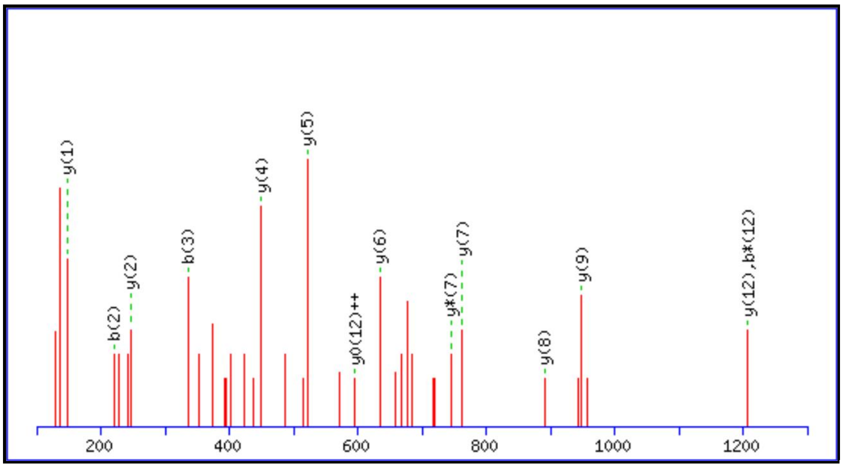
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGDSGEQIAGFVK**
Found in **P10619|PPGB_HUMAN**, Lysosomal protective protein OS=Homo sapiens GN=CTSA PE=1 SV=2

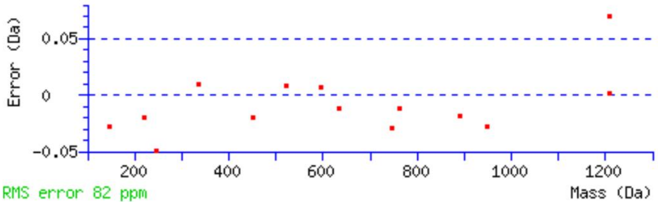
Match to Query 19656: 1369.609228 from(685.811890,2+)
Title: Locus:5.1.1.6609.3

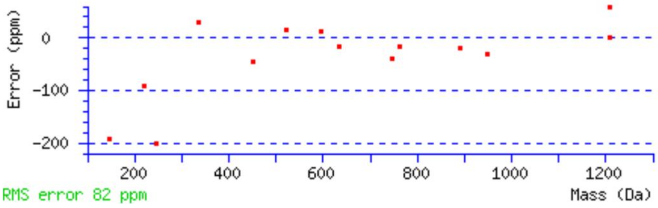
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1369.6514
Fixed modifications: Carbamidomethyl (C)
Ions Score: 75 **Expect:** 6.3e-007
Matches (Bold Red): 14/114 fragment ions using 22 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							13
2	**221.0921**	111.0497					G	**1207.5953**	604.3013	1190.5688	595.7880	1189.5848	**595.2960**	12
3	**336.1190**	168.5631			318.1084	159.5579	D	1150.5739	575.7906	1133.5473	567.2773	1132.5633	566.7853	11
4	423.1510	212.0792			405.1405	203.0739	S	1035.5469	518.2771	1018.5204	509.7638	1017.5364	509.2718	10
5	480.1725	240.5899			462.1619	231.5846	G	**948.5149**	474.7611	931.4884	466.2478	930.5043	465.7558	9
6	609.2151	305.1112			591.2045	296.1059	E	**891.4934**	446.2504	874.4669	437.7371	873.4829	437.2451	8
7	737.2737	369.1405	720.2471	360.6272	719.2631	360.1352	Q	**762.4509**	381.7291	**745.4243**	373.2158			7
8	850.3577	425.6825	833.3312	417.1692	832.3472	416.6772	I	**634.3923**	317.6998	617.3657	309.1865			6
9	921.3949	461.2011	904.3683	452.6878	903.3843	452.1958	A	**521.3082**	261.1577	504.2817	252.6445			5
10	978.4163	489.7118	961.3898	481.1985	960.4058	480.7065	G	**450.2711**	225.6392	433.2445	217.1259			4
11	1125.4847	563.2460	1108.4582	554.7327	1107.4742	554.2407	F	393.2496	197.1285	376.2231	188.6152			3
12	1224.5531	612.7802	**1207.5266**	604.2669	1206.5426	603.7749	V	**246.1812**	123.5942	229.1547	115.0810			2
13							K	**147.1128**	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
74.7	1369.6514	-0.0422	YGDSGEQIAGFVK

4.8	1369.6183	-0.0091	YADSLNDANMLK
4.3	1369.6514	-0.0422	QFEDELHPDLK
3.8	1369.6626	-0.0534	NFENTRESFVK
3.7	1369.6588	-0.0495	YAVSIMWELDK
1.4	1369.6734	-0.0642	GYLKCDISVMGK

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

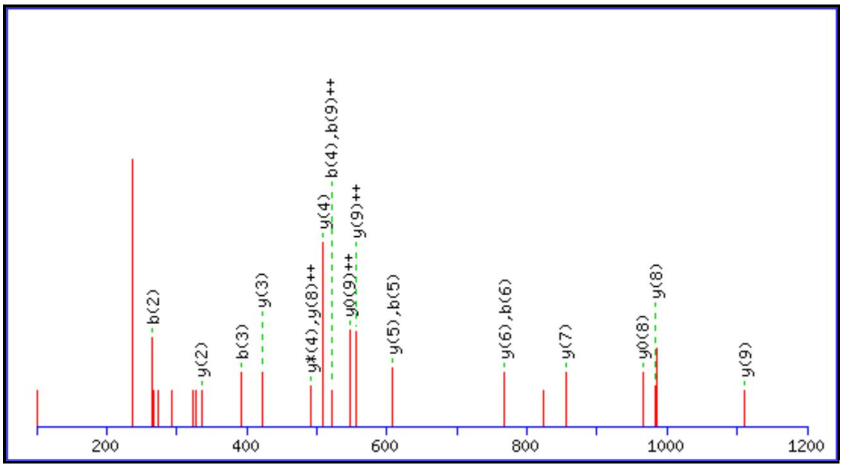
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TYQQSCVSSCR**
Found in **Q8IUC1|KR111_HUMAN**, Keratin-associated protein 11-1 OS=Homo sapiens GN=KRTAP11-1 PE=1 SV=1

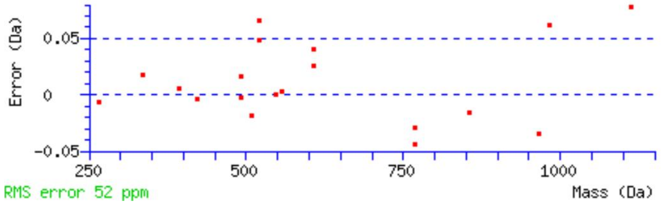
Match to Query 7646: 1374.527288 from(688.270920,2+)
Title: Locus:9.1.1.6301.2

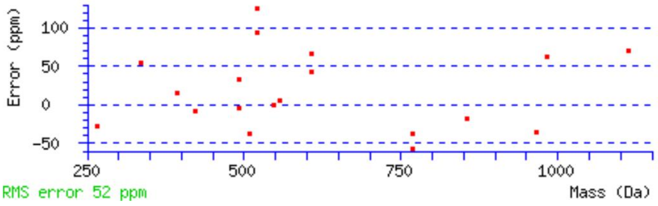
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1374.5656
Fixed modifications: Carbamidomethyl (C)
Ions Score: 58 **Expect:** 1e-005
Matches (Bold Red): 19/112 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	**265.1183**	133.0628			247.1077	124.0575	Y	1274.5252	637.7663	1257.4987	629.2530	1256.5147	628.7610	10
3	**393.1769**	197.0921	376.1503	188.5788	375.1663	188.0868	Q	**1111.4619**	**556.2346**	1094.4354	547.7213	1093.4513	**547.2293**	9
4	**521.2354**	261.1214	504.2089	252.6081	503.2249	252.1161	Q	**983.4033**	**492.2053**	966.3768	483.6920	**965.3928**	483.2000	8
5	**608.2675**	304.6374	591.2409	296.1241	590.2569	295.6321	S	**855.3447**	428.1760	838.3182	419.6627	837.3342	419.1707	7
6	**768.2981**	384.6527	751.2716	376.1394	750.2876	375.6474	C	**768.3127**	384.6600	751.2862	376.1467	750.3022	375.6547	6
7	867.3665	434.1869	850.3400	425.6736	849.3560	425.1816	V	**608.2821**	304.6447	591.2555	296.1314	590.2715	295.6394	5
8	954.3986	477.7029	937.3720	469.1896	936.3880	468.6976	S	**509.2137**	255.1105	**492.1871**	246.5972	491.2031	246.1052	4
9	1041.4306	**521.2189**	1024.4040	512.7057	1023.4200	512.2136	S	**422.1816**	211.5945	405.1551	203.0812	404.1711	202.5892	3
10	1201.4612	601.2343	1184.4347	592.7210	1183.4507	592.2290	C	**335.1496**	168.0784	318.1231	159.5652			2
11							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.0	1374.5656	-0.0384	TYQQSCVSSCR

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

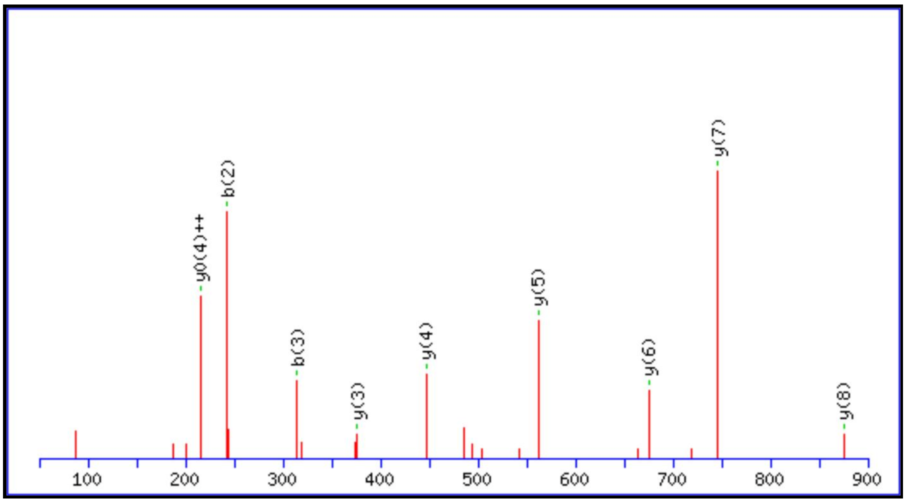
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEALDANSR**
Found in **P09496|CLCA_HUMAN**, Clathrin light chain A OS=Homo sapiens GN=CLTA PE=1 SV=1

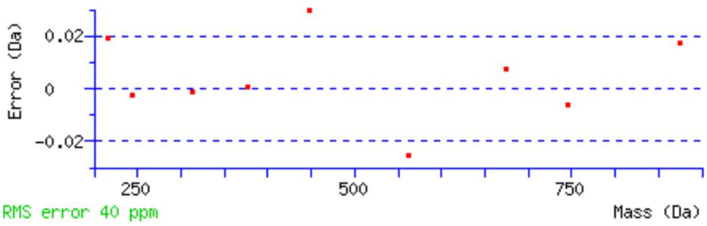
Match to Query 13962: 987.467208 from(494.740880,2+)
Title: Locus:9.1.1.6618.2

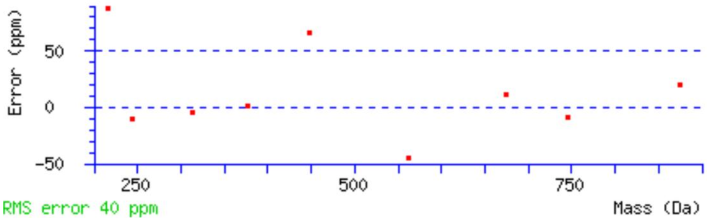
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 50 to 900 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 987.4985
Fixed modifications: Carbamidomethyl (C)
Ions Score: 53 **Expect:** 0.00015
Matches (Bold Red): 9/80 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							9
2	**243.1339**	122.0706			225.1234	113.0653	E	**875.4217**	438.2145	858.3952	429.7012	857.4112	429.2092	8
3	**314.1710**	157.5892			296.1605	148.5839	A	**746.3791**	373.6932	729.3526	365.1799	728.3686	364.6879	7
4	427.2551	214.1312			409.2445	205.1259	L	**675.3420**	338.1747	658.3155	329.6614	657.3315	329.1694	6
5	542.2821	271.6447			524.2715	262.6394	D	**562.2580**	281.6326	545.2314	273.1193	544.2474	272.6273	5
6	613.3192	307.1632			595.3086	298.1579	A	**447.2310**	224.1191	430.2045	215.6059	429.2205	**215.1139**	4
7	727.3621	364.1847	710.3355	355.6714	709.3515	355.1794	N	**376.1939**	188.6006	359.1674	180.0873	358.1833	179.5953	3
8	814.3941	407.7007	797.3676	399.1874	796.3836	398.6954	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
9							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of LEALDANSR

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.7	987.4985	-0.0313	LEALDANSR
19.2	987.4872	-0.0200	ELALEEER
10.4	987.4846	-0.0174	NKNQGSGAGR
8.2	987.4985	-0.0313	IEDSAQVAR
8.2	987.5059	-0.0387	LETPMELR
5.0	987.4946	-0.0274	ELELMPEK
5.0	987.4848	-0.0176	LAEHMFPK
4.8	987.4621	0.0051	TDEVPAGGSR
4.0	987.4509	0.0163	ELSPEEER
3.2	987.5025	-0.0353	LEYEGLHK

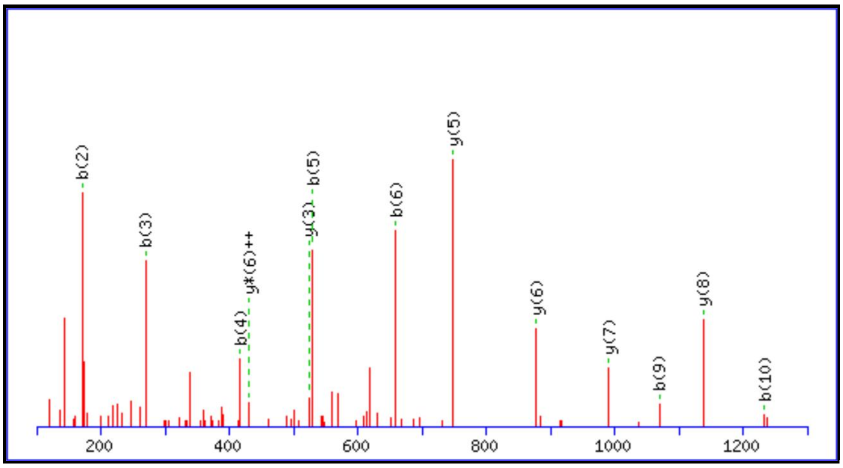
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVVFLEPQWYR**
Found in **P08637|FCG3A_HUMAN**, Low affinity immunoglobulin gamma Fc region receptor III-A OS=Homo sapiens GN=FCGR3A PE=1 SV=2

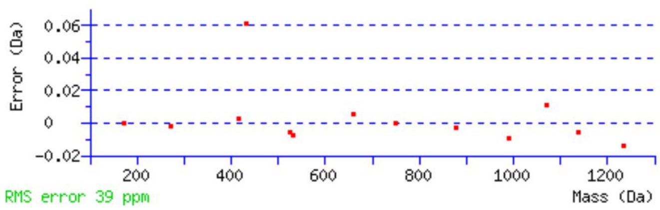
Match to Query 23608: 1406.694348 from(704.354450,2+)
Title: Locus:6.1.1.6080.2

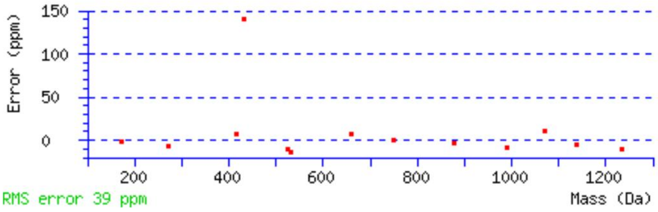
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range



```
Monoisotopic mass of neutral peptide Mr(calc): 1406.7347
Fixed modifications: Carbamidomethyl (C)
Ions Score: 73  Expect: 1.4e-006
Matches (Bold Red): 13/86 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	72.0444	36.5258					A							11
2	**171.1128**	86.0600					V	1336.7048	668.8561	1319.6783	660.3428	1318.6943	659.8508	10
3	**270.1812**	135.5942					V	1237.6364	619.3218	1220.6099	610.8086	1219.6259	610.3166	9
4	**417.2496**	209.1285					F	**1138.5680**	569.7876	1121.5415	561.2744	1120.5574	560.7824	8
5	**530.3337**	265.6705					L	**991.4996**	496.2534	974.4730	487.7402	973.4890	487.2482	7
6	**659.3763**	330.1918			641.3657	321.1865	E	**878.4155**	439.7114	861.3890	**431.1981**	860.4050	430.7061	6
7	756.4291	378.7182			738.4185	369.7129	P	**749.3729**	375.1901	732.3464	366.6768			5
8	884.4876	442.7475	867.4611	434.2342	866.4771	433.7422	Q	652.3202	326.6637	635.2936	318.1504			4
9	**1070.5669**	535.7871	1053.5404	527.2738	1052.5564	526.7818	W	**524.2616**	262.6344	507.2350	254.1212			3
10	**1233.6303**	617.3188	1216.6037	608.8055	1215.6197	608.3135	Y	338.1823	169.5948	321.1557	161.0815			2
11							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
73.4	1406.7347	-0.0403	AVVFLEPQWYR
19.3	1406.7379	-0.0435	GLVGPPGSRGNPGSR

13.2	1406.6897	0.0046	MLNDQLMLLER
12.9	1406.7194	-0.0250	YPLVSVNEAPYR
11.6	1406.6684	0.0259	SNRATAATAMNQR
7.2	1406.6976	-0.0033	LGFVDVQNCISR
6.3	1406.7261	-0.0318	MLEGDLVSKMLR
6.0	1406.6547	0.0396	VAMAMGSHPRYR
5.5	1406.6579	0.0365	GGGGDWPAGLTTYR
5.0	1406.7228	-0.0284	AVSCTPLYVEIR

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

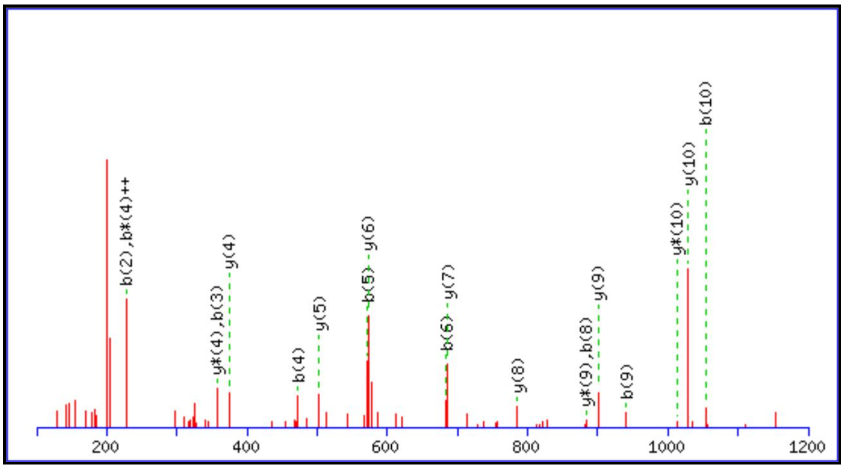
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NIEDVIAQGIGK**
Found in **P05387|RLA2_HUMAN**, 60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1

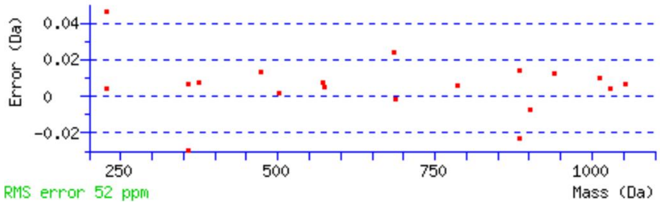
Match to Query 21010: 1255.652988 from(628.833770,2+)
Title: Locus:12.1.1.6455.3

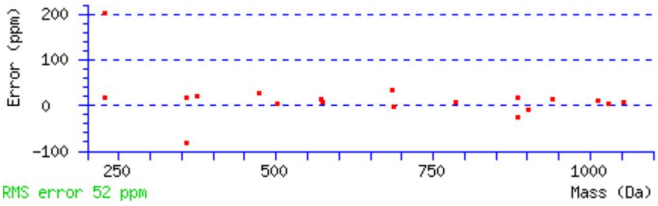
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1255.6772
Fixed modifications: Carbamidomethyl (C)
Ions Score: 71 **Expect:** 3e-006
Matches (Bold Red): 19/112 fragment ions using 22 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							12
2	**228.1343**	114.5708	211.1077	106.0575			I	1142.6416	571.8244	1125.6150	563.3111	1124.6310	562.8191	11
3	**357.1769**	179.0921	340.1503	170.5788	339.1663	170.0868	E	**1029.5575**	515.2824	**1012.5310**	506.7691	1011.5469	506.2771	10
4	**472.2038**	236.6055	455.1773	**228.0923**	454.1932	227.6003	D	**900.5149**	450.7611	**883.4884**	442.2478	882.5043	441.7558	9
5	**571.2722**	286.1397	554.2457	277.6265	553.2617	277.1345	V	**785.4880**	393.2476	768.4614	384.7343			8
6	**684.3563**	342.6818	667.3297	334.1685	666.3457	333.6765	I	**686.4196**	343.7134	669.3930	335.2001			7
7	755.3934	378.2003	738.3668	369.6871	737.3828	369.1951	A	**573.3355**	287.1714	556.3089	278.6581			6
8	**883.4520**	442.2296	866.4254	433.7164	865.4414	433.2243	Q	**502.2984**	251.6528	485.2718	243.1396			5
9	**940.4734**	470.7404	923.4469	462.2271	922.4629	461.7351	G	**374.2398**	187.6235	**357.2132**	179.1103			4
10	**1053.5575**	527.2824	1036.5310	518.7691	1035.5469	518.2771	I	317.2183	159.1128	300.1918	150.5995			3
11	1110.5790	555.7931	1093.5524	547.2798	1092.5684	546.7878	G	204.1343	102.5708	187.1077	94.0575			2
12							K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
70.6	1255.6772	-0.0242	NIEDVIAQGIGK
14.9	1255.6231	0.0299	DMPKVLHDSSK

12.3	1255.6006	0.0524	YEDMLSLLEK
8.3	1255.6884	-0.0354	LGDAITALQQAR
7.7	1255.6884	-0.0354	ARAEALQEALGK
7.5	1255.6772	-0.0242	VQEEIDLVVGR
6.2	1255.6958	-0.0428	LCPLSLTSLPR
5.8	1255.6093	0.0437	QVFPIMCAYK
5.5	1255.6561	-0.0031	LNGSITSPGWPK
3.9	1255.6231	0.0299	CHDVTAVVEVK

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

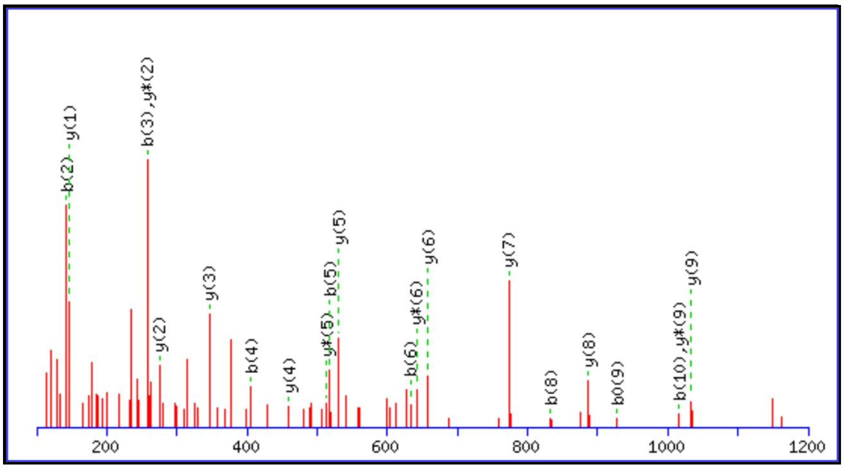
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AADFIDQALAQK**
Found in **P51452|DUS3_HUMAN**, Dual specificity protein phosphatase 3 OS=Homo sapiens GN=DUSP3 PE=1 SV=1

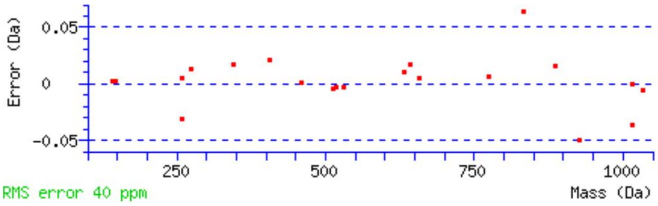
Match to Query 21660: 1289.648268 from(645.831410,2+)
Title: Locus:10.1.1.6692.3

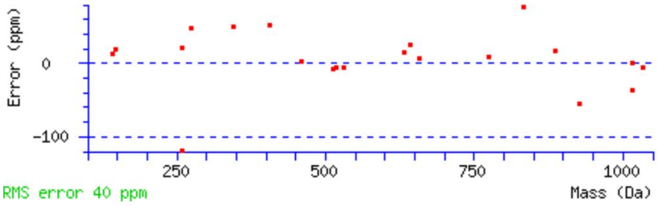
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1289.6615
Fixed modifications: Carbamidomethyl (C)
Ions Score: 60 **Expect:** 3.1e-005
Matches (Bold Red): 21/104 fragment ions using 38 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							12
2	**143.0815**	72.0444					A	1219.6317	610.3195	1202.6052	601.8062	1201.6212	601.3142	11
3	**258.1084**	129.5579			240.0979	120.5526	D	1148.5946	574.8009	1131.5681	566.2877	1130.5841	565.7957	10
4	**405.1769**	203.0921			387.1663	194.0868	F	**1033.5677**	517.2875	**1016.5411**	508.7742	1015.5571	508.2822	9
5	**518.2609**	259.6341			500.2504	250.6288	I	**886.4993**	443.7533	869.4727	435.2400	868.4887	434.7480	8
6	**633.2879**	317.1476			615.2773	308.1423	D	**773.4152**	387.2112	756.3886	378.6980	755.4046	378.2060	7
7	761.3464	381.1769	744.3199	372.6636	743.3359	372.1716	Q	**658.3883**	329.6978	**641.3617**	321.1845			6
8	**832.3836**	416.6954	815.3570	408.1821	814.3730	407.6901	A	**530.3297**	265.6685	**513.3031**	257.1552			5
9	945.4676	473.2375	928.4411	464.7242	**927.4571**	464.2322	L	**459.2926**	230.1499	442.2660	221.6366			4
10	**1016.5047**	508.7560	999.4782	500.2427	998.4942	499.7507	A	**346.2085**	173.6079	329.1819	165.0946			3
11	1144.5633	572.7853	1127.5368	564.2720	1126.5528	563.7800	Q	**275.1714**	138.0893	**258.1448**	129.5761			2
12							K	**147.1128**	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.3	1289.6615	-0.0133	AADFIDQALAQK
18.5	1289.6074	0.0408	CPFPAGSDLAQK

13.0	1289.7013	-0.0530	AEGTVVMKLAQK
9.7	1289.6687	-0.0205	NLSSASQATRQK
6.5	1289.6146	0.0336	GMSAQGGAPSRQK
6.5	1289.6463	0.0020	EDTQTLQSLQK
6.0	1289.6108	0.0375	CPPCLTSLSQK
4.9	1289.6656	-0.0173	EKNSYYVFLK
4.0	1289.6649	-0.0166	ESVTQIMKNPK
3.4	1289.6728	-0.0245	DFLRLQQENK

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

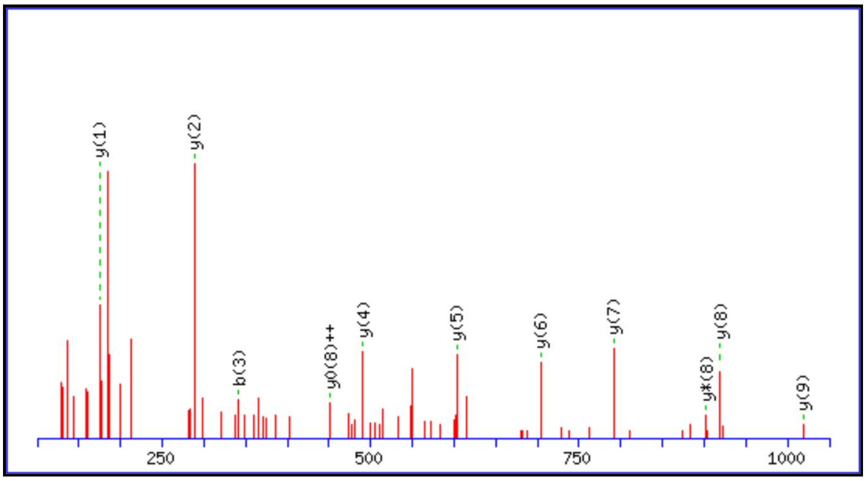
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVQSTLSDLR**
Found in **Q9BYN0|SRXN1_HUMAN**, Sulfiredoxin-1 OS=Homo sapiens GN=SRXN1 PE=1 SV=2

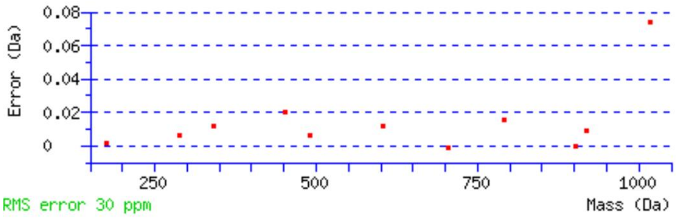
Match to Query 18342: 1130.598228 from(566.306390,2+)
Title: Locus:12.1.1.6171.2

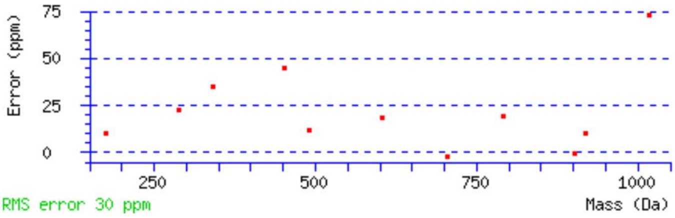
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1130.6295
Fixed modifications: Carbamidomethyl (C)
Ions Score: 59 **Expect:** 4.8e-005
Matches (Bold Red): 11/94 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	114.0913	57.5493					L							10
2	213.1598	107.0835					V	**1018.5527**	509.7800	1001.5262	501.2667	1000.5422	500.7747	9
3	**341.2183**	171.1128	324.1918	162.5995			Q	**919.4843**	460.2458	**902.4578**	451.7325	901.4738	**451.2405**	8
4	428.2504	214.6288	411.2238	206.1155	410.2398	205.6235	S	**791.4258**	396.2165	774.3992	387.7032	773.4152	387.2112	7
5	529.2980	265.1527	512.2715	256.6394	511.2875	256.1474	T	**704.3937**	352.7005	687.3672	344.1872	686.3832	343.6952	6
6	642.3821	321.6947	625.3556	313.1814	624.3715	312.6894	L	**603.3461**	302.1767	586.3195	293.6634	585.3355	293.1714	5
7	729.4141	365.2107	712.3876	356.6974	711.4036	356.2054	S	**490.2620**	245.6346	473.2354	237.1214	472.2514	236.6293	4
8	844.4411	422.7242	827.4145	414.2109	826.4305	413.7189	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	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





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.1	1130.6295	-0.0313	LVQSTLSDLR
11.5	1130.5576	0.0406	VIQPMGMSPR
10.7	1130.5866	0.0116	LVAGPSKCSGR
7.9	1130.5931	0.0051	KAEEALSDLR
5.7	1130.6448	-0.0465	LWTKIDLSR
5.7	1130.6230	-0.0248	VIRLSDCLR
5.7	1130.6448	-0.0466	VLVGEFAQIR
5.2	1130.5567	0.0415	QLESAIEDAR
5.2	1130.6084	-0.0102	LLNYAGEVPR
4.9	1130.5792	0.0190	LVGRNSDTNR

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

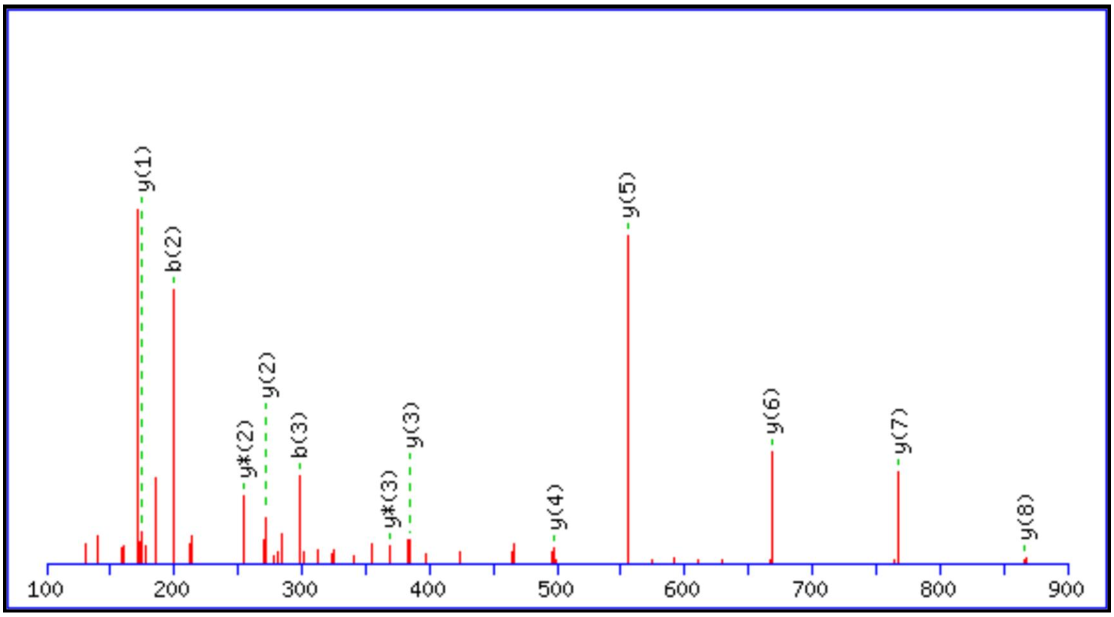
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVVLGLLPR**
Found in **Q15102|PA1B3_HUMAN**, Platelet-activating factor acetylhydrolase IB subunit gamma OS=Homo sapiens GN=PAFAH1B3 PE=1 SV=1

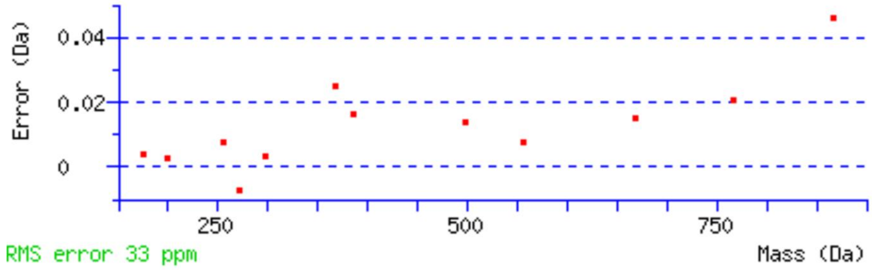
Match to Query 3719: 964.627448 from(483.321000,2+)
Title: Locus:9.1.1.6336.2

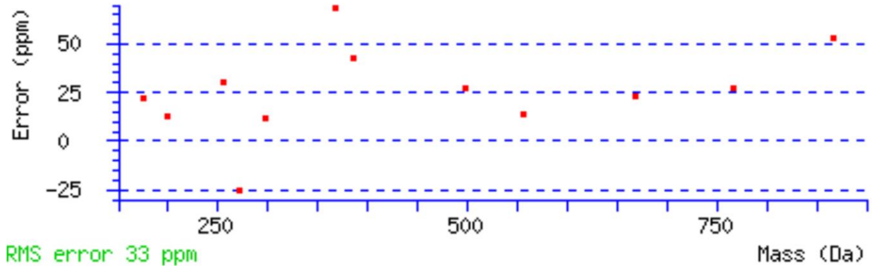
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 900 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 964.6433
Fixed modifications: Carbamidomethyl (C)
Ions Score: 58 **Expect:** 1e-005
Matches (Bold Red): 12/48 fragment ions using 27 most intense peaks

#	b	b^{++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	100.0757	50.5415	V					9
2	**199.1441**	100.0757	V	**866.5822**	433.7947	849.5557	425.2815	8
3	**298.2125**	149.6099	V	**767.5138**	384.2605	750.4872	375.7473	7
4	411.2966	206.1519	L	**668.4454**	334.7263	651.4188	326.2130	6
5	468.3180	234.6627	G	**555.3613**	278.1843	538.3348	269.6710	5
6	581.4021	291.2047	L	**498.3398**	249.6736	481.3133	241.1603	4
7	694.4862	347.7467	L	**385.2558**	193.1315	**368.2292**	184.6183	3
8	791.5389	396.2731	P	**272.1717**	136.5895	**255.1452**	128.0762	2
9			R	**175.1190**	88.0631	158.0924	79.5498	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.6	964.6433	-0.0159	VVVLGLLPR
6.5	964.5930	0.0344	VVKGRPGPR
4.0	964.6069	0.0205	IIAVATLHK

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

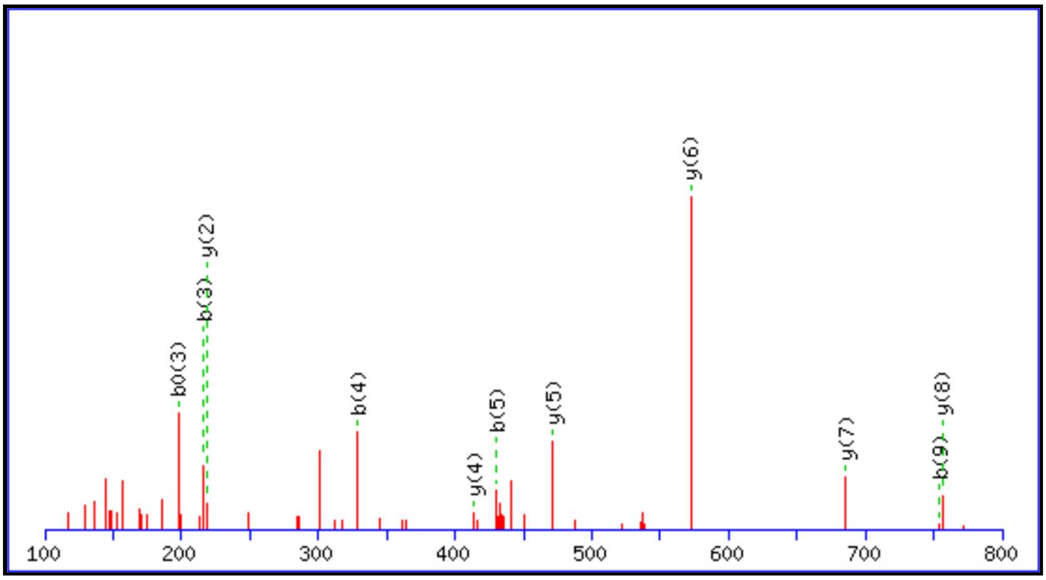
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSAITGPVAK**
Found in **P62829|RL23_HUMAN**, 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1

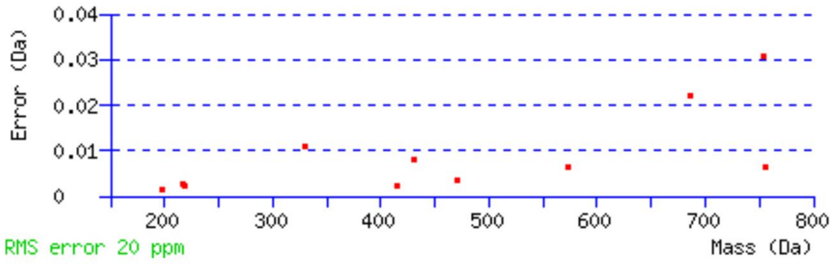
Match to Query 11810: 899.478848 from(450.746700,2+)
Title: Locus:12.1.1.5797.2

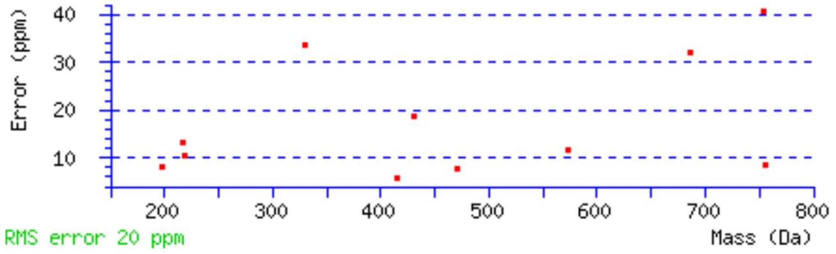
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 800 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 899.5076
Fixed modifications: Carbamidomethyl (C)
Ions Score: 56 **Expect:** 9.4e-005
Matches (Bold Red): 11/78 fragment ions using 15 most intense peaks

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180			G							10
2	145.0608	73.0340	127.0502	64.0287	S	843.4934	422.2504	826.4669	413.7371	825.4829	413.2451	9
3	**216.0979**	108.5526	**198.0873**	99.5473	A	**756.4614**	378.7343	739.4349	370.2211	738.4509	369.7291	8
4	**329.1819**	165.0946	311.1714	156.0893	I	**685.4243**	343.2158	668.3978	334.7025	667.4137	334.2105	7
5	**430.2296**	215.6185	412.2191	206.6132	T	**572.3402**	286.6738	555.3137	278.1605	554.3297	277.6685	6
6	487.2511	244.1292	469.2405	235.1239	G	**471.2926**	236.1499	454.2660	227.6366			5
7	584.3039	292.6556	566.2933	283.6503	P	**414.2711**	207.6392	397.2445	199.1259			4
8	683.3723	342.1898	665.3617	333.1845	V	317.2183	159.1128	300.1918	150.5995			3
9	**754.4094**	377.7083	736.3988	368.7030	A	**218.1499**	109.5786	201.1234	101.0653			2
10					K	147.1128	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.6	899.5076	-0.0288	GSAITGPVAK
9.5	899.5076	-0.0288	KAEPLASGK
8.0	899.5189	-0.0400	DNVVRVAK
7.9	899.4348	0.0440	EAQPEAGAK
7.5	899.4609	0.0180	KSFMMIK
7.5	899.4609	0.0180	KSFMMIK
7.5	899.4609	0.0180	KSFMMLK
7.5	899.4609	0.0180	KSFMMLK
6.8	899.4712	0.0076	DSPIGNLGK
5.8	899.4647	0.0142	REIHMAK

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

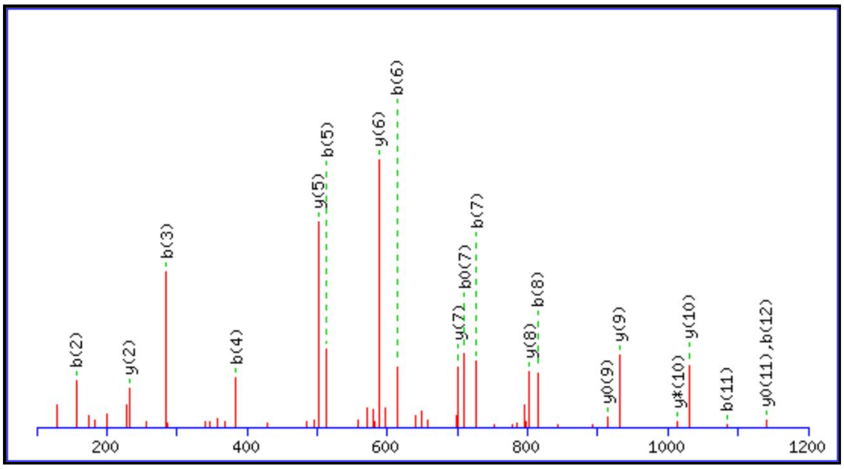
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVQVETISPGDGR**
Found in **P62942|FKB1A_HUMAN**, Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Homo sapiens GN=FKBP1A PE=1 SV=2

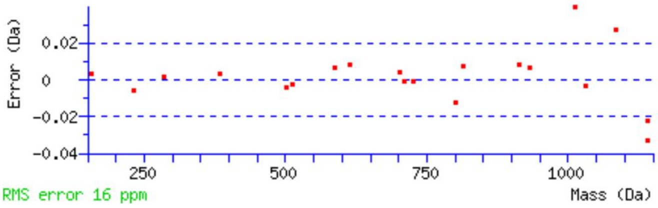
Match to Query 34264: 1313.635668 from(657.825110,2+)
Title: Locus:13.1.1.6308.2

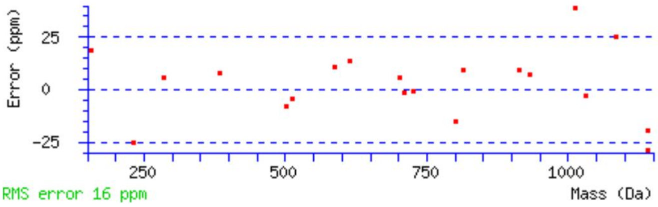
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1313.6576
Fixed modifications: Carbamidomethyl (C)
Ions Score: 88 **Expect:** 4.5e-008
Matches (Bold Red): 20/128 fragment ions using 22 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							13
2	**157.0972**	79.0522					V	1257.6434	629.3253	1240.6168	620.8120	1239.6328	620.3200	12
3	**285.1557**	143.0815	268.1292	134.5682			Q	1158.5749	579.7911	1141.5484	571.2778	**1140.5644**	570.7858	11
4	**384.2241**	192.6157	367.1976	184.1024			V	**1030.5164**	515.7618	**1013.4898**	507.2485	1012.5058	506.7565	10
5	**513.2667**	257.1370	496.2402	248.6237	495.2562	248.1317	E	**931.4480**	466.2276	914.4214	457.7143	**913.4374**	457.2223	9
6	**614.3144**	307.6608	597.2879	299.1476	596.3039	298.6556	T	**802.4054**	401.7063	785.3788	393.1930	784.3948	392.7010	8
7	**727.3985**	364.2029	710.3719	355.6896	**709.3879**	355.1976	I	**701.3577**	351.1825	684.3311	342.6692	683.3471	342.1772	7
8	**814.4305**	407.7189	797.4040	399.2056	796.4199	398.7136	S	**588.2736**	294.6404	571.2471	286.1272	570.2630	285.6352	6
9	911.4833	456.2453	894.4567	447.7320	893.4727	447.2400	P	**501.2416**	251.1244	484.2150	242.6112	483.2310	242.1191	5
10	968.5047	484.7560	951.4782	476.2427	950.4942	475.7507	G	404.1888	202.5980	387.1623	194.0848	386.1783	193.5928	4
11	**1083.5317**	542.2695	1066.5051	533.7562	1065.5211	533.2642	D	347.1674	174.0873	330.1408	165.5740	329.1568	165.0820	3
12	**1140.5531**	570.7802	1123.5266	562.2669	1122.5426	561.7749	G	**232.1404**	116.5738	215.1139	108.0606			2
13							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
87.8	1313.6576	-0.0219	GVQVETISPGDGR

13.8	1313.6324	0.0033	ARGDTGADEAVPR
10.0	1313.6688	-0.0331	VGQLRQDVEDR
7.8	1313.6687	-0.0331	LNELQEERQR
7.2	1313.6993	-0.0636	GKVTGFHNWIR
6.6	1313.6762	-0.0405	MLAAQGVDPGLAR
5.8	1313.6324	0.0033	QELRSNGEEPR
2.5	1313.6768	-0.0411	AWKVLTDYYR
2.5	1313.6939	-0.0582	KAELDIDALNGR
2.2	1313.6840	-0.0484	QPTWSRSSLPR

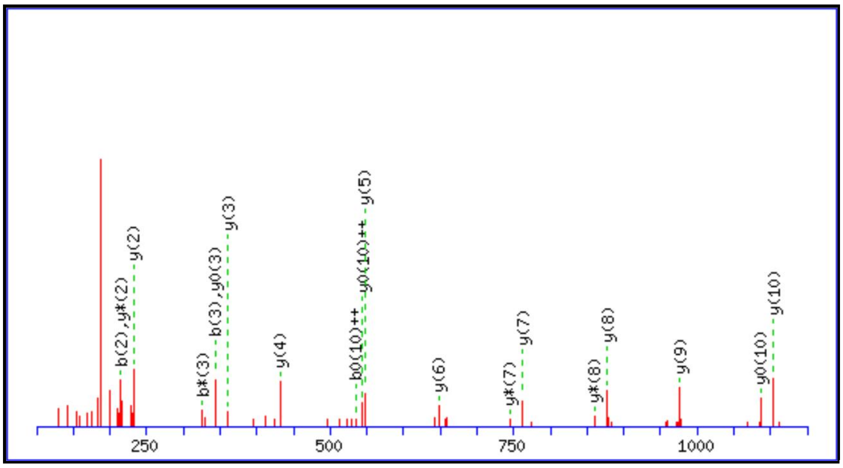
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TIQVDNTDAEGR**
Found in **P28838|AMPL_HUMAN**, Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3

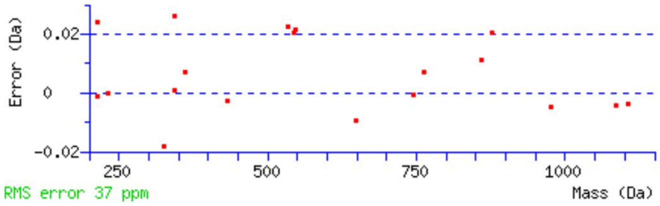
Match to Query 34398: 1317.626568 from(659.820560,2+)
Title: Locus:5.1.1.6129.3

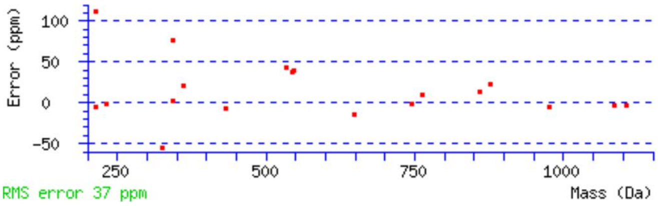
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1317.6161
Fixed modifications: Carbamidomethyl (C)
Ions Score: 84 **Expect:** 1.2e-007
Matches (Bold Red): 19/124 fragment ions using 21 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							12
2	**215.1390**	108.0731			197.1285	99.0679	I	1217.5757	609.2915	1200.5491	600.7782	1199.5651	600.2862	11
3	**343.1976**	172.1024	**326.1710**	163.5892	325.1870	163.0972	Q	**1104.4916**	552.7494	1087.4651	544.2362	**1086.4810**	**543.7442**	10
4	442.2660	221.6366	425.2395	213.1234	424.2554	212.6314	V	**976.4330**	488.7202	959.4065	480.2069	958.4225	479.7149	9
5	557.2930	279.1501	540.2664	270.6368	539.2824	270.1448	D	**877.3646**	439.1859	**860.3381**	430.6727	859.3540	430.1807	8
6	671.3359	336.1716	654.3093	327.6583	653.3253	327.1663	N	**762.3377**	381.6725	**745.3111**	373.1592	744.3271	372.6672	7
7	772.3836	386.6954	755.3570	378.1821	754.3730	377.6901	T	**648.2947**	324.6510	631.2682	316.1377	630.2842	315.6457	6
8	887.4105	444.2089	870.3840	435.6956	869.3999	435.2036	D	**547.2471**	274.1272	530.2205	265.6139	529.2365	265.1219	5
9	958.4476	479.7274	941.4211	471.2142	940.4371	470.7222	A	**432.2201**	216.6137	415.1936	208.1004	414.2096	207.6084	4
10	1087.4902	544.2487	1070.4637	535.7355	1069.4796	**535.2435**	E	**361.1830**	181.0951	344.1565	172.5819	**343.1724**	172.0899	3
11	1144.5117	572.7595	1127.4851	564.2462	1126.5011	563.7542	G	**232.1404**	116.5738	**215.1139**	108.0606			2
12							R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
83.9	1317.6161	0.0105	TIQVDNTDAEGR
29.2	1317.6161	0.0105	TVEINNTDAEGR

0.9	1317.6070	0.0195	WMMEGQRGAPR
0.9	1317.6731	-0.0465	WRWSGSVWVR
0.8	1317.6711	-0.0445	RLLLMEEEGGR
0.7	1317.6387	-0.0121	GEWTCKPIAEK
0.7	1317.6248	0.0018	VSNMFNLHAGGR
0.3	1317.6830	-0.0564	TIQHKYTNWK
0.3	1317.6048	0.0217	VSELTEEPDSGR

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

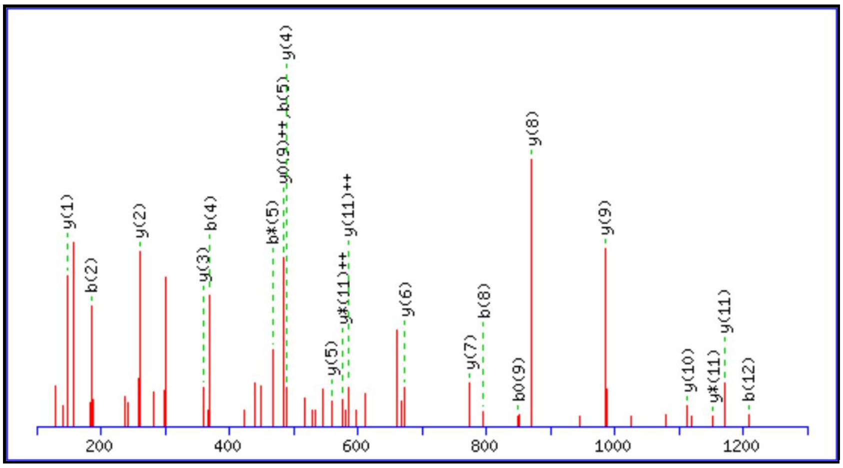
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALGQNPTNAEVLK**
Found in **P14649|MYL6B_HUMAN**, Myosin light chain 6B OS=Homo sapiens GN=MYL6B PE=1 SV=1

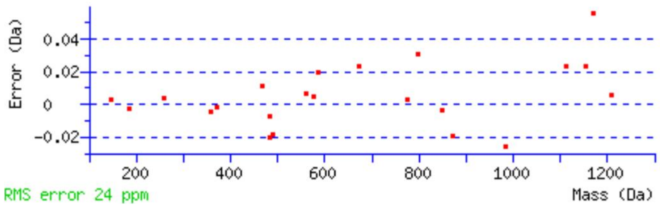
Match to Query 34828: 1353.709228 from(677.861890,2+)
Title: Locus:12.1.1.6777.2

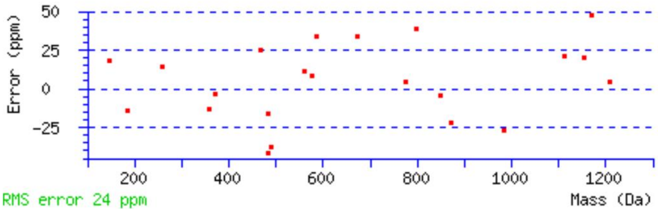
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1353.7252
Fixed modifications: Carbamidomethyl (C)
Ions Score: 77 **Expect:** 5.5e-007
Matches (Bold Red): 22/120 fragment ions using 43 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							13
2	**185.1285**	93.0679					L	1283.6954	642.3513	1266.6688	633.8381	1265.6848	633.3461	12
3	242.1499	121.5786					G	**1170.6113**	**585.8093**	**1153.5848**	**577.2960**	1152.6008	576.8040	11
4	**370.2085**	185.6079	353.1819	177.0946			Q	**1113.5899**	557.2986	1096.5633	548.7853	1095.5793	548.2933	10
5	**484.2514**	242.6293	**467.2249**	234.1161			N	**985.5313**	493.2693	968.5047	484.7560	967.5207	**484.2640**	9
6	581.3042	291.1557	564.2776	282.6425			P	**871.4884**	436.2478	854.4618	427.7345	853.4778	427.2425	8
7	682.3519	341.6796	665.3253	333.1663	664.3413	332.6743	T	**774.4356**	387.7214	757.4090	379.2082	756.4250	378.7162	7
8	**796.3948**	398.7010	779.3682	390.1878	778.3842	389.6958	N	**673.3879**	337.1976	656.3614	328.6843	655.3774	328.1923	6
9	867.4319	434.2196	850.4054	425.7063	**849.4213**	425.2143	A	**559.3450**	280.1761	542.3184	271.6629	541.3344	271.1709	5
10	996.4745	498.7409	979.4480	490.2276	978.4639	489.7356	E	**488.3079**	244.6576	471.2813	236.1443	470.2973	235.6523	4
11	1095.5429	548.2751	1078.5164	539.7618	1077.5323	539.2698	V	**359.2653**	180.1363	342.2387	171.6230			3
12	**1208.6270**	604.8171	1191.6004	596.3039	1190.6164	595.8118	L	**260.1969**	130.6021	243.1703	122.0888			2
13							K	**147.1128**	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
77.4	1353.7252	-0.0160	ALGQNPTNAEVLK

6.0	1353.6816	0.0276	SPDFYEEVKIK
5.5	1353.6520	0.0573	LQMSITEIMEK
4.8	1353.6459	0.0633	GQSCNNLPLSHK
3.4	1353.6850	0.0243	KMFEETAELLK
3.1	1353.6823	0.0269	KHATQGTMSHLK
0.7	1353.7625	-0.0532	AMHKCILKPLK
0.3	1353.6962	0.0130	YGMVAQVTQTLK
0.2	1353.7728	-0.0636	RAQQEQLLLQK

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

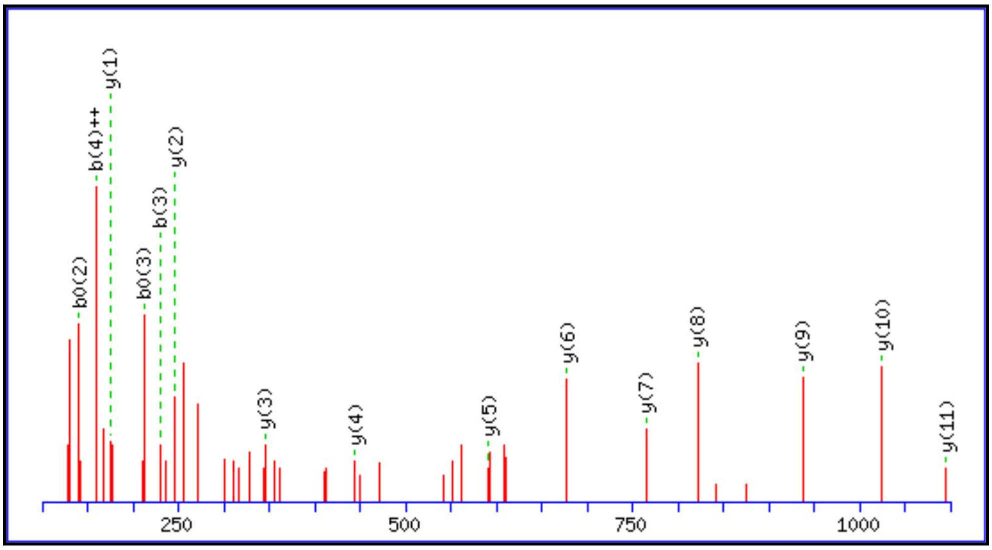
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASASDGSSFVVAR**
Found in **Q9H4G4|GAPR1_HUMAN**, Golgi-associated plant pathogenesis-related protein 1 OS=Homo sapiens GN=GLIPR2 PE=1 SV=3

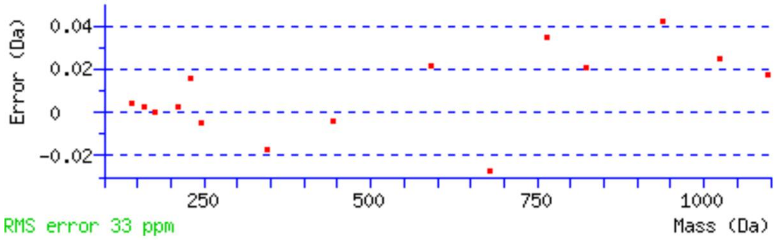
Match to Query 33118: 1252.601148 from(627.307850,2+)
Title: Locus:12.1.1.6739.3

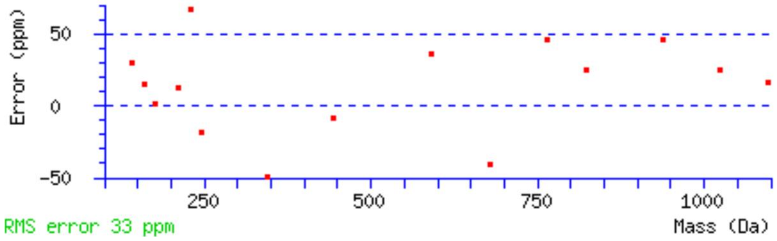
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1252.6048
Fixed modifications: Carbamidomethyl (C)
Ions Score: 76 **Expect:** 7.5e-007
Matches (Bold Red): 16/108 fragment ions using 35 most intense peaks

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.0444	36.5258			**A**							**13**
2	**159.0764**	80.0418	**141.0659**	71.0366	**S**	1182.5749	591.7911	1165.5484	583.2778	1164.5644	582.7858	**12**
3	**230.1135**	115.5604	**212.1030**	106.5551	**A**	**1095.5429**	548.2751	1078.5164	539.7618	1077.5323	539.2698	**11**
4	317.1456	**159.0764**	299.1350	150.0711	**S**	**1024.5058**	512.7565	1007.4792	504.2433	1006.4952	503.7513	**10**
5	432.1725	216.5899	414.1619	207.5846	**D**	**937.4738**	469.2405	920.4472	460.7272	919.4632	460.2352	**9**
6	489.1940	245.1006	471.1834	236.0953	**G**	**822.4468**	411.7271	805.4203	403.2138	804.4363	402.7218	**8**
7	576.2260	288.6166	558.2154	279.6114	**S**	**765.4254**	383.2163	748.3988	374.7030	747.4148	374.2110	**7**
8	663.2580	332.1326	645.2475	323.1274	**S**	**678.3933**	339.7003	661.3668	331.1870	660.3828	330.6950	**6**
9	810.3264	405.6669	792.3159	396.6616	**F**	**591.3613**	296.1843	574.3348	287.6710			**5**
10	909.3949	455.2011	891.3843	446.1958	**V**	**444.2929**	222.6501	427.2663	214.1368			**4**
11	1008.4633	504.7353	990.4527	495.7300	**V**	**345.2245**	173.1159	328.1979	164.6026			**3**
12	1079.5004	540.2538	1061.4898	531.2485	**A**	**246.1561**	123.5817	229.1295	115.0684			**2**
13					**R**	**175.1190**	88.0631	158.0924	79.5498			**1**





NCBI **BLAST** search of ASASDGSSFVVAR
(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	1252.6048	-0.0036	ASASDGSSFVVAR
2.4	1252.5969	0.0042	TGSKTDAVAEMK
0.9	1252.5718	0.0294	AGESVTLSCSSR

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

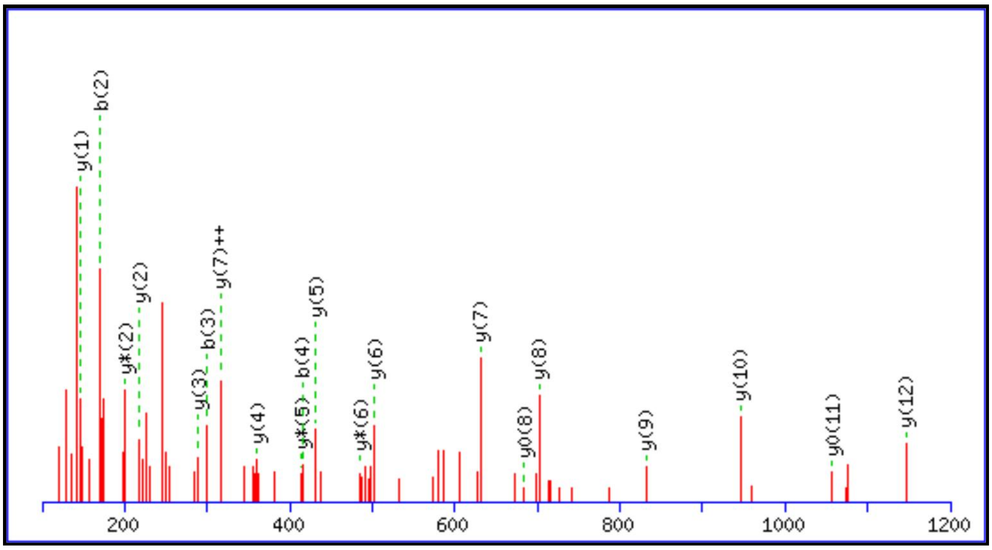
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VAEDEAEAAAAAK**
Found in **P08195|4F2_HUMAN**, 4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 PE=1 SV=3

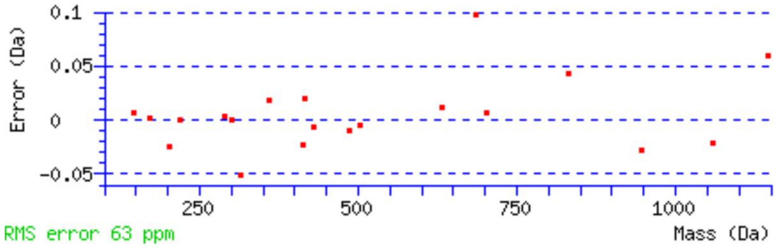
Match to Query 32969: 1244.606668 from(623.310610,2+)
Title: Locus:4.1.1.5813.3

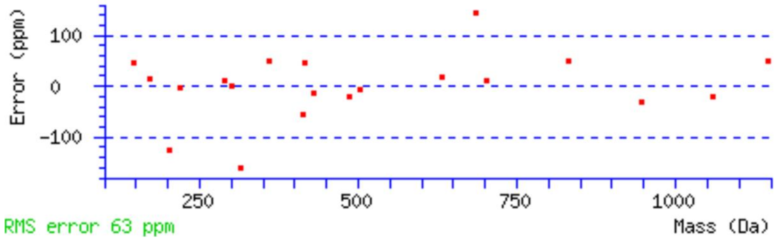
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1244.5884
Fixed modifications: Carbamidomethyl (C)
Ions Score: 59 **Expect:** 4.4e-005
Matches (Bold Red): 20/104 fragment ions using 56 most intense peaks

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415			**V**							**13**
2	**171.1128**	86.0600			**A**	**1146.5273**	573.7673	1129.5008	565.2540	1128.5168	564.7620	**12**
3	**300.1554**	150.5813	282.1448	141.5761	**E**	1075.4902	538.2487	1058.4637	529.7355	**1057.4796**	529.2435	**11**
4	**415.1823**	208.0948	397.1718	199.0895	**D**	**946.4476**	473.7274	929.4211	465.2142	928.4371	464.7222	**10**
5	544.2249	272.6161	526.2144	263.6108	**E**	**831.4207**	416.2140	814.3941	407.7007	813.4101	407.2087	**9**
6	615.2620	308.1347	597.2515	299.1294	**A**	**702.3781**	351.6927	685.3515	343.1794	**684.3675**	342.6874	**8**
7	744.3046	372.6560	726.2941	363.6507	**E**	**631.3410**	**316.1741**	614.3144	307.6608	613.3304	307.1688	**7**
8	815.3418	408.1745	797.3312	399.1692	**A**	**502.2984**	251.6528	**485.2718**	243.1396			**6**
9	886.3789	443.6931	868.3683	434.6878	**A**	**431.2613**	216.1343	**414.2347**	207.6210			**5**
10	957.4160	479.2116	939.4054	470.2063	**A**	**360.2241**	180.6157	343.1976	172.1024			**4**
11	1028.4531	514.7302	1010.4425	505.7249	**A**	**289.1870**	145.0972	272.1605	136.5839			**3**
12	1099.4902	550.2487	1081.4796	541.2435	**A**	**218.1499**	109.5786	**201.1234**	101.0653			**2**
13					**K**	**147.1128**	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.9	1244.5884	0.0183	VAEDEAEAAAAAK
5.2	1244.6473	-0.0406	TAELSLGRNER
4.5	1244.5932	0.0135	KSQAAPGSSPCR
4.3	1244.6361	-0.0294	TVTLDVDVNNR
2.2	1244.6547	-0.0480	SPSIMGILAANR
1.3	1244.6248	-0.0182	EDSVEAVGAQLK

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

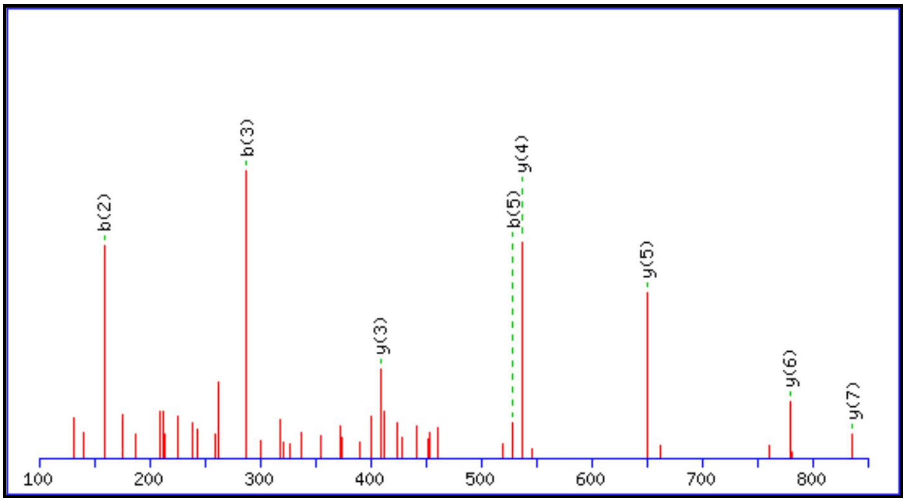
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TGEIQFSR**
Found in **Q86SJ6|DSG4_HUMAN**, Desmoglein-4 OS=Homo sapiens GN=DSG4 PE=1 SV=1

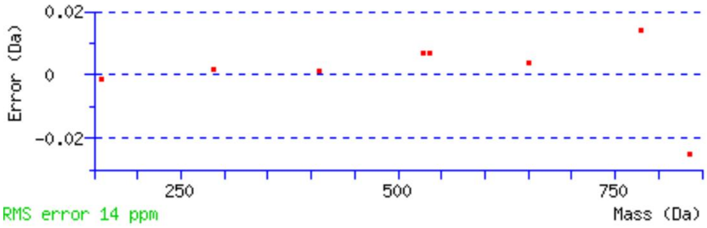
Match to Query 6637: 936.447428 from(469.230990,2+)
Title: Locus:13.1.1.6249.2

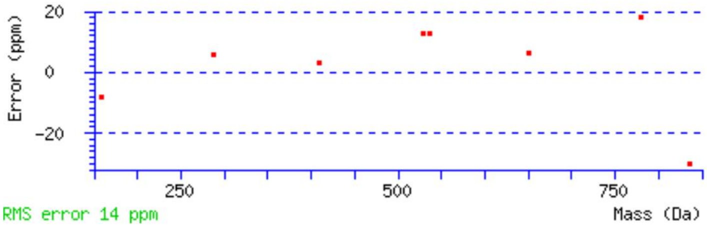
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 936.4665
Fixed modifications: Carbamidomethyl (C)
Ions Score: 52 **Expect:** 0.00045
Matches (Bold Red): 8/74 fragment ions using 9 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							8
2	**159.0764**	80.0418			141.0659	71.0366	G	**836.4261**	418.7167	819.3995	410.2034	818.4155	409.7114	7
3	**288.1190**	144.5631			270.1084	135.5579	E	**779.4046**	390.2060	762.3781	381.6927	761.3941	381.2007	6
4	401.2031	201.1052			383.1925	192.0999	I	**650.3620**	325.6847	633.3355	317.1714	632.3515	316.6794	5
5	**529.2617**	265.1345	512.2351	256.6212	511.2511	256.1292	Q	**537.2780**	269.1426	520.2514	260.6293	519.2674	260.1373	4
6	676.3301	338.6687	659.3035	330.1554	658.3195	329.6634	F	**409.2194**	205.1133	392.1928	196.6001	391.2088	196.1081	3
7	763.3621	382.1847	746.3355	373.6714	745.3515	373.1794	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
8							R	175.1190	88.0631	158.0924	79.5498			1





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

Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.2	936.4665	-0.0191	TGEIQFSR
16.9	936.4739	-0.0264	TWKLMDK
11.5	936.4222	0.0252	TVAEQDMK
6.1	936.4157	0.0317	MCNDLLR
5.5	936.4885	-0.0411	MGVLMSKR
5.1	936.4521	-0.0047	MLRQMDK
5.0	936.4665	-0.0190	TALENFSR
3.1	936.4777	-0.0303	SSSFRTPR
2.4	936.4149	0.0326	TGSESSVDR
2.0	936.4851	-0.0377	WTKSMLR

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

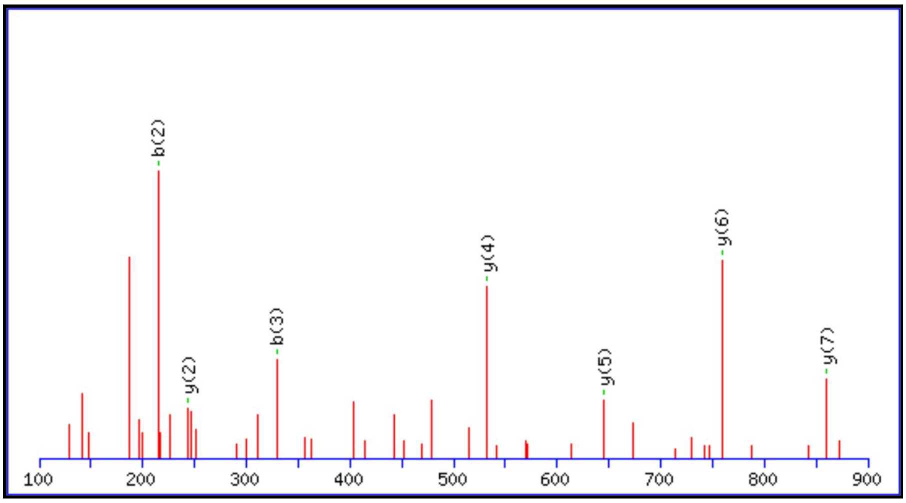
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITNIQCPK**
Found in **P80075|CCL8_HUMAN**, C-C motif chemokine 8 OS=Homo sapiens GN=CCL8 PE=1 SV=2

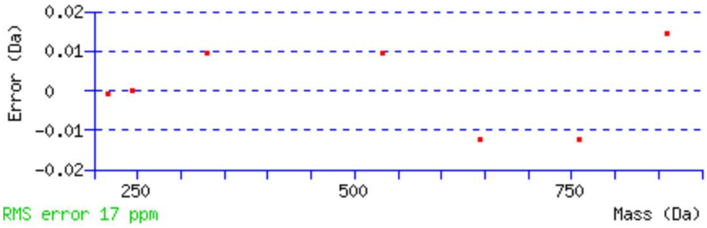
Match to Query 25315: 972.497628 from(487.256090,2+)
Title: Locus:13.1.1.5953.2

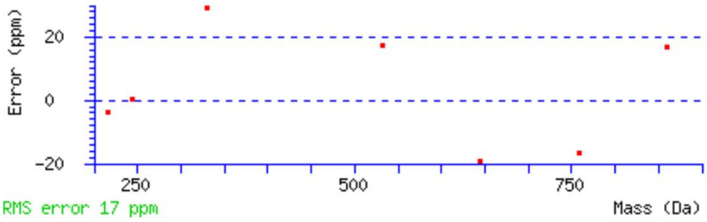
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 900 Da [Full range]



Monoisotopic mass of neutral peptide Mr(calc): 972.5062
Fixed modifications: Carbamidomethyl (C)
Ions Score: 52 **Expect:** 0.00026
Matches (Bold Red): 7/66 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	114.0913	57.5493					I							8
2	**215.1390**	108.0731			197.1285	99.0679	T	**860.4295**	430.7184	843.4029	422.2051	842.4189	421.7131	7
3	**329.1819**	165.0946	312.1554	156.5813	311.1714	156.0893	N	**759.3818**	380.1945	742.3552	371.6813			6
4	442.2660	221.6366	425.2395	213.1234	424.2554	212.6314	I	**645.3389**	323.1731	628.3123	314.6598			5
5	570.3246	285.6659	553.2980	277.1527	552.3140	276.6606	Q	**532.2548**	266.6310	515.2282	258.1178			4
6	730.3552	365.6813	713.3287	357.1680	712.3447	356.6760	C	404.1962	202.6017	387.1697	194.0885			3
7	827.4080	414.2076	810.3815	405.6944	809.3974	405.2024	P	**244.1656**	122.5864	227.1390	114.0731			2
8							K	147.1128	74.0600	130.0863	65.5468			1





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

Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.9	972.5062	-0.0086	ITNIQCPK
19.5	972.5240	-0.0264	LTNEVELR
16.4	972.5392	-0.0416	LTWNKSPK
11.3	972.5240	-0.0264	LTPEERTK
9.0	972.4989	-0.0012	LGTQSTGPGR
8.6	972.5240	-0.0264	TIIIEDNR
7.5	972.4988	-0.0012	EGGNQNKVK
6.8	972.4512	0.0464	VSNNAEDPK
6.6	972.4559	0.0417	NDVCRPGR
6.3	972.5352	-0.0376	ITGPSQRSK

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

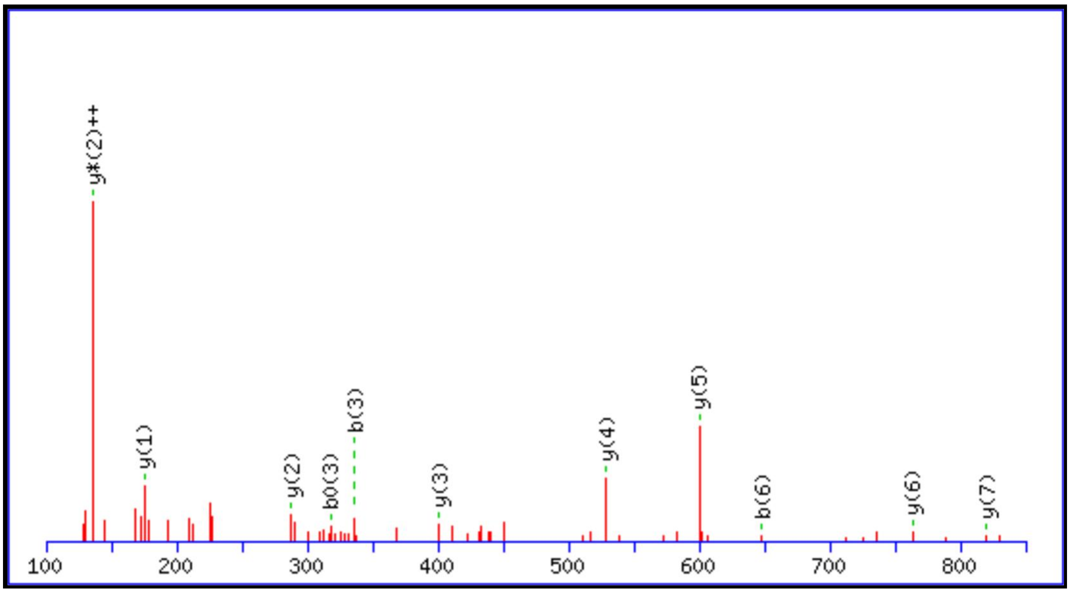
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DGYAQILR**
Found in **Q99798|ACON_HUMAN**, Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=2

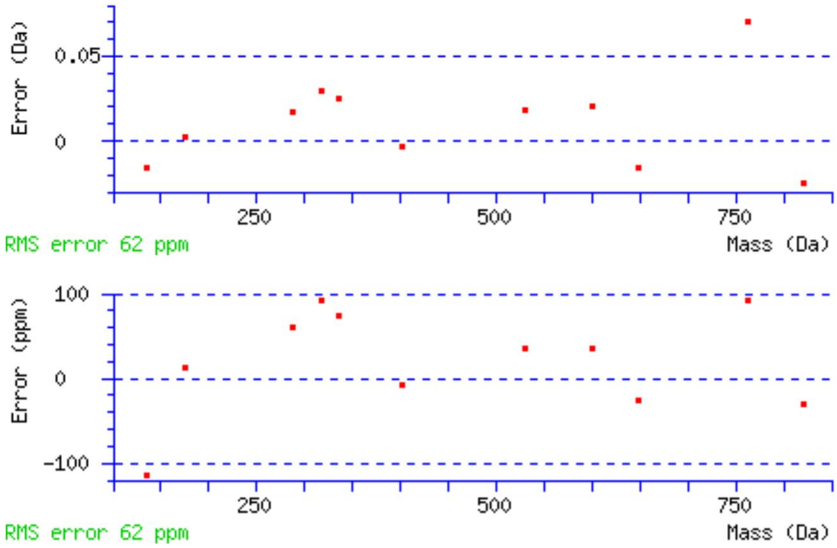
Match to Query 6622: 934.510468 from(468.262510,2+)
Title: Locus:4.1.1.6077.2

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 850 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 934.4872
Fixed modifications: Carbamidomethyl (C)
Ions Score: 50 **Expect:** 0.0012
Matches (Bold Red): 11/62 fragment ions using 23 most intense peaks

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	#
1	116.0342	58.5207			98.0237	49.5155	D					8
2	173.0557	87.0315			155.0451	78.0262	G	**820.4676**	410.7374	803.4410	402.2241	7
3	**336.1190**	168.5631			**318.1084**	159.5579	Y	**763.4461**	382.2267	746.4196	373.7134	6
4	407.1561	204.0817			389.1456	195.0764	A	**600.3828**	300.6950	583.3562	292.1817	5
5	535.2147	268.1110	518.1882	259.5977	517.2041	259.1057	Q	**529.3457**	265.1765	512.3191	256.6632	4
6	**648.2988**	324.6530	631.2722	316.1397	630.2882	315.6477	I	**401.2871**	201.1472	384.2605	192.6339	3
7	761.3828	381.1951	744.3563	372.6818	743.3723	372.1898	L	**288.2030**	144.6051	271.1765	**136.0919**	2
8							R	**175.1190**	88.0631	158.0924	79.5498	1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.6	934.4872	0.0233	DGYAQILR
18.6	934.4906	0.0199	DGKMSLLR
12.8	934.5236	-0.0131	NIEKYLR
11.5	934.4728	0.0377	AAMMNLLR
10.6	934.4906	0.0199	SCTSVILR
9.1	934.4728	0.0377	AAMMNLLR
8.2	934.4906	0.0199	GTMTGLALR
8.0	934.5236	-0.0131	VEQKYLR
7.8	934.5123	-0.0019	EEILYLR
7.8	934.5025	0.0080	FSLHYLR

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

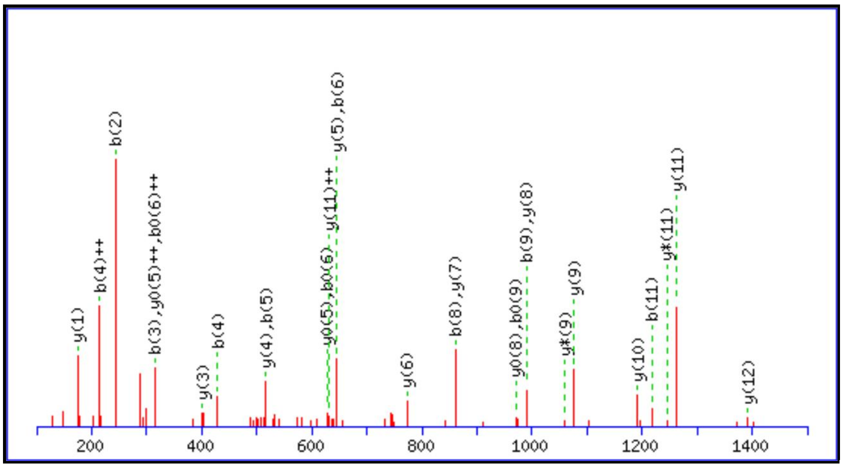
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IEADSESQEDIIR**
Found in **P55957|BID_HUMAN**, BH3-interacting domain death agonist OS=Homo sapiens GN=BID PE=1 SV=1

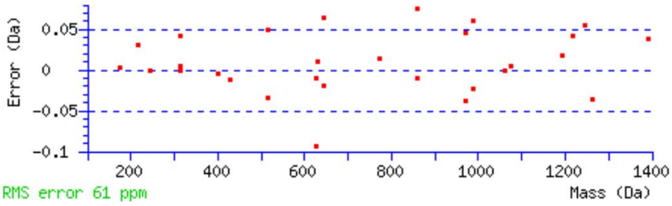
Match to Query 31634: 1503.681028 from(752.847790,2+)
Title: Locus:10.1.1.7036.2

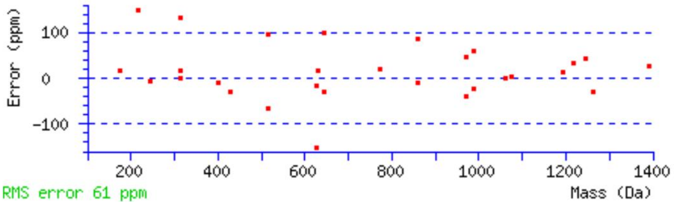
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1503.7052
Fixed modifications: Carbamidomethyl (C)
Ions Score: 103 **Expect:** 9.9e-010
Matches (Bold Red): 29/122 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	114.0913	57.5493					I							13
2	**243.1339**	122.0706			225.1234	113.0653	E	**1391.6285**	696.3179	1374.6019	687.8046	1373.6179	687.3126	12
3	**314.1710**	157.5892			296.1605	148.5839	A	**1262.5859**	**631.7966**	**1245.5594**	623.2833	1244.5753	622.7913	11
4	**429.1980**	**215.1026**			411.1874	206.0974	D	**1191.5488**	596.2780	1174.5222	587.7648	1173.5382	587.2727	10
5	**516.2300**	258.6186			498.2195	249.6134	S	**1076.5218**	538.7646	**1059.4953**	530.2513	1058.5113	529.7593	9
6	**645.2726**	323.1399			**627.2620**	**314.1347**	E	**989.4898**	495.2485	972.4633	486.7353	**971.4792**	486.2433	8
7	732.3046	366.6560			714.2941	357.6507	S	**860.4472**	430.7272	843.4207	422.2140	842.4367	421.7220	7
8	**860.3632**	430.6852	843.3367	422.1720	842.3527	421.6800	Q	**773.4152**	387.2112	756.3886	378.6980	755.4046	378.2060	6
9	**989.4058**	495.2065	972.3793	486.6933	**971.3952**	486.2013	E	**645.3566**	323.1819	628.3301	314.6687	**627.3461**	**314.1767**	5
10	1104.4328	552.7200	1087.4062	544.2067	1086.4222	543.7147	D	**516.3140**	258.6606	499.2875	250.1474	498.3035	249.6554	4
11	**1217.5168**	609.2620	1200.4903	600.7488	1199.5063	600.2568	I	**401.2871**	201.1472	384.2605	192.6339			3
12	1330.6009	665.8041	1313.5743	657.2908	1312.5903	656.7988	I	288.2030	144.6051	271.1765	136.0919			2
13							R	**175.1190**	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
103.2	1503.7052	-0.0242	IEADSESQEDIIR

18.6	1503.7239	-0.0428	LEAAETLEECALR
15.6	1503.7239	-0.0428	ELAMKAESGPNETK
14.2	1503.7165	-0.0354	KNSGEEEIDSLQR
7.8	1503.6446	0.0364	ELCAGPACNEVER
5.1	1503.7239	-0.0429	SDLIDQMNASGPIK
3.5	1503.7392	-0.0581	LEFDINICDLPR
3.2	1503.6915	-0.0105	IYSAYMDKASDPK
3.1	1503.7529	-0.0719	LTVSQGNTSVQQDK
2.1	1503.7464	-0.0653	NEGQRMETLTGLR

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

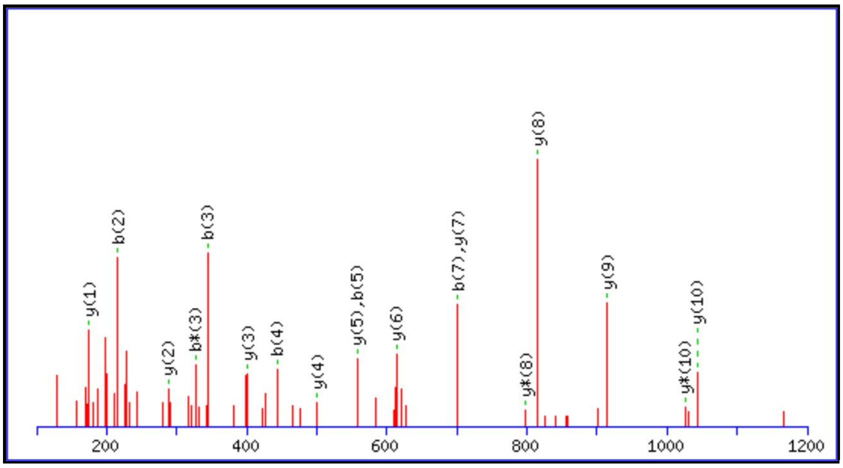
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TNQVNSGGVLLR**
Found in **P02747|C1QC_HUMAN**, Complement C1q subcomponent subunit C OS=Homo sapiens GN=C1QC PE=1 SV=3

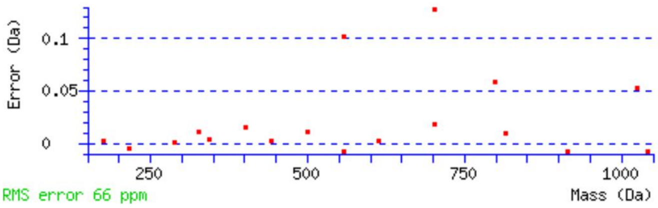
Match to Query 12934: 1256.650428 from(629.332490,2+)
Title: Locus:10.1.1.7000.2

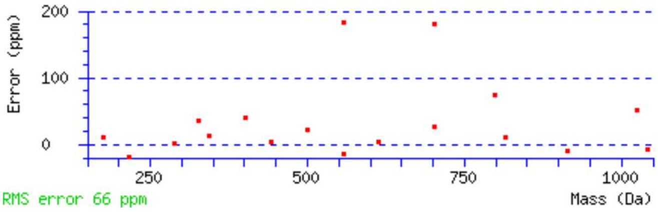
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1256.6837
Fixed modifications: Carbamidomethyl (C)
Ions Score: 103 **Expect:** 3.7e-009
Matches (Bold Red): 18/118 fragment ions using 21 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							12
2	**216.0979**	108.5526	199.0713	100.0393	198.0873	99.5473	N	1156.6433	578.8253	1139.6167	570.3120	1138.6327	569.8200	11
3	**344.1565**	172.5819	**327.1299**	164.0686	326.1459	163.5766	Q	**1042.6004**	521.8038	**1025.5738**	513.2905	1024.5898	512.7985	10
4	**443.2249**	222.1161	426.1983	213.6028	425.2143	213.1108	V	**914.5418**	457.7745	897.5152	449.2613	896.5312	448.7693	9
5	**557.2678**	279.1375	540.2413	270.6243	539.2572	270.1323	N	**815.4734**	408.2403	**798.4468**	399.7271	797.4628	399.2350	8
6	644.2998	322.6536	627.2733	314.1403	626.2893	313.6483	S	**701.4304**	351.2189	684.4039	342.7056	683.4199	342.2136	7
7	**701.3213**	351.1643	684.2947	342.6510	683.3107	342.1590	G	**614.3984**	307.7028	597.3719	299.1896			6
8	758.3428	379.6750	741.3162	371.1617	740.3322	370.6697	G	**557.3770**	279.1921	540.3504	270.6788			5
9	857.4112	429.2092	840.3846	420.6959	839.4006	420.2039	V	**500.3555**	250.6814	483.3289	242.1681			4
10	970.4952	485.7513	953.4687	477.2380	952.4847	476.7460	L	**401.2871**	201.1472	384.2605	192.6339			3
11	1083.5793	542.2933	1066.5528	533.7800	1065.5687	533.2880	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 TNQVNSGGVLLR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
103.2	1256.6837	-0.0333	TNQVNSGGVLLR
43.7	1256.6586	-0.0081	ASGAGGVGGGGGGKIR

14.5	1256.7023	-0.0519	QSLMKLERPR
11.8	1256.6336	0.0169	MLAPSGSPGVWR
6.9	1256.7088	-0.0584	DEVVKIQSLAR
6.9	1256.6109	0.0395	EPETNVAEGRR
6.3	1256.6514	-0.0009	VWQTVSPVEGR
6.3	1256.6837	-0.0332	TNQEIREIVR
5.1	1256.6724	-0.0220	QVQEKEDLLR
4.5	1256.5932	0.0573	DVNNHSMTAIR

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

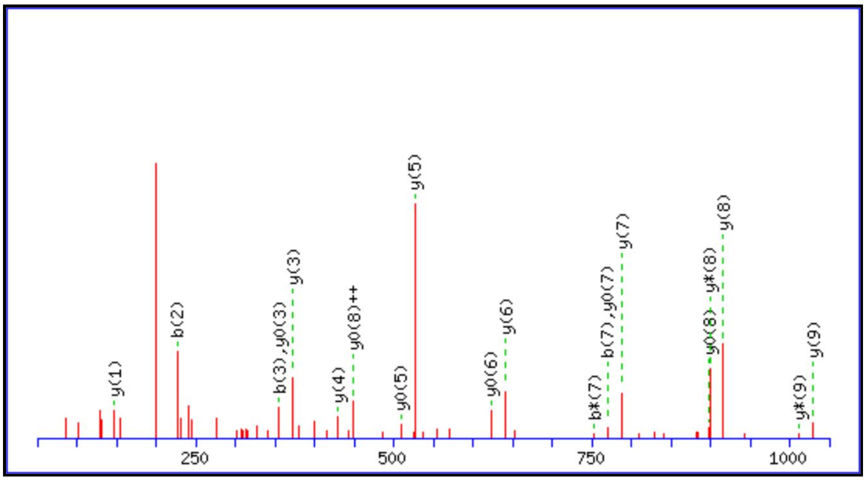
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIQFNPGPEK**
Found in **P46926|GNPI1_HUMAN**, Glucosamine-6-phosphate isomerase 1 OS=Homo sapiens GN=GNPDA1 PE=1 SV=1

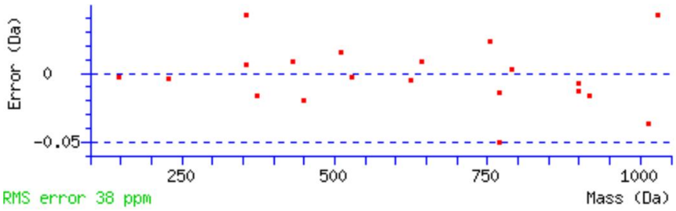
Match to Query 26541: 1141.596228 from(571.805390,2+)
Title: Locus:8.1.1.6743.2

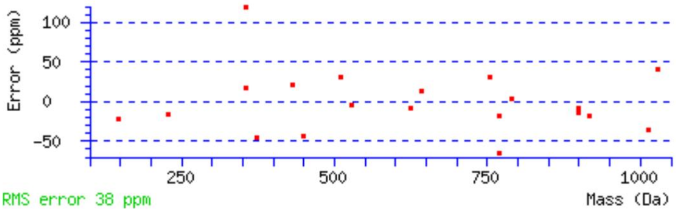
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 50 to 1050 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1141.6131
Fixed modifications: Carbamidomethyl (C)
Ions Score: 74 **Expect:** 1.5e-006
Matches (Bold Red): 20/86 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	114.0913	57.5493					I							10
2	**227.1754**	114.0913					I	**1029.5364**	515.2718	**1012.5098**	506.7585	1011.5258	506.2665	9
3	**355.2340**	178.1206	338.2074	169.6074			Q	**916.4523**	458.7298	**899.4258**	450.2165	**898.4417**	**449.7245**	8
4	502.3024	251.6548	485.2758	243.1416			F	**788.3937**	394.7005	771.3672	386.1872	**770.3832**	385.6952	7
5	616.3453	308.6763	599.3188	300.1630			N	**641.3253**	321.1663	624.2988	312.6530	**623.3148**	312.1610	6
6	713.3981	357.2027	696.3715	348.6894			P	**527.2824**	264.1448	510.2558	255.6316	**509.2718**	255.1396	5
7	**770.4196**	385.7134	**753.3930**	377.2001			G	**430.2296**	215.6185	413.2031	207.1052	412.2191	206.6132	4
8	867.4723	434.2398	850.4458	425.7265			P	**373.2082**	187.1077	356.1816	178.5944	**355.1976**	178.1024	3
9	996.5149	498.7611	979.4884	490.2478	978.5043	489.7558	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 IIQFNPGPEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
73.8	1141.6131	-0.0169	IIQFNPGPEK
28.1	1141.6455	-0.0492	IIQENERLK
19.4	1141.6342	-0.0380	LIKTENPAEK
19.4	1141.6203	-0.0241	LLQDNQRQK
11.9	1141.6019	-0.0057	LLFSADVSYK
8.3	1141.6091	-0.0129	ILKNAESDPR
6.0	1141.6416	-0.0454	ILVEEMAPLK
6.0	1141.6416	-0.0454	LLAIMPDELK
5.3	1141.5437	0.0525	HLMEKDPEK
4.5	1141.6343	-0.0381	EPTLVTGLQGK

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

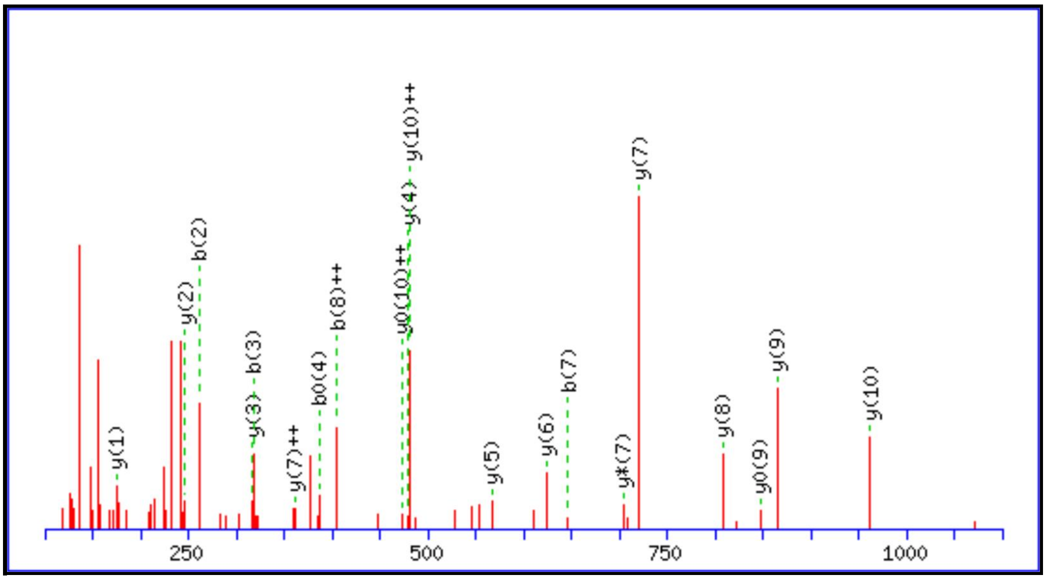
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YPGSPGSYAAR**
Found in **Q16769|QPCT_HUMAN**, Glutaminyl-peptide cyclotransferase OS=Homo sapiens GN=QPCT PE=1 SV=1

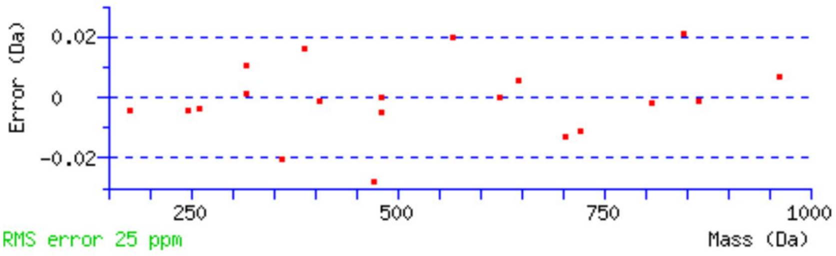
Match to Query 26058: 1124.514708 from(563.264630,2+)
Title: Locus:6.1.1.6100.2

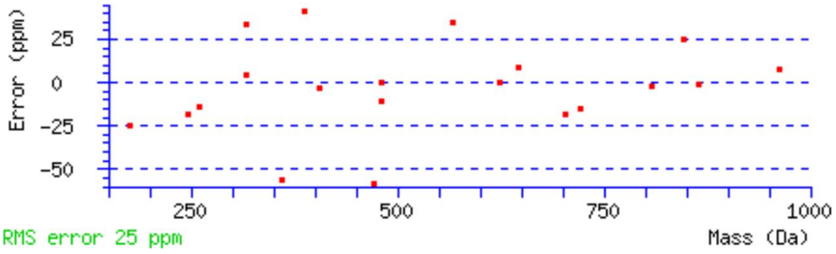
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1124.5251
Fixed modifications: Carbamidomethyl (C)
Ions Score: 70 **Expect:** 2.4e-006
Matches (Bold Red): 21/86 fragment ions using 43 most intense peaks

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389			Y							11
2	**261.1234**	131.0653			P	**962.4690**	**481.7381**	945.4425	473.2249	944.4585	**472.7329**	10
3	**318.1448**	159.5761			G	**865.4163**	433.2118	848.3897	424.6985	**847.4057**	424.2065	9
4	**405.1769**	203.0921	**387.1663**	194.0868	S	**808.3948**	404.7010	791.3682	396.1878	790.3842	395.6958	8
5	502.2296	251.6185	484.2191	242.6132	P	**721.3628**	**361.1850**	**704.3362**	352.6717	703.3522	352.1797	7
6	559.2511	280.1292	541.2405	271.1239	G	**624.3100**	312.6586	607.2835	304.1454	606.2994	303.6534	6
7	**646.2831**	323.6452	628.2726	314.6399	S	**567.2885**	284.1479	550.2620	275.6346	549.2780	275.1426	5
8	809.3464	**405.1769**	791.3359	396.1716	Y	**480.2565**	240.6319	463.2300	232.1186			4
9	880.3836	440.6954	862.3730	431.6901	A	**317.1932**	159.1002	300.1666	150.5870			3
10	951.4207	476.2140	933.4101	467.2087	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 YPGSPGSYAAR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
69.9	1124.5251	-0.0103	YPGSPGSYAAR
19.7	1124.5067	0.0081	MLGSRDMGAR
14.3	1124.5363	-0.0216	GYPSPGAHSPR
10.3	1124.5033	0.0114	EMGSQPHSPR
5.3	1124.4808	0.0339	YPEMDLDSR
5.0	1124.5570	-0.0423	LMVTMLTER
4.0	1124.5462	-0.0315	EEQVHLENK
2.9	1124.5648	-0.0501	KLYIDSCAR
2.0	1124.5172	-0.0025	MEAYEQVQK
1.4	1124.5141	0.0007	MIRDGCVMK

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

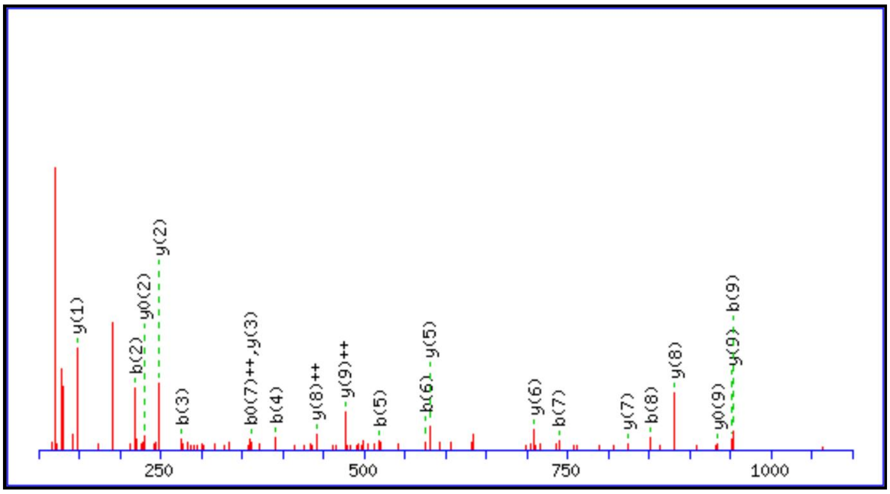
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FAGDKGYLTK**
Found in **P60903|S10AA_HUMAN**, Protein S100-A10 OS=Homo sapiens GN=S100A10 PE=1 SV=2

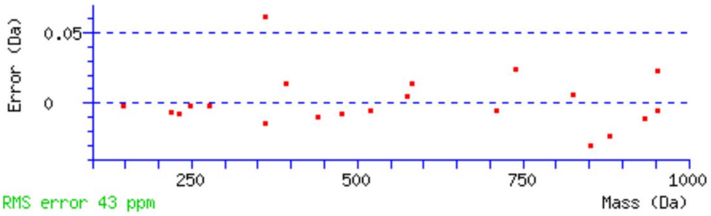
Match to Query 25371: 1098.529168 from(550.271860,2+)
Title: Locus:14.1.1.5894.3

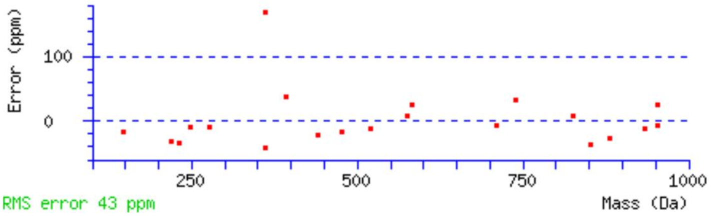
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1098.5710
Fixed modifications: Carbamidomethyl (C)
Ions Score: 53 **Expect:** 0.00014
Matches (Bold Red): 21/92 fragment ions using 44 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.0757	74.5415					F							10
2	**219.1128**	110.0600					A	**952.5098**	**476.7586**	935.4833	468.2453	**934.4993**	467.7533	9
3	**276.1343**	138.5708					G	**881.4727**	**441.2400**	864.4462	432.7267	863.4621	432.2347	8
4	**391.1612**	196.0842			373.1506	187.0790	D	**824.4512**	412.7293	807.4247	404.2160	806.4407	403.7240	7
5	**519.2562**	260.1317	502.2296	251.6185	501.2456	251.1264	K	**709.4243**	355.2158	692.3978	346.7025	691.4137	346.2105	6
6	**576.2776**	288.6425	559.2511	280.1292	558.2671	279.6372	G	**581.3293**	291.1683	564.3028	282.6550	563.3188	282.1630	5
7	**739.3410**	370.1741	722.3144	361.6608	721.3304	**361.1688**	Y	524.3079	262.6576	507.2813	254.1443	506.2973	253.6523	4
8	**852.4250**	426.7162	835.3985	418.2029	834.4145	417.7109	L	**361.2445**	181.1259	344.2180	172.6126	343.2340	172.1206	3
9	**953.4727**	477.2400	936.4462	468.7267	935.4621	468.2347	T	**248.1605**	124.5839	231.1339	116.0706	**230.1499**	115.5786	2
10							K	**147.1128**	74.0600	130.0863	65.5468			1





NCBI **BLAST** search of FAGDKGYLTK

(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	1098.5710	-0.0418	FAGDKGYLTK
21.1	1098.5492	-0.0200	MVSGAGISHPK
18.6	1098.4903	0.0389	MATFEIDEK
15.2	1098.4941	0.0350	HEQEGKDEK
8.8	1098.5743	-0.0452	VSGKMSTVFK
7.3	1098.5557	-0.0265	EVNGIPVEDK
6.7	1098.5015	0.0276	FAQDSEMKK
5.4	1098.5015	0.0276	ELRMYDEK
5.4	1098.5597	-0.0305	AFELSYLEK
5.1	1098.5379	-0.0088	MDPLHTIEK

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

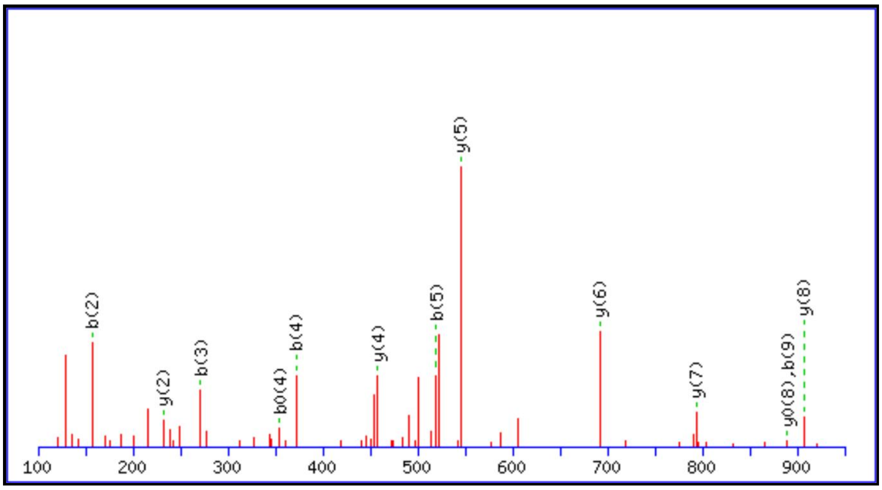
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVNTFSPEGR**
Found in **P28066|PSA5_HUMAN**, Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3

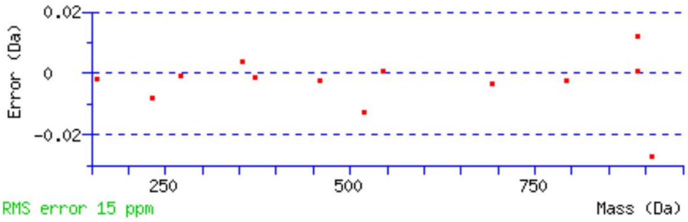
Match to Query 24206: 1062.484188 from(532.249370,2+)
Title: Locus:9.1.1.6569.3

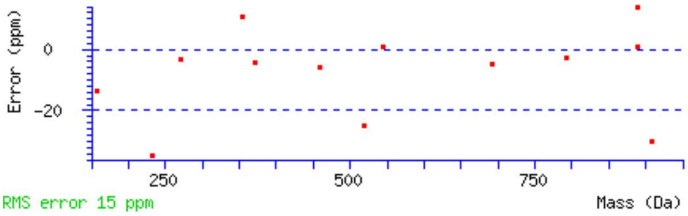
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1062.5094
Fixed modifications: Carbamidomethyl (C)
Ions Score: 52 **Expect:** 0.00014
Matches (Bold Red): 13/94 fragment ions using 18 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							10
2	**157.0972**	79.0522					V	1006.4952	503.7513	989.4687	495.2380	988.4847	494.7460	9
3	**271.1401**	136.0737	254.1135	127.5604			N	**907.4268**	454.2170	890.4003	445.7038	**889.4163**	445.2118	8
4	**372.1878**	186.5975	355.1612	178.0842	**354.1772**	177.5922	T	**793.3839**	397.1956	776.3573	388.6823	775.3733	388.1903	7
5	**519.2562**	260.1317	502.2296	251.6185	501.2456	251.1264	F	**692.3362**	346.6717	675.3097	338.1585	674.3257	337.6665	6
6	606.2882	303.6477	589.2617	295.1345	588.2776	294.6425	S	**545.2678**	273.1375	528.2413	264.6243	527.2572	264.1323	5
7	703.3410	352.1741	686.3144	343.6608	685.3304	343.1688	P	**458.2358**	229.6215	441.2092	221.1083	440.2252	220.6162	4
8	832.3836	416.6954	815.3570	408.1821	814.3730	407.6901	E	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	3
9	**889.4050**	445.2061	872.3785	436.6929	871.3945	436.2009	G	**232.1404**	116.5738	215.1139	108.0606			2
10							R	175.1190	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of GVNTFSPEGR

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.5	1062.5094	-0.0252	GVNTFSPEGR
20.5	1062.5094	-0.0252	GAKDFASDPR
14.8	1062.5128	-0.0286	KALTEECGR
14.7	1062.5280	-0.0438	RAAMDFPGAK
14.5	1062.5305	-0.0463	QLSESEKSR
11.4	1062.5128	-0.0286	NKEMEQLR
10.6	1062.4764	0.0078	AAMSASSEGPR
8.4	1062.4876	-0.0034	RLMQDDNR
8.3	1062.4730	0.0112	AKGDEDWSR
5.5	1062.5128	-0.0286	NQELLSMGR

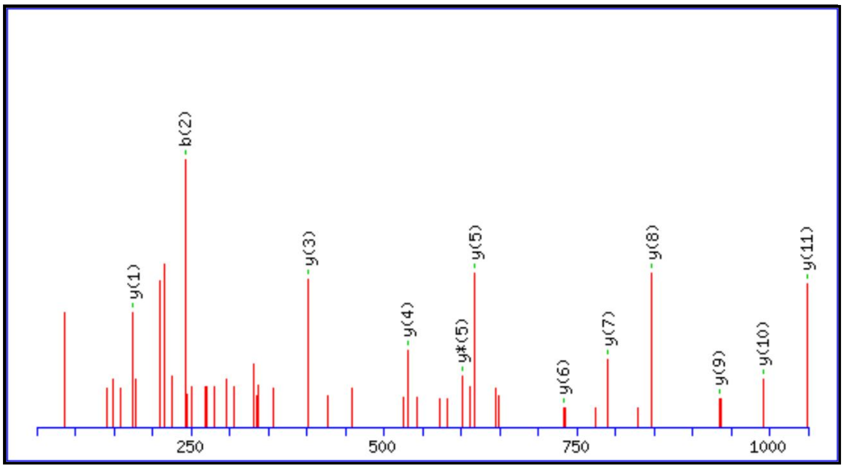
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEGGSGGDSEVQR**
Found in **P62195|PRS8_HUMAN**, 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1

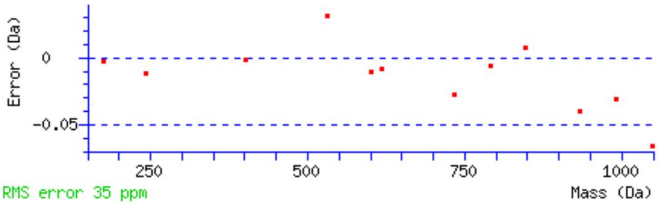
Match to Query 25155: 1289.583588 from(645.799070,2+)
Title: Locus:10.1.1.4947.2

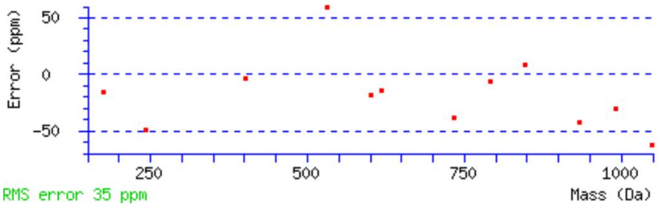
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 50 to 1050 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1289.5848
Fixed modifications: Carbamidomethyl (C)
Ions Score: 78 **Expect:** 2.9e-007
Matches (Bold Red): 12/114 fragment ions using 24 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	**243.1339**	122.0706			225.1234	113.0653	E	1177.5080	589.2576	1160.4814	580.7444	1159.4974	580.2523	12
3	300.1554	150.5813			282.1448	141.5761	G	**1048.4654**	524.7363	1031.4388	516.2231	1030.4548	515.7311	11
4	357.1769	179.0921			339.1663	170.0868	G	**991.4439**	496.2256	974.4174	487.7123	973.4334	487.2203	10
5	444.2089	222.6081			426.1983	213.6028	S	**934.4225**	467.7149	917.3959	459.2016	916.4119	458.7096	9
6	501.2304	251.1188			483.2198	242.1135	G	**847.3904**	424.1989	830.3639	415.6856	829.3799	415.1936	8
7	558.2518	279.6295			540.2413	270.6243	G	**790.3690**	395.6881	773.3424	387.1748	772.3584	386.6828	7
8	673.2788	337.1430			655.2682	328.1377	D	**733.3475**	367.1774	716.3210	358.6641	715.3369	358.1721	6
9	760.3108	380.6590			742.3002	371.6537	S	**618.3206**	309.6639	**601.2940**	301.1506	600.3100	300.6586	5
10	889.3534	445.1803			871.3428	436.1750	E	**531.2885**	266.1479	514.2620	257.6346	513.2780	257.1426	4
11	988.4218	494.7145			970.4112	485.7093	V	**402.2459**	201.6266	385.2194	193.1133			3
12	1116.4804	558.7438	1099.4538	550.2305	1098.4698	549.7385	Q	303.1775	152.0924	286.1510	143.5791			2
13							R	**175.1190**	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
78.0	1289.5848	-0.0012	LEGGSGGDSEVQR

10.5	1289.6397	-0.0562	ELLEQMERAR
0.2	1289.6398	-0.0562	KNIDALSGMEGR

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

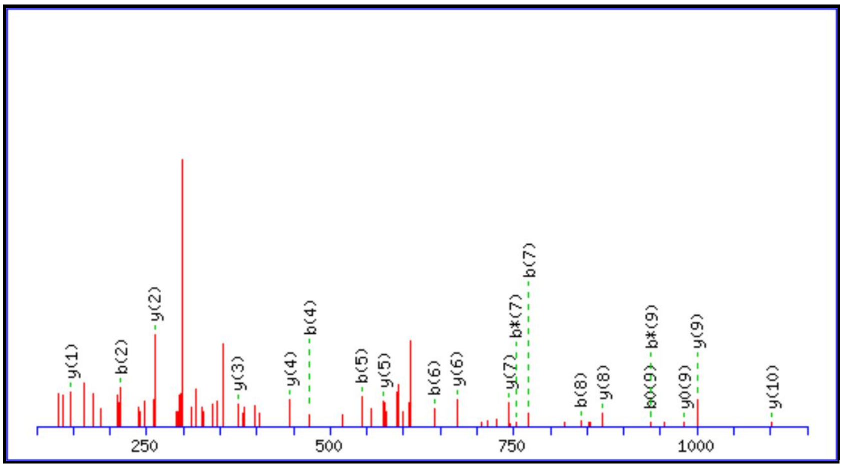
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTEQAVQAINK**
Found in **Q9BRF8|CPPED_HUMAN**, Calcineurin-like phosphoesterase domain-containing protein 1 OS=Homo sapiens GN=CPPED1 PE=1 SV=3

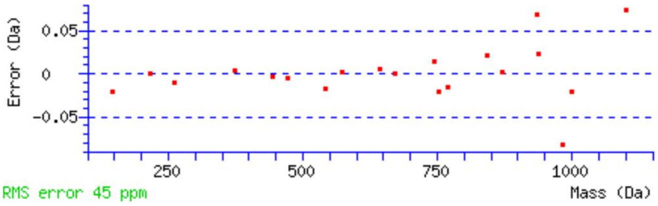
Match to Query 24134: 1213.655728 from(607.835140,2+)
Title: Locus:11.1.1.5300.2

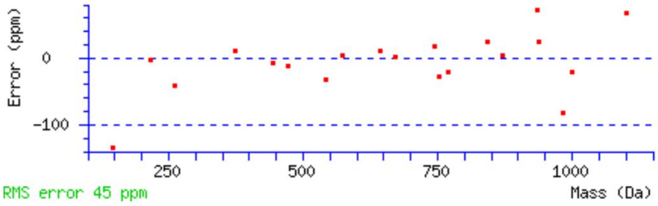
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1150 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1213.6666
Fixed modifications: Carbamidomethyl (C)
Ions Score: 59 **Expect:** 4.3e-005
Matches (Bold Red): 20/96 fragment ions using 49 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							11
2	**215.1390**	108.0731			197.1285	99.0679	T	**1101.5899**	551.2986	1084.5633	542.7853	1083.5793	542.2933	10
3	344.1816	172.5944			326.1710	163.5892	E	**1000.5422**	500.7747	983.5156	492.2615	**982.5316**	491.7694	9
4	**472.2402**	236.6237	455.2136	228.1105	454.2296	227.6185	Q	**871.4996**	436.2534	854.4730	427.7402			8
5	**543.2773**	272.1423	526.2508	263.6290	525.2667	263.1370	A	**743.4410**	372.2241	726.4145	363.7109			7
6	**642.3457**	321.6765	625.3192	313.1632	624.3352	312.6712	V	**672.4039**	336.7056	655.3774	328.1923			6
7	**770.4043**	385.7058	**753.3777**	377.1925	752.3937	376.7005	Q	**573.3355**	287.1714	556.3089	278.6581			5
8	**841.4414**	421.2243	824.4149	412.7111	823.4308	412.2191	A	**445.2769**	223.1421	428.2504	214.6288			4
9	954.5255	477.7664	**937.4989**	469.2531	**936.5149**	468.7611	I	**374.2398**	187.6235	357.2132	179.1103			3
10	1068.5684	534.7878	1051.5419	526.2746	1050.5578	525.7826	N	**261.1557**	131.0815	244.1292	122.5682			2
11							K	**147.1128**	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.9	1213.6666	-0.0109	LTEQAVQAINK
5.5	1213.7005	-0.0448	LLFNALKHMK

5.4	1213.7030	-0.0473	ITDDQLKILR
3.6	1213.6778	-0.0221	LQAEISQAARK
3.4	1213.6051	0.0506	LTNSRHGETTV
2.7	1213.6051	0.0506	QEPNGNSKVNK
0.0	1213.6666	-0.0109	LQQKVDELNK

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

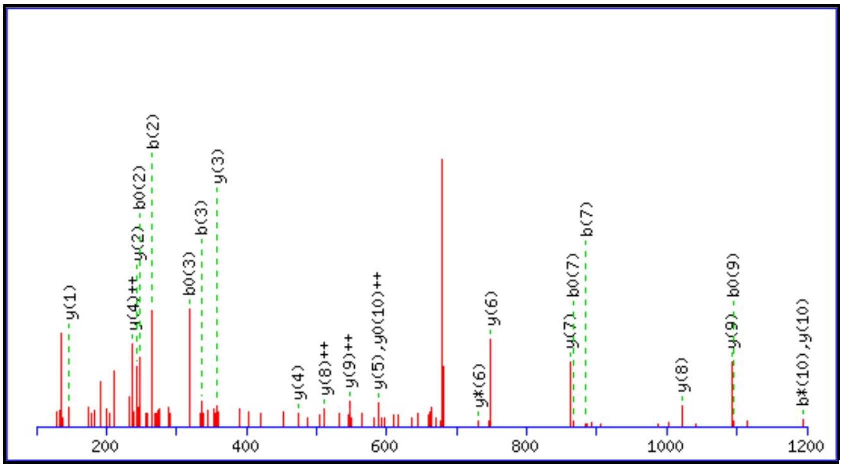
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YTACLCDDNPK**
Found in **P12273|PIP_HUMAN**, Prolactin-inducible protein OS=Homo sapiens GN=PIP PE=1 SV=1

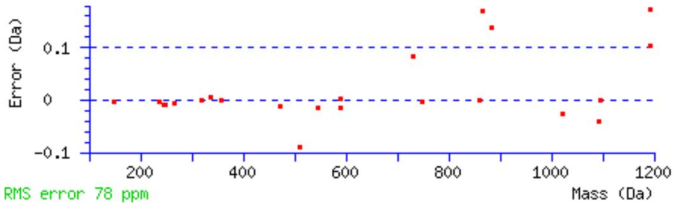
Match to Query 26108: 1355.557268 from(678.785910,2+)
Title: Locus:13.1.1.4919.2

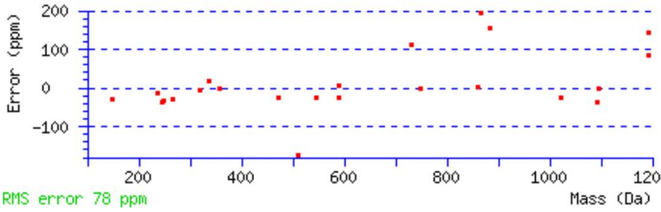
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1355.5486
Fixed modifications: Carbamidomethyl (C)
Ions Score: 56 **Expect:** 2e-005
Matches (Bold Red): 23/96 fragment ions using 51 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	164.0706	82.5389					Y							11
2	**265.1183**	133.0628			**247.1077**	124.0575	T	**1193.4925**	597.2499	1176.4660	588.7366	1175.4820	**588.2446**	10
3	**336.1554**	168.5813			**318.1448**	159.5761	A	**1092.4449**	**546.7261**	1075.4183	538.2128	1074.4343	537.7208	9
4	496.1860	248.5967			478.1755	239.5914	C	**1021.4077**	**511.2075**	1004.3812	502.6942	1003.3972	502.2022	8
5	609.2701	305.1387			591.2595	296.1334	L	**861.3771**	431.1922	844.3505	422.6789	843.3665	422.1869	7
6	769.3008	385.1540			751.2902	376.1487	C	**748.2930**	374.6502	**731.2665**	366.1369	730.2825	365.6449	6
7	**884.3277**	442.6675			**866.3171**	433.6622	D	**588.2624**	294.6348	571.2358	286.1216	570.2518	285.6295	5
8	999.3546	500.1810			981.3441	491.1757	D	**473.2354**	**237.1214**	456.2089	228.6081	455.2249	228.1161	4
9	1113.3976	557.2024	1096.3710	548.6892	**1095.3870**	548.1971	N	**358.2085**	179.6079	341.1819	171.0946			3
10	1210.4503	605.7288	**1193.4238**	597.2155	1192.4398	596.7235	P	**244.1656**	122.5864	227.1390	114.0731			2
11							K	**147.1128**	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.2	1355.5486	0.0087	YTACLCDDNPK

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

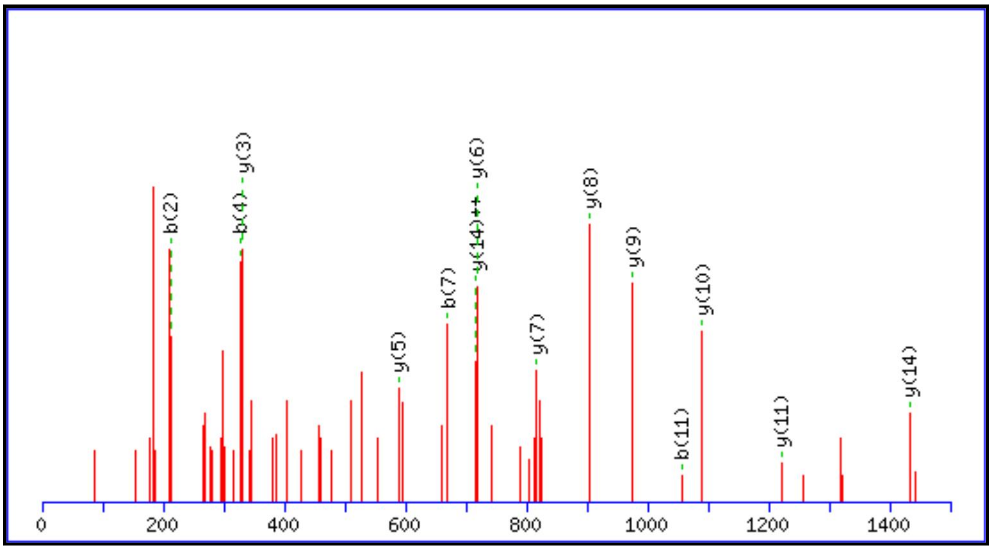
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LVGGPMDASVEEEGVR**
Found in **P01034|CYTC_HUMAN**, Cystatin-C OS=Homo sapiens GN=CST3 PE=1 SV=1

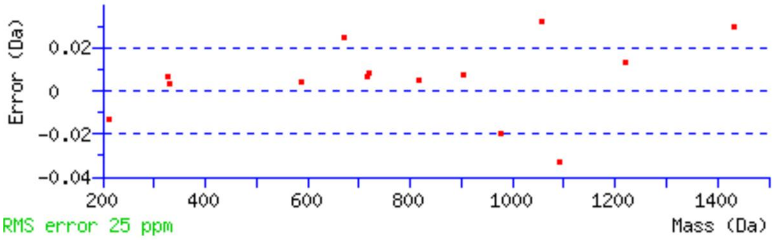
Match to Query 28165: 1643.777268 from(822.895910,2+)
Title: Locus:14.1.1.5320.3

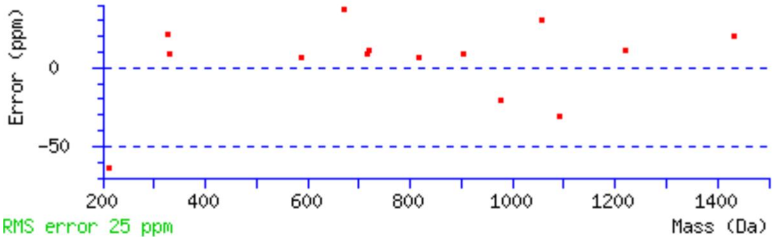
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 1500 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1643.7825
Fixed modifications: Carbamidomethyl (C)
Ions Score: 54 **Expect:** 0.0001
Matches (Bold Red): 14/132 fragment ions using 26 most intense peaks

#	b	b^{++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	114.0913	57.5493			L							16
2	**213.1598**	107.0835			V	1531.7057	766.3565	1514.6792	757.8432	1513.6951	757.3512	15
3	270.1812	135.5942			G	**1432.6373**	**716.8223**	1415.6107	708.3090	1414.6267	707.8170	14
4	**327.2027**	164.1050			G	1375.6158	688.3115	1358.5893	679.7983	1357.6053	679.3063	13
5	424.2554	212.6314			P	1318.5944	659.8008	1301.5678	651.2875	1300.5838	650.7955	12
6	555.2959	278.1516			M	**1221.5416**	611.2744	1204.5150	602.7612	1203.5310	602.2692	11
7	**670.3229**	335.6651	652.3123	326.6598	D	**1090.5011**	545.7542	1073.4746	537.2409	1072.4905	536.7489	10
8	741.3600	371.1836	723.3494	362.1783	A	**975.4742**	488.2407	958.4476	479.7274	957.4636	479.2354	9
9	828.3920	414.6996	810.3815	405.6944	S	**904.4371**	452.7222	887.4105	444.2089	886.4265	443.7169	8
10	927.4604	464.2339	909.4499	455.2286	V	**817.4050**	409.2061	800.3785	400.6929	799.3945	400.2009	7
11	**1056.5030**	528.7551	1038.4925	519.7499	E	**718.3366**	359.6719	701.3101	351.1587	700.3260	350.6667	6
12	1185.5456	593.2764	1167.5351	584.2712	E	**589.2940**	295.1506	572.2675	286.6374	571.2835	286.1454	5
13	1314.5882	657.7977	1296.5776	648.7925	E	460.2514	230.6293	443.2249	222.1161	442.2409	221.6241	4
14	1371.6097	686.3085	1353.5991	677.3032	G	**331.2088**	166.1081	314.1823	157.5948			3
15	1470.6781	735.8427	1452.6675	726.8374	V	274.1874	137.5973	257.1608	129.0840			2
16					R	175.1190	88.0631	158.0924	79.5498			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.7	1643.7825	-0.0052	LVGGPMDASVEEEGVR

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

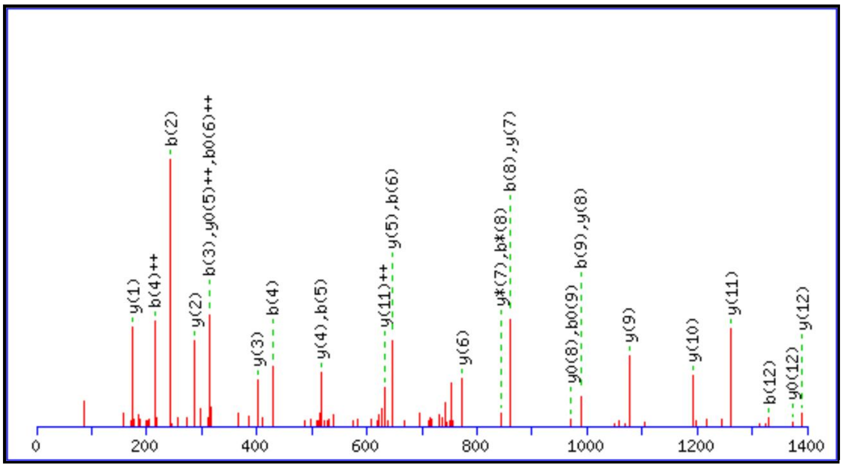
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **IEADSESQEDIIR**
Found in **P55957|BID_HUMAN**, BH3-interacting domain death agonist OS=Homo sapiens GN=BID PE=1 SV=1

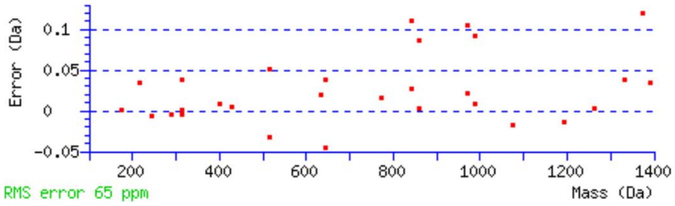
Match to Query 25637: 1503.713468 from(752.864010,2+)
Title: Locus:14.1.1.5184.3

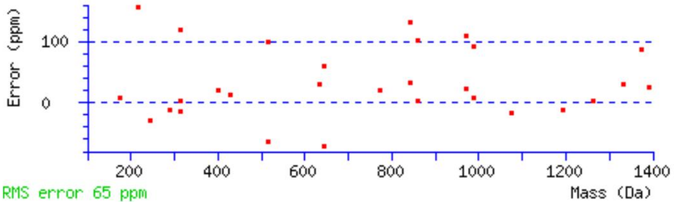
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 1400 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1503.7052
Fixed modifications: Carbamidomethyl (C)
Ions Score: 117 **Expect:** 5.4e-011
Matches (Bold Red): 29/122 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	114.0913	57.5493					**I**							**13**
2	**243.1339**	122.0706			225.1234	113.0653	**E**	**1391.6285**	696.3179	1374.6019	687.8046	**1373.6179**	687.3126	**12**
3	**314.1710**	157.5892			296.1605	148.5839	**A**	**1262.5859**	**631.7966**	1245.5594	623.2833	1244.5753	622.7913	**11**
4	**429.1980**	**215.1026**			411.1874	206.0974	**D**	**1191.5488**	596.2780	1174.5222	587.7648	1173.5382	587.2727	**10**
5	**516.2300**	258.6186			498.2195	249.6134	**S**	**1076.5218**	538.7646	1059.4953	530.2513	1058.5113	529.7593	**9**
6	**645.2726**	323.1399			627.2620	**314.1347**	**E**	**989.4898**	495.2485	972.4633	486.7353	**971.4792**	486.2433	**8**
7	732.3046	366.6560			714.2941	357.6507	**S**	**860.4472**	430.7272	**843.4207**	422.2140	842.4367	421.7220	**7**
8	**860.3632**	430.6852	**843.3367**	422.1720	842.3527	421.6800	**Q**	**773.4152**	387.2112	756.3886	378.6980	755.4046	378.2060	**6**
9	**989.4058**	495.2065	972.3793	486.6933	**971.3952**	486.2013	**E**	**645.3566**	323.1819	628.3301	314.6687	627.3461	**314.1767**	**5**
10	1104.4328	552.7200	1087.4062	544.2067	1086.4222	543.7147	**D**	**516.3140**	258.6606	499.2875	250.1474	498.3035	249.6554	**4**
11	1217.5168	609.2620	1200.4903	600.7488	1199.5063	600.2568	**I**	**401.2871**	201.1472	384.2605	192.6339			**3**
12	**1330.6009**	665.8041	1313.5743	657.2908	1312.5903	656.7988	**I**	**288.2030**	144.6051	271.1765	136.0919			**2**
13							**R**	**175.1190**	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
117.2	1503.7052	0.0082	IEADSESQEDIIR

21.3	1503.7165	-0.0030	KNSGEEEIDSLQR
19.7	1503.7239	-0.0104	LEAAETLEECALR
16.2	1503.7794	-0.0659	GESLFQGRGGLDLR
15.4	1503.7239	-0.0104	ELAMKAESGPNETK
14.2	1503.7392	-0.0257	LEFDINICDLPR
10.3	1503.6624	0.0511	GDCDPEVSAALQSR
9.4	1503.7681	-0.0546	ESPDYERIINLR
7.9	1503.7603	-0.0468	LETLIEVSVECGR
7.9	1503.6446	0.0689	ELCAGPACNEVER

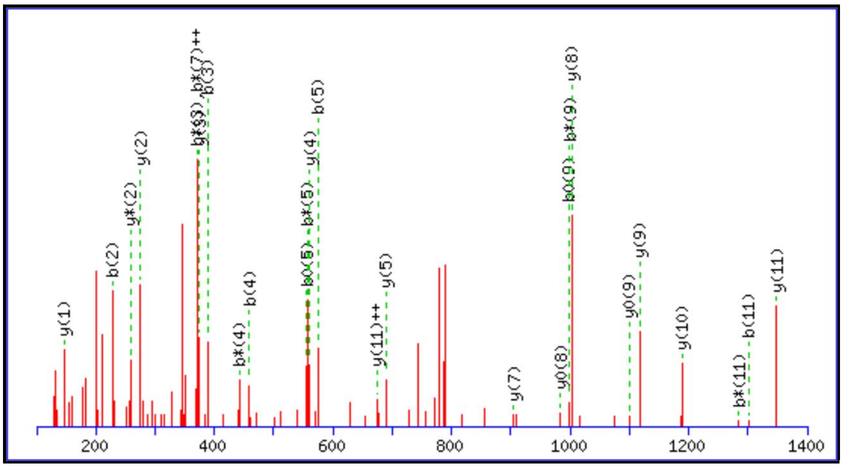
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QVCADPSEEWVQK**
Found in **P10147|CCL3_HUMAN**, C-C motif chemokine 3 OS=Homo sapiens GN=CCL3 PE=1 SV=1

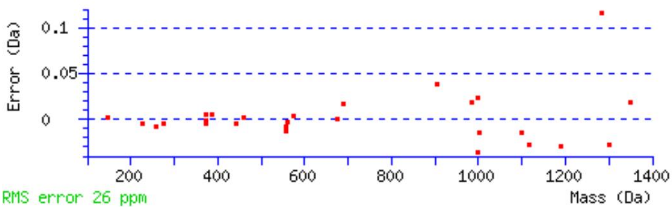
Match to Query 26063: 1574.713228 from(788.363890,2+)
Title: Locus:16.1.1.5061.2

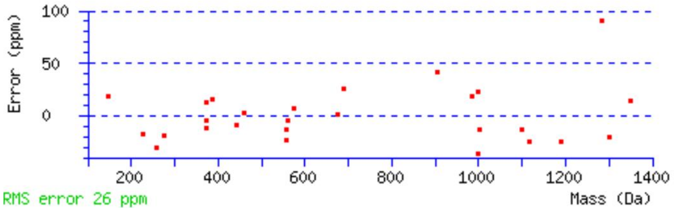
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1400 Da [Full range]



```
Monoisotopic mass of neutral peptide Mr(calc): 1574.7035
Fixed modifications: Carbamidomethyl (C)
Ions Score: 66  Expect: 5.3e-006
Matches (Bold Red): 27/128 fragment ions using 46 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							13
2	**228.1343**	114.5708	211.1077	106.0575			V	1447.6522	724.3297	1430.6257	715.8165	1429.6416	715.3245	12
3	**388.1649**	194.5861	**371.1384**	186.0728			C	**1348.5838**	**674.7955**	1331.5572	666.2823	1330.5732	665.7903	11
4	**459.2020**	230.1047	**442.1755**	221.5914			A	**1188.5531**	594.7802	1171.5266	586.2669	1170.5426	585.7749	10
5	**574.2290**	287.6181	**557.2024**	279.1049	**556.2184**	278.6128	D	**1117.5160**	559.2617	1100.4895	550.7484	**1099.5055**	550.2564	9
6	671.2817	336.1445	654.2552	327.6312	653.2712	327.1392	P	**1002.4891**	501.7482	985.4625	493.2349	**984.4785**	492.7429	8
7	758.3138	379.6605	741.2872	**371.1472**	740.3032	370.6552	S	**905.4363**	453.2218	888.4098	444.7085	887.4258	444.2165	7
8	887.3564	444.1818	870.3298	435.6685	869.3458	435.1765	E	818.4043	409.7058	801.3777	401.1925	800.3937	400.7005	6
9	1016.3990	508.7031	**999.3724**	500.1898	**998.3884**	499.6978	E	**689.3617**	345.1845	672.3352	336.6712	671.3511	336.1792	5
10	1202.4783	601.7428	1185.4517	593.2295	1184.4677	592.7375	W	**560.3191**	280.6632	543.2926	272.1499			4
11	**1301.5467**	651.2770	**1284.5201**	642.7637	1283.5361	642.2717	V	**374.2398**	187.6235	357.2132	179.1103			3
12	1429.6053	715.3063	1412.5787	706.7930	1411.5947	706.3010	Q	**275.1714**	138.0893	**258.1448**	129.5761			2
13							K	**147.1128**	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.9	1574.7035	0.0097	QVCADPSEEWVQK

4.8	1574.6527	0.0605	NCIGQQFAMSEMK
2.1	1574.7762	-0.0630	AFIQNSELIMHEK
1.0	1574.7311	-0.0179	EAEENDLSEEILGK

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

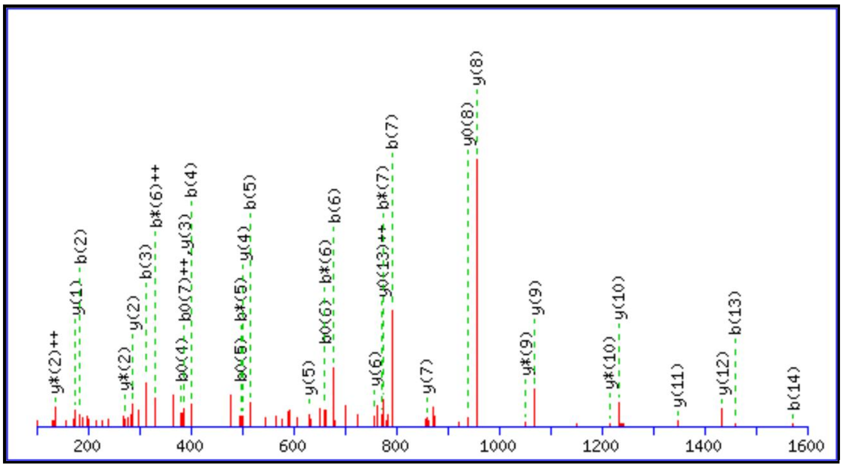
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IAQSDYIPTQQDVLR**
Found in **P04899|GNAI2_HUMAN**, Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3

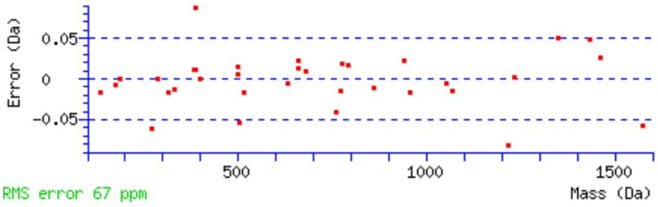
Match to Query 26647: 1745.896308 from(873.955430,2+)
Title: Locus:9.1.1.5211.2

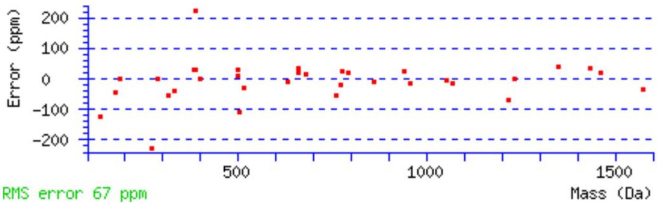
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1600 Da [Full range]



Monoisotopic mass of neutral peptide Mr(calc): 1745.8948
Fixed modifications: Carbamidomethyl (C)
Ions Score: 64 **Expect:** 1.1e-005
Matches (Bold Red): 34/152 fragment ions using 76 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							15
2	**185.1285**	93.0679					A	1633.8180	817.4127	1616.7915	808.8994	1615.8075	808.4074	14
3	**313.1870**	157.0972	296.1605	148.5839			Q	1562.7809	781.8941	1545.7544	773.3808	1544.7703	**772.8888**	13
4	**400.2191**	200.6132	383.1925	192.0999	**382.2085**	191.6079	S	**1434.7223**	717.8648	1417.6958	709.3515	1416.7118	708.8595	12
5	**515.2460**	258.1266	**498.2195**	249.6134	**497.2354**	249.1214	D	**1347.6903**	674.3488	1330.6638	665.8355	1329.6797	665.3435	11
6	**678.3093**	339.6583	**661.2828**	**331.1450**	**660.2988**	330.6530	Y	**1232.6634**	616.8353	**1215.6368**	608.3220	1214.6528	607.8300	10
7	**791.3934**	396.2003	**774.3668**	387.6871	773.3828	**387.1951**	I	**1069.6000**	535.3037	**1052.5735**	526.7904	1051.5895	526.2984	9
8	888.4462	444.7267	871.4196	436.2134	870.4356	435.7214	P	**956.5160**	478.7616	939.4894	470.2483	**938.5054**	469.7563	8
9	989.4938	495.2506	972.4673	486.7373	971.4833	486.2453	T	**859.4632**	430.2352	842.4367	421.7220	841.4526	421.2300	7
10	1117.5524	559.2798	1100.5259	550.7666	1099.5419	550.2746	Q	**758.4155**	379.7114	741.3890	371.1981	740.4050	370.7061	6
11	1245.6110	623.3091	1228.5844	614.7959	1227.6004	614.3039	Q	**630.3570**	315.6821	613.3304	307.1688	612.3464	306.6768	5
12	1360.6379	680.8226	1343.6114	672.3093	1342.6274	671.8173	D	**502.2984**	251.6528	485.2718	243.1395	484.2878	242.6475	4
13	**1459.7064**	730.3568	1442.6798	721.8435	1441.6958	721.3515	V	**387.2714**	194.1394	370.2449	185.6261			3
14	**1572.7904**	786.8988	1555.7639	778.3856	1554.7799	777.8936	L	**288.2030**	144.6051	**271.1765**	**136.0919**			2
15							R	**175.1190**	88.0631	158.0924	79.5498			1





NCBI **BLAST** search of IAQSDYIPTQQDVLR
(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	1745.8948	0.0015	IAQSDYIPTQQDVLR
7.8	1745.9723	-0.0760	VHALEQAPILCRALR
6.3	1745.9611	-0.0648	LTVHKVIHTGEKPCK
3.6	1745.9199	-0.0236	AQAEDYALVSAVATLPK
2.7	1745.8982	-0.0019	CKLLDVTGGLGTDELR
2.2	1745.8923	0.0040	LLFRFYDISSGCIR
2.0	1745.8544	0.0419	DERNQSIIVSGESGAGK
0.8	1745.8981	-0.0018	GQKLESMQLELDSLR

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

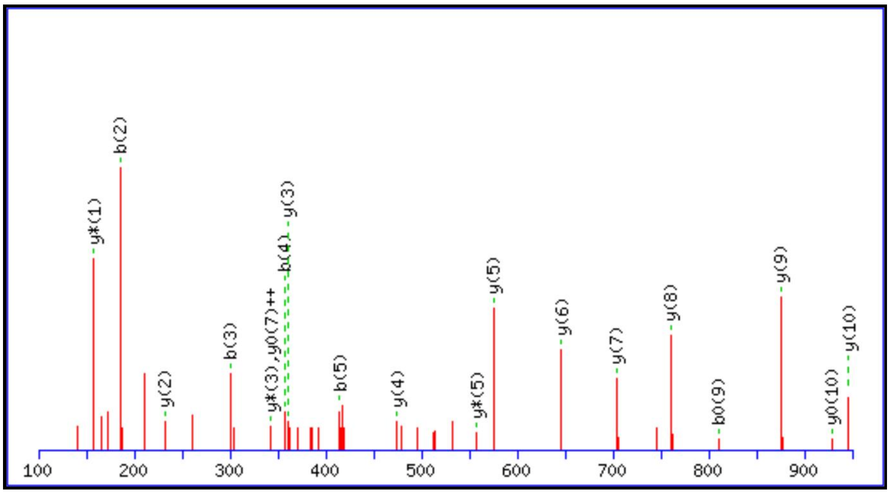
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LADGGATNQGR**
Found in **Q08380|LG3BP_HUMAN**, Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1

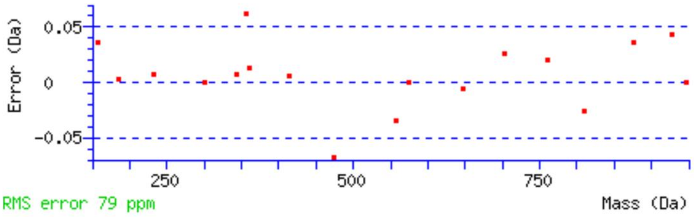
Match to Query 19548: 1058.521068 from(530.267810,2+)
Title: Locus:5.1.1.4612.2

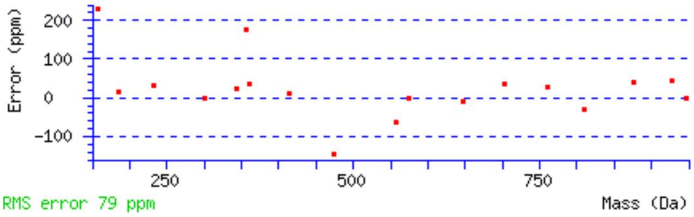
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1058.5105
Fixed modifications: Carbamidomethyl (C)
Ions Score: 60 **Expect:** 3.2e-005
Matches (Bold Red): 19/94 fragment ions using 38 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**							**11**
2	**185.1285**	93.0679					**A**	**946.4337**	473.7205	929.4072	465.2072	**928.4231**	464.7152	**10**
3	**300.1554**	150.5813			282.1448	141.5761	**D**	**875.3966**	438.2019	858.3700	429.6887	857.3860	429.1966	**9**
4	**357.1769**	179.0921			339.1663	170.0868	**G**	**760.3696**	380.6885	743.3431	372.1752	742.3591	371.6832	**8**
5	**414.1983**	207.6028			396.1878	198.5975	**G**	**703.3482**	352.1777	686.3216	343.6645	685.3376	**343.1724**	**7**
6	485.2354	243.1214			467.2249	234.1161	**A**	**646.3267**	323.6670	629.3002	315.1537	628.3161	314.6617	**6**
7	586.2831	293.6452			568.2726	284.6399	**T**	**575.2896**	288.1484	**558.2631**	279.6352	557.2790	279.1432	**5**
8	700.3260	350.6667	683.2995	342.1534	682.3155	341.6614	**N**	**474.2419**	237.6246	457.2154	229.1113			**4**
9	828.3846	414.6959	811.3581	406.1827	**810.3741**	405.6907	**Q**	**360.1990**	180.6031	**343.1724**	172.0899			**3**
10	885.4061	443.2067	868.3795	434.6934	867.3955	434.2014	**G**	**232.1404**	116.5738	215.1139	108.0606			**2**
11							**R**	175.1190	88.0631	**158.0924**	79.5498			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.3	1058.5105	0.0106	LADGGATNQGR
12.9	1058.5244	-0.0033	LAEEQEVNK
4.3	1058.5066	0.0144	GELGMSPPGSK
3.8	1058.5356	-0.0146	VISGGGEGEVR
2.8	1058.5244	-0.0033	ALEEDLNQK
0.1	1058.5356	-0.0145	IALQEDTNR
0.1	1058.5179	0.0032	IASDCQLPR
0.1	1058.5655	-0.0444	LAKNGICQR
0.1	1058.5066	0.0144	LANEPDLCK
0.1	1058.5291	-0.0080	LAQQVANCR

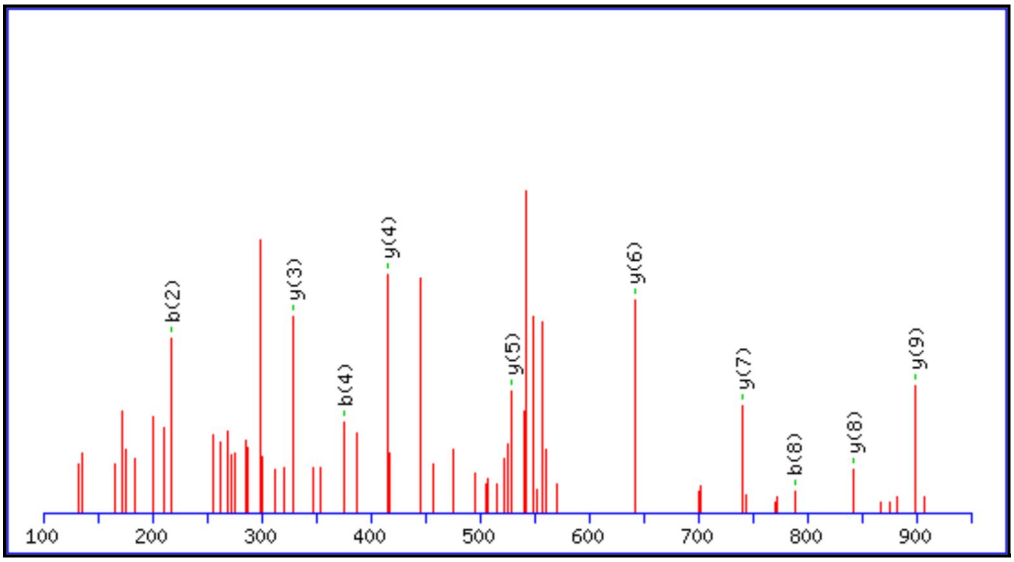
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GCGTVLLSGPR**
Found in **Q07020|RL18_HUMAN**, 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2

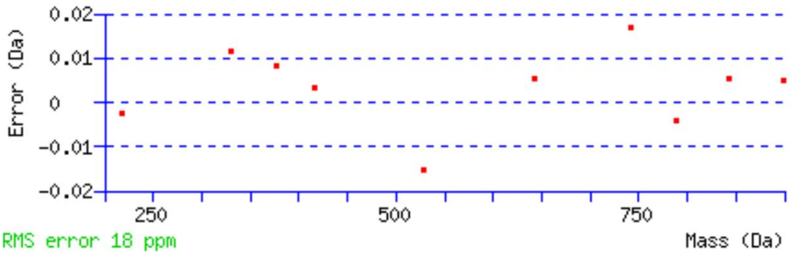
Match to Query 20902: 1115.578648 from(558.796600,2+)
Title: Locus:13.1.1.5200.3

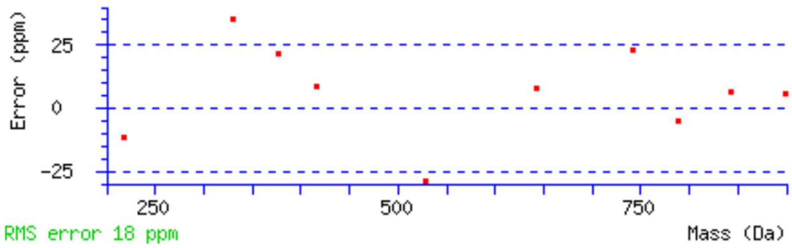
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1115.5757
Fixed modifications: Carbamidomethyl (C)
Ions Score: 54 **Expect:** 0.00014
Matches (Bold Red): 10/88 fragment ions using 16 most intense peaks

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180			**G**							**11**
2	**218.0594**	109.5333			**C**	1059.5615	530.2844	1042.5350	521.7711	1041.5510	521.2791	**10**
3	275.0809	138.0441			**G**	**899.5309**	450.2691	882.5043	441.7558	881.5203	441.2638	**9**
4	**376.1285**	188.5679	358.1180	179.5626	**T**	**842.5094**	421.7584	825.4829	413.2451	824.4989	412.7531	**8**
5	475.1969	238.1021	457.1864	229.0968	**V**	**741.4618**	371.2345	724.4352	362.7212	723.4512	362.2292	**7**
6	588.2810	294.6441	570.2704	285.6389	**L**	**642.3933**	321.7003	625.3668	313.1870	624.3828	312.6950	**6**
7	701.3651	351.1862	683.3545	342.1809	**L**	**529.3093**	265.1583	512.2827	256.6450	511.2987	256.1530	**5**
8	**788.3971**	394.7022	770.3865	385.6969	**S**	**416.2252**	208.6162	399.1987	200.1030	398.2146	199.6110	**4**
9	845.4186	423.2129	827.4080	414.2076	**G**	**329.1932**	165.1002	312.1666	156.5870			**3**
10	942.4713	471.7393	924.4608	462.7340	**P**	272.1717	136.5895	255.1452	128.0762			**2**
11					**R**	175.1190	88.0631	158.0924	79.5498			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.5	1115.5757	0.0029	GCGTVLLSGPR
17.7	1115.6186	-0.0400	SLQSLLGPSSK
9.5	1115.5571	0.0216	GDVGLVAENSR
6.5	1115.6186	-0.0400	NITEGLLTQK
2.8	1115.5935	-0.0148	QEASIQALTR
2.6	1115.5935	-0.0148	GVATSLGLNER
2.2	1115.6121	-0.0334	KAECLVALGR
2.1	1115.5935	-0.0148	SLQDSQLVAR
1.2	1115.6299	-0.0512	GSASIIIRGDK

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

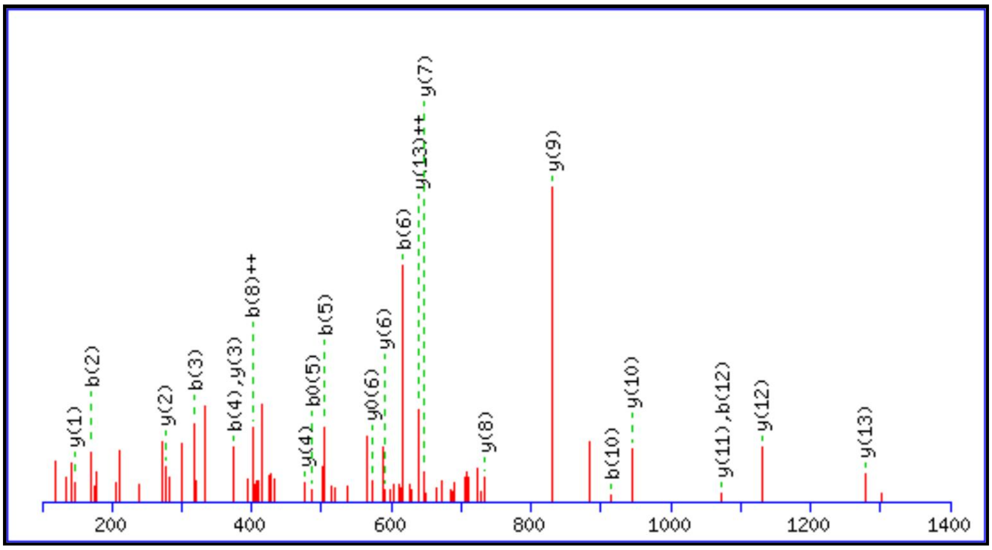
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVFGELPSGGGTVEK**
Found in **Q96C23|GALM_HUMAN**, Aldose 1-epimerase OS=Homo sapiens GN=GALM PE=1 SV=1

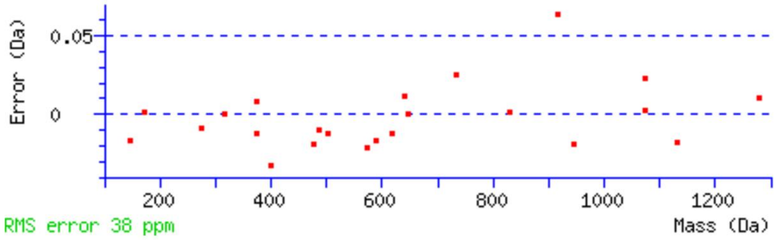
Match to Query 25283: 1446.732748 from(724.373650,2+)
Title: Locus:9.1.1.5175.3

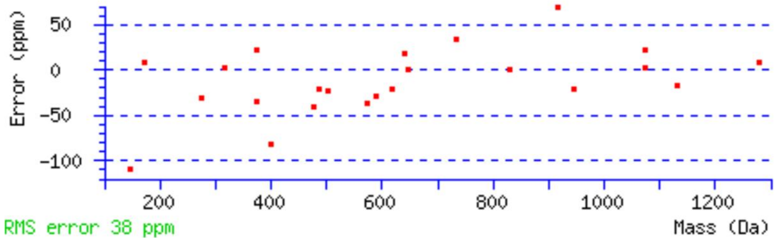
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1446.7355
Fixed modifications: Carbamidomethyl (C)
Ions Score: 54 **Expect:** 0.00014
Matches (Bold Red): 23/130 fragment ions using 68 most intense peaks

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258			**A**							**15**
2	**171.1128**	86.0600			**V**	1376.7056	688.8564	1359.6791	680.3432	1358.6951	679.8512	**14**
3	**318.1812**	159.5942			**F**	**1277.6372**	**639.3222**	1260.6107	630.8090	1259.6266	630.3170	**13**
4	**375.2027**	188.1050			**G**	**1130.5688**	565.7880	1113.5422	557.2748	1112.5582	556.7828	**12**
5	**504.2453**	252.6263	**486.2347**	243.6210	**E**	**1073.5473**	537.2773	1056.5208	528.7640	1055.5368	528.2720	**11**
6	**617.3293**	309.1683	599.3188	300.1630	**L**	**944.5047**	472.7560	927.4782	464.2427	926.4942	463.7507	**10**
7	714.3821	357.6947	696.3715	348.6894	**P**	**831.4207**	416.2140	814.3941	407.7007	813.4101	407.2087	**9**
8	801.4141	**401.2107**	783.4036	392.2054	**S**	**734.3679**	367.6876	717.3414	359.1743	716.3573	358.6823	**8**
9	858.4356	429.7214	840.4250	420.7162	**G**	**647.3359**	324.1716	630.3093	315.6583	629.3253	315.1663	**7**
10	**915.4571**	458.2322	897.4465	449.2269	**G**	**590.3144**	295.6608	573.2879	287.1476	**572.3039**	286.6556	**6**
11	972.4785	486.7429	954.4680	477.7376	**G**	533.2930	267.1501	516.2664	258.6368	515.2824	258.1448	**5**
12	**1073.5262**	537.2667	1055.5156	528.2615	**T**	**476.2715**	238.6394	459.2449	230.1261	458.2609	229.6341	**4**
13	1172.5946	586.8009	1154.5841	577.7957	**V**	**375.2238**	188.1155	358.1973	179.6023	357.2132	179.1103	**3**
14	1301.6372	651.3222	1283.6266	642.3170	**E**	**276.1554**	138.5813	259.1288	130.0681	258.1448	129.5761	**2**
15					**K**	**147.1128**	74.0600	130.0863	65.5468			**1**





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.6	1446.7355	-0.0027	AVFGELPSGGGTVEK
7.1	1446.7476	-0.0148	AVFHMQSVKCLK
5.3	1446.7983	-0.0656	GLFPRLENVGAFK
5.1	1446.7276	0.0051	GMITVTDPDLIEK
3.5	1446.7314	0.0013	KTTEENQELVTR
2.1	1446.8017	-0.0689	MKIDIHSHILPK
1.6	1446.6674	0.0654	AADMDLEWRQGR
1.6	1446.7653	-0.0325	RYLAIHGMETLK
0.6	1446.7579	-0.0252	AVDFLAANESRVR
0.6	1446.7388	-0.0061	MGVATTLQPPTTSK

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

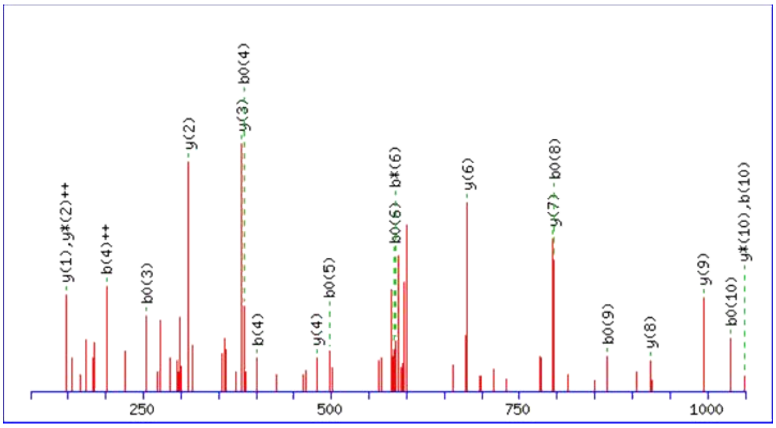
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAAENSLVAYK**
Found in **P62258|1433E_HUMAN**, 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1

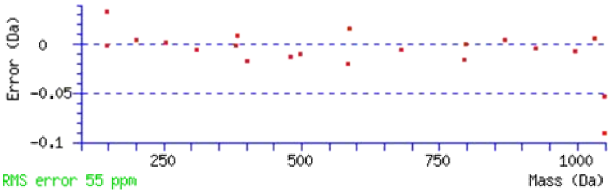
Match to Query 244: 1193.587028 from(597.800790,2+)
Title: Locus:1.1.1.4405.2

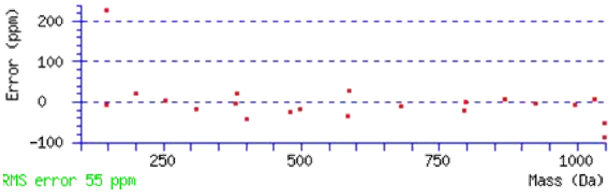
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1050 Da Full range



Monoisotopic mass of neutral peptide Mr(calc): 1193.5928
Fixed modifications: Carbamidomethyl (C)
Ions Score: 80 **Expect:** 4.6e-007
Matches (Bold Red): 22/102 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	130.0499	65.5286			112.0393	56.5233	E							11
2	**201.0870**	101.0471			183.0764	92.0418	A	1065.5575	533.2824	**1048.5310**	524.7691	1047.5469	524.2771	10
3	272.1241	136.5657			**254.1135**	127.5604	A	**994.5204**	497.7638	977.4938	489.2506	976.5098	488.7585	9
4	**401.1667**	**201.0870**			**383.1561**	192.0817	E	**923.4833**	462.2453	906.4567	453.7320	905.4727	453.2400	8
5	515.2096	258.1084	498.1831	249.5952	**497.1991**	249.1032	N	**794.4407**	397.7240	777.4141	389.2107	776.4301	388.7187	7
6	602.2416	301.6245	**585.2151**	293.1112	**584.2311**	292.6192	S	**680.3978**	340.7025	663.3712	332.1892	662.3872	331.6972	6
7	715.3257	358.1665	698.2992	349.6532	697.3151	349.1612	L	593.3657	297.1865	576.3392	288.6732			5
8	814.3941	407.7007	797.3676	399.1874	**796.3836**	398.6954	V	**480.2817**	240.6445	463.2551	232.1312			4
9	885.4312	443.2193	868.4047	434.7060	**867.4207**	434.2140	A	**381.2132**	191.1103	364.1867	182.5970			3
10	**1048.4946**	524.7509	1031.4680	516.2376	**1030.4840**	515.7456	Y	**310.1761**	155.5917	293.1496	**147.0784**			2
11							K	**147.1128**	74.0600	130.0863	65.5468			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
80.3	1193.5928	-0.0057	EAAENSLVAYK
6.9	1193.5598	0.0273	AEEEGVKMSAK
6.1	1193.6148	-0.0278	TVLSKMMGSPK
6.1	1193.6148	-0.0278	TVLSKMMGSPK
5.2	1193.5573	0.0297	ATLPPFMCNK

4.6	1193.5598	0.0272	DGDKDVMITGK
3.6	1193.6993	-0.1122	SLARHLTQLR
3.5	1193.7244	-0.1374	TVQTIVHRLK
3.0	1193.5135	0.0735	HPDMDEAVHK
2.5	1193.6404	-0.0534	NLVEELPQPR