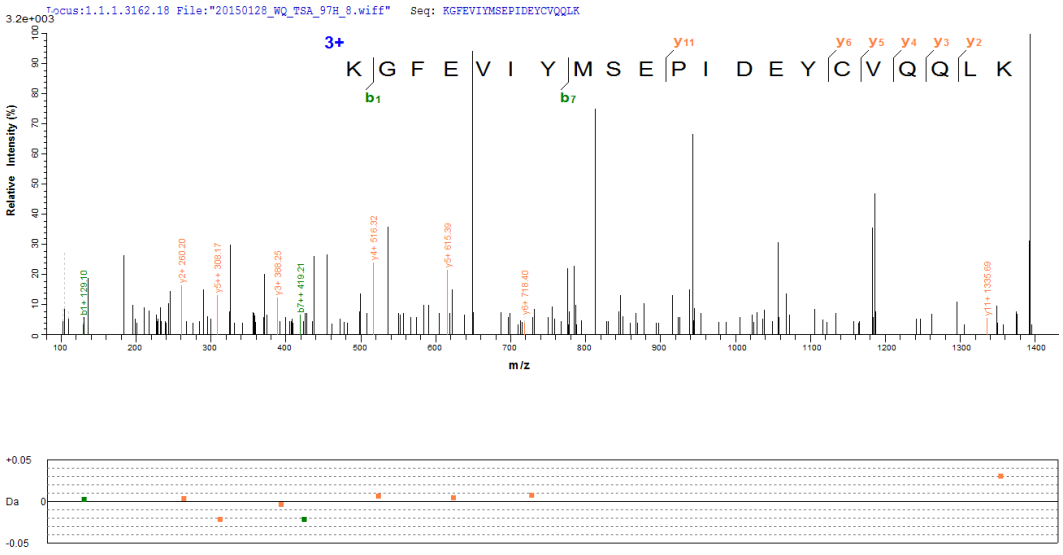
Ions Score: 36 **Expect:** 0.0076

Matches: 18/220 fragment ions using 52 most intense peaks

#	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							21
2	186.1237	93.5655	169.0972	85.0522			G	2448.1462	1224.5767	2431.1196	1216.0634	2430.1356	1215.5714	20
3	333.1921	167.0997	316.1656	158.5864			F	2391.1247	1196.0660	2374.0982	1187.5527	2373.1141	1187.0607	19
4	462.2347	231.6210	445.2082	223.1077	444.2241	222.6157	E	2244.0563	1122.5318	2227.0297	1114.0185	2226.0457	1113.5265	18
5	561.3031	281.1552	544.2766	272.6419	543.2926	272.1499	V	2115.0137	1058.0105	2097.9871	1049.4972	2097.0031	1049.0052	17
6	674.3872	337.6972	657.3606	329.1840	656.3766	328.6919	I	2015.9453	1008.4763	1998.9187	999.9630	1997.9347	999.4710	16
7	837.4505	419.2289	820.4240	410.7156	819.4400	410.2236	Y	1902.8612	951.9342	1885.8347	943.4210	1884.8507	942.9290	15
8	968.4910	484.7491	951.4645	476.2359	950.4804	475.7439	M	1739.7979	870.4026	1722.7713	861.8893	1721.7873	861.3973	14
9	1055.5230	528.2652	1038.4965	519.7519	1037.5125	519.2599	S	1608.7574	804.8823	1591.7309	796.3691	1590.7468	795.8771	13
10	1184.5656	592.7864	1167.5391	584.2732	1166.5551	583.7812	E	1521.7254	761.3663	1504.6988	752.8531	1503.7148	752.3610	12
11	1281.6184	641.3128	1264.5918	632.7996	1263.6078	632.3075	P	***1392.6828***	696.8450	1375.6562	688.3318	1374.6722	687.8397	11
12	1394.7025	697.8549	1377.6759	689.3416	1376.6919	688.8496	I	***1295.6300***	648.3186	1278.6035	639.8054	1277.6195	639.3134	10
13	1509.7294	755.3683	1492.7028	746.8551	1491.7188	746.3631	D	***1182.5460***	591.7766	1165.5194	583.2633	1164.5354	582.7713	9
14	1638.7720	819.8896	1621.7454	811.3764	1620.7614	810.8843	E	***1067.5190***	534.2631	1050.4925	525.7499	1049.5084	525.2579	8
15	1801.8353	901.4213	1784.8088	892.9080	1783.8248	892.4160	Y	***938.4764***	469.7418	921.4499	461.2286			7
16	1961.8660	981.4366	1944.8394	972.9233	1943.8554	972.4313	C	***775.4131***	**388.2102**	758.3865	379.6969			6
17	2060.9344	1030.9708	2043.9078	1022.4576	2042.9238	1021.9655	V	***615.3824***	**308.1949**	598.3559	299.6816			5
18	2188.9930	1095.0001	2171.9664	1086.4868	2170.9824	1085.9948	Q	***516.3140***	258.6607	499.2875	250.1474			4
19	2317.0515	1159.0294	2300.0250	1150.5161	2299.0410	1150.0241	Q	***388.2554***	194.6314	371.2289	186.1181			3
20	2430.1356	1215.5714	2413.1091	1207.0582	2412.1250	1206.5662	L	***260.1969***	130.6021	243.1703	122.0888			2
21							K	147.1128	74.0600	130.0863	65.5468			1



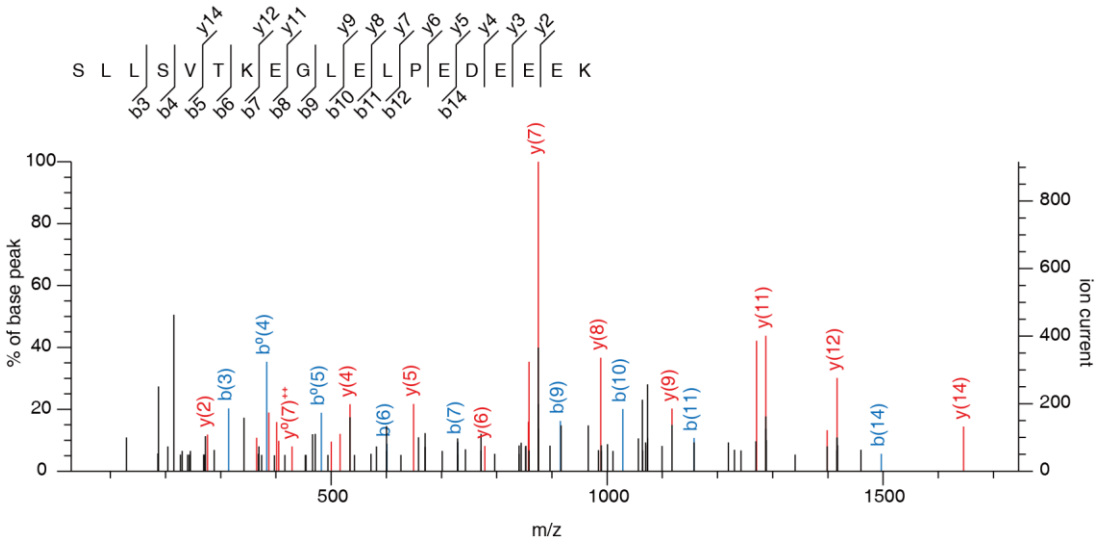
pLabel re-inspection:



Unique peptide 3: MS/MS Fragmentation of **SLLSVTKEGLELPEDEEEK**.

Spectrum 1: Found in **Q58FF6** in **MHCC97H-GSK1126** cell line (Ion Score cut-off=26).

Q58FF6



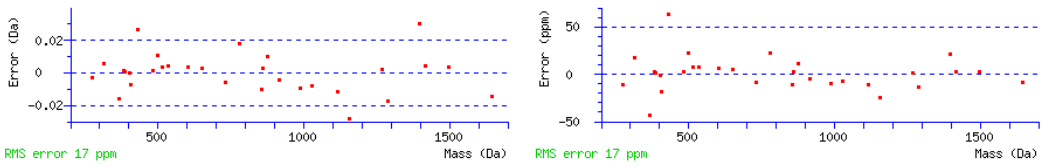
Monoisotopic mass of neutral peptide Mr (calc): 2144.0736

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

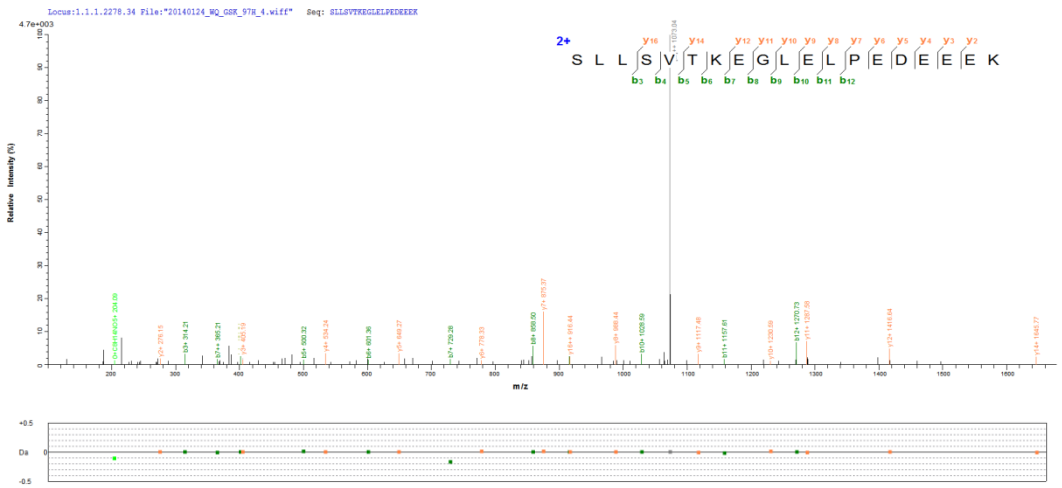
Ions Score: 65 **Expect:** 1.1e-005

Matches: 30/202 fragment ions using 77 most intense peaks

#	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	2058.0489	1029.5281	2041.0223	1021.0148	2040.0383	1020.5228	18
3	*314.2074*	157.6074			296.1969	148.6021	L	1944.9648	972.9860	1927.9383	964.4728	1926.9542	963.9808	17
4	*401.2395*	201.1234			383.2289	192.1181	S	1831.8807	916.4440	1814.8542	907.9307	1813.8702	907.4387	16
5	*500.3079*	250.6576			482.2973	241.6523	V	1744.8487	872.9280	1727.8222	864.4147	1726.8382	863.9227	15
6	*601.3556*	301.1814			583.3450	292.1761	T	*1645.7803*	823.3938	1628.7538	814.8805	1627.7697	814.3885	14
7	*729.4505*	365.2289	712.4240	356.7156	711.4400	356.2236	K	1544.7326	772.8700	1527.7061	764.3567	1526.7221	763.8647	13
8	*858.4931*	429.7502	841.4666	421.2369	840.4825	420.7449	E	*1416.6377*	708.8225	1399.6111	700.3092	1398.6271	699.8172	12
9	*915.5146*	458.2609	898.4880	449.7477	897.5040	449.2556	G	*1287.5951*	644.3012	1270.5685	635.7879	1269.5845	635.2959	11
10	*1028.5986*	514.8030	1011.5721	506.2897	1010.5881	505.7977	L	1230.5736	615.7904	1213.5471	607.2772	1212.5630	606.7852	10
11	*1157.6412*	579.3243	1140.6147	570.8110	1139.6307	570.3190	E	*1117.4895*	559.2484	1100.4630	550.7351	1099.4790	550.2431	9
12	*1270.7253*	635.8663	1253.6987	627.3530	1252.7147	626.8610	L	*988.4469*	494.7271	971.4204	486.2138	970.4364	485.7218	8
13	1367.7781	684.3927	1350.7515	675.8794	1349.7675	675.3874	P	*875.3629*	438.1851	858.3363	429.6718	857.3523	429.1798	7
14	*1496.8207*	748.9140	1479.7941	740.4007	1478.8101	739.9087	E	*778.3101*	389.6587	761.2836	381.1454	760.2996	380.6534	6
15	1611.8476	806.4274	1594.8210	797.9142	1593.8370	797.4222	D	*649.2675*	325.1374	632.2410	316.6241	631.2570	316.1321	5
16	1740.8902	870.9487	1723.8636	862.4355	1722.8796	861.9434	E	*534.2406*	267.6239	517.2140	259.1107	516.2300	258.6186	4
17	1869.9328	935.4700	1852.9062	926.9568	1851.9222	926.4647	E	*405.1980*	203.1026	388.1714	194.5894	387.1874	194.0974	3
18	1998.9754	999.9913	1981.9488	991.4781	1980.9648	990.9860	E	*276.1554*	138.5813	259.1288	130.0681	258.1448	129.5761	2
19							K	147.1128	74.0600	130.0863	65.5468			1

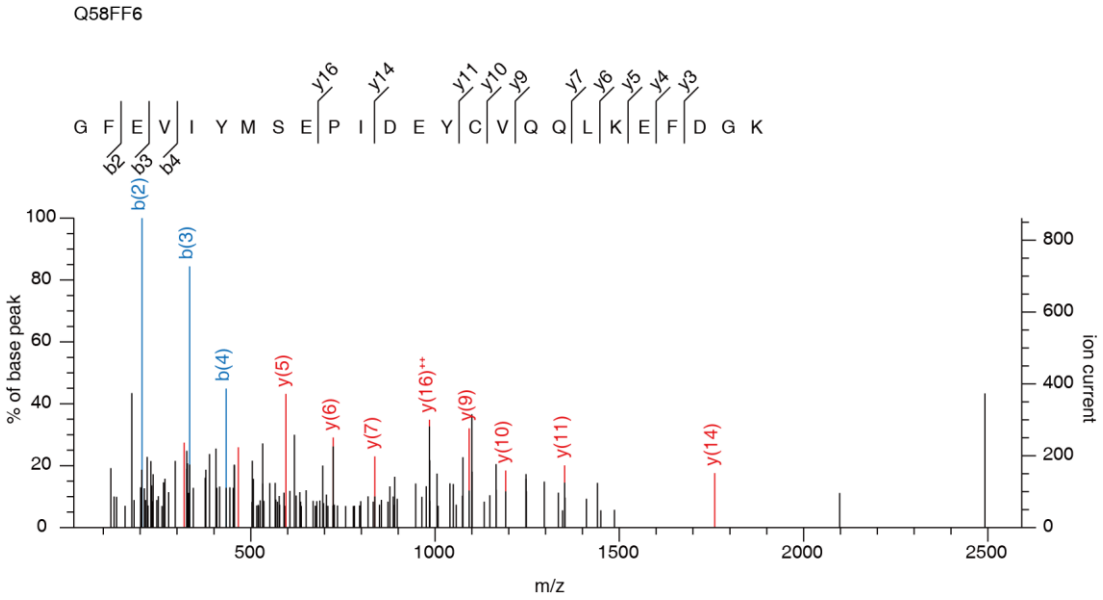


pLabel re-inspection:



Unique peptide 4: MS/MS Fragmentation of **GFEVIYMSEPIDEYCVQQLKEFDGK**.

Spectrum 3: Found in **Q58FF6** in **MHCC97H-GSK126** cell line (Ion Score cut-off=26).



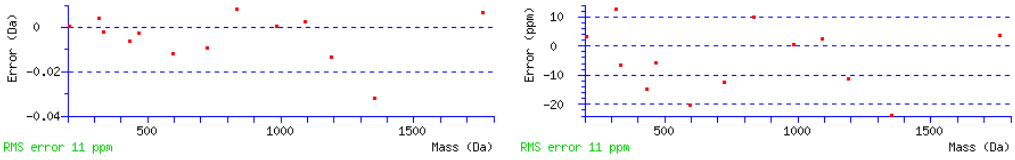
Monoisotopic mass of neutral peptide Mr (calc): 3023.3933

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

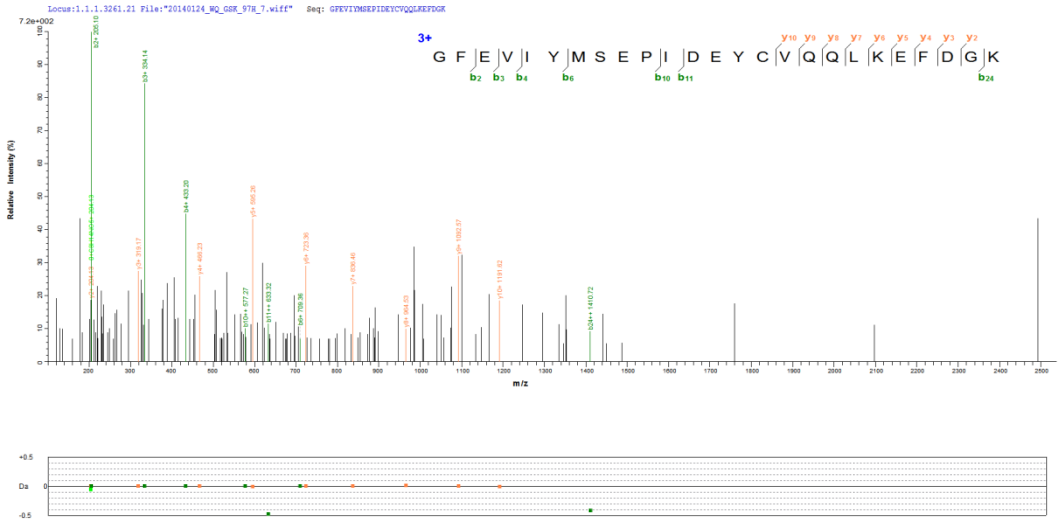
Ions Score: 40 **Expect:** 0.002

Matches: 13/248 fragment ions using 31 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							25
2	**205.0972**	103.0522					F	2967.3791	1484.1932	2950.3525	1475.6799	2949.3685	1475.1879	24
3	**334.1397**	167.5735			316.1292	158.5682	E	2820.3107	1410.6590	2803.2841	1402.1457	2802.3001	1401.6537	23
4	**433.2082**	217.1077			415.1976	208.1024	V	2691.2681	1346.1377	2674.2415	1337.6244	2673.2575	1337.1324	22
5	546.2922	273.6498			528.2817	264.6445	I	2592.1997	1296.6035	2575.1731	1288.0902	2574.1891	1287.5982	21
6	709.3556	355.1814			691.3450	346.1761	Y	2479.1156	1240.0614	2462.0890	1231.5482	2461.1050	1231.0562	20
7	840.3960	420.7017			822.3855	411.6964	M	2316.0523	1158.5298	2299.0257	1150.0165	2298.0417	1149.5245	19
8	927.4281	464.2177			909.4175	455.2124	S	2185.0118	1093.0095	2167.9852	1084.4963	2167.0012	1084.0042	18
9	1056.4707	528.7390			1038.4601	519.7337	E	2097.9797	1049.4935	2080.9532	1040.9802	2079.9692	1040.4882	17
10	1153.5234	577.2654			1135.5129	568.2601	P	1968.9372	**984.9722**	1951.9106	976.4589	1950.9266	975.9669	16
11	1266.6075	633.8074			1248.5969	624.8021	I	1871.8844	936.4458	1854.8578	927.9326	1853.8738	927.4406	15
12	1381.6344	691.3209			1363.6239	682.3156	D	***1758.8003***	879.9038	1741.7738	871.3905	1740.7898	870.8985	14
13	1510.6770	755.8421			1492.6665	746.8369	E	1643.7734	822.3903	1626.7468	813.8771	1625.7628	813.3850	13
14	1673.7404	837.3738			1655.7298	828.3685	Y	1514.7308	757.8690	1497.7042	749.3558	1496.7202	748.8638	12
15	1833.7710	917.3891			1815.7604	908.3839	C	***1351.6675***	676.3374	1334.6409	667.8241	1333.6569	667.3321	11
16	1932.8394	966.9233			1914.8289	957.9181	V	***1191.6368***	596.3220	1174.6103	587.8088	1173.6263	587.3168	10
17	2060.8980	1030.9526	2043.8714	1022.4394	2042.8874	1021.9474	Q	***1092.5684***	546.7878	1075.5419	538.2746	1074.5578	537.7826	9
18	2188.9566	1094.9819	2171.9300	1086.4686	2170.9460	1085.9766	Q	964.5098	482.7585	947.4833	474.2453	946.4993	473.7533	8
19	2302.0406	1151.5240	2285.0141	1143.0107	2284.0301	1142.5187	L	***836.4512***	418.7293	819.4247	410.2160	818.4407	409.7240	7
20	2430.1356	1215.5714	2413.1091	1207.0582	2412.1250	1206.5662	K	***723.3672***	362.1872	706.3406	353.6740	705.3566	353.1819	6
21	2559.1782	1280.0927	2542.1516	1271.5795	2541.1676	1271.0875	E	***595.2722***	298.1397	578.2457	289.6265	577.2617	289.1345	5
22	2706.2466	1353.6269	2689.2201	1345.1137	2688.2360	1344.6217	F	***466.2296***	233.6185	449.2031	225.1052	448.2191	224.6132	4
23	2821.2735	1411.1404	2804.2470	1402.6271	2803.2630	1402.1351	D	***319.1612***	160.0842	302.1347	151.5710	301.1506	151.0790	3
24	2878.2950	1439.6511	2861.2685	1431.1379	2860.2844	1430.6459	G	204.1343	102.5708	187.1077	94.0575			2
25							K	147.1128	74.0600	130.0863	65.5468			1



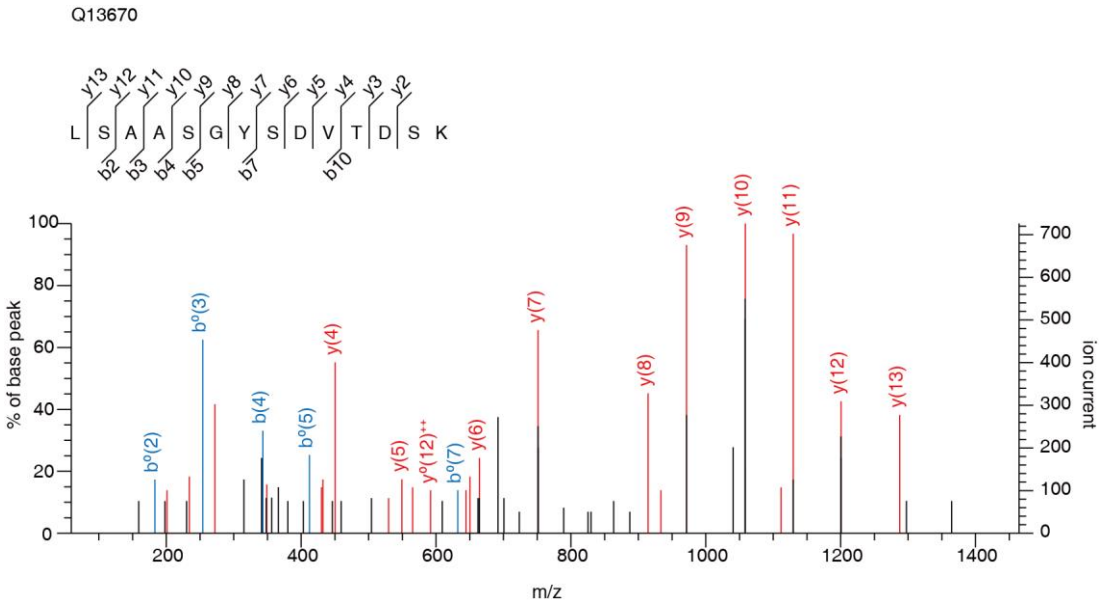
pLabel re-inspection:



No.29: **Q13670**, Putative postmeiotic segregation increased 2-like protein 11 OS=Homo sapiens GN=PMS2P11 **PE=5** SV=1.

Unique peptide: MS/MS Fragmentation of **LSAASGYSDVTDSK**.

Spectrum: Found in **Q13670** in **MHCC97H** cell line (Ion Score cut-off=29).



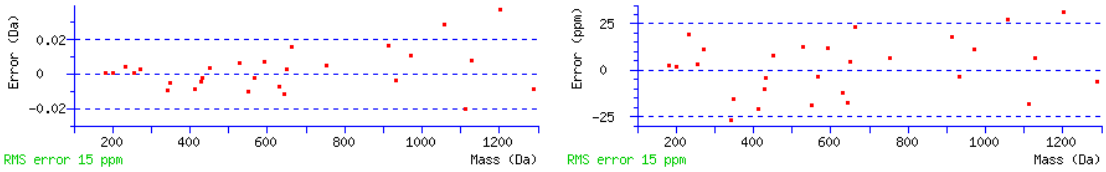
Monoisotopic mass of neutral peptide Mr (calc): 1399.6467

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

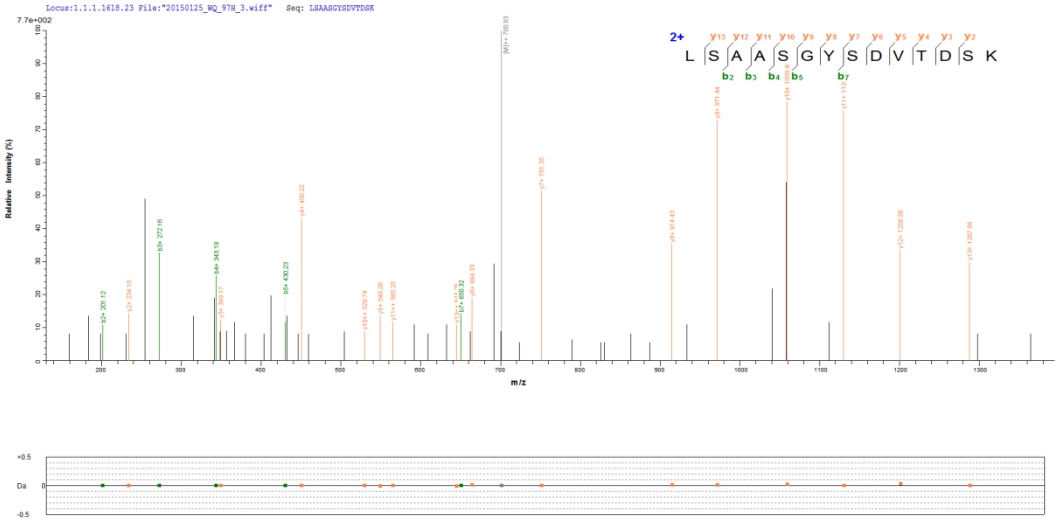
Ions Score: 104 **Expect:** 1.9e-010

Matches: 28/126 fragment ions using 50 most intense peaks

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							14
2	**201.1234**	101.0653	183.1128	92.0600	S	***1287.5699***	**644.2886**	1270.5434	635.7753	1269.5594	635.2833	13
3	**272.1605**	136.5839	254.1499	127.5786	A	***1200.5379***	600.7726	1183.5113	592.2593	1182.5273	591.7673	12
4	**343.1976**	172.1024	325.1870	163.0972	A	***1129.5008***	**565.2540**	1112.4742	556.7408	1111.4902	556.2487	11
5	**430.2296**	215.6184	412.2191	206.6132	S	***1058.4637***	**529.7355**	1041.4371	521.2222	1040.4531	520.7302	10
6	487.2511	244.1292	469.2405	235.1239	G	***971.4316***	486.2195	954.4051	477.7062	953.4211	477.2142	9
7	**650.3144**	325.6608	632.3039	316.6556	Y	***914.4102***	457.7087	897.3836	449.1954	896.3996	448.7034	8
8	737.3464	369.1769	719.3359	360.1716	S	***751.3468***	376.1771	734.3203	367.6638	733.3363	367.1718	7
9	852.3734	426.6903	834.3628	417.6850	D	***664.3148***	332.6610	647.2883	324.1478	646.3042	323.6558	6
10	951.4418	476.2245	933.4312	467.2193	V	***549.2879***	275.1476	532.2613	266.6343	531.2773	266.1423	5
11	1052.4895	526.7484	1034.4789	517.7431	T	***450.2195***	225.6134	433.1929	217.1001	432.2089	216.6081	4
12	1167.5164	584.2618	1149.5059	575.2566	D	***349.1718***	175.0895	332.1452	166.5763	331.1612	166.0842	3
13	1254.5485	627.7779	1236.5379	618.7726	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



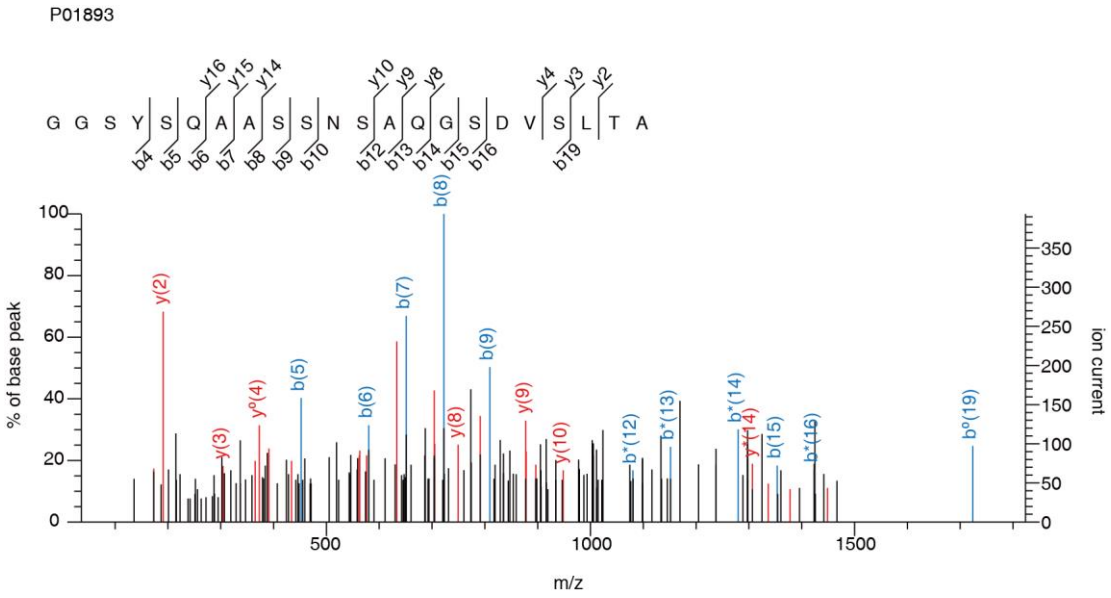
pLabel re-inspection:



No. 30: P01893, Putative HLA class I histocompatibility antigen, alpha chain H OS=Homo sapiens GN=HLA-H **PE=5** SV=3

Unique peptide 1:MS/MS Fragmentation of **GGSYSQAASSNSAQGSDVSLTA**

Spectrum 1: Found in **P01893** in **HCT116-TSA** cell line (Ion Score cut-off=27).



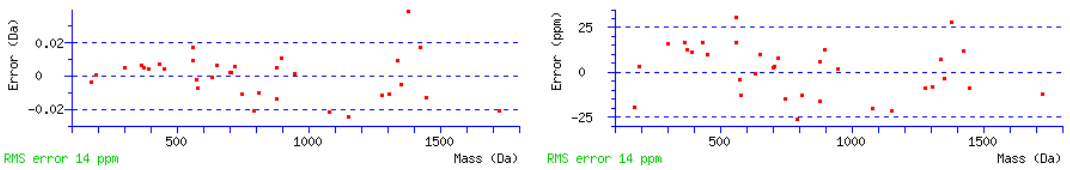
Monoisotopic mass of neutral peptide Mr(calc): 2043.8981

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

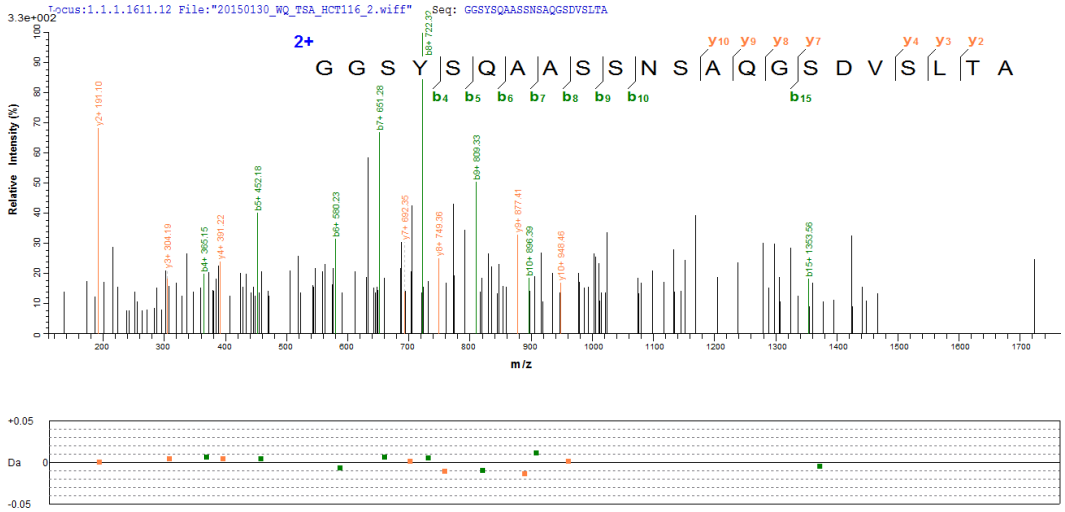
Ions Score: 31 **Expect:** 0.0062

Matches : 34/220 fragment ions using 105 most intense peaks

#	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	115.0502	58.0287					G	1987.8839	994.4456	1970.8574	985.9323	1969.8734	985.4403	21
3	202.0822	101.5448			184.0717	92.5395	S	1930.8625	965.9349	1913.8359	957.4216	1912.8519	956.9296	20
4	*365.1456*	183.0764			347.1350	174.0711	Y	1843.8304	922.4189	1826.8039	913.9056	1825.8199	913.4136	19
5	*452.1776*	226.5924			434.1670	217.5871	S	1680.7671	840.8872	1663.7406	832.3739	1662.7565	831.8819	18
6	*580.2362*	290.6217	563.2096	282.1084	562.2256	281.6164	Q	1593.7351	797.3712	1576.7085	788.8579	1575.7245	788.3659	17
7	*651.2733*	326.1403	634.2467	317.6270	633.2627	317.1350	A	1465.6765	733.3419	1448.6500	724.8286	1447.6659	724.3366	16
8	*722.3104*	361.6588	705.2838	353.1456	704.2998	352.6536	A	1394.6394	697.8233	1377.6128	689.3101	1376.6288	688.8181	15
9	*809.3424*	405.1748	792.3159	396.6616	791.3319	396.1696	S	1323.6023	662.3048	1306.5757	653.7915	1305.5917	653.2995	14
10	*896.3745*	448.6909	879.3479	440.1776	878.3639	439.6856	S	1236.5703	618.7888	1219.5437	610.2755	1218.5597	609.7835	13
11	1010.4174	505.7123	993.3908	497.1991	992.4068	496.7070	N	1149.5382	575.2727	1132.5117	566.7595	1131.5277	566.2675	12
12	1097.4494	549.2283	1080.4229	540.7151	1079.4388	540.2231	S	1035.4953	518.2513	1018.4687	509.7380	1017.4847	509.2460	11
13	1168.4865	584.7469	1151.4600	576.2336	1150.4760	575.7416	A	*948.4633*	474.7353	931.4367	466.2220	930.4527	465.7300	10
14	1296.5451	648.7762	1279.5185	640.2629	1278.5345	639.7709	Q	*877.4262*	439.2167	860.3996	430.7034	859.4156	430.2114	9
15	*1353.5666*	677.2869	1336.5400	668.7736	1335.5560	668.2816	G	*749.3676*	375.1874			731.3570	366.1821	8
16	1440.5986	720.8029	1423.5720	712.2897	1422.5880	711.7977	S	692.3461	346.6767			674.3355	337.6714	7
17	1555.6255	778.3164	1538.5990	769.8031	1537.6150	769.3111	D	605.3141	303.1607			587.3035	294.1554	6
18	1654.6939	827.8506	1637.6674	819.3373	1636.6834	818.8453	V	490.2871	245.6472			472.2766	236.6419	5
19	1741.7260	871.3666	1724.6994	862.8534	1723.7154	862.3613	S	*391.2187*	196.1130			373.2082	187.1077	4
20	1854.8100	927.9087	1837.7835	919.3954	1836.7995	918.9034	L	*304.1867*	152.5970			286.1761	143.5917	3
21	1955.8577	978.4325	1938.8312	969.9192	1937.8472	969.4272	T	*191.1026*	96.0550			173.0921	87.0497	2
22							A	90.0550	45.5311					1



pLabel re-inspection:

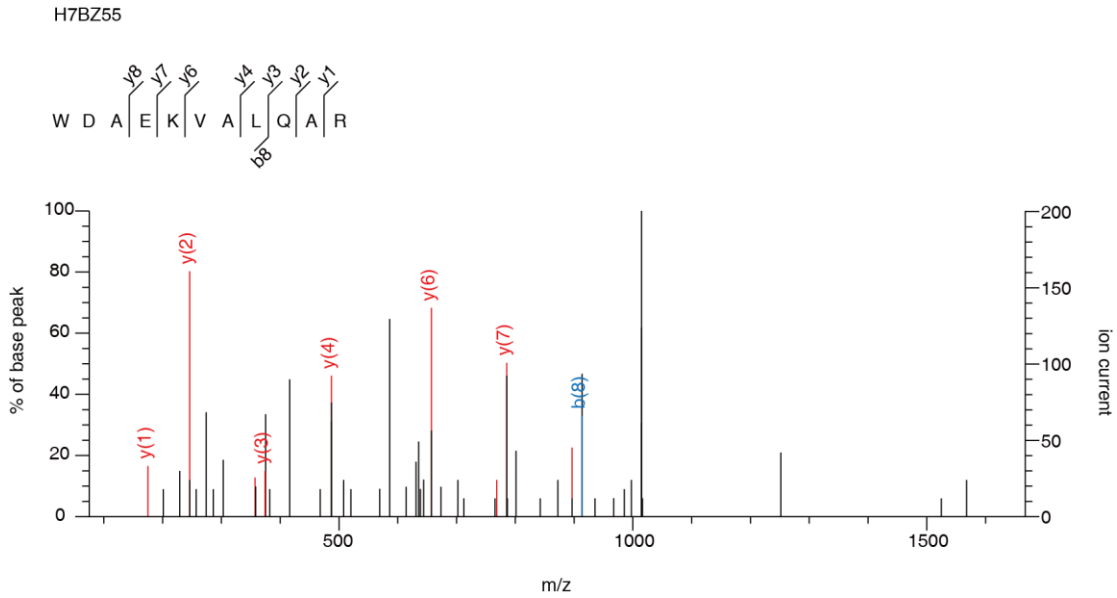


No. 31: H7BZ55, Putative ciliary rootlet coiled-coil protein-like 3 protein OS=Homo sapiens

PE=5 SV=2

Unique peptide 1: MS/MS Fragmentation of **WDAEKVALQAR**

Spectrum 1: Found in **H7BZ55** in **HCT116-S2101** cell line (Ion Score cut-off=27).



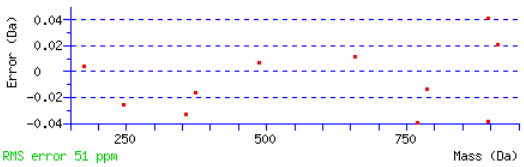
Monoisotopic mass of neutral peptide Mr(calc): 1285.6779

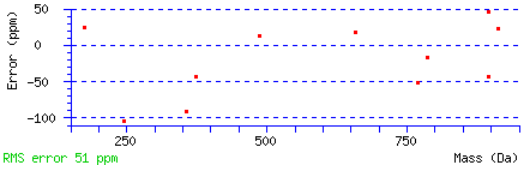
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Ions Score: 32 **Expect:** 0.025

Matches : 11/96 fragment ions using 28 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	187.0866	94.0469					W							11
2	302.1135	151.5604			284.1030	142.5551	D	1100.6058	550.8066	1083.5793	542.2933	1082.5953	541.8013	10
3	373.1506	187.0790			355.1401	178.0737	A	985.5789	493.2931	968.5524	484.7798	967.5683	484.2878	9
4	502.1932	251.6003			484.1827	242.5950	E	914.5418	457.7745	897.5152	449.2613	896.5312	448.7693	8
5	630.2882	315.6477	613.2617	307.1345	612.2776	306.6425	K	*785.4992*	393.2532	768.4726	384.7400			7
6	729.3566	365.1819	712.3301	356.6687	711.3461	356.1767	V	*657.4042*	329.2058	640.3777	320.6925			6
7	800.3937	400.7005	783.3672	392.1872	782.3832	391.6952	A	558.3358	279.6715	541.3093	271.1583			5
8	913.4778	457.2425	896.4512	448.7293	895.4672	448.2373	L	*487.2987*	244.1530	470.2722	235.6397			4
9	1041.5364	521.2718	1024.5098	512.7585	1023.5258	512.2665	Q	*374.2146*	187.6110	357.1881	179.0977			3
10	1112.5735	556.7904	1095.5469	548.2771	1094.5629	547.7851	A	*246.1561*	123.5817	229.1295	115.0684			2
11							R	*175.1190*	88.0631	158.0924	79.5498			1





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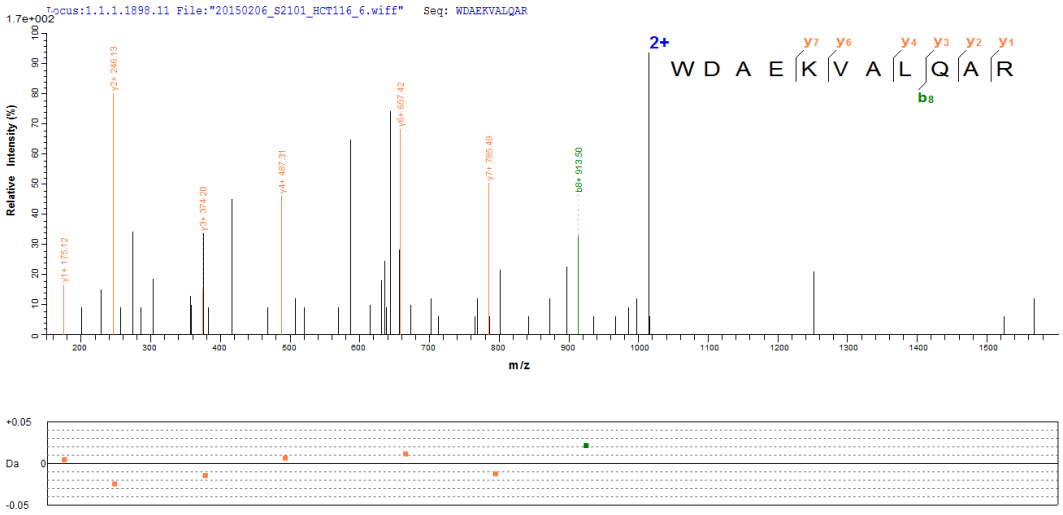
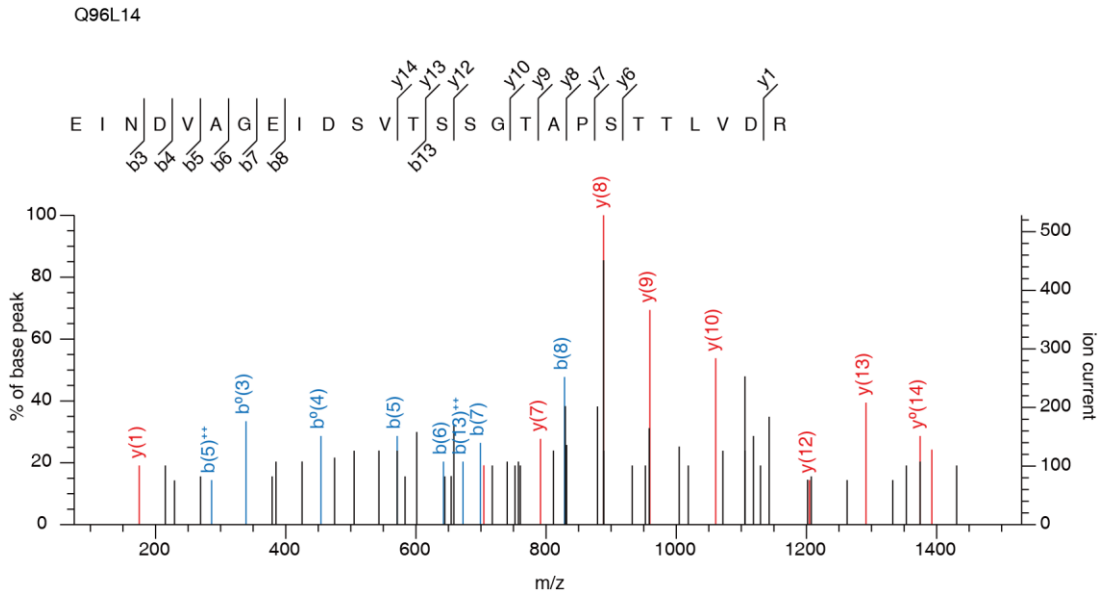


No. 32: Q96L14, UBAP1-MVB12-associated (UMA)-domain containing protein 1

OS=Homo sapiens GN=UMAD1 **PE=3** SV=1.

Unique peptide: MS/MS Fragmentation of **EINDVAGEIDSVTSSGTAPSTTLVDR**.

Spectrum: Found in **Q96L14** in **MHCC97H-S2101** cell line (Ion Score cut-off=28).



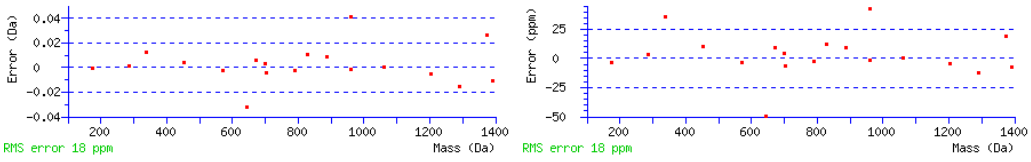
Monoisotopic mass of neutral peptide Mr (calc): 2633.2668

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

Ions Score: 34 **Expect:** 0.00071

Matches: 19/294 fragment ions using 48 most intense peaks

#	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							26
2	243.1339	122.0706			225.1234	113.0653	I	2505.2315	1253.1194	2488.2049	1244.6061	2487.2209	1244.1141	25
3	357.1769	179.0921	340.1503	170.5788	339.1663	170.0868	N	2392.1474	1196.5773	2375.1209	1188.0641	2374.1369	1187.5721	24
4	472.2038	236.6055	455.1773	228.0923	454.1932	227.6003	D	2278.1045	1139.5559	2261.0779	1131.0426	2260.0939	1130.5506	23
5	*571.2722*	**286.1397**	554.2457	277.6265	553.2617	277.1345	V	2163.0775	1082.0424	2146.0510	1073.5291	2145.0670	1073.0371	22
6	*642.3093*	321.6583	625.2828	313.1450	624.2988	312.6530	A	2064.0091	1032.5082	2046.9826	1023.9949	2045.9986	1023.5029	21
7	*699.3308*	350.1690	682.3042	341.6558	681.3202	341.1638	G	1992.9720	996.9896	1975.9455	988.4764	1974.9615	987.9844	20
8	*828.3734*	414.6903	811.3468	406.1771	810.3628	405.6850	E	1935.9506	968.4789	1918.9240	959.9656	1917.9400	959.4736	19
9	941.4575	471.2324	924.4309	462.7191	923.4469	462.2271	I	1806.9080	903.9576	1789.8814	895.4443	1788.8974	894.9523	18
10	1056.4844	528.7458	1039.4578	520.2326	1038.4738	519.7406	D	1693.8239	847.4156	1676.7974	838.9023	1675.8133	838.4103	17
11	1143.5164	572.2618	1126.4899	563.7486	1125.5059	563.2566	S	1578.7970	789.9021	1561.7704	781.3888	1560.7864	780.8968	16
12	1242.5848	621.7961	1225.5583	613.2828	1224.5743	612.7908	V	1491.7649	746.3861	1474.7384	737.8728	1473.7544	737.3808	15
13	1343.6325	**672.3199**	1326.6060	663.8066	1325.6220	663.3146	T	*1392.6965*	696.8519	1375.6700	688.3386	1374.6860	687.8466	14
14	1430.6645	715.8359	1413.6380	707.3226	1412.6540	706.8306	S	*1291.6488*	646.3281	1274.6223	637.8148	1273.6383	637.3228	13
15	1517.6966	759.3519	1500.6700	750.8386	1499.6860	750.3466	S	*1204.6168*	602.8120	1187.5903	594.2988	1186.6062	593.8068	12
16	1574.7180	787.8627	1557.6915	779.3494	1556.7075	778.8574	G	1117.5848	559.2960	1100.5582	550.7828	1099.5742	550.2907	11
17	1675.7657	838.3865	1658.7392	829.8732	1657.7552	829.3812	T	*1060.5633*	530.7853	1043.5368	522.2720	1042.5528	521.7800	10
18	1746.8028	873.9051	1729.7763	865.3918	1728.7923	864.8998	A	*959.5156*	480.2615	942.4891	471.7482	941.5051	471.2562	9
19	1843.8556	922.4314	1826.8290	913.9182	1825.8450	913.4262	P	*888.4785*	444.7429	871.4520	436.2296	870.4680	435.7376	8
20	1930.8876	965.9474	1913.8611	957.4342	1912.8771	956.9422	S	*791.4258*	396.2165	774.3992	387.7032	773.4152	387.2112	7
21	2031.9353	1016.4713	2014.9088	1007.9580	2013.9247	1007.4660	T	*704.3937*	352.7005	687.3672	344.1872	686.3832	343.6952	6
22	2132.9830	1066.9951	2115.9564	1058.4819	2114.9724	1057.9898	T	603.3461	302.1767	586.3195	293.6634	585.3355	293.1714	5
23	2246.0670	1123.5372	2229.0405	1115.0239	2228.0565	1114.5319	L	502.2984	251.6528	485.2718	243.1395	484.2878	242.6475	4
24	2345.1355	1173.0714	2328.1089	1164.5581	2327.1249	1164.0661	V	389.2143	195.1108	372.1878	186.5975	371.2037	186.1055	3
25	2460.1624	1230.5848	2443.1359	1222.0716	2442.1518	1221.5796	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
26							R	*175.1190*	88.0631	158.0924	79.5498			1



pLabel re-inspection: