Mascot Search Results

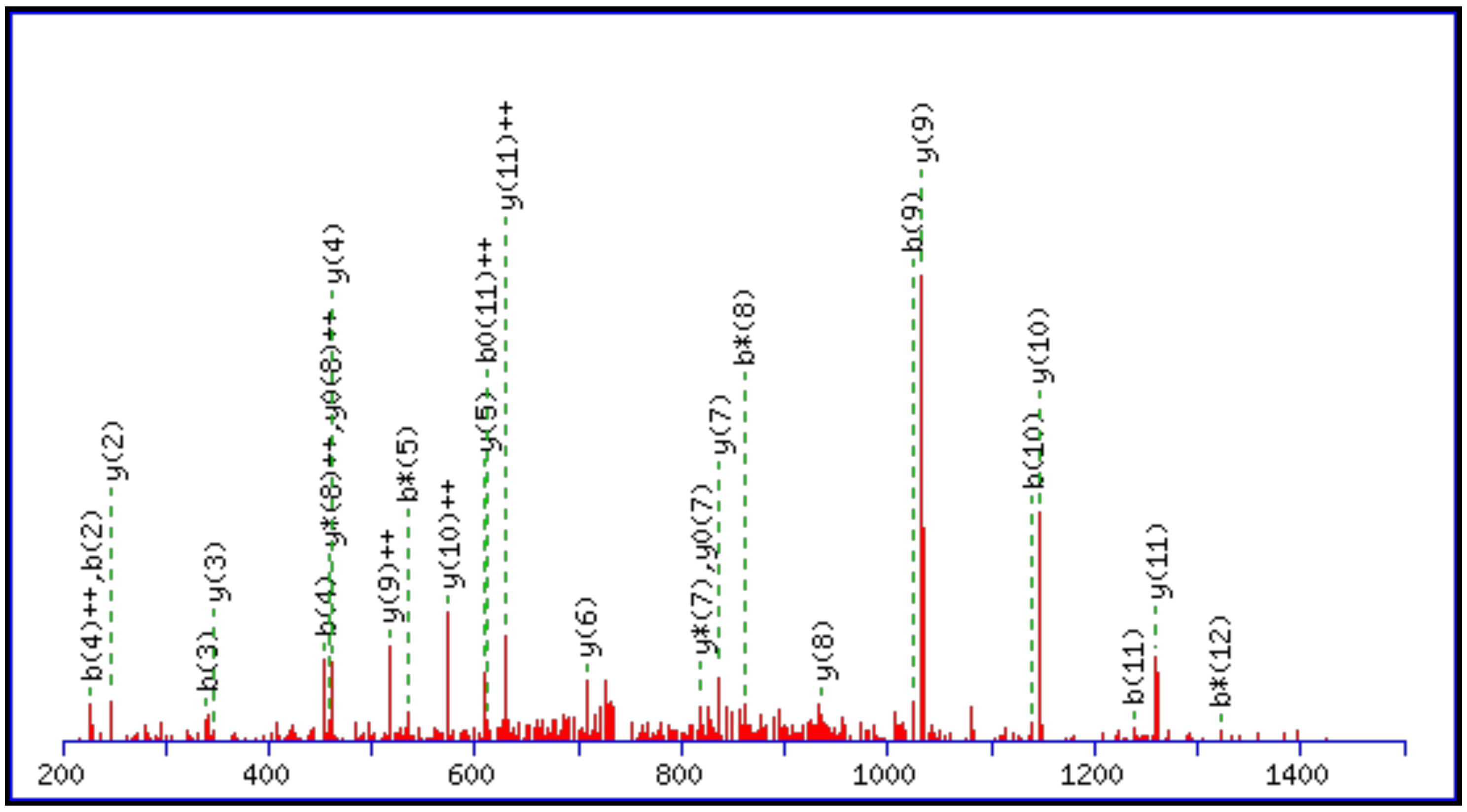
Figure S10

Peptide View

MS/MS Fragmentation of **ILLNPVQVFDVTK**
Found in **gi|9506541**, diacylglycerol kinase epsilon [Mus musculus]

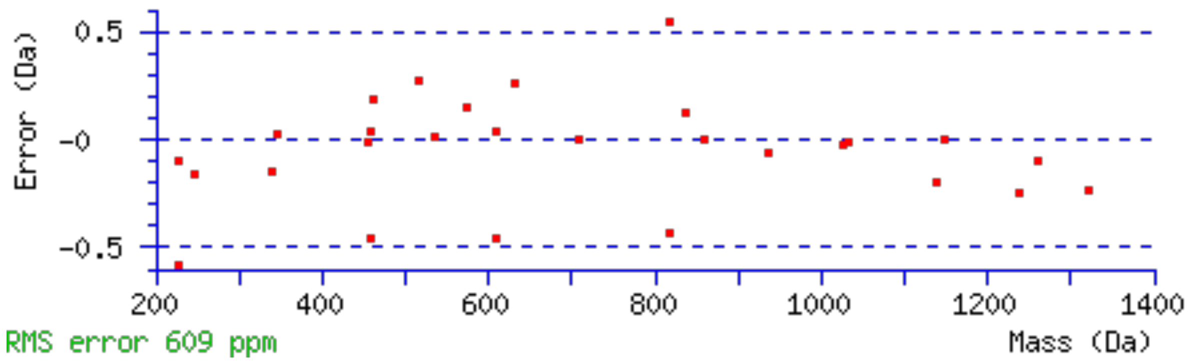
Match to Query 9320: 1485.805448 from(743.910000,2+) intensity(32282.5762) rtinseconds(2377.8054) index(6513)
Title: 15859_20130128_Glp1r_mouse.7857.7857.
Data file 15859_20130128_Glp1r_mouse.mgf

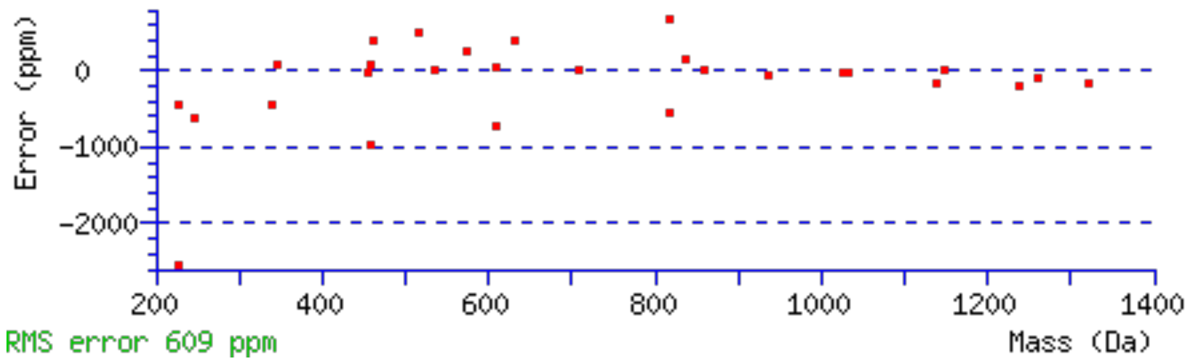
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1484.8603
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 63 **Expect:** 0.00041
Matches : 28/118 fragment ions using 49 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							13
2	**227.1754**	114.0913					L	1372.7835	686.8954	1355.7569	678.3821	1354.7729	677.8901	12
3	**340.2595**	170.6334					L	***1259.6994***	630.3533	1242.6729	621.8401	1241.6889	621.3481	11
4	**454.3024**	227.6548	437.2758	219.1416			N	***1146.6154***	573.8113	1129.5888	565.2980	1128.6048	564.8060	10
5	551.3552	276.1812	534.3286	267.6679			P	***1032.5724***	516.7899	1015.5459	508.2766	1014.5619	507.7846	9
6	650.4236	325.7154	633.3970	317.2022			V	***935.5197***	468.2635	918.4931	459.7502	917.5091	459.2582	8
7	778.4822	389.7447	761.4556	381.2314			Q	***836.4512***	418.7293	819.4247	410.2160	818.4407	409.7240	7
8	877.5506	439.2789	860.5240	430.7656			V	***708.3927***	354.7000	691.3661	346.1867	690.3821	345.6947	6
9	**1024.6190**	512.8131	1007.5924	504.2999			F	***609.3243***	305.1658	592.2977	296.6525	591.3137	296.1605	5
10	**1139.6459**	570.3266	1122.6194	561.8133	1121.6354	561.3213	D	***462.2558***	231.6316	445.2293	223.1183	444.2453	222.6263	4
11	**1238.7143**	619.8608	1221.6878	611.3475	1220.7038	610.8555	V	***347.2289***	174.1181	330.2023	165.6048	329.2183	165.1128	3
12	1339.7620	670.3846	1322.7355	661.8714	1321.7514	661.3794	T	***248.1605***	124.5839	231.1339	116.0706	230.1499	115.5786	2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ILLNPVQVFDVTK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.6	1484.8603	0.9452	ILLNPVQVFDVTK
17.4	1487.7766	-1.9711	QTLNVLEEVCKR
15.6	1485.7940	0.0115	ILNLRDQQFPDK
13.4	1485.8780	-0.0725	RALGPGIPHIINTK
13.1	1484.8715	0.9340	LLNIPINDIVHPK
12.8	1484.8450	0.9604	KPLDVTASSLVDLK
10.9	1484.7697	1.0357	IILNFTSMDLYR
10.8	1485.7948	0.0106	KVIGGMVWNPVMR
7.2	1485.7762	0.0292	LLINSVFHMGAER
6.5	1487.6602	-1.8548	VEINPPDDMEWK

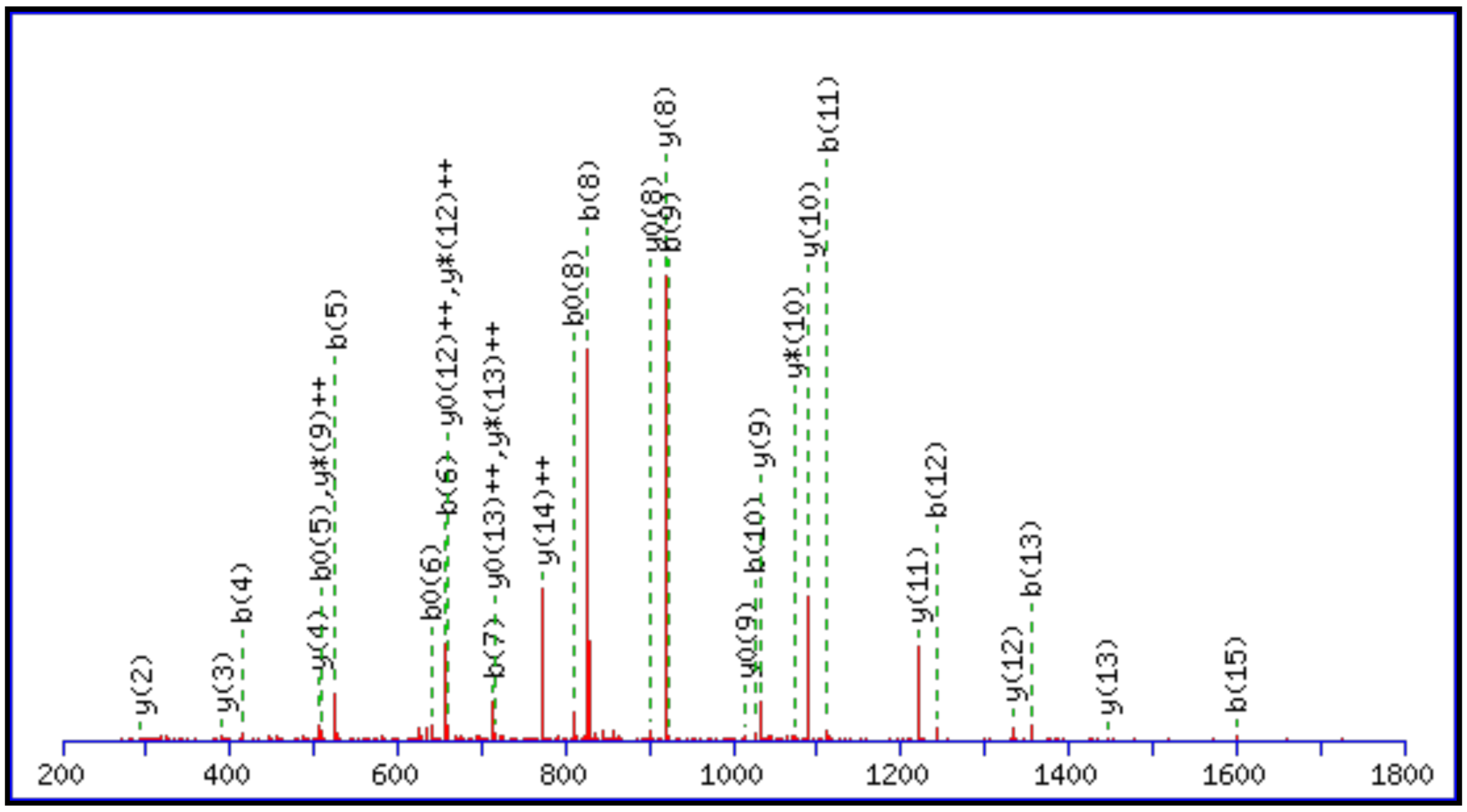
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SDPLLMGIPTSENPFK**
Found in **gi|13384618**, guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 [Mus musculus]

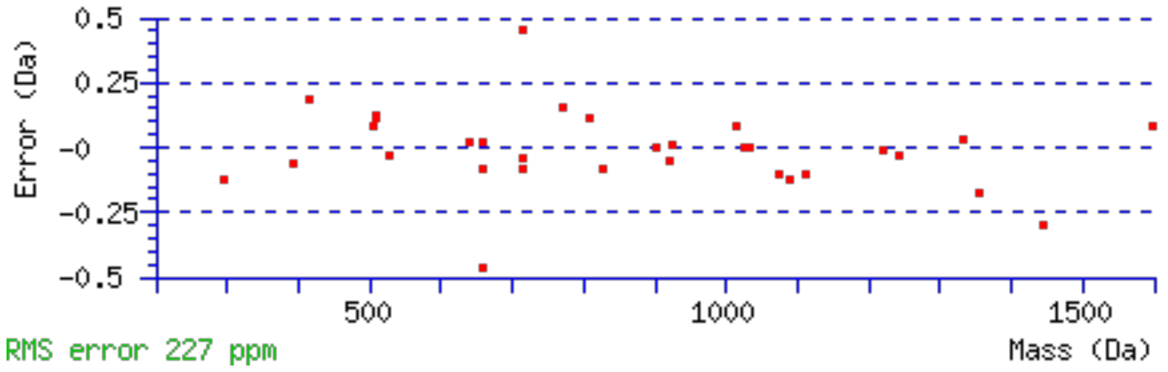
Match to Query 11651: 1745.545448 from(873.780000,2+) intensity(39879.7344) rtinseconds(2290.7407) index(6283)
Title: 15859_20130128_Glp1r_mouse.7581.7581.
Data file 15859_20130128_Glp1r_mouse.mgf

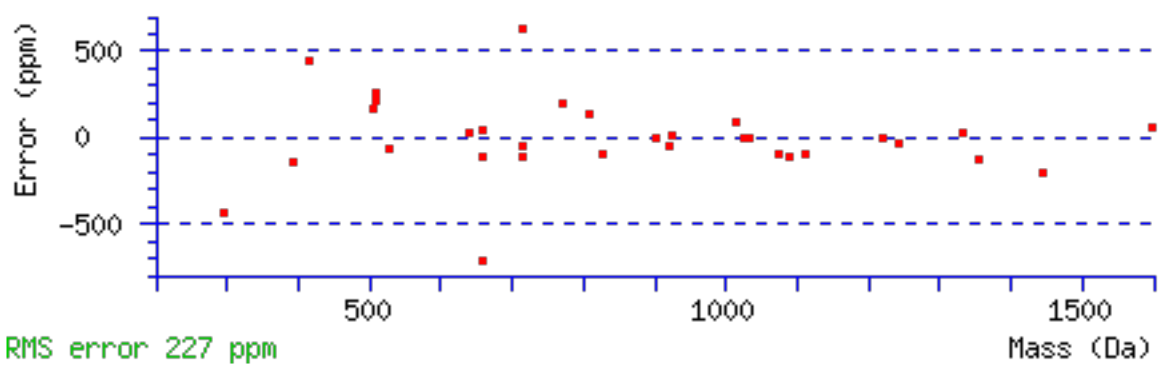
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1744.8706
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 67 **Expect:** 0.00014
Matches : 32/148 fragment ions using 55 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							16
2	203.0662	102.0368			185.0557	93.0315	D	1658.8458	829.9265	1641.8193	821.4133	1640.8353	820.9213	15
3	300.1190	150.5631			282.1084	141.5579	P	1543.8189	772.4131	1526.7923	763.8998	1525.8083	763.4078	14
4	***413.2031***	207.1052			395.1925	198.0999	L	***1446.7661***	723.8867	1429.7396	715.3734	1428.7555	714.8814	13
5	***526.2871***	263.6472			508.2766	254.6419	L	***1333.6821***	667.3447	1316.6555	658.8314	1315.6715	658.3394	12
6	***657.3276***	329.1675			639.3171	320.1622	M	***1220.5980***	610.8026	1203.5714	602.2894	1202.5874	601.7973	11
7	***714.3491***	357.6782			696.3385	348.6729	G	***1089.5575***	545.2824	1072.5310	536.7691	1071.5469	536.2771	10
8	***827.4332***	414.2202			809.4226	405.2149	I	***1032.5360***	516.7717	1015.5095	508.2584	1014.5255	507.7664	9
9	***924.4859***	462.7466			906.4754	453.7413	P	***919.4520***	460.2296	902.4254	451.7164	901.4414	451.2243	8
10	***1025.5336***	513.2704			1007.5230	504.2652	T	822.3992	411.7032	805.3727	403.1900	804.3886	402.6980	7
11	***1112.5656***	556.7864			1094.5551	547.7812	S	721.3515	361.1794	704.3250	352.6661	703.3410	352.1741	6
12	***1241.6082***	621.3077			1223.5977	612.3025	E	634.3195	317.6634	617.2930	309.1501	616.3089	308.6581	5
13	***1355.6511***	678.3292	1338.6246	669.8159	1337.6406	669.3239	N	***505.2769***	253.1421	488.2504	244.6288			4
14	1452.7039	726.8556	1435.6774	718.3423	1434.6933	717.8503	P	***391.2340***	196.1206	374.2074	187.6074			3
15	***1599.7723***	800.3898	1582.7458	791.8765	1581.7618	791.3845	F	***294.1812***	147.5942	277.1547	139.0810			2
16							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of SDPLLMGIPTSENPFK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.5	1744.8706	0.6749	SDPLLMGIPTSENPFK
13.4	1745.8618	-0.3163	ELLGNATQPTSCASGLK
7.9	1745.7340	-0.1885	HSEAEGSEKAQSDDEK
5.3	1744.7470	0.7985	NNVTPDMMEEMYKK
5.3	1744.7470	0.7985	NNVTPDMMEEMYKK
3.7	1745.9213	-0.3758	SGRLLVPAYTYHVDR
3.2	1744.9723	0.5731	HKFSTISTLGDISVLK
2.2	1747.9403	-2.3949	HRPAVVMDLIDLTPR
1.7	1746.9516	-1.4061	KLSGLSAFDIAEELVR
1.4	1744.0685	1.4770	VYIGKLNMILVQILK

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

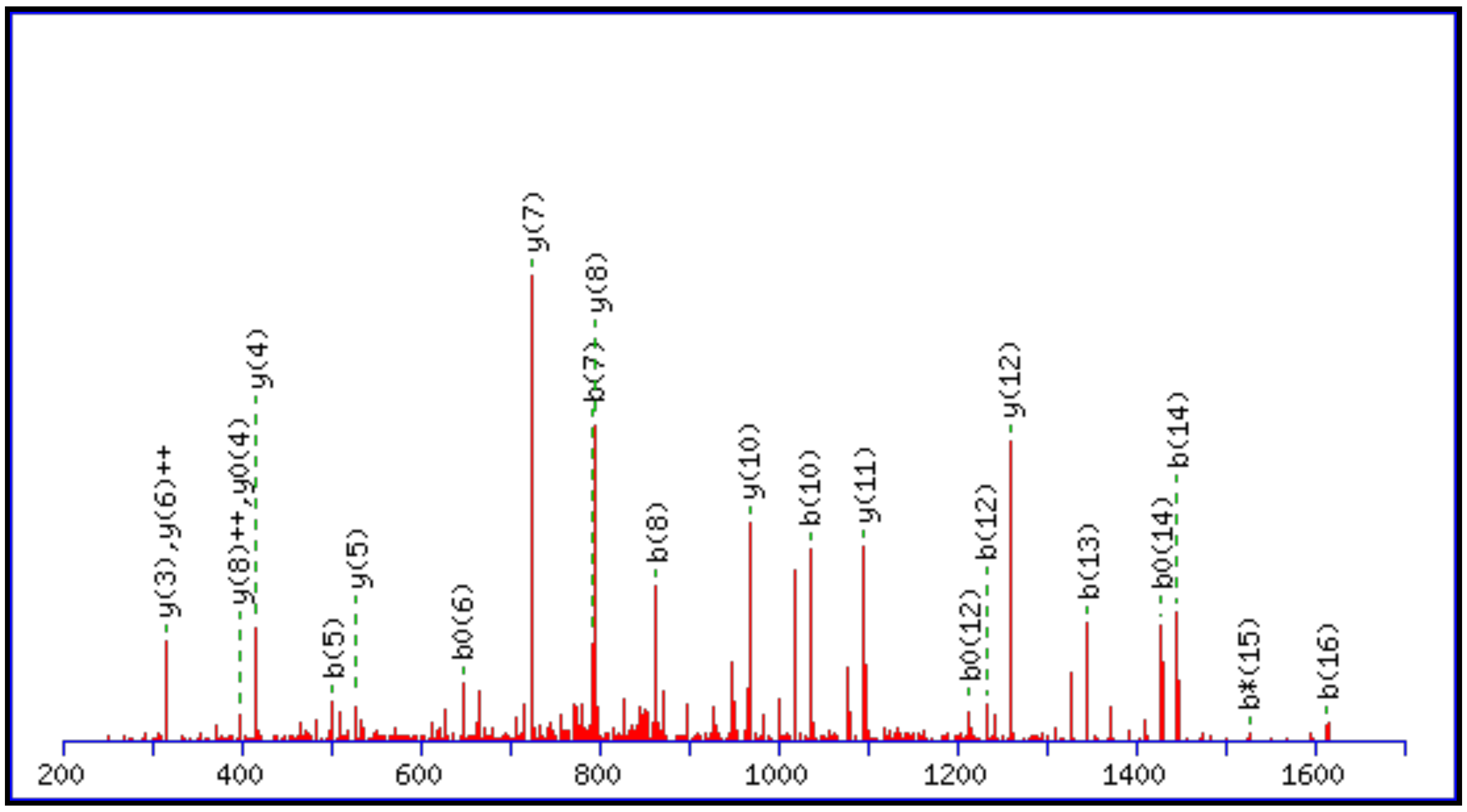
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ISSTLYQATAPVLTPAK**
Found in **gi|13384696**, keratinocyte-associated protein 2 [Mus musculus]

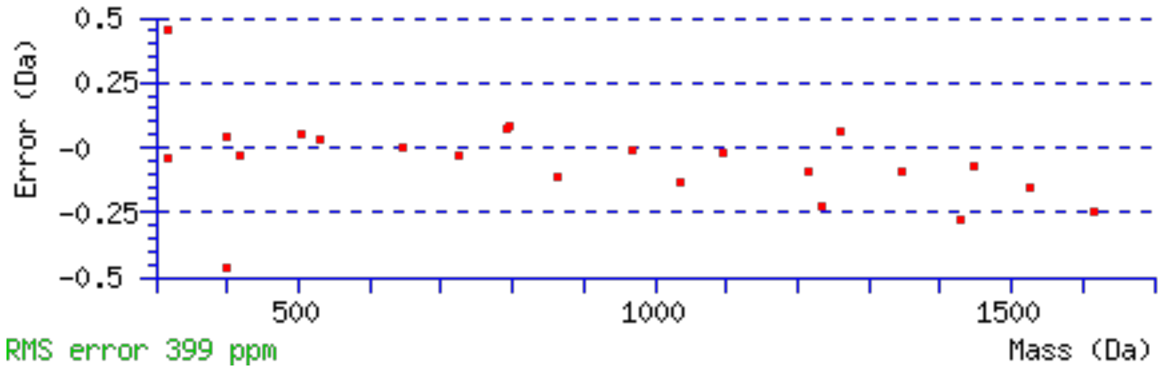
Match to Query 11744: 1760.645448 from(881.330000,2+) intensity(39946.9609) rtinseconds(1344.8266) index(3736)
Title: 15859_20130128_Glp1r_mouse.4524.4524.
Data file 15859_20130128_Glp1r_mouse.mgf

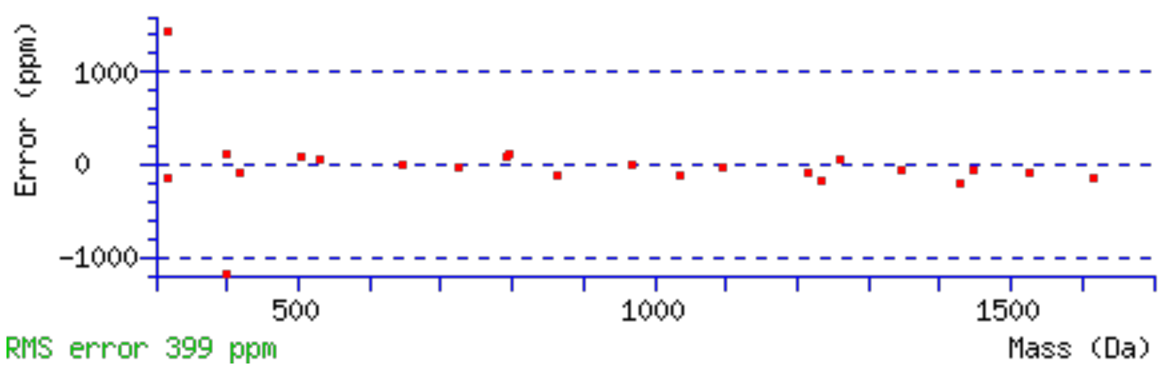
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1759.9720
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 70 **Expect:** 6.6e-05
Matches : 23/172 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							17
2	201.1234	101.0653			183.1128	92.0600	S	1647.8952	824.4512	1630.8687	815.9380	1629.8847	815.4460	16
3	288.1554	144.5813			270.1448	135.5761	S	1560.8632	780.9352	1543.8366	772.4220	1542.8526	771.9299	15
4	389.2031	195.1052			371.1925	186.0999	T	1473.8312	737.4192	1456.8046	728.9059	1455.8206	728.4139	14
5	***502.2871***	251.6472			484.2766	242.6419	L	1372.7835	686.8954	1355.7569	678.3821	1354.7729	677.8901	13
6	665.3505	333.1789			647.3399	324.1736	Y	***1259.6994***	630.3533	1242.6729	621.8401	1241.6889	621.3481	12
7	***793.4090***	397.2082	776.3825	388.6949	775.3985	388.2029	Q	***1096.6361***	548.8217	1079.6095	540.3084	1078.6255	539.8164	11
8	***864.4462***	432.7267	847.4196	424.2134	846.4356	423.7214	A	***968.5775***	484.7924	951.5510	476.2791	950.5669	475.7871	10
9	965.4938	483.2506	948.4673	474.7373	947.4833	474.2453	T	897.5404	449.2738	880.5138	440.7606	879.5298	440.2686	9
10	***1036.5310***	518.7691	1019.5044	510.2558	1018.5204	509.7638	A	***796.4927***	398.7500	779.4662	390.2367	778.4822	389.7447	8
11	1133.5837	567.2955	1116.5572	558.7822	1115.5732	558.2902	P	***725.4556***	363.2314	708.4291	354.7182	707.4450	354.2262	7
12	***1232.6521***	616.8297	1215.6256	608.3164	1214.6416	607.8244	V	628.4028	314.7051	611.3763	306.1918	610.3923	305.6998	6
13	***1345.7362***	673.3717	1328.7096	664.8585	1327.7256	664.3665	L	***529.3344***	265.1709	512.3079	256.6576	511.3239	256.1656	5
14	***1446.7839***	723.8956	1429.7573	715.3823	1428.7733	714.8903	T	***416.2504***	208.6288	399.2238	200.1155	398.2398	199.6235	4
15	1543.8366	772.4220	1526.8101	763.9087	1525.8261	763.4167	P	***315.2027***	158.1050	298.1761	149.5917			3
16	***1614.8738***	807.9405	1597.8472	799.4272	1596.8632	798.9352	A	218.1499	109.5786	201.1234	101.0653			2
17							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ISSTLYQATAPVLTPAK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
69.7	1759.9720	0.6735	ISSTLYQATAPVLTPAK
7.5	1758.8069	1.8385	CYLYQARDLPAMDK
6.3	1760.8801	-0.2346	TTMGLLVVHKEGEGMK
3.4	1759.8682	0.7773	APFYWDDAHRLIEK
3.4	1760.9165	-0.2710	VVTATGTLALGINMPCK
2.5	1759.9073	0.7382	AAQLCGAGMAAVVEKIR
2.1	1759.8887	0.7568	QLRMPNEVTSTDTIR
1.8	1762.9690	-2.3235	QGLIKQQQQIPNPSGK
1.4	1759.8662	0.7793	TGQELKEAALEPSMEK
0.2	1759.0356	1.6098	SGLLLHGPPGTGKTLLAK

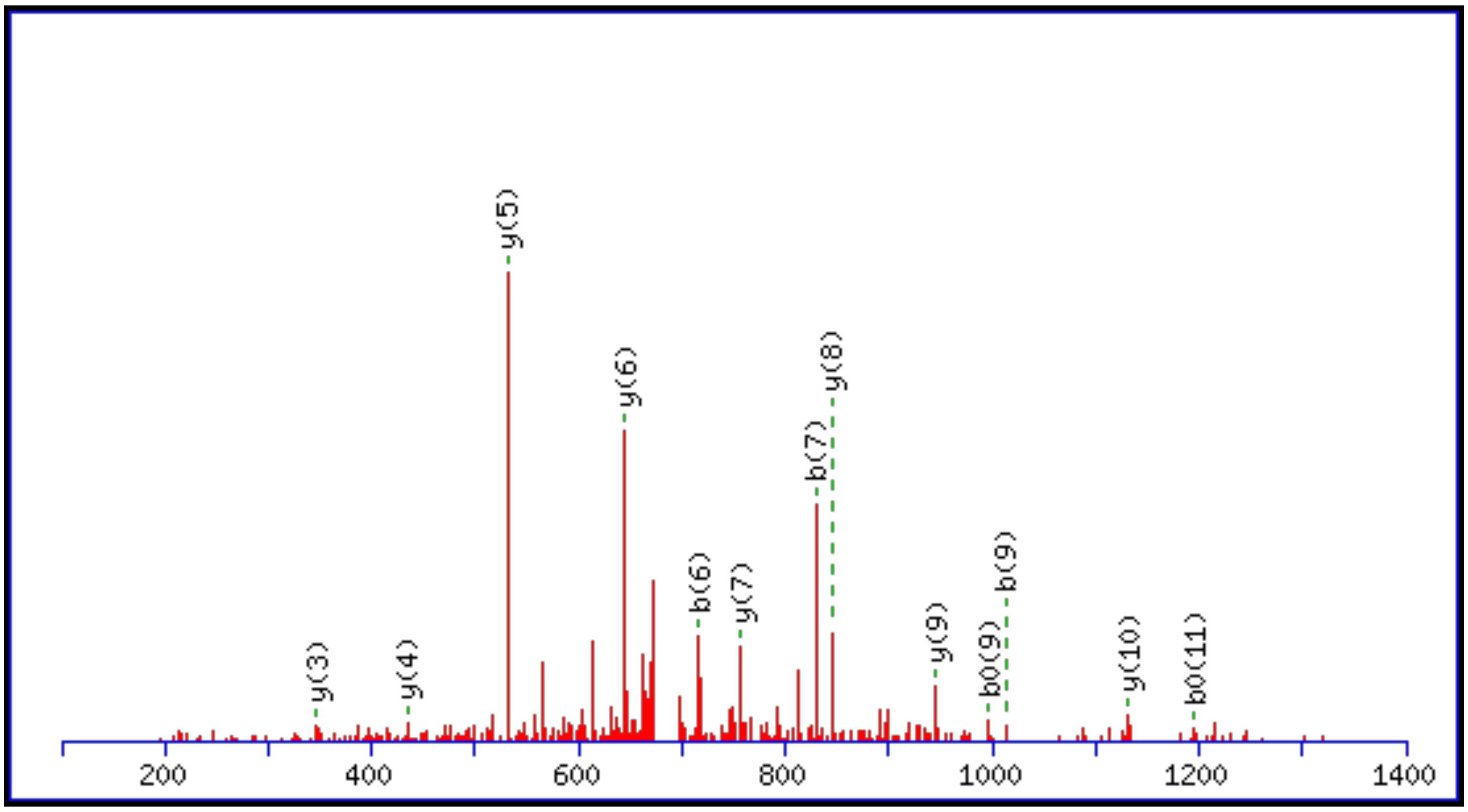
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDWTSLLPSSIK**
Found in **gi|30520239**, neutral cholesterol ester hydrolase 1 [Mus musculus]

Match to Query 6844: 1359.345448 from(680.680000,2+) intensity(8220.8672) rtinseconds(2822.01) index(7717)
Title: 16590_20130315_min6_glp1R_2hrp.09279.09279.0.dta
Data file 16590_20130315_min6_glp1R_2hrp.mgf

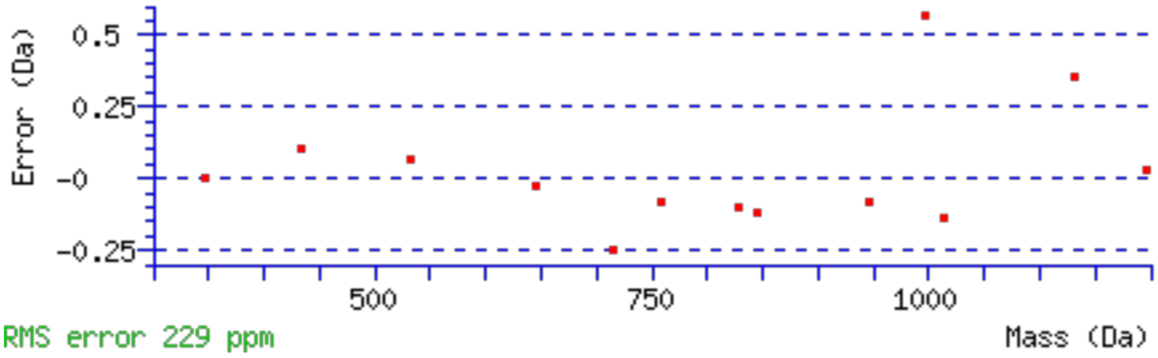
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●

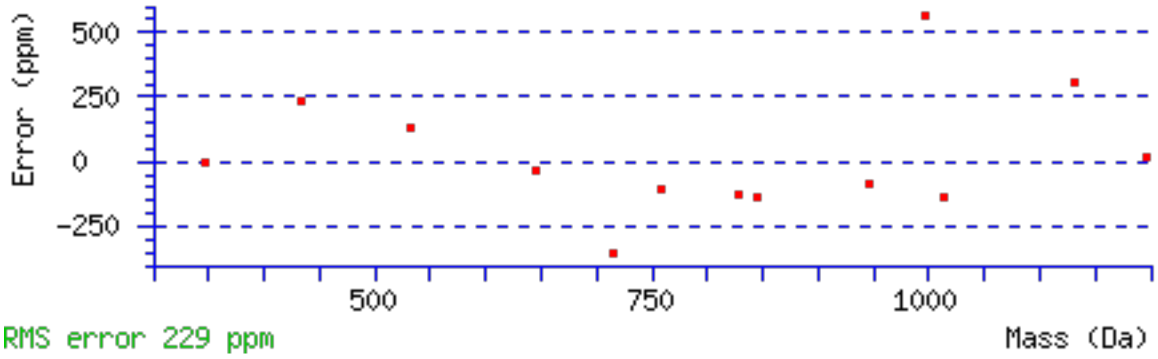


Monoisotopic mass of neutral peptide Mr(calc): 1358.7446
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 0.0033
Matches : 13/104 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							12
2	229.1183	115.0628	211.1077	106.0575	D	1246.6678	623.8375	1229.6412	615.3243	1228.6572	614.8322	11
3	415.1976	208.1024	397.1870	199.0972	W	***1131.6408***	566.3241	1114.6143	557.8108	1113.6303	557.3188	10
4	516.2453	258.6263	498.2347	249.6210	T	***945.5615***	473.2844	928.5350	464.7711	927.5510	464.2791	9
5	603.2773	302.1423	585.2667	293.1370	S	***844.5138***	422.7606	827.4873	414.2473	826.5033	413.7553	8
6	**716.3614**	358.6843	698.3508	349.6790	L	***757.4818***	379.2445	740.4553	370.7313	739.4713	370.2393	7
7	**829.4454**	415.2264	811.4349	406.2211	L	***644.3978***	322.7025	627.3712	314.1892	626.3872	313.6972	6
8	926.4982	463.7527	908.4876	454.7475	P	***531.3137***	266.1605	514.2871	257.6472	513.3031	257.1552	5
9	**1013.5302**	507.2687	995.5197	498.2635	S	***434.2609***	217.6341	417.2344	209.1208	416.2504	208.6288	4
10	1100.5623	550.7848	1082.5517	541.7795	S	***347.2289***	174.1181	330.2023	165.6048	329.2183	165.1128	3
11	1213.6463	607.3268	1195.6357	598.3215	I	260.1969	130.6021	243.1703	122.0888			2

12				K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LDWTSLLPSSIK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.0	1358.7446	0.6009	LDWTSLLPSSIK
12.7	1358.8173	0.5281	FAALITVLALAEK
9.8	1358.7531	0.5924	FQGLRARPSTAR
9.1	1360.7020	-1.3566	MELSQLLNEIR
8.4	1358.8021	0.5434	EKTLILLDVSTK
7.7	1358.5959	0.7496	YRGMGSLDAMDK
6.2	1357.7864	1.5591	MIATGGLLRISAR
4.7	1360.6809	-1.3355	FPKGTDATMLHK
4.3	1360.7384	-1.3930	VMLQVNGKELSK
3.7	1356.5438	2.8016	DCHVEPCPESK

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

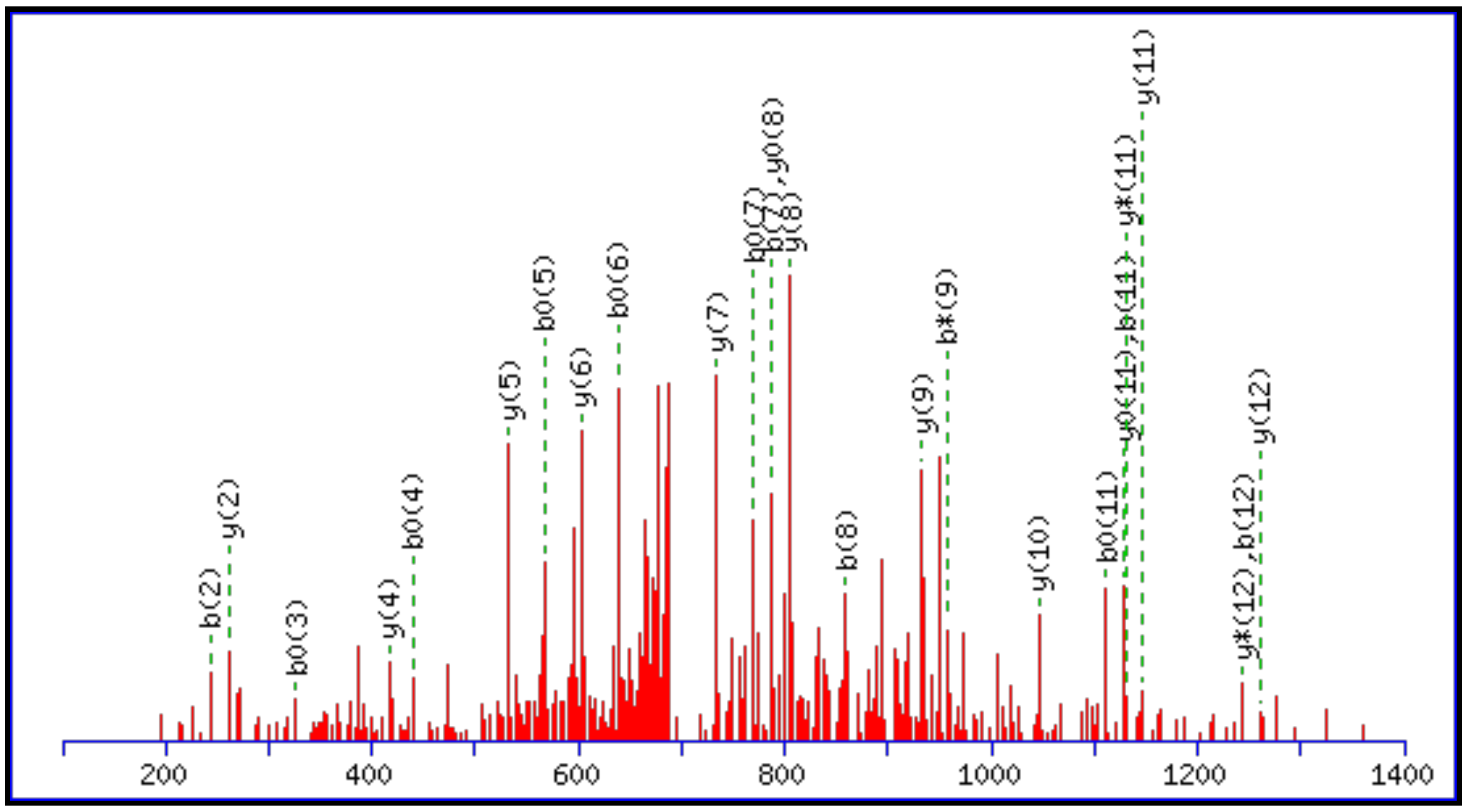
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELTLQAMADGVNK**
Found in **gi|6679229**, neuroendocrine convertase 2 precursor [Mus musculus]

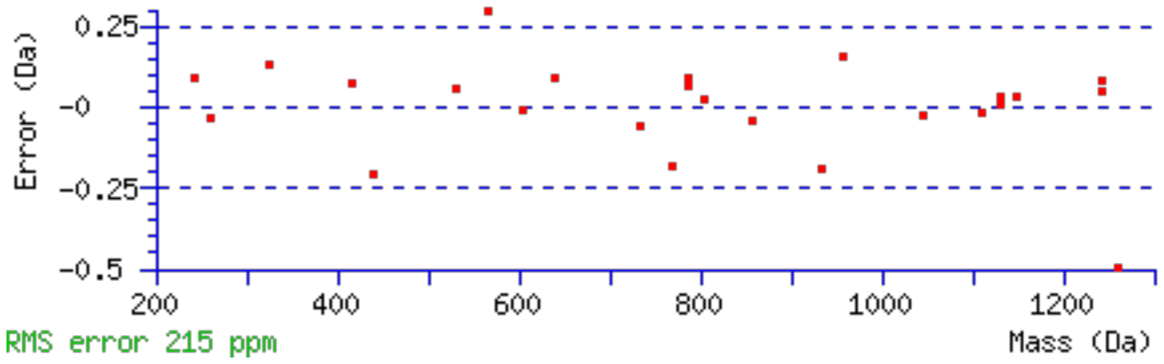
Match to Query 8404: 1389.725448 from(695.870000,2+) intensity(31416.9336) rtinseconds(1388.4489) index(3856)
Title: 15859_20130128_Glp1r_mouse.4668.4668.
Data file 15859_20130128_Glp1r_mouse.mgf

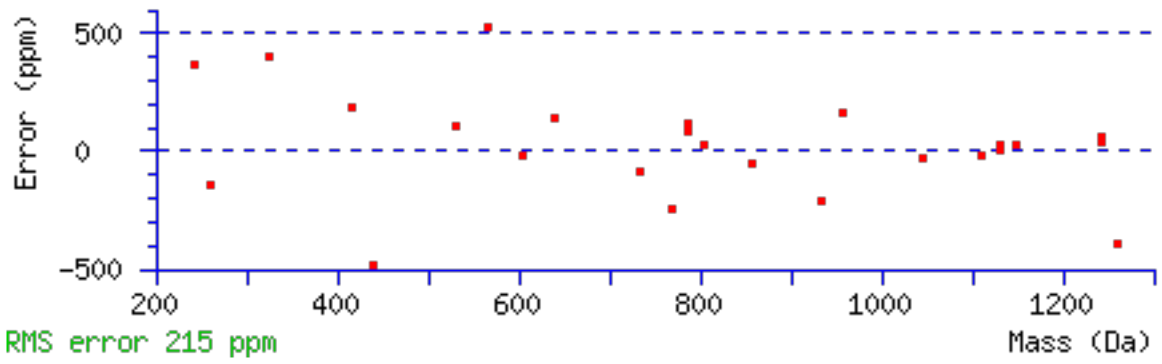
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1388.6969
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 64 **Expect:** 0.00035
Matches : 26/128 fragment ions using 47 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							13
2	**243.1339**	122.0706			225.1234	113.0653	L	***1260.6617***	630.8345	1243.6351	622.3212	1242.6511	621.8292	12
3	344.1816	172.5944			326.1710	163.5892	T	***1147.5776***	574.2924	1130.5510	565.7792	1129.5670	565.2871	11
4	457.2657	229.1365			439.2551	220.1312	L	***1046.5299***	523.7686	1029.5034	515.2553	1028.5193	514.7633	10
5	585.3243	293.1658	568.2977	284.6525	567.3137	284.1605	Q	***933.4458***	467.2266	916.4193	458.7133	915.4353	458.2213	9
6	656.3614	328.6843	639.3348	320.1710	638.3508	319.6790	A	***805.3873***	403.1973	788.3607	394.6840	787.3767	394.1920	8
7	**787.4019**	394.2046	770.3753	385.6913	769.3913	385.1993	M	***734.3502***	367.6787	717.3236	359.1654	716.3396	358.6734	7
8	**858.4390**	429.7231	841.4124	421.2098	840.4284	420.7178	A	***603.3097***	302.1585	586.2831	293.6452	585.2991	293.1532	6
9	973.4659	487.2366	956.4394	478.7233	955.4553	478.2313	D	***532.2726***	266.6399	515.2460	258.1266	514.2620	257.6346	5
10	1030.4874	515.7473	1013.4608	507.2341	1012.4768	506.7420	G	***417.2456***	209.1264	400.2191	200.6132			4
11	**1129.5558**	565.2815	1112.5292	556.7683	1111.5452	556.2762	V	360.2241	180.6157	343.1976	172.1024			3
12	**1243.5987**	622.3030	1226.5722	613.7897	1225.5882	613.2977	N	***261.1557***	131.0815	244.1292	122.5682			2
13							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of ELTLQAMADGVNK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.6	1388.6969	1.0285	ELTLQAMADGVNK
7.2	1388.6056	1.1199	DAETDGPEKGDQK
4.3	1389.6848	0.0406	IEQTNQTEKGSR
3.3	1388.7446	0.9809	AGIRVVMITGDNK
3.3	1389.7113	0.0142	EIHSQQVKEHR
2.6	1388.6606	1.0649	ELETQQPCKEK
2.2	1388.6572	1.0682	EDDGKGNFSPVPK
1.7	1387.7055	2.0199	QIEDLQGRTSNK
1.4	1390.7642	-1.0388	FLRQEMVIEVK
1.1	1387.6844	2.0410	AGGPRTFSEVPDR

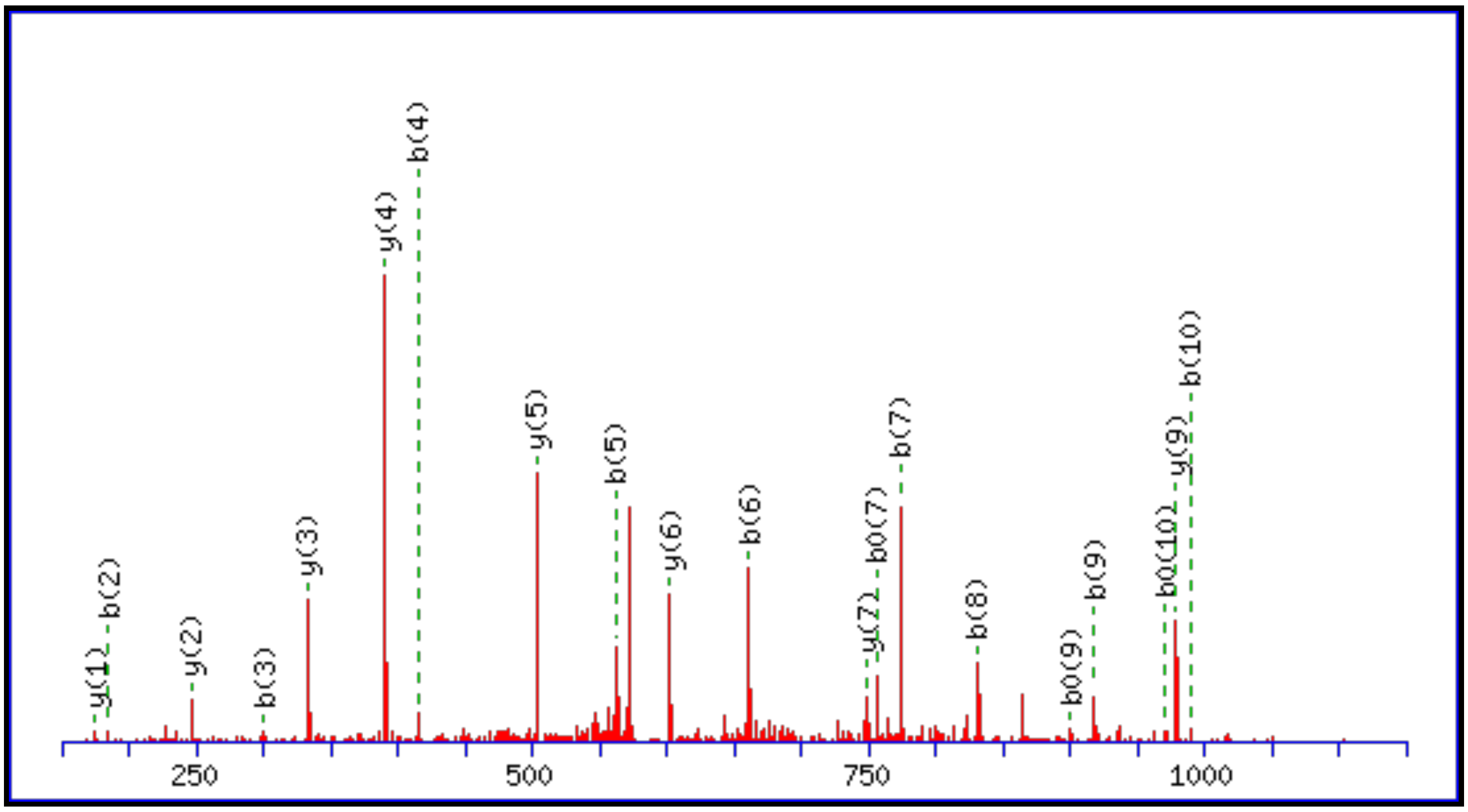
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALDDFVLGSAR**
Found in **gil20070422**, PRA1 family protein 2 [Mus musculus]

Match to Query 5497: 1164.525448 from(583.270000,2+) intensity(30006.5859) rtinseconds(1517.8133) index(4210)
Title: 15859_20130128_Glp1r_mouse.5093.5093.
Data file 15859_20130128_Glp1r_mouse.mgf

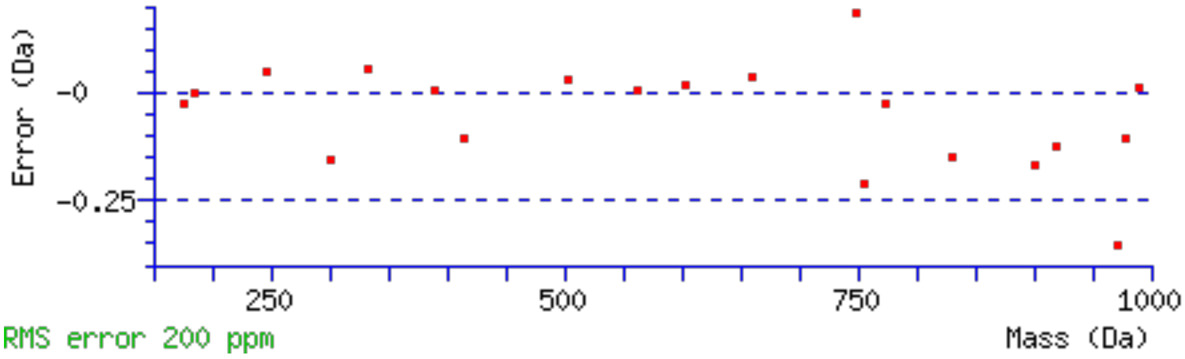
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●

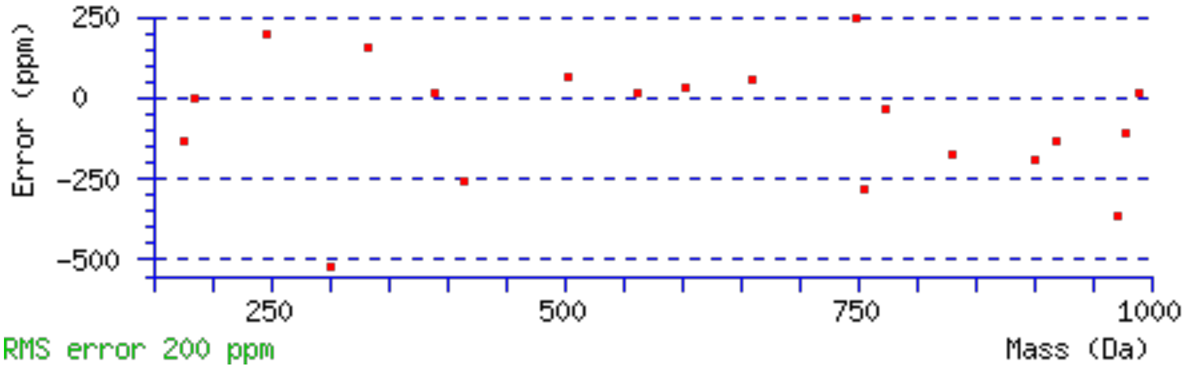


Monoisotopic mass of neutral peptide Mr(calc): 1162.5982
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 67 **Expect:** 0.0002
Matches : 20/92 fragment ions using 37 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258			A							11
2	***185.1285***	93.0679			L	1092.5684	546.7878	1075.5419	538.2746	1074.5578	537.7826	10
3	***300.1554***	150.5813	282.1448	141.5761	D	**979.4843**	490.2458	962.4578	481.7325	961.4738	481.2405	9
4	***415.1823***	208.0948	397.1718	199.0895	D	864.4574	432.7323	847.4308	424.2191	846.4468	423.7271	8
5	***562.2508***	281.6290	544.2402	272.6237	F	**749.4305**	375.2189	732.4039	366.7056	731.4199	366.2136	7
6	***661.3192***	331.1632	643.3086	322.1579	V	**602.3620**	301.6847	585.3355	293.1714	584.3515	292.6794	6
7	***774.4032***	387.7053	756.3927	378.7000	L	**503.2936**	252.1504	486.2671	243.6372	485.2831	243.1452	5
8	***831.4247***	416.2160	813.4141	407.2107	G	**390.2096**	195.6084	373.1830	187.0951	372.1990	186.6031	4
9	***918.4567***	459.7320	900.4462	450.7267	S	**333.1881**	167.0977	316.1615	158.5844	315.1775	158.0924	3
10	***989.4938***	495.2506	971.4833	486.2453	A	**246.1561**	123.5817	229.1295	115.0684			2

11					R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of ALDDFVLGSAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.9	1162.5982	1.9272	ALDDFVLGSAR
24.8	1162.5401	1.9854	GTSCPLSASGAR
15.8	1162.4924	2.0330	AEPSNCDGSVK
15.8	1162.4924	2.0330	MNSTPNENEK
15.8	1162.6207	1.9048	SGNVIFRGSAR
13.3	1162.5652	1.9602	LMESTDPSKR
12.6	1162.6710	1.8545	LLYGLTNTLR
12.1	1162.5553	1.9701	SPDFRPSMAR
11.5	1166.5311	-2.0057	DVDSLALCMK
10.0	1163.5796	0.9459	QGNPQHLSQR

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

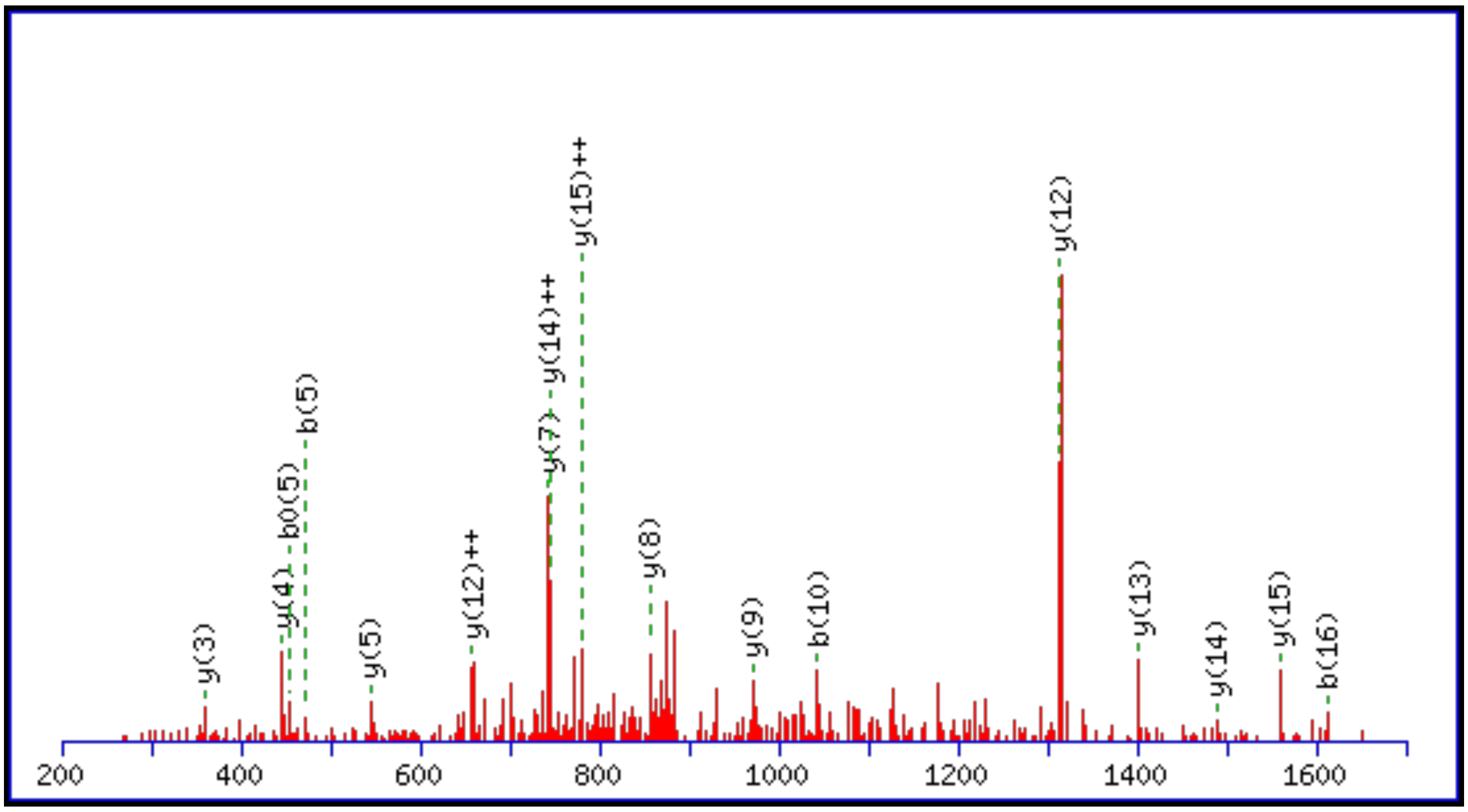
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIASSPDMDLPTVSALR**
Found in **gi|19526878**, pyrroline-5-carboxylate reductase 2 [Mus musculus]

Match to Query 11504: 1786.565448 from(894.290000,2+) intensity(16815.4043) rtinseconds(1898.64) index(5288)
Title: 16590_20130315_min6_glp1R_2hrp.06359.06359.0.dta
Data file 16590_20130315_min6_glp1R_2hrp.mgf

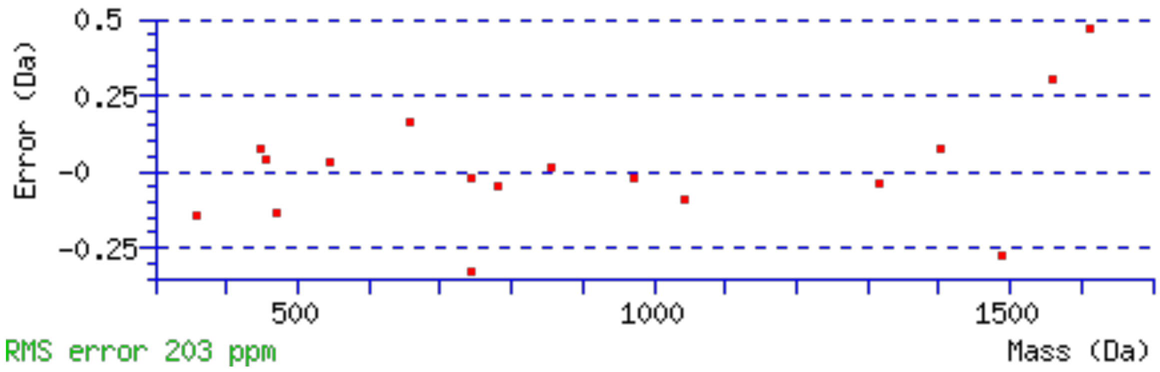
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

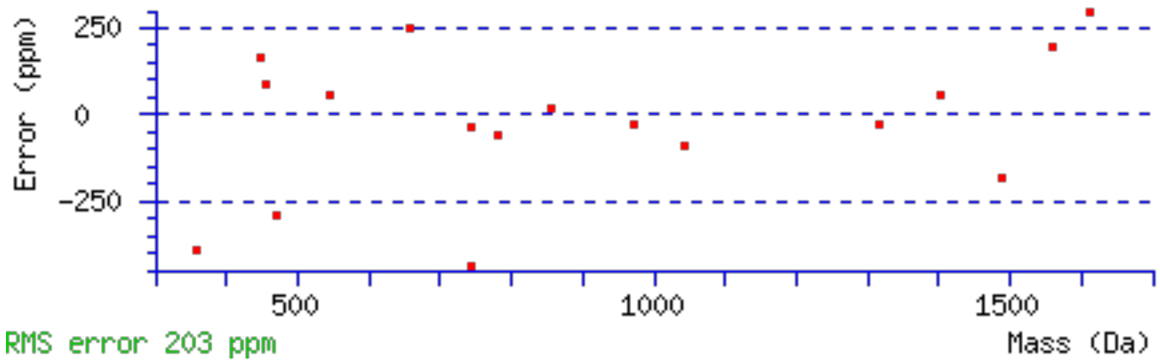


Monoisotopic mass of neutral peptide Mr(calc): 1784.9342
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 72 **Expect:** 4e-05
Matches : 17/148 fragment ions using 28 most intense peaks (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			I							17
2	227.1754	114.0913			I	1672.8574	836.9324	1655.8309	828.4191	1654.8469	827.9271	16
3	298.2125	149.6099			A	***1559.7734***	780.3903	1542.7468	771.8771	1541.7628	771.3850	15
4	385.2445	193.1259	367.2340	184.1206	S	***1488.7363***	744.8718	1471.7097	736.3585	1470.7257	735.8665	14
5	**472.2766**	236.6419	454.2660	227.6366	S	***1401.7042***	701.3558	1384.6777	692.8425	1383.6937	692.3505	13
6	569.3293	285.1683	551.3188	276.1630	P	***1314.6722***	657.8397	1297.6457	649.3265	1296.6616	648.8345	12
7	684.3563	342.6818	666.3457	333.6765	D	1217.6194	609.3134	1200.5929	600.8001	1199.6089	600.3081	11
8	815.3968	408.2020	797.3862	399.1967	M	1102.5925	551.7999	1085.5660	543.2866	1084.5819	542.7946	10
9	930.4237	465.7155	912.4131	456.7102	D	***971.5520***	486.2796	954.5255	477.7664	953.5415	477.2744	9
10	**1043.5078**	522.2575	1025.4972	513.2522	L	***856.5251***	428.7662	839.4985	420.2529	838.5145	419.7609	8
11	1140.5605	570.7839	1122.5500	561.7786	P	***743.4410***	372.2241	726.4145	363.7109	725.4305	363.2189	7

12	1241.6082	621.3077	1223.5977	612.3025	**T**	646.3883	323.6978	629.3617	315.1845	628.3777	314.6925	**6**
13	1340.6766	670.8420	1322.6661	661.8367	**V**	***545.3406***	273.1739	528.3140	264.6606	527.3300	264.1686	**5**
14	1427.7087	714.3580	1409.6981	705.3527	**S**	***446.2722***	223.6397	429.2456	215.1264	428.2616	214.6344	**4**
15	1498.7458	749.8765	1480.7352	740.8712	**A**	***359.2401***	180.1237	342.2136	171.6104			**3**
16	**1611.8298**	806.4186	1593.8193	797.4133	**L**	288.2030	144.6051	271.1765	136.0919			**2**
17					**R**	175.1190	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of IIASSPDMDLPTVSALR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
71.8	1784.9342	1.6312	IIASSPDMDLPTVSALR
10.8	1785.9083	0.6571	AENMHLTELYLSLPR
8.0	1784.9396	1.6258	IIARGFCIDGFTFLR
8.0	1784.9396	1.6258	ILARGFCVGEFTFLR
6.9	1786.8445	-0.2791	RESDGTPGGLASLENER
5.3	1784.9309	1.6346	EQTLEAAYVPVVVDPR
5.0	1785.9221	0.6434	SNPSVSSLLQKVDEQR
4.9	1786.9247	-0.3593	LDGEGITCIGNLEKLR
4.0	1785.8720	0.6935	ETSNFGFMLSSGKLPR
3.5	1786.8632	-0.2977	NNRSTSPVTDPSMPIR

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

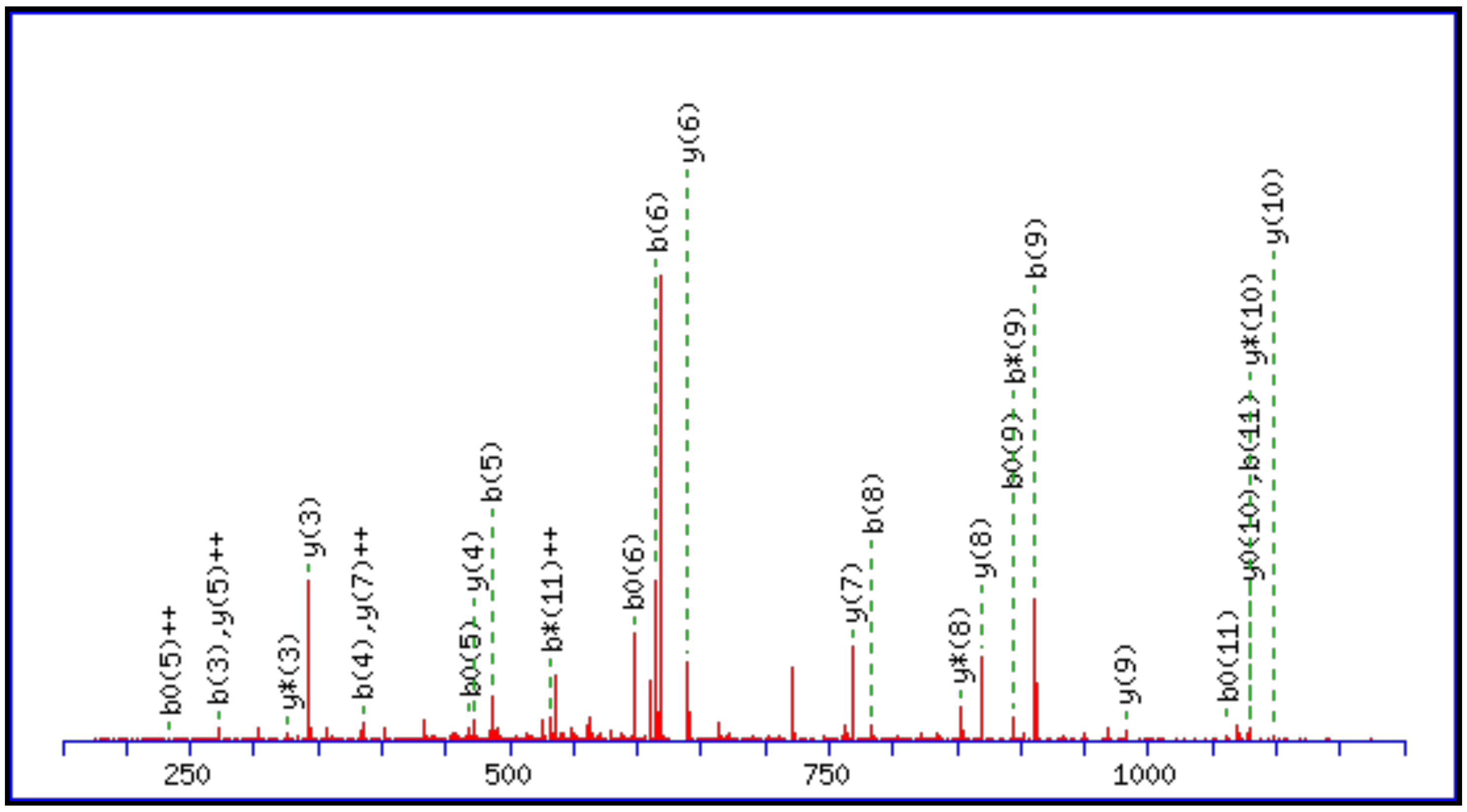
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVDLTEPAQPAR**
Found in **gi|13385374**, ras-related protein Rab-5A [Mus musculus]

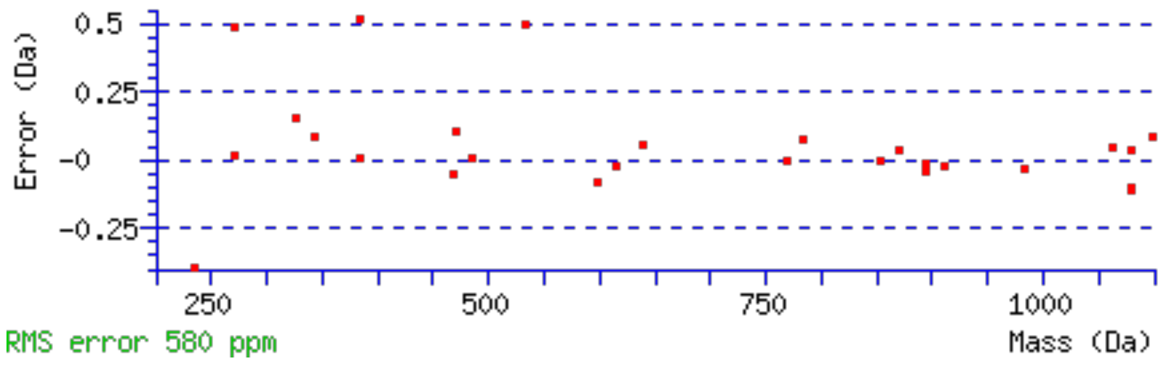
Match to Query 6087: 1253.245448 from(627.630000,2+) intensity(39021.2031) rtinseconds(759.023) index(2151)
Title: 17006_20130508_glp1R_lig_min6cells_num2.2586.2586.0.dta
Data file 17006_20130508_glp1R_lig_min6cells_num2.mgf

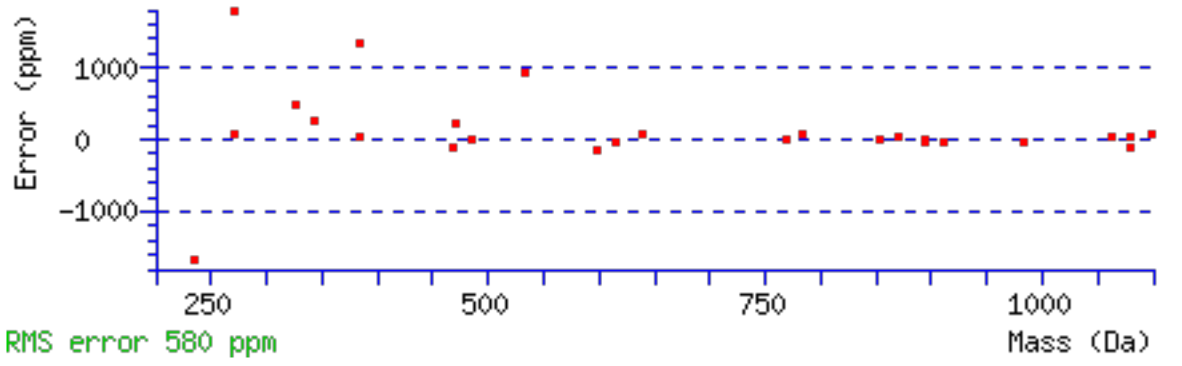
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1252.6412
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 38 **Expect:** 0.14
Matches : 27/100 fragment ions using 50 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180					G							12
2	157.0972	79.0522					V	1196.6270	598.8171	1179.6004	590.3039	1178.6164	589.8118	11
3	***272.1241***	136.5657			254.1135	127.5604	D	***1097.5586***	549.2829	1080.5320	540.7696	1079.5480	540.2776	10
4	***385.2082***	193.1077			367.1976	184.1024	L	***982.5316***	491.7694	965.5051	483.2562	964.5211	482.7642	9
5	***486.2558***	243.6316			468.2453	234.6263	T	***869.4476***	435.2274	852.4210	426.7141	851.4370	426.2221	8
6	***615.2984***	308.1529			597.2879	299.1476	E	***768.3999***	384.7036	751.3733	376.1903	750.3893	375.6983	7
7	712.3512	356.6792			694.3406	347.6740	P	***639.3573***	320.1823	622.3307	311.6690			6
8	***783.3883***	392.1978			765.3777	383.1925	A	542.3045	271.6559	525.2780	263.1426			5
9	***911.4469***	456.2271	894.4203	447.7138	893.4363	447.2218	Q	***471.2674***	236.1373	454.2409	227.6241			4
10	1008.4997	504.7535	991.4731	496.2402	990.4891	495.7482	P	***343.2088***	172.1081	326.1823	163.5948			3
11	***1079.5368***	540.2720	1062.5102	531.7587	1061.5262	531.2667	A	246.1561	123.5817	229.1295	115.0684			2
12							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of GVDLTEPAQPAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.8	1252.6412	0.6043	GVDLTEPAQPAR
25.6	1252.6452	0.6003	AISESYAFLPR
21.5	1252.6048	0.6407	ANTPTEPAAEPR
17.3	1252.7252	0.5203	VDGRLNITLPR
16.0	1253.6074	-0.3620	LAASFQSMEVR
14.9	1252.6048	0.6407	LEEQPGEQAPR
11.1	1252.7768	0.4687	KPFLRNLLPR
11.1	1253.5749	-0.3294	EGREHEDGGLR
10.7	1252.5870	0.6584	SLCAEGAYQVR
10.6	1252.6598	0.5857	GQPAVIMAVDPR

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

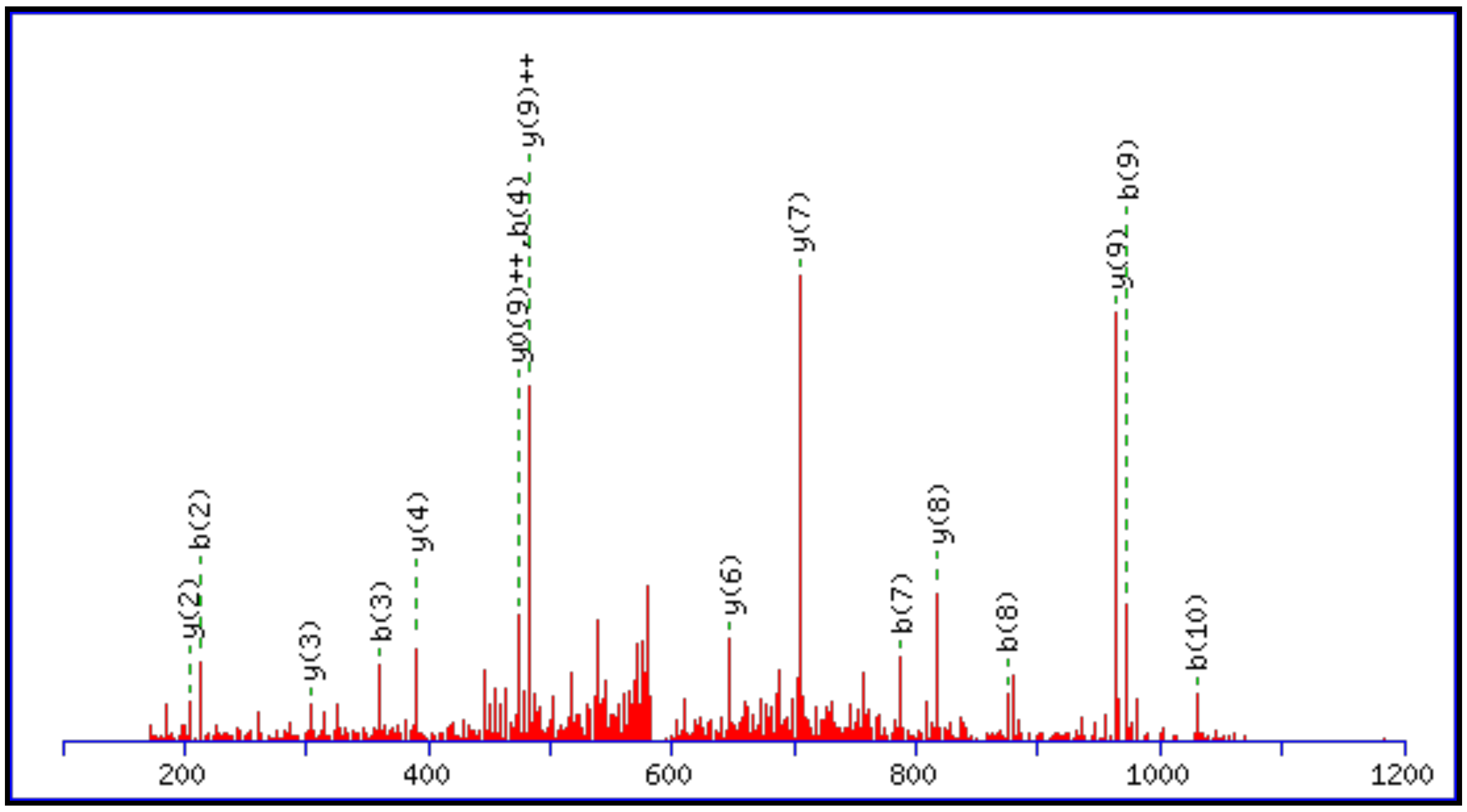
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVFLGEQSVGK**
Found in **gi|30424655**, ras-related protein Rab-6B [Mus musculus]

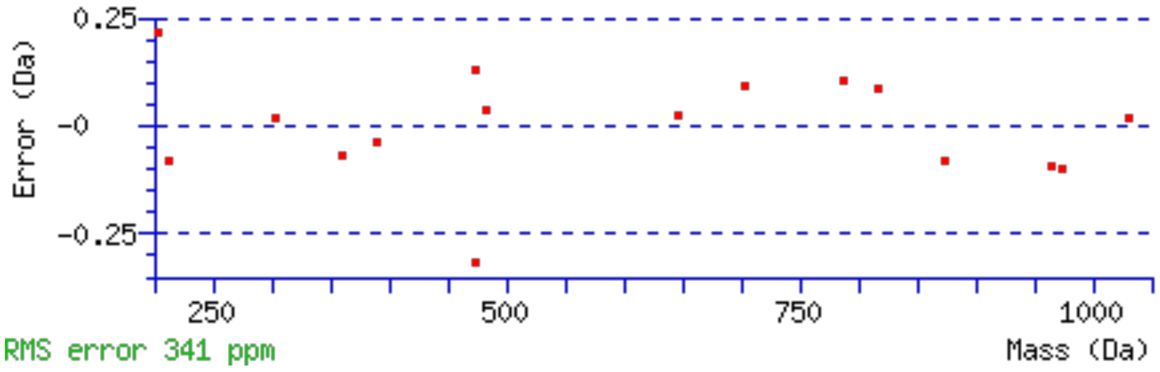
Match to Query 5650: 1175.765448 from(588.890000,2+) intensity(46726.2031) rtinseconds(1162.0777) index(3229)
Title: 15859_20130128_Glp1r_mouse.3916.3916.
Data file 15859_20130128_Glp1r_mouse.mgf

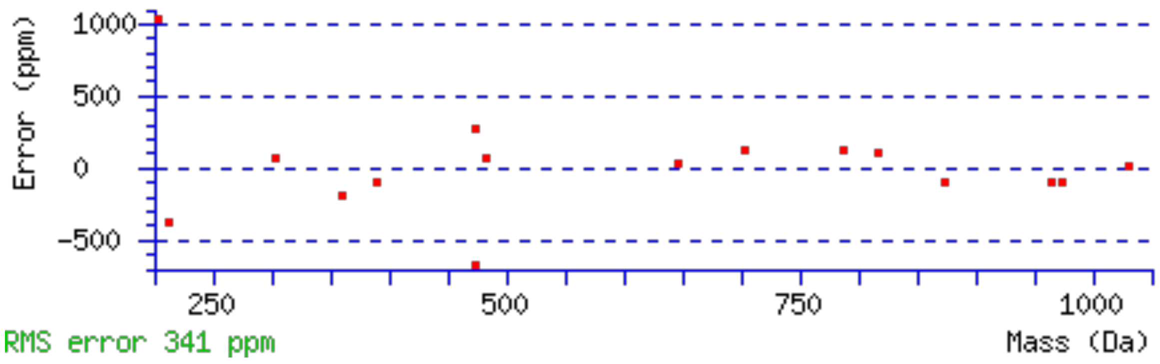
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1175.6550
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 50 **Expect:** 0.0091
Matches : 16/92 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							11
2	***213.1598***	107.0835					V	1063.5782	532.2928	1046.5517	523.7795	1045.5677	523.2875	10
3	***360.2282***	180.6177					F	***964.5098***	482.7585	947.4833	474.2453	946.4993	473.7533	9
4	***473.3122***	237.1598					L	***817.4414***	409.2243	800.4149	400.7111	799.4308	400.2191	8
5	530.3337	265.6705					G	***704.3573***	352.6823	687.3308	344.1690	686.3468	343.6770	7
6	659.3763	330.1918			641.3657	321.1865	E	***647.3359***	324.1716	630.3093	315.6583	629.3253	315.1663	6
7	***787.4349***	394.2211	770.4083	385.7078	769.4243	385.2158	Q	518.2933	259.6503	501.2667	251.1370	500.2827	250.6450	5
8	***874.4669***	437.7371	857.4403	429.2238	856.4563	428.7318	S	***390.2347***	195.6210	373.2082	187.1077	372.2241	186.6157	4
9	***973.5353***	487.2713	956.5088	478.7580	955.5247	478.2660	V	***303.2027***	152.1050	286.1761	143.5917			3
10	***1030.5568***	515.7820	1013.5302	507.2688	1012.5462	506.7767	G	***204.1343***	102.5708	187.1077	94.0575			2
11							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of LVFLGEQSVGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.2	1175.6550	0.1104	LVFLGEQSVGK
19.8	1175.6662	0.0992	LVISNPYSRK
14.1	1175.7026	0.0628	IAILGYRSVGK
11.3	1177.6013	-1.8358	DVMKTVVQDK
10.8	1173.6427	2.1227	IVLLGDMNVGK
10.5	1173.6104	2.1551	MEYKLSFIK
9.9	1175.5968	0.1686	DAVAMTDRLGK
8.7	1177.6707	-1.9052	TLLFISNDKK
8.5	1172.6037	3.1617	VQELESQVNK
8.1	1175.6815	0.0839	LVFRLWQSK

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

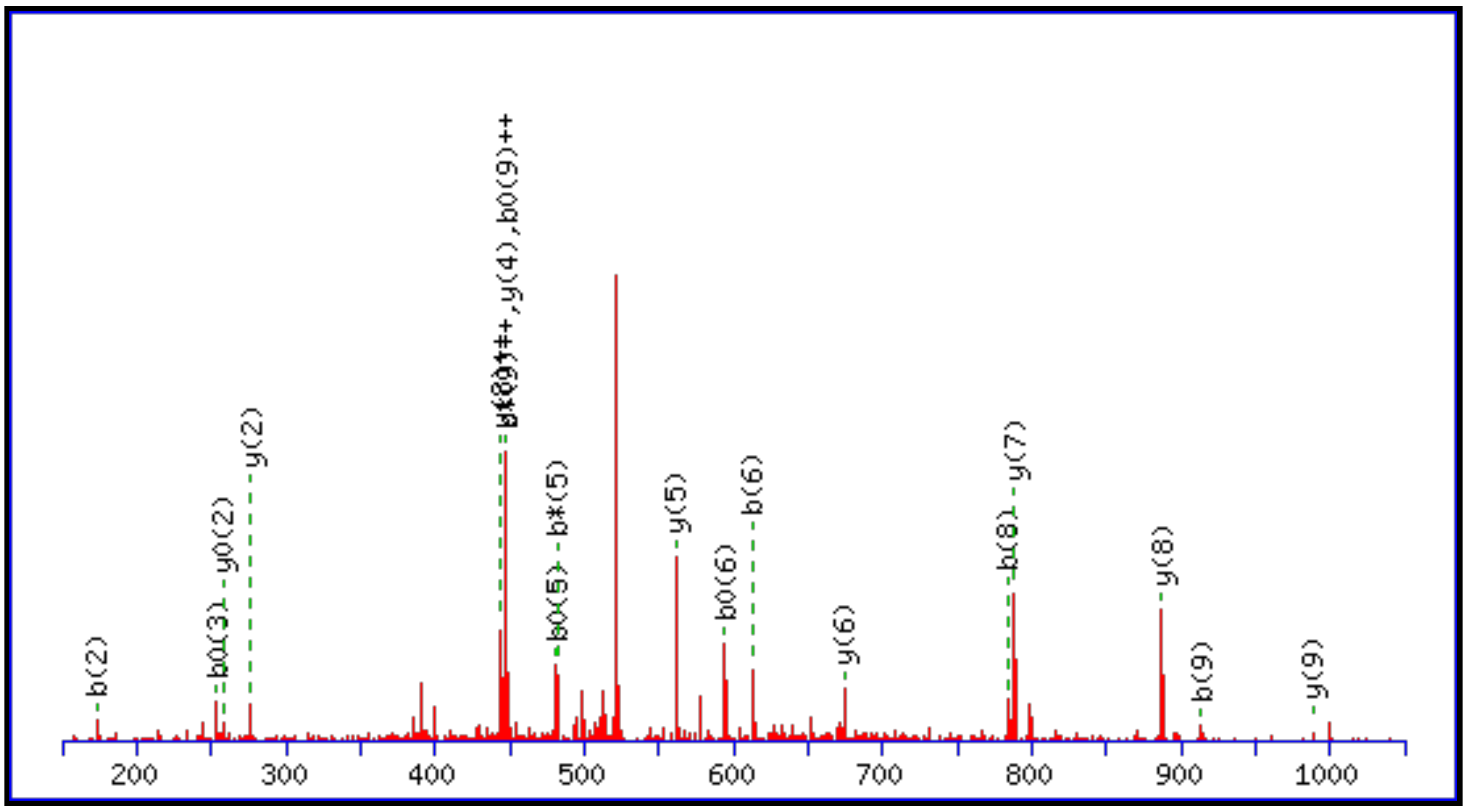
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ATVNLLGDEK**
Found in **gi|161016826**, receptor expression-enhancing protein 5 [Mus musculus]

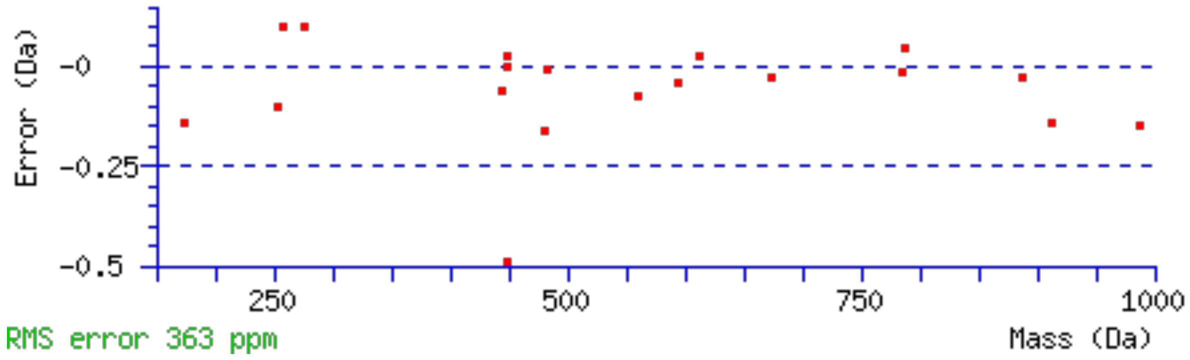
Match to Query 2941: 1060.205448 from(531.110000,2+) intensity(37886.5312) rtinseconds(566.534) index(1592)
Title: 16590_20130315_min6_glp1R_2hrp.01923.01923.0.dta
Data file 16590_20130315_min6_glp1R_2hrp.mgf

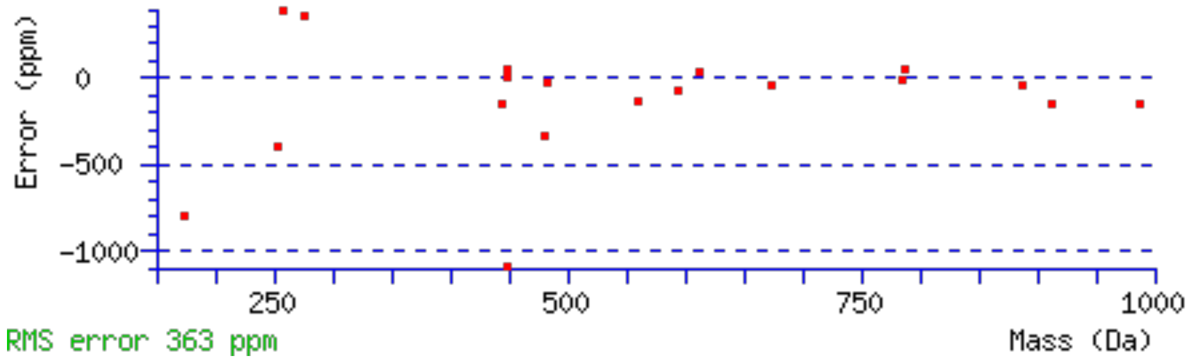
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1058.5608
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 53 **Expect:** 0.0055
Matches : 19/98 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258					**A**							**10**
2	**173.0921**	87.0497			155.0815	78.0444	**T**	***988.5310***	494.7691	971.5044	486.2558	970.5204	485.7638	**9**
3	272.1605	136.5839			254.1499	127.5786	**V**	***887.4833***	444.2453	870.4567	435.7320	869.4727	435.2400	**8**
4	386.2034	193.6053	369.1769	185.0921	368.1928	184.6001	**N**	***788.4149***	394.7111	771.3883	386.1978	770.4043	385.7058	**7**
5	499.2875	250.1474	482.2609	241.6341	481.2769	241.1421	**L**	***674.3719***	337.6896	657.3454	329.1763	656.3614	328.6843	**6**
6	**612.3715**	306.6894	595.3450	298.1761	594.3610	297.6841	**L**	***561.2879***	281.1476	544.2613	272.6343	543.2773	272.1423	**5**
7	669.3930	335.2001	652.3665	326.6869	651.3824	326.1949	**G**	***448.2038***	224.6055	431.1773	216.0923	430.1932	215.6003	**4**
8	**784.4199**	392.7136	767.3934	384.2003	766.4094	383.7083	**D**	391.1823	196.0948	374.1558	187.5815	373.1718	187.0895	**3**
9	**913.4625**	457.2349	896.4360	448.7216	895.4520	448.2296	**E**	***276.1554***	138.5813	259.1288	130.0681	258.1448	129.5761	**2**
10							**K**	147.1128	74.0600	130.0863	65.5468			**1**





NCBI **BLAST** search of ATVNLLGDEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.8	1058.5608	1.6447	ATVNLLGDEK
20.5	1058.5972	1.6083	EQQLLSTLK
17.7	1060.5335	-0.3281	MANDILVNR
15.4	1058.5608	1.6447	AKEGIEVGEK
14.1	1059.5825	0.6229	RETILWSR
13.9	1058.5972	1.6083	ATVLGTELQK
13.8	1058.5356	1.6698	AASRPEATEK
13.6	1059.5600	0.6454	ADSLLVWEK
11.6	1057.6131	2.5923	IRDLLDVSK
11.6	1057.6244	2.5811	LIRDLATTR

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

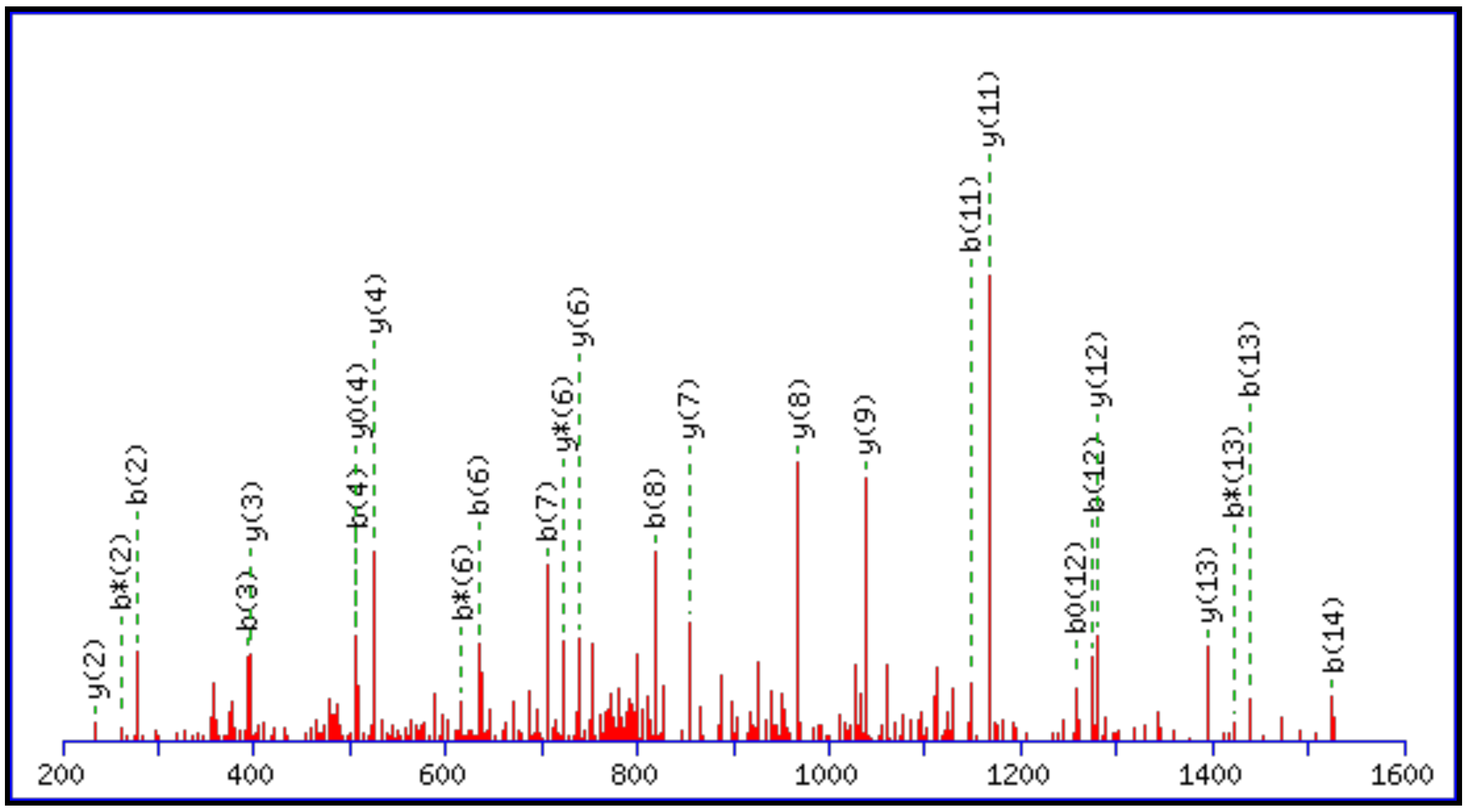
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NYDIGAALDTIQYSK**
Found in **gi|6754954**, sequestosome-1 [Mus musculus]

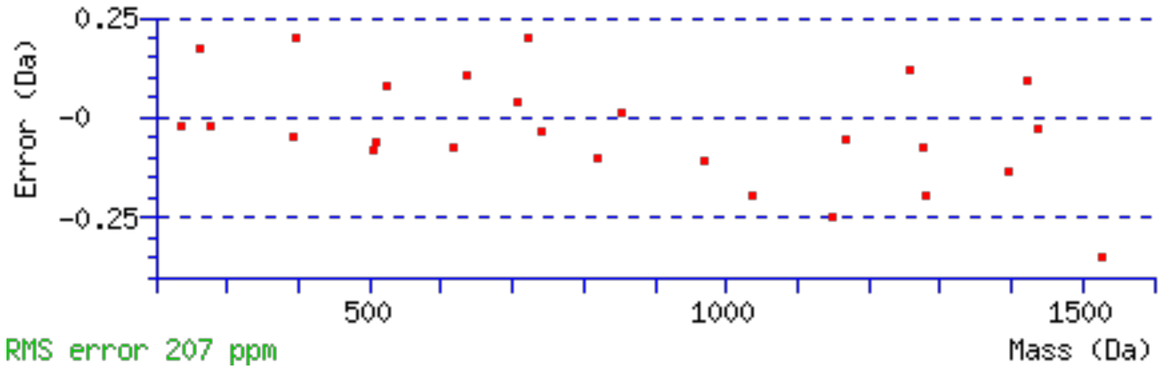
Match to Query 11061: 1671.405448 from(836.710000,2+) intensity(24918.2344) rtinseconds(1870.3582) index(5162)
Title: 15859_20130128_Glp1r_mouse.6235.6235.
Data file 15859_20130128_Glp1r_mouse.mgf

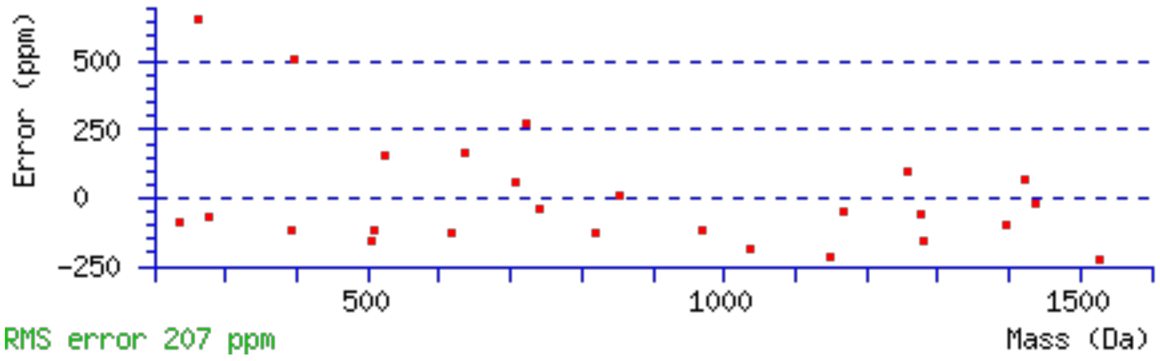
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [200] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1670.8151
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 76 **Expect:** 1.5e-05
Matches : 26/162 fragment ions using 39 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							15
2	***278.1135***	139.5604	261.0870	131.0471			Y	1557.7795	779.3934	1540.7530	770.8801	1539.7690	770.3881	14
3	***393.1405***	197.0739	376.1139	188.5606	375.1299	188.0686	D	***1394.7162***	697.8617	1377.6896	689.3485	1376.7056	688.8564	13
4	***506.2245***	253.6159	489.1980	245.1026	488.2140	244.6106	I	***1279.6892***	640.3483	1262.6627	631.8350	1261.6787	631.3430	12
5	563.2460	282.1266	546.2195	273.6134	545.2354	273.1214	G	***1166.6052***	583.8062	1149.5786	575.2930	1148.5946	574.8009	11
6	***634.2831***	317.6452	617.2566	309.1319	616.2726	308.6399	A	1109.5837	555.2955	1092.5572	546.7822	1091.5732	546.2902	10
7	***705.3202***	353.1638	688.2937	344.6505	687.3097	344.1585	A	***1038.5466***	519.7769	1021.5201	511.2637	1020.5360	510.7717	9
8	***818.4043***	409.7058	801.3777	401.1925	800.3937	400.7005	L	***967.5095***	484.2584	950.4829	475.7451	949.4989	475.2531	8
9	933.4312	467.2193	916.4047	458.7060	915.4207	458.2140	D	***854.4254***	427.7164	837.3989	419.2031	836.4149	418.7111	7
10	1034.4789	517.7431	1017.4524	509.2298	1016.4684	508.7378	T	***739.3985***	370.2029	722.3719	361.6896	721.3879	361.1976	6
11	***1147.5630***	574.2851	1130.5364	565.7719	1129.5524	565.2798	I	638.3508	319.6790	621.3243	311.1658	620.3402	310.6738	5
12	***1275.6216***	638.3144	1258.5950	629.8011	1257.6110	629.3091	Q	***525.2667***	263.1370	508.2402	254.6237	507.2562	254.1317	4
13	***1438.6849***	719.8461	1421.6583	711.3328	1420.6743	710.8408	Y	***397.2082***	199.1077	380.1816	190.5944	379.1976	190.1024	3
14	***1525.7169***	763.3621	1508.6904	754.8488	1507.7064	754.3568	S	***234.1448***	117.5761	217.1183	109.0628	216.1343	108.5708	2
15							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of NYDIGAALDTIQYSK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
76.1	1670.8151	0.5903	NYDIGAALDTIQYSK
16.3	1670.9719	0.4335	DLKQQLQALKPVYK
14.3	1670.8484	0.5571	MGVSRSAATVLAYAMK
6.8	1671.0083	0.3971	LVLRLQSDLQFVLK
6.1	1670.7424	0.6631	SADSEYQWVTSPSSK
4.5	1670.9290	0.4764	MVKLDIHTLAHHLK
3.9	1670.8820	0.5234	FIPRQPFAEYIYK
3.6	1670.8385	0.5670	NLRPEFMQMQHIK
3.1	1671.7893	-0.3838	FNSQSASYPQGYVPK
3.0	1670.6617	0.7437	SYEDDEDMDLQPSK

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

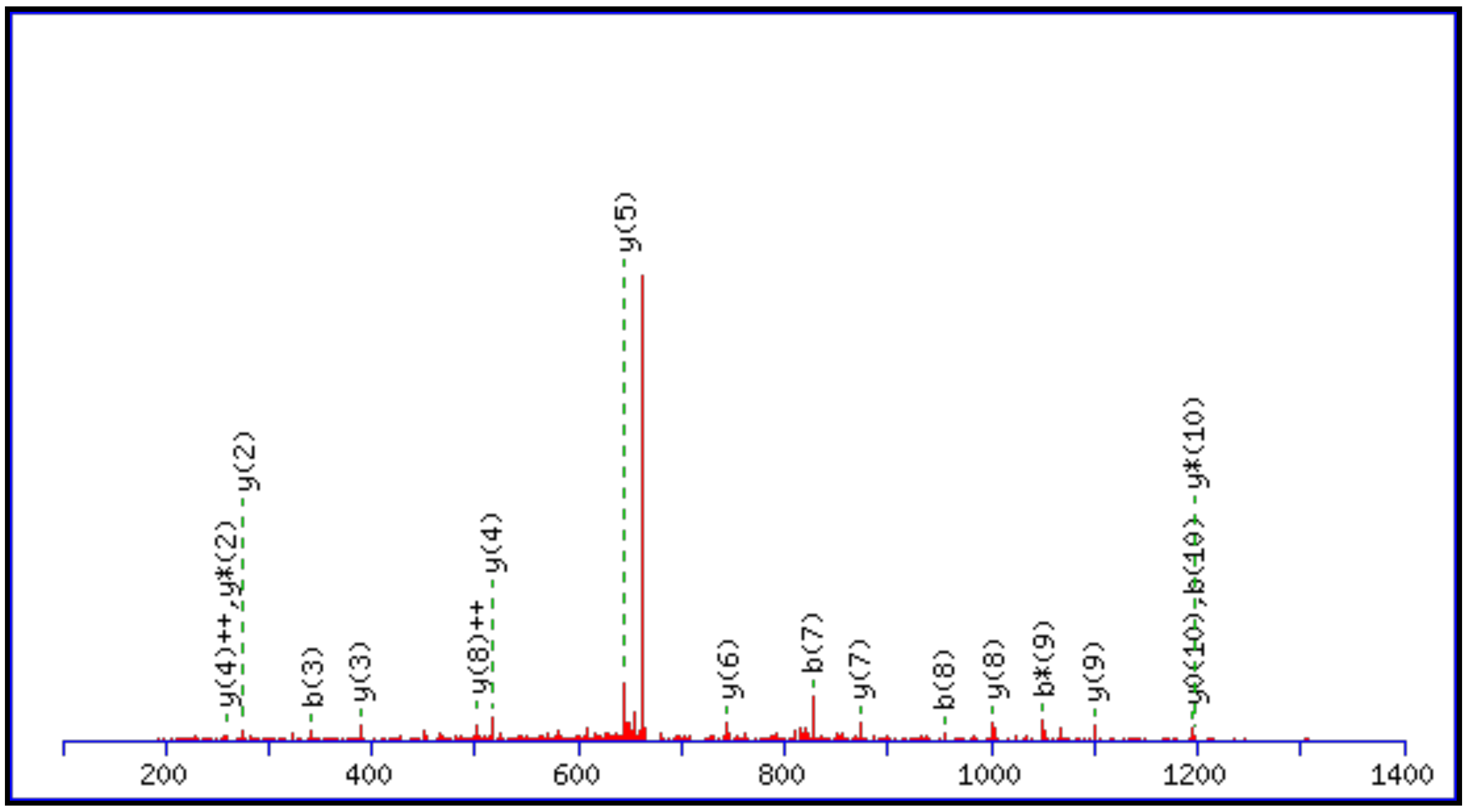
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLVEQVEQIQK**
Found in **gi|145966911**, transmembrane emp24 domain-containing protein 9 precursor [Mus musculus]

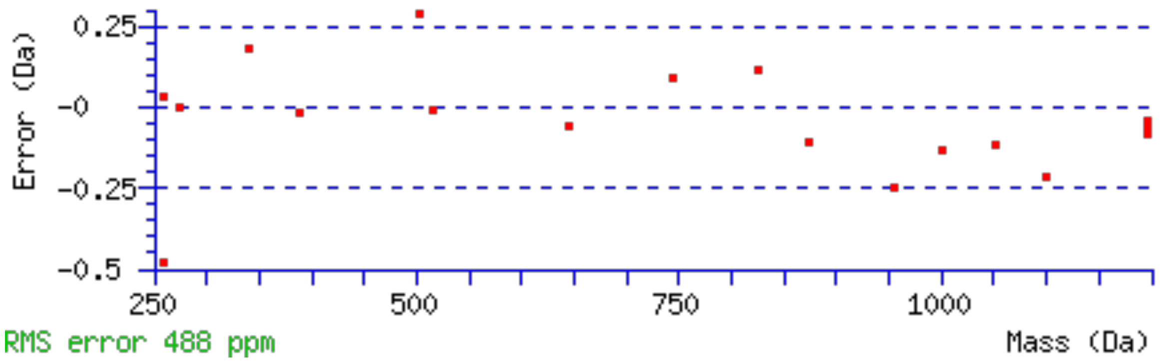
Match to Query 7849: 1341.445448 from(671.730000,2+) intensity(19227.2695) rtinseconds(662.292) index(1826)
Title: 15859_20130128_Glp1r_mouse.2231.2231.
Data file 15859_20130128_Glp1r_mouse.mgf

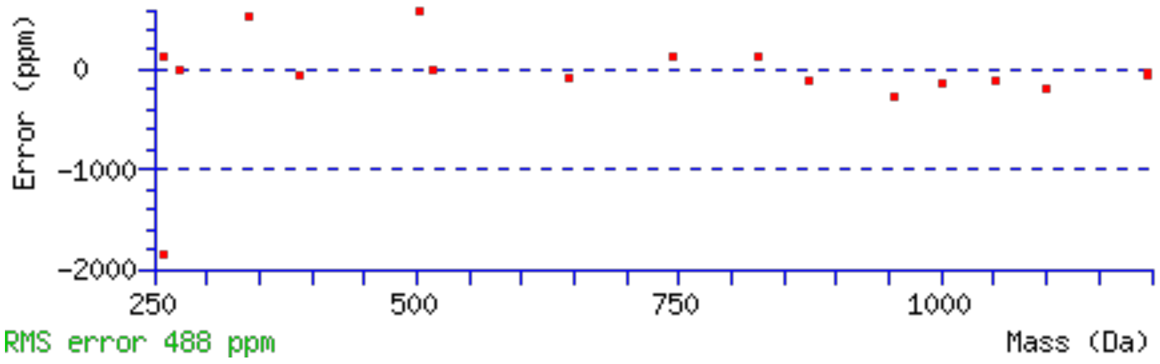
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1340.7300
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Ions Score: 65 **Expect:** 0.00027
Matches : 18/106 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							11
2	242.1499	121.5786	225.1234	113.0653			L	1213.6787	607.3430	1196.6521	598.8297	1195.6681	598.3377	10
3	**341.2183**	171.1128	324.1918	162.5995			V	***1100.5946***	550.8009	1083.5681	542.2877	1082.5841	541.7957	9
4	470.2609	235.6341	453.2344	227.1208	452.2504	226.6288	E	***1001.5262***	501.2667	984.4997	492.7535	983.5156	492.2615	8
5	598.3195	299.6634	581.2930	291.1501	580.3089	290.6581	Q	***872.4836***	436.7454	855.4571	428.2322	854.4730	427.7402	7
6	697.3879	349.1976	680.3614	340.6843	679.3774	340.1923	V	***744.4250***	372.7162	727.3985	364.2029	726.4145	363.7109	6
7	**826.4305**	413.7189	809.4040	405.2056	808.4199	404.7136	E	***645.3566***	323.1819	628.3301	314.6687	627.3461	314.1767	5
8	**954.4891**	477.7482	937.4625	469.2349	936.4785	468.7429	Q	***516.3140***	258.6607	499.2875	250.1474			4
9	1067.5732	534.2902	1050.5466	525.7769	1049.5626	525.2849	I	***388.2554***	194.6314	371.2289	186.1181			3
10	**1195.6317**	598.3195	1178.6052	589.8062	1177.6212	589.3142	Q	***275.1714***	138.0893	258.1448	129.5761			2
11							K	147.1128	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of QLVEQVEQIQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.7	1340.7300	0.7155	QLVEQVEQIQK
46.5	1340.7300	0.7155	QLLDQVEQIQK
19.4	1340.7300	0.7155	VQVEAIEGGALQK
14.2	1341.7292	-0.2838	EAHFLVEELKK
13.9	1340.8101	0.6353	MEASVILPILKK
12.7	1341.6888	-0.2434	NVVADQEAQIQK
11.0	1340.7776	0.6679	GLSELRQGLLQK
10.4	1340.6936	0.7519	DIAKNEGPELQK
10.3	1340.6659	0.7795	QIVSAVHYCHK
10.2	1340.7663	0.6791	QEVLQNLLKEK