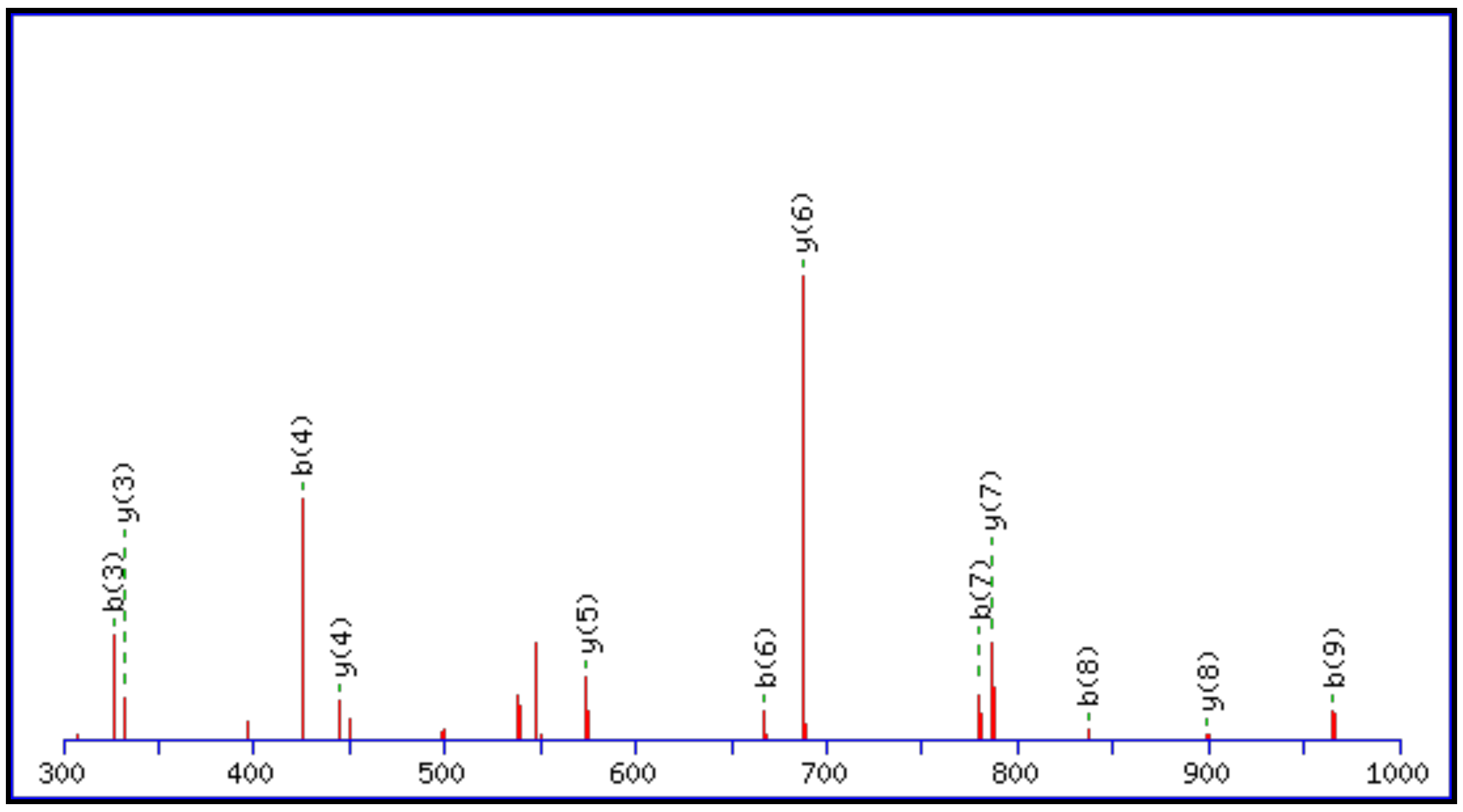
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DPLVIELGQK**
Found in **gi|354497358|ref|XP_003510787.1|**, PREDICTED: peptidyl-prolyl cis-trans isomerase FKBP11-like [Cricetulus griseus]

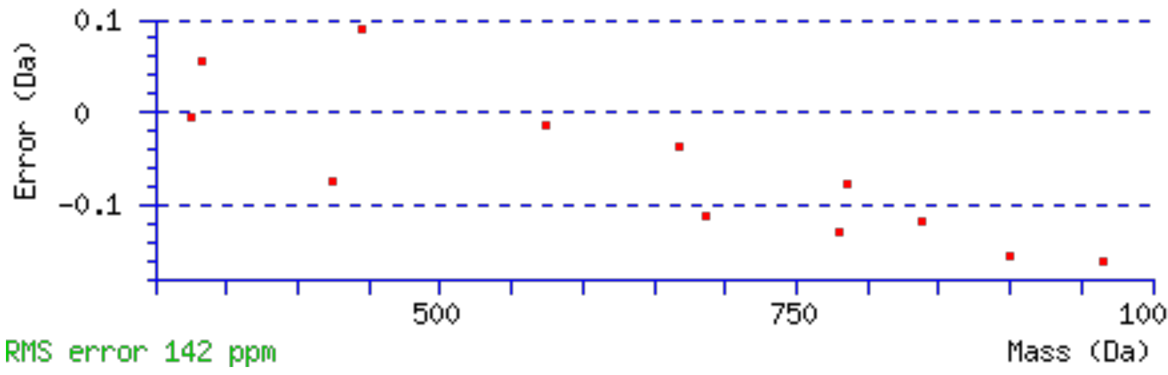
Match to Query 1907: 1112.685448 from(557.350000,2+) intensity(2865.8213) rtinseconds(2080.6358) index(5746)
Title: 17496_20120917_cho_glp1r_inj2.6900.6900.0.dta
Data file 17496_20120917_cho_glp1r_inj2.prh1.mgf

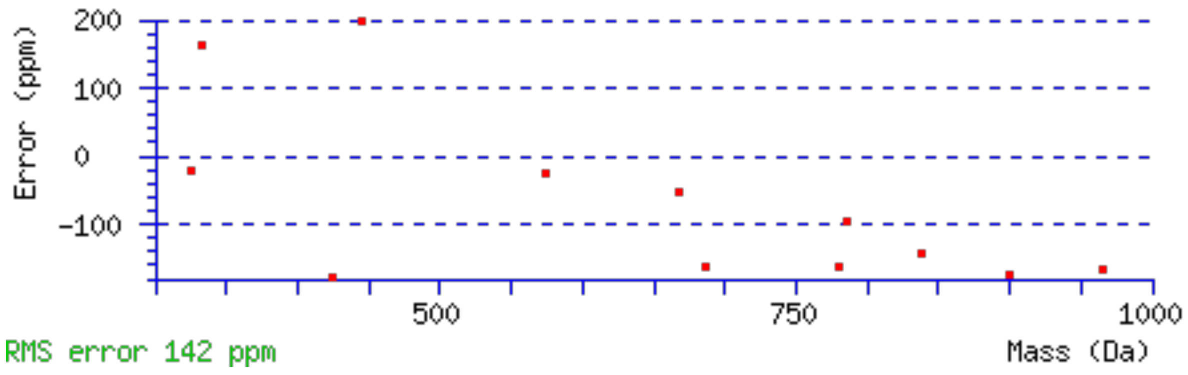
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1110.6285
Fixed modifications: Carboxymethyl (C) (apply to specified residues or termini only)
Ions Score: 54 **Expect:** 0.0041
Matches : 12/84 fragment ions using 20 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							10
2	213.0870	107.0471			195.0764	98.0418	P	996.6088	498.8080	979.5823	490.2948	978.5982	489.8028	9
3	***326.1710***	163.5892			308.1605	154.5839	L	***899.5560***	450.2817	882.5295	441.7684	881.5455	441.2764	8
4	***425.2395***	213.1234			407.2289	204.1181	V	***786.4720***	393.7396	769.4454	385.2264	768.4614	384.7343	7
5	538.3235	269.6654			520.3130	260.6601	I	***687.4036***	344.2054	670.3770	335.6921	669.3930	335.2001	6
6	***667.3661***	334.1867			649.3556	325.1814	E	***574.3195***	287.6634	557.2930	279.1501	556.3089	278.6581	5
7	***780.4502***	390.7287			762.4396	381.7234	L	***445.2769***	223.1421	428.2504	214.6288			4
8	***837.4716***	419.2395			819.4611	410.2342	G	***332.1928***	166.6001	315.1663	158.0868			3
9	***965.5302***	483.2688	948.5037	474.7555	947.5197	474.2635	Q	275.1714	138.0893	258.1448	129.5761			2
10							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.4	1110.6285	2.0570	DPLVIELGQK
22.1	1110.6761	2.0094	EVPVLRTGLK
22.1	1110.6649	2.0206	IVIVVPQDTK
18.4	1111.3736	1.3118	MMMMMMMK
18.1	1111.6601	1.0254	ALQLLLGAGEK
13.2	1111.5986	1.0869	TSSGLIEHIR
12.4	1111.5372	1.1483	IPAYENFMK

12.1	1111.5696	1.1159	ARVTMIDYK
11.5	1111.6713	1.0141	VLIRVAEANK
10.0	1111.6489	1.0366	DIPVDTVLLK

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

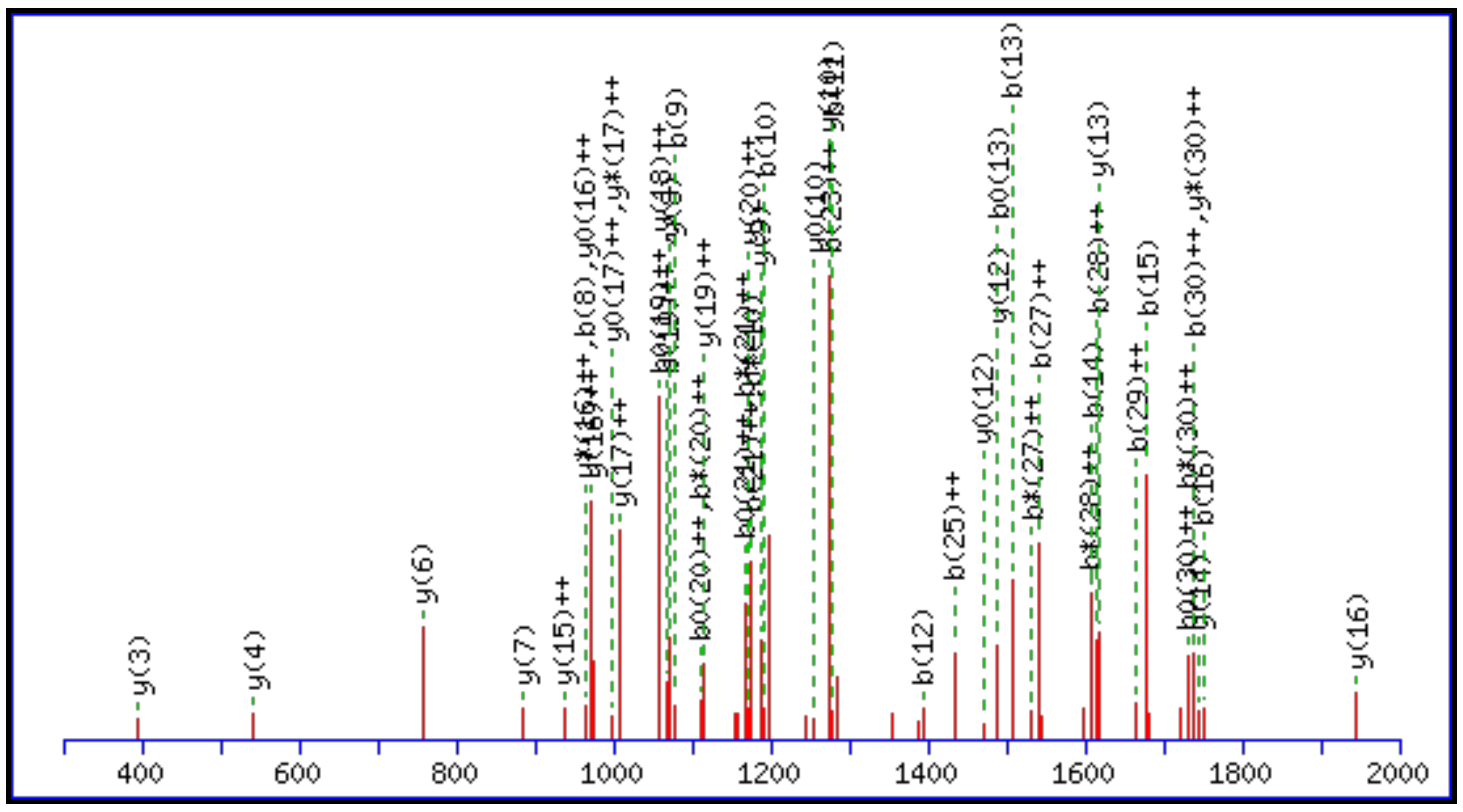
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EALKDEYDDLSDLTAAQQETLSDWESQFTFK**
Found in **gi|354475732|ref|XP_003500081.1|**, PREDICTED: membrane-associated progesterone receptor component 1-like [Cricetulus griseus]

Match to Query 15213: 3622.388172 from(1208.470000,3+) intensity(4439.7368) rtinseconds(3784.4942) index(10141)
Title: 17492_20120825_cho_glp1r_2hrp.12329.12329.0.dta
Data file 17492_20120825_cho_glp1r_2hrp.prh1.mgf

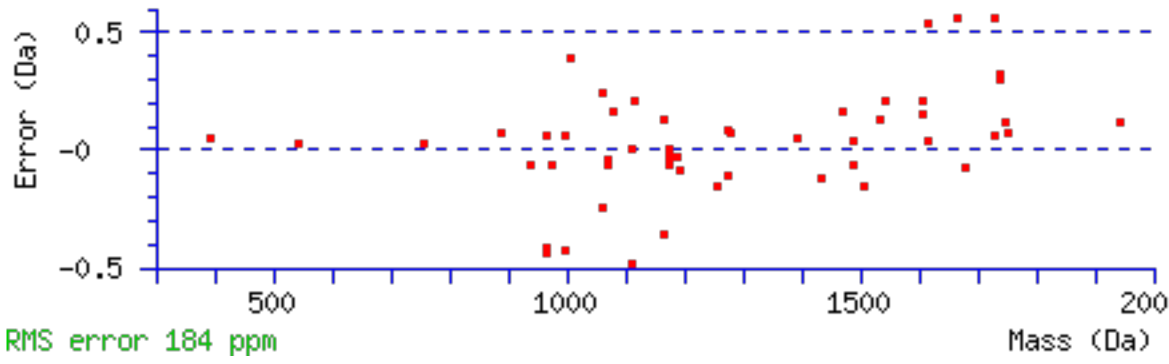
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

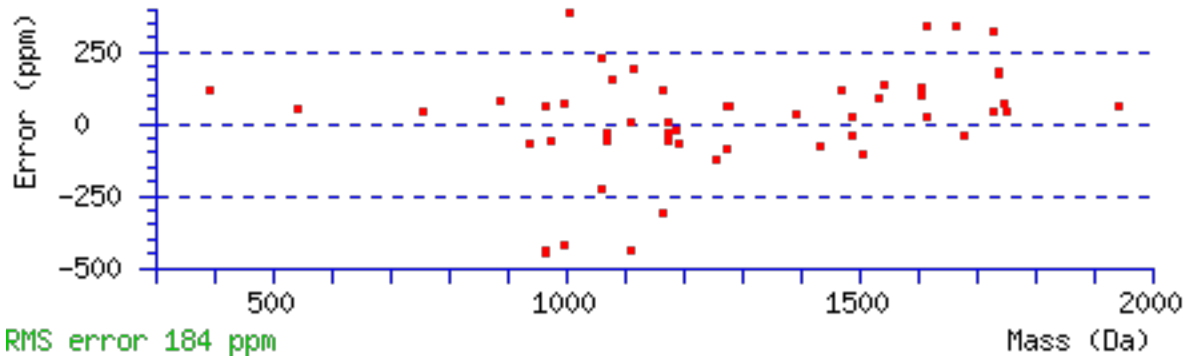


```
Monoisotopic mass of neutral peptide Mr(calc): 3622.6475
Fixed modifications: Carboxymethyl (C) (apply to specified residues or termini only)
Ions Score: 93  Expect: 2.3e-07
Matches : 52/350 fragment ions using 58 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.0499	65.5286			112.0393	56.5233	E							31
2	201.0870	101.0471			183.0764	92.0418	A	3494.6122	1747.8097	3477.5856	1739.2965	3476.6016	1738.8044	30
3	314.1710	157.5892			296.1605	148.5839	L	3423.5751	1712.2912	3406.5485	1703.7779	3405.5645	1703.2859	29
4	442.2660	221.6366	425.2395	213.1234	424.2554	212.6314	K	3310.4910	1655.7491	3293.4645	1647.2359	3292.4804	1646.7439	28
5	557.2930	279.1501	540.2664	270.6368	539.2824	270.1448	D	3182.3960	1591.7017	3165.3695	1583.1884	3164.3855	1582.6964	27
6	686.3355	343.6714	669.3090	335.1581	668.3250	334.6661	E	3067.3691	1534.1882	3050.3426	1525.6749	3049.3585	1525.1829	26
7	849.3989	425.2031	832.3723	416.6898	831.3883	416.1978	Y	2938.3265	1469.6669	2921.3000	1461.1536	2920.3159	1460.6616	25
8	***964.4258***	482.7165	947.3993	474.2033	946.4153	473.7113	D	2775.2632	1388.1352	2758.2366	1379.6220	2757.2526	1379.1299	24
9	***1079.4528***	540.2300	1062.4262	531.7167	1061.4422	531.2247	D	2660.2362	1330.6218	2643.2097	1322.1085	2642.2257	1321.6165	23
10	***1192.5368***	596.7721	1175.5103	588.2588	1174.5263	587.7668	L	2545.2093	1273.1083	2528.1827	1264.5950	2527.1987	1264.1030	22
11	***1279.5689***	640.2881	1262.5423	631.7748	1261.5583	631.2828	S	2432.1252	1216.5663	2415.0987	1208.0530	2414.1147	1207.5610	21
12	***1394.5958***	697.8015	1377.5692	689.2883	1376.5852	688.7963	D	2345.0932	1173.0502	2328.0667	1164.5370	2327.0826	1164.0450	20
13	***1507.6799***	754.3436	1490.6533	745.8303	1489.6693	745.3383	L	2230.0663	1115.5368	2213.0397	1107.0235	2212.0557	1106.5315	19
14	***1608.7275***	804.8674	1591.7010	796.3541	1590.7170	795.8621	T	2116.9822	1058.9947	2099.9556	1050.4815	2098.9716	1049.9895	18
15	***1679.7647***	840.3860	1662.7381	831.8727	1661.7541	831.3807	A	2015.9345	1008.4709	1998.9080	999.9576	1997.9239	999.4656	17
16	***1750.8018***	875.9045	1733.7752	867.3912	1732.7912	866.8992	A	***1944.8974***	972.9523	1927.8709	964.4391	1926.8868	963.9471	16
17	1878.8603	939.9338	1861.8338	931.4205	1860.8498	930.9285	Q	1873.8603	937.4338	1856.8337	928.9205	1855.8497	928.4285	15
18	2006.9189	1003.9631	1989.8924	995.4498	1988.9084	994.9578	Q	***1745.8017***	873.4045	1728.7752	864.8912	1727.7911	864.3992	14
19	2135.9615	**1068.4844**	2118.9350	1059.9711	2117.9510	1059.4791	E	***1617.7431***	809.3752	1600.7166	800.8619	1599.7326	800.3699	13
20	2237.0092	1119.0082	2219.9826	1110.4950	2218.9986	1110.0030	T	***1488.7005***	744.8539	1471.6740	736.3406	1470.6900	735.8486	12
21	2350.0933	**1175.5503**	2333.0667	1167.0370	2332.0827	1166.5450	L	1387.6529	694.3301	1370.6263	685.8168	1369.6423	685.3248	11
22	2437.1253	1219.0663	2420.0987	1210.5530	2419.1147	1210.0610	S	***1274.5688***	637.7880	1257.5422	629.2748	1256.5582	628.7828	10
23	2552.1522	**1276.5798**	2535.1257	1268.0665	2534.1417	1267.5745	D	***1187.5368***	594.2720	1170.5102	585.7587	1169.5262	585.2667	9
24	2738.2315	1369.6194	2721.2050	1361.1061	2720.2210	1360.6141	W	***1072.5098***	536.7585	1055.4833	528.2453	1054.4993	527.7533	8
25	2867.2741	**1434.1407**	2850.2476	1425.6274	2849.2636	1425.1354	E	***886.4305***	443.7189	869.4040	435.2056	868.4199	434.7136	7
26	2954.3062	1477.6567	2937.2796	1469.1434	2936.2956	1468.6514	S	***757.3879***	379.1976	740.3614	370.6843	739.3774	370.1923	6
27	3082.3647	**1541.6860**	3065.3382	1533.1727	3064.3542	1532.6807	Q	670.3559	335.6816	653.3293	327.1683	652.3453	326.6763	5
28	3229.4332	**1615.2202**	3212.4066	1606.7069	3211.4226	1606.2149	F	***542.2973***	271.6523	525.2708	263.1390	524.2867	262.6470	4
29	3330.4808	**1665.7441**	3313.4543	1657.2308	3312.4703	1656.7388	T	***395.2289***	198.1181	378.2023	189.6048	377.2183	189.1128	3
30	3477.5492	**1739.2783**	3460.5227	1730.7650	3459.5387	1730.2730	F	294.1812	147.5942	277.1547	139.0810			2

31						**K**	147.1128	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
93.3	3622.6475	-0.2593	EALKDEYDDLSDLTAAQQETLSDWESQFTFK
7.6	3620.7709	1.6173	LSSEDTPGEVMEQWIVQGDQPSTPGFIIYLLR
7.3	3622.8449	-0.4567	GEAMVAVITDVAAAYLKAGPSTLGPCMINAGSLVFK
7.0	3622.8882	-0.5001	EIDALTLRGSANYLDALQYLIDIELPTVQGYR
4.7	3619.7603	2.6278	ILEEEVTTLFELFDGHDTSGLKLMQEVEPER
4.7	3619.6030	2.7852	GLDTLEAVSSPTVETAMMEEDDGDVTPVASHDGTK
4.7	3619.6030	2.7852	GLDTLEAVSSPTVETAMMEEDDGDVTPVASHDGTK
4.2	3623.6247	-1.2365	DMVAGGGWFMTMNYGVHAVMYSYYALRAAGFR
3.3	3623.6247	-1.2365	DMVAGGGWFMTMNYGVHAVMYSYYALRAAGFR
2.5	3623.8648	-1.4766	FLFVIHEMVIIFTMKAALVHWFQMNHVYK

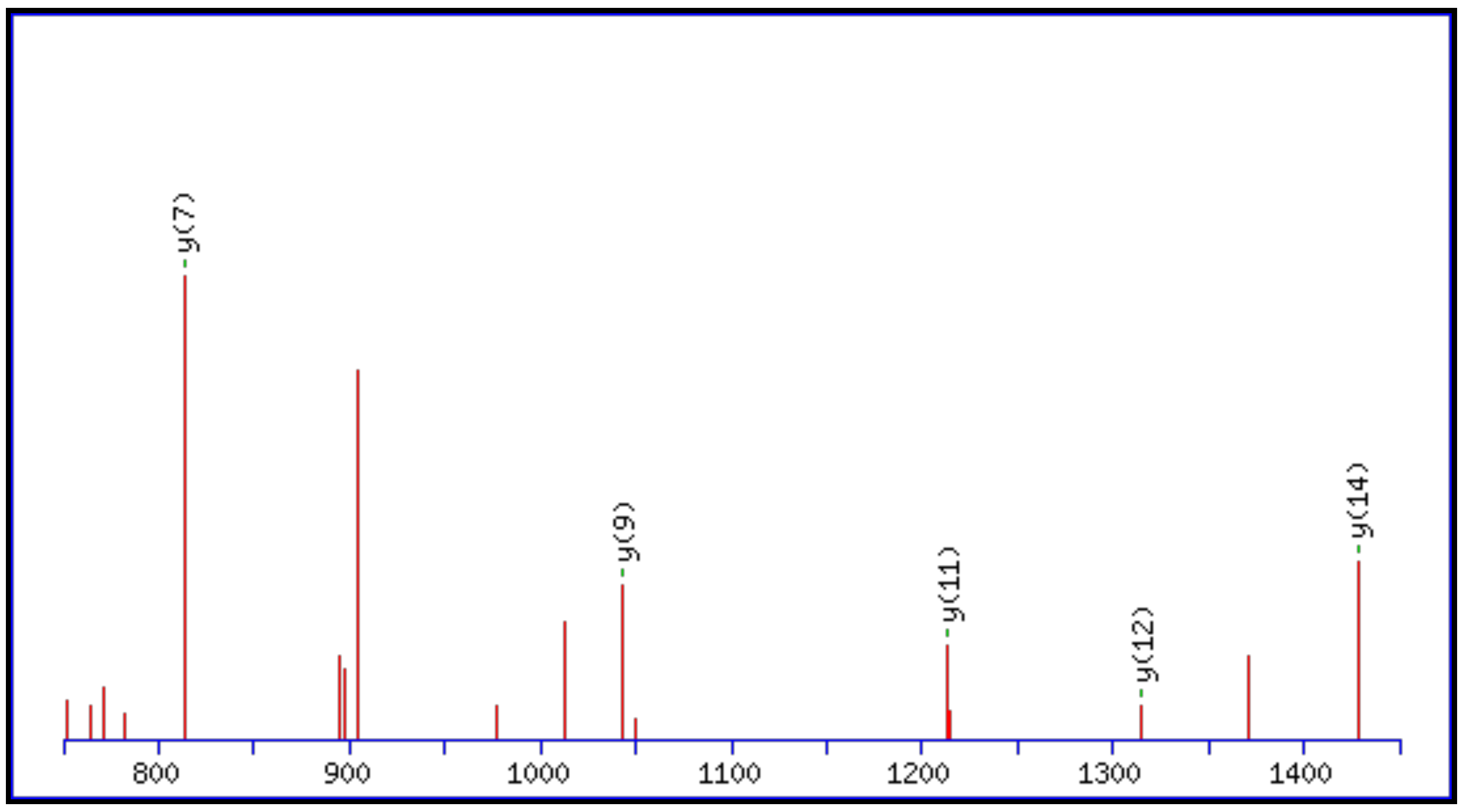
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGIIGGTGLDDPEILEGR**
Found in **gi|354493494|ref|XP_003508876.1|**, PREDICTED: S-methyl-5'-thioadenosine phosphorylase-like [Cricetulus griseus]

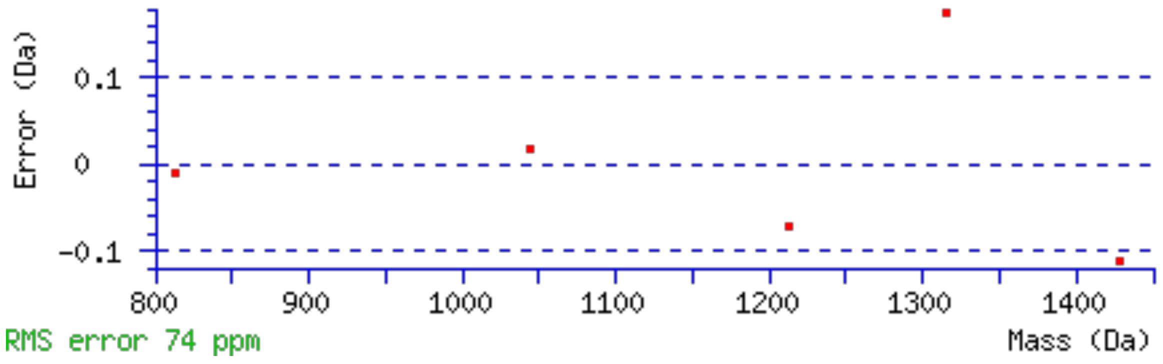
Match to Query 8207: 1824.625448 from(913.320000,2+) intensity(6016.0845) rtinseconds(2614.9864) index(7088)
Title: 17492_20120825_cho_glp1r_2hrp.8665.8665.0.dta
Data file 17492_20120825_cho_glp1r_2hrp.prh1.mgf

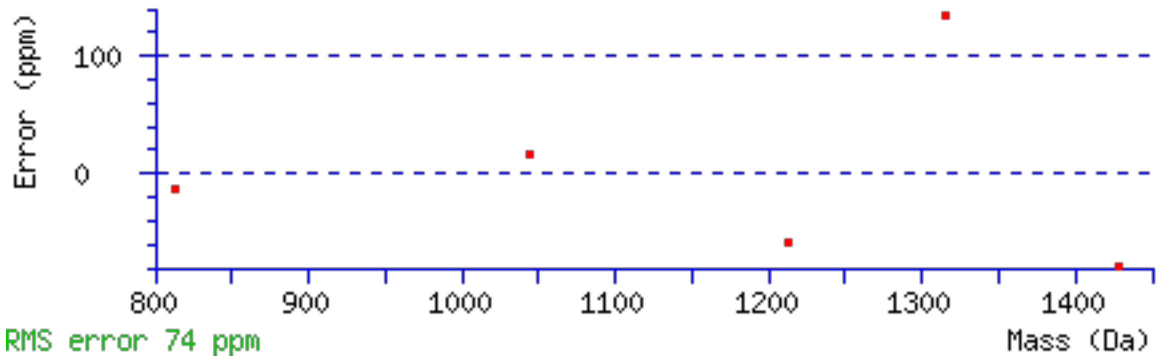
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 750 to 1450 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1823.9629
Fixed modifications: Carboxymethyl (C) (apply to specified residues or termini only)
Ions Score: 45 **Expect:** 0.024
Matches : 5/154 fragment ions using 6 most intense peaks (help)

#	b	b++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.0913	57.5493			I							18
2	171.1128	86.0600			G	1711.8861	856.4467	1694.8596	847.9334	1693.8755	847.4414	17
3	284.1969	142.6021			I	1654.8646	827.9360	1637.8381	819.4227	1636.8541	818.9307	16
4	397.2809	199.1441			I	1541.7806	771.3939	1524.7540	762.8807	1523.7700	762.3886	15
5	454.3024	227.6548			G	***1428.6965***	714.8519	1411.6700	706.3386	1410.6859	705.8466	14
6	511.3239	256.1656			G	1371.6751	686.3412	1354.6485	677.8279	1353.6645	677.3359	13
7	612.3715	306.6894	594.3610	297.6841	T	***1314.6536***	657.8304	1297.6270	649.3172	1296.6430	648.8251	12
8	669.3930	335.2001	651.3824	326.1949	G	***1213.6059***	607.3066	1196.5794	598.7933	1195.5953	598.3013	11
9	782.4771	391.7422	764.4665	382.7369	L	1156.5844	578.7959	1139.5579	570.2826	1138.5739	569.7906	10
10	897.5040	449.2556	879.4934	440.2504	D	***1043.5004***	522.2538	1026.4738	513.7406	1025.4898	513.2485	9
11	1012.5310	506.7691	994.5204	497.7638	D	928.4734	464.7404	911.4469	456.2271	910.4629	455.7351	8
12	1109.5837	555.2955	1091.5732	546.2902	P	***813.4465***	407.2269	796.4199	398.7136	795.4359	398.2216	7
13	1238.6263	619.8168	1220.6157	610.8115	E	716.3937	358.7005	699.3672	350.1872	698.3832	349.6952	6
14	1351.7104	676.3588	1333.6998	667.3535	I	587.3511	294.1792	570.3246	285.6659	569.3406	285.1739	5
15	1464.7944	732.9009	1446.7839	723.8956	L	474.2671	237.6372	457.2405	229.1239	456.2565	228.6319	4
16	1593.8370	797.4222	1575.8265	788.4169	E	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	3
17	1650.8585	825.9329	1632.8479	816.9276	G	232.1404	116.5738	215.1139	108.0606			2
18					R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.7	1823.9629	0.6626	IGIIGGTGLDDPEILEGR
7.0	1824.8927	-0.2673	IALEGEIGKEICSSYR
5.2	1824.8901	-0.2646	LRAGGGGPSAMAEVGQPDR
4.7	1823.7771	0.8483	PDNEVEEMVEEYVDK
4.5	1821.8050	2.8204	SENVTNGEMEAATAASPK
4.1	1822.8771	1.7484	VLREEEGPVSMAESFK
4.0	1826.9131	-2.2877	ALGQMNLGKEVHDMIR
3.4	1826.9097	-2.2843	SDQALGPLPPPAMHQPR
3.2	1826.8581	-2.2326	HSPQTESMISSIGNPAR
3.1	1824.8862	-0.2608	SMYNRVSDPLIVVCR

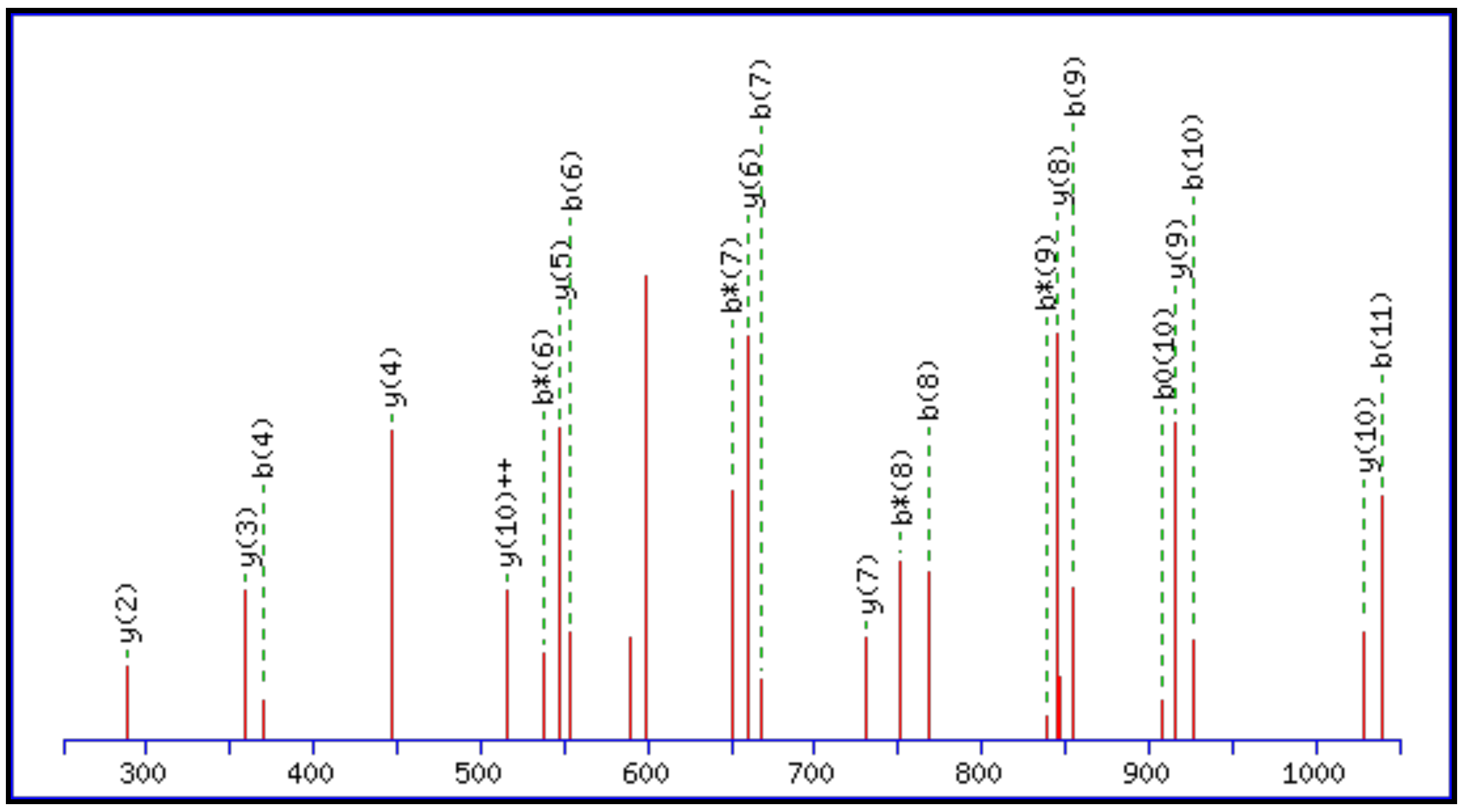
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALLANALTSALR**
Found in **gi|354503516|ref|XP_003513827.1|**, PREDICTED: transmembrane protein 33-like [Cricetulus griseus]

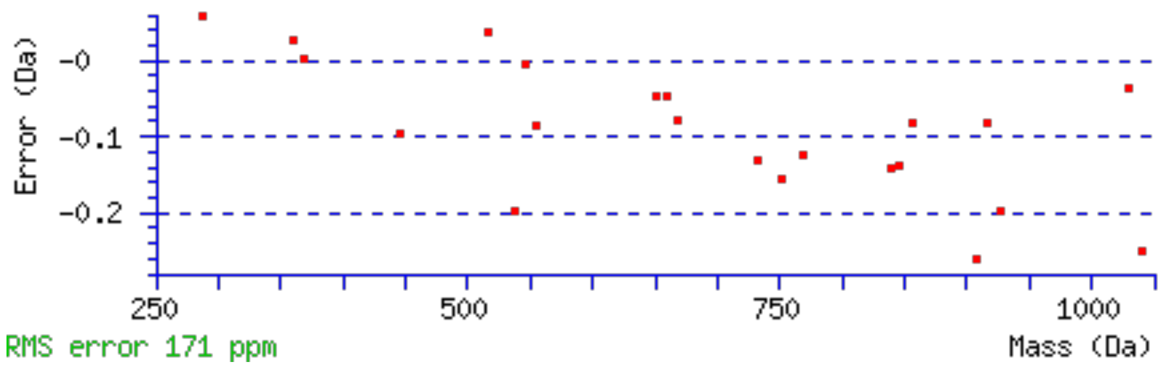
Match to Query 2953: 1212.225448 from(607.120000,2+) intensity(1455.7898) rtinseconds(2586.5322) index(7105)
Title: 17496_20120917_cho_glp1r_inj2.8530.8530.0.dta
Data file 17496_20120917_cho_glp1r_inj2.prh1.mgf

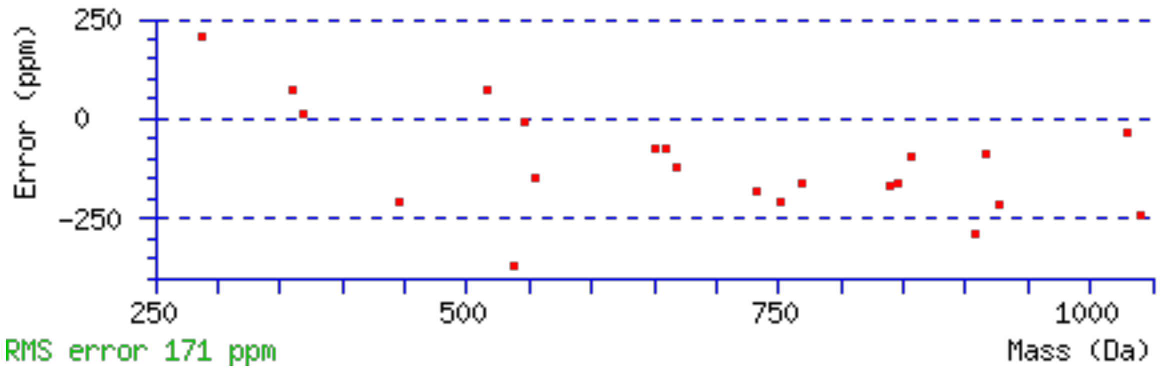
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 250 to 1050 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1212.7190
Fixed modifications: Carboxymethyl (C) (apply to specified residues or termini only)
Ions Score: 95  Expect: 3.6e-07
Matches : 22/104 fragment ions using 25 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							12
2	185.1285	93.0679					L	1142.6892	571.8482	1125.6626	563.3350	1124.6786	562.8429	11
3	298.2125	149.6099					L	***1029.6051***	515.3062	1012.5786	506.7929	1011.5946	506.3009	10
4	**369.2496**	185.1285					A	***916.5211***	458.7642	899.4945	450.2509	898.5105	449.7589	9
5	483.2926	242.1499	466.2660	233.6366			N	***845.4839***	423.2456	828.4574	414.7323	827.4734	414.2403	8
6	**554.3297**	277.6685	537.3031	269.1552			A	***731.4410***	366.2241	714.4145	357.7109	713.4305	357.2189	7
7	**667.4137**	334.2105	650.3872	325.6972			L	***660.4039***	330.7056	643.3774	322.1923	642.3933	321.7003	6
8	**768.4614**	384.7343	751.4349	376.2211	750.4509	375.7291	T	***547.3198***	274.1636	530.2933	265.6503	529.3093	265.1583	5
9	**855.4934**	428.2504	838.4669	419.7371	837.4829	419.2451	S	***446.2722***	223.6397	429.2456	215.1264	428.2616	214.6344	4
10	**926.5306**	463.7689	909.5040	455.2556	908.5200	454.7636	A	***359.2401***	180.1237	342.2136	171.6104			3
11	**1039.6146**	520.3109	1022.5881	511.7977	1021.6041	511.3057	L	***288.2030***	144.6051	271.1765	136.0919			2
12							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
94.7	1212.7190	-0.4935	ALLANALTSALR
14.3	1214.6407	-2.4153	WIAQDLSNLR
14.2	1212.6574	-0.4320	ARLAGEEQALR
13.7	1212.6107	-0.3853	GMFMLRGTLR
13.5	1209.6717	2.5537	GTISSTITFKR

12.2	1213.7030	-1.4776	LVPSDRTSLVK
12.1	1214.7234	-2.4980	VLSAQVGLSLTK
11.8	1211.6986	0.5268	GRGPGTGALSIVK
11.6	1209.6466	2.5789	NGALSLGLGSHGK
10.5	1212.6033	-0.3779	RTTSEVPMHR