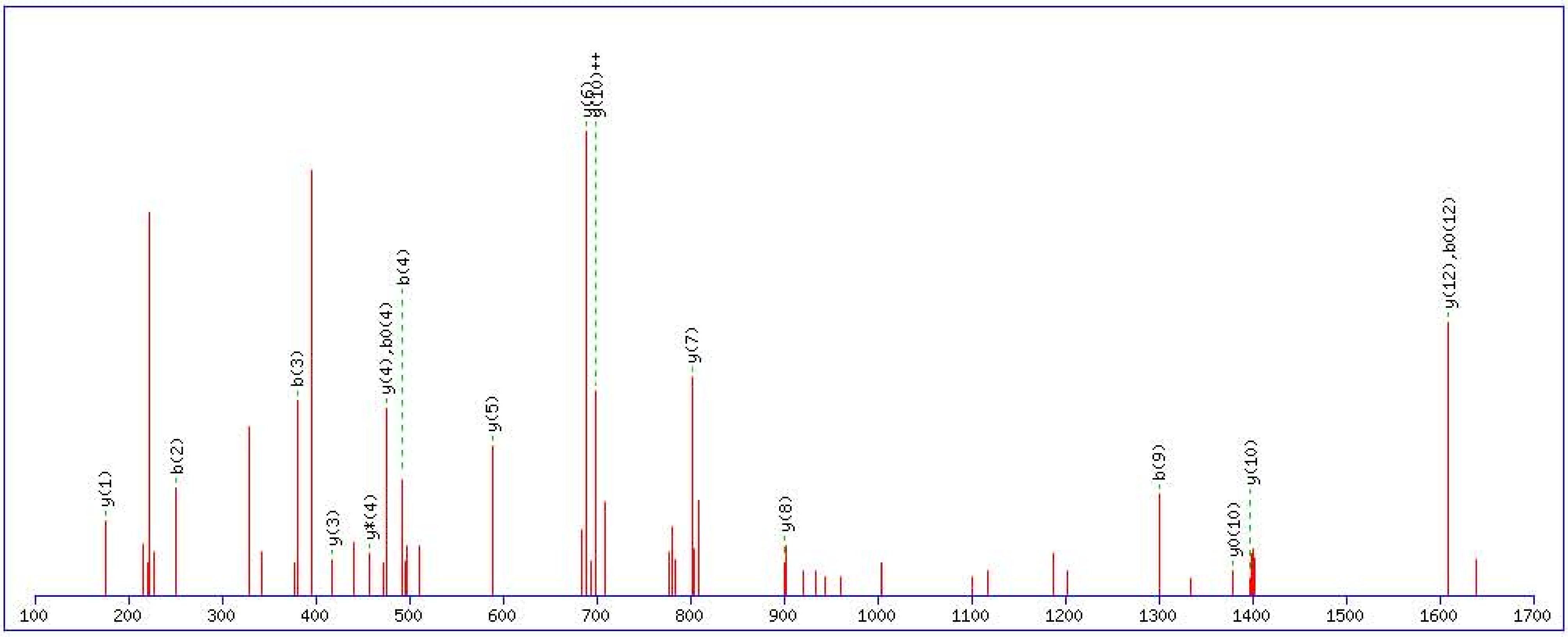
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SYELPDGQVITIGNER**
Found in **ACTA_HUMAN**, Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1

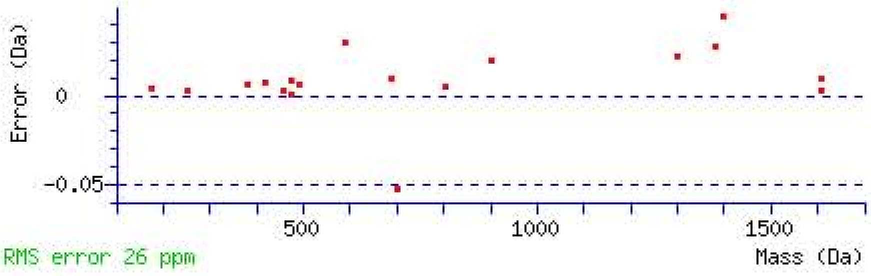
Match to Query 59545: 2101.062342 from(701.361390,3+) rtinseconds(2607) index(66818)
Title: Locus:1.1.1.2905.8 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

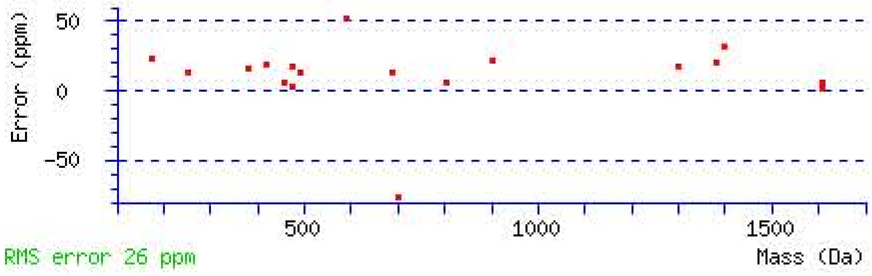
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2101.051376
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.0023
Matches : 18/164 fragment ions using 47 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							16
2	**251.102633**	126.054954			233.092068	117.049672	Y	2015.026640	1008.016958	1998.000091	999.503683	1997.016075	999.011675	15
3	**380.145226**	190.576251			362.134661	181.570969	E	1851.963311	926.485294	1834.936762	917.972019	1833.952746	917.480011	14
4	**493.229290**	247.118283			475.218725	238.113001	L	1722.920718	861.963997	1705.894169	853.450722	1704.910153	852.958714	13
5	590.282054	295.644665			572.271489	286.639383	P	***1609.836654***	805.421965	1592.810105	796.908691	1591.826089	796.416682	12
6	705.308997	353.158137			687.298432	344.152854	D	1512.783890	756.895583	1495.757341	748.382309	1494.773325	747.890300	11
7	762.330461	381.668869			744.319896	372.663586	G	***1397.756947***	699.382111	1380.730398	690.868837	1379.746382	690.376829	10
8	1201.555787	601.281532	1184.529238	592.768257	1183.545222	592.276249	Q	1340.735483	670.871379	1323.708934	662.358105	1322.724918	661.866097	9
9	**1300.624201**	650.815739	1283.597652	642.302464	1282.613636	641.810456	V	***901.510157***	451.258716	884.483608	442.745442	883.499592	442.253434	8
10	1413.708265	707.357771	1396.681716	698.844496	1395.697700	698.352488	I	***802.441743***	401.724509	785.415194	393.211235	784.431178	392.719227	7
11	1514.755944	757.881610	1497.729395	749.368336	1496.745379	748.876328	T	***689.357679***	345.182478	672.331130	336.669203	671.347114	336.177195	6
12	1627.840008	814.423642	1610.813459	805.910368	1609.829443	805.418359	I	***588.310000***	294.658638	571.283451	286.145363	570.299435	285.653355	5
13	1684.861472	842.934374	1667.834923	834.421099	1666.850907	833.929091	G	***475.225936***	238.116606	458.199387	229.603331	457.215371	229.111323	4
14	1798.904399	899.955837	1781.877850	891.442563	1780.893834	890.950555	N	***418.204472***	209.605874	401.177923	201.092600	400.193907	200.600592	3
15	1927.946992	964.477134	1910.920443	955.963860	1909.936427	955.471851	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
16							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.3	2101.051376	0.010966	SYELPDGQVITIGNER
3.1	2101.090240	-0.027898	SDDILEEGEKNLGNIKVTK

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

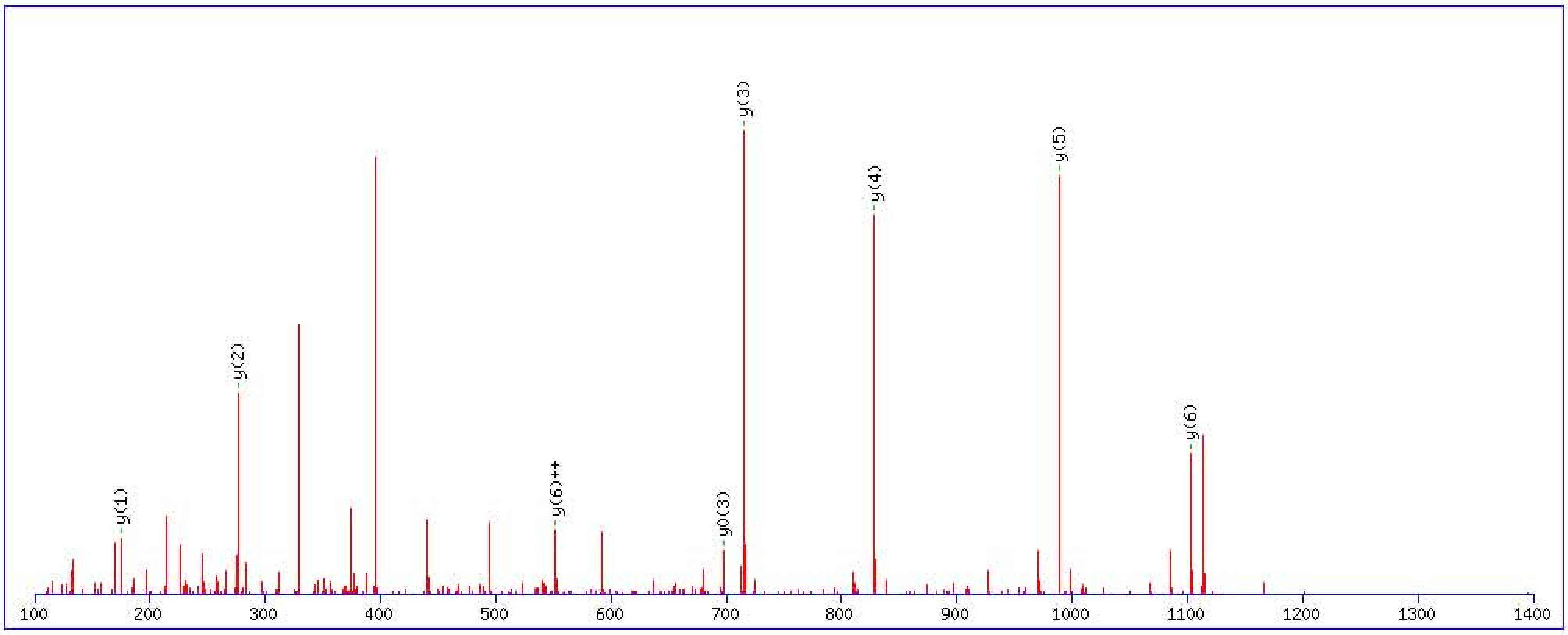
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNCLQTR**
Found in **AFAM_HUMAN**, Afamin OS=Homo sapiens GN=AFM PE=1 SV=1

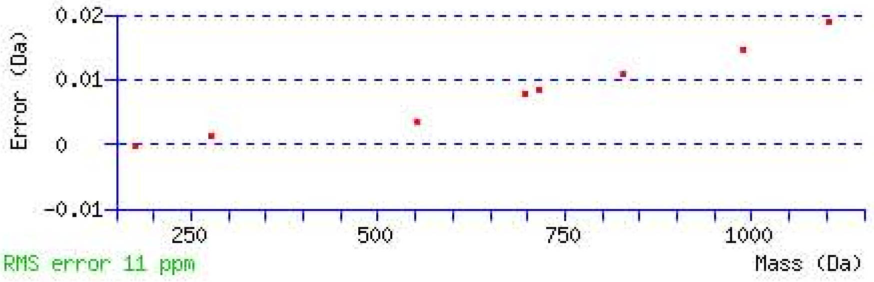
Match to Query 31707: 1200.616748 from(601.315650,2+) rtinseconds(1456) index(3705)
Title: Locus:1.1.1.2227.12 File:"2013-07-02 CLN FXIII 30 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

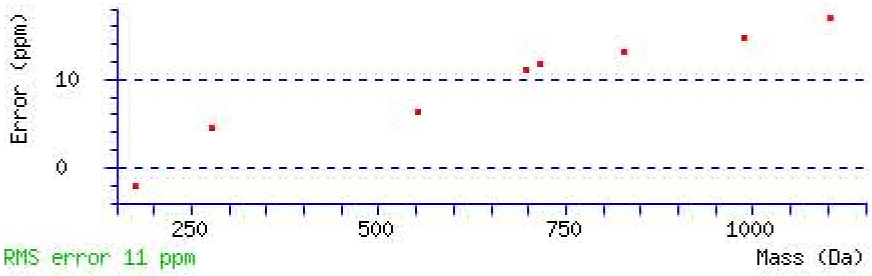
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1200.610733
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 48 **Expect:** 0.00013
Matches : 8/58 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							7
2	214.118617	107.562947	197.092068	99.049672			N	***1102.549597***	551.778437	1085.523048	543.265162	1084.539032	542.773154	6
3	374.149266	187.578271	357.122717	179.064997			C	***988.506670***	494.756973	971.480121	486.243698	970.496105	485.751691	5
4	487.233330	244.120303	470.206781	235.607029			L	***828.476021***	414.741649	811.449472	406.228374	810.465456	405.736366	4
5	926.458656	463.732966	909.432107	455.219692			Q	***715.391957***	358.199617	698.365408	349.686342	697.381392	349.194334	3
6	1027.506335	514.256806	1010.479786	505.743531	1009.495770	505.251523	T	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.581671	2
7							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.0	1200.610733	0.006015	VNCLQTR
6.2	1200.621948	-0.005200	VNMLKHCKR
5.9	1200.629822	-0.013074	VHHHGSKMLR
4.3	1200.628479	-0.011731	MVAALLGGGGEAR
3.7	1200.603333	0.013415	GRIAEPSVCGR
2.6	1200.632324	-0.015576	SRERSGGPVTR
1.3	1200.611191	0.005557	HDSHLAKHTR

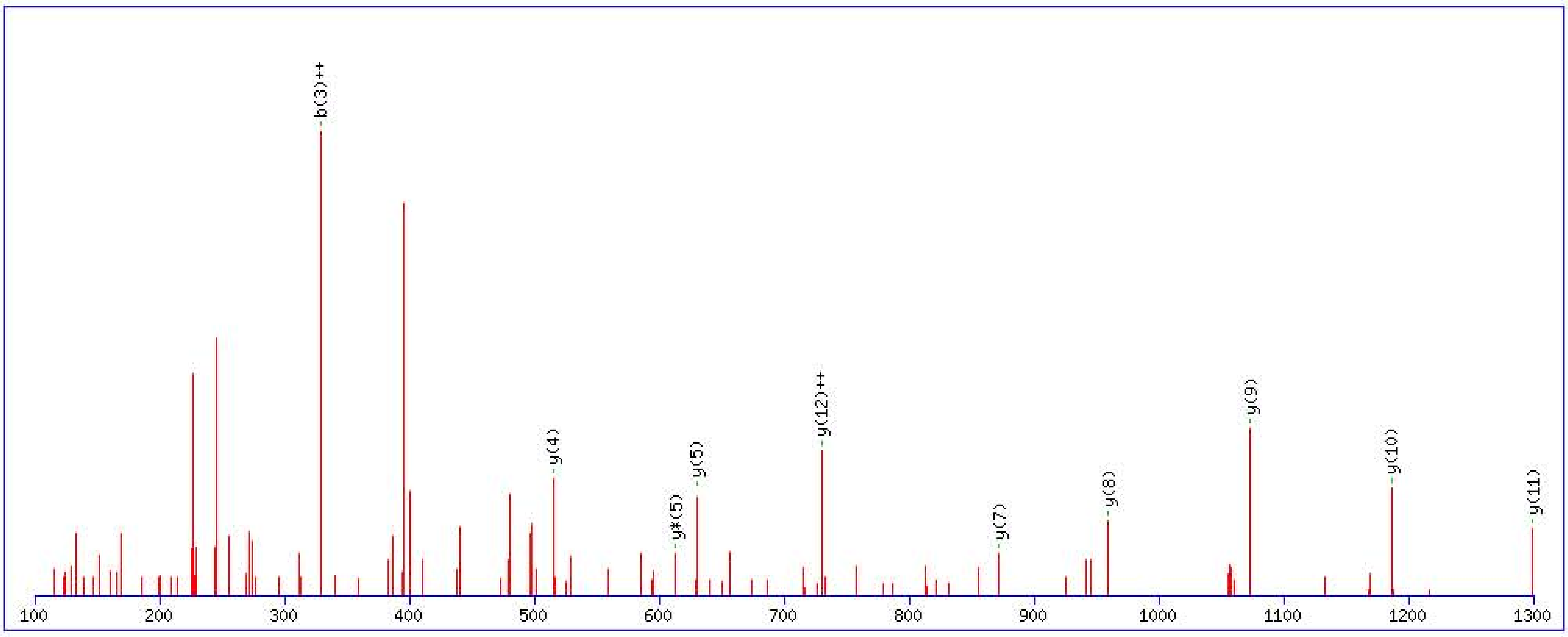
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQCIINSNKDDRPK**
Found in **AFAM_HUMAN**, Afamin OS=Homo sapiens GN=AFM PE=1 SV=1

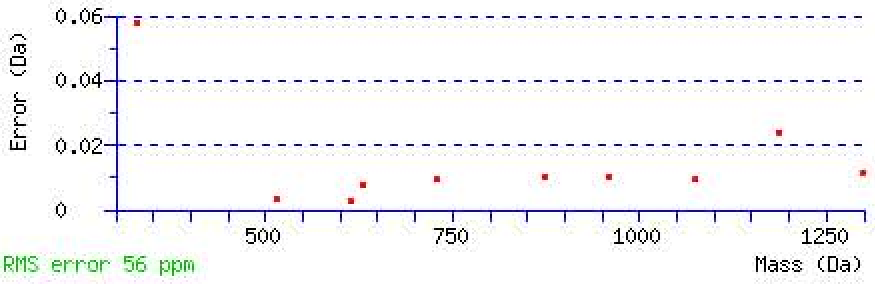
Match to Query 55559: 1954.976096 from(489.751300,4+) rtinseconds(1326) index(2686)
Title: Locus:1.1.1.2182.14 File:"2013-07-02 CLN FXIII 30 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

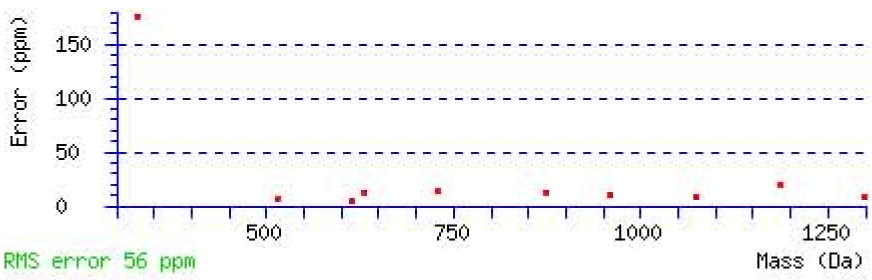
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1954.971680
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 54 **Expect:** 8.7e-006
Matches : 10/136 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							14
2	497.254066	249.130671	480.227517	240.617397			Q	1898.957513	949.982395	1881.930964	941.469120	1880.946948	940.977112	13
3	657.284715	**329.145996**	640.258166	320.632721			C	1459.732187	730.369732	1442.705638	721.856457	1441.721622	721.364449	12
4	770.368779	385.688028	753.342230	377.174753			I	***1299.701538***	650.354407	1282.674989	641.841133	1281.690973	641.349125	11
5	883.452843	442.230060	866.426294	433.716785			I	***1186.617474***	593.812375	1169.590925	585.299101	1168.606909	584.807093	10
6	997.495770	499.251523	980.469221	490.738249			N	***1073.533410***	537.270343	1056.506861	528.757069	1055.522845	528.265061	9
7	1084.527798	542.767537	1067.501249	534.254263	1066.517233	533.762255	S	***959.490483***	480.248880	942.463934	471.735605	941.479918	471.243597	8
8	1198.570725	599.789001	1181.544176	591.275726	1180.560160	590.783718	N	***872.458455***	436.732866	855.431906	428.219591	854.447890	427.727583	7
9	1326.665688	663.836482	1309.639139	655.323208	1308.655123	654.831200	K	758.415528	379.711402	741.388979	371.198128	740.404963	370.706120	6
10	1441.692631	721.349954	1424.666082	712.836679	1423.682066	712.344671	D	***630.320565***	315.663921	613.294016	307.150646	612.310000	306.658638	5
11	1556.719574	778.863425	1539.693025	770.350151	1538.709009	769.858143	D	***515.293622***	258.150449	498.267073	249.637175	497.283057	249.145167	4
12	1712.820685	856.913981	1695.794136	848.400706	1694.810120	847.908698	R	400.266679	200.636977	383.240130	192.123703			3
13	1809.873449	905.440363	1792.846900	896.927088	1791.862884	896.435080	P	244.165568	122.586422	227.139019	114.073148			2
14							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.4	1954.971680	0.004416	GQCIINSNKDDRPK
0.4	1955.004227	-0.028131	TVQEQMSALQAK

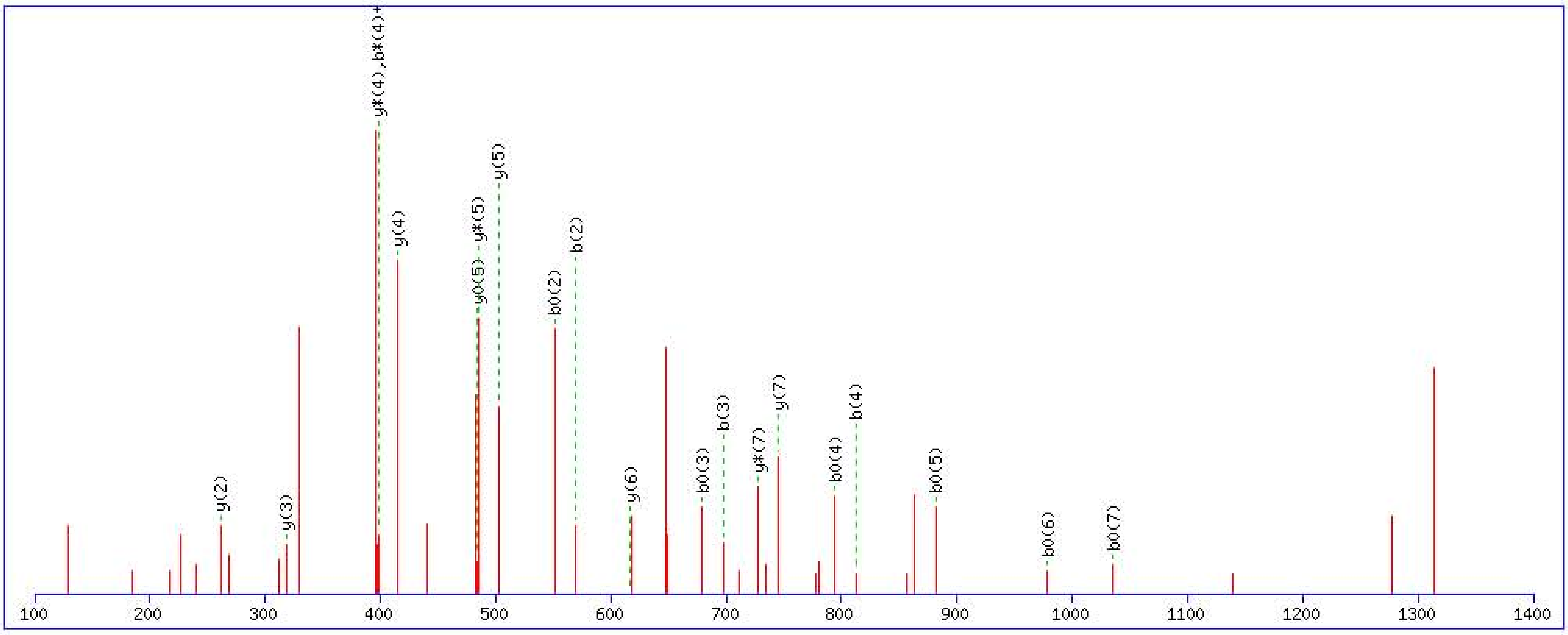
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQQDSPGNK**
Found in **A2AP_HUMAN**, Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3

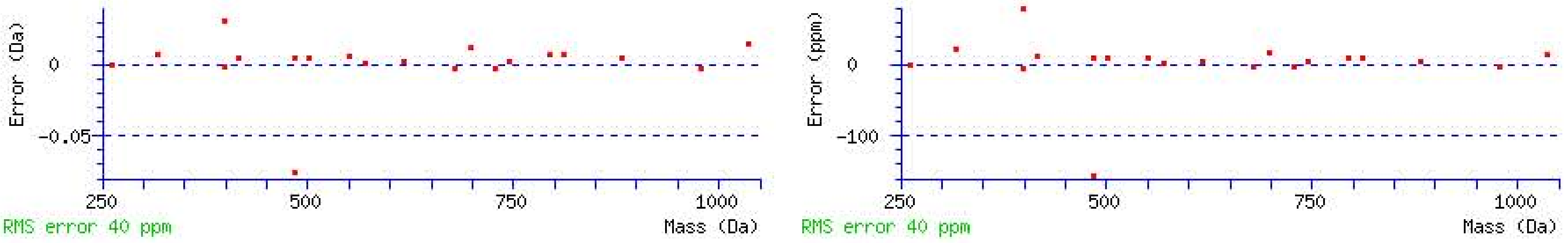
Match to Query 35523: 1312.617668 from(657.316110,2+) rtinseconds(1132) index(1231)
Title: Locus:1.1.1.2114.25 File:"2013-07-02 CLN FXIII 30 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

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



```
Monoisotopic mass of neutral peptide Mr(calc): 1312.608139
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.0026
Matches : 20/86 fragment ions using 40 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							9
2	**569.275195**	285.141236	552.248646	276.627961	551.264630	276.135953	Q	1184.572834	592.790055	1167.546285	584.276780	1166.562269	583.784772	8
3	**697.333773**	349.170525	680.307224	340.657250	679.323208	340.165242	Q	***745.347508***	373.177392	728.320959	364.664117	727.336943	364.172109	7
4	**812.360716**	406.683996	795.334167	398.170722	794.350151	397.678714	D	***617.288930***	309.148103	600.262381	300.634828	599.278365	300.142820	6
5	899.392744	450.200010	882.366195	441.686736	881.382179	441.194728	S	***502.261987***	251.634631	485.235438	243.121357	484.251422	242.629349	5
6	996.445508	498.726392	979.418959	490.213118	978.434943	489.721110	P	***415.229959***	208.118617	398.203410	199.605343			4
7	1053.466972	527.237124	1036.440423	518.723850	1035.456407	518.231841	G	***318.177195***	159.592235	301.150646	151.078961			3
8	1167.509899	584.258587	1150.483350	575.745313	1149.499334	575.253305	N	***261.155731***	131.081503	244.129182	122.568229			2
9							K	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.8	1312.608139	0.009529	EQQDSPGNK
19.1	1312.608139	0.009529	EQQDSPGNK
3.2	1312.608154	0.009514	KIGSFDETCTR

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

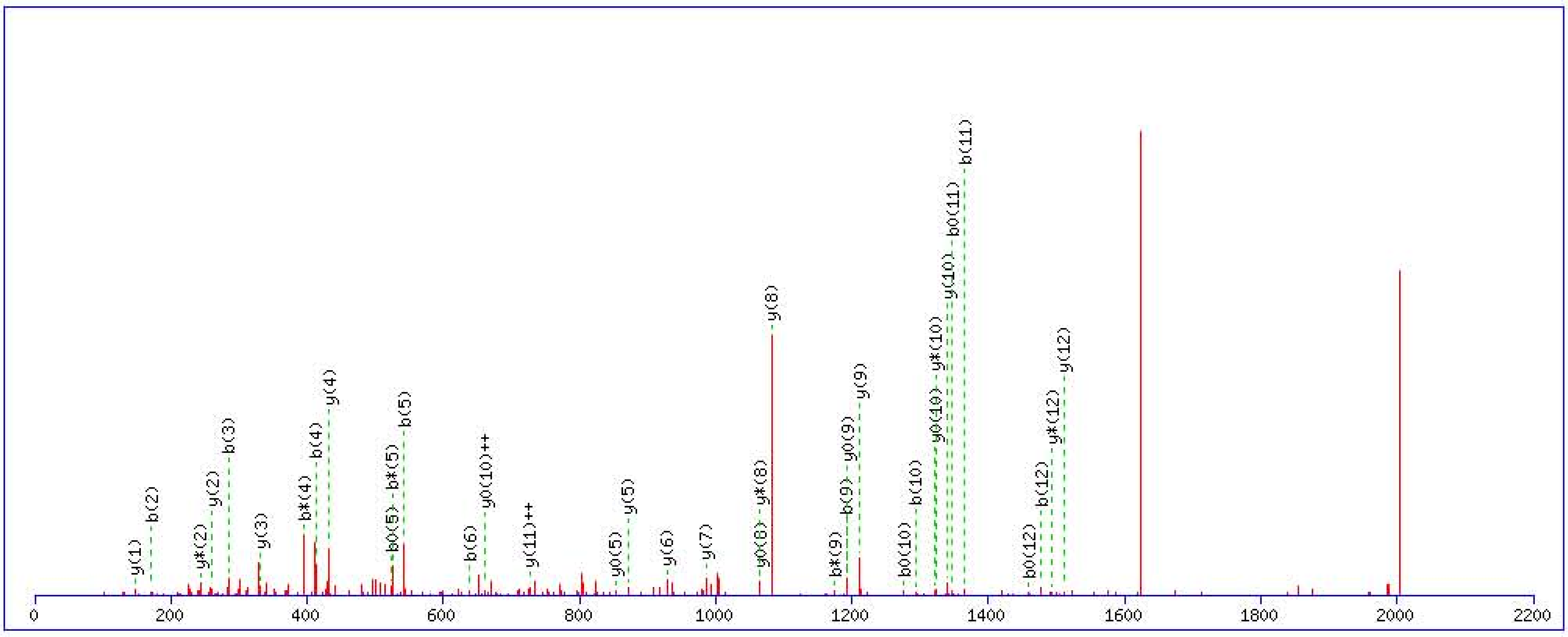
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGNQEPGGQTALK**
Found in **A2AP_HUMAN**, Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3

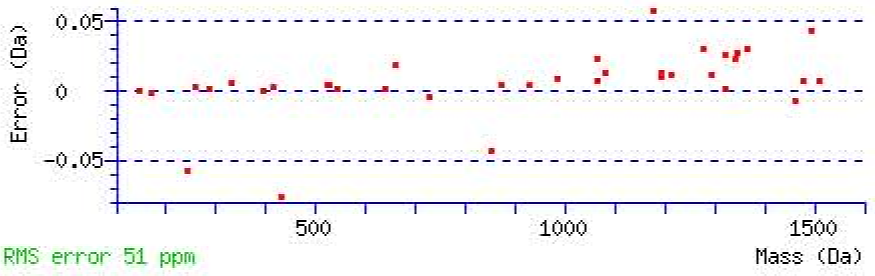
Match to Query 47030: 1622.858448 from(812.436500,2+) rtinseconds(1565) index(4469)
Title: Locus:1.1.1.2265.13 File:"2013-07-02 CLN FXIII 30 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

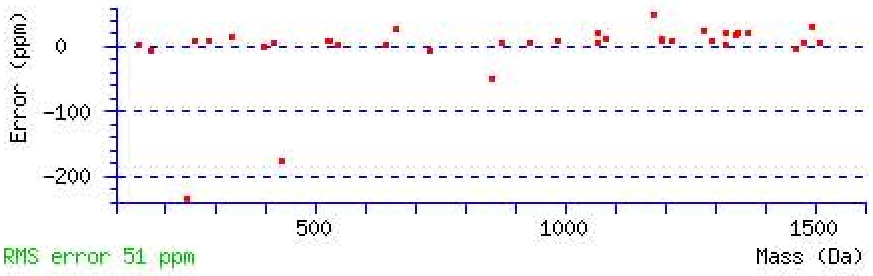
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1622.845016
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9     : Biotin:Thermo-21345 (Q)
Ions Score: 45  Expect: 0.00049
Matches : 37/126 fragment ions using 106 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							13
2	**171.112804**	86.060040					G	***1510.768241***	755.887759	1493.741692	747.374484	1492.757676	746.882476	12
3	**285.155731**	143.081504	268.129182	134.568229			N	1453.746777	727.377027	1436.720228	718.863752	1435.736212	718.371744	11
4	**413.214309**	207.110793	396.187760	198.597518			Q	***1339.703850***	670.355563	1322.677301	661.842289	1321.693285	661.350281	10
5	**542.256902**	271.632089	525.230353	263.118815	524.246337	262.626807	E	***1211.645272***	606.326274	1194.618723	597.813000	1193.634707	597.320991	9
6	**639.309666**	320.158471	622.283117	311.645197	621.299101	311.153189	P	***1082.602679***	541.804978	1065.576130	533.291703	1064.592114	532.799695	8
7	696.331130	348.669203	679.304581	340.155929	678.320565	339.663921	G	***985.549915***	493.278596	968.523366	484.765321	967.539350	484.273313	7
8	753.352594	377.179935	736.326045	368.666661	735.342029	368.174653	G	***928.528451***	464.767864	911.501902	456.254589	910.517886	455.762581	6
9	**1192.577920**	596.792598	1175.551371	588.279324	1174.567355	587.787316	Q	***871.506987***	436.257132	854.480438	427.743857	853.496422	427.251849	5
10	**1293.625599**	647.316438	1276.599050	638.803163	1275.615034	638.311155	T	***432.281661***	216.644468	415.255112	208.131194	414.271096	207.639186	4
11	**1364.662713**	682.834995	1347.636164	674.321720	1346.652148	673.829712	A	***331.233982***	166.120629	314.207433	157.607354			3
12	**1477.746777**	739.377027	1460.720228	730.863752	1459.736212	730.371744	L	***260.196868***	130.602072	243.170319	122.088797			2
13							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.6	1622.845016	0.013432	LGNQEPGGQTALK
24.3	1622.845016	0.013432	LGNQEPGGQTALK
8.7	1622.881409	-0.022961	TVDPEQARGVLK
2.3	1622.863632	-0.005184	KRMILSTISWMGGK
0.5	1622.860260	-0.001812	EHSAFQAPAVKK
0.2	1622.878021	-0.019573	RLQPPDFIDPLANK
0.1	1622.864288	-0.005840	FPLPSMYRALVWK
0.1	1622.849045	0.009403	IPMPDFDLHLKGPK

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

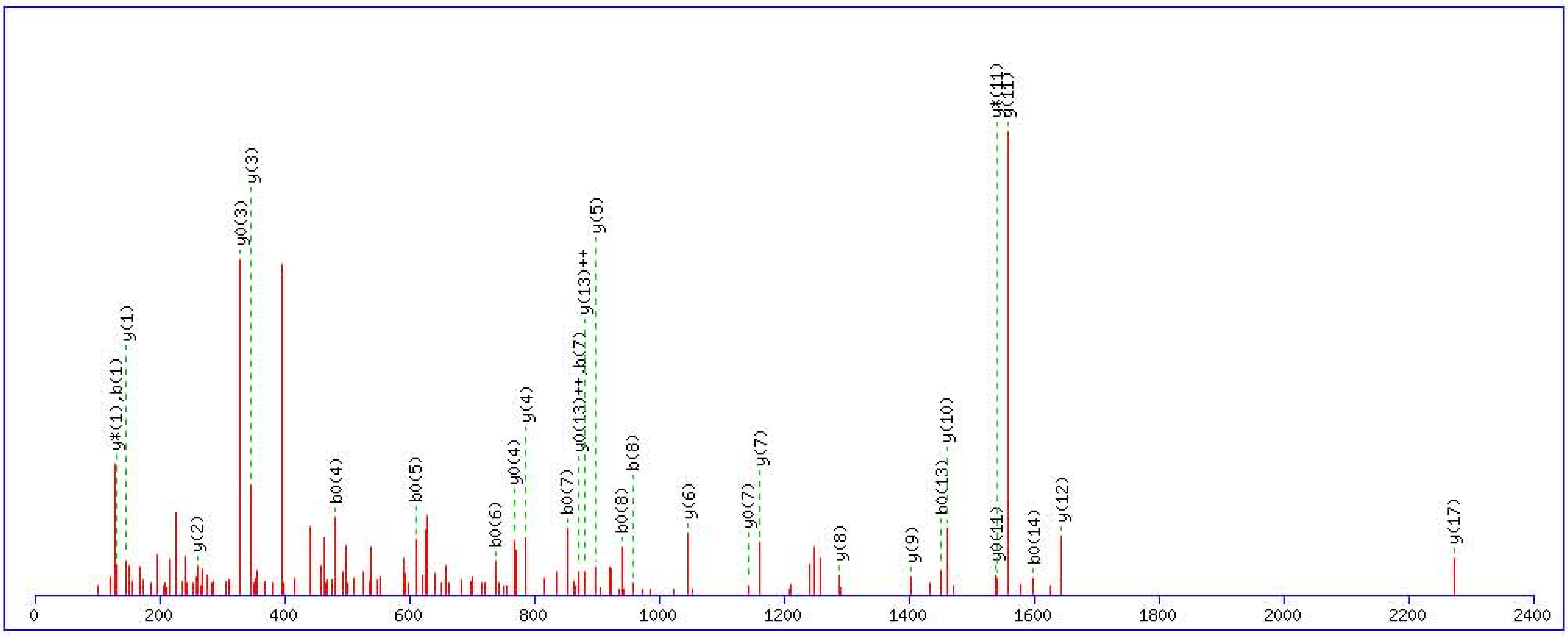
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of ELKEQQDSPGNKDFLQSLK
Found in A2AP_HUMAN, Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3

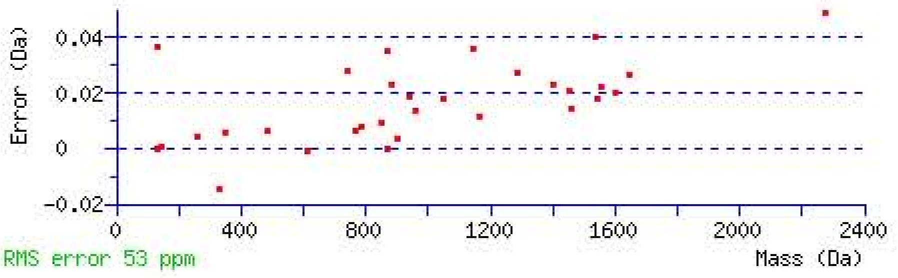
Match to Query 68820: 2514.304456 from(629.583390,4+) rtinseconds(1869) index(6425)
Title: Locus:1.1.1.2371.19 File:"2013-07-02 CLN FXIII 30 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

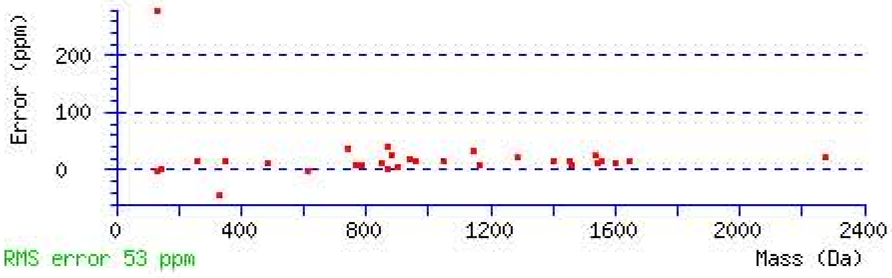
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2514.278793
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16     : Biotin:Thermo-21345 (Q)
Ions Score: 62  Expect: 1.5e-006
Matches : 31/208 fragment ions using 68 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	**130.049869**	65.528572			112.039304	56.523290	E							19
2	243.133933	122.070605			225.123368	113.065322	L	2386.243508	1193.625392	2369.216959	1185.112117	2368.232943	1184.620109	18
3	371.228896	186.118086	354.202347	177.604812	353.218331	177.112804	K	***2273.159444***	1137.083360	2256.132895	1128.570085	2255.148879	1128.078077	17
4	500.271489	250.639383	483.244940	242.126108	482.260924	241.634100	E	2145.064481	1073.035878	2128.037932	1064.522604	2127.053916	1064.030596	16
5	628.330067	314.668672	611.303518	306.155397	610.319502	305.663389	Q	2016.021888	1008.514582	1998.995339	1000.001308	1998.011323	999.509300	15
6	756.388645	378.697961	739.362096	370.184686	738.378080	369.692678	Q	1887.963310	944.485293	1870.936761	935.972019	1869.952745	935.480011	14
7	**871.415588**	436.211432	854.389039	427.698158	853.405023	427.206150	D	1759.904732	880.456004	1742.878183	871.942730	1741.894167	871.450722	13
8	**958.447616**	479.727446	941.421067	471.214172	940.437051	470.722164	S	***1644.877789***	822.942533	1627.851240	814.429258	1626.867224	813.937250	12
9	1055.500380	528.253828	1038.473831	519.740554	1037.489815	519.248545	P	***1557.845761***	779.426519	1540.819212	770.913244	1539.835196	770.421236	11
10	1112.521844	556.764560	1095.495295	548.251285	1094.511279	547.759277	G	***1460.792997***	730.900137	1443.766448	722.386862	1442.782432	721.894854	10
11	1226.564771	613.786023	1209.538222	605.272749	1208.554206	604.780741	N	***1403.771533***	702.389405	1386.744984	693.876130	1385.760968	693.384122	9
12	1354.659734	677.833505	1337.633185	669.320230	1336.649169	668.828222	K	***1289.728606***	645.367941	1272.702057	636.854667	1271.718041	636.362659	8
13	1469.686677	735.346976	1452.660128	726.833702	1451.676112	726.341694	D	***1161.633643***	581.320460	1144.607094	572.807185	1143.623078	572.315177	7
14	1616.755091	808.881184	1599.728542	800.367909	1598.744526	799.875901	F	***1046.606700***	523.806988	1029.580151	515.293714	1028.596135	514.801706	6
15	1729.839155	865.423215	1712.812606	856.909941	1711.828590	856.417933	L	***899.538286***	450.272781	882.511737	441.759507	881.527721	441.267499	5
16	2169.064481	1085.035878	2152.037932	1076.522604	2151.053916	1076.030596	Q	***786.454222***	393.730749	769.427673	385.217475	768.443657	384.725467	4
17	2256.096509	1128.551892	2239.069960	1120.038618	2238.085944	1119.546610	S	***347.228896***	174.118086	330.202347	165.604812	329.218331	165.112804	3
18	2369.180573	1185.093925	2352.154024	1176.580650	2351.170008	1176.088642	L	***260.196868***	130.602072	243.170319	122.088798			2
19							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.1	2514.278793	0.025663	ELKEQQDSPGNKDFLQSLK
0.0	2514.268951	0.035505	GNSGPPGIVGQKGDPGYPGPAGPK

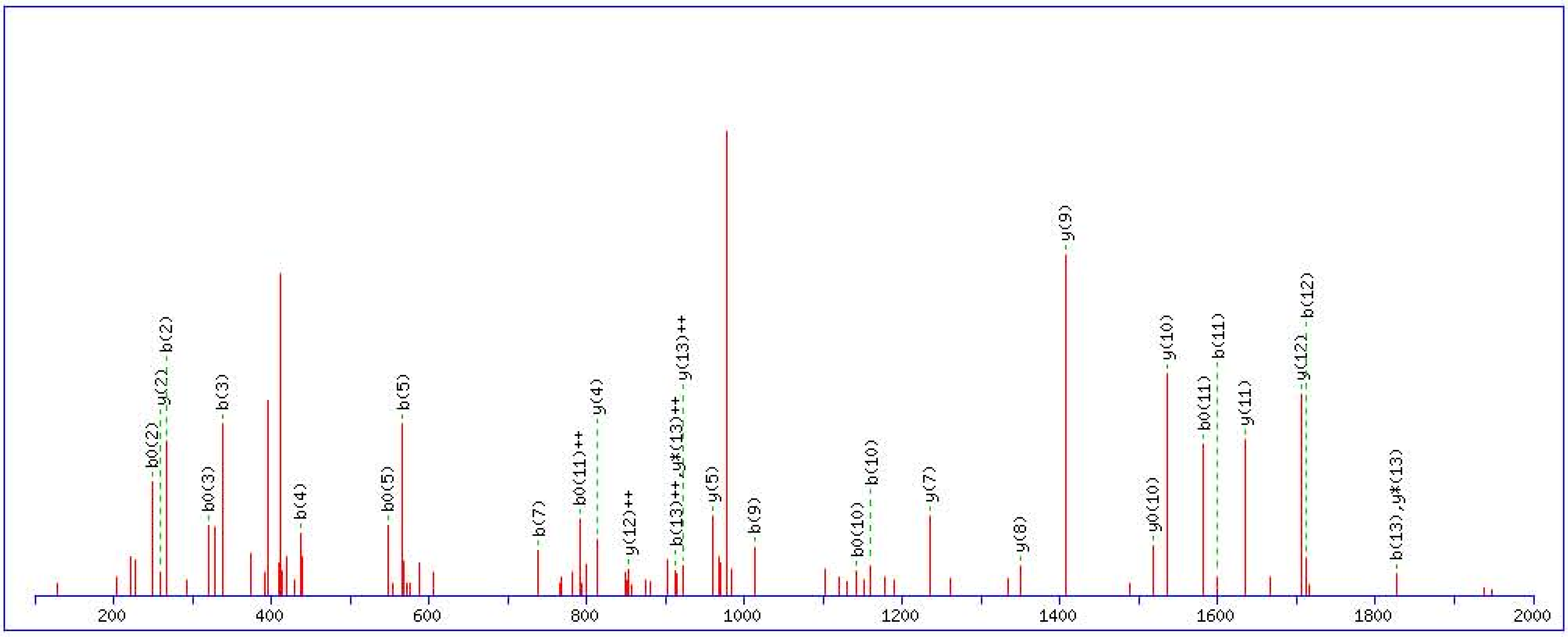
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EHAVEGDCDFQLLK**
Found in **FETUA_HUMAN**, Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1

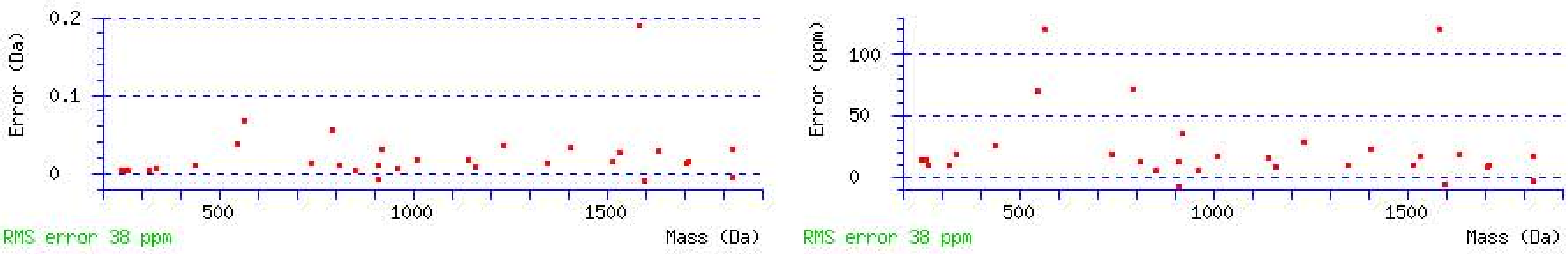
Match to Query 56031: 1970.947228 from(986.480890,2+) rtinseconds(2044) index(7635)
Title: Locus:1.1.1.2432.15 File:"2013-07-02 CLN FXIII 30 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1970.923019
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 56  Expect: 2.5e-005
Matches : 31/126 fragment ions using 56 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							14
2	*267.108781*	134.058028			249.098216	125.052746	H	1842.887704	921.947490	1825.861155	913.434216	1824.877139	912.942207	13
3	*338.145895*	169.576585			320.135330	160.571303	A	**1705.828792**	853.418034	1688.802243	844.904760	1687.818227	844.412752	12
4	*437.214309*	219.110792			419.203744	210.105510	V	**1634.791678**	817.899477	1617.765129	809.386203	1616.781113	808.894195	11
5	*566.256902*	283.632089			548.246337	274.626807	E	**1535.723264**	768.365270	1518.696715	759.851996	1517.712699	759.359988	10
6	623.278366	312.142821			605.267801	303.137539	G	**1406.680671**	703.843974	1389.654122	695.330699	1388.670106	694.838691	9
7	*738.305309*	369.656293			720.294744	360.651010	D	**1349.659207**	675.333241	1332.632658	666.819967	1331.648642	666.327959	8
8	898.335958	449.671617			880.325393	440.666335	C	**1234.632264**	617.819770	1217.605715	609.306496	1216.621699	608.814488	7
9	*1013.362901*	507.185089			995.352336	498.179806	D	1074.601615	537.804446	1057.575066	529.291171	1056.591050	528.799163	6
10	*1160.431315*	580.719296			1142.420750	571.714013	F	**959.574672**	480.290974	942.548123	471.777700			5
11	*1599.656641*	800.331959	1582.630092	791.818684	1581.646076	791.326676	Q	**812.506258**	406.756767	795.479709	398.243493			4
12	*1712.740705*	856.873991	1695.714156	848.360716	1694.730140	847.868708	L	373.280932	187.144104	356.254383	178.630829			3
13	*1825.824769*	913.416023	1808.798220	904.902748	1807.814204	904.410740	L	**260.196868**	130.602072	243.170319	122.088797			2
14							K	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.5	1970.923019	0.024209	EHAVEGDCDFQLLK
7.0	1970.963882	-0.016654	EHWLYPQQITTNQWK
6.7	1970.944138	0.003090	STTMEHPSLGQLSEK
3.4	1970.965729	-0.018501	EAINGQREDTGDQQGLLK
2.8	1970.965881	-0.018653	EDKDPQKMYATIYELK

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

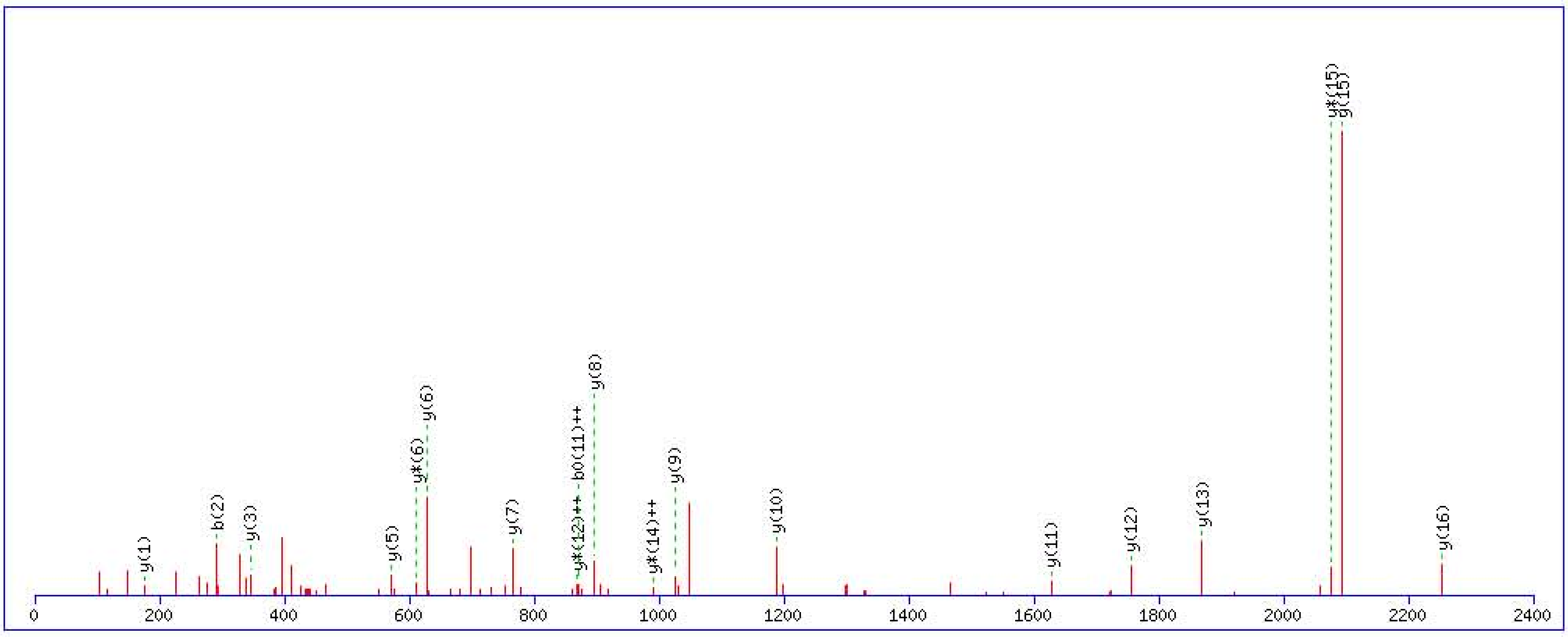
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MCPQLQQYEMHGPEGLR**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

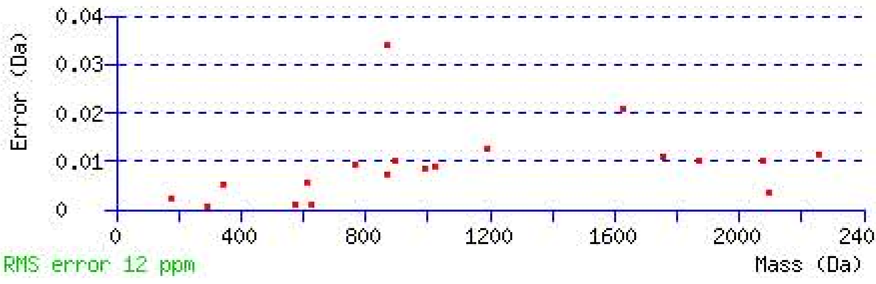
Match to Query 65421: 2384.096202 from(795.706010,3+) rtinseconds(2025) index(63247)
Title: Locus:1.1.1.2702.17 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

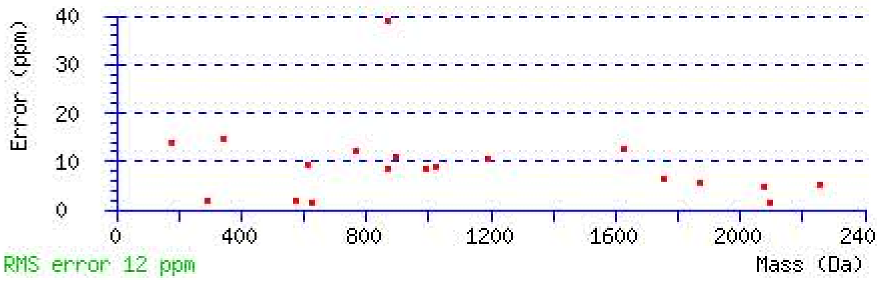
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2384.089767
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 55  Expect: 3.8e-005
Matches : 19/164 fragment ions using 54 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	132.047761	66.527518					M							17
2	292.078410	146.542843					C	***2254.056579***	1127.531927	2237.030030	1119.018653	2236.046014	1118.526645	16
3	389.131174	195.069225					P	***2094.025930***	1047.516603	2076.999381	1039.003328	2076.015365	1038.511320	15
4	517.189752	259.098514	500.163203	250.585240			Q	1996.973166	998.990221	1979.946617	990.476947	1978.962601	989.984939	14
5	630.273816	315.640546	613.247267	307.127272			L	***1868.914588***	934.960932	1851.888039	926.447658	1850.904023	925.955650	13
6	758.332394	379.669835	741.305845	371.156561			Q	***1755.830524***	878.418900	1738.803975	869.905626	1737.819959	869.413618	12
7	1197.557720	599.282498	1180.531171	590.769224			Q	***1627.771946***	814.389611	1610.745397	805.876337	1609.761381	805.384329	11
8	1360.621049	680.814163	1343.594500	672.300888			Y	***1188.546620***	594.776948	1171.520071	586.263674	1170.536055	585.771666	10
9	1489.663642	745.335459	1472.637093	736.822185	1471.653077	736.330177	E	***1025.483291***	513.245284	1008.456742	504.732009	1007.472726	504.240001	9
10	1620.704127	810.855702	1603.677578	802.342427	1602.693562	801.850419	M	***896.440698***	448.723987	879.414149	440.210713	878.430133	439.718705	8
11	1757.763039	879.385158	1740.736490	870.871883	1739.752474	870.379875	H	***765.400213***	383.203745	748.373664	374.690470	747.389648	374.198462	7
12	1814.784503	907.895890	1797.757954	899.382615	1796.773938	898.890607	G	***628.341301***	314.674289	611.314752	306.161014	610.330736	305.669006	6
13	1911.837267	956.422272	1894.810718	947.908997	1893.826702	947.416989	P	***571.319837***	286.163557	554.293288	277.650282	553.309272	277.158274	5
14	2040.879860	1020.943568	2023.853311	1012.430294	2022.869295	1011.938286	E	474.267073	237.637175	457.240524	229.123900	456.256508	228.631892	4
15	2097.901324	1049.454300	2080.874775	1040.941025	2079.890759	1040.449017	G	***345.224480***	173.115878	328.197931	164.602603			3
16	2210.985388	1105.996332	2193.958839	1097.483057	2192.974823	1096.991049	L	288.203016	144.605146	271.176467	136.091872			2
17							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.2	2384.089767	0.006435	MCPQLQQYEMHGPEGLR
47.4	2384.089767	0.006435	MCPQLQQYEMHGPEGLR
28.7	2384.089767	0.006435	MCPQLQQYEMHGPEGLR

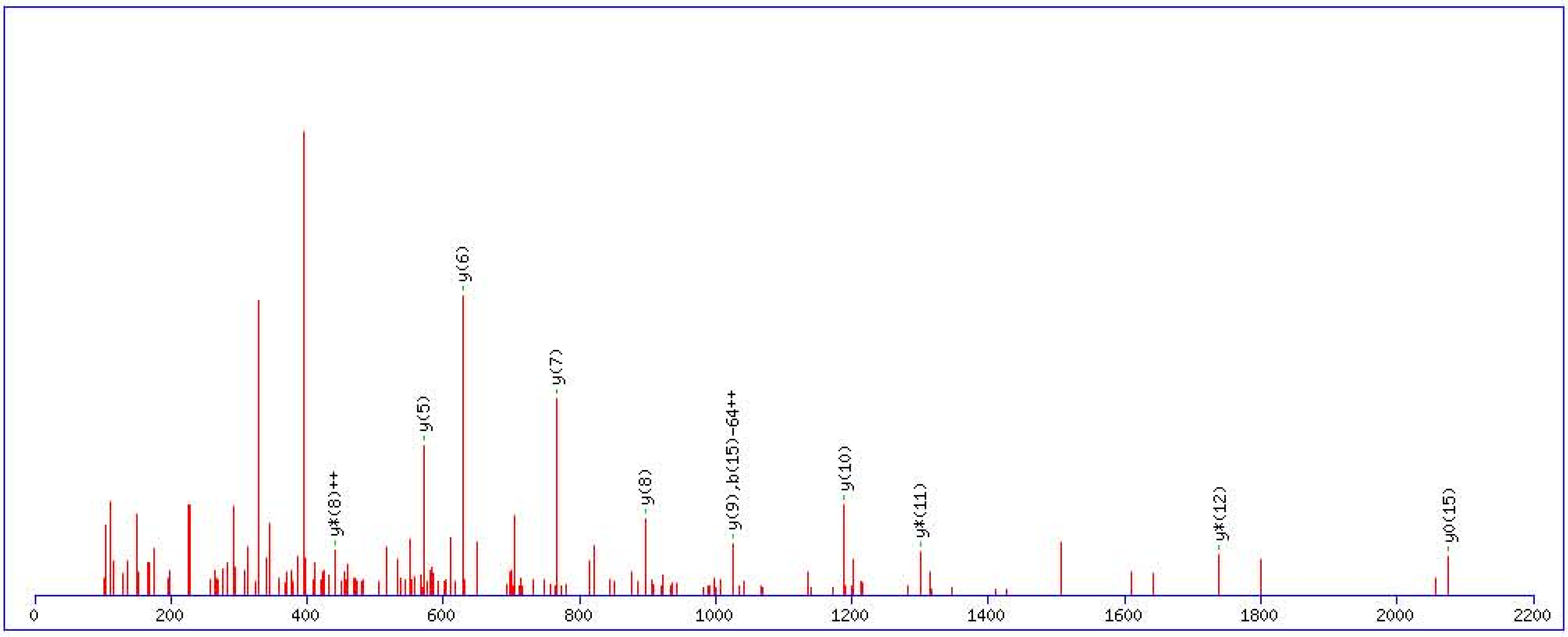
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MCPQLQQYEMHGPEGLR**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

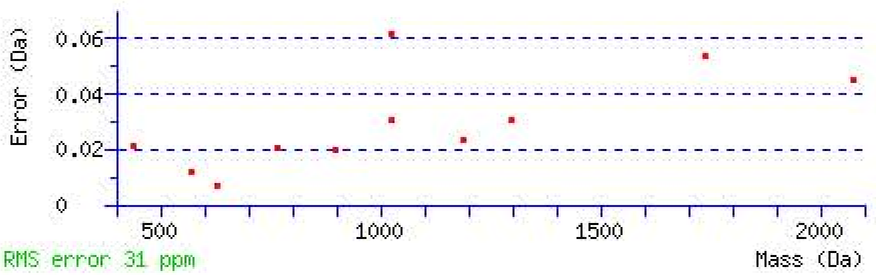
Match to Query 65710: 2400.113696 from(601.035700,4+) rtinseconds(1993) index(25212)
Title: Locus:1.1.1.2546.8 File:"2013-07-02 CLN FXIII 30 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

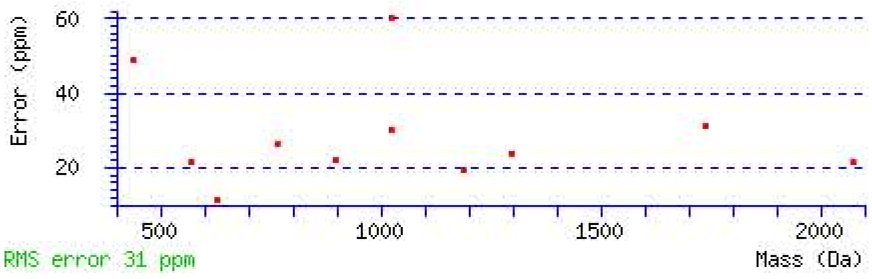
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2400.084686
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 26 **Expect:** 0.038
Matches : 11/238 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.042676	74.524976					M							17
2	308.073325	154.540301					C	2254.056579	1127.531927	2237.030030	1119.018653	2236.046014	1118.526645	16
3	405.126089	203.066683					P	2094.025930	1047.516603	2076.999381	1039.003328	2076.015365	1038.511320	15
4	533.184667	267.095972	516.158118	258.582697			Q	1996.973166	998.990221	1979.946617	990.476947	1978.962601	989.984939	14
5	646.268731	323.638004	629.242182	315.124729			L	1868.914588	934.960932	1851.888039	926.447658	1850.904023	925.955650	13
6	1085.494057	543.250667	1068.467508	534.737392			Q	1755.830524	878.418900	1738.803975	869.905626	1737.819959	869.413618	12
7	1213.552635	607.279956	1196.526086	598.766681			Q	1316.605198	658.806237	1299.578649	650.292963	1298.594633	649.800955	11
8	1376.615964	688.811620	1359.589415	680.298346			Y	***1188.546620***	594.776948	1171.520071	586.263674	1170.536055	585.771666	10
9	1505.658557	753.332917	1488.632008	744.819642	1487.647992	744.327634	E	***1025.483291***	513.245284	1008.456742	504.732009	1007.472726	504.240001	9
10	1636.699042	818.853159	1619.672493	810.339885	1618.688477	809.847877	M	***896.440698***	448.723987	879.414149	440.210713	878.430133	439.718705	8
11	1773.757954	887.382615	1756.731405	878.869341	1755.747389	878.377333	H	***765.400213***	383.203745	748.373664	374.690470	747.389648	374.198462	7
12	1830.779418	915.893347	1813.752869	907.380073	1812.768853	906.888065	G	***628.341301***	314.674289	611.314752	306.161014	610.330736	305.669006	6
13	1927.832182	964.419729	1910.805633	955.906455	1909.821617	955.414447	P	***571.319837***	286.163557	554.293288	277.650282	553.309272	277.158274	5
14	2056.874775	1028.941026	2039.848226	1020.427751	2038.864210	1019.935743	E	474.267073	237.637175	457.240524	229.123900	456.256508	228.631892	4
15	2113.896239	1057.451758	2096.869690	1048.938483	2095.885674	1048.446475	G	345.224480	173.115878	328.197931	164.602603			3
16	2226.980303	1113.993790	2209.953754	1105.480515	2208.969738	1104.988507	L	288.203016	144.605146	271.176467	136.091872			2
17							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.2	2400.084686	0.029010	MCPQLQQYEMHGPEGLR
26.1	2400.084686	0.029010	MCPQLQQYEMHGPEGLR
24.0	2400.084686	0.029010	MCPQLQQYEMHGPEGLR

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

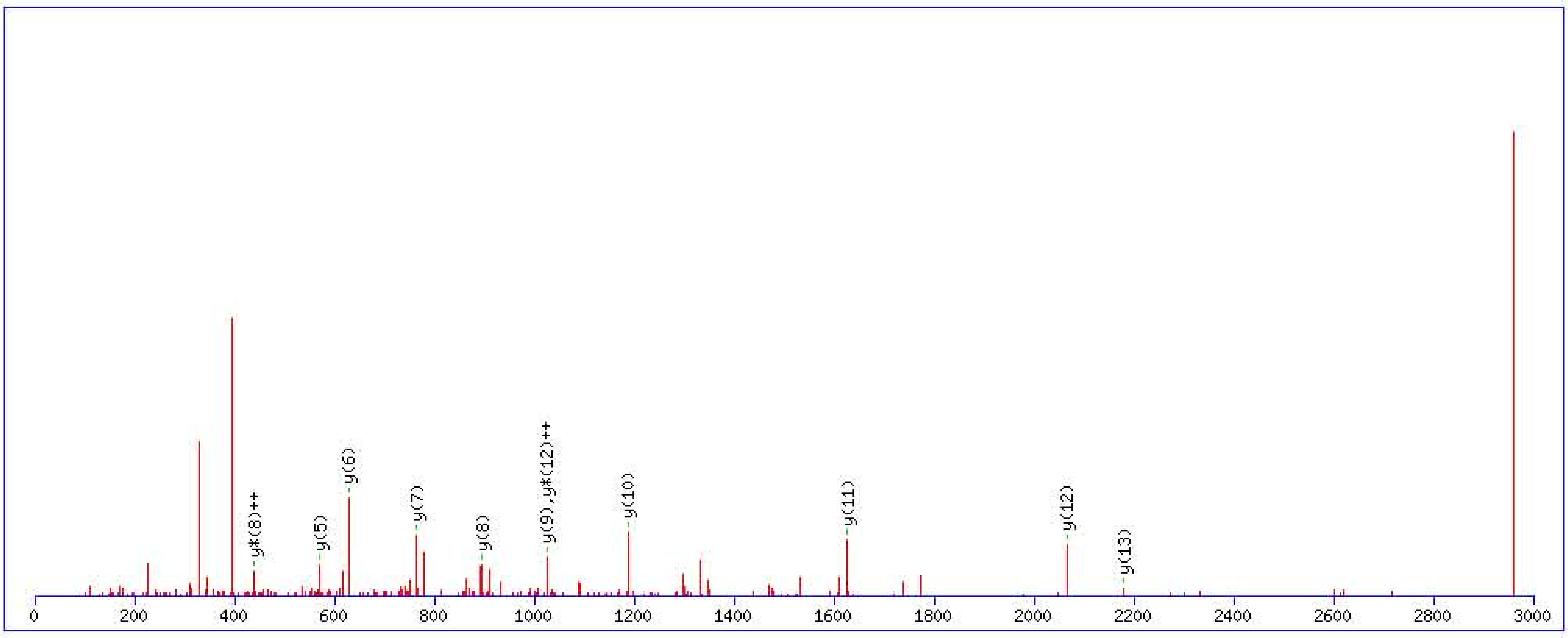
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPKMCPQLQQYEMHGPEGLR**
Found in **A2MG_HUMAN**, Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3

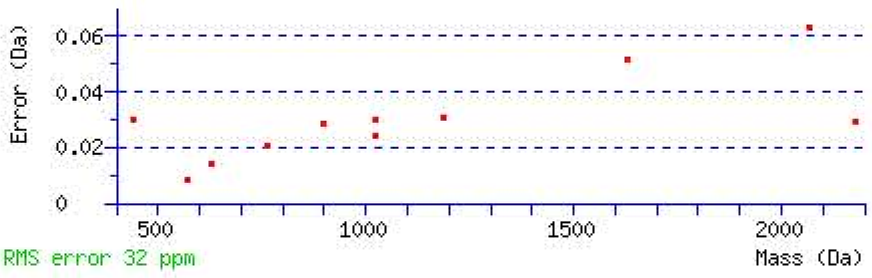
Match to Query 74962: 3064.527936 from(767.139260,4+) rtinseconds(2099) index(44636)
Title: Locus:1.1.1.2759.16 File:"2013-07-02 CLN FXIII 30 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

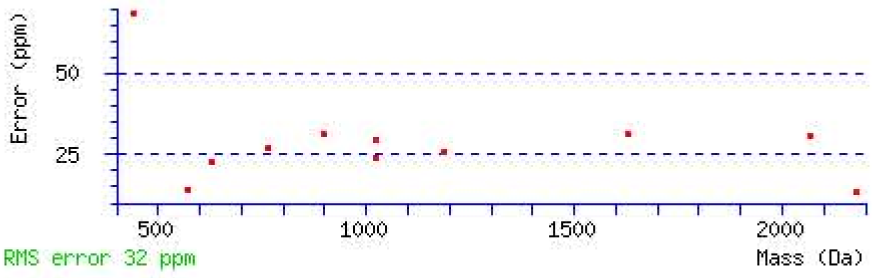
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3064.494110
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Q9 : Biotin:Thermo-21345 (Q)
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 35 **Expect:** 0.0099
Matches : 11/298 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.102239	65.054757	112.075690	56.541483			K							20
2	226.155003	113.581139	209.128454	105.067865			P	2937.406454	1469.206865	2920.379905	1460.693590	2919.395889	1460.201582	19
3	354.249966	177.628621	337.223417	169.115347			K	2840.353690	1420.680483	2823.327141	1412.167208	2822.343125	1411.675200	18
4	501.285366	251.146321	484.258817	242.633047			M	2712.258727	1356.633001	2695.232178	1348.119727	2694.248162	1347.627719	17
5	661.316015	331.161646	644.289466	322.648371			C	2565.223327	1283.115302	2548.196778	1274.602027	2547.212762	1274.110019	16
6	758.368779	379.688028	741.342230	371.174753			P	2405.192678	1203.099977	2388.166129	1194.586702	2387.182113	1194.094694	15
7	886.427357	443.717317	869.400808	435.204042			Q	2308.139914	1154.573595	2291.113365	1146.060320	2290.129349	1145.568312	14
8	999.511421	500.259349	982.484872	491.746074			L	***2180.081336***	1090.544306	2163.054787	1082.031031	2162.070771	1081.539023	13
9	1438.736747	719.872012	1421.710198	711.358737			Q	***2066.997272***	1034.002274	2049.970723	1025.488999	2048.986707	1024.996991	12
10	1877.962073	939.484675	1860.935524	930.971400			Q	***1627.771946***	814.389611	1610.745397	805.876337	1609.761381	805.384329	11
11	2041.025402	1021.016339	2023.998853	1012.503065			Y	***1188.546620***	594.776948	1171.520071	586.263674	1170.536055	585.771666	10
12	2170.067995	1085.537636	2153.041446	1077.024361	2152.057430	1076.532353	E	***1025.483291***	513.245284	1008.456742	504.732009	1007.472726	504.240001	9
13	2301.108480	1151.057878	2284.081931	1142.544604	2283.097915	1142.052596	M	***896.440698***	448.723987	879.414149	440.210713	878.430133	439.718705	8
14	2438.167392	1219.587334	2421.140843	1211.074060	2420.156827	1210.582052	H	***765.400213***	383.203745	748.373664	374.690470	747.389648	374.198462	7
15	2495.188856	1248.098066	2478.162307	1239.584791	2477.178291	1239.092784	G	***628.341301***	314.674289	611.314752	306.161014	610.330736	305.669006	6
16	2592.241620	1296.624448	2575.215071	1288.111173	2574.231055	1287.619166	P	***571.319837***	286.163557	554.293288	277.650282	553.309272	277.158274	5
17	2721.284213	1361.145745	2704.257664	1352.632470	2703.273648	1352.140462	E	474.267073	237.637175	457.240524	229.123900	456.256508	228.631892	4
18	2778.305677	1389.656477	2761.279128	1381.143202	2760.295112	1380.651194	G	345.224480	173.115878	328.197931	164.602603			3
19	2891.389741	1446.198509	2874.363192	1437.685234	2873.379176	1437.193226	L	288.203016	144.605146	271.176467	136.091872			2
20							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.5	3064.494110	0.033826	KPKMCPQLQQYEMHGPEGLR
17.7	3064.494110	0.033826	KPKMCPQLQQYEMHGPEGLR
12.4	3064.494110	0.033826	KPKMCPQLQQYEMHGPEGLR
1.4	3064.494110	0.033826	KPKMCPQLQQYEMHGPEGLR

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

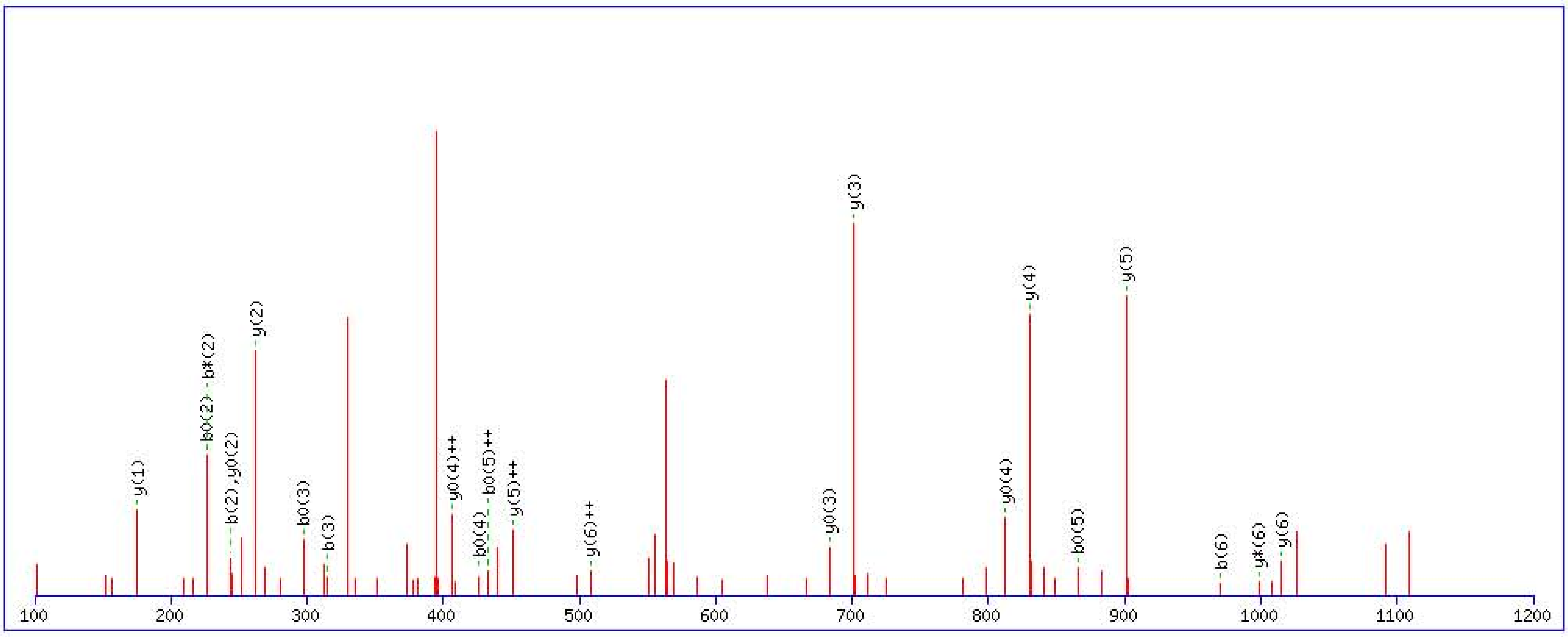
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ENAEQSR**
Found in **ANT3_HUMAN**, Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1

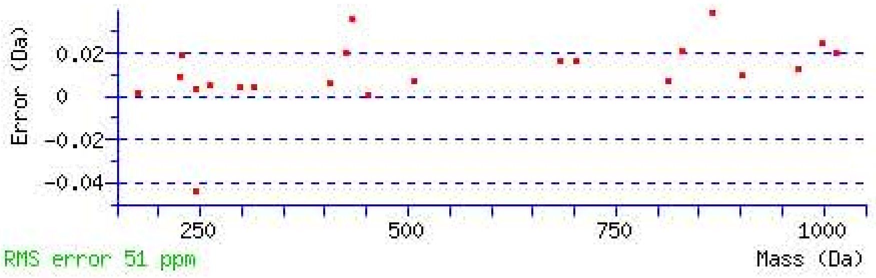
Match to Query 29310: 1143.545108 from(572.779830,2+) rtinseconds(1117) index(19082)
Title: Locus:1.1.1.2241.15 File:"2013-07-02 CLN FXIII 30 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

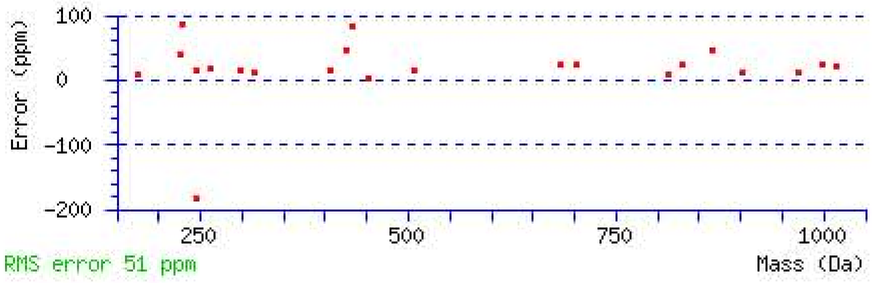
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1143.534225
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.026
Matches : 22/68 fragment ions using 52 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	**E**							7
2	**244.092796**	122.550036	227.066247	114.036762	226.082231	113.544754	**N**	***1015.498940***	508.253108	998.472391	499.739834	997.488375	499.247826	6
3	**315.129910**	158.068593	298.103361	149.555319	297.119345	149.063311	**A**	***901.456013***	451.231645	884.429464	442.718370	883.445448	442.226362	5
4	444.172503	222.589890	427.145954	214.076615	426.161938	213.584607	**E**	***830.418899***	415.713088	813.392350	407.199813	812.408334	406.707805	4
5	883.397829	442.202553	866.371280	433.689278	865.387264	433.197270	**Q**	***701.376306***	351.191791	684.349757	342.678517	683.365741	342.186509	3
6	**970.429857**	485.718567	953.403308	477.205292	952.419292	476.713284	**S**	***262.150980***	131.579128	245.124431	123.065853	244.140415	122.573845	2
7							**R**	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.8	1143.534225	0.010883	ENAEQSR
14.1	1143.552017	-0.006909	VDDGTGREAPK
11.9	1143.549500	-0.004392	WQEQSR
9.5	1143.552002	-0.006894	SSSALDSPAGPR
8.5	1143.551987	-0.006879	ELNGSEAATPR
6.2	1143.549316	-0.004208	SRSRSHSGDR
3.3	1143.556717	-0.011609	THLRCQSSR
3.1	1143.544815	0.000293	DPDPEFPTVK
3.1	1143.552017	-0.006909	GREDGDAPVTK
1.7	1143.530899	0.014209	TPFPDSSTHR

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

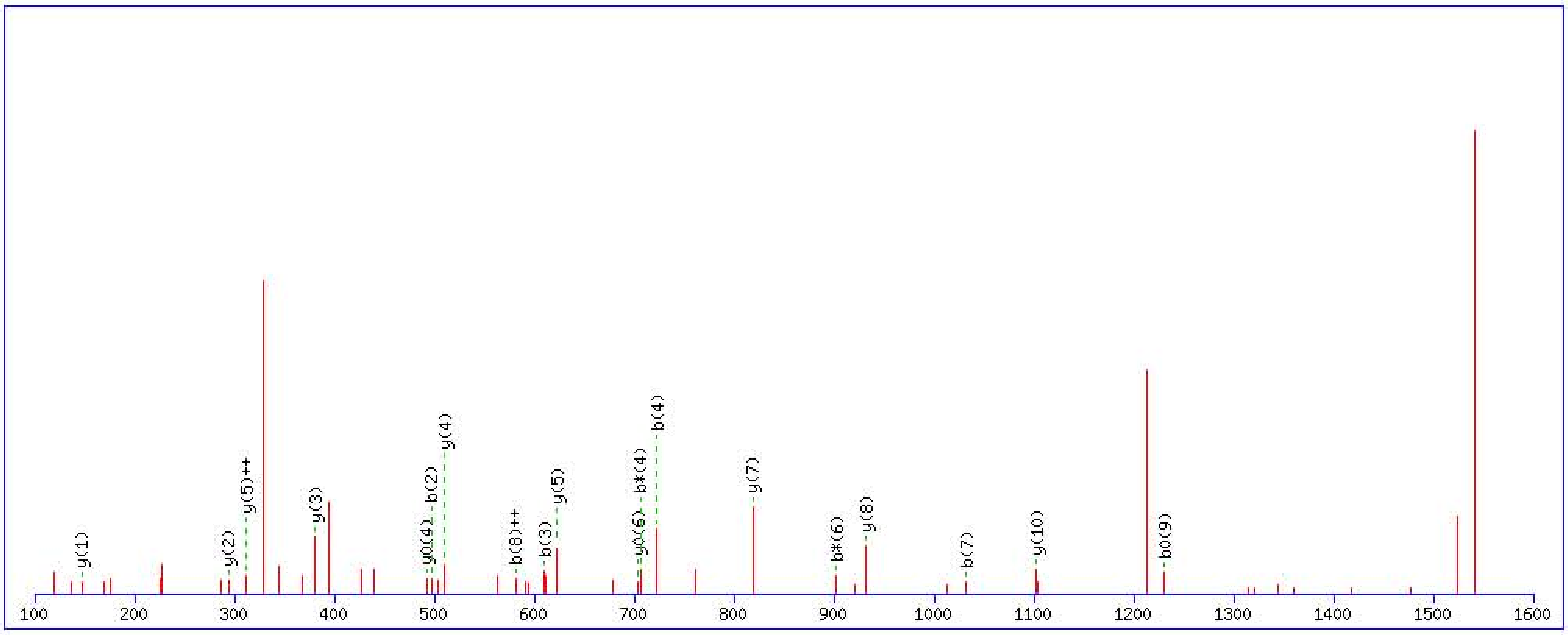
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QGLLPVLESFK**
Found in **APOA1_HUMAN**, Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1

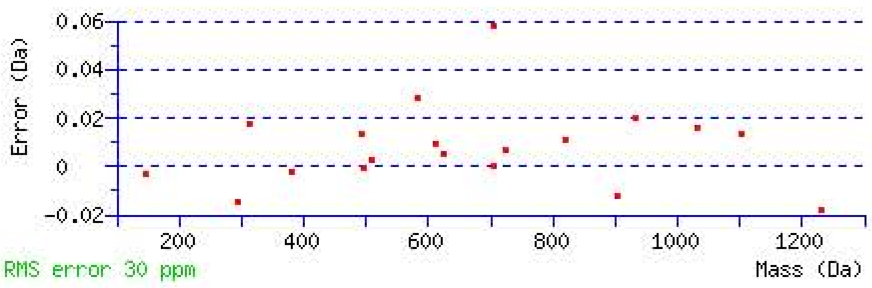
Match to Query 43726: 1540.882188 from(771.448370,2+) rtinseconds(2811) index(85393)
Title: Locus:1.1.1.2857.14 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

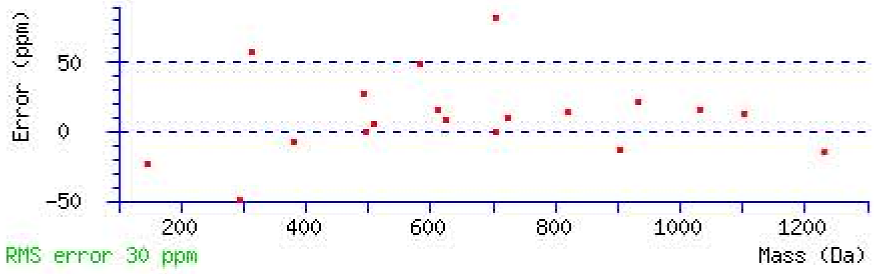
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1540.868713
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.0014
Matches : 19/102 fragment ions using 49 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	440.232602	220.619939	423.206053	212.106664			Q							11
2	**497.254066**	249.130671	480.227517	240.617396			G	***1102.650673***	551.828975	1085.624124	543.315700	1084.640108	542.823692	10
3	**610.338130**	305.672703	593.311581	297.159428			L	1045.629209	523.318243	1028.602660	514.804968	1027.618644	514.312960	9
4	**723.422194**	362.214735	706.395645	353.701461			L	***932.545145***	466.776211	915.518596	458.262936	914.534580	457.770928	8
5	820.474958	410.741117	803.448409	402.227843			P	***819.461081***	410.234179	802.434532	401.720904	801.450516	401.228896	7
6	919.543372	460.275324	902.516823	451.762049			V	722.408317	361.707797	705.381768	353.194522	704.397752	352.702514	6
7	**1032.627436**	516.817356	1015.600887	508.304082			L	***623.339903***	312.173590	606.313354	303.660315	605.329338	303.168307	5
8	1161.670029	581.338653	1144.643480	572.825378	1143.659464	572.333370	E	***510.255839***	255.631558	493.229290	247.118283	492.245274	246.626275	4
9	1248.702057	624.854667	1231.675508	616.341392	1230.691492	615.849384	S	***381.213246***	191.110261	364.186697	182.596987	363.202681	182.104979	3
10	1395.770471	698.388874	1378.743922	689.875599	1377.759906	689.383591	F	***294.181218***	147.594247	277.154669	139.080973			2
11							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.2	1540.868713	0.013475	QGLLPVLESFK
3.7	1540.894531	-0.012343	QAVLSMVRKAK
0.7	1540.891174	-0.008986	QVLALRIDFR

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

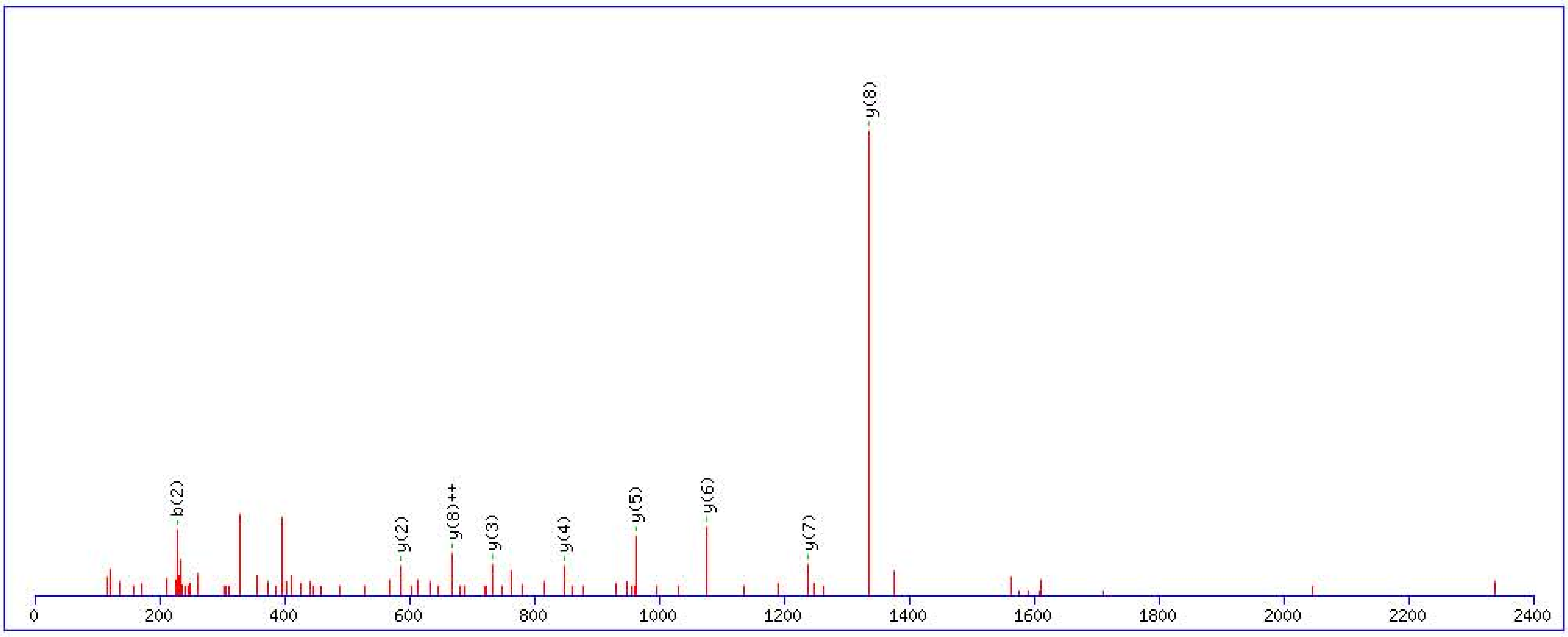
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQPYLDDFQK**
Found in **APOA1_HUMAN**, Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1

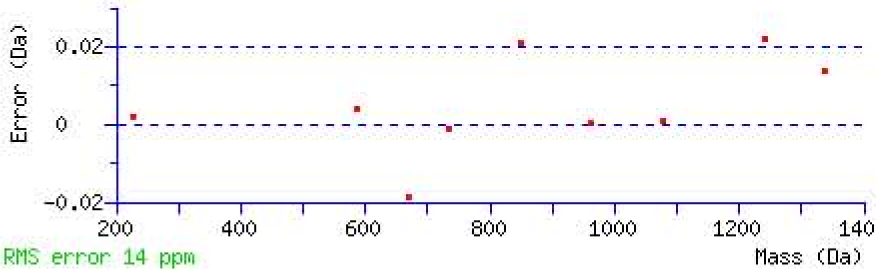
Match to Query 44254: 1562.786548 from(782.400550,2+) rtinseconds(2200) index(81627)
Title: Locus:1.1.1.2645.22 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

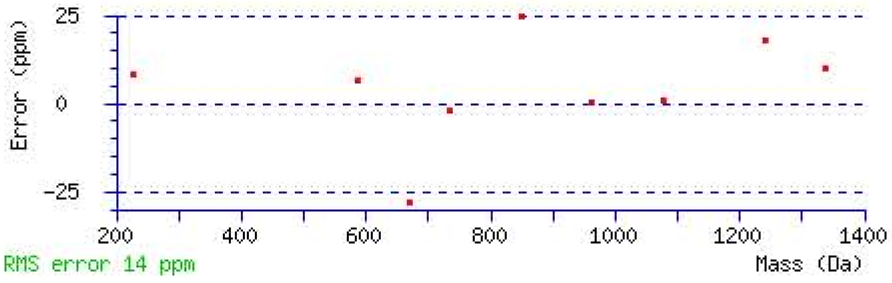
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1562.780304
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 52 **Expect:** 0.0001
Matches : 9/90 fragment ions using 13 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					V							10
2	**228.134268**	114.570772	211.107719	106.057498			Q	1464.719165	732.863221	1447.692616	724.349946	1446.708600	723.857938	9
3	325.187032	163.097154	308.160483	154.583879			P	***1336.660587***	668.833932	1319.634038	660.320657	1318.650022	659.828649	8
4	488.250361	244.628818	471.223812	236.115544			Y	***1239.607823***	620.307550	1222.581274	611.794275	1221.597258	611.302267	7
5	601.334425	301.170851	584.307876	292.657576			L	***1076.544494***	538.775885	1059.517945	530.262611	1058.533929	529.770603	6
6	716.361368	358.684322	699.334819	350.171047	698.350803	349.679039	D	***963.460430***	482.233853	946.433881	473.720579	945.449865	473.228571	5
7	831.388311	416.197793	814.361762	407.684519	813.377746	407.192511	D	***848.433487***	424.720382	831.406938	416.207107	830.422922	415.715099	4
8	978.456725	489.732000	961.430176	481.218726	960.446160	480.726718	F	***733.406544***	367.206910	716.379995	358.693636			3
9	1417.682051	709.344664	1400.655502	700.831389	1399.671486	700.339381	Q	***586.338130***	293.672703	569.311581	285.159429			2
10							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VQPYLDDFQK
(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	1562.780304	0.006244	VQPYLDDFQK
9.4	1562.808624	-0.022076	LNSPTTTSQIMARK
2.2	1562.804764	-0.018216	QVEELLMAMEKVK
1.5	1562.768860	0.017688	LNFGASLQQTAEER
1.3	1562.805252	-0.018704	RATIVSLEDFEQR
0.8	1562.787521	-0.000973	VQLVDNVYCIGQR
0.8	1562.804764	-0.018216	QVEELLMAMEKVK
0.5	1562.769714	0.016834	YAVMRAAEMHQLK

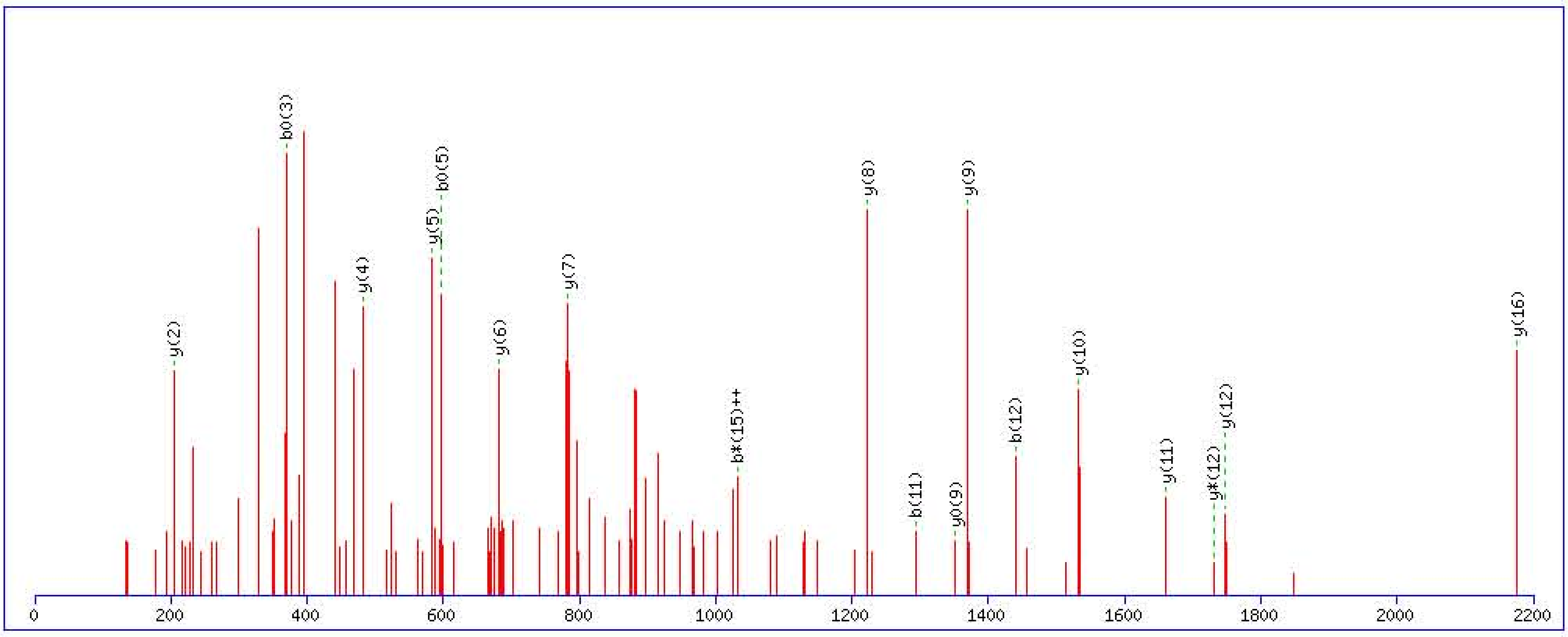
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EPCVESLVSQYFQTVTDYGK**
Found in **APOA2_HUMAN**, Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1

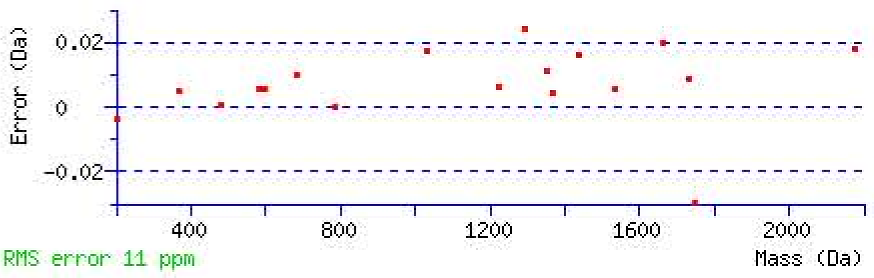
Match to Query 70246: 2660.267862 from(887.763230,3+) rtinseconds(3095) index(69855)
Title: Locus:1.1.1.3071.13 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

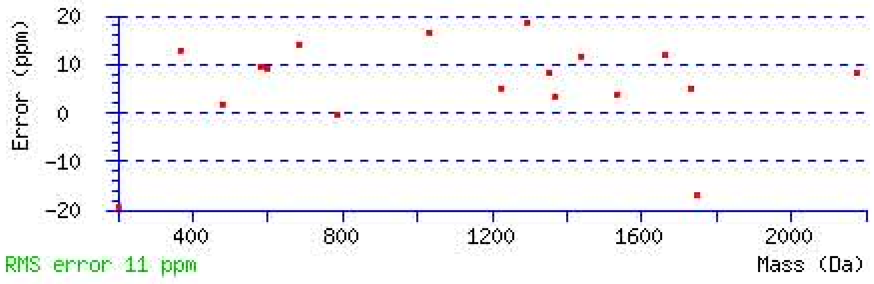
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2660.250244
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 60  Expect: 2.5e-006
Matches : 18/204 fragment ions using 34 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							20
2	227.102633	114.054954			209.092068	105.049672	P	2532.214913	1266.611094	2515.188364	1258.097820	2514.204348	1257.605812	19
3	387.133282	194.070279			369.122717	185.064997	C	2435.162149	1218.084712	2418.135600	1209.571438	2417.151584	1209.079430	18
4	486.201696	243.604486			468.191131	234.599204	V	2275.131500	1138.069388	2258.104951	1129.556113	2257.120935	1129.064105	17
5	615.244289	308.125783			597.233724	299.120500	E	***2176.063086***	1088.535181	2159.036537	1080.021906	2158.052521	1079.529898	16
6	702.276317	351.641797			684.265752	342.636514	S	2047.020493	1024.013885	2029.993944	1015.500610	2029.009928	1015.008602	15
7	815.360381	408.183829			797.349816	399.178546	L	1959.988465	980.497871	1942.961916	971.984596	1941.977900	971.492588	14
8	914.428795	457.718036			896.418230	448.712753	V	1846.904401	923.955839	1829.877852	915.442564	1828.893836	914.950556	13
9	1001.460823	501.234050			983.450258	492.228767	S	***1747.835987***	874.421632	1730.809438	865.908357	1729.825422	865.416349	12
10	1129.519401	565.263339	1112.492852	556.750064	1111.508836	556.258056	Q	***1660.803959***	830.905618	1643.777410	822.392343	1642.793394	821.900335	11
11	**1292.582730**	646.795003	1275.556181	638.281729	1274.572165	637.789721	Y	***1532.745381***	766.876329	1515.718832	758.363054	1514.734816	757.871046	10
12	**1439.651144**	720.329210	1422.624595	711.815936	1421.640579	711.323928	F	***1369.682052***	685.344664	1352.655503	676.831390	1351.671487	676.339382	9
13	1878.876470	939.941873	1861.849921	931.428599	1860.865905	930.936591	Q	***1222.613638***	611.810457	1205.587089	603.297183	1204.603073	602.805175	8
14	1979.924149	990.465713	1962.897600	981.952438	1961.913584	981.460430	T	***783.388312***	392.197794	766.361763	383.684519	765.377747	383.192511	7
15	2078.992563	1039.999920	2061.966014	1031.486645	2060.981998	1030.994637	V	***682.340633***	341.673954	665.314084	333.160680	664.330068	332.668672	6
16	2180.040242	1090.523759	2163.013693	1082.010484	2162.029677	1081.518476	T	***583.272219***	292.139747	566.245670	283.626473	565.261654	283.134465	5
17	2295.067185	1148.037230	2278.040636	1139.523956	2277.056620	1139.031948	D	***482.224540***	241.615908	465.197991	233.102633	464.213975	232.610625	4
18	2458.130514	1229.568895	2441.103965	1221.055620	2440.119949	1220.563612	Y	367.197597	184.102436	350.171048	175.589162			3
19	2515.151978	1258.079627	2498.125429	1249.566352	2497.141413	1249.074344	G	***204.134268***	102.570772	187.107719	94.057497			2
20							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.2	2660.250244	0.017618	EPCVESLVSQYFQTVTDYGK
26.3	2660.250244	0.017618	EPCVESLVSQYFQTVTDYGK
0.4	2660.289917	-0.022055	EAKDMLYKMLSENFMSLQEIPK

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

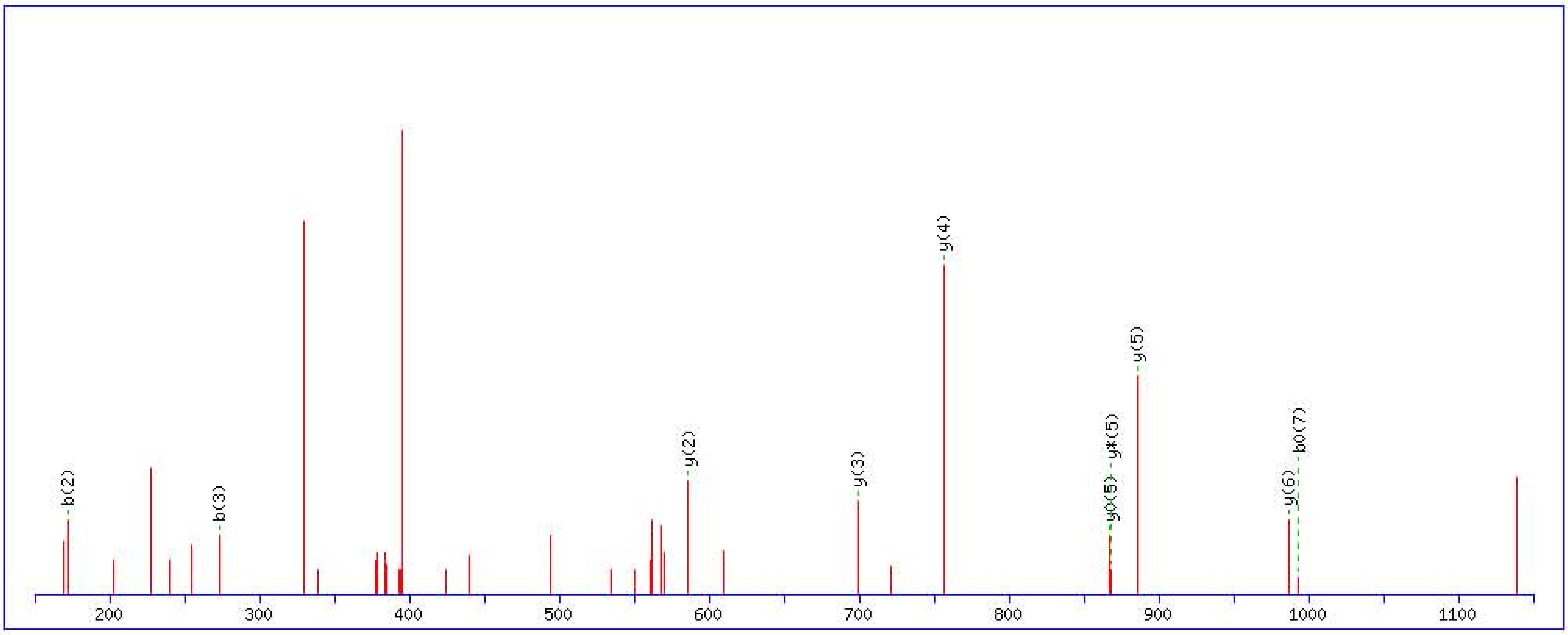
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNTEGLQK**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

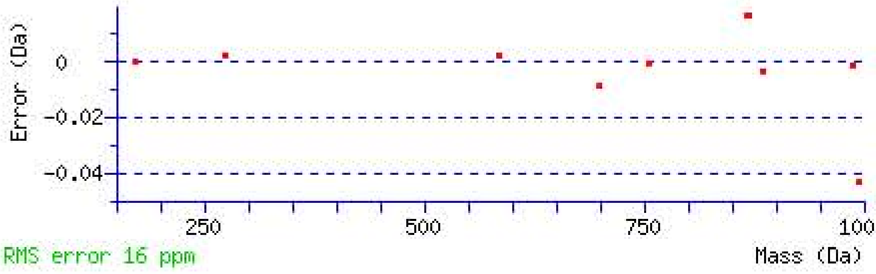
Match to Query 29838: 1156.586588 from(579.300570,2+) rtinseconds(1451) index(76533)
Title: Locus:1.1.1.2384.24 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

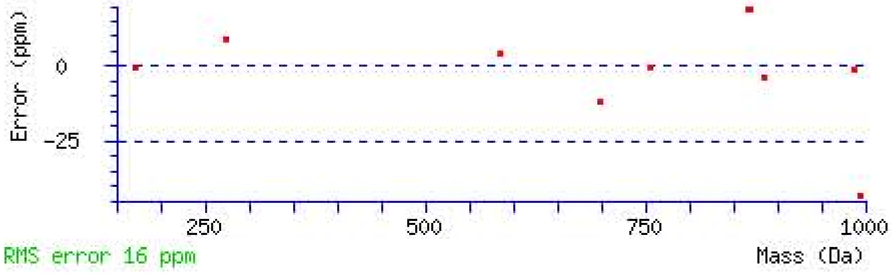
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1156.591034
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 32 **Expect:** 0.012
Matches : 10/70 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.028740	29.518008					G							8
2	**172.071667**	86.539471	155.045118	78.026197			N	1100.576857	550.792067	1083.550308	542.278792	1082.566292	541.786784	7
3	**273.119346**	137.063311	256.092797	128.550037	255.108781	128.058029	T	***986.533930***	493.770603	969.507381	485.257329	968.523365	484.765321	6
4	402.161939	201.584608	385.135390	193.071333	384.151374	192.579325	E	***885.486251***	443.246764	868.459702	434.733489	867.475686	434.241481	5
5	459.183403	230.095339	442.156854	221.582065	441.172838	221.090057	G	***756.443658***	378.725467	739.417109	370.212193			4
6	572.267467	286.637372	555.240918	278.124097	554.256902	277.632089	L	***699.422194***	350.214735	682.395645	341.701461			3
7	1011.492793	506.250035	994.466244	497.736760	993.482228	497.244752	Q	***586.338130***	293.672703	569.311581	285.159429			2
8							K	147.112804	74.060040	130.086255	65.546766			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.9	1156.591034	-0.004446	GNTEGLQK

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

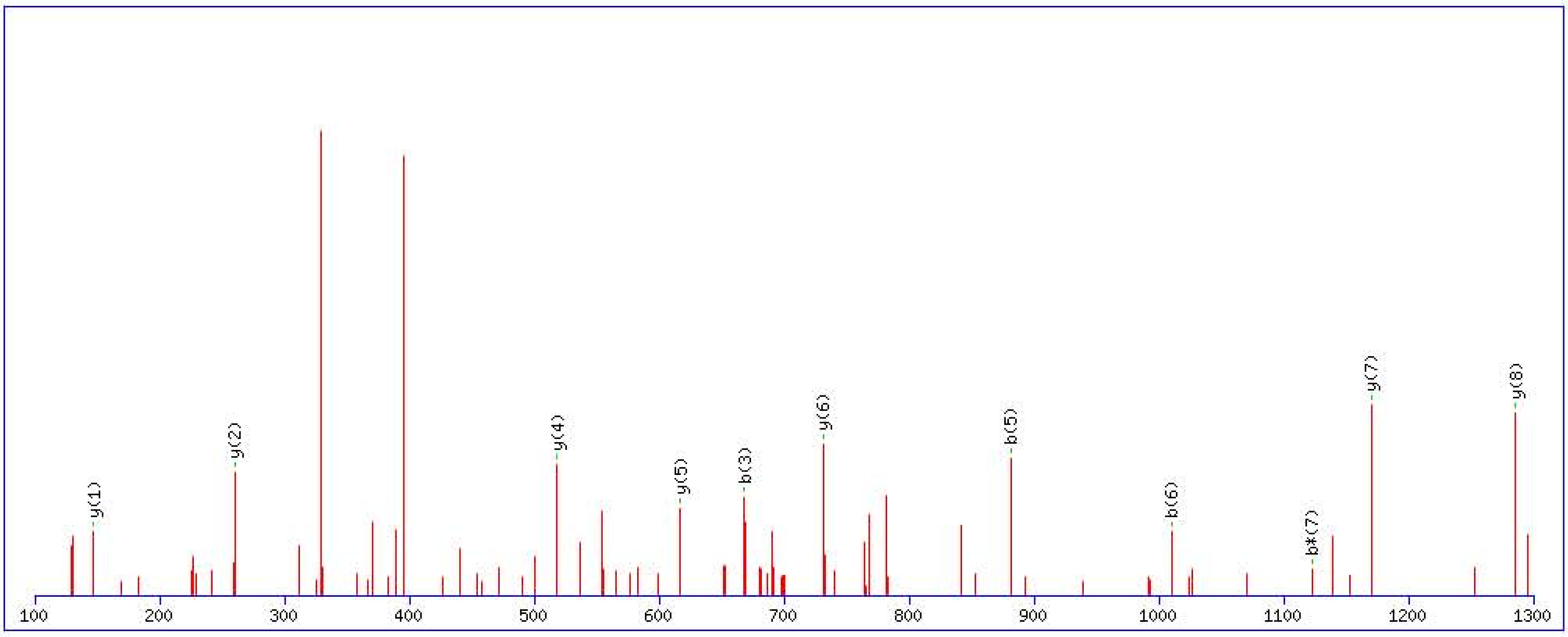
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IDQNVEELK**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

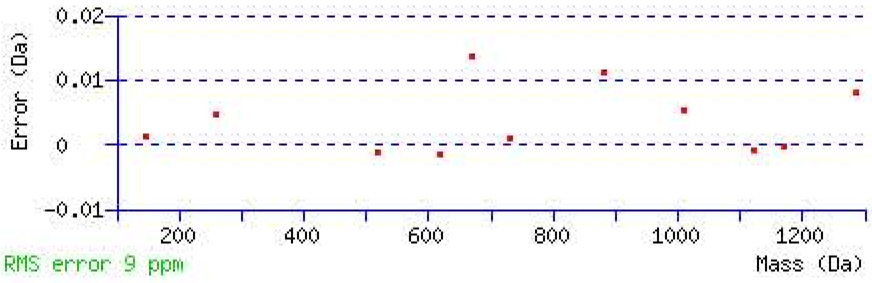
Match to Query 38844: 1397.726468 from(699.870510,2+) rtinseconds(1855) index(79251)
Title: Locus:1.1.1.2525.18 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

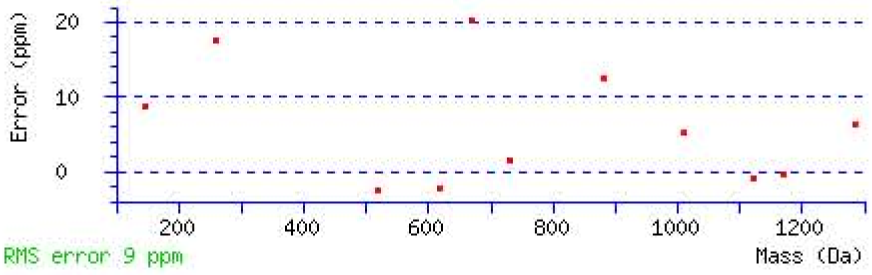
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1397.722427
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 65 **Expect:** 9.1e-006
Matches : 11/86 fragment ions using 12 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							9
2	229.118283	115.062779			211.107718	106.057497	D	*1285.645664*	643.326470	1268.619115	634.813196	1267.635099	634.321187	8
3	**668.343609**	334.675443	651.317060	326.162168	650.333044	325.670160	Q	*1170.618721*	585.812998	1153.592172	577.299724	1152.608156	576.807716	7
4	782.386536	391.696906	765.359987	383.183631	764.375971	382.691623	N	*731.393395*	366.200335	714.366846	357.687061	713.382830	357.195053	6
5	**881.454950**	441.231113	864.428401	432.717838	863.444385	432.225830	V	*617.350468*	309.178872	600.323919	300.665597	599.339903	300.173589	5
6	**1010.497543**	505.752410	993.470994	497.239135	992.486978	496.747127	E	*518.282054*	259.644665	501.255505	251.131390	500.271489	250.639382	4
7	1139.540136	570.273706	1122.513587	561.760431	1121.529571	561.268423	E	389.239461	195.123368	372.212912	186.610094	371.228896	186.118086	3
8	1252.624200	626.815738	1235.597651	618.302463	1234.613635	617.810455	L	*260.196868*	130.602072	243.170319	122.088797			2
9							K	*147.112804*	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.5	1397.722427	0.004041	IDQNVEELK
13.5	1397.744873	-0.018405	QRREEELK
11.4	1397.734329	-0.007861	LYTHSYLGFGLK
9.8	1397.744873	-0.018405	MLEKARHQELK
8.4	1397.733658	-0.007190	QNITNQLEK
8.3	1397.715042	0.011426	LQESQPGNAVIDK
7.9	1397.722412	0.004056	QLEAQLEEK
7.0	1397.733658	-0.007190	EVDQREALK
6.4	1397.744904	-0.018436	SSGPQRAGSLK
5.9	1397.733658	-0.007190	NQQTENLLK

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

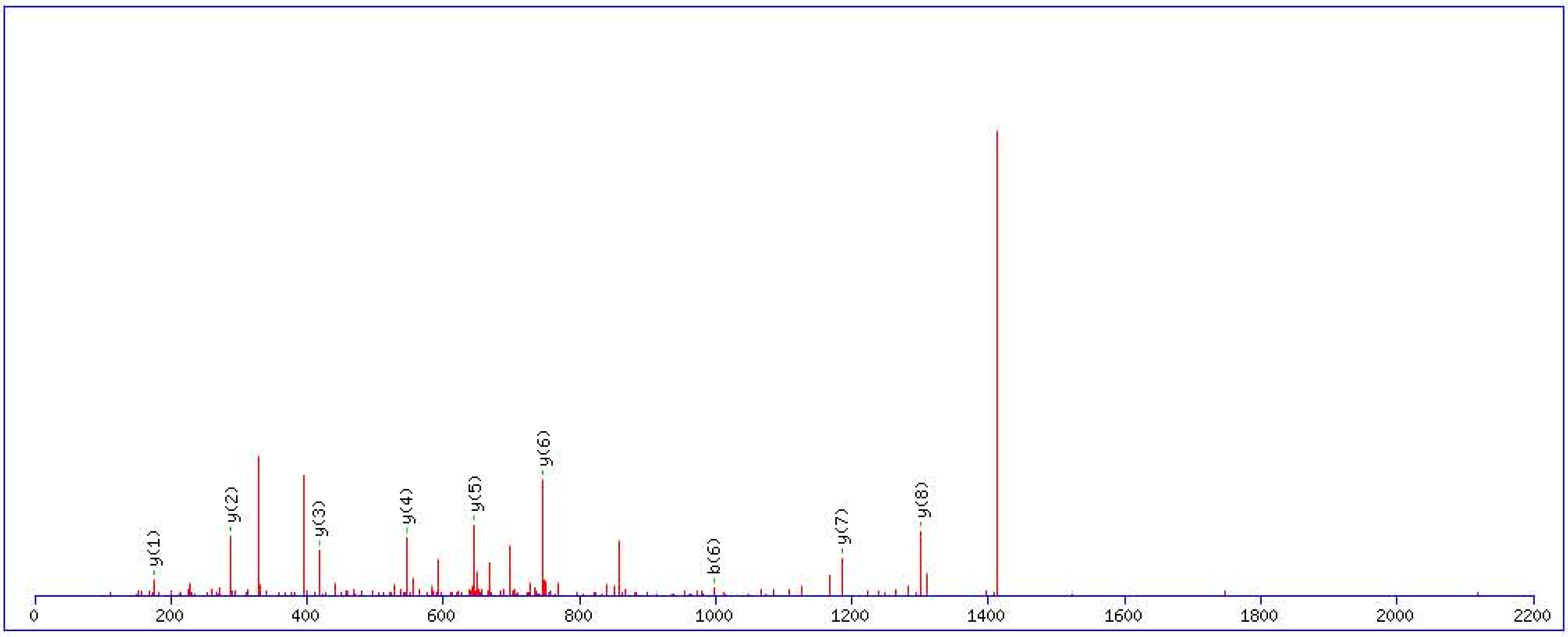
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IDQTVEELR**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

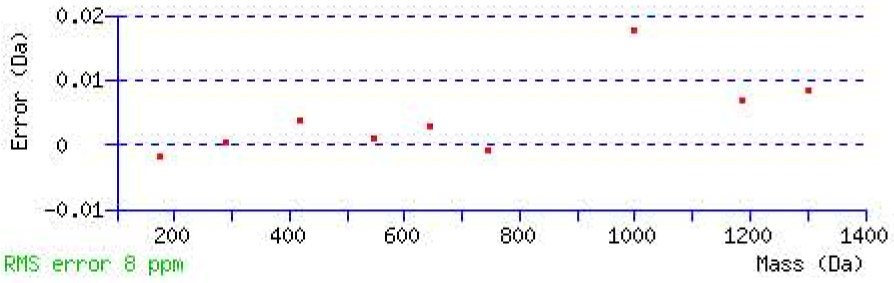
Match to Query 39801: 1412.736128 from(707.375340,2+) rtinseconds(1926) index(79697)
Title: Locus:1.1.1.2550.15 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

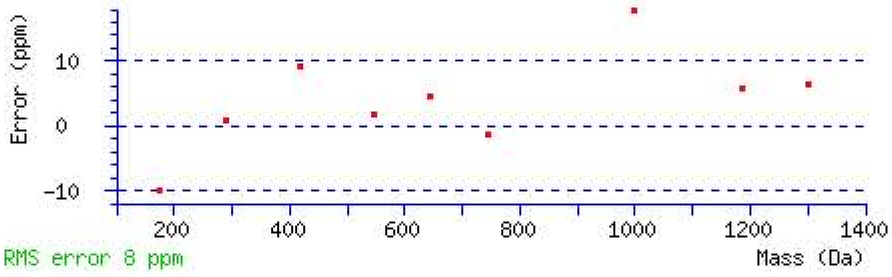
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1412.733337
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 69 **Expect:** 3.3e-006
Matches : 9/86 fragment ions using 13 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					I							9
2	229.118283	115.062779			211.107718	106.057497	D	***1300.656564***	650.831920	1283.630015	642.318646	1282.645999	641.826638	8
3	668.343609	334.675443	651.317060	326.162168	650.333044	325.670160	Q	***1185.629621***	593.318449	1168.603072	584.805174	1167.619056	584.313166	7
4	769.391288	385.199282	752.364739	376.686008	751.380723	376.194000	T	***746.404295***	373.705786	729.377746	365.192511	728.393730	364.700503	6
5	868.459702	434.733489	851.433153	426.220215	850.449137	425.728207	V	***645.356616***	323.181946	628.330067	314.668672	627.346051	314.176664	5
6	**997.502295**	499.254786	980.475746	490.741511	979.491730	490.249503	E	***546.288202***	273.647739	529.261653	265.134465	528.277637	264.642457	4
7	1126.544888	563.776082	1109.518339	555.262808	1108.534323	554.770800	E	***417.245609***	209.126442	400.219060	200.613168	399.235044	200.121160	3
8	1239.628952	620.318114	1222.602403	611.804840	1221.618387	611.312832	L	***288.203016***	144.605146	271.176467	136.091871			2
9							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
69.1	1412.733337	0.002791	IDQTVEELR
15.4	1412.744537	-0.008409	IPPEKMRELER
8.8	1412.741211	-0.005083	KVTIYSFTGNQR
8.7	1412.734665	0.001463	MPADWRQQLLR
6.2	1412.733322	0.002806	LSEEIDQLR
5.4	1412.737167	-0.001039	ARPEDVISEGRGK
4.5	1412.719391	0.016737	LKAEMDEHRLR
4.2	1412.752441	-0.016313	QVHIPPNPQDLR
3.4	1412.752411	-0.016283	LLEIQADYHRR
3.1	1412.752396	-0.016268	AEKPKLHYSNAR

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

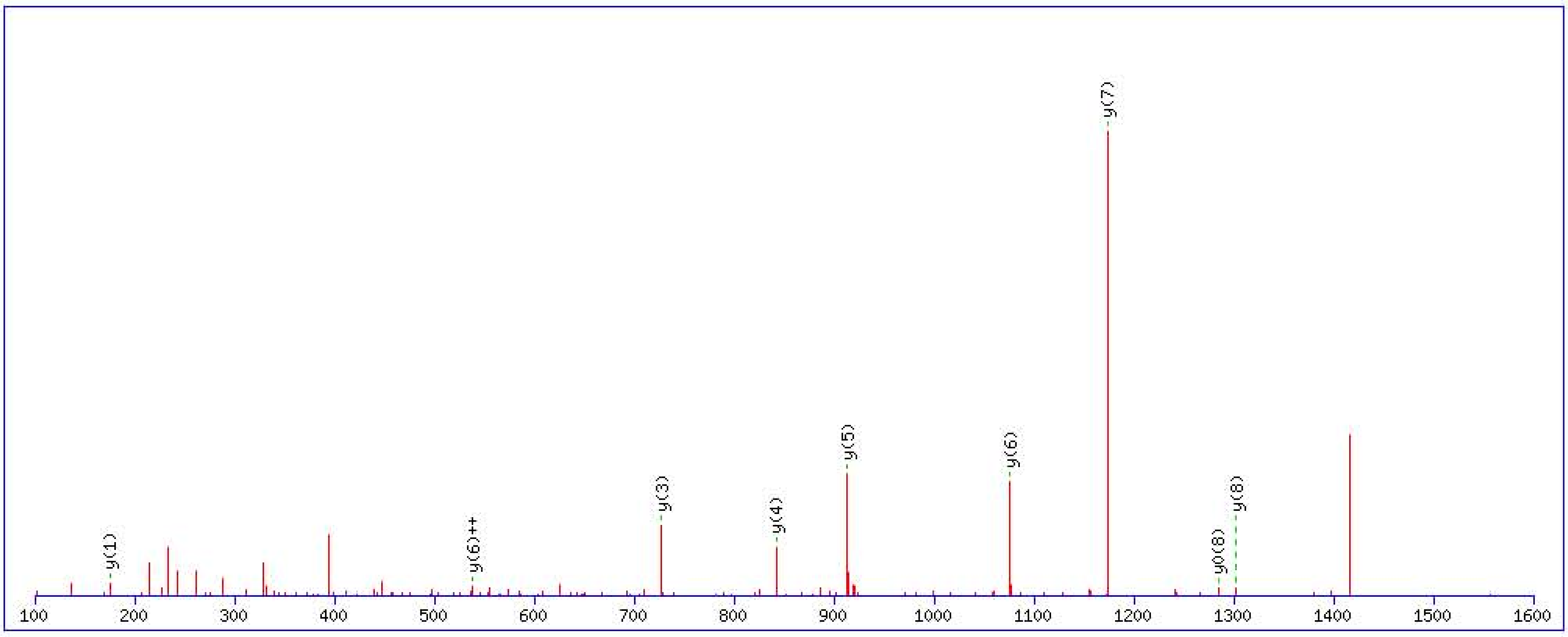
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LEPYADQLR**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

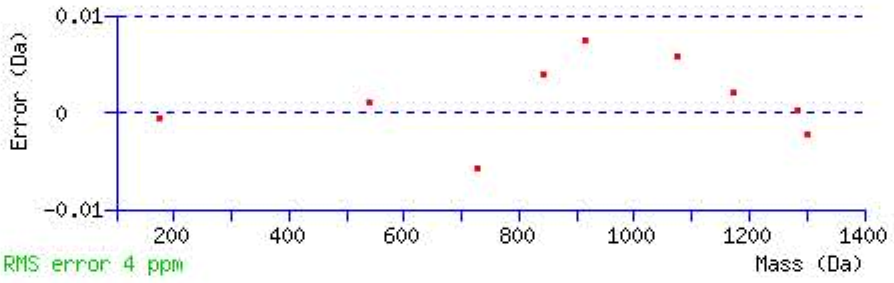
Match to Query 39827: 1414.730288 from(708.372420,2+) rtinseconds(2005) index(80337)
Title: Locus:1.1.1.2577.11 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

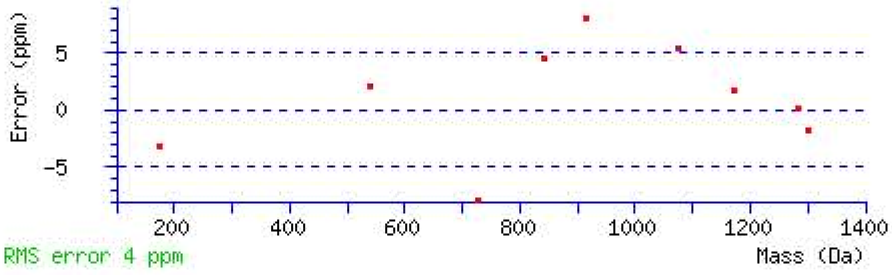
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1414.727844
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 56  Expect: 3.6e-005
Matches : 9/76 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							9
2	243.133933	122.070605			225.123368	113.065322	E	***1302.651085***	651.829181	1285.624536	643.315906	1284.640520	642.823898	8
3	340.186697	170.596987			322.176132	161.591704	P	***1173.608492***	587.307884	1156.581943	578.794610	1155.597927	578.302602	7
4	503.250026	252.128651			485.239461	243.123369	Y	***1076.555728***	538.781502	1059.529179	530.268228	1058.545163	529.776220	6
5	574.287140	287.647208			556.276575	278.641926	A	***913.492399***	457.249838	896.465850	448.736563	895.481834	448.244555	5
6	689.314083	345.160680			671.303518	336.155397	D	***842.455285***	421.731281	825.428736	413.218006	824.444720	412.725998	4
7	1128.539409	564.773343	1111.512860	556.260068	1110.528844	555.768060	Q	***727.428342***	364.217809	710.401793	355.704535			3
8	1241.623473	621.315375	1224.596924	612.802100	1223.612908	612.310092	L	288.203016	144.605146	271.176467	136.091871			2
9							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.8	1414.727844	0.002444	LEPYADQLR
7.9	1414.712585	0.017703	EISTEEQLR
5.0	1414.731689	-0.001401	NKAEFHQSVISR
4.1	1414.716400	0.013888	LEEDARLEERR
2.7	1414.735062	-0.004774	IQLMQEVDRQR
1.5	1414.741547	-0.011259	LEKENLEERQK
0.3	1414.741577	-0.011289	LETVQADNIREK
0.3	1414.741577	-0.011289	ELDVEVSRLEAR

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

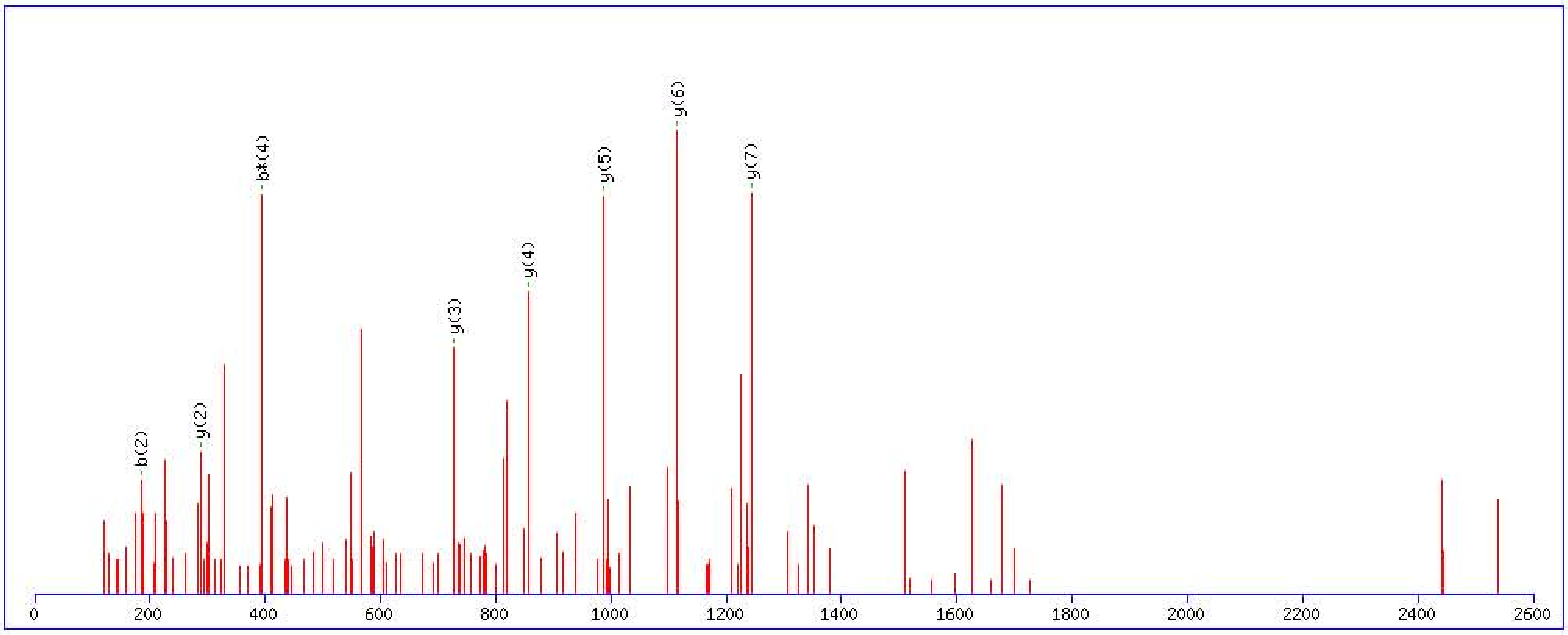
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALVQQMEQLR**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

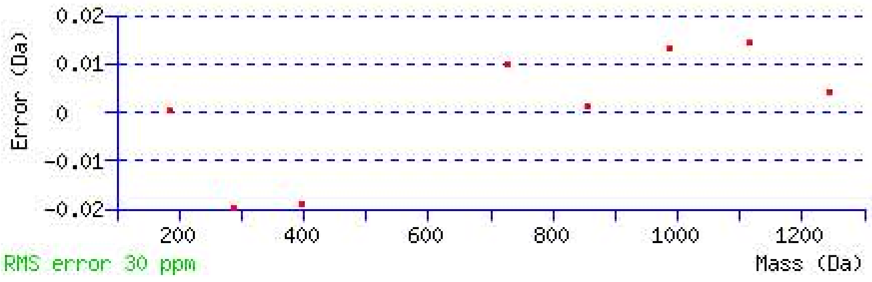
Match to Query 43378: 1525.821028 from(763.917790,2+) rtinseconds(2139) index(81204)
Title: Locus:1.1.1.2624.14 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

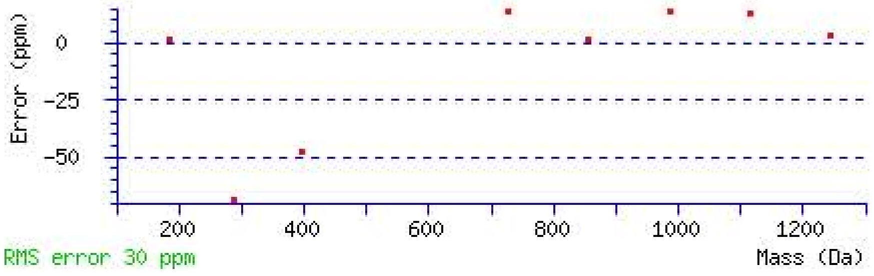
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1525.810867
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 38 **Expect:** 0.0008
Matches : 8/84 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							10
2	**185.128454**	93.067865					L	1455.781054	728.394165	1438.754505	719.880890	1437.770489	719.388882	9
3	284.196868	142.602072					V	1342.696990	671.852133	1325.670441	663.338858	1324.686425	662.846850	8
4	412.255446	206.631361	395.228897	198.118087			Q	***1243.628576***	622.317926	1226.602027	613.804651	1225.618011	613.312643	7
5	540.314024	270.660650	523.287475	262.147376			Q	***1115.569998***	558.288637	1098.543449	549.775362	1097.559433	549.283354	6
6	671.354509	336.180893	654.327960	327.667618			M	***987.511420***	494.259348	970.484871	485.746073	969.500855	485.254065	5
7	800.397102	400.702189	783.370553	392.188915	782.386537	391.696907	E	***856.470935***	428.739105	839.444386	420.225831	838.460370	419.733823	4
8	1239.622428	620.314852	1222.595879	611.801578	1221.611863	611.309569	Q	***727.428342***	364.217809	710.401793	355.704534			3
9	1352.706492	676.856884	1335.679943	668.343609	1334.695927	667.851601	L	***288.203016***	144.605146	271.176467	136.091871			2
10							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.3	1525.810867	0.010161	ALVQQMEQLR
10.2	1525.810867	0.010161	ALVQQMEQLR
5.1	1525.807495	0.013533	WPPQQLMLSAALR
1.8	1525.817383	0.003645	IPSNILLPEDKCK

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

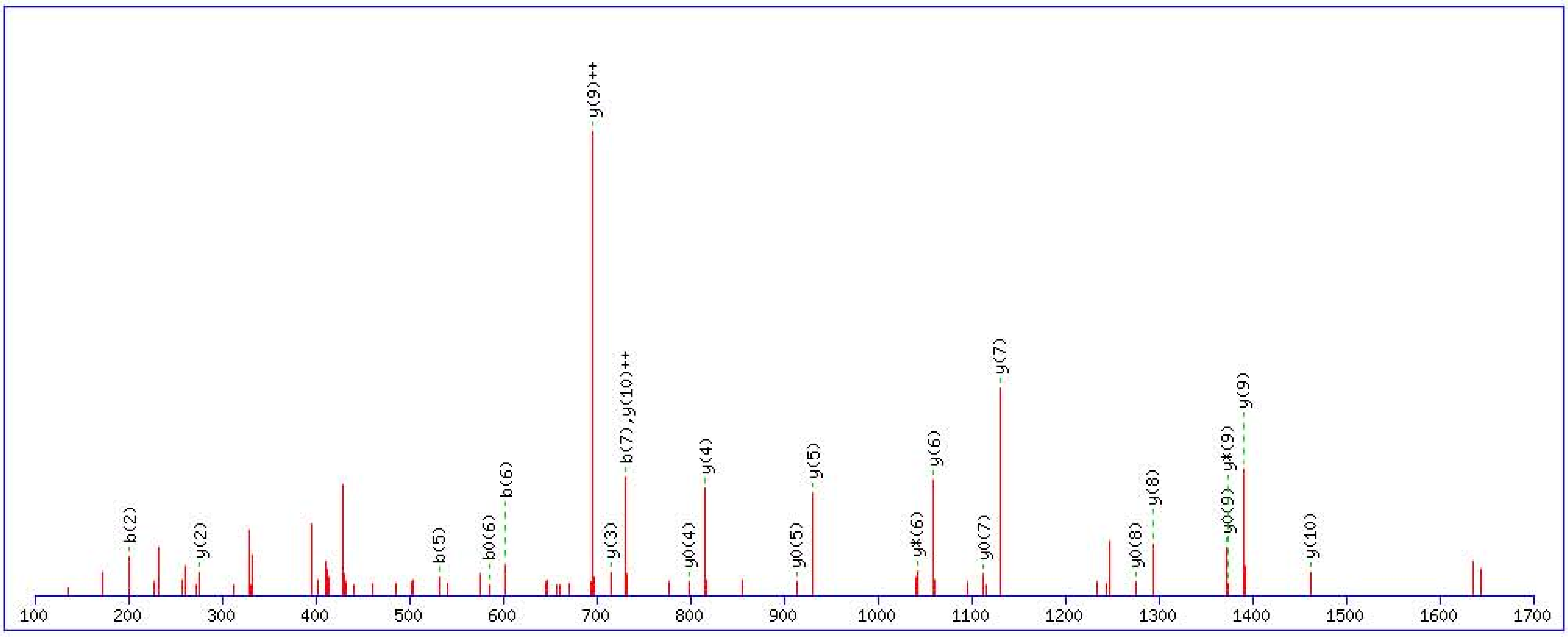
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLAPYAQDTQEK**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

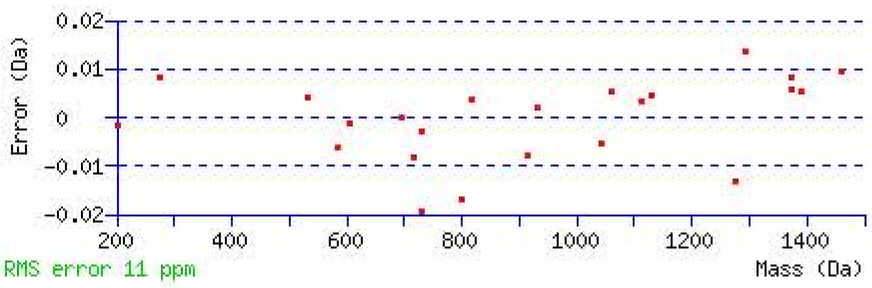
Match to Query 48601: 1660.815828 from(831.415190,2+) rtinseconds(1766) index(78668)
Title: Locus:1.1.1.2494.19 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

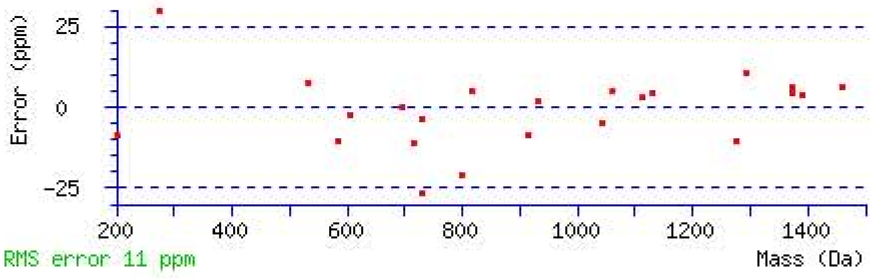
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1660.813034
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 48 **Expect:** 5.4e-005
Matches : 23/118 fragment ions using 47 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	88.039304	44.523290			70.028739	35.518008	S							12
2	**201.123368**	101.065322			183.112803	92.060039	L	1574.788308	787.897792	1557.761759	779.384518	1556.777743	778.892510	11
3	272.160482	136.583879			254.149917	127.578596	A	***1461.704244***	731.355760	1444.677695	722.842486	1443.693679	722.350478	10
4	369.213246	185.110261			351.202681	176.104978	P	***1390.667130***	695.837203	1373.640581	687.323929	1372.656565	686.831921	9
5	**532.276575**	266.641926			514.266010	257.636643	Y	***1293.614366***	647.310821	1276.587817	638.797547	1275.603801	638.305539	8
6	**603.313689**	302.160483			585.303124	293.155200	A	***1130.551037***	565.779157	1113.524488	557.265882	1112.540472	556.773874	7
7	**731.372267**	366.189772	714.345718	357.676497	713.361702	357.184489	Q	***1059.513923***	530.260600	1042.487374	521.747325	1041.503358	521.255317	6
8	846.399210	423.703243	829.372661	415.189969	828.388645	414.697961	D	***931.455345***	466.231311	914.428796	457.718036	913.444780	457.226028	5
9	947.446889	474.227083	930.420340	465.713808	929.436324	465.221800	T	***816.428402***	408.717839	799.401853	400.204565	798.417837	399.712557	4
10	1386.672215	693.839746	1369.645666	685.326471	1368.661650	684.834463	Q	***715.380723***	358.194000	698.354174	349.680725	697.370158	349.188717	3
11	1515.714808	758.361042	1498.688259	749.847768	1497.704243	749.355760	E	***276.155397***	138.581337	259.128848	130.068062	258.144832	129.576054	2
12							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.4	1660.813034	0.002794	SLAPYAQDTQEK
19.6	1660.813034	0.002794	SLAPYAQDTQEK
2.9	1660.820908	-0.005080	SLARAGFYYTGVNDK

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

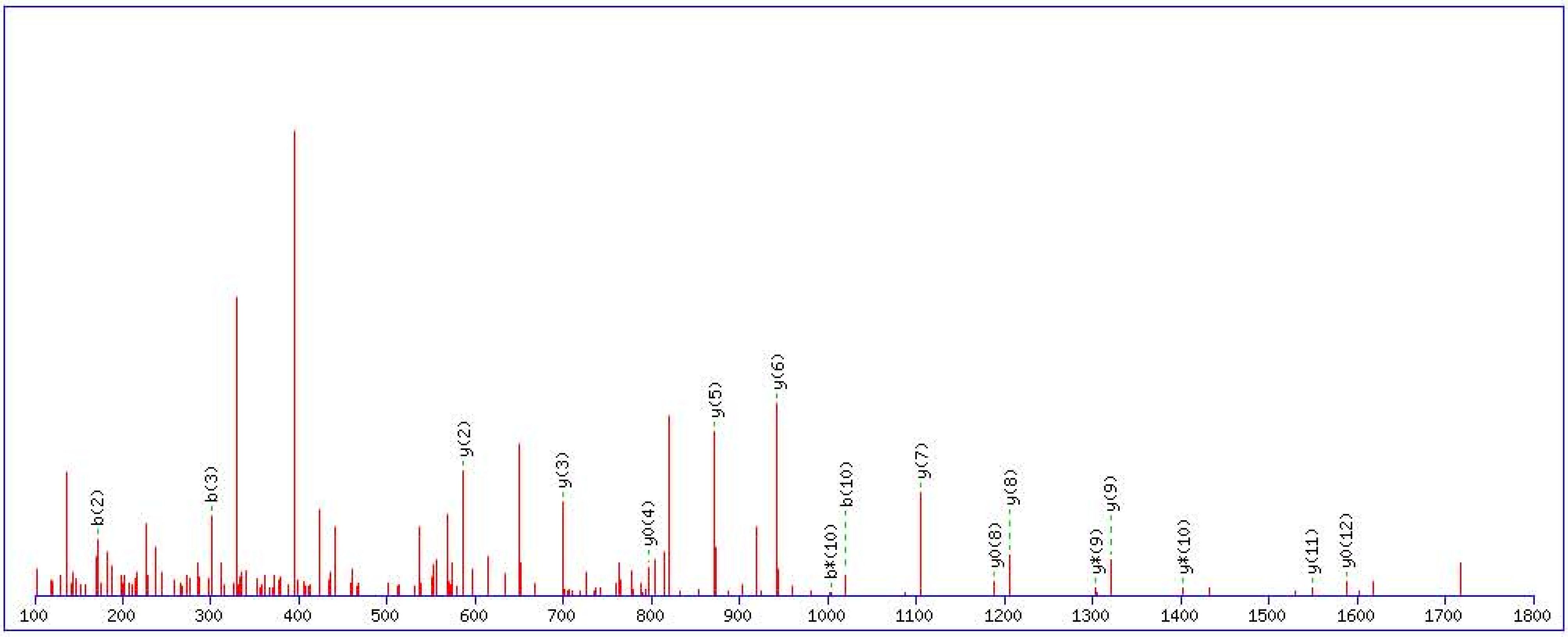
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGEVNTYAGDLQK**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

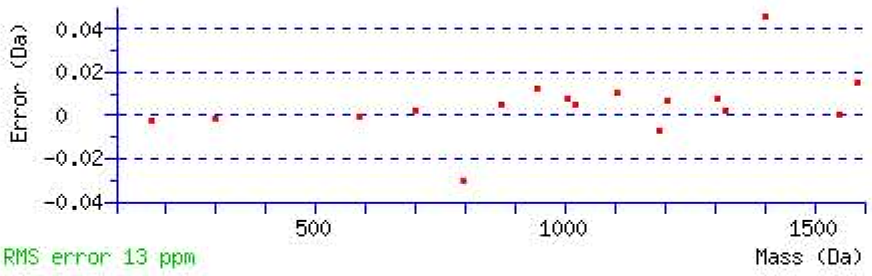
Match to Query 50002: 1717.869342 from(573.630390,3+) rtinseconds(2012) index(80382)
Title: Locus:1.1.1.2580.8 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

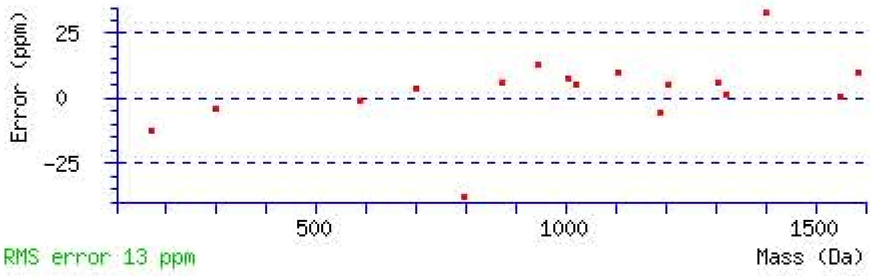
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1717.870895
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 44  Expect: 8.5e-005
Matches : 17/126 fragment ions using 30 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					L							13
2	**171.112804**	86.060040					G	1605.794121	803.400699	1588.767572	794.887424	1587.783556	794.395416	12
3	**300.155397**	150.581336			282.144832	141.576054	E	***1548.772657***	774.889967	1531.746108	766.376692	1530.762092	765.884684	11
4	399.223811	200.115544			381.213246	191.110261	V	1419.730064	710.368670	1402.703515	701.855396	1401.719499	701.363388	10
5	513.266738	257.137007	496.240189	248.623733	495.256173	248.131725	N	***1320.661650***	660.834463	1303.635101	652.321189	1302.651085	651.829181	9
6	614.314417	307.660847	597.287868	299.147572	596.303852	298.655564	T	***1206.618723***	603.813000	1189.592174	595.299725	1188.608158	594.807717	8
7	777.377746	389.192511	760.351197	380.679237	759.367181	380.187229	Y	***1105.571044***	553.289160	1088.544495	544.775886	1087.560479	544.283878	7
8	848.414860	424.711068	831.388311	416.197794	830.404295	415.705786	A	***942.507715***	471.757496	925.481166	463.244221	924.497150	462.752213	6
9	905.436324	453.221800	888.409775	444.708526	887.425759	444.216518	G	***871.470601***	436.238939	854.444052	427.725664	853.460036	427.233656	5
10	**1020.463267**	510.735272	1003.436718	502.221997	1002.452702	501.729989	D	814.449137	407.728207	797.422588	399.214932	796.438572	398.722924	4
11	1133.547331	567.277304	1116.520782	558.764029	1115.536766	558.272021	L	***699.422194***	350.214735	682.395645	341.701461			3
12	1572.772657	786.889967	1555.746108	778.376692	1554.762092	777.884684	Q	***586.338130***	293.672703	569.311581	285.159429			2
13							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.0	1717.870895	-0.001553	LGEVNTYAGDLQK
0.6	1717.855606	0.013736	VANAEEKLMDDLLNK

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

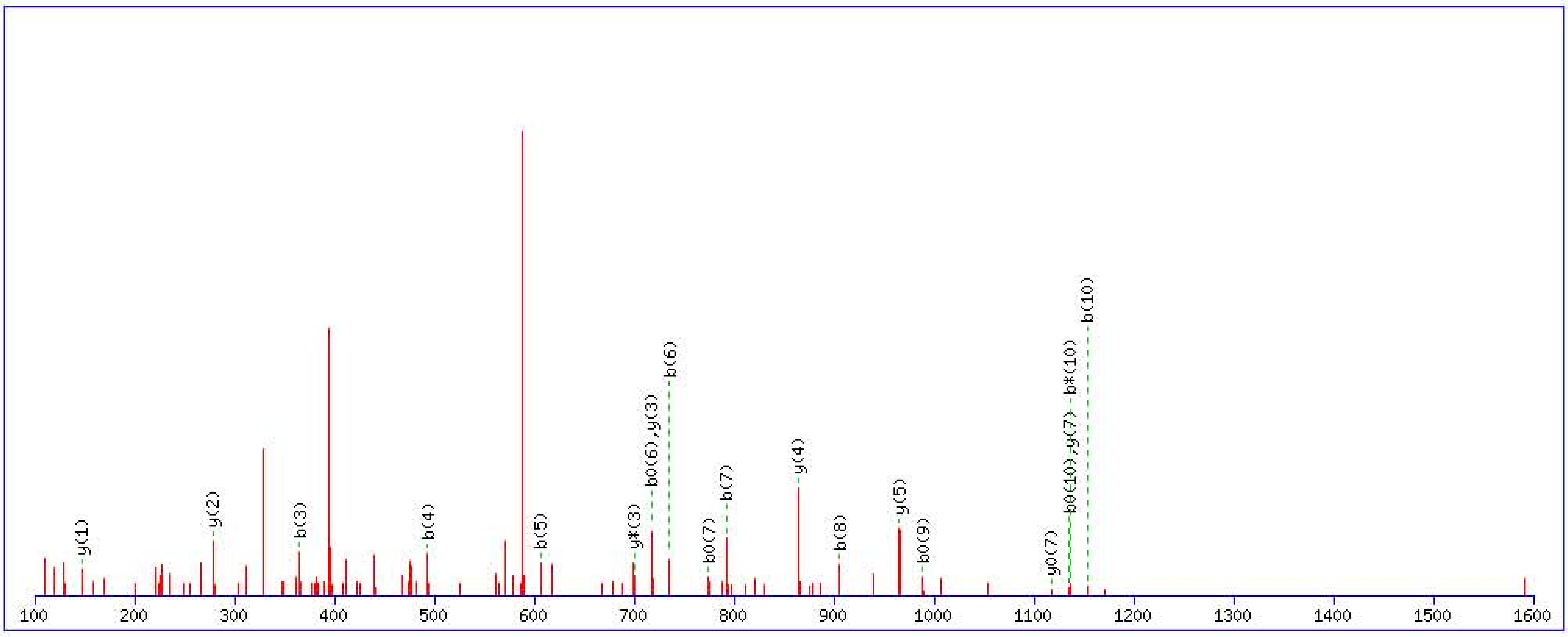
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LNHQLEGLTFQMK**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

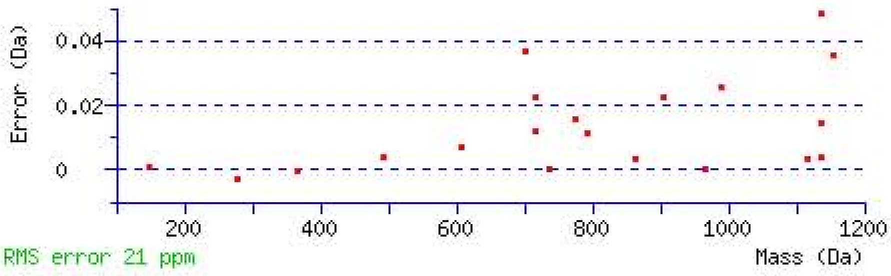
Match to Query 53766: 1868.970012 from(623.997280,3+) rtinseconds(2161) index(81336)
Title: Locus:1.1.1.2632.9 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

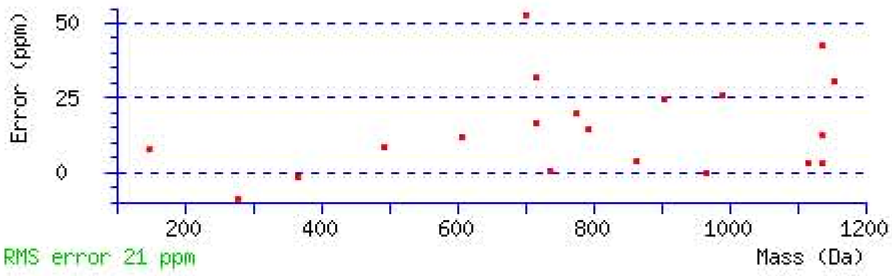
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1868.964081
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.0014
Matches : 20/124 fragment ions using 42 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	114.091340	57.549308					L							13
2	228.134267	114.570771	211.107718	106.057497			N	1756.887310	878.947293	1739.860761	870.434019	1738.876745	869.942011	12
3	***365.193179***	183.100227	348.166630	174.586953			H	1642.844383	821.925830	1625.817834	813.412555	1624.833818	812.920547	11
4	***493.251757***	247.129516	476.225208	238.616242			Q	1505.785471	753.396374	1488.758922	744.883099	1487.774906	744.391091	10
5	***606.335821***	303.671549	589.309272	295.158274			L	1377.726893	689.367085	1360.700344	680.853810	1359.716328	680.361802	9
6	***735.378414***	368.192845	718.351865	359.679571	717.367849	359.187563	E	1264.642829	632.825053	1247.616280	624.311778	1246.632264	623.819770	8
7	***792.399878***	396.703577	775.373329	388.190303	774.389313	387.698295	G	***1135.600236***	568.303756	1118.573687	559.790482	1117.589671	559.298474	7
8	***905.483942***	453.245609	888.457393	444.732335	887.473377	444.240327	L	1078.578772	539.793024	1061.552223	531.279750	1060.568207	530.787742	6
9	1006.531621	503.769449	989.505072	495.256174	988.521056	494.764166	T	***965.494708***	483.250992	948.468159	474.737718	947.484143	474.245710	5
10	***1153.600035***	577.303656	1136.573486	568.790381	1135.589470	568.298373	F	***864.447029***	432.727153	847.420480	424.213878			4
11	1592.825361	796.916319	1575.798812	788.403044	1574.814796	787.911036	Q	***717.378615***	359.192946	700.352066	350.679671			3
12	1723.865846	862.436561	1706.839297	853.923287	1705.855281	853.431279	M	***278.153289***	139.580282	261.126740	131.067008			2
13							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.8	1868.964081	0.005931	LNHQLEGLTFQMK
0.4	1868.977798	-0.007786	RGGMLGEPEPLTEKALR

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

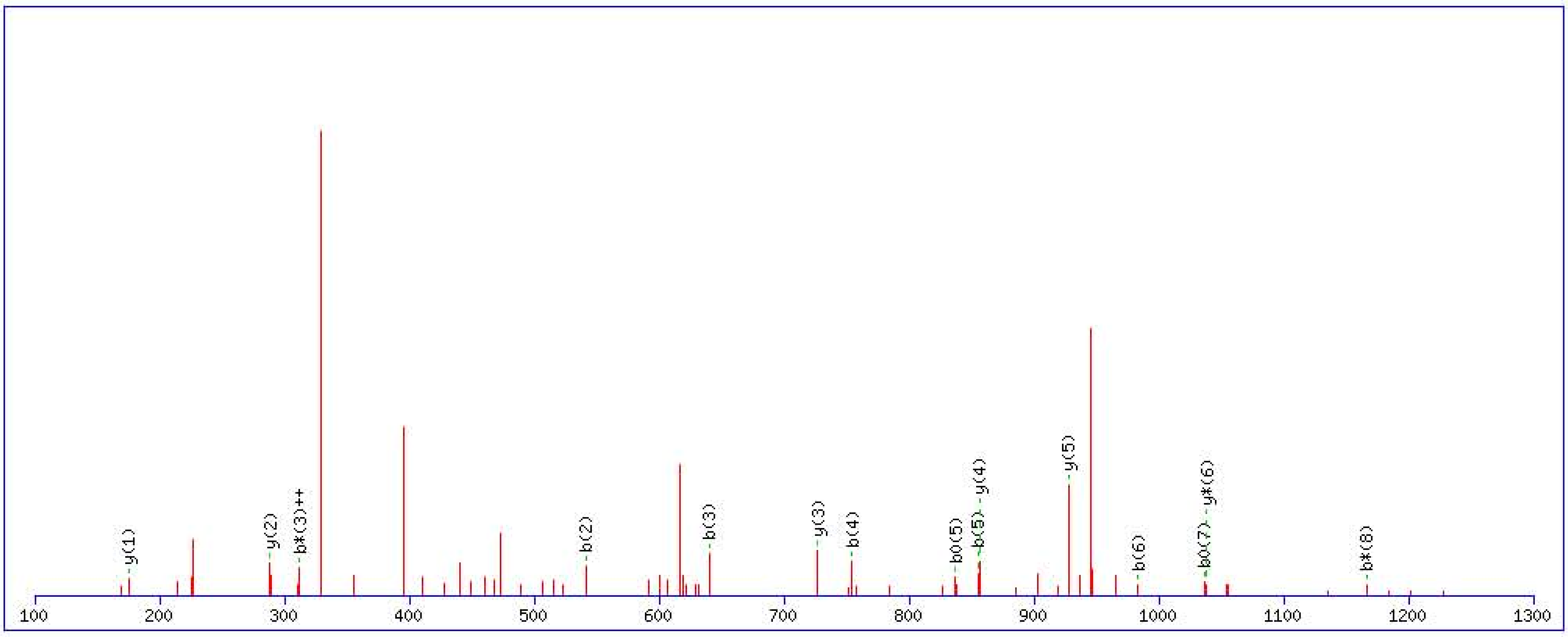
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TQVNTQAEQLR**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

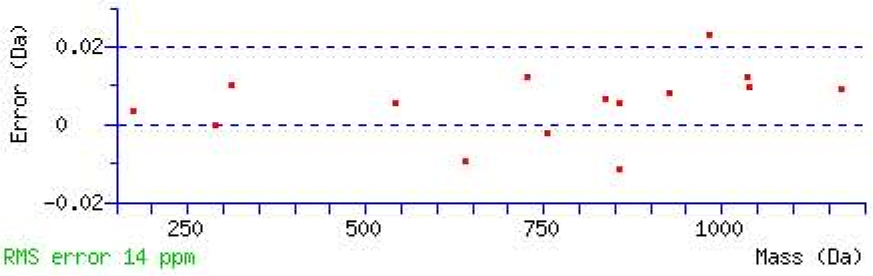
Match to Query 54530: 1908.989112 from(637.336980,3+) rtinseconds(1944) index(79845)
Title: Locus:1.1.1.2556.19 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

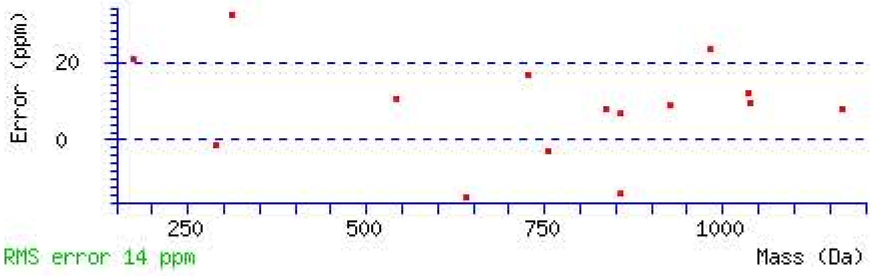
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1908.991364
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2     : Biotin:Thermo-21345 (Q)
Q9     : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.034
Matches : 15/112 fragment ions using 32 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							11
2	***541.280281***	271.143779	524.253732	262.630504	523.269716	262.138496	Q	1808.950973	904.979125	1791.924424	896.465850	1790.940408	895.973842	10
3	***640.348695***	320.677986	623.322146	312.164711	622.338130	311.672703	V	1369.725647	685.366462	1352.699098	676.853187	1351.715082	676.361179	9
4	***754.391622***	377.699449	737.365073	369.186174	736.381057	368.694166	N	1270.657233	635.832255	1253.630684	627.318980	1252.646668	626.826972	8
5	***855.439301***	428.223289	838.412752	419.710014	837.428736	419.218006	T	1156.614306	578.810791	1139.587757	570.297517	1138.603741	569.805509	7
6	***983.497879***	492.252578	966.471330	483.739303	965.487314	483.247295	Q	1055.566627	528.286952	1038.540078	519.773677	1037.556062	519.281669	6
7	1054.534993	527.771135	1037.508444	519.257860	1036.524428	518.765852	A	***927.508049***	464.257663	910.481500	455.744388	909.497484	455.252380	5
8	1183.577586	592.292431	1166.551037	583.779157	1165.567021	583.287149	E	***856.470935***	428.739106	839.444386	420.225831	838.460370	419.733823	4
9	1622.802912	811.905094	1605.776363	803.391820	1604.792347	802.899812	Q	***727.428342***	364.217809	710.401793	355.704535			3
10	1735.886976	868.447126	1718.860427	859.933852	1717.876411	859.441844	L	***288.203016***	144.605146	271.176467	136.091871			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.2	1908.991364	-0.002252	TQVNTQAEQLR
12.1	1908.991364	-0.002252	TQVNTQAEQLR
10.1	1908.974045	0.015067	SAQWAINRVAMEIQHR
3.4	1909.015610	-0.026498	SSIALTAPDAAADPKEKPK
2.4	1908.991364	-0.002252	TQVNTQAEQLR

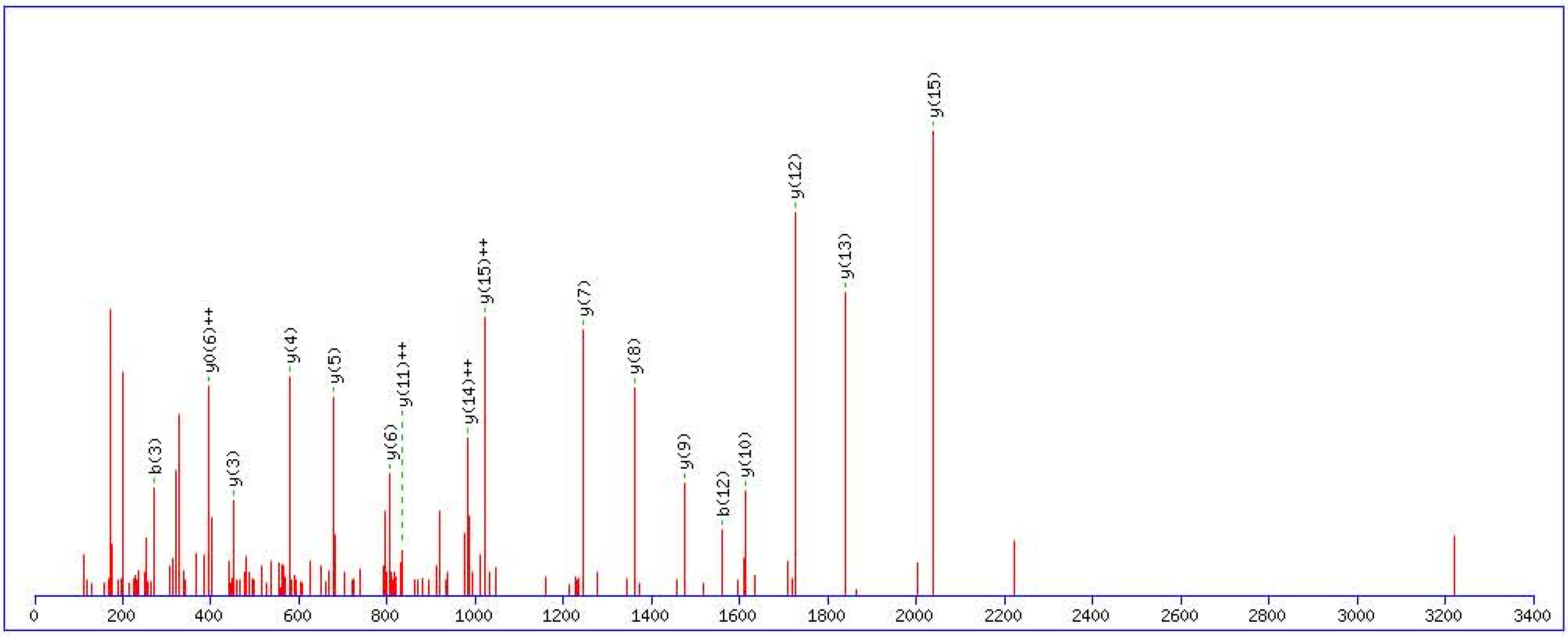
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SLAELGGHLDQQVEEFR**
Found in **APOA4_HUMAN**, Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3

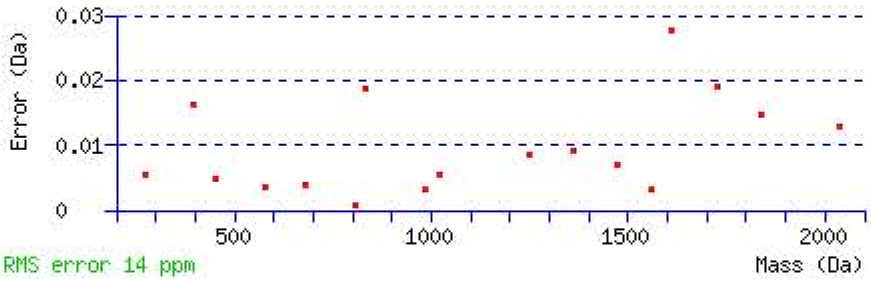
Match to Query 62503: 2238.116202 from(747.046010,3+) rtinseconds(2232) index(64606)
Title: Locus:1.1.1.2774.19 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

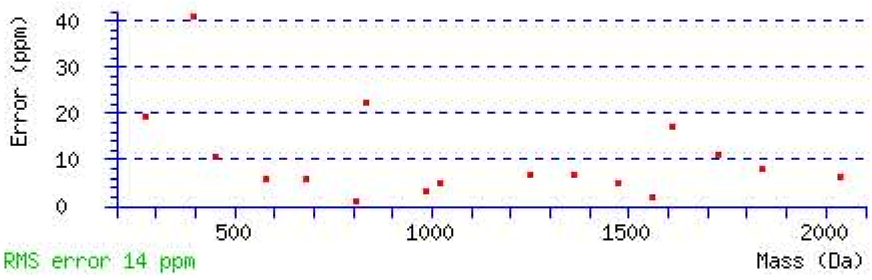
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2238.110291
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 97  Expect: 5.1e-009
Matches : 17/168 fragment ions using 21 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							17
2	201.123368	101.065322			183.112803	92.060039	L	2152.085552	1076.546414	2135.059003	1068.033139	2134.074987	1067.541131	16
3	**272.160482**	136.583879			254.149917	127.578596	A	***2039.001488***	1020.004382	2021.974939	1011.491108	2020.990923	1010.999100	15
4	401.203075	201.105175			383.192510	192.099893	E	1967.964374	984.485825	1950.937825	975.972551	1949.953809	975.480543	14
5	514.287139	257.647208			496.276574	248.641925	L	***1838.921781***	919.964529	1821.895232	911.451254	1820.911216	910.959246	13
6	571.308603	286.157940			553.298038	277.152657	G	***1725.837717***	863.422497	1708.811168	854.909222	1707.827152	854.417214	12
7	628.330067	314.668672			610.319502	305.663389	G	1668.816253	834.911765	1651.789704	826.398490	1650.805688	825.906482	11
8	765.388979	383.198128			747.378414	374.192845	H	***1611.794789***	806.401033	1594.768240	797.887758	1593.784224	797.395750	10
9	878.473043	439.740160			860.462478	430.734877	L	***1474.735877***	737.871577	1457.709328	729.358302	1456.725312	728.866294	9
10	993.499986	497.253631			975.489421	488.248349	D	***1361.651813***	681.329545	1344.625264	672.816270	1343.641248	672.324262	8
11	1432.725312	716.866294	1415.698763	708.353020	1414.714747	707.861012	Q	***1246.624870***	623.816073	1229.598321	615.302799	1228.614305	614.810791	7
12	**1560.783890**	780.895583	1543.757341	772.382309	1542.773325	771.890301	Q	***807.399544***	404.203410	790.372995	395.690136	789.388979	395.198128	6
13	1659.852304	830.429790	1642.825755	821.916516	1641.841739	821.424508	V	***679.340966***	340.174121	662.314417	331.660846	661.330401	331.168838	5
14	1788.894897	894.951087	1771.868348	886.437812	1770.884332	885.945804	E	***580.272552***	290.639914	563.246003	282.126639	562.261987	281.634631	4
15	1917.937490	959.472383	1900.910941	950.959109	1899.926925	950.467101	E	***451.229959***	226.118617	434.203410	217.605343	433.219394	217.113335	3
16	2065.005904	1033.006590	2047.979355	1024.493316	2046.995339	1024.001307	F	322.187366	161.597321	305.160817	153.084046			2
17							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
97.3	2238.110291	0.005911	SLAELGGHLDQQVEEFR
77.5	2238.110291	0.005911	SLAELGGHLDQQVEEFR

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

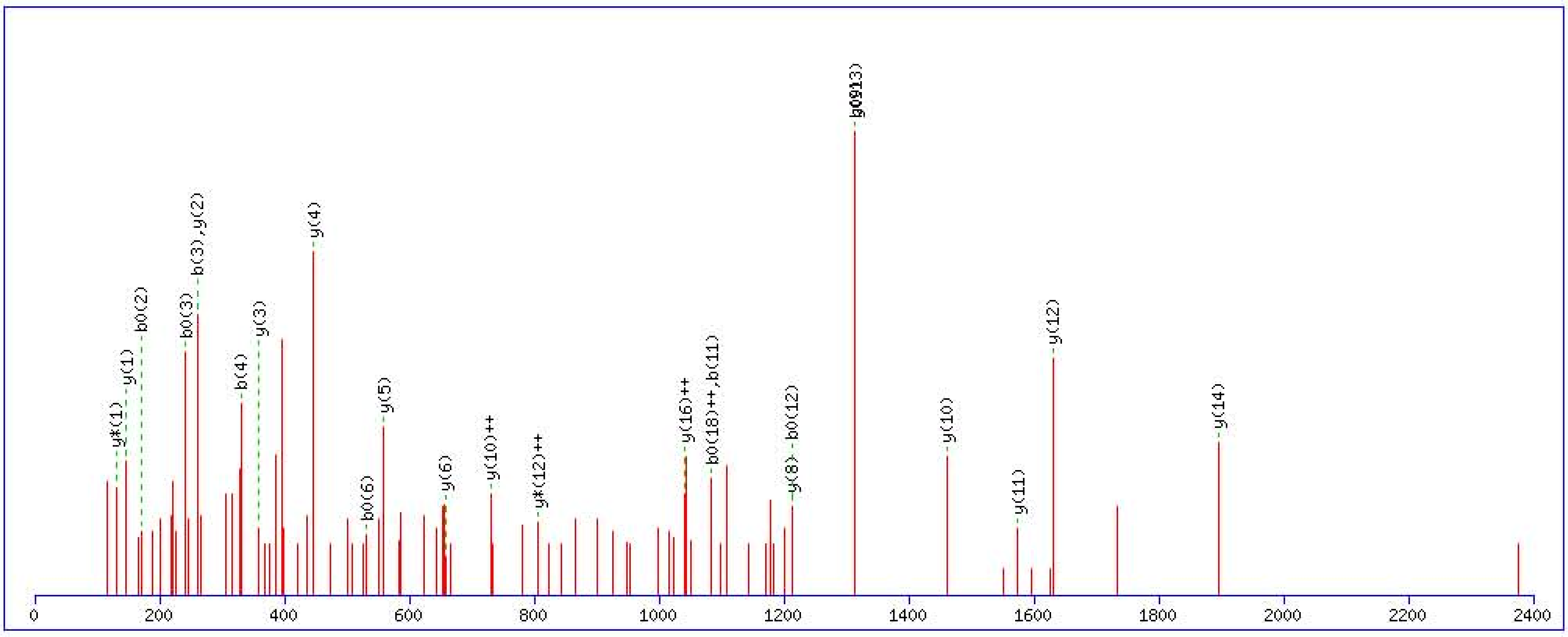
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **STAAMSTYTGIFTDQVLSVLK**
Found in **APOC2_HUMAN**, Apolipoprotein C-II OS=Homo sapiens GN=APOC2 PE=1 SV=1

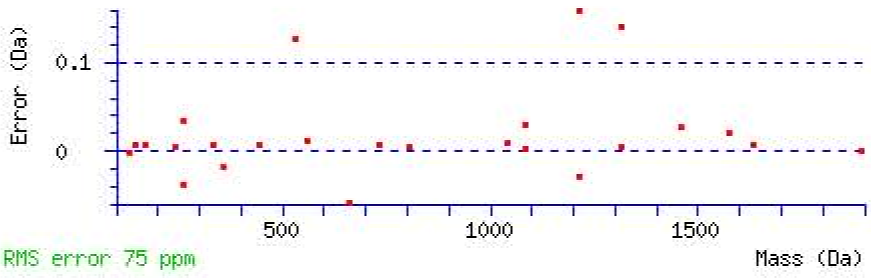
Match to Query 69173: 2543.316192 from(848.779340,3+) rtinseconds(3190) index(70586)
Title: Locus:1.1.1.3103.17 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

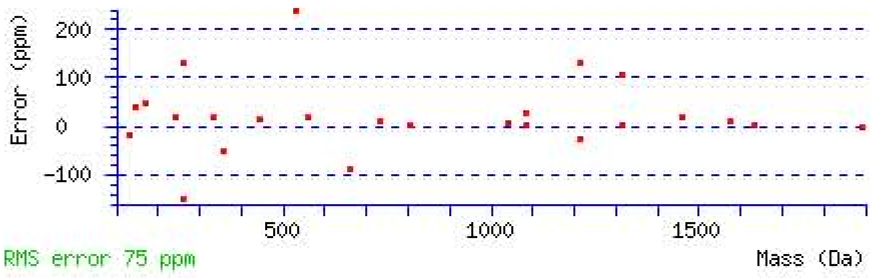
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2543.301544
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15 : Biotin:Thermo-21345 (Q)
Ions Score: 37 **Expect:** 0.0053
Matches : 25/206 fragment ions using 76 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	88.039304	44.523290			70.028739	35.518008	S							21
2	189.086983	95.047129			171.076418	86.041847	T	2457.276785	1229.142030	2440.250236	1220.628756	2439.266220	1220.136748	20
3	**260.124097**	130.565686			242.113532	121.560404	A	2356.229106	1178.618191	2339.202557	1170.104916	2338.218541	1169.612908	19
4	**331.161211**	166.084243			313.150646	157.078961	A	2285.191992	1143.099634	2268.165443	1134.586359	2267.181427	1134.094351	18
5	462.201696	231.604486			444.191131	222.599203	M	2214.154878	1107.581077	2197.128329	1099.067802	2196.144313	1098.575794	17
6	549.233724	275.120500			531.223159	266.115217	S	2083.114393	1042.060834	2066.087844	1033.547560	2065.103828	1033.055552	16
7	650.281403	325.644340			632.270838	316.639057	T	1996.082365	998.544821	1979.055816	990.031546	1978.071800	989.539538	15
8	813.344732	407.176004			795.334167	398.170722	Y	***1895.034686***	948.020981	1878.008137	939.507707	1877.024121	939.015699	14
9	914.392411	457.699844			896.381846	448.694561	T	1731.971357	866.489317	1714.944808	857.976042	1713.960792	857.484034	13
10	971.413875	486.210576			953.403310	477.205293	G	***1630.923678***	815.965477	1613.897129	807.452203	1612.913113	806.960195	12
11	**1084.497939**	542.752608			1066.487374	533.747325	I	***1573.902214***	787.454745	1556.875665	778.941471	1555.891649	778.449463	11
12	1231.566353	616.286815			1213.555788	607.281532	F	***1460.818150***	730.912713	1443.791601	722.399439	1442.807585	721.907431	10
13	1332.614032	666.810654			1314.603467	657.805372	T	***1313.749736***	657.378506	1296.723187	648.865232	1295.739171	648.373224	9
14	1447.640975	724.324126			1429.630410	715.318843	D	***1212.702057***	606.854667	1195.675508	598.341392	1194.691492	597.849384	8
15	1886.866301	943.936789	1869.839752	935.423514	1868.855736	934.931506	Q	1097.675114	549.341195	1080.648565	540.827921	1079.664549	540.335913	7
16	1985.934715	993.470996	1968.908166	984.957721	1967.924150	984.465713	V	***658.449788***	329.728532	641.423239	321.215258	640.439223	320.723250	6
17	2099.018779	1050.013027	2081.992230	1041.499753	2081.008214	1041.007745	L	***559.381374***	280.194325	542.354825	271.681051	541.370809	271.189043	5
18	2186.050807	1093.529041	2169.024258	1085.015767	2168.040242	1084.523759	S	***446.297310***	223.652293	429.270761	215.139019	428.286745	214.647011	4
19	2285.119221	1143.063248	2268.092672	1134.549974	2267.108656	1134.057966	V	***359.265282***	180.136279	342.238733	171.623004			3
20	2398.203285	1199.605280	2381.176736	1191.092006	2380.192720	1190.599998	L	***260.196868***	130.602072	243.170319	122.088798			2
21							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.3	2543.301544	0.014648	STAAMSTYTGIFTDQVLSVLK

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

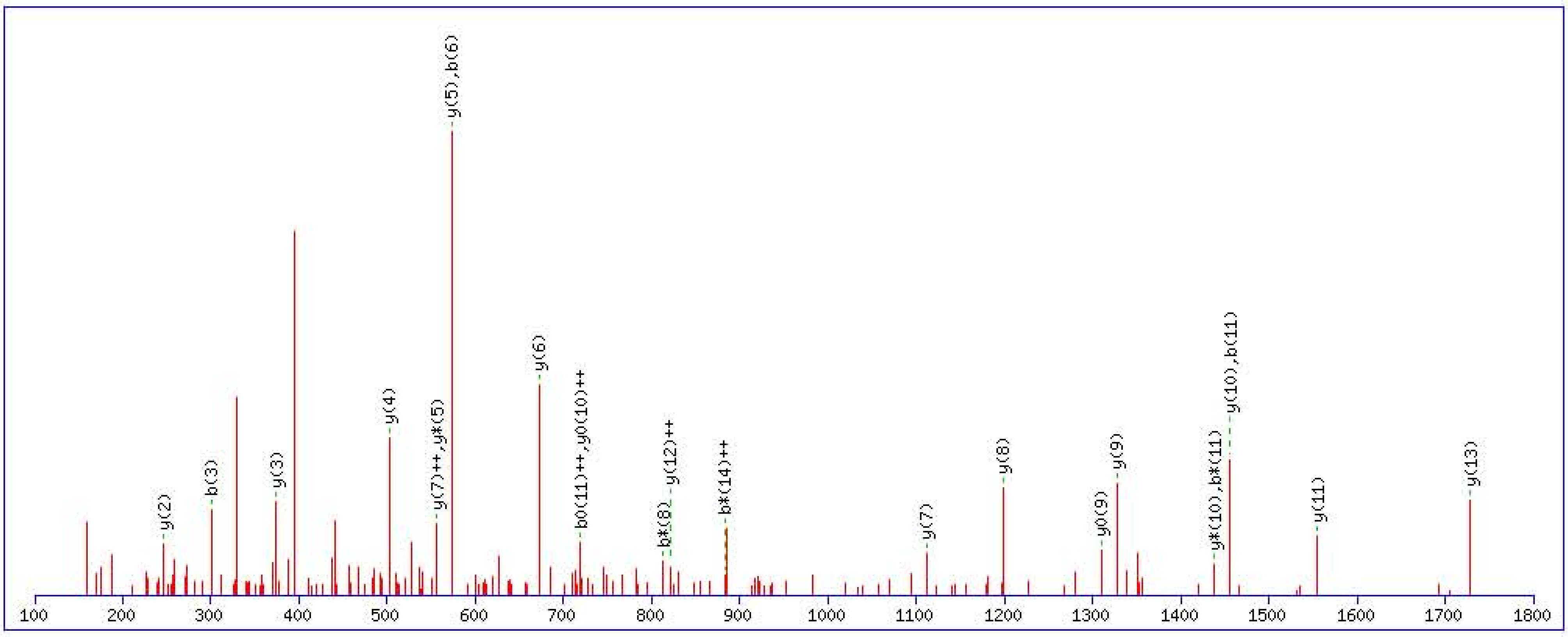
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DALSSVQESQVAQQAR**
Found in **APOC3_HUMAN**, Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=1 SV=1

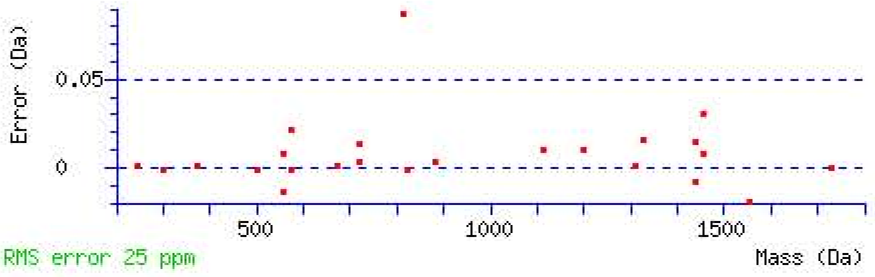
Match to Query 57955: 2027.009322 from(676.677050,3+) rtinseconds(1940) index(62695)
Title: Locus:1.1.1.2673.16 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

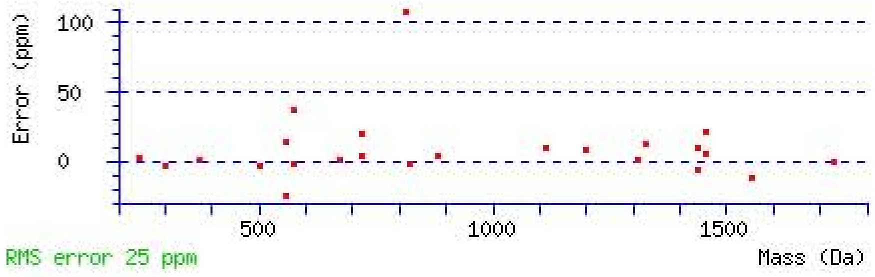
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2027.010574
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 77  Expect: 1.1e-007
Matches : 24/154 fragment ions using 30 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							16
2	187.071333	94.039304			169.060768	85.034022	A	1912.990923	956.999100	1895.964374	948.485825	1894.980358	947.993817	15
3	**300.155397**	150.581336			282.144832	141.576054	L	1841.953809	921.480543	1824.927260	912.967268	1823.943244	912.475260	14
4	387.187425	194.097351			369.176860	185.092068	S	***1728.869745***	864.938511	1711.843196	856.425236	1710.859180	855.933228	13
5	474.219453	237.613364			456.208888	228.608082	S	1641.837717	821.422497	1624.811168	812.909222	1623.827152	812.417214	12
6	**573.287867**	287.147572			555.277302	278.142289	V	***1554.805689***	777.906483	1537.779140	769.393208	1536.795124	768.901200	11
7	701.346445	351.176861	684.319896	342.663586	683.335880	342.171578	Q	***1455.737275***	728.372276	1438.710726	719.859001	1437.726710	719.366993	10
8	830.389038	415.698157	813.362489	407.184883	812.378473	406.692875	E	***1327.678697***	664.342987	1310.652148	655.829712	1309.668132	655.337704	9
9	917.421066	459.214171	900.394517	450.700897	899.410501	450.208889	S	***1198.636104***	599.821690	1181.609555	591.308416	1180.625539	590.816408	8
10	1356.646392	678.826834	1339.619843	670.313560	1338.635827	669.821551	Q	***1111.604076***	556.305676	1094.577527	547.792402			7
11	**1455.714806**	728.361041	1438.688257	719.847767	1437.704241	719.355758	V	***672.378750***	336.693013	655.352201	328.179739			6
12	1526.751920	763.879598	1509.725371	755.366324	1508.741355	754.874315	A	***573.310336***	287.158806	556.283787	278.645532			5
13	1654.810498	827.908887	1637.783949	819.395613	1636.799933	818.903605	Q	***502.273222***	251.640249	485.246673	243.126975			4
14	1782.869076	891.938176	1765.842527	883.424902	1764.858511	882.932894	Q	***374.214644***	187.610960	357.188095	179.097686			3
15	1853.906190	927.456733	1836.879641	918.943459	1835.895625	918.451451	A	***246.156066***	123.581671	229.129517	115.068396			2
16							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of DALSSVQESQVAQQAR
(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	2027.010574	-0.001252	DALSSVQESQVAQQAR
76.7	2027.010574	-0.001252	DALSSVQESQVAQQAR
64.0	2027.010574	-0.001252	DALSSVQESQVAQQAR
35.2	2027.010574	-0.001252	DALSSVQESQVAQQAR
3.2	2027.021805	-0.012483	VASVESQGQEISGNRR

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

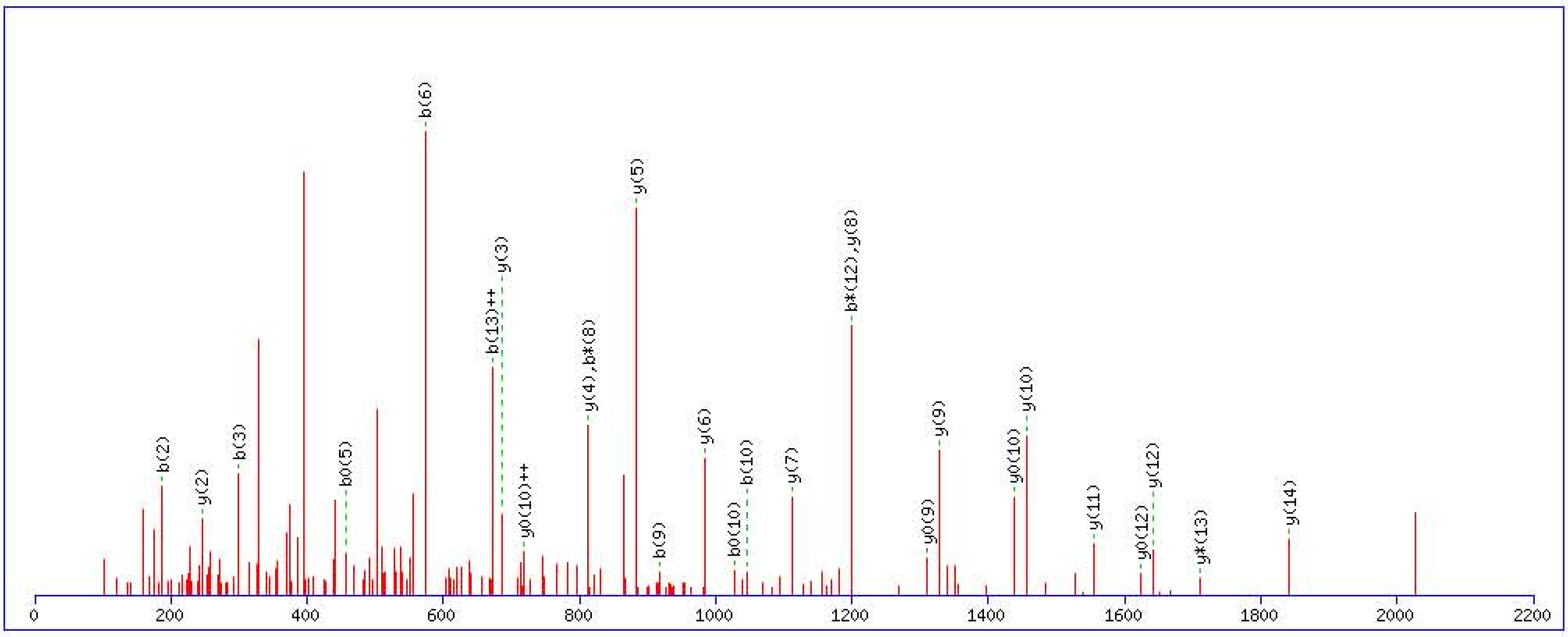
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DALSSVQESQVAQQAR**
Found in **APOC3_HUMAN**, Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=1 SV=1

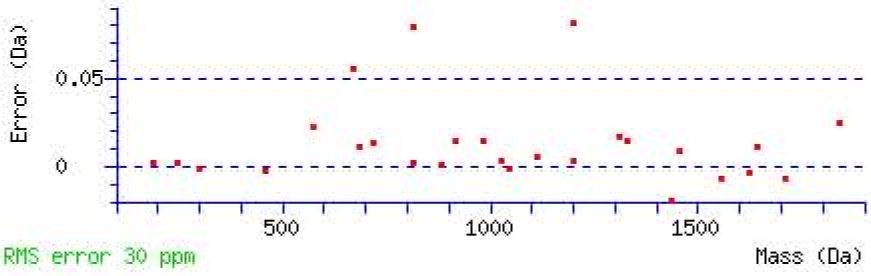
Match to Query 57956: 2027.009322 from(676.677050,3+) rtinseconds(1932) index(62620)
Title: Locus:1.1.1.2670.16 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

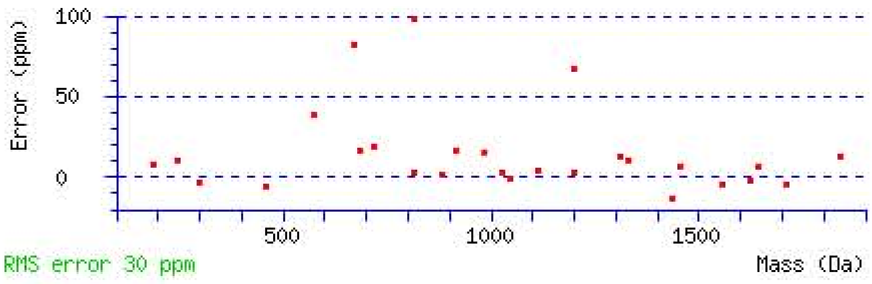
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2027.010574
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 95  Expect: 7.3e-009
Matches : 27/154 fragment ions using 33 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	116.034219	58.520748			98.023654	49.515465	D							16
2	**187.071333**	94.039304			169.060768	85.034022	A	1912.990923	956.999100	1895.964374	948.485825	1894.980358	947.993817	15
3	**300.155397**	150.581336			282.144832	141.576054	L	***1841.953809***	921.480543	1824.927260	912.967268	1823.943244	912.475260	14
4	387.187425	194.097351			369.176860	185.092068	S	1728.869745	864.938511	1711.843196	856.425236	1710.859180	855.933228	13
5	474.219453	237.613364			456.208888	228.608082	S	***1641.837717***	821.422497	1624.811168	812.909222	1623.827152	812.417214	12
6	**573.287867**	287.147572			555.277302	278.142289	V	***1554.805689***	777.906483	1537.779140	769.393208	1536.795124	768.901200	11
7	701.346445	351.176861	684.319896	342.663586	683.335880	342.171578	Q	***1455.737275***	728.372276	1438.710726	719.859001	1437.726710	719.366993	10
8	830.389038	415.698157	813.362489	407.184883	812.378473	406.692875	E	***1327.678697***	664.342987	1310.652148	655.829712	1309.668132	655.337704	9
9	**917.421066**	459.214171	900.394517	450.700897	899.410501	450.208889	S	***1198.636104***	599.821690	1181.609555	591.308416	1180.625539	590.816408	8
10	**1045.479644**	523.243460	1028.453095	514.730186	1027.469079	514.238178	Q	***1111.604076***	556.305676	1094.577527	547.792402			7
11	1144.548058	572.777667	1127.521509	564.264393	1126.537493	563.772385	V	***983.545498***	492.276387	966.518949	483.763113			6
12	1215.585172	608.296224	1198.558623	599.782950	1197.574607	599.290942	A	***884.477084***	442.742180	867.450535	434.228906			5
13	1343.643750	672.325513	1326.617201	663.812239	1325.633185	663.320230	Q	***813.439970***	407.223623	796.413421	398.710349			4
14	1782.869076	891.938176	1765.842527	883.424902	1764.858511	882.932894	Q	***685.381392***	343.194334	668.354843	334.681060			3
15	1853.906190	927.456733	1836.879641	918.943459	1835.895625	918.451451	A	***246.156066***	123.581671	229.129517	115.068396			2
16							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
95.4	2027.010574	-0.001252	DALSSVQESQVAQQAR
93.8	2027.010574	-0.001252	DALSSVQESQVAQQAR
91.7	2027.010574	-0.001252	DALSSVQESQVAQQAR
46.6	2027.010574	-0.001252	DALSSVQESQVAQQAR

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

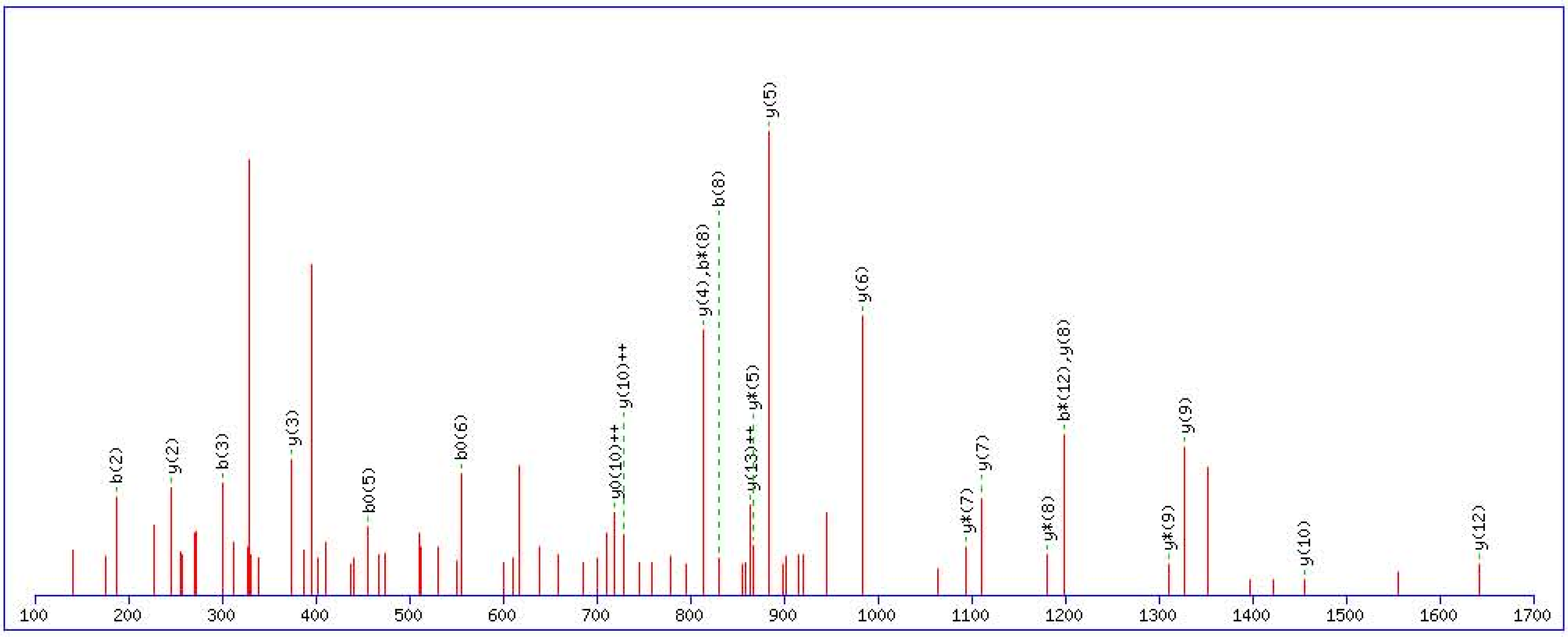
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DALSSVQESQVAQQAR**
Found in **APOC3_HUMAN**, Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=1 SV=1

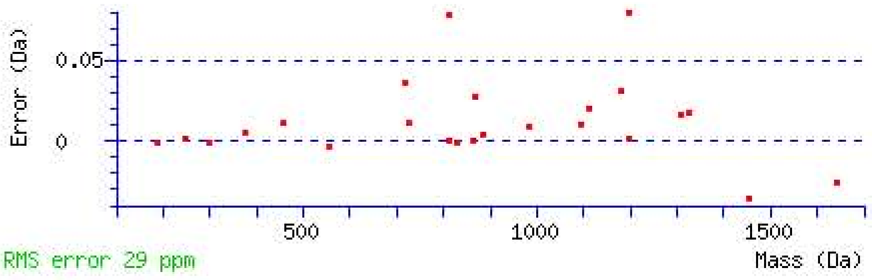
Match to Query 57957: 2027.010582 from(676.677470,3+) rtinseconds(1885) index(62223)
Title: Locus:1.1.1.2654.19 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

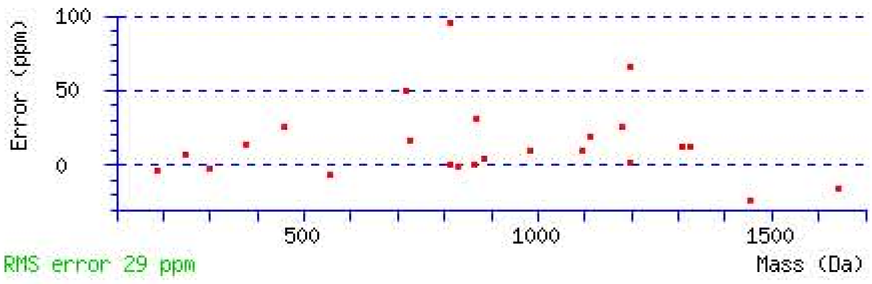
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2027.010574
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 58  Expect: 3.6e-005
Matches : 24/154 fragment ions using 39 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							16
2	**187.071333**	94.039304			169.060768	85.034022	A	1912.990923	956.999100	1895.964374	948.485825	1894.980358	947.993817	15
3	**300.155397**	150.581336			282.144832	141.576054	L	1841.953809	921.480543	1824.927260	912.967268	1823.943244	912.475260	14
4	387.187425	194.097351			369.176860	185.092068	S	1728.869745	864.938511	1711.843196	856.425236	1710.859180	855.933228	13
5	474.219453	237.613364			456.208888	228.608082	S	***1641.837717***	821.422497	1624.811168	812.909222	1623.827152	812.417214	12
6	573.287867	287.147572			555.277302	278.142289	V	1554.805689	777.906483	1537.779140	769.393208	1536.795124	768.901200	11
7	701.346445	351.176861	684.319896	342.663586	683.335880	342.171578	Q	***1455.737275***	728.372276	1438.710726	719.859001	1437.726710	719.366993	10
8	**830.389038**	415.698157	813.362489	407.184883	812.378473	406.692875	E	***1327.678697***	664.342987	1310.652148	655.829712	1309.668132	655.337704	9
9	917.421066	459.214171	900.394517	450.700897	899.410501	450.208889	S	***1198.636104***	599.821690	1181.609555	591.308416	1180.625539	590.816408	8
10	1045.479644	523.243460	1028.453095	514.730186	1027.469079	514.238178	Q	***1111.604076***	556.305676	1094.577527	547.792402			7
11	1144.548058	572.777667	1127.521509	564.264393	1126.537493	563.772385	V	***983.545498***	492.276387	966.518949	483.763113			6
12	1215.585172	608.296224	1198.558623	599.782950	1197.574607	599.290942	A	***884.477084***	442.742180	867.450535	434.228906			5
13	1654.810498	827.908887	1637.783949	819.395613	1636.799933	818.903605	Q	***813.439970***	407.223623	796.413421	398.710349			4
14	1782.869076	891.938176	1765.842527	883.424902	1764.858511	882.932894	Q	***374.214644***	187.610960	357.188095	179.097686			3
15	1853.906190	927.456733	1836.879641	918.943459	1835.895625	918.451451	A	***246.156066***	123.581671	229.129517	115.068396			2
16							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.5	2027.010574	0.000008	DALSSVQESQVAQQAR
48.8	2027.010574	0.000008	DALSSVQESQVAQQAR
35.1	2027.010574	0.000008	DALSSVQESQVAQQAR
8.3	2027.010574	0.000008	DALSSVQESQVAQQAR

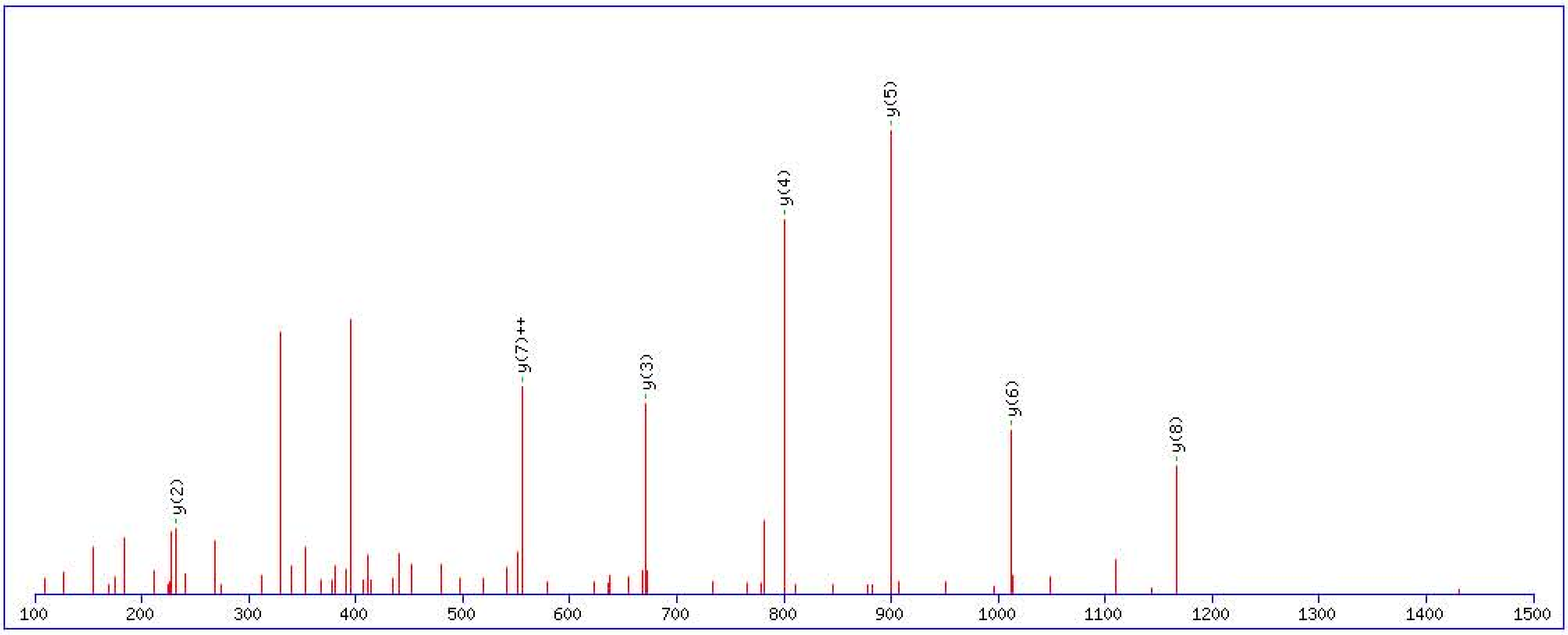
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGPLVEQGR**
Found in **APOE_HUMAN**, Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1

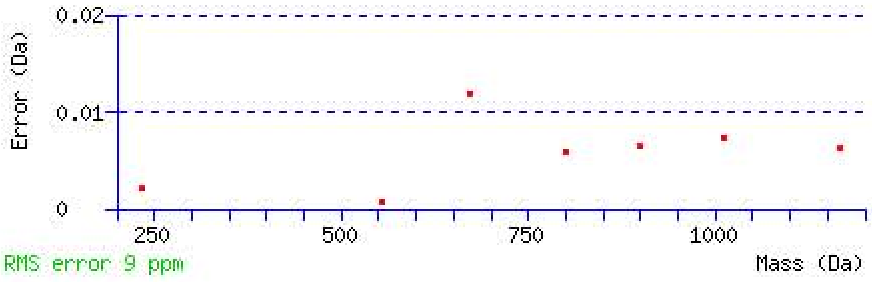
Match to Query 34434: 1278.710368 from(640.362460,2+) rtinseconds(1949) index(62767)
Title: Locus:1.1.1.2676.13 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

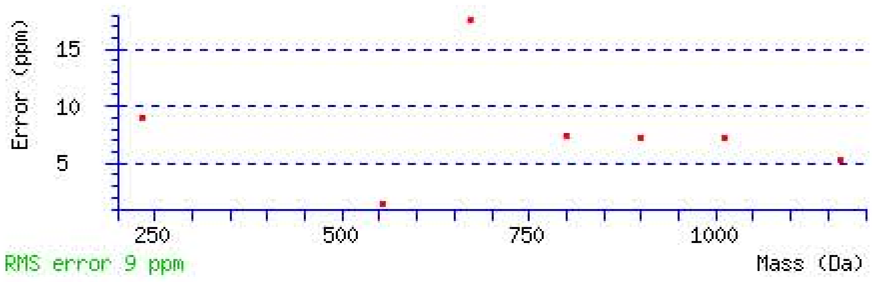
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1278.711823
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 44 **Expect:** 0.00054
Matches : 7/68 fragment ions using 11 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					L							9
2	171.112804	86.060040					G	***1166.635041***	583.821159	1149.608492	575.307884	1148.624476	574.815876	8
3	268.165568	134.586422					P	1109.613577	555.310426	1092.587028	546.797152	1091.603012	546.305144	7
4	381.249632	191.128454					L	***1012.560813***	506.784044	995.534264	498.270770	994.550248	497.778762	6
5	480.318046	240.662661					V	***899.476749***	450.242012	882.450200	441.728738	881.466184	441.236730	5
6	609.360639	305.183958			591.350074	296.178675	E	***800.408335***	400.707805	783.381786	392.194531	782.397770	391.702523	4
7	1048.585965	524.796621	1031.559416	516.283346	1030.575400	515.791338	Q	***671.365742***	336.186509	654.339193	327.673234			3
8	1105.607429	553.307352	1088.580880	544.794078	1087.596864	544.302070	G	***232.140416***	116.573846	215.113867	108.060571			2
9							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.0	1278.711823	-0.001455	LGPLVEQGR

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

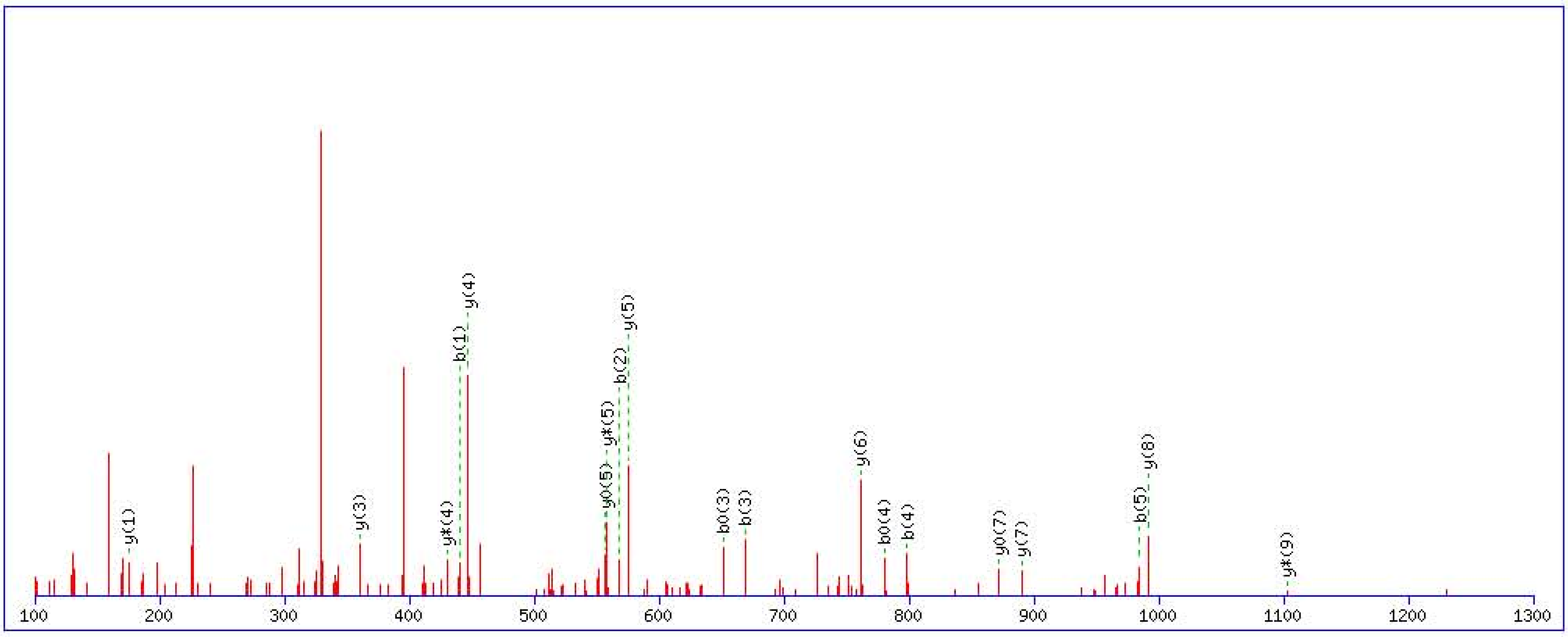
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QQTEWQSGQR**
Found in **APOE_HUMAN**, Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1

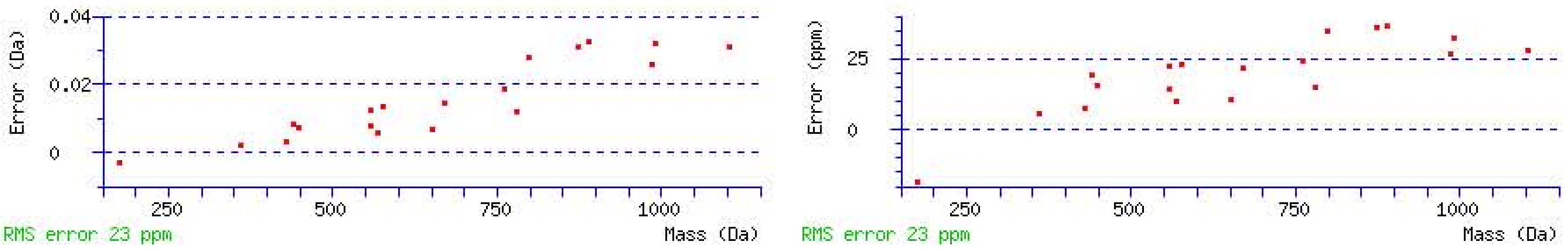
Match to Query 44033: 1557.754452 from(520.258760,3+) rtinseconds(1536) index(40681)
Title: Locus:1.1.1.2563.18 File:"2013-07-02 CLN FXIII 30 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1557.735809
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1     : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.0039
Matches : 19/98 fragment ions using 38 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	**440.232602**	220.619939	423.206053	212.106664			Q							10
2	**568.291180**	284.649228	551.264631	276.135954			Q	1119.517763	560.262520	1102.491214	551.749245	1101.507198	551.257237	9
3	**669.338859**	335.173068	652.312310	326.659793	651.328294	326.167785	T	***991.459185***	496.233231	974.432636	487.719956	973.448620	487.227948	8
4	**798.381452**	399.694364	781.354903	391.181090	780.370887	390.689082	E	***890.411506***	445.709391	873.384957	437.196117	872.400941	436.704109	7
5	**984.460765**	492.734021	967.434216	484.220746	966.450200	483.728738	W	***761.368913***	381.188095	744.342364	372.674820	743.358348	372.182812	6
6	1112.519343	556.763310	1095.492794	548.250035	1094.508778	547.758027	Q	***575.289600***	288.148438	558.263051	279.635164	557.279035	279.143156	5
7	1199.551371	600.279324	1182.524822	591.766049	1181.540806	591.274041	S	***447.231022***	224.119149	430.204473	215.605875	429.220457	215.113867	4
8	1256.572835	628.790056	1239.546286	620.276781	1238.562270	619.784773	G	***360.198994***	180.603135	343.172445	172.089860			3
9	1384.631413	692.819345	1367.604864	684.306070	1366.620848	683.814062	Q	303.177530	152.092403	286.150981	143.579129			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.6	1557.735809	0.018643	QQTEWQSGQR
28.9	1557.735809	0.018643	QQTEWQSGQR
5.7	1557.768158	-0.013706	SIQQTMARQSHQK
4.1	1557.747040	0.007412	AFSHCSSLTKHQR
3.8	1557.745697	0.008755	GSSLFMDTEKSGKR

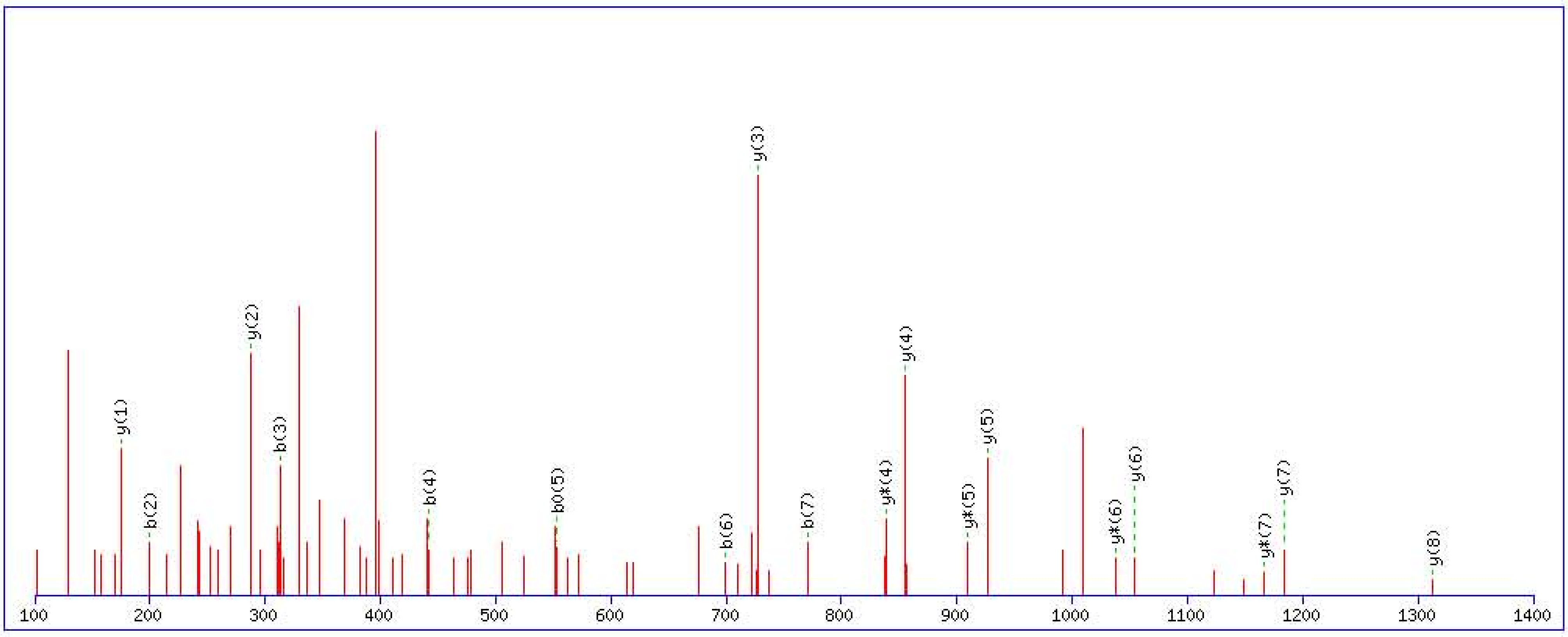
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AKLEEQAQQIR**
Found in **APOE_HUMAN**, Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1

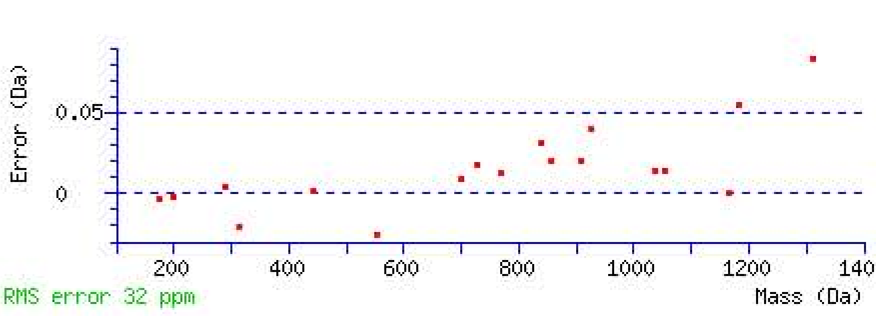
Match to Query 47073: 1623.886512 from(542.302780,3+) rtinseconds(1467) index(40205)
Title: Locus:1.1.1.2539.21 File:"2013-07-02 CLN FXIII 30 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

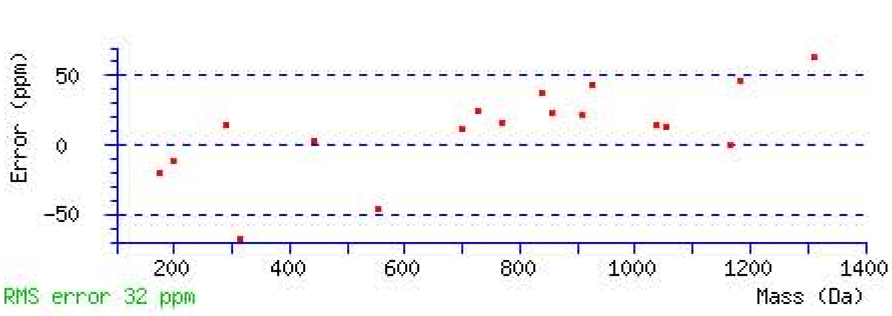
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1623.876617
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 0.00095
Matches : 18/100 fragment ions using 34 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							11
2	**200.139353**	100.573315	183.112804	92.060040			K	1553.846825	777.427050	1536.820276	768.913776	1535.836260	768.421768	10
3	**313.223417**	157.115346	296.196868	148.602072			L	1425.751862	713.379569	1408.725313	704.866294	1407.741297	704.374286	9
4	**442.266010**	221.636643	425.239461	213.123369	424.255445	212.631361	E	***1312.667798***	656.837537	1295.641249	648.324262	1294.657233	647.832254	8
5	571.308603	286.157940	554.282054	277.644665	553.298038	277.152657	E	***1183.625205***	592.316240	1166.598656	583.802966	1165.614640	583.310958	7
6	**699.367181**	350.187229	682.340632	341.673954	681.356616	341.181946	Q	***1054.582612***	527.794944	1037.556063	519.281670			6
7	**770.404295**	385.705786	753.377746	377.192511	752.393730	376.700503	A	***926.524034***	463.765655	909.497485	455.252380			5
8	898.462873	449.735075	881.436324	441.221800	880.452308	440.729792	Q	***855.486920***	428.247098	838.460371	419.733823			4
9	1337.688199	669.347737	1320.661650	660.834463	1319.677634	660.342455	Q	***727.428342***	364.217809	710.401793	355.704534			3
10	1450.772263	725.889769	1433.745714	717.376495	1432.761698	716.884487	I	***288.203016***	144.605146	271.176467	136.091871			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
43.4	1623.876617	0.009895	AKLEEQAQQIR
31.8	1623.876617	0.009895	AKLEEQAQQIR
18.3	1623.877502	0.009010	QMKAQQLR
11.2	1623.877502	0.009010	QMKAQQLR
8.7	1623.876617	0.009895	AKLEEQAQQIR
3.8	1623.869247	0.017265	KEADGDLPQRVQLR
3.3	1623.866745	0.019767	QAQAQPHLPPAR
2.5	1623.876617	0.009895	QAEEAVAKLQAR
2.4	1623.865402	0.021110	KLKLPGDSSLMTYR
2.1	1623.877502	0.009010	AQKMQQLR

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

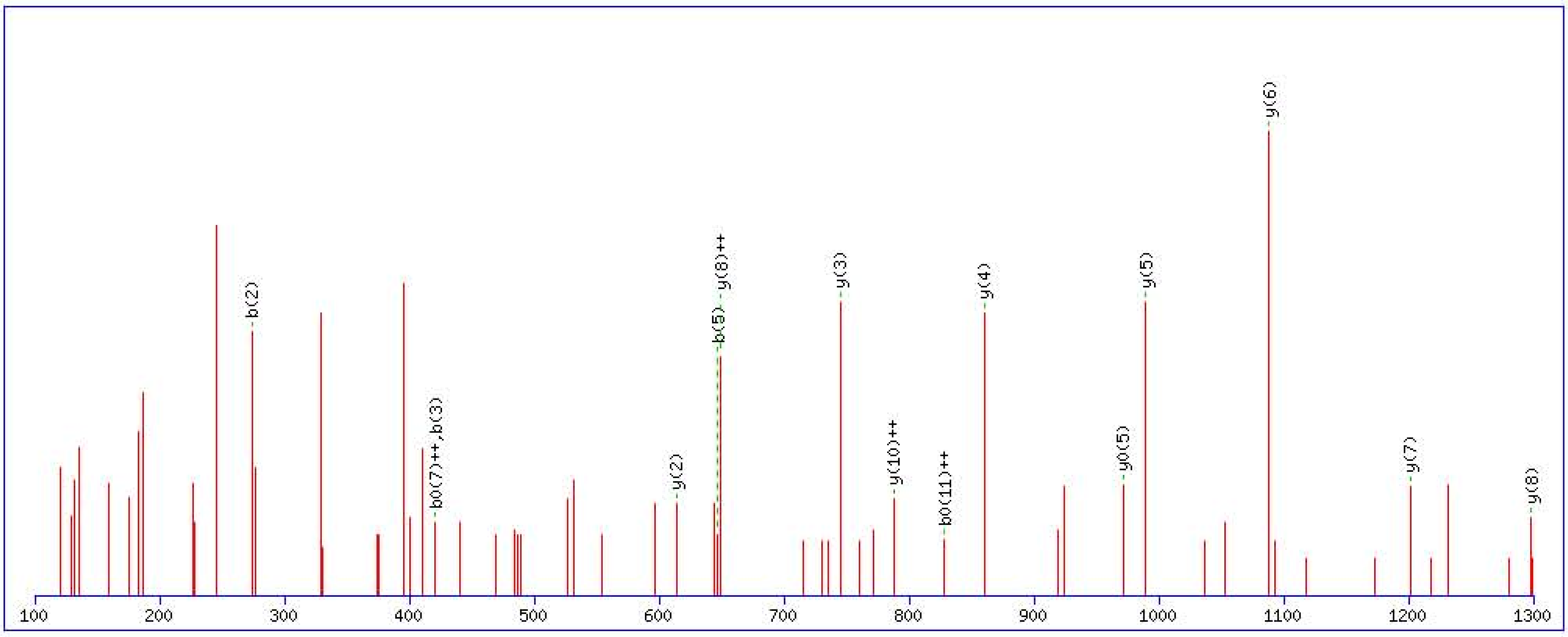
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SWFEPLVEDMQR**
Found in **APOE_HUMAN**, Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1

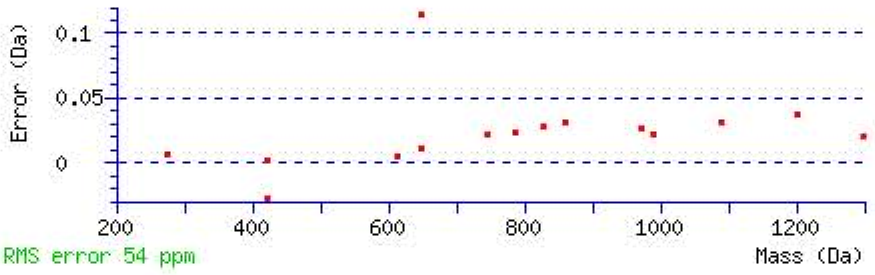
Match to Query 53233: 1846.899702 from(616.640510,3+) rtinseconds(2778) index(12259)
Title: Locus:1.1.1.2687.12 File:"2013-07-02 CLN FXIII 30 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

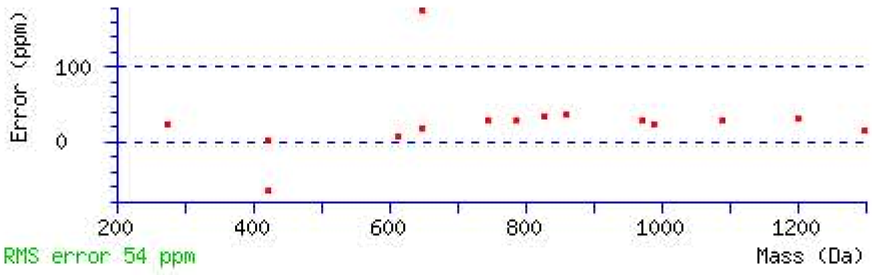
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1846.874603
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 25  Expect: 0.034
Matches : 15/106 fragment ions using 36 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							12
2	**274.118617**	137.562947			256.108052	128.557664	W	1760.849861	880.928568	1743.823312	872.415294	1742.839296	871.923286	11
3	**421.187031**	211.097153			403.176466	202.091871	F	1574.770548	787.888912	1557.743999	779.375638	1556.759983	778.883629	10
4	550.229624	275.618450			532.219059	266.613168	E	1427.702134	714.354705	1410.675585	705.841431	1409.691569	705.349422	9
5	**647.282388**	324.144832			629.271823	315.139550	P	***1298.659541***	649.833409	1281.632992	641.320134	1280.648976	640.828126	8
6	760.366452	380.686864			742.355887	371.681582	L	***1201.606777***	601.307027	1184.580228	592.793752	1183.596212	592.301744	7
7	859.434866	430.221071			841.424301	421.215789	V	***1088.522713***	544.764995	1071.496164	536.251720	1070.512148	535.759712	6
8	988.477459	494.742368			970.466894	485.737085	E	***989.454299***	495.230788	972.427750	486.717513	971.443734	486.225505	5
9	1103.504402	552.255839			1085.493837	543.250557	D	***860.411706***	430.709491	843.385157	422.196216	842.401141	421.704208	4
10	1234.544887	617.776082			1216.534322	608.770799	M	***745.384763***	373.196020	728.358214	364.682745			3
11	1673.770213	837.388745	1656.743664	828.875470	1655.759648	828.383462	Q	***614.344278***	307.675777	597.317729	299.162503			2
12							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.2	1846.874603	0.025099	SWFEPLVEDMQR
9.2	1846.895721	0.003981	LQLEETMPSPYGR
3.3	1846.909470	-0.009768	RATASLDTPEGAIMGDVK

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

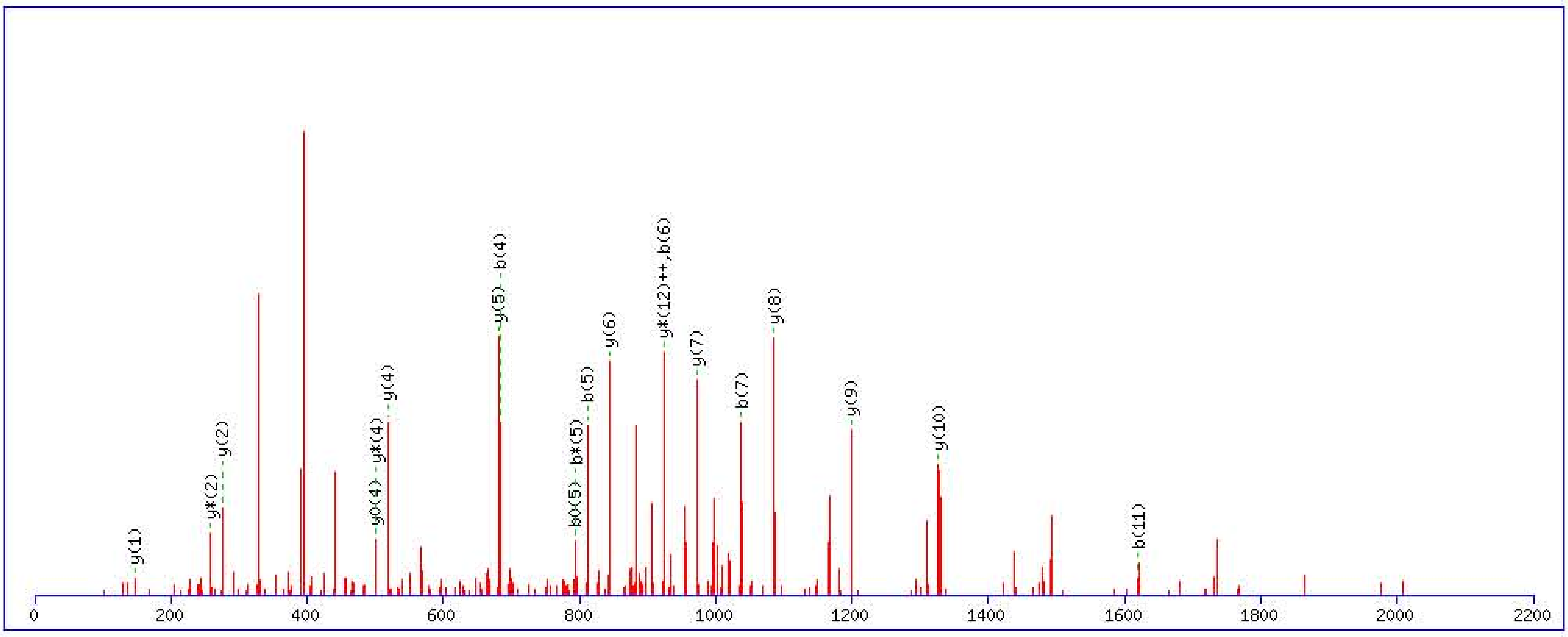
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SGVQQLIQYYQDQK**
Found in **APOF_HUMAN**, Apolipoprotein F OS=Homo sapiens GN=APOF PE=1 SV=2

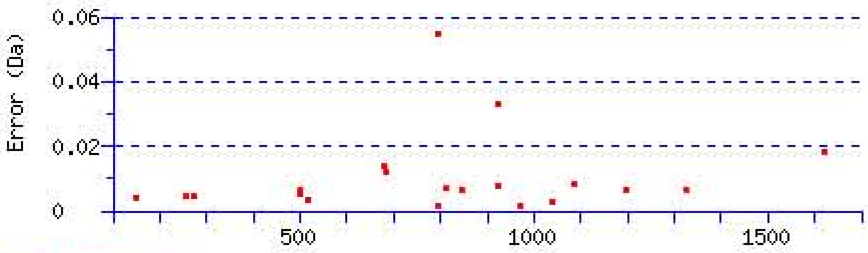
Match to Query 57599: 2008.020548 from(1005.017550,2+) rtinseconds(2459) index(65964)
Title: Locus:1.1.1.2853.16 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●

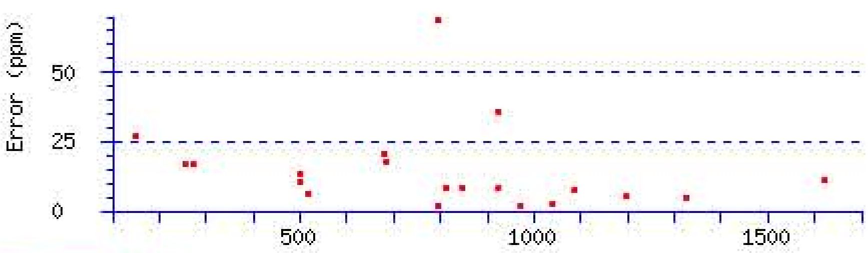


```
Monoisotopic mass of neutral peptide Mr(calc): 2008.008789
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 47  Expect: 0.00014
Matches : 20/146 fragment ions using 36 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							14
2	145.060768	73.034022			127.050203	64.028740	G	1921.984049	961.495663	1904.957500	952.982388	1903.973484	952.490380	13
3	244.129182	122.568229			226.118617	113.562947	V	1864.962585	932.984931	1847.936036	924.471656	1846.952020	923.979648	12
4	**683.354508**	342.180892	666.327959	333.667618	665.343943	333.175610	Q	1765.894171	883.450724	1748.867622	874.937449	1747.883606	874.445441	11
5	**811.413086**	406.210181	794.386537	397.696907	793.402521	397.204899	Q	***1326.668845***	663.838061	1309.642296	655.324786	1308.658280	654.832778	10
6	**924.497150**	462.752213	907.470601	454.238939	906.486585	453.746931	L	***1198.610267***	599.808772	1181.583718	591.295497	1180.599702	590.803489	9
7	**1037.581214**	519.294245	1020.554665	510.780971	1019.570649	510.288963	I	***1085.526203***	543.266740	1068.499654	534.753465	1067.515638	534.261457	8
8	1165.639792	583.323534	1148.613243	574.810260	1147.629227	574.318252	Q	***972.442139***	486.724708	955.415590	478.211433	954.431574	477.719425	7
9	1328.703121	664.855199	1311.676572	656.341924	1310.692556	655.849916	Y	***844.383561***	422.695419	827.357012	414.182144	826.372996	413.690136	6
10	1491.766450	746.386863	1474.739901	737.873589	1473.755885	737.381581	Y	***681.320232***	341.163754	664.293683	332.650480	663.309667	332.158472	5
11	**1619.825028**	810.416152	1602.798479	801.902878	1601.814463	801.410870	Q	***518.256903***	259.632090	501.230354	251.118815	500.246338	250.626807	4
12	1734.851971	867.929624	1717.825422	859.416349	1716.841406	858.924341	D	390.198325	195.602800	373.171776	187.089526	372.187760	186.597518	3
13	1862.910549	931.958913	1845.884000	923.445638	1844.899984	922.953630	Q	***275.171382***	138.089329	258.144833	129.576054			2
14							K	***147.112804***	74.060040	130.086255	65.546765			1



RMS error 21 ppm



RMS error 21 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.7	2008.008789	0.011759	SGVQQLIQYYQDQK
36.0	2008.008789	0.011759	SGVQQLIQYYQDQK
14.2	2008.008789	0.011759	SGVQQLIQYYQDQK
5.2	2008.037766	-0.017218	NYEDSVIQSVFRAKPQK
3.5	2008.037308	-0.016760	VVPVSLSELYLLQCNMK
3.0	2008.048523	-0.027975	KLTIIFKNMQECIDQK
2.8	2008.037277	-0.016729	IEELQEQLEQK
1.9	2008.005630	0.014918	ITQRMVCAGYKEGGK
1.8	2007.998215	0.022333	QQLNLRTHMADENK
1.8	2007.998215	0.022333	QQLNLRTHMADENK

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

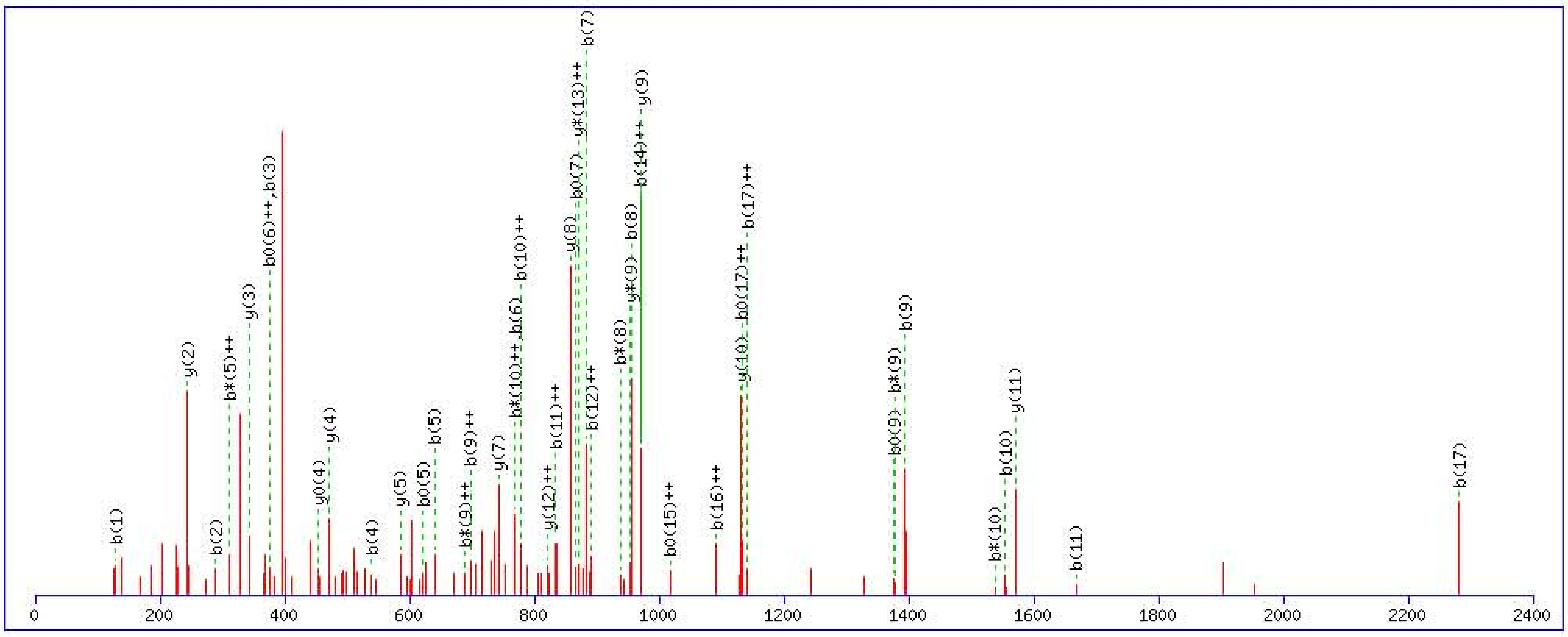
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KCSYTEDAQCIDGTIEVPK**
Found in **APOH_HUMAN**, Beta-2-glycoprotein 1 OS=Homo sapiens GN=APOH PE=1 SV=3

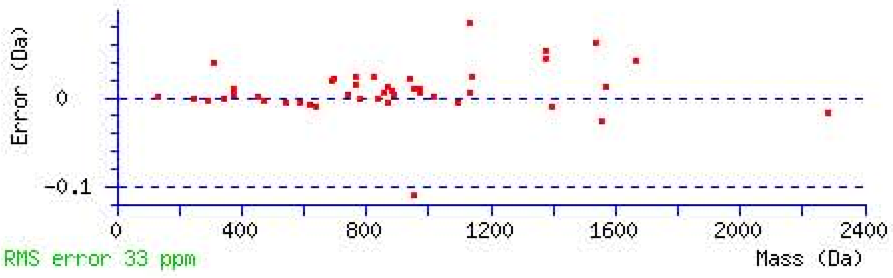
Match to Query 68929: 2524.173462 from(842.398430,3+) rtinseconds(1996) index(80285)
Title: Locus:1.1.1.2574.25 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

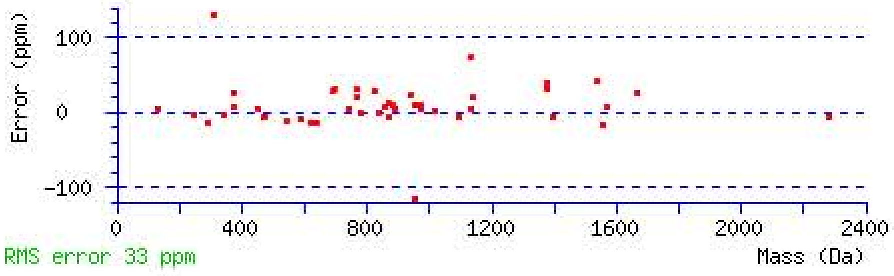
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2524.164780
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 61 **Expect:** 1.2e-005
Matches : 44/206 fragment ions using 83 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	*129.102239*	65.054757	112.075690	56.541483			K							19
2	*289.132888*	145.070082	272.106339	136.556808			C	2397.077099	1199.042187	2380.050550	1190.528913	2379.066534	1190.036905	18
3	*376.164916*	188.586096	359.138367	180.072822	358.154351	179.580814	S	2237.046450	1119.026863	2220.019901	1110.513588	2219.035885	1110.021580	17
4	*539.228245*	270.117761	522.201696	261.604486	521.217680	261.112478	Y	2150.014422	1075.510849	2132.987873	1066.997574	2132.003857	1066.505566	16
5	*640.275924*	320.641600	623.249375	312.128326	622.265359	311.636318	T	1986.951093	993.979185	1969.924544	985.465910	1968.940528	984.973902	15
6	*769.318517*	385.162897	752.291968	376.649622	751.307952	376.157614	E	1885.903414	943.455345	1868.876865	934.942071	1867.892849	934.450063	14
7	*884.345460*	442.676368	867.318911	434.163094	866.334895	433.671086	D	1756.860821	878.934049	1739.834272	870.420774	1738.850256	869.928766	13
8	*955.382574*	478.194925	938.356025	469.681650	937.372009	469.189642	A	1641.833878	821.420577	1624.807329	812.907303	1623.823313	812.415295	12
9	*1394.607900*	**697.807588**	1377.581351	689.294314	1376.597335	688.802306	Q	*1570.796764*	785.902020	1553.770215	777.388746	1552.786199	776.896738	11
10	*1554.638549*	**777.822913**	1537.612000	769.309638	1536.627984	768.817630	C	*1131.571438*	566.289357	1114.544889	557.776083	1113.560873	557.284075	10
11	*1667.722613*	**834.364945**	1650.696064	825.851670	1649.712048	825.359662	I	*971.540789*	486.274033	954.514240	477.760758	953.530224	477.268750	9
12	1782.749556	**891.878416**	1765.723007	883.365142	1764.738991	882.873134	D	*858.456725*	429.732001	841.430176	421.218726	840.446160	420.726718	8
13	1839.771020	920.389148	1822.744471	911.875874	1821.760455	911.383866	G	*743.429782*	372.218529	726.403233	363.705255	725.419217	363.213247	7
14	1940.818699	**970.912988**	1923.792150	962.399713	1922.808134	961.907705	T	686.408318	343.707797	669.381769	335.194523	668.397753	334.702515	6
15	2053.902763	1027.455019	2036.876214	1018.941745	2035.892198	1018.449737	I	*585.360639*	293.183958	568.334090	284.670683	567.350074	284.178675	5
16	2182.945356	**1091.976316**	2165.918807	1083.463041	2164.934791	1082.971034	E	*472.276575*	236.641925	455.250026	228.128651	454.266010	227.636643	4
17	*2282.013770*	**1141.510523**	2264.987221	1132.997248	2264.003205	1132.505240	V	*343.233982*	172.120629	326.207433	163.607354			3
18	2379.066534	1190.036905	2362.039985	1181.523630	2361.055969	1181.031622	P	*244.165568*	122.586422	227.139019	114.073148			2
19							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.6	2524.164780	0.008682	KCSYTEDAQCIDGTIEVPK

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

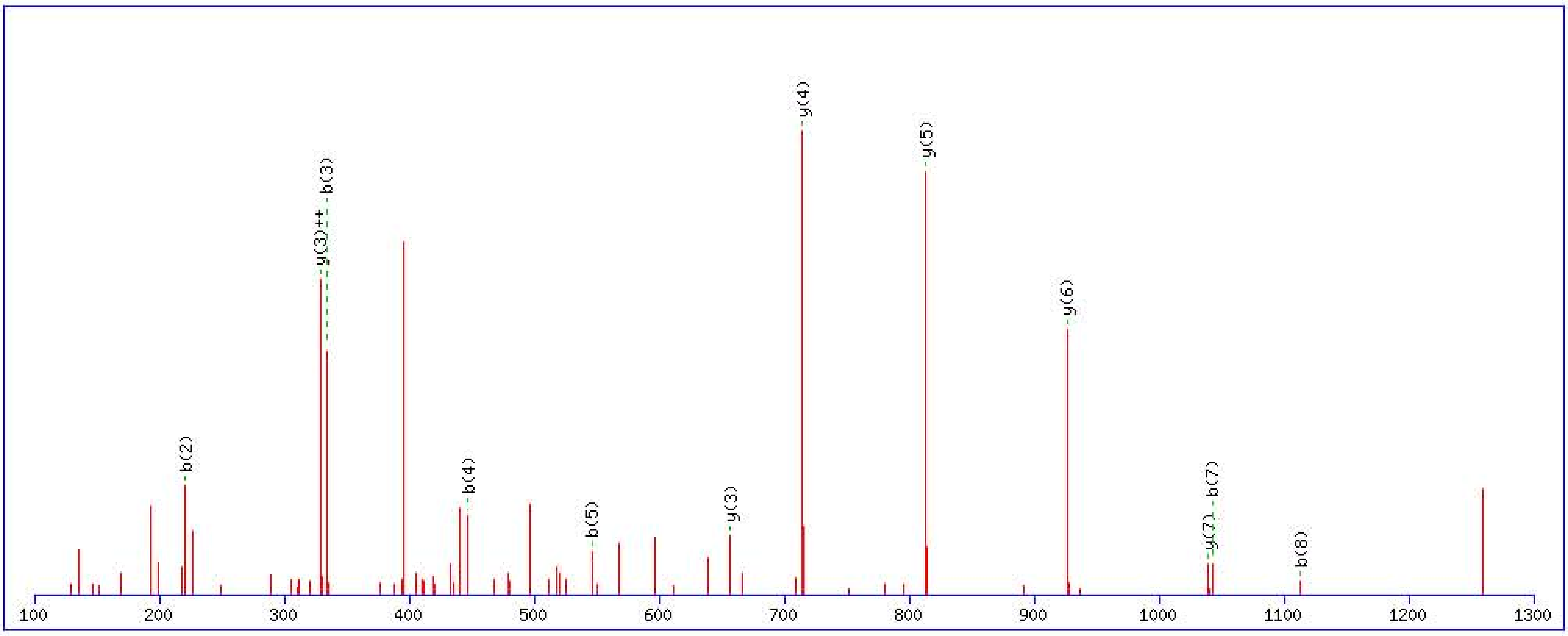
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GYILVGQAK**
Found in **C4BPA_HUMAN**, C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

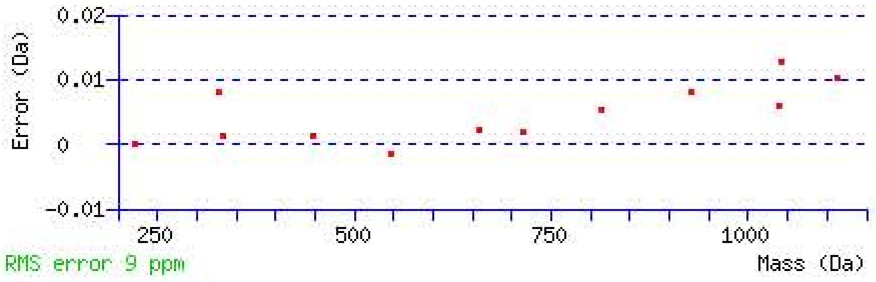
Match to Query 33696: 1258.712588 from(630.363570,2+) rtinseconds(2018) index(63192)
Title: Locus:1.1.1.2700.7 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

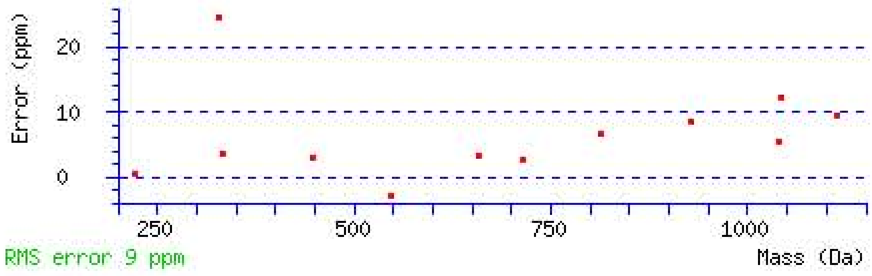
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1258.710754
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 29  Expect: 0.021
Matches : 12/52 fragment ions using 28 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	58.028740	29.518008			G					9
2	***221.092069***	111.049673			Y	1202.696579	601.851928	1185.670030	593.338653	8
3	***334.176133***	167.591704			I	***1039.633250***	520.320263	1022.606701	511.806989	7
4	***447.260197***	224.133737			L	***926.549186***	463.778231	909.522637	455.264957	6
5	***546.328611***	273.667944			V	***813.465122***	407.236199	796.438573	398.722925	5
6	603.350075	302.178676			G	***714.396708***	357.701992	697.370159	349.188718	4
7	***1042.575401***	521.791339	1025.548852	513.278064	Q	***657.375244***	***329.191260***	640.348695	320.677986	3
8	***1113.612515***	557.309896	1096.585966	548.796621	A	218.149918	109.578597	201.123369	101.065322	2
9					K	147.112804	74.060040	130.086255	65.546765	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.6	1258.710754	0.001834	GYILVGQAK
10.4	1258.717941	-0.005353	RILAKVQEMR
8.6	1258.721970	-0.009382	GYILQAKR

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

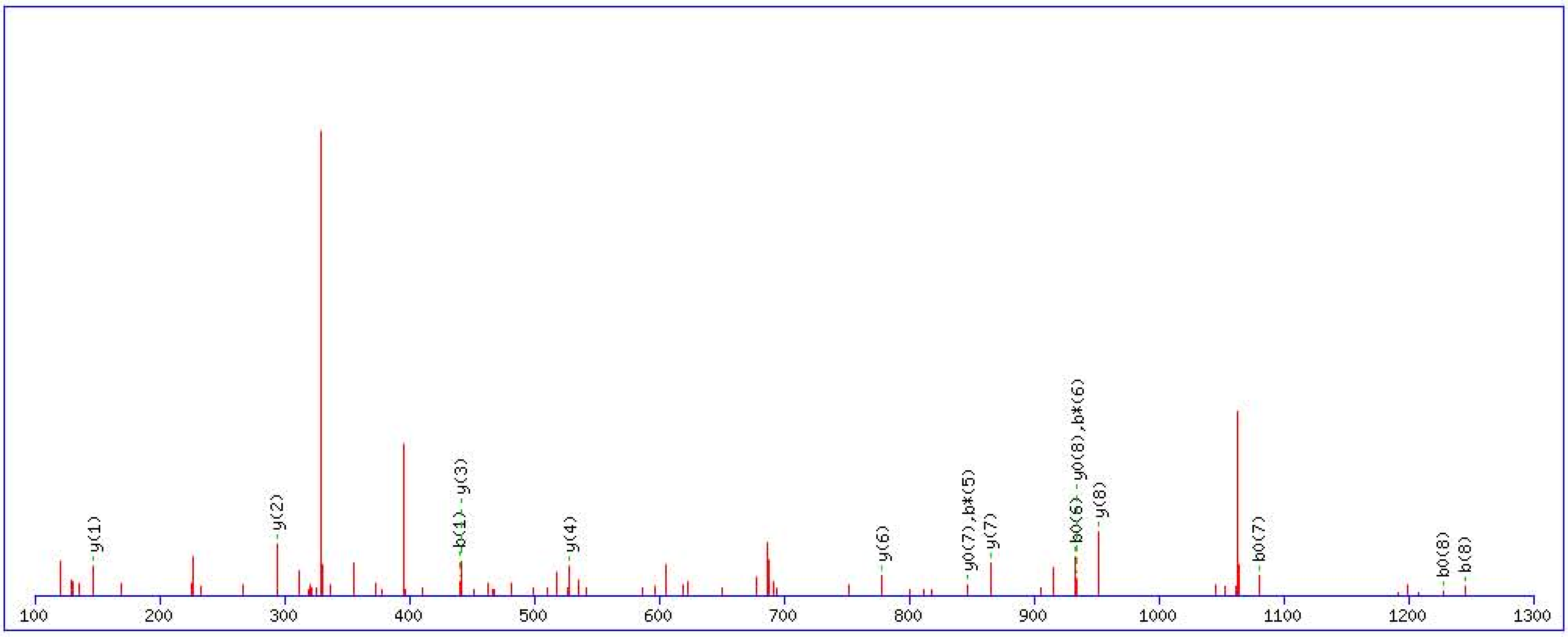
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QSSSYSFFK**
Found in **C4BPA_HUMAN**, C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2

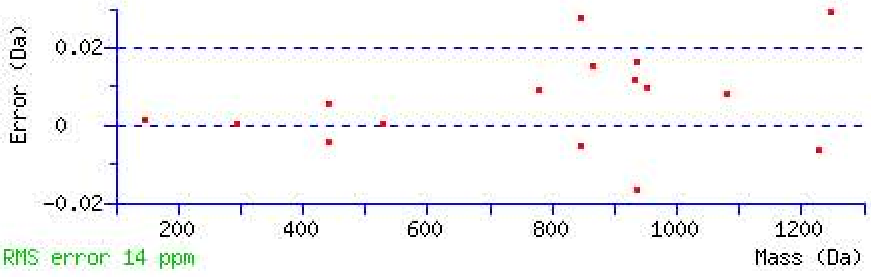
Match to Query 38507: 1390.665768 from(696.340160,2+) rtinseconds(2117) index(63848)
Title: Locus:1.1.1.2734.18 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

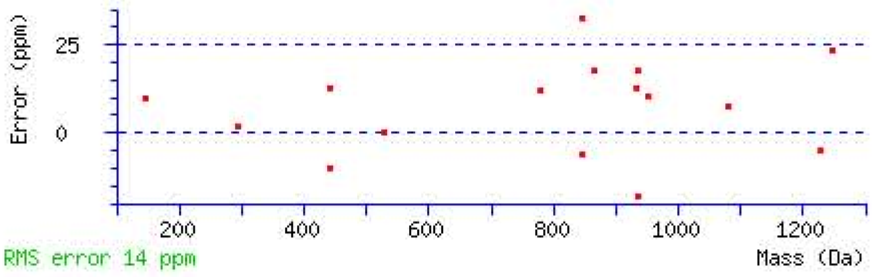
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1390.659119
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1     : Biotin:Thermo-21345 (Q)
Ions Score: 33  Expect: 0.0046
Matches : 16/88 fragment ions using 35 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**440.232602**	220.619939	423.206053	212.106664			Q							9
2	527.264630	264.135953	510.238081	255.622679	509.254065	255.130671	S	***952.441073***	476.724175	935.414524	468.210900	934.430508	467.718892	8
3	614.296658	307.651967	597.270109	299.138692	596.286093	298.646684	S	***865.409045***	433.208161	848.382496	424.694886	847.398480	424.202878	7
4	701.328686	351.167981	684.302137	342.654706	683.318121	342.162698	S	***778.377017***	389.692147	761.350468	381.178872	760.366452	380.686864	6
5	864.392015	432.699645	847.365466	424.186371	846.381450	423.694363	Y	691.344989	346.176133	674.318440	337.662858	673.334424	337.170850	5
6	951.424043	476.215659	934.397494	467.702385	933.413478	467.210377	S	***528.281660***	264.644468	511.255111	256.131194	510.271095	255.639186	4
7	1098.492457	549.749866	1081.465908	541.236592	1080.481892	540.744584	F	***441.249632***	221.128454	424.223083	212.615180			3
8	**1245.560871**	623.284073	1228.534322	614.770799	1227.550306	614.278791	F	***294.181218***	147.594247	277.154669	139.080973			2
9							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.8	1390.659119	0.006649	QSSSYSFFK
7.4	1390.676208	-0.010440	AEKSSSTDQK
3.5	1390.676208	-0.010440	LTENNSQPLMTK
2.0	1390.669678	-0.003910	CAPASIRLMDNK
1.3	1390.673706	-0.007938	TLNADLMMFAHK
1.2	1390.673721	-0.007953	QPNCSSLFK

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

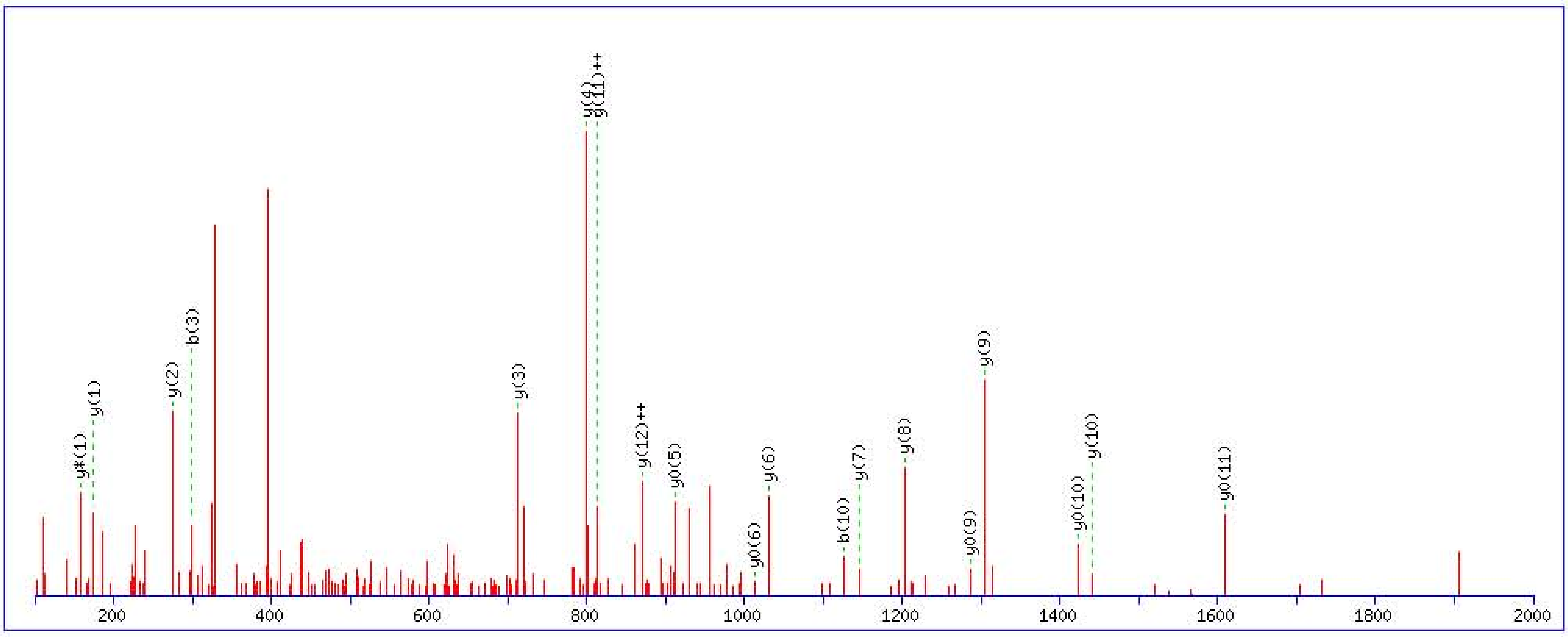
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NALWHTGDTESQVR**
Found in **COMP_HUMAN**, Cartilage oligomeric matrix protein OS=Homo sapiens GN=COMP PE=1 SV=2

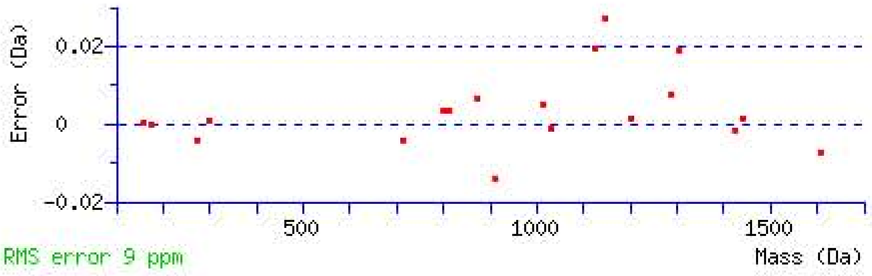
Match to Query 54890: 1923.926082 from(642.315970,3+) rtinseconds(1732) index(61233)
Title: Locus:1.1.1.2601.12 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

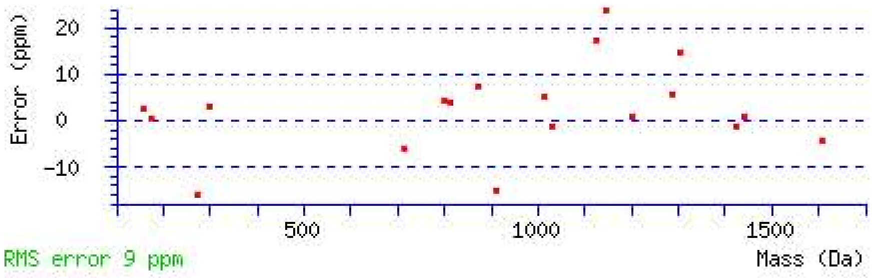
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1923.926132
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12 : Biotin:Thermo-21345 (Q)
Ions Score: 53 **Expect:** 2.9e-005
Matches : 19/140 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							14
2	186.087317	93.547296	169.060768	85.034022			A	1810.890481	905.948879	1793.863932	897.435604	1792.879916	896.943596	13
3	**299.171381**	150.089328	282.144832	141.576054			L	1739.853367	870.430322	1722.826818	861.917047	1721.842802	861.425039	12
4	485.250694	243.128985	468.224145	234.615711			W	1626.769303	813.888290	1609.742754	805.375015	1608.758738	804.883007	11
5	622.309606	311.658441	605.283057	303.145167			H	***1440.689990***	720.848633	1423.663441	712.335359	1422.679425	711.843351	10
6	723.357285	362.182281	706.330736	353.669006	705.346720	353.176998	T	***1303.631078***	652.319177	1286.604529	643.805903	1285.620513	643.313895	9
7	780.378749	390.693013	763.352200	382.179738	762.368184	381.687730	G	***1202.583399***	601.795338	1185.556850	593.282063	1184.572834	592.790055	8
8	895.405692	448.206484	878.379143	439.693210	877.395127	439.201202	D	***1145.561935***	573.284606	1128.535386	564.771331	1127.551370	564.279323	7
9	996.453371	498.730324	979.426822	490.217049	978.442806	489.725041	T	***1030.534992***	515.771134	1013.508443	507.257860	1012.524427	506.765852	6
10	**1125.495964**	563.251620	1108.469415	554.738346	1107.485399	554.246337	E	929.487313	465.247295	912.460764	456.734020	911.476748	456.242012	5
11	1212.527992	606.767634	1195.501443	598.254360	1194.517427	597.762352	S	***800.444720***	400.725998	783.418171	392.212724	782.434155	391.720716	4
12	1651.753318	826.380297	1634.726769	817.867023	1633.742753	817.375015	Q	***713.412692***	357.209984	696.386143	348.696710			3
13	1750.821732	875.914504	1733.795183	867.401230	1732.811167	866.909222	V	***274.187366***	137.597321	257.160817	129.084047			2
14							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.6	1923.926132	-0.000050	NALWHTGDTESQVR
4.0	1923.928635	-0.002553	SDNTTLPAPASNQGPTTPR
0.3	1923.909531	0.016551	NLEAVETLGSTSTICSDK

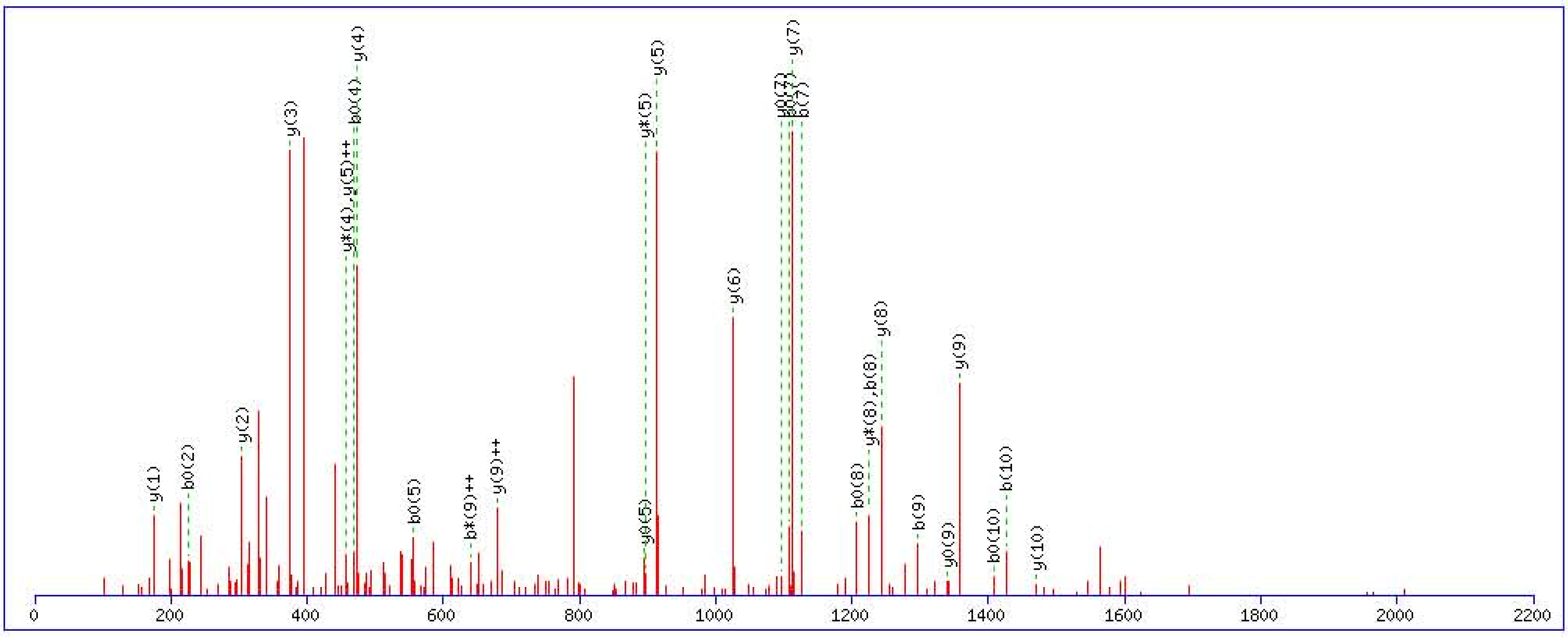
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELDESLQVAER**
Found in **CLUS_HUMAN**, Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1

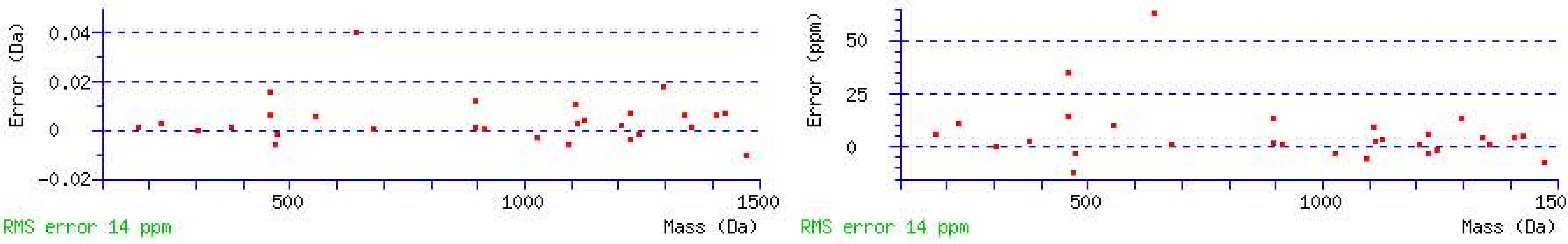
Match to Query 46050: 1598.800168 from(800.407360,2+) rtinseconds(1944) index(62723)
Title: Locus:1.1.1.2674.19 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1598.797379
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 56  Expect: 5.2e-005
Matches : 29/106 fragment ions using 60 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							11
2	243.133933	122.070605			225.123368	113.065322	L	*1470.762091*	735.884684	1453.735542	727.371409	1452.751526	726.879401	10
3	358.160876	179.584076			340.150311	170.578794	D	*1357.678027*	679.342652	1340.651478	670.829377	1339.667462	670.337369	9
4	487.203469	244.105373			469.192904	235.100090	E	*1242.651084*	621.829180	1225.624535	613.315906	1224.640519	612.823898	8
5	574.235497	287.621387			556.224932	278.616104	S	*1113.608491*	557.307884	1096.581942	548.794609	1095.597926	548.302601	7
6	687.319561	344.163419			669.308996	335.158136	L	*1026.576463*	513.791870	1009.549914	505.278595	1008.565898	504.786587	6
7	**1126.544887**	563.776082	1109.518338	555.262807	1108.534322	554.770799	Q	*913.492399*	457.249838	896.465850	448.736563	895.481834	448.244555	5
8	**1225.613301**	613.310289	1208.586752	604.797014	1207.602736	604.305006	V	*474.267073*	237.637175	457.240524	229.123900	456.256508	228.631892	4
9	**1296.650415**	648.828846	1279.623866	640.315571	1278.639850	639.823563	A	*375.198659*	188.102968	358.172110	179.589693	357.188094	179.097685	3
10	**1425.693008**	713.350142	1408.666459	704.836868	1407.682443	704.344860	E	*304.161545*	152.584411	287.134996	144.071136	286.150980	143.579128	2
11							R	*175.118952*	88.063114	158.092403	79.549839			1



NCBI **BLAST** search of ELDESLQVAER
(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	1598.797379	0.002789	ELDESLQVAER
9.9	1598.790024	0.010144	VTAEGDSHTEVVISR
7.6	1598.797379	0.002789	LEESDVLQEAR
4.2	1598.823883	-0.023715	TPTEKVEKMFPHR
3.6	1598.802094	-0.001926	ELVSRCGEMLHIR
3.1	1598.797409	0.002759	EDVDDLVSQLR
2.9	1598.783478	0.016690	EDSVQRSTPNR
2.9	1598.819138	-0.018970	EYFLSEIDEAKKK
2.6	1598.817352	-0.017184	QLNLMKWTLCHR
1.9	1598.776932	0.023236	FPIDYPYSPPTFR

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

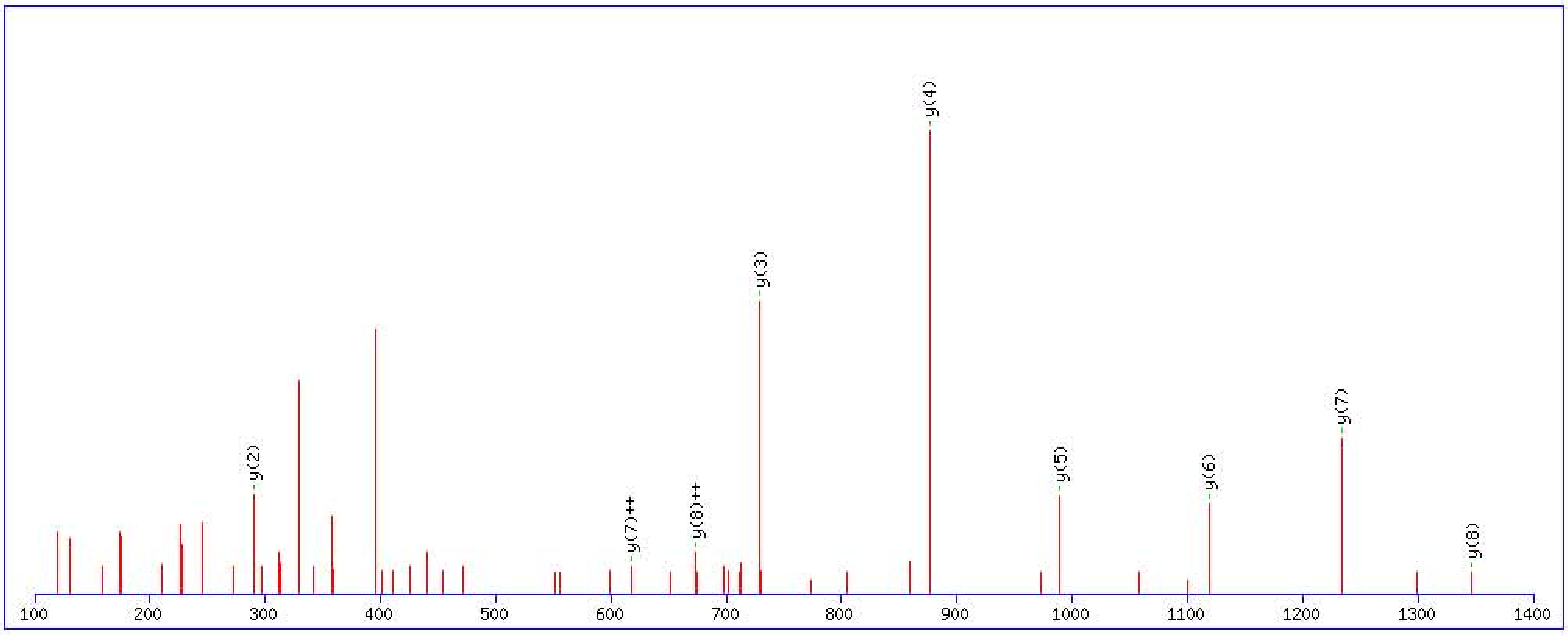
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ASSIIDELFQDR**
Found in **CLUS_HUMAN**, Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1

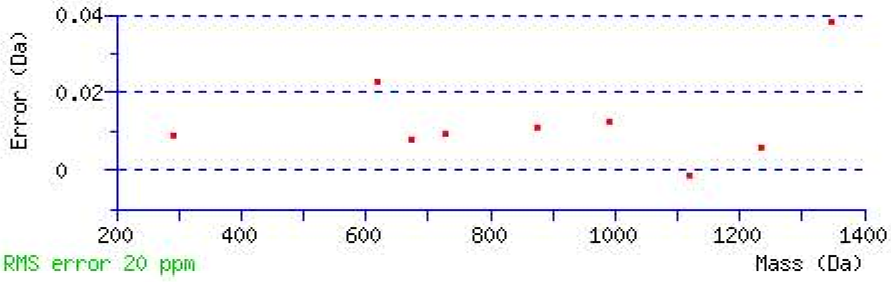
Match to Query 49675: 1703.861382 from(568.961070,3+) rtinseconds(2786) index(68148)
Title: Locus:1.1.1.2966.3 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

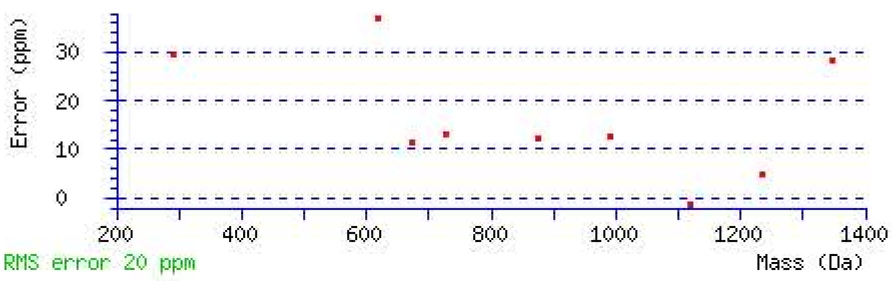
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1703.855240
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10    : Biotin:Thermo-21345 (Q)
Ions Score: 54  Expect: 0.00011
Matches : 9/110 fragment ions using 12 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							12
2	159.076418	80.041847			141.065853	71.036564	S	1633.825419	817.416348	1616.798870	808.903073	1615.814854	808.411065	11
3	246.108446	123.557861			228.097881	114.552578	S	1546.793391	773.900333	1529.766842	765.387059	1528.782826	764.895051	10
4	359.192510	180.099893			341.181945	171.094610	I	1459.761363	730.384320	1442.734814	721.871045	1441.750798	721.379037	9
5	472.276574	236.641925			454.266009	227.636642	I	***1346.677299***	673.842288	1329.650750	665.329013	1328.666734	664.837005	8
6	587.303517	294.155397			569.292952	285.150114	D	***1233.593235***	617.300256	1216.566686	608.786981	1215.582670	608.294973	7
7	716.346110	358.676693			698.335545	349.671411	E	***1118.566292***	559.786784	1101.539743	551.273510	1100.555727	550.781501	6
8	829.430174	415.218725			811.419609	406.213443	L	***989.523699***	495.265488	972.497150	486.752213	971.513134	486.260205	5
9	976.498588	488.752932			958.488023	479.747650	F	***876.439635***	438.723456	859.413086	430.210181	858.429070	429.718173	4
10	1415.723914	708.365595	1398.697365	699.852321	1397.713349	699.360312	Q	***729.371221***	365.189249	712.344672	356.675974	711.360656	356.183966	3
11	1530.750857	765.879067	1513.724308	757.365792	1512.740292	756.873784	D	***290.145895***	145.576585	273.119346	137.063311	272.135330	136.571303	2
12							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.9	1703.855240	0.006142	ASSIIDELFQDR

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

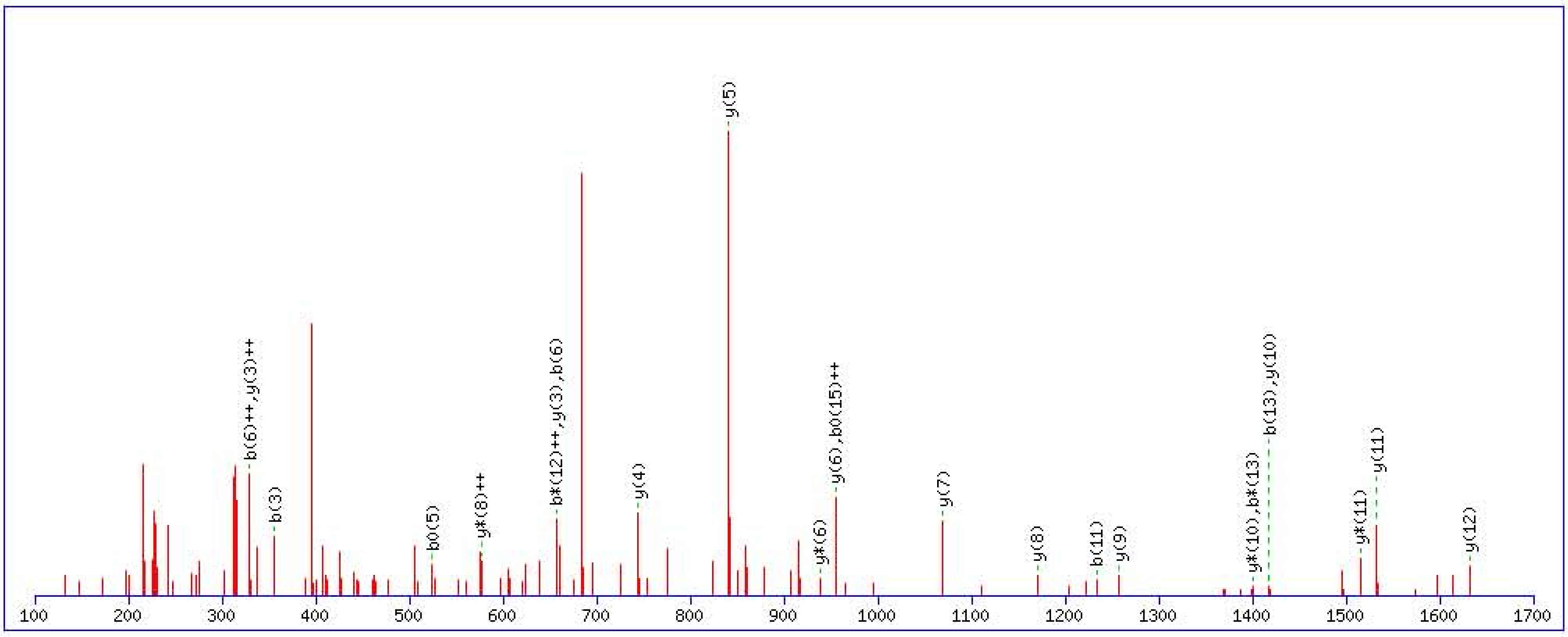
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EILSVDCSTNNPSQAK**
Found in **CLUS_HUMAN**, Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1

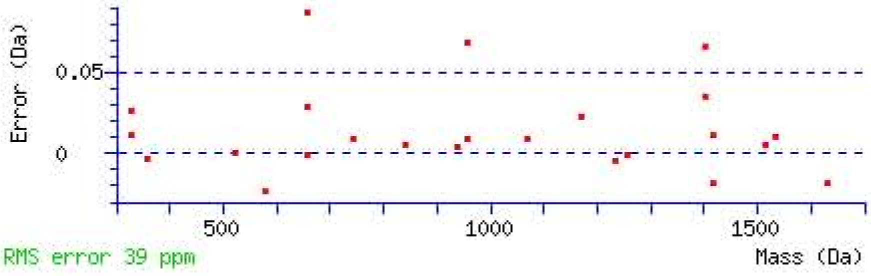
Match to Query 58961: 2072.987382 from(692.003070,3+) rtinseconds(1791) index(61651)
Title: Locus:1.1.1.2621.22 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

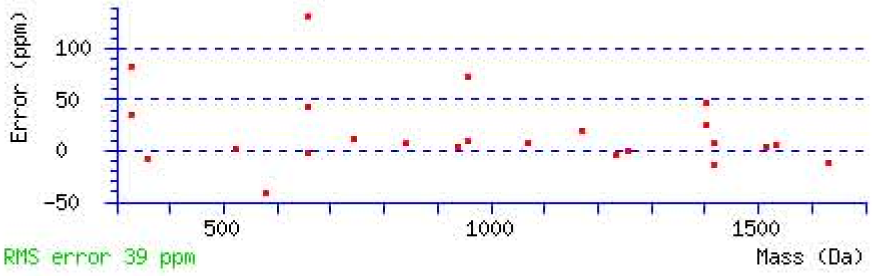
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2072.987061
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14 : Biotin:Thermo-21345 (Q)
Ions Score: 60 **Expect:** 3.4e-006
Matches : 24/156 fragment ions using 30 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							16
2	243.133933	122.070605			225.123368	113.065322	I	1944.951759	972.979517	1927.925210	964.466243	1926.941194	963.974235	15
3	**356.217997**	178.612637			338.207432	169.607354	L	1831.867695	916.437485	1814.841146	907.924211	1813.857130	907.432203	14
4	443.250025	222.128650			425.239460	213.123368	S	1718.783631	859.895454	1701.757082	851.382179	1700.773066	850.890171	13
5	542.318439	271.662858			524.307874	262.657575	V	***1631.751603***	816.379439	1614.725054	807.866165	1613.741038	807.374157	12
6	**657.345382**	329.176329			639.334817	320.171046	D	***1532.683189***	766.845233	1515.656640	758.331958	1514.672624	757.839950	11
7	817.376031	409.191654			799.365466	400.186371	C	***1417.656246***	709.331761	1400.629697	700.818487	1399.645681	700.326479	10
8	904.408059	452.707668			886.397494	443.702385	S	***1257.625597***	629.316437	1240.599048	620.803162	1239.615032	620.311154	9
9	1005.455738	503.231507			987.445173	494.226225	T	***1170.593569***	585.800422	1153.567020	577.287148	1152.583004	576.795140	8
10	1119.498665	560.252971	1102.472116	551.739696	1101.488100	551.247688	N	***1069.545890***	535.276583	1052.519341	526.763309	1051.535325	526.271301	7
11	**1233.541592**	617.274434	1216.515043	608.761160	1215.531027	608.269152	N	***955.502963***	478.255119	938.476414	469.741845	937.492398	469.249837	6
12	1330.594356	665.800816	1313.567807	657.287542	1312.583791	656.795534	P	***841.460036***	421.233656	824.433487	412.720381	823.449471	412.228373	5
13	**1417.626384**	709.316830	1400.599835	700.803556	1399.615819	700.311548	S	***744.407272***	372.707274	727.380723	364.193999	726.396707	363.701991	4
14	1856.851710	928.929493	1839.825161	920.416219	1838.841145	919.924211	Q	***657.375244***	329.191260	640.348695	320.677985			3
15	1927.888824	964.448050	1910.862275	955.934776	1909.878259	955.442768	A	218.149918	109.578597	201.123369	101.065322			2
16							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of EILSVDCSTNNPSQAK
(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	2072.987061	0.000321	EILSVDCSTNNPSQAK
1.9	2073.012680	-0.025298	TLVLDFETEGERNSPNPR

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

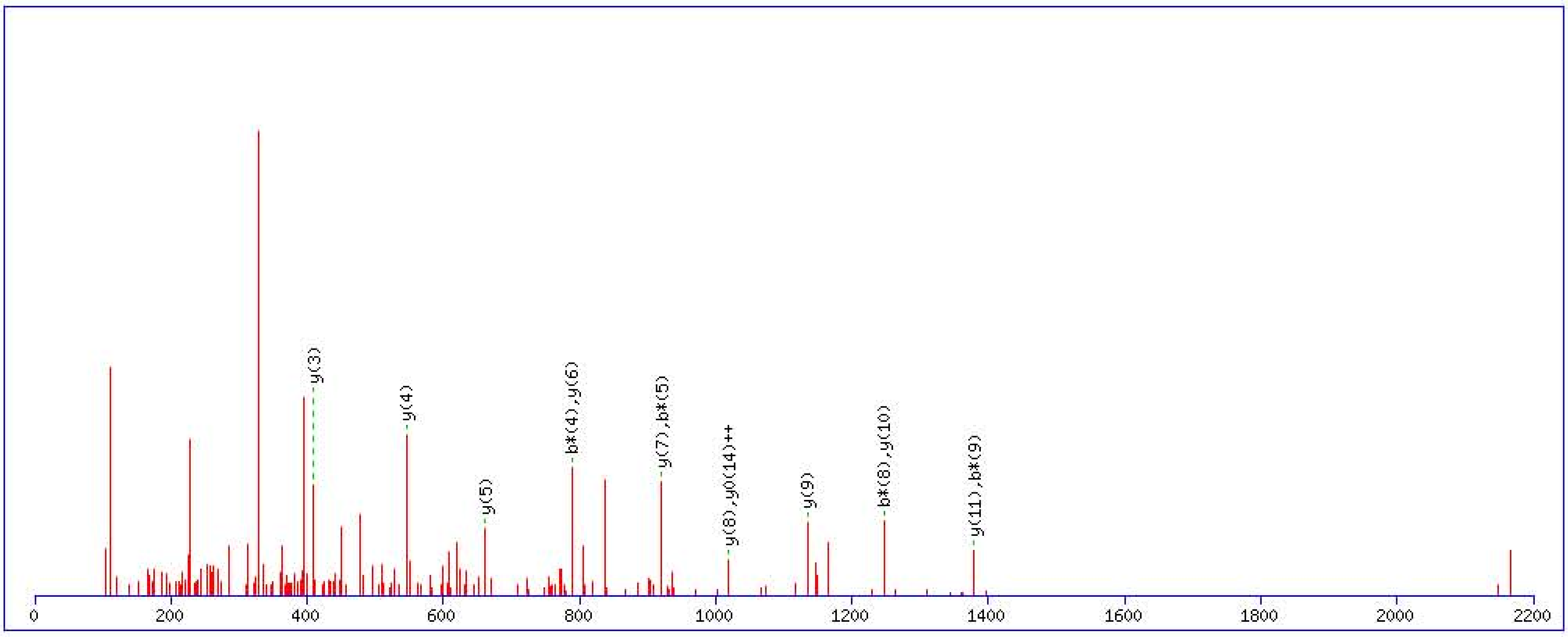
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QQTHMLDVMQDHFSR**
Found in **CLUS_HUMAN**, Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1

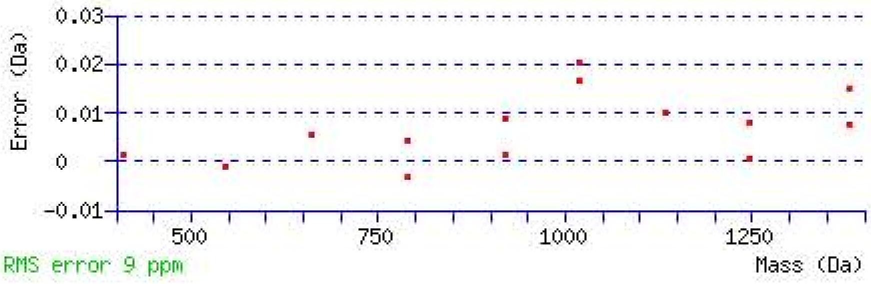
Match to Query 61224: 2183.004816 from(546.758480,4+) rtinseconds(1992) index(63056)
Title: Locus:1.1.1.2691.6 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

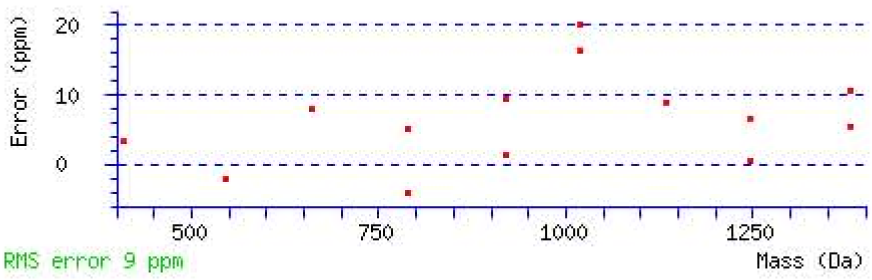
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2183.007446
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 66 **Expect:** 3.5e-006
Matches : 14/162 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	129.065854	65.036565	112.039305	56.523291			Q							15
2	568.291180	284.649228	551.264631	276.135954			Q	2055.956135	1028.481705	2038.929586	1019.968431	2037.945570	1019.476423	14
3	669.338859	335.173068	652.312310	326.659793	651.328294	326.167785	T	1616.730809	808.869043	1599.704260	800.355768	1598.720244	799.863760	13
4	806.397771	403.702524	789.371222	395.189249	788.387206	394.697241	H	1515.683130	758.345203	1498.656581	749.831929	1497.672565	749.339921	12
5	937.438256	469.222766	920.411707	460.709492	919.427691	460.217484	M	***1378.624218***	689.815747	1361.597669	681.302473	1360.613653	680.810465	11
6	1050.522320	525.764798	1033.495771	517.251524	1032.511755	516.759516	L	***1247.583733***	624.295505	1230.557184	615.782230	1229.573168	615.290222	10
7	1165.549263	583.278270	1148.522714	574.764995	1147.538698	574.272987	D	***1134.499669***	567.753473	1117.473120	559.240198	1116.489104	558.748190	9
8	1264.617677	632.812477	1247.591128	624.299202	1246.607112	623.807194	V	***1019.472726***	510.240001	1002.446177	501.726727	1001.462161	501.234719	8
9	1395.658162	698.332719	1378.631613	689.819445	1377.647597	689.327437	M	***920.404312***	460.705794	903.377763	452.192520	902.393747	451.700512	7
10	1523.716740	762.362008	1506.690191	753.848734	1505.706175	753.356726	Q	***789.363827***	395.185552	772.337278	386.672277	771.353262	386.180269	6
11	1638.743683	819.875480	1621.717134	811.362205	1620.733118	810.870197	D	***661.305249***	331.156263	644.278700	322.642988	643.294684	322.150980	5
12	1775.802595	888.404936	1758.776046	879.891661	1757.792030	879.399653	H	***546.278306***	273.642791	529.251757	265.129517	528.267741	264.637509	4
13	1922.871009	961.939143	1905.844460	953.425868	1904.860444	952.933860	F	***409.219394***	205.113335	392.192845	196.600061	391.208829	196.108053	3
14	2009.903037	1005.455157	1992.876488	996.941882	1991.892472	996.449874	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
15							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.5	2183.007446	-0.002630	QQTHMLDVMQDHFSR
65.5	2183.007446	-0.002630	QQTHMLDVMQDHFSR

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

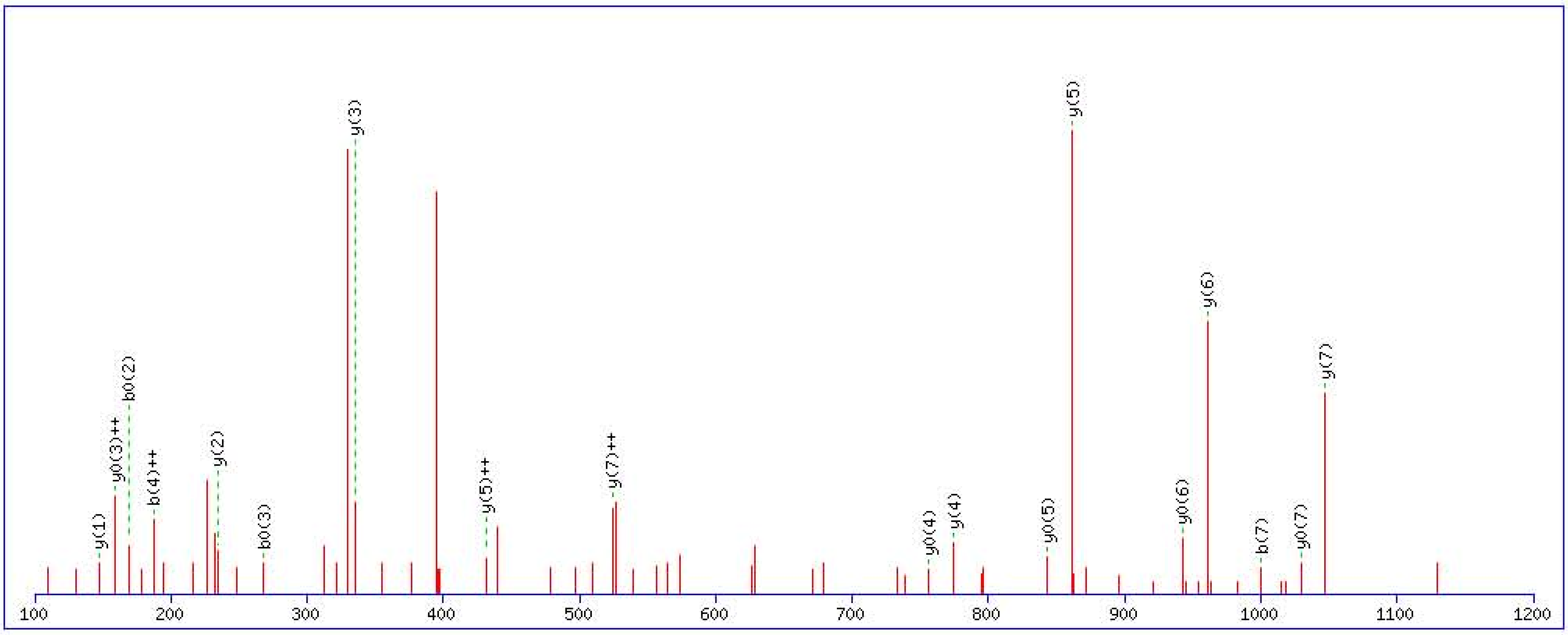
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSVSQTSK**
Found in **FA9_HUMAN**, Coagulation factor IX OS=Homo sapiens GN=F9 PE=1 SV=2

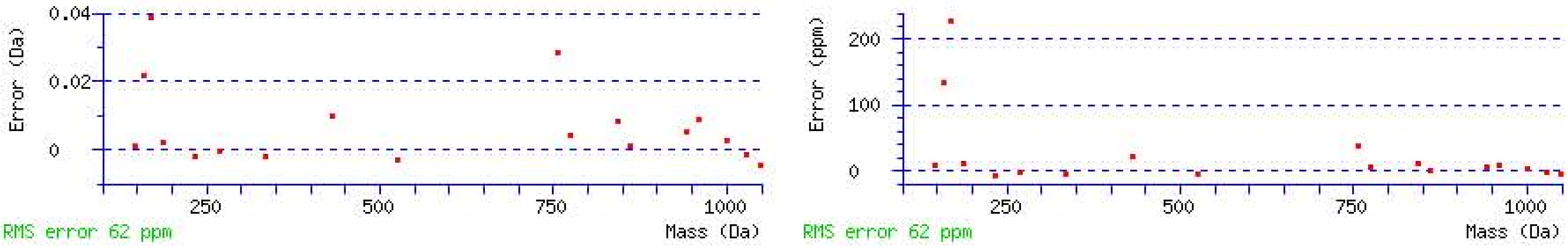
Match to Query 29415: 1145.607808 from(573.811180,2+) rtinseconds(1397) index(58756)
Title: Locus:1.1.1.2484.20 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

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



```
Monoisotopic mass of neutral peptide Mr(calc): 1145.611450
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.004
Matches : 19/72 fragment ions using 41 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							8
2	**187.107718**	94.057497			169.097153	85.052214	S	***1047.550307***	524.278792	1030.523758	515.765517	1029.539742	515.273509	7
3	286.176132	143.591704			268.165567	134.586422	V	***960.518279***	480.762778	943.491730	472.249503	942.507714	471.757495	6
4	373.208160	187.107718			355.197595	178.102435	S	***861.449865***	431.228571	844.423316	422.715296	843.439300	422.223288	5
5	812.433486	406.720381	795.406937	398.207107	794.422921	397.715099	Q	***774.417837***	387.712557	757.391288	379.199282	756.407272	378.707274	4
6	913.481165	457.244221	896.454616	448.730946	895.470600	448.238938	T	***335.192511***	168.099893	318.165962	159.586619	317.181946	159.094611	3
7	**1000.513193**	500.760235	983.486644	492.246960	982.502628	491.754952	S	***234.144832***	117.576054	217.118283	109.062779	216.134267	108.570771	2
8							K	***147.112804***	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.0	1145.611450	-0.003642	VSVSQTSK
10.9	1145.592819	0.014989	VSDGVTKSPEK
8.5	1145.611420	-0.003612	KSIMVQSPEK
2.8	1145.623337	-0.015529	WVDGGKPLFK
2.4	1145.622650	-0.014842	VDNAMSRLLK

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

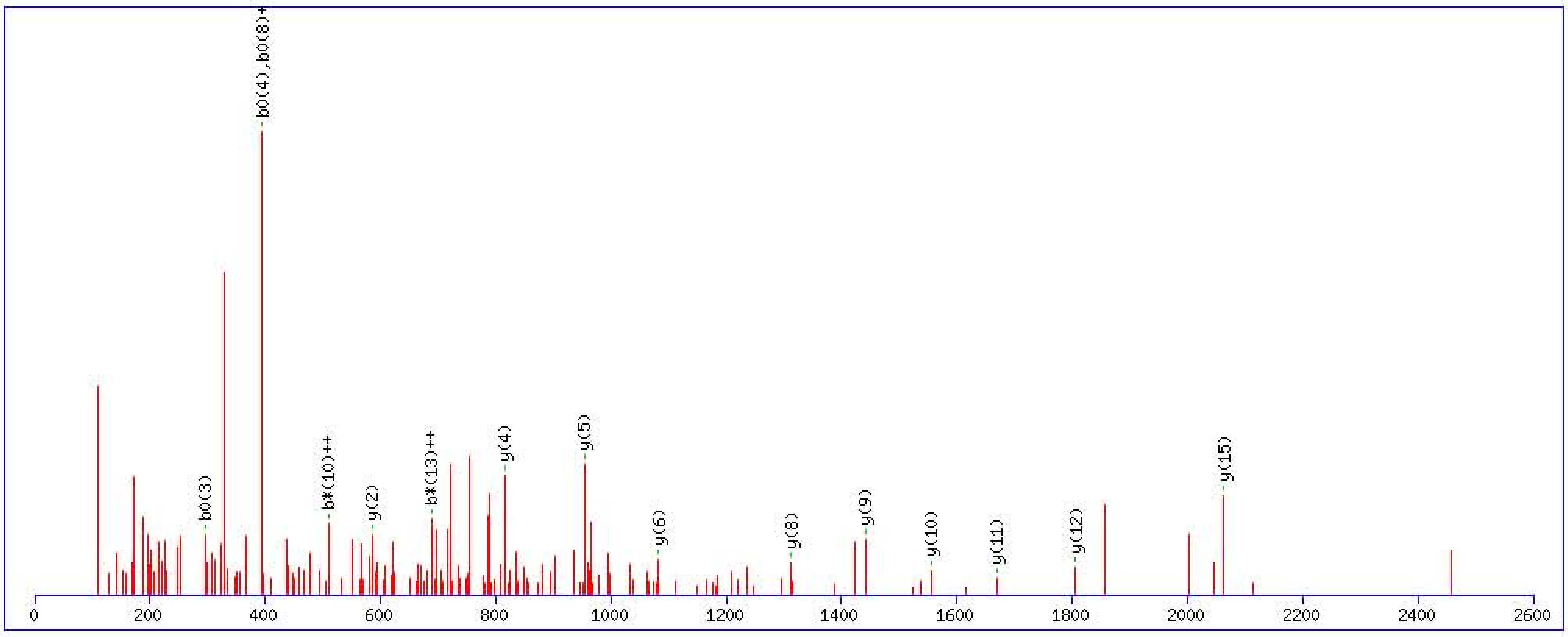
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ITVVAGEHNIEETEHTEQK**
Found in **FA9_HUMAN**, Coagulation factor IX OS=Homo sapiens GN=F9 PE=1 SV=2

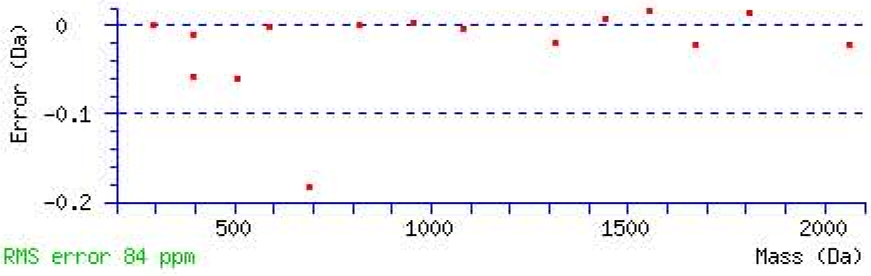
Match to Query 67654: 2474.203696 from(619.558200,4+) rtinseconds(1589) index(60208)
Title: Locus:1.1.1.2551.14 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

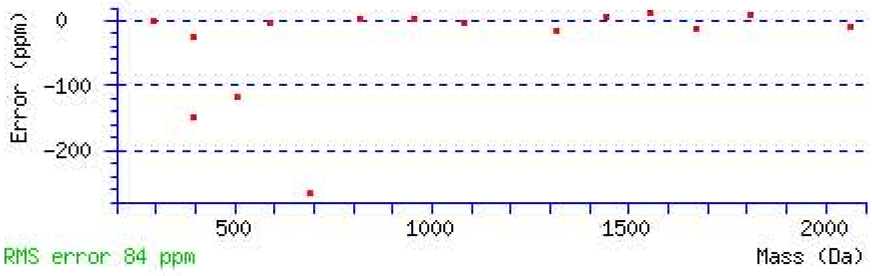
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2474.211121
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18     : Biotin:Thermo-21345 (Q)
Ions Score: 55  Expect: 8.4e-005
Matches : 15/194 fragment ions using 22 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							19
2	215.139019	108.073147			197.128454	99.067865	T	2362.134353	1181.570814	2345.107804	1173.057540	2344.123788	1172.565532	18
3	314.207433	157.607354			296.196868	148.602072	V	2261.086674	1131.046975	2244.060125	1122.533700	2243.076109	1122.041692	17
4	413.275847	207.141561			395.265282	198.136279	V	2162.018260	1081.512768	2144.991711	1072.999493	2144.007695	1072.507485	16
5	484.312961	242.660119			466.302396	233.654836	A	***2062.949846***	1031.978561	2045.923297	1023.465286	2044.939281	1022.973278	15
6	541.334425	271.170851			523.323860	262.165568	G	1991.912732	996.460004	1974.886183	987.946730	1973.902167	987.454722	14
7	670.377018	335.692147			652.366453	326.686865	E	1934.891268	967.949272	1917.864719	959.435998	1916.880703	958.943990	13
8	807.435930	404.221603			789.425365	395.216321	H	***1805.848675***	903.427976	1788.822126	894.914701	1787.838110	894.422693	12
9	921.478857	461.243067	904.452308	452.729792	903.468292	452.237784	N	***1668.789763***	834.898520	1651.763214	826.385245	1650.779198	825.893237	11
10	1034.562921	517.785099	1017.536372	509.271824	1016.552356	508.779816	I	***1554.746836***	777.877056	1537.720287	769.363782	1536.736271	768.871774	10
11	1163.605514	582.306395	1146.578965	573.793121	1145.594949	573.301113	E	***1441.662772***	721.335024	1424.636223	712.821750	1423.652207	712.329742	9
12	1292.648107	646.827692	1275.621558	638.314417	1274.637542	637.822409	E	***1312.620179***	656.813728	1295.593630	648.300453	1294.609614	647.808445	8
13	1393.695786	697.351531	1376.669237	688.838257	1375.685221	688.346249	T	1183.577586	592.292431	1166.551037	583.779157	1165.567021	583.287149	7
14	1522.738379	761.872828	1505.711830	753.359553	1504.727814	752.867545	E	***1082.529907***	541.768592	1065.503358	533.255317	1064.519342	532.763309	6
15	1659.797291	830.402284	1642.770742	821.889009	1641.786726	821.397001	H	***953.487314***	477.247295	936.460765	468.734021	935.476749	468.242013	5
16	1760.844970	880.926123	1743.818421	872.412849	1742.834405	871.920841	T	***816.428402***	408.717839	799.401853	400.204565	798.417837	399.712557	4
17	1889.887563	945.447420	1872.861014	936.934145	1871.876998	936.442137	E	715.380723	358.194000	698.354174	349.680725	697.370158	349.188717	3
18	2329.112889	1165.060082	2312.086340	1156.546808	2311.102324	1156.054800	Q	***586.338130***	293.672703	569.311581	285.159429			2
19							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.6	2474.211121	-0.007425	ITVVAGEHNIEETEHTEQK

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

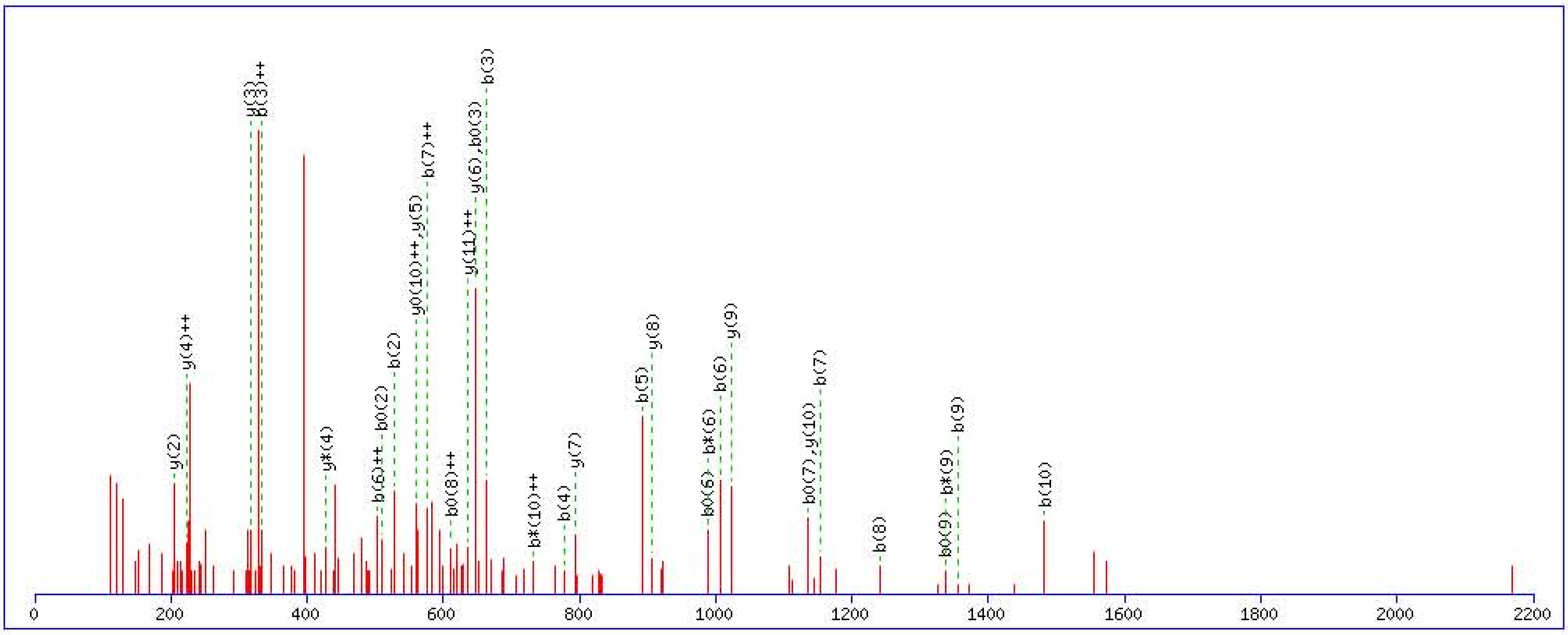
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SQHLDNFSNQIGK**
Found in **FA5_HUMAN**, Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4

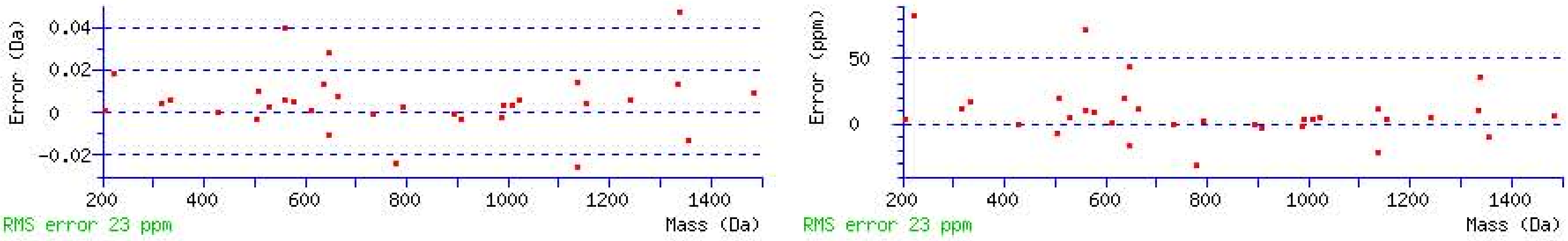
Match to Query 52060: 1797.880722 from(600.300850,3+) rtinseconds(1737) index(61277)
Title: Locus:1.1.1.2603.8 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1797.883194
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 40  Expect: 0.0019
Matches : 33/132 fragment ions using 62 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							13
2	***527.264630***	264.135953	510.238081	255.622679	509.254065	255.130671	Q	1711.858451	856.432863	1694.831902	847.919589	1693.847886	847.427581	12
3	***664.323542***	**332.665409**	647.296993	324.152134	646.312977	323.660126	H	1272.633125	636.820200	1255.606576	628.306926	1254.622560	627.814918	11
4	***777.407606***	389.207441	760.381057	380.694166	759.397041	380.202159	L	**1135.574213**	568.290744	1118.547664	559.777470	1117.563648	559.285462	10
5	***892.434549***	446.720913	875.408000	438.207638	874.423984	437.715630	D	**1022.490149**	511.748712	1005.463600	503.235438	1004.479584	502.743430	9
6	***1006.477476***	**503.742376**	989.450927	495.229101	988.466911	494.737093	N	**907.463206**	454.235241	890.436657	445.721966	889.452641	445.229958	8
7	***1153.545890***	**577.276583**	1136.519341	568.763308	1135.535325	568.271300	F	**793.420279**	397.213777	776.393730	388.700503	775.409714	388.208495	7
8	***1240.577918***	620.792597	1223.551369	612.279323	1222.567353	611.787314	S	**646.351865**	323.679570	629.325316	315.166296	628.341300	314.674288	6
9	***1354.620845***	677.814060	1337.594296	669.300786	1336.610280	668.808778	N	**559.319837**	280.163556	542.293288	271.650282			5
10	***1482.679423***	741.843349	1465.652874	733.330075	1464.668858	732.838067	Q	445.276910	223.142093	428.250361	214.628818			4
11	1595.763487	798.385381	1578.736938	789.872107	1577.752922	789.380099	I	**317.218332**	159.112804	300.191783	150.599529			3
12	1652.784951	826.896113	1635.758402	818.382839	1634.774386	817.890831	G	**204.134268**	102.570772	187.107719	94.057497			2
13							K	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.4	1797.883194	-0.002472	SQHLDNFSNQIGK

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

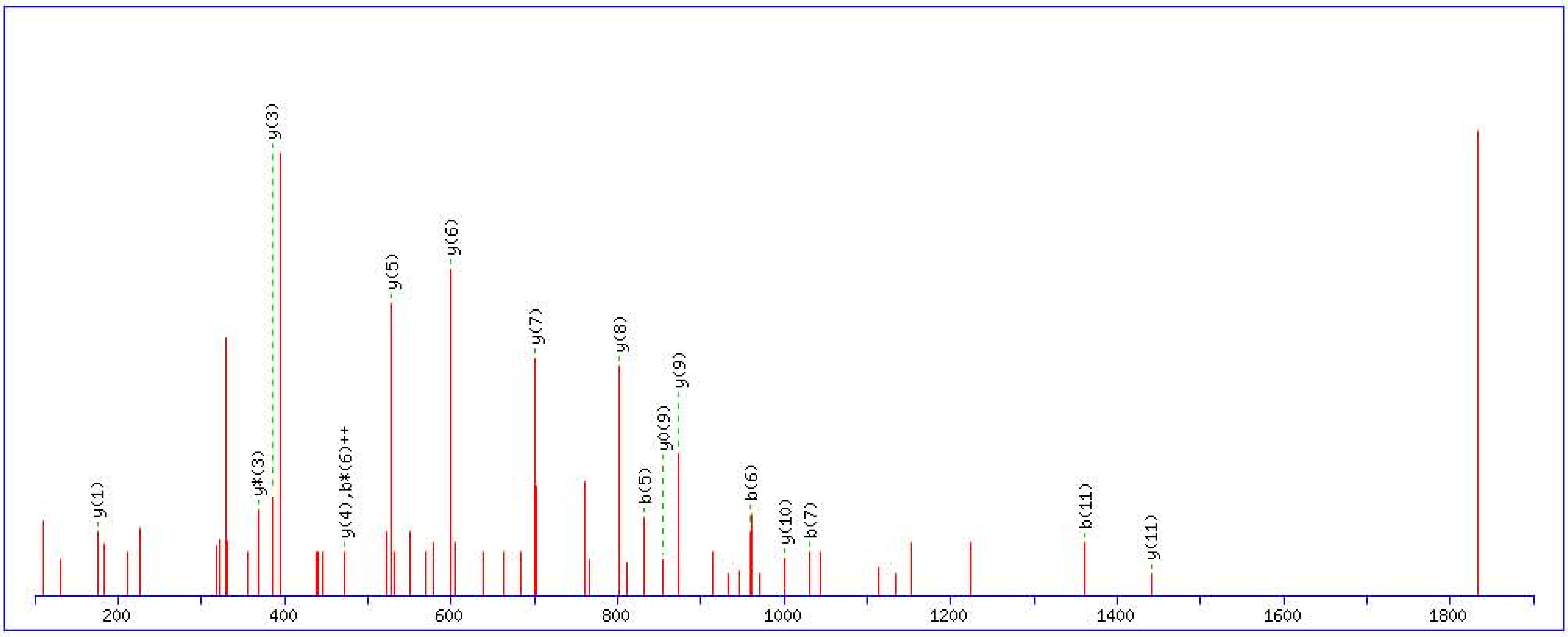
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **APSHQQATTAGSPLR**
Found in **FA5_HUMAN**, Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4

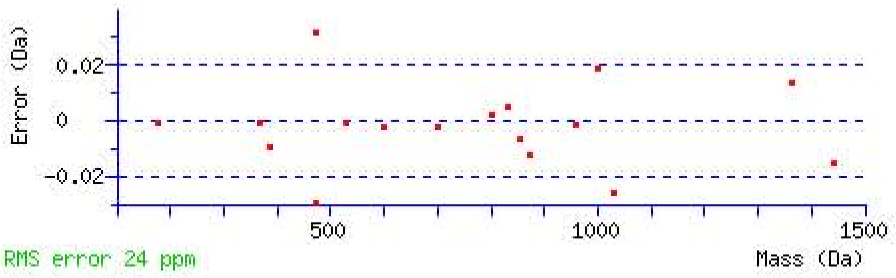
Match to Query 52837: 1831.932342 from(611.651390,3+) rtinseconds(1383) index(58635)
Title: Locus:1.1.1.2479.24 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

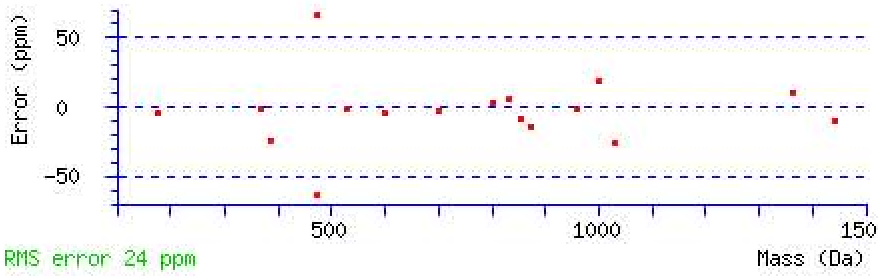
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1831.936295
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 45 **Expect:** 0.00093
Matches : 17/150 fragment ions using 44 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							15
2	169.097154	85.052215					P	1761.906466	881.456871	1744.879917	872.943597	1743.895901	872.451588	14
3	256.129182	128.568229			238.118617	119.562947	S	1664.853702	832.930489	1647.827153	824.417215	1646.843137	823.925206	13
4	393.188094	197.097685			375.177529	188.092402	H	1577.821674	789.414475	1560.795125	780.901200	1559.811109	780.409192	12
5	**832.413420**	416.710348	815.386871	408.197073	814.402855	407.705065	Q	***1440.762762***	720.885019	1423.736213	712.371744	1422.752197	711.879736	11
6	**960.471998**	480.739637	943.445449	472.226362	942.461433	471.734354	Q	***1001.537436***	501.272356	984.510887	492.759081	983.526871	492.267073	10
7	**1031.509112**	516.258194	1014.482563	507.744919	1013.498547	507.252911	A	***873.478858***	437.243067	856.452309	428.729792	855.468293	428.237784	9
8	1132.556791	566.782034	1115.530242	558.268759	1114.546226	557.776751	T	***802.441744***	401.724510	785.415195	393.211235	784.431179	392.719227	8
9	1233.604470	617.305873	1216.577921	608.792599	1215.593905	608.300591	T	***701.394065***	351.200671	684.367516	342.687396	683.383500	342.195388	7
10	1304.641584	652.824430	1287.615035	644.311156	1286.631019	643.819147	A	***600.346386***	300.676831	583.319837	292.163556	582.335821	291.671548	6
11	**1361.663048**	681.335162	1344.636499	672.821888	1343.652483	672.329879	G	***529.309272***	265.158274	512.282723	256.644999	511.298707	256.152991	5
12	1448.695076	724.851176	1431.668527	716.337902	1430.684511	715.845893	S	***472.287808***	236.647542	455.261259	228.134267	454.277243	227.642259	4
13	1545.747840	773.377558	1528.721291	764.864284	1527.737275	764.372276	P	***385.255780***	193.131528	368.229231	184.618253			3
14	1658.831904	829.919590	1641.805355	821.406316	1640.821339	820.914307	L	288.203016	144.605146	271.176467	136.091871			2
15							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
44.7	1831.936295	-0.003953	APSHQQATTAGSPLR
39.8	1831.936295	-0.003953	APSHQQATTAGSPLR

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

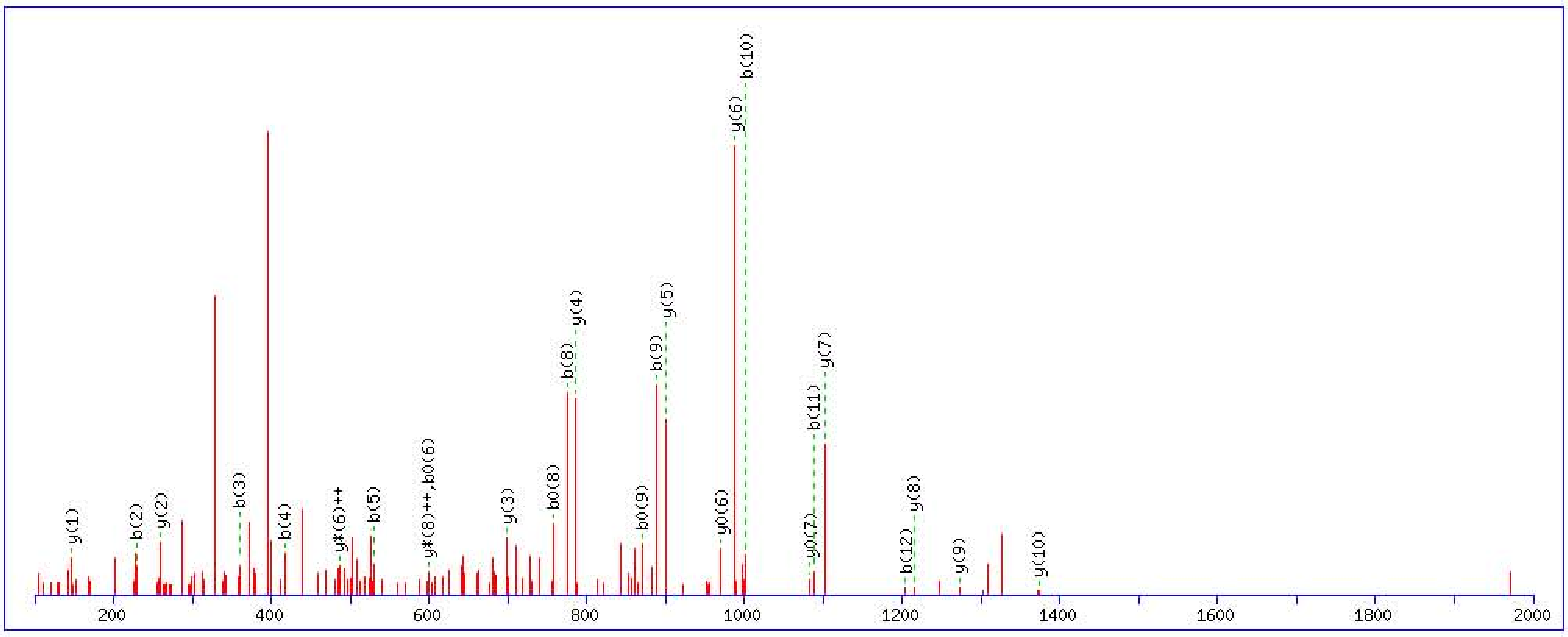
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MPMGLSTGIISDSQIK**
Found in **FA5_HUMAN**, Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4

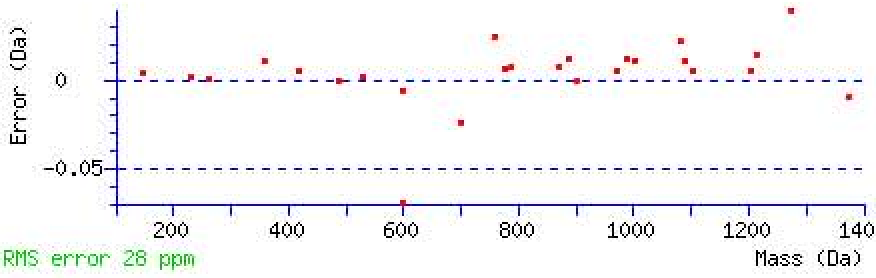
Match to Query 56324: 1988.022192 from(663.681340,3+) rtinseconds(2443) index(65899)
Title: Locus:1.1.1.2848.6 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

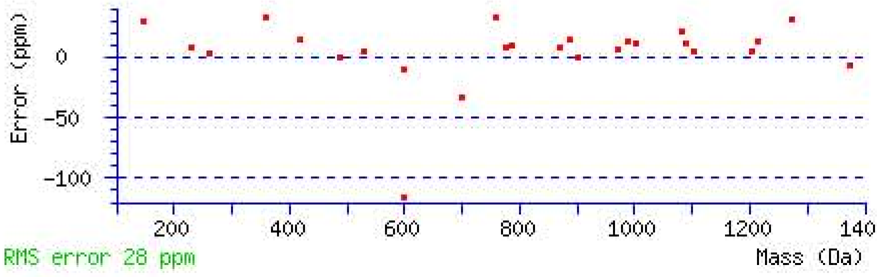
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1988.014465
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 56  Expect: 1.5e-005
Matches : 26/138 fragment ions using 60 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	132.047761	66.527518					M							16
2	***229.100525***	115.053900					P	1857.981269	929.494273	1840.954720	920.980998	1839.970704	920.488990	15
3	***360.141010***	180.574143					M	1760.928505	880.967891	1743.901956	872.454616	1742.917940	871.962608	14
4	***417.162474***	209.084875					G	1629.888020	815.447648	1612.861471	806.934374	1611.877455	806.442366	13
5	***530.246538***	265.626907					L	1572.866556	786.936916	1555.840007	778.423642	1554.855991	777.931634	12
6	617.278566	309.142921			599.268001	300.137638	S	1459.782492	730.394884	1442.755943	721.881610	1441.771927	721.389602	11
7	718.326245	359.666761			700.315680	350.661478	T	***1372.750464***	686.878870	1355.723915	678.365596	1354.739899	677.873588	10
8	***775.347709***	388.177493			757.337144	379.172210	G	***1271.702785***	636.355031	1254.676236	627.841756	1253.692220	627.349748	9
9	***888.431773***	444.719525			870.421208	435.714242	I	***1214.681321***	607.844299	1197.654772	599.331024	1196.670756	598.839016	8
10	***1001.515837***	501.261557			983.505272	492.256274	I	***1101.597257***	551.302267	1084.570708	542.788992	1083.586692	542.296984	7
11	***1088.547865***	544.777571			1070.537300	535.772288	S	***988.513193***	494.760235	971.486644	486.246960	970.502628	485.754952	6
12	***1203.574808***	602.291042			1185.564243	593.285760	D	***901.481165***	451.244221	884.454616	442.730946	883.470600	442.238938	5
13	1290.606836	645.807056			1272.596271	636.801774	S	***786.454222***	393.730749	769.427673	385.217475	768.443657	384.725467	4
14	1729.832162	865.419719	1712.805613	856.906445	1711.821597	856.414437	Q	***699.422194***	350.214735	682.395645	341.701461			3
15	1842.916226	921.961751	1825.889677	913.448477	1824.905661	912.956469	I	***260.196868***	130.602072	243.170319	122.088797			2
16							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.0	1988.014465	0.007727	MPMGLSTGIISDSQIK
4.2	1988.051315	-0.029123	IVHQSLNIMNSFSQKVK
1.4	1988.051331	-0.029139	MTHKLVFLEDGTSQVRK
0.3	1987.998535	0.023657	VCAQCRVFLRGTHAWK

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

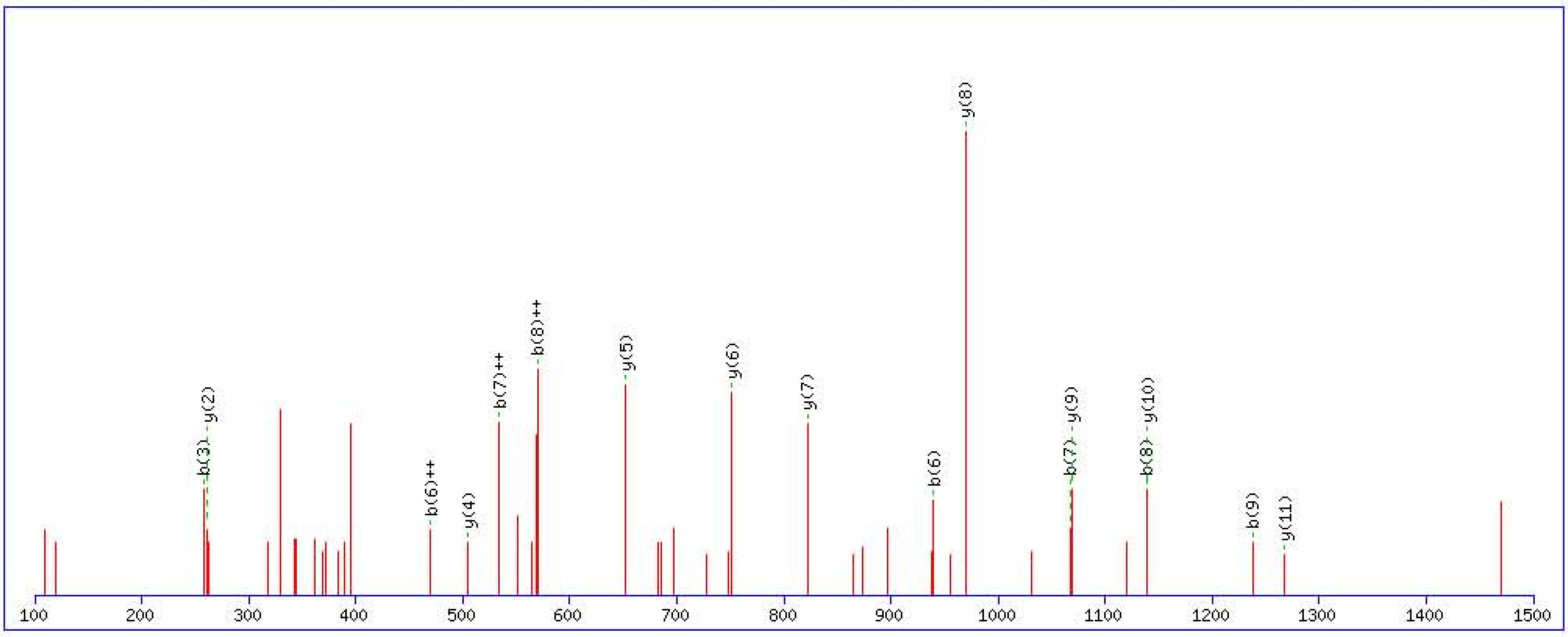
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AADIEQQAVFAVFDENK**
Found in **FA5_HUMAN**, Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4

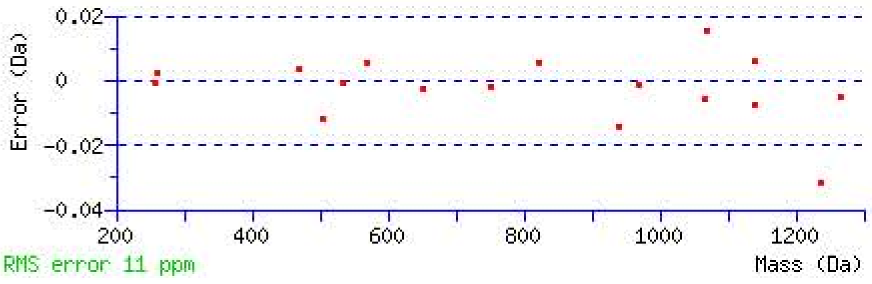
Match to Query 61688: 2205.087642 from(736.036490,3+) rtinseconds(2725) index(67669)
Title: Locus:1.1.1.2945.17 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

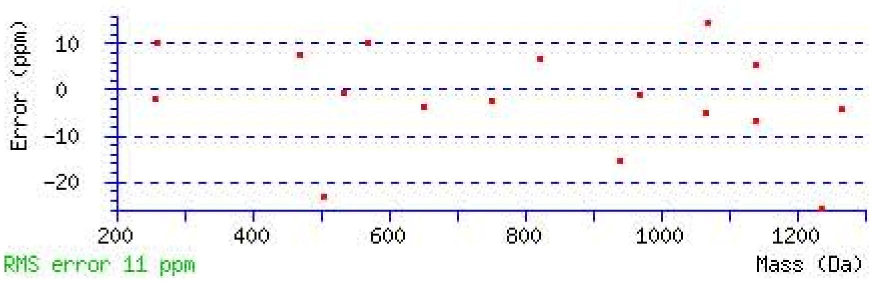
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2205.077591
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 61  Expect: 4e-006
Matches : 17/174 fragment ions using 25 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							17
2	143.081504	72.044390					A	2135.047769	1068.027522	2118.021220	1059.514248	2117.037204	1059.022240	16
3	**258.108447**	129.557862			240.097882	120.552579	D	2064.010655	1032.508965	2046.984106	1023.995691	2046.000090	1023.503683	15
4	371.192511	186.099894			353.181946	177.094611	I	1948.983712	974.995494	1931.957163	966.482220	1930.973147	965.990212	14
5	500.235104	250.621190			482.224539	241.615908	E	1835.899648	918.453462	1818.873099	909.940188	1817.889083	909.448180	13
6	**939.460430**	**470.233853**	922.433881	461.720579	921.449865	461.228571	Q	1706.857055	853.932166	1689.830506	845.418891	1688.846490	844.926883	12
7	**1067.519008**	**534.263142**	1050.492459	525.749868	1049.508443	525.257860	Q	***1267.631729***	634.319503	1250.605180	625.806228	1249.621164	625.314220	11
8	**1138.556122**	**569.781699**	1121.529573	561.268425	1120.545557	560.776416	A	***1139.573151***	570.290214	1122.546602	561.776939	1121.562586	561.284931	10
9	**1237.624536**	619.315906	1220.597987	610.802632	1219.613971	610.310624	V	***1068.536037***	534.771657	1051.509488	526.258382	1050.525472	525.766374	9
10	1384.692950	692.850113	1367.666401	684.336839	1366.682385	683.844831	F	***969.467623***	485.237450	952.441074	476.724175	951.457058	476.232167	8
11	1455.730064	728.368670	1438.703515	719.855396	1437.719499	719.363388	A	***822.399209***	411.703243	805.372660	403.189968	804.388644	402.697960	7
12	1554.798478	777.902877	1537.771929	769.389603	1536.787913	768.897595	V	***751.362095***	376.184686	734.335546	367.671411	733.351530	367.179403	6
13	1701.866892	851.437084	1684.840343	842.923810	1683.856327	842.431802	F	***652.293681***	326.650479	635.267132	318.137204	634.283116	317.645196	5
14	1816.893835	908.950556	1799.867286	900.437281	1798.883270	899.945273	D	***505.225267***	253.116271	488.198718	244.602997	487.214702	244.110989	4
15	1945.936428	973.471852	1928.909879	964.958578	1927.925863	964.466570	E	390.198324	195.602800	373.171775	187.089525	372.187759	186.597517	3
16	2059.979355	1030.493315	2042.952806	1021.980041	2041.968790	1021.488033	N	***261.155731***	131.081503	244.129182	122.568229			2
17							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.4	2205.077591	0.010051	AADIEQQAVFAVFDENK
44.6	2205.077591	0.010051	AADIEQQAVFAVFDENK
3.8	2205.063492	0.024150	GERGEPGIRGEDGRPGQEGPR
3.1	2205.080063	0.007579	EKENDELDIQLKVFDENK

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

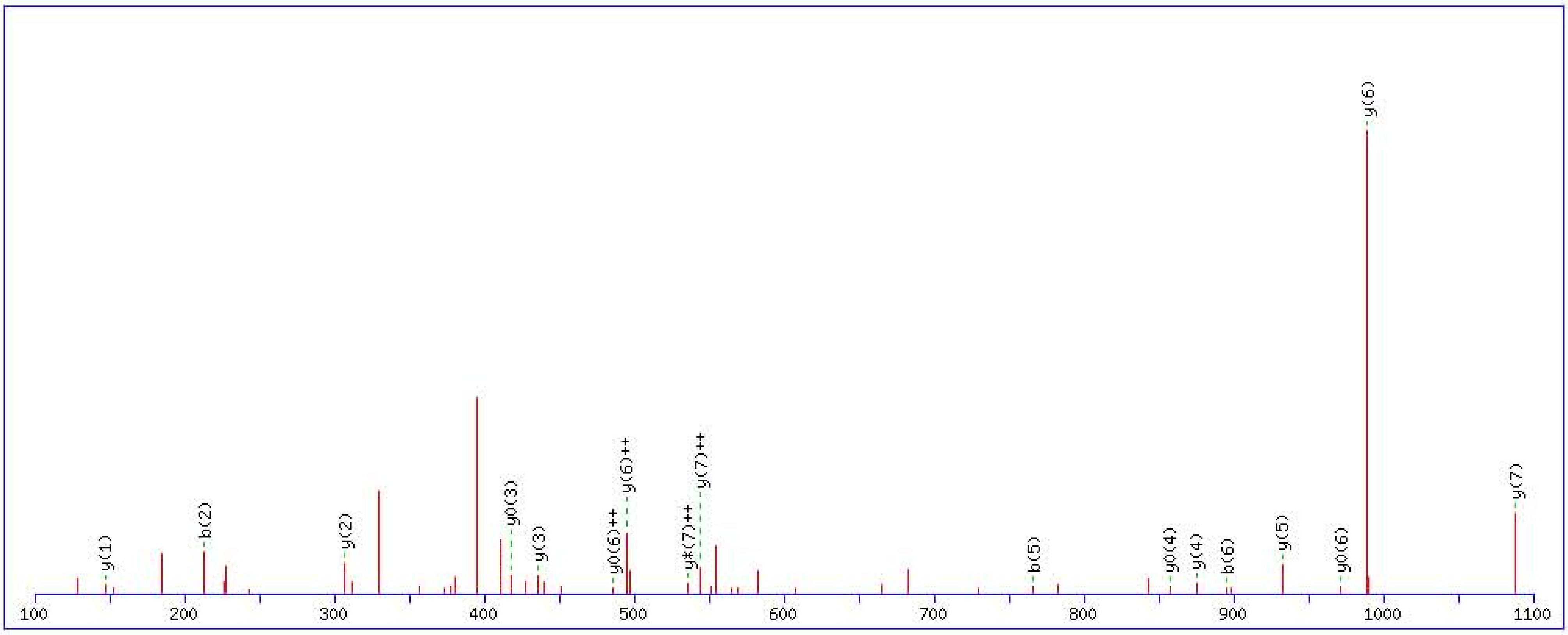
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IVGGQECK**
Found in **FA10_HUMAN**, Coagulation factor X OS=Homo sapiens GN=F10 PE=1 SV=2

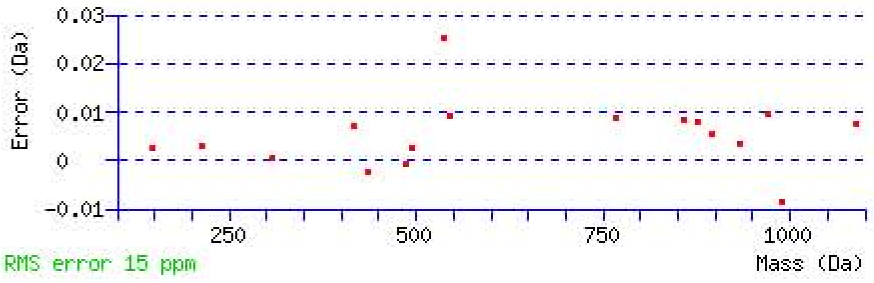
Match to Query 31703: 1200.596328 from(601.305440,2+) rtinseconds(1397) index(58759)
Title: Locus:1.1.1.2484.23 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

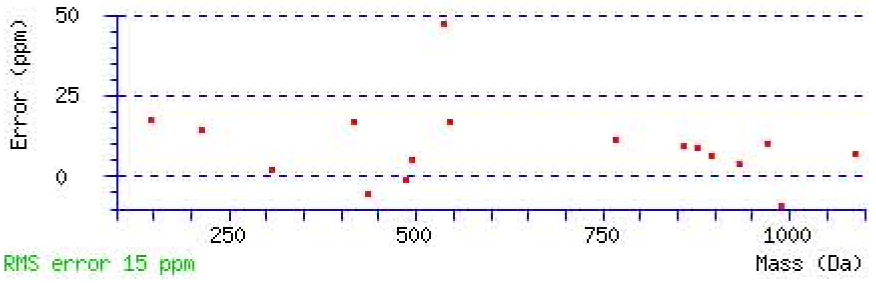
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1200.599503
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.0012
Matches : 17/62 fragment ions using 42 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					I							8
2	**213.159754**	107.083515					V	***1088.522714***	544.764995	1071.496165	536.251721	1070.512149	535.759713	7
3	270.181218	135.594247					G	***989.454300***	495.230788	972.427751	486.717514	971.443735	486.225506	6
4	327.202682	164.104979					G	***932.432836***	466.720056	915.406287	458.206782	914.422271	457.714774	5
5	**766.428008**	383.717642	749.401459	375.204368			Q	***875.411372***	438.209324	858.384823	429.696050	857.400807	429.204042	4
6	**895.470601**	448.238939	878.444052	439.725664	877.460036	439.233656	E	***436.186046***	218.596661	419.159497	210.083386	418.175481	209.591378	3
7	1055.501250	528.254263	1038.474701	519.740989	1037.490685	519.248981	C	***307.143453***	154.075364	290.116904	145.562090			2
8							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.5	1200.599503	-0.003175	IVGGQECK
3.2	1200.596100	0.000228	LVKYMYDNR
1.4	1200.599503	-0.003175	LIQGDGCK

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

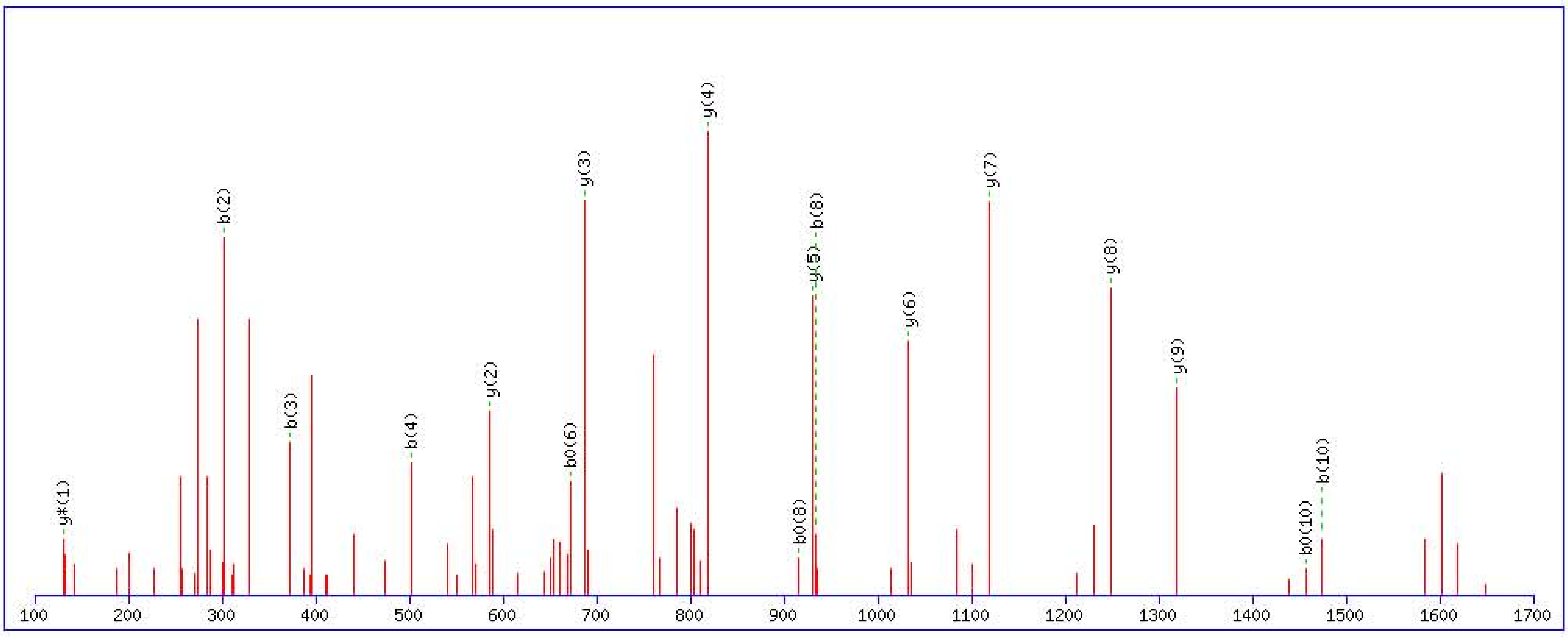
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DWAESTLMTQK**
Found in **FA10_HUMAN**, Coagulation factor X OS=Homo sapiens GN=F10 PE=1 SV=2

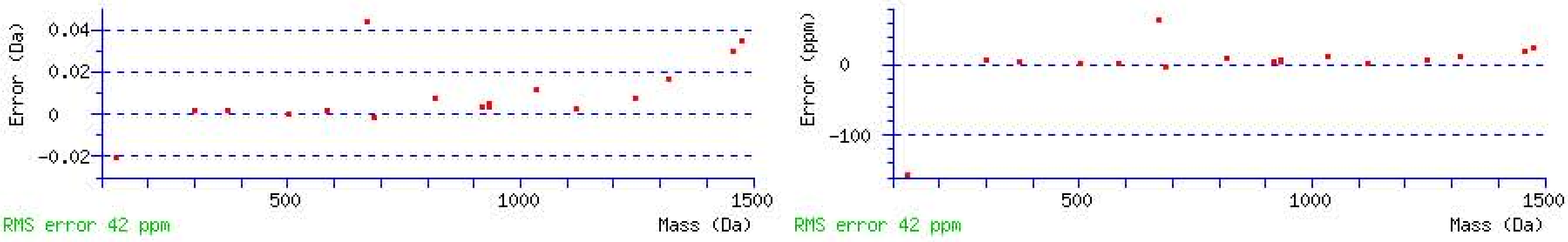
Match to Query 46800: 1619.778288 from(810.896420,2+) rtinseconds(2263) index(64820)
Title: Locus:1.1.1.2785.15 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1619.768738
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 60  Expect: 2.1e-005
Matches : 17/98 fragment ions using 26 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							11
2	**302.113532**	151.560404			284.102967	142.555122	W	1505.749085	753.378180	1488.722536	744.864906	1487.738520	744.372898	10
3	**373.150646**	187.078961			355.140081	178.073679	A	***1319.669772***	660.338524	1302.643223	651.825250	1301.659207	651.333241	9
4	**502.193239**	251.600258			484.182674	242.594975	E	***1248.632658***	624.819967	1231.606109	616.306693	1230.622093	615.814685	8
5	589.225267	295.116272			571.214702	286.110989	S	***1119.590065***	560.298671	1102.563516	551.785396	1101.579500	551.293388	7
6	690.272946	345.640111			672.262381	336.634829	T	***1032.558037***	516.782657	1015.531488	508.269382	1014.547472	507.777374	6
7	803.357010	402.182143			785.346445	393.176861	L	***931.510358***	466.258817	914.483809	457.745543	913.499793	457.253535	5
8	**934.397495**	467.702386			916.386930	458.697103	M	***818.426294***	409.716785	801.399745	401.203510	800.415729	400.711502	4
9	1035.445174	518.226225			1017.434609	509.220942	T	***687.385809***	344.196543	670.359260	335.683268	669.375244	335.191260	3
10	**1474.670500**	737.838888	1457.643951	729.325614	1456.659935	728.833605	Q	***586.338130***	293.672703	569.311581	285.159429			2
11							K	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.8	1619.768738	0.009550	DWAESTLMTQK
10.8	1619.783340	-0.005052	MLGNEICLCIVGNK
5.7	1619.793686	-0.015398	MEQPTSSINGEKRK
5.0	1619.793716	-0.015428	LVCAVGSRNGTEETK
3.9	1619.775909	0.002379	EEQCREMERLIK
3.3	1619.768738	0.009550	AFAPDSIQDSMK
3.3	1619.782440	-0.004152	GDAEEMAQKKQEIK
0.6	1619.790329	-0.012041	EAGEQGPHGSLGPKEK
0.2	1619.782455	-0.004167	NTEVNLMLNDGKEK

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

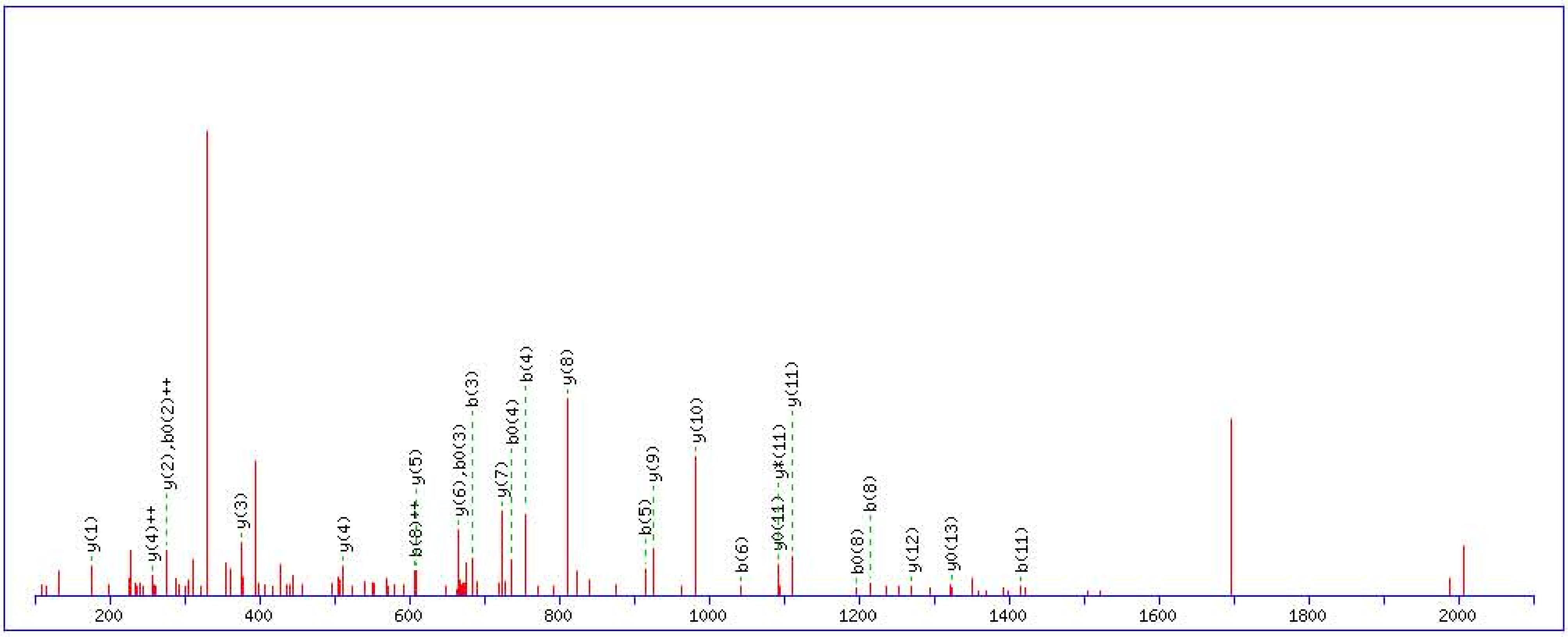
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QEDACQGDSGGPHVTR**
Found in **FA10_HUMAN**, Coagulation factor X OS=Homo sapiens GN=F10 PE=1 SV=2

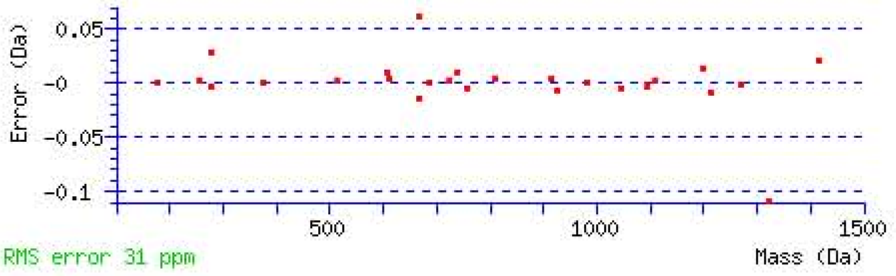
Match to Query 57890: 2023.881792 from(675.634540,3+) rtinseconds(1279) index(57912)
Title: Locus:1.1.1.2443.23 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

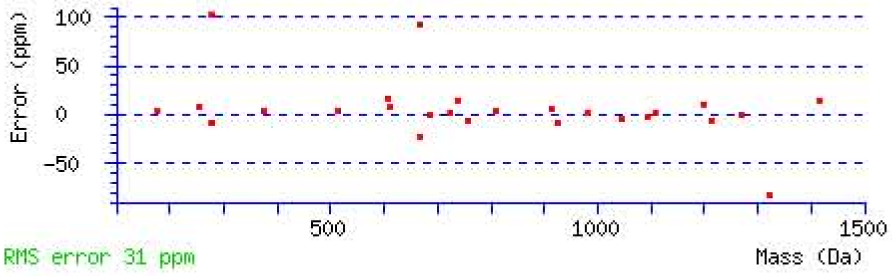
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2023.884033
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 75 **Expect:** 1.5e-007
Matches : 27/176 fragment ions using 45 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	440.232602	220.619939	423.206053	212.106664			Q							16
2	569.275195	285.141236	552.248646	276.627961	551.264630	276.135953	E	1585.665961	793.336618	1568.639412	784.823344	1567.655396	784.331336	15
3	**684.302138**	342.654707	667.275589	334.141433	666.291573	333.649425	D	1456.623368	728.815322	1439.596819	720.302047	1438.612803	719.810039	14
4	**755.339252**	378.173264	738.312703	369.659989	737.328687	369.167982	A	1341.596425	671.301851	1324.569876	662.788576	1323.585860	662.296568	13
5	**915.369901**	458.188589	898.343352	449.675314	897.359336	449.183306	C	***1270.559311***	635.783294	1253.532762	627.270019	1252.548746	626.778011	12
6	**1043.428479**	522.217877	1026.401930	513.704603	1025.417914	513.212595	Q	***1110.528662***	555.767969	1093.502113	547.254695	1092.518097	546.762686	11
7	1100.449943	550.728609	1083.423394	542.215335	1082.439378	541.723327	G	***982.470084***	491.738680	965.443535	483.225406	964.459519	482.733398	10
8	**1215.476886**	608.242081	1198.450337	599.728807	1197.466321	599.236798	D	***925.448620***	463.227948	908.422071	454.714674	907.438055	454.222666	9
9	1302.508914	651.758095	1285.482365	643.244821	1284.498349	642.752813	S	***810.421677***	405.714477	793.395128	397.201202	792.411112	396.709194	8
10	1359.530378	680.268827	1342.503829	671.755553	1341.519813	671.263544	G	***723.389649***	362.198463	706.363100	353.685188	705.379084	353.193180	7
11	**1416.551842**	708.779559	1399.525293	700.266284	1398.541277	699.774276	G	***666.368185***	333.687731	649.341636	325.174456	648.357620	324.682448	6
12	1513.604606	757.305941	1496.578057	748.792667	1495.594041	748.300658	P	***609.346721***	305.176999	592.320172	296.663724	591.336156	296.171716	5
13	1650.663518	825.835397	1633.636969	817.322122	1632.652953	816.830114	H	***512.293957***	256.650617	495.267408	248.137342	494.283392	247.645334	4
14	1749.731932	875.369604	1732.705383	866.856330	1731.721367	866.364321	V	***375.235045***	188.121161	358.208496	179.607886	357.224480	179.115878	3
15	1850.779611	925.893443	1833.753062	917.380169	1832.769046	916.888161	T	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.581671	2
16							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
75.2	2023.884033	-0.002241	QEDACQGDSGGPHVTR
53.6	2023.884033	-0.002241	QEDACQGDSGGPHVTR

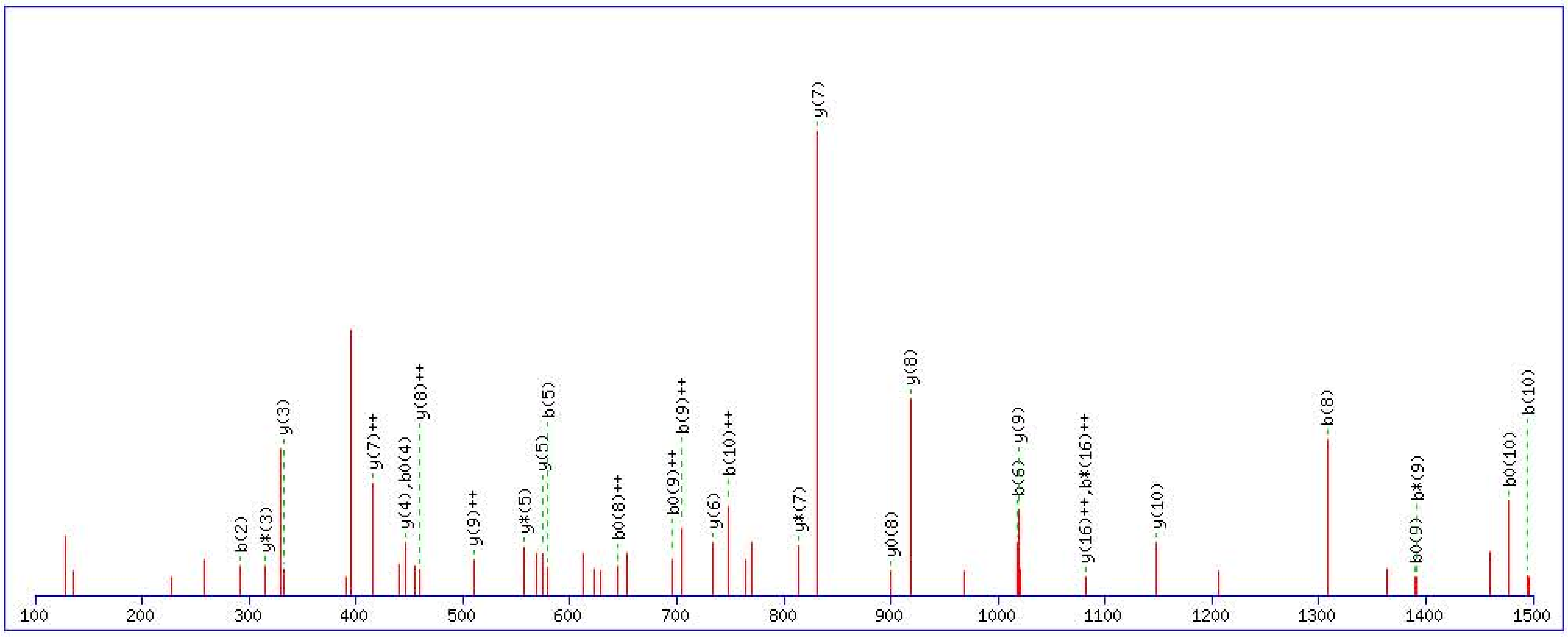
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YKDGDQCETSPCQNQGK**
Found in **FA10_HUMAN**, Coagulation factor X OS=Homo sapiens GN=F10 PE=1 SV=2

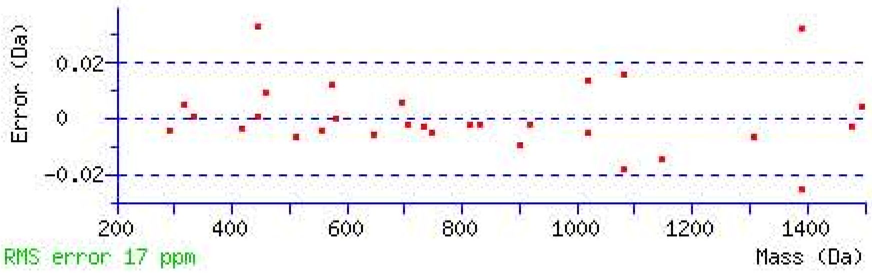
Match to Query 64665: 2324.981082 from(776.000970,3+) rtinseconds(1248) index(57718)
Title: Locus:1.1.1.2432.17 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

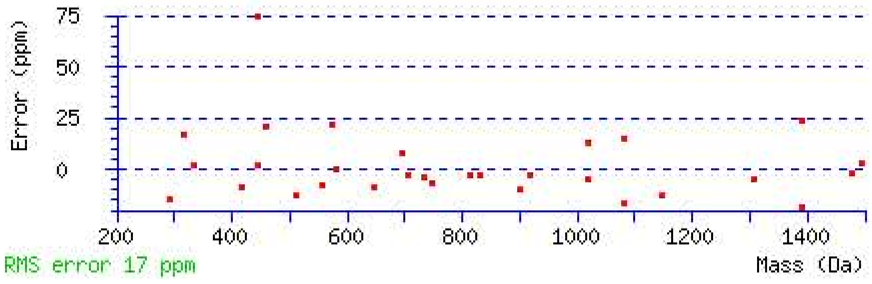
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2324.982407
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 41 **Expect:** 0.00021
Matches : 30/172 fragment ions using 49 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940					Y							17
2	***292.165568***	146.586422	275.139019	138.073148			K	2162.926352	1081.966814	2145.899803	1073.453539	2144.915787	1072.961531	16
3	407.192511	204.099894	390.165962	195.586619	389.181946	195.094611	D	2034.831389	1017.919333	2017.804840	1009.406058	2016.820824	1008.914050	15
4	464.213975	232.610626	447.187426	224.097351	446.203410	223.605343	G	1919.804446	960.405861	1902.777897	951.892587	1901.793881	951.400579	14
5	***579.240918***	290.124097	562.214369	281.610823	561.230353	281.118815	D	1862.782982	931.895129	1845.756433	923.381855	1844.772417	922.889847	13
6	***1018.466244***	509.736760	1001.439695	501.223486	1000.455679	500.731478	Q	1747.756039	874.381658	1730.729490	865.868383	1729.745474	865.376375	12
7	1178.496893	589.752085	1161.470344	581.238810	1160.486328	580.746802	C	1308.530713	654.768995	1291.504164	646.255720	1290.520148	645.763712	11
8	***1307.539486***	654.273381	1290.512937	645.760107	1289.528921	645.268098	E	***1148.500064***	574.753670	1131.473515	566.240396	1130.489499	565.748388	10
9	1408.587165	**704.797220**	1391.560616	696.283946	1390.576600	695.791938	T	***1019.457471***	510.232374	1002.430922	501.719099	1001.446906	501.227091	9
10	***1495.619193***	**748.313235**	1478.592644	739.799960	1477.608628	739.307952	S	***918.409792***	459.708534	901.383243	451.195260	900.399227	450.703252	8
11	1592.671957	796.839617	1575.645408	788.326342	1574.661392	787.834334	P	***831.377764***	416.192520	814.351215	407.679246			7
12	1752.702606	876.854941	1735.676057	868.341667	1734.692041	867.849659	C	***734.325000***	367.666138	717.298451	359.152864			6
13	1880.761184	940.884230	1863.734635	932.370956	1862.750619	931.878948	Q	***574.294351***	287.650814	557.267802	279.137539			5
14	1994.804111	997.905694	1977.777562	989.392419	1976.793546	988.900411	N	***446.235773***	223.621524	429.209224	215.108250			4
15	2122.862689	1061.934982	2105.836140	1053.421708	2104.852124	1052.929700	Q	***332.192846***	166.600061	315.166297	158.086787			3
16	2179.884153	1090.445714	2162.857604	1081.932440	2161.873588	1081.440432	G	204.134268	102.570772	187.107719	94.057497			2
17							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.8	2324.982407	-0.001325	YKDGDQCETSPCQNQGK

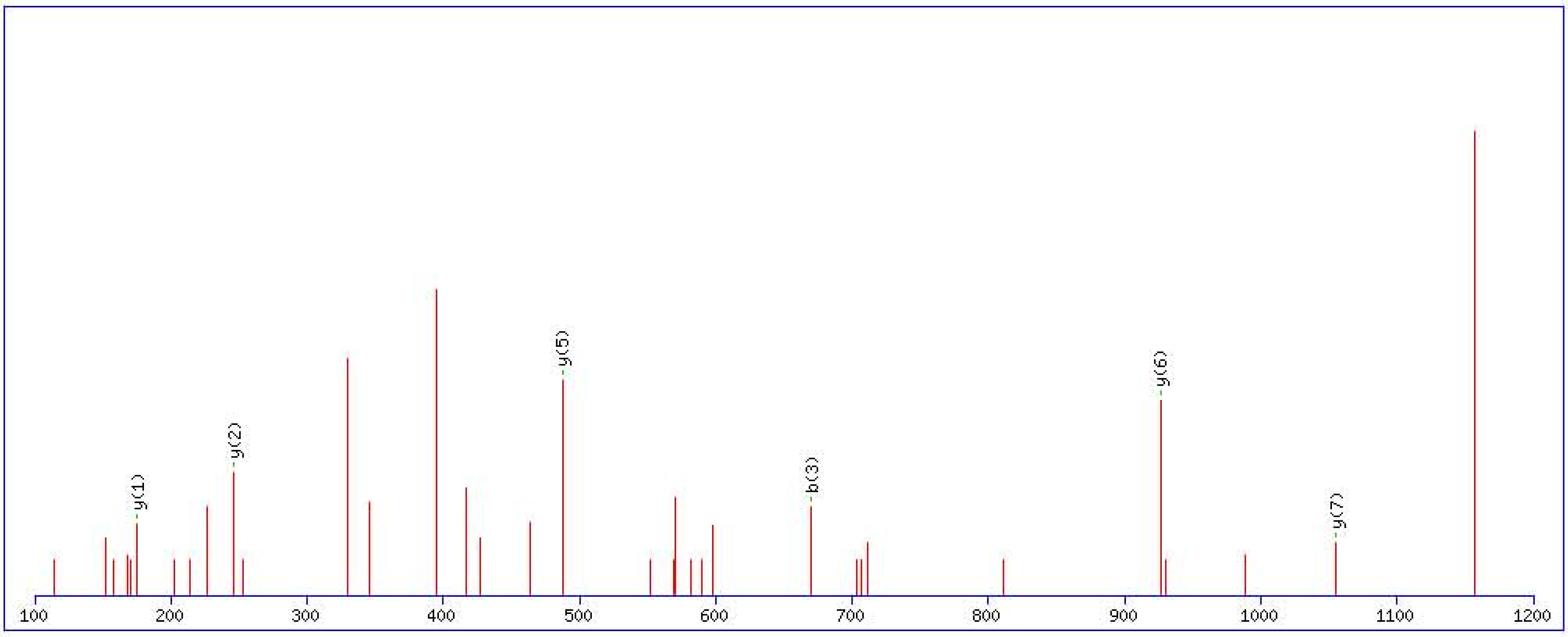
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEQAAVAR**
Found in **FA12_HUMAN**, Coagulation factor XII OS=Homo sapiens GN=F12 PE=1 SV=3

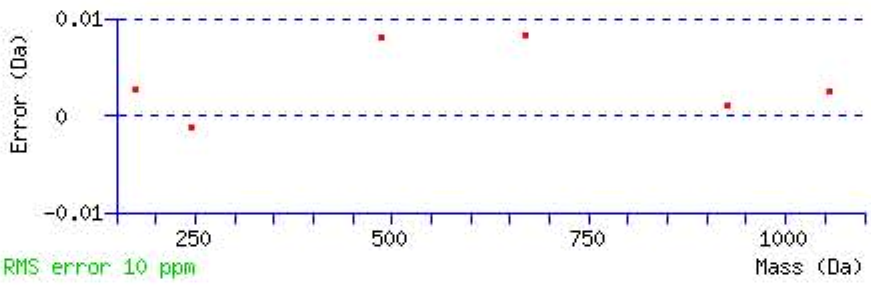
Match to Query 29816: 1155.602668 from(578.808610,2+) rtinseconds(1416) index(76230)
Title: Locus:1.1.1.2372.21 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

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

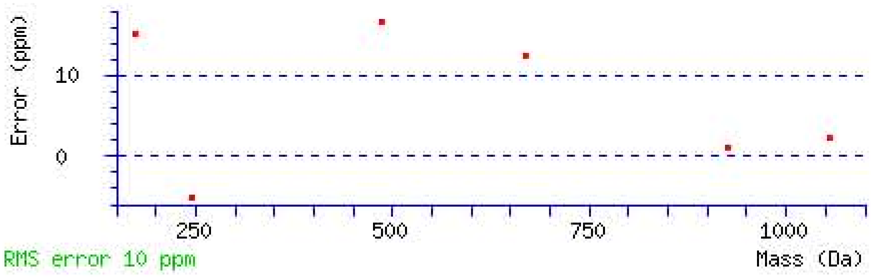


```
Monoisotopic mass of neutral peptide Mr(calc): 1155.607010
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.0032
Matches : 6/68 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							8
2	231.097548	116.052412			213.086983	107.047130	E	***1055.566627***	528.286951	1038.540078	519.773677	1037.556062	519.281669	7
3	**670.322874**	335.665075	653.296325	327.151801	652.312309	326.659793	Q	***926.524034***	463.765655	909.497485	455.252380			6
4	741.359988	371.183632	724.333439	362.670358	723.349423	362.178350	A	***487.298708***	244.152992	470.272159	235.639717			5
5	812.397102	406.702189	795.370553	398.188915	794.386537	397.696907	A	416.261594	208.634435	399.235045	200.121160			4
6	911.465516	456.236396	894.438967	447.723121	893.454951	447.231113	V	345.224480	173.115878	328.197931	164.602603			3
7	982.502630	491.754953	965.476081	483.241678	964.492065	482.749670	A	***246.156066***	123.581671	229.129517	115.068396			2
8							R	***175.118952***	88.063114	158.092403	79.549839			1



RMS error 10 ppm



RMS error 10 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.6	1155.607010	-0.004342	TEQAAVAR
11.3	1155.610855	-0.008187	GAGAGLSRPGSAR
9.4	1155.599594	0.003074	TKESKHEAAR
8.7	1155.588379	0.014289	TEVPLAENQR
6.9	1155.588394	0.014274	VEQIEAGTPGR
5.7	1155.607025	-0.004357	VQDSAVAR
1.6	1155.618256	-0.015588	TGQIDRR

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

{MATRIX SCIENCE}

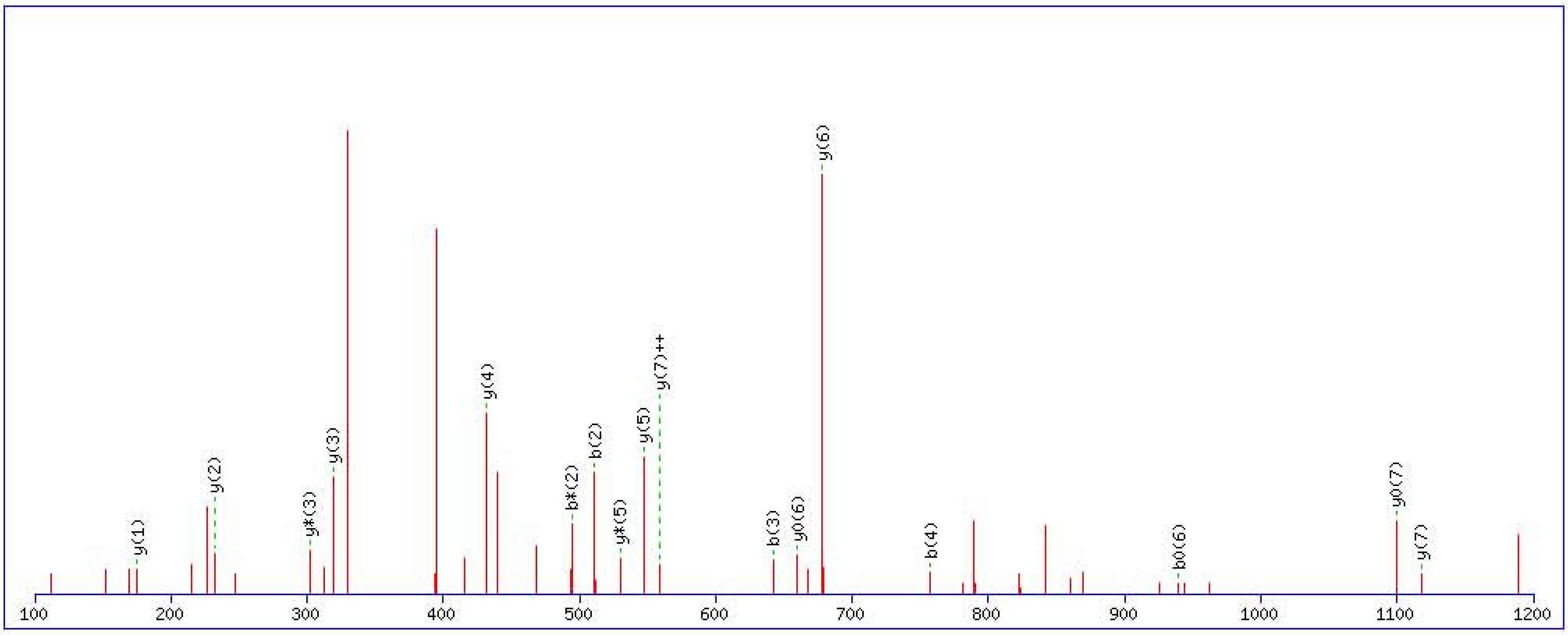
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AQMDLSGR**
Found in **F13A_HUMAN**, Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4

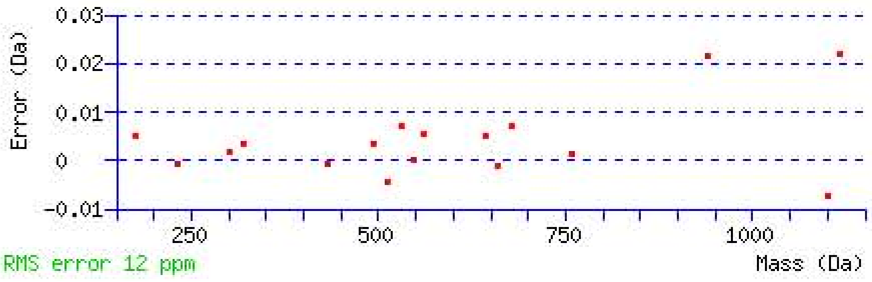
Match to Query 31313: 1187.577748 from(594.796150,2+) rtinseconds(1765) index(78661)
Title: Locus:1.1.1.2494.12 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

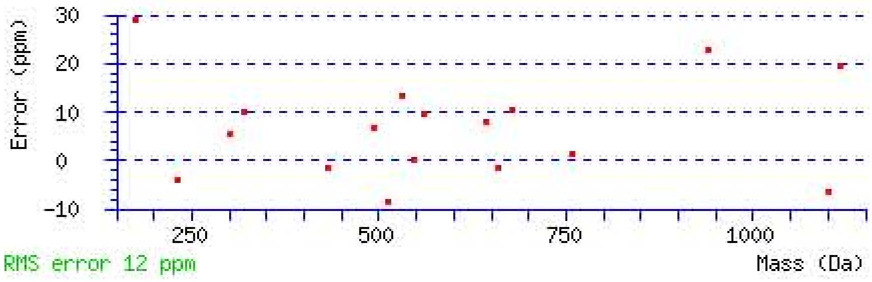
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1187.579086
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 34 **Expect:** 0.00069
Matches : 17/72 fragment ions using 38 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							8
2	**511.269716**	256.138496	494.243167	247.625221			Q	***1117.549262***	559.278269	1100.522713	550.764995	1099.538697	550.272987	7
3	**642.310201**	321.658739	625.283652	313.145464			M	***678.323936***	339.665606	661.297387	331.152332	660.313371	330.660324	6
4	**757.337144**	379.172210	740.310595	370.658935	739.326579	370.166927	D	***547.283451***	274.145364	530.256902	265.632089	529.272886	265.140081	5
5	870.421208	435.714242	853.394659	427.200967	852.410643	426.708959	L	***432.256508***	216.631892	415.229959	208.118617	414.245943	207.626609	4
6	957.453236	479.230256	940.426687	470.716981	939.442671	470.224973	S	***319.172444***	160.089860	302.145895	151.576585	301.161879	151.084577	3
7	1014.474700	507.740988	997.448151	499.227713	996.464135	498.735705	G	***232.140416***	116.573846	215.113867	108.060571			2
8							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.5	1187.579086	-0.001338	AQMDLSGR
0.7	1187.578201	-0.000453	SSLENEPSLGR
0.2	1187.578217	-0.000469	SKSNEGADGPVK

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

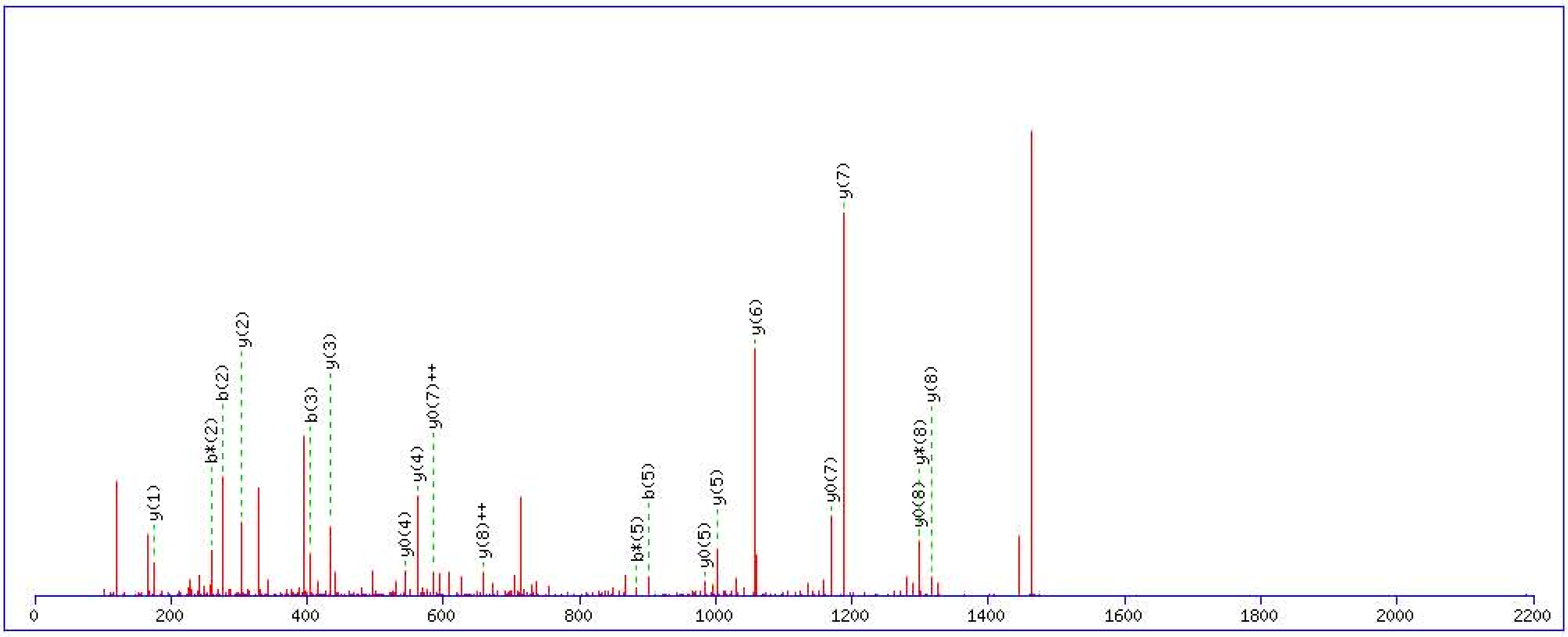
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FQEGQEEER**
Found in **F13A_HUMAN**, Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4

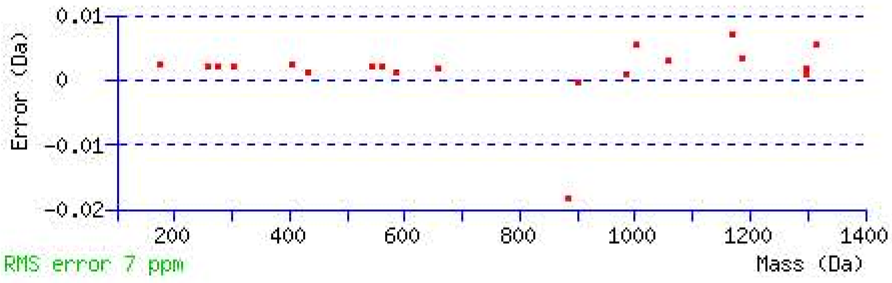
Match to Query 41409: 1461.654448 from(731.834500,2+) rtinseconds(1443) index(59118)
Title: Locus:1.1.1.2500.15 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

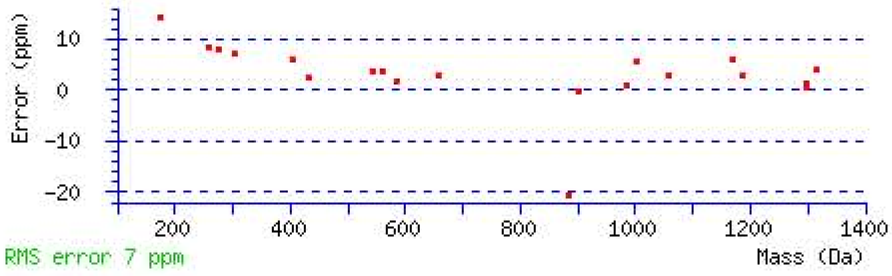
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1461.655807
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 43  Expect: 0.00039
Matches : 20/88 fragment ions using 42 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					F							9
2	**276.134268**	138.570772	259.107719	130.057497			Q	***1315.594692***	658.300984	1298.568143	649.787710	1297.584127	649.295702	8
3	**405.176861**	203.092068	388.150312	194.578794	387.166296	194.086786	E	***1187.536114***	594.271695	1170.509565	585.758421	1169.525549	585.266413	7
4	462.198325	231.602800	445.171776	223.089526	444.187760	222.597518	G	***1058.493521***	529.750399	1041.466972	521.237124	1040.482956	520.745116	6
5	**901.423651**	451.215464	884.397102	442.702189	883.413086	442.210181	Q	***1001.472057***	501.239667	984.445508	492.726392	983.461492	492.234384	5
6	1030.466244	515.736760	1013.439695	507.223485	1012.455679	506.731477	E	***562.246731***	281.627004	545.220182	273.113729	544.236166	272.621721	4
7	1159.508837	580.258057	1142.482288	571.744782	1141.498272	571.252774	E	***433.204138***	217.105707	416.177589	208.592433	415.193573	208.100425	3
8	1288.551430	644.779353	1271.524881	636.266079	1270.540865	635.774071	E	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	2
9							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.6	1461.655807	-0.001359	FQEGQEEER
12.2	1461.640564	0.013884	NSGTQSDGEEK
7.6	1461.655807	-0.001359	FQEGQEEER
6.2	1461.640564	0.013884	VMTDVAGNPEEER
4.5	1461.648392	0.006056	HREELSDYEER
2.8	1461.637161	0.017287	ESELQWQEEER

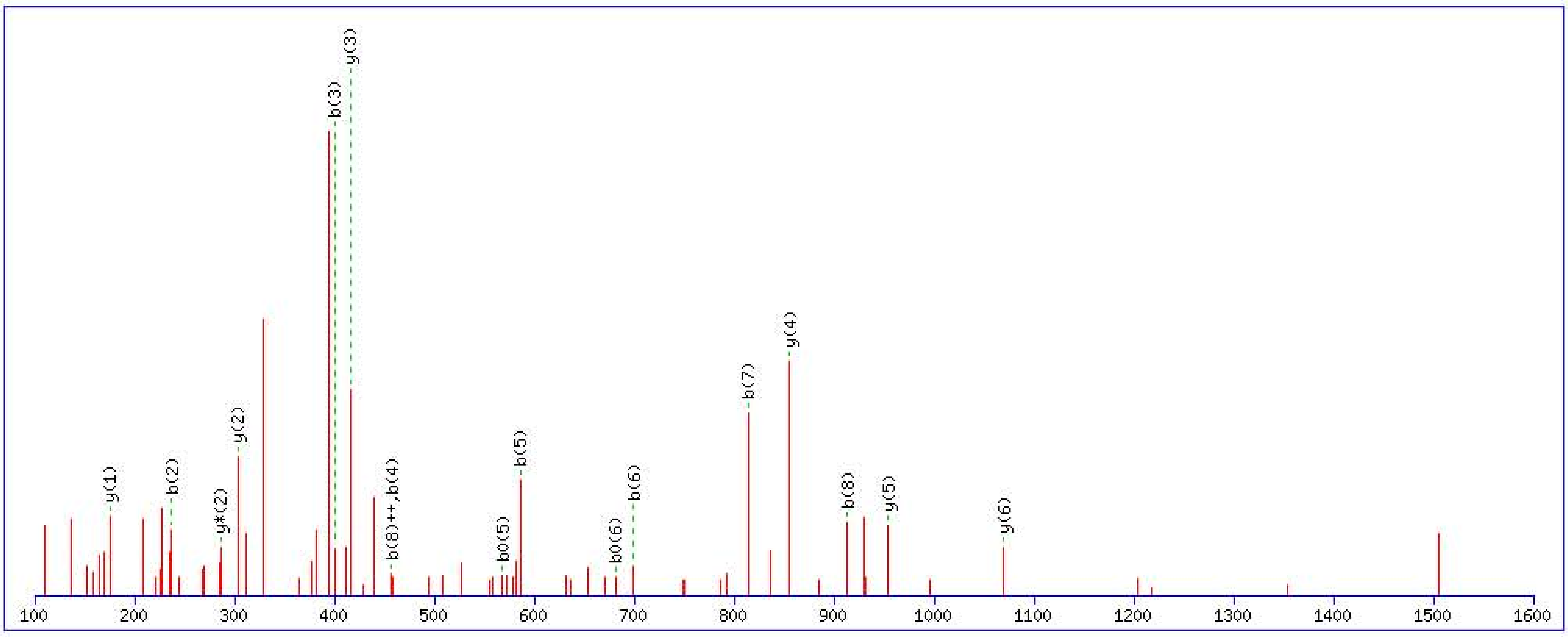
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HVYGELDVQIQR**
Found in **F13A_HUMAN**, Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4

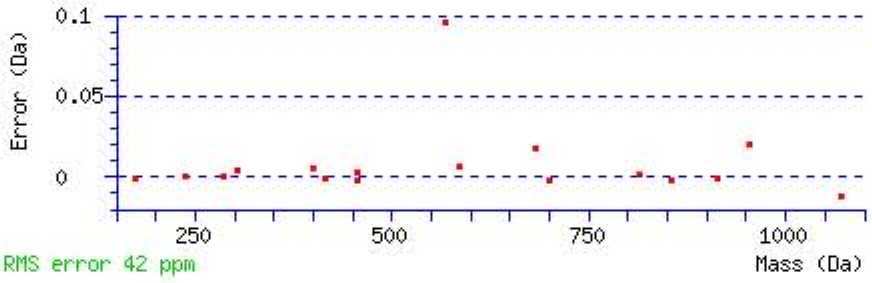
Match to Query 51335: 1766.911572 from(589.977800,3+) rtinseconds(1955) index(62815)
Title: Locus:1.1.1.2678.11 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

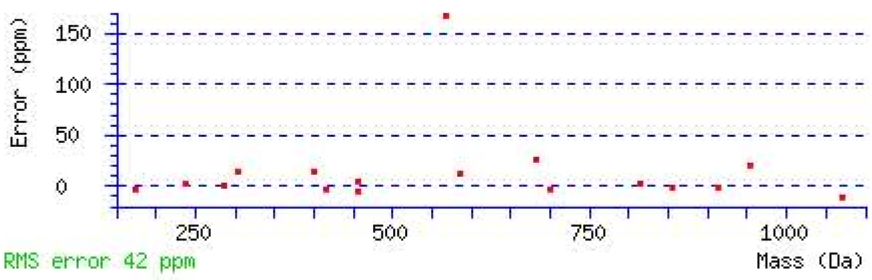
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1766.913773
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 27 **Expect:** 0.0074
Matches : 17/98 fragment ions using 49 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	138.066188	69.536732					H							12
2	***237.134602***	119.070939					V	1630.862141	815.934708	1613.835592	807.421434	1612.851576	806.929426	11
3	***400.197931***	200.602603					Y	1531.793727	766.400501	1514.767178	757.887227	1513.783162	757.395219	10
4	***457.219395***	229.113335					G	1368.730398	684.868837	1351.703849	676.355563	1350.719833	675.863554	9
5	***586.261988***	293.634632			568.251423	284.629349	E	1311.708934	656.358105	1294.682385	647.844830	1293.698369	647.352822	8
6	***699.346052***	350.176664			681.335487	341.171382	L	1182.666341	591.836808	1165.639792	583.323534	1164.655776	582.831526	7
7	***814.372995***	407.690136			796.362430	398.684853	D	***1069.582277***	535.294776	1052.555728	526.781502	1051.571712	526.289494	6
8	***913.441409***	457.224342			895.430844	448.219060	V	***954.555334***	477.781305	937.528785	469.268030			5
9	1352.666735	676.837006	1335.640186	668.323731	1334.656170	667.831723	Q	***855.486920***	428.247098	838.460371	419.733823			4
10	1465.750799	733.379037	1448.724250	724.865763	1447.740234	724.373755	I	***416.261594***	208.634435	399.235045	200.121160			3
11	1593.809377	797.408326	1576.782828	788.895052	1575.798812	788.403044	Q	***303.177530***	152.092403	286.150981	143.579128			2
12							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.6	1766.913773	-0.002201	HVYGELDVQIQR
15.4	1766.913773	-0.002201	HVYGELDVQIQR
3.9	1766.888138	0.023434	IMQNGTILYTMR

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

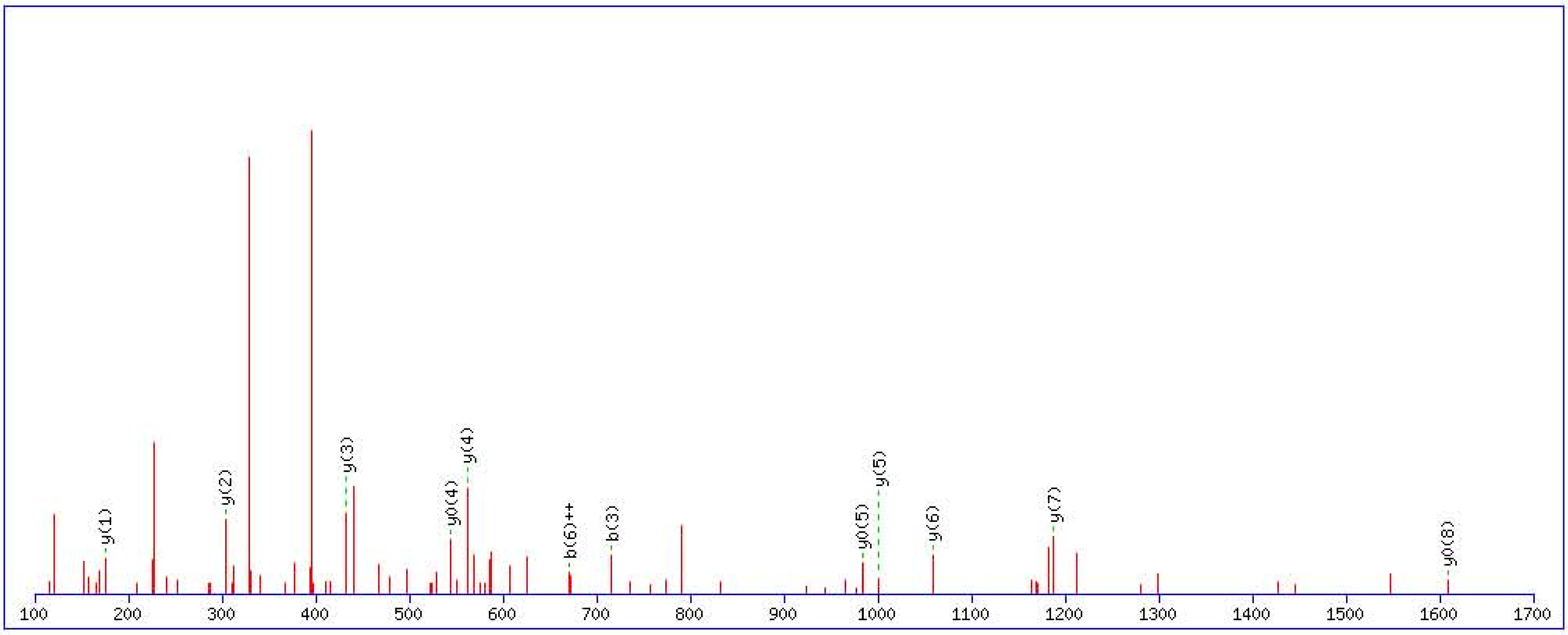
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FQEGQEEER**
Found in **F13A_HUMAN**, Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4

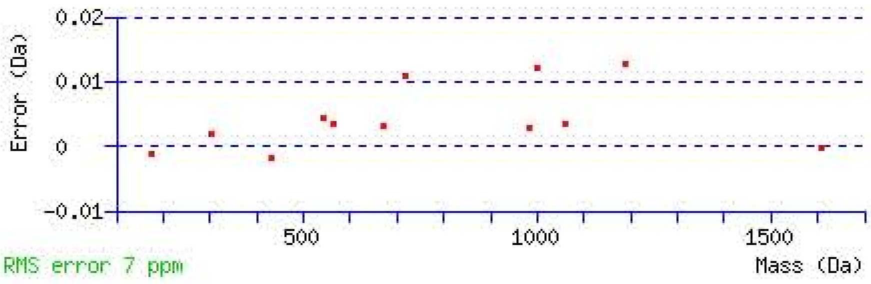
Match to Query 51514: 1772.822952 from(591.948260,3+) rtinseconds(1827) index(61836)
Title: Locus:1.1.1.2634.9 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

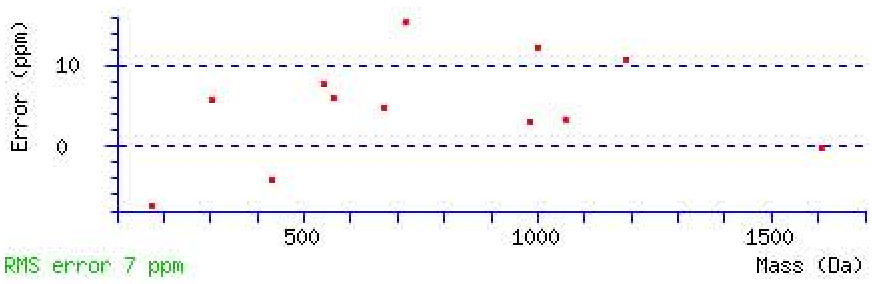
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1772.822556
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.029
Matches : 12/88 fragment ions using 26 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	148.075690	74.541483					F							9
2	587.301016	294.154146	570.274467	285.640872			Q	1626.761440	813.884358	1609.734891	805.371084	1608.750875	804.879076	8
3	716.343609	358.675443	699.317060	350.162168	698.333044	349.670160	E	***1187.536114***	594.271695	1170.509565	585.758421	1169.525549	585.266413	7
4	773.365073	387.186175	756.338524	378.672900	755.354508	378.180892	G	***1058.493521***	529.750399	1041.466972	521.237124	1040.482956	520.745116	6
5	1212.590399	606.798837	1195.563850	598.285563	1194.579834	597.793555	Q	***1001.472057***	501.239667	984.445508	492.726392	983.461492	492.234384	5
6	1341.632992	671.320134	1324.606443	662.806860	1323.622427	662.314852	E	***562.246731***	281.627004	545.220182	273.113729	544.236166	272.621721	4
7	1470.675585	735.841431	1453.649036	727.328156	1452.665020	726.836148	E	***433.204138***	217.105707	416.177589	208.592433	415.193573	208.100425	3
8	1599.718178	800.362727	1582.691629	791.849453	1581.707613	791.357445	E	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	2
9							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.7	1772.822556	0.000396	FQEGQEEER
17.3	1772.803909	0.019043	ESELQWQEEER

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

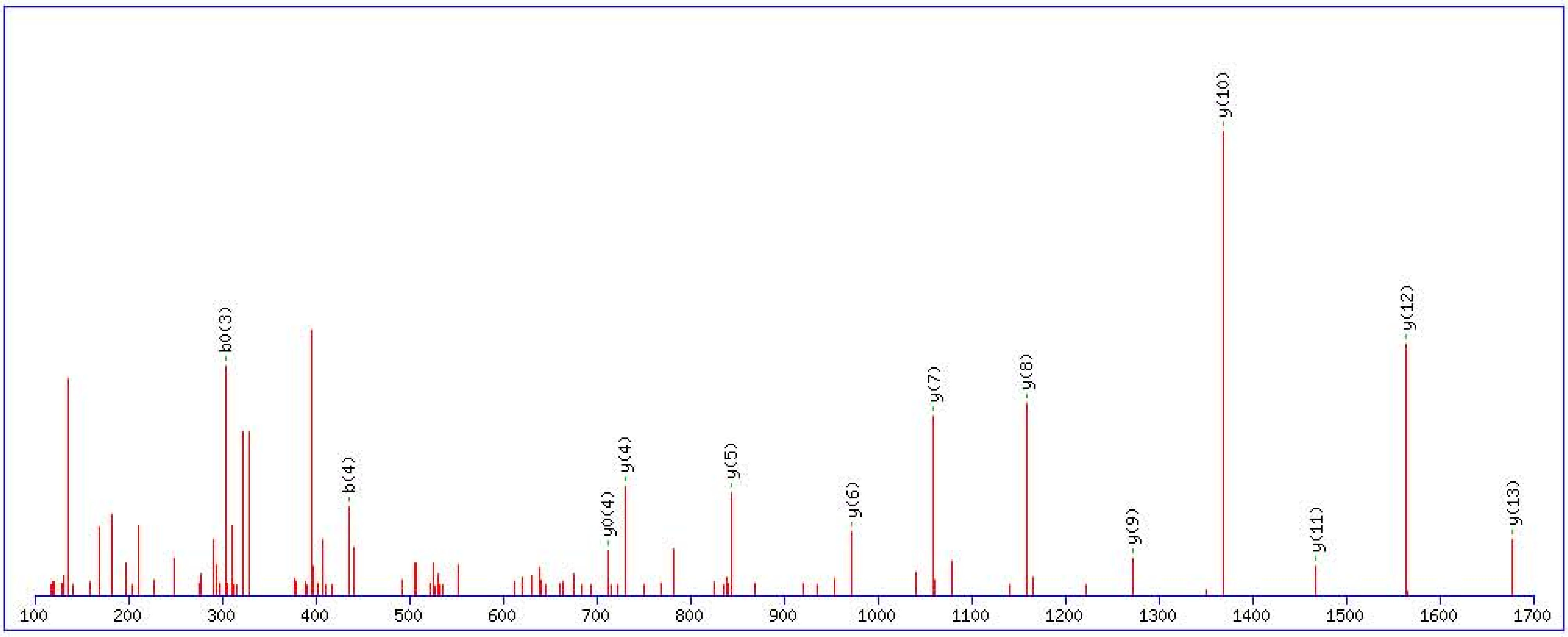
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GTYIPVPIVSELQSGK**
Found in **F13A_HUMAN**, Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4

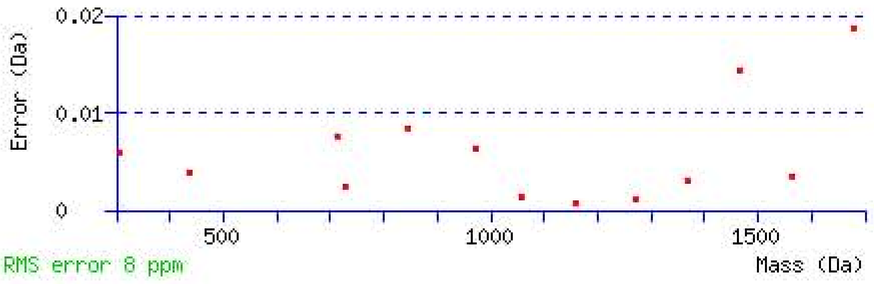
Match to Query 56584: 1998.095832 from(667.039220,3+) rtinseconds(2745) index(67835)
Title: Locus:1.1.1.2952.8 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

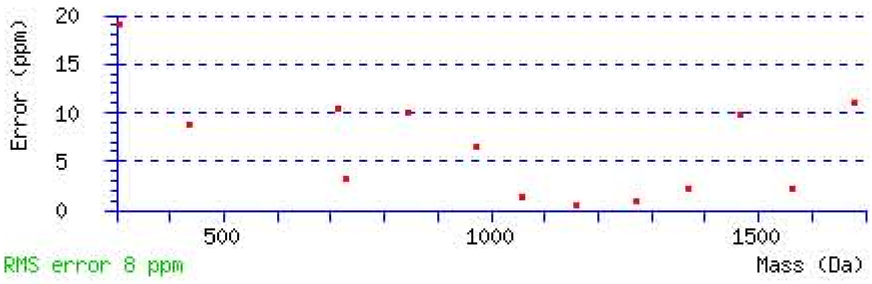
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1998.085983
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 78  Expect: 5.3e-008
Matches : 13/150 fragment ions using 16 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							16
2	159.076419	80.041847			141.065854	71.036565	T	1942.071799	971.539538	1925.045250	963.026263	1924.061234	962.534255	15
3	322.139748	161.573512			304.129183	152.568230	Y	1841.024120	921.015698	1823.997571	912.502424	1823.013555	912.010416	14
4	435.223812	218.115544			417.213247	209.110262	I	***1677.960791***	839.484034	1660.934242	830.970759	1659.950226	830.478751	13
5	532.276576	266.641926			514.266011	257.636644	P	***1564.876727***	782.942002	1547.850178	774.428727	1546.866162	773.936719	12
6	631.344990	316.176133			613.334425	307.170851	V	***1467.823963***	734.415620	1450.797414	725.902345	1449.813398	725.410337	11
7	728.397754	364.702515			710.387189	355.697233	P	***1368.755549***	684.881413	1351.729000	676.368138	1350.744984	675.876130	10
8	841.481818	421.244547			823.471253	412.239265	I	***1271.702785***	636.355031	1254.676236	627.841756	1253.692220	627.349748	9
9	940.550232	470.778754			922.539667	461.773472	V	***1158.618721***	579.812999	1141.592172	571.299724	1140.608156	570.807716	8
10	1027.582260	514.294768			1009.571695	505.289486	S	***1059.550307***	530.278792	1042.523758	521.765517	1041.539742	521.273509	7
11	1156.624853	578.816065			1138.614288	569.810782	E	***972.518279***	486.762777	955.491730	478.249503	954.507714	477.757495	6
12	1269.708917	635.358096			1251.698352	626.352814	L	***843.475686***	422.241481	826.449137	413.728207	825.465121	413.236199	5
13	1708.934243	854.970759	1691.907694	846.457485	1690.923678	845.965477	Q	***730.391622***	365.699449	713.365073	357.186175	712.381057	356.694167	4
14	1795.966271	898.486774	1778.939722	889.973499	1777.955706	889.481491	S	291.166296	146.086786	274.139747	137.573512	273.155731	137.081504	3
15	1852.987735	926.997505	1835.961186	918.484231	1834.977170	917.992223	G	204.134268	102.570772	187.107719	94.057497			2
16							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
78.2	1998.085983	0.009849	GTYIPVPIVSELQSGK
0.6	1998.099731	-0.003899	GDEVVVELVENGKKVTVGK

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

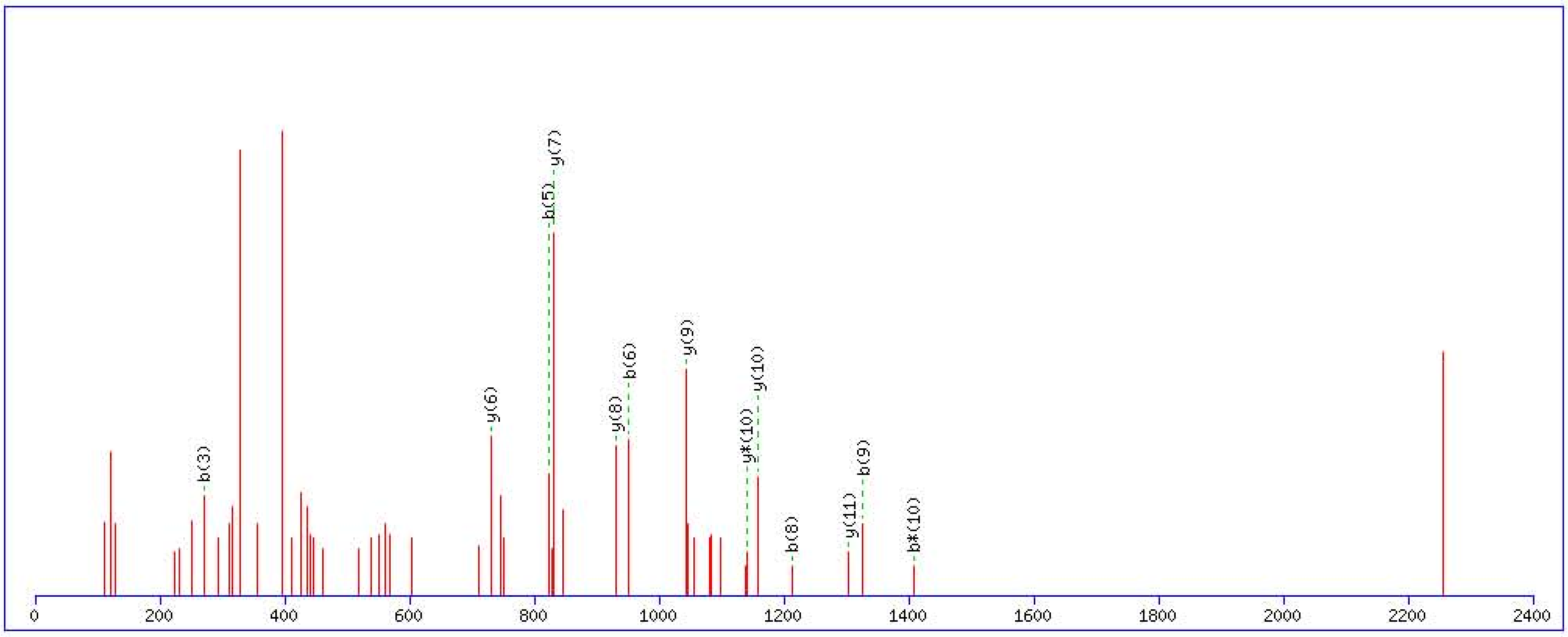
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GVNLQEFLNVTSVHLFK**
Found in **F13A_HUMAN**, Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4

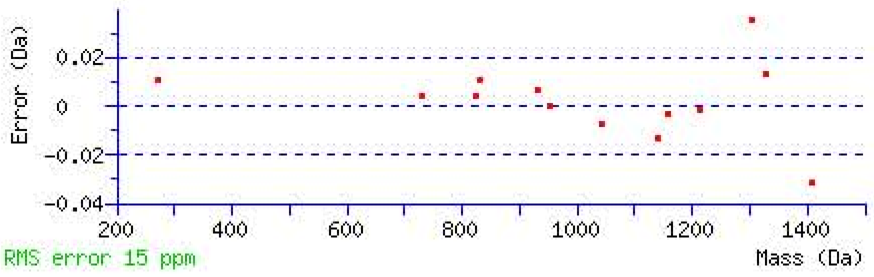
Match to Query 62919: 2255.224422 from(752.748750,3+) rtinseconds(2950) index(69247)
Title: Locus:1.1.1.3021.11 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

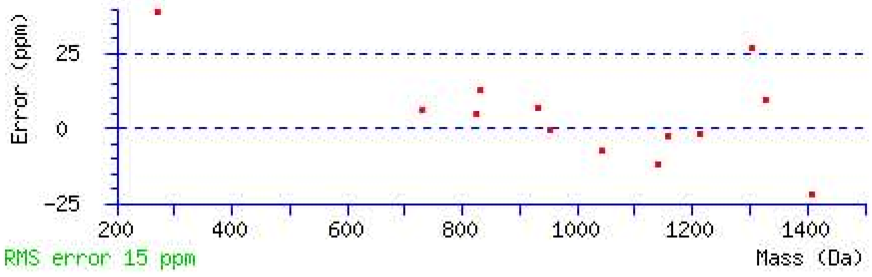
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2255.213654
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5 : Biotin:Thermo-21345 (Q)
Ions Score: 31 **Expect:** 0.017
Matches : 13/168 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							17
2	157.097154	79.052215					V	2199.199458	1100.103367	2182.172909	1091.590092	2181.188893	1091.098084	16
3	***271.140081***	136.073679	254.113532	127.560404			N	2100.131044	1050.569160	2083.104495	1042.055885	2082.120479	1041.563877	15
4	384.224145	192.615711	367.197596	184.102436			L	1986.088117	993.547697	1969.061568	985.034422	1968.077552	984.542414	14
5	***823.449471***	412.228374	806.422922	403.715099			Q	1873.004053	937.005665	1855.977504	928.492390	1854.993488	928.000382	13
6	***952.492064***	476.749670	935.465515	468.236396	934.481499	467.744388	E	1433.778727	717.393002	1416.752178	708.879727	1415.768162	708.387719	12
7	1099.560478	550.283877	1082.533929	541.770603	1081.549913	541.278595	F	***1304.736134***	652.871705	1287.709585	644.358431	1286.725569	643.866423	11
8	***1212.644542***	606.825909	1195.617993	598.312635	1194.633977	597.820627	L	***1157.667720***	579.337498	1140.641171	570.824224	1139.657155	570.332216	10
9	***1326.687469***	663.847373	1309.660920	655.334098	1308.676904	654.842090	N	***1044.583656***	522.795466	1027.557107	514.282192	1026.573091	513.790184	9
10	1425.755883	713.381580	1408.729334	704.868305	1407.745318	704.376297	V	***930.540729***	465.774003	913.514180	457.260728	912.530164	456.768720	8
11	1526.803562	763.905419	1509.777013	755.392145	1508.792997	754.900137	T	***831.472315***	416.239796	814.445766	407.726521	813.461750	407.234513	7
12	1613.835590	807.421433	1596.809041	798.908159	1595.825025	798.416151	S	***730.424636***	365.715956	713.398087	357.202682	712.414071	356.710674	6
13	1712.904004	856.955640	1695.877455	848.442366	1694.893439	847.950358	V	643.392608	322.199942	626.366059	313.686668			5
14	1849.962916	925.485096	1832.936367	916.971822	1831.952351	916.479814	H	544.324194	272.665735	527.297645	264.152461			4
15	1963.046980	982.027128	1946.020431	973.513854	1945.036415	973.021846	L	407.265282	204.136279	390.238733	195.623004			3
16	2110.115394	1055.561335	2093.088845	1047.048060	2092.104829	1046.556052	F	294.181218	147.594247	277.154669	139.080973			2
17							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.5	2255.213654	0.010768	GVNLQEFLNVTSVHLFK

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

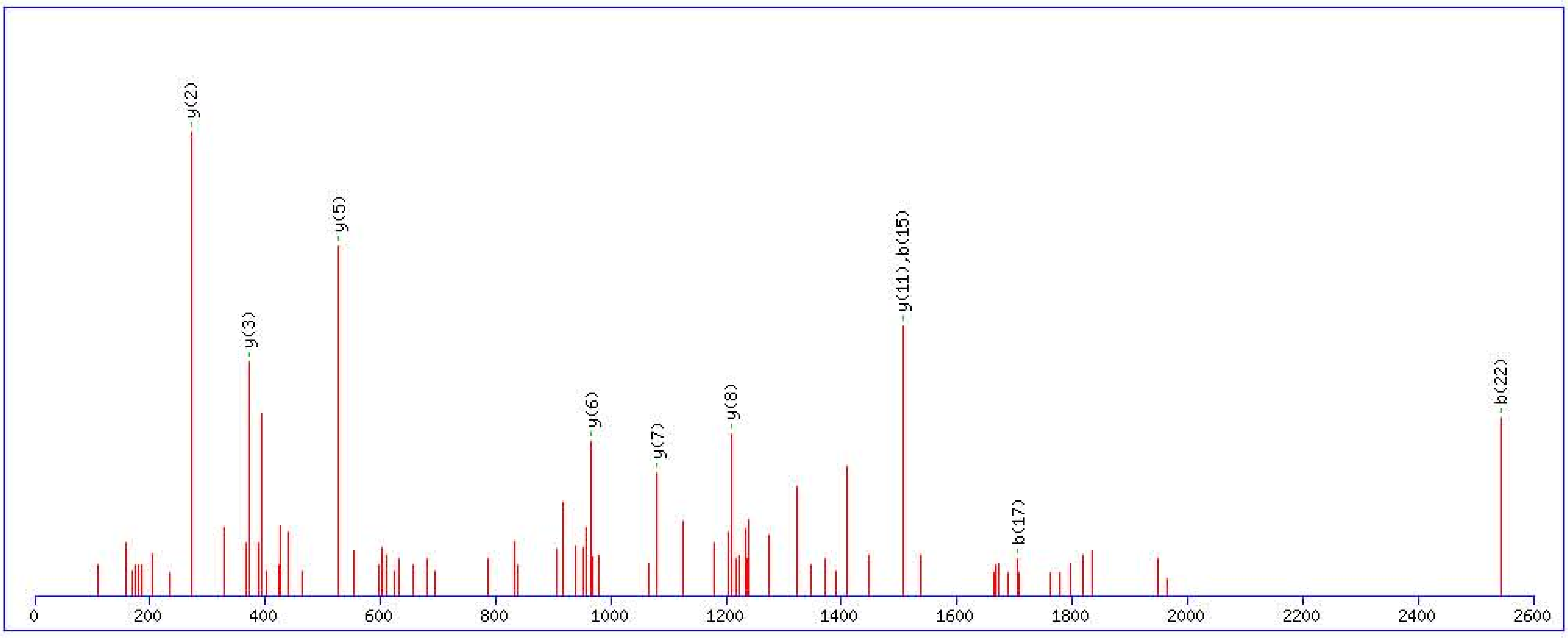
Mascot Search Results

Peptide View

MS/MS Fragmentation of **AVPPNNSNAAEDDLPTVELQGVVPR**
Found in **F13A_HUMAN**, Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4

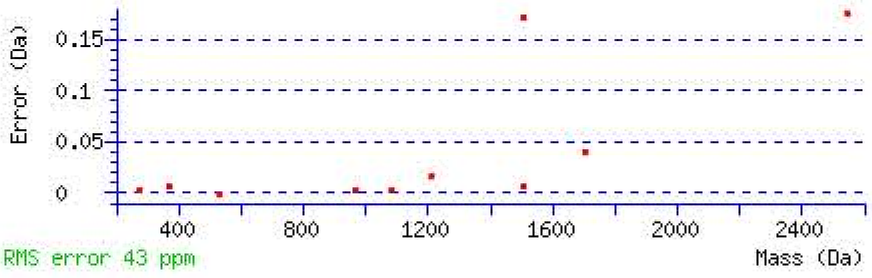
Match to Query 73467: 2912.479962 from(971.833930,3+) rtinseconds(2494) index(66169)
Title: Locus:1.1.1.2865.25 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

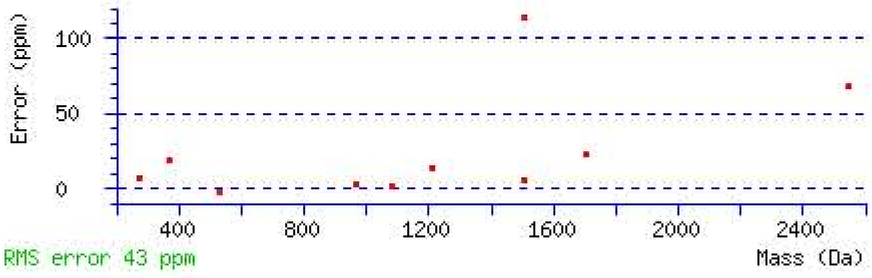
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2912.470200
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q20     : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.043
Matches : 10/254 fragment ions using 20 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							25
2	171.112804	86.060040					V	2842.440370	1421.723823	2825.413821	1413.210548	2824.429805	1412.718540	24
3	268.165568	134.586422					P	2743.371956	1372.189616	2726.345407	1363.676341	2725.361391	1363.184333	23
4	365.218332	183.112804					P	2646.319192	1323.663234	2629.292643	1315.149959	2628.308627	1314.657951	22
5	479.261259	240.134267	462.234710	231.620993			N	2549.266428	1275.136852	2532.239879	1266.623577	2531.255863	1266.131569	21
6	593.304186	297.155731	576.277637	288.642457			N	2435.223501	1218.115388	2418.196952	1209.602114	2417.212936	1209.110106	20
7	680.336214	340.671745	663.309665	332.158471	662.325649	331.666463	S	2321.180574	1161.093925	2304.154025	1152.580650	2303.170009	1152.088642	19
8	794.379141	397.693209	777.352592	389.179934	776.368576	388.687926	N	2234.148546	1117.577911	2217.121997	1109.064636	2216.137981	1108.572628	18
9	865.416255	433.211766	848.389706	424.698491	847.405690	424.206483	A	2120.105619	1060.556447	2103.079070	1052.043173	2102.095054	1051.551165	17
10	936.453369	468.730323	919.426820	460.217048	918.442804	459.725040	A	2049.068505	1025.037890	2032.041956	1016.524616	2031.057940	1016.032608	16
11	1065.495962	533.251619	1048.469413	524.738345	1047.485397	524.246336	E	1978.031391	989.519333	1961.004842	981.006059	1960.020826	980.514051	15
12	1180.522905	590.765091	1163.496356	582.251816	1162.512340	581.759808	D	1848.988798	924.998037	1831.962249	916.484762	1830.978233	915.992754	14
13	1295.549848	648.278562	1278.523299	639.765288	1277.539283	639.273280	D	1733.961855	867.484565	1716.935306	858.971291	1715.951290	858.479283	13
14	1408.633912	704.820594	1391.607363	696.307320	1390.623347	695.815312	L	1618.934912	809.971094	1601.908363	801.457819	1600.924347	800.965811	12
15	**1505.686676**	753.346976	1488.660127	744.833702	1487.676111	744.341694	P	***1505.850848***	753.429062	1488.824299	744.915787	1487.840283	744.423779	11
16	1606.734355	803.870816	1589.707806	795.357541	1588.723790	794.865533	T	1408.798084	704.902680	1391.771535	696.389405	1390.787519	695.897397	10
17	**1705.802769**	853.405023	1688.776220	844.891748	1687.792204	844.399740	V	1307.750405	654.378840	1290.723856	645.865566	1289.739840	645.373558	9
18	1834.845362	917.926319	1817.818813	909.413045	1816.834797	908.921037	E	***1208.681991***	604.844633	1191.655442	596.331359	1190.671426	595.839351	8
19	1947.929426	974.468351	1930.902877	965.955077	1929.918861	965.463069	L	***1079.639398***	540.323337	1062.612849	531.810062			7
20	2387.154752	1194.081014	2370.128203	1185.567739	2369.144187	1185.075731	Q	***966.555334***	483.781305	949.528785	475.268030			6
21	2444.176216	1222.591746	2427.149667	1214.078471	2426.165651	1213.586463	G	***527.330008***	264.168642	510.303459	255.655367			5
22	**2543.244630**	1272.125953	2526.218081	1263.612678	2525.234065	1263.120670	V	470.308544	235.657910	453.281995	227.144635			4
23	2642.313044	1321.660160	2625.286495	1313.146885	2624.302479	1312.654877	V	***371.240130***	186.123703	354.213581	177.610428			3
24	2739.365808	1370.186542	2722.339259	1361.673267	2721.355243	1361.181259	P	***272.171716***	136.589496	255.145167	128.076221			2
25							R	175.118952	88.063114	158.092403	79.549839			1



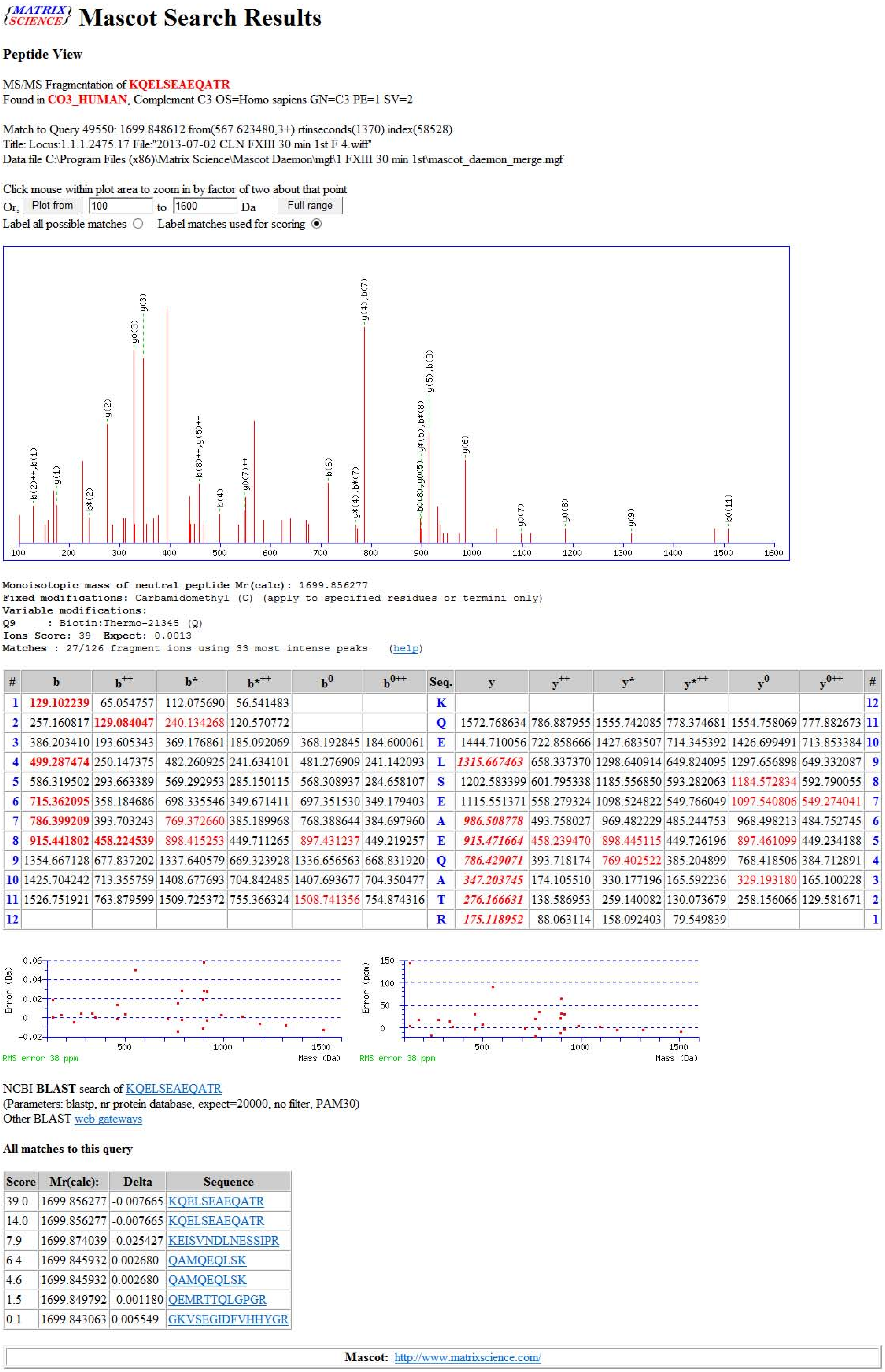


NCBI **BLAST** search of AVPPNNSNAAEDDLPTVELQGVVPR
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.5	2912.470200	0.009762	AVPPNNSNAAEDDLPTVELQGVVPR

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



{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **KQELSEAEQATR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

Match to Query 49550: 1699.848612 from(567.623480,3+) rtinseconds(1370) index(58528)
Title: Locus:1.1.1.2475.17 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1699.856277
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9     : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.0013
Matches : 27/126 fragment ions using 33 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**129.102239**	65.054757	112.075690	56.541483			K							12
2	257.160817	**129.084047**	240.134268	120.570772			Q	1572.768634	786.887955	1555.742085	778.374681	1554.758069	777.882673	11
3	386.203410	193.605343	369.176861	185.092069	368.192845	184.600061	E	1444.710056	722.858666	1427.683507	714.345392	1426.699491	713.853384	10
4	**499.287474**	250.147375	482.260925	241.634101	481.276909	241.142093	L	***1315.667463***	658.337370	1298.640914	649.824095	1297.656898	649.332087	9
5	586.319502	293.663389	569.292953	285.150115	568.308937	284.658107	S	1202.583399	601.795338	1185.556850	593.282063	1184.572834	592.790055	8
6	**715.362095**	358.184686	698.335546	349.671411	697.351530	349.179403	E	1115.551371	558.279324	1098.524822	549.766049	1097.540806	549.274041	7
7	**786.399209**	393.703243	769.372660	385.189968	768.388644	384.697960	A	***986.508778***	493.758027	969.482229	485.244753	968.498213	484.752745	6
8	**915.441802**	**458.224539**	898.415253	449.711265	897.431237	449.219257	E	***915.471664***	458.239470	898.445115	449.726196	897.461099	449.234188	5
9	1354.667128	677.837202	1337.640579	669.323928	1336.656563	668.831920	Q	***786.429071***	393.718174	769.402522	385.204899	768.418506	384.712891	4
10	1425.704242	713.355759	1408.677693	704.842485	1407.693677	704.350477	A	***347.203745***	174.105510	330.177196	165.592236	329.193180	165.100228	3
11	1526.751921	763.879599	1509.725372	755.366324	1508.741356	754.874316	T	***276.166631***	138.586953	259.140082	130.073679	258.156066	129.581671	2
12							R	***175.118952***	88.063114	158.092403	79.549839			1

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.0	1699.856277	-0.007665	KQELSEAEQATR
14.0	1699.856277	-0.007665	KQELSEAEQATR
7.9	1699.874039	-0.025427	KEISVNDLNESSIPR
6.4	1699.845932	0.002680	QAMQEQLSK
4.6	1699.845932	0.002680	QAMQEQLSK
1.5	1699.849792	-0.001180	QEMRTTQLGPGR
0.1	1699.843063	0.005549	GKVSEGIDFVHHYGR

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

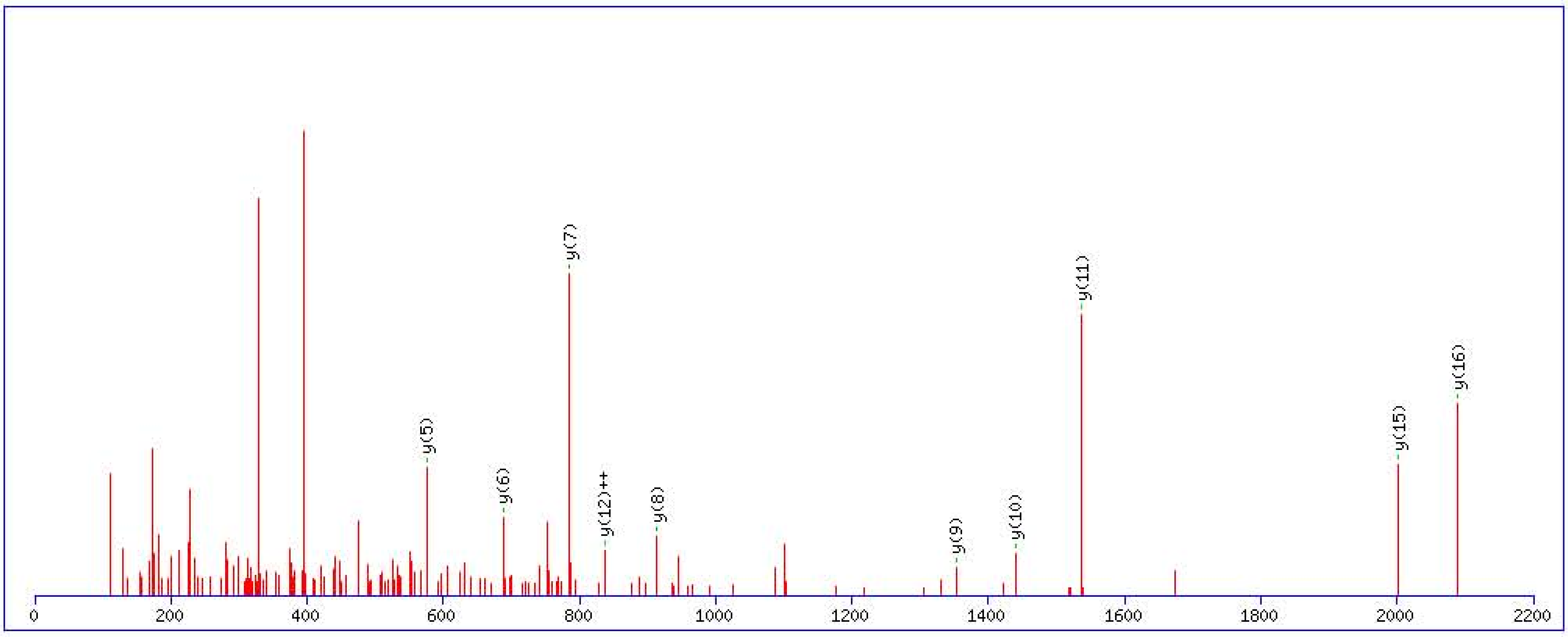
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSINTHPSQKPLSITVR**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

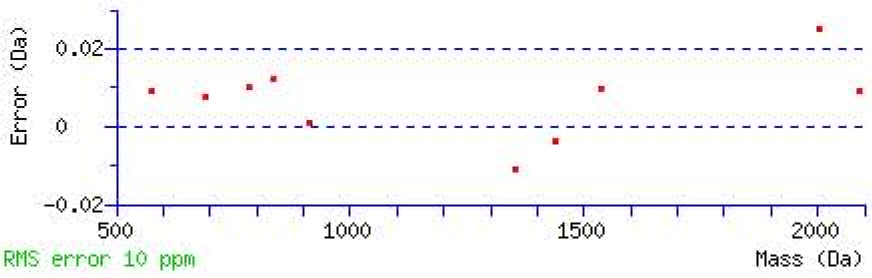
Match to Query 61624: 2201.232616 from(551.315430,4+) rtinseconds(1861) index(62043)
Title: Locus:1.1.1.2646.8 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

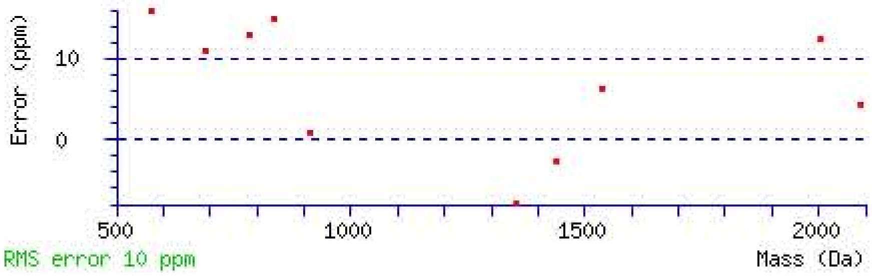
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2201.235428
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 5.5e-005
Matches : 10/180 fragment ions using 18 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							17
2	201.123368	101.065322			183.112803	92.060039	S	***2089.158656***	1045.082966	2072.132107	1036.569691	2071.148091	1036.077683	16
3	314.207432	157.607354			296.196867	148.602071	I	***2002.126628***	1001.566952	1985.100079	993.053678	1984.116063	992.561669	15
4	428.250359	214.628818	411.223810	206.115543	410.239794	205.623535	N	1889.042564	945.024920	1872.016015	936.511646	1871.031999	936.019638	14
5	529.298038	265.152657	512.271489	256.639383	511.287473	256.147375	T	1774.999637	888.003456	1757.973088	879.490182	1756.989072	878.998174	13
6	666.356950	333.682113	649.330401	325.168838	648.346385	324.676830	H	1673.951958	837.479617	1656.925409	828.966343	1655.941393	828.474334	12
7	763.409714	382.208495	746.383165	373.695221	745.399149	373.203213	P	***1536.893046***	768.950161	1519.866497	760.436887	1518.882481	759.944878	11
8	850.441742	425.724509	833.415193	417.211234	832.431177	416.719226	S	***1439.840282***	720.423779	1422.813733	711.910505	1421.829717	711.418496	10
9	1289.667068	645.337172	1272.640519	636.823898	1271.656503	636.331889	Q	***1352.808254***	676.907765	1335.781705	668.394491	1334.797689	667.902483	9
10	1417.762031	709.384654	1400.735482	700.871379	1399.751466	700.379371	K	***913.582928***	457.295102	896.556379	448.781828	895.572363	448.289820	8
11	1514.814795	757.911036	1497.788246	749.397761	1496.804230	748.905753	P	***785.487965***	393.247621	768.461416	384.734346	767.477400	384.242338	7
12	1627.898859	814.453067	1610.872310	805.939793	1609.888294	805.447785	L	***688.435201***	344.721239	671.408652	336.207964	670.424636	335.715956	6
13	1714.930887	857.969082	1697.904338	849.455807	1696.920322	848.963799	S	***575.351137***	288.179207	558.324588	279.665932	557.340572	279.173924	5
14	1828.014951	914.511113	1810.988402	905.997839	1810.004386	905.505831	I	488.319109	244.663192	471.292560	236.149918	470.308544	235.657910	4
15	1929.062630	965.034953	1912.036081	956.521679	1911.052065	956.029670	T	375.235045	188.121161	358.208496	179.607886	357.224480	179.115878	3
16	2028.131044	1014.569160	2011.104495	1006.055886	2010.120479	1005.563878	V	274.187366	137.597321	257.160817	129.084047			2
17							R	175.118952	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of LSINTHPSQKPLSITVR
(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	2201.235428	-0.002812	LSINTHPSQKPLSITVR

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

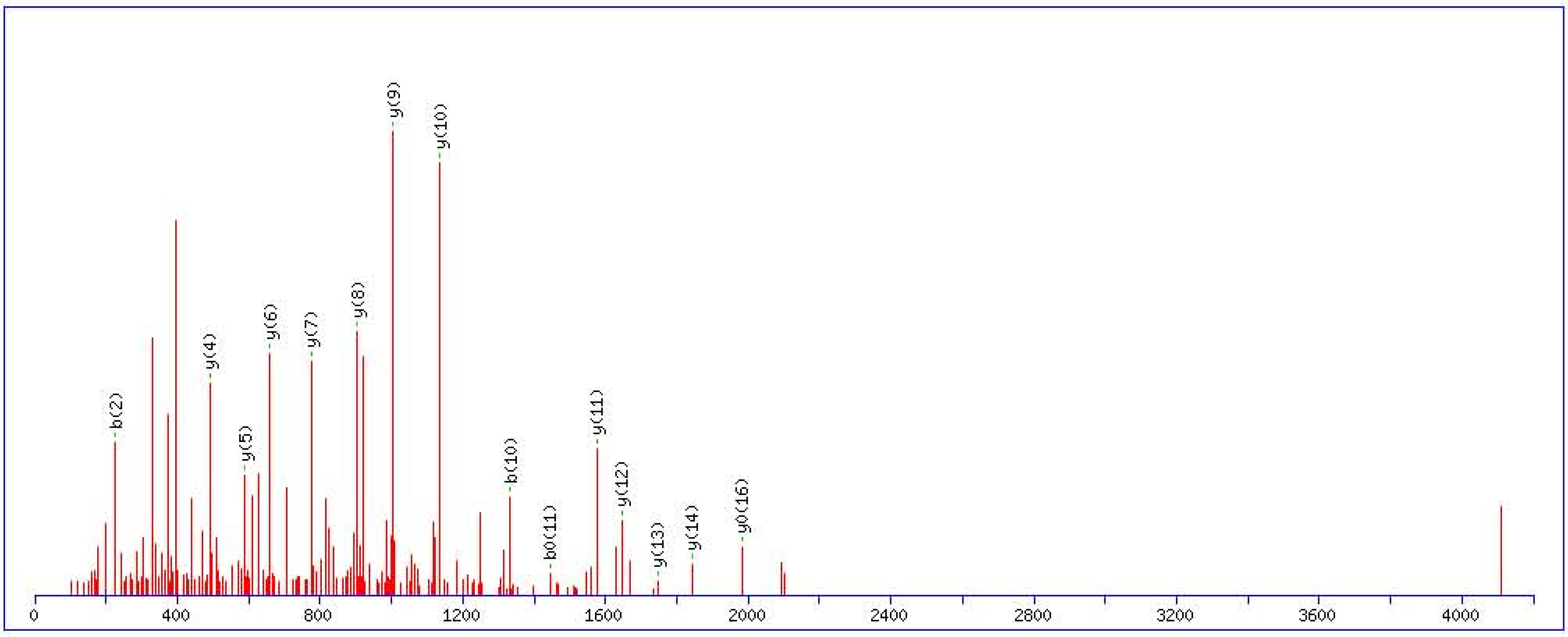
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ILLQGTPVAQMTEDAVDAER**
Found in **CO3_HUMAN**, Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2

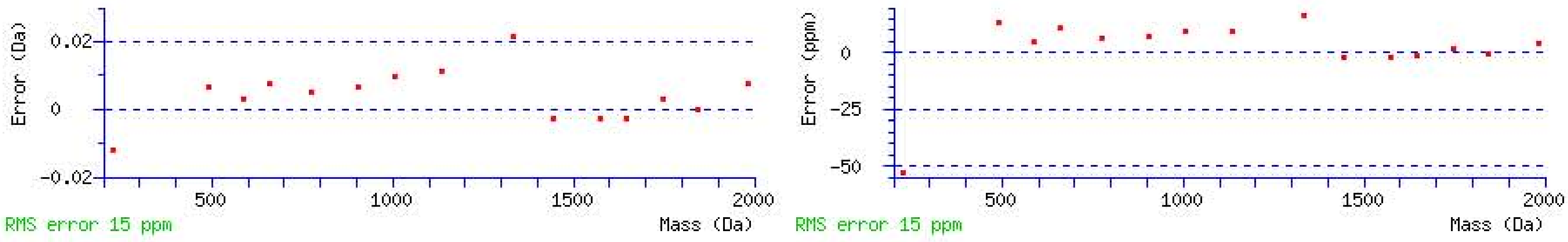
Match to Query 67474: 2467.258272 from(823.426700,3+) rtinseconds(2634) index(66934)
Title: Locus:1.1.1.2914.4 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 4200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2467.245071
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10    : Biotin:Thermo-21345 (Q)
Ions Score: 82  Expect: 2e-007
Matches : 15/210 fragment ions using 21 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							20
2	**227.175404**	114.091340					L	2355.168297	1178.087786	2338.141748	1169.574512	2337.157732	1169.082504	19
3	340.259468	170.633372					L	2242.084233	1121.545754	2225.057684	1113.032480	2224.073668	1112.540472	18
4	468.318046	234.662661	451.291497	226.149386			Q	2129.000169	1065.003722	2111.973620	1056.490448	2110.989604	1055.998440	17
5	525.339510	263.173393	508.312961	254.660119			G	2000.941591	1000.974434	1983.915042	992.461159	1982.931026	991.969151	16
6	626.387189	313.697233	609.360640	305.183958	608.376624	304.691950	T	1943.920127	972.463702	1926.893578	963.950427	1925.909562	963.458419	15
7	723.439953	362.223615	706.413404	353.710340	705.429388	353.218332	P	***1842.872448***	921.939862	1825.845899	913.426588	1824.861883	912.934580	14
8	822.508367	411.757822	805.481818	403.244547	804.497802	402.752539	V	***1745.819684***	873.413480	1728.793135	864.900206	1727.809119	864.408198	13
9	893.545481	447.276379	876.518932	438.763104	875.534916	438.271096	A	***1646.751270***	823.879273	1629.724721	815.365999	1628.740705	814.873991	12
10	**1332.770807**	666.889042	1315.744258	658.375767	1314.760242	657.883759	Q	***1575.714156***	788.360716	1558.687607	779.847442	1557.703591	779.355434	11
11	1463.811292	732.409284	1446.784743	723.896010	1445.800727	723.404002	M	***1136.488830***	568.748053	1119.462281	560.234779	1118.478265	559.742771	10
12	1564.858971	782.933124	1547.832422	774.419849	1546.848406	773.927841	T	***1005.448345***	503.227811	988.421796	494.714536	987.437780	494.222528	9
13	1693.901564	847.454420	1676.875015	838.941146	1675.890999	838.449138	E	***904.400666***	452.703971	887.374117	444.190697	886.390101	443.698689	8
14	1808.928507	904.967892	1791.901958	896.454617	1790.917942	895.962609	D	***775.358073***	388.182675	758.331524	379.669400	757.347508	379.177392	7
15	1879.965621	940.486449	1862.939072	931.973174	1861.955056	931.481166	A	***660.331130***	330.669203	643.304581	322.155929	642.320565	321.663921	6
16	1979.034035	990.020656	1962.007486	981.507381	1961.023470	981.015373	V	***589.294016***	295.150646	572.267467	286.637372	571.283451	286.145364	5
17	2094.060978	1047.534127	2077.034429	1039.020852	2076.050413	1038.528844	D	***490.225602***	245.616439	473.199053	237.103165	472.215037	236.611157	4
18	2165.098092	1083.052684	2148.071543	1074.539409	2147.087527	1074.047402	A	375.198659	188.102968	358.172110	179.589693	357.188094	179.097685	3
19	2294.140685	1147.573981	2277.114136	1139.060706	2276.130120	1138.568698	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
20							R	175.118952	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
81.6	2467.245071	0.013201	ILLQGTPVAQMTEDAVDAER
32.2	2467.245071	0.013201	ILLQGTPVAQMTEDAVDAER

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

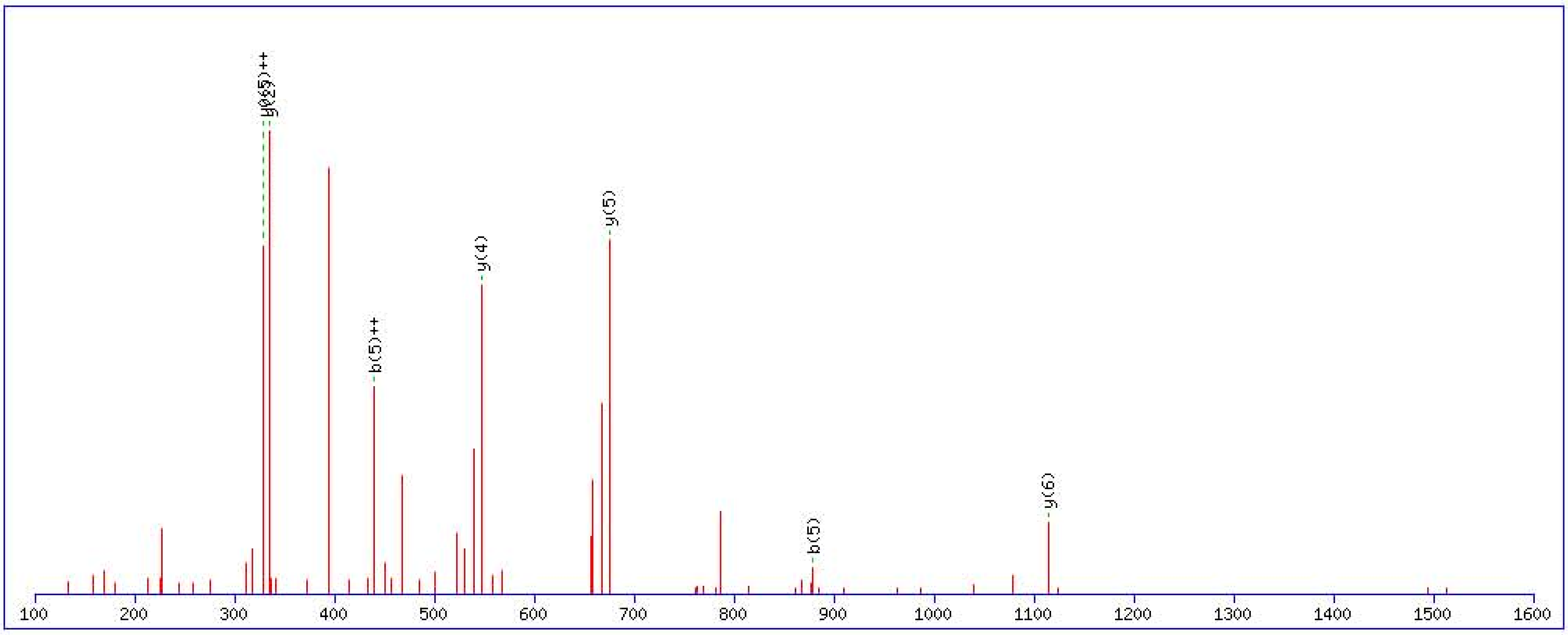
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQQPDCR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

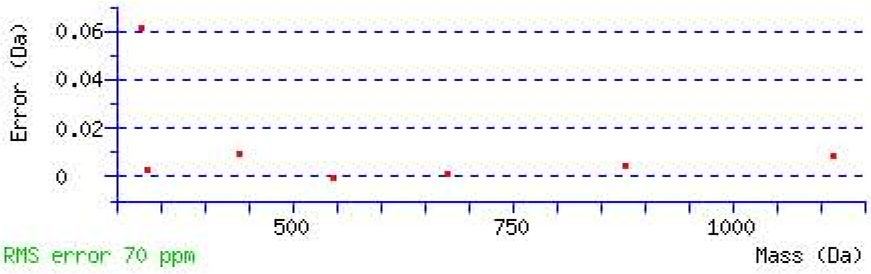
Match to Query 32107: 1212.579748 from(607.297150,2+) rtinseconds(1259) index(57781)
Title: Locus:1.1.1.2436.15 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

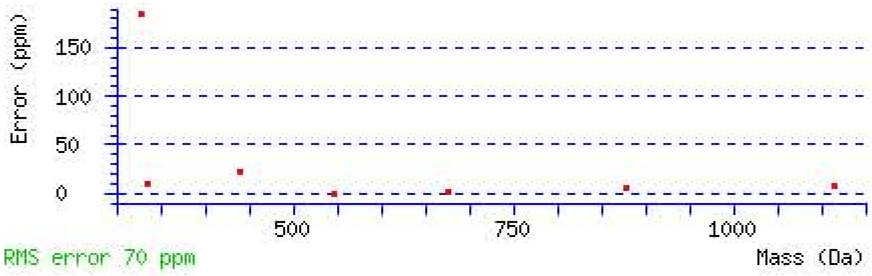
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1600 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1212.574356
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 27 **Expect:** 0.0082
Matches : 7/58 fragment ions using 10 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					V							7
2	539.301016	270.154146	522.274467	261.640872			Q	***1114.513212***	557.760244	1097.486663	549.246970	1096.502647	548.754962	6
3	667.359594	334.183435	650.333045	325.670161			Q	***675.287886***	338.147581	658.261337	329.634307	657.277321	329.142299	5
4	764.412358	382.709817	747.385809	374.196543			P	***547.229308***	274.118292	530.202759	265.605018	529.218743	265.113010	4
5	**879.439301**	**440.223289**	862.412752	431.710014	861.428736	431.218006	D	450.176544	225.591910	433.149995	217.078635	432.165979	216.586627	3
6	1039.469950	520.238613	1022.443401	511.725339	1021.459385	511.233331	C	***335.149601***	168.078438	318.123052	159.565164			2
7							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.9	1212.574356	0.005392	VQQPDCR
11.7	1212.574356	0.005392	VQQPDCR
4.7	1212.596115	-0.016367	YFVEAGAMAVR

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

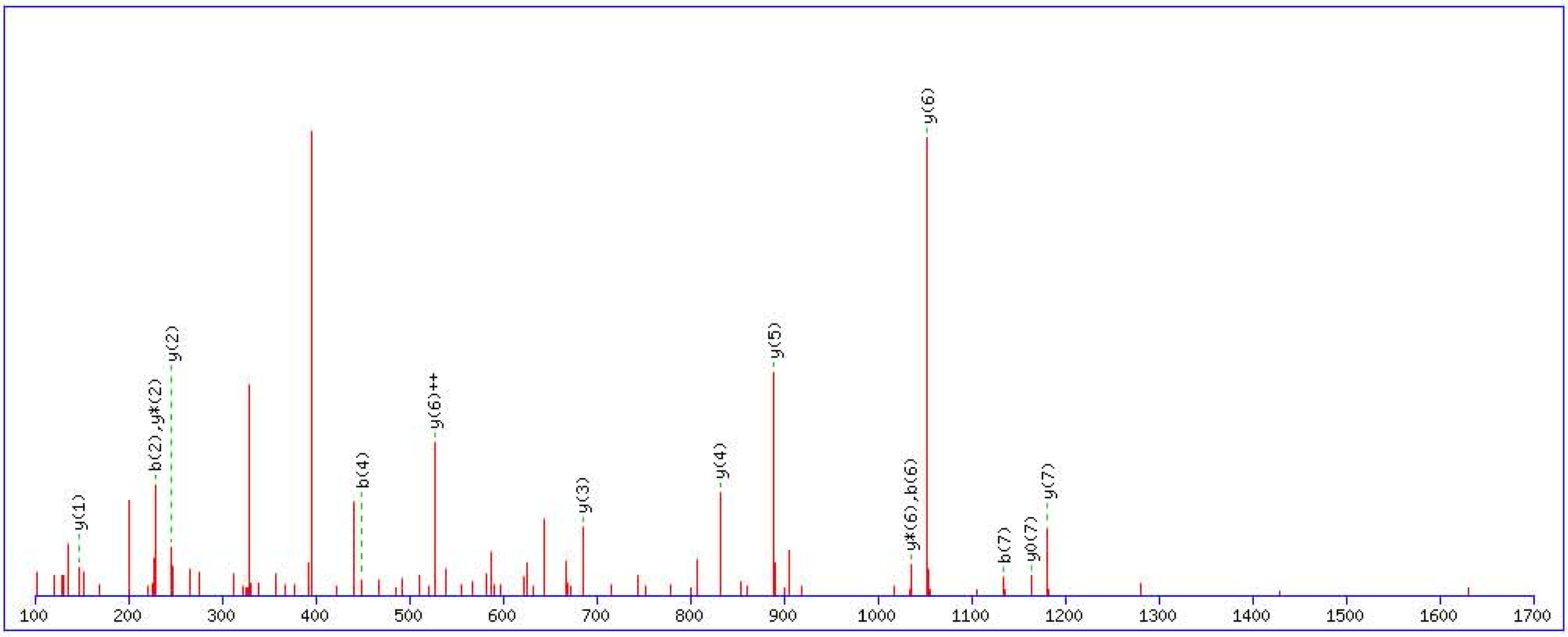
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VEYGFQVK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

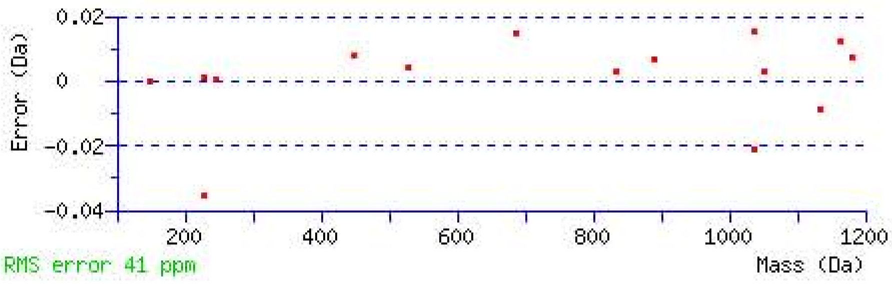
Match to Query 34490: 1279.663528 from(640.839040,2+) rtinseconds(1964) index(62890)
Title: Locus:1.1.1.2681.11 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

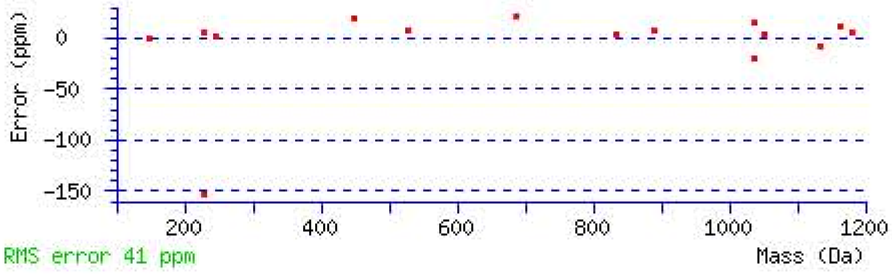
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1279.663483
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6      : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.012
Matches : 15/60 fragment ions using 32 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							8
2	**229.118283**	115.062780			211.107718	106.057497	E	***1181.602344***	591.304810	1164.575795	582.791536	1163.591779	582.299528	7
3	392.181612	196.594444			374.171047	187.589162	Y	***1052.559751***	526.783514	1035.533202	518.270239			6
4	**449.203076**	225.105176			431.192511	216.099894	G	***889.496422***	445.251849	872.469873	436.738575			5
5	596.271490	298.639383			578.260925	289.634101	F	***832.474958***	416.741117	815.448409	408.227843			4
6	**1035.496816**	518.252046	1018.470267	509.738772	1017.486251	509.246764	Q	***685.406544***	343.206910	668.379995	334.693636			3
7	**1134.565230**	567.786253	1117.538681	559.272979	1116.554665	558.780971	V	***246.181218***	123.594247	229.154669	115.080973			2
8							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.6	1279.663483	0.000045	VEYGFQVK
10.5	1279.681229	-0.017701	EVTVKEWYVK
5.2	1279.663483	0.000045	QFVGYLDK
4.4	1279.659470	0.004058	VCSFGKQVVEK
3.4	1279.677216	-0.013688	VFKTEDTQGKK
0.8	1279.666824	-0.003296	VKEWSLMIMK
0.3	1279.652039	0.011489	QAVRSYNSEVK
0.2	1279.652924	0.010604	MVARVWSLMR
0.1	1279.659424	0.004104	VECLYEALKR

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

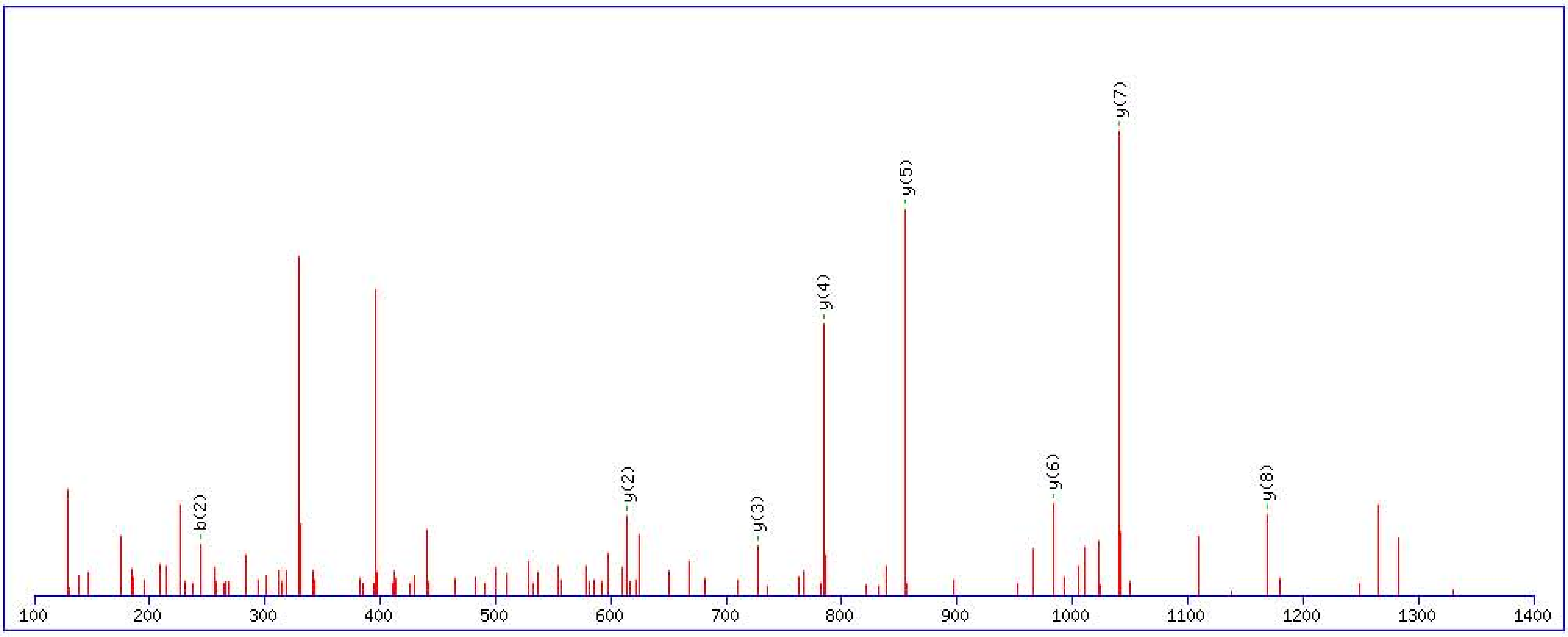
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DKGQAGLQR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

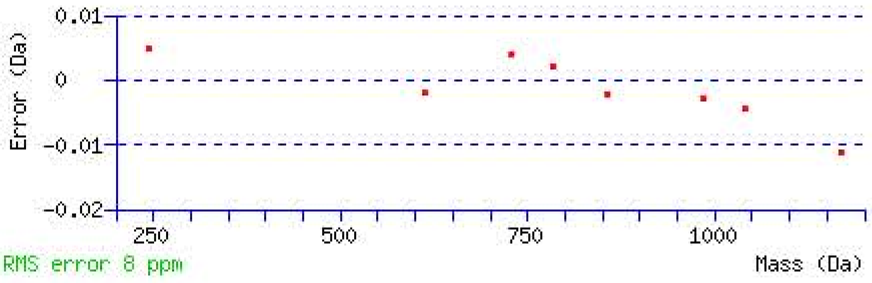
Match to Query 34737: 1282.679888 from(642.347220,2+) rtinseconds(1299) index(58067)
Title: Locus:1.1.1.2450.18 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

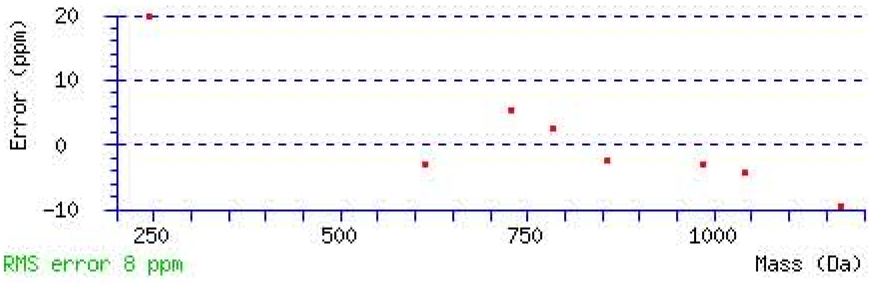
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1282.681580
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 59  Expect: 2.7e-005
Matches : 8/78 fragment ions using 12 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	#
1	116.034219	58.520748			98.023654	49.515465	D					9
2	**244.129182**	122.568229	227.102633	114.054955	226.118617	113.562947	K	***1168.661925***	584.834600	1151.635376	576.321326	8
3	301.150646	151.078961	284.124097	142.565687	283.140081	142.073679	G	***1040.566962***	520.787119	1023.540413	512.273844	7
4	429.209224	215.108250	412.182675	206.594976	411.198659	206.102968	Q	***983.545498***	492.276387	966.518949	483.763112	6
5	500.246338	250.626807	483.219789	242.113532	482.235773	241.621524	A	***855.486920***	428.247098	838.460371	419.733823	5
6	557.267802	279.137539	540.241253	270.624265	539.257237	270.132257	G	***784.449806***	392.728541	767.423257	384.215266	4
7	670.351866	335.679571	653.325317	327.166297	652.341301	326.674289	L	***727.428342***	364.217809	710.401793	355.704534	3
8	1109.577192	555.292234	1092.550643	546.778960	1091.566627	546.286951	Q	***614.344278***	307.675777	597.317729	299.162502	2
9							R	175.118952	88.063114	158.092403	79.549839	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.5	1282.681580	-0.001692	DKGQAGLQR
13.0	1282.688095	-0.008207	KPTKPESQSPGK
11.7	1282.662933	0.016955	QKNEGRPETPK
10.6	1282.670334	0.009554	ELEGQIQR
7.7	1282.681580	-0.001692	DKGQAGLQR
5.6	1282.674194	0.005694	QGEGQSRLVPGR
5.3	1282.685623	-0.005735	VWVDGIQR
4.8	1282.670334	0.009554	QDLEAQIR
3.6	1282.676834	0.003054	KALEDEKPEPK
3.1	1282.670319	0.009569	MAAPEQPLAISR

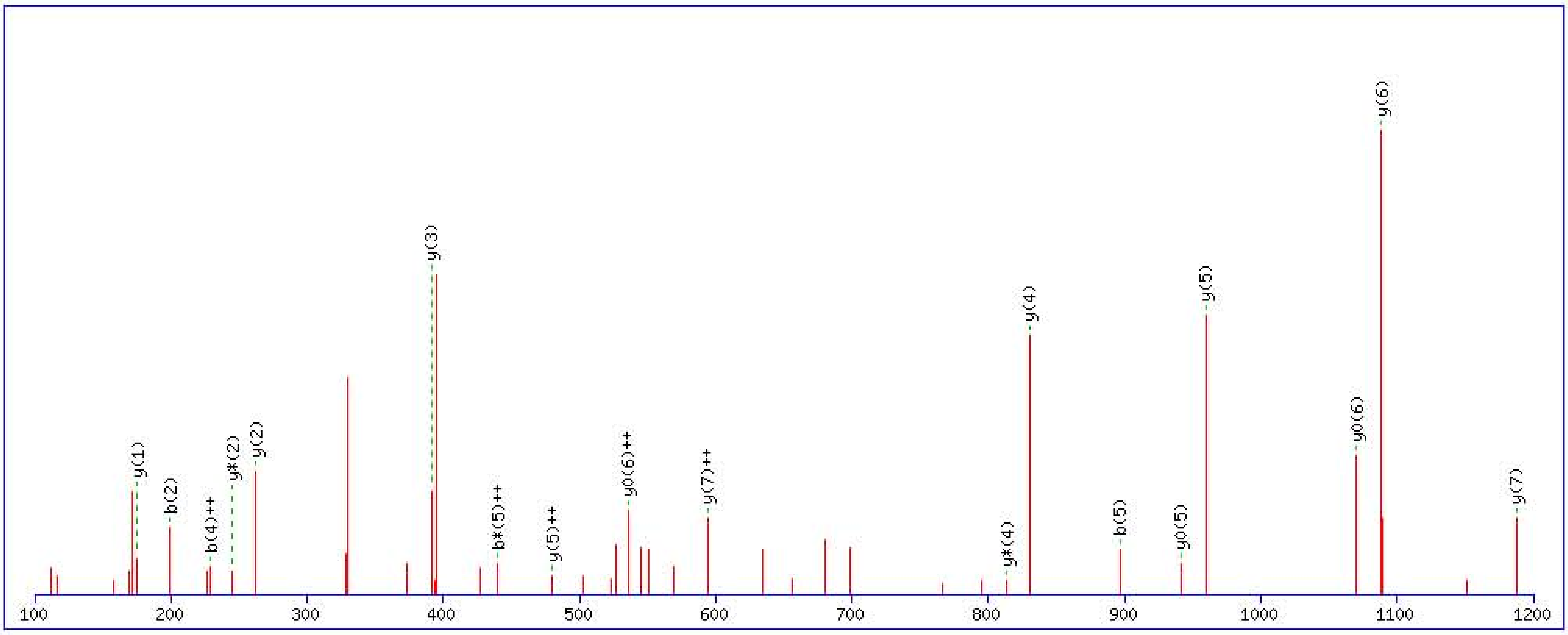
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVEEQESR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

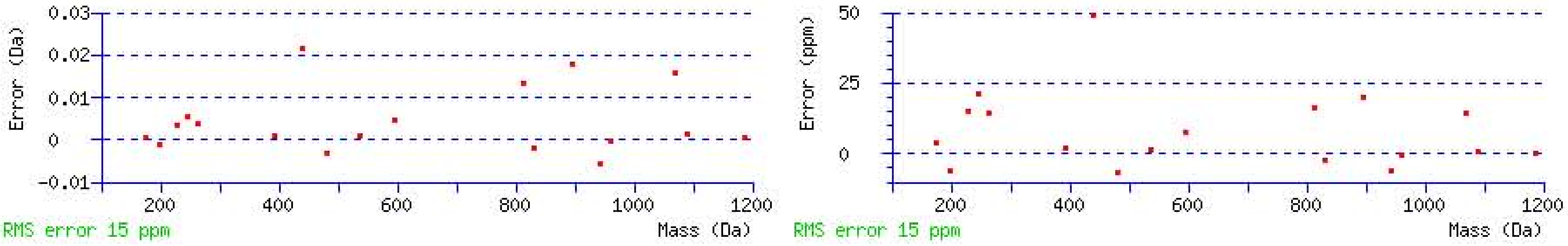
Match to Query 34842: 1285.625228 from(643.819890,2+) rtinseconds(1333) index(58250)
Title: Locus:1.1.1.2462.22 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

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



```
Monoisotopic mass of neutral peptide Mr(calc): 1285.633621
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 45  Expect: 0.00051
Matches : 18/70 fragment ions using 30 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							8
2	**199.144104**	100.075690					V	***1187.572499***	594.289888	1170.545950	585.776613	1169.561934	585.284605	7
3	328.186697	164.596987			310.176132	155.591704	E	***1088.504085***	544.755681	1071.477536	536.242406	1070.493520	535.750398	6
4	457.229290	229.118283			439.218725	220.113001	E	***959.461492***	480.234384	942.434943	471.721110	941.450927	471.229102	5
5	**896.454616**	448.730946	879.428067	440.217672	878.444051	439.725664	Q	***830.418899***	415.713088	813.392350	407.199813	812.408334	406.707805	4
6	1025.497209	513.252243	1008.470660	504.738968	1007.486644	504.246960	E	***391.193573***	196.100425	374.167024	187.587150	373.183008	187.095142	3
7	1112.529237	556.768257	1095.502688	548.254982	1094.518672	547.762974	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
8							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.3	1285.633621	-0.008393	VVEEQESR

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

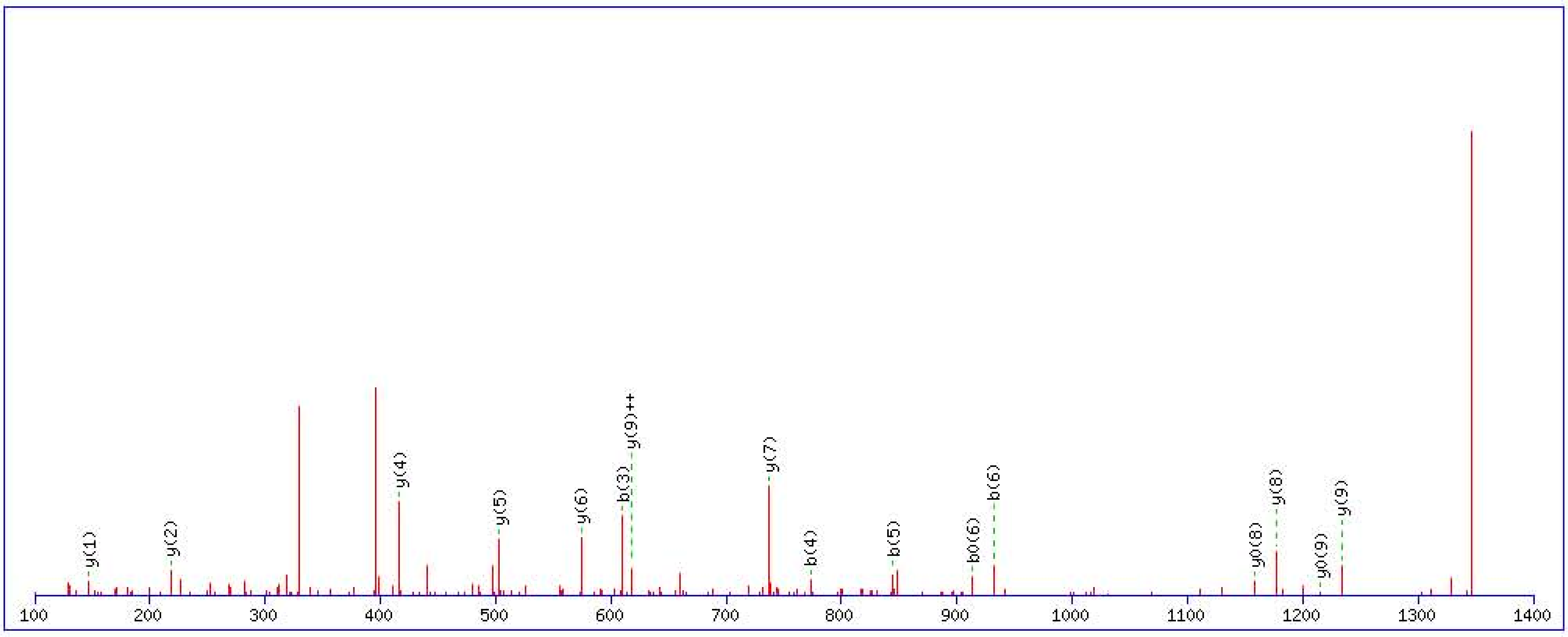
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGQYASPTAK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

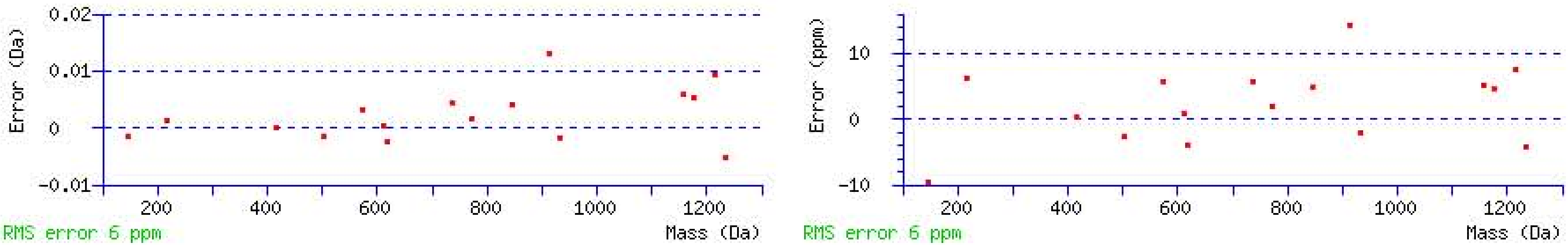
Match to Query 36303: 1345.702868 from(673.858710,2+) rtinseconds(1569) index(60066)
Title: Locus:1.1.1.2544.17 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

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



```
Monoisotopic mass of neutral peptide Mr(calc): 1345.706390
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 57  Expect: 5.9e-005
Matches : 16/90 fragment ions using 26 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							10
2	171.112804	86.060040					G	***1233.629622***	617.318449	1216.603073	608.805175	1215.619057	608.313167	9
3	**610.338130**	305.672703	593.311581	297.159429			Q	***1176.608158***	588.807717	1159.581609	580.294443	1158.597593	579.802435	8
4	**773.401459**	387.204368	756.374910	378.691093			Y	***737.382832***	369.195054	720.356283	360.681780	719.372267	360.189772	7
5	**844.438573**	422.722925	827.412024	414.209650			A	***574.319503***	287.663389	557.292954	279.150115	556.308938	278.658107	6
6	**931.470601**	466.238939	914.444052	457.725664	913.460036	457.233656	S	***503.282389***	252.144832	486.255840	243.631558	485.271824	243.139550	5
7	1028.523365	514.765321	1011.496816	506.252046	1010.512800	505.760038	P	***416.250361***	208.628818	399.223812	200.115544	398.239796	199.623536	4
8	1129.571044	565.289160	1112.544495	556.775886	1111.560479	556.283878	T	319.197597	160.102436	302.171048	151.589162	301.187032	151.097154	3
9	1200.608158	600.807717	1183.581609	592.294443	1182.597593	591.802435	A	***218.149918***	109.578597	201.123369	101.065322			2
10							K	***147.112804***	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.9	1345.706390	-0.003522	LGQYASPTAK
25.0	1345.706390	-0.003522	LGQYDQALK
10.6	1345.692474	0.010394	VASCRYPALGPR
9.3	1345.706406	-0.003538	QGLYTPQTK
3.7	1345.708862	-0.005994	LTESEEELLRK
3.4	1345.713608	-0.010740	NGMLLTGGGKDRK
2.3	1345.720993	-0.018125	QVGMICERLLK
1.8	1345.683746	0.019122	QDASTLISDLQR
1.2	1345.717636	-0.014768	QMPQPTFTLRK
0.5	1345.720108	-0.017240	KQEEEVSTLRK

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

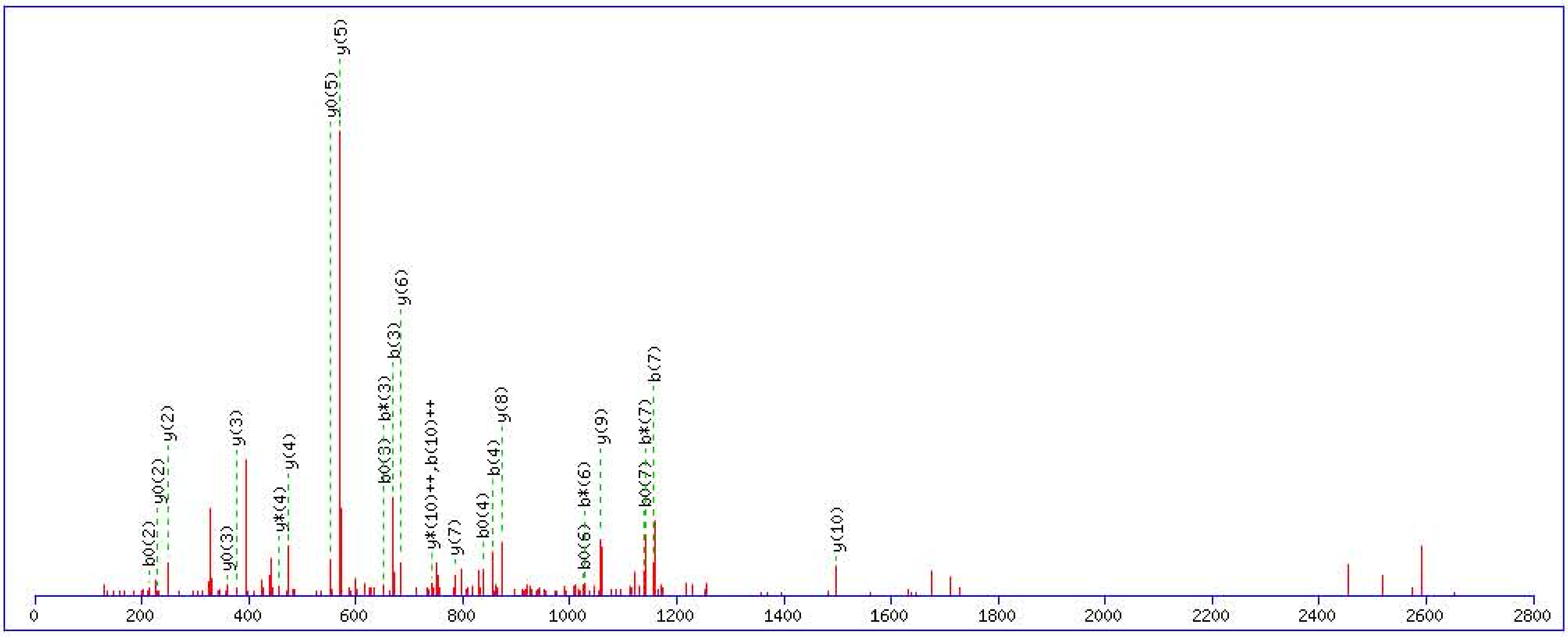
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TEQWSTLPPETK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

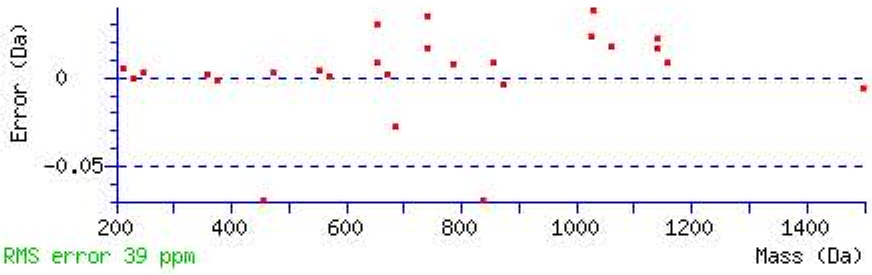
Match to Query 50183: 1726.869408 from(864.441980,2+) rtinseconds(1997) index(63074)
Title: Locus:1.1.1.2692.14 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

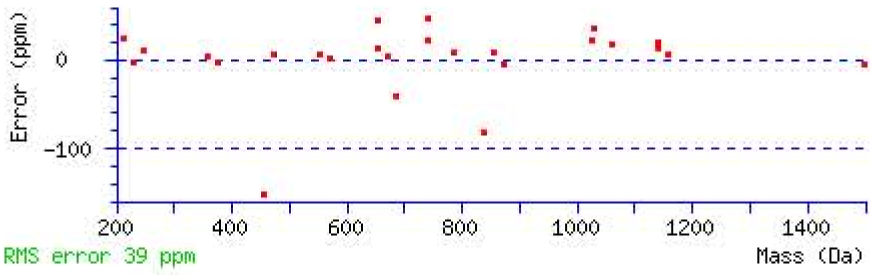
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1726.860001
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.013
Matches : 26/126 fragment ions using 82 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							12
2	231.097548	116.052412			213.086983	107.047130	E	1626.819607	813.913442	1609.793058	805.400167	1608.809042	804.908159	11
3	**670.322874**	335.665075	653.296325	327.151801	652.312309	326.659793	Q	***1497.777014***	749.392145	1480.750465	740.878871	1479.766449	740.386863	10
4	**856.402187**	428.704732	839.375638	420.191457	838.391622	419.699449	W	***1058.551688***	529.779482	1041.525139	521.266208	1040.541123	520.774200	9
5	943.434215	472.220746	926.407666	463.707471	925.423650	463.215463	S	***872.472375***	436.739826	855.445826	428.226551	854.461810	427.734543	8
6	1044.481894	522.744585	1027.455345	514.231311	1026.471329	513.739303	T	***785.440347***	393.223812	768.413798	384.710537	767.429782	384.218529	7
7	**1157.565958**	579.286617	1140.539409	570.773343	1139.555393	570.281334	L	***684.392668***	342.699972	667.366119	334.186698	666.382103	333.694690	6
8	1254.618722	627.812999	1237.592173	619.299725	1236.608157	618.807716	P	***571.308604***	286.157940	554.282055	277.644666	553.298039	277.152658	5
9	1351.671486	676.339381	1334.644937	667.826107	1333.660921	667.334098	P	***474.255840***	237.631558	457.229291	229.118284	456.245275	228.626276	4
10	1480.714079	740.860678	1463.687530	732.347403	1462.703514	731.855395	E	***377.203076***	189.105176	360.176527	180.591902	359.192511	180.099894	3
11	1581.761758	791.384517	1564.735209	782.871243	1563.751193	782.379235	T	***248.160483***	124.583879	231.133934	116.070605	230.149918	115.578597	2
12							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.1	1726.860001	0.009407	TEQWSTLPPETK
7.4	1726.849960	0.019448	TERFGQGGAGPVGGQGPR
3.8	1726.867188	0.002221	KDHAEMQAVIDAKQK
0.3	1726.871216	-0.001808	NLNTKLQMYFQSPK

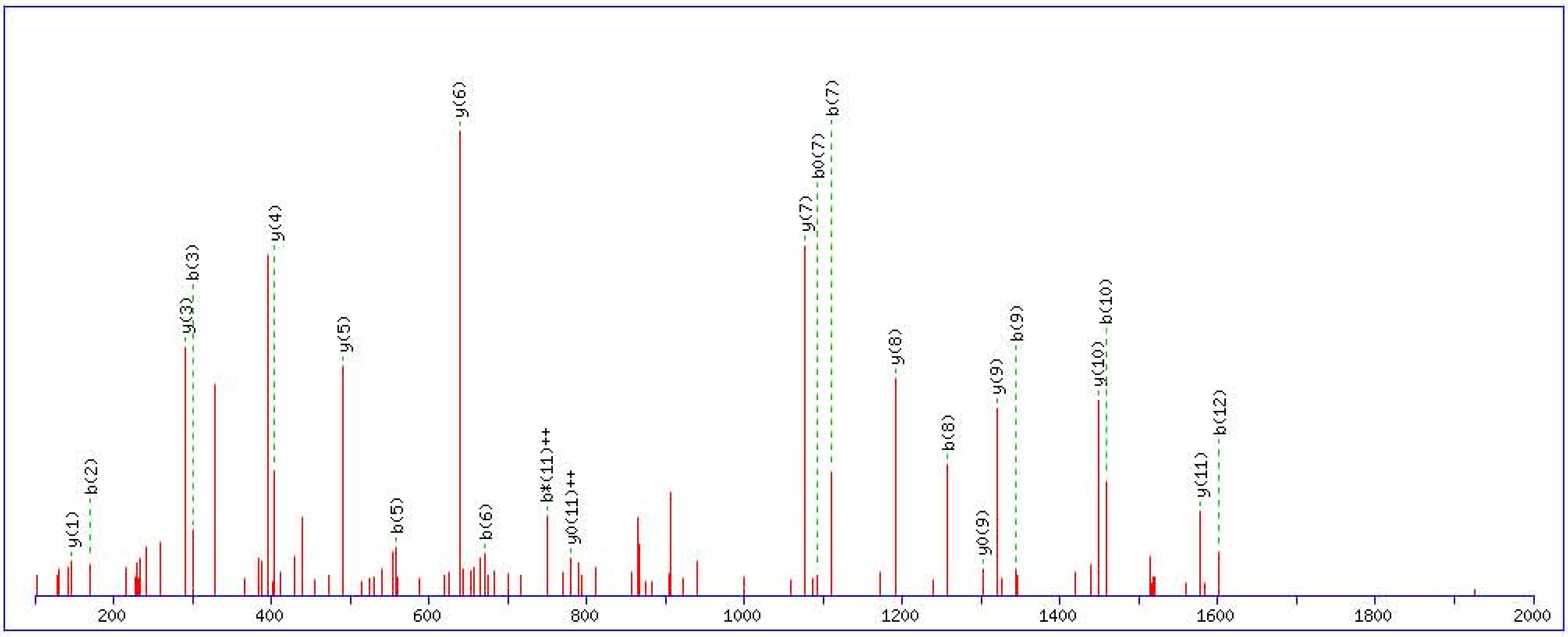
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GLEEELQFSLGSK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

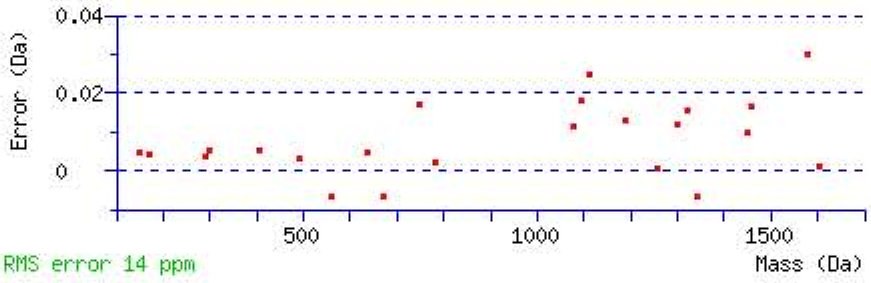
Match to Query 50803: 1746.897668 from(874.456110,2+) rtinseconds(2522) index(66377)
Title: Locus:1.1.1.2875.8 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

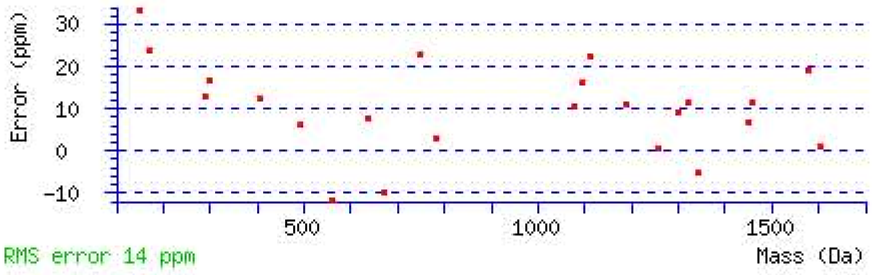
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1746.886200
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 88  Expect: 2.7e-008
Matches : 23/126 fragment ions using 30 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							13
2	**171.112804**	86.060040					L	1690.872035	845.939656	1673.845486	837.426381	1672.861470	836.934373	12
3	**300.155397**	150.581336			282.144832	141.576054	E	***1577.787971***	789.397624	1560.761422	780.884349	1559.777406	780.392341	11
4	429.197990	215.102633			411.187425	206.097351	E	***1448.745378***	724.876327	1431.718829	716.363053	1430.734813	715.871045	10
5	**558.240583**	279.623930			540.230018	270.618647	E	***1319.702785***	660.355031	1302.676236	651.841756	1301.692220	651.349748	9
6	**671.324647**	336.165962			653.314082	327.160679	L	***1190.660192***	595.833734	1173.633643	587.320460	1172.649627	586.828452	8
7	**1110.549973**	555.778624	1093.523424	547.265350	1092.539408	546.773342	Q	***1077.576128***	539.291702	1060.549579	530.778428	1059.565563	530.286419	7
8	**1257.618387**	629.312832	1240.591838	620.799557	1239.607822	620.307549	F	***638.350802***	319.679039	621.324253	311.165765	620.340237	310.673757	6
9	**1344.650415**	672.828846	1327.623866	664.315571	1326.639850	663.823563	S	***491.282388***	246.144832	474.255839	237.631557	473.271823	237.139549	5
10	**1457.734479**	729.370878	1440.707930	720.857603	1439.723914	720.365595	L	***404.250360***	202.628818	387.223811	194.115543	386.239795	193.623535	4
11	1514.755943	757.881609	1497.729394	749.368335	1496.745378	748.876327	G	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.081504	3
12	**1601.787971**	801.397624	1584.761422	792.884349	1583.777406	792.392341	S	234.144832	117.576054	217.118283	109.062780	216.134267	108.570772	2
13							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
88.1	1746.886200	0.011468	GLEEELQFSLGSK
7.0	1746.887558	0.010110	AVQSKAFCAGGLAPGWK
2.8	1746.886185	0.011483	DLIDTYLLHMEKEK
1.6	1746.918533	-0.020865	AKLQMTEAALALSEQK
0.8	1746.876999	0.020669	TWRAQRMSQTR

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

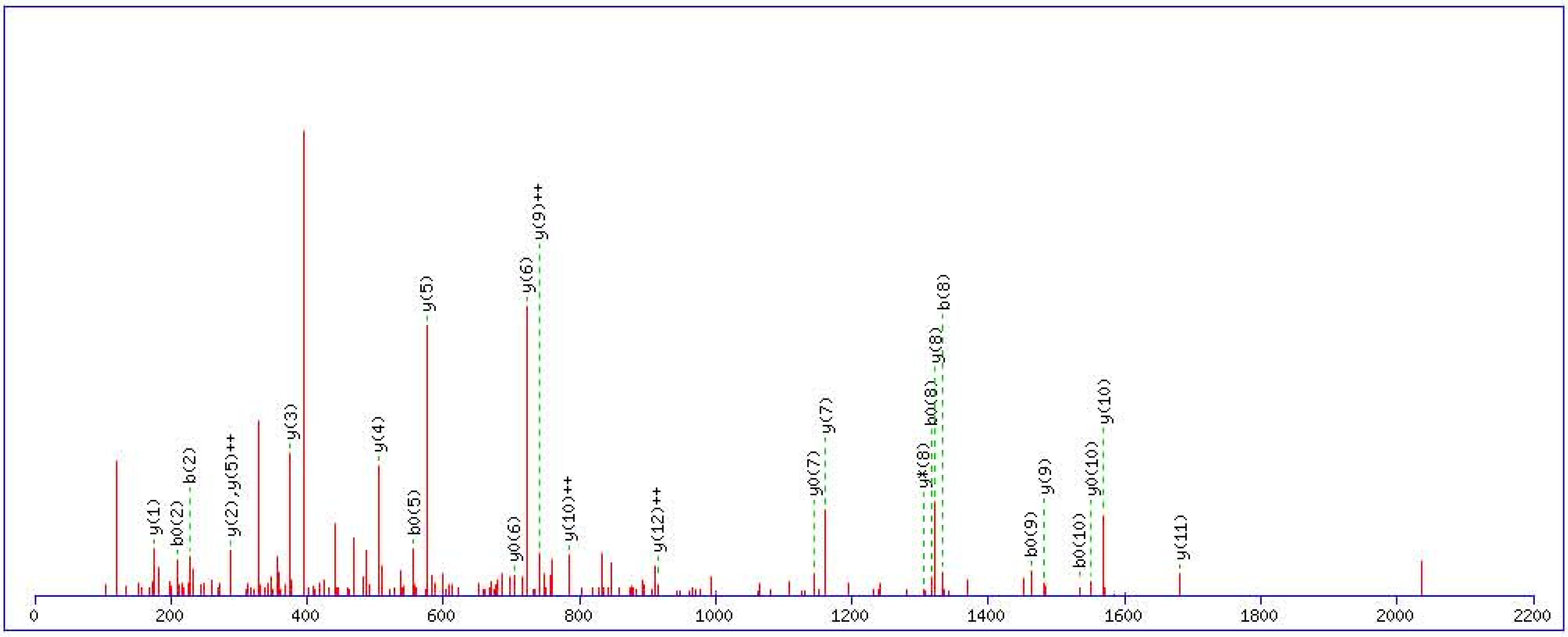
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EPFLSCCQFAESLR**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

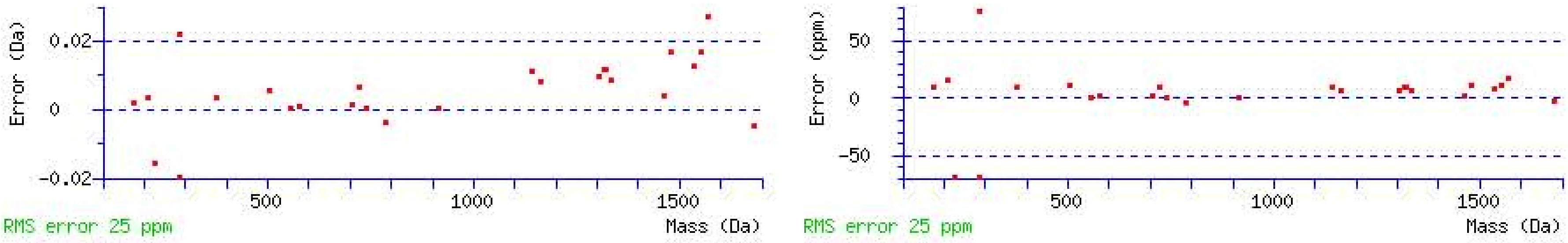
Match to Query 58583: 2053.953402 from(685.658410,3+) rtinseconds(2464) index(65980)
Title: Locus:1.1.1.2855.5 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2053.942368
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 64  Expect: 5.5e-006
Matches : 26/138 fragment ions using 47 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							14
2	**227.102633**	114.054954			209.092068	105.049672	P	1925.907059	963.457168	1908.880510	954.943893	1907.896494	954.451885	13
3	374.171047	187.589161			356.160482	178.583879	F	1828.854295	914.930786	1811.827746	906.417511	1810.843730	905.925503	12
4	487.255111	244.131193			469.244546	235.125911	L	***1681.785881***	841.396579	1664.759332	832.883304	1663.775316	832.391296	11
5	574.287139	287.647208			556.276574	278.641925	S	***1568.701817***	784.854547	1551.675268	776.341272	1550.691252	775.849264	10
6	734.317788	367.662532			716.307223	358.657250	C	***1481.669789***	741.338533	1464.643240	732.825258	1463.659224	732.333250	9
7	894.348437	447.677857			876.337872	438.672574	C	***1321.639140***	661.323208	1304.612591	652.809934	1303.628575	652.317926	8
8	**1333.573763**	667.290520	1316.547214	658.777245	1315.563198	658.285237	Q	***1161.608491***	581.307884	1144.581942	572.794609	1143.597926	572.302601	7
9	1480.642177	740.824727	1463.615628	732.311452	1462.631612	731.819444	F	***722.383165***	361.695221	705.356616	353.181946	704.372600	352.689938	6
10	1551.679291	776.343284	1534.652742	767.830009	1533.668726	767.338001	A	***575.314751***	288.161014	558.288202	279.647739	557.304186	279.155731	5
11	1680.721884	840.864580	1663.695335	832.351306	1662.711319	831.859298	E	***504.277637***	252.642457	487.251088	244.129182	486.267072	243.637174	4
12	1767.753912	884.380594	1750.727363	875.867320	1749.743347	875.375312	S	***375.235044***	188.121160	358.208495	179.607885	357.224479	179.115877	3
13	1880.837976	940.922626	1863.811427	932.409352	1862.827411	931.917344	L	***288.203016***	144.605146	271.176467	136.091871			2
14							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.1	2053.942368	0.011034	EPFLSCCQFAESLR

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

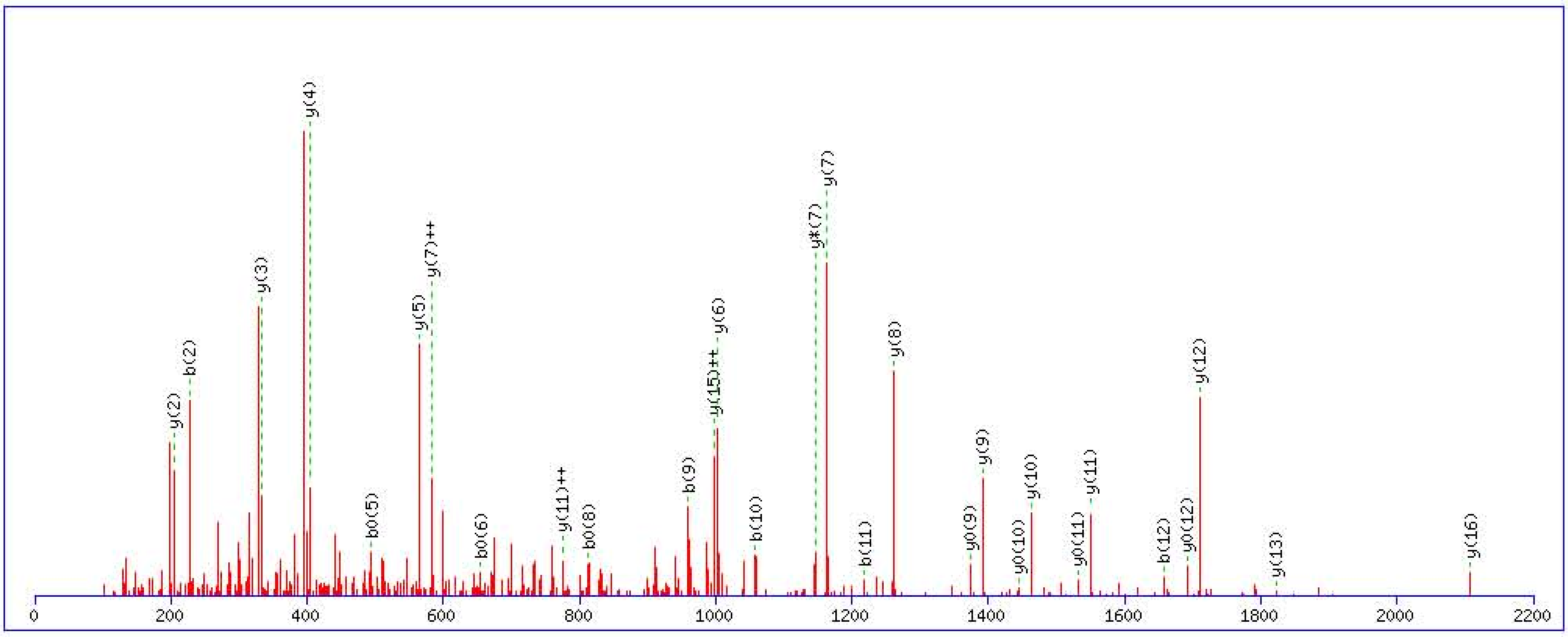
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLATLCSAEVCQCAEGK**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

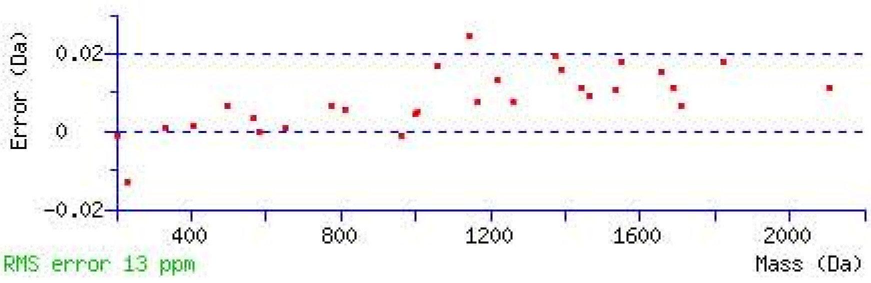
Match to Query 62090: 2220.043392 from(741.021740,3+) rtinseconds(2099) index(63713)
Title: Locus:1.1.1.2728.8 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

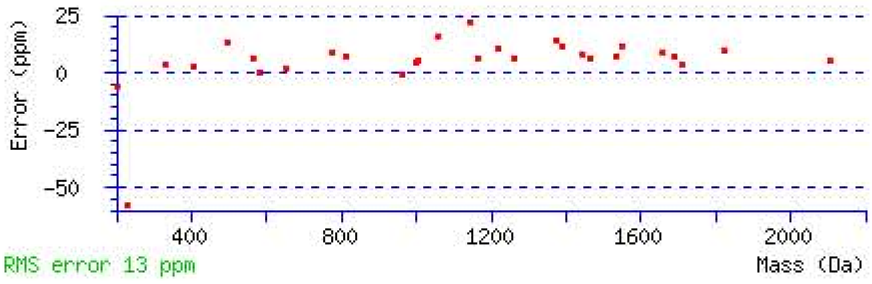
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [0] to [2200] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2220.041092
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12    : Biotin:Thermo-21345 (Q)
Ions Score: 74  Expect: 2.2e-007
Matches : 29/160 fragment ions using 56 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							17
2	**227.175404**	114.091340					L	***2107.964318***	1054.485797	2090.937769	1045.972522	2089.953753	1045.480514	16
3	298.212518	149.609897					A	1994.880254	997.943765	1977.853705	989.430491	1976.869689	988.938483	15
4	399.260197	200.133737			381.249632	191.128454	T	1923.843140	962.425208	1906.816591	953.911934	1905.832575	953.419926	14
5	512.344261	256.675769			494.333696	247.670486	L	***1822.795461***	911.901369	1805.768912	903.388094	1804.784896	902.896086	13
6	672.374910	336.691093			654.364345	327.685811	C	***1709.711397***	855.359337	1692.684848	846.846062	1691.700832	846.354054	12
7	759.406938	380.207107			741.396373	371.201825	S	***1549.680748***	775.344012	1532.654199	766.830738	1531.670183	766.338730	11
8	830.444052	415.725664			812.433487	406.720382	A	***1462.648720***	731.827998	1445.622171	723.314724	1444.638155	722.822716	10
9	**959.486645**	480.246961			941.476080	471.241678	E	***1391.611606***	696.309441	1374.585057	687.796167	1373.601041	687.304159	9
10	**1058.555059**	529.781168			1040.544494	520.775885	V	***1262.569013***	631.788145	1245.542464	623.274870	1244.558448	622.782862	8
11	**1218.585708**	609.796492			1200.575143	600.791210	C	***1163.500599***	582.253938	1146.474050	573.740663	1145.490034	573.248655	7
12	**1657.811034**	829.409155	1640.784485	820.895881	1639.800469	820.403873	Q	***1003.469950***	502.238613	986.443401	493.725339	985.459385	493.233331	6
13	1817.841683	909.424480	1800.815134	900.911205	1799.831118	900.419197	C	***564.244624***	282.625950	547.218075	274.112676	546.234059	273.620668	5
14	1888.878797	944.943037	1871.852248	936.429762	1870.868232	935.937754	A	***404.213975***	202.610626	387.187426	194.097351	386.203410	193.605343	4
15	2017.921390	1009.464333	2000.894841	1000.951059	1999.910825	1000.459051	E	***333.176861***	167.092069	316.150312	158.578794	315.166296	158.086786	3
16	2074.942854	1037.975065	2057.916305	1029.461790	2056.932289	1028.969782	G	***204.134268***	102.570772	187.107719	94.057497			2
17							K	147.112804	74.060040	130.086255	65.546765			1



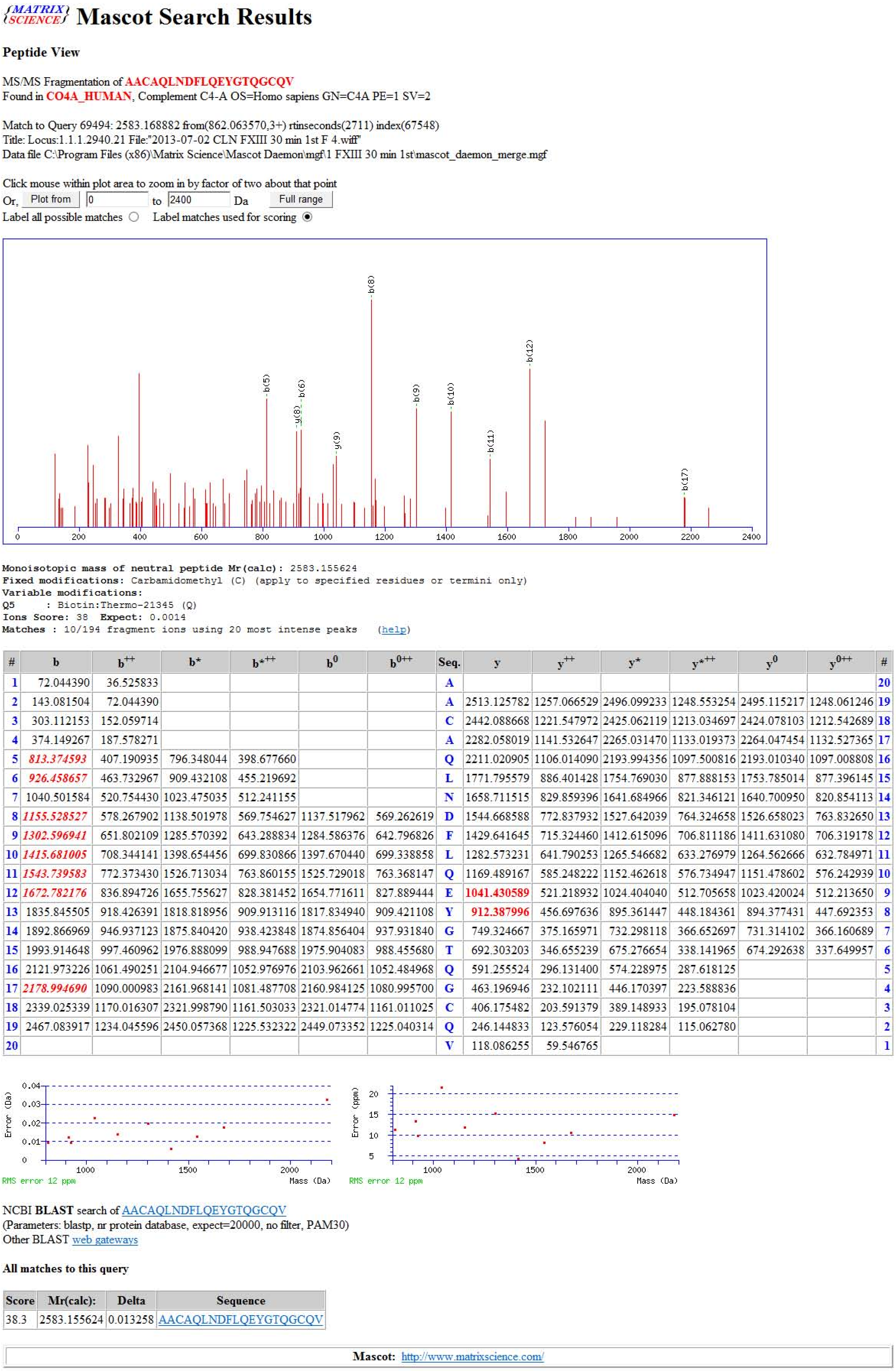


NCBI **BLAST** search of LLATLCSAEVCQCAEGK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
74.4	2220.041092	0.002300	LLATLCSAEVCQCAEGK
3.4	2220.048080	-0.004688	EPQEGAELPEATGTTSHR

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



Mascot Search Results

Peptide View

MS/MS Fragmentation of **AACAQLNDFLQEYGTQGCQV**
Found in **CO4A_HUMAN**, Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2

Match to Query 69494: 2583.168882 from(862.063570,3+) rtinseconds(2711) index(67548)
Title: Locus:1.1.1.2940.21 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 2583.155624
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 38  Expect: 0.0014
Matches : 10/194 fragment ions using 20 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							20
2	143.081504	72.044390					A	2513.125782	1257.066529	2496.099233	1248.553254	2495.115217	1248.061246	19
3	303.112153	152.059714					C	2442.088668	1221.547972	2425.062119	1213.034697	2424.078103	1212.542689	18
4	374.149267	187.578271					A	2282.058019	1141.532647	2265.031470	1133.019373	2264.047454	1132.527365	17
5	*813.374593*	407.190935	796.348044	398.677660			Q	2211.020905	1106.014090	2193.994356	1097.500816	2193.010340	1097.008808	16
6	*926.458657*	463.732967	909.432108	455.219692			L	1771.795579	886.401428	1754.769030	877.888153	1753.785014	877.396145	15
7	1040.501584	520.754430	1023.475035	512.241155			N	1658.711515	829.859396	1641.684966	821.346121	1640.700950	820.854113	14
8	*1155.528527*	578.267902	1138.501978	569.754627	1137.517962	569.262619	D	1544.668588	772.837932	1527.642039	764.324658	1526.658023	763.832650	13
9	*1302.596941*	651.802109	1285.570392	643.288834	1284.586376	642.796826	F	1429.641645	715.324460	1412.615096	706.811186	1411.631080	706.319178	12
10	*1415.681005*	708.344141	1398.654456	699.830866	1397.670440	699.338858	L	1282.573231	641.790253	1265.546682	633.276979	1264.562666	632.784971	11
11	*1543.739583*	772.373430	1526.713034	763.860155	1525.729018	763.368147	Q	1169.489167	585.248222	1152.462618	576.734947	1151.478602	576.242939	10
12	*1672.782176*	836.894726	1655.755627	828.381452	1654.771611	827.889444	E	1041.430589	521.218932	1024.404040	512.705658	1023.420024	512.213650	9
13	1835.845505	918.426391	1818.818956	909.913116	1817.834940	909.421108	Y	912.387996	456.697636	895.361447	448.184361	894.377431	447.692353	8
14	1892.866969	946.937123	1875.840420	938.423848	1874.856404	937.931840	G	749.324667	375.165971	732.298118	366.652697	731.314102	366.160689	7
15	1993.914648	997.460962	1976.888099	988.947688	1975.904083	988.455680	T	692.303203	346.655239	675.276654	338.141965	674.292638	337.649957	6
16	2121.973226	1061.490251	2104.946677	1052.976976	2103.962661	1052.484968	Q	591.255524	296.131400	574.228975	287.618125			5
17	*2178.994690*	1090.000983	2161.968141	1081.487708	2160.984125	1080.995700	G	463.196946	232.102111	446.170397	223.588836			4
18	2339.025339	1170.016307	2321.998790	1161.503033	2321.014774	1161.011025	C	406.175482	203.591379	389.148933	195.078104			3
19	2467.083917	1234.045596	2450.057368	1225.532322	2449.073352	1225.040314	Q	246.144833	123.576054	229.118284	115.062780			2
20							V	118.086255	59.546765					1

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.3	2583.155624	0.013258	AACAQLNDFLQEYGTQGCQV

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

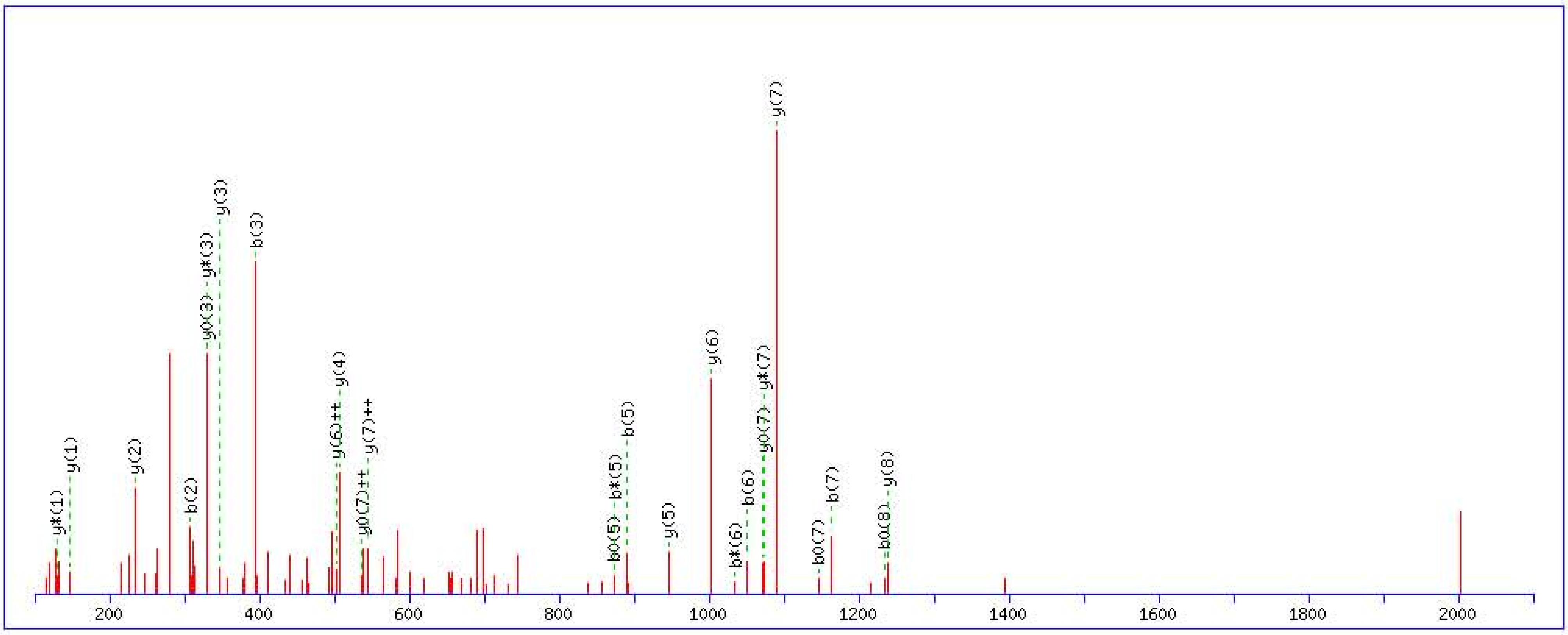
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **CFSGQCISK**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

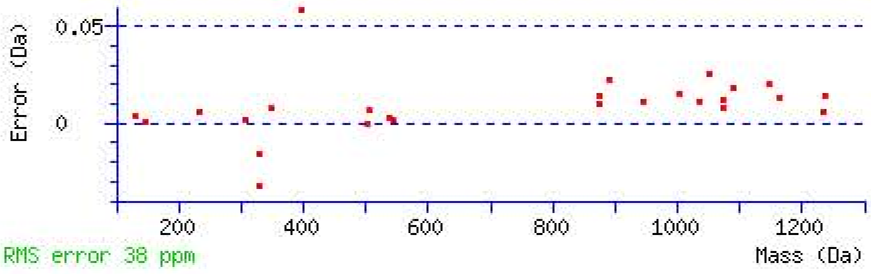
Match to Query 38827: 1396.642768 from(699.328660,2+) rtinseconds(1616) index(4754)
Title: Locus:1.1.1.2283.15 File:"2013-07-02 CLN FXIII 30 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

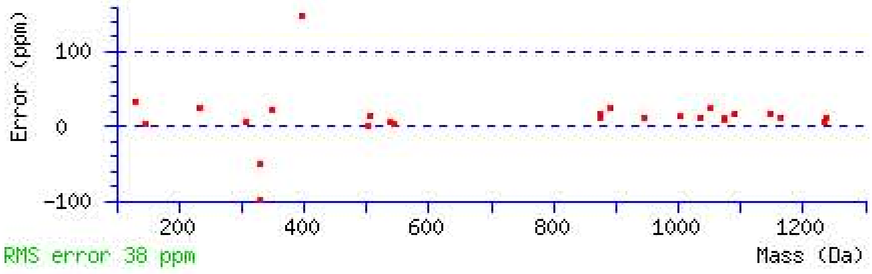
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1396.630157
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 40  Expect: 0.00025
Matches : 26/82 fragment ions using 58 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	161.037925	81.022600					C							9
2	**308.106339**	154.556807					F	***1237.606777***	619.307027	1220.580228	610.793752	1219.596212	610.301744	8
3	**395.138367**	198.072821			377.127802	189.067539	S	***1090.538363***	545.772819	1073.511814	537.259545	1072.527798	536.767537	7
4	452.159831	226.583553			434.149266	217.578271	G	***1003.506335***	502.256806	986.479786	493.743531	985.495770	493.251523	6
5	**891.385157**	446.196217	874.358608	437.682942	873.374592	437.190934	Q	***946.484871***	473.746074	929.458322	465.232799	928.474306	464.740791	5
6	**1051.415806**	526.211541	1034.389257	517.698267	1033.405241	517.206258	C	***507.259545***	254.133410	490.232996	245.620136	489.248980	245.128128	4
7	**1164.499870**	582.753573	1147.473321	574.240298	1146.489305	573.748290	I	***347.228896***	174.118086	330.202347	165.604811	329.218331	165.112803	3
8	1251.531898	626.269587	1234.505349	617.756313	1233.521333	617.264304	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
9							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.7	1396.630157	0.012611	CFSGQCISK
1.2	1396.629272	0.013496	QLSQAEATDFCK

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

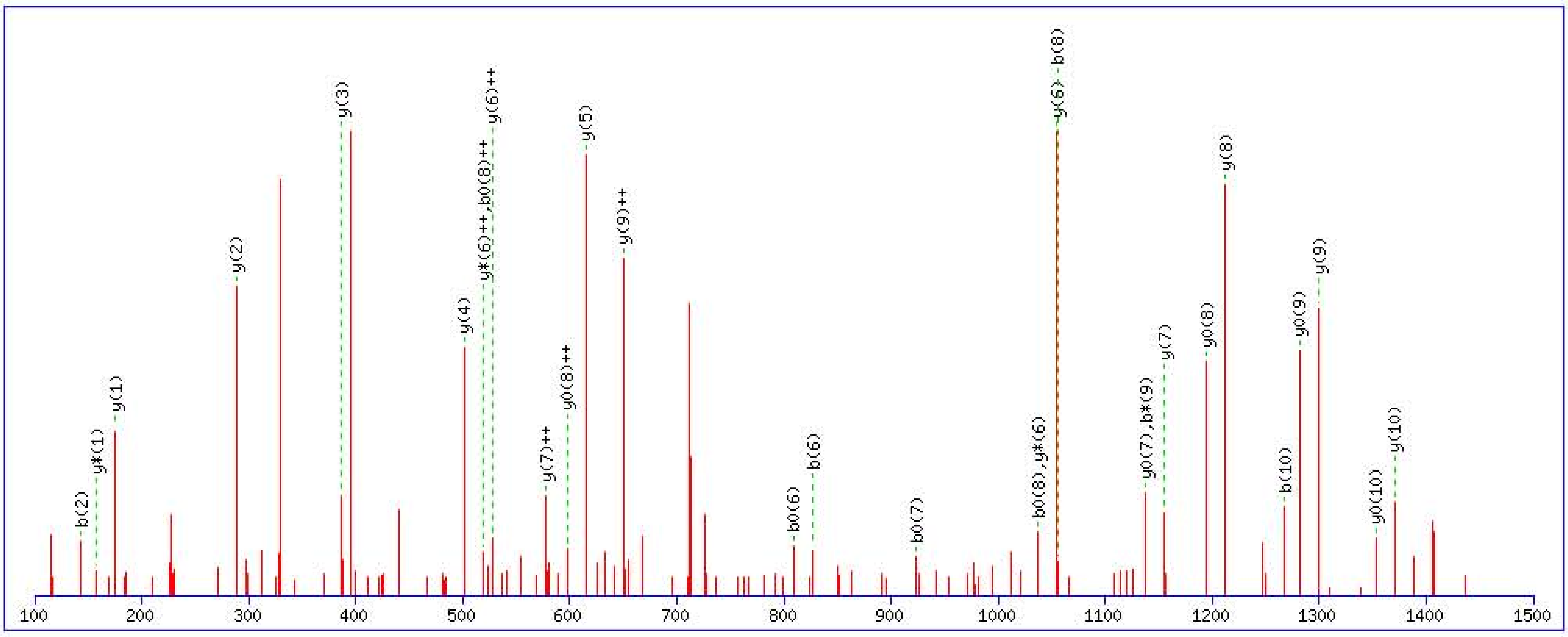
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AASGTQNNVLR**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

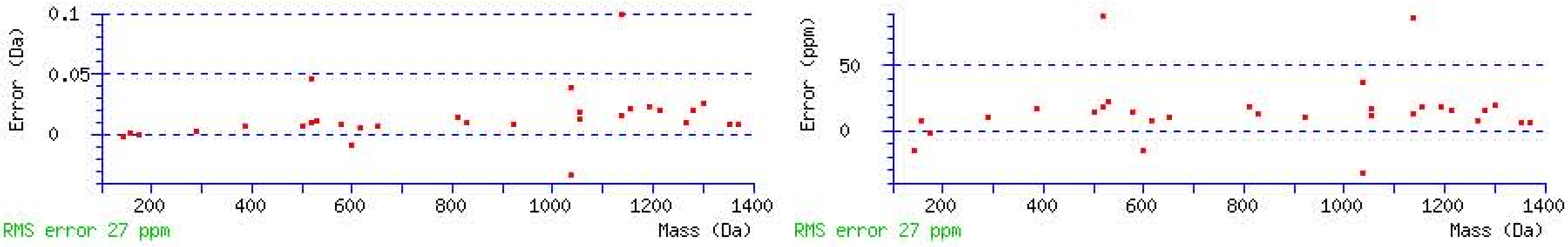
Match to Query 40834: 1440.759988 from(721.387270,2+) rtinseconds(1522) index(4165)
Title: Locus:1.1.1.2250.22 File:"2013-07-02 CLN FXIII 30 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1440.750717
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 68  Expect: 2.2e-006
Matches : 30/94 fragment ions using 53 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							11
2	**143.081504**	72.044390					A	***1370.720895***	685.864086	1353.694346	677.350811	1352.710330	676.858803	10
3	230.113532	115.560404			212.102967	106.555121	S	***1299.683781***	650.345529	1282.657232	641.832254	1281.673216	641.340246	9
4	287.134996	144.071136			269.124431	135.065854	G	***1212.651753***	606.829515	1195.625204	598.316240	1194.641188	597.824232	8
5	388.182675	194.594976			370.172110	185.589693	T	***1155.630289***	578.318783	1138.603740	569.805508	1137.619724	569.313500	7
6	**827.408001**	414.207639	810.381452	405.694364	809.397436	405.202356	Q	***1054.582610***	527.794943	1037.556061	519.281669			6
7	941.450928	471.229102	924.424379	462.715828	923.440363	462.223820	N	***615.357284***	308.182280	598.330735	299.669006			5
8	**1055.493855**	528.250566	1038.467306	519.737291	1037.483290	519.245283	N	***501.314357***	251.160816	484.287808	242.647542			4
9	1154.562269	577.784773	1137.535720	569.271498	1136.551704	568.779490	V	***387.271430***	194.139353	370.244881	185.626078			3
10	**1267.646333**	634.326805	1250.619784	625.813530	1249.635768	625.321522	L	***288.203016***	144.605146	271.176467	136.091871			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
67.8	1440.750717	0.009271	AASGTQNNVLR
7.0	1440.739487	0.020501	AAVTGQDEAIR
4.2	1440.750717	0.009271	TQMQHGLISIAAR
2.9	1440.754745	0.005243	WEATQQVLR
2.2	1440.754745	0.005243	WEATQQVLR
1.3	1440.750732	0.009256	DGQLVTEGRR

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

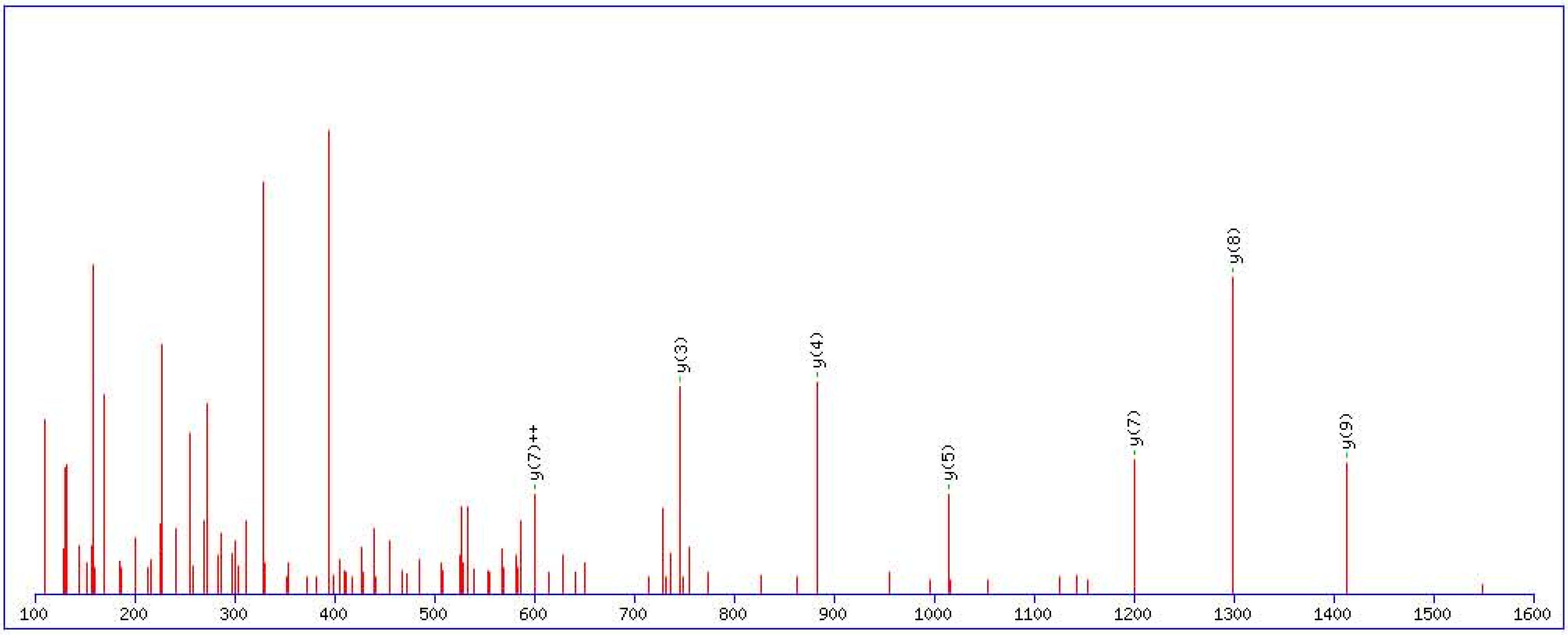
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WLVGEMHCQK**
Found in **CO7_HUMAN**, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

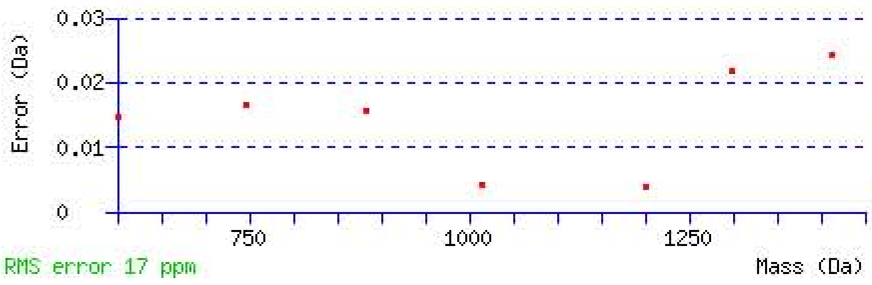
Match to Query 46010: 1597.767912 from(533.596580,3+) rtinseconds(1851) index(6293)
Title: Locus:1.1.1.2365.12 File:"2013-07-02 CLN FXIII 30 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

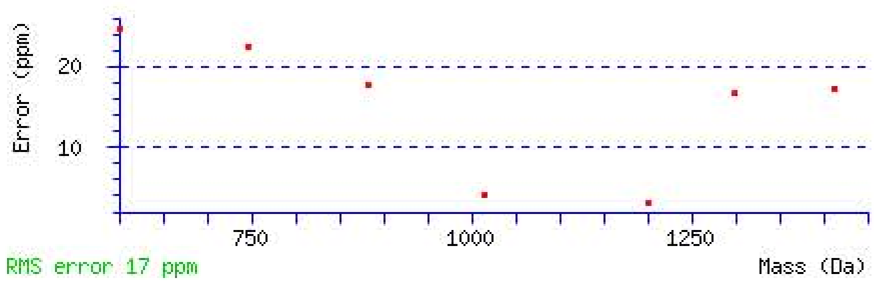
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1597.756744
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.0023
Matches : 7/74 fragment ions using 14 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	187.086589	94.046932					W							10
2	300.170653	150.588965					L	*1412.684711*	706.845994	1395.658162	698.332719	1394.674146	697.840711	9
3	399.239067	200.123172					V	*1299.600647*	650.303962	1282.574098	641.790687	1281.590082	641.298679	8
4	456.260531	228.633904					G	*1200.532233*	600.769755	1183.505684	592.256480	1182.521668	591.764472	7
5	585.303124	293.155200			567.292559	284.149918	E	1143.510769	572.259023	1126.484220	563.745748	1125.500204	563.253740	6
6	716.343609	358.675443			698.333044	349.670160	M	*1014.468176*	507.737726	997.441627	499.224452			5
7	853.402521	427.204899			835.391956	418.199616	H	*883.427691*	442.217484	866.401142	433.704209			4
8	1013.433170	507.220223			995.422605	498.214941	C	*746.368779*	373.688028	729.342230	365.174753			3
9	1452.658496	726.832886	1435.631947	718.319612	1434.647931	717.827604	Q	586.338130	293.672703	569.311581	285.159429			2
10							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.2	1597.756744	0.011168	WLVGEMHCQK
2.0	1597.763718	0.004194	LWKDEGRWEHDK

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

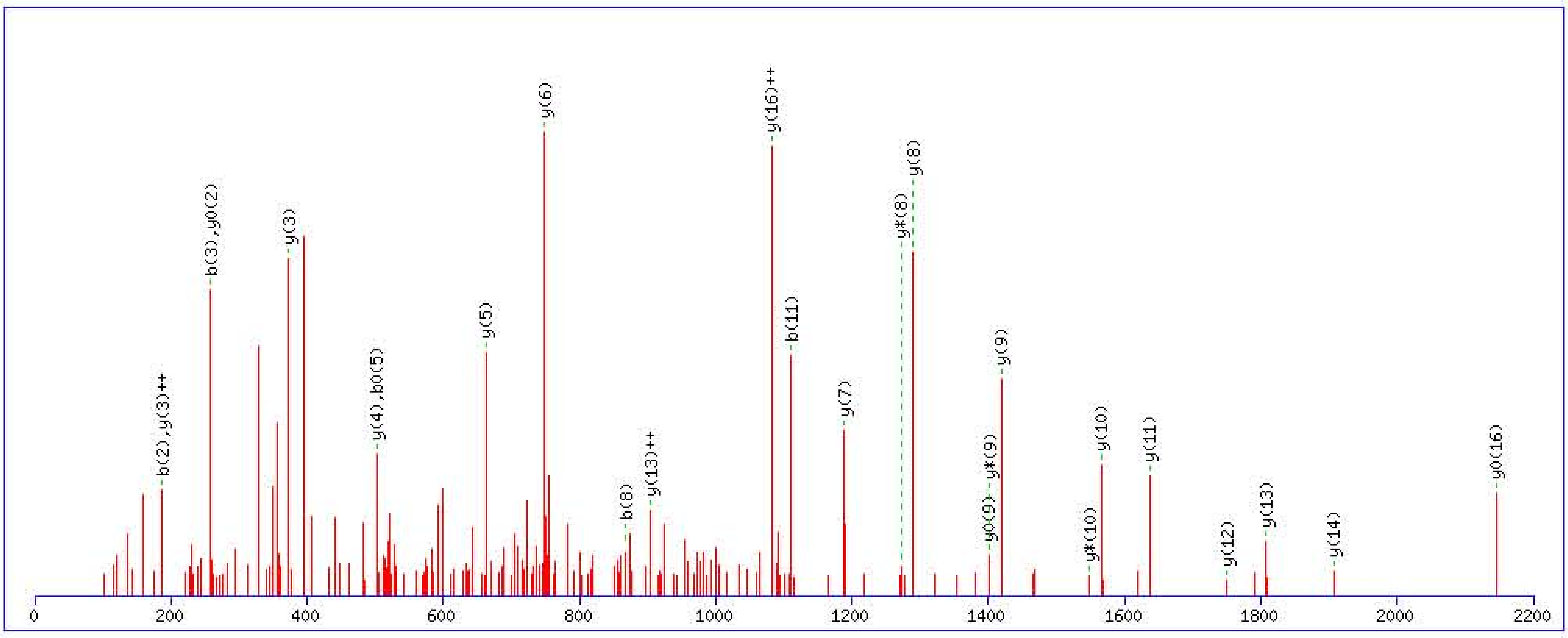
Mascot Search Results

Peptide View

MS/MS Fragmentation of SVAVYGQYGGQPCVGNAFETQSCEPTR
Found in CO7_HUMAN, Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2

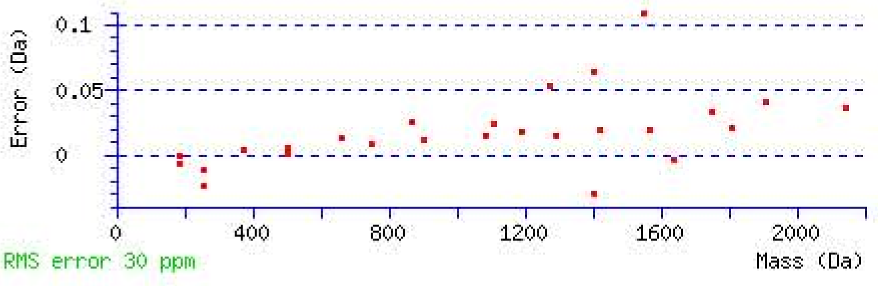
Match to Query 78005: 3272.512296 from(819.135350,4+) rtinseconds(2145) index(8258)
Title: Locus:1.1.1.2467.26 File:"2013-07-02 CLN FXIII 30 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

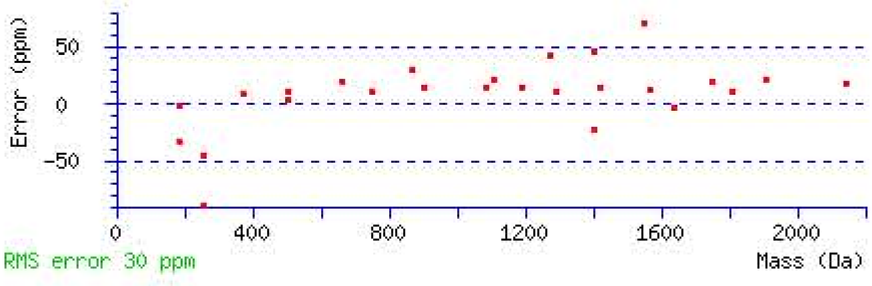
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3272.468933
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q21     : Biotin:Thermo-21345 (Q)
Ions Score: 69  Expect: 1.8e-006
Matches : 26/298 fragment ions using 39 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							27
2	**187.107718**	94.057497			169.097153	85.052214	V	3186.444157	1593.725716	3169.417608	1585.212442	3168.433592	1584.720434	26
3	**258.144832**	129.576054			240.134267	120.570772	A	3087.375743	1544.191509	3070.349194	1535.678235	3069.365178	1535.186227	25
4	357.213246	179.110261			339.202681	170.104979	V	3016.338629	1508.672952	2999.312080	1500.159678	2998.328064	1499.667670	24
5	520.276575	260.641926			502.266010	251.636643	Y	2917.270215	1459.138745	2900.243666	1450.625471	2899.259650	1450.133463	23
6	577.298039	289.152658			559.287474	280.147375	G	2754.206886	1377.607081	2737.180337	1369.093806	2736.196321	1368.601798	22
7	705.356617	353.181947	688.330068	344.668672	687.346052	344.176664	Q	2697.185422	1349.096349	2680.158873	1340.583074	2679.174857	1340.091066	21
8	**868.419946**	434.713611	851.393397	426.200337	850.409381	425.708329	Y	2569.126844	1285.067060	2552.100295	1276.553785	2551.116279	1276.061777	20
9	925.441410	463.224343	908.414861	454.711069	907.430845	454.219061	G	2406.063515	1203.535395	2389.036966	1195.022121	2388.052950	1194.530113	19
10	982.462874	491.735075	965.436325	483.221801	964.452309	482.729793	G	2349.042051	1175.024663	2332.015502	1166.511389	2331.031486	1166.019381	18
11	**1110.521452**	555.764364	1093.494903	547.251090	1092.510887	546.759082	Q	2292.020587	1146.513931	2274.994038	1138.000657	2274.010022	1137.508649	17
12	1207.574216	604.290746	1190.547667	595.777472	1189.563651	595.285464	P	2163.962009	1082.484642	2146.935460	1073.971368	2145.951444	1073.479360	16
13	1367.604865	684.306071	1350.578316	675.792796	1349.594300	675.300788	C	2066.909245	1033.958260	2049.882696	1025.444986	2048.898680	1024.952978	15
14	1466.673279	733.840278	1449.646730	725.327003	1448.662714	724.834995	V	***1906.878596***	953.942936	1889.852047	945.429662	1888.868031	944.937654	14
15	1523.694743	762.351010	1506.668194	753.837735	1505.684178	753.345727	G	***1807.810182***	904.408729	1790.783633	895.895455	1789.799617	895.403446	13
16	1637.737670	819.372473	1620.711121	810.859199	1619.727105	810.367191	N	***1750.788718***	875.897997	1733.762169	867.384723	1732.778153	866.892715	12
17	1708.774784	854.891030	1691.748235	846.377756	1690.764219	845.885748	A	***1636.745791***	818.876534	1619.719242	810.363259	1618.735226	809.871251	11
18	1855.843198	928.425237	1838.816649	919.911963	1837.832633	919.419955	F	***1565.708677***	783.357977	1548.682128	774.844702	1547.698112	774.352694	10
19	1984.885791	992.946534	1967.859242	984.433259	1966.875226	983.941251	E	***1418.640263***	709.823770	1401.613714	701.310495	1400.629698	700.818487	9
20	2085.933470	1043.470373	2068.906921	1034.957098	2067.922905	1034.465090	T	***1289.597670***	645.302473	1272.571121	636.789199	1271.587105	636.297190	8
21	2525.158796	1263.083036	2508.132247	1254.569761	2507.148231	1254.077754	Q	***1188.549991***	594.778634	1171.523442	586.265359	1170.539426	585.773351	7
22	2612.190824	1306.599050	2595.164275	1298.085776	2594.180259	1297.593768	S	***749.324665***	375.165970	732.298116	366.652696	731.314100	366.160688	6
23	2772.221473	1386.614374	2755.194924	1378.101100	2754.210908	1377.609092	C	***662.292637***	331.649956	645.266088	323.136682	644.282072	322.644674	5
24	2901.264066	1451.135671	2884.237517	1442.622396	2883.253501	1442.130389	E	***502.261988***	251.634632	485.235439	243.121357	484.251423	242.629349	4
25	2998.316830	1499.662053	2981.290281	1491.148778	2980.306265	1490.656771	P	***373.219395***	187.113335	356.192846	178.600061	355.208830	178.108053	3
26	3099.364509	1550.185892	3082.337960	1541.672618	3081.353944	1541.180610	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
27							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.7	3272.468933	0.043363	SVAVYGQYGGQPCVGNAFETQSCEPTR
5.5	3272.468933	0.043363	SVAVYGQYGGQPCVGNAFETQSCEPTR

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

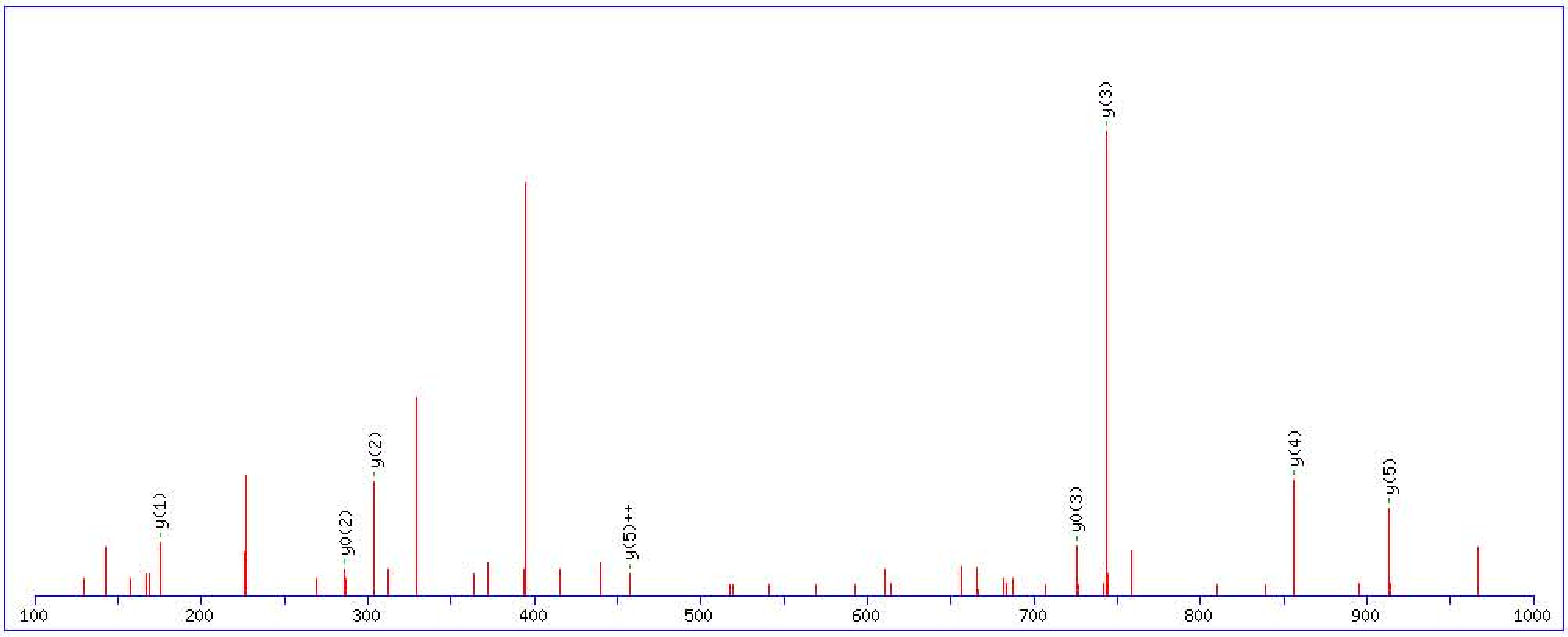
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AGIQER**
Found in **CO8A_HUMAN**, Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2

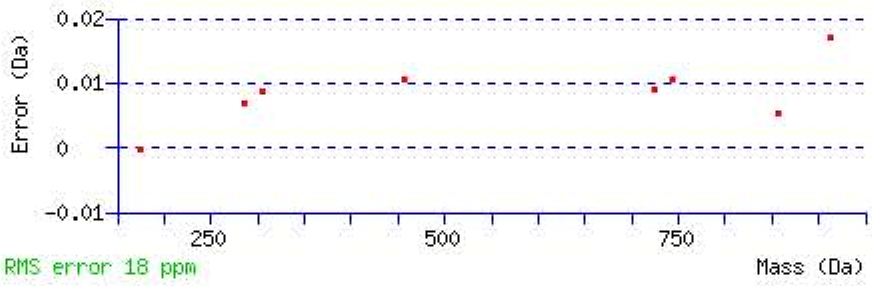
Match to Query 21529: 983.531308 from(492.772930,2+) rtinseconds(1387) index(20899)
Title: Locus:1.1.1.2335.18 File:"2013-07-02 CLN FXIII 30 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

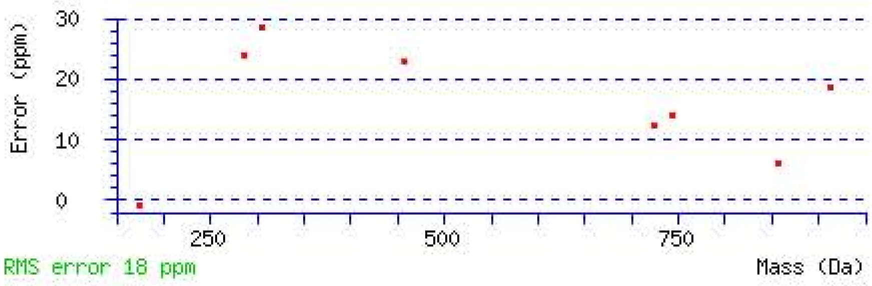
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 983.522217
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.032
Matches : 8/44 fragment ions using 17 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							6
2	129.065854	65.036565					G	***913.492399***	457.249838	896.465850	448.736563	895.481834	448.244555	5
3	242.149918	121.578597					I	***856.470935***	428.739106	839.444386	420.225831	838.460370	419.733823	4
4	681.375244	341.191260	664.348695	332.677986			Q	***743.386871***	372.197074	726.360322	363.683799	725.376306	363.191791	3
5	810.417837	405.712557	793.391288	397.199282	792.407272	396.707274	E	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	2
6							R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.9	983.522217	0.009091	AGIQER
25.2	983.522217	0.009091	AGLEQR
16.9	983.522217	0.009091	QIQER
16.9	983.522217	0.009091	QLQER
14.6	983.522217	0.009091	QLEQR
8.0	983.522217	0.009091	IQQER
8.0	983.522217	0.009091	LQQER
7.4	983.544678	-0.013370	LKSHGMRR
6.9	983.522232	0.009076	QLCLHVSK
6.7	983.522202	0.009106	KLMENPPR

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

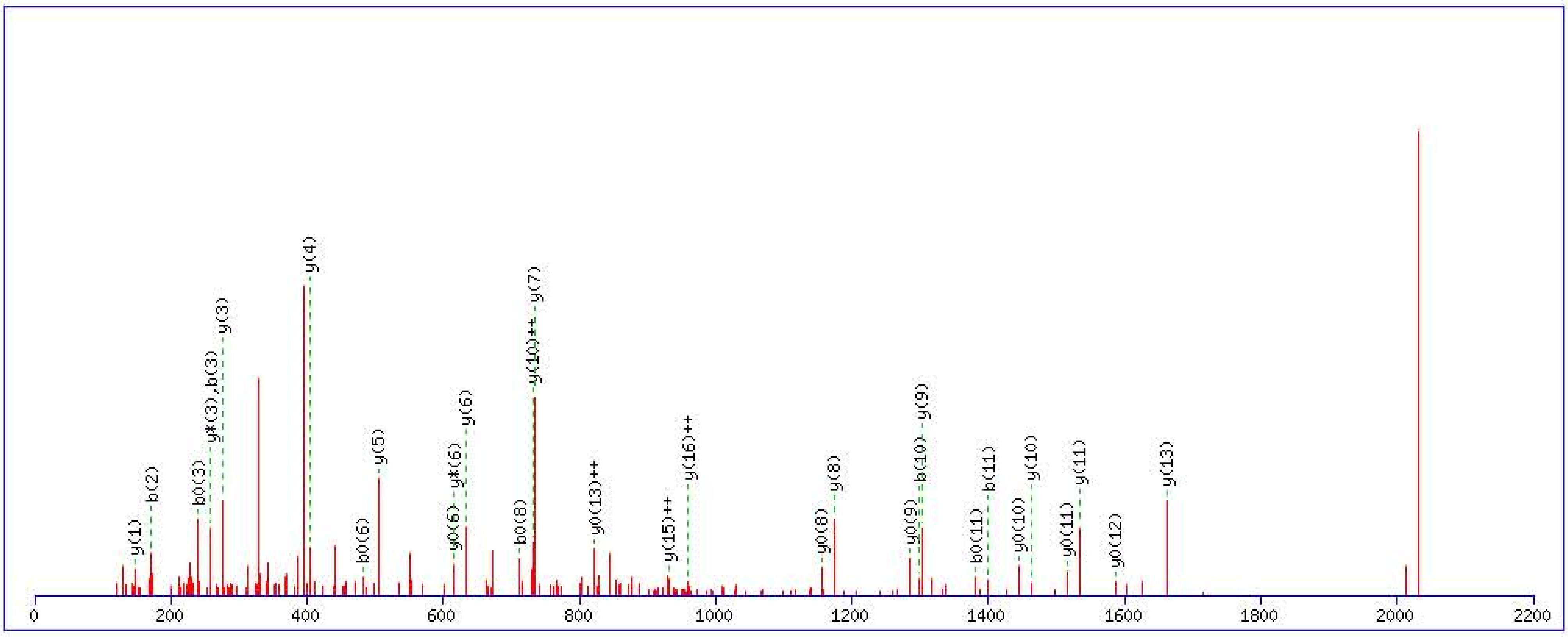
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGSLGAACEQTQTEGAK**
Found in **CO8A_HUMAN**, Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2

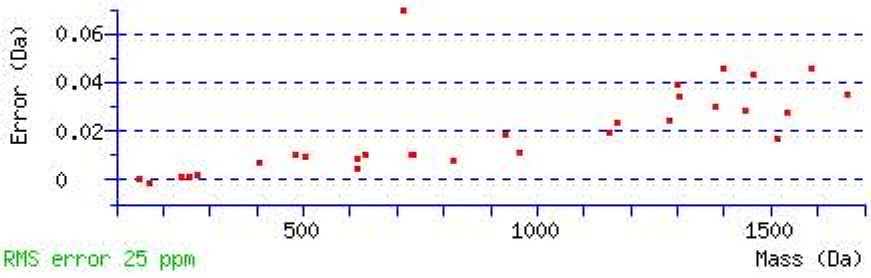
Match to Query 58027: 2031.005082 from(678.008970,3+) rtinseconds(1702) index(23158)
Title: Locus:1.1.1.2445.12 File:"2013-07-02 CLN FXIII 30 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

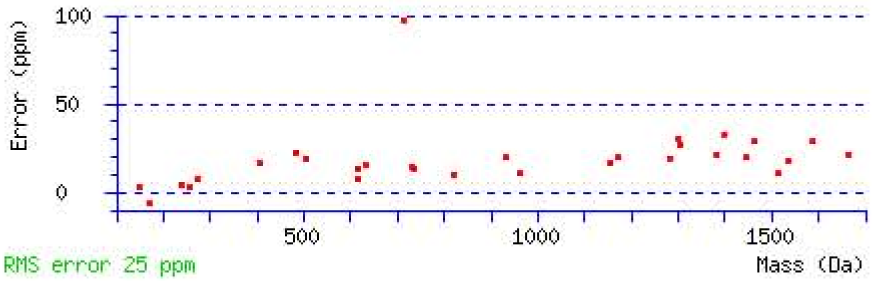
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2030.976501
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 70  Expect: 2.8e-006
Matches : 31/164 fragment ions using 49 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							17
2	**171.112804**	86.060040					G	1918.899727	959.953502	1901.873178	951.440227	1900.889162	950.948219	16
3	**258.144832**	129.576054			240.134267	120.570772	S	1861.878263	931.442770	1844.851714	922.929495	1843.867698	922.437487	15
4	371.228896	186.118086			353.218331	177.112804	L	1774.846235	887.926756	1757.819686	879.413481	1756.835670	878.921473	14
5	428.250360	214.628818			410.239795	205.623536	G	***1661.762171***	831.384724	1644.735622	822.871449	1643.751606	822.379441	13
6	499.287474	250.147375			481.276909	241.142093	A	1604.740707	802.873992	1587.714158	794.360717	1586.730142	793.868709	12
7	570.324588	285.665932			552.314023	276.660650	A	***1533.703593***	767.355435	1516.677044	758.842160	1515.693028	758.350152	11
8	730.355237	365.681257			712.344672	356.675974	C	***1462.666479***	731.836878	1445.639930	723.323603	1444.655914	722.831595	10
9	859.397830	430.202553			841.387265	421.197271	E	***1302.635830***	651.821553	1285.609281	643.308279	1284.625265	642.816270	9
10	**1298.623156**	649.815216	1281.596607	641.301942	1280.612591	640.809934	Q	***1173.593237***	587.300257	1156.566688	578.786982	1155.582672	578.294974	8
11	**1399.670835**	700.339056	1382.644286	691.825781	1381.660270	691.333773	T	***734.367911***	367.687594	717.341362	359.174319	716.357346	358.682311	7
12	1527.729413	764.368345	1510.702864	755.855070	1509.718848	755.363062	Q	***633.320232***	317.163754	616.293683	308.650480	615.309667	308.158472	6
13	1628.777092	814.892184	1611.750543	806.378910	1610.766527	805.886902	T	***505.261654***	253.134465	488.235105	244.621190	487.251089	244.129182	5
14	1757.819685	879.413481	1740.793136	870.900206	1739.809120	870.408198	E	***404.213975***	202.610625	387.187426	194.097351	386.203410	193.605343	4
15	1814.841149	907.924213	1797.814600	899.410938	1796.830584	898.918930	G	***275.171382***	138.089329	258.144833	129.576054			3
16	1885.878263	943.442770	1868.851714	934.929495	1867.867698	934.437487	A	218.149918	109.578597	201.123369	101.065322			2
17							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of LGSLGAACEQTQTEGAK
(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	2030.976501	0.028581	LGSLGAACEQTQTEGAK
41.3	2030.976501	0.028581	LGSLGAACEQTQTEGAK

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

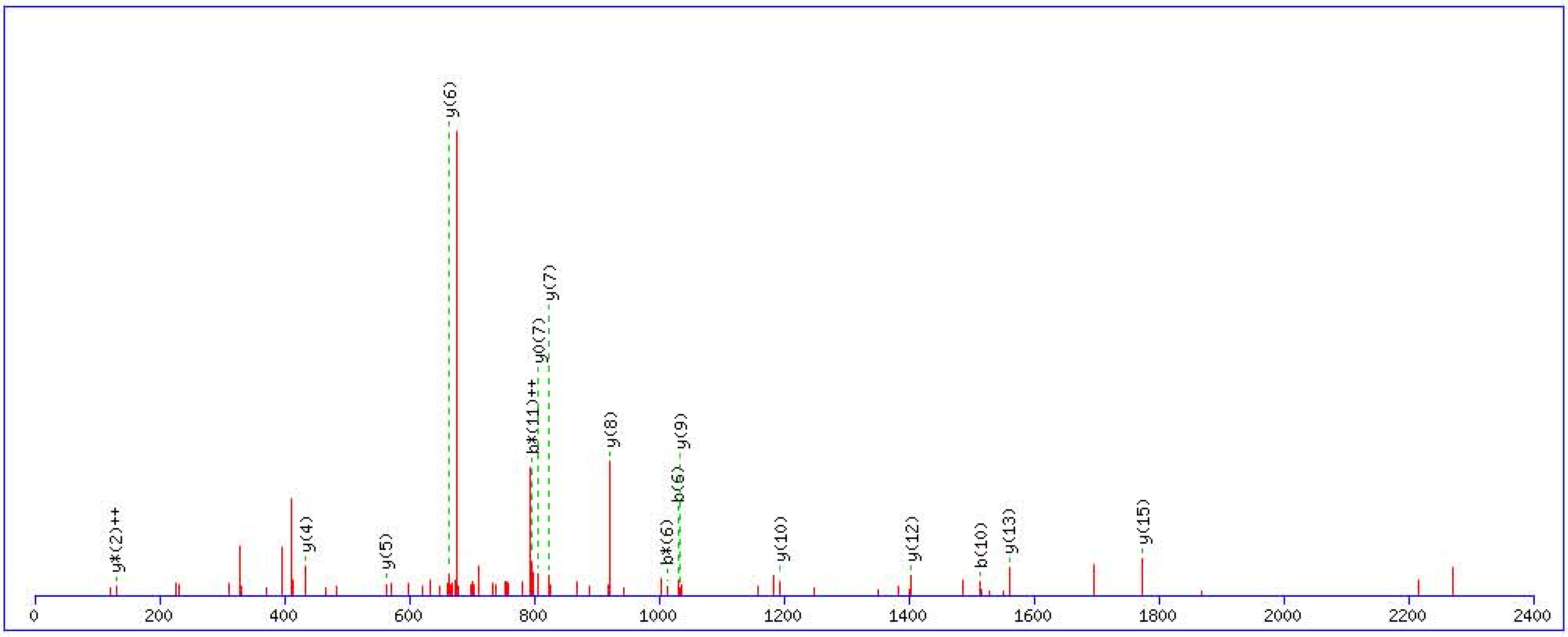
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **YGQTIRPICLPCTEGTTR**
Found in **CFAB_HUMAN**, Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2

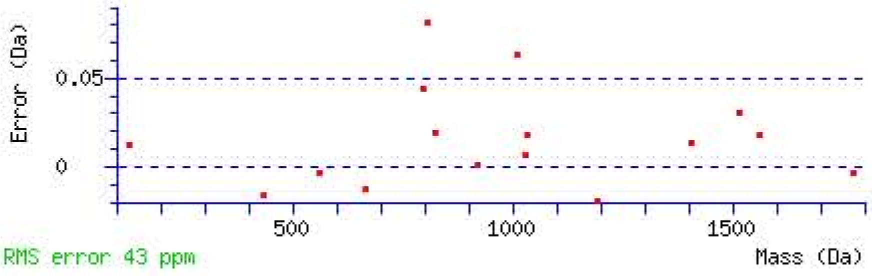
Match to Query 66717: 2433.212742 from(812.078190,3+) rtinseconds(2087) index(80870)
Title: Locus:1.1.1.2606.15 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●

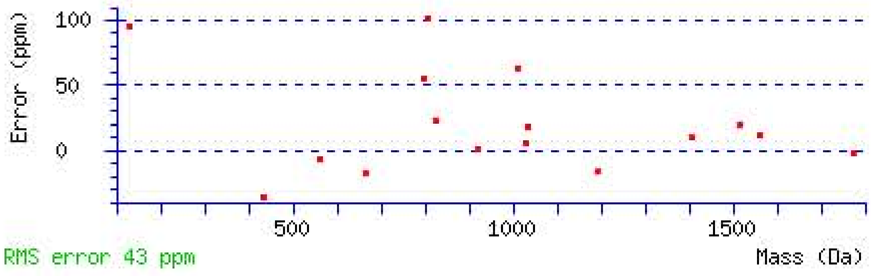


Monoisotopic mass of neutral peptide Mr(calc): 2433.196701
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 26 **Expect:** 0.076
Matches : 16/192 fragment ions using 56 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940					Y							18
2	221.092069	111.049673					G	2271.140644	1136.073960	2254.114095	1127.560685	2253.130079	1127.068677	17
3	660.317395	330.662336	643.290846	322.149061			Q	2214.119180	1107.563228	2197.092631	1099.049953	2196.108615	1098.557945	16
4	761.365074	381.186175	744.338525	372.672901	743.354509	372.180893	T	***1774.893854***	887.950565	1757.867305	879.437290	1756.883289	878.945282	15
5	874.449138	437.728207	857.422589	429.214933	856.438573	428.722925	I	1673.846175	837.426725	1656.819626	828.913451	1655.835610	828.421443	14
6	**1030.550249**	515.778763	1013.523700	507.265488	1012.539684	506.773480	R	***1560.762111***	780.884693	1543.735562	772.371419	1542.751546	771.879411	13
7	1127.603013	564.305145	1110.576464	555.791870	1109.592448	555.299862	P	***1404.661000***	702.834138	1387.634451	694.320863	1386.650435	693.828855	12
8	1240.687077	620.847177	1223.660528	612.333902	1222.676512	611.841894	I	1307.608236	654.307756	1290.581687	645.794481	1289.597671	645.302473	11
9	1400.717726	700.862501	1383.691177	692.349227	1382.707161	691.857219	C	***1194.524172***	597.765724	1177.497623	589.252449	1176.513607	588.760441	10
10	**1513.801790**	757.404533	1496.775241	748.891259	1495.791225	748.399250	L	***1034.493523***	517.750399	1017.466974	509.237125	1016.482958	508.745117	9
11	1610.854554	805.930915	1593.828005	797.417641	1592.843989	796.925633	P	***921.409459***	461.208367	904.382910	452.695093	903.398894	452.203085	8
12	1770.885203	885.946240	1753.858654	877.432965	1752.874638	876.940957	C	***824.356695***	412.681985	807.330146	404.168711	806.346130	403.676703	7
13	1871.932882	936.470079	1854.906333	927.956805	1853.922317	927.464797	T	***664.326046***	332.666661	647.299497	324.153386	646.315481	323.661378	6
14	2000.975475	1000.991376	1983.948926	992.478101	1982.964910	991.986093	E	***563.278367***	282.142821	546.251818	273.629547	545.267802	273.137539	5
15	2057.996939	1029.502107	2040.970390	1020.988833	2039.986374	1020.496825	G	***434.235774***	217.621525	417.209225	209.108250	416.225209	208.616242	4
16	2159.044618	1080.025947	2142.018069	1071.512672	2141.034053	1071.020664	T	377.214310	189.110793	360.187761	180.597518	359.203745	180.105510	3
17	2260.092297	1130.549786	2243.065748	1122.036512	2242.081732	1121.544504	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
18							R	175.118952	88.063114	158.092403	79.549839			1



RMS error 43 ppm



RMS error 43 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.8	2433.196701	0.016041	YGQTIRPICLPCTEGTTR

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

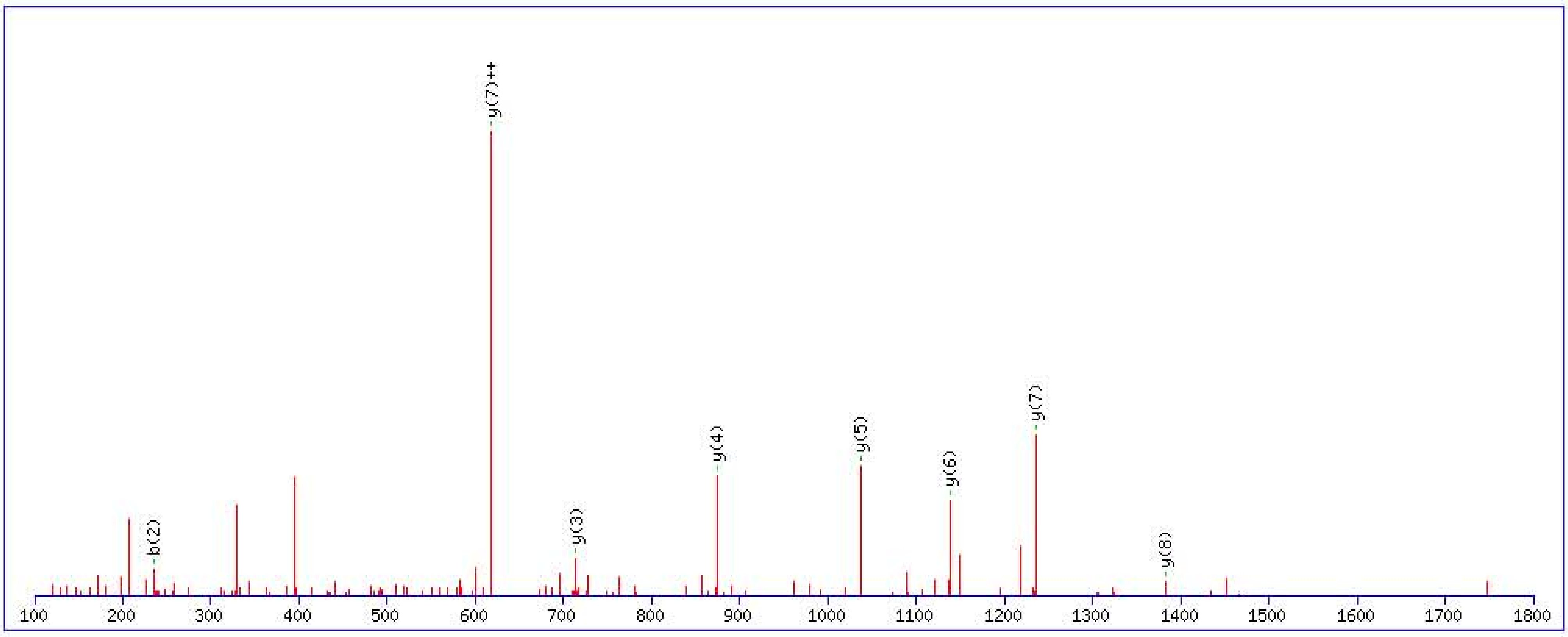
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFPTYCQQK**
Found in **CFAI_HUMAN**, Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2

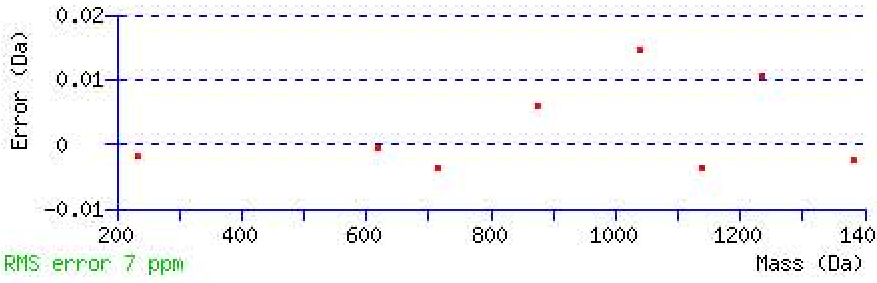
Match to Query 41664: 1468.686948 from(735.350750,2+) rtinseconds(1847) index(79206)
Title: Locus:1.1.1.2522.17 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

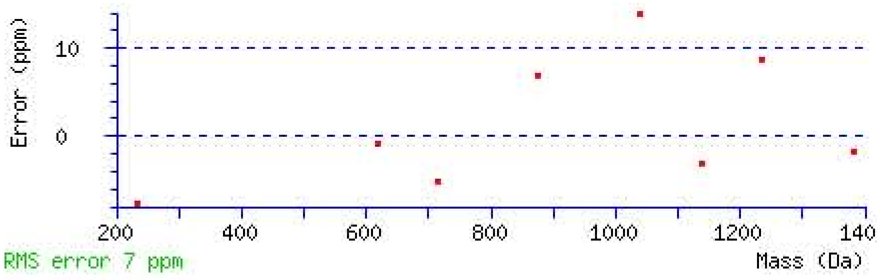
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1468.684296
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 40 **Expect:** 0.00089
Matches : 8/74 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							9
2	**235.107718**	118.057497			217.097153	109.052214	F	***1382.659543***	691.833410	1365.632994	683.320135	1364.648978	682.828127	8
3	332.160482	166.583879			314.149917	157.578596	P	***1235.591129***	618.299203	1218.564580	609.785928	1217.580564	609.293920	7
4	433.208161	217.107718			415.197596	208.102436	T	***1138.538365***	569.772821	1121.511816	561.259546	1120.527800	560.767538	6
5	596.271490	298.639383			578.260925	289.634101	Y	***1037.490686***	519.248981	1020.464137	510.735707			5
6	756.302139	378.654708			738.291574	369.649425	C	***874.427357***	437.717317	857.400808	429.204042			4
7	884.360717	442.683997	867.334168	434.170722	866.350152	433.678714	Q	***714.396708***	357.701992	697.370159	349.188718			3
8	1323.586043	662.296660	1306.559494	653.783385	1305.575478	653.291377	Q	586.338130	293.672703	569.311581	285.159428			2
9							K	147.112804	74.060040	130.086255	65.546765			1



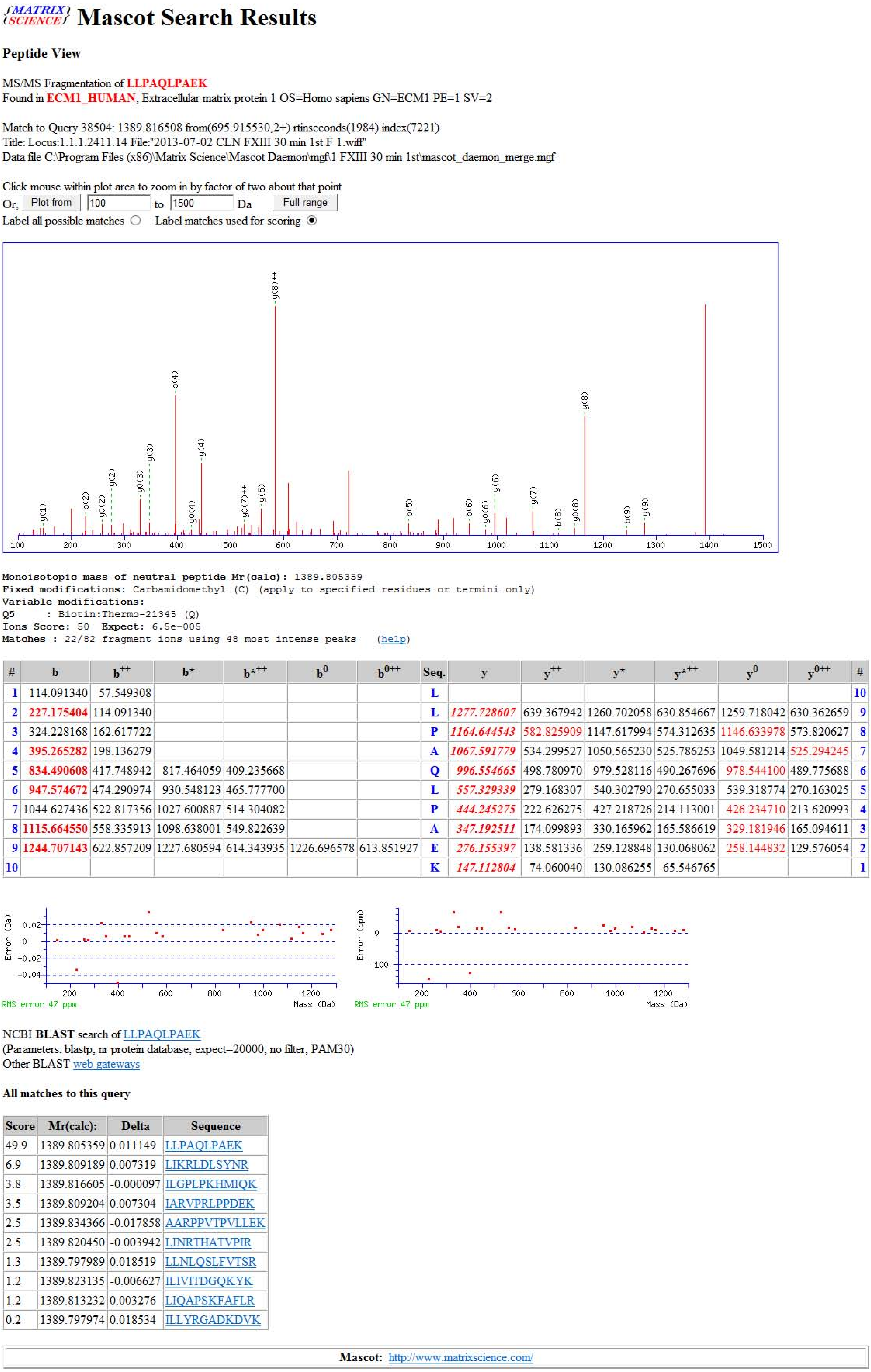


NCBI **BLAST** search of SFPTYCQQK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.3	1468.684296	0.002652	SFPTYCQQK
40.3	1468.684296	0.002652	SFPTYCQQK
7.3	1468.691498	-0.004550	ESDCLVCRKFR
3.1	1468.671524	0.015424	MEAETGSSVETGKK
2.7	1468.672394	0.014554	IMQSSQSMSK
1.2	1468.688126	-0.001178	FSIPSMTEHHAGR
1.2	1468.666336	0.020612	SMAQHVHNMDKR
0.1	1468.680252	0.006696	YAKGNGDCALLCK
0.1	1468.698029	-0.011081	SFLEGTMQVAQSR
0.1	1468.695511	-0.008563	SFLYCNQAR

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



Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLPAQLPAEK**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

Match to Query 38504: 1389.816508 from(695.915530,2+) rtinseconds(1984) index(7221)
Title: Locus:1.1.1.2411.14 File:"2013-07-02 CLN FXIII 30 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1389.805359
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 50  Expect: 6.5e-005
Matches : 22/82 fragment ions using 48 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					L							10
2	**227.175404**	114.091340					L	***1277.728607***	639.367942	1260.702058	630.854667	1259.718042	630.362659	9
3	324.228168	162.617722					P	***1164.644543***	582.825909	1147.617994	574.312635	1146.633978	573.820627	8
4	**395.265282**	198.136279					A	***1067.591779***	534.299527	1050.565230	525.786253	1049.581214	525.294245	7
5	**834.490608**	417.748942	817.464059	409.235668			Q	***996.554665***	498.780970	979.528116	490.267696	978.544100	489.775688	6
6	**947.574672**	474.290974	930.548123	465.777700			L	***557.329339***	279.168307	540.302790	270.655033	539.318774	270.163025	5
7	1044.627436	522.817356	1027.600887	514.304082			P	***444.245275***	222.626275	427.218726	214.113001	426.234710	213.620993	4
8	**1115.664550**	558.335913	1098.638001	549.822639			A	***347.192511***	174.099893	330.165962	165.586619	329.181946	165.094611	3
9	**1244.707143**	622.857209	1227.680594	614.343935	1226.696578	613.851927	E	***276.155397***	138.581336	259.128848	130.068062	258.144832	129.576054	2
10							K	***147.112804***	74.060040	130.086255	65.546765			1

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.9	1389.805359	0.011149	LLPAQLPAEK
6.9	1389.809189	0.007319	LIKRLDLSYNR
3.8	1389.816605	-0.000097	ILGPLPKHMIQK
3.5	1389.809204	0.007304	IARVPRLPPDEK
2.5	1389.834366	-0.017858	AARPPVTPVLLEK
2.5	1389.820450	-0.003942	LINRTHATVPIR
1.3	1389.797989	0.018519	LLNLQSLFVTSR
1.2	1389.823135	-0.006627	ILIVITDGQKYK
1.2	1389.813232	0.003276	LIQAPSKFAFLR
0.2	1389.797974	0.018534	ILLYRGADKDVK

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

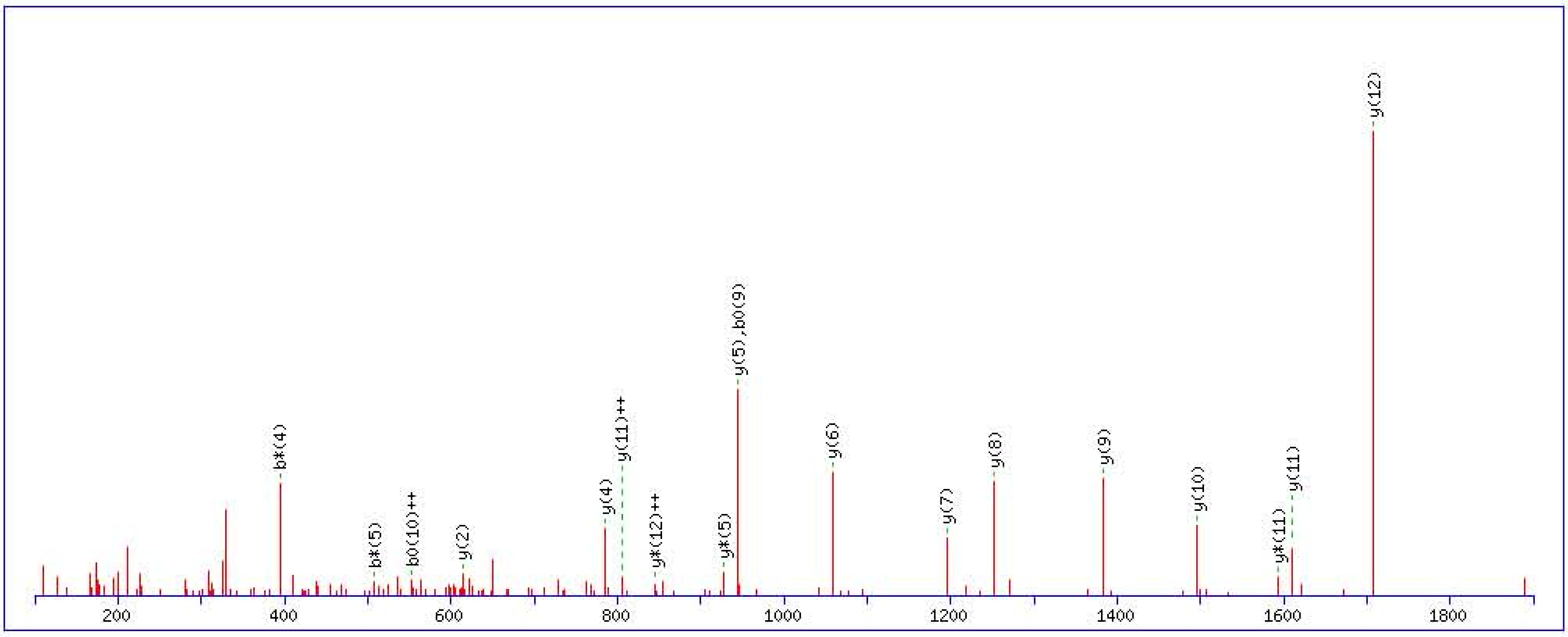
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VTPNLMGHLCGNQR**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

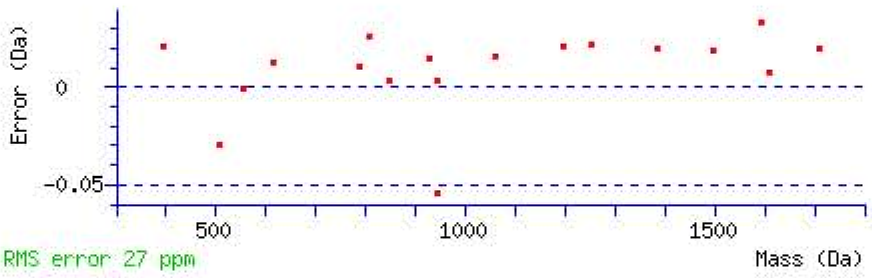
Match to Query 54456: 1906.950912 from(636.657580,3+) rtinseconds(1856) index(6330)
Title: Locus:1.1.1.2367.11 File:"2013-07-02 CLN FXIII 30 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

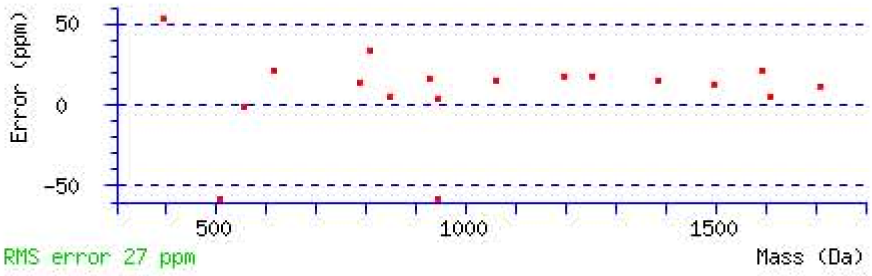
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1900 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1906.932816
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 55  Expect: 7.8e-005
Matches : 18/124 fragment ions using 32 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							14
2	201.123369	101.065322			183.112804	92.060040	T	1808.871677	904.939477	1791.845128	896.426202	1790.861112	895.934194	13
3	298.176133	149.591704			280.165568	140.586422	P	***1707.823998***	854.415637	1690.797449	845.902363			12
4	412.219060	206.613168	395.192511	198.099894	394.208495	197.607886	N	***1610.771234***	805.889255	1593.744685	797.375981			11
5	525.303124	263.155200	508.276575	254.641926	507.292559	254.149918	L	***1496.728307***	748.867792	1479.701758	740.354517			10
6	656.343609	328.675443	639.317060	320.162168	638.333044	319.670160	M	***1383.644243***	692.325760	1366.617694	683.812485			9
7	713.365073	357.186175	696.338524	348.672900	695.354508	348.180892	G	***1252.603758***	626.805517	1235.577209	618.292243			8
8	850.423985	425.715631	833.397436	417.202356	832.413420	416.710348	H	***1195.582294***	598.294785	1178.555745	589.781511			7
9	963.508049	482.257663	946.481500	473.744388	945.497484	473.252380	L	***1058.523382***	529.765329	1041.496833	521.252055			6
10	1123.538698	562.272987	1106.512149	553.759713	1105.528133	553.267705	C	***945.439318***	473.223297	928.412769	464.710023			5
11	1180.560162	590.783719	1163.533613	582.270445	1162.549597	581.778437	G	***785.408669***	393.207973	768.382120	384.694698			4
12	1294.603089	647.805183	1277.576540	639.291908	1276.592524	638.799900	N	728.387205	364.697241	711.360656	356.183966			3
13	1733.828415	867.417846	1716.801866	858.904571	1715.817850	858.412563	Q	***614.344278***	307.675777	597.317729	299.162503			2
14							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.1	1906.932816	0.018096	VTPNLMGHLCGNQR

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

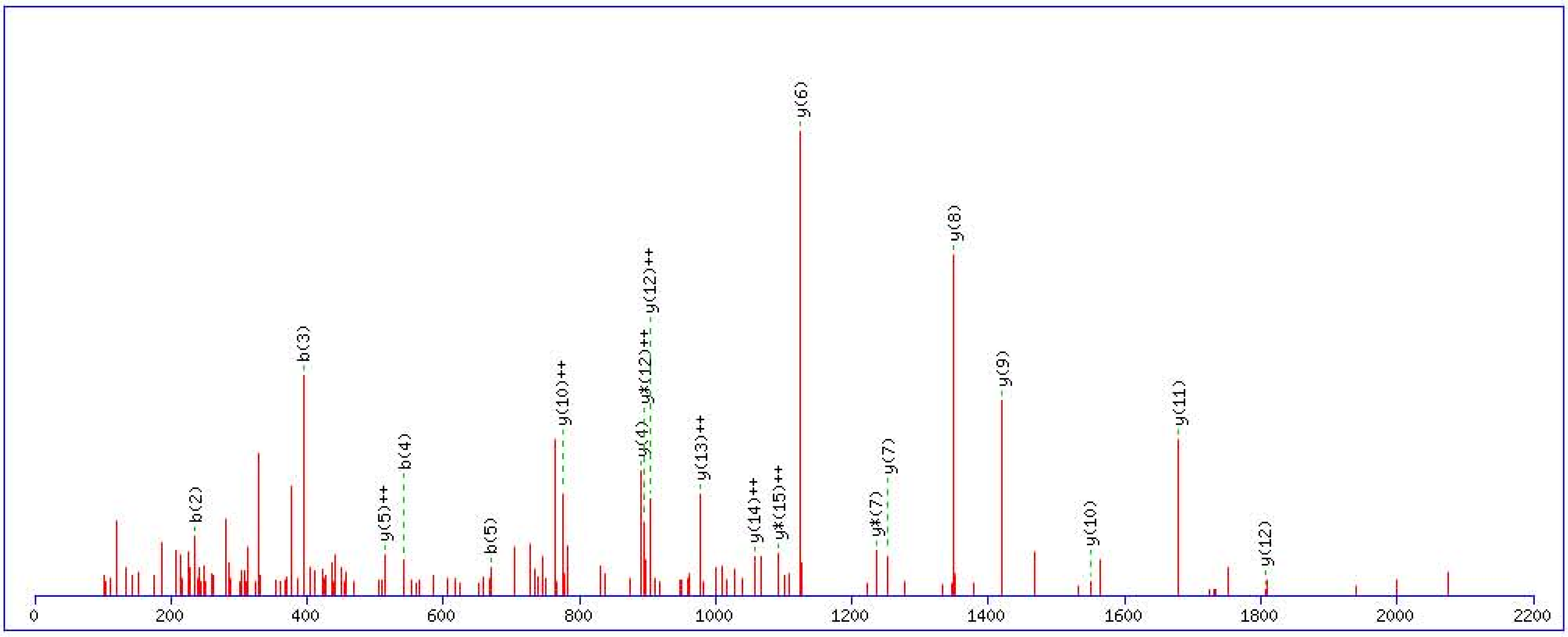
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FSCFQEEAPQPHYQLR**
Found in **ECM1_HUMAN**, Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2

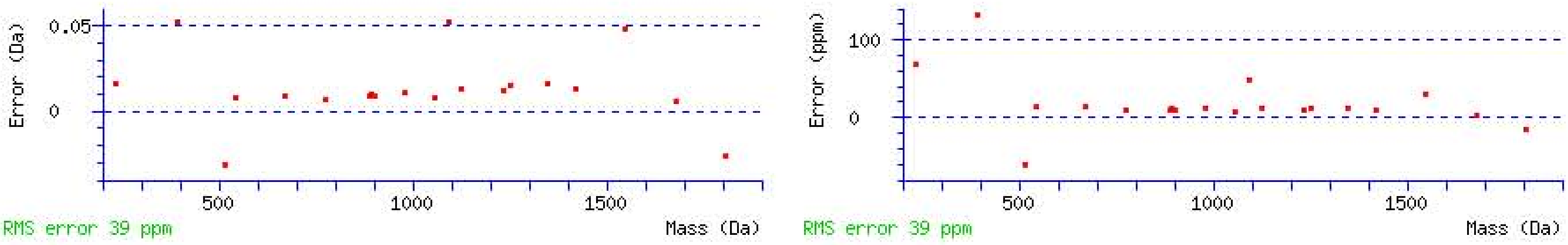
Match to Query 64979: 2347.111032 from(783.377620,3+) rtinseconds(1907) index(6720)
Title: Locus:1.1.1.2384.17 File:"2013-07-02 CLN FXIII 30 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2347.087784
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.0024
Matches : 20/152 fragment ions using 38 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					F							16
2	**235.107718**	118.057497			217.097153	109.052214	S	2201.026658	1101.016967	2184.000109	1092.503692	2183.016093	1092.011684	15
3	**395.138367**	198.072821			377.127802	189.067539	C	2113.994630	1057.500953	2096.968081	1048.987678	2095.984065	1048.495670	14
4	**542.206781**	271.607029			524.196216	262.601746	F	1953.963981	977.485629	1936.937432	968.972354	1935.953416	968.480346	13
5	**670.265359**	335.636318	653.238810	327.123043	652.254794	326.631035	Q	***1806.895567***	903.951422	1789.869018	895.438147	1788.885002	894.946139	12
6	799.307952	400.157614	782.281403	391.644340	781.297387	391.152332	E	***1678.836989***	839.922133	1661.810440	831.408858	1660.826424	830.916850	11
7	928.350545	464.678911	911.323996	456.165636	910.339980	455.673628	E	***1549.794396***	775.400836	1532.767847	766.887562	1531.783831	766.395554	10
8	999.387659	500.197468	982.361110	491.684193	981.377094	491.192185	A	***1420.751803***	710.879540	1403.725254	702.366265			9
9	1096.440423	548.723850	1079.413874	540.210575	1078.429858	539.718567	P	***1349.714689***	675.360983	1332.688140	666.847708			8
10	1224.499001	612.753138	1207.472452	604.239864	1206.488436	603.747856	Q	***1252.661925***	626.834601	1235.635376	618.321326			7
11	1321.551765	661.279520	1304.525216	652.766246	1303.541200	652.274238	P	***1124.603347***	562.805312	1107.576798	554.292037			6
12	1458.610677	729.808976	1441.584128	721.295702	1440.600112	720.803694	H	1027.550583	514.278930	1010.524034	505.765655			5
13	1621.674006	811.340641	1604.647457	802.827367	1603.663441	802.335358	Y	***890.491671***	445.749474	873.465122	437.236199			4
14	2060.899332	1030.953304	2043.872783	1022.440030	2042.888767	1021.948022	Q	727.428342	364.217809	710.401793	355.704535			3
15	2173.983396	1087.495336	2156.956847	1078.982061	2155.972831	1078.490053	L	288.203016	144.605146	271.176467	136.091872			2
16							R	175.118952	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.2	2347.087784	0.023248	FSCFQEEAPQPHYQLR
18.9	2347.087784	0.023248	FSCFQEEAPQPHYQLR

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

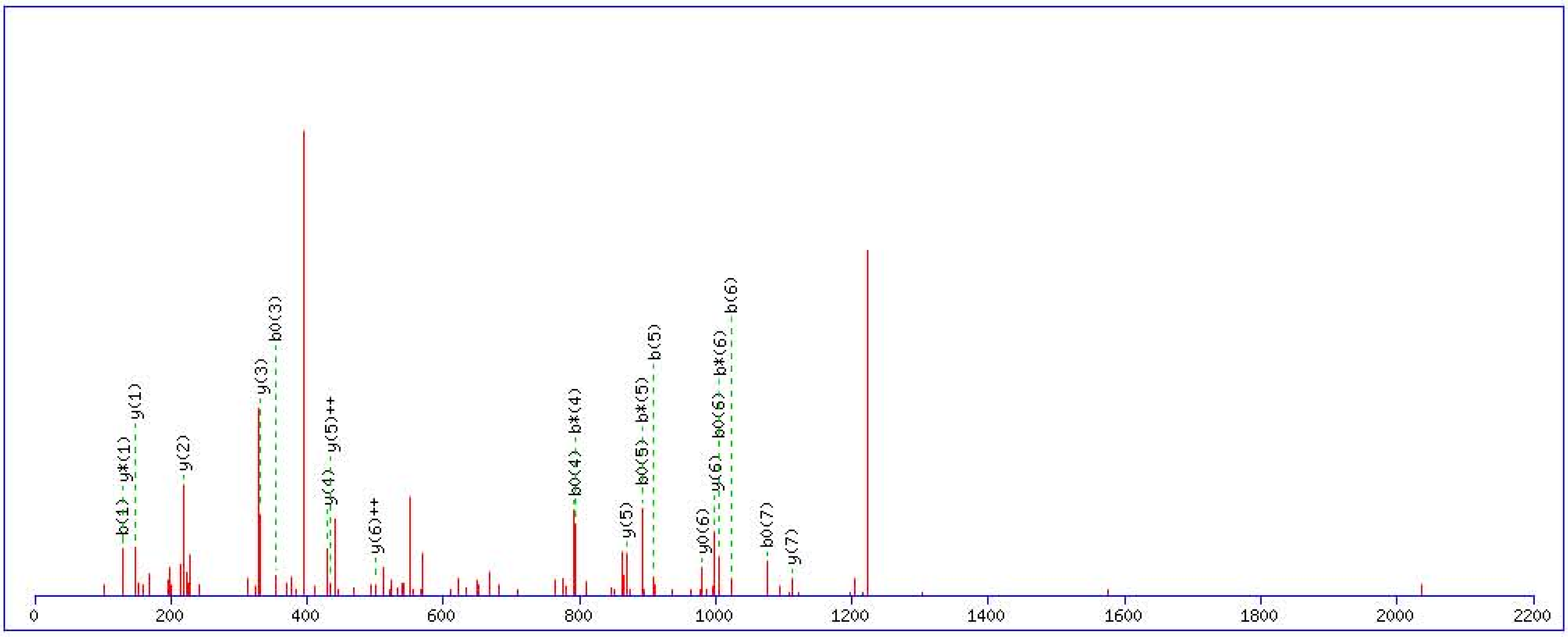
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLEQVIAK**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

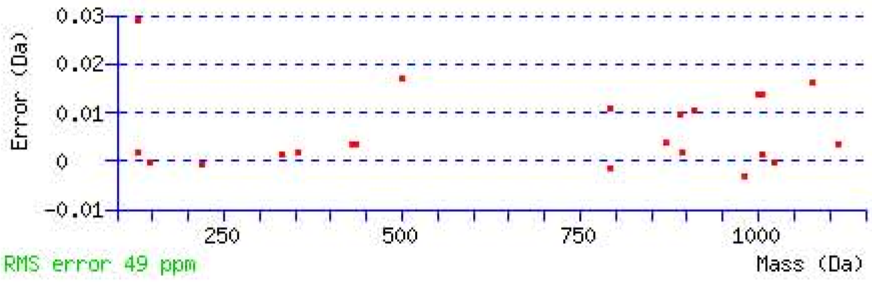
Match to Query 32978: 1238.701808 from(620.358180,2+) rtinseconds(1749) index(61357)
Title: Locus:1.1.1.2607.13 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

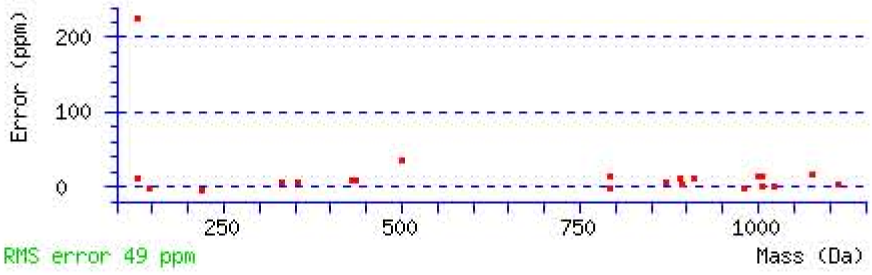
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1238.705658
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4     : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.0052
Matches : 22/70 fragment ions using 47 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	**129.065854**	65.036565	112.039305	56.523291			Q							8
2	242.149918	121.578597	225.123369	113.065323			L	***1111.654379***	556.330828	1094.627830	547.817553	1093.643814	547.325545	7
3	371.192511	186.099894	354.165962	177.586619	353.181946	177.094611	E	***998.570315***	499.788796	981.543766	491.275521	980.559750	490.783513	6
4	810.417837	405.712557	793.391288	397.199282	792.407272	396.707274	Q	***869.527722***	435.267499	852.501173	426.754225			5
5	**909.486251**	455.246764	892.459702	446.733489	891.475686	446.241481	V	***430.302396***	215.654836	413.275847	207.141562			4
6	**1022.570315**	511.788796	1005.543766	503.275521	1004.559750	502.783513	I	***331.233982***	166.120629	314.207433	157.607355			3
7	1093.607429	547.307353	1076.580880	538.794078	1075.596864	538.302070	A	***218.149918***	109.578597	201.123369	101.065323			2
8							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.9	1238.705658	-0.003850	QLEQVIAK
15.3	1238.705658	-0.003850	QLEQVIAK
11.0	1238.687027	0.014781	KEETQPPVALK
9.4	1238.698257	0.003551	IHADASSKVLAK
7.6	1238.702301	-0.000493	DVFKKGFSIAK
6.6	1238.716904	-0.015096	DRVQVAIK
5.1	1238.705658	-0.003850	QIAQEIVK
4.6	1238.691040	0.010768	LYKEFIDLAK
4.3	1238.698273	0.003535	GHVTQLKESLK
3.0	1238.716888	-0.015080	KRILCPLDPK

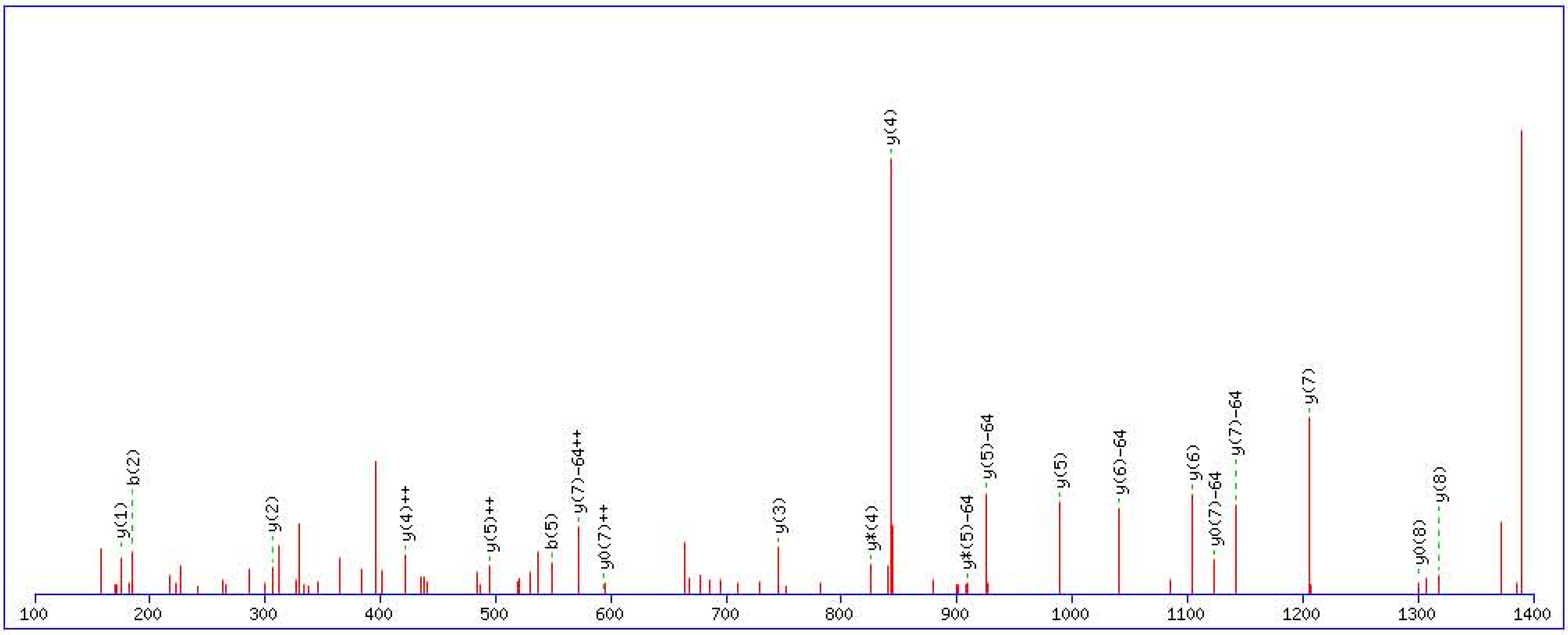
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALTDMPQMR**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

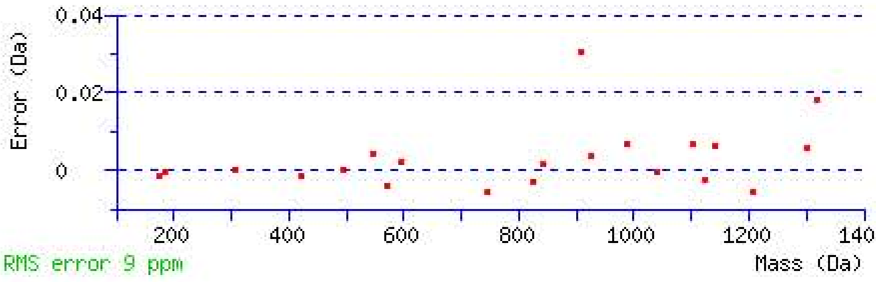
Match to Query 38327: 1388.657568 from(695.336060,2+) rtinseconds(1677) index(60797)
Title: Locus:1.1.1.2582.10 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

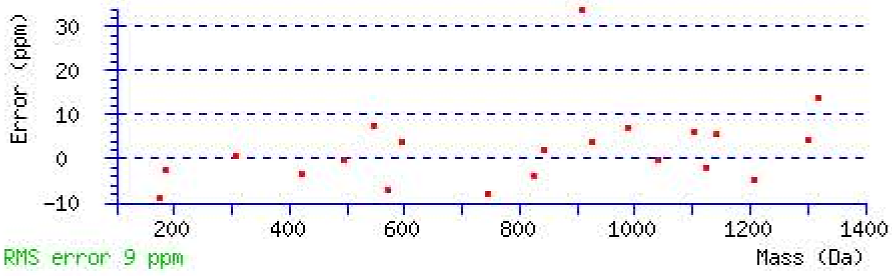
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1400] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1388.661438
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5      : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 56  Expect: 1.2e-005
Matches : 21/112 fragment ions using 35 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.044390	36.525833					A							9
2	**185.128454**	93.067865					L	***1318.631613***	659.819445	1301.605064	651.306170	1300.621048	650.814162	8
3	286.176133	143.591704			268.165568	134.586422	T	***1205.547549***	603.277413	1188.521000	594.764138	1187.536984	594.272130	7
4	401.203076	201.105176			383.192511	192.099894	D	***1104.499870***	552.753573	1087.473321	544.240298	1086.489305	543.748290	6
5	**548.238476**	274.622876			530.227911	265.617594	M	***989.472927***	495.240102	972.446378	486.726827			5
6	645.291240	323.149258			627.280675	314.143976	P	***842.437527***	421.722402	825.410978	413.209127			4
7	1084.516566	542.761921	1067.490017	534.248647	1066.506001	533.756639	Q	***745.384763***	373.196020	728.358214	364.682745			3
8	1215.557051	608.282164	1198.530502	599.768889	1197.546486	599.276881	M	***306.159437***	153.583356	289.132888	145.070082			2
9							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.7	1388.661438	-0.003870	ALTDMPQMR
19.3	1388.661438	-0.003870	ALTDMPQMR
3.0	1388.660568	-0.003000	SEMTASPLVGPER

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

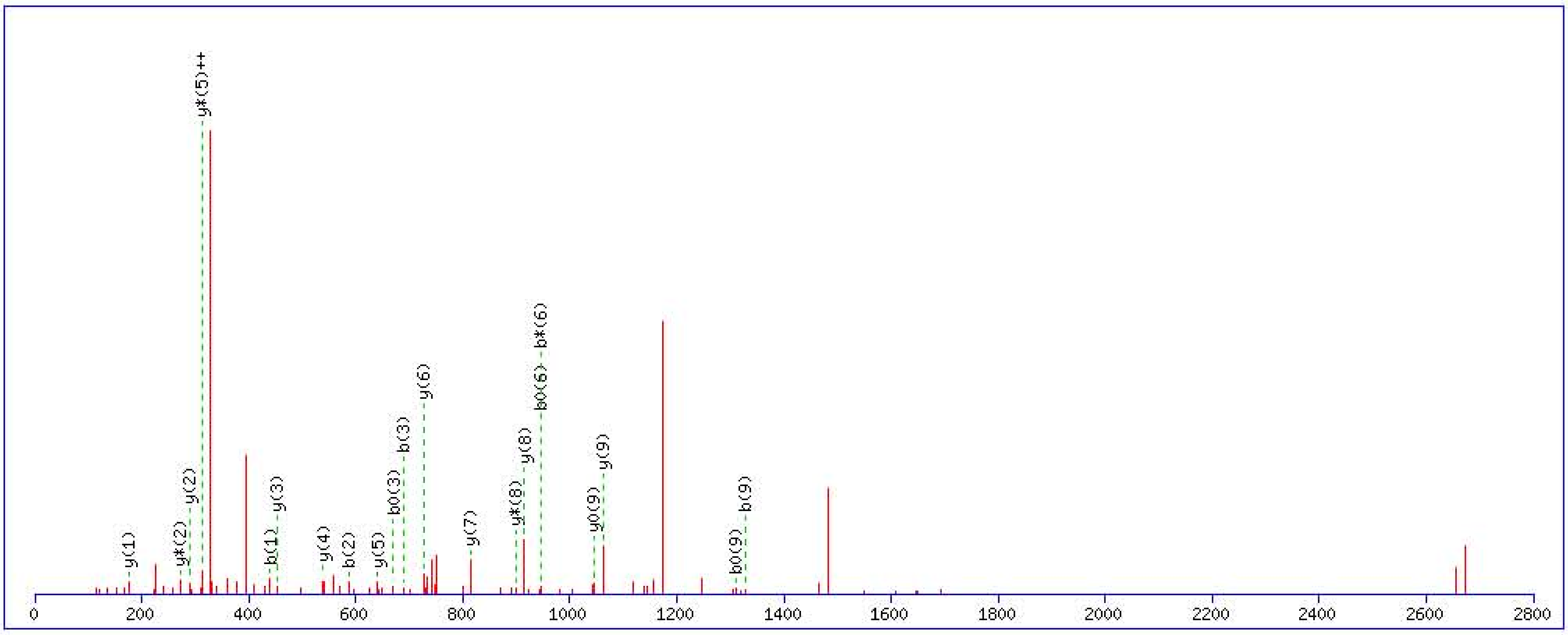
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QFTSSTSYNR**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

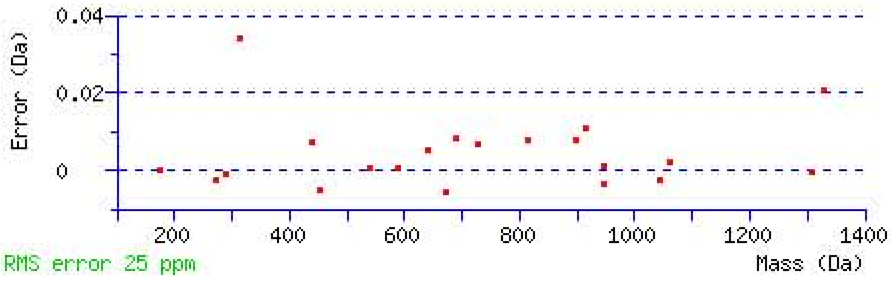
Match to Query 42577: 1500.699268 from(751.356910,2+) rtinseconds(1698) index(60953)
Title: Locus:1.1.1.2589.12 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

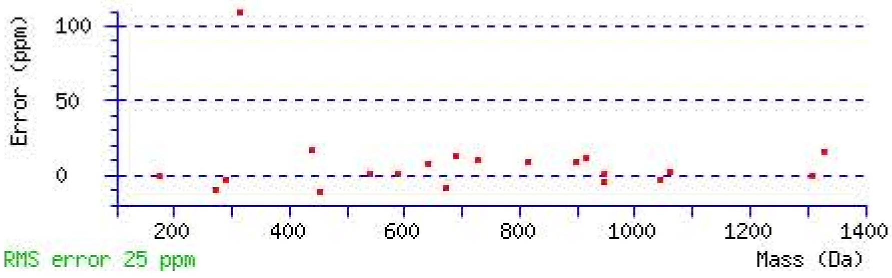
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1500.703110
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1 : Biotin:Thermo-21345 (Q)
Ions Score: 37 **Expect:** 0.00053
Matches : 21/98 fragment ions using 61 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	**440.232602**	220.619939	423.206053	212.106664			Q							10
2	**587.301016**	294.154146	570.274467	285.640872			F	***1062.485064***	531.746170	1045.458515	523.232896	1044.474499	522.740887	9
3	**688.348695**	344.677986	671.322146	336.164711	670.338130	335.672703	T	***915.416650***	458.211963	898.390101	449.698689	897.406085	449.206681	8
4	775.380723	388.194000	758.354174	379.680725	757.370158	379.188717	S	***814.368971***	407.688124	797.342422	399.174849	796.358406	398.682841	7
5	862.412751	431.710014	845.386202	423.196739	844.402186	422.704731	S	***727.336943***	364.172110	710.310394	355.658835	709.326378	355.166827	6
6	963.460430	482.233853	946.433881	473.720578	945.449865	473.228570	T	***640.304915***	320.656096	623.278366	312.142821	622.294350	311.650813	5
7	1050.492458	525.749867	1033.465909	517.236593	1032.481893	516.744584	S	***539.257236***	270.132256	522.230687	261.618982	521.246671	261.126974	4
8	1213.555787	607.281532	1196.529238	598.768257	1195.545222	598.276249	Y	***452.225208***	226.616242	435.198659	218.102967			3
9	**1327.598714**	664.302995	1310.572165	655.789721	1309.588149	655.297712	N	***289.161879***	145.084577	272.135330	136.571303			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.6	1500.703110	-0.003842	QFTSSTSYNR
1.6	1500.699768	-0.000500	AEAGSGGPGFTFTFR
1.5	1500.710464	-0.011196	LYYMVAPSAEAMR
0.4	1500.714355	-0.015087	EEIALGGGGFCVHR

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

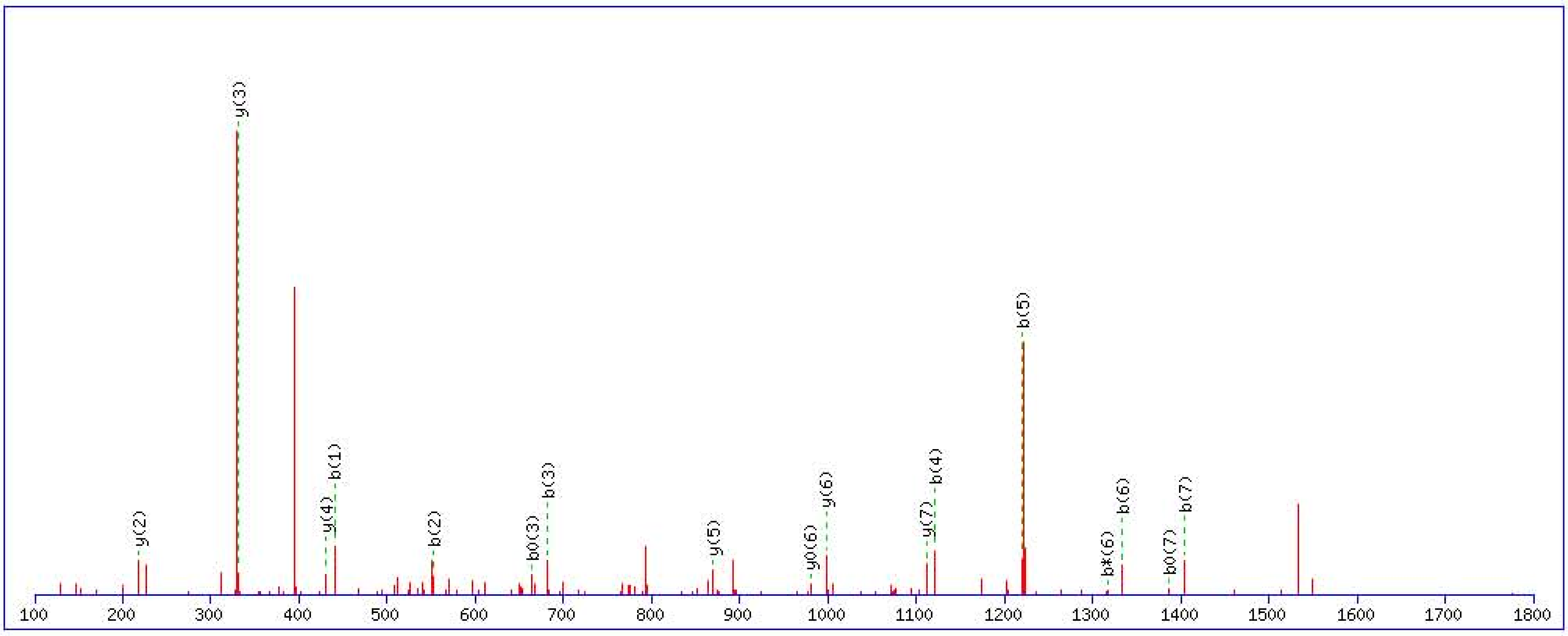
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLEQVIAK**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

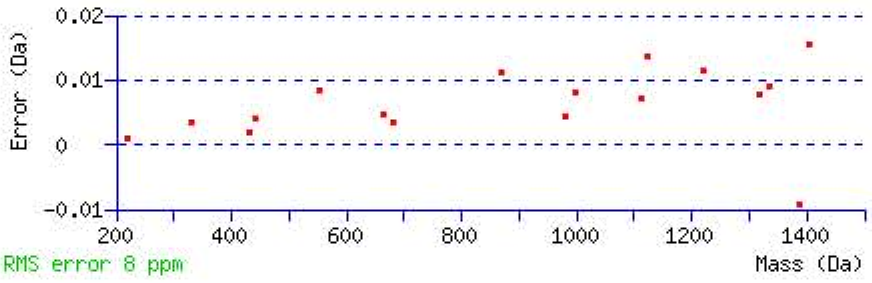
Match to Query 43910: 1549.881288 from(775.947920,2+) rtinseconds(2105) index(63753)
Title: Locus:1.1.1.2730.18 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

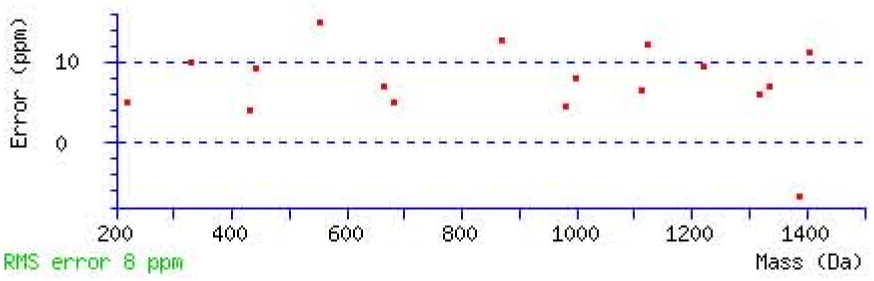
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1549.872406
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.012
Matches : 17/70 fragment ions using 43 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	440.232602	220.619939	423.206053	212.106664			Q							8
2	553.316666	277.161971	536.290117	268.648697			L	1111.654379	556.330828	1094.627830	547.817553	1093.643814	547.325545	7
3	682.359259	341.683268	665.332710	333.169993	664.348694	332.677985	E	998.570315	499.788796	981.543766	491.275521	980.559750	490.783513	6
4	1121.584585	561.295931	1104.558036	552.782656	1103.574020	552.290648	Q	869.527722	435.267499	852.501173	426.754225			5
5	1220.652999	610.830138	1203.626450	602.316863	1202.642434	601.824855	V	430.302396	215.654836	413.275847	207.141561			4
6	1333.737063	667.372170	1316.710514	658.858895	1315.726498	658.366887	I	331.233982	166.120629	314.207433	157.607354			3
7	1404.774177	702.890727	1387.747628	694.377452	1386.763612	693.885444	A	218.149918	109.578597	201.123369	101.065322			2
8							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.2	1549.872406	0.008882	QLEQVIAK
7.2	1549.861633	0.019655	KLSRPFQSEIFAK
7.2	1549.886810	-0.005522	YVIGIGVGAGAYVLAK
6.2	1549.886795	-0.005507	KGNLVYIIDFGLAK
2.3	1549.861618	0.019670	TAEKLYRTAWIAK
2.1	1549.893967	-0.012679	LIRENHELKSAIK
1.9	1549.862991	0.018297	AAWLRVFQHLGPR
1.5	1549.876236	0.005052	QLEGRLALPSR
1.3	1549.865005	0.016283	KSLAGMLTPYVARK
0.9	1549.876251	0.005037	LVDINLVRCHALK

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

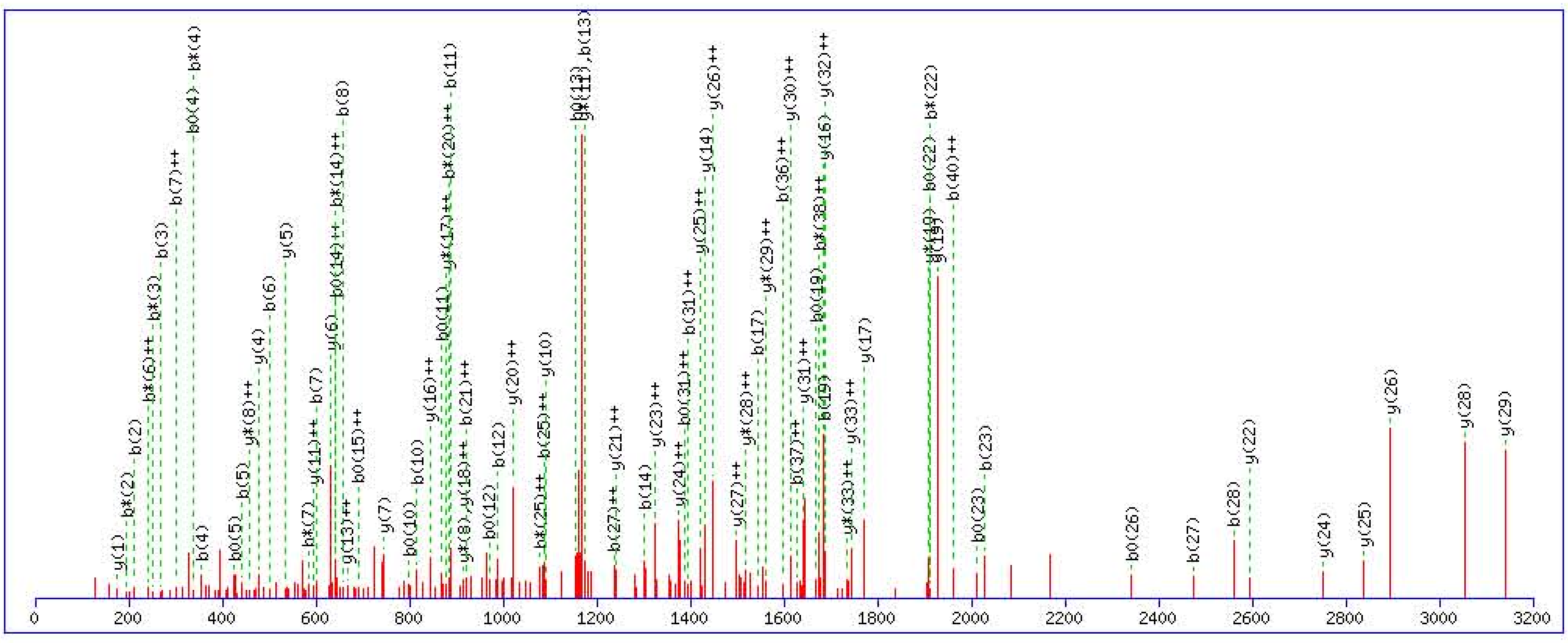
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NPGSSGTGGTATWKPGSSGPGSTGSWNSGSSGTGSTGNQNPGSPRPGSTGTWNPGSSER**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

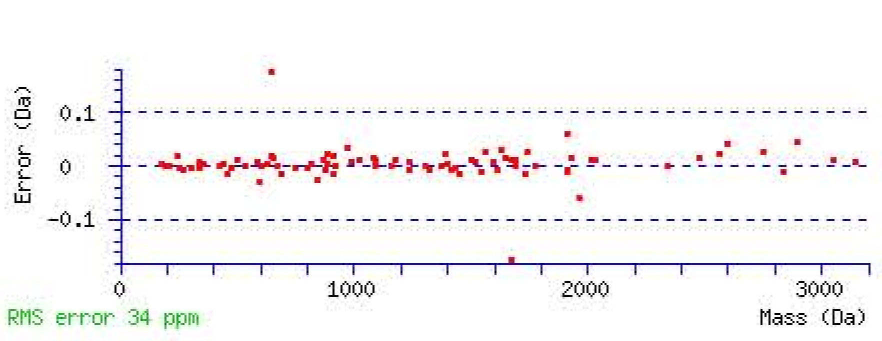
Match to Query 89944: 5844.643070 from(1169.935890,5+) rtinseconds(1751) index(61364)
Title: Locus:1.1.1.2607.20 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

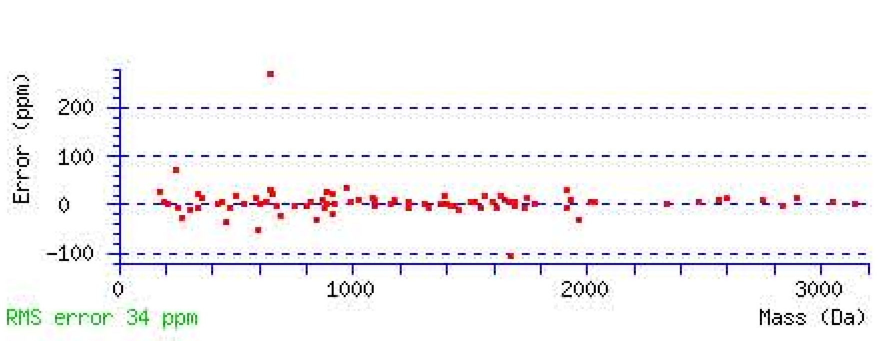
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 5844.608032
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q39 : Biotin:Thermo-21345 (Q)
Ions Score: 91 **Expect:** 3.9e-009
Matches : 87/688 fragment ions using 188 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							59
2	***212.102967***	106.555121	195.076418	98.041847			P	5731.572302	2866.289789	5714.545753	2857.776515	5713.561737	2857.284507	58
3	***269.124431***	135.065853	252.097882	126.552579			G	5634.519538	2817.763407	5617.492989	2809.250133	5616.508973	2808.758125	57
4	***356.156459***	178.581867	339.129910	170.068593	338.145894	169.576585	S	5577.498074	2789.252675	5560.471525	2780.739401	5559.487509	2780.247393	56
5	***443.188487***	222.097881	426.161938	213.584607	425.177922	213.092599	S	5490.466046	2745.736661	5473.439497	2737.223387	5472.455481	2736.731379	55
6	***500.209951***	250.608613	483.183402	242.095339	482.199386	241.603331	G	5403.434018	2702.220647	5386.407469	2693.707373	5385.423453	2693.215365	54
7	***601.257630***	**301.132453**	584.231081	292.619178	583.247065	292.127170	T	5346.412554	2673.709915	5329.386005	2665.196641	5328.401989	2664.704633	53
8	***658.279094***	329.643185	641.252545	321.129910	640.268529	320.637903	G	5245.364875	2623.186076	5228.338326	2614.672801	5227.354310	2614.180793	52
9	715.300558	358.153917	698.274009	349.640643	697.289993	349.148635	G	5188.343411	2594.675344	5171.316862	2586.162069	5170.332846	2585.670061	51
10	***816.348237***	408.677757	799.321688	400.164482	798.337672	399.672474	T	5131.321947	2566.164612	5114.295398	2557.651337	5113.311382	2557.159329	50
11	***887.385351***	444.196314	870.358802	435.683039	869.374786	435.191031	A	5030.274268	2515.640772	5013.247719	2507.127498	5012.263703	2506.635490	49
12	***988.433030***	494.720153	971.406481	486.206879	970.422465	485.714871	T	4959.237154	2480.122215	4942.210605	2471.608941	4941.226589	2471.116933	48
13	***1174.512343***	587.759810	1157.485794	579.246535	1156.501778	578.754527	W	4858.189475	2429.598376	4841.162926	2421.085101	4840.178910	2420.593093	47
14	***1302.607306***	651.807291	1285.580757	643.294017	1284.596741	642.802009	K	4672.110162	2336.558719	4655.083613	2328.045445	4654.099597	2327.553437	46
15	1399.660070	700.333673	1382.633521	691.820399	1381.649505	691.328391	P	4544.015199	2272.511238	4526.988650	2263.997963	4526.004634	2263.505955	45
16	1456.681534	728.844405	1439.654985	720.331131	1438.670969	719.839123	G	4446.962435	2223.984856	4429.935886	2215.471581	4428.951870	2214.979573	44
17	***1543.713562***	772.360419	1526.687013	763.847145	1525.702997	763.355137	S	4389.940971	2195.474124	4372.914422	2186.960849	4371.930406	2186.468841	43
18	1630.745590	815.876433	1613.719041	807.363159	1612.735025	806.871151	S	4302.908943	2151.958110	4285.882394	2143.444835	4284.898378	2142.952827	42
19	***1687.767054***	844.387165	1670.740505	835.873891	1669.756489	835.381883	G	4215.876915	2108.442096	4198.850366	2099.928821	4197.866350	2099.436813	41
20	1784.819818	892.913547	1767.793269	884.400273	1766.809253	883.908265	P	4158.855451	2079.931364	4141.828902	2071.418089	4140.844886	2070.926081	40
21	1841.841282	**921.424279**	1824.814733	912.911005	1823.830717	912.418997	G	4061.802687	2031.404982	4044.776138	2022.891707	4043.792122	2022.399699	39
22	1928.873310	964.940293	1911.846761	956.427019	1910.862745	955.935011	S	4004.781223	2002.894250	3987.754674	1994.380975	3986.770658	1993.888967	38
23	***2029.920989***	1015.464133	2012.894440	1006.950858	2011.910424	1006.458850	T	3917.749195	1959.378236	3900.722646	1950.864961	3899.738630	1950.372953	37
24	2086.942453	1043.974865	2069.915904	1035.461590	2068.931888	1034.969582	G	3816.701516	1908.854396	3799.674967	1900.341122	3798.690951	1899.849114	36
25	2173.974481	**1087.490879**	2156.947932	1078.977604	2155.963916	1078.485596	S	3759.680052	1880.343664	3742.653503	1871.830389	3741.669487	1871.338382	35
26	2360.053794	1180.530535	2343.027245	1172.017261	2342.043229	1171.525253	W	3672.648024	1836.827650	3655.621475	1828.314375	3654.637459	1827.822367	34
27	***2474.096721***	**1237.551999**	2457.070172	1229.038724	2456.086156	1228.546716	N	3486.568711	1743.787993	3469.542162	1735.274719	3468.558146	1734.782711	33
28	***2561.128749***	1281.068013	2544.102200	1272.554738	2543.118184	1272.062730	S	3372.525784	1686.766530	3355.499235	1678.253255	3354.515219	1677.761247	32
29	2618.150213	1309.578745	2601.123664	1301.065470	2600.139648	1300.573462	G	3285.493756	1643.250516	3268.467207	1634.737241	3267.483191	1634.245233	31
30	2705.182241	1353.094759	2688.155692	1344.581484	2687.171676	1344.089476	S	3228.472292	1614.739784	3211.445743	1606.226509	3210.461727	1605.734501	30
31	2792.214269	**1396.610773**	2775.187720	1388.097498	2774.203704	1387.605490	S	***3141.440264***	1571.223770	3124.413715	1562.710495	3123.429699	1562.218487	29
32	2849.235733	1425.121505	2832.209184	1416.608230	2831.225168	1416.116222	G	***3054.408236***	1527.707756	3037.381687	1519.194481	3036.397671	1518.702473	28
33	2950.283412	1475.645344	2933.256863	1467.132069	2932.272847	1466.640062	T	2997.386772	1499.197024	2980.360223	1490.683749	2979.376207	1490.191741	27
34	3007.304876	1504.156076	2990.278327	1495.642801	2989.294311	1495.150794	G	***2896.339093***	1448.673184	2879.312544	1440.159910	2878.328528	1439.667902	26
35	3094.336904	1547.672090	3077.310355	1539.158815	3076.326339	1538.666808	S	***2839.317629***	1420.162453	2822.291080	1411.649178	2821.307064	1411.157170	25
36	3195.384583	**1598.195929**	3178.358034	1589.682655	3177.374018	1589.190647	T	***2752.285601***	1376.646438	2735.259052	1368.133164	2734.275036	1367.641156	24
37	3252.406047	**1626.706661**	3235.379498	1618.193387	3234.395482	1617.701379	G	2651.237922	1326.122599	2634.211373	1317.609325	2633.227357	1317.117317	23
38	3366.448974	1683.728125	3349.422425	1675.214850	3348.438409	1674.722842	N	***2594.216458***	1297.611867	2577.189909	1289.098593	2576.205893	1288.606585	22
39	3805.674300	1903.340788	3788.647751	1894.827513	3787.663735	1894.335506	Q	2480.173531	1240.590404	2463.146982	1232.077129	2462.162966	1231.585121	21
40	3919.717227	**1960.362252**	3902.690678	1951.848977	3901.706662	1951.356969	N	2040.948205	1020.977741	2023.921656	1012.464466	2022.937640	1011.972458	20
41	4016.769991	2008.888634	3999.743442	2000.375359	3998.759426	1999.883351	P	***1926.905278***	963.956277	1909.878729	955.443003	1908.894713	954.950995	19
42	4073.791455	2037.399365	4056.764906	2028.886091	4055.780890	2028.394083	G	1829.852514	915.429895	1812.825965	906.916621	1811.841949	906.424613	18
43	4160.823483	2080.915380	4143.796934	2072.402105	4142.812918	2071.910097	S	***1772.831050***	886.919163	1755.804501	878.405889	1754.820485	877.913881	17
44	4257.876247	2129.441762	4240.849698	2120.928487	4239.865682	2120.436479	P	***1685.799022***	843.403149	1668.772473	834.889875	1667.788457	834.397867	16
45	4413.977358	2207.492317	4396.950809	2198.979043	4395.966793	2198.487035	R	1588.746258	794.876767	1571.719709	786.363493	1570.735693	785.871485	15
46	4511.030122	2256.018699	4494.003573	2247.505425	4493.019557	2247.013417	P	***1432.645147***	716.826212	1415.618598	708.312937	1414.634582	707.820929	14
47	4568.051586	2284.529431	4551.025037	2276.016157	4550.041021	2275.524149	G	1335.592383	668.299830	1318.565834	659.786555	1317.581818	659.294547	13
48	4655.083614	2328.045445	4638.057065	2319.532171	4637.073049	2319.040163	S	1278.570919	639.789098	1261.544370	631.275823	1260.560354	630.783815	12
49	4756.131293	2378.569285	4739.104744	2370.056010	4738.120728	2369.564002	T	1191.538891	596.273084	1174.512342	587.759809	1173.528326	587.267801	11
50	4813.152757	2407.080017	4796.126208	2398.566742	4795.142192	2398.074734	G	***1090.491212***	545.749244	1073.464663	537.235970	1072.480647	536.743962	10
51	4914.200436	2457.603856	4897.173887	2449.090582	4896.189871	2448.598574	T	1033.469748	517.238512	1016.443199	508.725238	1015.459183	508.233230	9
52	5100.279749	2550.643513	5083.253200	2542.130238	5082.269184	2541.638230	W	932.422069	466.714673	915.395520	458.201398	914.411504	457.709390	8
53	5214.322676	2607.664976	5197.296127	2599.151702	5196.312111	2598.659694	N	***746.342756***	373.675016	729.316207	365.161742	728.332191	364.669734	7
54	5311.375440	2656.191358	5294.348891	2647.678084	5293.364875	2647.186076	P	***632.299829***	316.653552	615.273280	308.140278	614.289264	307.648270	6
55	5368.396904	2684.702090	5351.370355	2676.188816	5350.386339	2675.696808	G	***535.247065***	268.127170	518.220516	259.613896	517.236500	259.121888	5
56	5455.428932	2728.218104	5438.402383	2719.704830	5437.418367	2719.212822	S	***478.225601***	239.616438	461.199052	231.103164	460.215036	230.611156	4
57	5542.460960	2771.734118	5525.434411	2763.220844	5524.450395	2762.728836	S	391.193573	196.100424	374.167024	187.587150	373.183008	187.095142	3
58	5671.503553	2836.255415	5654.477004	2827.742140	5653.492988	2827.250132	E	304.161545	152.584411	287.134996	144.071136	286.150980	143.579128	2
59							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
91.0	5844.608032	0.035038	NPGSSGTGGTATWKPGSSGPGSTGSWNSGSSGTGSTGNQNPGSPRPGSTGTWNPGSSER

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

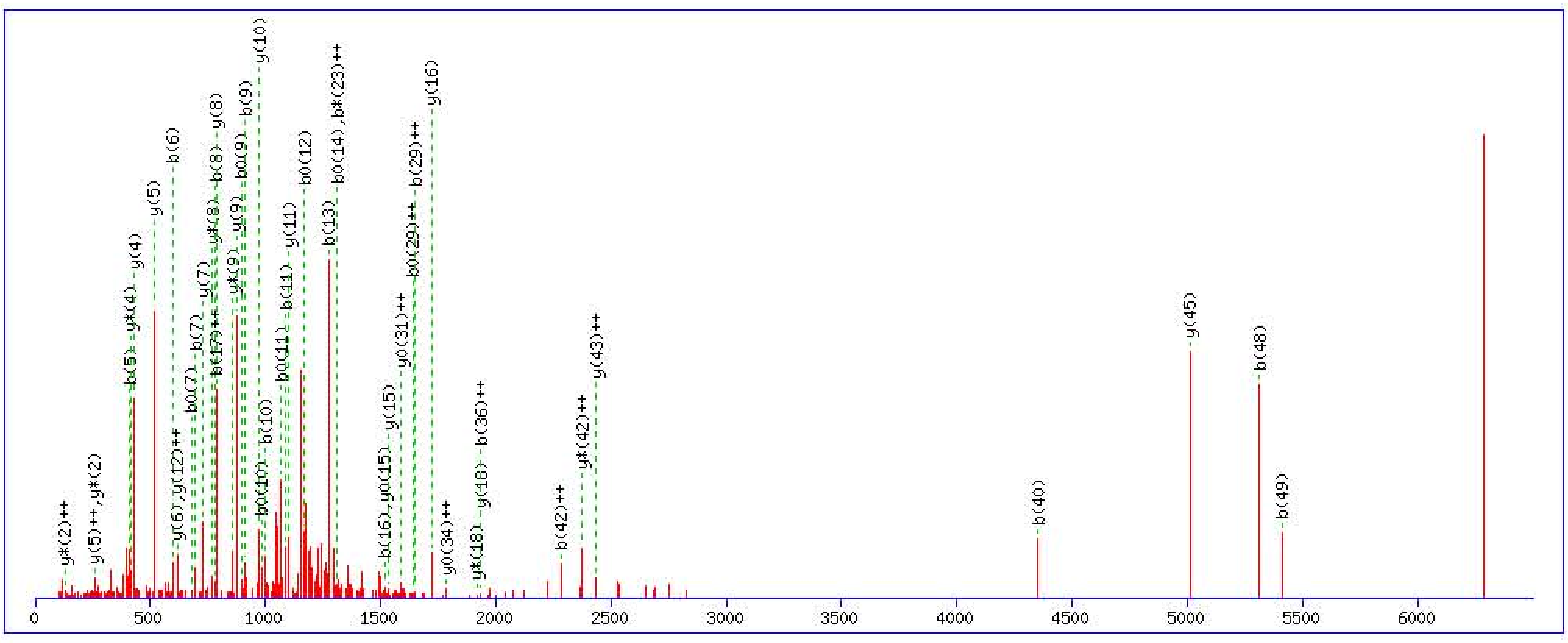
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSAGHWTSESSVSGSTGQWHSESGSFRPDSPGSGNARPNNPDWGTFEEVSGNVSPGTR**
Found in **FIBA_HUMAN**, Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2

Match to Query 90471: 6284.823864 from(1048.477920,6+) rtinseconds(2045) index(63379)
Title: Locus:1.1.1.2709.19 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 6500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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Monoisotopic mass of neutral peptide Mr(calc): 6284.792847
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18    : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.002
Matches : 49/646 fragment ions using 113 most intense peaks   (help)
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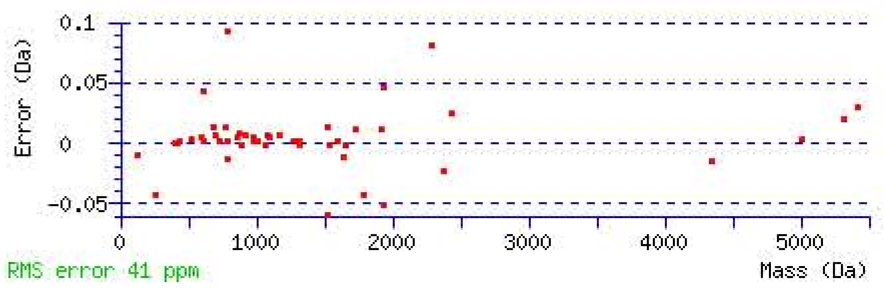
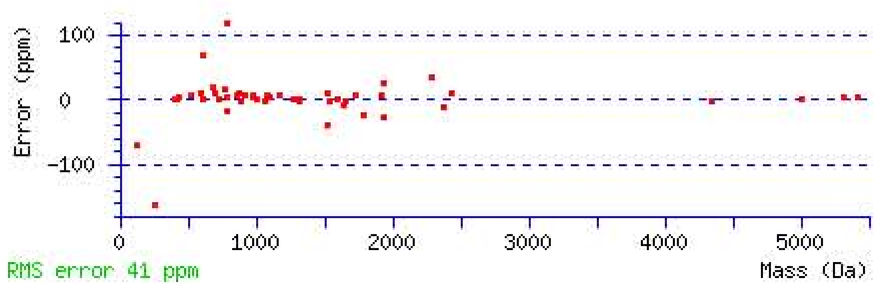
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							58
2	145.060768	73.034022			127.050203	64.028740	S	6228.778603	3114.892940	6211.752054	3106.379665	6210.768038	3105.887657	57
3	216.097882	108.552579			198.087317	99.547296	A	6141.746575	3071.376926	6124.720026	3062.863651	6123.736010	3062.371643	56
4	273.119346	137.063311			255.108781	128.058029	G	6070.709461	3035.858369	6053.682912	3027.345094	6052.698896	3026.853086	55
5	***410.178258***	205.592767			392.167693	196.587484	H	6013.687997	3007.347637	5996.661448	2998.834362	5995.677432	2998.342354	54
6	***596.257571***	298.632424			578.247006	289.627141	W	5876.629085	2938.818181	5859.602536	2930.304906	5858.618520	2929.812898	53
7	***697.305250***	349.156263			679.294685	340.150981	T	5690.549772	2845.778524	5673.523223	2837.265250	5672.539207	2836.773242	52
8	***784.337278***	392.672277			766.326713	383.666995	S	5589.502093	2795.254685	5572.475544	2786.741410	5571.491528	2786.249402	51
9	***913.379871***	457.193574			895.369306	448.188291	E	5502.470065	2751.738671	5485.443516	2743.225396	5484.459500	2742.733388	50
10	***1000.411899***	500.709588			982.401334	491.704305	S	5373.427472	2687.217374	5356.400923	2678.704100	5355.416907	2678.212092	49
11	***1087.443927***	544.225602			1069.433362	535.220319	S	5286.395444	2643.701360	5269.368895	2635.188086	5268.384879	2634.696078	48
12	1186.512341	593.759809			1168.501776	584.754526	V	5199.363416	2600.185346	5182.336867	2591.672072	5181.352851	2591.180064	47
13	***1273.544369***	637.275823			1255.533804	628.270540	S	5100.295002	2550.651139	5083.268453	2542.137865	5082.284437	2541.645857	46
14	1330.565833	665.786555			1312.555268	656.781272	G	***5013.262974***	2507.135125	4996.236425	2498.621851	4995.252409	2498.129843	45
15	1417.597861	709.302569			1399.587296	700.297286	S	4956.241510	2478.624393	4939.214961	2470.111119	4938.230945	2469.619111	44
16	***1518.645540***	759.826408			1500.634975	750.821126	T	4869.209482	2435.108379	4852.182933	2426.595105	4851.198917	2426.103097	43
17	1575.667004	**788.337140**			1557.656439	779.331858	G	4768.161803	2384.584540	4751.135254	2376.071265	4750.151238	2375.579257	42
18	2014.892330	1007.949803	1997.865781	999.436529	1996.881765	998.944521	Q	4711.140339	2356.073808	4694.113790	2347.560533	4693.129774	2347.068525	41
19	2200.971643	1100.989460	2183.945094	1092.476185	2182.961078	1091.984177	W	4271.915013	2136.461145	4254.888464	2127.947870	4253.904448	2127.455862	40
20	2338.030555	1169.518916	2321.004006	1161.005641	2320.019990	1160.513633	H	4085.835700	2043.421488	4068.809151	2034.908214	4067.825135	2034.416206	39
21	2425.062583	1213.034930	2408.036034	1204.521655	2407.052018	1204.029647	S	3948.776788	1974.892032	3931.750239	1966.378758	3930.766223	1965.886750	38
22	2554.105176	1277.556226	2537.078627	1269.042952	2536.094611	1268.550944	E	3861.744760	1931.376018	3844.718211	1922.862744	3843.734195	1922.370736	37
23	2641.137204	1321.072240	2624.110655	1312.558966	2623.126639	1312.066958	S	3732.702167	1866.854722	3715.675618	1858.341447	3714.691602	1857.849439	36
24	2698.158668	1349.582972	2681.132119	1341.069698	2680.148103	1340.577690	G	3645.670139	1823.338708	3628.643590	1814.825433	3627.659574	1814.333425	35
25	2785.190696	1393.098986	2768.164147	1384.585712	2767.180131	1384.093704	S	3588.648675	1794.827976	3571.622126	1786.314701	3570.638110	1785.822693	34
26	2932.259110	1466.633193	2915.232561	1458.119919	2914.248545	1457.627911	F	3501.616647	1751.311962	3484.590098	1742.798687	3483.606082	1742.306679	33
27	3088.360221	1544.683749	3071.333672	1536.170474	3070.349656	1535.678466	R	3354.548233	1677.777755	3337.521684	1669.264480	3336.537668	1668.772472	32
28	3185.412985	1593.210131	3168.386436	1584.696856	3167.402420	1584.204848	P	3198.447122	1599.727199	3181.420573	1591.213925	3180.436557	1590.721917	31
29	3300.439928	**1650.723602**	3283.413379	1642.210327	3282.429363	1641.718320	D	3101.394358	1551.200817	3084.367809	1542.687543	3083.383793	1542.195535	30
30	3387.471956	1694.239616	3370.445407	1685.726342	3369.461391	1685.234334	S	2986.367415	1493.687346	2969.340866	1485.174071	2968.356850	1484.682063	29
31	3484.524720	1742.765998	3467.498171	1734.252724	3466.514155	1733.760716	P	2899.335387	1450.171332	2882.308838	1441.658057	2881.324822	1441.166049	28
32	3541.546184	1771.276730	3524.519635	1762.763456	3523.535619	1762.271448	G	2802.282623	1401.644950	2785.256074	1393.131675	2784.272058	1392.639667	27
33	3628.578212	1814.792744	3611.551663	1806.279470	3610.567647	1805.787462	S	2745.261159	1373.134218	2728.234610	1364.620943	2727.250594	1364.128935	26
34	3685.599676	1843.303476	3668.573127	1834.790202	3667.589111	1834.298194	G	2658.229131	1329.618204	2641.202582	1321.104929	2640.218566	1320.612921	25
35	3799.642603	1900.324940	3782.616054	1891.811665	3781.632038	1891.319657	N	2601.207667	1301.107472	2584.181118	1292.594197	2583.197102	1292.102189	24
36	3870.679717	**1935.843497**	3853.653168	1927.330222	3852.669152	1926.838214	A	2487.164740	1244.086008	2470.138191	1235.572734	2469.154175	1235.080726	23
37	4026.780828	2013.894052	4009.754279	2005.380778	4008.770263	2004.888770	R	2416.127626	1208.567451	2399.101077	1200.054177	2398.117061	1199.562169	22
38	4123.833592	2062.420434	4106.807043	2053.907160	4105.823027	2053.415152	P	2260.026515	1130.516896	2242.999966	1122.003621	2242.015950	1121.511613	21
39	4237.876519	2119.441898	4220.849970	2110.928623	4219.865954	2110.436615	N	2162.973751	1081.990514	2145.947202	1073.477239	2144.963186	1072.985231	20
40	***4351.919446***	2176.463361	4334.892897	2167.950087	4333.908881	2167.458079	N	2048.930824	1024.969050	2031.904275	1016.455776	2030.920259	1015.963768	19
41	4448.972210	2224.989743	4431.945661	2216.476469	4430.961645	2215.984461	P	***1934.887897***	967.947587	1917.861348	959.434312	1916.877332	958.942304	18
42	4563.999153	**2282.503215**	4546.972604	2273.989940	4545.988588	2273.497932	D	1837.835133	919.421205	1820.808584	910.907930	1819.824568	910.415922	17
43	4750.078466	2375.542871	4733.051917	2367.029597	4732.067901	2366.537589	W	***1722.808190***	861.907733	1705.781641	853.394459	1704.797625	852.902451	16
44	4807.099930	2404.053603	4790.073381	2395.540329	4789.089365	2395.048321	G	***1536.728877***	768.868077	1519.702328	760.354802	1518.718312	759.862794	15
45	4908.147609	2454.577443	4891.121060	2446.064168	4890.137044	2445.572160	T	1479.707413	740.357345	1462.680864	731.844070	1461.696848	731.352062	14
46	5055.216023	2528.111650	5038.189474	2519.598375	5037.205458	2519.106367	F	1378.659734	689.833505	1361.633185	681.320231	1360.649169	680.828223	13
47	5184.258616	2592.632946	5167.232067	2584.119672	5166.248051	2583.627664	E	1231.591320	616.299298	1214.564771	607.786024	1213.580755	607.294016	12
48	***5313.301209***	2657.154243	5296.274660	2648.640968	5295.290644	2648.148960	E	***1102.548727***	551.778002	1085.522178	543.264727	1084.538162	542.772719	11
49	***5412.369623***	2706.688450	5395.343074	2698.175175	5394.359058	2697.683167	V	***973.506134***	487.256705	956.479585	478.743431	955.495569	478.251423	10
50	5499.401651	2750.204464	5482.375102	2741.691189	5481.391086	2741.199181	S	***874.437720***	437.722498	857.411171	429.209224	856.427155	428.717216	9
51	5556.423115	2778.715196	5539.396566	2770.201921	5538.412550	2769.709913	G	***787.405692***	394.206484	770.379143	385.693210	769.395127	385.201202	8
52	5670.466042	2835.736659	5653.439493	2827.223385	5652.455477	2826.731377	N	***730.384228***	365.695752	713.357679	357.182478	712.373663	356.690470	7
53	5769.534456	2885.270866	5752.507907	2876.757592	5751.523891	2876.265584	V	***616.341301***	308.674289	599.314752	300.161014	598.330736	299.669006	6
54	5856.566484	2928.786880	5839.539935	2920.273606	5838.555919	2919.781598	S	***517.272887***	259.140082	500.246338	250.626807	499.262322	250.134799	5
55	5953.619248	2977.313262	5936.592699	2968.799988	5935.608683	2968.307980	P	***430.240859***	215.624068	413.214310	207.110793	412.230294	206.618785	4
56	6010.640712	3005.823994	5993.614163	2997.310720	5992.630147	2996.818712	G	333.188095	167.097686	316.161546	158.584411	315.177530	158.092403	3
57	6111.688391	3056.347834	6094.661842	3047.834559	6093.677826	3047.342551	T	276.166631	138.586954	259.140082	130.073679	258.156066	129.581671	2
58							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
33.6	6284.792847	0.031017	GSAGHWTSESSVSGSTGQWHSESGSFRPDSPGSGNARPNNPDWGTFEEVSGNVSPGTR

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

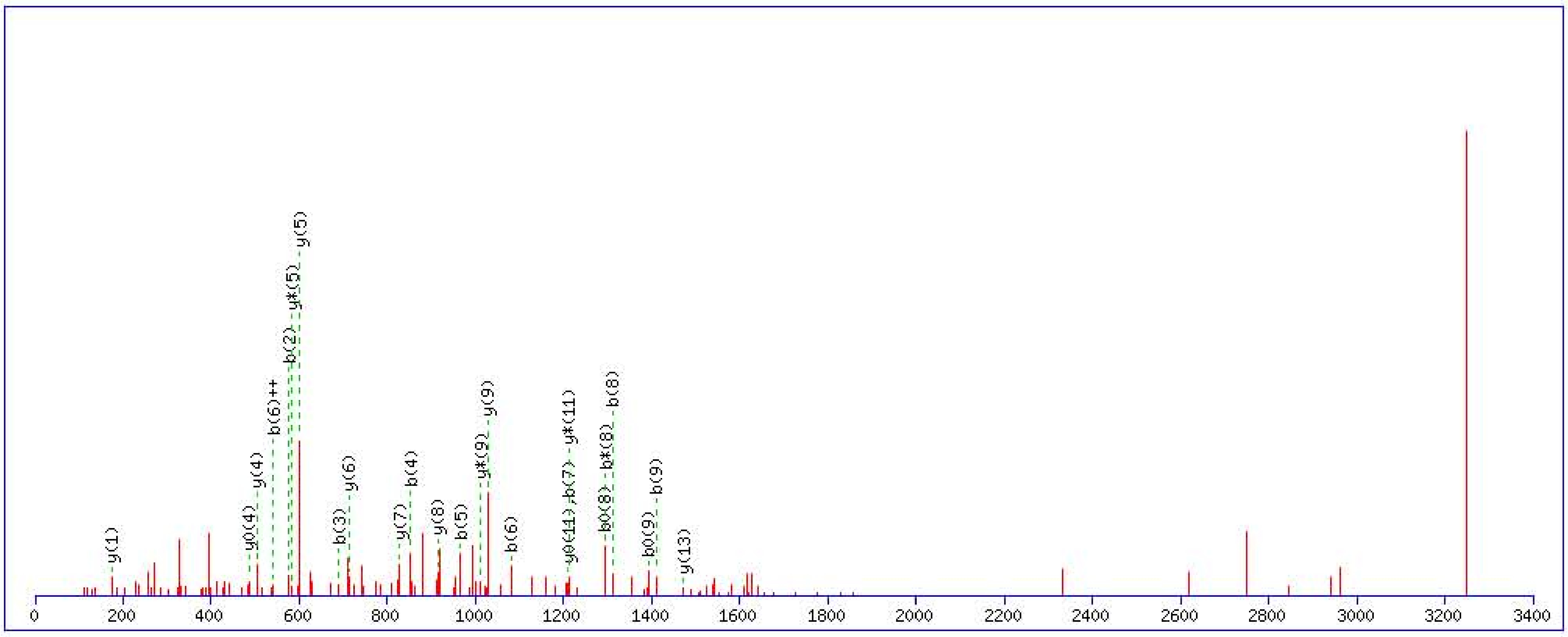
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQLYIDETVNSNIPTNLR**
Found in **FIBB_HUMAN**, Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2

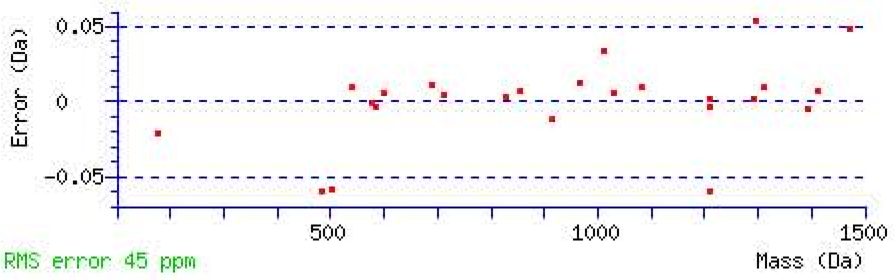
Match to Query 66763: 2437.250352 from(813.424060,3+) rtinseconds(2149) index(64059)
Title: Locus:1.1.1.2745.25 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

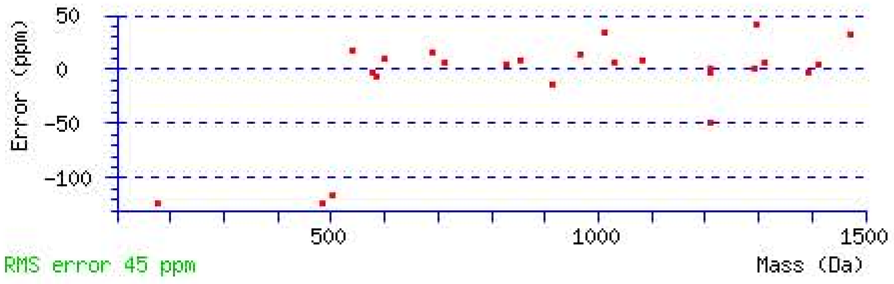
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2437.242355
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 25 **Expect:** 0.08
Matches : 25/186 fragment ions using 84 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	138.066188	69.536732					H							18
2	***577.291514***	289.149395	560.264965	280.636121			Q	2301.190744	1151.099010	2284.164195	1142.585735	2283.180179	1142.093727	17
3	***690.375578***	345.691427	673.349029	337.178153			L	1861.965418	931.486347	1844.938869	922.973073	1843.954853	922.481065	16
4	***853.438907***	427.223092	836.412358	418.709817			Y	1748.881354	874.944315	1731.854805	866.431041	1730.870789	865.939033	15
5	***966.522971***	483.765124	949.496422	475.251849			I	1585.818025	793.412651	1568.791476	784.899376	1567.807460	784.407368	14
6	***1081.549914***	541.278595	1064.523365	532.765321	1063.539349	532.273312	D	***1472.733961***	736.870619	1455.707412	728.357344	1454.723396	727.865336	13
7	***1210.592507***	605.799892	1193.565958	597.286617	1192.581942	596.794609	E	1357.707018	679.357147	1340.680469	670.843873	1339.696453	670.351865	12
8	***1311.640186***	656.323731	1294.613637	647.810457	1293.629621	647.318449	T	1228.664425	614.835851	1211.637876	606.322576	1210.653860	605.830568	11
9	***1410.708600***	705.857938	1393.682051	697.344664	1392.698035	696.852656	V	1127.616746	564.312011	1110.590197	555.798737	1109.606181	555.306729	10
10	1524.751527	762.879402	1507.724978	754.366127	1506.740962	753.874119	N	***1028.548332***	514.777804	1011.521783	506.264530	1010.537767	505.772522	9
11	1611.783555	806.395416	1594.757006	797.882141	1593.772990	797.390133	S	***914.505405***	457.756341	897.478856	449.243066	896.494840	448.751058	8
12	1725.826482	863.416879	1708.799933	854.903605	1707.815917	854.411597	N	***827.473377***	414.240327	810.446828	405.727052	809.462812	405.235044	7
13	1838.910546	919.958911	1821.883997	911.445637	1820.899981	910.953629	I	***713.430450***	357.218863	696.403901	348.705589	695.419885	348.213581	6
14	1935.963310	968.485293	1918.936761	959.972019	1917.952745	959.480011	P	***600.346386***	300.676831	583.319837	292.163557	582.335821	291.671549	5
15	2037.010989	1019.009133	2019.984440	1010.495858	2019.000424	1010.003850	T	***503.293622***	252.150449	486.267073	243.637175	485.283057	243.145167	4
16	2151.053916	1076.030596	2134.027367	1067.517321	2133.043351	1067.025313	N	402.245943	201.626610	385.219394	193.113335			3
17	2264.137980	1132.572628	2247.111431	1124.059353	2246.127415	1123.567345	L	288.203016	144.605146	271.176467	136.091872			2
18							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.4	2437.242355	0.007997	HQLYIDETVNSNIPTNLR

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

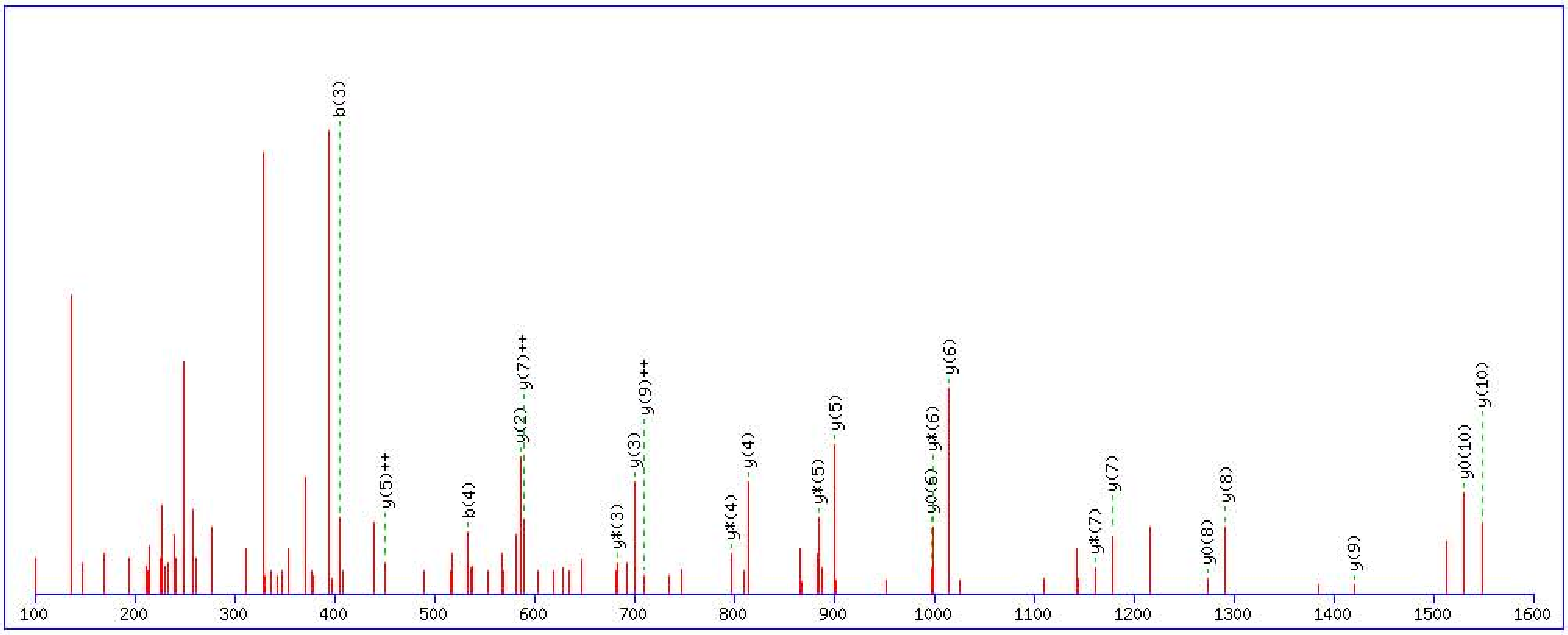
Mascot Search Results

Peptide View

MS/MS Fragmentation of **YLQEIYNSNNQK**
Found in **FIBG_HUMAN**, Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3

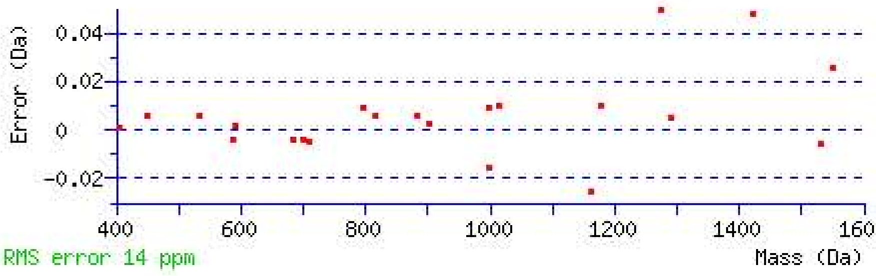
Match to Query 52726: 1823.888922 from(608.970250,3+) rtinseconds(1829) index(61853)
Title: Locus:1.1.1.2635.9 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

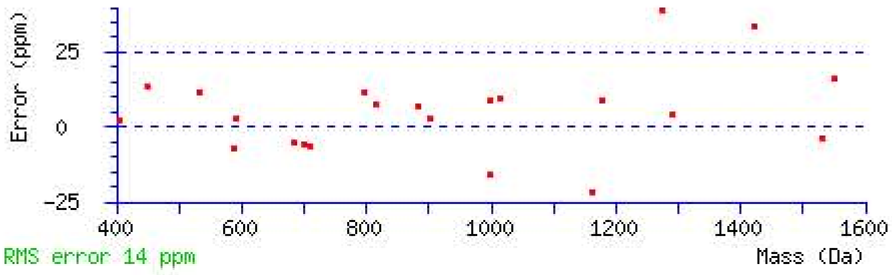
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1823.887573
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 0.00028
Matches : 22/114 fragment ions using 40 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	164.070605	82.538940					Y							12
2	277.154669	139.080973					L	1661.831567	831.419422	1644.805018	822.906147	1643.821002	822.414139	11
3	**405.213247**	203.110262	388.186698	194.596987			Q	***1548.747503***	774.877390	1531.720954	766.364115	1530.736938	765.872107	10
4	**534.255840**	267.631558	517.229291	259.118284	516.245275	258.626276	E	***1420.688925***	710.848100	1403.662376	702.334826	1402.678360	701.842818	9
5	647.339904	324.173590	630.313355	315.660316	629.329339	315.168308	I	***1291.646332***	646.326804	1274.619783	637.813530	1273.635767	637.321522	8
6	810.403233	405.705255	793.376684	397.191980	792.392668	396.699972	Y	***1178.562268***	589.784772	1161.535719	581.271498	1160.551703	580.779489	7
7	924.446160	462.726718	907.419611	454.213443	906.435595	453.721435	N	***1015.498939***	508.253108	998.472390	499.739833	997.488374	499.247825	6
8	1011.478188	506.242732	994.451639	497.729457	993.467623	497.237449	S	***901.456012***	451.231644	884.429463	442.718370	883.445447	442.226362	5
9	1125.521115	563.264196	1108.494566	554.750921	1107.510550	554.258913	N	***814.423984***	407.715630	797.397435	399.202356			4
10	1239.564042	620.285659	1222.537493	611.772385	1221.553477	611.280376	N	***700.381057***	350.694167	683.354508	342.180892			3
11	1678.789368	839.898322	1661.762819	831.385048	1660.778803	830.893039	Q	***586.338130***	293.672703	569.311581	285.159429			2
12							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.7	1823.887573	0.001349	YLQEIYNSNNQK

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

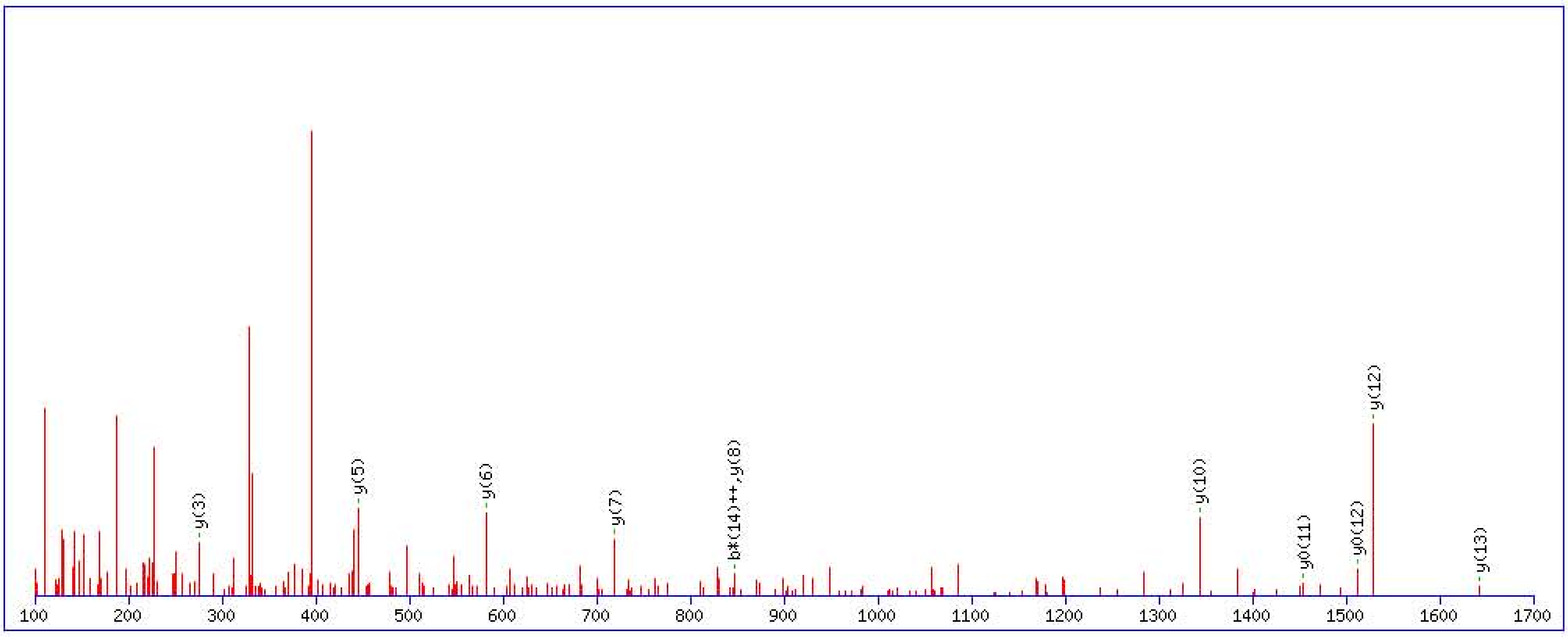
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTIGEGQQHHLGGAK**
Found in **FIBG_HUMAN**, Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3

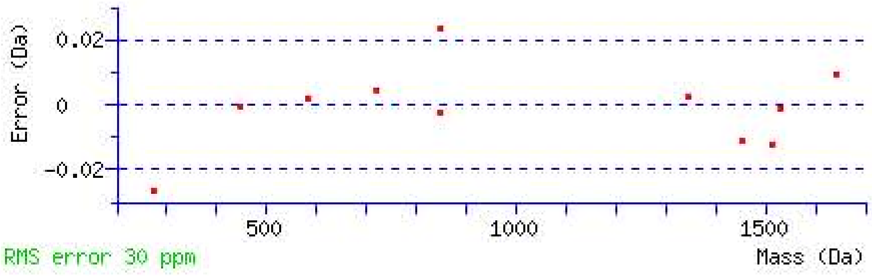
Match to Query 53566: 1855.965456 from(464.998640,4+) rtinseconds(1485) index(59428)
Title: Locus:1.1.1.2515.7 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

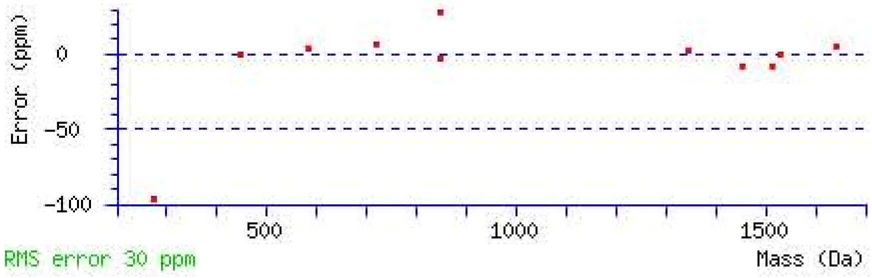
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1855.972687
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 29 **Expect:** 0.037
Matches : 11/134 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							15
2	215.139019	108.073147			197.128454	99.067865	T	1743.895902	872.451589	1726.869353	863.938314	1725.885337	863.446306	14
3	328.223083	164.615179			310.212518	155.609897	I	***1642.848223***	821.927749	1625.821674	813.414475	1624.837658	812.922467	13
4	385.244547	193.125911			367.233982	184.120629	G	***1529.764159***	765.385717	1512.737610	756.872443	1511.753594	756.380435	12
5	514.287140	257.647208			496.276575	248.641926	E	1472.742695	736.874985	1455.716146	728.361711	1454.732130	727.869703	11
6	571.308604	286.157940			553.298039	277.152658	G	***1343.700102***	672.353689	1326.673553	663.840414			10
7	1010.533930	505.770603	993.507381	497.257329	992.523365	496.765321	Q	1286.678638	643.842957	1269.652089	635.329682			9
8	1138.592508	569.799892	1121.565959	561.286618	1120.581943	560.794609	Q	***847.453312***	424.230294	830.426763	415.717019			8
9	1275.651420	638.329348	1258.624871	629.816074	1257.640855	629.324065	H	***719.394734***	360.201005	702.368185	351.687730			7
10	1412.710332	706.858804	1395.683783	698.345530	1394.699767	697.853521	H	***582.335822***	291.671549	565.309273	283.158274			6
11	1525.794396	763.400836	1508.767847	754.887561	1507.783831	754.395553	L	***445.276910***	223.142093	428.250361	214.628818			5
12	1582.815860	791.911568	1565.789311	783.398293	1564.805295	782.906285	G	332.192846	166.600061	315.166297	158.086786			4
13	1639.837324	820.422300	1622.810775	811.909025	1621.826759	811.417017	G	***275.171382***	138.089329	258.144833	129.576054			3
14	1710.874438	855.940857	1693.847889	847.427582	1692.863873	846.935574	A	218.149918	109.578597	201.123369	101.065322			2
15							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.7	1855.972687	-0.007231	LTIGEGQQHHLGGAK
23.1	1855.972687	-0.007231	LTIGEGQQHHLGGAK

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

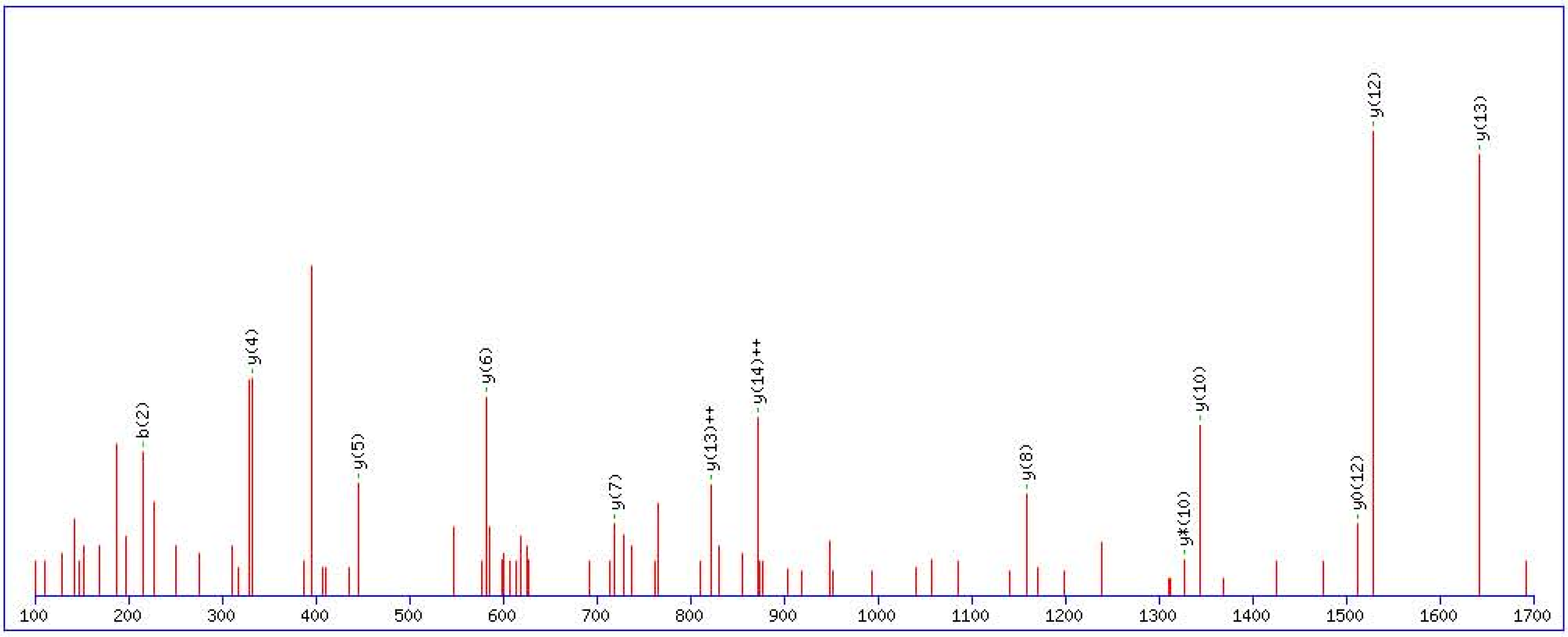
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTIGEGQQHHLGGAK**
Found in **FIBG_HUMAN**, Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3

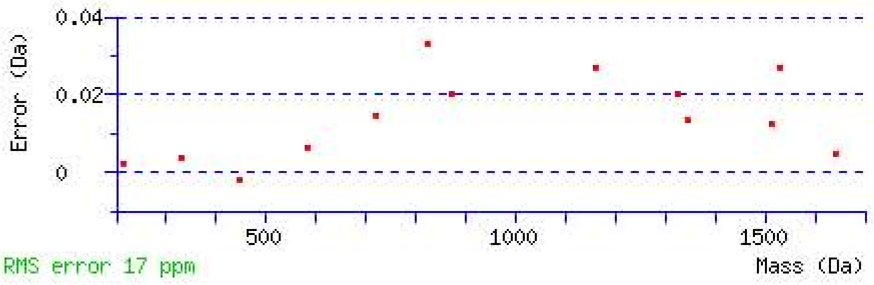
Match to Query 53574: 1855.983582 from(619.668470,3+) rtinseconds(1433) index(3529)
Title: Locus:1.1.1.2219.23 File:"2013-07-02 CLN FXIII 30 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

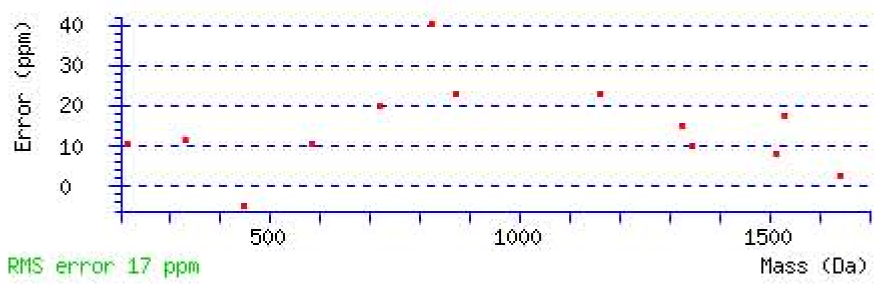
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1855.972687
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 35  Expect: 0.0007
Matches : 13/134 fragment ions using 31 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							15
2	215.139019	108.073147			197.128454	99.067865	T	1743.895902	872.451589	1726.869353	863.938314	1725.885337	863.446306	14
3	328.223083	164.615179			310.212518	155.609897	I	***1642.848223***	821.927749	1625.821674	813.414475	1624.837658	812.922467	13
4	385.244547	193.125911			367.233982	184.120629	G	***1529.764159***	765.385717	1512.737610	756.872443	1511.753594	756.380435	12
5	514.287140	257.647208			496.276575	248.641926	E	1472.742695	736.874985	1455.716146	728.361711	1454.732130	727.869703	11
6	571.308604	286.157940			553.298039	277.152658	G	***1343.700102***	672.353689	1326.673553	663.840414			10
7	699.367182	350.187229	682.340633	341.673955	681.356617	341.181947	Q	1286.678638	643.842957	1269.652089	635.329682			9
8	1138.592508	569.799892	1121.565959	561.286618	1120.581943	560.794609	Q	***1158.620060***	579.813668	1141.593511	571.300393			8
9	1275.651420	638.329348	1258.624871	629.816074	1257.640855	629.324065	H	***719.394734***	360.201005	702.368185	351.687730			7
10	1412.710332	706.858804	1395.683783	698.345530	1394.699767	697.853521	H	***582.335822***	291.671549	565.309273	283.158274			6
11	1525.794396	763.400836	1508.767847	754.887561	1507.783831	754.395553	L	***445.276910***	223.142093	428.250361	214.628818			5
12	1582.815860	791.911568	1565.789311	783.398293	1564.805295	782.906285	G	***332.192846***	166.600061	315.166297	158.086786			4
13	1639.837324	820.422300	1622.810775	811.909025	1621.826759	811.417017	G	275.171382	138.089329	258.144833	129.576054			3
14	1710.874438	855.940857	1693.847889	847.427582	1692.863873	846.935574	A	218.149918	109.578597	201.123369	101.065322			2
15							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.0	1855.972687	0.010895	LTIGEGQQHHLGGAK
25.7	1855.972687	0.010895	LTIGEGQQHHLGGAK
1.4	1856.000519	-0.016937	TIVVTTILESPYVMYK

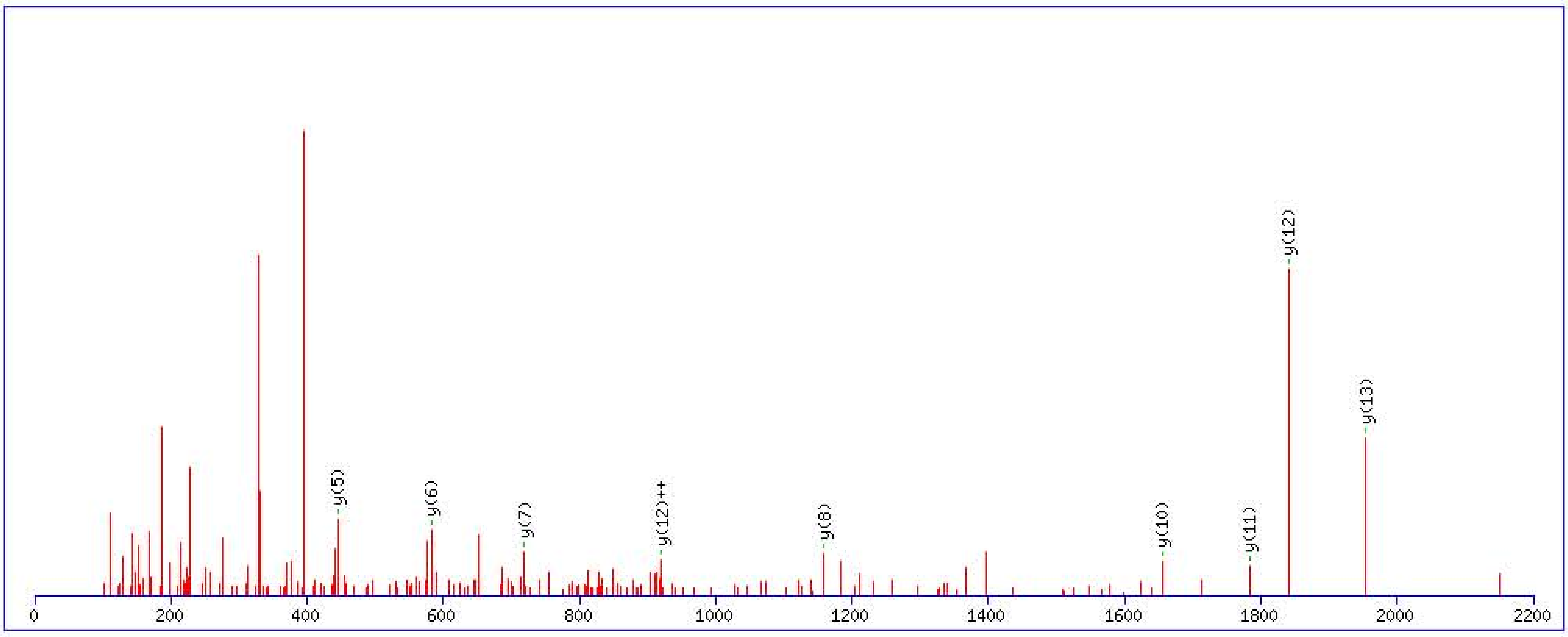
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LTIGEGQQHHLGGAK**
Found in **FIBG_HUMAN**, Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3

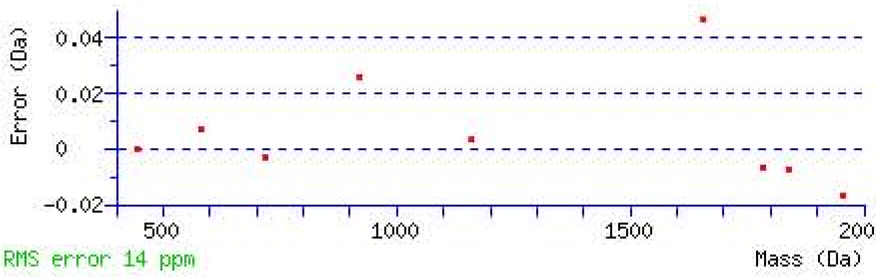
Match to Query 60870: 2167.135816 from(542.791230,4+) rtinseconds(1787) index(61617)
Title: Locus:1.1.1.2620.13 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

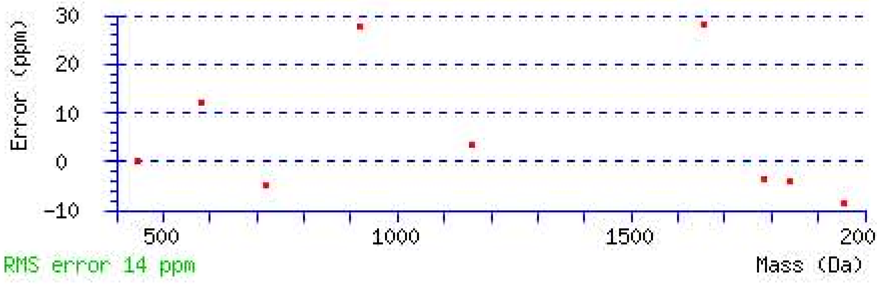
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2167.139435
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7     : Biotin:Thermo-21345 (Q)
Q8     : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0046
Matches : 9/134 fragment ions using 20 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							15
2	215.139019	108.073147			197.128454	99.067865	T	2055.062650	1028.034963	2038.036101	1019.521688	2037.052085	1019.029680	14
3	328.223083	164.615179			310.212518	155.609897	I	***1954.014971***	977.511123	1936.988422	968.997849	1936.004406	968.505841	13
4	385.244547	193.125911			367.233982	184.120629	G	***1840.930907***	920.969091	1823.904358	912.455817	1822.920342	911.963809	12
5	514.287140	257.647208			496.276575	248.641926	E	***1783.909443***	892.458359	1766.882894	883.945085	1765.898878	883.453077	11
6	571.308604	286.157940			553.298039	277.152658	G	***1654.866850***	827.937063	1637.840301	819.423788			10
7	1010.533930	505.770603	993.507381	497.257329	992.523365	496.765321	Q	1597.845386	799.426331	1580.818837	790.913056			9
8	1449.759256	725.383266	1432.732707	716.869992	1431.748691	716.377984	Q	***1158.620060***	579.813668	1141.593511	571.300393			8
9	1586.818168	793.912722	1569.791619	785.399448	1568.807603	784.907440	H	***719.394734***	360.201005	702.368185	351.687730			7
10	1723.877080	862.442178	1706.850531	853.928904	1705.866515	853.436895	H	***582.335822***	291.671549	565.309273	283.158274			6
11	1836.961144	918.984210	1819.934595	910.470936	1818.950579	909.978927	L	***445.276910***	223.142093	428.250361	214.628818			5
12	1893.982608	947.494942	1876.956059	938.981667	1875.972043	938.489659	G	332.192846	166.600061	315.166297	158.086786			4
13	1951.004072	976.005674	1933.977523	967.492399	1932.993507	967.000391	G	275.171382	138.089329	258.144833	129.576054			3
14	2022.041186	1011.524231	2005.014637	1003.010956	2004.030621	1002.518948	A	218.149918	109.578597	201.123369	101.065322			2
15							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.4	2167.139435	-0.003619	LTIGEGQQHHLGGAK

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

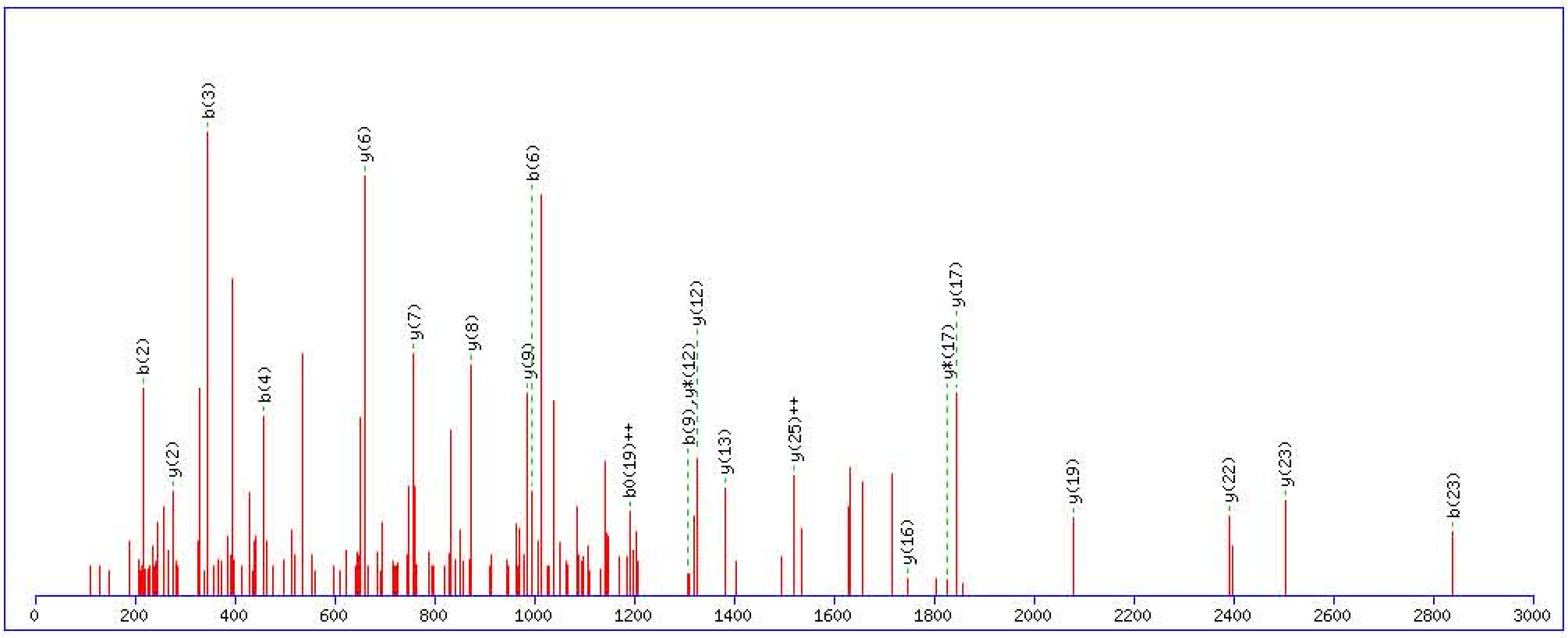
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TDELPQLVTLPHPNLHGPEILDVPSTVQK**
Found in **FINC_HUMAN**, Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4

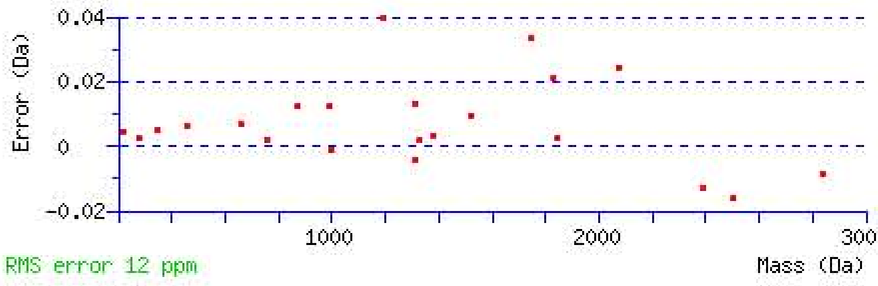
Match to Query 79729: 3497.881536 from(875.477660,4+) rtinseconds(2574) index(66541)
Title: Locus:1.1.1.2893.21 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

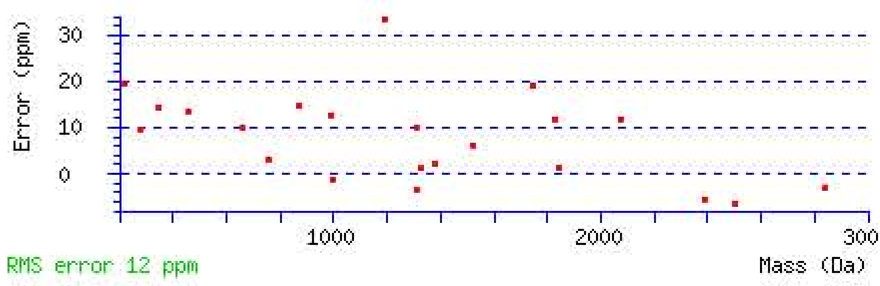
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3497.859238
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 57  Expect: 2.9e-005
Matches : 22/320 fragment ions using 40 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							29
2	***217.081898***	109.044587			199.071333	100.039304	D	3397.818827	1699.413051	3380.792278	1690.899777	3379.808262	1690.407769	28
3	***346.124491***	173.565883			328.113926	164.560601	E	3282.791884	1641.899580	3265.765335	1633.386305	3264.781319	1632.894297	27
4	***459.208555***	230.107915			441.197990	221.102633	L	3153.749291	1577.378283	3136.722742	1568.865009	3135.738726	1568.373001	26
5	556.261319	278.634298			538.250754	269.629015	P	3040.665227	1520.836251	3023.638678	1512.322977	3022.654662	1511.830969	25
6	***995.486645***	498.246961	978.460096	489.733686	977.476080	489.241678	Q	2943.612463	1472.309869	2926.585914	1463.796595	2925.601898	1463.304587	24
7	1108.570709	554.788993	1091.544160	546.275718	1090.560144	545.783710	L	***2504.387137***	1252.697206	2487.360588	1244.183932	2486.376572	1243.691924	23
8	1207.639123	604.323200	1190.612574	595.809925	1189.628558	595.317917	V	***2391.303073***	1196.155174	2374.276524	1187.641900	2373.292508	1187.149892	22
9	***1308.686802***	654.847039	1291.660253	646.333765	1290.676237	645.841757	T	2292.234659	1146.620967	2275.208110	1138.107693	2274.224094	1137.615685	21
10	1421.770866	711.389071	1404.744317	702.875797	1403.760301	702.383789	L	2191.186980	1096.097128	2174.160431	1087.583853	2173.176415	1087.091845	20
11	1518.823630	759.915453	1501.797081	751.402179	1500.813065	750.910171	P	***2078.102916***	1039.555096	2061.076367	1031.041821	2060.092351	1030.549813	19
12	1655.882542	828.444909	1638.855993	819.931635	1637.871977	819.439627	H	1981.050152	991.028714	1964.023603	982.515440	1963.039587	982.023432	18
13	1752.935306	876.971291	1735.908757	868.458017	1734.924741	867.966009	P	***1843.991240***	922.499258	1826.964691	913.985984	1825.980675	913.493976	17
14	1866.978233	933.992755	1849.951684	925.479480	1848.967668	924.987472	N	***1746.938476***	873.972876	1729.911927	865.459602	1728.927911	864.967594	16
15	1980.062297	990.534787	1963.035748	982.021512	1962.051732	981.529504	L	1632.895549	816.951413	1615.869000	808.438138	1614.884984	807.946130	15
16	2117.121209	1059.064242	2100.094660	1050.550968	2099.110644	1050.058960	H	1519.811485	760.409381	1502.784936	751.896106	1501.800920	751.404098	14
17	2174.142673	1087.574974	2157.116124	1079.061700	2156.132108	1078.569692	G	***1382.752573***	691.879925	1365.726024	683.366650	1364.742008	682.874642	13
18	2271.195437	1136.101356	2254.168888	1127.588082	2253.184872	1127.096074	P	***1325.731109***	663.369193	1308.704560	654.855918	1307.720544	654.363910	12
19	2400.238030	1200.622653	2383.211481	1192.109378	2382.227465	1191.617370	E	1228.678345	614.842811	1211.651796	606.329536	1210.667780	605.837528	11
20	2513.322094	1257.164685	2496.295545	1248.651410	2495.311529	1248.159402	I	1099.635752	550.321514	1082.609203	541.808240	1081.625187	541.316231	10
21	2626.406158	1313.706717	2609.379609	1305.193442	2608.395593	1304.701435	L	***986.551688***	493.779482	969.525139	485.266207	968.541123	484.774199	9
22	2741.433101	1371.220188	2724.406552	1362.706914	2723.422536	1362.214906	D	***873.467624***	437.237450	856.441075	428.724175	855.457059	428.232167	8
23	***2840.501515***	1420.754395	2823.474966	1412.241121	2822.490950	1411.749113	V	***758.440681***	379.723978	741.414132	371.210704	740.430116	370.718696	7
24	2937.554279	1469.280777	2920.527730	1460.767503	2919.543714	1460.275495	P	***659.372267***	330.189772	642.345718	321.676497	641.361702	321.184489	6
25	3024.586307	1512.796791	3007.559758	1504.283517	3006.575742	1503.791509	S	562.319503	281.663389	545.292954	273.150115	544.308938	272.658107	5
26	3125.633986	1563.320631	3108.607437	1554.807356	3107.623421	1554.315348	T	475.287475	238.147375	458.260926	229.634101	457.276910	229.142093	4
27	3224.702400	1612.854838	3207.675851	1604.341563	3206.691835	1603.849555	V	374.239796	187.623536	357.213247	179.110261			3
28	3352.760978	1676.884127	3335.734429	1668.370852	3334.750413	1667.878844	Q	***275.171382***	138.089329	258.144833	129.576055			2
29							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.5	3497.859238	0.022298	TDELPQLVTLPHPNLHGPEILDVPSTVQK

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

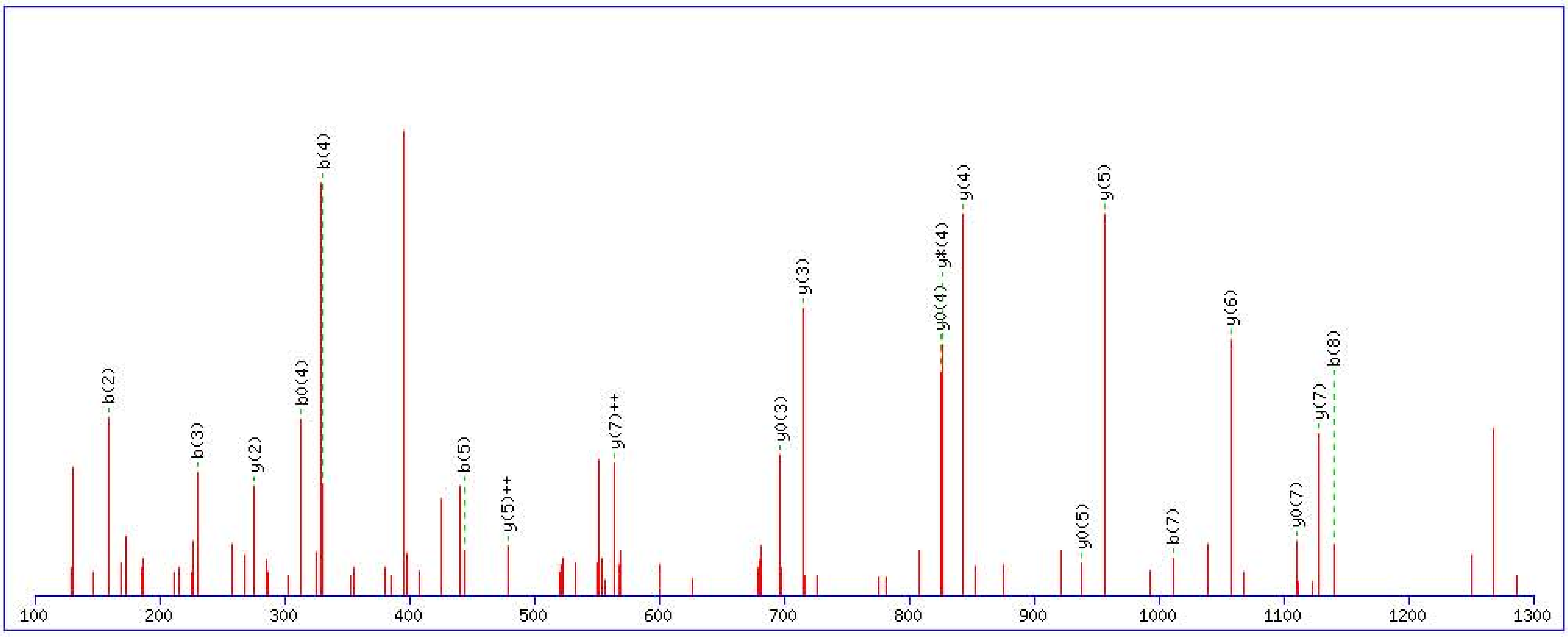
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SAATLQQEK**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

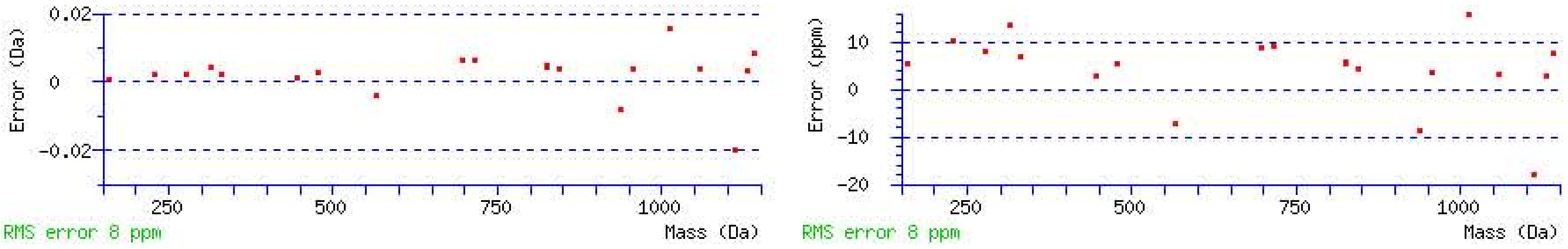
Match to Query 34844: 1285.666248 from(643.840400,2+) rtinseconds(1457) index(59220)
Title: Locus:1.1.1.2505.18 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1285.669998
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 41 **Expect:** 0.0014
Matches : 20/84 fragment ions using 33 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							9
2	***159.076418***	80.041847			141.065853	71.036564	A	1199.645272	600.326274	1182.618723	591.813000	1181.634707	591.320991	8
3	***230.113532***	115.560404			212.102967	106.555121	A	***1128.608158***	564.807717	1111.581609	556.294443	1110.597593	555.802435	7
4	***331.161211***	166.084243			313.150646	157.078961	T	***1057.571044***	529.289160	1040.544495	520.775886	1039.560479	520.283878	6
5	***444.245275***	222.626275			426.234710	213.620993	L	***956.523365***	478.765321	939.496816	470.252046	938.512800	469.760038	5
6	572.303853	286.655565	555.277304	278.142290	554.293288	277.650282	Q	***843.439301***	422.223289	826.412752	413.710014	825.428736	413.218006	4
7	***1011.529179***	506.268228	994.502630	497.754953	993.518614	497.262945	Q	***715.380723***	358.194000	698.354174	349.680725	697.370158	349.188717	3
8	***1140.571772***	570.789524	1123.545223	562.276250	1122.561207	561.784242	E	***276.155397***	138.581336	259.128848	130.068062	258.144832	129.576054	2
9							K	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.8	1285.669998	-0.003750	SAATLQQEK
33.8	1285.669998	-0.003750	SAATLQQEK
9.7	1285.652237	0.014011	AMQIQEQK
6.5	1285.669998	-0.003750	ASLDQGKEK
4.3	1285.652252	0.013996	VCALEQQK
4.2	1285.651367	0.014881	LLQAVENGDAEK
4.0	1285.649582	0.016666	SVPCPRCVRR
3.7	1285.652252	0.013996	VCALEQQK
3.0	1285.648880	0.017368	MYEFAGRLVGK
3.0	1285.652237	0.014011	AMQIQEQK

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

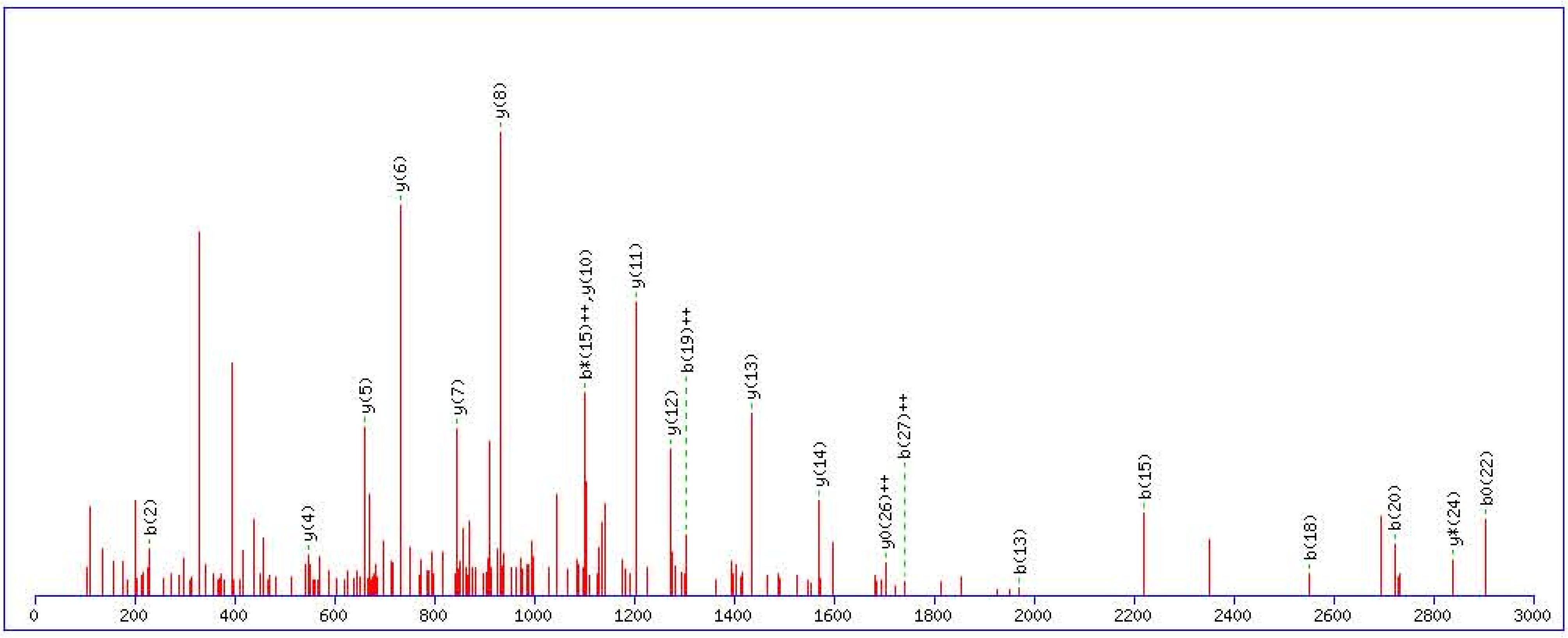
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MVQEQCCHSQLEELHCATGISLANEQDR**
Found in **FBLN1_HUMAN**, Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4

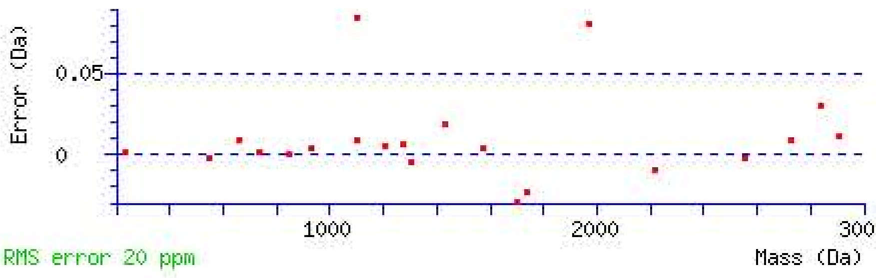
Match to Query 80863: 3653.630216 from(914.414830,4+) rtinseconds(1962) index(62874)
Title: Locus:1.1.1.2680.20 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

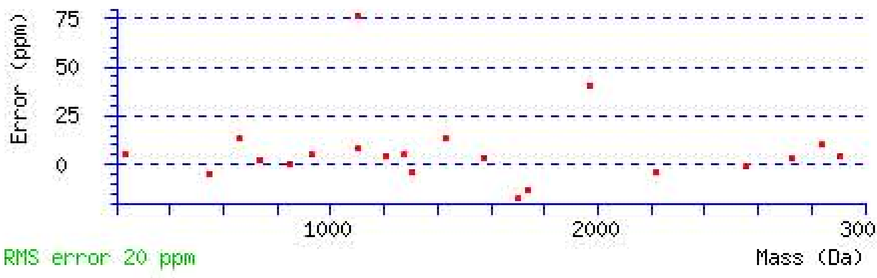
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3653.615311
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 64 **Expect:** 1.9e-006
Matches : 21/312 fragment ions using 26 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	132.047761	66.527518					M							28
2	**231.116175**	116.061725					V	3523.582122	1762.294699	3506.555573	1753.781424	3505.571557	1753.289416	27
3	670.341501	335.674389	653.314952	327.161114			Q	3424.513708	1712.760492	3407.487159	1704.247217	3406.503143	1703.755209	26
4	799.384094	400.195685	782.357545	391.682411	781.373529	391.190403	E	2985.288382	1493.147829	2968.261833	1484.634554	2967.277817	1484.142546	25
5	927.442672	464.224974	910.416123	455.711700	909.432107	455.219692	Q	2856.245789	1428.626532	2839.219240	1420.113258	2838.235224	1419.621250	24
6	1087.473321	544.240299	1070.446772	535.727024	1069.462756	535.235016	C	2728.187211	1364.597243	2711.160662	1356.083969	2710.176646	1355.591961	23
7	1247.503970	624.255623	1230.477421	615.742349	1229.493405	615.250341	C	2568.156562	1284.581919	2551.130013	1276.068644	2550.145997	1275.576636	22
8	1384.562882	692.785079	1367.536333	684.271805	1366.552317	683.779797	H	2408.125913	1204.566594	2391.099364	1196.053320	2390.115348	1195.561312	21
9	1471.594910	736.301093	1454.568361	727.787819	1453.584345	727.295811	S	2271.067001	1136.037138	2254.040452	1127.523864	2253.056436	1127.031856	20
10	1599.653488	800.330382	1582.626939	791.817108	1581.642923	791.325100	Q	2184.034973	1092.521124	2167.008424	1084.007850	2166.024408	1083.515842	19
11	1712.737552	856.872414	1695.711003	848.359140	1694.726987	847.867132	L	2055.976395	1028.491835	2038.949846	1019.978561	2037.965830	1019.486553	18
12	1841.780145	921.393711	1824.753596	912.880436	1823.769580	912.388428	E	1942.892331	971.949804	1925.865782	963.436529	1924.881766	962.944521	17
13	**1970.822738**	985.915007	1953.796189	977.401733	1952.812173	976.909725	E	1813.849738	907.428507	1796.823189	898.915233	1795.839173	898.423225	16
14	2083.906802	1042.457039	2066.880253	1033.943764	2065.896237	1033.451756	L	1684.807145	842.907211	1667.780596	834.393936	1666.796580	833.901928	15
15	**2220.965714**	1110.986495	2203.939165	1102.473220	2202.955149	1101.981212	H	***1571.723081***	786.365179	1554.696532	777.851904	1553.712516	777.359896	14
16	2380.996363	1191.001819	2363.969814	1182.488545	2362.985798	1181.996537	C	***1434.664169***	717.835723	1417.637620	709.322448	1416.653604	708.830440	13
17	2452.033477	1226.520376	2435.006928	1218.007102	2434.022912	1217.515094	A	***1274.633520***	637.820398	1257.606971	629.307124	1256.622955	628.815116	12
18	**2553.081156**	1277.044216	2536.054607	1268.530941	2535.070591	1268.038933	T	***1203.596406***	602.301841	1186.569857	593.788567	1185.585841	593.296559	11
19	2610.102620	**1305.554948**	2593.076071	1297.041673	2592.092055	1296.549665	G	***1102.548727***	551.778002	1085.522178	543.264727	1084.538162	542.772719	10
20	**2723.186684**	1362.096980	2706.160135	1353.583705	2705.176119	1353.091697	I	1045.527263	523.267270	1028.500714	514.753995	1027.516698	514.261987	9
21	2810.218712	1405.612994	2793.192163	1397.099719	2792.208147	1396.607711	S	***932.443199***	466.725238	915.416650	458.211963	914.432634	457.719955	8
22	2923.302776	1462.155026	2906.276227	1453.641751	2905.292211	1453.149743	L	***845.411171***	423.209224	828.384622	414.695949	827.400606	414.203941	7
23	2994.339890	1497.673583	2977.313341	1489.160308	2976.329325	1488.668301	A	***732.327107***	366.667192	715.300558	358.153917	714.316542	357.661909	6
24	3108.382817	1554.695047	3091.356268	1546.181772	3090.372252	1545.689764	N	***661.289993***	331.148635	644.263444	322.635360	643.279428	322.143352	5
25	3237.425410	1619.216343	3220.398861	1610.703069	3219.414845	1610.211061	E	***547.247066***	274.127171	530.220517	265.613897	529.236501	265.121889	4
26	3365.483988	1683.245632	3348.457439	1674.732358	3347.473423	1674.240350	Q	418.204473	209.605874	401.177924	201.092600	400.193908	200.600592	3
27	3480.510931	**1740.759104**	3463.484382	1732.245829	3462.500366	1731.753821	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
28							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.2	3653.615311	0.014905	MVQEQCCHSQLEELHCATGISLANEQDR
61.4	3653.615311	0.014905	MVQEQCCHSQLEELHCATGISLANEQDR
61.4	3653.615311	0.014905	MVQEQCCHSQLEELHCATGISLANEQDR
3.3	3653.684525	-0.054309	FTDRETEAAAGTLAHMGFAPPTSFSHFTDQELR

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

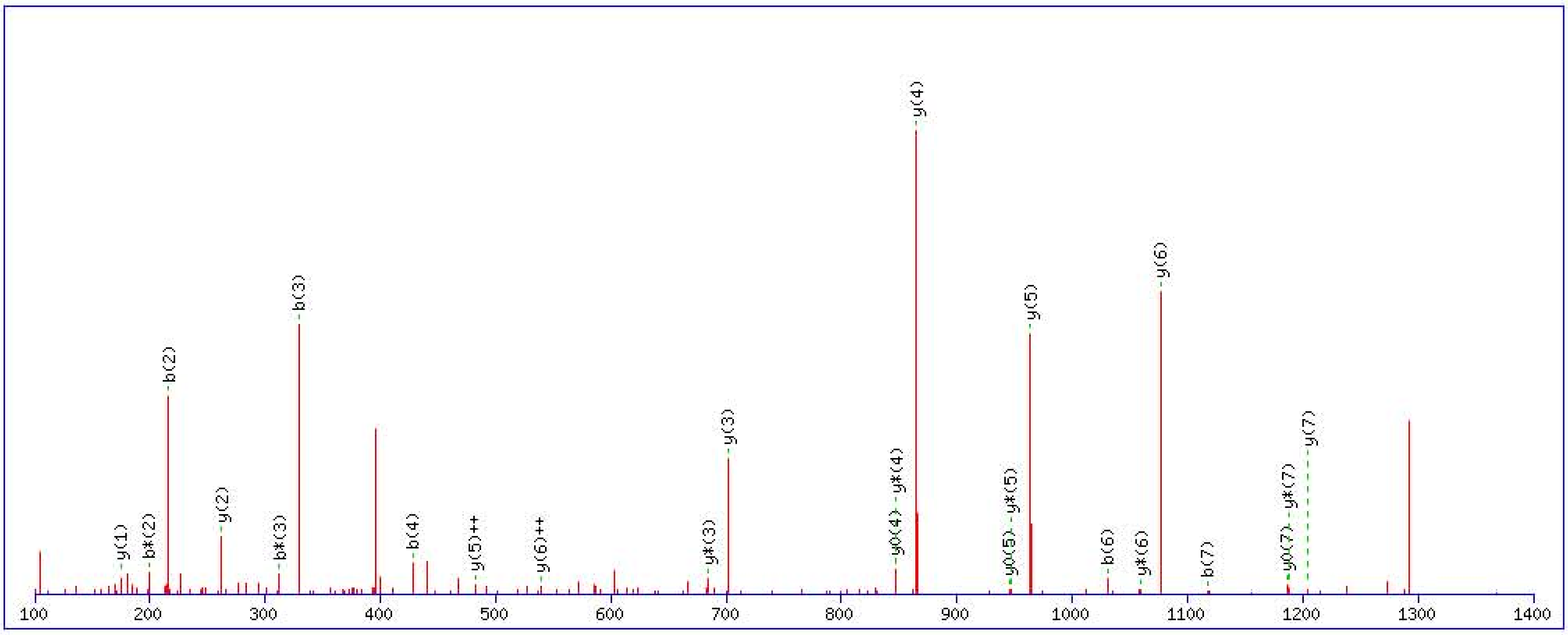
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

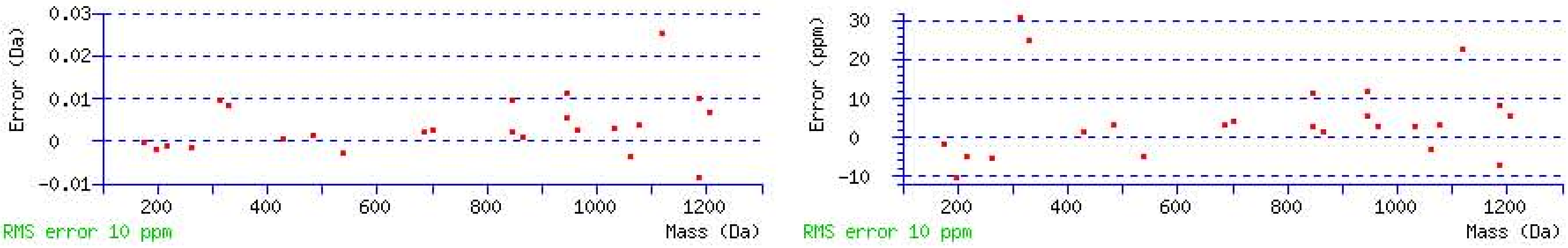
Match to Query 35015: 1290.670728 from(646.342640,2+) rtinseconds(1680) index(60818)
Title: Locus:1.1.1.2583.6 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

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



Monoisotopic mass of neutral peptide Mr(calc): 1290.675430
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 37 **Expect:** 0.0011
Matches : 24/80 fragment ions using 48 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							8
2	**216.097882**	108.552579	199.071333	100.039305	198.087317	99.547296	Q	***1204.650691***	602.828984	1187.624142	594.315709	1186.640126	593.823701	7
3	**329.181946**	165.094611	312.155397	156.581336	311.171381	156.089328	L	***1076.592113***	538.799695	1059.565564	530.286420	1058.581548	529.794412	6
4	**428.250360**	214.628818	411.223811	206.115544	410.239795	205.623536	V	***963.508049***	482.257663	946.481500	473.744388	945.497484	473.252380	5
5	591.313689	296.160483	574.287140	287.647208	573.303124	287.155200	Y	***864.439635***	432.723456	847.413086	424.210181	846.429070	423.718173	4
6	**1030.539015**	515.773146	1013.512466	507.259871	1012.528450	506.767863	Q	***701.376306***	351.191791	684.349757	342.678517	683.365741	342.186509	3
7	**1117.571043**	559.289160	1100.544494	550.775885	1099.560478	550.283877	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
8							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.1	1290.675430	-0.004702	SQLVYQSR
5.2	1290.685303	-0.014575	SQISELNLLMK
3.4	1290.652771	0.017957	SLGAQSSKAGETR
1.5	1290.656799	0.013929	SKSSSTTYFKR
0.3	1290.668045	0.002683	SSGKFISSVHSR

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

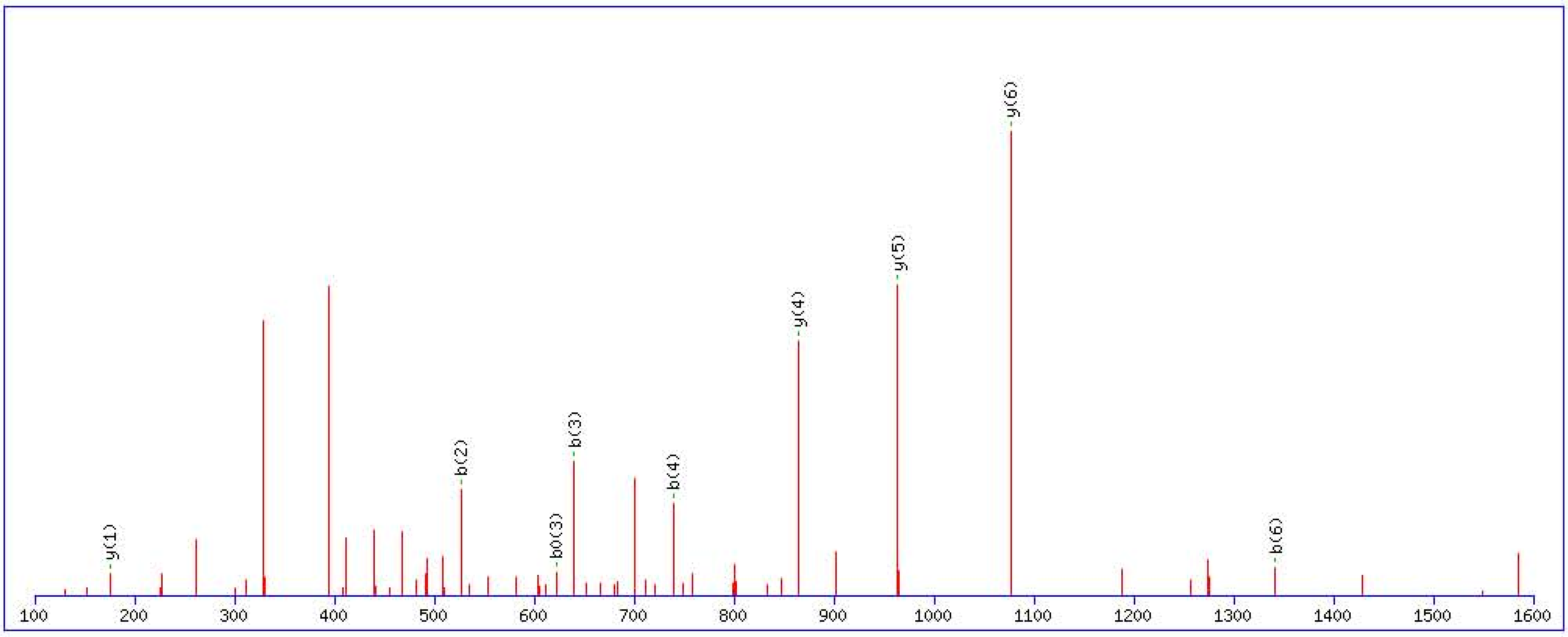
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

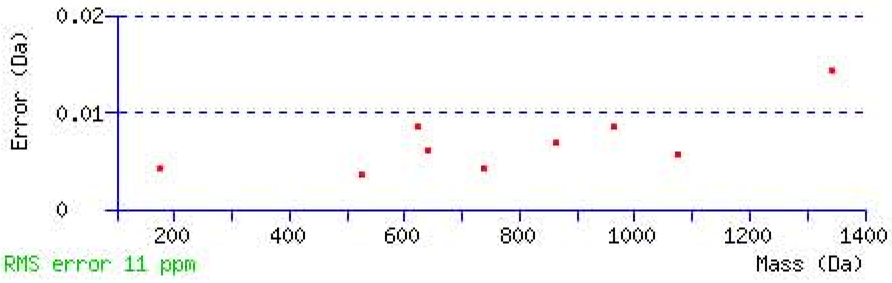
Match to Query 46123: 1601.849408 from(801.931980,2+) rtinseconds(2053) index(63430)
Title: Locus:1.1.1.2712.19 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

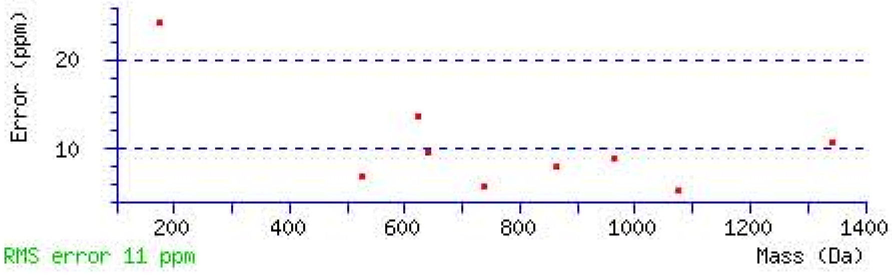
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1601.842178
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2     : Biotin:Thermo-21345 (Q)
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.035
Matches : 9/80 fragment ions using 14 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							8
2	***527.264630***	264.135953	510.238081	255.622679	509.254065	255.130671	Q	1515.817439	758.412358	1498.790890	749.899083	1497.806874	749.407075	7
3	***640.348694***	320.677985	623.322145	312.164711	622.338129	311.672703	L	***1076.592113***	538.799695	1059.565564	530.286420	1058.581548	529.794412	6
4	***739.417108***	370.212192	722.390559	361.698917	721.406543	361.206909	V	***963.508049***	482.257663	946.481500	473.744388	945.497484	473.252380	5
5	902.480437	451.743856	885.453888	443.230582	884.469872	442.738574	Y	***864.439635***	432.723456	847.413086	424.210181	846.429070	423.718173	4
6	***1341.705763***	671.356520	1324.679214	662.843245	1323.695198	662.351237	Q	701.376306	351.191791	684.349757	342.678517	683.365741	342.186509	3
7	1428.737791	714.872534	1411.711242	706.359259	1410.727226	705.867251	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
8							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.3	1601.842178	0.007230	SQLVYQSR
12.8	1601.846024	0.003384	RFVLSCSLLSHQR
9.7	1601.834763	0.014645	QMLEALNFLHSKR
3.9	1601.841995	0.007413	RPGTMTLQDGRKSR
3.6	1601.867126	-0.017718	RLGLAQKLMDQASR
2.8	1601.855881	-0.006473	ELQRLQQAETMKK
2.8	1601.852051	-0.002643	SQISELNLLMK
1.7	1601.826050	0.023358	SSPGEIVEERATVTK

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

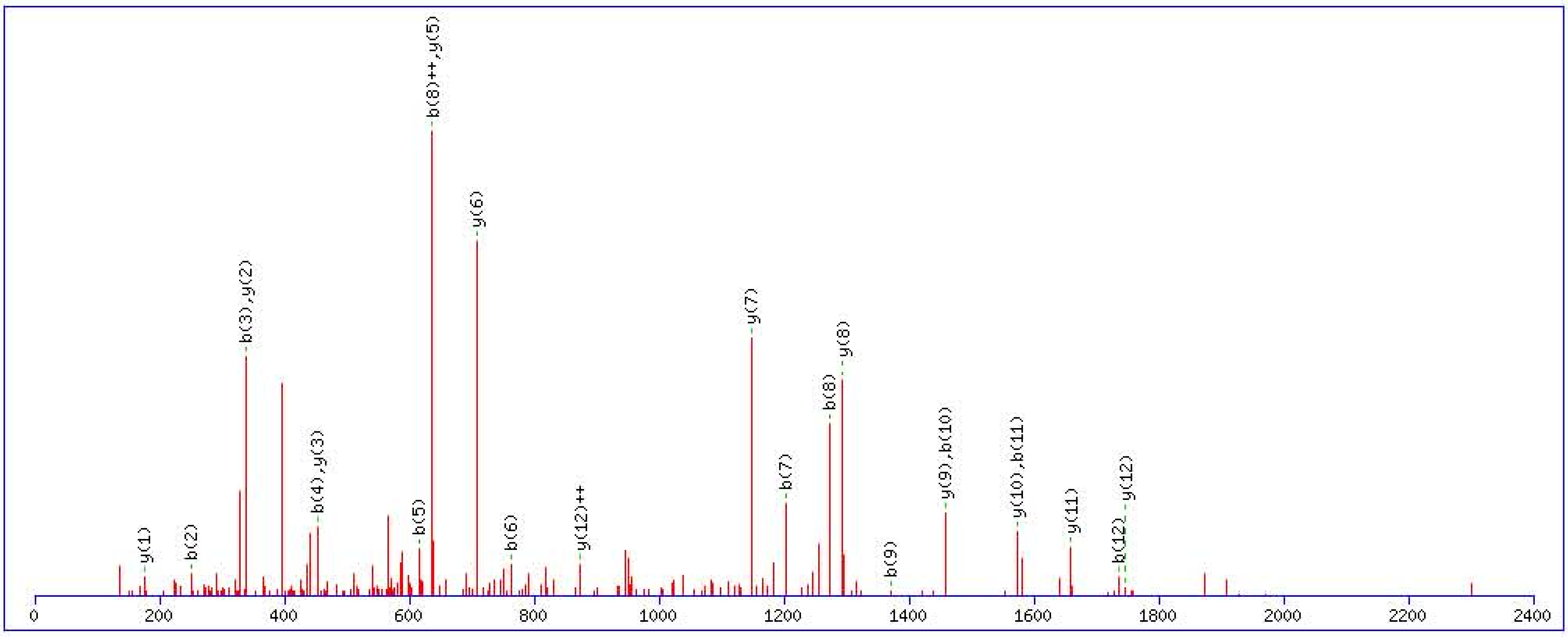
{MATRIX SCIENCE} Mascot Search Results

Peptide View

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

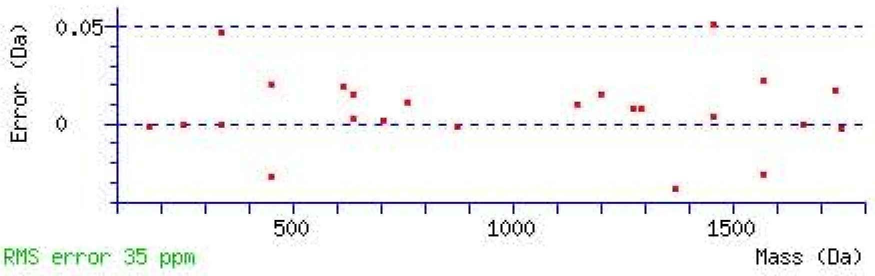
Match to Query 54520: 1908.846268 from(955.430410,2+) rtinseconds(2076) index(63588)
Title: Locus:1.1.1.2720.10 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

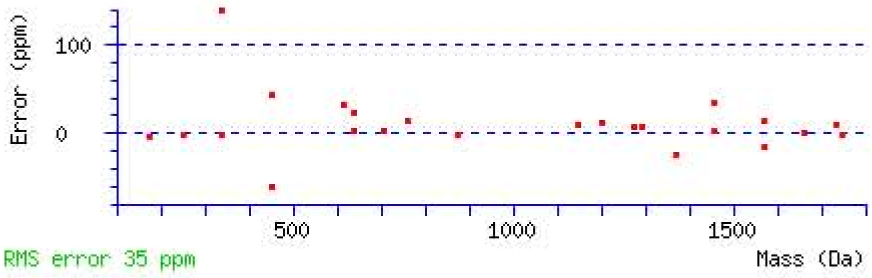
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1908.835236
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 78  Expect: 6e-008
Matches : 24/126 fragment ions using 35 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.070605	82.538940					Y							13
2	*251.102633*	126.054954			233.092068	117.049672	S	*1746.779198*	873.893237	1729.752649	865.379963	1728.768633	864.887955	12
3	*338.134661*	169.570968			320.124096	160.565686	S	*1659.747170*	830.377223	1642.720621	821.863949	1641.736605	821.371941	11
4	*453.161604*	227.084440			435.151039	218.079158	D	*1572.715142*	786.861209	1555.688593	778.347935	1554.704577	777.855927	10
5	*616.224933*	308.616105			598.214368	299.610822	Y	*1457.688199*	729.347738	1440.661650	720.834463	1439.677634	720.342455	9
6	*763.293347*	382.150312			745.282782	373.145029	F	*1294.624870*	647.816073	1277.598321	639.302799	1276.614305	638.810791	8
7	*1202.518673*	601.762975	1185.492124	593.249700	1184.508108	592.757692	Q	*1147.556456*	574.281866	1130.529907	565.768592	1129.545891	565.276584	7
8	*1273.555787*	637.281532	1256.529238	628.768257	1255.545222	628.276249	A	*708.331130*	354.669203	691.304581	346.155929	690.320565	345.663921	6
9	*1370.608551*	685.807914	1353.582002	677.294639	1352.597986	676.802631	P	*637.294016*	319.150646	620.267467	310.637372	619.283451	310.145364	5
10	*1457.640579*	729.323928	1440.614030	720.810653	1439.630014	720.318645	S	540.241252	270.624264	523.214703	262.110990	522.230687	261.618982	4
11	*1572.667522*	786.837399	1555.640973	778.324125	1554.656957	777.832117	D	*453.209224*	227.108250	436.182675	218.594976	435.198659	218.102968	3
12	*1735.730851*	868.369064	1718.704302	859.855789	1717.720286	859.363781	Y	*338.182281*	169.594778	321.155732	161.081504			2
13							R	*175.118952*	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
77.7	1908.835236	0.011032	YSSDYFQAPSDYR
0.7	1908.868927	-0.022659	YSSYRSHDHYQR

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

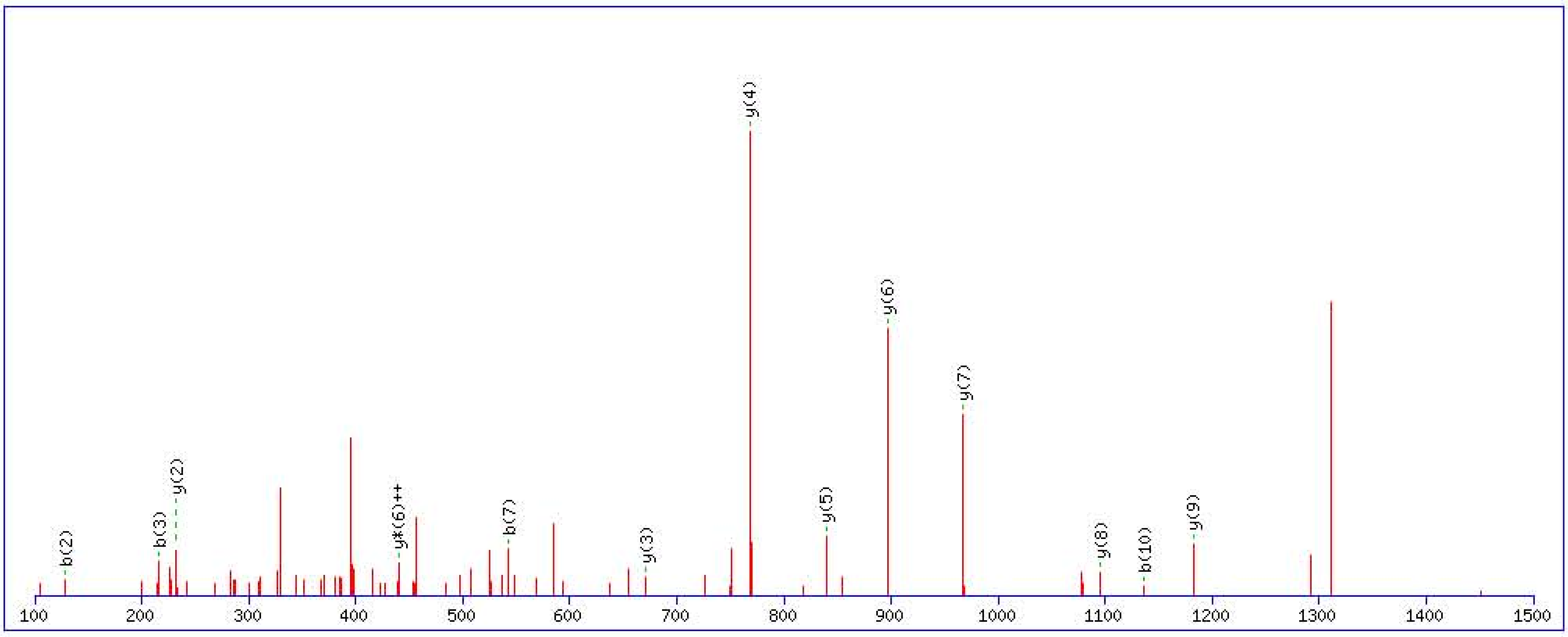
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GASQAGAPQGR**
Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

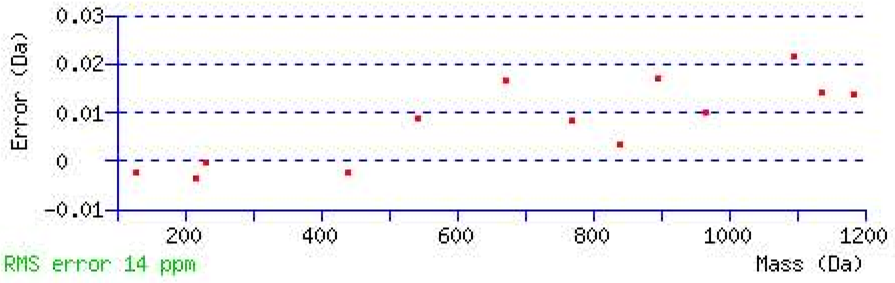
Match to Query 35477: 1309.662988 from(655.838770,2+) rtinseconds(1215) index(1880)
Title: Locus:1.1.1.2143.19 File:"2013-07-02 CLN FXIII 30 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

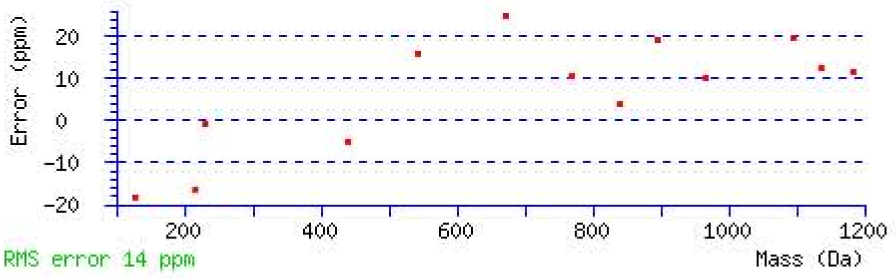
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1309.656097
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 59  Expect: 8.1e-006
Matches : 13/94 fragment ions using 23 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							11
2	**129.065854**	65.036565					A	1253.641918	627.324597	1236.615369	618.811323	1235.631353	618.319315	10
3	**216.097882**	108.552579			198.087317	99.547296	S	***1182.604804***	591.806040	1165.578255	583.292765	1164.594239	582.800757	9
4	344.156460	172.581868	327.129911	164.068593	326.145895	163.576585	Q	***1095.572776***	548.290026	1078.546227	539.776752			8
5	415.193574	208.100425	398.167025	199.587150	397.183009	199.095142	A	***967.514198***	484.260737	950.487649	475.747462			7
6	472.215038	236.611157	455.188489	228.097882	454.204473	227.605874	G	***896.477084***	448.742180	879.450535	440.228906			6
7	**543.252152**	272.129714	526.225603	263.616440	525.241587	263.124432	A	***839.455620***	420.231448	822.429071	411.718173			5
8	640.304916	320.656096	623.278367	312.142822	622.294351	311.650814	P	***768.418506***	384.712891	751.391957	376.199616			4
9	1079.530242	540.268759	1062.503693	531.755485	1061.519677	531.263477	Q	***671.365742***	336.186509	654.339193	327.673234			3
10	**1136.551706**	568.779491	1119.525157	560.266217	1118.541141	559.774208	G	***232.140416***	116.573846	215.113867	108.060571			2
11							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.7	1309.656097	0.006891	GASQAGAPQGR
28.2	1309.656097	0.006891	GASQAGAPQGR
4.2	1309.681900	-0.018912	KAPDFVFYAPR
0.5	1309.648682	0.014306	KSTHRNPEDAR

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

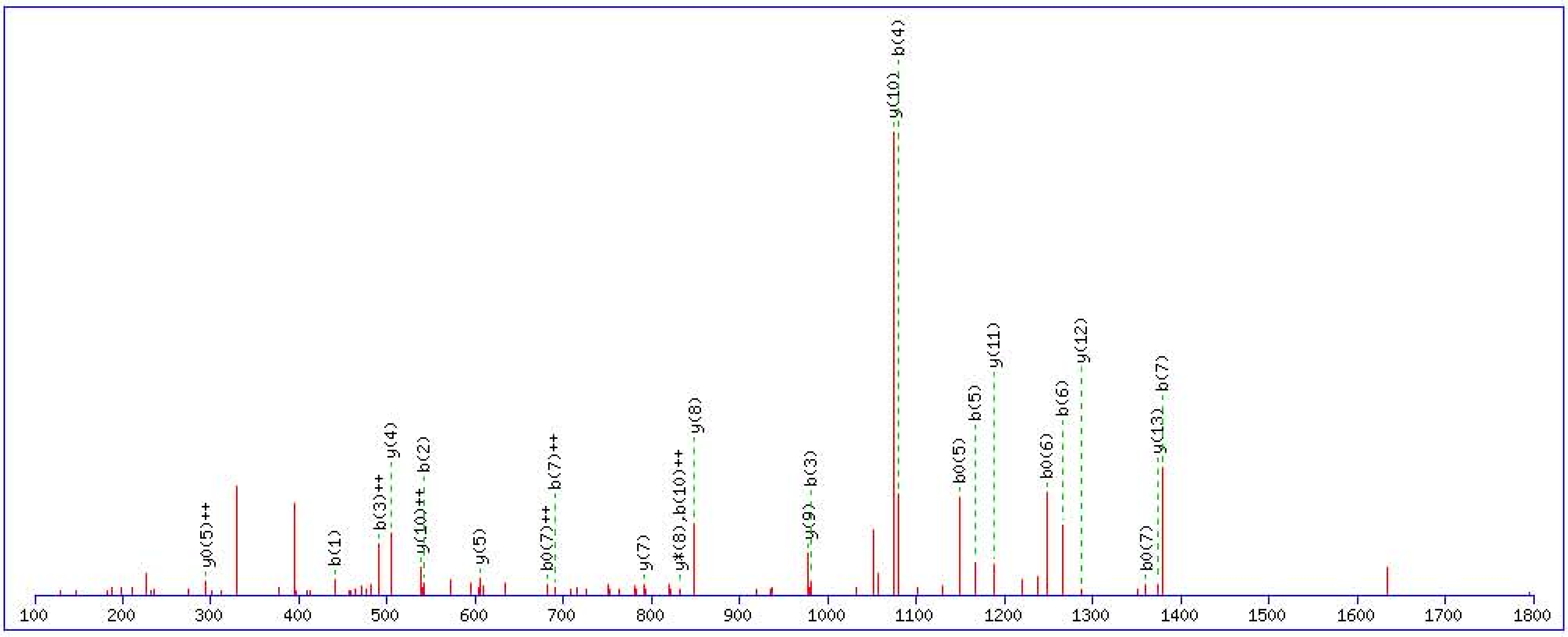
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QTQVSVLPEGGETPLFK**
Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

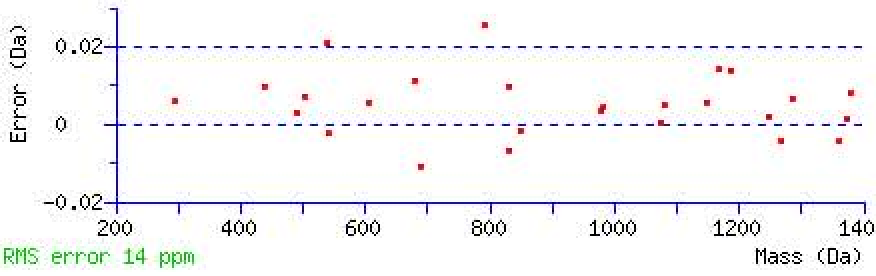
Match to Query 67053: 2451.302562 from(818.108130,3+) rtinseconds(2585) index(66625)
Title: Locus:1.1.1.2897.15 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●

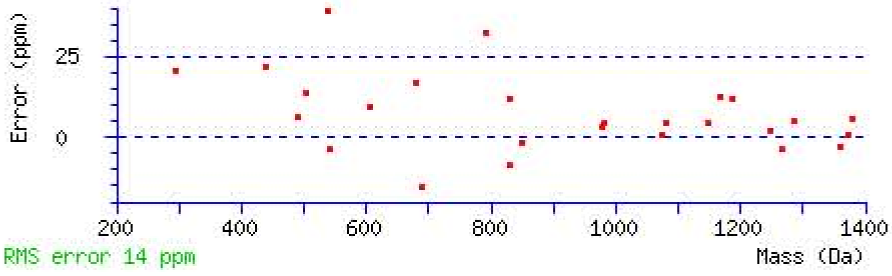


```
Monoisotopic mass of neutral peptide Mr(calc): 2451.290588
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 46  Expect: 0.00011
Matches : 27/182 fragment ions using 54 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***440.232602***	220.619939	423.206053	212.106664			Q							17
2	***541.280281***	271.143779	524.253732	262.630504	523.269716	262.138496	T	2013.072528	1007.039902	1996.045979	998.526628	1995.061963	998.034620	16
3	***980.505607***	**490.756442**	963.479058	482.243167	962.495042	481.751159	Q	1912.024849	956.516063	1894.998300	948.002788	1894.014284	947.510780	15
4	***1079.574021***	540.290649	1062.547472	531.777374	1061.563456	531.285366	V	1472.799523	736.903400	1455.772974	728.390125	1454.788958	727.898117	14
5	***1166.606049***	583.806663	1149.579500	575.293388	1148.595484	574.801380	S	***1373.731109***	687.369193	1356.704560	678.855918	1355.720544	678.363910	13
6	***1265.674463***	633.340870	1248.647914	624.827595	1247.663898	624.335587	V	***1286.699081***	643.853179	1269.672532	635.339904	1268.688516	634.847896	12
7	***1378.758527***	**689.882902**	1361.731978	681.369627	1360.747962	680.877619	L	***1187.630667***	594.318971	1170.604118	585.805697	1169.620102	585.313689	11
8	1475.811291	738.409284	1458.784742	729.896009	1457.800726	729.404001	P	***1074.546603***	537.776940	1057.520054	529.263665	1056.536038	528.771657	10
9	1604.853884	802.930580	1587.827335	794.417306	1586.843319	793.925298	E	***977.493839***	489.250558	960.467290	480.737283	959.483274	480.245275	9
10	1661.875348	**831.441312**	1644.848799	822.928038	1643.864783	822.436030	G	***848.451246***	424.729261	831.424697	416.215986	830.440681	415.723978	8
11	1718.896812	859.952044	1701.870263	851.438770	1700.886247	850.946762	G	***791.429782***	396.218529	774.403233	387.705254	773.419217	387.213246	7
12	1847.939405	924.473341	1830.912856	915.960066	1829.928840	915.468058	E	734.408318	367.707797	717.381769	359.194523	716.397753	358.702515	6
13	1948.987084	974.997180	1931.960535	966.483906	1930.976519	965.991898	T	***605.365725***	303.186500	588.339176	294.673226	587.355160	294.181218	5
14	2046.039848	1023.523562	2029.013299	1015.010288	2028.029283	1014.518280	P	***504.318046***	252.662661	487.291497	244.149386			4
15	2159.123912	1080.065594	2142.097363	1071.552319	2141.113347	1071.060311	L	407.265282	204.136279	390.238733	195.623004			3
16	2306.192326	1153.599801	2289.165777	1145.086526	2288.181761	1144.594518	F	***294.181218***	147.594247	277.154669	139.080972			2
17							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 14 ppm



RMS error 14 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
45.7	2451.290588	0.011974	QTQVSVLPEGGETPLFK
3.5	2451.301590	0.000972	ATKRISHMPSRPELSAVATDLR
2.3	2451.277130	0.025432	GFPSDTQLLDLRRNHFPSVPR

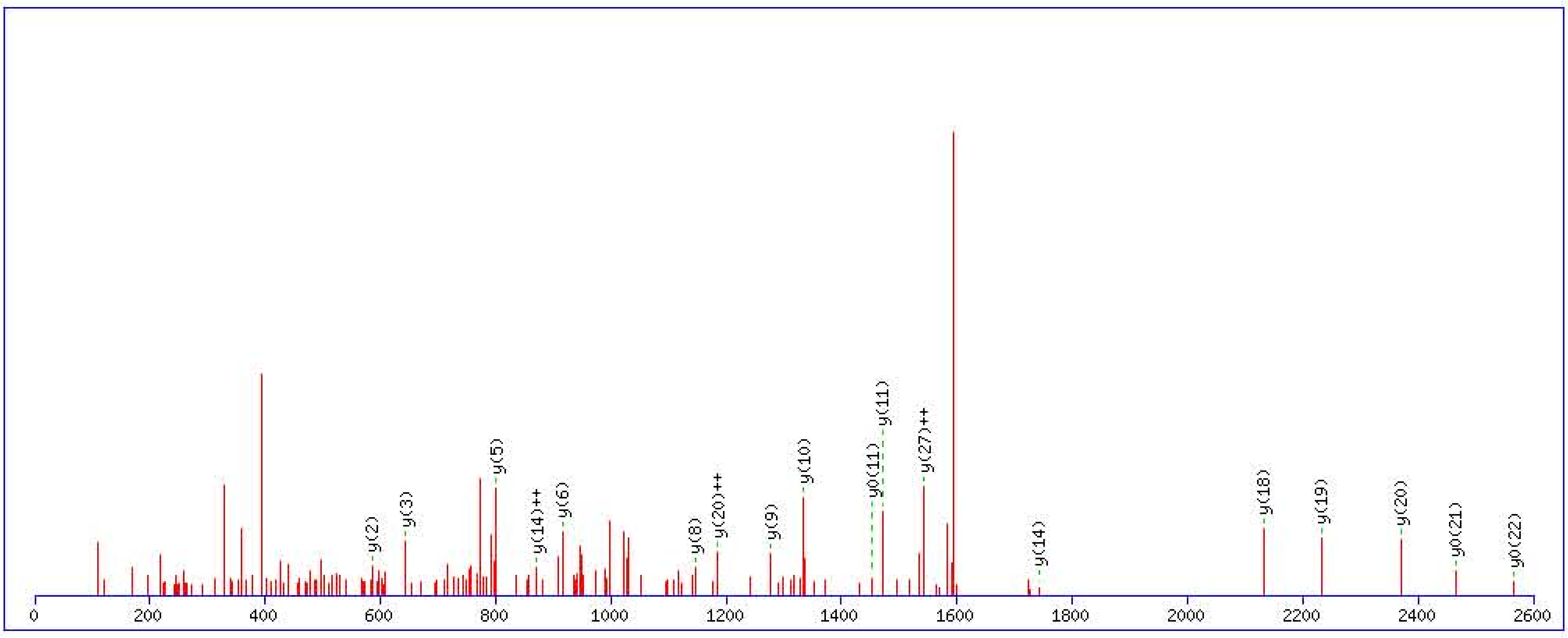
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VPFDAATLHTSTAMAAQHGMDDDGTGQK**
Found in **GELS_HUMAN**, Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1

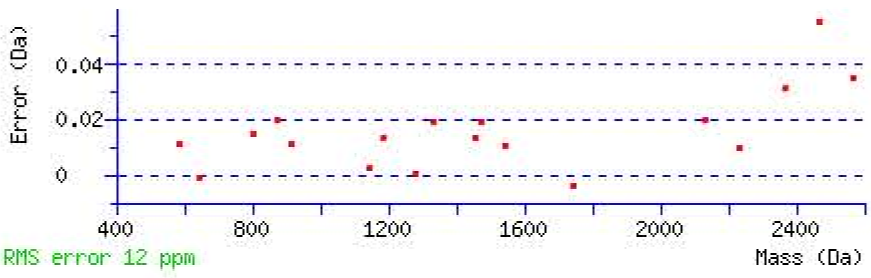
Match to Query 76056: 3183.478056 from(796.876790,4+) rtinseconds(1929) index(6869)
Title: Locus:1.1.1.2392.22 File:"2013-07-02 CLN FXIII 30 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

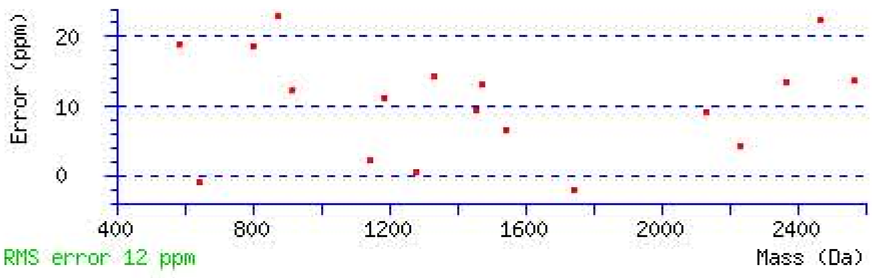
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3183.442383
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q27    : Biotin:Thermo-21345 (Q)
Ions Score: 61  Expect: 1.2e-005
Matches : 18/280 fragment ions using 37 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							28
2	197.128454	99.067865					P	3085.381222	1543.194249	3068.354673	1534.680974	3067.370657	1534.188966	27
3	344.196868	172.602072					F	2988.328458	1494.667867	2971.301909	1486.154592	2970.317893	1485.662584	26
4	459.223811	230.115543			441.213246	221.110261	D	2841.260044	1421.133660	2824.233495	1412.620385	2823.249479	1412.128377	25
5	530.260925	265.634101			512.250360	256.628818	A	2726.233101	1363.620188	2709.206552	1355.106914	2708.222536	1354.614906	24
6	601.298039	301.152658			583.287474	292.147375	A	2655.195987	1328.101631	2638.169438	1319.588357	2637.185422	1319.096349	23
7	702.345718	351.676497			684.335153	342.671215	T	2584.158873	1292.583074	2567.132324	1284.069800	2566.148308	1283.577792	22
8	815.429782	408.218529			797.419217	399.213247	L	2483.111194	1242.059235	2466.084645	1233.545960	2465.100629	1233.053952	21
9	952.488694	476.747985			934.478129	467.742703	H	***2370.027130***	1185.517203	2353.000581	1177.003928	2352.016565	1176.511920	20
10	1053.536373	527.271824			1035.525808	518.266542	T	***2232.968218***	1116.987747	2215.941669	1108.474472	2214.957653	1107.982464	19
11	1140.568401	570.787839			1122.557836	561.782556	S	***2131.920539***	1066.463907	2114.893990	1057.950633	2113.909974	1057.458625	18
12	1241.616080	621.311678			1223.605515	612.306396	T	2044.888511	1022.947893	2027.861962	1014.434619	2026.877946	1013.942611	17
13	1312.653194	656.830235			1294.642629	647.824952	A	1943.840832	972.424054	1926.814283	963.910779	1925.830267	963.418771	16
14	1443.693679	722.350478			1425.683114	713.345195	M	1872.803718	936.905497	1855.777169	928.392222	1854.793153	927.900214	15
15	1514.730793	757.869035			1496.720228	748.863752	A	***1741.763233***	871.385254	1724.736684	862.871980	1723.752668	862.379972	14
16	1585.767907	793.387591			1567.757342	784.382309	A	1670.726119	835.866697	1653.699570	827.353423	1652.715554	826.861415	13
17	1713.826485	857.416880	1696.799936	848.903606	1695.815920	848.411598	Q	1599.689005	800.348140	1582.662456	791.834866	1581.678440	791.342858	12
18	1850.885397	925.946336	1833.858848	917.433062	1832.874832	916.941054	H	***1471.630427***	736.318851	1454.603878	727.805577	1453.619862	727.313569	11
19	1907.906861	954.457068	1890.880312	945.943794	1889.896296	945.451786	G	***1334.571515***	667.789395	1317.544966	659.276121	1316.560950	658.784113	10
20	2038.947346	1019.977311	2021.920797	1011.464036	2020.936781	1010.972028	M	***1277.550051***	639.278663	1260.523502	630.765389	1259.539486	630.273381	9
21	2153.974289	1077.490782	2136.947740	1068.977508	2135.963724	1068.485500	D	***1146.509566***	573.758421	1129.483017	565.245146	1128.499001	564.753138	8
22	2269.001232	1135.004254	2251.974683	1126.490979	2250.990667	1125.998971	D	1031.482623	516.244949	1014.456074	507.731675	1013.472058	507.239667	7
23	2384.028175	1192.517725	2367.001626	1184.004451	2366.017610	1183.512443	D	***916.455680***	458.731478	899.429131	450.218203	898.445115	449.726195	6
24	2441.049639	1221.028457	2424.023090	1212.515183	2423.039074	1212.023175	G	***801.428737***	401.218007	784.402188	392.704732	783.418172	392.212724	5
25	2542.097318	1271.552297	2525.070769	1263.039022	2524.086753	1262.547014	T	744.407273	372.707275	727.380724	364.194000	726.396708	363.701992	4
26	2599.118782	1300.063029	2582.092233	1291.549754	2581.108217	1291.057746	G	***643.359594***	322.183435	626.333045	313.670161			3
27	3038.344108	1519.675692	3021.317559	1511.162417	3020.333543	1510.670409	Q	***586.338130***	293.672703	569.311581	285.159429			2
28							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
61.2	3183.442383	0.035673	VPFDAATLHTSTAMAAQHGMDDDGTGQK
13.5	3183.442383	0.035673	VPFDAATLHTSTAMAAQHGMDDDGTGQK

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

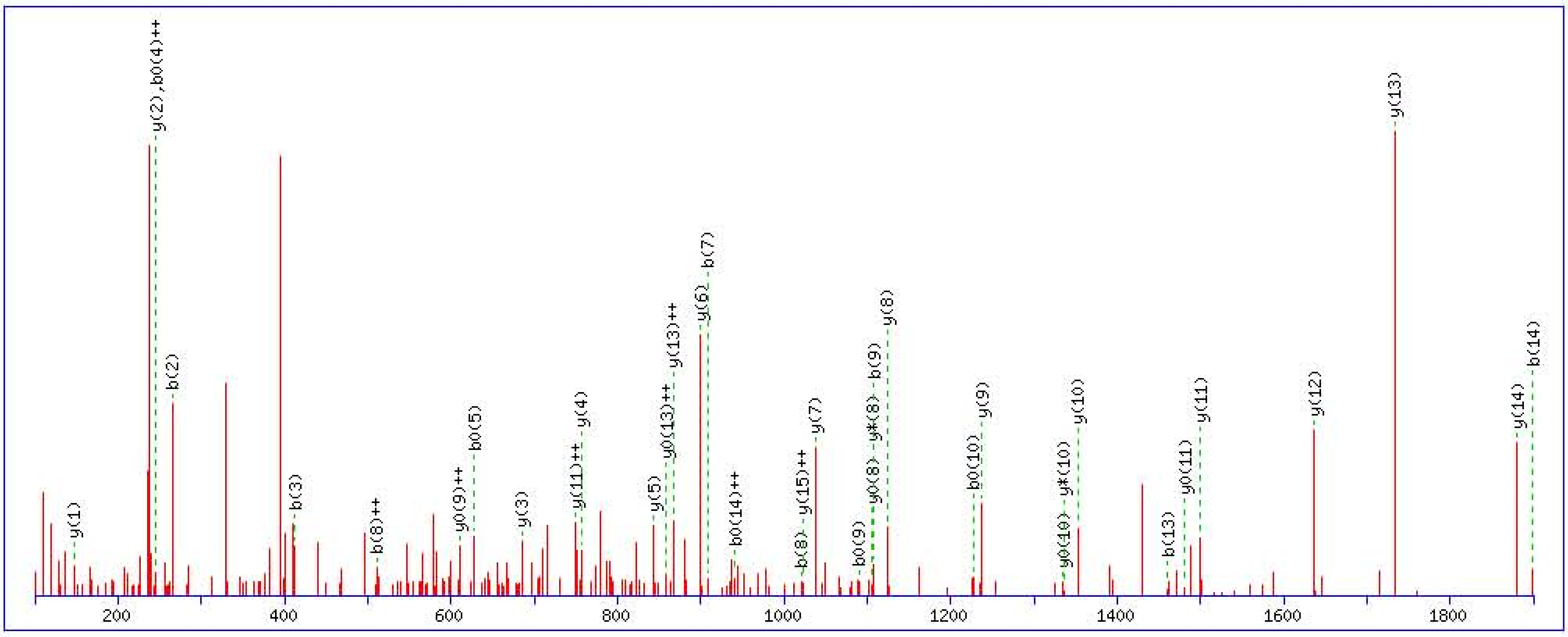
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TYFPHFDLSHGSAQVK**
Found in **HBA_HUMAN**, Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2

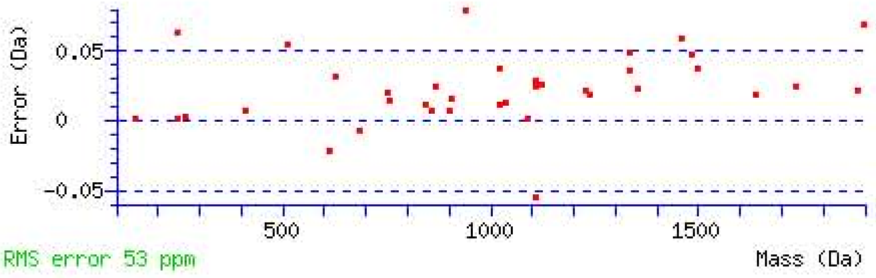
Match to Query 60369: 2144.074482 from(715.698770,3+) rtinseconds(2044) index(7633)
Title: Locus:1.1.1.2432.13 File:"2013-07-02 CLN FXIII 30 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

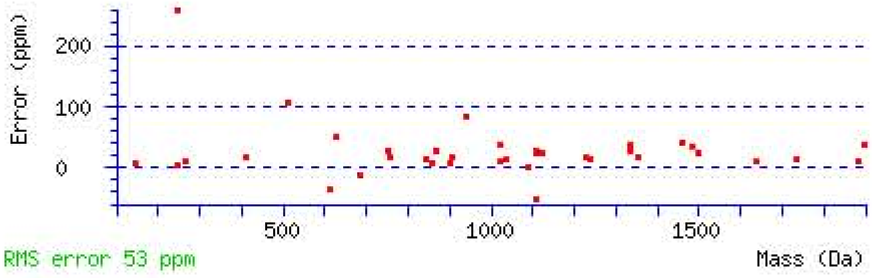
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2144.051346
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14 : Biotin:Thermo-21345 (Q)
Ions Score: 40 **Expect:** 0.0031
Matches : 37/146 fragment ions using 136 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							16
2	**265.118284**	133.062780			247.107719	124.057498	Y	2044.010930	1022.509103	2026.984381	1013.995829	2026.000365	1013.503821	15
3	**412.186698**	206.596987			394.176133	197.591705	F	***1880.947601***	940.977438	1863.921052	932.464164	1862.937036	931.972156	14
4	509.239462	255.123369			491.228897	246.118087	P	***1733.879187***	867.443231	1716.852638	858.929957	1715.868622	858.437949	13
5	646.298374	323.652825			628.287809	314.647543	H	***1636.826423***	818.916849	1619.799874	810.403575	1618.815858	809.911567	12
6	793.366788	397.187032			775.356223	388.181750	F	***1499.767511***	750.387393	1482.740962	741.874119	1481.756946	741.382111	11
7	**908.393731**	454.700504			890.383166	445.695221	D	***1352.699097***	676.853186	1335.672548	668.339912	1334.688532	667.847904	10
8	**1021.477795**	511.242536			1003.467230	502.237253	L	***1237.672154***	619.339715	1220.645605	610.826441	1219.661589	610.334433	9
9	**1108.509823**	554.758550			1090.499258	545.753267	S	***1124.588090***	562.797683	1107.561541	554.284409	1106.577525	553.792400	8
10	1245.568735	623.288006			1227.558170	614.282723	H	***1037.556062***	519.281669	1020.529513	510.768394	1019.545497	510.276386	7
11	1302.590199	651.798738			1284.579634	642.793455	G	***900.497150***	450.752213	883.470601	442.238938	882.486585	441.746930	6
12	1389.622227	695.314752			1371.611662	686.309469	S	***843.475686***	422.241481	826.449137	413.728207	825.465121	413.236199	5
13	**1460.659341**	730.833309			1442.648776	721.828026	A	***756.443658***	378.725467	739.417109	370.212192			4
14	**1899.884667**	950.445972	1882.858118	941.932697	1881.874102	941.440689	Q	***685.406544***	343.206910	668.379995	334.693635			3
15	1998.953081	999.980179	1981.926532	991.466904	1980.942516	990.974896	V	***246.181218***	123.594247	229.154669	115.080972			2
16							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.7	2144.051346	0.023136	TYFPHFDLSHGSAQVK

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

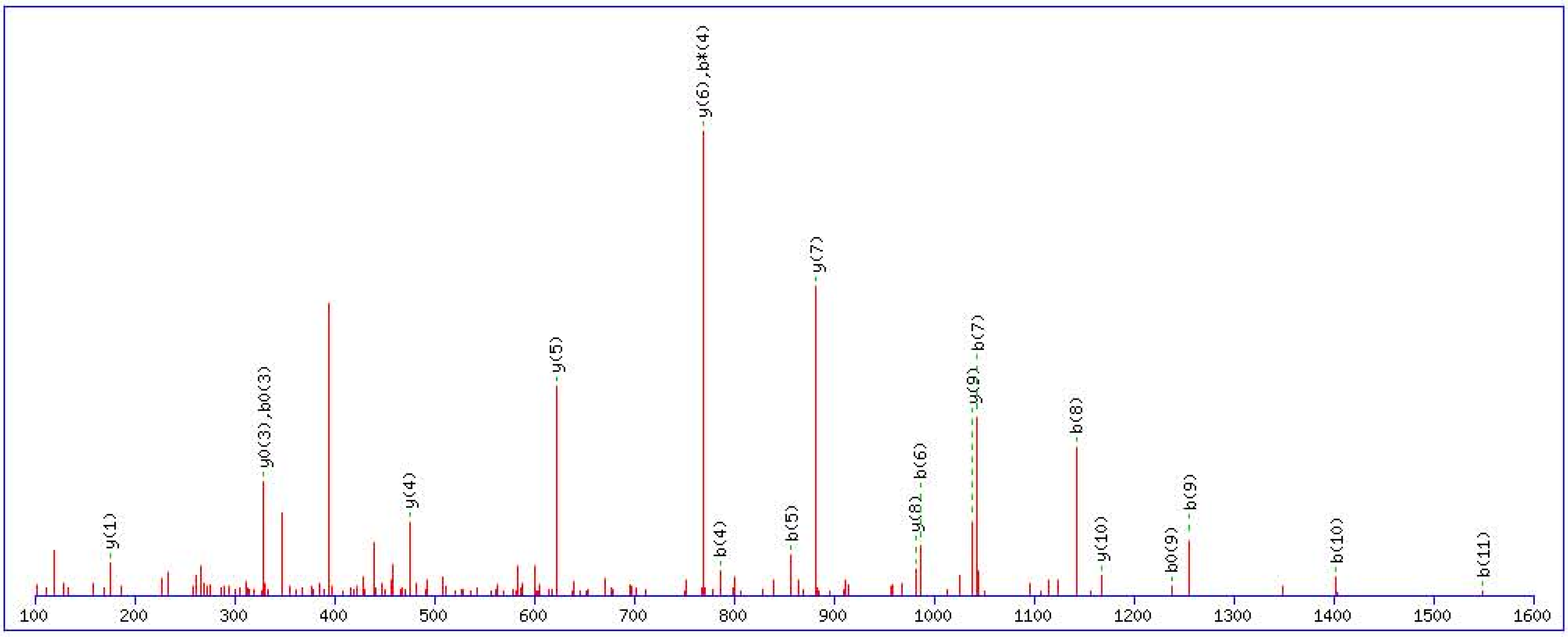
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GECQAEGVLFFQGDR**
Found in **HEMO_HUMAN**, Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

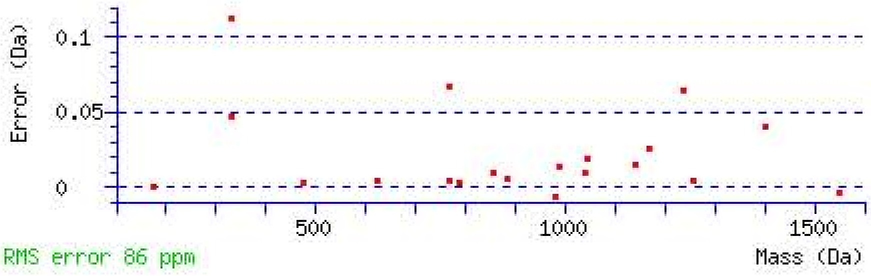
Match to Query 57874: 2022.939312 from(675.320380,3+) rtinseconds(2426) index(83184)
Title: Locus:1.1.1.2724.7 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

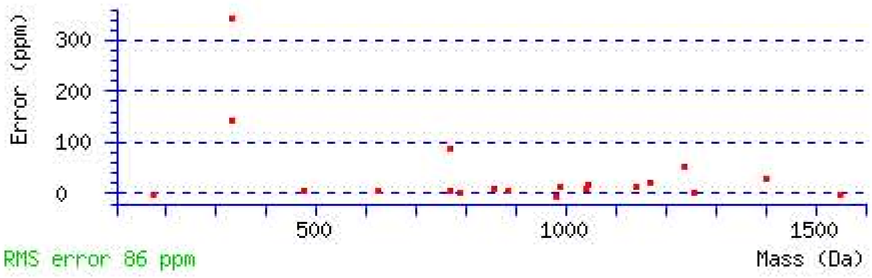
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2022.929184
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 55  Expect: 7.2e-006
Matches : 20/158 fragment ions using 28 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.028740	29.518008					G							15
2	187.071333	94.039305			169.060768	85.034022	E	1966.914982	983.961129	1949.888433	975.447855	1948.904417	974.955847	14
3	347.101982	174.054629			329.091417	165.049347	C	1837.872389	919.439833	1820.845840	910.926558	1819.861824	910.434550	13
4	***786.327308***	393.667292	769.300759	385.154018	768.316743	384.662010	Q	1677.841740	839.424508	1660.815191	830.911234	1659.831175	830.419226	12
5	***857.364422***	429.185849	840.337873	420.672575	839.353857	420.180567	A	1238.616414	619.811845	1221.589865	611.298571	1220.605849	610.806563	11
6	***986.407015***	493.707146	969.380466	485.193871	968.396450	484.701863	E	***1167.579300***	584.293288	1150.552751	575.780014	1149.568735	575.288006	10
7	***1043.428479***	522.217878	1026.401930	513.704603	1025.417914	513.212595	G	***1038.536707***	519.771992	1021.510158	511.258717	1020.526142	510.766709	9
8	***1142.496893***	571.752085	1125.470344	563.238810	1124.486328	562.746802	V	***981.515243***	491.261260	964.488694	482.747985	963.504678	482.255977	8
9	***1255.580957***	628.294117	1238.554408	619.780842	1237.570392	619.288834	L	***882.446829***	441.727053	865.420280	433.213778	864.436264	432.721770	7
10	***1402.649371***	701.828324	1385.622822	693.315049	1384.638806	692.823041	F	***769.362765***	385.185021	752.336216	376.671746	751.352200	376.179738	6
11	***1549.717785***	775.362531	1532.691236	766.849256	1531.707220	766.357248	F	***622.294351***	311.650814	605.267802	303.137539	604.283786	302.645531	5
12	1677.776363	839.391820	1660.749814	830.878545	1659.765798	830.386537	Q	***475.225937***	238.116606	458.199388	229.603332	457.215372	229.111324	4
13	1734.797827	867.902552	1717.771278	859.389277	1716.787262	858.897269	G	347.167359	174.087317	330.140810	165.574043	329.156794	165.082035	3
14	1849.824770	925.416023	1832.798221	916.902749	1831.814205	916.410741	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
15							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
55.2	2022.929184	0.010128	GECQAEGVLFFQGDR
3.4	2022.929184	0.010128	GECQAEGVLFFQGDR
0.4	2022.914581	0.024731	SGKWYFEFEVVTGGDMR

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

{MATRIX SCIENCE}

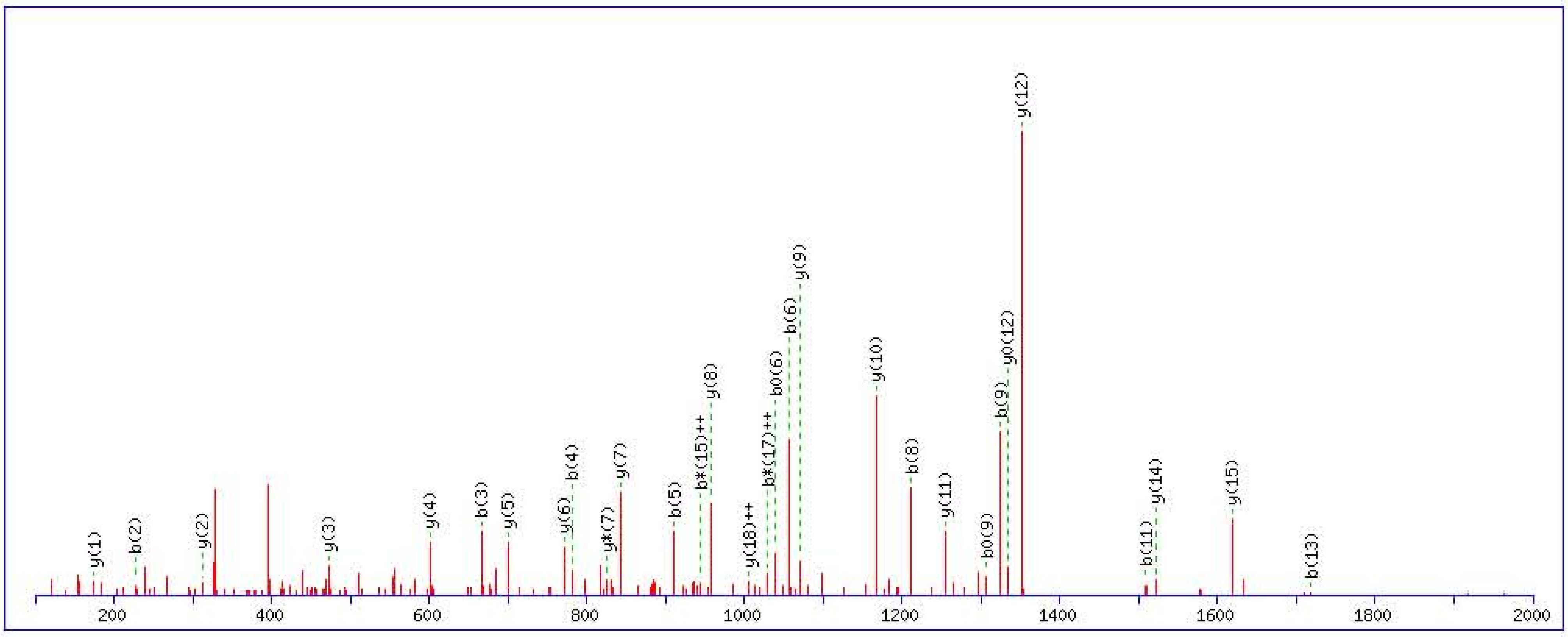
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LLQDEFPGIPSPLDAAVECHR**
Found in **HEMO_HUMAN**, Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

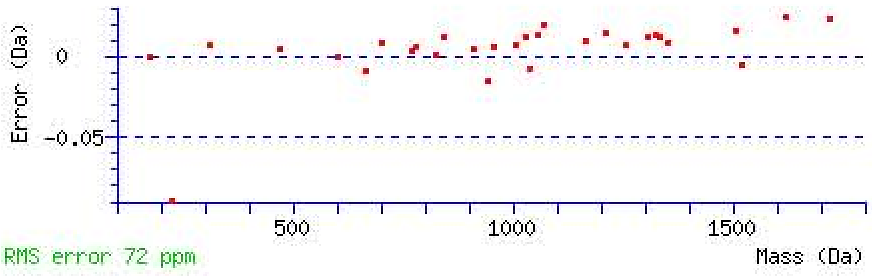
Match to Query 70387: 2674.348632 from(892.456820,3+) rtinseconds(2656) index(84237)
Title: Locus:1.1.1.2804.14 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

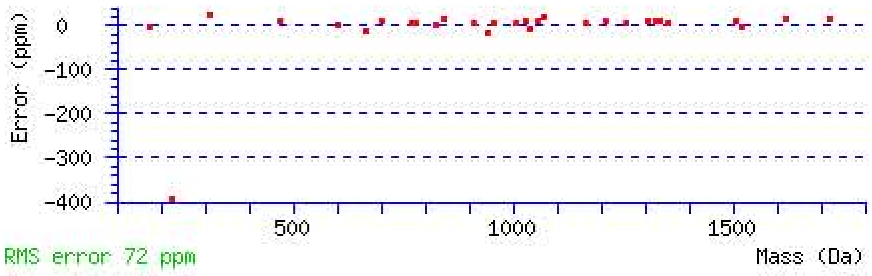
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2674.324722
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 79  Expect: 4.1e-008
Matches : 30/224 fragment ions using 63 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							21
2	***227.175404***	114.091340					L	2562.247943	1281.627609	2545.221394	1273.114335	2544.237378	1272.622327	20
3	***666.400730***	333.704003	649.374181	325.190729			Q	2449.163879	1225.085577	2432.137330	1216.572303	2431.153314	1216.080295	19
4	***781.427673***	391.217475	764.401124	382.704200	763.417108	382.212192	D	2009.938553	1005.472914	1992.912004	996.959640	1991.927988	996.467632	18
5	***910.470266***	455.738771	893.443717	447.225497	892.459701	446.733489	E	1894.911610	947.959443	1877.885061	939.446169	1876.901045	938.954160	17
6	***1057.538680***	529.272978	1040.512131	520.759704	1039.528115	520.267696	F	1765.869017	883.438146	1748.842468	874.924872	1747.858452	874.432864	16
7	1154.591444	577.799360	1137.564895	569.286086	1136.580879	568.794078	P	***1618.800603***	809.903939	1601.774054	801.390665	1600.790038	800.898657	15
8	***1211.612908***	606.310092	1194.586359	597.796818	1193.602343	597.304810	G	***1521.747839***	761.377557	1504.721290	752.864283	1503.737274	752.372275	14
9	***1324.696972***	662.852124	1307.670423	654.338850	1306.686407	653.846841	I	1464.726375	732.866825	1447.699826	724.353551	1446.715810	723.861543	13
10	1421.749736	711.378506	1404.723187	702.865232	1403.739171	702.373223	P	***1351.642311***	676.324793	1334.615762	667.811519	1333.631746	667.319511	12
11	***1508.781764***	754.894520	1491.755215	746.381246	1490.771199	745.889238	S	***1254.589547***	627.798411	1237.562998	619.285137	1236.578982	618.793129	11
12	1605.834528	803.420902	1588.807979	794.907628	1587.823963	794.415620	P	***1167.557519***	584.282397	1150.530970	575.769123	1149.546954	575.277115	10
13	***1718.918592***	859.962934	1701.892043	851.449660	1700.908027	850.957652	L	***1070.504755***	535.756015	1053.478206	527.242741	1052.494190	526.750733	9
14	1833.945535	917.476406	1816.918986	908.963131	1815.934970	908.471123	D	***957.420691***	479.213983	940.394142	470.700709	939.410126	470.208701	8
15	1904.982649	952.994963	1887.956100	944.481688	1886.972084	943.989680	A	***842.393748***	421.700512	825.367199	413.187237	824.383183	412.695229	7
16	1976.019763	988.513520	1958.993214	980.000245	1958.009198	979.508237	A	***771.356634***	386.181955	754.330085	377.668680	753.346069	377.176672	6
17	2075.088177	1038.047726	2058.061628	1029.534452	2057.077612	1029.042444	V	***700.319520***	350.663398	683.292971	342.150123	682.308955	341.658115	5
18	2204.130770	1102.569023	2187.104221	1094.055748	2186.120205	1093.563740	E	***601.251106***	301.129191	584.224557	292.615916	583.240541	292.123908	4
19	2364.161419	1182.584347	2347.134870	1174.071073	2346.150854	1173.579065	C	***472.208513***	236.607894	455.181964	228.094620			3
20	2501.220331	1251.113803	2484.193782	1242.600529	2483.209766	1242.108521	H	***312.177864***	156.592570	295.151315	148.079295			2
21							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
78.8	2674.324722	0.023910	LLQDEFPGIPSPLDAAVECHR
0.0	2674.320724	0.027908	VSVETSPPQTAAQDPQGQGR

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

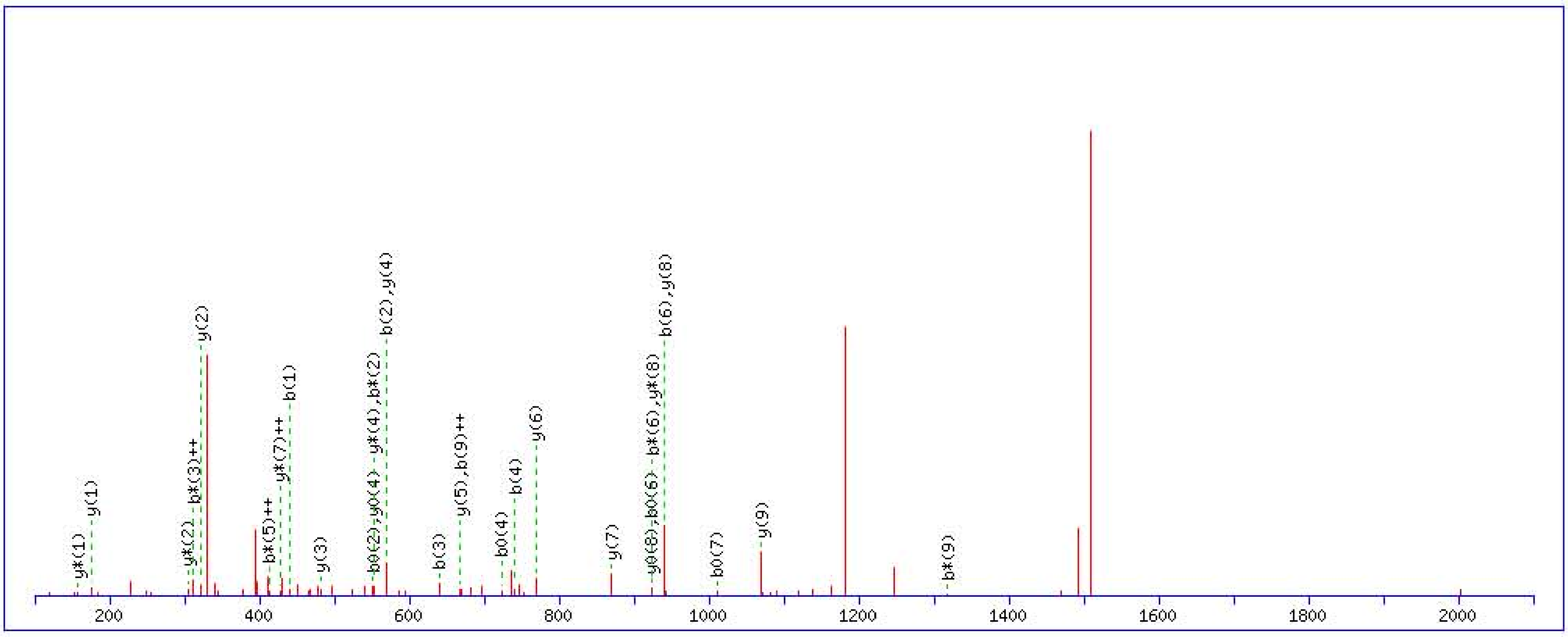
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QEATTVSCFR**
Found in **HGFL_HUMAN**, Hepatocyte growth factor-like protein OS=Homo sapiens GN=MST1 PE=1 SV=2

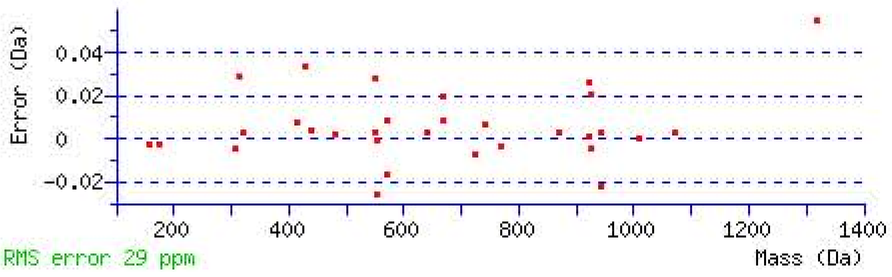
Match to Query 42902: 1508.711468 from(755.363010,2+) rtinseconds(1780) index(78783)
Title: Locus:1.1.1.2499.17 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

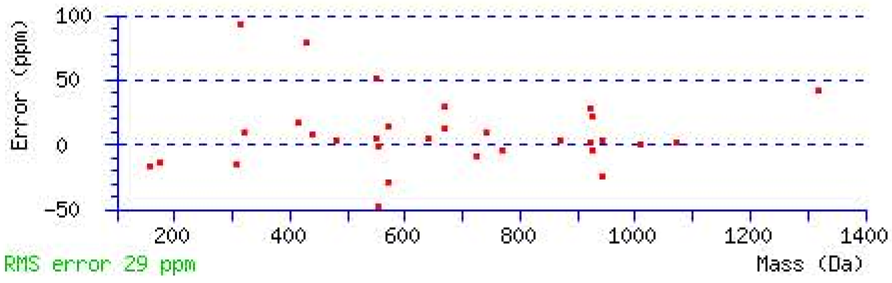
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1508.711578
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 40  Expect: 0.00043
Matches : 31/100 fragment ions using 65 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	**440.232602**	220.619939	423.206053	212.106664			Q							10
2	**569.275195**	285.141236	552.248646	276.627961	551.264630	276.135953	E	***1070.493522***	535.750399	1053.466973	527.237125	1052.482957	526.745117	9
3	**640.312309**	320.659793	623.285760	312.146518	622.301744	311.654510	A	***941.450929***	471.229103	924.424380	462.715828	923.440364	462.223820	8
4	**741.359988**	371.183632	724.333439	362.670358	723.349423	362.178350	T	***870.413815***	435.710546	853.387266	427.197271	852.403250	426.705263	7
5	842.407667	421.707472	825.381118	413.194197	824.397102	412.702189	T	***769.366136***	385.186706	752.339587	376.673432	751.355571	376.181424	6
6	**941.476081**	471.241679	924.449532	462.728404	923.465516	462.236396	V	***668.318457***	334.662867	651.291908	326.149592	650.307892	325.657584	5
7	1028.508109	514.757693	1011.481560	506.244418	1010.497544	505.752410	S	***569.250043***	285.128660	552.223494	276.615385	551.239478	276.123377	4
8	1188.538758	594.773017	1171.512209	586.259743	1170.528193	585.767735	C	***482.218015***	241.612646	465.191466	233.099371			3
9	1335.607172	668.307224	1318.580623	659.793950	1317.596607	659.301942	F	***322.187366***	161.597321	305.160817	153.084047			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.5	1508.711578	-0.000110	QEATTVSCFR
3.4	1508.726624	-0.015156	RDGQLQRMNYGR
2.9	1508.708191	0.003277	EYGSMYTVHLGPR
2.9	1508.711380	0.000088	RTASGGRTEQGMSR
2.0	1508.732681	-0.021213	KEAMKVSSQPCTK
0.9	1508.711548	-0.000080	QMSKYPSGER
0.4	1508.719437	-0.007969	TFSWKSSLTCHR

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

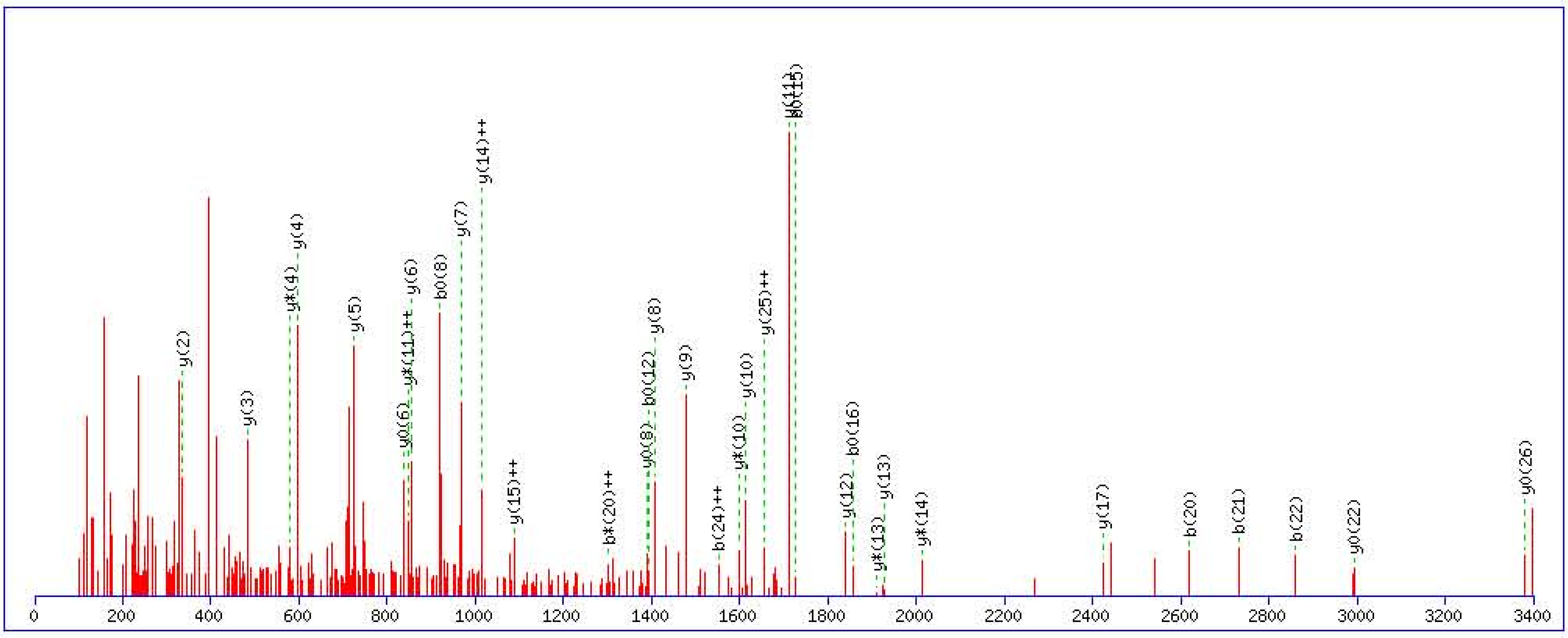
Mascot Search Results

Peptide View

MS/MS Fragmentation of **WSAETPHKPQFTFTSEPHAQLEENFCR**
Found in **HGFL_HUMAN**, Hepatocyte growth factor-like protein OS=Homo sapiens GN=MST1 PE=1 SV=2

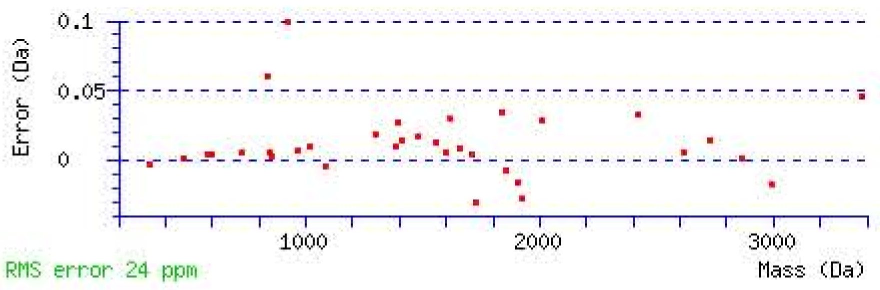
Match to Query 80579: 3584.673020 from(717.941880,5+) rtinseconds(2036) index(80514)
Title: Locus:1.1.1.2588.17 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

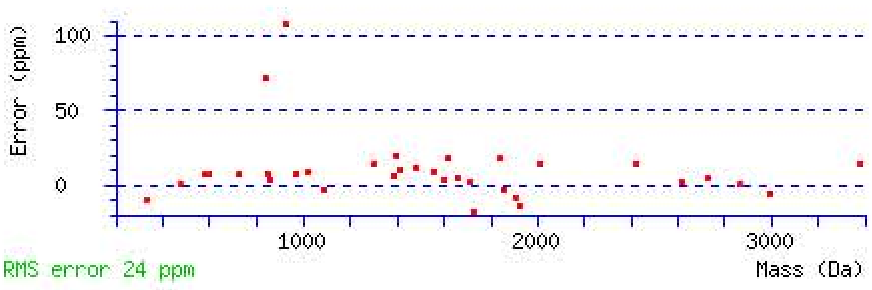
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3584.660538
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q20 : Biotin:Thermo-21345 (Q)
Ions Score: 51 **Expect:** 0.00012
Matches : 34/288 fragment ions using 69 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	187.086589	94.046932					W							27
2	274.118617	137.562947			256.108052	128.557664	S	3399.588510	1700.297893	3382.561961	1691.784618	3381.577945	1691.292610	26
3	345.155731	173.081504			327.145166	164.076221	A	3312.556482	1656.781879	3295.529933	1648.268605	3294.545917	1647.776597	25
4	474.198324	237.602800			456.187759	228.597518	E	3241.519368	1621.263322	3224.492819	1612.750047	3223.508803	1612.258040	24
5	575.246003	288.126640			557.235438	279.121357	T	3112.476775	1556.742026	3095.450226	1548.228751	3094.466210	1547.736743	23
6	672.298767	336.653022			654.288202	327.647739	P	3011.429096	1506.218186	2994.402547	1497.704912	2993.418531	1497.212904	22
7	809.357679	405.182478			791.347114	396.177195	H	2914.376332	1457.691804	2897.349783	1449.178530	2896.365767	1448.686522	21
8	937.452642	469.229959	920.426093	460.716685	919.442077	460.224677	K	2777.317420	1389.162348	2760.290871	1380.649074	2759.306855	1380.157066	20
9	1034.505406	517.756341	1017.478857	509.243067	1016.494841	508.751059	P	2649.222457	1325.114867	2632.195908	1316.601592	2631.211892	1316.109584	19
10	1162.563984	581.785630	1145.537435	573.272356	1144.553419	572.780348	Q	2552.169693	1276.588485	2535.143144	1268.075210	2534.159128	1267.583202	18
11	1309.632398	655.319837	1292.605849	646.806563	1291.621833	646.314555	F	***2424.111115***	1212.559196	2407.084566	1204.045921	2406.100550	1203.553913	17
12	1410.680077	705.843677	1393.653528	697.330402	1392.669512	696.838394	T	2277.042701	1139.024988	2260.016152	1130.511714	2259.032136	1130.019706	16
13	1557.748491	779.377884	1540.721942	770.864609	1539.737926	770.372601	F	2175.995022	1088.501149	2158.968473	1079.987874	2157.984457	1079.495866	15
14	1658.796170	829.901723	1641.769621	821.388449	1640.785605	820.896441	T	2028.926608	1014.966942	2011.900059	1006.453668	2010.916043	1005.961660	14
15	1745.828198	873.417737	1728.801649	864.904463	1727.817633	864.412455	S	***1927.878929***	964.443103	1910.852380	955.929828	1909.868364	955.437820	13
16	1874.870791	937.939034	1857.844242	929.425759	1856.860226	928.933751	E	***1840.846901***	920.927089	1823.820352	912.413814	1822.836336	911.921806	12
17	1971.923555	986.465416	1954.897006	977.952141	1953.912990	977.460133	P	***1711.804308***	856.405792	1694.777759	847.892518	1693.793743	847.400510	11
18	2108.982467	1054.994872	2091.955918	1046.481597	2090.971902	1045.989589	H	***1614.751544***	807.879410	1597.724995	799.366136	1596.740979	798.874128	10
19	2180.019581	1090.513429	2162.993032	1082.000154	2162.009016	1081.508146	A	***1477.692632***	739.349954	1460.666083	730.836680	1459.682067	730.344672	9
20	**2619.244907**	1310.126092	2602.218358	1301.612817	2601.234342	1301.120809	Q	***1406.655518***	703.831397	1389.628969	695.318123	1388.644953	694.826115	8
21	**2732.328971**	1366.668124	2715.302422	1358.154849	2714.318406	1357.662841	L	***967.430192***	484.218734	950.403643	475.705460	949.419627	475.213452	7
22	**2861.371564**	1431.189420	2844.345015	1422.676146	2843.360999	1422.184138	E	***854.346128***	427.676702	837.319579	419.163427	836.335563	418.671419	6
23	2990.414157	1495.710717	2973.387608	1487.197442	2972.403592	1486.705434	E	***725.303535***	363.155405	708.276986	354.642131	707.292970	354.150123	5
24	3104.457084	1552.732180	3087.430535	1544.218906	3086.446519	1543.726898	N	***596.260942***	298.634109	579.234393	290.120834			4
25	3251.525498	1626.266387	3234.498949	1617.753113	3233.514933	1617.261105	F	***482.218015***	241.612645	465.191466	233.099371			3
26	3411.556147	1706.281712	3394.529598	1697.768437	3393.545582	1697.276429	C	***335.149601***	168.078438	318.123052	159.565164			2
27							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.3	3584.660538	0.012482	WSAETPHKPQFTFTSEPHAQLEENFCR
1.9	3584.660538	0.012482	WSAETPHKPQFTFTSEPHAQLEENFCR

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

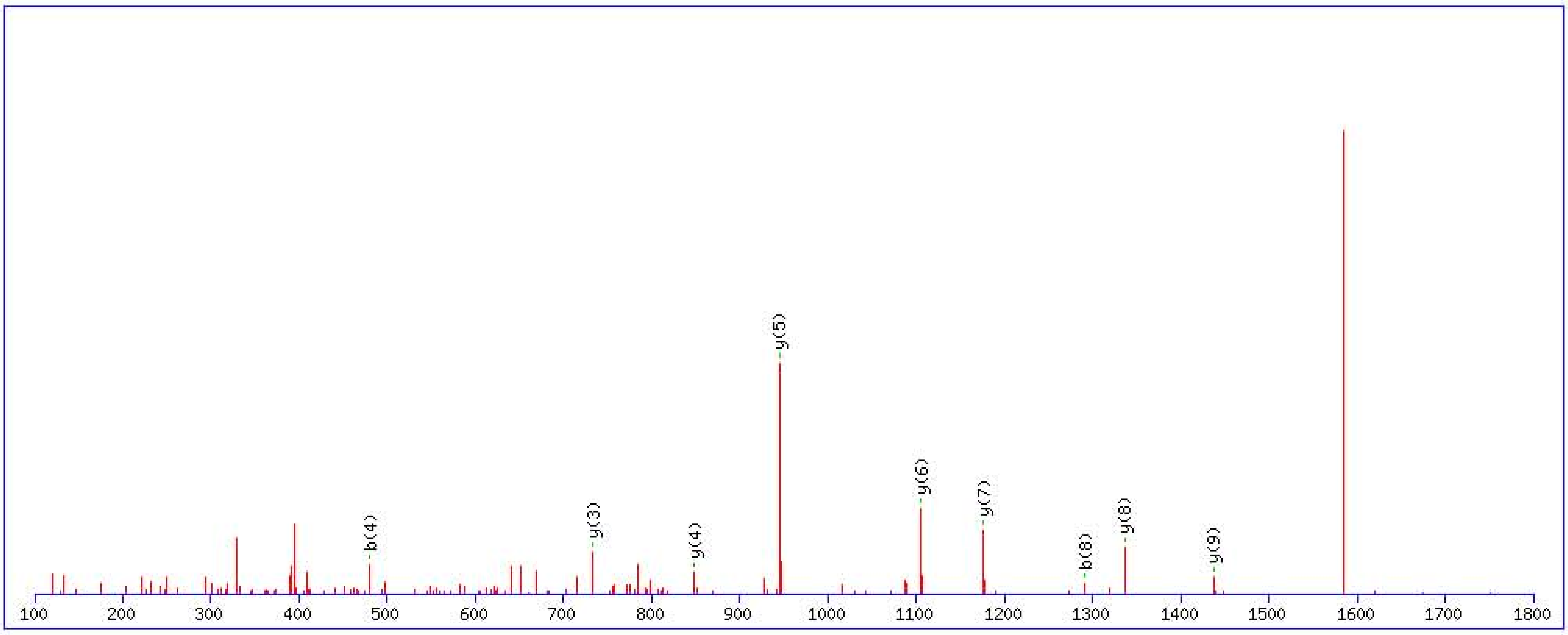
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FTCACPDQFK**
Found in **HABP2_HUMAN**, Hyaluronan-binding protein 2 OS=Homo sapiens GN=HABP2 PE=1 SV=1

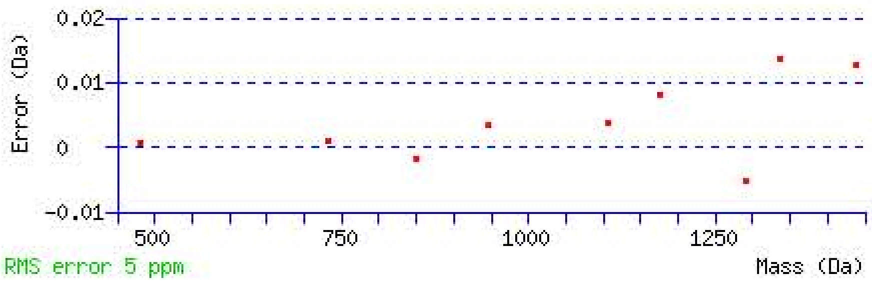
Match to Query 45270: 1583.696408 from(792.855480,2+) rtinseconds(1854) index(61996)
Title: Locus:1.1.1.2643.18 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

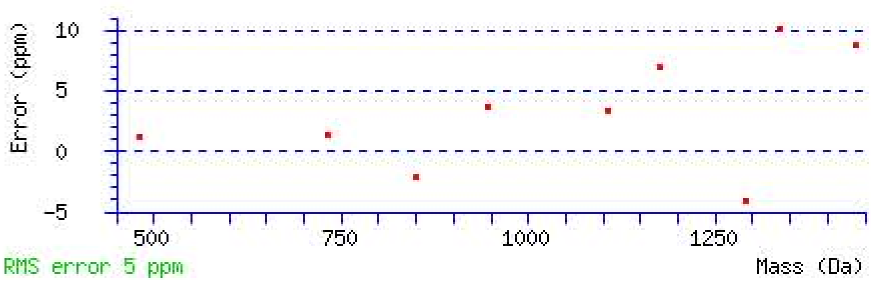
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1583.693497
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 49 **Expect:** 7.6e-005
Matches : 9/86 fragment ions using 14 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	148.075690	74.541483					F							10
2	249.123369	125.065322			231.112804	116.060040	T	***1437.632342***	719.319809	1420.605793	710.806535	1419.621777	710.314527	9
3	409.154018	205.080647			391.143453	196.075365	C	***1336.584663***	668.795970	1319.558114	660.282695	1318.574098	659.790687	8
4	**480.191132**	240.599204			462.180567	231.593921	A	***1176.554014***	588.780645	1159.527465	580.267371	1158.543449	579.775363	7
5	640.221781	320.614529			622.211216	311.609246	C	***1105.516900***	553.262088	1088.490351	544.748814	1087.506335	544.256806	6
6	737.274545	369.140911			719.263980	360.135628	P	***945.486251***	473.246764	928.459702	464.733489	927.475686	464.241481	5
7	852.301488	426.654382			834.290923	417.649100	D	***848.433487***	424.720382	831.406938	416.207107	830.422922	415.715099	4
8	**1291.526814**	646.267045	1274.500265	637.753771	1273.516249	637.261763	Q	***733.406544***	367.206910	716.379995	358.693636			3
9	1438.595228	719.801252	1421.568679	711.287978	1420.584663	710.795970	F	294.181218	147.594247	277.154669	139.080973			2
10							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.5	1583.693497	0.002911	FTCACPDQFK
4.6	1583.703827	-0.007419	FKDACGKSEDWNK

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

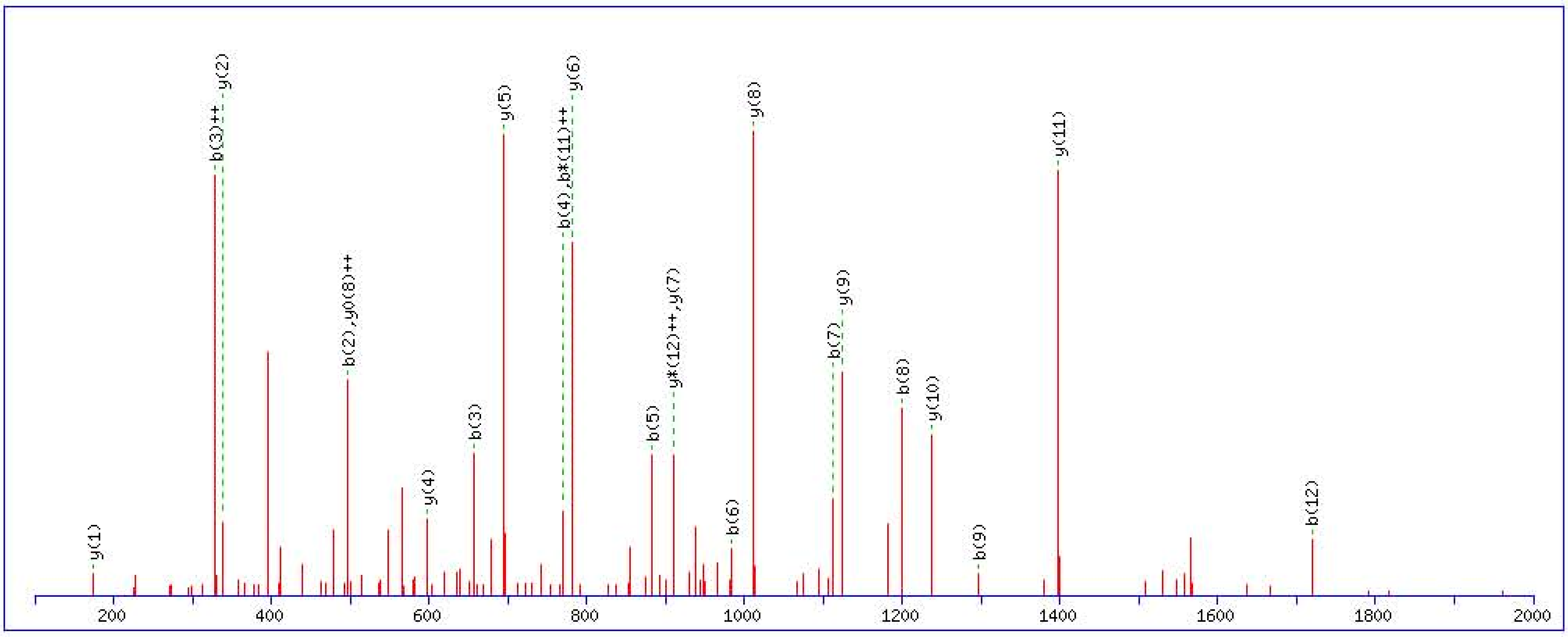
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQCLITQSPPYYR**
Found in **HABP2_HUMAN**, Hyaluronan-binding protein 2 OS=Homo sapiens GN=HABP2 PE=1 SV=1

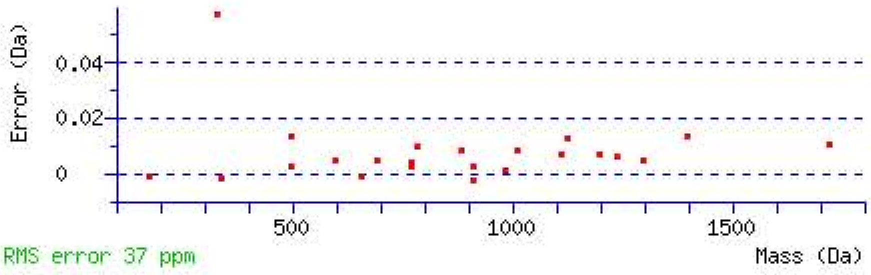
Match to Query 54156: 1892.938288 from(947.476420,2+) rtinseconds(2079) index(63606)
Title: Locus:1.1.1.2721.12 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

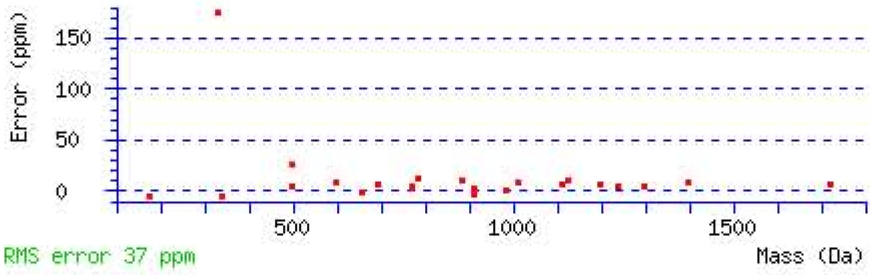
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1892.927704
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 66  Expect: 9.7e-007
Matches : 23/122 fragment ions using 32 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							13
2	**497.254066**	249.130671	480.227517	240.617397			Q	1836.913526	918.960401	1819.886977	910.447127	1818.902961	909.955119	12
3	**657.284715**	329.145996	640.258166	320.632721			C	***1397.688200***	699.347738	1380.661651	690.834464	1379.677635	690.342456	11
4	**770.368779**	385.688028	753.342230	377.174753			L	***1237.657551***	619.332414	1220.631002	610.819139	1219.646986	610.327131	10
5	**883.452843**	442.230060	866.426294	433.716785			I	***1124.573487***	562.790382	1107.546938	554.277107	1106.562922	553.785099	9
6	**984.500522**	492.753899	967.473973	484.240625	966.489957	483.748617	T	***1011.489423***	506.248350	994.462874	497.735075	993.478858	497.243067	8
7	**1112.559100**	556.783188	1095.532551	548.269914	1094.548535	547.777906	Q	***910.441744***	455.724510	893.415195	447.211236	892.431179	446.719228	7
8	**1199.591128**	600.299202	1182.564579	591.785928	1181.580563	591.293920	S	***782.383166***	391.695221	765.356617	383.181947	764.372601	382.689939	6
9	**1296.643892**	648.825584	1279.617343	640.312310	1278.633327	639.820302	P	***695.351138***	348.179207	678.324589	339.665933			5
10	1393.696656	697.351966	1376.670107	688.838692	1375.686091	688.346684	P	***598.298374***	299.652825	581.271825	291.139551			4
11	1556.759985	778.883631	1539.733436	770.370356	1538.749420	769.878348	Y	501.245610	251.126443	484.219061	242.613169			3
12	**1719.823314**	860.415295	1702.796765	851.902021	1701.812749	851.410013	Y	***338.182281***	169.594778	321.155732	161.081504			2
13							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
66.3	1892.927704	0.010584	GQCLITQSPPYYR
13.7	1892.927704	0.010584	GQCLITQSPPYYR
2.1	1892.910400	0.027888	SSRNYFGAQPHYR
1.8	1892.963882	-0.025594	SGREQAEPRTPAQR
1.3	1892.938065	0.000223	AQESVGFLDPAPAANPGPR

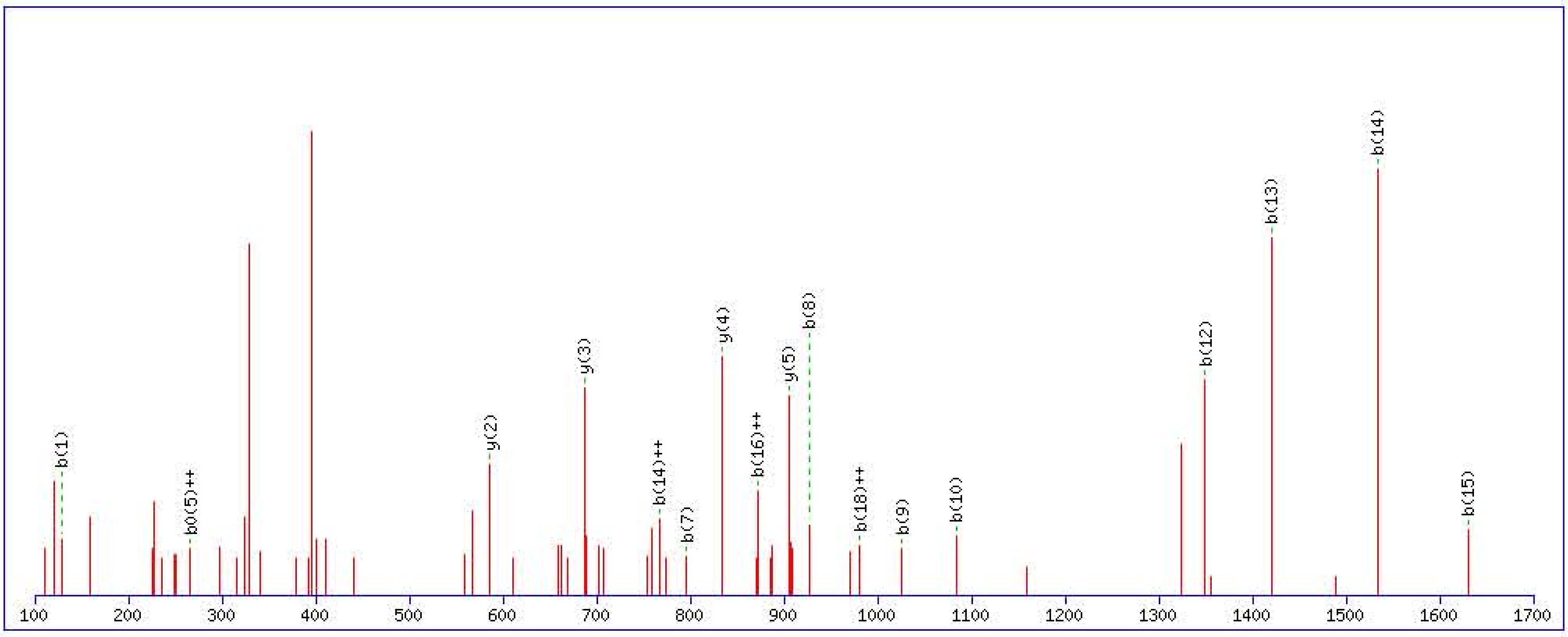
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KGDTFSCMVGHEALPLAFTQK**
Found in **IGHA1_HUMAN**, Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2

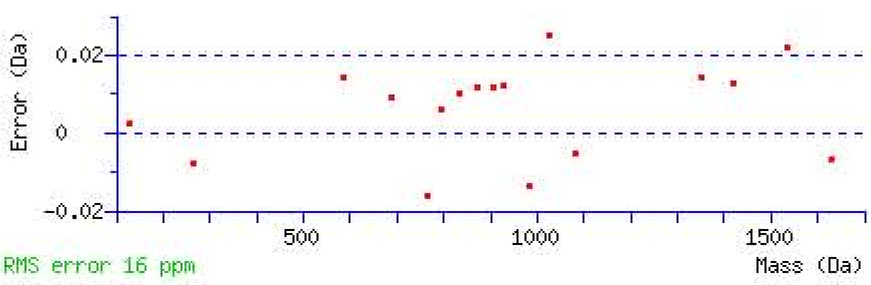
Match to Query 70123: 2647.305856 from(662.833740,4+) rtinseconds(2340) index(65285)
Title: Locus:1.1.1.2812.14 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

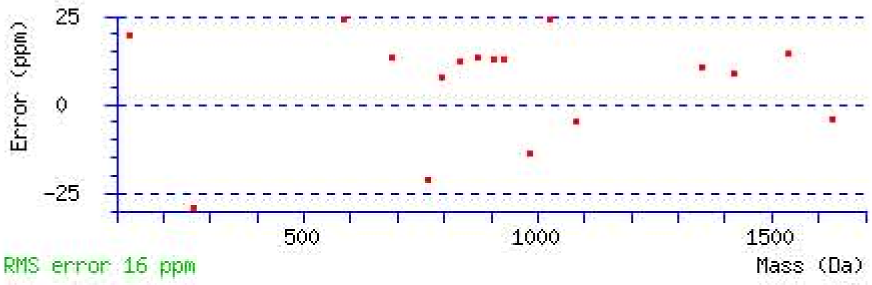
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2647.296082
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q20     : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0012
Matches : 17/232 fragment ions using 42 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***129.102239***	65.054757	112.075690	56.541483			K							21
2	186.123703	93.565489	169.097154	85.052215			G	2520.208388	1260.607832	2503.181839	1252.094557	2502.197823	1251.602549	20
3	301.150646	151.078961	284.124097	142.565687	283.140081	142.073679	D	2463.186924	1232.097100	2446.160375	1223.583825	2445.176359	1223.091817	19
4	402.198325	201.602801	385.171776	193.089526	384.187760	192.597518	T	2348.159981	1174.583628	2331.133432	1166.070354	2330.149416	1165.578346	18
5	549.266739	275.137008	532.240190	266.623733	531.256174	266.131725	F	2247.112302	1124.059789	2230.085753	1115.546514	2229.101737	1115.054506	17
6	636.298767	318.653022	619.272218	310.139747	618.288202	309.647739	S	2100.043888	1050.525582	2083.017339	1042.012307	2082.033323	1041.520299	16
7	***796.329416***	398.668346	779.302867	390.155072	778.318851	389.663064	C	2013.011860	1007.009568	1995.985311	998.496294	1995.001295	998.004286	15
8	***927.369901***	464.188589	910.343352	455.675314	909.359336	455.183306	M	1852.981211	926.994244	1835.954662	918.480969	1834.970646	917.988961	14
9	***1026.438315***	513.722796	1009.411766	505.209521	1008.427750	504.717513	V	1721.940726	861.474001	1704.914177	852.960727	1703.930161	852.468719	13
10	***1083.459779***	542.233528	1066.433230	533.720253	1065.449214	533.228245	G	1622.872312	811.939794	1605.845763	803.426520	1604.861747	802.934512	12
11	1220.518691	610.762984	1203.492142	602.249709	1202.508126	601.757701	H	1565.850848	783.429062	1548.824299	774.915788	1547.840283	774.423780	11
12	***1349.561284***	675.284280	1332.534735	666.771006	1331.550719	666.278998	E	1428.791936	714.899606	1411.765387	706.386332	1410.781371	705.894324	10
13	***1420.598398***	710.802837	1403.571849	702.289563	1402.587833	701.797555	A	1299.749343	650.378310	1282.722794	641.865035	1281.738778	641.373027	9
14	***1533.682462***	**767.344869**	1516.655913	758.831595	1515.671897	758.339587	L	1228.712229	614.859753	1211.685680	606.346478	1210.701664	605.854470	8
15	***1630.735226***	815.871251	1613.708677	807.357977	1612.724661	806.865969	P	1115.628165	558.317721	1098.601616	549.804446	1097.617600	549.312438	7
16	1743.819290	**872.413283**	1726.792741	863.900009	1725.808725	863.408000	L	1018.575401	509.791339	1001.548852	501.278064	1000.564836	500.786056	6
17	1814.856404	907.931840	1797.829855	899.418566	1796.845839	898.926557	A	***905.491337***	453.249307	888.464788	444.736032	887.480772	444.244024	5
18	1961.924818	**981.466047**	1944.898269	972.952773	1943.914253	972.460764	F	***834.454223***	417.730750	817.427674	409.217475	816.443658	408.725467	4
19	2062.972497	1031.989886	2045.945948	1023.476612	2044.961932	1022.984604	T	***687.385809***	344.196543	670.359260	335.683268	669.375244	335.191260	3
20	2502.197823	1251.602549	2485.171274	1243.089275	2484.187258	1242.597267	Q	***586.338130***	293.672703	569.311581	285.159429			2
21							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.5	2647.296082	0.009774	KGDTFSCMVGHEALPLAFTQK
5.1	2647.281662	0.024194	AAVLACQACCMLAIFLSMLVSYR
0.8	2647.285706	0.020150	QKYGLCVIFLSCTMMPNFK

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

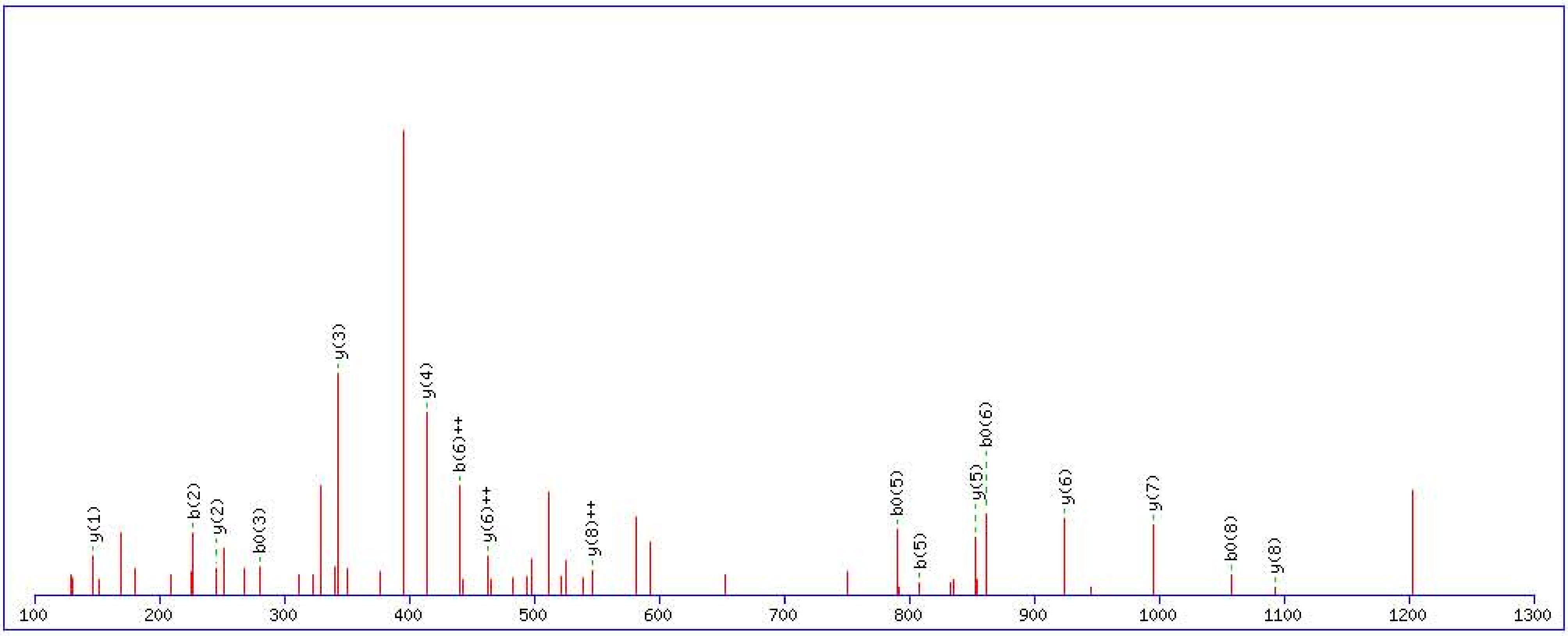
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of EPAAQAPVK
Found in IGHD_HUMAN, Ig delta chain C region OS=Homo sapiens GN=IGHD PE=1 SV=2

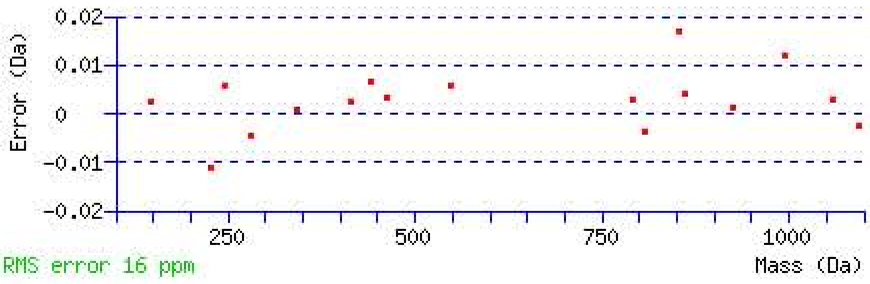
Match to Query 32301: 1220.655328 from(611.334940,2+) rtinseconds(1464) index(76638)
Title: Locus:1.1.1.2389.14 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

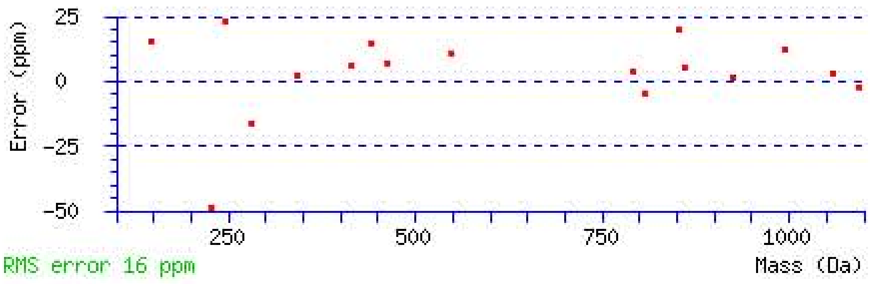
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1220.658707
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5     : Biotin:Thermo-21345 (Q)
Ions Score: 62  Expect: 1.1e-005
Matches : 17/72 fragment ions using 27 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	#
1	130.049869	65.528572			112.039304	56.523290	E					9
2	**227.102633**	114.054954			209.092068	105.049672	P	***1092.623414***	546.815345	1075.596865	538.302071	8
3	298.139747	149.573512			280.129182	140.568229	A	***995.570650***	498.288963	978.544101	489.775689	7
4	369.176861	185.092068			351.166296	176.086786	A	***924.533536***	462.770406	907.506987	454.257132	6
5	**808.402187**	404.704732	791.375638	396.191457	790.391622	395.699449	Q	***853.496422***	427.251849	836.469873	418.738575	5
6	879.439301	440.223289	862.412752	431.710014	861.428736	431.218006	A	***414.271096***	207.639186	397.244547	199.125911	4
7	976.492065	488.749671	959.465516	480.236396	958.481500	479.744388	P	***343.233982***	172.120629	326.207433	163.607354	3
8	1075.560479	538.283878	1058.533930	529.770603	1057.549914	529.278595	V	***246.181218***	123.594247	229.154669	115.080972	2
9							K	***147.112804***	74.060040	130.086255	65.546765	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.2	1220.658707	-0.003379	EPAAQAPVK
15.0	1220.658722	-0.003394	EQNVPVPK
6.5	1220.637589	0.017739	NHMFFIAITK
2.1	1220.651321	0.004007	GQVLIAASSYGR
0.0	1220.643463	0.011865	EMDLLRTTVK

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

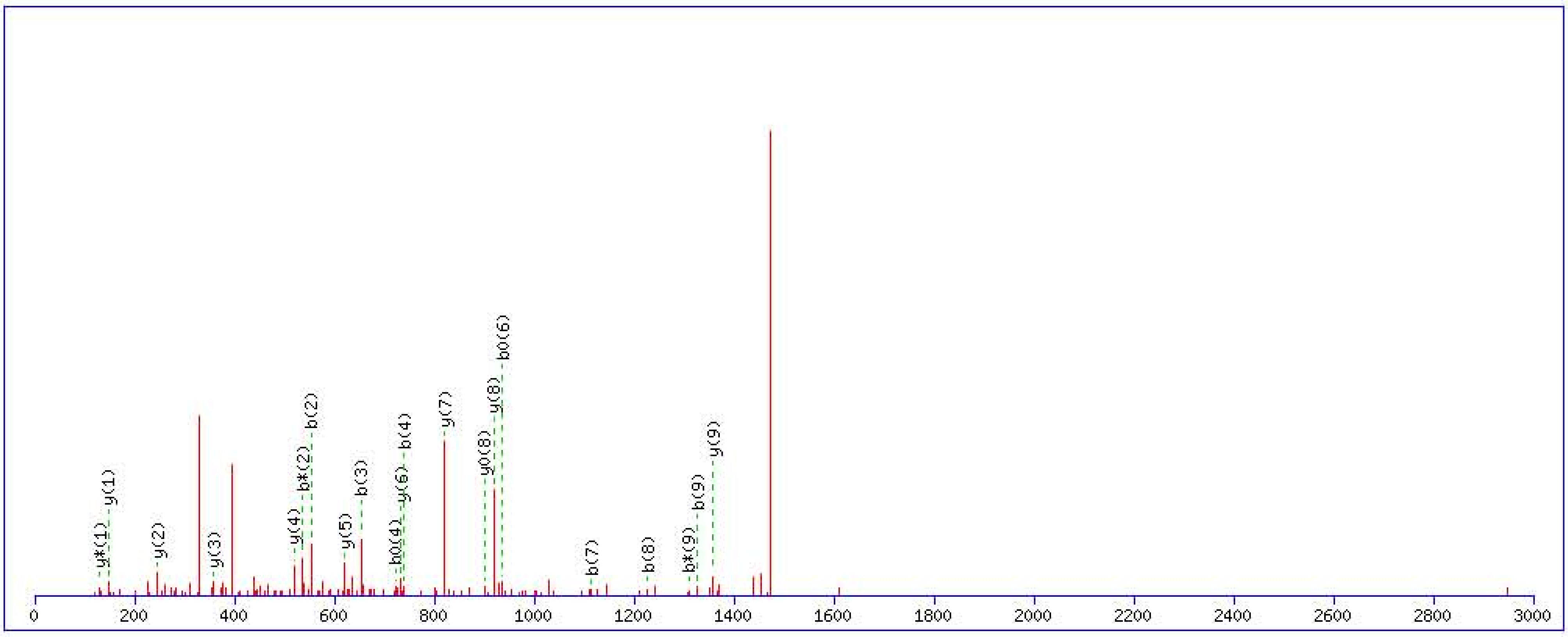
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NQVSLTCLVK**
Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

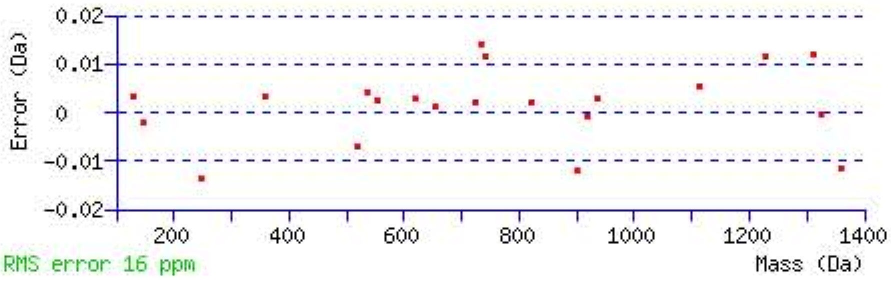
Match to Query 41797: 1471.793768 from(736.904160,2+) rtinseconds(2244) index(81981)
Title: Locus:1.1.1.2661.9 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

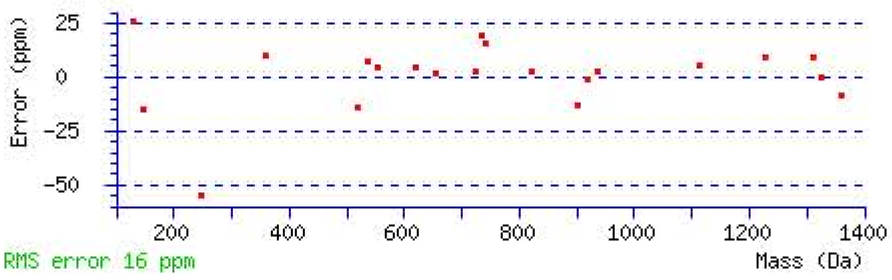
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1471.789093
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 54  Expect: 4.7e-005
Matches : 21/94 fragment ions using 42 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							10
2	**554.275529**	277.641403	537.248980	269.128128			Q	***1358.753442***	679.880359	1341.726893	671.367085	1340.742877	670.875076	9
3	**653.343943**	327.175610	636.317394	318.662335			V	***919.528116***	460.267696	902.501567	451.754421	901.517551	451.262413	8
4	**740.375971**	370.691623	723.349422	362.178349	722.365406	361.686341	S	***820.459702***	410.733489	803.433153	402.220215	802.449137	401.728207	7
5	853.460035	427.233656	836.433486	418.720381	835.449470	418.228373	L	***733.427674***	367.217475	716.401125	358.704201	715.417109	358.212193	6
6	954.507714	477.757495	937.481165	469.244220	936.497149	468.752212	T	***620.343610***	310.675443	603.317061	302.162169	602.333045	301.670161	5
7	**1114.538363**	557.772819	1097.511814	549.259545	1096.527798	548.767537	C	***519.295931***	260.151604	502.269382	251.638329			4
8	**1227.622427**	614.314851	1210.595878	605.801577	1209.611862	605.309569	L	***359.265282***	180.136279	342.238733	171.623004			3
9	**1326.690841**	663.849058	1309.664292	655.335784	1308.680276	654.843776	V	***246.181218***	123.594247	229.154669	115.080973			2
10							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.0	1471.789093	0.004675	NQVSLTCLVK
7.5	1471.797592	-0.003824	KYFWDRAFLVK
4.7	1471.803467	-0.009699	EKQGPLLDLFGQK
4.6	1471.792908	0.000860	NITINCVKGINAR
2.8	1471.799438	-0.005670	EVELDRLRDTVK
2.6	1471.792221	0.001547	NESIIPLSPFEVK
2.3	1471.806793	-0.013025	AAALLAKQAEMEVK
1.2	1471.777847	0.015921	QLDMELVSVK

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

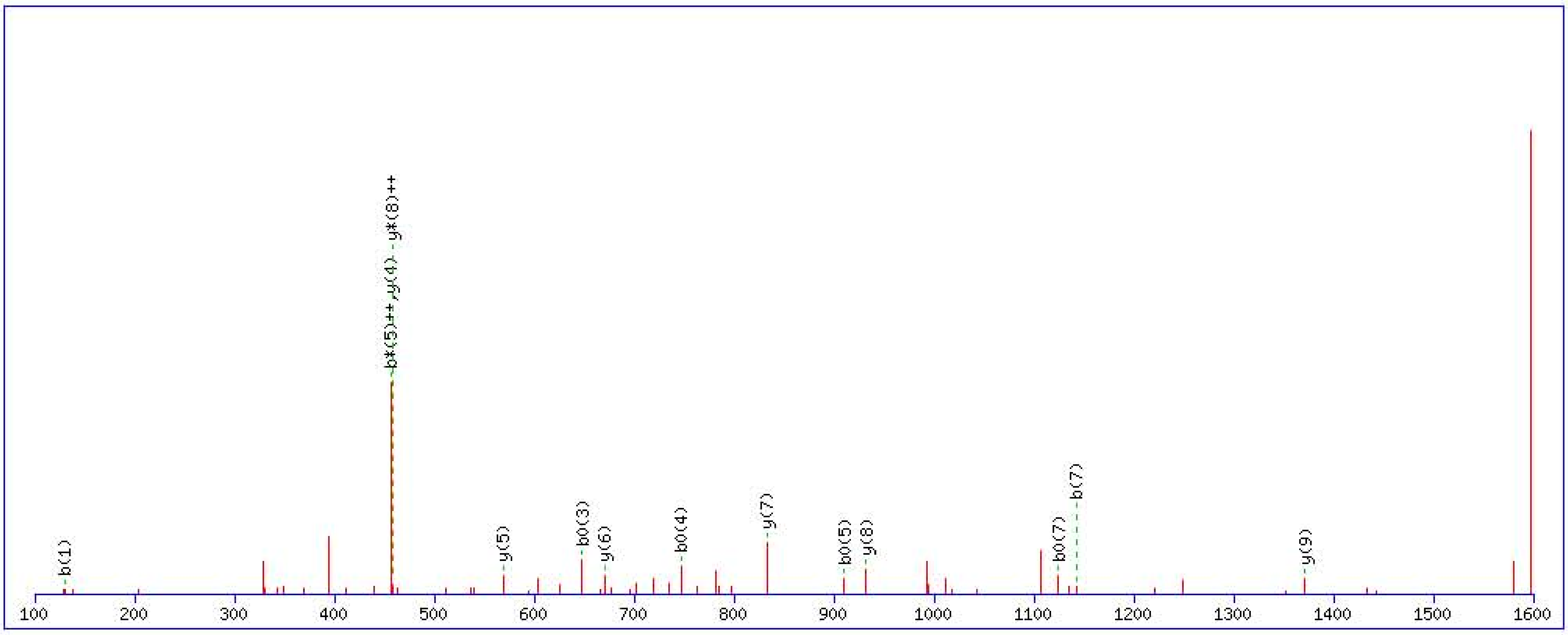
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EPQVYTLPPSR**
Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

Match to Query 45999: 1596.832228 from(799.423390,2+) rtinseconds(1989) index(80222)
Title: Locus:1.1.1.2572.12 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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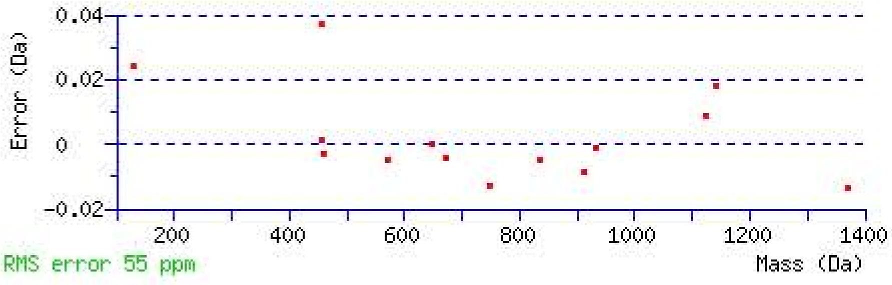
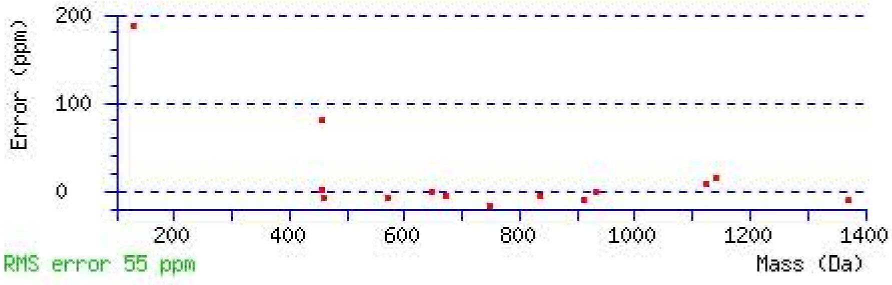
Monoisotopic mass of neutral peptide Mr(calc): 1596.833389
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.0045
Matches : 14/114 fragment ions using 27 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**130.049869**	65.528572			112.039304	56.523290	E							11
2	227.102633	114.054954			209.092068	105.049672	P	1468.798084	734.902680	1451.771535	726.389406	1450.787519	725.897398	10
3	666.327959	333.667618	649.301410	325.154343	648.317394	324.662335	Q	***1371.745320***	686.376298	1354.718771	677.863024	1353.734755	677.371016	9
4	765.396373	383.201825	748.369824	374.688550	747.385808	374.196542	V	***932.519994***	466.763635	915.493445	458.250361	914.509429	457.758353	8
5	928.459702	464.733489	911.433153	456.220215	910.449137	455.728207	Y	***833.451580***	417.229428	816.425031	408.716154	815.441015	408.224146	7
6	1029.507381	515.257329	1012.480832	506.744054	1011.496816	506.252046	T	***670.388251***	335.697764	653.361702	327.184489	652.377686	326.692481	6
7	**1142.591445**	571.799361	1125.564896	563.286086	1124.580880	562.794078	L	***569.340572***	285.173924	552.314023	276.660650	551.330007	276.168642	5
8	1239.644209	620.325743	1222.617660	611.812468	1221.633644	611.320460	P	***456.256508***	228.631892	439.229959	220.118618	438.245943	219.626610	4
9	1336.696973	668.852125	1319.670424	660.338850	1318.686408	659.846842	P	359.203744	180.105510	342.177195	171.592236	341.193179	171.100228	3
10	1423.729001	712.368139	1406.702452	703.854864	1405.718436	703.362856	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
11							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.0	1596.833389	-0.001161	EPQVYTLPPSR
0.7	1596.825974	0.006254	KLSDLEAQWAPSPR

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

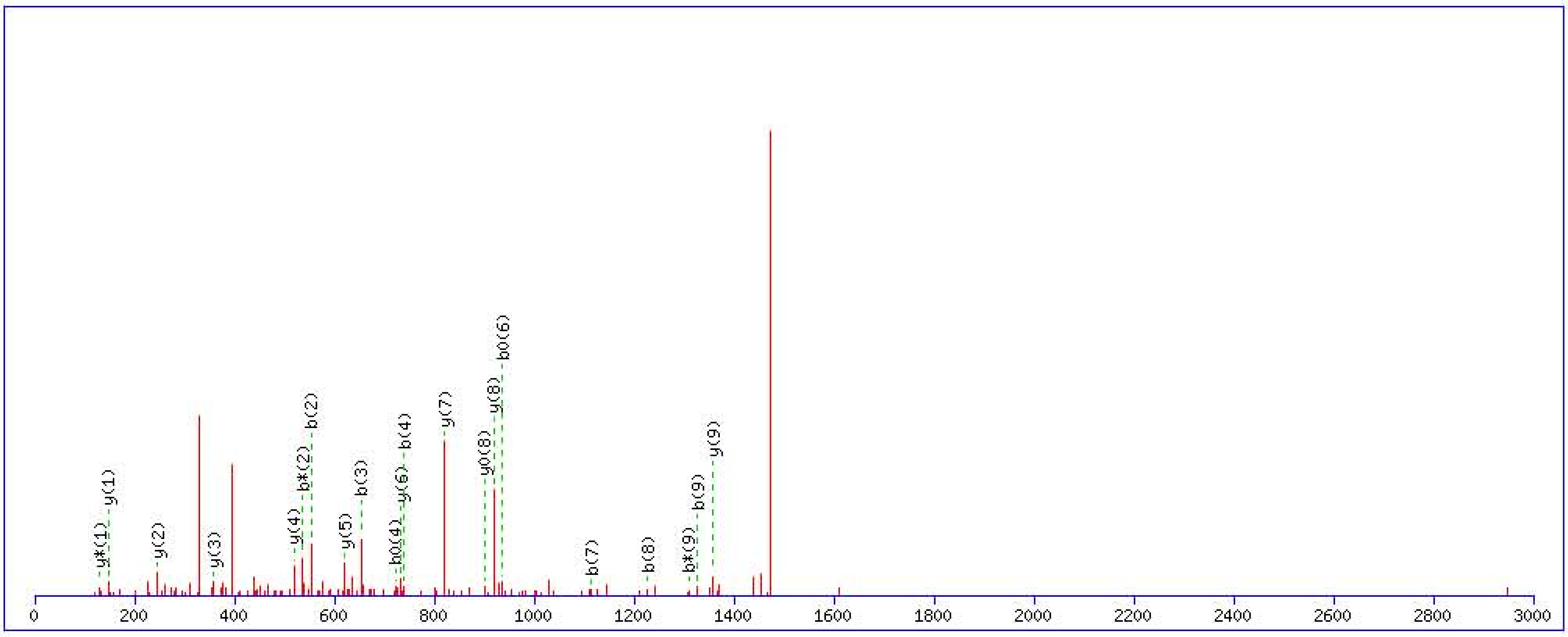
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NQVSLTCLVK**
Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

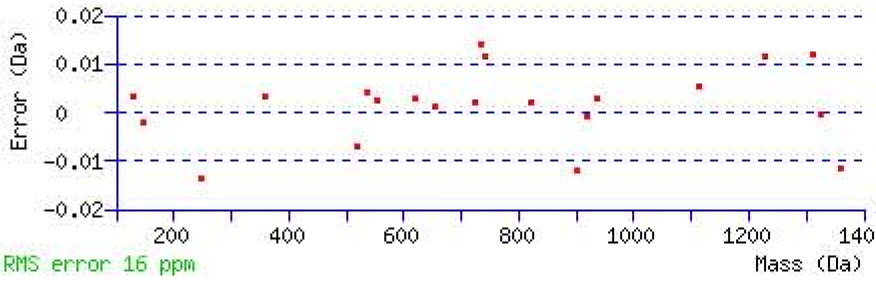
Match to Query 41797: 1471.793768 from(736.904160,2+) rtinseconds(2244) index(81981)
Title: Locus:1.1.1.2661.9 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

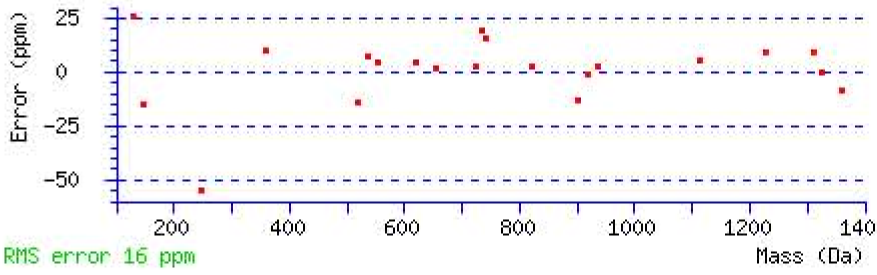
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1471.789093
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 54 **Expect:** 4.7e-005
Matches : 21/94 fragment ions using 42 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							10
2	**554.275529**	277.641403	537.248980	269.128128			Q	***1358.753442***	679.880359	1341.726893	671.367085	1340.742877	670.875076	9
3	**653.343943**	327.175610	636.317394	318.662335			V	***919.528116***	460.267696	902.501567	451.754421	901.517551	451.262413	8
4	**740.375971**	370.691623	723.349422	362.178349	722.365406	361.686341	S	***820.459702***	410.733489	803.433153	402.220215	802.449137	401.728207	7
5	853.460035	427.233656	836.433486	418.720381	835.449470	418.228373	L	***733.427674***	367.217475	716.401125	358.704201	715.417109	358.212193	6
6	954.507714	477.757495	937.481165	469.244220	936.497149	468.752212	T	***620.343610***	310.675443	603.317061	302.162169	602.333045	301.670161	5
7	**1114.538363**	557.772819	1097.511814	549.259545	1096.527798	548.767537	C	***519.295931***	260.151604	502.269382	251.638329			4
8	**1227.622427**	614.314851	1210.595878	605.801577	1209.611862	605.309569	L	***359.265282***	180.136279	342.238733	171.623004			3
9	**1326.690841**	663.849058	1309.664292	655.335784	1308.680276	654.843776	V	***246.181218***	123.594247	229.154669	115.080973			2
10							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.0	1471.789093	0.004675	NQVSLTCLVK
7.5	1471.797592	-0.003824	KYFWDRAFLVK
4.7	1471.803467	-0.009699	EKQGPLLDLFGQK
4.6	1471.792908	0.000860	NITINCVKGINAR
2.8	1471.799438	-0.005670	EVELDRLRDTVK
2.6	1471.792221	0.001547	NESIIPLSPFEVK
2.3	1471.806793	-0.013025	AAALLAKQAEMEVK
1.2	1471.777847	0.015921	QLDMELVSVK

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

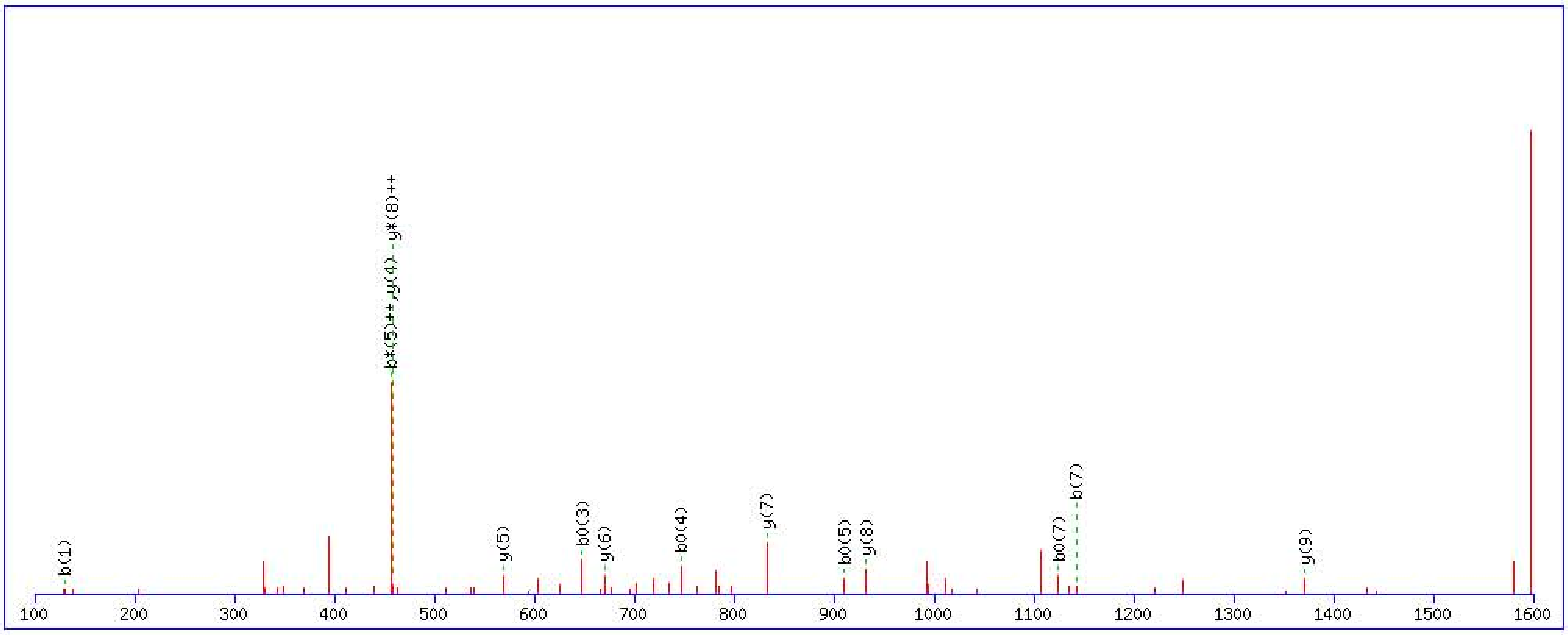
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EPQVYTLPPSR**
Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

Match to Query 45999: 1596.832228 from(799.423390,2+) rtinseconds(1989) index(80222)
Title: Locus:1.1.1.2572.12 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1600] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



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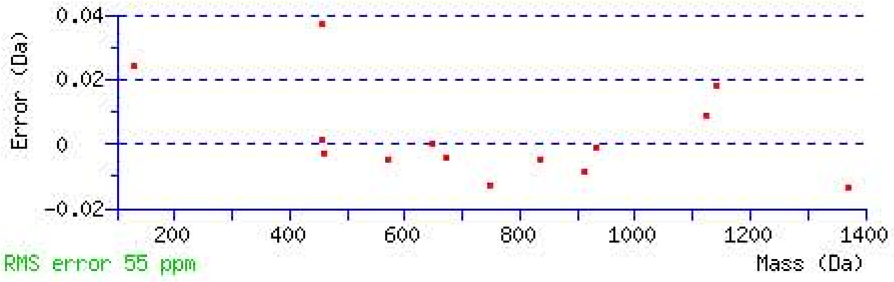
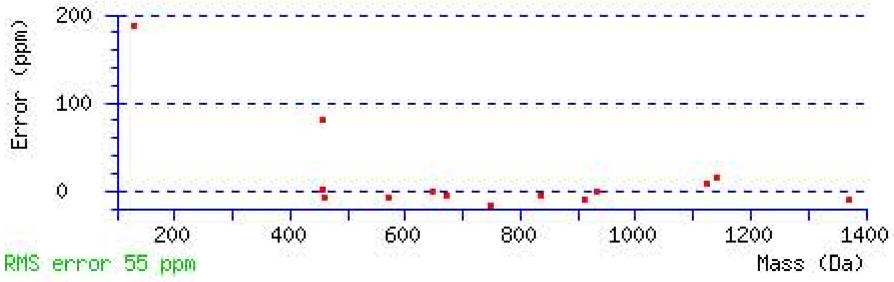
Monoisotopic mass of neutral peptide Mr(calc): 1596.833389
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.0045
Matches : 14/114 fragment ions using 27 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**130.049869**	65.528572			112.039304	56.523290	E							11
2	227.102633	114.054954			209.092068	105.049672	P	1468.798084	734.902680	1451.771535	726.389406	1450.787519	725.897398	10
3	666.327959	333.667618	649.301410	325.154343	648.317394	324.662335	Q	***1371.745320***	686.376298	1354.718771	677.863024	1353.734755	677.371016	9
4	765.396373	383.201825	748.369824	374.688550	747.385808	374.196542	V	***932.519994***	466.763635	915.493445	458.250361	914.509429	457.758353	8
5	928.459702	464.733489	911.433153	456.220215	910.449137	455.728207	Y	***833.451580***	417.229428	816.425031	408.716154	815.441015	408.224146	7
6	1029.507381	515.257329	1012.480832	506.744054	1011.496816	506.252046	T	***670.388251***	335.697764	653.361702	327.184489	652.377686	326.692481	6
7	**1142.591445**	571.799361	1125.564896	563.286086	1124.580880	562.794078	L	***569.340572***	285.173924	552.314023	276.660650	551.330007	276.168642	5
8	1239.644209	620.325743	1222.617660	611.812468	1221.633644	611.320460	P	***456.256508***	228.631892	439.229959	220.118618	438.245943	219.626610	4
9	1336.696973	668.852125	1319.670424	660.338850	1318.686408	659.846842	P	359.203744	180.105510	342.177195	171.592236	341.193179	171.100228	3
10	1423.729001	712.368139	1406.702452	703.854864	1405.718436	703.362856	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
11							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.0	1596.833389	-0.001161	EPQVYTLPPSR
0.7	1596.825974	0.006254	KLSDLEAQWAPSPR

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

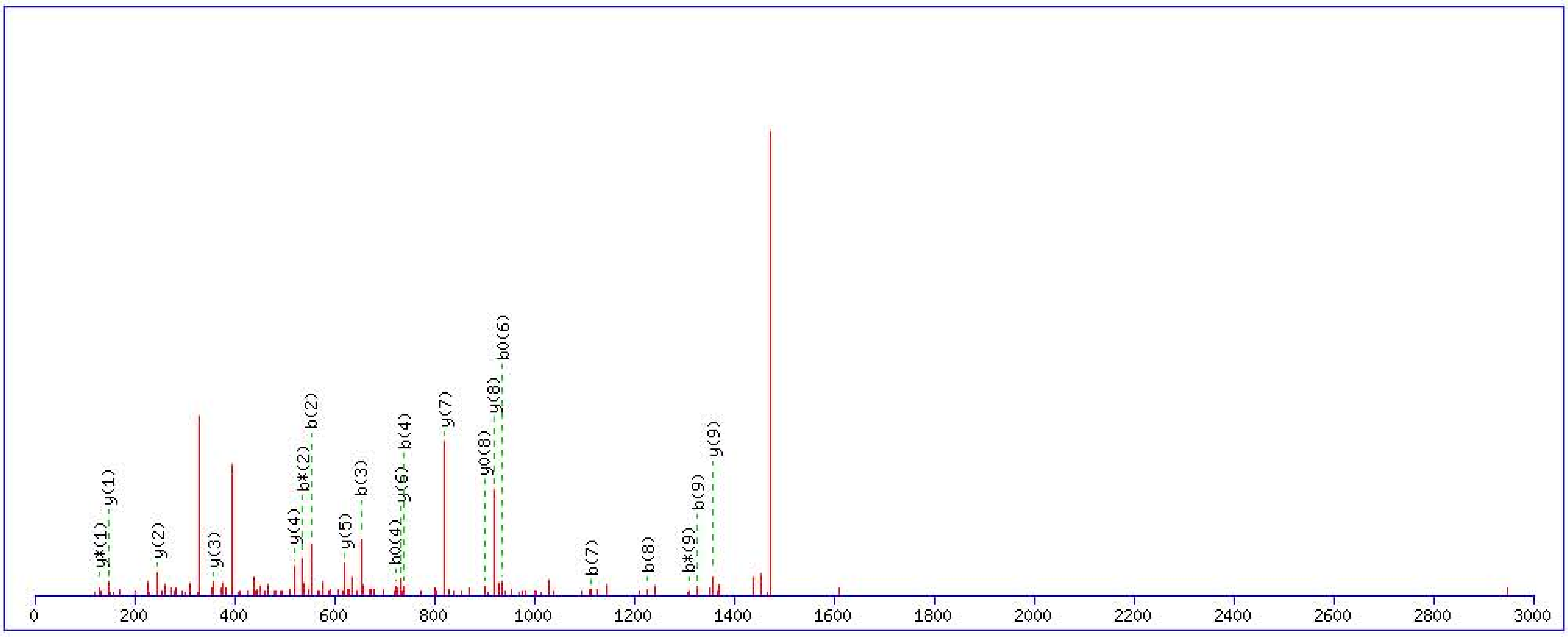
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NQVSLTCLVK**
Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

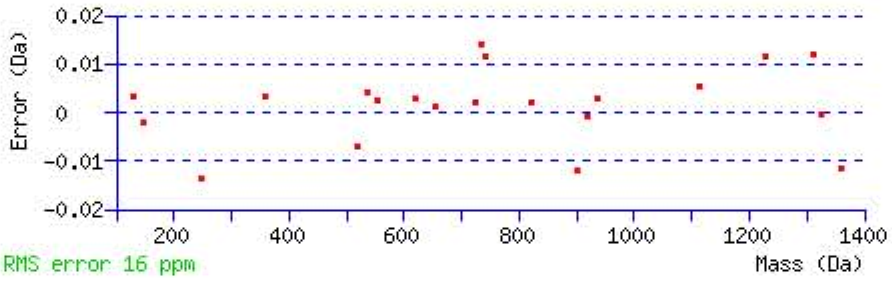
Match to Query 41797: 1471.793768 from(736.904160,2+) rtinseconds(2244) index(81981)
Title: Locus:1.1.1.2661.9 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

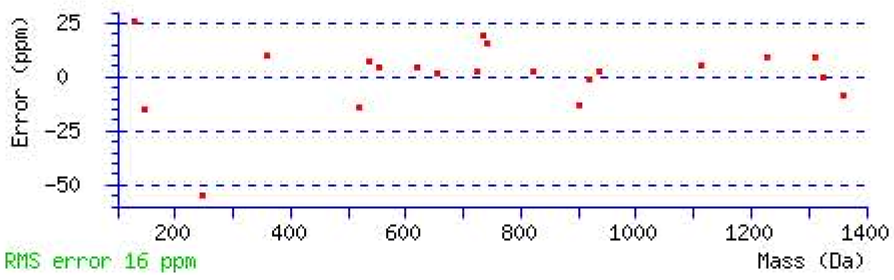
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1471.789093
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 54 **Expect:** 4.7e-005
Matches : 21/94 fragment ions using 42 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							10
2	**554.275529**	277.641403	537.248980	269.128128			Q	***1358.753442***	679.880359	1341.726893	671.367085	1340.742877	670.875076	9
3	**653.343943**	327.175610	636.317394	318.662335			V	***919.528116***	460.267696	902.501567	451.754421	901.517551	451.262413	8
4	**740.375971**	370.691623	723.349422	362.178349	722.365406	361.686341	S	***820.459702***	410.733489	803.433153	402.220215	802.449137	401.728207	7
5	853.460035	427.233656	836.433486	418.720381	835.449470	418.228373	L	***733.427674***	367.217475	716.401125	358.704201	715.417109	358.212193	6
6	954.507714	477.757495	937.481165	469.244220	936.497149	468.752212	T	***620.343610***	310.675443	603.317061	302.162169	602.333045	301.670161	5
7	**1114.538363**	557.772819	1097.511814	549.259545	1096.527798	548.767537	C	***519.295931***	260.151604	502.269382	251.638329			4
8	**1227.622427**	614.314851	1210.595878	605.801577	1209.611862	605.309569	L	***359.265282***	180.136279	342.238733	171.623004			3
9	**1326.690841**	663.849058	1309.664292	655.335784	1308.680276	654.843776	V	***246.181218***	123.594247	229.154669	115.080973			2
10							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
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4.6	1471.792908	0.000860	NITINCVKGINAR
2.8	1471.799438	-0.005670	EVELDRLRDTVK
2.6	1471.792221	0.001547	NESIIPLSPFEVK
2.3	1471.806793	-0.013025	AAALLAKQAEMEVK
1.2	1471.777847	0.015921	QLDMELVSVK

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

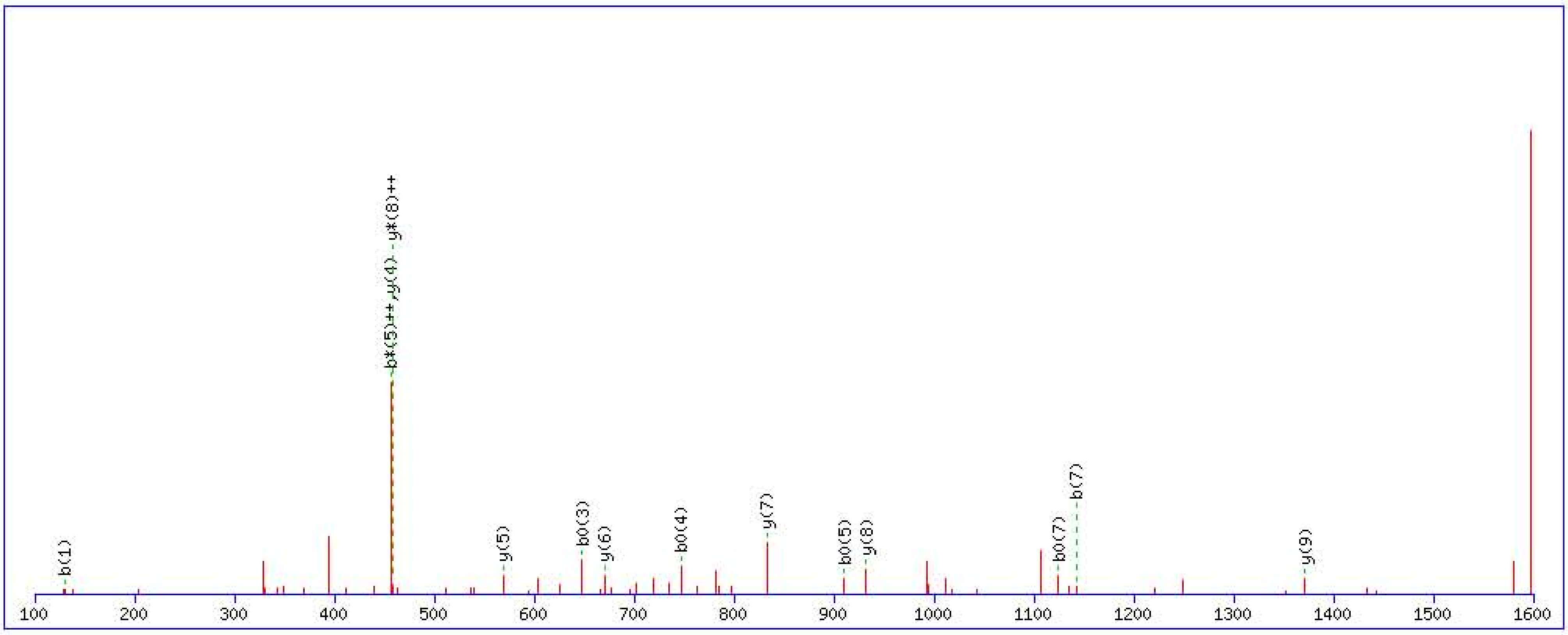
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EPQVYTLPPSR**
Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

Match to Query 45999: 1596.832228 from(799.423390,2+) rtinseconds(1989) index(80222)
Title: Locus:1.1.1.2572.12 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



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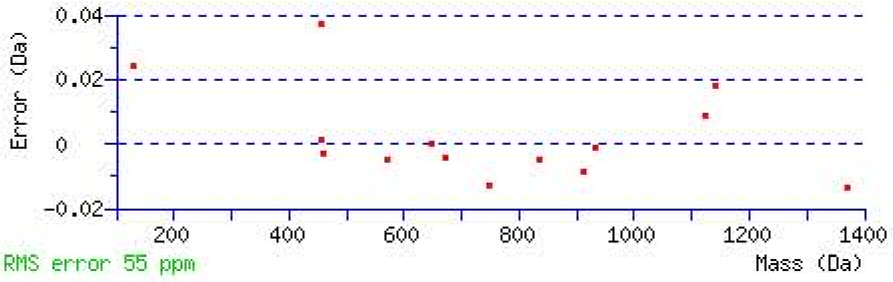
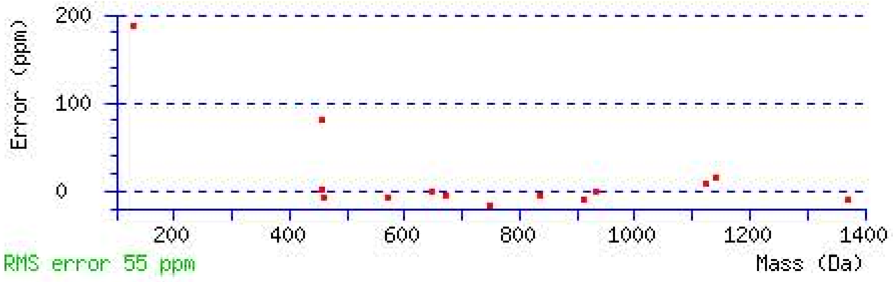
Monoisotopic mass of neutral peptide Mr(calc): 1596.833389
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.0045
Matches : 14/114 fragment ions using 27 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**130.049869**	65.528572			112.039304	56.523290	E							11
2	227.102633	114.054954			209.092068	105.049672	P	1468.798084	734.902680	1451.771535	726.389406	1450.787519	725.897398	10
3	666.327959	333.667618	649.301410	325.154343	648.317394	324.662335	Q	***1371.745320***	686.376298	1354.718771	677.863024	1353.734755	677.371016	9
4	765.396373	383.201825	748.369824	374.688550	747.385808	374.196542	V	***932.519994***	466.763635	915.493445	458.250361	914.509429	457.758353	8
5	928.459702	464.733489	911.433153	456.220215	910.449137	455.728207	Y	***833.451580***	417.229428	816.425031	408.716154	815.441015	408.224146	7
6	1029.507381	515.257329	1012.480832	506.744054	1011.496816	506.252046	T	***670.388251***	335.697764	653.361702	327.184489	652.377686	326.692481	6
7	**1142.591445**	571.799361	1125.564896	563.286086	1124.580880	562.794078	L	***569.340572***	285.173924	552.314023	276.660650	551.330007	276.168642	5
8	1239.644209	620.325743	1222.617660	611.812468	1221.633644	611.320460	P	***456.256508***	228.631892	439.229959	220.118618	438.245943	219.626610	4
9	1336.696973	668.852125	1319.670424	660.338850	1318.686408	659.846842	P	359.203744	180.105510	342.177195	171.592236	341.193179	171.100228	3
10	1423.729001	712.368139	1406.702452	703.854864	1405.718436	703.362856	S	262.150980	131.579128	245.124431	123.065854	244.140415	122.573846	2
11							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.0	1596.833389	-0.001161	EPQVYTLPPSR
0.7	1596.825974	0.006254	KLSDLEAQWAPSPR

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

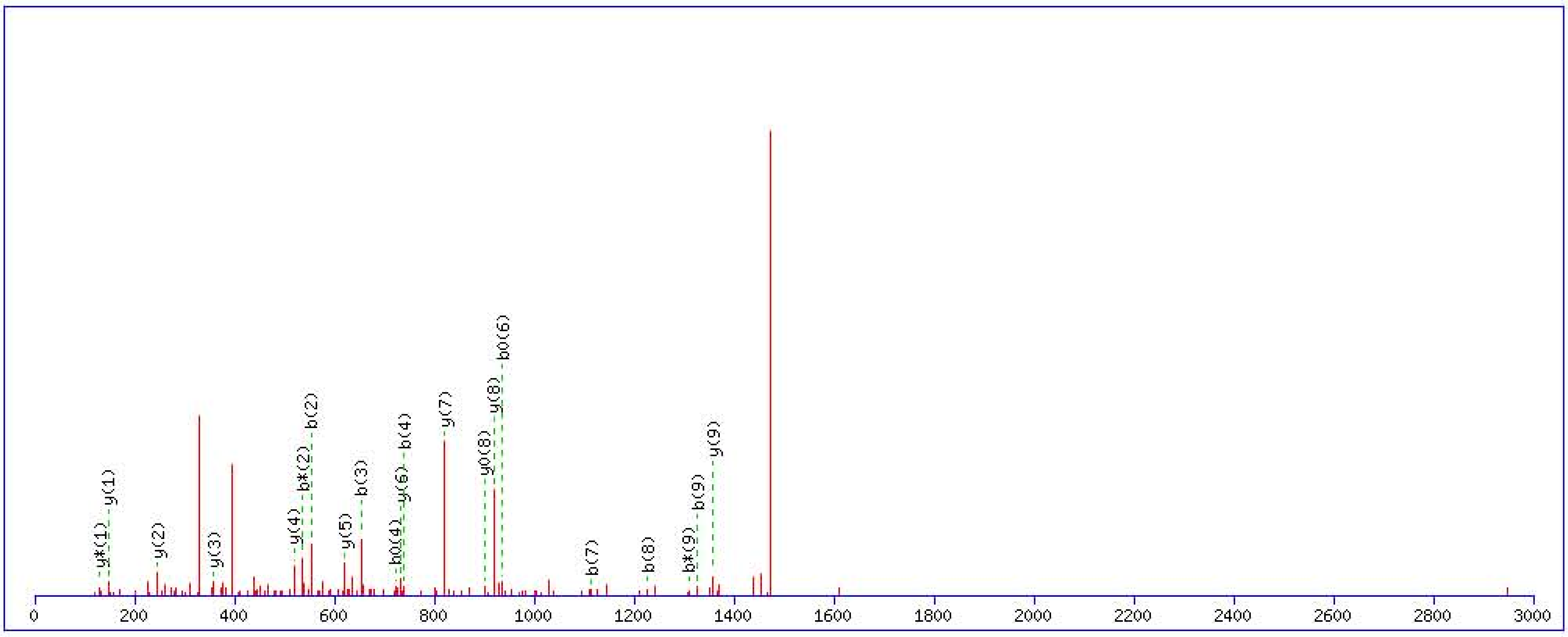
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **NQVSLTCLVK**
Found in **IGHG1_HUMAN**, Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

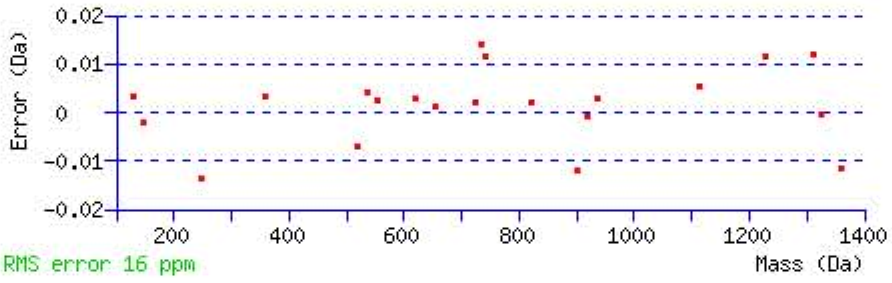
Match to Query 41797: 1471.793768 from(736.904160,2+) rtinseconds(2244) index(81981)
Title: Locus:1.1.1.2661.9 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

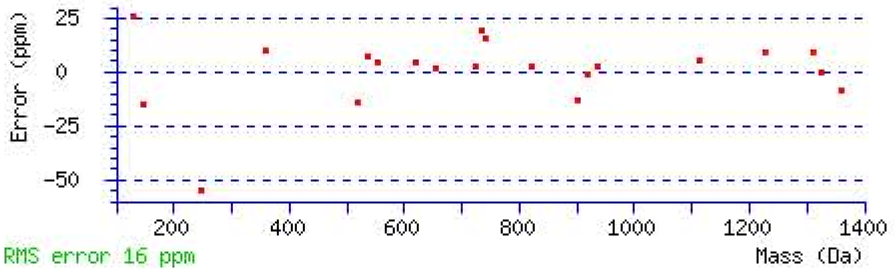
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1471.789093
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 54 **Expect:** 4.7e-005
Matches : 21/94 fragment ions using 42 most intense peaks (help)

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							10
2	**554.275529**	277.641403	537.248980	269.128128			Q	***1358.753442***	679.880359	1341.726893	671.367085	1340.742877	670.875076	9
3	**653.343943**	327.175610	636.317394	318.662335			V	***919.528116***	460.267696	902.501567	451.754421	901.517551	451.262413	8
4	**740.375971**	370.691623	723.349422	362.178349	722.365406	361.686341	S	***820.459702***	410.733489	803.433153	402.220215	802.449137	401.728207	7
5	853.460035	427.233656	836.433486	418.720381	835.449470	418.228373	L	***733.427674***	367.217475	716.401125	358.704201	715.417109	358.212193	6
6	954.507714	477.757495	937.481165	469.244220	936.497149	468.752212	T	***620.343610***	310.675443	603.317061	302.162169	602.333045	301.670161	5
7	**1114.538363**	557.772819	1097.511814	549.259545	1096.527798	548.767537	C	***519.295931***	260.151604	502.269382	251.638329			4
8	**1227.622427**	614.314851	1210.595878	605.801577	1209.611862	605.309569	L	***359.265282***	180.136279	342.238733	171.623004			3
9	**1326.690841**	663.849058	1309.664292	655.335784	1308.680276	654.843776	V	***246.181218***	123.594247	229.154669	115.080973			2
10							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.0	1471.789093	0.004675	NQVSLTCLVK
7.5	1471.797592	-0.003824	KYFWDRAFLVK
4.7	1471.803467	-0.009699	EKQGPLLDLFGQK
4.6	1471.792908	0.000860	NITINCVKGINAR
2.8	1471.799438	-0.005670	EVELDRLRDTVK
2.6	1471.792221	0.001547	NESIIPLSPFEVK
2.3	1471.806793	-0.013025	AAALLAKQAEMEVK
1.2	1471.777847	0.015921	QLDMELVSVK

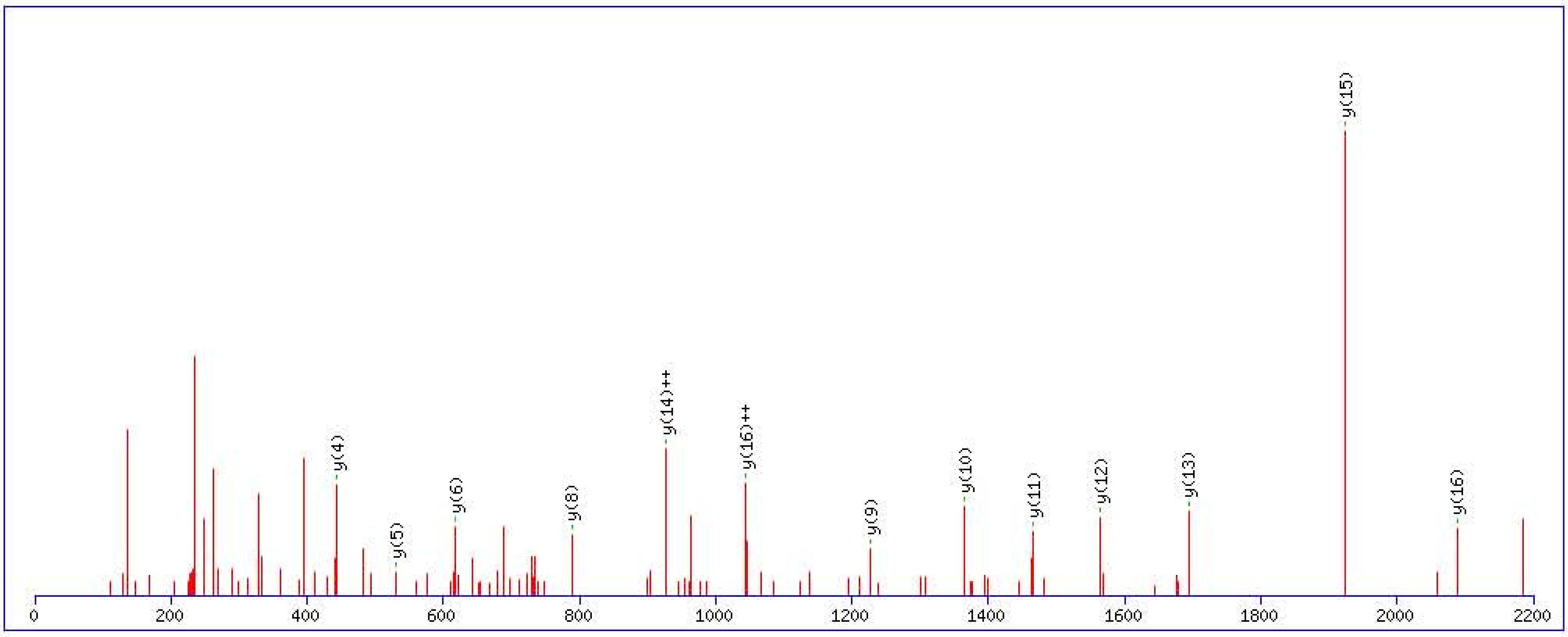
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VYACEVTHQGLSSPVTK**
Found in **IGKC_HUMAN**, Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1

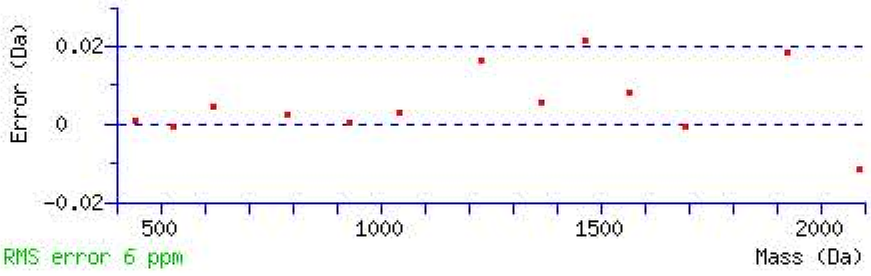
Match to Query 61335: 2186.091072 from(729.704300,3+) rtinseconds(1797) index(78900)
Title: Locus:1.1.1.2505.17 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

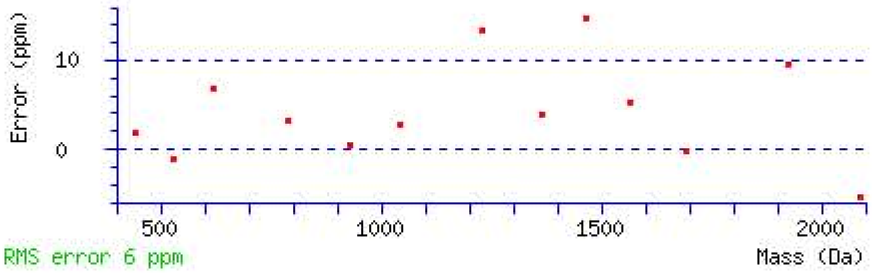
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2186.086411
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9 : Biotin:Thermo-21345 (Q)
Ions Score: 88 **Expect:** 4.1e-008
Matches : 13/166 fragment ions using 18 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							17
2	263.139019	132.073148					Y	***2088.025261***	1044.516268	2070.998712	1036.002994	2070.014696	1035.510986	16
3	334.176133	167.591704					A	***1924.961932***	962.984604	1907.935383	954.471330	1906.951367	953.979322	15
4	494.206782	247.607029					C	1853.924818	927.466047	1836.898269	918.952773	1835.914253	918.460765	14
5	623.249375	312.128326			605.238810	303.123043	E	***1693.894169***	847.450723	1676.867620	838.937448	1675.883604	838.445440	13
6	722.317789	361.662533			704.307224	352.657250	V	***1564.851576***	782.929426	1547.825027	774.416152	1546.841011	773.924144	12
7	823.365468	412.186372			805.354903	403.181090	T	***1465.783162***	733.395219	1448.756613	724.881945	1447.772597	724.389937	11
8	960.424380	480.715828			942.413815	471.710546	H	***1364.735483***	682.871380	1347.708934	674.358105	1346.724918	673.866097	10
9	1399.649706	700.328491	1382.623157	691.815217	1381.639141	691.323208	Q	***1227.676571***	614.341924	1210.650022	605.828649	1209.666006	605.336641	9
10	1456.671170	728.839223	1439.644621	720.325948	1438.660605	719.833940	G	***788.451245***	394.729261	771.424696	386.215986	770.440680	385.723978	8
11	1569.755234	785.381255	1552.728685	776.867980	1551.744669	776.375972	L	731.429781	366.218529	714.403232	357.705254	713.419216	357.213246	7
12	1656.787262	828.897269	1639.760713	820.383994	1638.776697	819.891986	S	***618.345717***	309.676497	601.319168	301.163222	600.335152	300.671214	6
13	1743.819290	872.413283	1726.792741	863.900009	1725.808725	863.408000	S	***531.313689***	266.160483	514.287140	257.647208	513.303124	257.155200	5
14	1840.872054	920.939665	1823.845505	912.426391	1822.861489	911.934382	P	***444.281661***	222.644469	427.255112	214.131194	426.271096	213.639186	4
15	1939.940468	970.473872	1922.913919	961.960598	1921.929903	961.468590	V	347.228897	174.118087	330.202348	165.604812	329.218332	165.112804	3
16	2040.988147	1020.997712	2023.961598	1012.484437	2022.977582	1011.992429	T	248.160483	124.583880	231.133934	116.070605	230.149918	115.578597	2
17							K	147.112804	74.060040	130.086255	65.546766			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
88.4	2186.086411	0.004661	VYACEVTHQGLSSPVTK

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

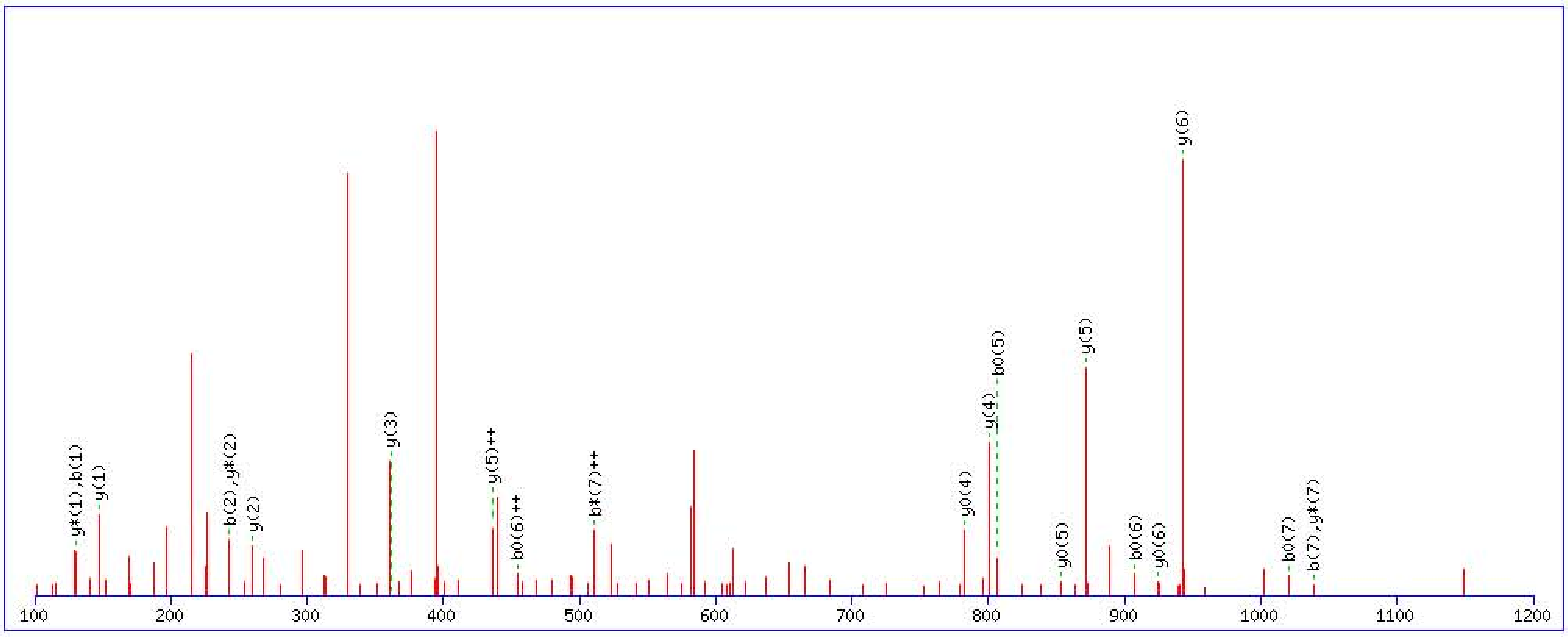
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ELAAQTIK**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

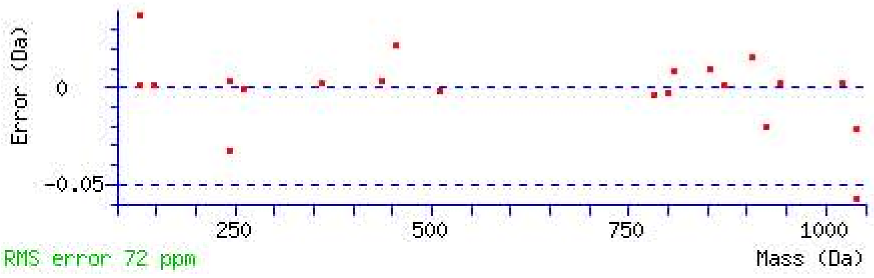
Match to Query 31190: 1183.661668 from(592.838110,2+) rtinseconds(1709) index(61046)
Title: Locus:1.1.1.2593.9 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

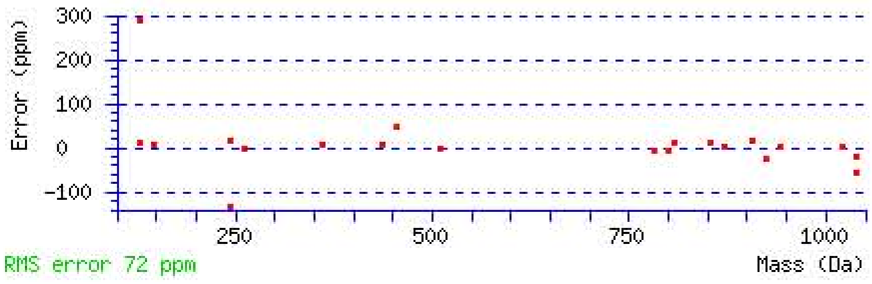
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1183.663452
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 27  Expect: 0.043
Matches : 21/72 fragment ions using 40 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	**130.049869**	65.528572			112.039304	56.523290	E							8
2	**243.133933**	122.070605			225.123368	113.065322	L	1055.628165	528.317720	1038.601616	519.804446	1037.617600	519.312438	7
3	314.171047	157.589161			296.160482	148.583879	A	***942.544101***	471.775689	925.517552	463.262414	924.533536	462.770406	6
4	385.208161	193.107718			367.197596	184.102436	A	***871.506987***	436.257132	854.480438	427.743857	853.496422	427.251849	5
5	824.433487	412.720382	807.406938	404.207107	806.422922	403.715099	Q	***800.469873***	400.738575	783.443324	392.225300	782.459308	391.733292	4
6	925.481166	463.244221	908.454617	454.730947	907.470601	454.238939	T	***361.244547***	181.125911	344.217998	172.612637	343.233982	172.120629	3
7	**1038.565230**	519.786253	1021.538681	511.272978	1020.554665	510.780970	I	***260.196868***	130.602072	243.170319	122.088797			2
8							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.1	1183.663452	-0.001784	ELAAQTIK
18.7	1183.663452	-0.001784	ELAAQITK
10.3	1183.649551	0.012117	KVCGHKQSLK
9.0	1183.663452	-0.001784	LEQAATLK
7.8	1183.660080	0.001588	AIEAVAISPWK
6.1	1183.656937	0.004731	MRPQTLK
5.9	1183.667282	-0.005614	GKQASEPALRK
5.4	1183.663467	-0.001799	TQLSPSIK
4.6	1183.674683	-0.013015	ELRQLSK
4.4	1183.667282	-0.005614	QLLRALEEGR

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

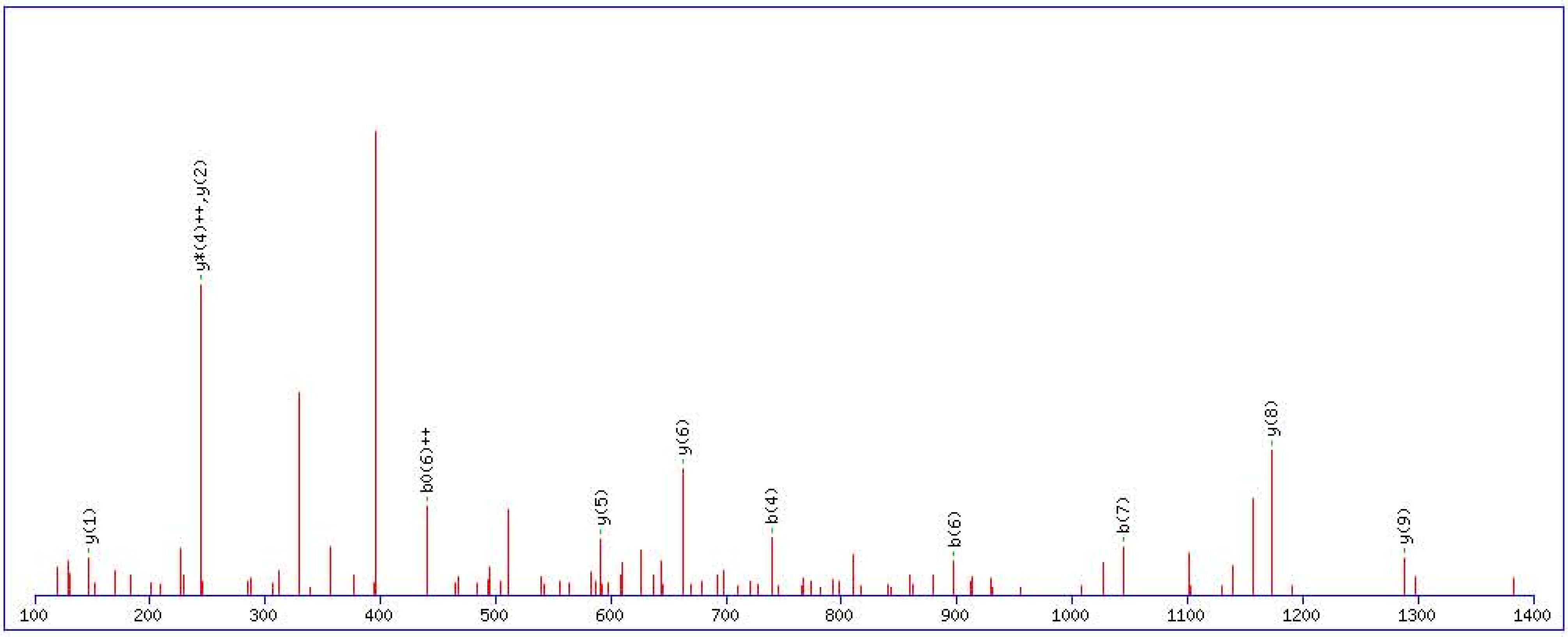
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LDAQASFLPK**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

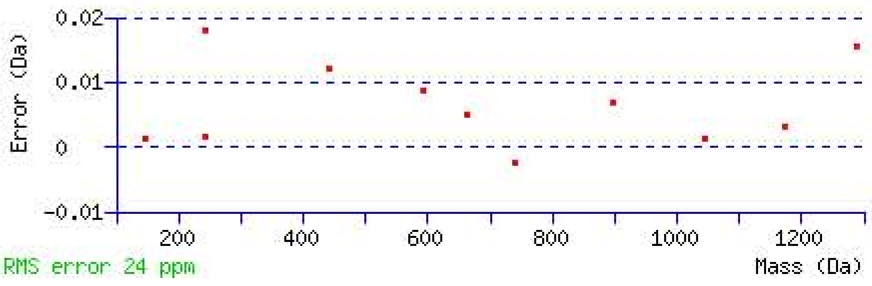
Match to Query 38880: 1399.755788 from(700.885170,2+) rtinseconds(2177) index(64284)
Title: Locus:1.1.1.2755.15 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

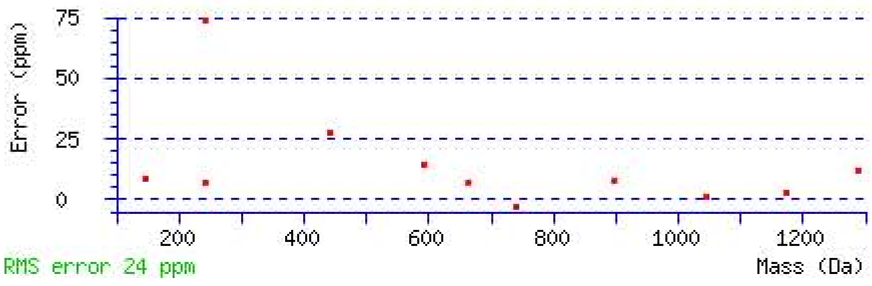
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1399.753342
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 49  Expect: 0.00034
Matches : 11/92 fragment ions using 13 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							10
2	229.118283	115.062779			211.107718	106.057497	D	***1287.676571***	644.341924	1270.650022	635.828649	1269.666006	635.336641	9
3	300.155397	150.581336			282.144832	141.576054	A	***1172.649628***	586.828452	1155.623079	578.315178	1154.639063	577.823169	8
4	***739.380723***	370.194000	722.354174	361.680725	721.370158	361.188717	Q	1101.612514	551.309895	1084.585965	542.796621	1083.601949	542.304612	7
5	810.417837	405.712557	793.391288	397.199282	792.407272	396.707274	A	***662.387188***	331.697232	645.360639	323.183957	644.376623	322.691949	6
6	***897.449865***	449.228570	880.423316	440.715296	879.439300	440.223288	S	***591.350074***	296.178675	574.323525	287.665400	573.339509	287.173392	5
7	***1044.518279***	522.762777	1027.491730	514.249503	1026.507714	513.757495	F	504.318046	252.662661	487.291497	244.149386			4
8	1157.602343	579.304809	1140.575794	570.791535	1139.591778	570.299527	L	357.249632	179.128454	340.223083	170.615179			3
9	1254.655107	627.831191	1237.628558	619.317917	1236.644542	618.825909	P	***244.165568***	122.586422	227.139019	114.073148			2
10							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
48.8	1399.753342	0.002446	LDAQASFLPK
12.5	1399.745972	0.009816	IDAATGIPVTTWR
5.7	1399.755814	-0.000026	KTELGPLKEEEK
5.2	1399.746811	0.008977	FKMPKIHMSGPK
5.0	1399.738083	0.017705	LQKEEVTDK
4.0	1399.756729	-0.000941	QGTMPVSLLK
4.0	1399.738083	0.017705	QASDLSLIDK
2.8	1399.741913	0.013875	DLQEVKAAARDGK
2.7	1399.771973	-0.016185	IWQGMLTIK
2.7	1399.756714	-0.000926	LSQVPMSALK

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

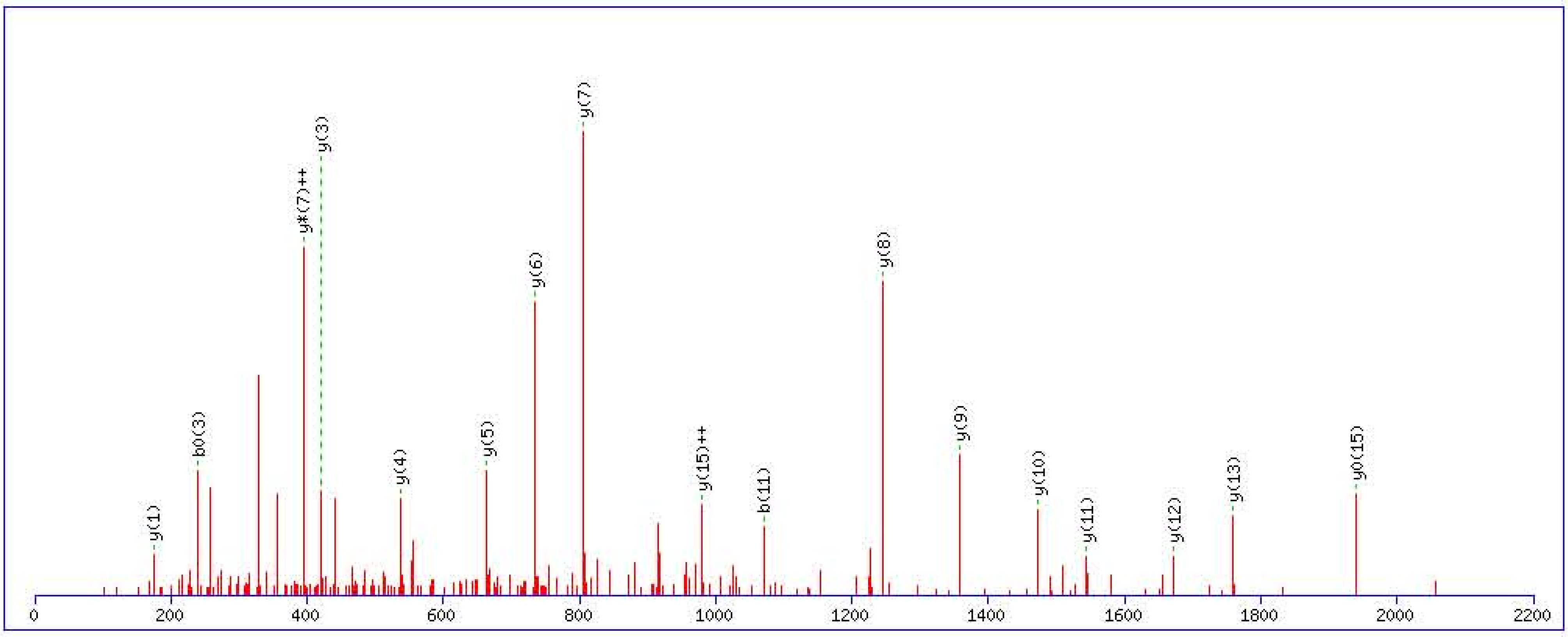
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSLVQASEANLQAAQDFVR**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

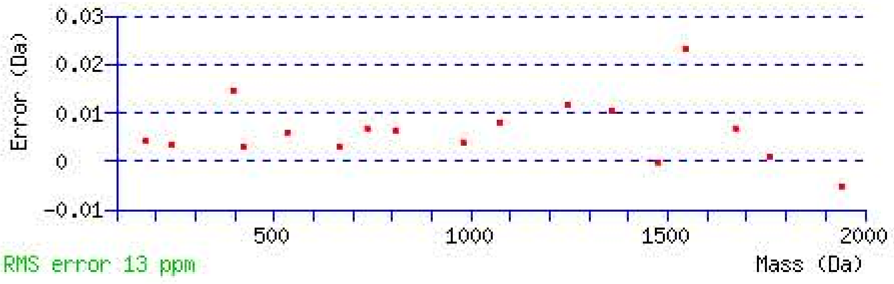
Match to Query 64410: 2314.185312 from(772.402380,3+) rtinseconds(2516) index(66353)
Title: Locus:1.1.1.2873.9 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

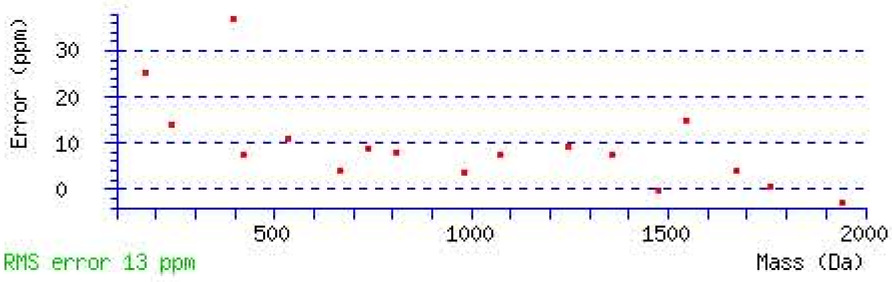
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2314.173950
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 97  Expect: 2.1e-009
Matches : 17/200 fragment ions using 20 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							19
2	145.060768	73.034022			127.050203	64.028740	S	2258.159779	1129.583527	2241.133230	1121.070253	2240.149214	1120.578245	18
3	258.144832	129.576054			240.134267	120.570772	L	2171.127751	1086.067513	2154.101202	1077.554239	2153.117186	1077.062231	17
4	357.213246	179.110261			339.202681	170.104979	V	2058.043687	1029.525481	2041.017138	1021.012207	2040.033122	1020.520199	16
5	485.271824	243.139550	468.245275	234.626276	467.261259	234.134268	Q	1958.975273	979.991275	1941.948724	971.478000	1940.964708	970.985992	15
6	556.308938	278.658107	539.282389	270.144833	538.298373	269.652825	A	1830.916695	915.961986	1813.890146	907.448711	1812.906130	906.956703	14
7	643.340966	322.174121	626.314417	313.660847	625.330401	313.168839	S	***1759.879581***	880.443429	1742.853032	871.930154	1741.869016	871.438146	13
8	772.383559	386.695418	755.357010	378.182143	754.372994	377.690135	E	***1672.847553***	836.927415	1655.821004	828.414140	1654.836988	827.922132	12
9	843.420673	422.213975	826.394124	413.700700	825.410108	413.208692	A	***1543.804960***	772.406118	1526.778411	763.892844	1525.794395	763.400836	11
10	957.463600	479.235438	940.437051	470.722164	939.453035	470.230156	N	***1472.767846***	736.887561	1455.741297	728.374287	1454.757281	727.882279	10
11	1070.547664	535.777470	1053.521115	527.264196	1052.537099	526.772187	L	***1358.724919***	679.866098	1341.698370	671.352823	1340.714354	670.860815	9
12	1509.772990	755.390133	1492.746441	746.876859	1491.762425	746.384851	Q	***1245.640855***	623.324066	1228.614306	614.810791	1227.630290	614.318783	8
13	1580.810104	790.908690	1563.783555	782.395416	1562.799539	781.903408	A	***806.415529***	403.711403	789.388980	395.198128	788.404964	394.706120	7
14	1651.847218	826.427247	1634.820669	817.913973	1633.836653	817.421965	A	***735.378415***	368.192846	718.351866	359.679571	717.367850	359.187563	6
15	1779.905796	890.456536	1762.879247	881.943262	1761.895231	881.451254	Q	***664.341301***	332.674289	647.314752	324.161014	646.330736	323.669006	5
16	1894.932739	947.970008	1877.906190	939.456733	1876.922174	938.964725	D	***536.282723***	268.645000	519.256174	260.131725	518.272158	259.639717	4
17	2042.001153	1021.504215	2024.974604	1012.990940	2023.990588	1012.498932	F	***421.255780***	211.131528	404.229231	202.618253			3
18	2141.069567	1071.038421	2124.043018	1062.525147	2123.059002	1062.033139	V	274.187366	137.597321	257.160817	129.084046			2
19							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
97.1	2314.173950	0.011362	GSLVQASEANLQAAQDFVR
49.3	2314.173950	0.011362	GSLVQASEANLQAAQDFVR
22.2	2314.173950	0.011362	GSLVQASEANLQAAQDFVR
4.2	2314.178635	0.006677	NKDRPAMQLYQPGARSR
0.2	2314.153702	0.031610	FAKFQHQVEMGSQR

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

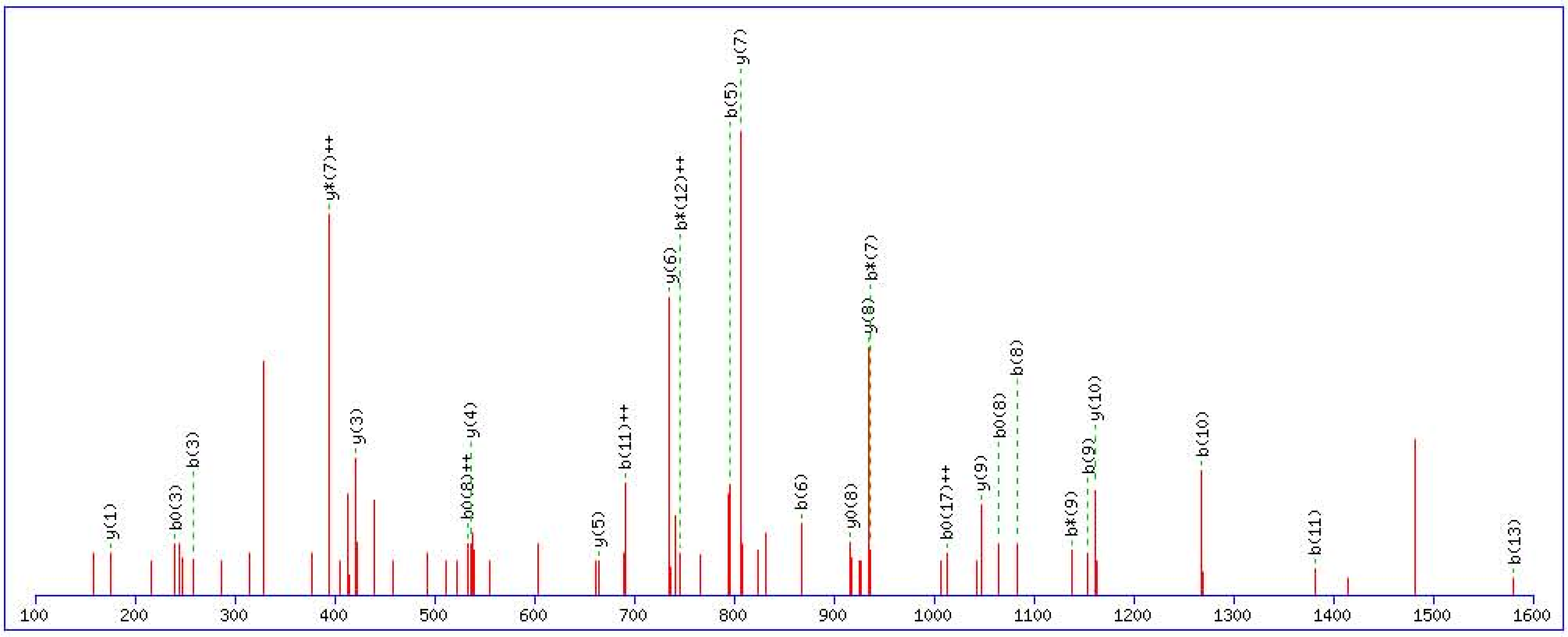
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSLVQASEANLQAAQDFVR**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

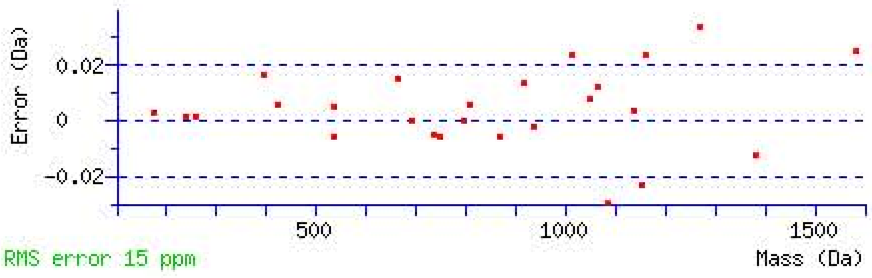
Match to Query 64412: 2314.192212 from(772.404680,3+) rtinseconds(2478) index(66053)
Title: Locus:1.1.1.2860.12 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

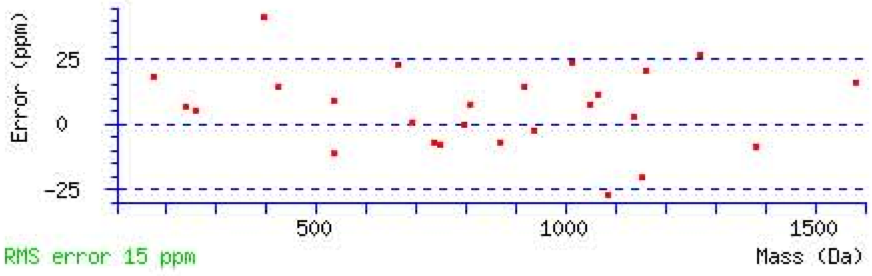
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2314.173950
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5     : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 0.00046
Matches : 27/200 fragment ions using 56 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							19
2	145.060768	73.034022			127.050203	64.028740	S	2258.159779	1129.583527	2241.133230	1121.070253	2240.149214	1120.578245	18
3	***258.144832***	129.576054			240.134267	120.570772	L	2171.127751	1086.067513	2154.101202	1077.554239	2153.117186	1077.062231	17
4	357.213246	179.110261			339.202681	170.104979	V	2058.043687	1029.525481	2041.017138	1021.012207	2040.033122	1020.520199	16
5	***796.438572***	398.722924	779.412023	390.209650	778.428007	389.717642	Q	1958.975273	979.991274	1941.948724	971.478000	1940.964708	970.985992	15
6	***867.475686***	434.241481	850.449137	425.728207	849.465121	425.236199	A	1519.749947	760.378611	1502.723398	751.865337	1501.739382	751.373329	14
7	954.507714	477.757495	937.481165	469.244220	936.497149	468.752212	S	1448.712833	724.860054	1431.686284	716.346780	1430.702268	715.854772	13
8	***1083.550307***	542.278792	1066.523758	533.765517	1065.539742	533.273509	E	1361.680805	681.344040	1344.654256	672.830766	1343.670240	672.338758	12
9	***1154.587421***	577.797349	1137.560872	569.284074	1136.576856	568.792066	A	1232.638212	616.822744	1215.611663	608.309469	1214.627647	607.817461	11
10	***1268.630348***	634.818812	1251.603799	626.305538	1250.619783	625.813529	N	***1161.601098***	581.304187	1144.574549	572.790912	1143.590533	572.298904	10
11	***1381.714412***	691.360844	1364.687863	682.847569	1363.703847	682.355561	L	***1047.558171***	524.282723	1030.531622	515.769449	1029.547606	515.277441	9
12	1509.772990	755.390133	1492.746441	746.876858	1491.762425	746.384850	Q	***934.474107***	467.740692	917.447558	459.227417	916.463542	458.735409	8
13	***1580.810104***	790.908690	1563.783555	782.395415	1562.799539	781.903407	A	***806.415529***	403.711403	789.388980	395.198128	788.404964	394.706120	7
14	1651.847218	826.427247	1634.820669	817.913972	1633.836653	817.421964	A	***735.378415***	368.192846	718.351866	359.679571	717.367850	359.187563	6
15	1779.905796	890.456536	1762.879247	881.943261	1761.895231	881.451253	Q	***664.341301***	332.674289	647.314752	324.161014	646.330736	323.669006	5
16	1894.932739	947.970007	1877.906190	939.456733	1876.922174	938.964725	D	***536.282723***	268.645000	519.256174	260.131725	518.272158	259.639717	4
17	2042.001153	1021.504215	2024.974604	1012.990940	2023.990588	1012.498932	F	***421.255780***	211.131528	404.229231	202.618253			3
18	2141.069567	1071.038421	2124.043018	1062.525147	2123.059002	1062.033139	V	274.187366	137.597321	257.160817	129.084046			2
19							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.8	2314.173950	0.018262	GSLVQASEANLQAAQDFVR
9.1	2314.173950	0.018262	GSLVQASEANLQAAQDFVR

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

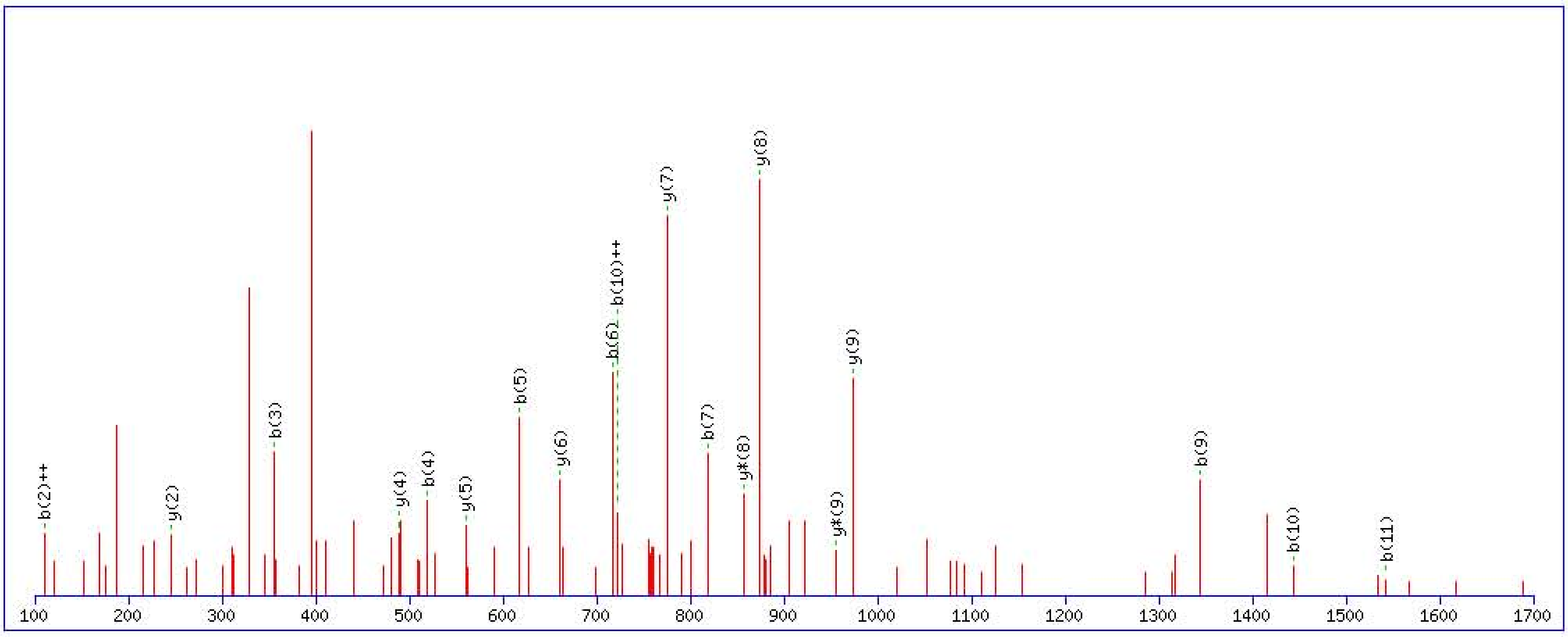
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **FAHYVVTSQVVNTANEAR**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

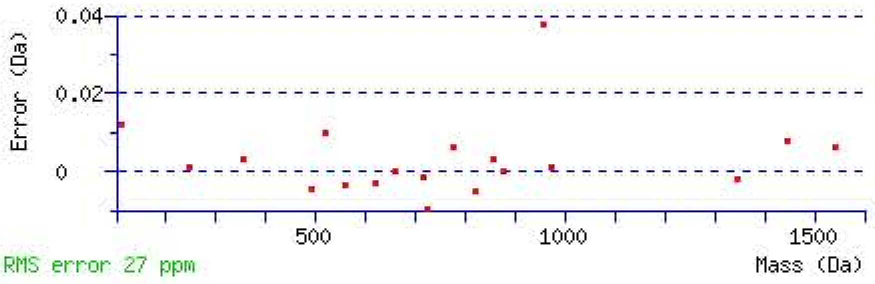
Match to Query 64465: 2316.170112 from(773.063980,3+) rtinseconds(1929) index(62599)
Title: Locus:1.1.1.2669.20 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

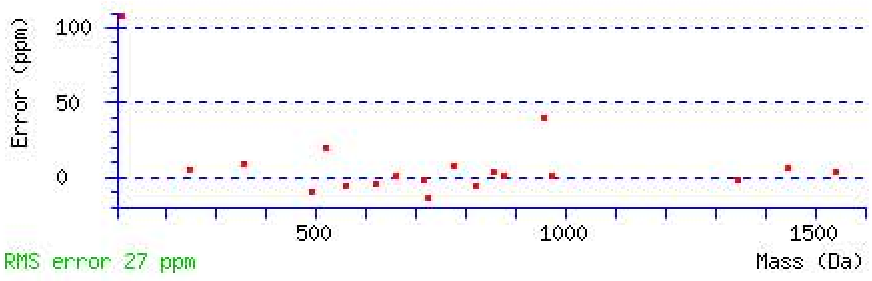
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2316.168488
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 40  Expect: 0.0025
Matches : 19/172 fragment ions using 44 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	148.075690	74.541483					F							18
2	219.112804	**110.060040**					A	2170.107350	1085.557313	2153.080801	1077.044038	2152.096785	1076.552030	17
3	***356.171716***	178.589496					H	2099.070236	1050.038756	2082.043687	1041.525481	2081.059671	1041.033473	16
4	***519.235045***	260.121161					Y	1962.011324	981.509300	1944.984775	972.996026	1944.000759	972.504018	15
5	***618.303459***	309.655368					V	1798.947995	899.977636	1781.921446	891.464361	1780.937430	890.972353	14
6	***717.371873***	359.189575					V	1699.879581	850.443429	1682.853032	841.930154	1681.869016	841.438146	13
7	***818.419552***	409.713414			800.408987	400.708132	T	1600.811167	800.909222	1583.784618	792.395947	1582.800602	791.903939	12
8	905.451580	453.229428			887.441015	444.224146	S	1499.763488	750.385382	1482.736939	741.872108	1481.752923	741.380100	11
9	***1344.676906***	672.842091	1327.650357	664.328817	1326.666341	663.836808	Q	1412.731460	706.869368	1395.704911	698.356094	1394.720895	697.864086	10
10	***1443.745320***	**722.376298**	1426.718771	713.863024	1425.734755	713.371016	V	***973.506134***	487.256705	956.479585	478.743431	955.495569	478.251423	9
11	***1542.813734***	771.910505	1525.787185	763.397231	1524.803169	762.905223	V	***874.437720***	437.722498	857.411171	429.209224	856.427155	428.717216	8
12	1656.856661	828.931969	1639.830112	820.418694	1638.846096	819.926686	N	***775.369306***	388.188291	758.342757	379.675017	757.358741	379.183009	7
13	1757.904340	879.455808	1740.877791	870.942534	1739.893775	870.450526	T	***661.326379***	331.166828	644.299830	322.653553	643.315814	322.161545	6
14	1828.941454	914.974365	1811.914905	906.461091	1810.930889	905.969083	A	***560.278700***	280.642988	543.252151	272.129714	542.268135	271.637706	5
15	1942.984381	971.995829	1925.957832	963.482554	1924.973816	962.990546	N	***489.241586***	245.124431	472.215037	236.611157	471.231021	236.119149	4
16	2072.026974	1036.517125	2055.000425	1028.003850	2054.016409	1027.511842	E	375.198659	188.102968	358.172110	179.589693	357.188094	179.097685	3
17	2143.064088	1072.035682	2126.037539	1063.522407	2125.053523	1063.030399	A	***246.156066***	123.581671	229.129517	115.068397			2
18							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.3	2316.168488	0.001624	FAHYVVTSQVVNTANEAR

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

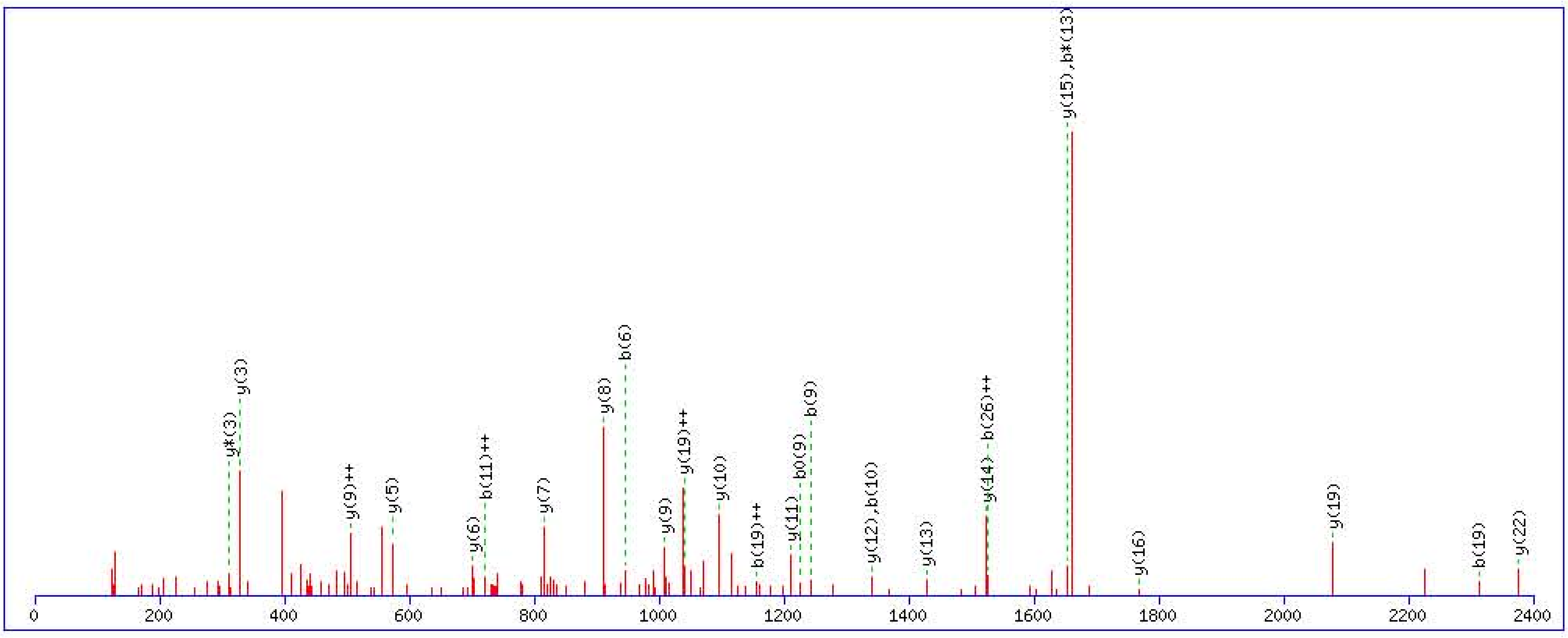
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GMADQDGLKPTIDKPSEDSPPLEMLGPR**
Found in **ITIH1_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3

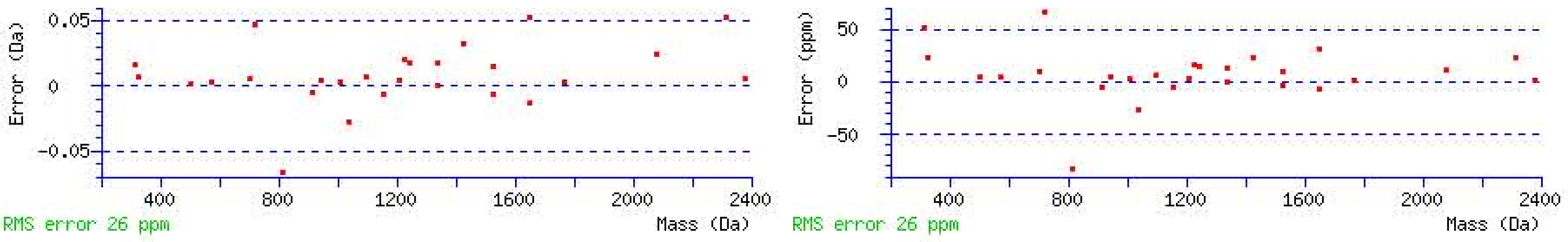
Match to Query 78369: 3320.631376 from(831.165120,4+) rtinseconds(2128) index(63909)
Title: Locus:1.1.1.2738.17 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3320.609070
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2     : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Q5     : Biotin:Thermo-21345 (Q)
Ions Score: 109  Expect: 6.2e-011
Matches : 27/452 fragment ions using 37 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	58.028740	29.518008					G							28
2	205.064140	103.035708					M	3264.594900	1632.801088	3247.568351	1624.287813	3246.584335	1623.795805	27
3	276.101254	138.554265					A	3117.559500	1559.283388	3100.532951	1550.770113	3099.548935	1550.278105	26
4	391.128197	196.067737			373.117632	187.062454	D	3046.522386	1523.764831	3029.495837	1515.251556	3028.511821	1514.759548	25
5	830.353523	415.680400	813.326974	407.167125	812.342958	406.675117	Q	2931.495443	1466.251359	2914.468894	1457.738085	2913.484878	1457.246077	24
6	**945.380466**	473.193871	928.353917	464.680597	927.369901	464.188589	D	2492.270117	1246.638696	2475.243568	1238.125422	2474.259552	1237.633414	23
7	1002.401930	501.704603	985.375381	493.191329	984.391365	492.699321	G	***2377.243174***	1189.125225	2360.216625	1180.611950	2359.232609	1180.119942	22
8	1115.485994	558.246635	1098.459445	549.733361	1097.475429	549.241353	L	2320.221710	1160.614493	2303.195161	1152.101218	2302.211145	1151.609210	21
9	**1243.580957**	622.294117	1226.554408	613.780842	1225.570392	613.288834	K	2207.137646	1104.072461	2190.111097	1095.559186	2189.127081	1095.067178	20
10	**1340.633721**	670.820499	1323.607172	662.307224	1322.623156	661.815216	P	***2079.042683***	1040.024980	2062.016134	1031.511705	2061.032118	1031.019697	19
11	1441.681400	**721.344338**	1424.654851	712.831064	1423.670835	712.339056	T	1981.989919	991.498598	1964.963370	982.985323	1963.979354	982.493315	18
12	1554.765464	777.886370	1537.738915	769.373096	1536.754899	768.881088	I	1880.942240	940.974758	1863.915691	932.461484	1862.931675	931.969476	17
13	1669.792407	835.399842	1652.765858	826.886567	1651.781842	826.394559	D	***1767.858176***	884.432726	1750.831627	875.919452	1749.847611	875.427444	16
14	1797.887370	899.447323	1780.860821	890.934049	1779.876805	890.442041	K	***1652.831233***	826.919255	1635.804684	818.405980	1634.820668	817.913972	15
15	1894.940134	947.973705	1877.913585	939.460431	1876.929569	938.968423	P	***1524.736270***	762.871773	1507.709721	754.358499	1506.725705	753.866491	14
16	1981.972162	991.489719	1964.945613	982.976445	1963.961597	982.484437	S	***1427.683506***	714.345391	1410.656957	705.832117	1409.672941	705.340109	13
17	2111.014755	1056.011016	2093.988206	1047.497741	2093.004190	1047.005733	E	***1340.651478***	670.829377	1323.624929	662.316103	1322.640913	661.824095	12
18	2226.041698	1113.524487	2209.015149	1105.011212	2208.031133	1104.519204	D	***1211.608885***	606.308081	1194.582336	597.794806	1193.598320	597.302798	11
19	**2313.073726**	**1157.040501**	2296.047177	1148.527226	2295.063161	1148.035218	S	***1096.581942***	548.794609	1079.555393	540.281335	1078.571377	539.789327	10
20	2410.126490	1205.566883	2393.099941	1197.053608	2392.115925	1196.561600	P	***1009.549914***	505.278595	992.523365	496.765321	991.539349	496.273313	9
21	2507.179254	1254.093265	2490.152705	1245.579990	2489.168689	1245.087983	P	***912.497150***	456.752213	895.470601	448.238939	894.486585	447.746931	8
22	2620.263318	1310.635297	2603.236769	1302.122023	2602.252753	1301.630015	L	***815.444386***	408.225831	798.417837	399.712557	797.433821	399.220549	7
23	2749.305911	1375.156594	2732.279362	1366.643319	2731.295346	1366.151311	E	***702.360322***	351.683799	685.333773	343.170525	684.349757	342.678517	6
24	2880.346396	1440.676836	2863.319847	1432.163562	2862.335831	1431.671554	M	***573.317729***	287.162503	556.291180	278.649228			5
25	2993.430460	1497.218868	2976.403911	1488.705594	2975.419895	1488.213586	L	442.277244	221.642260	425.250695	213.128986			4
26	3050.451924	**1525.729600**	3033.425375	1517.216326	3032.441359	1516.724318	G	***329.193180***	165.100228	312.166631	156.586953			3
27	3147.504688	1574.255982	3130.478139	1565.742708	3129.494123	1565.250700	P	272.171716	136.589496	255.145167	128.076221			2
28							R	175.118952	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
109.2	3320.609070	0.022306	GMADQDGLKPTIDKPSEDSPPLEMLGPR
0.3	3320.645462	-0.014086	QDIGDILHQIMTITDQSLDEAQAK

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

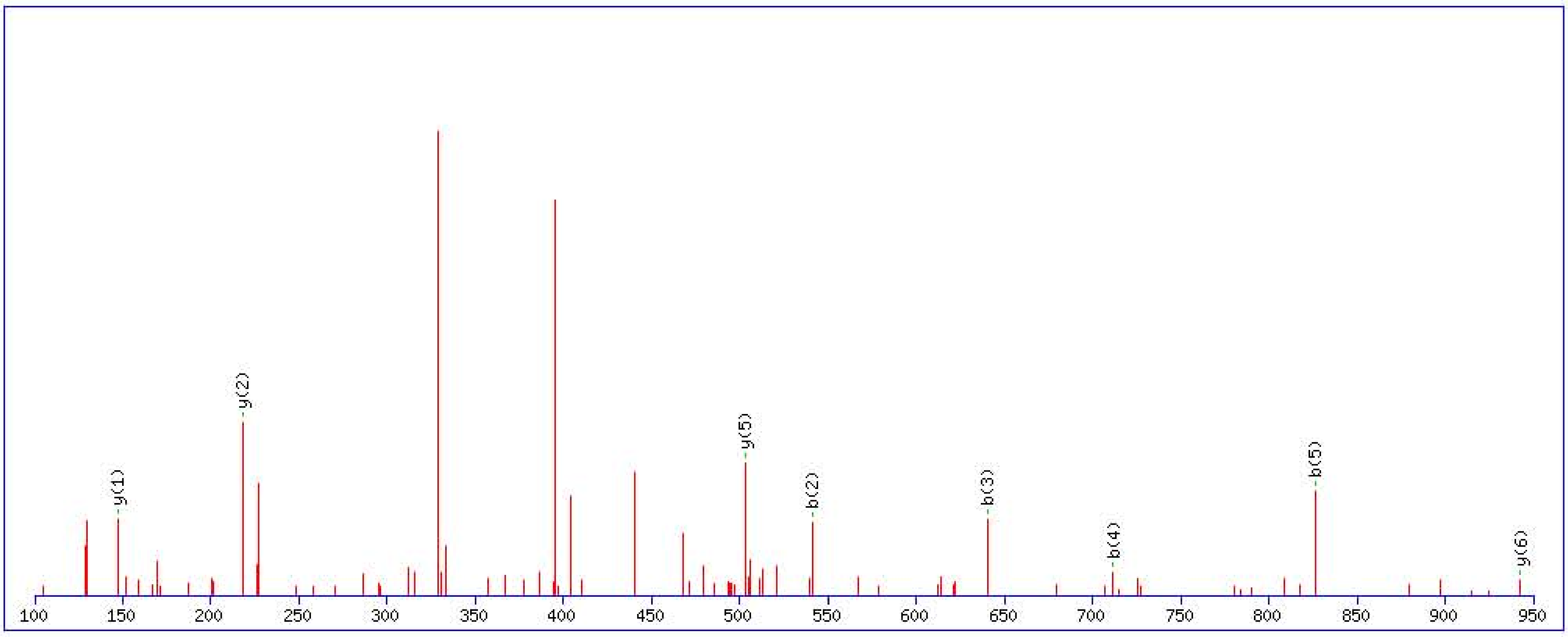
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TQVADAK**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

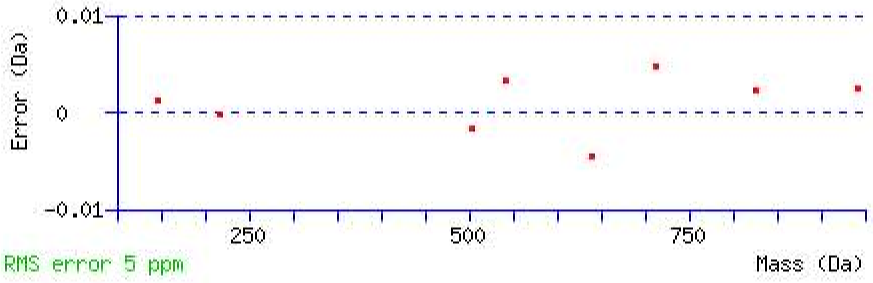
Match to Query 24156: 1042.544968 from(522.279760,2+) rtinseconds(1273) index(57861)
Title: Locus:1.1.1.2441.18 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

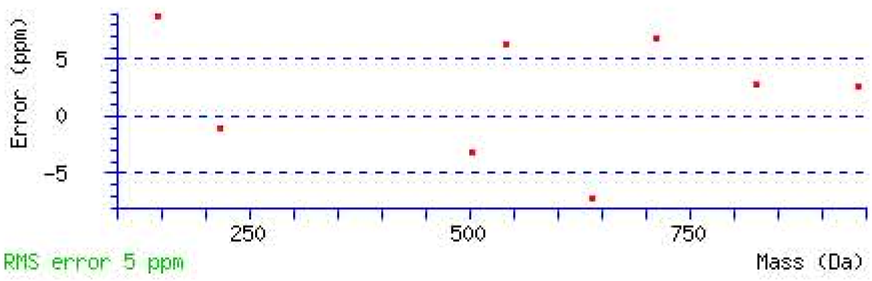
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 950 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1042.548111
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2     : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.0019
Matches : 8/66 fragment ions using 9 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							7
2	***541.280281***	271.143779	524.253732	262.630504	523.269716	262.138496	Q	***942.507715***	471.757496	925.481166	463.244221	924.497150	462.752213	6
3	***640.348695***	320.677986	623.322146	312.164711	622.338130	311.672703	V	***503.282389***	252.144832	486.255840	243.631558	485.271824	243.139550	5
4	***711.385809***	356.196543	694.359260	347.683268	693.375244	347.191260	A	404.213975	202.610625	387.187426	194.097351	386.203410	193.605343	4
5	***826.412752***	413.710014	809.386203	405.196739	808.402187	404.704731	D	333.176861	167.092068	316.150312	158.578794	315.166296	158.086786	3
6	897.449866	449.228571	880.423317	440.715296	879.439301	440.223288	A	***218.149918***	109.578597	201.123369	101.065322			2
7							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.4	1042.548111	-0.003143	TQVADAK
17.6	1042.529480	0.015488	TSPQPESGIK
15.4	1042.540726	0.004242	KPVSEVGDGR
12.2	1042.548096	-0.003128	SLQADAK
10.7	1042.540680	0.004288	EAEKRPADK
10.0	1042.544724	0.000244	WKGIEPGEK
8.0	1042.540680	0.004288	TPEERAAAAK
7.5	1042.540680	0.004288	SLENPAERK
7.2	1042.548080	-0.003112	KEQEAK
7.2	1042.548080	-0.003112	KQEEAK

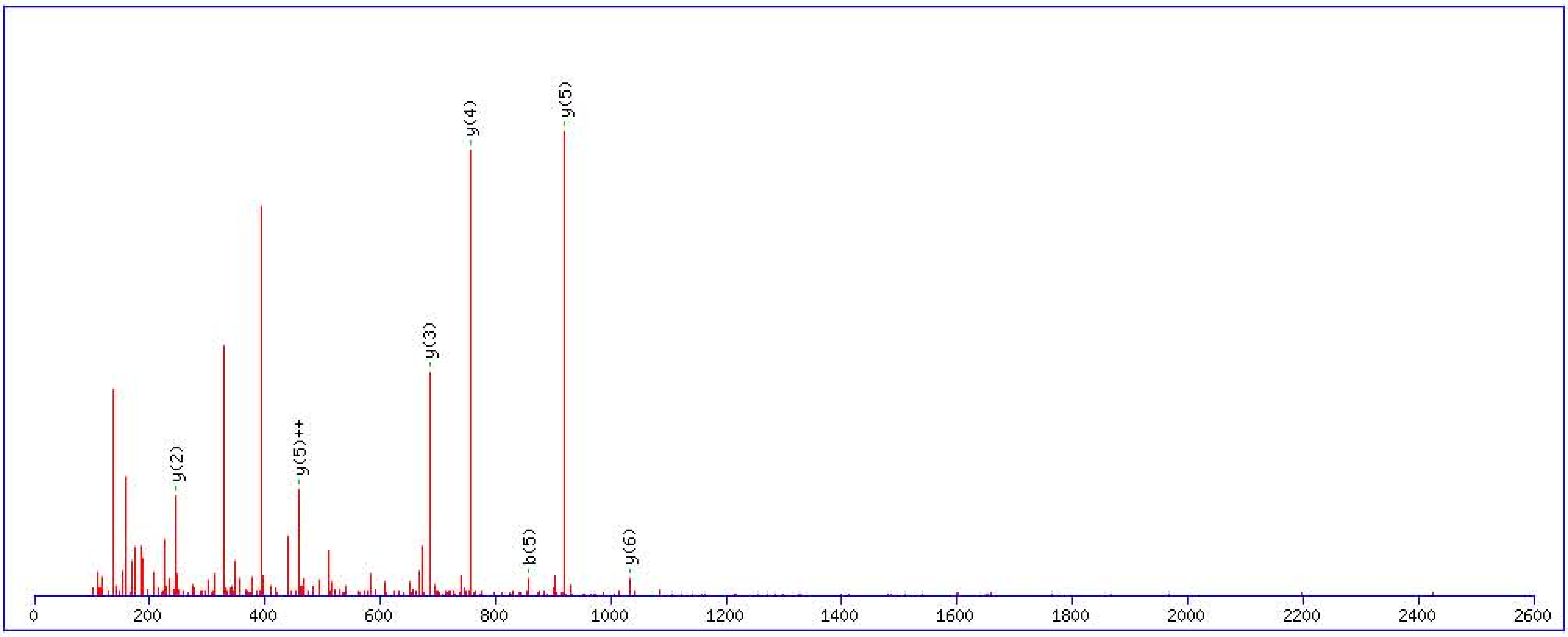
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ALYAQAR**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

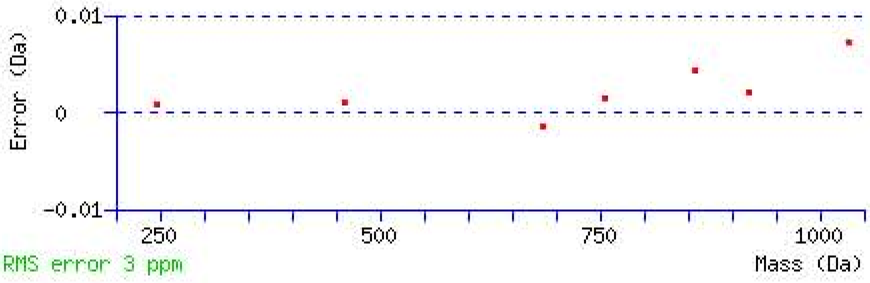
Match to Query 26247: 1102.591248 from(552.302900,2+) rtinseconds(1628) index(60439)
Title: Locus:1.1.1.2565.5 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

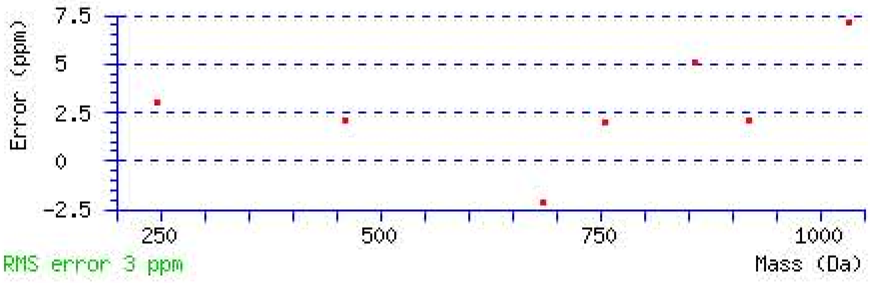
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1102.595703
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5     : Biotin:Thermo-21345 (Q)
Ions Score: 37  Expect: 0.0035
Matches : 7/40 fragment ions using 10 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	Seq.	y	y^{++}	y^{*}	y^{*++}	#
1	72.044390	36.525833			A					7
2	185.128454	93.067865			L	***1032.565899***	516.786588	1015.539350	508.273313	6
3	348.191783	174.599529			Y	***919.481835***	460.244556	902.455286	451.731281	5
4	419.228897	210.118087			A	***756.418506***	378.712891	739.391957	370.199617	4
5	**858.454223**	429.730750	841.427674	421.217475	Q	***685.381392***	343.194334	668.354843	334.681060	3
6	929.491337	465.249307	912.464788	456.736032	A	***246.156066***	123.581671	229.129517	115.068397	2
7					R	175.118952	88.063114	158.092403	79.549840	1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
37.4	1102.595703	-0.004455	ALYAQAR
10.5	1102.602234	-0.010986	AIELGYNPVK
6.0	1102.580475	0.010773	SPQMVSAIVR
4.4	1102.580460	0.010788	AMVENVTLAR
3.6	1102.588333	0.002915	SPYGLTPRGR
1.7	1102.591660	-0.000412	AMKRLEEAR
1.5	1102.584305	0.006943	QSSQRGLTAR
1.3	1102.598221	-0.006973	DDLKATLTAR
0.3	1102.602921	-0.011673	LLRQRMDR

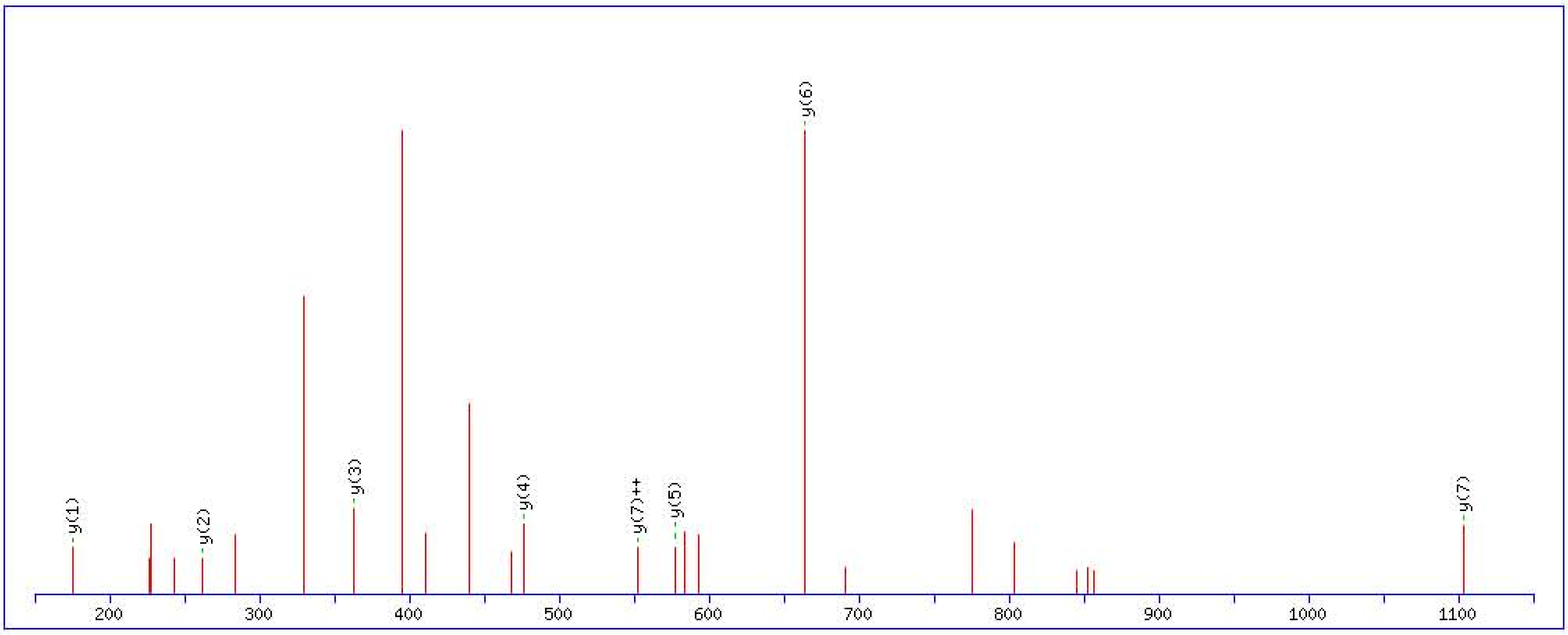
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQSTITSR**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

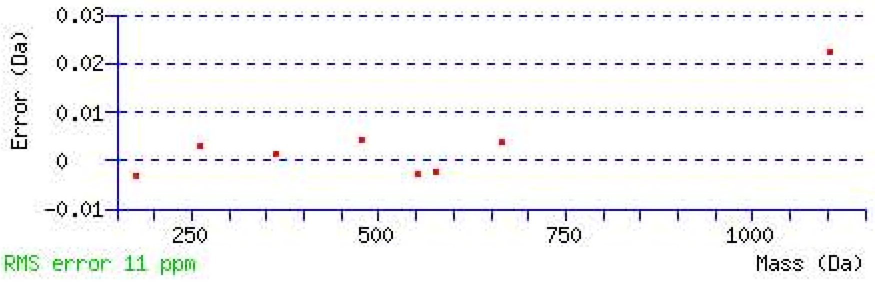
Match to Query 31716: 1201.645228 from(601.829890,2+) rtinseconds(1469) index(59321)
Title: Locus:1.1.1.2509.19 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

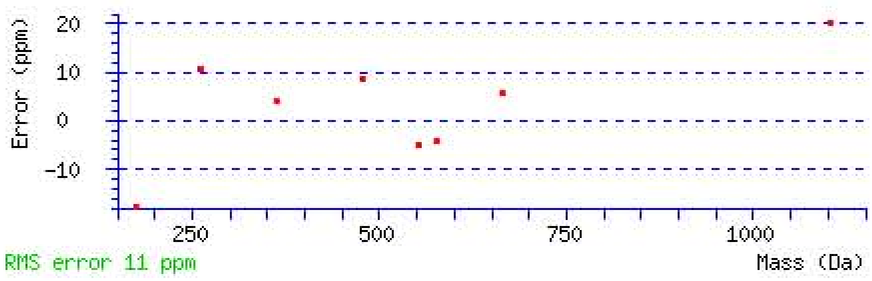
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1201.648895
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 32 **Expect:** 0.0053
Matches : 8/76 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							8
2	539.301016	270.154146	522.274467	261.640872			Q	*1103.587756*	552.297516	1086.561207	543.784242	1085.577191	543.292234	7
3	626.333044	313.670160	609.306495	305.156886	608.322479	304.664878	S	*664.362430*	332.684853	647.335881	324.171579	646.351865	323.679571	6
4	727.380723	364.194000	710.354174	355.680725	709.370158	355.188717	T	*577.330402*	289.168839	560.303853	280.655565	559.319837	280.163557	5
5	840.464787	420.736032	823.438238	412.222757	822.454222	411.730749	I	*476.282723*	238.645000	459.256174	230.131725	458.272158	229.639717	4
6	941.512466	471.259871	924.485917	462.746597	923.501901	462.254589	T	*363.198659*	182.102968	346.172110	173.589693	345.188094	173.097685	3
7	1028.544494	514.775885	1011.517945	506.262611	1010.533929	505.770603	S	*262.150980*	131.579128	245.124431	123.065854	244.140415	122.573846	2
8							R	*175.118952*	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
32.5	1201.648895	-0.003667	VQSTITSR
7.9	1201.638992	0.006236	VQPPSHAR
6.5	1201.641479	0.003749	VSIKDNQKDR
6.4	1201.638992	0.006236	VQGREFR
6.4	1201.660767	-0.015539	VWKPQLFER
3.1	1201.648895	-0.003667	VALGVPDMTKR

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

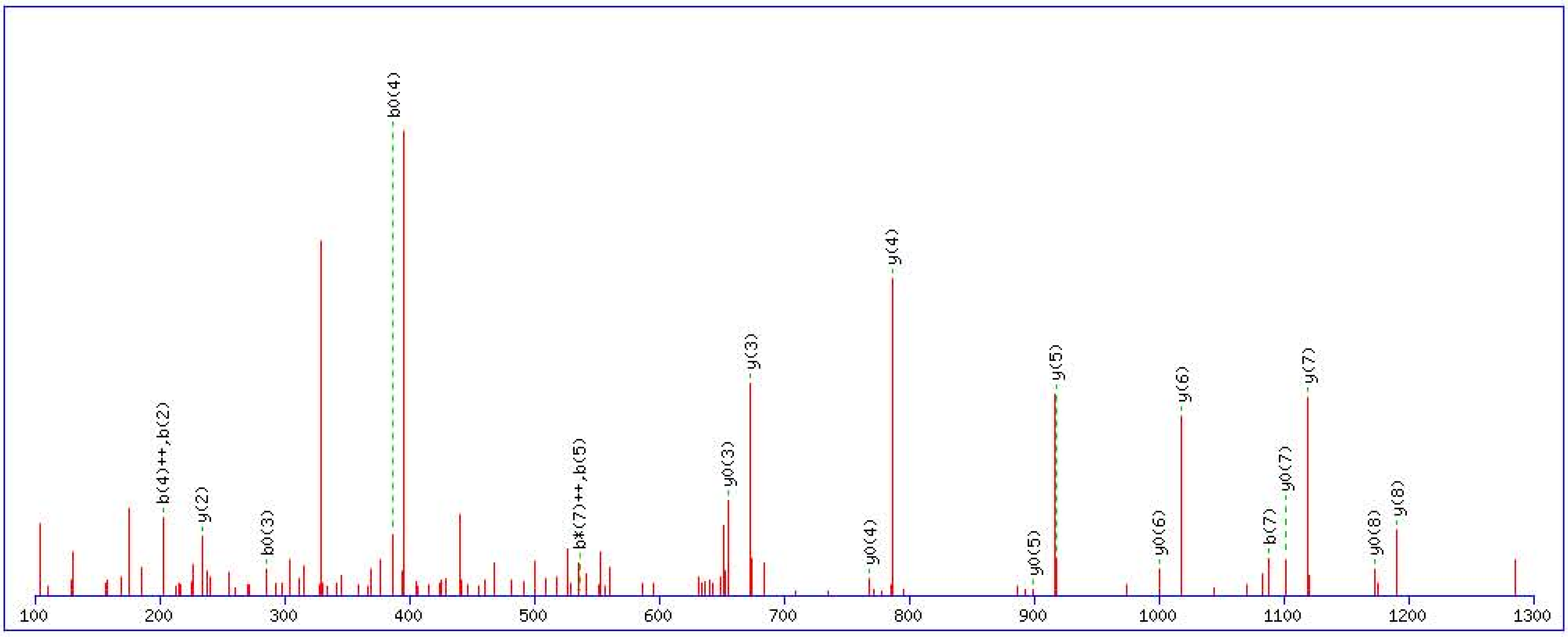
Mascot Search Results

Peptide View

MS/MS Fragmentation of **MATTMIQSK**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

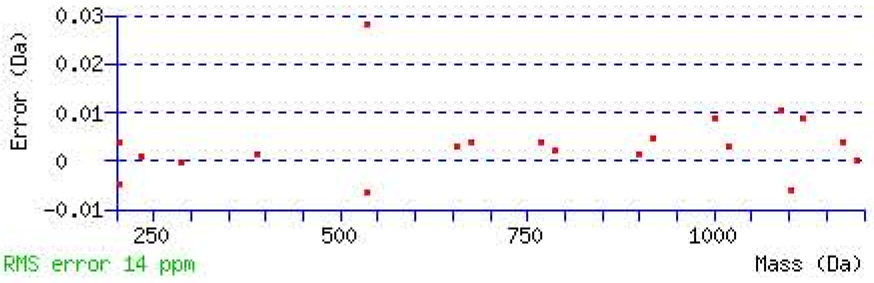
Match to Query 35670: 1320.658408 from(661.336480,2+) rtinseconds(1706) index(61024)
Title: Locus:1.1.1.2592.12 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

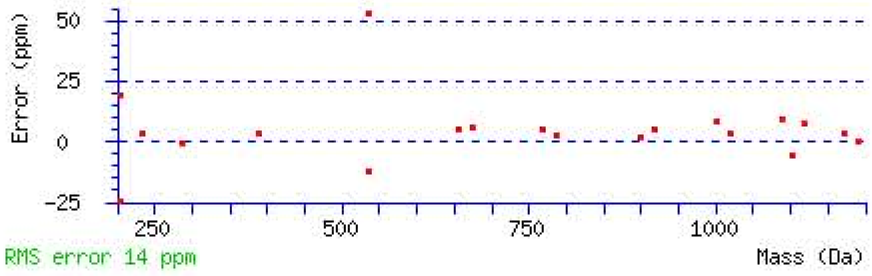
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1320.660370
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 42 **Expect:** 0.00048
Matches : 20/78 fragment ions using 34 most intense peaks (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	132.047761	66.527518					M							9
2	**203.084875**	102.046075					A	***1190.627179***	595.817228	1173.600630	587.303953	1172.616614	586.811945	8
3	304.132554	152.569915			286.121989	143.564632	T	***1119.590065***	560.298671	1102.563516	551.785396	1101.579500	551.293388	7
4	405.180233	203.093754			387.169668	194.088472	T	***1018.542386***	509.774831	1001.515837	501.261557	1000.531821	500.769549	6
5	**536.220718**	268.613997			518.210153	259.608715	M	***917.494707***	459.250992	900.468158	450.737717	899.484142	450.245709	5
6	649.304782	325.156029			631.294217	316.150747	I	***786.454222***	393.730749	769.427673	385.217475	768.443657	384.725467	4
7	**1088.530108**	544.768692	1071.503559	536.255418	1070.519543	535.763410	Q	***673.370158***	337.188717	656.343609	328.675443	655.359593	328.183435	3
8	1175.562136	588.284706	1158.535587	579.771432	1157.551571	579.279424	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
9							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.0	1320.660370	-0.001962	MATTMIQSK
6.4	1320.643082	0.015326	MADSQRFR
5.5	1320.670715	-0.012307	IAPKASMAGASSSK
4.5	1320.640854	0.017554	EPSEKLESTSSK
2.2	1320.675461	-0.017053	RMRLVVDGMGR
1.3	1320.674759	-0.016351	QSTEFAISK

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

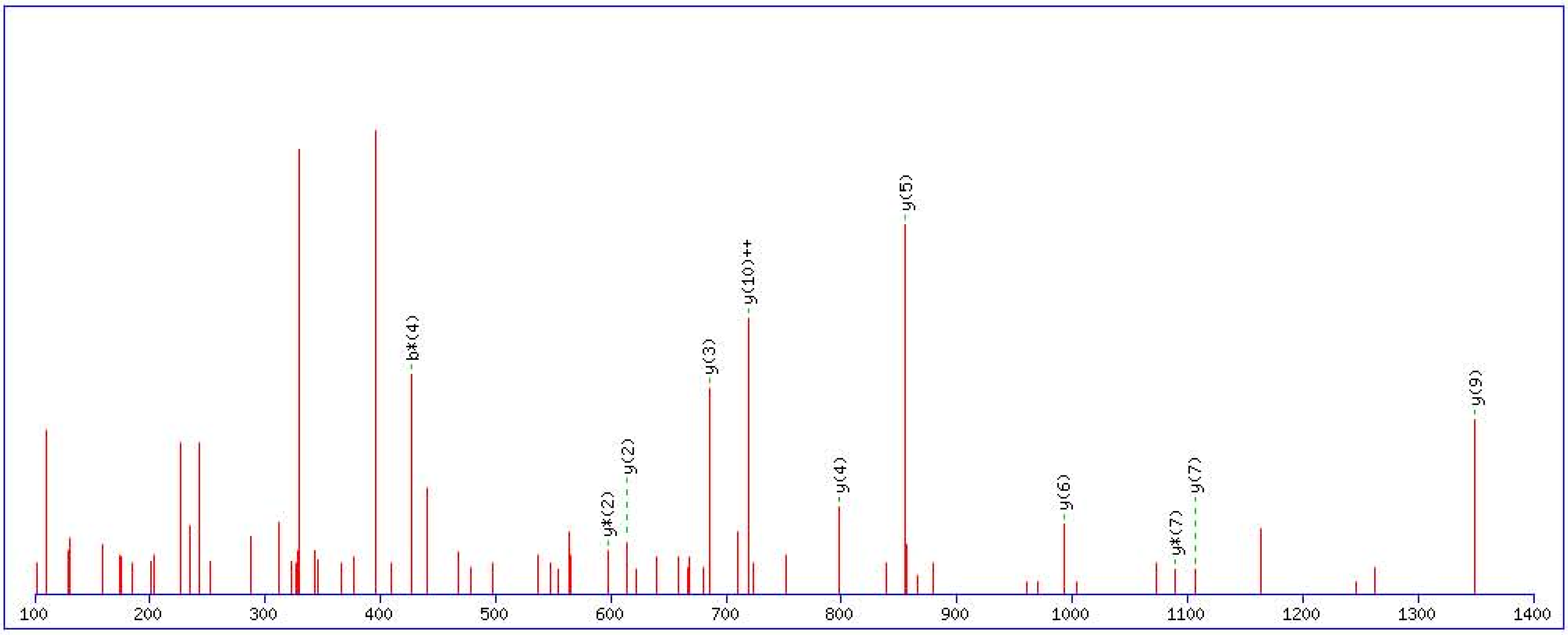
Mascot Search Results

Peptide View

MS/MS Fragmentation of **LSNENHGIAQR**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

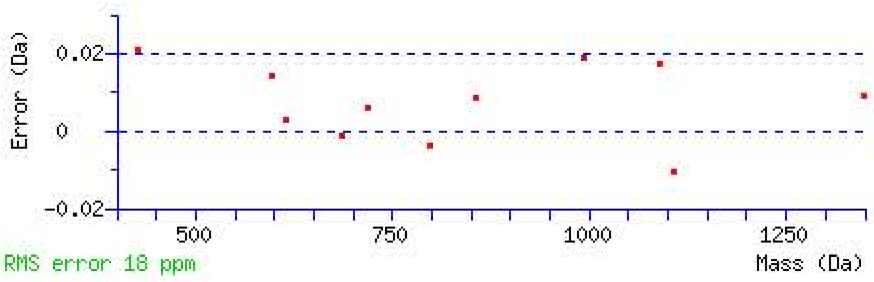
Match to Query 43869: 1548.775782 from(517.265870,3+) rtinseconds(1376) index(58578)
Title: Locus:1.1.1.2477.17 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

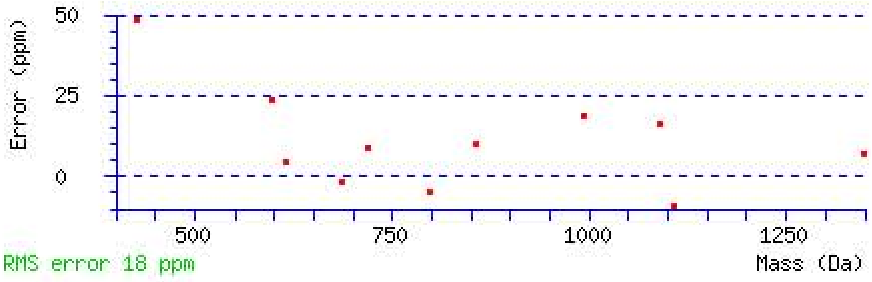
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1548.783066
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 30 **Expect:** 0.0044
Matches : 11/100 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							11
2	201.123368	101.065322			183.112803	92.060039	S	1436.706307	718.856792	1419.679758	710.343517	1418.695742	709.851509	10
3	315.166295	158.086785	298.139746	149.573511	297.155730	149.081503	N	***1349.674279***	675.340778	1332.647730	666.827503	1331.663714	666.335495	9
4	444.208888	222.608082	427.182339	214.094808	426.198323	213.602800	E	1235.631352	618.319314	1218.604803	609.806040	1217.620787	609.314032	8
5	558.251815	279.629546	541.225266	271.116271	540.241250	270.624263	N	***1106.588759***	553.798018	1089.562210	545.284743			7
6	695.310727	348.159002	678.284178	339.645727	677.300162	339.153719	H	***992.545832***	496.776554	975.519283	488.263280			6
7	752.332191	376.669734	735.305642	368.156459	734.321626	367.664451	G	***855.486920***	428.247098	838.460371	419.733824			5
8	865.416255	433.211766	848.389706	424.698491	847.405690	424.206483	I	***798.465456***	399.736366	781.438907	391.223092			4
9	936.453369	468.730323	919.426820	460.217048	918.442804	459.725040	A	***685.381392***	343.194334	668.354843	334.681060			3
10	1375.678695	688.342986	1358.652146	679.829711	1357.668130	679.337703	Q	***614.344278***	307.675777	597.317729	299.162503			2
11							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.9	1548.783066	-0.007284	LSNENHGIAQR
4.8	1548.782394	-0.006612	IIPPYTDDAFEIR

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

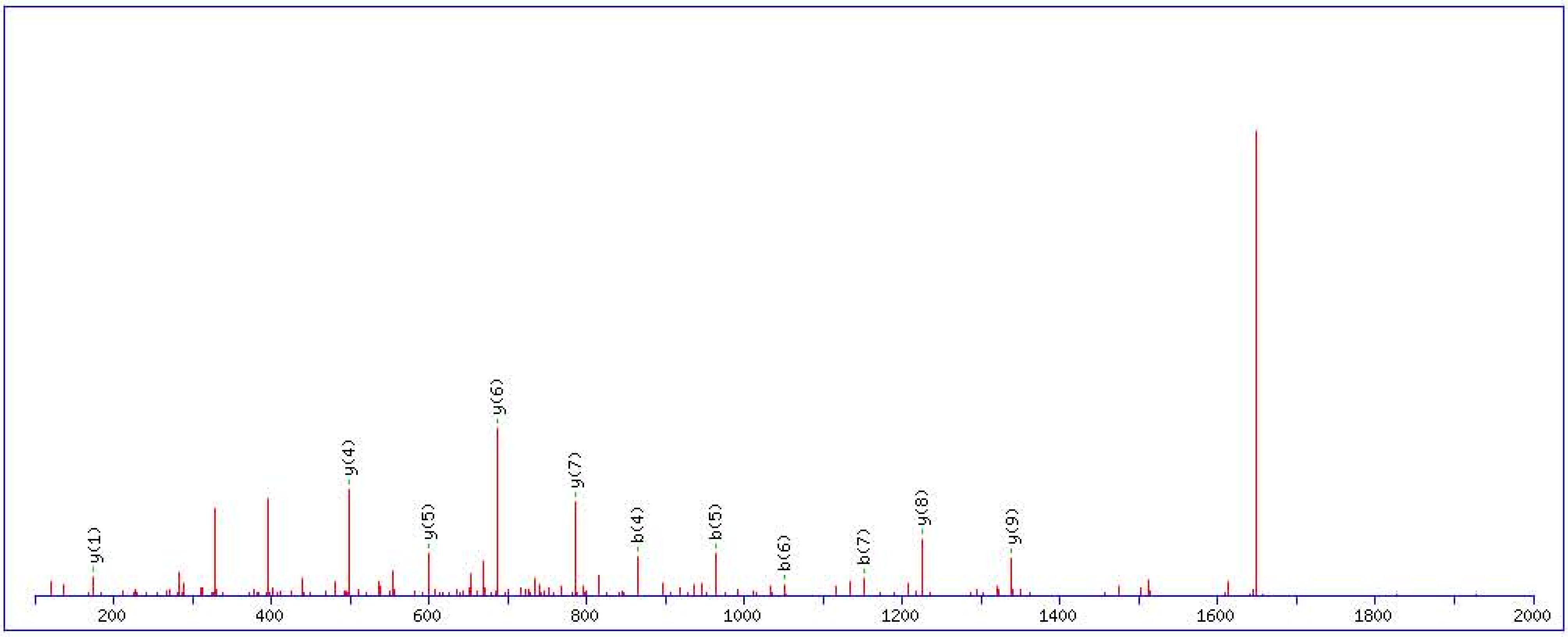
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FYNQVSTPLLR**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

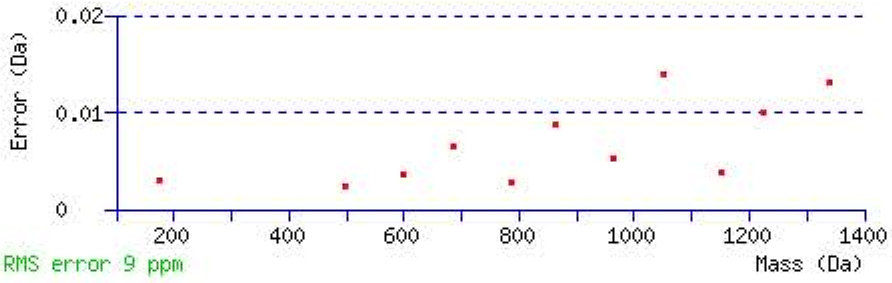
Match to Query 48329: 1647.886428 from(824.950490,2+) rtinseconds(2268) index(64853)
Title: Locus:1.1.1.2787.10 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

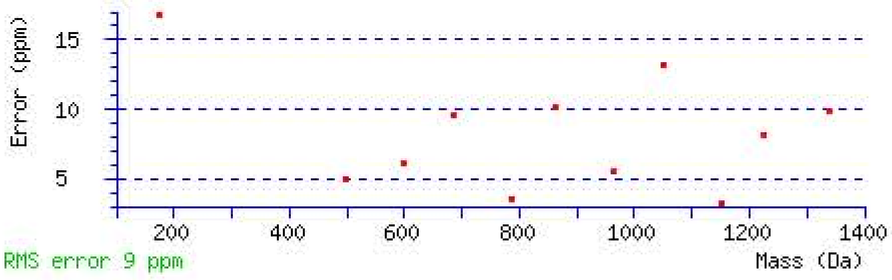
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1647.880676
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4      : Biotin:Thermo-21345 (Q)
Ions Score: 53  Expect: 4.5e-005
Matches : 11/98 fragment ions using 16 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					F							11
2	311.139019	156.073148					Y	1501.819547	751.413411	1484.792998	742.900137	1483.808982	742.408129	10
3	425.181946	213.094611	408.155397	204.581337			N	***1338.756218***	669.881747	1321.729669	661.368472	1320.745653	660.876464	9
4	**864.407272**	432.707274	847.380723	424.194000			Q	***1224.713291***	612.860283	1207.686742	604.347009	1206.702726	603.855001	8
5	**963.475686**	482.241481	946.449137	473.728207			V	***785.487965***	393.247620	768.461416	384.734346	767.477400	384.242338	7
6	**1050.507714**	525.757495	1033.481165	517.244221	1032.497149	516.752213	S	***686.419551***	343.713414	669.393002	335.200139	668.408986	334.708131	6
7	**1151.555393**	576.281335	1134.528844	567.768060	1133.544828	567.276052	T	***599.387523***	300.197399	582.360974	291.684125	581.376958	291.192117	5
8	1248.608157	624.807717	1231.581608	616.294442	1230.597592	615.802434	P	***498.339844***	249.673560	481.313295	241.160285			4
9	1361.692221	681.349749	1344.665672	672.836474	1343.681656	672.344466	L	401.287080	201.147178	384.260531	192.633903			3
10	1474.776285	737.891780	1457.749736	729.378506	1456.765720	728.886498	L	288.203016	144.605146	271.176467	136.091871			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.9	1647.880676	0.005752	FYNQVSTPLLR
6.1	1647.887878	-0.001450	TLNQQLTNHIR
4.8	1647.887878	-0.001450	TLNQQLTNHIR
2.8	1647.910339	-0.023911	LMRPRREGGPPGGLR
2.8	1647.873260	0.013168	AFKELPVNAQNYVR
1.6	1647.903137	-0.016709	EVRIMRWFGLVSR
0.2	1647.895264	-0.008836	MKPILLQGHER

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

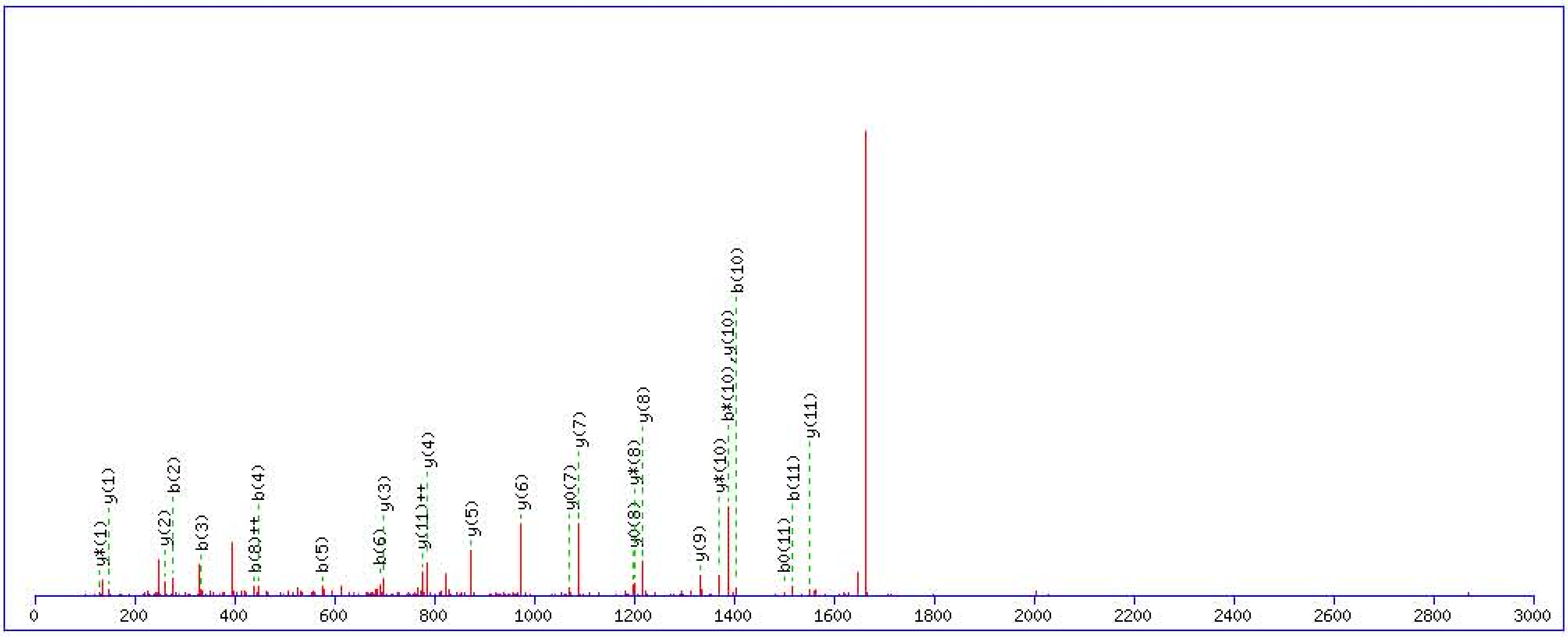
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IYGNQDTSSQLK**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

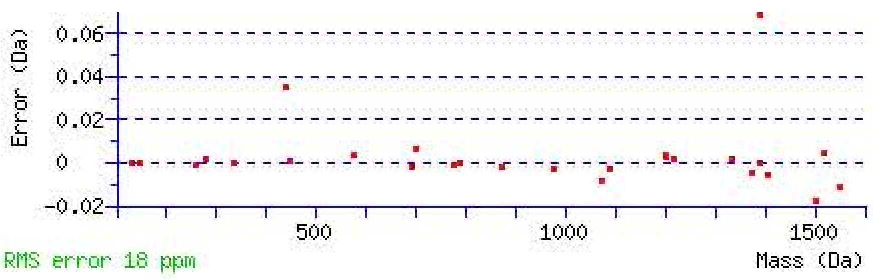
Match to Query 48671: 1663.824828 from(832.919690,2+) rtinseconds(1621) index(60403)
Title: Locus:1.1.1.2562.13 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

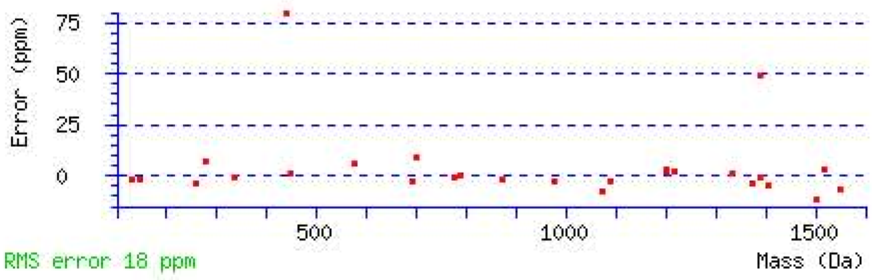
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1663.823944
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10    : Biotin:Thermo-21345 (Q)
Ions Score: 72  Expect: 3.3e-007
Matches : 27/110 fragment ions using 48 most intense peaks   (help)
```

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	114.091340	57.549308					I							12
2	**277.154669**	139.080973					Y	***1551.747170***	776.377223	1534.720621	767.863948	1533.736605	767.371940	11
3	**334.176133**	167.591704					G	***1388.683841***	694.845558	1371.657292	686.332284	1370.673276	685.840276	10
4	**448.219060**	224.613168	431.192511	216.099894			N	***1331.662377***	666.334826	1314.635828	657.821552	1313.651812	657.329544	9
5	**576.277638**	288.642457	559.251089	280.129183			Q	***1217.619450***	609.313363	1200.592901	600.800088	1199.608885	600.308080	8
6	**691.304581**	346.155929	674.278032	337.642654	673.294016	337.150646	D	***1089.560872***	545.284074	1072.534323	536.770799	1071.550307	536.278791	7
7	792.352260	396.679768	775.325711	388.166494	774.341695	387.674486	T	***974.533929***	487.770602	957.507380	479.257328	956.523364	478.765320	6
8	879.384288	440.195782	862.357739	431.682507	861.373723	431.190499	S	***873.486250***	437.246763	856.459701	428.733488	855.475685	428.241480	5
9	966.416316	483.711796	949.389767	475.198521	948.405751	474.706513	S	***786.454222***	393.730749	769.427673	385.217474	768.443657	384.725466	4
10	**1405.641642**	703.324459	1388.615093	694.811184	1387.631077	694.319176	Q	***699.422194***	350.214735	682.395645	341.701460			3
11	**1518.725706**	759.866491	1501.699157	751.353216	1500.715141	750.861208	L	***260.196868***	130.602072	243.170319	122.088797			2
12							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
72.0	1663.823944	0.000884	IYGNQDTSSQLK
16.3	1663.823944	0.000884	IYGNQDTSSQLK
2.8	1663.821442	0.003386	LYGCFLRVYMQSK
2.4	1663.827957	-0.003129	EEAFLHVAVDMYLK
1.8	1663.806198	0.018630	INGTWNGMIGEVVMK

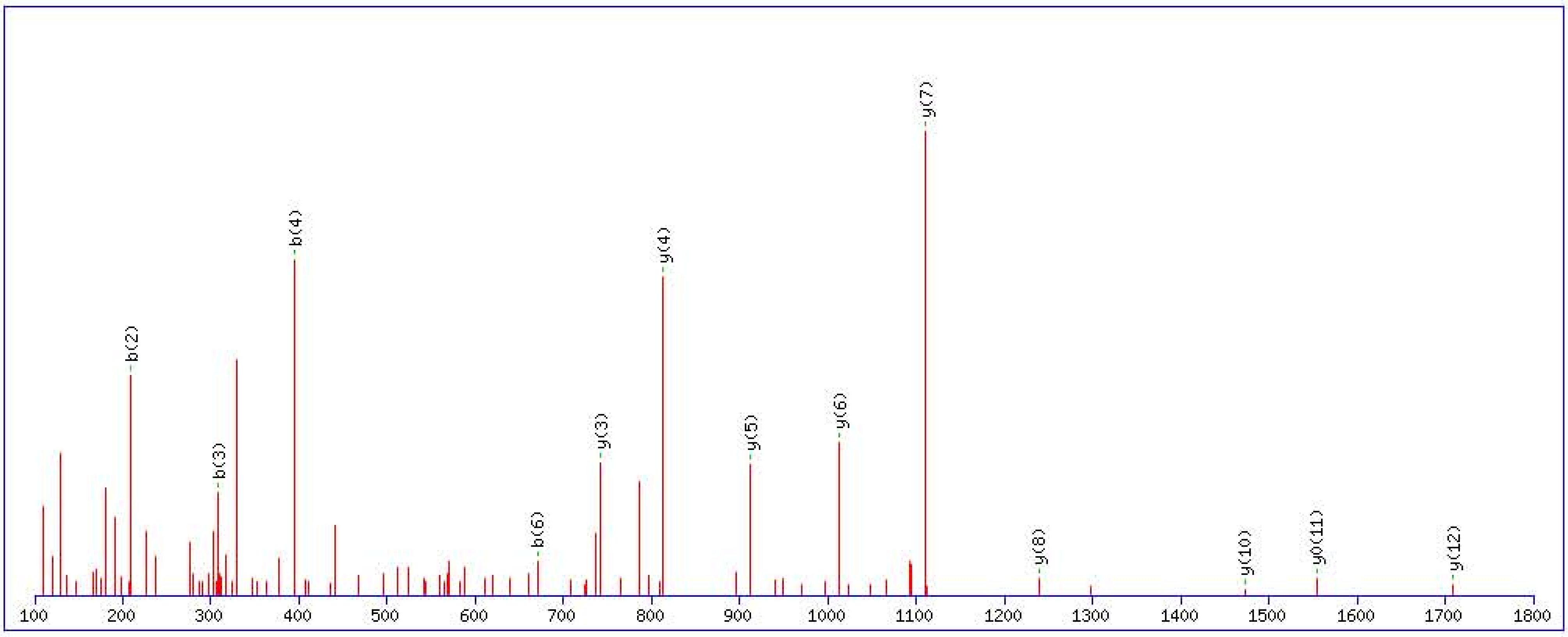
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AHVSFKPTVAQQR**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

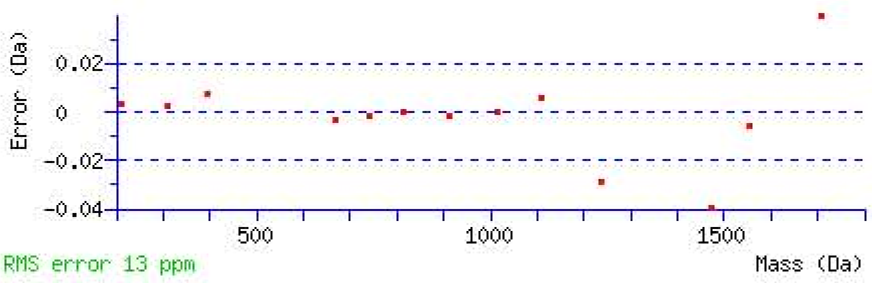
Match to Query 51673: 1778.957142 from(593.992990,3+) rtinseconds(1486) index(59437)
Title: Locus:1.1.1.2515.16 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

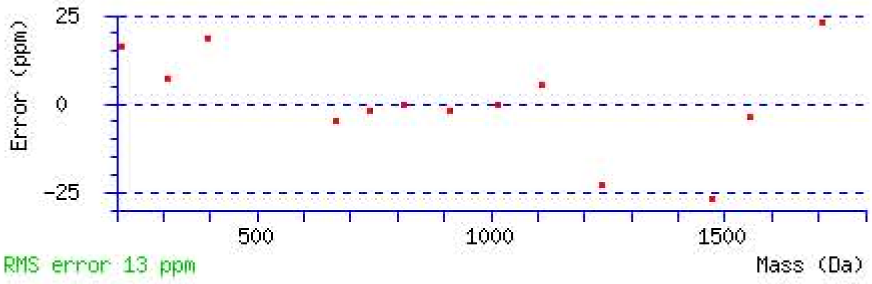
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1778.961395
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 69  Expect: 2.5e-006
Matches : 13/118 fragment ions using 15 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							13
2	**209.103302**	105.055289					H	***1708.931558***	854.969417	1691.905009	846.456143	1690.920993	845.964135	12
3	**308.171716**	154.589496					V	1571.872646	786.439961	1554.846097	777.926687	1553.862081	777.434679	11
4	**395.203744**	198.105510			377.193179	189.100227	S	***1472.804232***	736.905754	1455.777683	728.392480	1454.793667	727.900472	10
5	542.272158	271.639717			524.261593	262.634435	F	1385.772204	693.389740	1368.745655	684.876466	1367.761639	684.384458	9
6	**670.367121**	335.687199	653.340572	327.173924	652.356556	326.681916	K	***1238.703790***	619.855533	1221.677241	611.342259	1220.693225	610.850251	8
7	767.419885	384.213581	750.393336	375.700306	749.409320	375.208298	P	***1110.608827***	555.808052	1093.582278	547.294777	1092.598262	546.802769	7
8	868.467564	434.737420	851.441015	426.224146	850.456999	425.732138	T	***1013.556063***	507.281670	996.529514	498.768395	995.545498	498.276387	6
9	967.535978	484.271627	950.509429	475.758353	949.525413	475.266345	V	***912.508384***	456.757830	895.481835	448.244556			5
10	1038.573092	519.790184	1021.546543	511.276910	1020.562527	510.784902	A	***813.439970***	407.223623	796.413421	398.710349			4
11	1166.631670	583.819473	1149.605121	575.306199	1148.621105	574.814191	Q	***742.402856***	371.705066	725.376307	363.191792			3
12	1605.856996	803.432136	1588.830447	794.918862	1587.846431	794.426854	Q	614.344278	307.675777	597.317729	299.162503			2
13							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
69.4	1778.961395	-0.004253	AHVSFKPTVAQQR
69.4	1778.961395	-0.004253	AHVSFKPTVAQQR

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

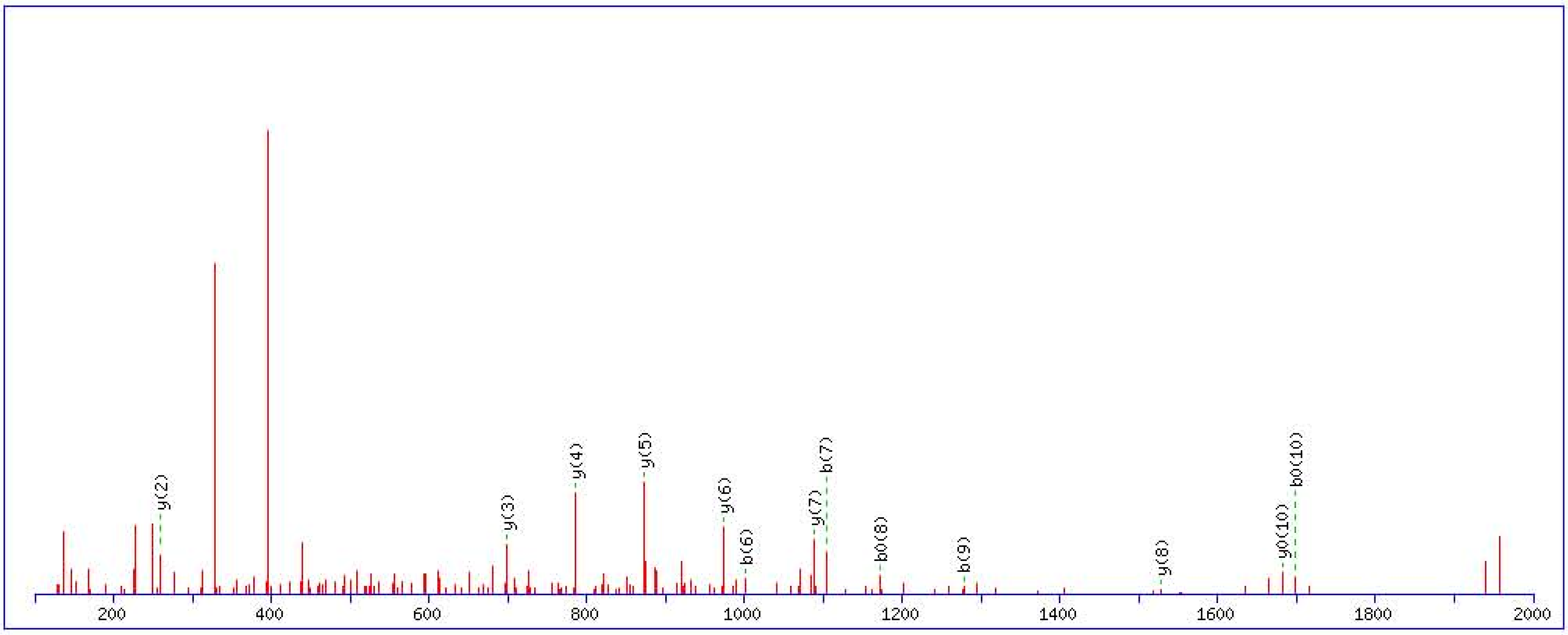
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IYGNQDTSSQLK**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

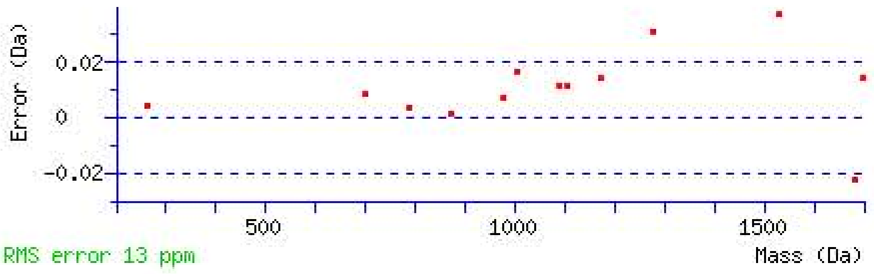
Match to Query 56086: 1974.995652 from(659.339160,3+) rtinseconds(1975) index(62983)
Title: Locus:1.1.1.2685.4 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

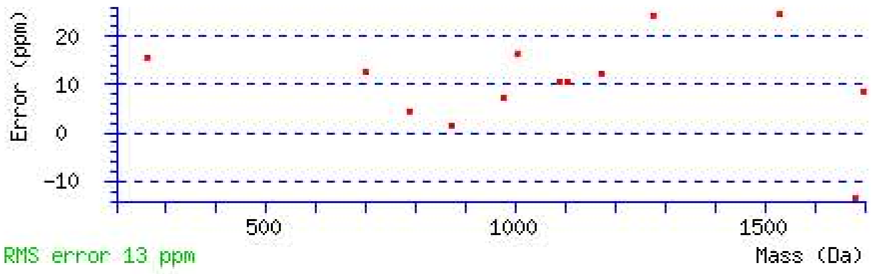
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1974.990692
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 25  Expect: 0.077
Matches : 13/110 fragment ions using 34 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							12
2	277.154669	139.080973					Y	1862.913918	931.960597	1845.887369	923.447323	1844.903353	922.955315	11
3	334.176133	167.591704					G	1699.850589	850.428933	1682.824040	841.915658	1681.840024	841.423650	10
4	448.219060	224.613168	431.192511	216.099894			N	1642.829125	821.918201	1625.802576	813.404926	1624.818560	812.912918	9
5	887.444386	444.225831	870.417837	435.712557			Q	***1528.786198***	764.896737	1511.759649	756.383463	1510.775633	755.891455	8
6	**1002.471329**	501.739303	985.444780	493.226028	984.460764	492.734020	D	***1089.560872***	545.284074	1072.534323	536.770800	1071.550307	536.278792	7
7	**1103.519008**	552.263142	1086.492459	543.749868	1085.508443	543.257860	T	***974.533929***	487.770603	957.507380	479.257328	956.523364	478.765320	6
8	1190.551036	595.779156	1173.524487	587.265882	1172.540471	586.773874	S	***873.486250***	437.246763	856.459701	428.733489	855.475685	428.241481	5
9	**1277.583064**	639.295170	1260.556515	630.781896	1259.572499	630.289888	S	***786.454222***	393.730749	769.427673	385.217475	768.443657	384.725467	4
10	1716.808390	858.907833	1699.781841	850.394559	1698.797825	849.902551	Q	***699.422194***	350.214735	682.395645	341.701461			3
11	1829.892454	915.449865	1812.865905	906.936591	1811.881889	906.444583	L	***260.196868***	130.602072	243.170319	122.088797			2
12							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.4	1974.990692	0.004960	IYGNQDTSSQLK

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

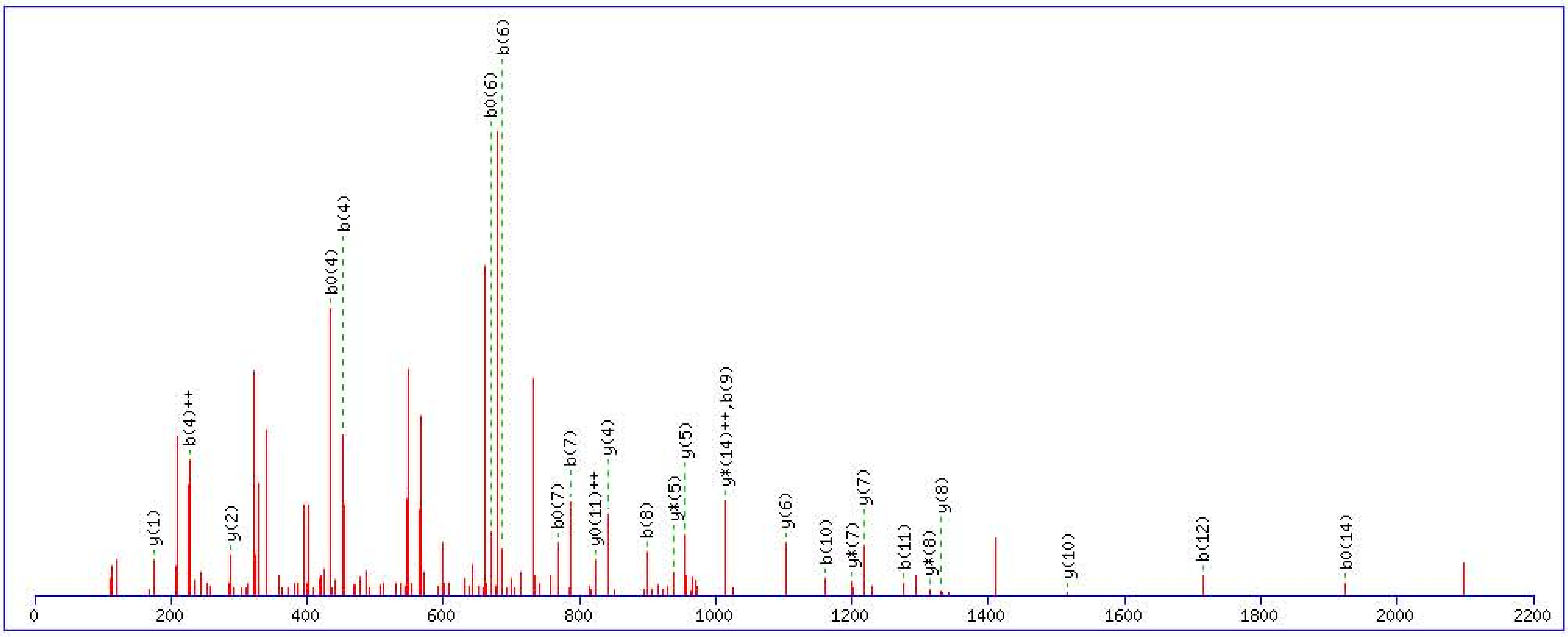
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AEDHFSVIDFNQNIR**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

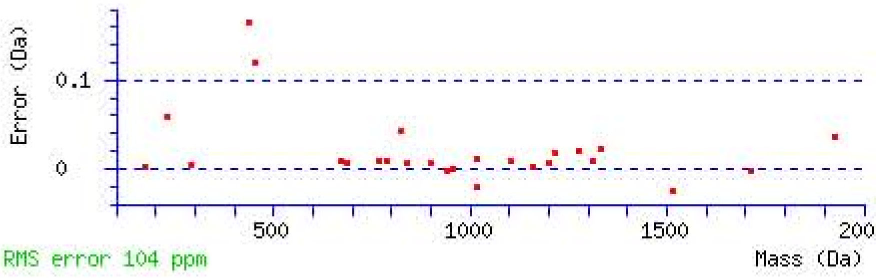
Match to Query 59853: 2115.024762 from(706.015530,3+) rtinseconds(2265) index(64833)
Title: Locus:1.1.1.2786.8 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

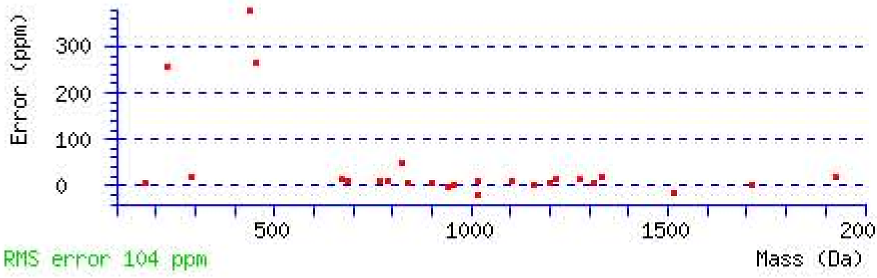
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2115.020752
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12 : Biotin:Thermo-21345 (Q)
Ions Score: 36 **Expect:** 0.0023
Matches : 26/134 fragment ions using 55 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							15
2	201.086983	101.047130			183.076418	92.041847	E	2044.990921	1022.999099	2027.964372	1014.485824	2026.980356	1013.993816	14
3	316.113926	158.560601			298.103361	149.555319	D	1915.948328	958.477802	1898.921779	949.964528	1897.937763	949.472519	13
4	***453.172838***	227.090057			435.162273	218.084775	H	1800.921385	900.964331	1783.894836	892.451056	1782.910820	891.959048	12
5	600.241252	300.624264			582.230687	291.618982	F	1663.862473	832.434874	1646.835924	823.921600	1645.851908	823.429592	11
6	***687.273280***	344.140278			669.262715	335.134996	S	***1516.794059***	758.900668	1499.767510	750.387393	1498.783494	749.895385	10
7	***786.341694***	393.674485			768.331129	384.669202	V	1429.762031	715.384654	1412.735482	706.871379	1411.751466	706.379371	9
8	***899.425758***	450.216517			881.415193	441.211234	I	***1330.693617***	665.850447	1313.667068	657.337172	1312.683052	656.845164	8
9	***1014.452701***	507.729988			996.442136	498.724706	D	***1217.609553***	609.308415	1200.583004	600.795140	1199.598988	600.303132	7
10	***1161.521115***	581.264196			1143.510550	572.258913	F	***1102.582610***	551.794943	1085.556061	543.281669			6
11	***1275.564042***	638.285659	1258.537493	629.772385	1257.553477	629.280376	N	***955.514196***	478.260736	938.487647	469.747462			5
12	***1714.789368***	857.898322	1697.762819	849.385048	1696.778803	848.893039	Q	***841.471269***	421.239273	824.444720	412.725998			4
13	1828.832295	914.919785	1811.805746	906.406511	1810.821730	905.914503	N	402.245943	201.626610	385.219394	193.113335			3
14	1941.916359	971.461817	1924.889810	962.948543	1923.905794	962.456535	I	***288.203016***	144.605146	271.176467	136.091872			2
15							R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.6	2115.020752	0.004010	AEDHFSVIDFNQNIR
7.6	2115.027237	-0.002475	KYSDYIKGSNLDAPEPYR

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

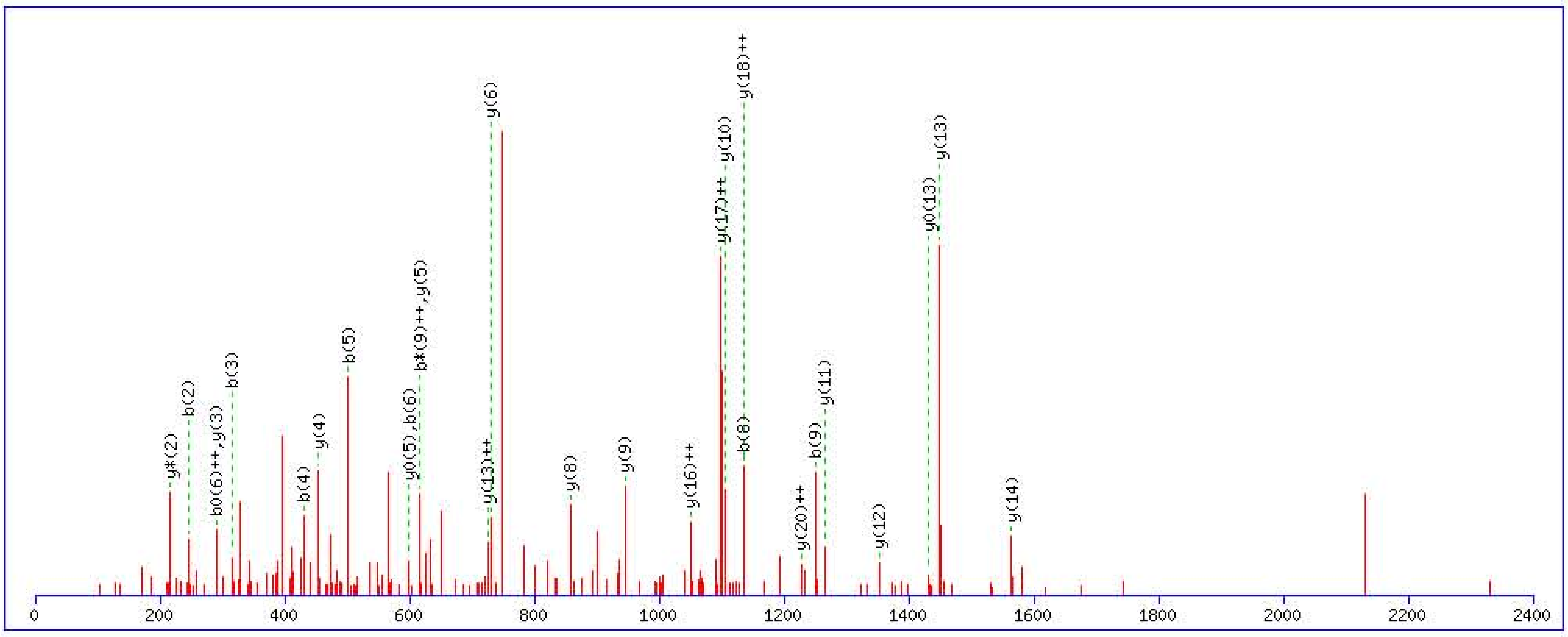
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **MLADAPPQDPSCCSGALYYGSK**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

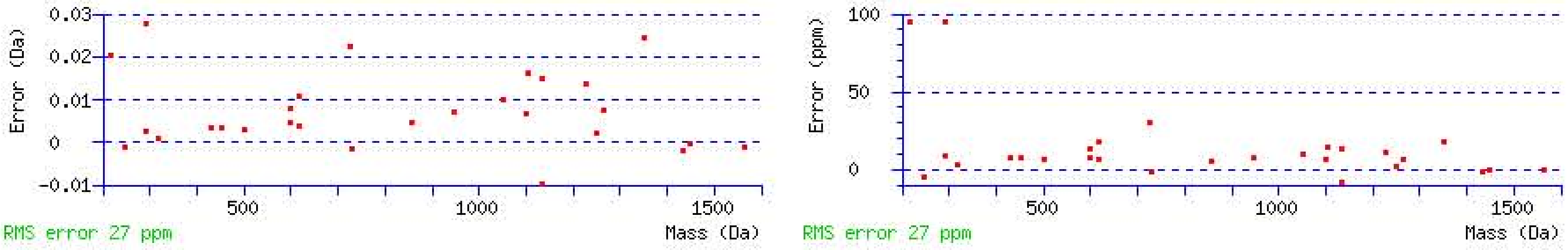
Match to Query 70616: 2698.203642 from(900.408490,3+) rtinseconds(2091) index(63671)
Title: Locus:1.1.1.2725.17 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2698.189941
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 61  Expect: 6.9e-006
Matches : 28/230 fragment ions using 50 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	132.047761	66.527518					M							22
2	***245.131825***	123.069550					L	2568.156746	1284.582011	2551.130197	1276.068736	2550.146181	1275.576728	21
3	***316.168939***	158.588107					A	2455.072682	1228.039979	2438.046133	1219.526704	2437.062117	1219.034696	20
4	***431.195882***	216.101579			413.185317	207.096296	D	2384.035568	1192.521422	2367.009019	1184.008148	2366.025003	1183.516140	19
5	***502.232996***	251.620136			484.222431	242.614854	A	2269.008625	1135.007950	2251.982076	1126.494676	2250.998060	1126.002668	18
6	***599.285760***	300.146518			581.275195	291.141236	P	2197.971511	1099.489394	2180.944962	1090.976119	2179.960946	1090.484111	17
7	696.338524	348.672900			678.327959	339.667618	P	2100.918747	1050.963012	2083.892198	1042.449737	2082.908182	1041.957729	16
8	***1135.563850***	568.285563	1118.537301	559.772289	1117.553285	559.280281	Q	2003.865983	1002.436630	1986.839434	993.923355	1985.855418	993.431347	15
9	***1250.590793***	625.799035	1233.564244	617.285760	1232.580228	616.793752	D	***1564.640657***	782.823967	1547.614108	774.310692	1546.630092	773.818684	14
10	1347.643557	674.325417	1330.617008	665.812142	1329.632992	665.320134	P	***1449.613714***	725.310495	1432.587165	716.797221	1431.603149	716.305213	13
11	1434.675585	717.841431	1417.649036	709.328156	1416.665020	708.836148	S	***1352.560950***	676.784113	1335.534401	668.270839	1334.550385	667.778831	12
12	1594.706234	797.856755	1577.679685	789.343481	1576.695669	788.851473	C	***1265.528922***	633.268099	1248.502373	624.754825	1247.518357	624.262817	11
13	1754.736883	877.872080	1737.710334	869.358805	1736.726318	868.866797	C	***1105.498273***	553.252775	1088.471724	544.739500	1087.487708	544.247492	10
14	1841.768911	921.388094	1824.742362	912.874819	1823.758346	912.382811	S	***945.467624***	473.237450	928.441075	464.724176	927.457059	464.232168	9
15	1898.790375	949.898826	1881.763826	941.385551	1880.779810	940.893543	G	***858.435596***	429.721436	841.409047	421.208162	840.425031	420.716154	8
16	1969.827489	985.417383	1952.800940	976.904108	1951.816924	976.412100	A	801.414132	401.210704	784.387583	392.697430	783.403567	392.205422	7
17	2082.911553	1041.959415	2065.885004	1033.446140	2064.900988	1032.954132	L	***730.377018***	365.692147	713.350469	357.178873	712.366453	356.686865	6
18	2245.974882	1123.491079	2228.948333	1114.977805	2227.964317	1114.485797	Y	***617.292954***	309.150115	600.266405	300.636841	599.282389	300.144833	5
19	2409.038211	1205.022744	2392.011662	1196.509469	2391.027646	1196.017461	Y	***454.229625***	227.618451	437.203076	219.105176	436.219060	218.613168	4
20	2466.059675	1233.533476	2449.033126	1225.020201	2448.049110	1224.528193	G	***291.166296***	146.086786	274.139747	137.573512	273.155731	137.081504	3
21	2553.091703	1277.049490	2536.065154	1268.536215	2535.081138	1268.044207	S	234.144832	117.576054	217.118283	109.062780	216.134267	108.570772	2
22							K	147.112804	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
60.5	2698.189941	0.013701	MLADAPPQDPSCCSGALYYGSK

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

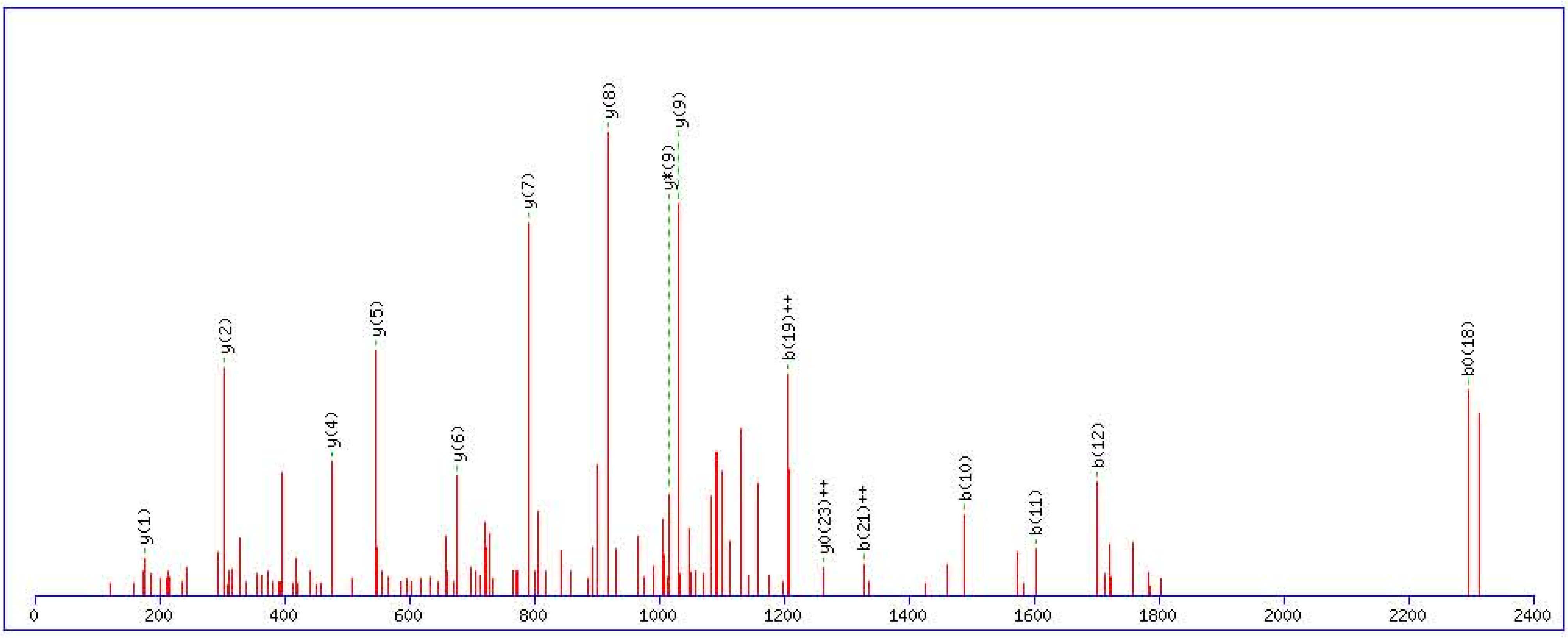
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SILQMSLDHHIVTPLTSLVIENEAGDER**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

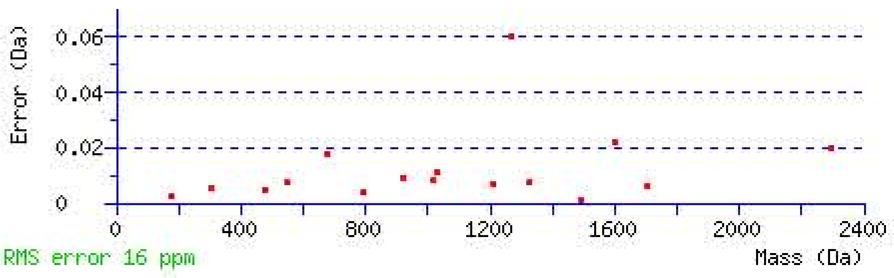
Match to Query 79291: 3443.762896 from(861.948000,4+) rtinseconds(2612) index(66855)
Title: Locus:1.1.1.2906.20 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

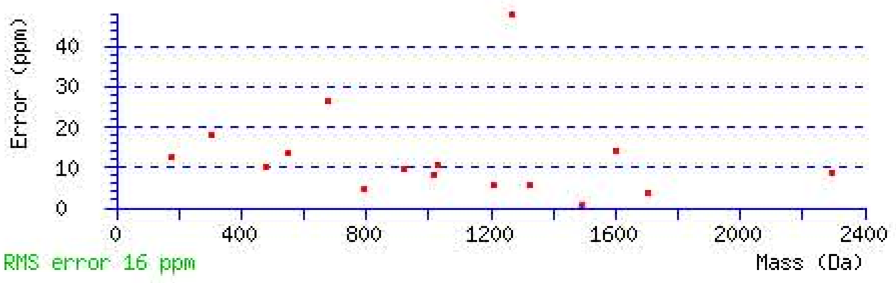
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3443.742859
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4     : Biotin:Thermo-21345 (Q)
M5     : Oxidation (M), with neutral losses 0.000000(shown in table), 63.998285
Ions Score: 58  Expect: 3.8e-006
Matches : 16/478 fragment ions using 18 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							28
2	201.123368	101.065322			183.112803	92.060039	I	3357.718126	1679.362701	3340.691577	1670.849426	3339.707561	1670.357418	27
3	314.207432	157.607354			296.196867	148.602071	L	3244.634062	1622.820669	3227.607513	1614.307394	3226.623497	1613.815386	26
4	753.432758	377.220017	736.406209	368.706743	735.422193	368.214735	Q	3131.549998	1566.278637	3114.523449	1557.765362	3113.539433	1557.273354	25
5	900.468158	450.737717	883.441609	442.224443	882.457593	441.732435	M	2692.324672	1346.665974	2675.298123	1338.152699	2674.314107	1337.660691	24
6	987.500186	494.253731	970.473637	485.740456	969.489621	485.248448	S	2545.289272	1273.148274	2528.262723	1264.634999	2527.278707	1264.142991	23
7	1100.584250	550.795763	1083.557701	542.282489	1082.573685	541.790480	L	2458.257244	1229.632260	2441.230695	1221.118985	2440.246679	1220.626977	22
8	1215.611193	608.309235	1198.584644	599.795960	1197.600628	599.303952	D	2345.173180	1173.090228	2328.146631	1164.576953	2327.162615	1164.084945	21
9	1352.670105	676.838690	1335.643556	668.325416	1334.659540	667.833408	H	2230.146237	1115.576756	2213.119688	1107.063482	2212.135672	1106.571474	20
10	**1489.729017**	745.368146	1472.702468	736.854872	1471.718452	736.362864	H	2093.087325	1047.047300	2076.060776	1038.534026	2075.076760	1038.042018	19
11	**1602.813081**	801.910178	1585.786532	793.396904	1584.802516	792.904896	I	1956.028413	978.517845	1939.001864	970.004570	1938.017848	969.512562	18
12	**1701.881495**	851.444385	1684.854946	842.931111	1683.870930	842.439103	V	1842.944349	921.975813	1825.917800	913.462538	1824.933784	912.970530	17
13	1802.929174	901.968225	1785.902625	893.454951	1784.918609	892.962942	T	1743.875935	872.441606	1726.849386	863.928331	1725.865370	863.436323	16
14	1899.981938	950.494607	1882.955389	941.981333	1881.971373	941.489324	P	1642.828256	821.917766	1625.801707	813.404492	1624.817691	812.912484	15
15	2013.066002	1007.036639	1996.039453	998.523364	1995.055437	998.031356	L	1545.775492	773.391384	1528.748943	764.878110	1527.764927	764.386102	14
16	2114.113681	1057.560478	2097.087132	1049.047204	2096.103116	1048.555196	T	1432.691428	716.849352	1415.664879	708.336078	1414.680863	707.844070	13
17	2201.145709	1101.076492	2184.119160	1092.563218	2183.135144	1092.071210	S	1331.643749	666.325513	1314.617200	657.812238	1313.633184	657.320230	12
18	2314.229773	1157.618524	2297.203224	1149.105250	2296.219208	1148.613242	L	1244.611721	622.809499	1227.585172	614.296224	1226.601156	613.804216	11
19	2413.298187	**1207.152731**	2396.271638	1198.639457	2395.287622	1198.147449	V	1131.527657	566.267467	1114.501108	557.754192	1113.517092	557.262184	10
20	2526.382251	1263.694763	2509.355702	1255.181489	2508.371686	1254.689481	I	***1032.459243***	516.733260	1015.432694	508.219985	1014.448678	507.727977	9
21	2655.424844	**1328.216060**	2638.398295	1319.702785	2637.414279	1319.210777	E	***919.375179***	460.191228	902.348630	451.677953	901.364614	451.185945	8
22	2769.467771	1385.237523	2752.441222	1376.724249	2751.457206	1376.232241	N	***790.332586***	395.669931	773.306037	387.156657	772.322021	386.664649	7
23	2898.510364	1449.758820	2881.483815	1441.245545	2880.499799	1440.753537	E	***676.289659***	338.648468	659.263110	330.135193	658.279094	329.643185	6
24	2969.547478	1485.277377	2952.520929	1476.764102	2951.536913	1476.272094	A	***547.247066***	274.127171	530.220517	265.613897	529.236501	265.121889	5
25	3026.568942	1513.788109	3009.542393	1505.274834	3008.558377	1504.782826	G	***476.209952***	238.608614	459.183403	230.095339	458.199387	229.603331	4
26	3141.595885	1571.301580	3124.569336	1562.788306	3123.585320	1562.296298	D	419.188488	210.097882	402.161939	201.584607	401.177923	201.092599	3
27	3270.638478	1635.822877	3253.611929	1627.309602	3252.627913	1626.817594	E	***304.161545***	152.584411	287.134996	144.071136	286.150980	143.579128	2
28							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
57.9	3443.742859	0.020037	SILQMSLDHHIVTPLTSLVIENEAGDER
0.1	3443.760620	0.002276	AIVNSALKLYSQDKTGMVDFALESGGGSILSTR

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

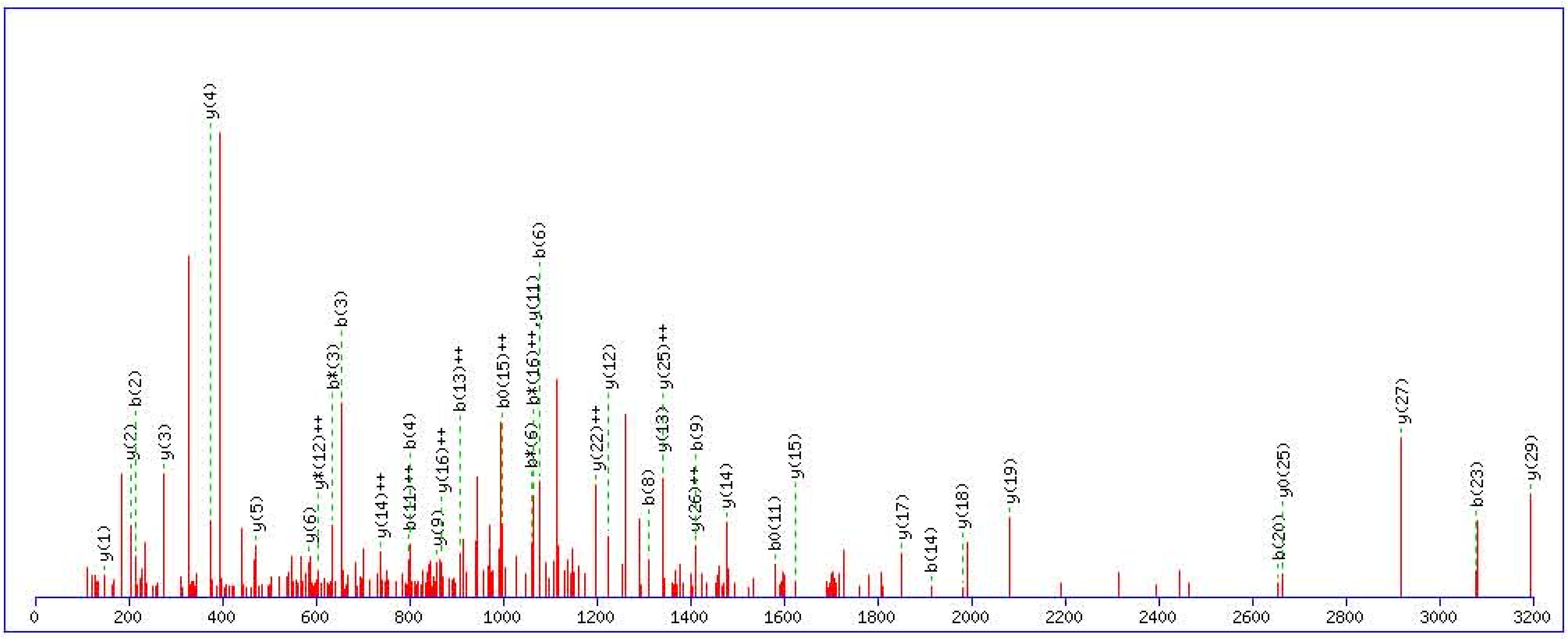
Mascot Search Results

Peptide View

MS/MS Fragmentation of **NVQFNYPHTSVTDVTQNNFHNYFGGSEIVVAGK**
Found in **ITIH2_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2

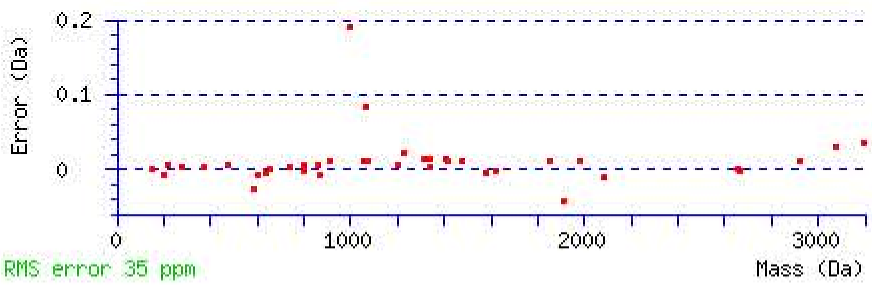
Match to Query 82544: 3993.930256 from(999.489840,4+) rtinseconds(2364) index(65447)
Title: Locus:1.1.1.2820.21 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

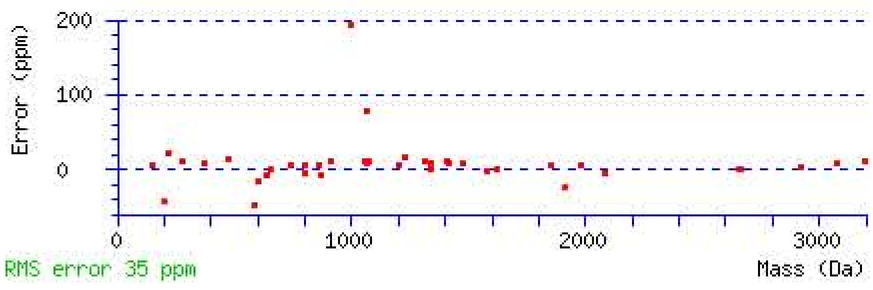
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3993.910858
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 59  Expect: 2.7e-005
Matches : 40/356 fragment ions using 102 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	115.050203	58.028740	98.023654	49.515465			N							33
2	***214.118617***	107.562947	197.092068	99.049672			V	3880.875173	1940.941224	3863.848624	1932.427950	3862.864608	1931.935942	32
3	***653.343943***	327.175610	636.317394	318.662335			Q	3781.806759	1891.407017	3764.780210	1882.893743	3763.796194	1882.401735	31
4	***800.412357***	400.709817	783.385808	392.196542			F	3342.581433	1671.794354	3325.554884	1663.281080	3324.570868	1662.789072	30
5	914.455284	457.731280	897.428735	449.218006			N	***3195.513019***	1598.260147	3178.486470	1589.746873	3177.502454	1589.254865	29
6	***1077.518613***	539.262945	1060.492064	530.749670			Y	3081.470092	1541.238684	3064.443543	1532.725409	3063.459527	1532.233401	28
7	1174.571377	587.789327	1157.544828	579.276052			P	***2918.406763***	1459.707019	2901.380214	1451.193745	2900.396198	1450.701737	27
8	***1311.630289***	656.318783	1294.603740	647.805508			H	2821.353999	1411.180637	2804.327450	1402.667363	2803.343434	1402.175355	26
9	***1412.677968***	706.842622	1395.651419	698.329348	1394.667403	697.837339	T	2684.295087	1342.651181	2667.268538	1334.137907	2666.284522	1333.645899	25
10	1499.709996	750.358636	1482.683447	741.845362	1481.699431	741.353354	S	2583.247408	1292.127342	2566.220859	1283.614067	2565.236843	1283.122059	24
11	1598.778410	**799.892843**	1581.751861	791.379569	1580.767845	790.887561	V	2496.215380	1248.611328	2479.188831	1240.098053	2478.204815	1239.606045	23
12	1699.826089	850.416683	1682.799540	841.903408	1681.815524	841.411400	T	2397.146966	1199.077121	2380.120417	1190.563846	2379.136401	1190.071838	22
13	1814.853032	**907.930154**	1797.826483	899.416880	1796.842467	898.924872	D	2296.099287	1148.553281	2279.072738	1140.040007	2278.088722	1139.547999	21
14	***1913.921446***	957.464361	1896.894897	948.951087	1895.910881	948.459079	V	2181.072344	1091.039810	2164.045795	1082.526535	2163.061779	1082.034527	20
15	2014.969125	1007.988201	1997.942576	999.474926	1996.958560	998.982918	T	***2082.003930***	1041.505603	2064.977381	1032.992328	2063.993365	1032.500320	19
16	2143.027703	1072.017490	2126.001154	1063.504215	2125.017138	1063.012207	Q	***1980.956251***	990.981763	1963.929702	982.468489	1962.945686	981.976481	18
17	2257.070630	1129.038953	2240.044081	1120.525678	2239.060065	1120.033671	N	***1852.897673***	926.952474	1835.871124	918.439200	1834.887108	917.947192	17
18	2371.113557	1186.060417	2354.087008	1177.547142	2353.102992	1177.055134	N	1738.854746	869.931011	1721.828197	861.417736	1720.844181	860.925728	16
19	2518.181971	1259.594623	2501.155422	1251.081349	2500.171406	1250.589341	F	***1624.811819***	812.909547	1607.785270	804.396273	1606.801254	803.904265	15
20	***2655.240883***	1328.124079	2638.214334	1319.610805	2637.230318	1319.118797	H	***1477.743405***	739.375340	1460.716856	730.862066	1459.732840	730.370058	14
21	2769.283810	1385.145543	2752.257261	1376.632268	2751.273245	1376.140260	N	***1340.684493***	670.845885	1323.657944	662.332610	1322.673928	661.840602	13
22	2932.347139	1466.677207	2915.320590	1458.163933	2914.336574	1457.671925	Y	***1226.641566***	613.824421	1209.615017	605.311147	1208.631001	604.819139	12
23	***3079.415553***	1540.211414	3062.389004	1531.698140	3061.404988	1531.206132	F	***1063.578237***	532.292757	1046.551688	523.779482	1045.567672	523.287474	11
24	3136.437017	1568.722146	3119.410468	1560.208872	3118.426452	1559.716864	G	916.509823	458.758550	899.483274	450.245275	898.499258	449.753267	10
25	3193.458481	1597.232878	3176.431932	1588.719604	3175.447916	1588.227596	G	***859.488359***	430.247818	842.461810	421.734543	841.477794	421.242535	9
26	3280.490509	1640.748892	3263.463960	1632.235618	3262.479944	1631.743610	S	802.466895	401.737086	785.440346	393.223811	784.456330	392.731803	8
27	3409.533102	1705.270189	3392.506553	1696.756914	3391.522537	1696.264906	E	715.434867	358.221072	698.408318	349.707797	697.424302	349.215789	7
28	3522.617166	1761.812221	3505.590617	1753.298946	3504.606601	1752.806938	I	***586.392274***	293.699775	569.365725	285.186501			6
29	3621.685580	1811.346428	3604.659031	1802.833153	3603.675015	1802.341145	V	***473.308210***	237.157743	456.281661	228.644468			5
30	3720.753994	1860.880635	3703.727445	1852.367360	3702.743429	1851.875352	V	***374.239796***	187.623536	357.213247	179.110261			4
31	3791.791108	1896.399192	3774.764559	1887.885917	3773.780543	1887.393909	A	***275.171382***	138.089329	258.144833	129.576055			3
32	3848.812572	1924.909924	3831.786023	1916.396649	3830.802007	1915.904641	G	***204.134268***	102.570772	187.107719	94.057497			2
33							K	***147.112804***	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of NVQFNYPHTSVTDVTQNNFHNYFGGSEIVVAGK
(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	3993.910858	0.019398	NVQFNYPHTSVTDVTQNNFHNYFGGSEIVVAGK
14.6	3993.910858	0.019398	NVQFNYPHTSVTDVTQNNFHNYFGGSEIVVAGK

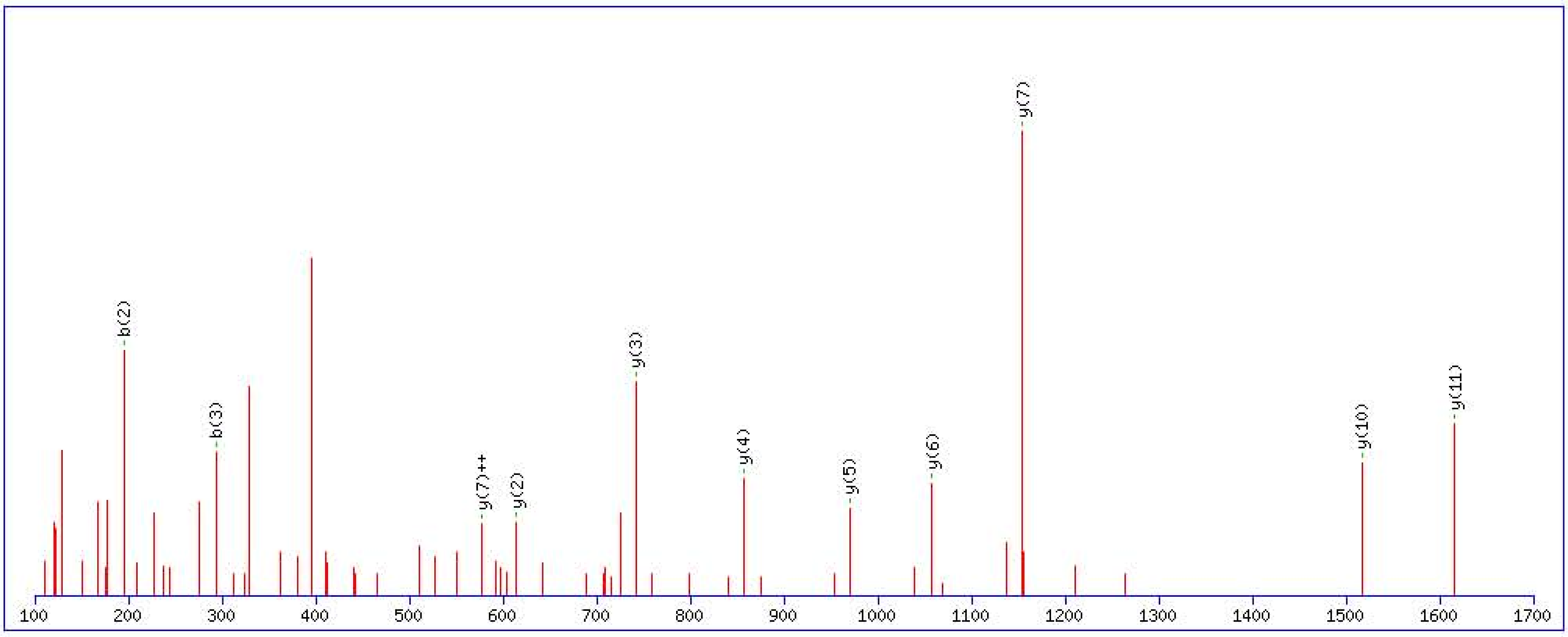
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GHVSFKPSLDQQR**
Found in **ITIH3_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2

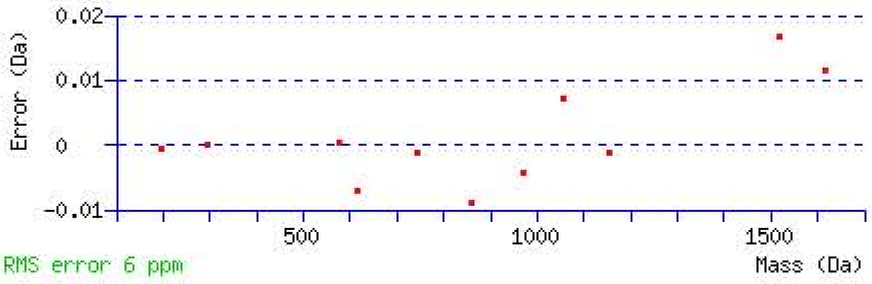
Match to Query 52341: 1808.929512 from(603.983780,3+) rtinseconds(1551) index(59911)
Title: Locus:1.1.1.2538.9 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

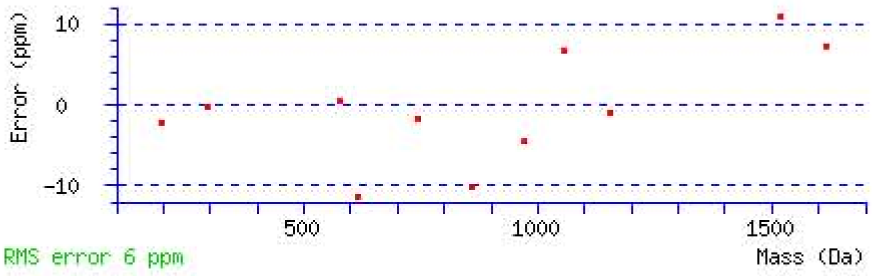
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1808.935577
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 65  Expect: 8.3e-006
Matches : 11/122 fragment ions using 14 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.028740	29.518008					G							13
2	**195.087652**	98.047464					H	1752.921386	876.964331	1735.894837	868.451057	1734.910821	867.959049	12
3	**294.156066**	147.581671					V	***1615.862474***	808.434875	1598.835925	799.921601	1597.851909	799.429593	11
4	381.188094	191.097685			363.177529	182.092403	S	***1516.794060***	758.900668	1499.767511	750.387394	1498.783495	749.895386	10
5	528.256508	264.631892			510.245943	255.626610	F	1429.762032	715.384654	1412.735483	706.871380	1411.751467	706.379372	9
6	656.351471	328.679374	639.324922	320.166099	638.340906	319.674091	K	1282.693618	641.850447	1265.667069	633.337173	1264.683053	632.845165	8
7	753.404235	377.205756	736.377686	368.692481	735.393670	368.200473	P	***1154.598655***	577.802966	1137.572106	569.289691	1136.588090	568.797683	7
8	840.436263	420.721770	823.409714	412.208495	822.425698	411.716487	S	***1057.545891***	529.276584	1040.519342	520.763309	1039.535326	520.271301	6
9	953.520327	477.263802	936.493778	468.750527	935.509762	468.258519	L	***970.513863***	485.760570	953.487314	477.247295	952.503298	476.755287	5
10	1068.547270	534.777273	1051.520721	526.263999	1050.536705	525.771991	D	***857.429799***	429.218538	840.403250	420.705263	839.419234	420.213255	4
11	1196.605848	598.806562	1179.579299	590.293288	1178.595283	589.801279	Q	***742.402856***	371.705066	725.376307	363.191792			3
12	1635.831174	818.419225	1618.804625	809.905951	1617.820609	809.413943	Q	***614.344278***	307.675777	597.317729	299.162503			2
13							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.8	1808.935577	-0.006065	GHVSFKPSLDQQR
50.0	1808.935577	-0.006065	GHVSFKPSLDQQR

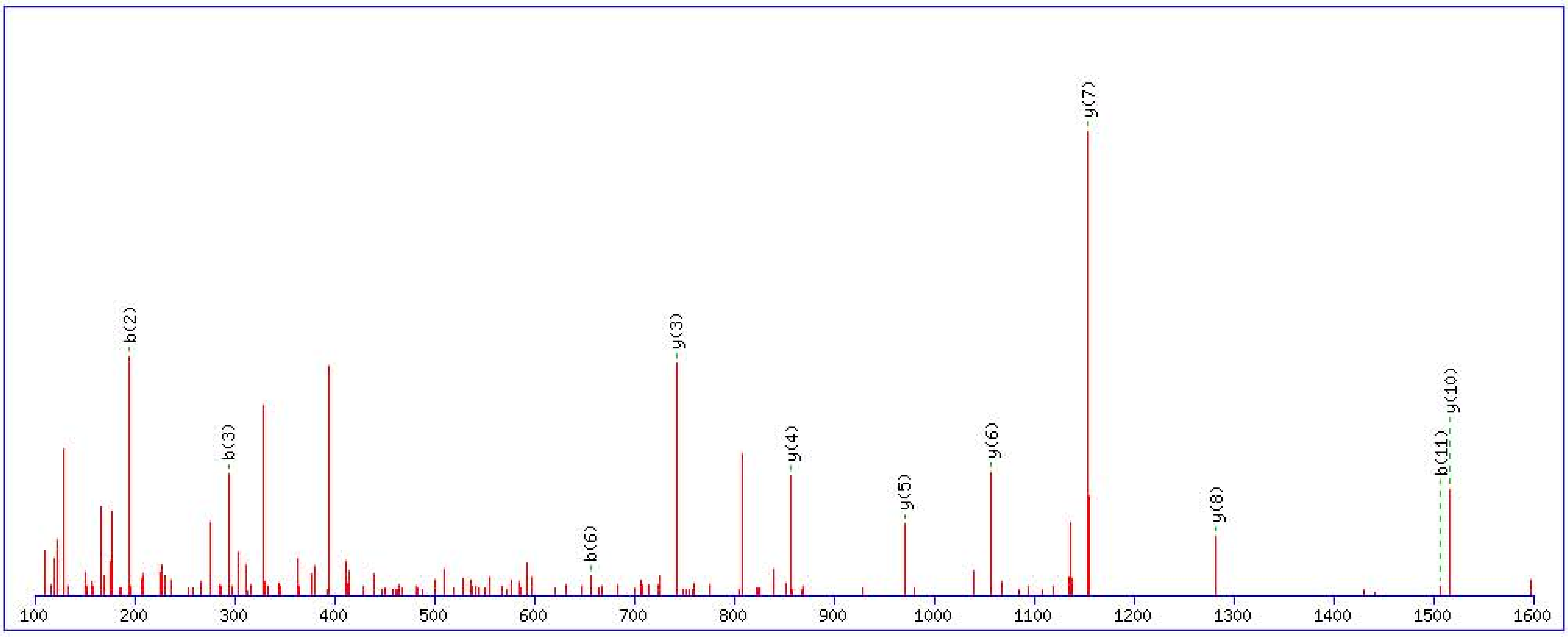
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GHVSFKPSLDQQR**
Found in **ITIH3_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2

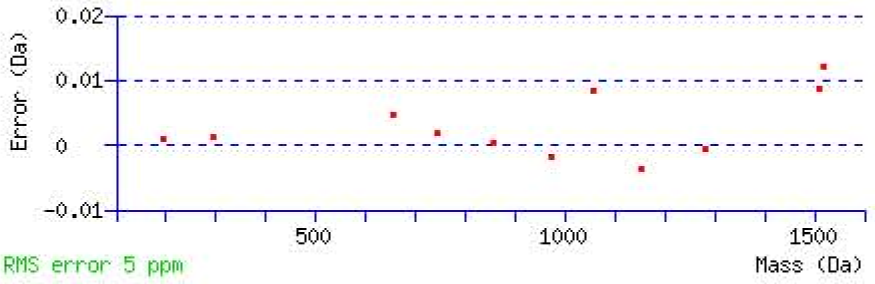
Match to Query 52342: 1808.931522 from(603.984450,3+) rtinseconds(1574) index(60107)
Title: Locus:1.1.1.2546.8 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

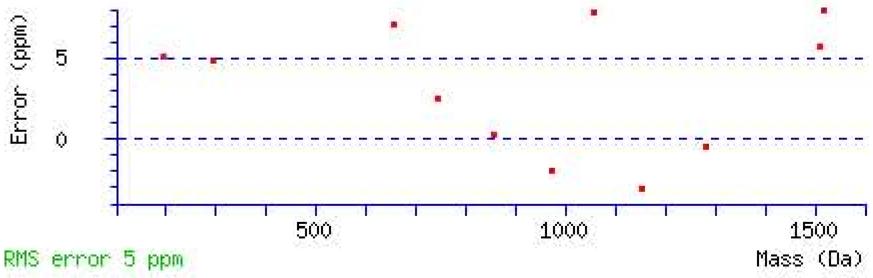
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1808.935577
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11 : Biotin:Thermo-21345 (Q)
Ions Score: 54 **Expect:** 0.0001
Matches : 11/122 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							13
2	***195.087652***	98.047464					H	1752.921386	876.964331	1735.894837	868.451057	1734.910821	867.959049	12
3	***294.156066***	147.581671					V	1615.862474	808.434875	1598.835925	799.921601	1597.851909	799.429593	11
4	381.188094	191.097685			363.177529	182.092403	S	***1516.794060***	758.900668	1499.767511	750.387394	1498.783495	749.895386	10
5	528.256508	264.631892			510.245943	255.626610	F	1429.762032	715.384654	1412.735483	706.871380	1411.751467	706.379372	9
6	***656.351471***	328.679374	639.324922	320.166099	638.340906	319.674091	K	***1282.693618***	641.850447	1265.667069	633.337173	1264.683053	632.845165	8
7	753.404235	377.205756	736.377686	368.692481	735.393670	368.200473	P	***1154.598655***	577.802966	1137.572106	569.289691	1136.588090	568.797683	7
8	840.436263	420.721770	823.409714	412.208495	822.425698	411.716487	S	***1057.545891***	529.276584	1040.519342	520.763309	1039.535326	520.271301	6
9	953.520327	477.263802	936.493778	468.750527	935.509762	468.258519	L	***970.513863***	485.760570	953.487314	477.247295	952.503298	476.755287	5
10	1068.547270	534.777273	1051.520721	526.263999	1050.536705	525.771991	D	***857.429799***	429.218538	840.403250	420.705263	839.419234	420.213255	4
11	***1507.772596***	754.389936	1490.746047	745.876662	1489.762031	745.384654	Q	***742.402856***	371.705066	725.376307	363.191792			3
12	1635.831174	818.419225	1618.804625	809.905951	1617.820609	809.413943	Q	303.177530	152.092403	286.150981	143.579129			2
13							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
53.9	1808.935577	-0.004055	GHVSFKPSLDQQR
49.8	1808.935577	-0.004055	GHVSFKPSLDQQR

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

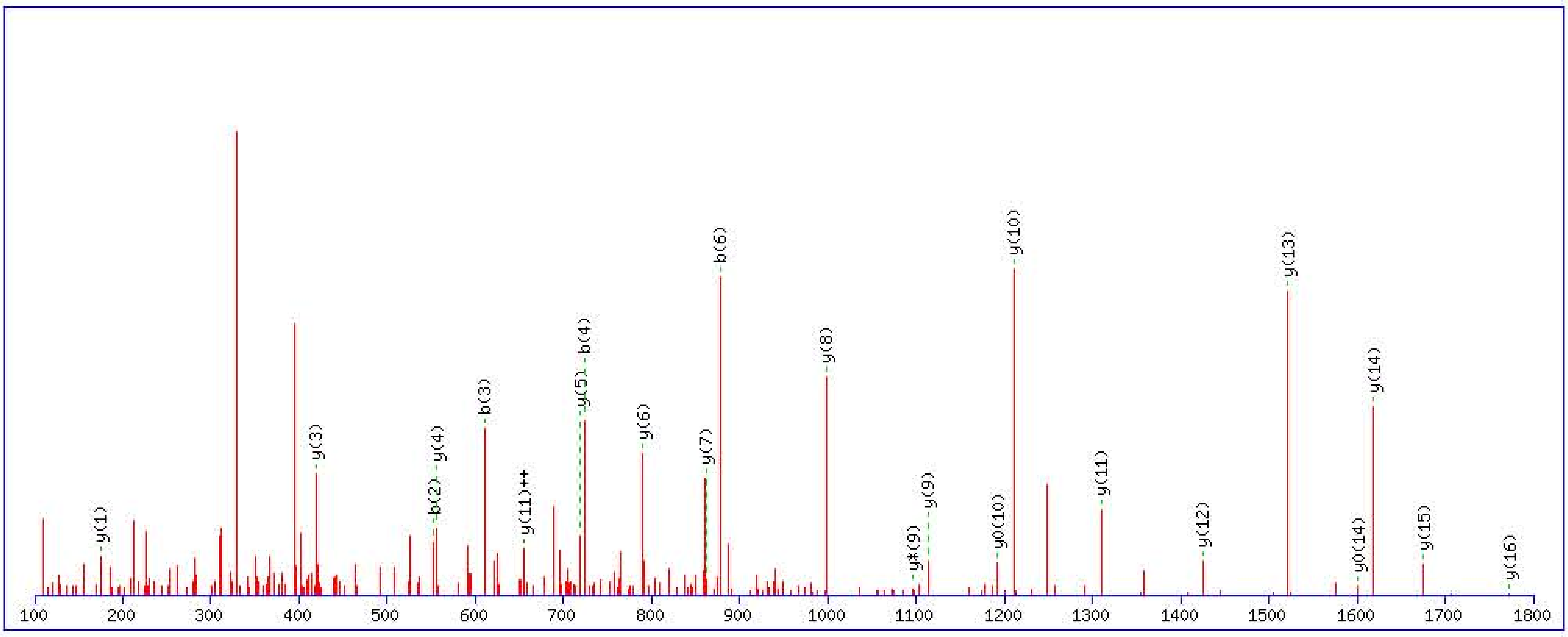
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLGLPGPPDVPDHAAYHPFR**
Found in **ITIH4_HUMAN**, Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4

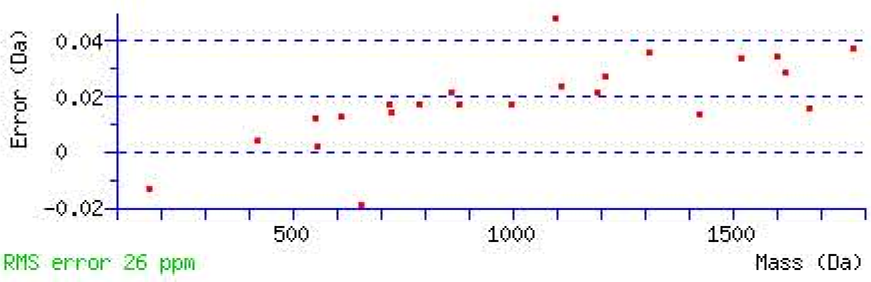
Match to Query 68367: 2494.282016 from(624.577780,4+) rtinseconds(2127) index(8127)
Title: Locus:1.1.1.2461.15 File:"2013-07-02 CLN FXIII 30 min 1st F 1.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

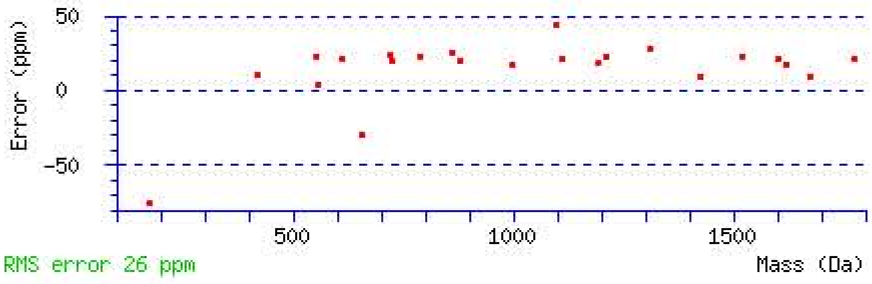
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] 100 to 1800 Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2494.257980
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 87  Expect: 2.1e-008
Matches : 23/196 fragment ions using 49 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	440.232602	220.619939	423.206053	212.106664			Q							20
2	**553.316666**	277.161971	536.290117	268.648697			L	2056.039923	1028.523599	2039.013374	1020.010325	2038.029358	1019.518317	19
3	**610.338130**	305.672703	593.311581	297.159429			G	1942.955859	971.981568	1925.929310	963.468293	1924.945294	962.976285	18
4	**723.422194**	362.214735	706.395645	353.701461			L	1885.934395	943.470836	1868.907846	934.957561	1867.923830	934.465553	17
5	820.474958	410.741117	803.448409	402.227843			P	***1772.850331***	886.928804	1755.823782	878.415529	1754.839766	877.923521	16
6	**877.496422**	439.251849	860.469873	430.738575			G	***1675.797567***	838.402422	1658.771018	829.889147	1657.787002	829.397139	15
7	974.549186	487.778231	957.522637	479.264957			P	***1618.776103***	809.891690	1601.749554	801.378415	1600.765538	800.886407	14
8	1071.601950	536.304613	1054.575401	527.791339			P	***1521.723339***	761.365308	1504.696790	752.852033	1503.712774	752.360025	13
9	1186.628893	593.818085	1169.602344	585.304810	1168.618328	584.812802	D	***1424.670575***	712.838926	1407.644026	704.325651	1406.660010	703.833643	12
10	1285.697307	643.352292	1268.670758	634.839017	1267.686742	634.347009	V	***1309.643632***	655.325454	1292.617083	646.812180	1291.633067	646.320172	11
11	1382.750071	691.878674	1365.723522	683.365399	1364.739506	682.873391	P	***1210.575218***	605.791247	1193.548669	597.277973	1192.564653	596.785964	10
12	1497.777014	749.392145	1480.750465	740.878871	1479.766449	740.386863	D	***1113.522454***	557.264865	1096.495905	548.751591	1095.511889	548.259582	9
13	1634.835926	817.921601	1617.809377	809.408327	1616.825361	808.916319	H	***998.495511***	499.751393	981.468962	491.238119			8
14	1705.873040	853.440158	1688.846491	844.926884	1687.862475	844.434876	A	***861.436599***	431.221937	844.410050	422.708663			7
15	1776.910154	888.958715	1759.883605	880.445441	1758.899589	879.953433	A	***790.399485***	395.703380	773.372936	387.190106			6
16	1939.973483	970.490380	1922.946934	961.977105	1921.962918	961.485097	Y	***719.362371***	360.184823	702.335822	351.671549			5
17	2077.032395	1039.019836	2060.005846	1030.506561	2059.021830	1030.014553	H	***556.299042***	278.653159	539.272493	270.139884			4
18	2174.085159	1087.546218	2157.058610	1079.032943	2156.074594	1078.540935	P	***419.240130***	210.123703	402.213581	201.610428			3
19	2321.153573	1161.080424	2304.127024	1152.567150	2303.143008	1152.075142	F	322.187366	161.597321	305.160817	153.084046			2
20							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
87.1	2494.257980	0.024036	QLGLPGPPDVPDHAAYHPFR
5.0	2494.256424	0.025592	SPHRESLPGLSSTATPGNPALYSR
2.0	2494.278381	0.003635	MSAPLDAALHALQEEQARLKMR

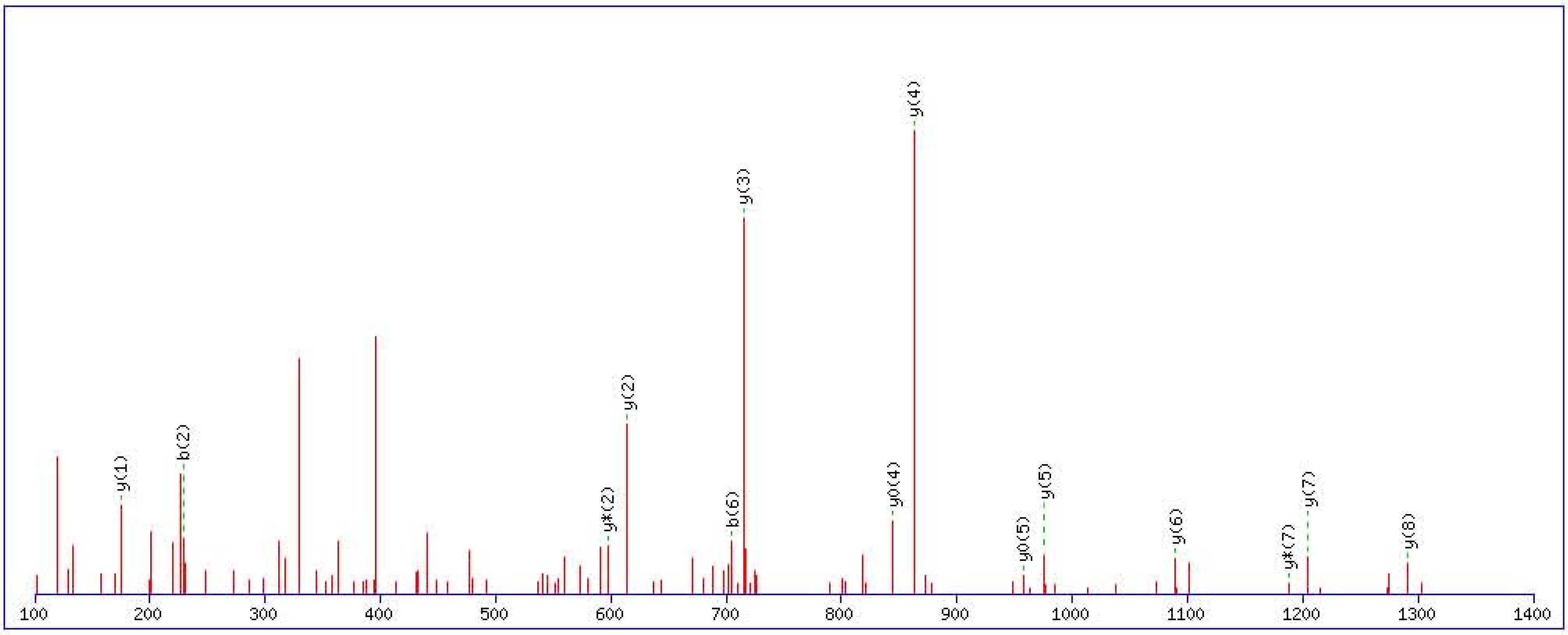
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VECSDNLFTQR**
Found in **MASP1_HUMAN**, Mannan-binding lectin serine protease 1 OS=Homo sapiens GN=MASP1 PE=1 SV=3

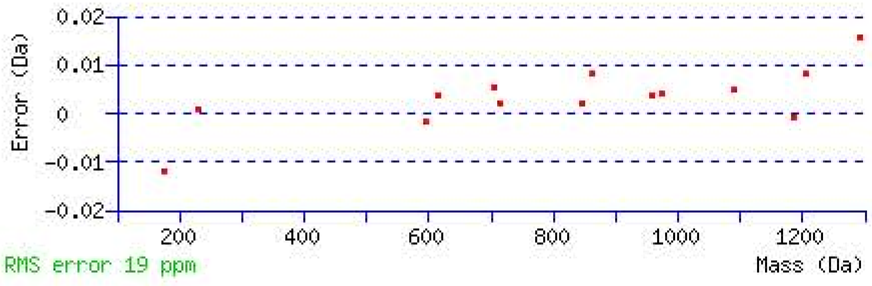
Match to Query 49008: 1678.780272 from(560.600700,3+) rtinseconds(2083) index(63629)
Title: Locus:1.1.1.2723.3 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

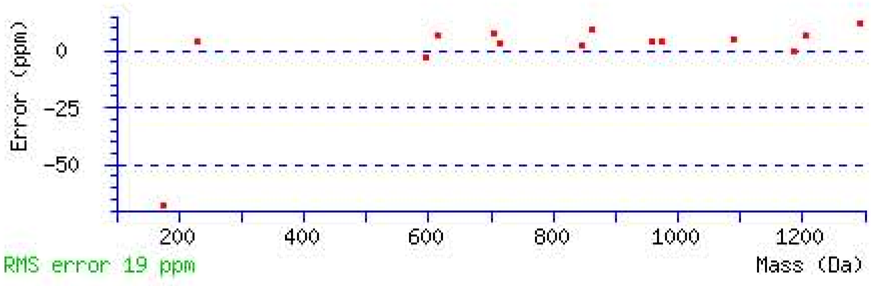
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1678.780716
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 49 **Expect:** 0.00014
Matches : 14/104 fragment ions using 24 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					V							11
2	**229.118283**	115.062780			211.107718	106.057497	E	1580.719575	790.863426	1563.693026	782.350151	1562.709010	781.858143	10
3	389.148932	195.078104			371.138367	186.072822	C	1451.676982	726.342129	1434.650433	717.828855	1433.666417	717.336847	9
4	476.180960	238.594118			458.170395	229.588835	S	***1291.646333***	646.326805	1274.619784	637.813530	1273.635768	637.321522	8
5	591.207903	296.107590			573.197338	287.102307	D	***1204.614305***	602.810791	1187.587756	594.297516	1186.603740	593.805508	7
6	**705.250830**	353.129053	688.224281	344.615778	687.240265	344.123770	N	***1089.587362***	545.297319	1072.560813	536.784045	1071.576797	536.292037	6
7	818.334894	409.671085	801.308345	401.157810	800.324329	400.665802	L	***975.544435***	488.275856	958.517886	479.762581	957.533870	479.270573	5
8	965.403308	483.205292	948.376759	474.692017	947.392743	474.200009	F	***862.460371***	431.733824	845.433822	423.220549	844.449806	422.728541	4
9	1066.450987	533.729131	1049.424438	525.215857	1048.440422	524.723849	T	***715.391957***	358.199617	698.365408	349.686342	697.381392	349.194334	3
10	1505.676313	753.341795	1488.649764	744.828520	1487.665748	744.336512	Q	***614.344278***	307.675777	597.317729	299.162503			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
49.5	1678.780716	-0.000444	VECSDNLFTQR

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

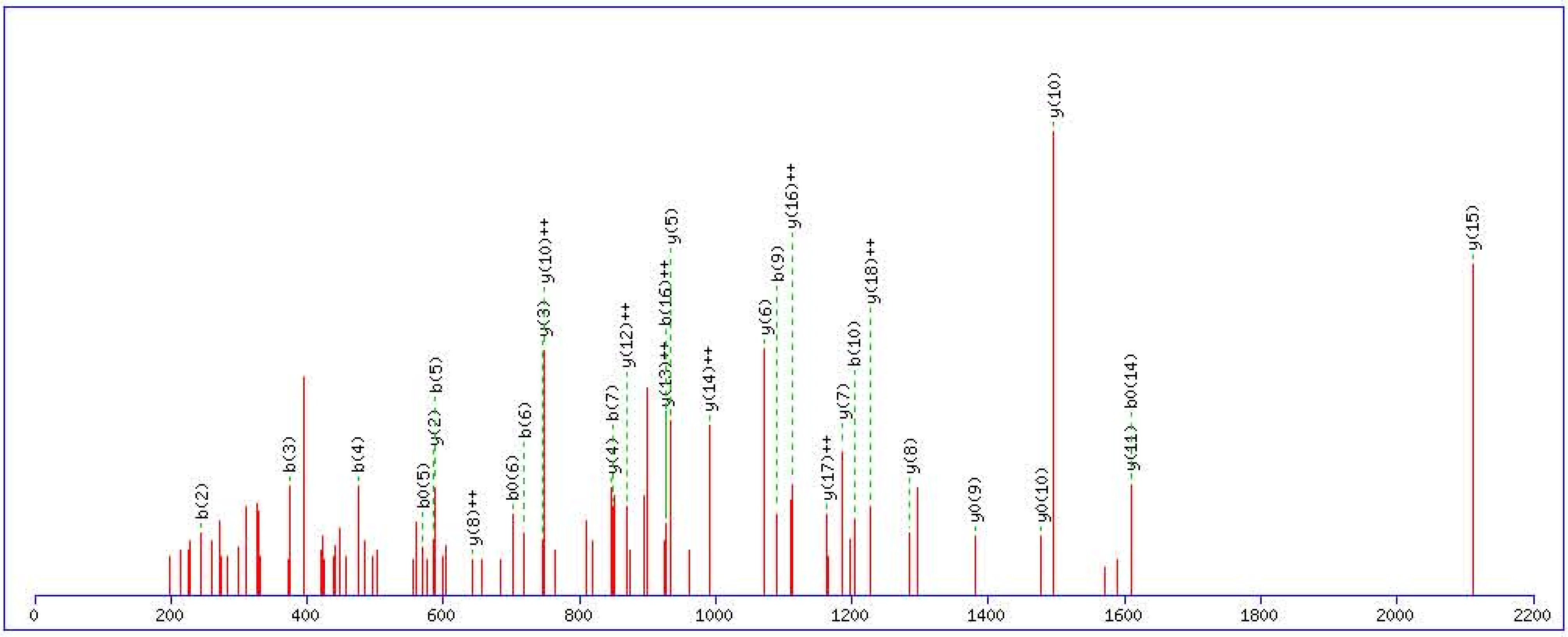
Mascot Search Results

Peptide View

MS/MS Fragmentation of **FPETLMEIEIPIVDHSTCQK**
Found in **MASP1_HUMAN**, Mannan-binding lectin serine protease 1 OS=Homo sapiens GN=MASP1 PE=1 SV=3

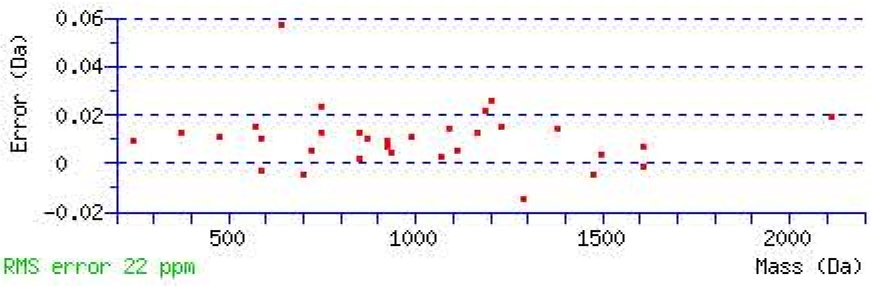
Match to Query 70607: 2697.334572 from(900.118800,3+) rtinseconds(2729) index(67699)
Title: Locus:1.1.1.2946.22 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

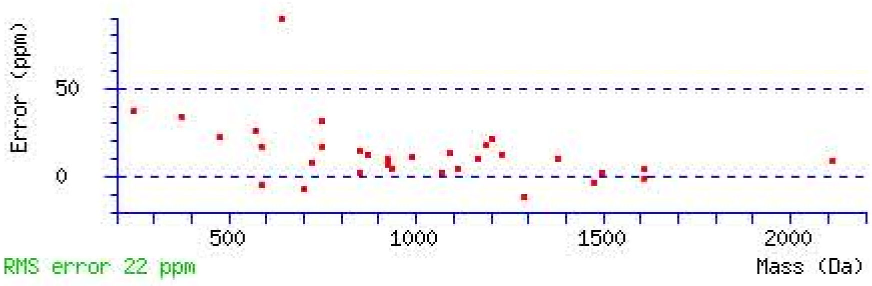
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2697.321609
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q19 : Biotin:Thermo-21345 (Q)
Ions Score: 52 **Expect:** 1.9e-005
Matches : 32/182 fragment ions using 68 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.075690	74.541483					F							20
2	**245.128454**	123.067865					P	2551.260482	1276.133879	2534.233933	1267.620604	2533.249917	1267.128596	19
3	**374.171047**	187.589161			356.160482	178.583879	E	2454.207718	1227.607497	2437.181169	1219.094222	2436.197153	1218.602214	18
4	**475.218726**	238.113001			457.208161	229.107719	T	2325.165125	1163.086200	2308.138576	1154.572926	2307.154560	1154.080918	17
5	**588.302790**	294.655033			570.292225	285.649751	L	2224.117446	1112.562361	2207.090897	1104.049086	2206.106881	1103.557078	16
6	**719.343275**	360.175276			701.332710	351.169993	M	***2111.033382***	1056.020329	2094.006833	1047.507054	2093.022817	1047.015046	15
7	**848.385868**	424.696572			830.375303	415.691290	E	1979.992897	990.500087	1962.966348	981.986812	1961.982332	981.494804	14
8	961.469932	481.238604			943.459367	472.233322	I	1850.950304	925.978790	1833.923755	917.465516	1832.939739	916.973508	13
9	**1090.512525**	545.759901			1072.501960	536.754618	E	1737.866240	869.436758	1720.839691	860.923484	1719.855675	860.431476	12
10	**1203.596589**	602.301933			1185.586024	593.296650	I	***1608.823647***	804.915462	1591.797098	796.402187	1590.813082	795.910179	11
11	1300.649353	650.828315			1282.638788	641.823032	P	***1495.739583***	748.373430	1478.713034	739.860155	1477.729018	739.368147	10
12	1413.733417	707.370346			1395.722852	698.365064	I	1398.686819	699.847048	1381.660270	691.333773	1380.676254	690.841765	9
13	1512.801831	756.904554			1494.791266	747.899271	V	***1285.602755***	643.305016	1268.576206	634.791741	1267.592190	634.299733	8
14	1627.828774	814.418025			1609.818209	805.412743	D	***1186.534341***	593.770809	1169.507792	585.257534	1168.523776	584.765526	7
15	1764.887686	882.947481			1746.877121	873.942199	H	***1071.507398***	536.257337	1054.480849	527.744063	1053.496833	527.252055	6
16	1851.919714	926.463495			1833.909149	917.458213	S	***934.448486***	467.727881	917.421937	459.214607	916.437921	458.722599	5
17	1952.967393	976.987335			1934.956828	967.982052	T	***847.416458***	424.211867	830.389909	415.698593	829.405893	415.206585	4
18	2112.998042	1057.002659			2094.987477	1047.997376	C	***746.368779***	373.688028	729.342230	365.174753			3
19	2552.223368	1276.615322	2535.196819	1268.102047	2534.212803	1267.610039	Q	***586.338130***	293.672703	569.311581	285.159429			2
20							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.0	2697.321609	0.012963	FPETLMEIEIPIVDHSTCQK
1.5	2697.325470	0.009102	KDAATTVCSKFNGFDQQTLQK
1.5	2697.325470	0.009102	KDAATTVCSKFNGFDQQTLQK

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

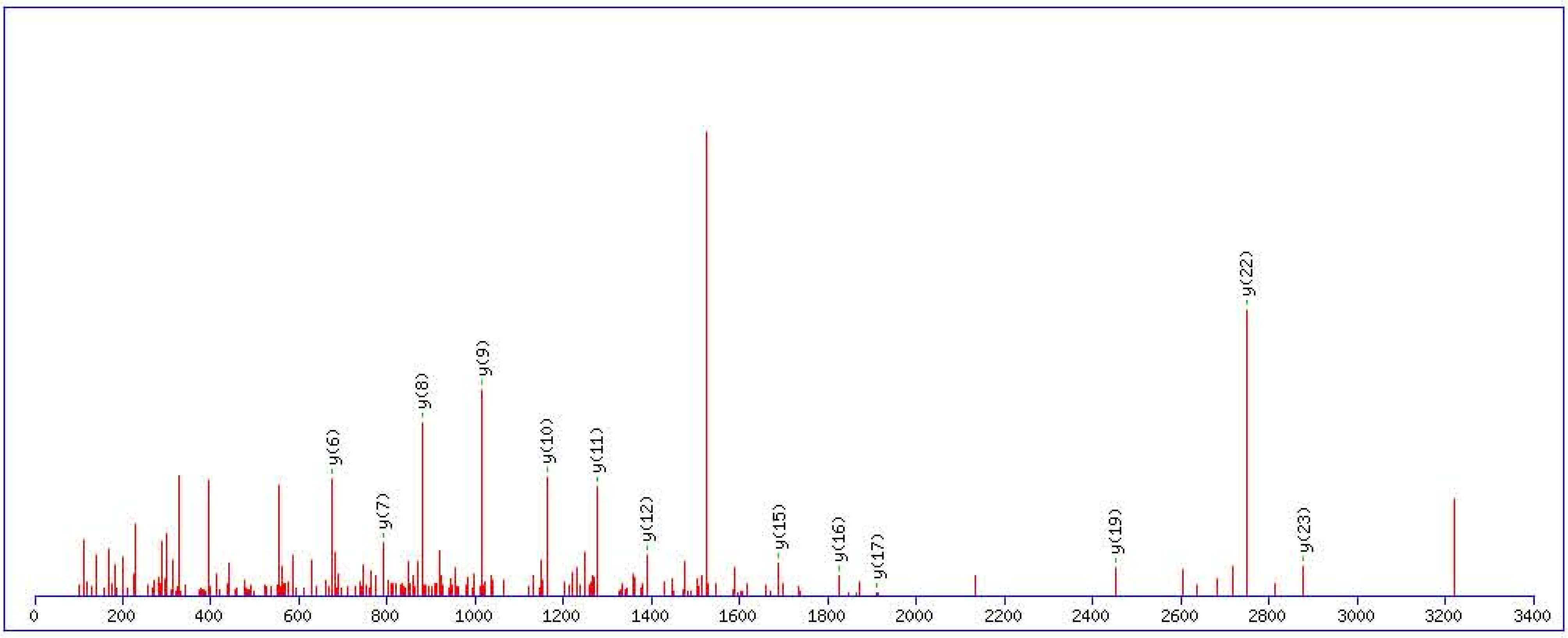
Mascot Search Results

Peptide View

MS/MS Fragmentation of **APEPISTQSHSVLILFHSDNSGENR**
Found in **MASP1_HUMAN**, Mannan-binding lectin serine protease 1 OS=Homo sapiens GN=MASP1 PE=1 SV=3

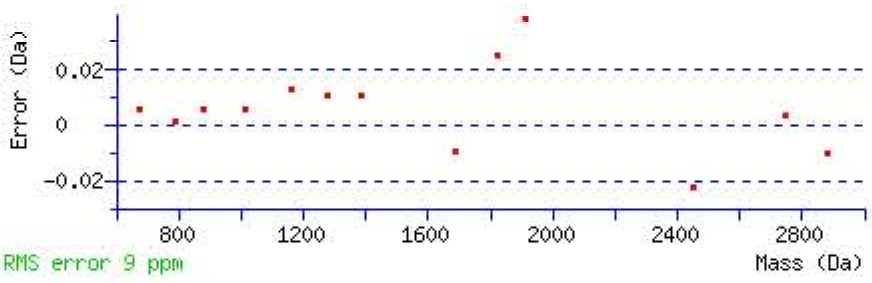
Match to Query 74857: 3045.505936 from(762.383760,4+) rtinseconds(2238) index(64649)
Title: Locus:1.1.1.2776.12 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

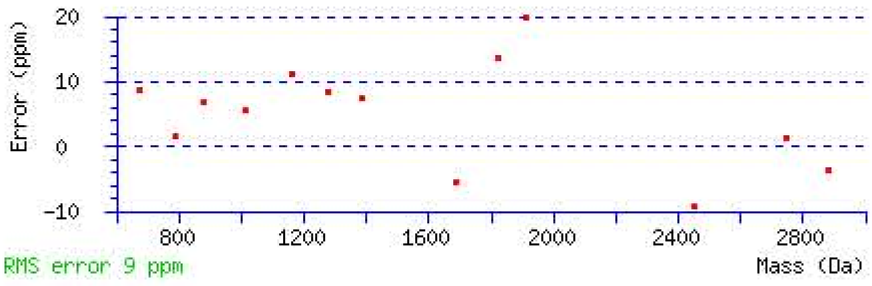
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3045.497803
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 82  Expect: 1.8e-007
Matches : 13/266 fragment ions using 24 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							25
2	169.097154	85.052215					P	2975.467980	1488.237628	2958.441431	1479.724353	2957.457415	1479.232345	24
3	298.139747	149.573512			280.129182	140.568229	E	***2878.415216***	1439.711246	2861.388667	1431.197971	2860.404651	1430.705963	23
4	395.192511	198.099894			377.181946	189.094611	P	***2749.372623***	1375.189949	2732.346074	1366.676675	2731.362058	1366.184667	22
5	508.276575	254.641926			490.266010	245.636643	I	2652.319859	1326.663567	2635.293310	1318.150293	2634.309294	1317.658285	21
6	595.308603	298.157940			577.298038	289.152657	S	2539.235795	1270.121535	2522.209246	1261.608261	2521.225230	1261.116253	20
7	696.356282	348.681779			678.345717	339.676497	T	***2452.203767***	1226.605521	2435.177218	1218.092247	2434.193202	1217.600239	19
8	1135.581608	568.294442	1118.555059	559.781168	1117.571043	559.289160	Q	2351.156088	1176.081682	2334.129539	1167.568407	2333.145523	1167.076399	18
9	1222.613636	611.810456	1205.587087	603.297182	1204.603071	602.805174	S	***1911.930762***	956.469019	1894.904213	947.955745	1893.920197	947.463737	17
10	1359.672548	680.339912	1342.645999	671.826638	1341.661983	671.334630	H	***1824.898734***	912.953005	1807.872185	904.439731	1806.888169	903.947723	16
11	1446.704576	723.855926	1429.678027	715.342652	1428.694011	714.850644	S	***1687.839822***	844.423549	1670.813273	835.910275	1669.829257	835.418267	15
12	1545.772990	773.390133	1528.746441	764.876859	1527.762425	764.384851	V	1600.807794	800.907535	1583.781245	792.394261	1582.797229	791.902253	14
13	1658.857054	829.932165	1641.830505	821.418891	1640.846489	820.926883	L	1501.739380	751.373328	1484.712831	742.860054	1483.728815	742.368045	13
14	1771.941118	886.474197	1754.914569	877.960923	1753.930553	877.468915	I	***1388.655316***	694.831296	1371.628767	686.318022	1370.644751	685.826014	12
15	1885.025182	943.016229	1867.998633	934.502955	1867.014617	934.010947	L	***1275.571252***	638.289264	1258.544703	629.775990	1257.560687	629.283982	11
16	2032.093596	1016.550436	2015.067047	1008.037162	2014.083031	1007.545154	F	***1162.487188***	581.747232	1145.460639	573.233958	1144.476623	572.741950	10
17	2169.152508	1085.079892	2152.125959	1076.566617	2151.141943	1076.074610	H	***1015.418774***	508.213025	998.392225	499.699751	997.408209	499.207743	9
18	2256.184536	1128.595906	2239.157987	1120.082631	2238.173971	1119.590624	S	***878.359862***	439.683569	861.333313	431.170295	860.349297	430.678287	8
19	2371.211479	1186.109377	2354.184930	1177.596103	2353.200914	1177.104095	D	***791.327834***	396.167555	774.301285	387.654280	773.317269	387.162272	7
20	2485.254406	1243.130841	2468.227857	1234.617566	2467.243841	1234.125558	N	***676.300891***	338.654084	659.274342	330.140809	658.290326	329.648801	6
21	2572.286434	1286.646855	2555.259885	1278.133580	2554.275869	1277.641572	S	562.257964	281.632620	545.231415	273.119346	544.247399	272.627338	5
22	2629.307898	1315.157587	2612.281349	1306.644312	2611.297333	1306.152304	G	475.225936	238.116606	458.199387	229.603331	457.215371	229.111323	4
23	2758.350491	1379.678884	2741.323942	1371.165609	2740.339926	1370.673601	E	418.204472	209.605874	401.177923	201.092600	400.193907	200.600592	3
24	2872.393418	1436.700347	2855.366869	1428.187072	2854.382853	1427.695064	N	289.161879	145.084577	272.135330	136.571303			2
25							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
81.8	3045.497803	0.008133	APEPISTQSHSVLILFHSDNSGENR

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

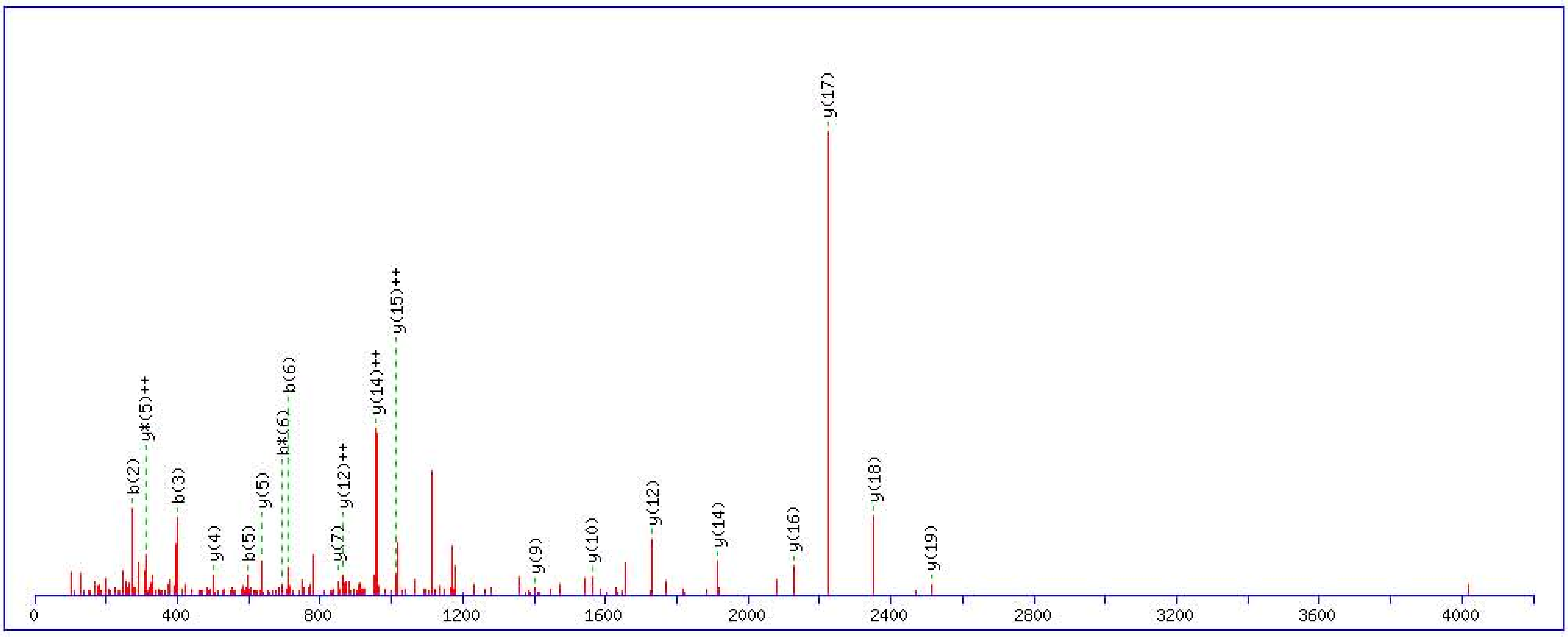
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LCQPVLPSPACQLVLHQILK**
Found in **PMEL_HUMAN**, Melanocyte protein PMEL OS=Homo sapiens GN=PMEL PE=1 SV=2

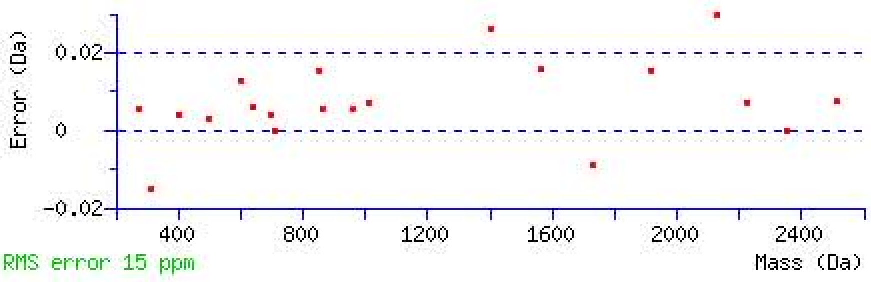
Match to Query 69958: 2624.453952 from(875.825260,3+) rtinseconds(2632) index(66928)
Title: Locus:1.1.1.2913.10 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

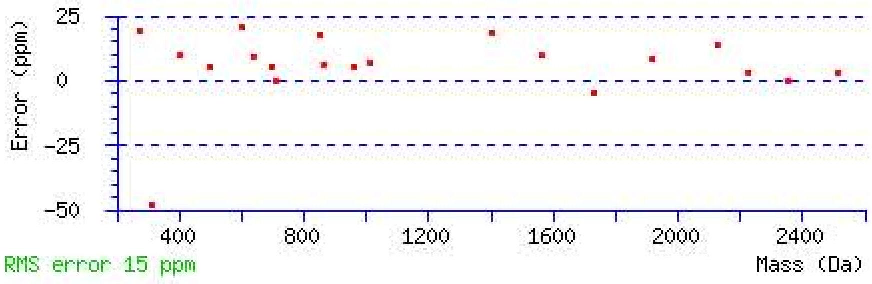
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 4200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2624.436859
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 7.6e-005
Matches : 20/186 fragment ions using 44 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							20
2	**274.121989**	137.564632					C	***2512.360078***	1256.683677	2495.333529	1248.170402	2494.349513	1247.678394	19
3	**402.180567**	201.593921	385.154018	193.080647			Q	***2352.329429***	1176.668352	2335.302880	1168.155078	2334.318864	1167.663070	18
4	499.233331	250.120303	482.206782	241.607029			P	***2224.270851***	1112.639063	2207.244302	1104.125789	2206.260286	1103.633781	17
5	**598.301745**	299.654511	581.275196	291.141236			V	***2127.218087***	1064.112681	2110.191538	1055.599407	2109.207522	1055.107399	16
6	**711.385809**	356.196543	694.359260	347.683268			L	2028.149673	1014.578475	2011.123124	1006.065200	2010.139108	1005.573192	15
7	808.438573	404.722925	791.412024	396.209650			P	***1915.065609***	958.036443	1898.039060	949.523168	1897.055044	949.031160	14
8	895.470601	448.238939	878.444052	439.725664	877.460036	439.233656	S	1818.012845	909.510061	1800.986296	900.996786	1800.002280	900.504778	13
9	992.523365	496.765321	975.496816	488.252046	974.512800	487.760038	P	***1730.980817***	865.994047	1713.954268	857.480772			12
10	1063.560479	532.283878	1046.533930	523.770603	1045.549914	523.278595	A	1633.928053	817.467665	1616.901504	808.954390			11
11	1223.591128	612.299202	1206.564579	603.785928	1205.580563	603.293920	C	***1562.890939***	781.949108	1545.864390	773.435833			10
12	1662.816454	831.911865	1645.789905	823.398591	1644.805889	822.906583	Q	***1402.860290***	701.933783	1385.833741	693.420509			9
13	1775.900518	888.453897	1758.873969	879.940623	1757.889953	879.448614	L	963.634964	482.321120	946.608415	473.807846			8
14	1874.968932	937.988104	1857.942383	929.474830	1856.958367	928.982822	V	***850.550900***	425.779088	833.524351	417.265814			7
15	1988.052996	994.530136	1971.026447	986.016862	1970.042431	985.524853	L	751.482486	376.244881	734.455937	367.731607			6
16	2125.111908	1063.059592	2108.085359	1054.546317	2107.101343	1054.054309	H	***638.398422***	319.702849	621.371873	311.189575			5
17	2253.170486	1127.088881	2236.143937	1118.575606	2235.159921	1118.083598	Q	***501.339510***	251.173393	484.312961	242.660119			4
18	2366.254550	1183.630913	2349.228001	1175.117638	2348.243985	1174.625630	I	373.280932	187.144104	356.254383	178.630830			3
19	2479.338614	1240.172945	2462.312065	1231.659670	2461.328049	1231.167663	L	260.196868	130.602072	243.170319	122.088798			2
20							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.2	2624.436859	0.017093	LCQPVLPSPACQLVLHQILK
23.7	2624.436859	0.017093	LCQPVLPSPACQLVLHQILK

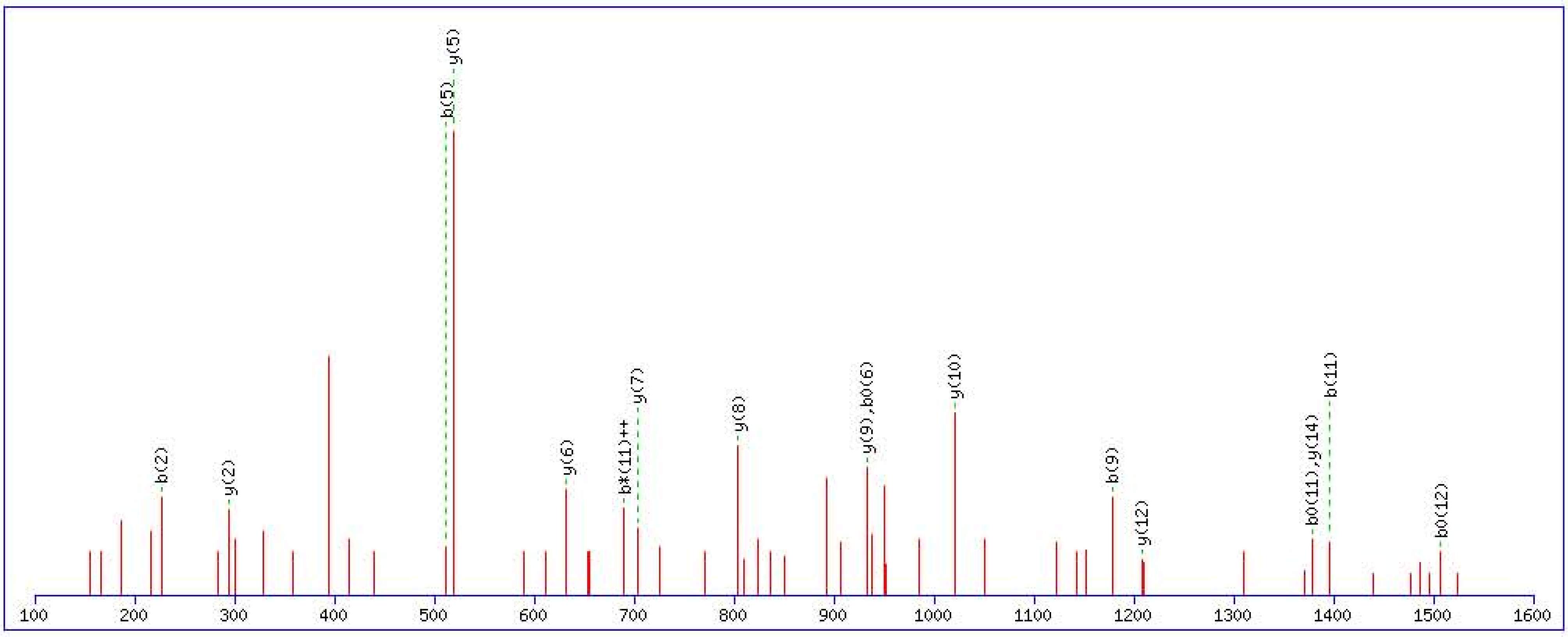
{MATRIX} {SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **IIGLDQVAGMSETALPGAFK**
Found in **MYH9_HUMAN**, Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4

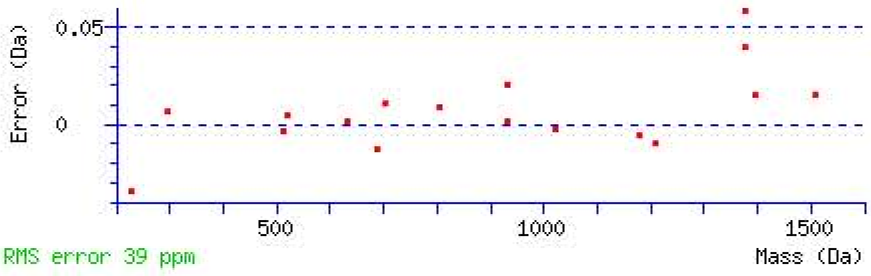
Match to Query 64715: 2328.213552 from(777.078460,3+) rtinseconds(2823) index(68457)
Title: Locus:1.1.1.2978.12 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●

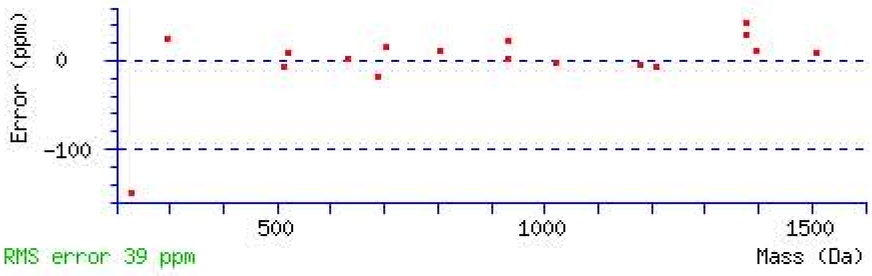


```
Monoisotopic mass of neutral peptide Mr(calc): 2328.222153
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 0.00022
Matches : 17/196 fragment ions using 27 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	114.091340	57.549308					I							20
2	**227.175404**	114.091340					I	2216.145376	1108.576326	2199.118827	1100.063051	2198.134811	1099.571043	19
3	284.196868	142.602072					G	2103.061312	1052.034294	2086.034763	1043.521019	2085.050747	1043.029011	18
4	397.280932	199.144104					L	2046.039848	1023.523562	2029.013299	1015.010288	2028.029283	1014.518279	17
5	**512.307875**	256.657576			494.297310	247.652293	D	1932.955784	966.981530	1915.929235	958.468255	1914.945219	957.976247	16
6	951.533201	476.270239	934.506652	467.756964	933.522636	467.264956	Q	1817.928841	909.468058	1800.902292	900.954784	1799.918276	900.462776	15
7	1050.601615	525.804446	1033.575066	517.291171	1032.591050	516.799163	V	***1378.703515***	689.855395	1361.676966	681.342121	1360.692950	680.850113	14
8	1121.638729	561.323003	1104.612180	552.809728	1103.628164	552.317720	A	1279.635101	640.321188	1262.608552	631.807914	1261.624536	631.315906	13
9	**1178.660193**	589.833734	1161.633644	581.320460	1160.649628	580.828452	G	***1208.597987***	604.802631	1191.571438	596.289357	1190.587422	595.797349	12
10	1309.700678	655.353977	1292.674129	646.840703	1291.690113	646.348694	M	1151.576523	576.291900	1134.549974	567.778625	1133.565958	567.286617	11
11	**1396.732706**	698.869991	1379.706157	690.356717	1378.722141	689.864709	S	***1020.536038***	510.771657	1003.509489	502.258382	1002.525473	501.766374	10
12	1525.775299	763.391288	1508.748750	754.878013	1507.764734	754.386005	E	***933.504010***	467.255643	916.477461	458.742368	915.493445	458.250360	9
13	1626.822978	813.915127	1609.796429	805.401853	1608.812413	804.909845	T	***804.461417***	402.734346	787.434868	394.221072	786.450852	393.729064	8
14	1697.860092	849.433684	1680.833543	840.920410	1679.849527	840.428402	A	***703.413738***	352.210507	686.387189	343.697232			7
15	1810.944156	905.975716	1793.917607	897.462442	1792.933591	896.970434	L	***632.376624***	316.691950	615.350075	308.178675			6
16	1907.996920	954.502098	1890.970371	945.988824	1889.986355	945.496816	P	***519.292560***	260.149918	502.266011	251.636643			5
17	1965.018384	983.012830	1947.991835	974.499556	1947.007819	974.007547	G	422.239796	211.623536	405.213247	203.110261			4
18	2036.055498	1018.531387	2019.028949	1010.018113	2018.044933	1009.526105	A	365.218332	183.112804	348.191783	174.599529			3
19	2183.123912	1092.065594	2166.097363	1083.552319	2165.113347	1083.060311	F	***294.181218***	147.594247	277.154669	139.080972			2
20							K	147.112804	74.060040	130.086255	65.546765			1



RMS error 39 ppm



RMS error 39 ppm

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.0	2328.222153	-0.008601	IIGLDQVAGMSETALPGAFK

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

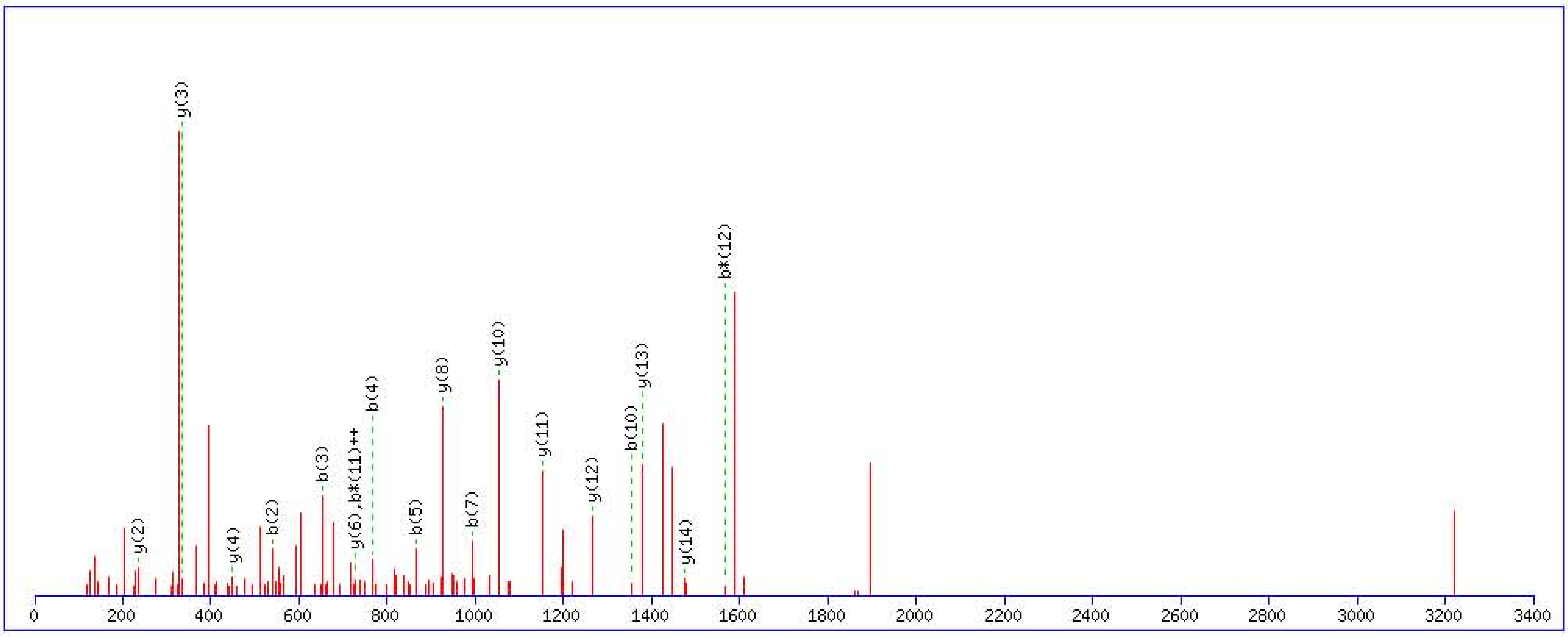
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QVLLVGAPTYDDVSK**
Found in **PHLD_HUMAN**, Phosphatidylinositol-glycan-specific phospholipase D OS=Homo sapiens GN=GPLD1 PE=1 SV=3

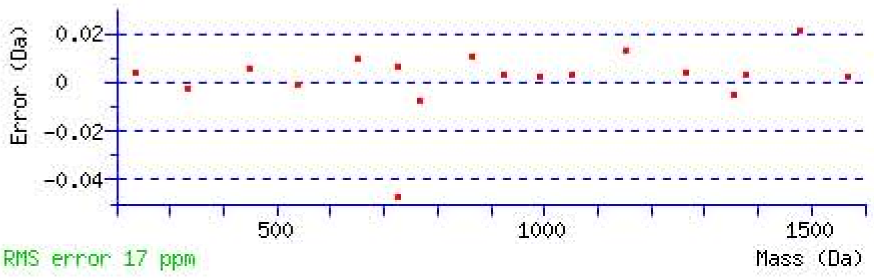
Match to Query 54694: 1915.029308 from(958.521930,2+) rtinseconds(2294) index(64997)
Title: Locus:1.1.1.2796.11 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

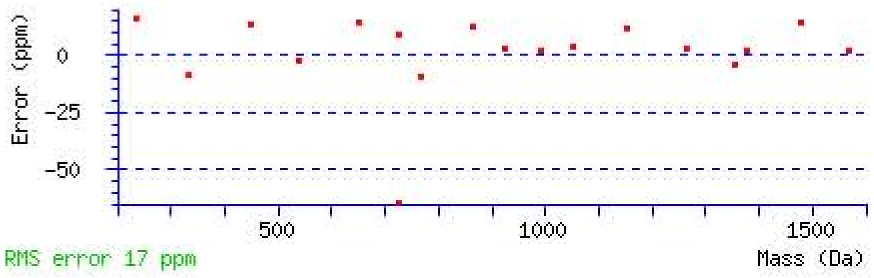
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1915.012497
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 34  Expect: 0.0029
Matches : 18/150 fragment ions using 59 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	440.232602	220.619939	423.206053	212.106664			Q							15
2	**539.301016**	270.154146	522.274467	261.640872			V	***1476.794438***	738.900857	1459.767889	730.387583	1458.783873	729.895575	14
3	**652.385080**	326.696178	635.358531	318.182904			L	***1377.726024***	689.366650	1360.699475	680.853376	1359.715459	680.361368	13
4	**765.469144**	383.238210	748.442595	374.724936			L	***1264.641960***	632.824618	1247.615411	624.311344	1246.631395	623.819336	12
5	**864.537558**	432.772417	847.511009	424.259143			V	***1151.557896***	576.282586	1134.531347	567.769312	1133.547331	567.277304	11
6	921.559022	461.283149	904.532473	452.769875			G	***1052.489482***	526.748379	1035.462933	518.235105	1034.478917	517.743097	10
7	**992.596136**	496.801706	975.569587	488.288432			A	995.468018	498.237647	978.441469	489.724373	977.457453	489.232365	9
8	1089.648900	545.328088	1072.622351	536.814814			P	***924.430904***	462.719090	907.404355	454.205816	906.420339	453.713808	8
9	1190.696579	595.851927	1173.670030	587.338653	1172.686014	586.846645	T	827.378140	414.192708	810.351591	405.679434	809.367575	405.187426	7
10	**1353.759908**	677.383592	1336.733359	668.870318	1335.749343	668.378310	Y	***726.330461***	363.668869	709.303912	355.155594	708.319896	354.663586	6
11	1468.786851	734.897064	1451.760302	726.383789	1450.776286	725.891781	D	563.267132	282.137204	546.240583	273.623930	545.256567	273.131922	5
12	1583.813794	792.410535	1566.787245	783.897261	1565.803229	783.405253	D	***448.240189***	224.623733	431.213640	216.110458	430.229624	215.618450	4
13	1682.882208	841.944742	1665.855659	833.431468	1664.871643	832.939460	V	***333.213246***	167.110261	316.186697	158.596987	315.202681	158.104979	3
14	1769.914236	885.460756	1752.887687	876.947482	1751.903671	876.455474	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
15							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
34.3	1915.012497	0.016811	QVLLVGAPTYDDVSK
7.0	1915.027710	0.001598	DYPIYLLKFKQCLSK
2.9	1915.008438	0.020870	VIQKNQEETTSISK

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

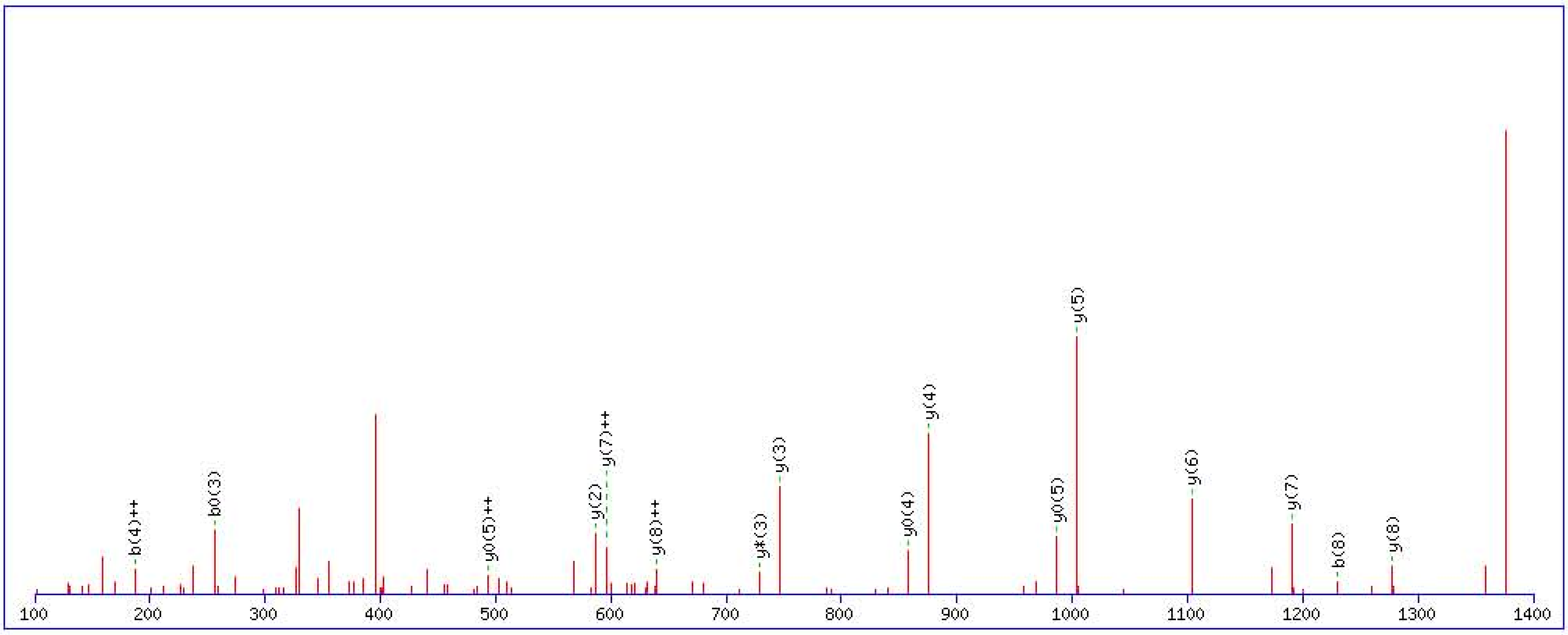
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VSSVEECQK**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

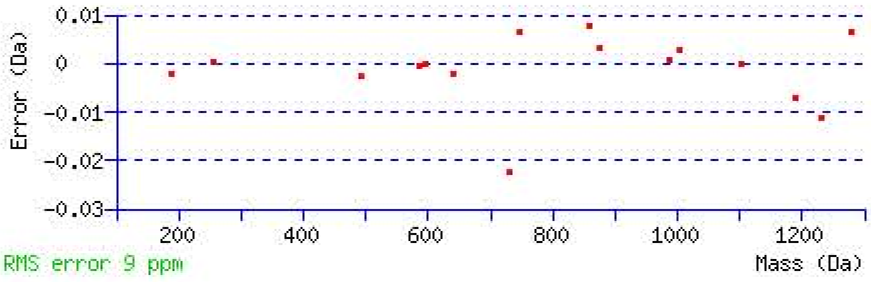
Match to Query 38014: 1375.644448 from(688.829500,2+) rtinseconds(1408) index(76160)
Title: Locus:1.1.1.2369.26 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

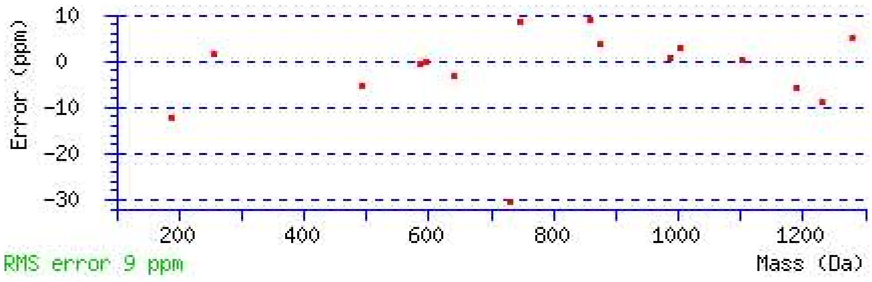
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1375.647568
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 51 **Expect:** 8e-005
Matches : 17/74 fragment ions using 25 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							9
2	**187.107718**	94.057497			169.097153	85.052214	S	***1277.586435***	639.296856	1260.559886	630.783581	1259.575870	630.291573	8
3	274.139746	137.573511			256.129181	128.568229	S	***1190.554407***	595.780842	1173.527858	587.267567	1172.543842	586.775559	7
4	373.208160	187.107718			355.197595	178.102436	V	***1103.522379***	552.264828	1086.495830	543.751553	1085.511814	543.259545	6
5	502.250753	251.629015			484.240188	242.623732	E	***1004.453965***	502.730621	987.427416	494.217346	986.443400	493.725338	5
6	631.293346	316.150311			613.282781	307.145029	E	***875.411372***	438.209324	858.384823	429.696050	857.400807	429.204042	4
7	791.323995	396.165636			773.313430	387.160353	C	***746.368779***	373.688028	729.342230	365.174753			3
8	**1230.549321**	615.778299	1213.522772	607.265024	1212.538756	606.773016	Q	***586.338130***	293.672703	569.311581	285.159429			2
9							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.3	1375.647568	-0.003120	VSSVEECQK
7.2	1375.662827	-0.018379	GFSIPECQK
0.5	1375.644196	0.000252	DFQESSPQK

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

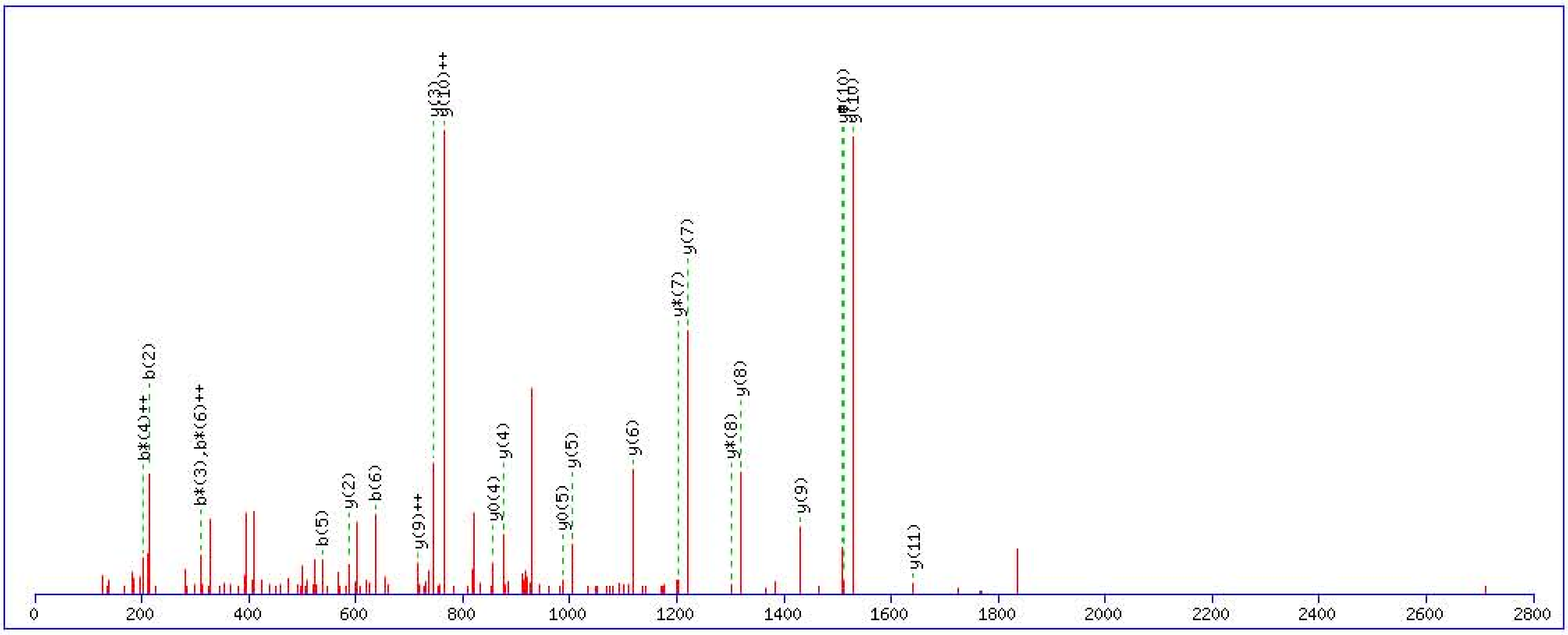
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VNIPLVTNEECQK**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

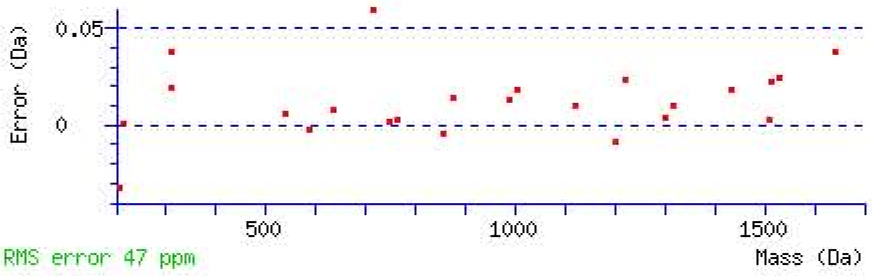
Match to Query 53502: 1853.956008 from(927.985280,2+) rtinseconds(2163) index(81348)
Title: Locus:1.1.1.2632.21 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

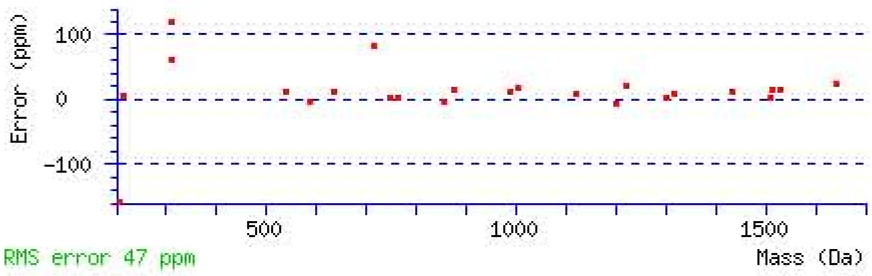
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1853.937927
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12 : Biotin:Thermo-21345 (Q)
Ions Score: 56 **Expect:** 7.2e-005
Matches : 24/124 fragment ions using 47 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	100.075690	50.541483					V							13
2	**214.118617**	107.562947	197.092068	99.049672			N	1755.876804	878.442040	1738.850255	869.928766	1737.866239	869.436758	12
3	327.202681	164.104978	310.176132	155.591704			I	***1641.833877***	821.420577	1624.807328	812.907302	1623.823312	812.415294	11
4	424.255445	212.631360	407.228896	204.118086			P	***1528.749813***	764.878545	1511.723264	756.365270	1510.739248	755.873262	10
5	**537.339509**	269.173393	520.312960	260.660118			L	***1431.697049***	716.352163	1414.670500	707.838888	1413.686484	707.346880	9
6	**636.407923**	318.707600	619.381374	310.194325			V	***1318.612985***	659.810131	1301.586436	651.296856	1300.602420	650.804848	8
7	737.455602	369.231439	720.429053	360.718165	719.445037	360.226157	T	***1219.544571***	610.275924	1202.518022	601.762649	1201.534006	601.270641	7
8	851.498529	426.252903	834.471980	417.739628	833.487964	417.247620	N	***1118.496892***	559.752084	1101.470343	551.238810	1100.486327	550.746802	6
9	980.541122	490.774199	963.514573	482.260924	962.530557	481.768916	E	***1004.453965***	502.730621	987.427416	494.217346	986.443400	493.725338	5
10	1109.583715	555.295496	1092.557166	546.782221	1091.573150	546.290213	E	***875.411372***	438.209324	858.384823	429.696050	857.400807	429.204042	4
11	1269.614364	635.310820	1252.587815	626.797546	1251.603799	626.305538	C	***746.368779***	373.688028	729.342230	365.174753			3
12	1708.839690	854.923483	1691.813141	846.410209	1690.829125	845.918201	Q	***586.338130***	293.672703	569.311581	285.159429			2
13							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of VNIPLVTNEECQK
(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	1853.937927	0.018081	VNIPLVTNEECQK

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

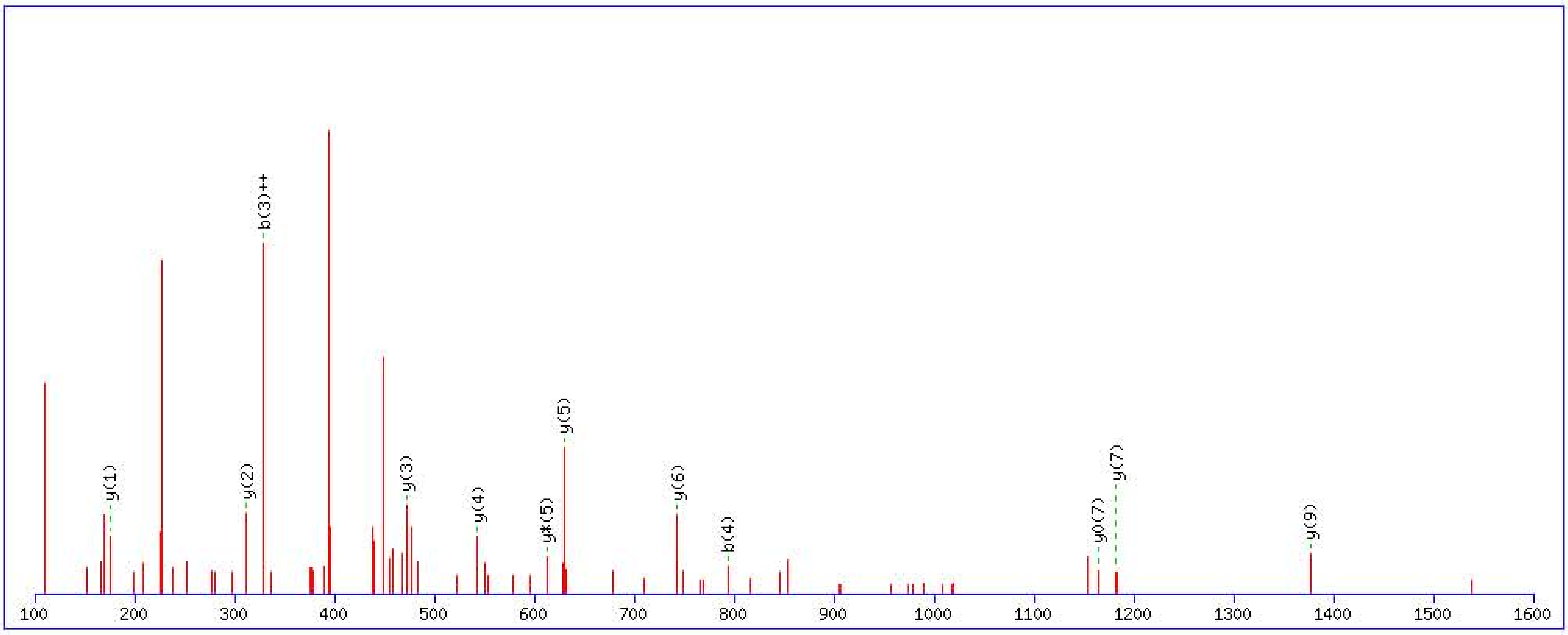
Mascot Search Results

Peptide View

MS/MS Fragmentation of **QCGHQISACHR**
Found in **KLKB1_HUMAN**, Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1

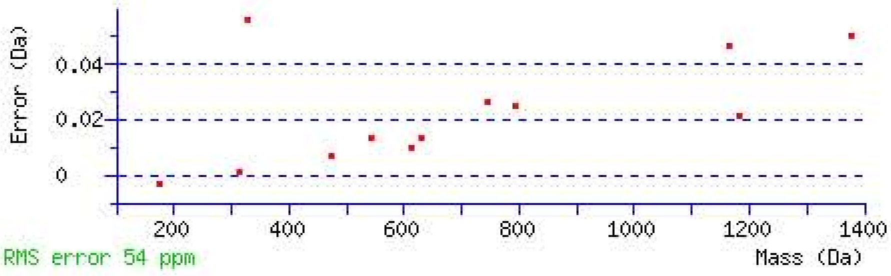
Match to Query 56078: 1974.940296 from(494.742350,4+) rtinseconds(1438) index(39952)
Title: Locus:1.1.1.2529.18 File:"2013-07-02 CLN FXIII 30 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

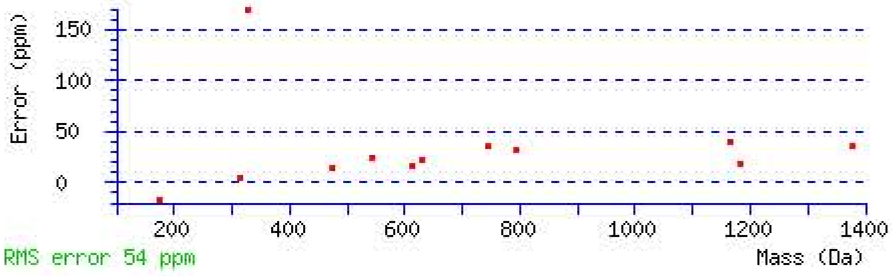
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1974.916122
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.051
Matches : 12/100 fragment ions using 34 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	440.232602	220.619939	423.206053	212.106664			Q							11
2	600.263251	300.635264	583.236702	292.121989			C	1536.698070	768.852673	1519.671521	760.339399	1518.687505	759.847391	10
3	657.284715	329.145996	640.258166	320.632721			G	***1376.667421***	688.837349	1359.640872	680.324074	1358.656856	679.832066	9
4	794.343627	397.675452	777.317078	389.162177			H	1319.645957	660.326617	1302.619408	651.813342	1301.635392	651.321334	8
5	1233.568953	617.288115	1216.542404	608.774840			Q	***1182.587045***	591.797161	1165.560496	583.283886	1164.576480	582.791878	7
6	1346.653017	673.830147	1329.626468	665.316872			I	***743.361719***	372.184498	726.335170	363.671223	725.351154	363.179215	6
7	1433.685045	717.346161	1416.658496	708.832886	1415.674480	708.340878	S	***630.277655***	315.642466	613.251106	307.129191	612.267090	306.637183	5
8	1504.722159	752.864718	1487.695610	744.351443	1486.711594	743.859435	A	***543.245627***	272.126452	526.219078	263.613177			4
9	1664.752808	832.880042	1647.726259	824.366768	1646.742243	823.874760	C	***472.208513***	236.607894	455.181964	228.094620			3
10	1801.811720	901.409498	1784.785171	892.896224	1783.801155	892.404216	H	***312.177864***	156.592570	295.151315	148.079295			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
25.5	1974.916122	0.024174	QCGHQISACHR

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

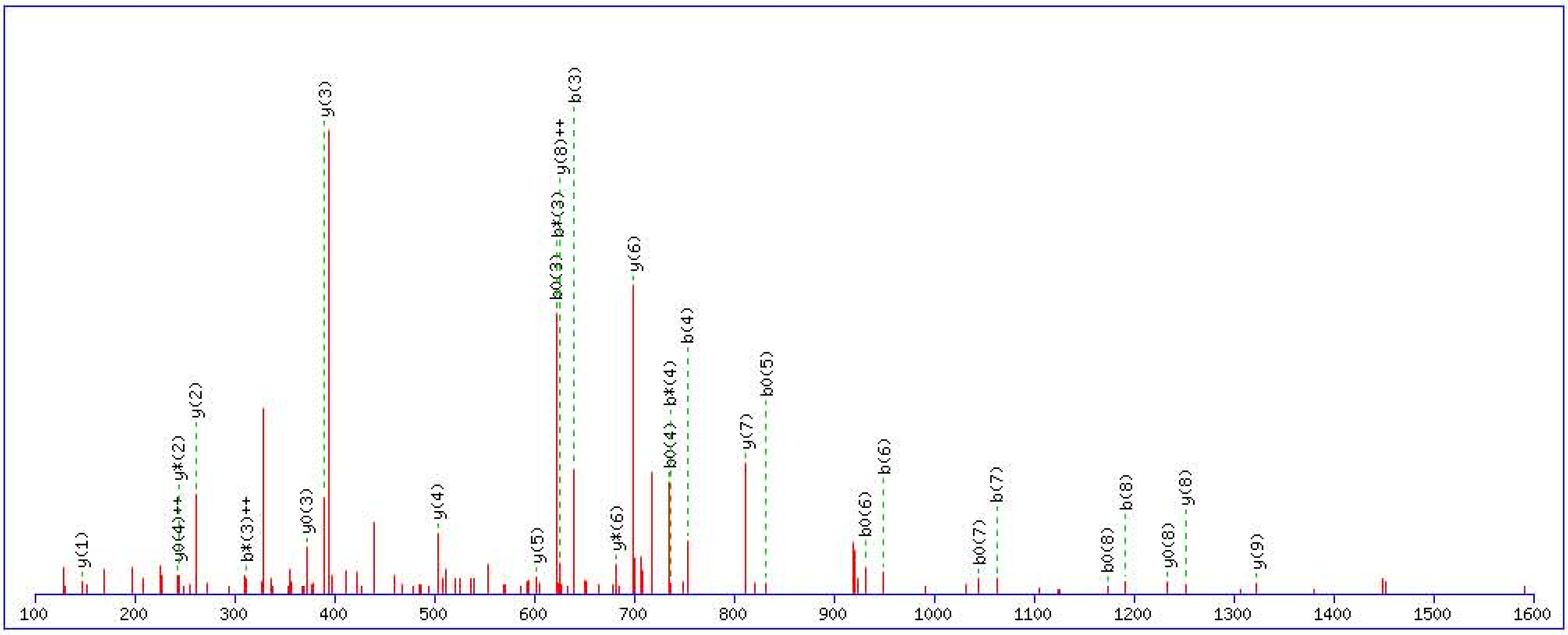
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EAQLPVIENK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

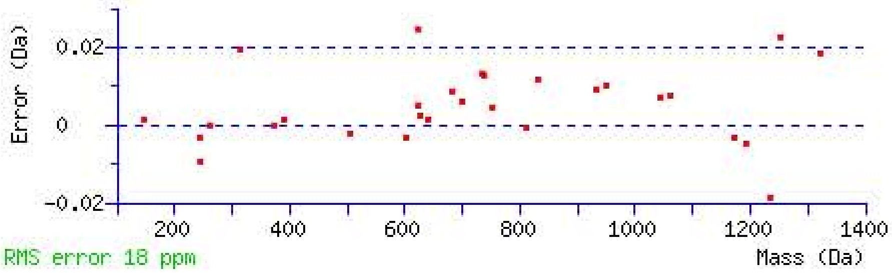
Match to Query 41157: 1450.787968 from(726.401260,2+) rtinseconds(2034) index(80498)
Title: Locus:1.1.1.2587.16 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

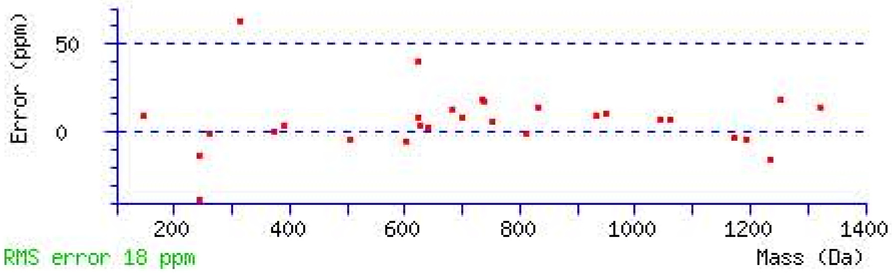
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1450.785355
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 40  Expect: 0.00039
Matches : 29/100 fragment ions using 70 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							10
2	201.086983	101.047130			183.076418	92.041847	A	*1322.750070*	661.878673	1305.723521	653.365398	1304.739505	652.873390	9
3	**640.312309**	320.659793	623.285760	312.146518	622.301744	311.654510	Q	*1251.712956*	626.360116	1234.686407	617.846841	1233.702391	617.354833	8
4	**753.396373**	377.201825	736.369824	368.688550	735.385808	368.196542	L	*812.487630*	406.747453	795.461081	398.234178	794.477065	397.742170	7
5	850.449137	425.728207	833.422588	417.214932	832.438572	416.722924	P	*699.403566*	350.205421	682.377017	341.692146	681.393001	341.200138	6
6	**949.517551**	475.262414	932.491002	466.749139	931.506986	466.257131	V	*602.350802*	301.679039	585.324253	293.165764	584.340237	292.673756	5
7	**1062.601615**	531.804446	1045.575066	523.291171	1044.591050	522.799163	I	*503.282388*	252.144832	486.255839	243.631557	485.271823	243.139549	4
8	**1191.644208**	596.325742	1174.617659	587.812468	1173.633643	587.320459	E	*390.198324*	195.602800	373.171775	187.089525	372.187759	186.597517	3
9	1305.687135	653.347205	1288.660586	644.833931	1287.676570	644.341923	N	*261.155731*	131.081503	244.129182	122.568229			2
10							K	*147.112804*	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.4	1450.785355	0.002613	EAQLPVIENK
3.9	1450.804459	-0.016491	AFLEVNRPQIHK
1.2	1450.777985	0.009983	AGTPSPIQLQSPAGK
0.3	1450.779312	0.008656	AFNQTSHLIRHK

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

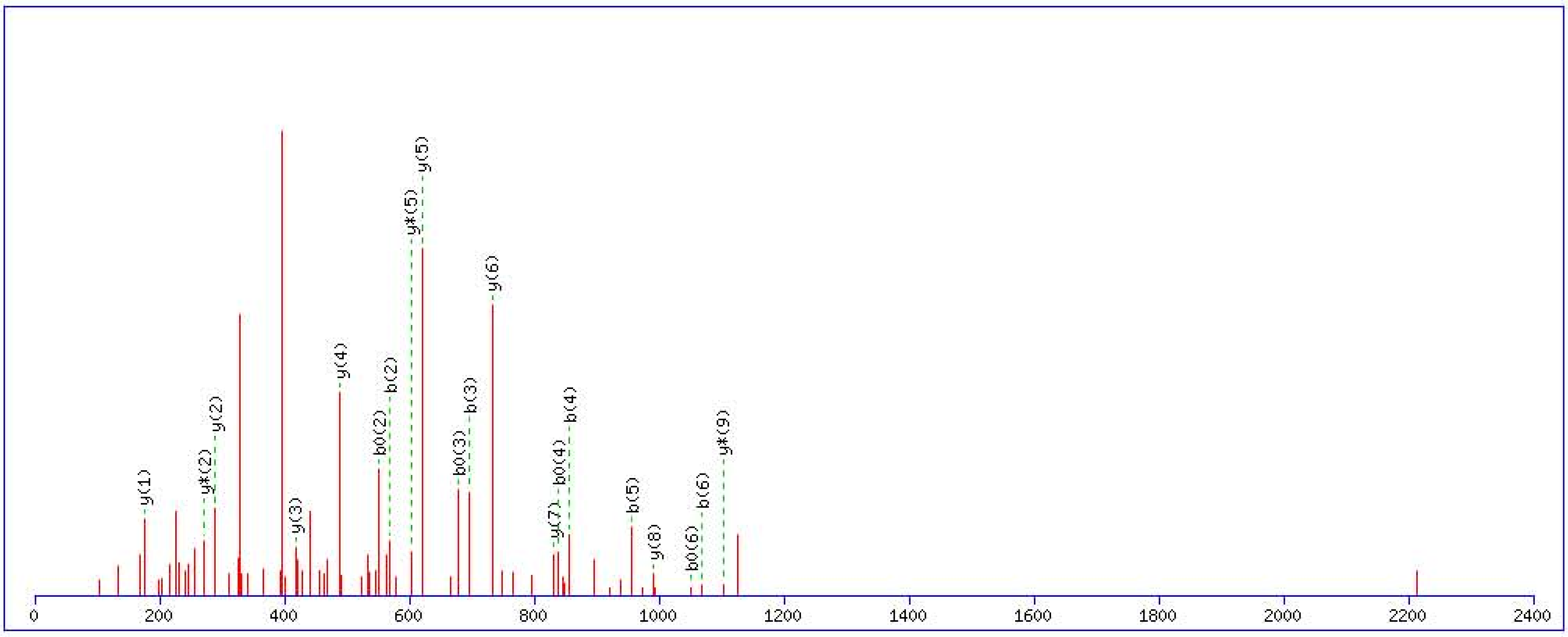
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQQCVIMAENR**
Found in **PLGB_HUMAN**, Plasminogen-like protein B OS=Homo sapiens GN=PLGLB1 PE=1 SV=1

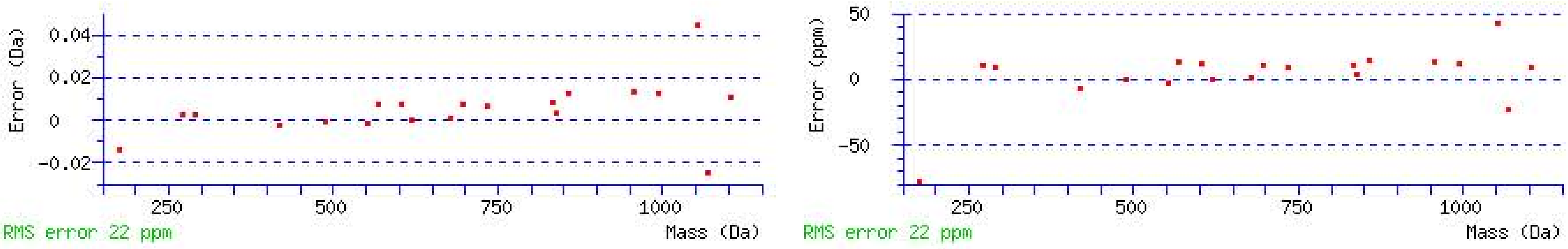
Match to Query 49259: 1687.780752 from(563.600860,3+) rtinseconds(1834) index(79144)
Title: Locus:1.1.1.2518.14 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1687.784393
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 51 **Expect:** 5.2e-005
Matches : 20/114 fragment ions using 31 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.049869	65.528572			112.039304	56.523290	E							11
2	**569.275195**	285.141236	552.248646	276.627961	551.264630	276.135953	Q	1559.749102	780.378189	1542.722553	771.864915	1541.738537	771.372907	10
3	**697.333773**	349.170525	680.307224	340.657250	679.323208	340.165242	Q	1120.523776	560.765526	1103.497227	552.252252	1102.513211	551.760244	9
4	**857.364422**	429.185849	840.337873	420.672575	839.353857	420.180567	C	***992.465198***	496.736237	975.438649	488.222963	974.454633	487.730955	8
5	**956.432836**	478.720056	939.406287	470.206782	938.422271	469.714774	V	***832.434549***	416.720913	815.408000	408.207638	814.423984	407.715630	7
6	**1069.516900**	535.262088	1052.490351	526.748814	1051.506335	526.256806	I	***733.366135***	367.186706	716.339586	358.673431	715.355570	358.181423	6
7	1200.557385	600.782331	1183.530836	592.269056	1182.546820	591.777048	M	***620.282071***	310.644674	603.255522	302.131399	602.271506	301.639391	5
8	1271.594499	636.300888	1254.567950	627.787613	1253.583934	627.295605	A	***489.241586***	245.124431	472.215037	236.611156	471.231021	236.119148	4
9	1400.637092	700.822184	1383.610543	692.308910	1382.626527	691.816902	E	***418.204472***	209.605874	401.177923	201.092600	400.193907	200.600592	3
10	1514.680019	757.843648	1497.653470	749.330373	1496.669454	748.838365	N	***289.161879***	145.084577	272.135330	136.571303			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
50.7	1687.784393	-0.003641	EQQCVIMAENR
44.8	1687.784393	-0.003641	EQQCVIMAENR
4.8	1687.758408	0.022344	ADGSCSTDFKTTRSR
3.7	1687.773666	0.007086	TTGPPSGQMPDNPPHR
1.8	1687.787552	-0.006800	SDAYVCPLYKTSER
0.6	1687.787552	-0.006800	GASEDGEYFLMIRGK

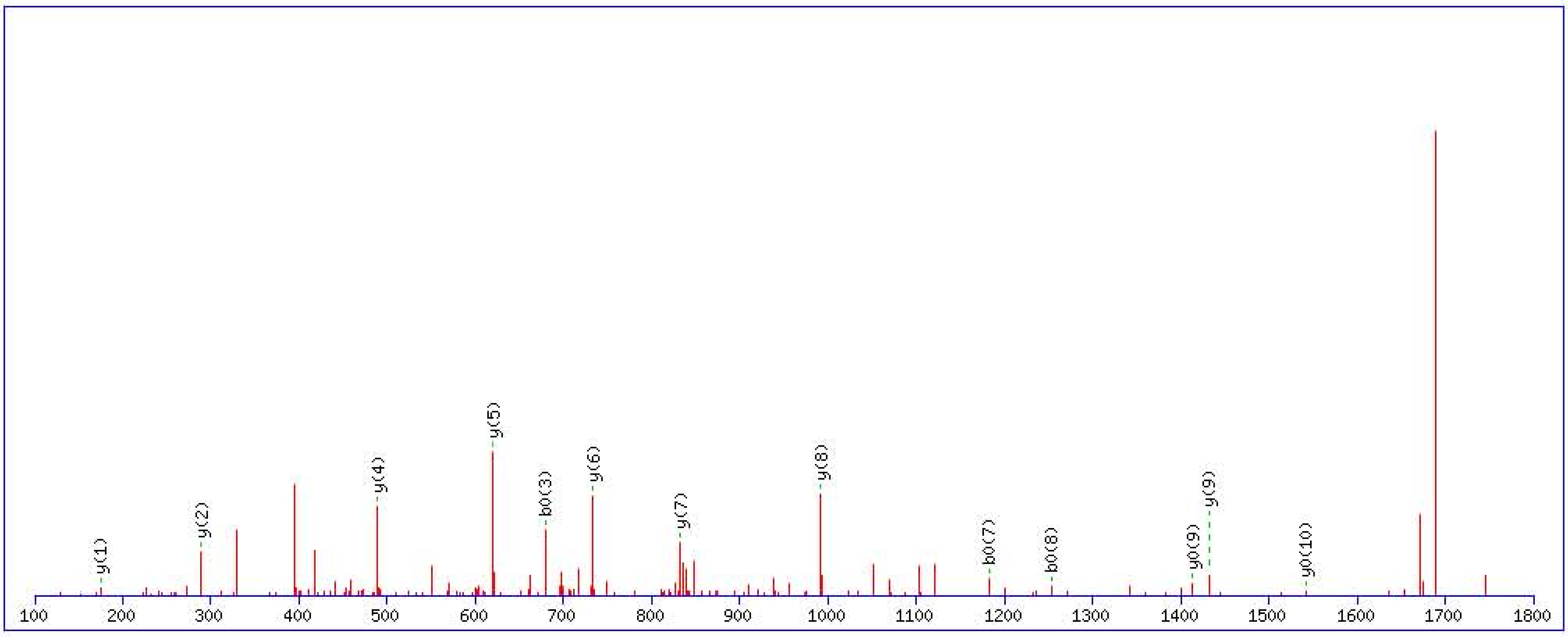
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQQCVIMAENR**
Found in **PLGB_HUMAN**, Plasminogen-like protein B OS=Homo sapiens GN=PLGLB1 PE=1 SV=1

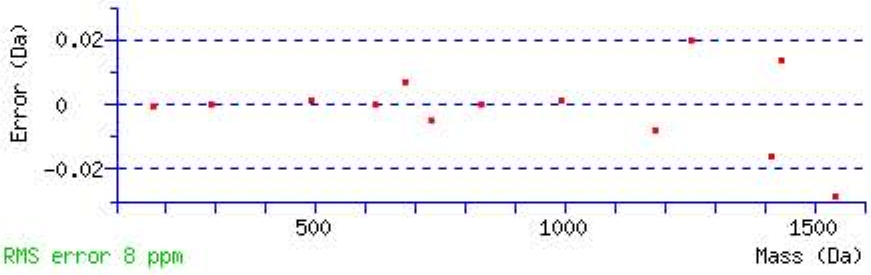
Match to Query 49260: 1687.788968 from(844.901760,2+) rtinseconds(1827) index(79090)
Title: Locus:1.1.1.2515.26 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

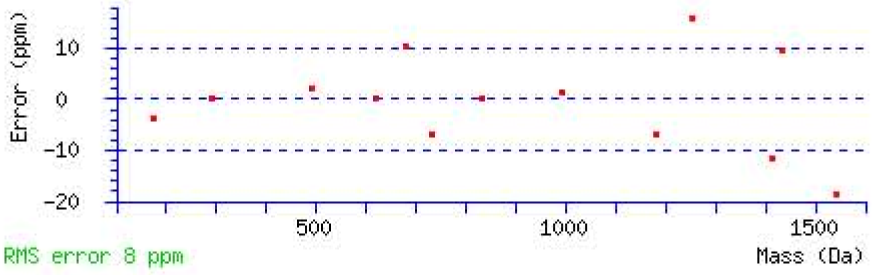
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1687.784393
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 60 **Expect:** 1.3e-005
Matches : 13/114 fragment ions using 16 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							11
2	258.108447	129.557862	241.081898	121.044587	240.097882	120.552579	Q	1559.749102	780.378189	1542.722553	771.864915	1541.738537	771.372907	10
3	697.333773	349.170525	680.307224	340.657250	679.323208	340.165242	Q	***1431.690524***	716.348900	1414.663975	707.835626	1413.679959	707.343618	9
4	857.364422	429.185849	840.337873	420.672575	839.353857	420.180567	C	***992.465198***	496.736237	975.438649	488.222963	974.454633	487.730955	8
5	956.432836	478.720056	939.406287	470.206782	938.422271	469.714774	V	***832.434549***	416.720913	815.408000	408.207638	814.423984	407.715630	7
6	1069.516900	535.262088	1052.490351	526.748814	1051.506335	526.256806	I	***733.366135***	367.186706	716.339586	358.673431	715.355570	358.181423	6
7	1200.557385	600.782331	1183.530836	592.269056	1182.546820	591.777048	M	***620.282071***	310.644674	603.255522	302.131399	602.271506	301.639391	5
8	1271.594499	636.300888	1254.567950	627.787613	1253.583934	627.295605	A	***489.241586***	245.124431	472.215037	236.611156	471.231021	236.119148	4
9	1400.637092	700.822184	1383.610543	692.308910	1382.626527	691.816902	E	418.204472	209.605874	401.177923	201.092600	400.193907	200.600592	3
10	1514.680019	757.843648	1497.653470	749.330373	1496.669454	748.838365	N	***289.161879***	145.084577	272.135330	136.571303			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.5	1687.784393	0.004575	EQQCVIMAENR
56.3	1687.784393	0.004575	EQQCVIMAENR
7.2	1687.813370	-0.024402	MKQSPALAPEERCR
6.5	1687.773666	0.015302	TTGPPSGQMPDNPPHR
5.5	1687.781006	0.007962	ELMAWNQAENR
2.1	1687.773193	0.015775	FGAVCTCMEKATGLK
1.9	1687.788254	0.000714	SQCHLSPISRSCTR

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

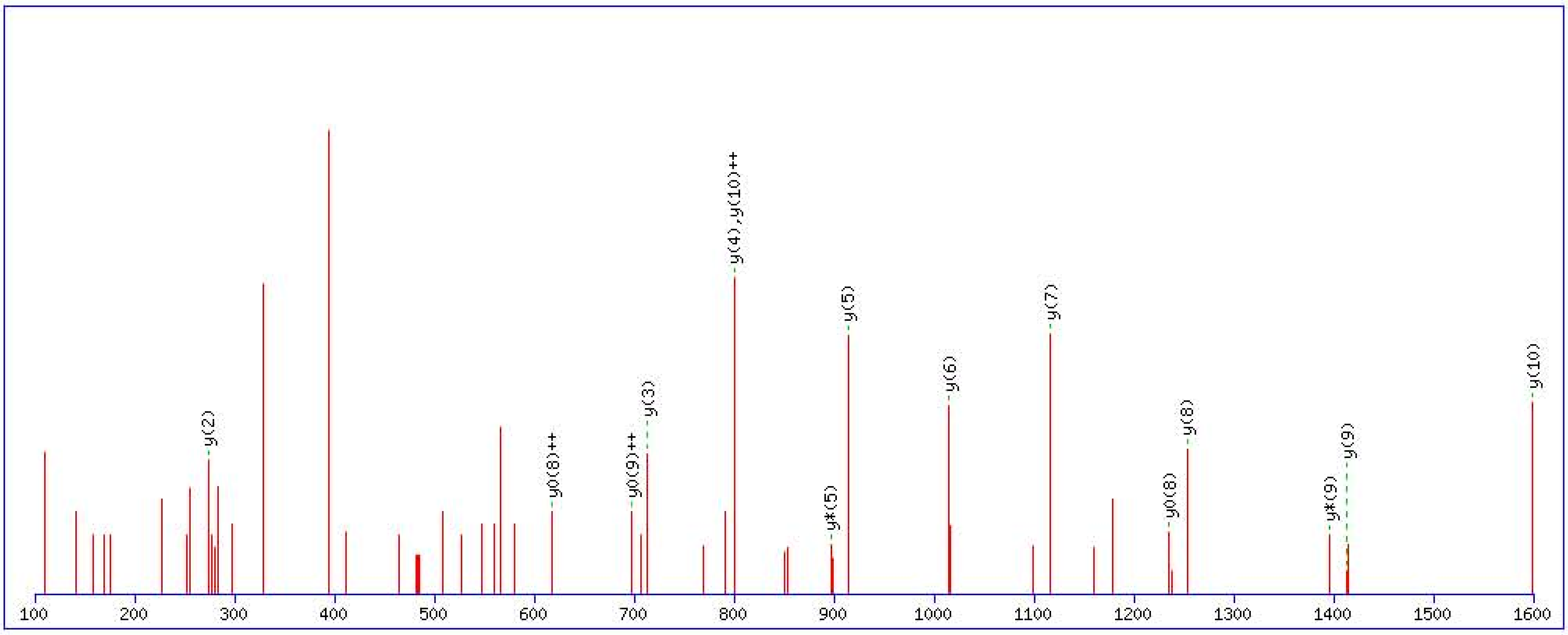
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **APWCHTTNSQVR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

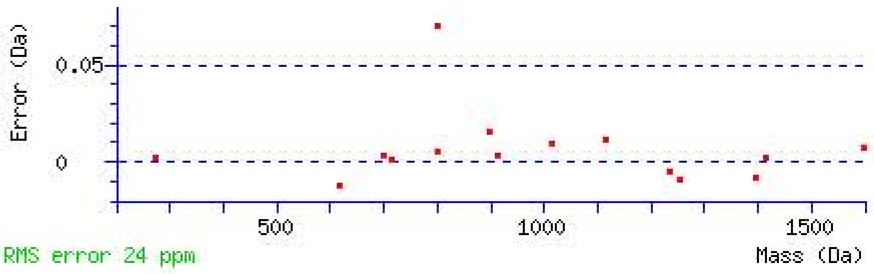
Match to Query 51325: 1766.830242 from(589.950690,3+) rtinseconds(1548) index(77267)
Title: Locus:1.1.1.2418.18 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

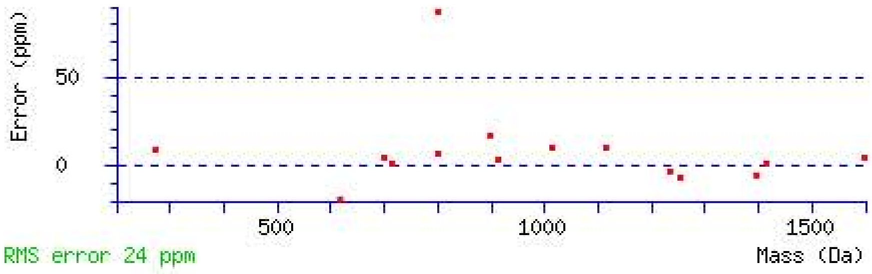
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1766.834488
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 54 **Expect:** 6.1e-005
Matches : 15/102 fragment ions using 27 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							12
2	169.097154	85.052215					P	1696.804643	848.905960	1679.778094	840.392685	1678.794078	839.900677	11
3	355.176467	178.091872					W	***1599.751879***	800.379578	1582.725330	791.866303	1581.741314	791.374295	10
4	515.207116	258.107196					C	***1413.672566***	707.339921	1396.646017	698.826647	1395.662001	698.334639	9
5	652.266028	326.636652					H	***1253.641917***	627.324597	1236.615368	618.811322	1235.631352	618.319314	8
6	753.313707	377.160492			735.303142	368.155209	T	***1116.583005***	558.795141	1099.556456	550.281866	1098.572440	549.789858	7
7	854.361386	427.684331			836.350821	418.679049	T	***1015.535326***	508.271301	998.508777	499.758027	997.524761	499.266019	6
8	968.404313	484.705795	951.377764	476.192520	950.393748	475.700512	N	***914.487647***	457.747462	897.461098	449.234187	896.477082	448.742179	5
9	1055.436341	528.221809	1038.409792	519.708534	1037.425776	519.216526	S	***800.444720***	400.725998	783.418171	392.212724	782.434155	391.720716	4
10	1494.661667	747.834472	1477.635118	739.321197	1476.651102	738.829189	Q	***713.412692***	357.209984	696.386143	348.696710			3
11	1593.730081	797.368679	1576.703532	788.855404	1575.719516	788.363396	V	***274.187366***	137.597321	257.160817	129.084047			2
12							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
54.3	1766.834488	-0.004246	APWCHTTNSQVR

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

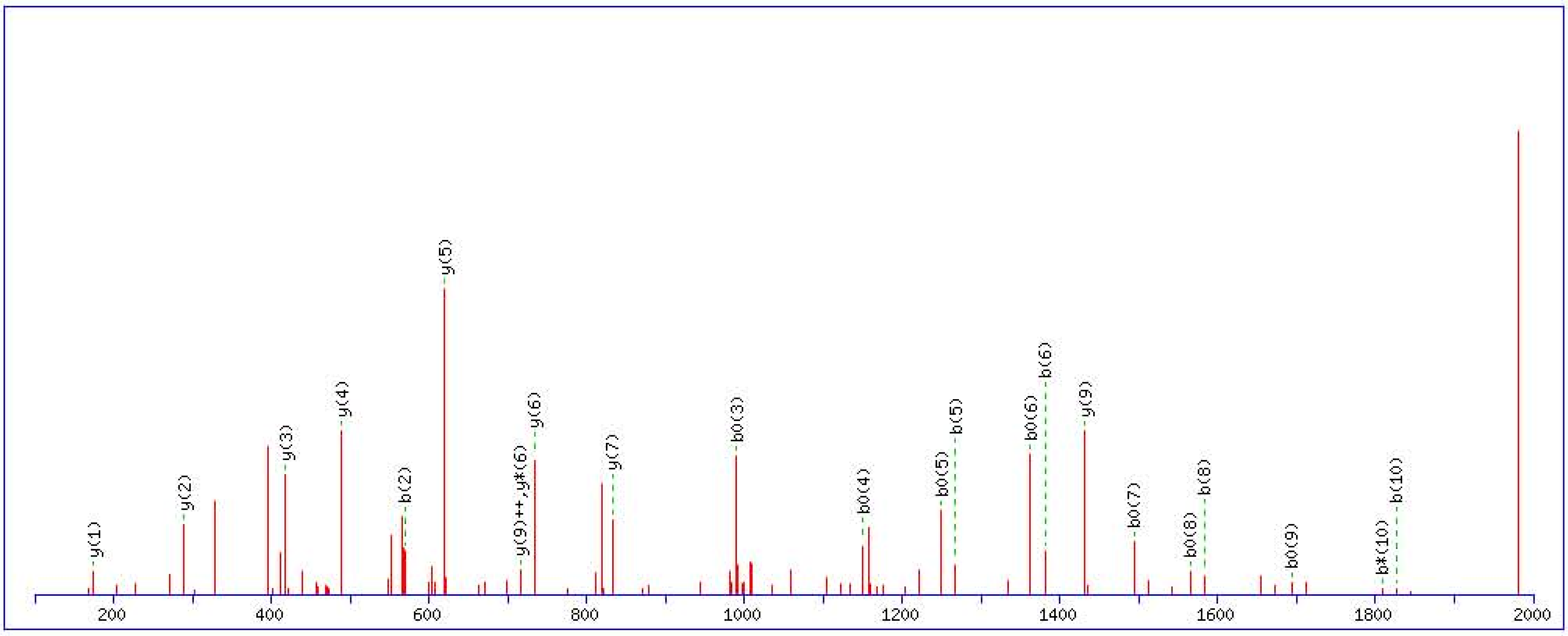
Mascot Search Results

Peptide View

MS/MS Fragmentation of **EQQCVIMAENR**
Found in **PLGB_HUMAN**, Plasminogen-like protein B OS=Homo sapiens GN=PLGLB1 PE=1 SV=1

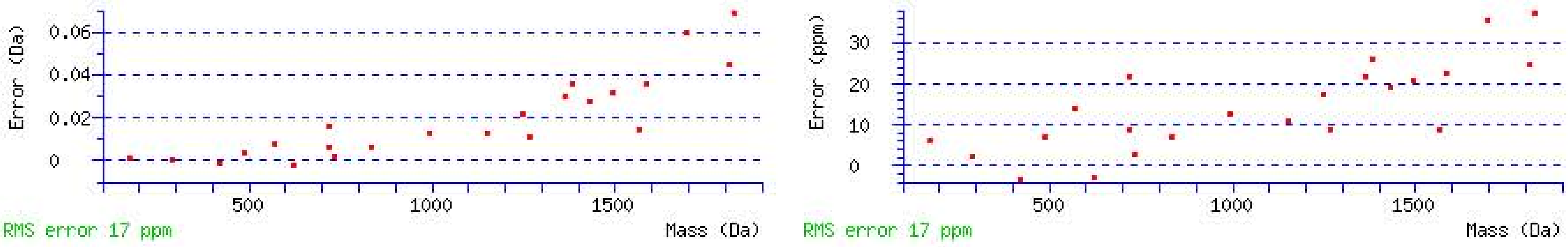
Match to Query 56607: 1998.977308 from(1000.495930,2+) rtinseconds(2137) index(81190)
Title: Locus:1.1.1.2623.25 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [2000] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1998.951141
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 48  Expect: 0.00038
Matches : 23/114 fragment ions using 35 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							11
2	**569.275195**	285.141236	552.248646	276.627961	551.264630	276.135953	Q	1870.915850	935.961563	1853.889301	927.448288	1852.905285	926.956280	10
3	1008.500521	504.753899	991.473972	496.240624	990.489956	495.748616	Q	***1431.690524***	716.348900	1414.663975	707.835625	1413.679959	707.343617	9
4	1168.531170	584.769223	1151.504621	576.255949	1150.520605	575.763940	C	992.465198	496.736237	975.438649	488.222962	974.454633	487.730954	8
5	**1267.599584**	634.303430	1250.573035	625.790156	1249.589019	625.298148	V	***832.434549***	416.720912	815.408000	408.207638	814.423984	407.715630	7
6	**1380.683648**	690.845462	1363.657099	682.332188	1362.673083	681.840179	I	***733.366135***	367.186705	716.339586	358.673431	715.355570	358.181423	6
7	1511.724133	756.365704	1494.697584	747.852430	1493.713568	747.360422	M	***620.282071***	310.644673	603.255522	302.131399	602.271506	301.639391	5
8	**1582.761247**	791.884261	1565.734698	783.370987	1564.750682	782.878979	A	***489.241586***	245.124431	472.215037	236.611156	471.231021	236.119148	4
9	1711.803840	856.405558	1694.777291	847.892283	1693.793275	847.400275	E	***418.204472***	209.605874	401.177923	201.092599	400.193907	200.600591	3
10	**1825.846767**	913.427021	1808.820218	904.913747	1807.836202	904.421739	N	***289.161879***	145.084577	272.135330	136.571303			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
47.9	1998.951141	0.026167	EQQCVIMAENR
11.7	1999.001053	-0.023745	QLPPTEKESTRIVDSWN
7.1	1998.960159	0.017149	SSTLSSSSMSLSPKLCAEK
2.4	1998.950912	0.026396	YEAKQLRTFYQMYDK
1.4	1998.976746	0.000562	NMTAQNYTYAIRSR
0.6	1998.958130	0.019178	RAGDVYYREATDPAMLR

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

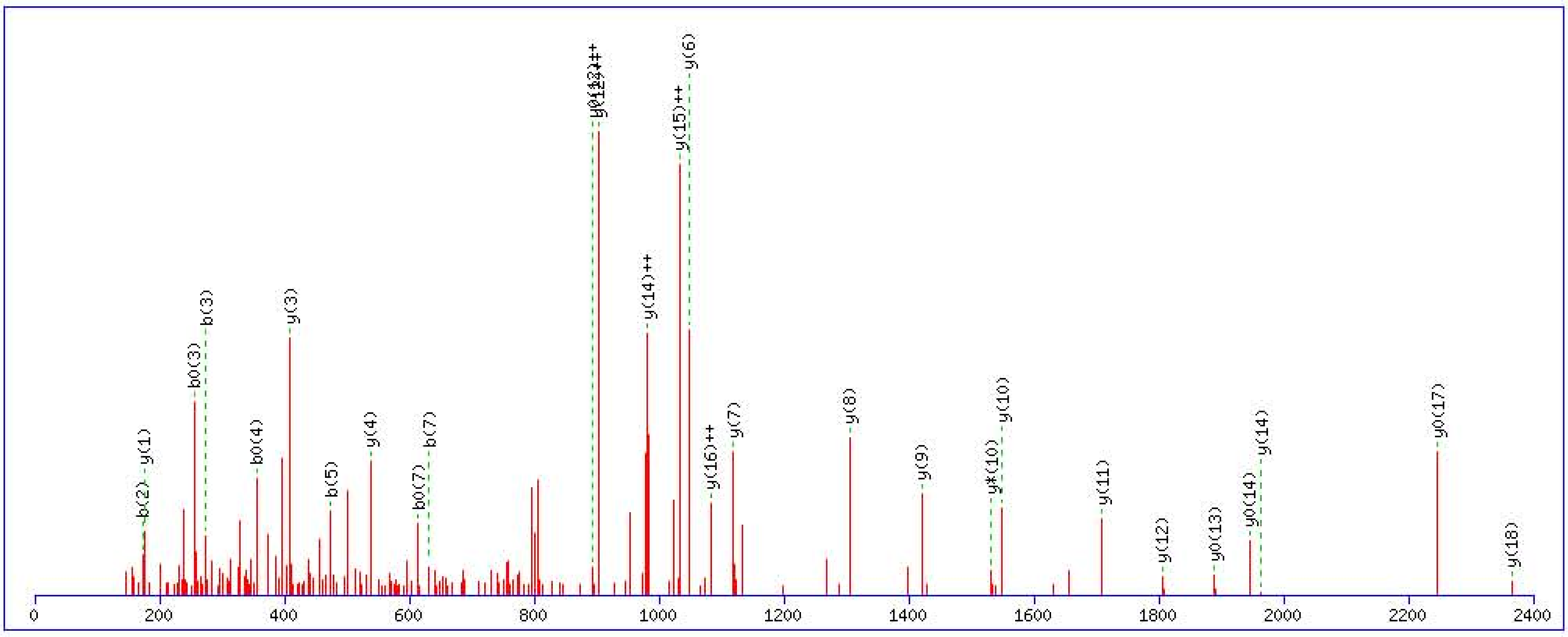
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ATTVTGTPCQDWAAQEPHR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

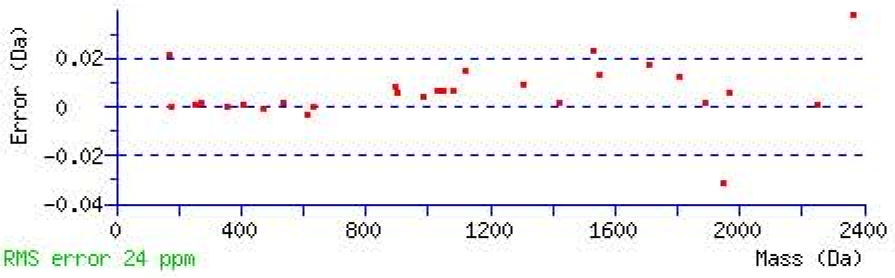
Match to Query 66749: 2436.142542 from(813.054790,3+) rtinseconds(1874) index(79361)
Title: Locus:1.1.1.2532.10 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

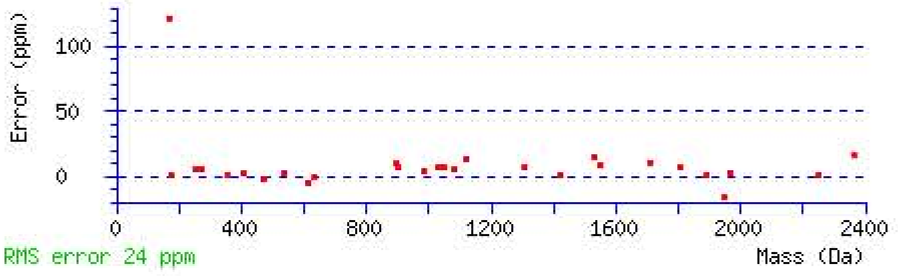
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2436.131470
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15    : Biotin:Thermo-21345 (Q)
Ions Score: 63  Expect: 7.7e-006
Matches : 28/190 fragment ions using 55 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.044390	36.525833					A							19
2	**173.092069**	87.049672			155.081504	78.044390	T	***2366.101616***	1183.554446	2349.075067	1175.041171	2348.091051	1174.549163	18
3	**274.139748**	137.573512			256.129183	128.568230	T	2265.053937	1133.030606	2248.027388	1124.517332	2247.043372	1124.025324	17
4	373.208162	187.107719			355.197597	178.102437	V	2164.006258	1082.506767	2146.979709	1073.993492	2145.995693	1073.501484	16
5	**474.255841**	237.631559			456.245276	228.626276	T	2064.937844	1032.972560	2047.911295	1024.459285	2046.927279	1023.967277	15
6	531.277305	266.142291			513.266740	257.137008	G	***1963.890165***	982.448721	1946.863616	973.935446	1945.879600	973.443438	14
7	**632.324984**	316.666130			614.314419	307.660848	T	1906.868701	953.937989	1889.842152	945.424714	1888.858136	944.932706	13
8	729.377748	365.192512			711.367183	356.187230	P	***1805.821022***	903.414149	1788.794473	894.900875	1787.810457	894.408867	12
9	889.408397	445.207837			871.397832	436.202554	C	***1708.768258***	854.887767	1691.741709	846.374493	1690.757693	845.882485	11
10	1017.466975	509.237126	1000.440426	500.723851	999.456410	500.231843	Q	***1548.737609***	774.872443	1531.711060	766.359168	1530.727044	765.867160	10
11	1132.493918	566.750597	1115.467369	558.237323	1114.483353	557.745315	D	***1420.679031***	710.843154	1403.652482	702.329879	1402.668466	701.837871	9
12	1318.573231	659.790254	1301.546682	651.276979	1300.562666	650.784971	W	***1305.652088***	653.329682	1288.625539	644.816408	1287.641523	644.324400	8
13	1389.610345	695.308811	1372.583796	686.795536	1371.599780	686.303528	A	***1119.572775***	560.290026	1102.546226	551.776751	1101.562210	551.284743	7
14	1460.647459	730.827368	1443.620910	722.314093	1442.636894	721.822085	A	***1048.535661***	524.771469	1031.509112	516.258194	1030.525096	515.766186	6
15	1899.872785	950.440031	1882.846236	941.926756	1881.862220	941.434748	Q	977.498547	489.252912	960.471998	480.739637	959.487982	480.247629	5
16	2028.915378	1014.961327	2011.888829	1006.448053	2010.904813	1005.956045	E	***538.273221***	269.640249	521.246672	261.126974	520.262656	260.634966	4
17	2125.968142	1063.487709	2108.941593	1054.974434	2107.957577	1054.482427	P	***409.230628***	205.118952	392.204079	196.605677			3
18	2263.027054	1132.017165	2246.000505	1123.503890	2245.016489	1123.011883	H	312.177864	156.592570	295.151315	148.079295			2
19							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
63.4	2436.131470	0.011072	ATTVTGTPCQDWAAQEPHR
27.2	2436.131470	0.011072	ATTVTGTPCQDWAAQEPHR

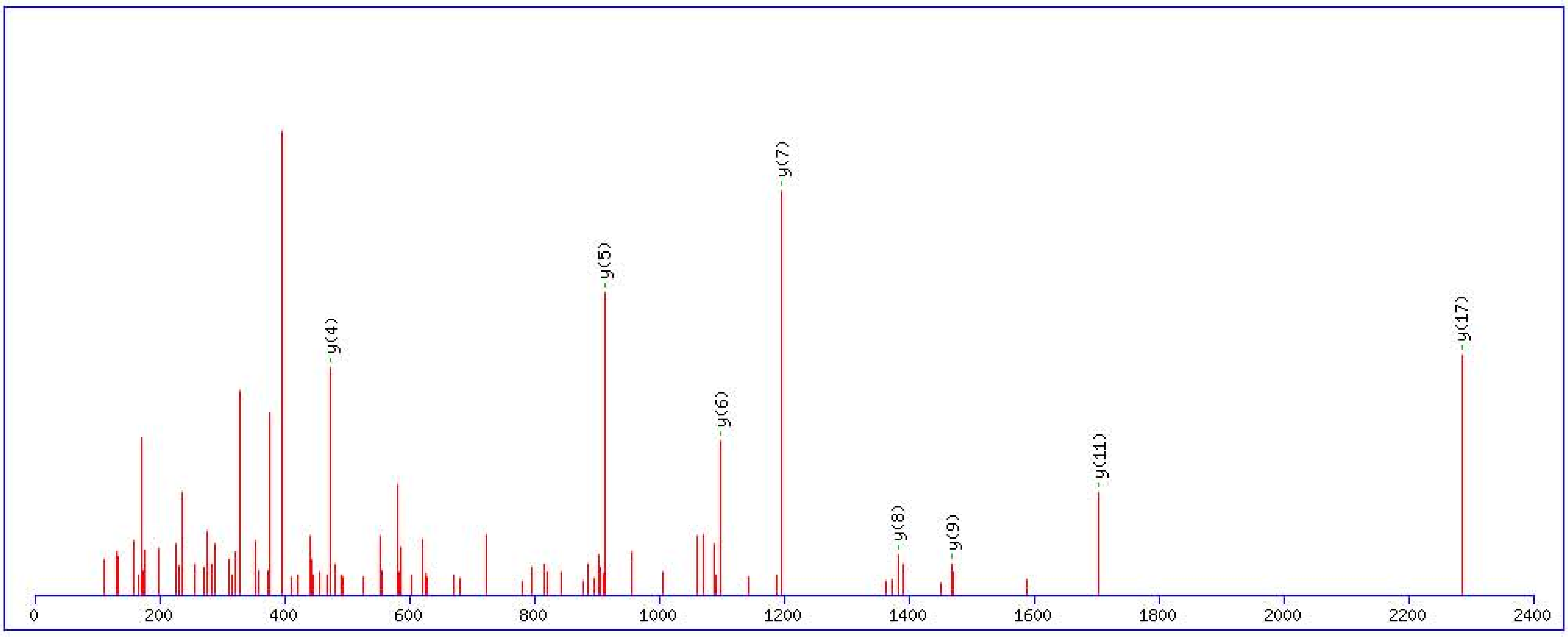
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VVGGCVAHPHSWPWQVSLR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

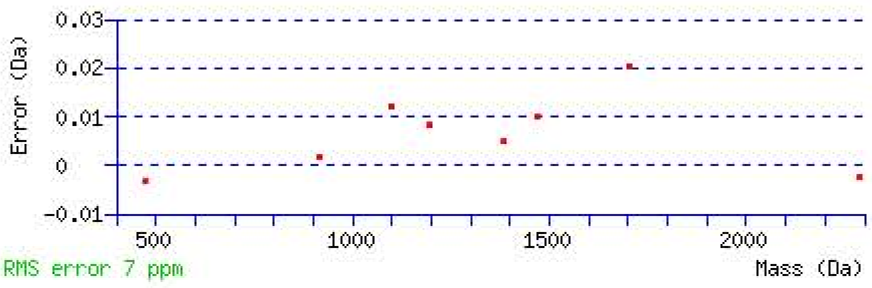
Match to Query 67892: 2482.256416 from(621.571380,4+) rtinseconds(2208) index(81698)
Title: Locus:1.1.1.2648.18 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

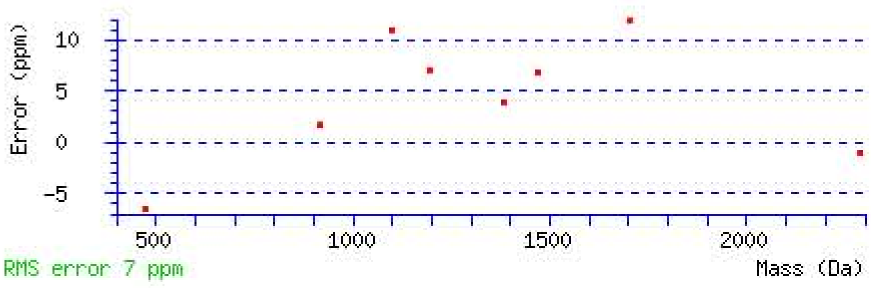
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2482.251480
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q15    : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.002
Matches : 8/164 fragment ions using 16 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							19
2	199.144104	100.075690					V	2384.190309	1192.598792	2367.163760	1184.085518	2366.179744	1183.593510	18
3	256.165568	128.586422					G	***2285.121895***	1143.064585	2268.095346	1134.551311	2267.111330	1134.059303	17
4	313.187032	157.097154					G	2228.100431	1114.553853	2211.073882	1106.040579	2210.089866	1105.548571	16
5	473.217681	237.112479					C	2171.078967	1086.043121	2154.052418	1077.529847	2153.068402	1077.037839	15
6	572.286095	286.646686					V	2011.048318	1006.027797	1994.021769	997.514523	1993.037753	997.022515	14
7	643.323209	322.165243					A	1911.979904	956.493590	1894.953355	947.980316	1893.969339	947.488308	13
8	780.382121	390.694699					H	1840.942790	920.975033	1823.916241	912.461759	1822.932225	911.969751	12
9	877.434885	439.221081					P	***1703.883878***	852.445577	1686.857329	843.932303	1685.873313	843.440295	11
10	1014.493797	507.750537					H	1606.831114	803.919195	1589.804565	795.405921	1588.820549	794.913913	10
11	1101.525825	551.266550			1083.515260	542.261268	S	***1469.772202***	735.389739	1452.745653	726.876465	1451.761637	726.384457	9
12	1287.605138	644.306207			1269.594573	635.300924	W	***1382.740174***	691.873725	1365.713625	683.360451	1364.729609	682.868443	8
13	1384.657902	692.832589			1366.647337	683.827306	P	***1196.660861***	598.834069	1179.634312	590.320794	1178.650296	589.828786	7
14	1570.737215	785.872245			1552.726650	776.866963	W	***1099.608097***	550.307687	1082.581548	541.794412	1081.597532	541.302404	6
15	2009.962541	1005.484909	1992.935992	996.971634	1991.951976	996.479626	Q	***913.528784***	457.268030	896.502235	448.754756	895.518219	448.262748	5
16	2109.030955	1055.019115	2092.004406	1046.505841	2091.020390	1046.013833	V	***474.303458***	237.655367	457.276909	229.142092	456.292893	228.650084	4
17	2196.062983	1098.535129	2179.036434	1090.021855	2178.052418	1089.529847	S	375.235044	188.121160	358.208495	179.607886	357.224479	179.115878	3
18	2309.147047	1155.077161	2292.120498	1146.563887	2291.136482	1146.071879	L	288.203016	144.605146	271.176467	136.091872			2
19							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.0	2482.251480	0.004936	VVGGCVAHPHSWPWQVSLR

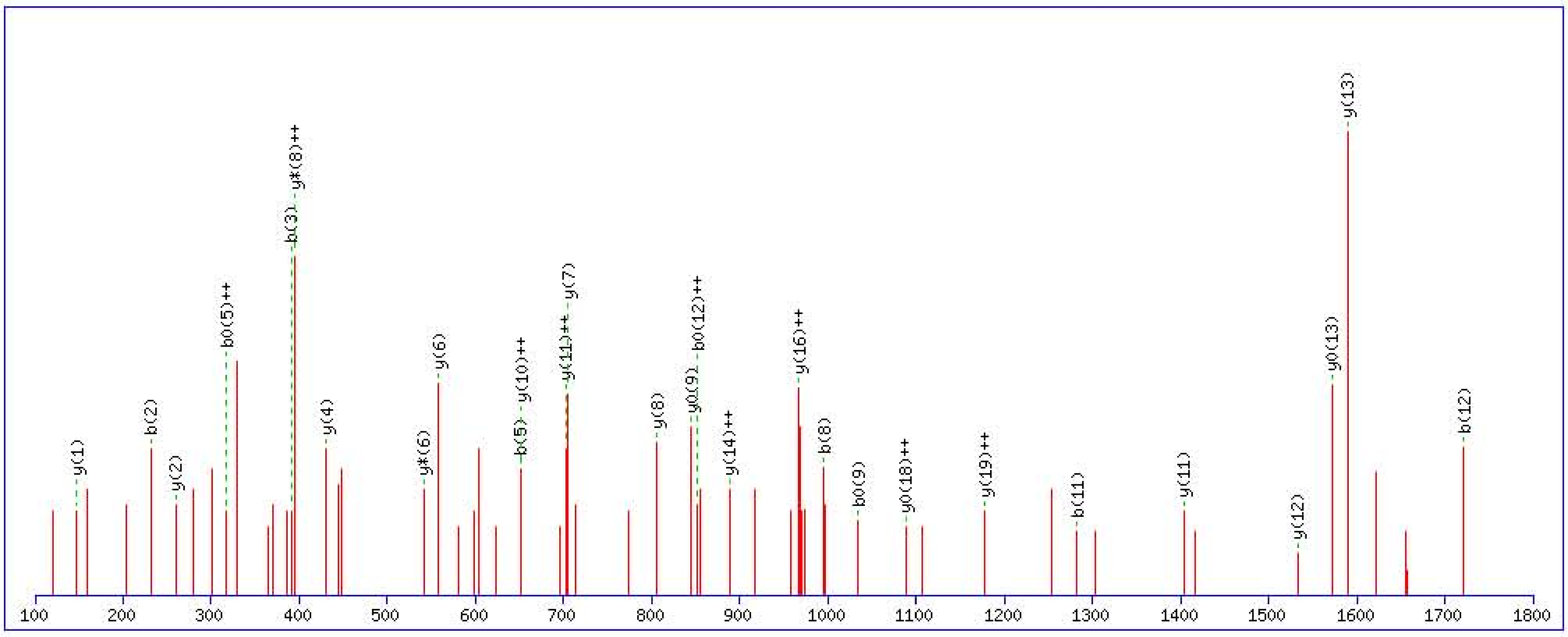
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TECFITGWGETQGTFGAGLLK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

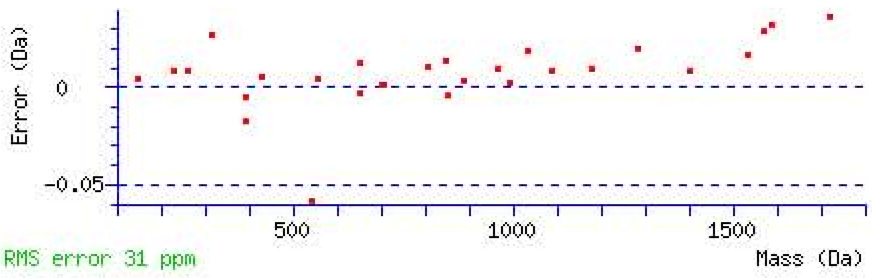
Match to Query 69497: 2583.280482 from(862.100770,3+) rtinseconds(2809) index(85372)
Title: Locus:1.1.1.2856.18 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

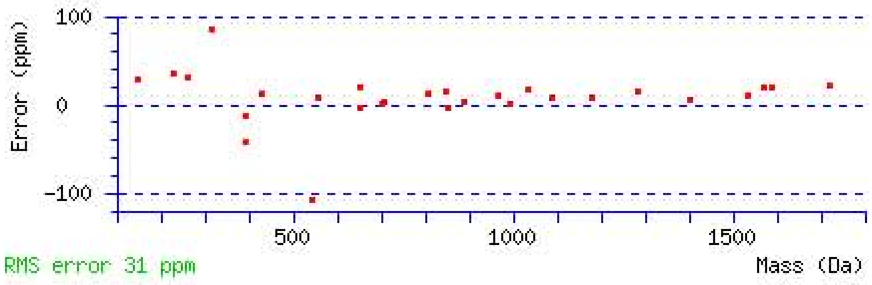
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2583.250198
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12 : Biotin:Thermo-21345 (Q)
Ions Score: 46 **Expect:** 0.0006
Matches : 28/204 fragment ions using 56 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	102.054955	51.531116			84.044390	42.525833	T							21
2	***231.097548***	116.052412			213.086983	107.047130	E	2483.209769	1242.108522	2466.183220	1233.595248	2465.199204	1233.103240	20
3	***391.128197***	196.067737			373.117632	187.062454	C	2354.167176	1177.587226	2337.140627	1169.073951	2336.156611	1168.581943	19
4	538.196611	269.601944			520.186046	260.596661	F	2194.136527	1097.571901	2177.109978	1089.058627	2176.125962	1088.566619	18
5	***651.280675***	326.143976			633.270110	317.138693	I	2047.068113	1024.037695	2030.041564	1015.524420	2029.057548	1015.032412	17
6	752.328354	376.667815			734.317789	367.662533	T	1933.984049	967.495663	1916.957500	958.982388	1915.973484	958.490380	16
7	809.349818	405.178547			791.339253	396.173265	G	1832.936370	916.971823	1815.909821	908.458549	1814.925805	907.966541	15
8	***995.429131***	498.218204			977.418566	489.212921	W	1775.914906	888.461091	1758.888357	879.947817	1757.904341	879.455809	14
9	1052.450595	526.728936			1034.440030	517.723653	G	***1589.835593***	795.421435	1572.809044	786.908160	1571.825028	786.416152	13
10	1181.493188	591.250232			1163.482623	582.244950	E	***1532.814129***	766.910703	1515.787580	758.397428	1514.803564	757.905420	12
11	***1282.540867***	641.774072			1264.530302	632.768789	T	***1403.771536***	702.389406	1386.744987	693.876132	1385.760971	693.384124	11
12	***1721.766193***	861.386735	1704.739644	852.873460	1703.755628	852.381452	Q	1302.723857	651.865567	1285.697308	643.352292	1284.713292	642.860284	10
13	1778.787657	889.897467	1761.761108	881.384192	1760.777092	880.892184	G	863.498531	432.252904	846.471982	423.739629	845.487966	423.247621	9
14	1879.835336	940.421306	1862.808787	931.908032	1861.824771	931.416024	T	***806.477067***	403.742172	789.450518	395.228897	788.466502	394.736889	8
15	2026.903750	1013.955513	2009.877201	1005.442239	2008.893185	1004.950231	F	***705.429388***	353.218332	688.402839	344.705058			7
16	2083.925214	1042.466245	2066.898665	1033.952970	2065.914649	1033.460962	G	***558.360974***	279.684125	541.334425	271.170851			6
17	2154.962328	1077.984802	2137.935779	1069.471527	2136.951763	1068.979519	A	501.339510	251.173393	484.312961	242.660119			5
18	2211.983792	1106.495534	2194.957243	1097.982259	2193.973227	1097.490251	G	***430.302396***	215.654836	413.275847	207.141562			4
19	2325.067856	1163.037566	2308.041307	1154.524291	2307.057291	1154.032283	L	373.280932	187.144104	356.254383	178.630830			3
20	2438.151920	1219.579598	2421.125371	1211.066324	2420.141355	1210.574316	L	***260.196868***	130.602072	243.170319	122.088798			2
21							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
46.3	2583.250198	0.030284	TECFITGWGETQGTFGAGLLK

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

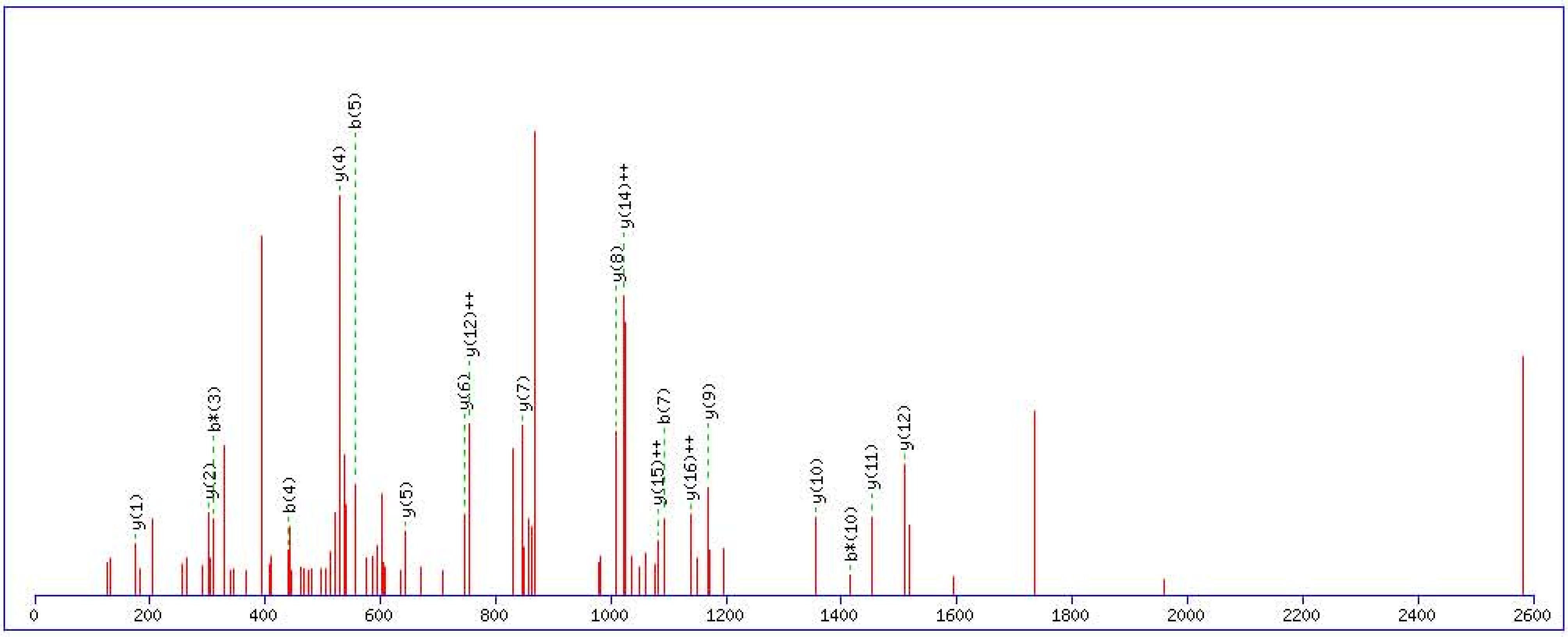
MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **NPDNDPQGPWCYTTDPEKR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

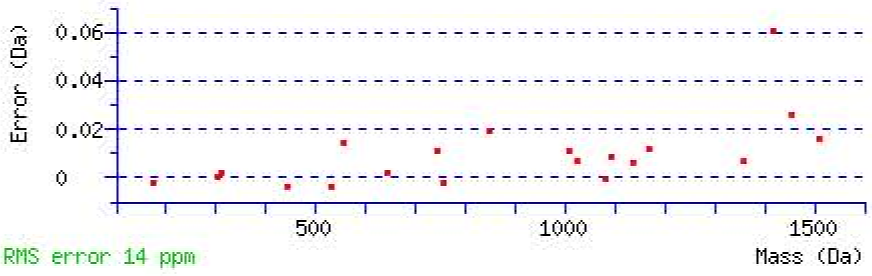
Match to Query 69723: 2600.154192 from(867.725340,3+) rtinseconds(1967) index(80050)
Title: Locus:1.1.1.2564.24 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

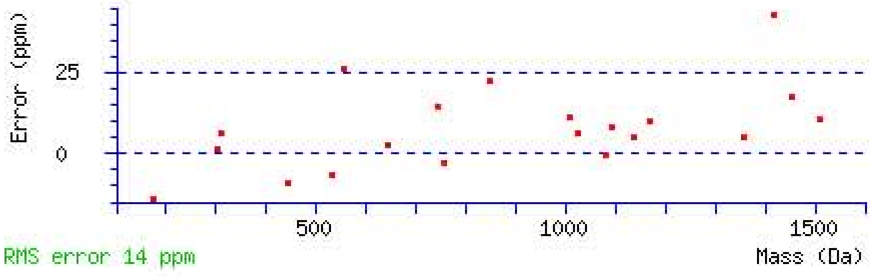
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2600.142410
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7 : Biotin:Thermo-21345 (Q)
Ions Score: 56 **Expect:** 1.7e-005
Matches : 20/208 fragment ions using 41 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.050203	58.028740	98.023654	49.515465			N							19
2	212.102967	106.555121	195.076418	98.041847			P	2487.106759	1244.057017	2470.080210	1235.543743	2469.096194	1235.051735	18
3	327.129910	164.068593	310.103361	155.555319	309.119345	155.063311	D	2390.053995	1195.530635	2373.027446	1187.017361	2372.043430	1186.525353	17
4	**441.172837**	221.090057	424.146288	212.576782	423.162272	212.084774	N	2275.027052	1138.017164	2258.000503	1129.503889	2257.016487	1129.011881	16
5	**556.199780**	278.603528	539.173231	270.090254	538.189215	269.598246	D	2160.984125	1080.995700	2143.957576	1072.482426	2142.973560	1071.990418	15
6	653.252544	327.129910	636.225995	318.616636	635.241979	318.124628	P	2045.957182	1023.482229	2028.930633	1014.968955	2027.946617	1014.476946	14
7	**1092.477870**	546.742573	1075.451321	538.229299	1074.467305	537.737290	Q	1948.904418	974.955847	1931.877869	966.442572	1930.893853	965.950564	13
8	1149.499334	575.253305	1132.472785	566.740030	1131.488769	566.248022	G	***1509.679092***	755.343184	1492.652543	746.829910	1491.668527	746.337902	12
9	1246.552098	623.779687	1229.525549	615.266413	1228.541533	614.774404	P	***1452.657628***	726.832452	1435.631079	718.319178	1434.647063	717.827170	11
10	1432.631411	716.819343	1415.604862	708.306069	1414.620846	707.814061	W	***1355.604864***	678.306070	1338.578315	669.792796	1337.594299	669.300788	10
11	1592.662060	796.834668	1575.635511	788.321394	1574.651495	787.829385	C	***1169.525551***	585.266414	1152.499002	576.753139	1151.514986	576.261131	9
12	1755.725389	878.366333	1738.698840	869.853058	1737.714824	869.361050	Y	***1009.494902***	505.251089	992.468353	496.737815	991.484337	496.245807	8
13	1856.773068	928.890172	1839.746519	920.376898	1838.762503	919.884889	T	***846.431573***	423.719425	829.405024	415.206150	828.421008	414.714142	7
14	1957.820747	979.414012	1940.794198	970.900737	1939.810182	970.408729	T	***745.383894***	373.195585	728.357345	364.682311	727.373329	364.190303	6
15	2072.847690	1036.927483	2055.821141	1028.414208	2054.837125	1027.922200	D	***644.336215***	322.671746	627.309666	314.158471	626.325650	313.666463	5
16	2169.900454	1085.453865	2152.873905	1076.940590	2151.889889	1076.448582	P	***529.309272***	265.158274	512.282723	256.645000	511.298707	256.152992	4
17	2298.943047	1149.975161	2281.916498	1141.461887	2280.932482	1140.969879	E	432.256508	216.631892	415.229959	208.118618	414.245943	207.626610	3
18	2427.038010	1214.022643	2410.011461	1205.509368	2409.027445	1205.017360	K	***303.213915***	152.110595	286.187366	143.597321			2
19							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.4	2600.142410	0.011782	NPDNDPQGPWCYTTDPEKR

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

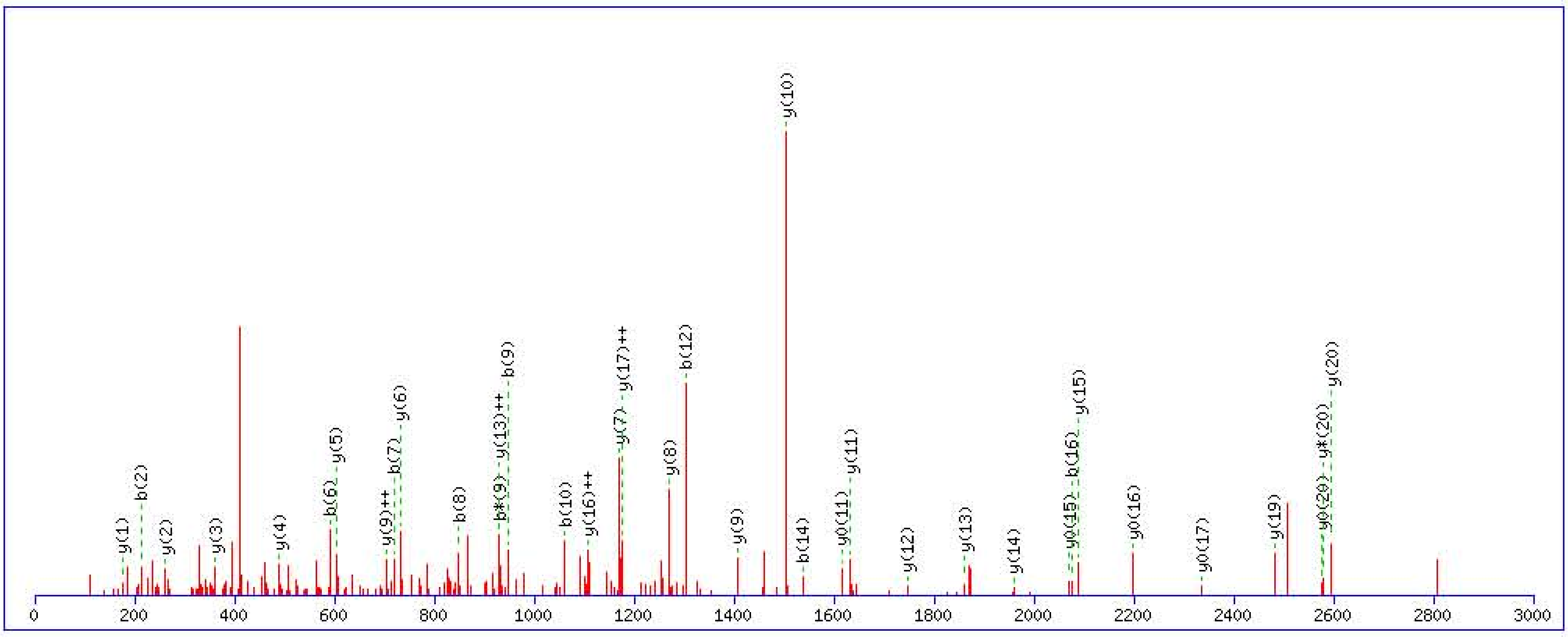
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VILGAHQEVNLEPHVQEIEVSR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

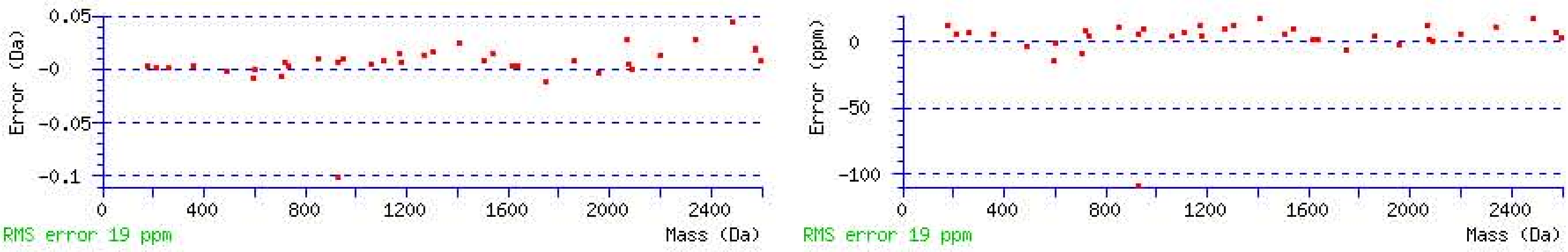
Match to Query 71857: 2806.497552 from(936.506460,3+) rtinseconds(2070) index(80740)
Title: Locus:1.1.1.2600.12 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2806.479965
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q16 : Biotin:Thermo-21345 (Q)
Ions Score: 109 **Expect:** 2.4e-010
Matches : 37/224 fragment ions using 65 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							22
2	**213.159754**	107.083515					I	2708.418847	1354.713061	2691.392298	1346.199787	2690.408282	1345.707779	21
3	326.243818	163.625547					L	***2595.334783***	1298.171029	2578.308234	1289.657755	2577.324218	1289.165747	20
4	383.265282	192.136279					G	***2482.250719***	1241.628997	2465.224170	1233.115723	2464.240154	1232.623715	19
5	454.302396	227.654836					A	2425.229255	1213.118265	2408.202706	1204.604991	2407.218690	1204.112983	18
6	**591.361308**	296.184292					H	2354.192141	1177.599708	2337.165592	1169.086434	2336.181576	1168.594426	17
7	**719.419886**	360.213581	702.393337	351.700307			Q	2217.133229	1109.070252	2200.106680	1100.556978	2199.122664	1100.064970	16
8	**848.462479**	424.734878	831.435930	416.221603	830.451914	415.729595	E	***2089.074651***	1045.040963	2072.048102	1036.527689	2071.064086	1036.035681	15
9	**947.530893**	474.269085	930.504344	465.755810	929.520328	465.263802	V	***1960.032058***	980.519667	1943.005509	972.006393	1942.021493	971.514385	14
10	**1061.573820**	531.290548	1044.547271	522.777274	1043.563255	522.285266	N	***1860.963644***	930.985460	1843.937095	922.472186	1842.953079	921.980178	13
11	1174.657884	587.832580	1157.631335	579.319306	1156.647319	578.827297	L	***1746.920717***	873.963997	1729.894168	865.450722	1728.910152	864.958714	12
12	**1303.700477**	652.353877	1286.673928	643.840602	1285.689912	643.348594	E	***1633.836653***	817.421965	1616.810104	808.908690	1615.826088	808.416682	11
13	1400.753241	700.880259	1383.726692	692.366984	1382.742676	691.874976	P	***1504.794060***	752.900668	1487.767511	744.387394	1486.783495	743.895386	10
14	**1537.812153**	769.409715	1520.785604	760.896440	1519.801588	760.404432	H	***1407.741296***	704.374286	1390.714747	695.861012	1389.730731	695.369004	9
15	1636.880567	818.943922	1619.854018	810.430647	1618.870002	809.938639	V	***1270.682384***	635.844830	1253.655835	627.331556	1252.671819	626.839548	8
16	**2076.105893**	1038.556584	2059.079344	1030.043310	2058.095328	1029.551302	Q	***1171.613970***	586.310623	1154.587421	577.797349	1153.603405	577.305341	7
17	2205.148486	1103.077881	2188.121937	1094.564606	2187.137921	1094.072598	E	***732.388644***	366.697960	715.362095	358.184686	714.378079	357.692678	6
18	2318.232550	1159.619913	2301.206001	1151.106638	2300.221985	1150.614631	I	***603.346051***	302.176664	586.319502	293.663389	585.335486	293.171381	5
19	2447.275143	1224.141210	2430.248594	1215.627935	2429.264578	1215.135927	E	***490.261987***	245.634631	473.235438	237.121357	472.251422	236.629349	4
20	2546.343557	1273.675417	2529.317008	1265.162142	2528.332992	1264.670134	V	***361.219394***	181.113335	344.192845	172.600060	343.208829	172.108052	3
21	2633.375585	1317.191431	2616.349036	1308.678156	2615.365020	1308.186148	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
22							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
109.1	2806.479965	0.017587	VILGAHQEVNLEPHVQEIEVSR
8.8	2806.479965	0.017587	VILGAHQEVNLEPHVQEIEVSR

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

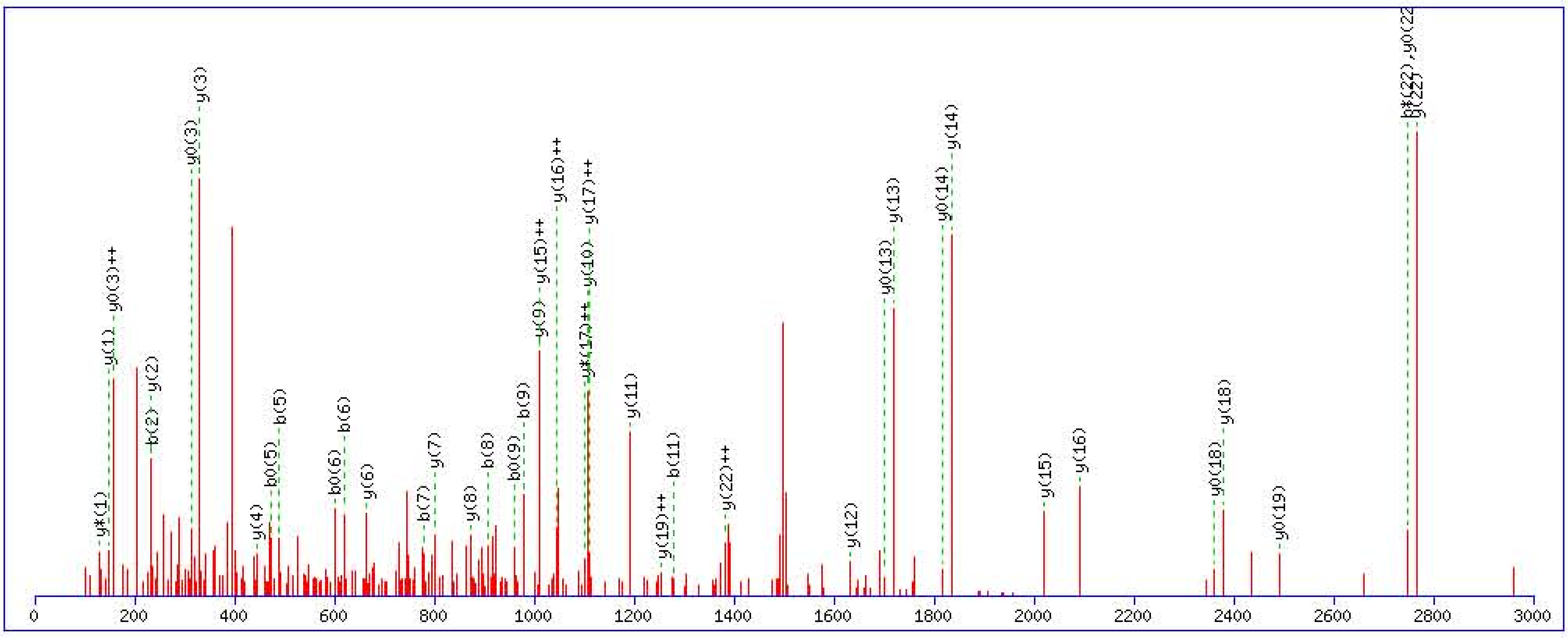
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TMSGLECQAWDSQSPHAHGYIPSK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

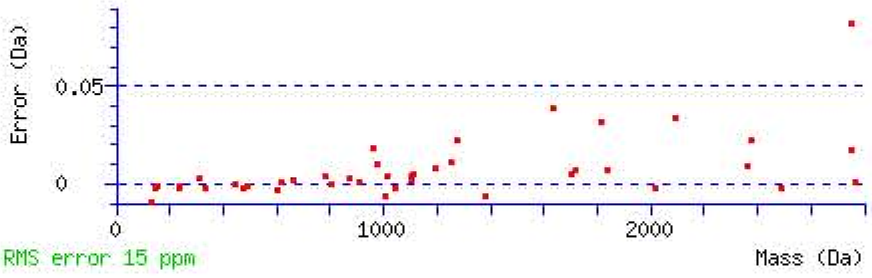
Match to Query 74390: 2997.367976 from(750.349270,4+) rtinseconds(1976) index(80123)
Title: Locus:1.1.1.2567.22 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

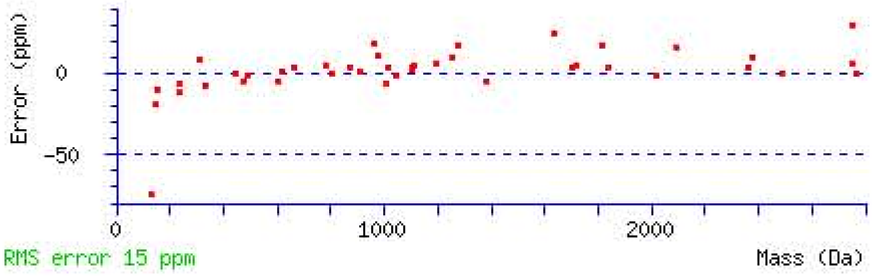
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2997.357162
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13 : Biotin:Thermo-21345 (Q)
Ions Score: 75 **Expect:** 3.8e-007
Matches : 42/260 fragment ions using 105 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							24
2	**233.095440**	117.051358			215.084875	108.046076	M	2897.316768	1449.162022	2880.290219	1440.648748	2879.306203	1440.156740	23
3	320.127468	160.567372			302.116903	151.562089	S	***2766.276283***	1383.641780	2749.249734	1375.128505	2748.265718	1374.636497	22
4	377.148932	189.078104			359.138367	180.072821	G	2679.244255	1340.125766	2662.217706	1331.612491	2661.233690	1331.120483	21
5	**490.232996**	245.620136			472.222431	236.614853	L	2622.222791	1311.615034	2605.196242	1303.101759	2604.212226	1302.609751	20
6	**619.275589**	310.141433			601.265024	301.136150	E	2509.138727	1255.073002	2492.112178	1246.559727	2491.128162	1246.067719	19
7	**779.306238**	390.156757			761.295673	381.151475	C	***2380.096134***	1190.551705	2363.069585	1182.038431	2362.085569	1181.546423	18
8	**907.364816**	454.186046	890.338267	445.672772	889.354251	445.180764	Q	2220.065485	1110.536381	2203.038936	1102.023106	2202.054920	1101.531098	17
9	**978.401930**	489.704603	961.375381	481.191329	960.391365	480.699321	A	***2092.006907***	1046.507092	2074.980358	1037.993817	2073.996342	1037.501809	16
10	1164.481243	582.744260	1147.454694	574.230985	1146.470678	573.738977	W	***2020.969793***	1010.988535	2003.943244	1002.475260	2002.959228	1001.983252	15
11	**1279.508186**	640.257731	1262.481637	631.744457	1261.497621	631.252449	D	***1834.890480***	917.948878	1817.863931	909.435604	1816.879915	908.943596	14
12	1366.540214	683.773745	1349.513665	675.260471	1348.529649	674.768463	S	***1719.863537***	860.435407	1702.836988	851.922132	1701.852972	851.430124	13
13	1805.765540	903.386408	1788.738991	894.873134	1787.754975	894.381126	Q	***1632.831509***	816.919393	1615.804960	808.406118	1614.820944	807.914110	12
14	1892.797568	946.902422	1875.771019	938.389148	1874.787003	937.897140	S	***1193.606183***	597.306730	1176.579634	588.793455	1175.595618	588.301447	11
15	1989.850332	995.428804	1972.823783	986.915530	1971.839767	986.423522	P	***1106.574155***	553.790716	1089.547606	545.277441	1088.563590	544.785433	10
16	2126.909244	1063.958260	2109.882695	1055.444986	2108.898679	1054.952978	H	***1009.521391***	505.264334	992.494842	496.751059	991.510826	496.259051	9
17	2197.946358	1099.476817	2180.919809	1090.963543	2179.935793	1090.471535	A	***872.462479***	436.734878	855.435930	428.221603	854.451914	427.729595	8
18	2335.005270	1168.006273	2317.978721	1159.492999	2316.994705	1159.000991	H	***801.425365***	401.216321	784.398816	392.703046	783.414800	392.211038	7
19	2392.026734	1196.517005	2375.000185	1188.003731	2374.016169	1187.511723	G	***664.366453***	332.686865	647.339904	324.173590	646.355888	323.681582	6
20	2555.090063	1278.048670	2538.063514	1269.535395	2537.079498	1269.043387	Y	607.344989	304.176133	590.318440	295.662858	589.334424	295.170850	5
21	2668.174127	1334.590702	2651.147578	1326.077427	2650.163562	1325.585419	I	***444.281660***	222.644468	427.255111	214.131194	426.271095	213.639186	4
22	2765.226891	1383.117084	2748.200342	1374.603809	2747.216326	1374.111801	P	***331.197596***	166.102436	314.171047	157.589162	313.187031	157.097154	3
23	2852.258919	1426.633098	2835.232370	1418.119823	2834.248354	1417.627815	S	***234.144832***	117.576054	217.118283	109.062780	216.134267	108.570772	2
24							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
75.0	2997.357162	0.010814	TMSGLECQAWDSQSPHAHGYIPSK
30.1	2997.357162	0.010814	TMSGLECQAWDSQSPHAHGYIPSK

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

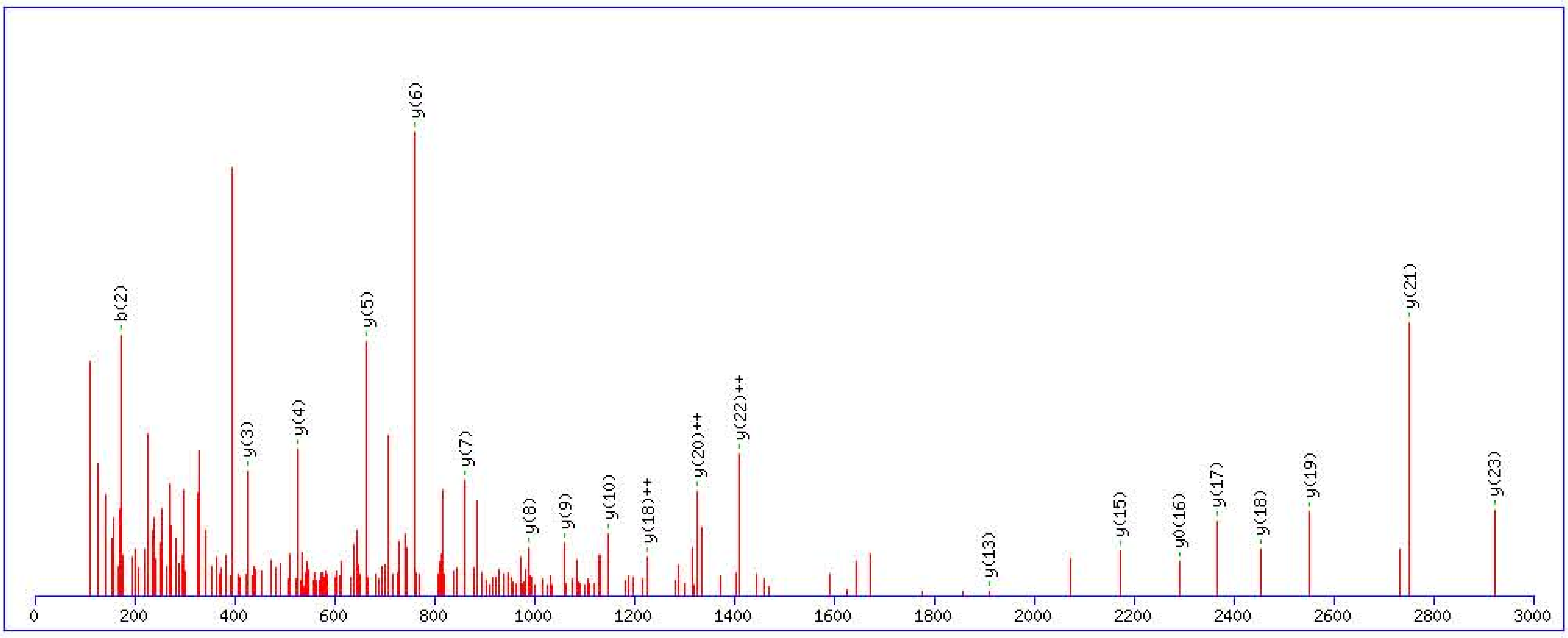
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNVAVTVSGHTCQHWSAQTPHTHNR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

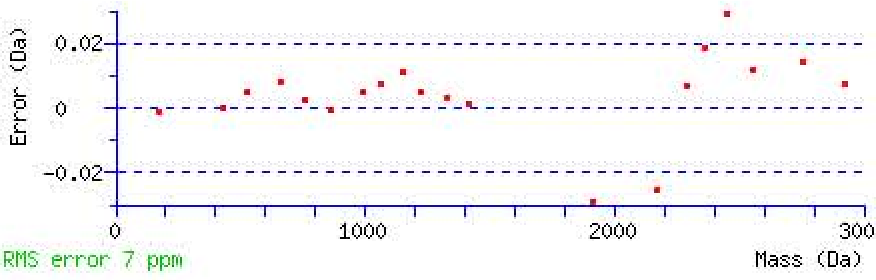
Match to Query 75169: 3092.444720 from(619.496220,5+) rtinseconds(1464) index(76640)
Title: Locus:1.1.1.2389.16 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

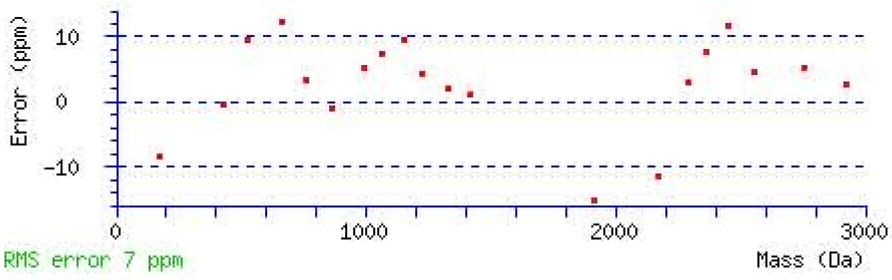
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3092.457016
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 115  Expect: 5.2e-011
Matches : 20/270 fragment ions using 27 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							25
2	172.071667	86.539471	155.045118	78.026197			N	3036.442790	1518.725033	3019.416241	1510.211758	3018.432225	1509.719750	24
3	271.140081	136.073679	254.113532	127.560404			V	***2922.399863***	1461.703569	2905.373314	1453.190295	2904.389298	1452.698287	23
4	342.177195	171.592236	325.150646	163.078961			A	2823.331449	1412.169362	2806.304900	1403.656088	2805.320884	1403.164080	22
5	441.245609	221.126443	424.219060	212.613168			V	***2752.294335***	1376.650805	2735.267786	1368.137531	2734.283770	1367.645523	21
6	542.293288	271.650282	525.266739	263.137008	524.282723	262.645000	T	2653.225921	1327.116598	2636.199372	1318.603324	2635.215356	1318.111316	20
7	641.361702	321.184489	624.335153	312.671215	623.351137	312.179207	V	***2552.178242***	1276.592759	2535.151693	1268.079484	2534.167677	1267.587476	19
8	728.393730	364.700503	711.367181	356.187229	710.383165	355.695221	S	***2453.109828***	1227.058552	2436.083279	1218.545277	2435.099263	1218.053269	18
9	785.415194	393.211235	768.388645	384.697961	767.404629	384.205953	G	***2366.077800***	1183.542538	2349.051251	1175.029263	2348.067235	1174.537255	17
10	922.474106	461.740691	905.447557	453.227417	904.463541	452.735409	H	2309.056336	1155.031806	2292.029787	1146.518531	2291.045771	1146.026523	16
11	1023.521785	512.264530	1006.495236	503.751256	1005.511220	503.259248	T	***2171.997424***	1086.502350	2154.970875	1077.989075	2153.986859	1077.497067	15
12	1183.552434	592.279855	1166.525885	583.766581	1165.541869	583.274572	C	2070.949745	1035.978510	2053.923196	1027.465236	2052.939180	1026.973228	14
13	1622.777760	811.892518	1605.751211	803.379244	1604.767195	802.887236	Q	***1910.919096***	955.963186	1893.892547	947.449911	1892.908531	946.957903	13
14	1759.836672	880.421974	1742.810123	871.908700	1741.826107	871.416692	H	1471.693770	736.350523	1454.667221	727.837248	1453.683205	727.345240	12
15	1945.915985	973.461631	1928.889436	964.948356	1927.905420	964.456348	W	1334.634858	667.821067	1317.608309	659.307792	1316.624293	658.815784	11
16	2032.948013	1016.977645	2015.921464	1008.464370	2014.937448	1007.972362	S	***1148.555545***	574.781410	1131.528996	566.268136	1130.544980	565.776128	10
17	2103.985127	1052.496201	2086.958578	1043.982927	2085.974562	1043.490919	A	***1061.523517***	531.265396	1044.496968	522.752122	1043.512952	522.260114	9
18	2232.043705	1116.525490	2215.017156	1108.012216	2214.033140	1107.520208	Q	***990.486403***	495.746839	973.459854	487.233565	972.475838	486.741557	8
19	2333.091384	1167.049330	2316.064835	1158.536055	2315.080819	1158.044047	T	***862.427825***	431.717550	845.401276	423.204276	844.417260	422.712268	7
20	2430.144148	1215.575712	2413.117599	1207.062437	2412.133583	1206.570429	P	***761.380146***	381.193711	744.353597	372.680436	743.369581	372.188428	6
21	2567.203060	1284.105168	2550.176511	1275.591893	2549.192495	1275.099885	H	***664.327382***	332.667329	647.300833	324.154054	646.316817	323.662046	5
22	2668.250739	1334.629007	2651.224190	1326.115733	2650.240174	1325.623725	T	***527.268470***	264.137873	510.241921	255.624598	509.257905	255.132590	4
23	2805.309651	1403.158463	2788.283102	1394.645189	2787.299086	1394.153181	H	***426.220791***	213.614033	409.194242	205.100759			3
24	2919.352578	1460.179927	2902.326029	1451.666652	2901.342013	1451.174644	N	289.161879	145.084577	272.135330	136.571303			2
25							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
115.0	3092.457016	-0.012296	GNVAVTVSGHTCQHWSAQTPHTHNR
73.1	3092.457016	-0.012296	GNVAVTVSGHTCQHWSAQTPHTHNR

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

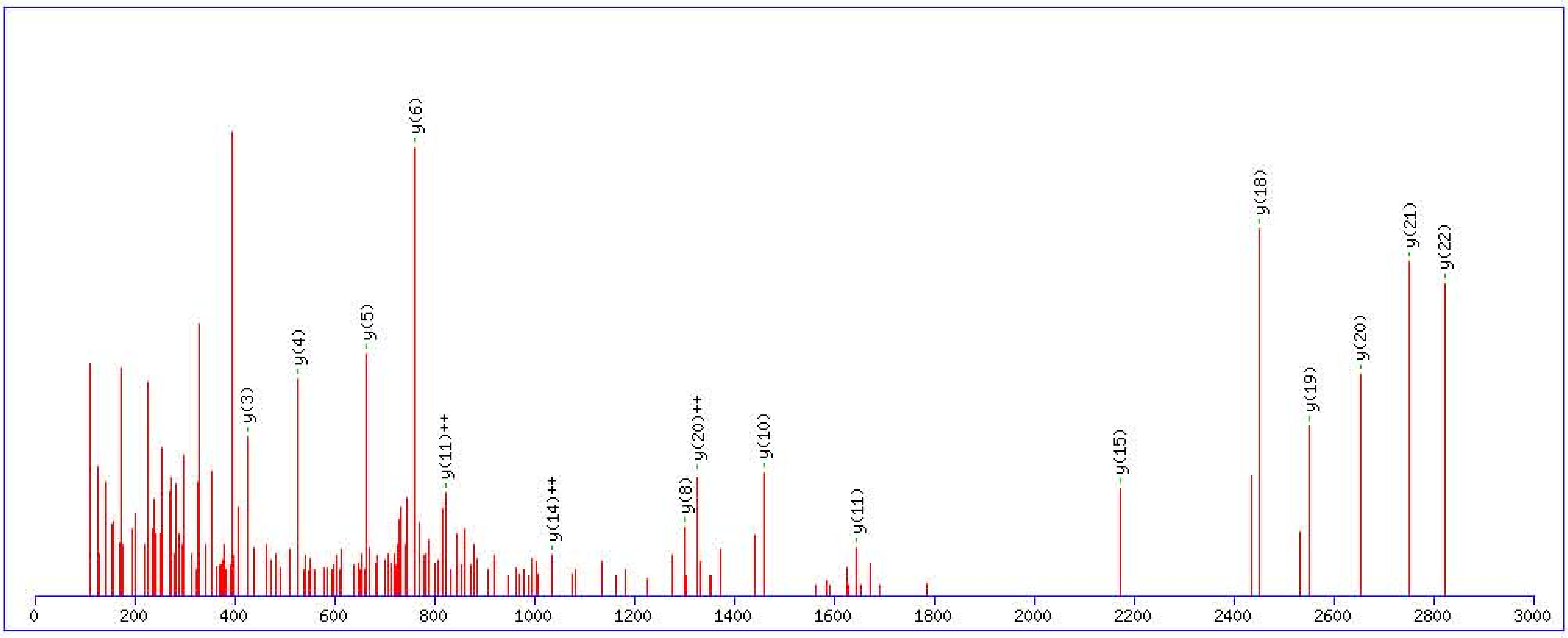
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNVAVTVSGHTCQHWSAQTPHTHNR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

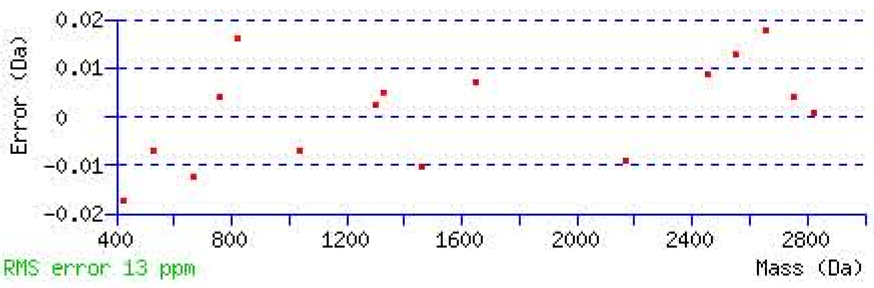
Match to Query 75170: 3092.450170 from(619.497310,5+) rtinseconds(1442) index(76458)
Title: Locus:1.1.1.2381.24 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

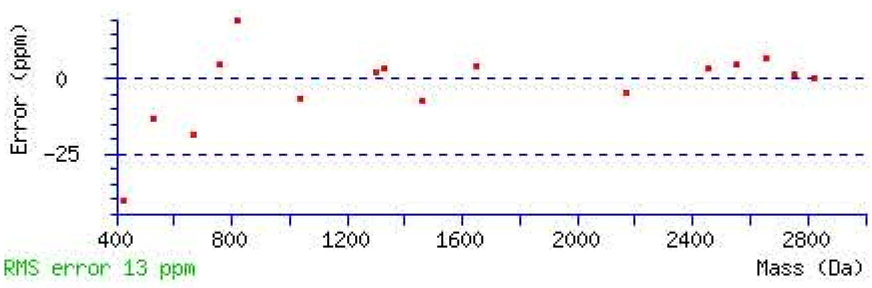
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3092.457016
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q18 : Biotin:Thermo-21345 (Q)
Ions Score: 95 **Expect:** 6e-009
Matches : 16/270 fragment ions using 23 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							25
2	172.071667	86.539471	155.045118	78.026197			N	3036.442790	1518.725033	3019.416241	1510.211758	3018.432225	1509.719750	24
3	271.140081	136.073679	254.113532	127.560404			V	2922.399863	1461.703569	2905.373314	1453.190295	2904.389298	1452.698287	23
4	342.177195	171.592236	325.150646	163.078961			A	***2823.331449***	1412.169362	2806.304900	1403.656088	2805.320884	1403.164080	22
5	441.245609	221.126443	424.219060	212.613168			V	***2752.294335***	1376.650805	2735.267786	1368.137531	2734.283770	1367.645523	21
6	542.293288	271.650282	525.266739	263.137008	524.282723	262.645000	T	***2653.225921***	1327.116598	2636.199372	1318.603324	2635.215356	1318.111316	20
7	641.361702	321.184489	624.335153	312.671215	623.351137	312.179207	V	***2552.178242***	1276.592759	2535.151693	1268.079484	2534.167677	1267.587476	19
8	728.393730	364.700503	711.367181	356.187229	710.383165	355.695221	S	***2453.109828***	1227.058552	2436.083279	1218.545277	2435.099263	1218.053269	18
9	785.415194	393.211235	768.388645	384.697961	767.404629	384.205953	G	2366.077800	1183.542538	2349.051251	1175.029263	2348.067235	1174.537255	17
10	922.474106	461.740691	905.447557	453.227417	904.463541	452.735409	H	2309.056336	1155.031806	2292.029787	1146.518531	2291.045771	1146.026523	16
11	1023.521785	512.264530	1006.495236	503.751256	1005.511220	503.259248	T	***2171.997424***	1086.502350	2154.970875	1077.989075	2153.986859	1077.497067	15
12	1183.552434	592.279855	1166.525885	583.766581	1165.541869	583.274572	C	2070.949745	1035.978510	2053.923196	1027.465236	2052.939180	1026.973228	14
13	1311.611012	656.309144	1294.584463	647.795870	1293.600447	647.303862	Q	1910.919096	955.963186	1893.892547	947.449911	1892.908531	946.957903	13
14	1448.669924	724.838600	1431.643375	716.325326	1430.659359	715.833318	H	1782.860518	891.933897	1765.833969	883.420622	1764.849953	882.928614	12
15	1634.749237	817.878257	1617.722688	809.364982	1616.738672	808.872974	W	***1645.801606***	823.404441	1628.775057	814.891166	1627.791041	814.399158	11
16	1721.781265	861.394271	1704.754716	852.880996	1703.770700	852.388988	S	***1459.722293***	730.364784	1442.695744	721.851510	1441.711728	721.359502	10
17	1792.818379	896.912828	1775.791830	888.399553	1774.807814	887.907545	A	1372.690265	686.848770	1355.663716	678.335496	1354.679700	677.843488	9
18	2232.043705	1116.525490	2215.017156	1108.012216	2214.033140	1107.520208	Q	***1301.653151***	651.330213	1284.626602	642.816939	1283.642586	642.324931	8
19	2333.091384	1167.049330	2316.064835	1158.536055	2315.080819	1158.044047	T	862.427825	431.717550	845.401276	423.204276	844.417260	422.712268	7
20	2430.144148	1215.575712	2413.117599	1207.062437	2412.133583	1206.570429	P	***761.380146***	381.193711	744.353597	372.680436	743.369581	372.188428	6
21	2567.203060	1284.105168	2550.176511	1275.591893	2549.192495	1275.099885	H	***664.327382***	332.667329	647.300833	324.154054	646.316817	323.662046	5
22	2668.250739	1334.629007	2651.224190	1326.115733	2650.240174	1325.623725	T	***527.268470***	264.137873	510.241921	255.624598	509.257905	255.132590	4
23	2805.309651	1403.158463	2788.283102	1394.645189	2787.299086	1394.153181	H	***426.220791***	213.614033	409.194242	205.100759			3
24	2919.352578	1460.179927	2902.326029	1451.666652	2901.342013	1451.174644	N	289.161879	145.084577	272.135330	136.571303			2
25							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
94.6	3092.457016	-0.006846	GNVAVTVSGHTCQHWSAQTPHTHNR
52.2	3092.457016	-0.006846	GNVAVTVSGHTCQHWSAQTPHTHNR

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

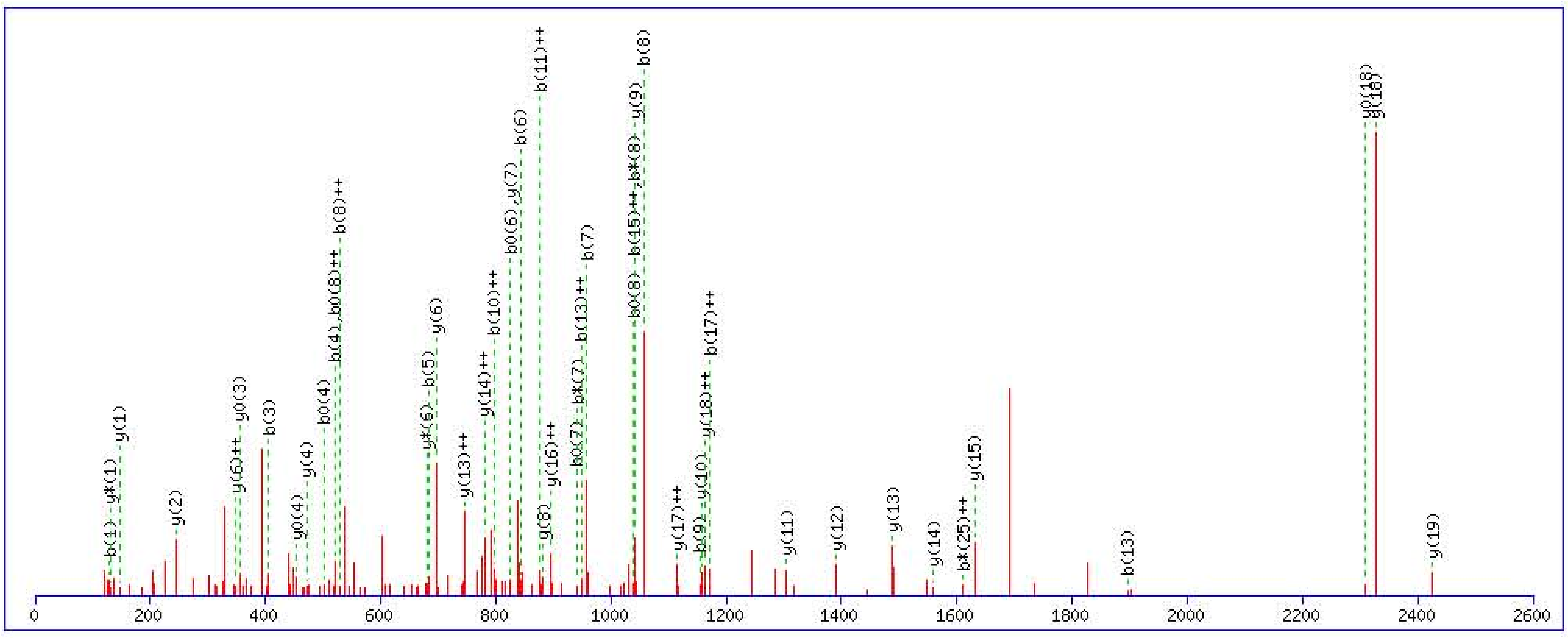
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KLYDYCDVPQCAAPSFDCGKPQVEPK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

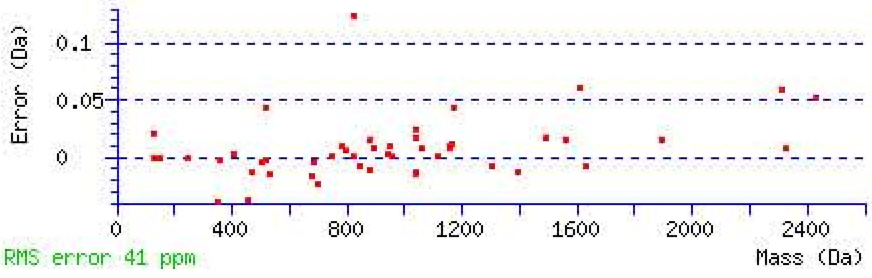
Match to Query 78684: 3382.564816 from(846.648480,4+) rtinseconds(1993) index(80250)
Title: Locus:1.1.1.2573.15 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

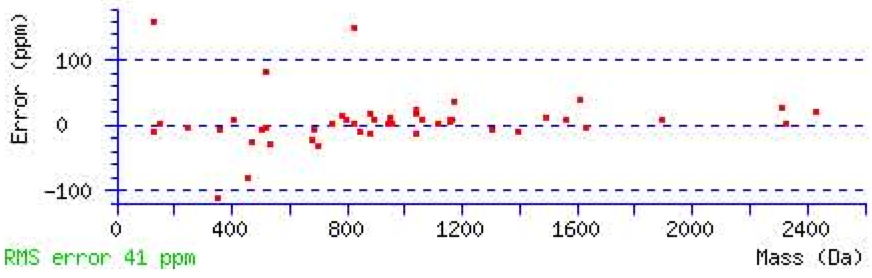
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3382.549469
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10    : Biotin:Thermo-21345 (Q)
Ions Score: 56  Expect: 6.1e-006
Matches : 49/290 fragment ions using 123 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***129.102239***	65.054757	112.075690	56.541483			K							26
2	242.186303	121.596790	225.159754	113.083515			L	3255.461780	1628.234528	3238.435231	1619.721253	3237.451215	1619.229245	25
3	***405.249632***	203.128454	388.223083	194.615180			Y	3142.377716	1571.692496	3125.351167	1563.179221	3124.367151	1562.687213	24
4	***520.276575***	260.641926	503.250026	252.128651	502.266010	251.636643	D	2979.314387	1490.160831	2962.287838	1481.647557	2961.303822	1481.155549	23
5	***683.339904***	342.173590	666.313355	333.660316	665.329339	333.168308	Y	2864.287444	1432.647360	2847.260895	1424.134085	2846.276879	1423.642077	22
6	***843.370553***	422.188915	826.344004	413.675640	825.359988	413.183632	C	2701.224115	1351.115695	2684.197566	1342.602421	2683.213550	1342.110413	21
7	***958.397496***	479.702386	941.370947	471.189112	940.386931	470.697104	D	2541.193466	1271.100371	2524.166917	1262.587096	2523.182901	1262.095088	20
8	***1057.465910***	**529.236593**	1040.439361	520.723319	1039.455345	520.231311	V	***2426.166523***	1213.586899	2409.139974	1205.073625	2408.155958	1204.581617	19
9	***1154.518674***	577.762975	1137.492125	569.249701	1136.508109	568.757693	P	***2327.098109***	1164.052692	2310.071560	1155.539418	2309.087544	1155.047410	18
10	1593.744000	**797.375638**	1576.717451	788.862364	1575.733435	788.370356	Q	2230.045345	1115.526310	2213.018796	1107.013036	2212.034780	1106.521028	17
11	1753.774649	**877.390963**	1736.748100	868.877688	1735.764084	868.385680	C	1790.820019	895.913647	1773.793470	887.400373	1772.809454	886.908365	16
12	1824.811763	912.909520	1807.785214	904.396245	1806.801198	903.904237	A	***1630.789370***	815.898323	1613.762821	807.385048	1612.778805	806.893040	15
13	***1895.848877***	**948.428077**	1878.822328	939.914802	1877.838312	939.422794	A	***1559.752256***	780.379766	1542.725707	771.866491	1541.741691	771.374483	14
14	1992.901641	996.954459	1975.875092	988.441184	1974.891076	987.949176	P	***1488.715142***	744.861209	1471.688593	736.347934	1470.704577	735.855926	13
15	2079.933669	**1040.470472**	2062.907120	1031.957198	2061.923104	1031.465190	S	***1391.662378***	696.334827	1374.635829	687.821552	1373.651813	687.329544	12
16	2227.002083	1114.004679	2209.975534	1105.491405	2208.991518	1104.999397	F	***1304.630350***	652.818813	1287.603801	644.305538	1286.619785	643.813530	11
17	2342.029026	**1171.518151**	2325.002477	1163.004876	2324.018461	1162.512868	D	***1157.561936***	579.284606	1140.535387	570.771331	1139.551371	570.279323	10
18	2502.059675	1251.533475	2485.033126	1243.020201	2484.049110	1242.528193	C	***1042.534993***	521.771135	1025.508444	513.257860	1024.524428	512.765852	9
19	2559.081139	1280.044207	2542.054590	1271.530933	2541.070574	1271.038925	G	***882.504344***	441.755810	865.477795	433.242536	864.493779	432.750528	8
20	2687.176102	1344.091689	2670.149553	1335.578414	2669.165537	1335.086406	K	***825.482880***	413.245078	808.456331	404.731804	807.472315	404.239796	7
21	2784.228866	1392.618071	2767.202317	1384.104796	2766.218301	1383.612788	P	***697.387917***	349.197597	680.361368	340.684322	679.377352	340.192314	6
22	2912.287444	1456.647360	2895.260895	1448.134085	2894.276879	1447.642077	Q	600.335153	300.671215	583.308604	292.157940	582.324588	291.665932	5
23	3011.355858	1506.181567	2994.329309	1497.668292	2993.345293	1497.176284	V	***472.276575***	236.641925	455.250026	228.128651	454.266010	227.636643	4
24	3140.398451	1570.702863	3123.371902	1562.189589	3122.387886	1561.697581	E	373.208161	187.107719	356.181612	178.594444	355.197596	178.102436	3
25	3237.451215	1619.229245	3220.424666	1610.715971	3219.440650	1610.223963	P	***244.165568***	122.586422	227.139019	114.073148			2
26							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.5	3382.549469	0.015347	KLYDYCDVPQCAAPSFDCGKPQVEPK
7.9	3382.549469	0.015347	KLYDYCDVPQCAAPSFDCGKPQVEPK
0.9	3382.580414	-0.015598	HLYPNTPYAYTFWTYMMNARSKNVGWR
0.9	3382.580414	-0.015598	HLYPNTPYAYTFWTYMMNARSKNVGWR

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

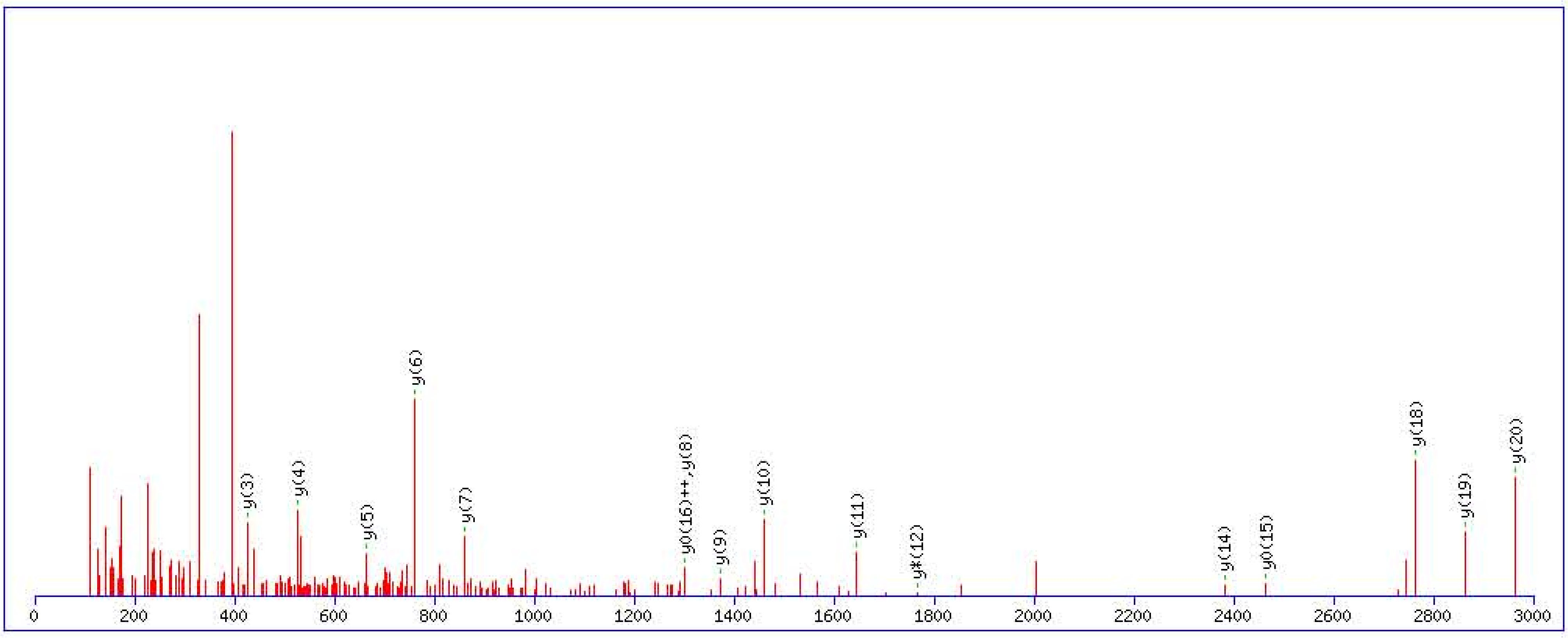
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNVAVTVSGHTCQHWSAQTPHTHNR**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

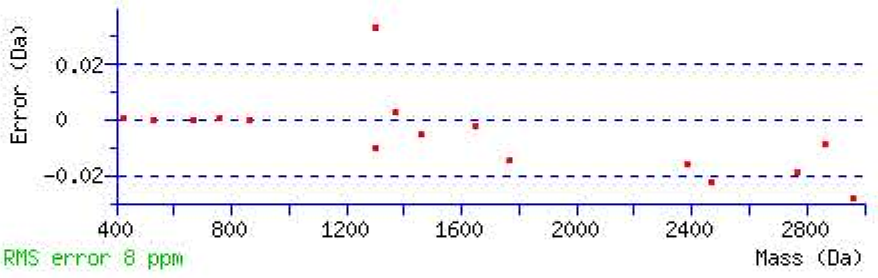
Match to Query 78967: 3403.612284 from(568.275990,6+) rtinseconds(1674) index(78081)
Title: Locus:1.1.1.2462.11 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

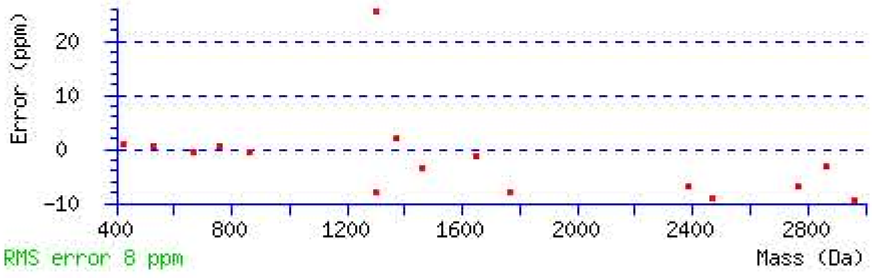
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3403.623764
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Q18     : Biotin:Thermo-21345 (Q)
Ions Score: 83  Expect: 1e-007
Matches : 16/270 fragment ions using 24 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							25
2	172.071667	86.539471	155.045118	78.026197			N	3347.609538	1674.308407	3330.582989	1665.795132	3329.598973	1665.303124	24
3	271.140081	136.073679	254.113532	127.560404			V	3233.566611	1617.286943	3216.540062	1608.773669	3215.556046	1608.281661	23
4	342.177195	171.592236	325.150646	163.078961			A	3134.498197	1567.752736	3117.471648	1559.239462	3116.487632	1558.747454	22
5	441.245609	221.126443	424.219060	212.613168			V	3063.461083	1532.234179	3046.434534	1523.720905	3045.450518	1523.228897	21
6	542.293288	271.650282	525.266739	263.137008	524.282723	262.645000	T	***2964.392669***	1482.699972	2947.366120	1474.186698	2946.382104	1473.694690	20
7	641.361702	321.184489	624.335153	312.671215	623.351137	312.179207	V	***2863.344990***	1432.176133	2846.318441	1423.662858	2845.334425	1423.170850	19
8	728.393730	364.700503	711.367181	356.187229	710.383165	355.695221	S	***2764.276576***	1382.641926	2747.250027	1374.128651	2746.266011	1373.636643	18
9	785.415194	393.211235	768.388645	384.697961	767.404629	384.205953	G	2677.244548	1339.125912	2660.217999	1330.612637	2659.233983	1330.120629	17
10	922.474106	461.740691	905.447557	453.227417	904.463541	452.735409	H	2620.223084	1310.615180	2603.196535	1302.101905	2602.212519	1301.609897	16
11	1023.521785	512.264530	1006.495236	503.751256	1005.511220	503.259248	T	2483.164172	1242.085724	2466.137623	1233.572449	2465.153607	1233.080441	15
12	1183.552434	592.279855	1166.525885	583.766581	1165.541869	583.274572	C	***2382.116493***	1191.561884	2365.089944	1183.048610	2364.105928	1182.556602	14
13	1622.777760	811.892518	1605.751211	803.379244	1604.767195	802.887236	Q	2222.085844	1111.546560	2205.059295	1103.033285	2204.075279	1102.541277	13
14	1759.836672	880.421974	1742.810123	871.908700	1741.826107	871.416692	H	1782.860518	891.933897	1765.833969	883.420622	1764.849953	882.928614	12
15	1945.915985	973.461631	1928.889436	964.948356	1927.905420	964.456348	W	***1645.801606***	823.404441	1628.775057	814.891166	1627.791041	814.399158	11
16	2032.948013	1016.977645	2015.921464	1008.464370	2014.937448	1007.972362	S	***1459.722293***	730.364784	1442.695744	721.851510	1441.711728	721.359502	10
17	2103.985127	1052.496201	2086.958578	1043.982927	2085.974562	1043.490919	A	***1372.690265***	686.848770	1355.663716	678.335496	1354.679700	677.843488	9
18	2543.210453	1272.108865	2526.183904	1263.595590	2525.199888	1263.103582	Q	***1301.653151***	651.330213	1284.626602	642.816939	1283.642586	642.324931	8
19	2644.258132	1322.632704	2627.231583	1314.119429	2626.247567	1313.627421	T	***862.427825***	431.717550	845.401276	423.204276	844.417260	422.712268	7
20	2741.310896	1371.159086	2724.284347	1362.645811	2723.300331	1362.153803	P	***761.380146***	381.193711	744.353597	372.680436	743.369581	372.188428	6
21	2878.369808	1439.688542	2861.343259	1431.175267	2860.359243	1430.683259	H	***664.327382***	332.667329	647.300833	324.154054	646.316817	323.662046	5
22	2979.417487	1490.212381	2962.390938	1481.699107	2961.406922	1481.207099	T	***527.268470***	264.137873	510.241921	255.624598	509.257905	255.132590	4
23	3116.476399	1558.741837	3099.449850	1550.228563	3098.465834	1549.736555	H	***426.220791***	213.614033	409.194242	205.100759			3
24	3230.519326	1615.763301	3213.492777	1607.250026	3212.508761	1606.758018	N	289.161879	145.084577	272.135330	136.571303			2
25							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
83.4	3403.623764	-0.011480	GNVAVTVSGHTCQHWSAQTPHTHNR

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

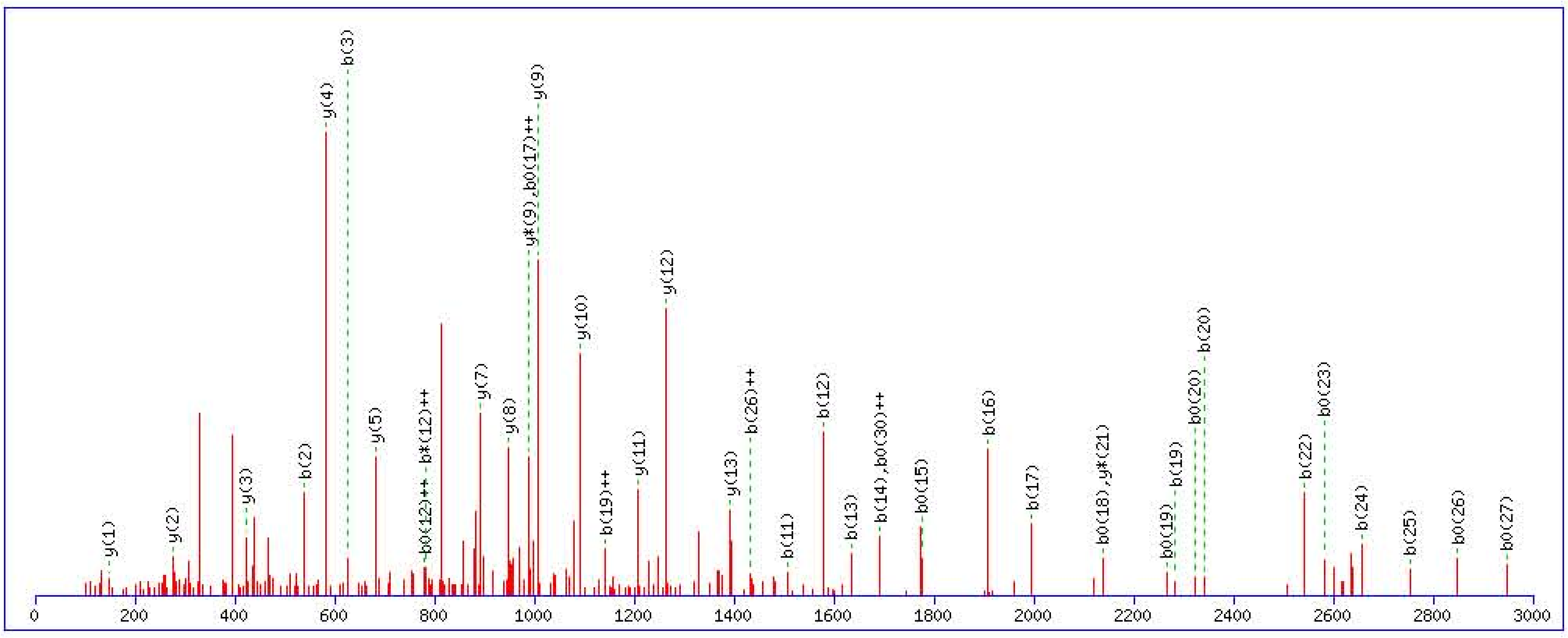
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VQSTELCAGHLAGGTDSCQGDSGGPLVCFEK**
Found in **PLMN_HUMAN**, Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2

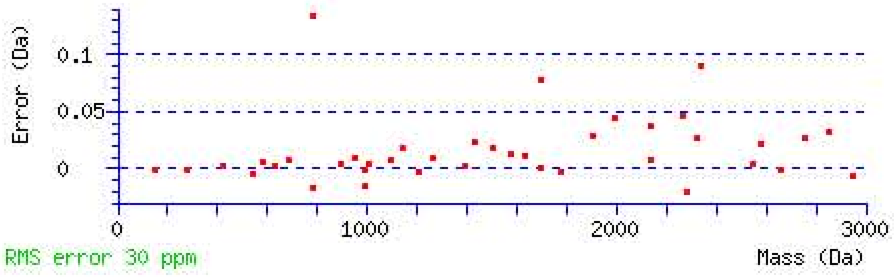
Match to Query 80114: 3547.624336 from(887.913360,4+) rtinseconds(2180) index(81457)
Title: Locus:1.1.1.2638.26 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

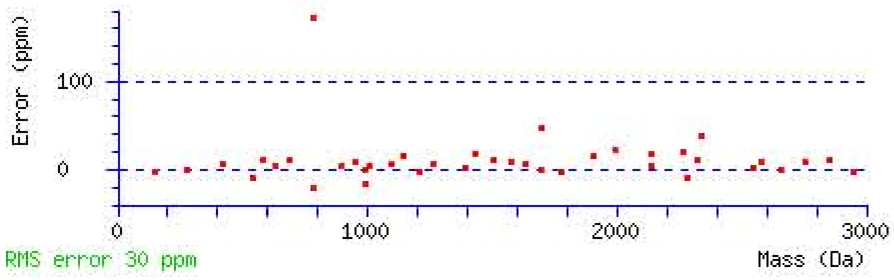
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3547.584061
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2 : Biotin:Thermo-21345 (Q)
Ions Score: 117 **Expect:** 2.1e-011
Matches : 40/352 fragment ions using 50 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							31
2	***539.301016***	270.154146	522.274467	261.640872			Q	3449.522877	1725.265076	3432.496328	1716.751802	3431.512312	1716.259794	30
3	***626.333044***	313.670160	609.306495	305.156886	608.322479	304.664878	S	3010.297551	1505.652413	2993.271002	1497.139139	2992.286986	1496.647131	29
4	727.380723	364.194000	710.354174	355.680725	709.370158	355.188717	T	2923.265523	1462.136399	2906.238974	1453.623125	2905.254958	1453.131117	28
5	856.423316	428.715296	839.396767	420.202022	838.412751	419.710014	E	2822.217844	1411.612560	2805.191295	1403.099285	2804.207279	1402.607277	27
6	969.507380	485.257328	952.480831	476.744054	951.496815	476.252046	L	2693.175251	1347.091263	2676.148702	1338.577989	2675.164686	1338.085981	26
7	1129.538029	565.272653	1112.511480	556.759378	1111.527464	556.267370	C	2580.091187	1290.549231	2563.064638	1282.035957	2562.080622	1281.543949	25
8	1200.575143	600.791210	1183.548594	592.277935	1182.564578	591.785927	A	2420.060538	1210.533907	2403.033989	1202.020632	2402.049973	1201.528624	24
9	1257.596607	629.301942	1240.570058	620.788667	1239.586042	620.296659	G	2349.023424	1175.015350	2331.996875	1166.502075	2331.012859	1166.010067	23
10	1394.655519	697.831397	1377.628970	689.318123	1376.644954	688.826115	H	2292.001960	1146.504618	2274.975411	1137.991343	2273.991395	1137.499335	22
11	***1507.739583***	754.373429	1490.713034	745.860155	1489.729018	745.368147	L	2154.943048	1077.975162	2137.916499	1069.461887	2136.932483	1068.969879	21
12	***1578.776697***	789.891986	1561.750148	781.378712	1560.766132	780.886704	A	2041.858984	1021.433130	2024.832435	1012.919855	2023.848419	1012.427847	20
13	***1635.798161***	818.402718	1618.771612	809.889444	1617.787596	809.397436	G	1970.821870	985.914573	1953.795321	977.401298	1952.811305	976.909290	19
14	***1692.819625***	846.913450	1675.793076	838.400176	1674.809060	837.908168	G	1913.800406	957.403841	1896.773857	948.890566	1895.789841	948.398558	18
15	1793.867304	897.437290	1776.840755	888.924015	1775.856739	888.432007	T	1856.778942	928.893109	1839.752393	920.379835	1838.768377	919.887826	17
16	***1908.894247***	954.950761	1891.867698	946.437487	1890.883682	945.945479	D	1755.731263	878.369269	1738.704714	869.855995	1737.720698	869.363987	16
17	***1995.926275***	998.466775	1978.899726	989.953501	1977.915710	989.461493	S	1640.704320	820.855798	1623.677771	812.342523	1622.693755	811.850515	15
18	2155.956924	1078.482100	2138.930375	1069.968825	2137.946359	1069.476817	C	1553.672292	777.339784	1536.645743	768.826509	1535.661727	768.334501	14
19	***2284.015502***	**1142.511389**	2266.988953	1133.998114	2266.004937	1133.506106	Q	***1393.641643***	697.324459	1376.615094	688.811185	1375.631078	688.319177	13
20	***2341.036966***	1171.022121	2324.010417	1162.508846	2323.026401	1162.016838	G	***1265.583065***	633.295170	1248.556516	624.781896	1247.572500	624.289888	12
21	2456.063909	1228.535592	2439.037360	1220.022318	2438.053344	1219.530310	D	***1208.561601***	604.784438	1191.535052	596.271164	1190.551036	595.779156	11
22	***2543.095937***	1272.051606	2526.069388	1263.538332	2525.085372	1263.046324	S	***1093.534658***	547.270967	1076.508109	538.757692	1075.524093	538.265684	10
23	2600.117401	1300.562338	2583.090852	1292.049064	2582.106836	1291.557056	G	***1006.502630***	503.754953	989.476081	495.241678	988.492065	494.749670	9
24	***2657.138865***	1329.073070	2640.112316	1320.559796	2639.128300	1320.067788	G	***949.481166***	475.244221	932.454617	466.730946	931.470601	466.238938	8
25	***2754.191629***	1377.599452	2737.165080	1369.086178	2736.181064	1368.594170	P	***892.459702***	446.733489	875.433153	438.220214	874.449137	437.728206	7
26	2867.275693	**1434.141484**	2850.249144	1425.628210	2849.265128	1425.136202	L	795.406938	398.207107	778.380389	389.693832	777.396373	389.201824	6
27	2966.344107	1483.675691	2949.317558	1475.162417	2948.333542	1474.670409	V	***682.322874***	341.665075	665.296325	333.151800	664.312309	332.659792	5
28	3126.374756	1563.691016	3109.348207	1555.177741	3108.364191	1554.685733	C	***583.254460***	292.130868	566.227911	283.617593	565.243895	283.125585	4
29	3273.443170	1637.225223	3256.416621	1628.711948	3255.432605	1628.219940	F	***423.223811***	212.115543	406.197262	203.602269	405.213246	203.110261	3
30	3402.485763	1701.746519	3385.459214	1693.233245	3384.475198	1692.741237	E	***276.155397***	138.581337	259.128848	130.068062	258.144832	129.576054	2
31							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
117.4	3547.584061	0.040275	VQSTELCAGHLAGGTDSCQGDSGGPLVCFEK
45.5	3547.584061	0.040275	VQSTELCAGHLAGGTDSCQGDSGGPLVCFEK

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

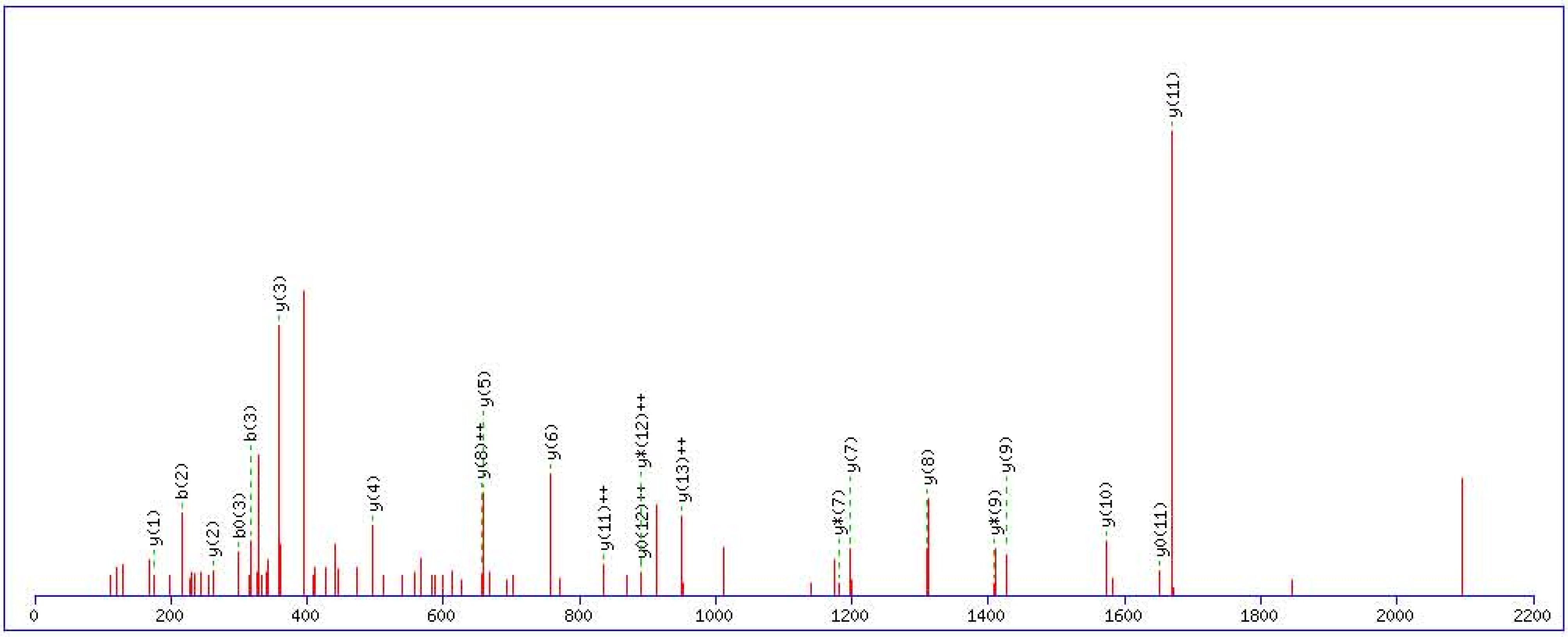
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TNTQPFDLQVYHPSR**
Found in **LRP1_HUMAN**, Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapiens GN=LRP1 PE=1 SV=2

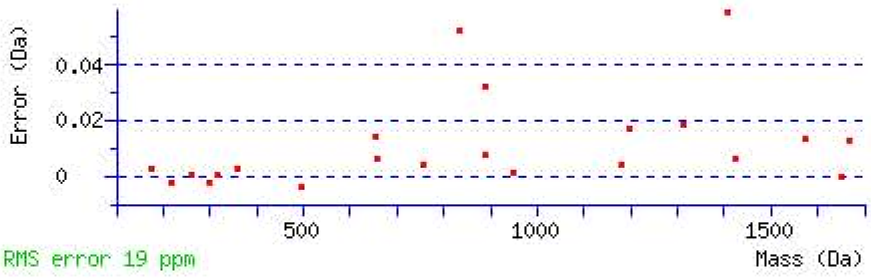
Match to Query 59830: 2113.048242 from(705.356690,3+) rtinseconds(2075) index(63582)
Title: Locus:1.1.1.2720.4 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

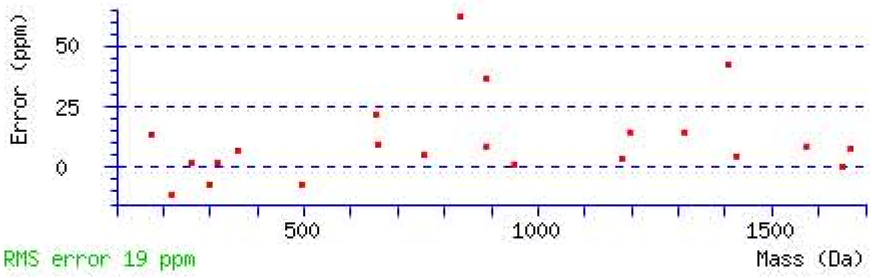
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2200 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2113.041504
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9     : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 0.00016
Matches : 22/164 fragment ions using 53 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							15
2	**216.097882**	108.552579	199.071333	100.039305	198.087317	99.547296	N	2013.001094	1007.004185	1995.974545	998.490911	1994.990529	997.998903	14
3	**317.145561**	159.076418	300.119012	150.563144	299.134996	150.071136	T	1898.958167	949.982722	1881.931618	941.469447	1880.947602	940.977439	13
4	445.204139	223.105707	428.177590	214.592433	427.193574	214.100425	Q	1797.910488	899.458882	1780.883939	890.945608	1779.899923	890.453600	12
5	542.256903	271.632090	525.230354	263.118815	524.246338	262.626807	P	***1669.851910***	835.429593	1652.825361	826.916319	1651.841345	826.424311	11
6	689.325317	345.166297	672.298768	336.653022	671.314752	336.161014	F	***1572.799146***	786.903211	1555.772597	778.389937	1554.788581	777.897929	10
7	804.352260	402.679768	787.325711	394.166494	786.341695	393.674486	D	***1425.730732***	713.369004	1408.704183	704.855730	1407.720167	704.363722	9
8	917.436324	459.221800	900.409775	450.708526	899.425759	450.216518	L	***1310.703789***	655.855533	1293.677240	647.342258	1292.693224	646.850250	8
9	1356.661650	678.834463	1339.635101	670.321189	1338.651085	669.829181	Q	***1197.619725***	599.313501	1180.593176	590.800226	1179.609160	590.308218	7
10	1455.730064	728.368670	1438.703515	719.855396	1437.719499	719.363388	V	***758.394399***	379.700838	741.367850	371.187563	740.383834	370.695555	6
11	1618.793393	809.900335	1601.766844	801.387060	1600.782828	800.895052	Y	***659.325985***	330.166631	642.299436	321.653356	641.315420	321.161348	5
12	1755.852305	878.429791	1738.825756	869.916516	1737.841740	869.424508	H	***496.262656***	248.634966	479.236107	240.121692	478.252091	239.629684	4
13	1852.905069	926.956173	1835.878520	918.442898	1834.894504	917.950890	P	***359.203744***	180.105510	342.177195	171.592236	341.193179	171.100228	3
14	1939.937097	970.472187	1922.910548	961.958912	1921.926532	961.466904	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
15							R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
52.1	2113.041504	0.006738	TNTQPFDLQVYHPSR
8.0	2113.041504	0.006738	TNTQPFDLQVYHPSR

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

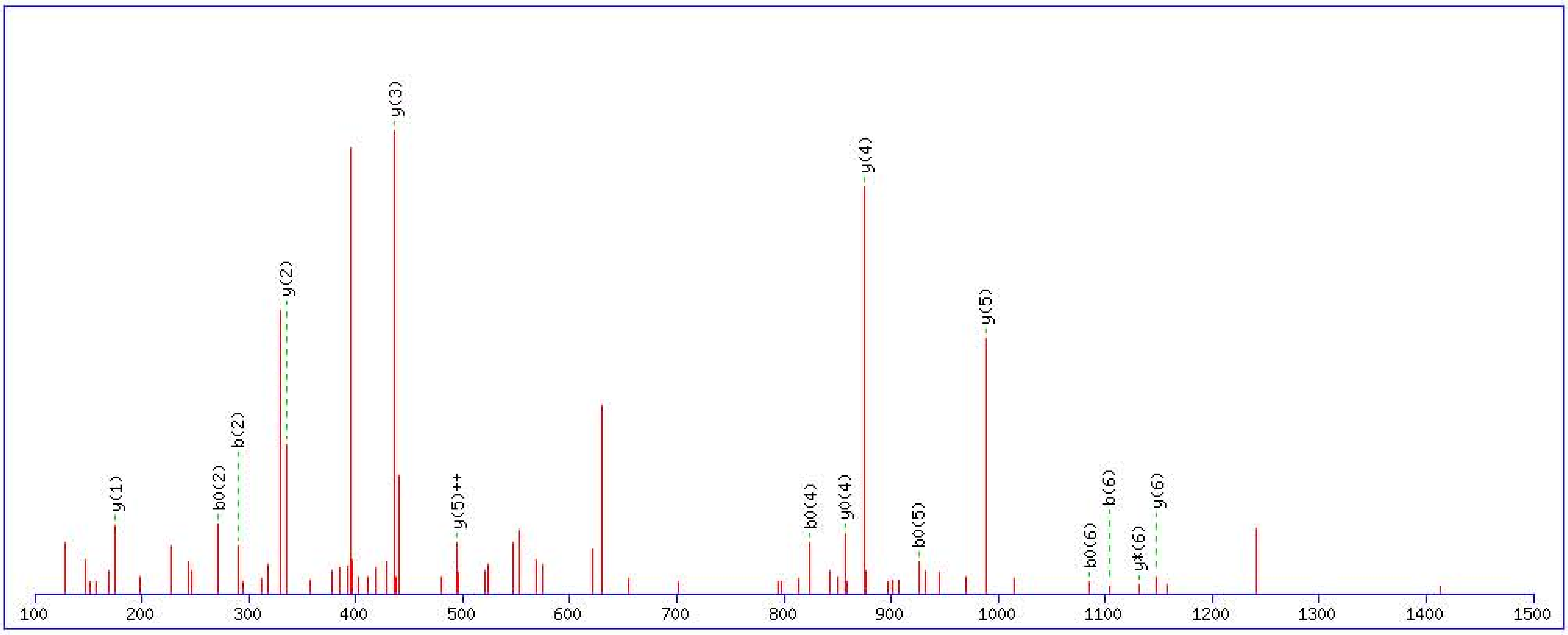
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ECLQTCR**
Found in **AMBP_HUMAN**, Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

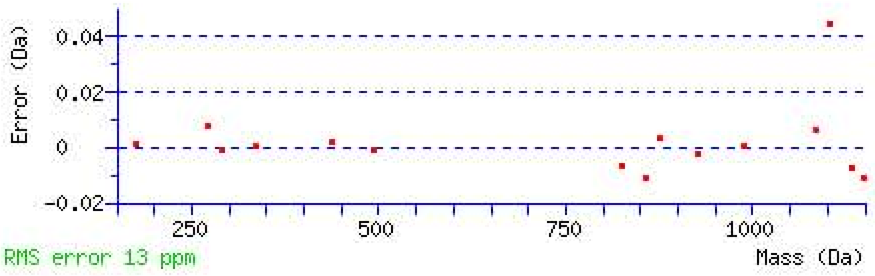
Match to Query 34363: 1276.570328 from(639.292440,2+) rtinseconds(1466) index(59296)
Title: Locus:1.1.1.2508.19 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

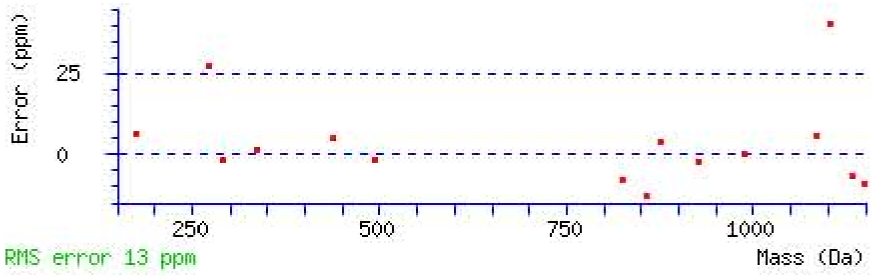
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1276.572632
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4     : Biotin:Thermo-21345 (Q)
Ions Score: 32  Expect: 0.004
Matches : 15/62 fragment ions using 33 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							7
2	**290.080518**	145.543897			272.069953	136.538615	C	***1148.537319***	574.772298	1131.510770	566.259023	1130.526754	565.767015	6
3	403.164582	202.085929			385.154017	193.080647	L	***988.506670***	494.756973	971.480121	486.243699	970.496105	485.751691	5
4	842.389908	421.698592	825.363359	413.185318	824.379343	412.693310	Q	***875.422606***	438.214941	858.396057	429.701667	857.412041	429.209659	4
5	943.437587	472.222432	926.411038	463.709157	925.427022	463.217149	T	***436.197280***	218.602278	419.170731	210.089003	418.186715	209.596995	3
6	**1103.468236**	552.237756	1086.441687	543.724482	1085.457671	543.232474	C	***335.149601***	168.078438	318.123052	159.565164			2
7							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
31.6	1276.572632	-0.002304	ECLQTCR
8.8	1276.583862	-0.013534	KMSLSCHVCR
8.6	1276.579605	-0.009277	EEQRSPFNDR
7.0	1276.571762	-0.001434	AGAESPTMSVDGR
6.5	1276.569229	0.001099	MTGRYEMYAR
5.3	1276.560516	0.009812	QQVPSEDSMEK
4.8	1276.553116	0.017212	EDLDNASKDDR

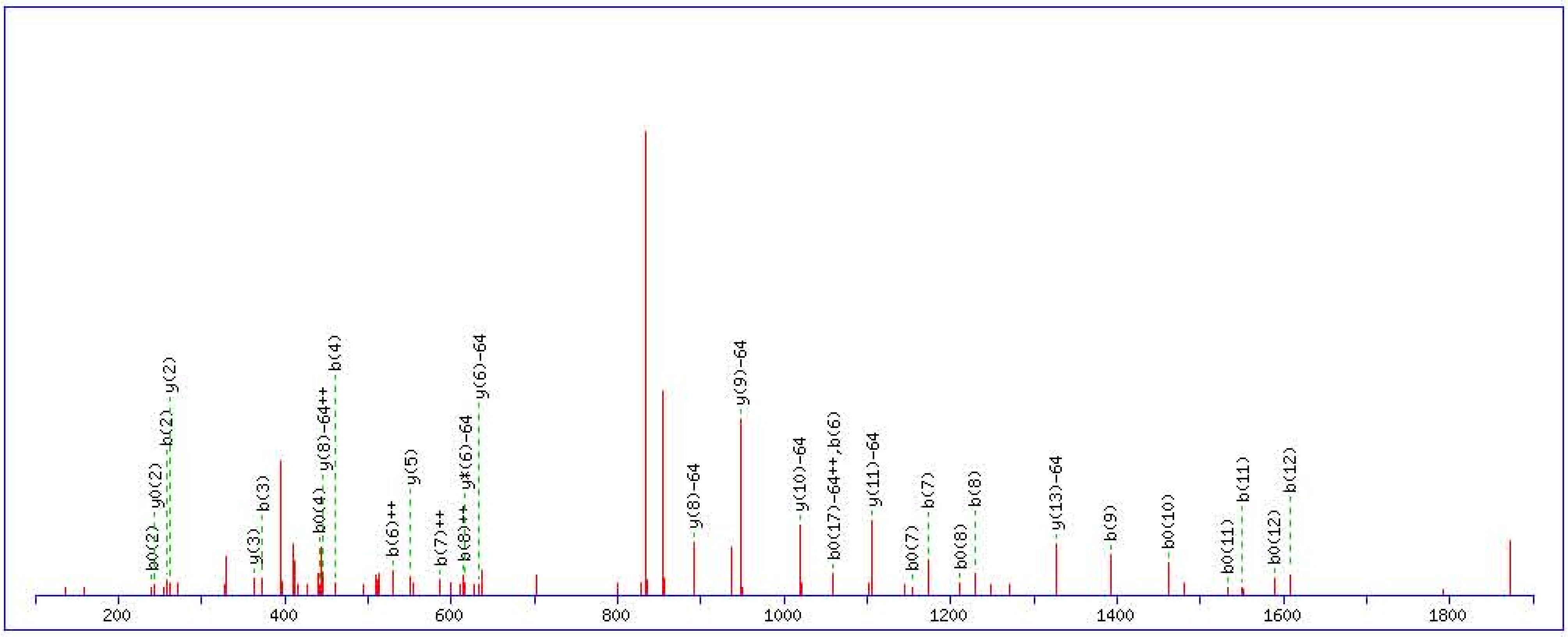
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KEDSCQLGYSAGPCMGMTSR**
Found in **AMBP_HUMAN**, Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1

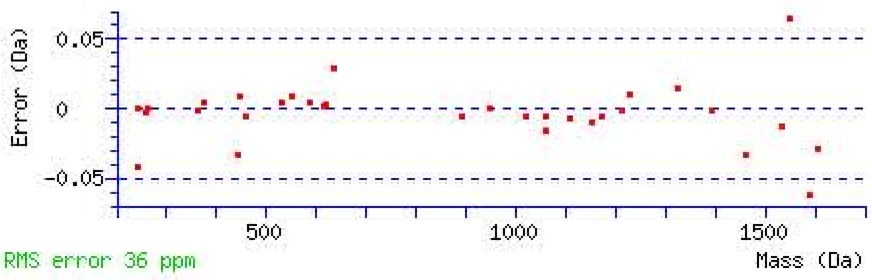
Match to Query 69322: 2561.097522 from(854.706450,3+) rtinseconds(1501) index(59545)
Title: Locus:1.1.1.2520.21 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

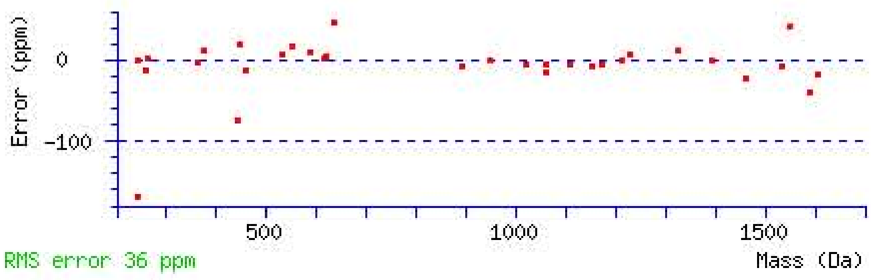
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2561.084106
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
M15    : Oxidation (M), with neutral losses 63.998285(shown in table), 0.000000
Ions Score: 36  Expect: 0.00099
Matches : 32/338 fragment ions using 80 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	129.102239	65.054757	112.075690	56.541483			K							20
2	***258.144832***	129.576054	241.118283	121.062780	240.134267	120.570772	E	2369.998138	1185.502707	2352.971589	1176.989432	2351.987573	1176.497424	19
3	***373.171775***	187.089526	356.145226	178.576251	355.161210	178.084243	D	2240.955545	1120.981410	2223.928996	1112.468136	2222.944980	1111.976128	18
4	***460.203803***	230.605540	443.177254	222.092265	442.193238	221.600257	S	2125.928602	1063.467939	2108.902053	1054.954664	2107.918037	1054.462656	17
5	620.234452	310.620864	603.207903	302.107590	602.223887	301.615582	C	2038.896574	1019.951925	2021.870025	1011.438650	2020.886009	1010.946642	16
6	***1059.459778***	**530.233527**	1042.433229	521.720253	1041.449213	521.228245	Q	1878.865925	939.936600	1861.839376	931.423326	1860.855360	930.931318	15
7	***1172.543842***	**586.775559**	1155.517293	578.262285	1154.533277	577.770277	L	1439.640599	720.323937	1422.614050	711.810663	1421.630034	711.318655	14
8	***1229.565306***	**615.286291**	1212.538757	606.773017	1211.554741	606.281008	G	***1326.556535***	663.781905	1309.529986	655.268631	1308.545970	654.776623	13
9	***1392.628635***	696.817956	1375.602086	688.304681	1374.618070	687.812673	Y	1269.535071	635.271174	1252.508522	626.757899	1251.524506	626.265891	12
10	1479.660663	740.333970	1462.634114	731.820695	1461.650098	731.328687	S	***1106.471742***	553.739509	1089.445193	545.226235	1088.461177	544.734226	11
11	***1550.697777***	775.852527	1533.671228	767.339252	1532.687212	766.847244	A	***1019.439714***	510.223495	1002.413165	501.710220	1001.429149	501.218212	10
12	***1607.719241***	804.363259	1590.692692	795.849984	1589.708676	795.357976	G	***948.402600***	474.704938	931.376051	466.191663	930.392035	465.699655	9
13	1704.772005	852.889641	1687.745456	844.376366	1686.761440	843.884358	P	***891.381136***	446.194206	874.354587	437.680931	873.370571	437.188923	8
14	1864.802654	932.904965	1847.776105	924.391691	1846.792089	923.899683	C	794.328372	397.667824	777.301823	389.154549	776.317807	388.662541	7
15	1947.839769	974.423523	1930.813220	965.910248	1929.829204	965.418240	M	***634.297723***	317.652499	617.271174	309.139225	616.287158	308.647217	6
16	2004.861233	1002.934255	1987.834684	994.420980	1986.850668	993.928972	G	***551.260608***	276.133942	534.234059	267.620667	533.250043	267.128659	5
17	2135.901718	1068.454497	2118.875169	1059.941222	2117.891153	1059.449214	M	494.239144	247.623210	477.212595	239.109935	476.228579	238.617927	4
18	2236.949397	1118.978336	2219.922848	1110.465062	2218.938832	1109.973054	T	***363.198659***	182.102967	346.172110	173.589693	345.188094	173.097685	3
19	2323.981425	1162.494350	2306.954876	1153.981076	2305.970860	1153.489068	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
20							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.7	2561.084106	0.013416	KEDSCQLGYSAGPCMGMTSR
28.8	2561.084106	0.013416	KEDSCQLGYSAGPCMGMTSR

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

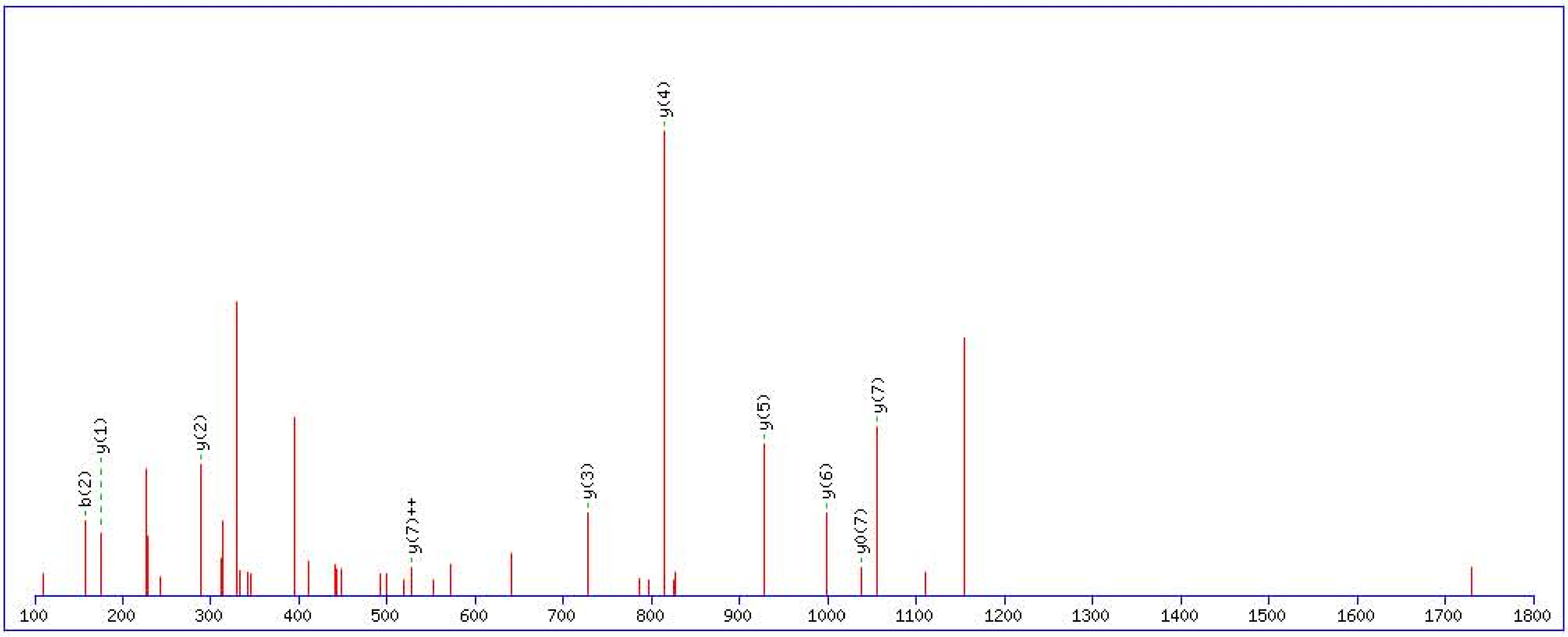
Mascot Search Results

Peptide View

MS/MS Fragmentation of **VGALSQLR**
Found in **MENT_HUMAN**, Protein MENT OS=Homo sapiens GN=MENT PE=2 SV=1

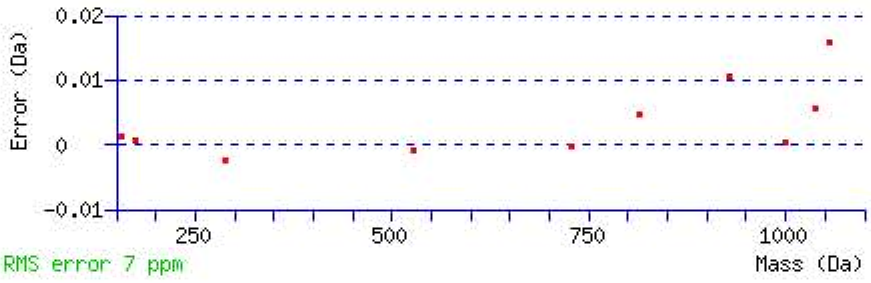
Match to Query 29792: 1153.660228 from(577.837390,2+) rtinseconds(1920) index(62518)
Title: Locus:1.1.1.2666.14 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

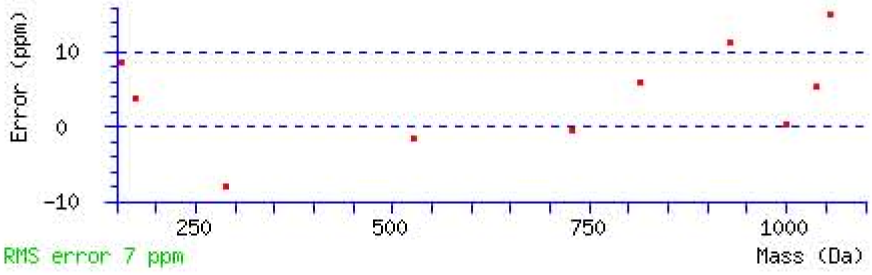
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1153.664139
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6 : Biotin:Thermo-21345 (Q)
Ions Score: 42 **Expect:** 0.00088
Matches : 10/60 fragment ions using 19 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							8
2	157.097154	79.052215					G	***1055.603012***	528.305144	1038.576463	519.791870	1037.592447	519.299862	7
3	228.134268	114.570772					A	***998.581548***	499.794412	981.554999	491.281138	980.570983	490.789130	6
4	341.218332	171.112804					L	***927.544434***	464.275855	910.517885	455.762581	909.533869	455.270573	5
5	428.250360	214.628818			410.239795	205.623535	S	***814.460370***	407.733823	797.433821	399.220549	796.449805	398.728541	4
6	867.475686	434.241481	850.449137	425.728207	849.465121	425.236199	Q	***727.428342***	364.217809	710.401793	355.704535			3
7	980.559750	490.783513	963.533201	482.270239	962.549185	481.778231	L	***288.203016***	144.605146	271.176467	136.091872			2
8							R	***175.118952***	88.063114	158.092403	79.549840			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
42.0	1153.664139	-0.003911	VGALSQLR
8.8	1153.675354	-0.015126	RALLSQR
8.8	1153.675369	-0.015141	RALTVQR
8.6	1153.664124	-0.003896	VKQEALR
5.6	1153.645477	0.014751	RALAAPVAEEK
5.1	1153.645523	0.014705	GGLSVAVPGEIR
4.5	1153.650864	0.009364	LWQRPWLR
1.0	1153.645493	0.014735	NLLKLDPADR
0.1	1153.656723	0.003505	RPSADPGKKAK

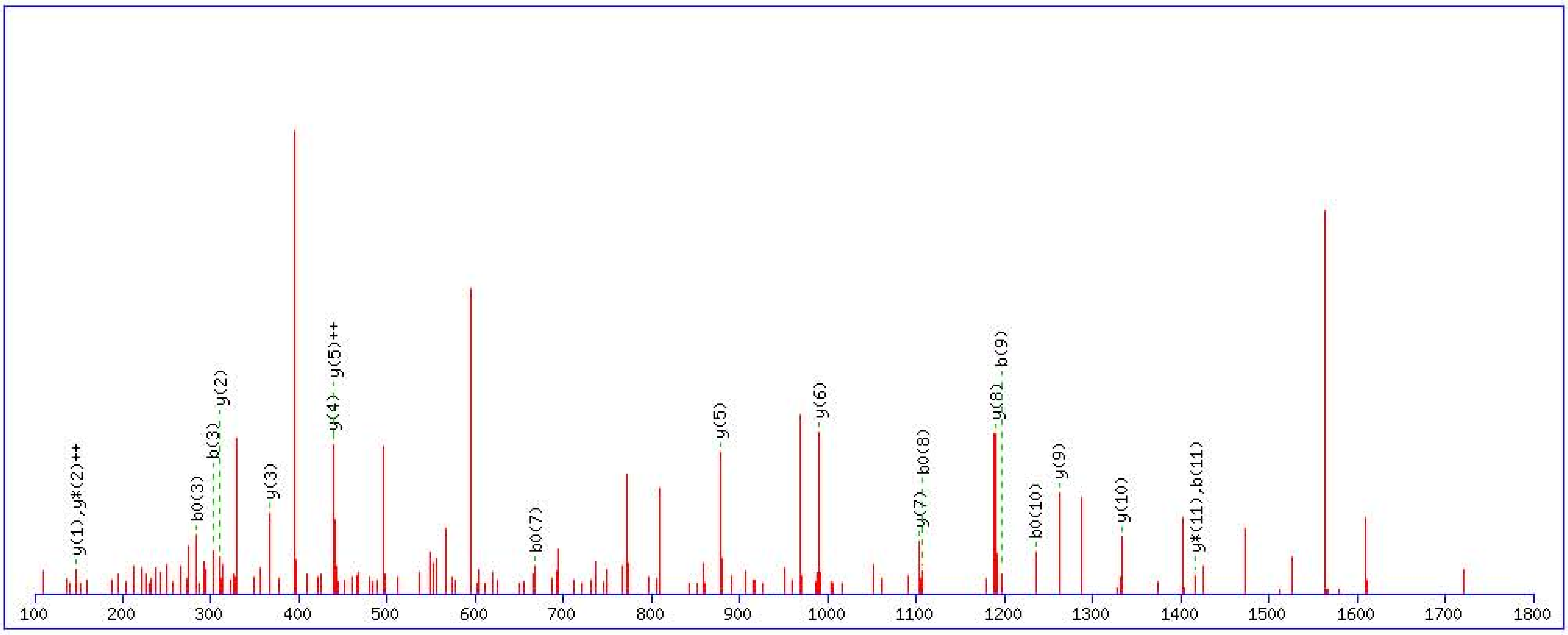
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **ETAASLLQAGYK**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

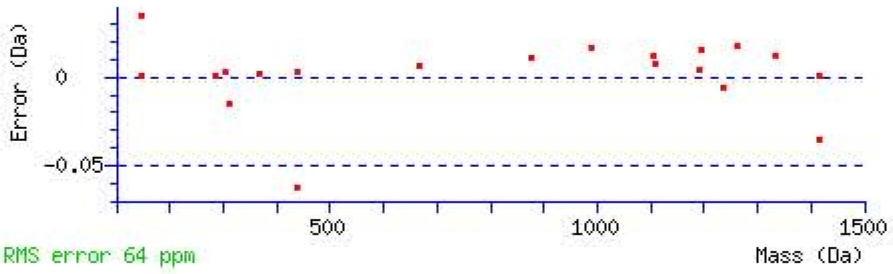
Match to Query 44160: 1561.813428 from(781.913990,2+) rtinseconds(2117) index(63853)
Title: Locus:1.1.1.2734.23 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

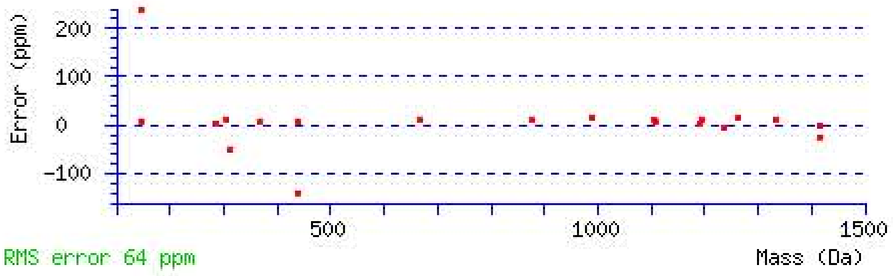
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1561.817383
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 42 **Expect:** 0.0016
Matches : 20/104 fragment ions using 57 most intense peaks (help)

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#
1	130.049869	65.528572			112.039304	56.523290	E							12
2	231.097548	116.052412			213.086983	107.047130	T	1433.782100	717.394688	1416.755551	708.881414	1415.771535	708.389406	11
3	**302.134662**	151.570969			284.124097	142.565687	A	***1332.734421***	666.870848	1315.707872	658.357574	1314.723856	657.865566	10
4	373.171776	187.089526			355.161211	178.084243	A	***1261.697307***	631.352292	1244.670758	622.839017	1243.686742	622.347009	9
5	460.203804	230.605540			442.193239	221.600257	S	***1190.660193***	595.833734	1173.633644	587.320460	1172.649628	586.828452	8
6	573.287868	287.147572			555.277303	278.142290	L	***1103.628165***	552.317721	1086.601616	543.804446			7
7	686.371932	343.689604			668.361367	334.684322	L	***990.544101***	495.775689	973.517552	487.262414			6
8	1125.597258	563.302267	1108.570709	554.788993	1107.586693	554.296985	Q	***877.460037***	439.233657	860.433488	430.720382			5
9	**1196.634372**	598.820824	1179.607823	590.307550	1178.623807	589.815541	A	***438.234711***	219.620993	421.208162	211.107719			4
10	1253.655836	627.331556	1236.629287	618.818282	1235.645271	618.326273	G	***367.197597***	184.102436	350.171048	175.589162			3
11	**1416.719165**	708.863221	1399.692616	700.349946	1398.708600	699.857938	Y	***310.176133***	155.591705	293.149584	147.078430			2
12							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.6	1561.817383	-0.003955	ETAASLLQAGYK

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

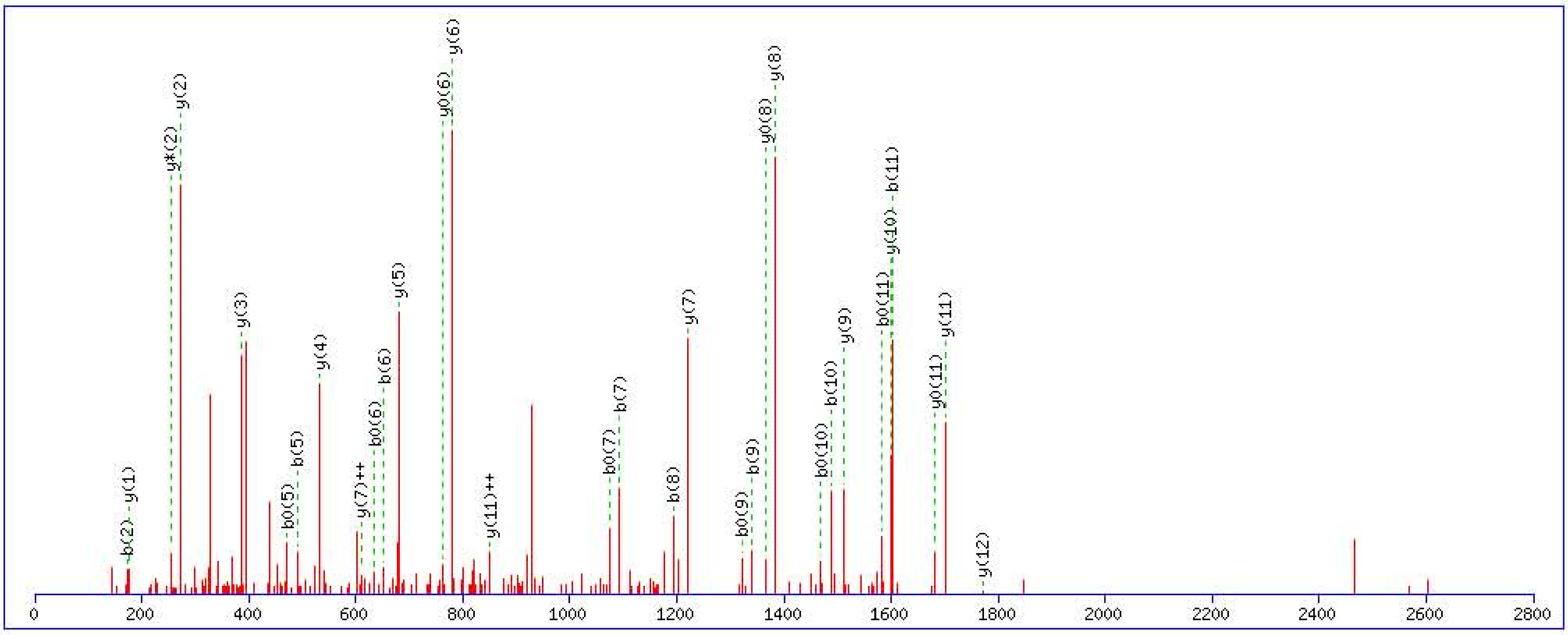
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **TATSEYQTFFNPR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

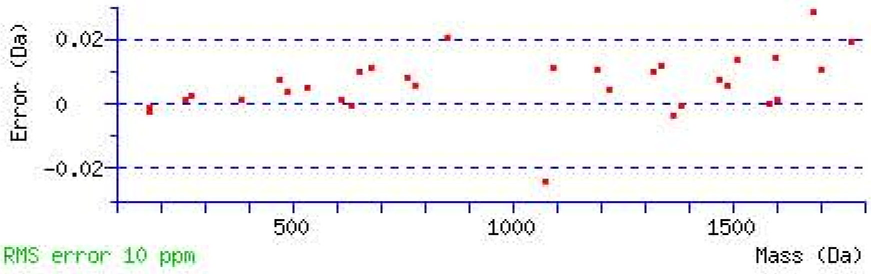
Match to Query 53843: 1871.896248 from(936.955400,2+) rtinseconds(2251) index(64738)
Title: Locus:1.1.1.2781.11 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

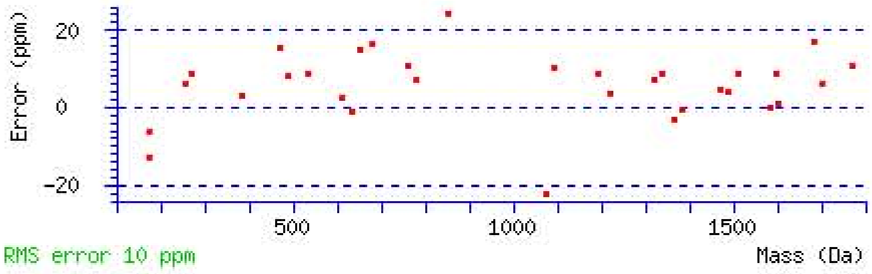
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1871.887619
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 90  Expect: 1.9e-008
Matches : 32/122 fragment ions using 50 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							13
2	**173.092069**	87.049672			155.081504	78.044390	A	***1771.847219***	886.427248	1754.820670	877.913973	1753.836654	877.421965	12
3	274.139748	137.573512			256.129183	128.568230	T	***1700.810105***	850.908691	1683.783556	842.395416	1682.799540	841.903408	11
4	361.171776	181.089526			343.161211	172.084243	S	***1599.762426***	800.384851	1582.735877	791.871577	1581.751861	791.379569	10
5	**490.214369**	245.610822			472.203804	236.605540	E	***1512.730398***	756.868837	1495.703849	748.355563	1494.719833	747.863555	9
6	**653.277698**	327.142487			635.267133	318.137205	Y	***1383.687805***	692.347541	1366.661256	683.834266	1365.677240	683.342258	8
7	**1092.503024**	546.755150	1075.476475	538.241876	1074.492459	537.749868	Q	***1220.624476***	610.815876	1203.597927	602.302602	1202.613911	601.810594	7
8	**1193.550703**	597.278990	1176.524154	588.765715	1175.540138	588.273707	T	***781.399150***	391.203213	764.372601	382.689939	763.388585	382.197931	6
9	**1340.619117**	670.813197	1323.592568	662.299922	1322.608552	661.807914	F	***680.351471***	340.679374	663.324922	332.166099			5
10	**1487.687531**	744.347404	1470.660982	735.834129	1469.676966	735.342121	F	***533.283057***	267.145167	516.256508	258.631892			4
11	**1601.730458**	801.368867	1584.703909	792.855593	1583.719893	792.363585	N	***386.214643***	193.610959	369.188094	185.097685			3
12	1698.783222	849.895249	1681.756673	841.381975	1680.772657	840.889967	P	***272.171716***	136.589496	255.145167	128.076221			2
13							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
90.2	1871.887619	0.008629	TATSEYQTFFNPR

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

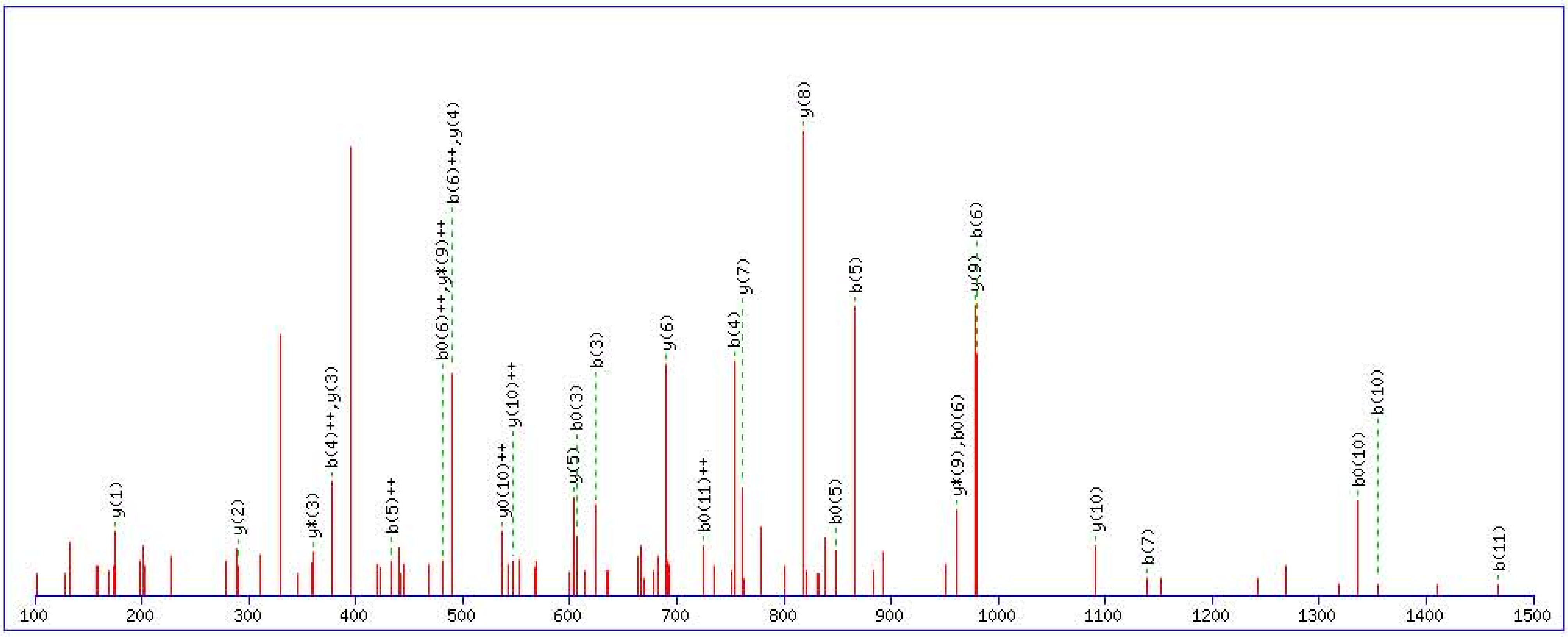
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPQELLCGASLISDR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

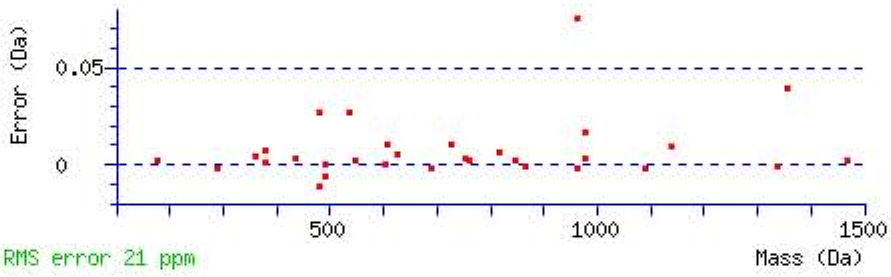
Match to Query 55583: 1955.991132 from(653.004320,3+) rtinseconds(2469) index(66008)
Title: Locus:1.1.1.2857.9 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

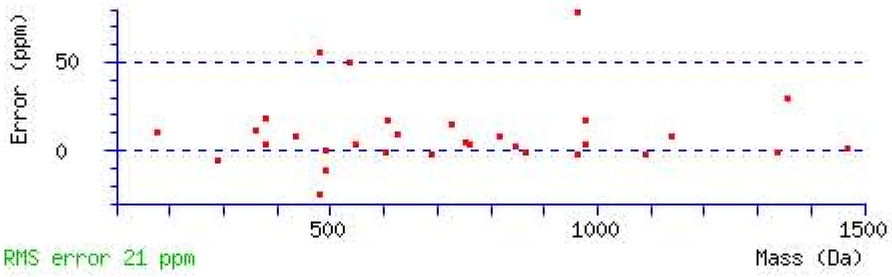
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1955.980850
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 58 **Expect:** 1.3e-005
Matches : 31/162 fragment ions using 46 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							15
2	185.092068	93.049672			167.081503	84.044389	P	1869.956117	935.481697	1852.929568	926.968422	1851.945552	926.476414	14
3	**624.317394**	312.662335	607.290845	304.149061	606.306829	303.657053	Q	1772.903353	886.955314	1755.876804	878.442040	1754.892788	877.950032	13
4	**753.359987**	**377.183632**	736.333438	368.670357	735.349422	368.178349	E	1333.678027	667.342652	1316.651478	658.829377	1315.667462	658.337369	12
5	**866.444051**	**433.725664**	849.417502	425.212389	848.433486	424.720381	L	1204.635434	602.821355	1187.608885	594.308081	1186.624869	593.816073	11
6	**979.528115**	**490.267696**	962.501566	481.754421	961.517550	481.262413	L	***1091.551370***	546.279323	1074.524821	537.766049	1073.540805	537.274040	10
7	**1139.558764**	570.283020	1122.532215	561.769746	1121.548199	561.277738	C	***978.467306***	489.737291	961.440757	481.224017	960.456741	480.732009	9
8	1196.580228	598.793752	1179.553679	590.280478	1178.569663	589.788470	G	***818.436657***	409.721967	801.410108	401.208692	800.426092	400.716684	8
9	1267.617342	634.312309	1250.590793	625.799035	1249.606777	625.307027	A	***761.415193***	381.211235	744.388644	372.697960	743.404628	372.205952	7
10	**1354.649370**	677.828323	1337.622821	669.315049	1336.638805	668.823041	S	***690.378079***	345.692678	673.351530	337.179403	672.367514	336.687395	6
11	**1467.733434**	734.370355	1450.706885	725.857081	1449.722869	725.365073	L	***603.346051***	302.176664	586.319502	293.663389	585.335486	293.171381	5
12	1580.817498	790.912387	1563.790949	782.399113	1562.806933	781.907104	I	***490.261987***	245.634631	473.235438	237.121357	472.251422	236.629349	4
13	1667.849526	834.428401	1650.822977	825.915127	1649.838961	825.423118	S	***377.177923***	189.092600	360.151374	180.579325	359.167358	180.087317	3
14	1782.876469	891.941873	1765.849920	883.428598	1764.865904	882.936590	D	***290.145895***	145.576585	273.119346	137.063311	272.135330	136.571303	2
15							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
58.4	1955.980850	0.010282	SPQELLCGASLISDR
6.3	1955.966949	0.024183	EQQPGKCEGTRTVR
6.3	1955.966949	0.024183	EQQPGKCEGTRTVR
4.0	1956.006470	-0.015338	AILRVAELSSDDFHLDR

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

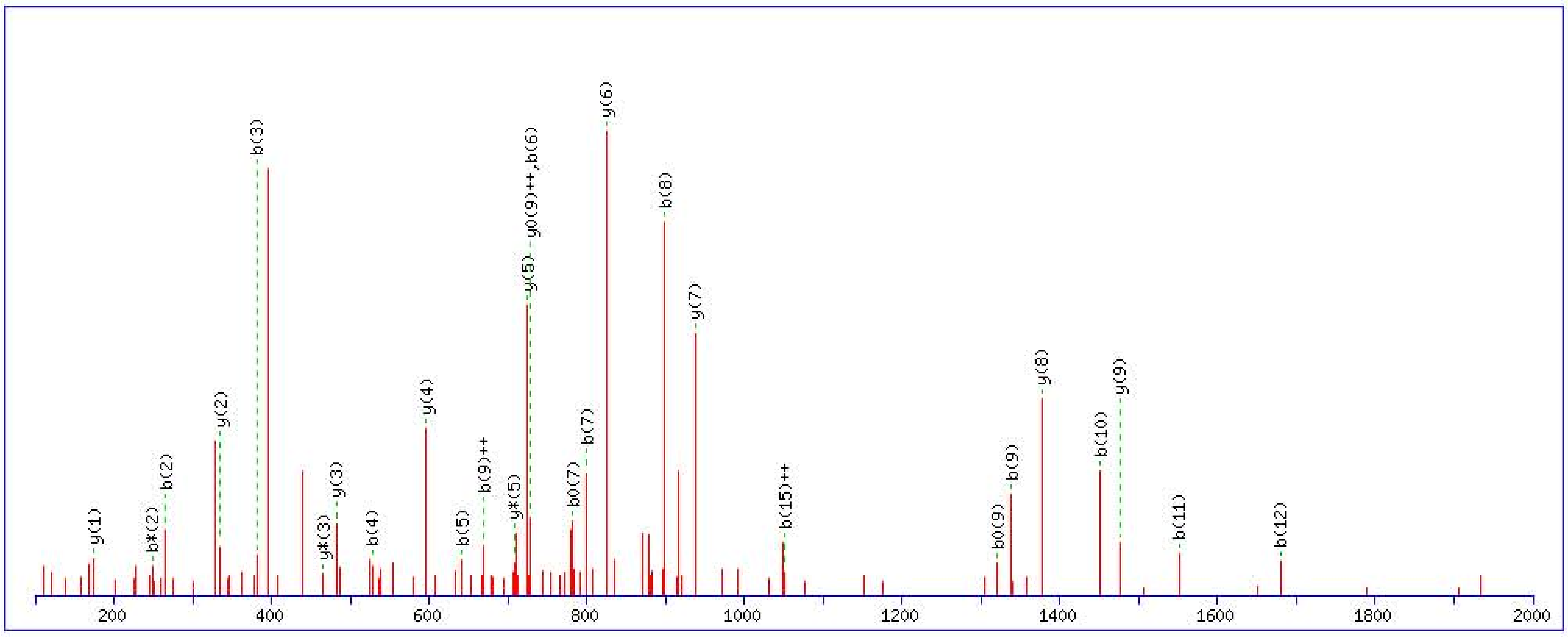
Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQDFNSAVQLVENFCR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

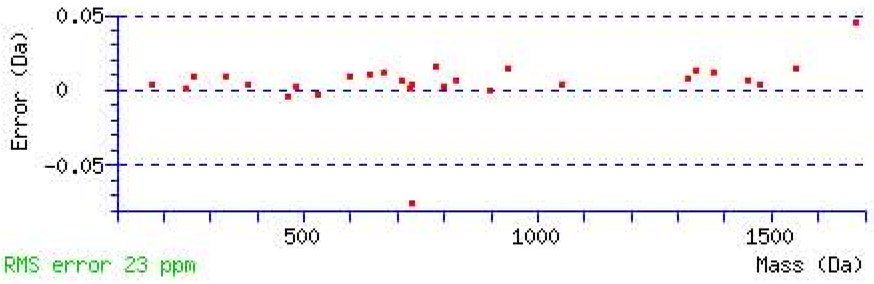
Match to Query 63463: 2274.074742 from(759.032190,3+) rtinseconds(2487) index(66111)
Title: Locus:1.1.1.2863.17 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

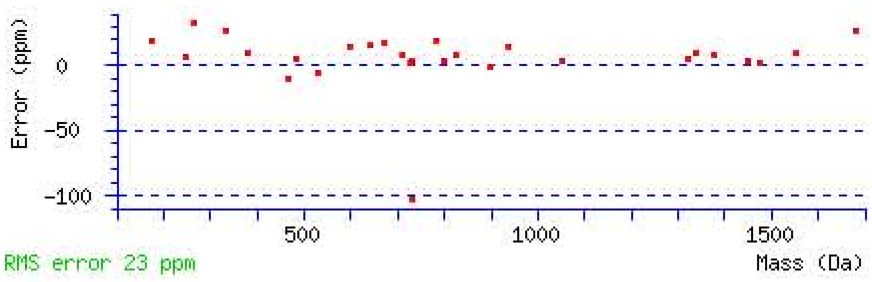
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2274.067398
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 60  Expect: 2e-005
Matches : 28/166 fragment ions using 56 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	138.066188	69.536732					H							16
2	***266.124766***	133.566021	249.098217	125.052746			Q	2138.015757	1069.511516	2120.989208	1060.998242	2120.005192	1060.506234	15
3	***381.151709***	191.079492	364.125160	182.566218	363.141144	182.074210	D	2009.957179	1005.482228	1992.930630	996.968953	1991.946614	996.476945	14
4	***528.220123***	264.613700	511.193574	256.100425	510.209558	255.608417	F	1894.930236	947.968756	1877.903687	939.455482	1876.919671	938.963474	13
5	***642.263050***	321.635163	625.236501	313.121889	624.252485	312.629881	N	1747.861822	874.434549	1730.835273	865.921275	1729.851257	865.429267	12
6	***729.295078***	365.151177	712.268529	356.637903	711.284513	356.145895	S	1633.818895	817.413086	1616.792346	808.899811	1615.808330	808.407803	11
7	***800.332192***	400.669734	783.305643	392.156459	782.321627	391.664451	A	1546.786867	773.897072	1529.760318	765.383797	1528.776302	764.891789	10
8	***899.400606***	450.203941	882.374057	441.690666	881.390041	441.198658	V	***1475.749753***	738.378515	1458.723204	729.865240	1457.739188	729.373232	9
9	***1338.625932***	**669.816604**	1321.599383	661.303330	1320.615367	660.811322	Q	***1376.681339***	688.844308	1359.654790	680.331033	1358.670774	679.839025	8
10	***1451.709996***	726.358636	1434.683447	717.845362	1433.699431	717.353354	L	***937.456013***	469.231645	920.429464	460.718370	919.445448	460.226362	7
11	***1550.778410***	775.892843	1533.751861	767.379569	1532.767845	766.887561	V	***824.371949***	412.689613	807.345400	404.176338	806.361384	403.684330	6
12	***1679.821003***	840.414140	1662.794454	831.900865	1661.810438	831.408857	E	***725.303535***	363.155406	708.276986	354.642131	707.292970	354.150123	5
13	1793.863930	897.435603	1776.837381	888.922329	1775.853365	888.430321	N	***596.260942***	298.634109	579.234393	290.120835			4
14	1940.932344	970.969810	1923.905795	962.456536	1922.921779	961.964528	F	***482.218015***	241.612646	465.191466	233.099371			3
15	2100.962993	**1050.985135**	2083.936444	1042.471860	2082.952428	1041.979852	C	***335.149601***	168.078438	318.123052	159.565164			2
16							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
59.9	2274.067398	0.007344	HQDFNSAVQLVENFCR
19.1	2274.067398	0.007344	HQDFNSAVQLVENFCR

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

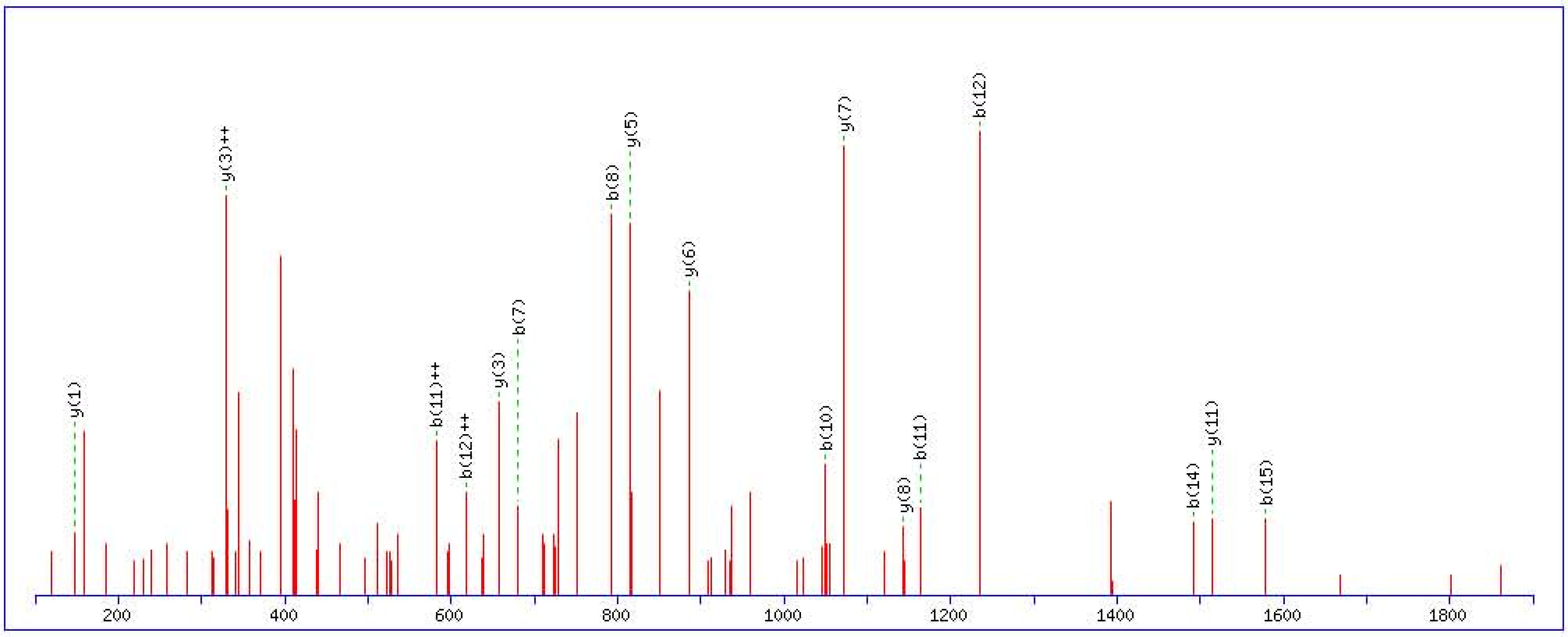
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **LAVTTHGLPCLAWASAQAK**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

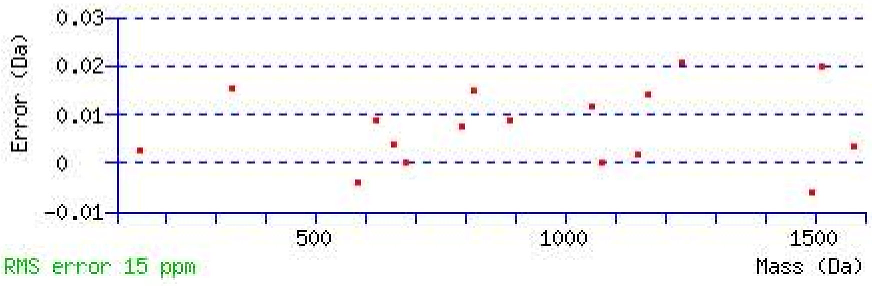
Match to Query 64234: 2305.218312 from(769.413380,3+) rtinseconds(2358) index(65394)
Title: Locus:1.1.1.2818.17 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

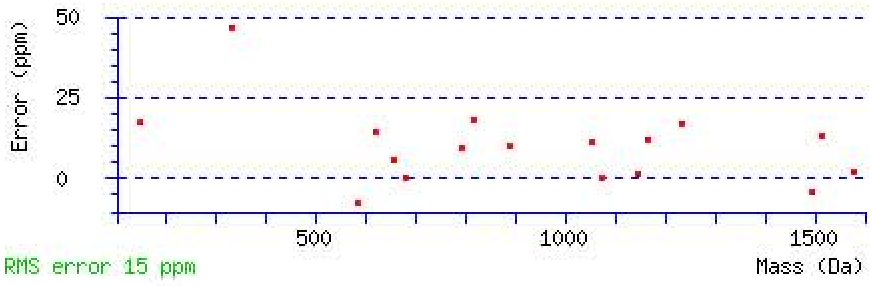
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2305.207504
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q17 : Biotin:Thermo-21345 (Q)
Ions Score: 40 **Expect:** 0.00021
Matches : 17/170 fragment ions using 32 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					L							19
2	185.128454	93.067865					A	2193.130730	1097.069003	2176.104181	1088.555728	2175.120165	1088.063720	18
3	284.196868	142.602072					V	2122.093616	1061.550446	2105.067067	1053.037171	2104.083051	1052.545163	17
4	385.244547	193.125912			367.233982	184.120629	T	2023.025202	1012.016239	2005.998653	1003.502965	2005.014637	1003.010957	16
5	486.292226	243.649751			468.281661	234.644469	T	1921.977523	961.492400	1904.950974	952.979125	1903.966958	952.487117	15
6	623.351138	312.179207			605.340573	303.173925	H	1820.929844	910.968560	1803.903295	902.455286	1802.919279	901.963278	14
7	***680.372602***	340.689939			662.362037	331.684657	G	1683.870932	842.439104	1666.844383	833.925830	1665.860367	833.433822	13
8	***793.456666***	397.231971			775.446101	388.226689	L	1626.849468	813.928372	1609.822919	805.415098	1608.838903	804.923090	12
9	890.509430	445.758353			872.498865	436.753071	P	***1513.765404***	757.386340	1496.738855	748.873066	1495.754839	748.381058	11
10	***1050.540079***	525.773678			1032.529514	516.768395	C	1416.712640	708.859958	1399.686091	700.346684	1398.702075	699.854675	10
11	***1163.624143***	**582.315710**			1145.613578	573.310427	L	1256.681991	628.844634	1239.655442	620.331359	1238.671426	619.839351	9
12	***1234.661257***	**617.834267**			1216.650692	608.828984	A	***1143.597927***	572.302602	1126.571378	563.789327	1125.587362	563.297319	8
13	1420.740570	710.873923			1402.730005	701.868640	W	***1072.560813***	536.784045	1055.534264	528.270770	1054.550248	527.778762	7
14	***1491.777684***	746.392480			1473.767119	737.387197	A	***886.481500***	443.744388	869.454951	435.231114	868.470935	434.739106	6
15	***1578.809712***	789.908494			1560.799147	780.903212	S	***815.444386***	408.225831	798.417837	399.712557	797.433821	399.220549	5
16	1649.846826	825.427051			1631.836261	816.421768	A	728.412358	364.709817	711.385809	356.196543			4
17	2089.072152	1045.039714	2072.045603	1036.526439	2071.061587	1036.034431	Q	***657.375244***	329.191260	640.348695	320.677986			3
18	2160.109266	1080.558271	2143.082717	1072.044996	2142.098701	1071.552988	A	218.149918	109.578597	201.123369	101.065323			2
19							K	***147.112804***	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.0	2305.207504	0.010808	LAVTTHGLPCLAWASAQAK
0.8	2305.184830	0.033482	QAAASATQTIAAAQHAASTPK
0.2	2305.236481	-0.018169	STLSQHLRIHTGEKPYK

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

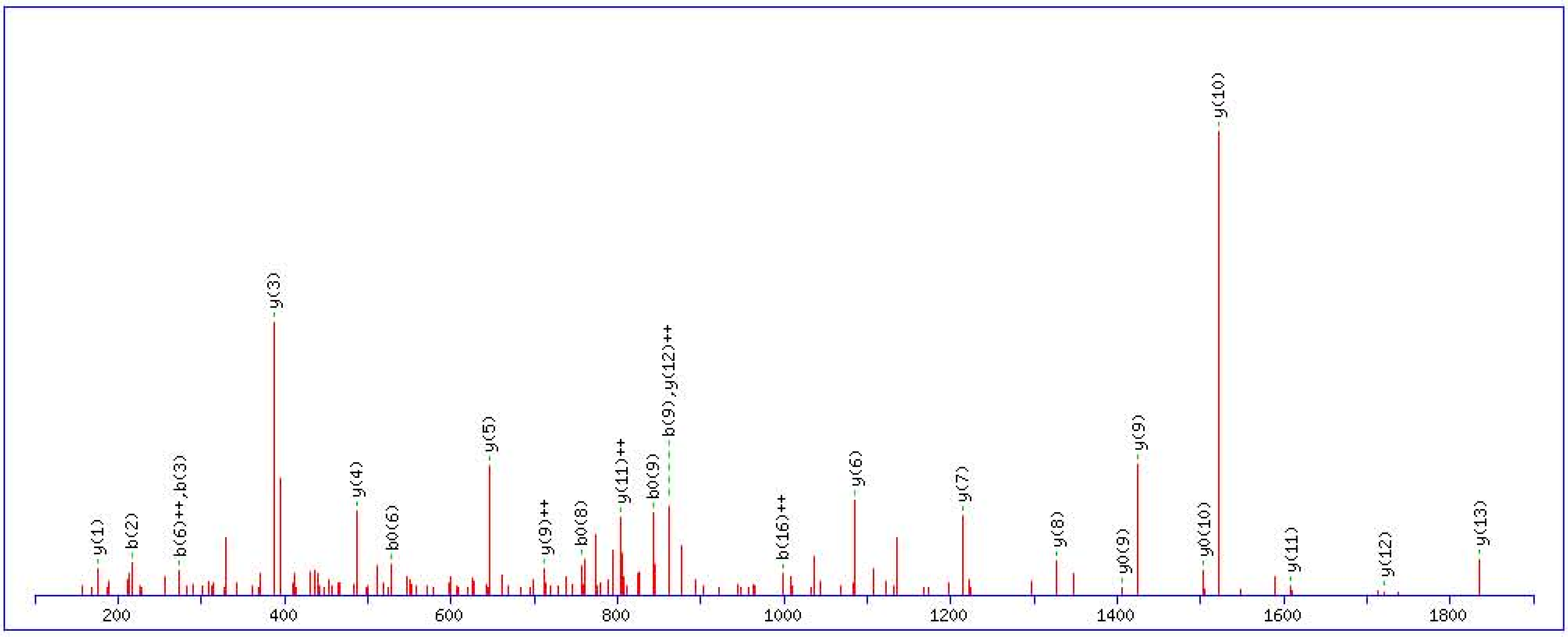
Mascot Search Results

Peptide View

MS/MS Fragmentation of **SEGSSVNLSPPLEQCVPDR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

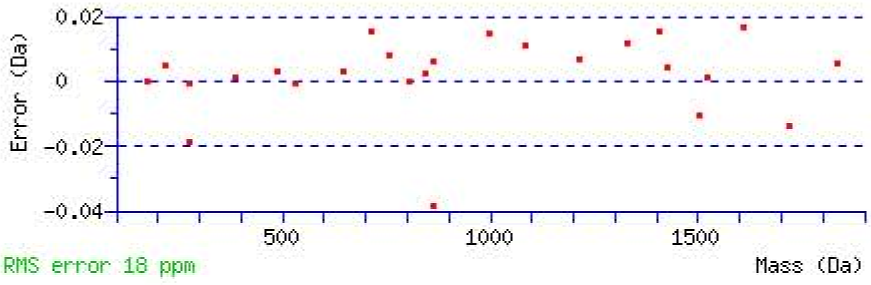
Match to Query 65388: 2381.142582 from(794.721470,3+) rtinseconds(2146) index(64031)
Title: Locus:1.1.1.2744.22 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

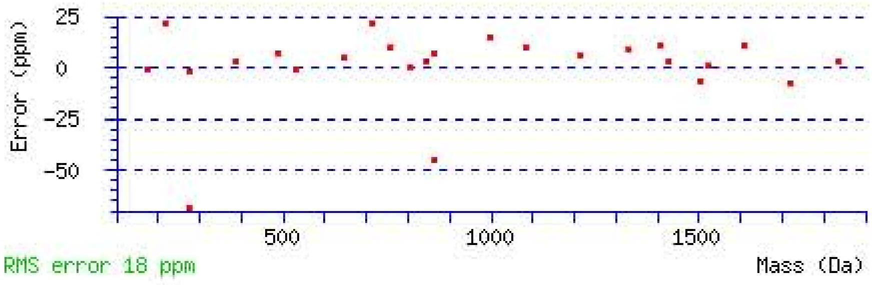
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2381.135529
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q14     : Biotin:Thermo-21345 (Q)
Ions Score: 88  Expect: 3e-008
Matches : 25/202 fragment ions using 33 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							19
2	**217.081897**	109.044586			199.071332	100.039304	E	2295.110779	1148.059027	2278.084230	1139.545753	2277.100214	1139.053745	18
3	**274.103361**	137.555319			256.092796	128.550036	G	2166.068186	1083.537731	2149.041637	1075.024456	2148.057621	1074.532448	17
4	361.135389	181.071332			343.124824	172.066050	S	2109.046722	1055.026999	2092.020173	1046.513724	2091.036157	1046.021716	16
5	448.167417	224.587346			430.156852	215.582064	S	2022.014694	1011.510985	2004.988145	1002.997711	2004.004129	1002.505703	15
6	547.235831	**274.121554**			529.225266	265.116271	V	1934.982666	967.994971	1917.956117	959.481697	1916.972101	958.989689	14
7	661.278758	331.143017	644.252209	322.629742	643.268193	322.137734	N	***1835.914252***	918.460764	1818.887703	909.947490	1817.903687	909.455482	13
8	774.362822	387.685049	757.336273	379.171774	756.352257	378.679766	L	***1721.871325***	861.439301	1704.844776	852.926026	1703.860760	852.434018	12
9	**861.394850**	431.201063	844.368301	422.687788	843.384285	422.195780	S	***1608.787261***	804.897269	1591.760712	796.383994	1590.776696	795.891986	11
10	958.447614	479.727445	941.421065	471.214170	940.437049	470.722162	P	***1521.755233***	761.381255	1504.728684	752.867980	1503.744668	752.375972	10
11	1055.500378	528.253827	1038.473829	519.740553	1037.489813	519.248544	P	***1424.702469***	712.854873	1407.675920	704.341598	1406.691904	703.849590	9
12	1168.584442	584.795859	1151.557893	576.282584	1150.573877	575.790576	L	***1327.649705***	664.328491	1310.623156	655.815216	1309.639140	655.323208	8
13	1297.627035	649.317155	1280.600486	640.803881	1279.616470	640.311873	E	***1214.565641***	607.786459	1197.539092	599.273184	1196.555076	598.781176	7
14	1736.852361	868.929819	1719.825812	860.416544	1718.841796	859.924536	Q	***1085.523048***	543.265162	1068.496499	534.751888	1067.512483	534.259880	6
15	1896.883010	948.945143	1879.856461	940.431869	1878.872445	939.939861	C	***646.297722***	323.652499	629.271173	315.139225	628.287157	314.647217	5
16	1995.951424	**998.479350**	1978.924875	989.966076	1977.940859	989.474068	V	***486.267073***	243.637174	469.240524	235.123900	468.256508	234.631892	4
17	2093.004188	1047.005732	2075.977639	1038.492457	2074.993623	1038.000449	P	***387.198659***	194.102967	370.172110	185.589693	369.188094	185.097685	3
18	2208.031131	1104.519203	2191.004582	1096.005929	2190.020566	1095.513921	D	290.145895	145.576585	273.119346	137.063311	272.135330	136.571303	2
19							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
88.5	2381.135529	0.007053	SEGSSVNLSPPLEQCVPDR

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

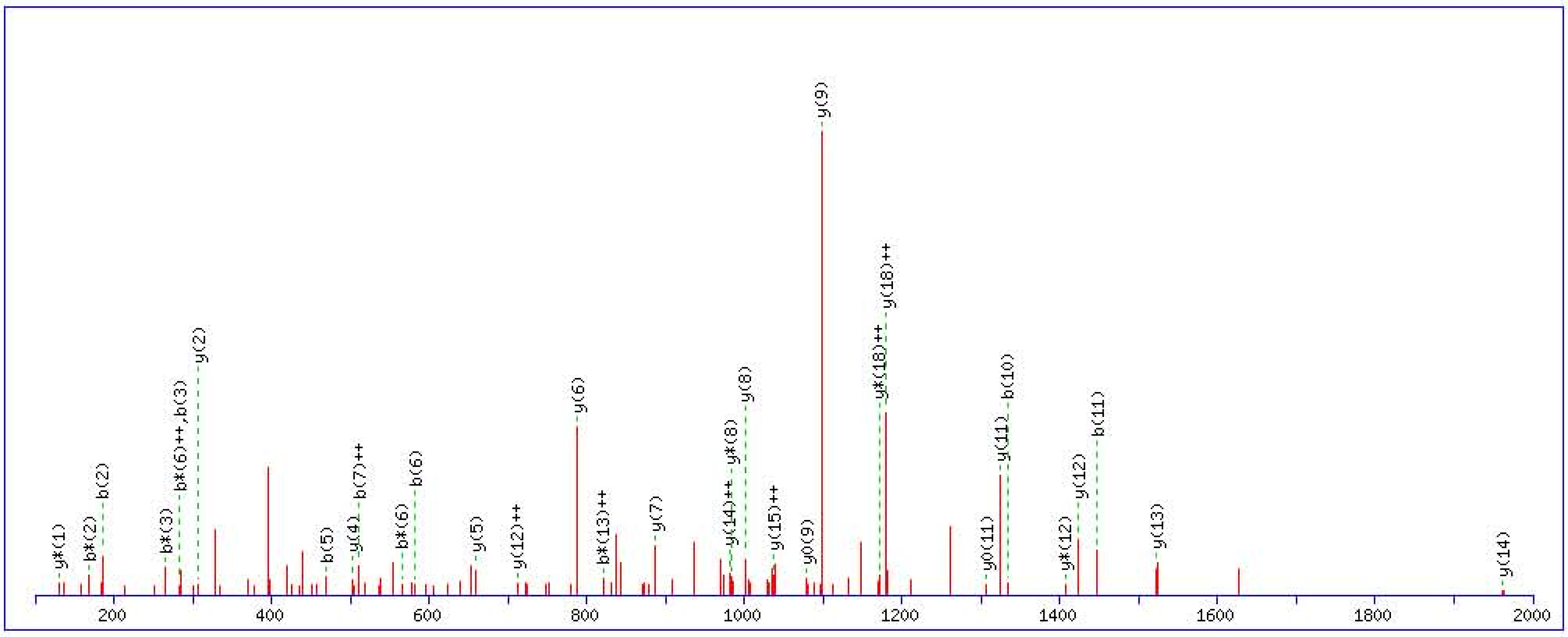
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQPSVLQVVNLPIVERPVCK**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

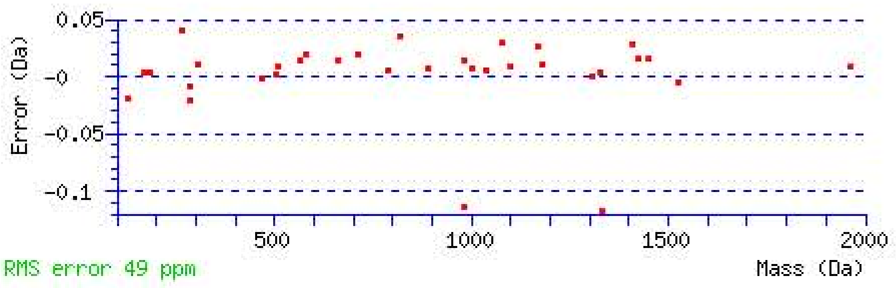
Match to Query 69164: 2542.427562 from(848.483130,3+) rtinseconds(2511) index(66317)
Title: Locus:1.1.1.2871.23 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

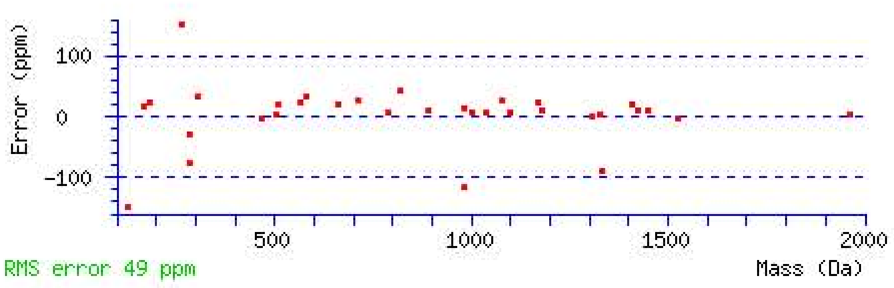
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2542.412766
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 42  Expect: 0.00045
Matches : 33/210 fragment ions using 78 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.028740	29.518008					G							20
2	***186.087318***	93.547297	169.060769	85.034023			Q	2486.398570	1243.702923	2469.372021	1235.189648	2468.388005	1234.697640	19
3	***283.140082***	142.073679	266.113533	133.560405			P	2358.339992	1179.673634	2341.313443	1171.160359	2340.329427	1170.668351	18
4	370.172110	185.589693	353.145561	177.076419	352.161545	176.584411	S	2261.287228	1131.147252	2244.260679	1122.633977	2243.276663	1122.141969	17
5	***469.240524***	235.123900	452.213975	226.610626	451.229959	226.118618	V	2174.255200	1087.631238	2157.228651	1079.117963	2156.244635	1078.625955	16
6	***582.324588***	291.665932	565.298039	283.152658	564.314023	282.660650	L	2075.186786	1038.097031	2058.160237	1029.583756	2057.176221	1029.091748	15
7	1021.549914	511.278595	1004.523365	502.765321	1003.539349	502.273313	Q	***1962.102722***	981.554999	1945.076173	973.041724	1944.092157	972.549716	14
8	1120.618328	560.812802	1103.591779	552.299528	1102.607763	551.807520	V	***1522.877396***	761.942336	1505.850847	753.429061	1504.866831	752.937053	13
9	1219.686742	610.347009	1202.660193	601.833735	1201.676177	601.341727	V	***1423.808982***	712.408129	1406.782433	703.894854	1405.798417	703.402846	12
10	***1333.729669***	667.368473	1316.703120	658.855198	1315.719104	658.363190	N	***1324.740568***	662.873922	1307.714019	654.360647	1306.730003	653.868639	11
11	***1446.813733***	723.910505	1429.787184	715.397230	1428.803168	714.905222	L	1210.697641	605.852458	1193.671092	597.339184	1192.687076	596.847176	10
12	1543.866497	772.436887	1526.839948	763.923612	1525.855932	763.431604	P	***1097.613577***	549.310426	1080.587028	540.797152	1079.603012	540.305144	9
13	1656.950561	828.978918	1639.924012	820.465644	1638.939996	819.973636	I	***1000.560813***	500.784044	983.534264	492.270770	982.550248	491.778762	8
14	1756.018975	878.513126	1738.992426	869.999851	1738.008410	869.507843	V	***887.476749***	444.242012	870.450200	435.728738	869.466184	435.236730	7
15	1885.061568	943.034422	1868.035019	934.521147	1867.051003	934.029139	E	***788.408335***	394.707805	771.381786	386.194531	770.397770	385.702523	6
16	2041.162679	1021.084977	2024.136130	1012.571703	2023.152114	1012.079695	R	***659.365742***	330.186509	642.339193	321.673234			5
17	2138.215443	1069.611359	2121.188894	1061.098085	2120.204878	1060.606077	P	***503.264631***	252.135953	486.238082	243.622679			4
18	2237.283857	1119.145566	2220.257308	1110.632292	2219.273292	1110.140284	V	406.211867	203.609571	389.185318	195.096297			3
19	2397.314506	1199.160891	2380.287957	1190.647616	2379.303941	1190.155608	C	***307.143453***	154.075364	290.116904	145.562090			2
20							K	147.112804	74.060040	130.086255	65.546765			1



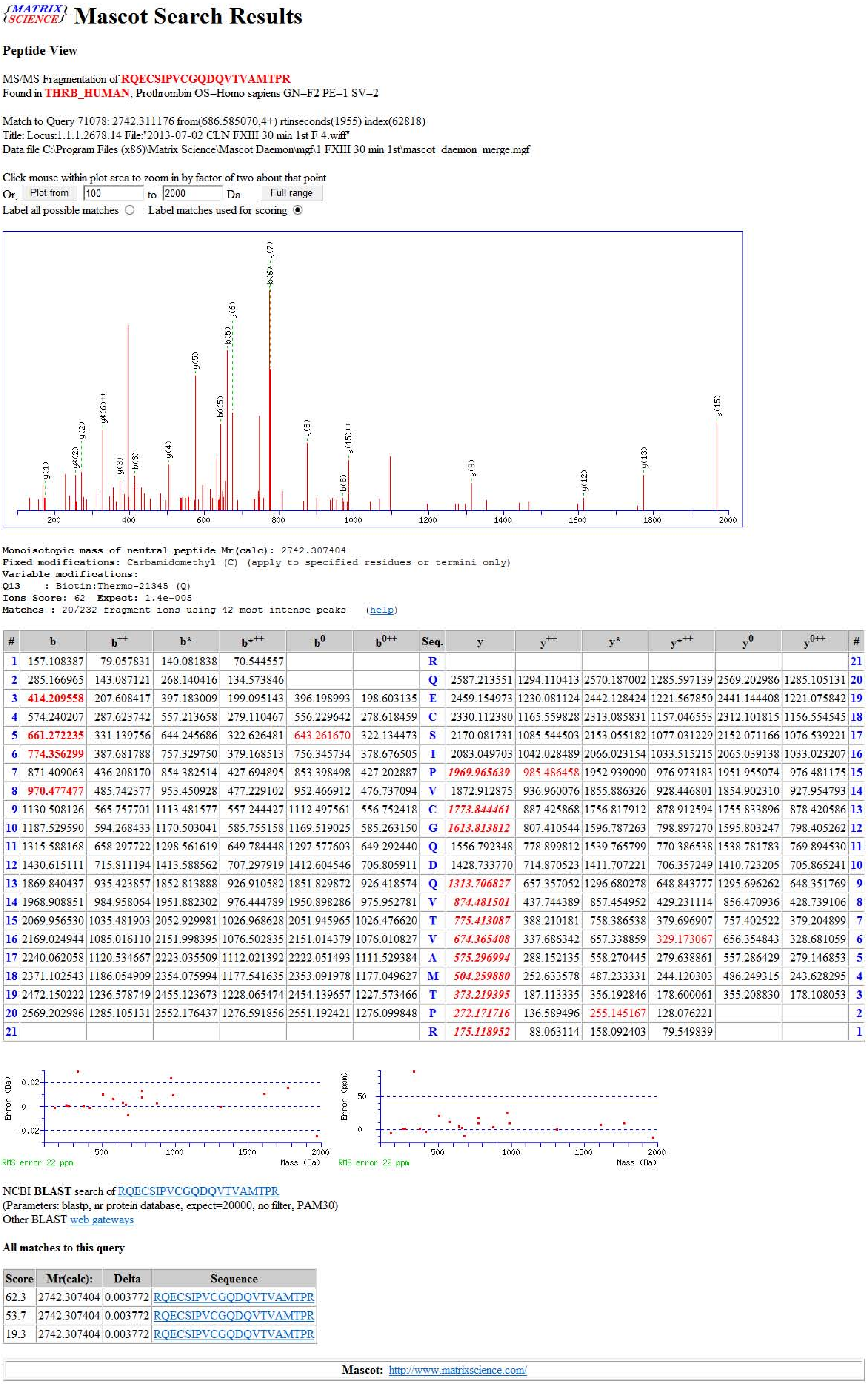


NCBI **BLAST** search of GQPSVLQVVNLPIVERPVCK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
41.9	2542.412766	0.014796	GQPSVLQVVNLPIVERPVCK
20.7	2542.412766	0.014796	GQPSVLQVVNLPIVERPVCK

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



Mascot Search Results

Peptide View

MS/MS Fragmentation of **RQECSIPVCGQDQVTVAMTPR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

Match to Query 71078: 2742.311176 from(686.585070,4+) rtinseconds(1955) index(62818)
Title: Locus:1.1.1.2678.14 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 2742.307404
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13     : Biotin:Thermo-21345 (Q)
Ions Score: 62  Expect: 1.4e-005
Matches : 20/232 fragment ions using 42 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	157.108387	79.057831	140.081838	70.544557			R							21
2	285.166965	143.087121	268.140416	134.573846			Q	2587.213551	1294.110413	2570.187002	1285.597139	2569.202986	1285.105131	20
3	**414.209558**	207.608417	397.183009	199.095143	396.198993	198.603135	E	2459.154973	1230.081124	2442.128424	1221.567850	2441.144408	1221.075842	19
4	574.240207	287.623742	557.213658	279.110467	556.229642	278.618459	C	2330.112380	1165.559828	2313.085831	1157.046553	2312.101815	1156.554545	18
5	**661.272235**	331.139756	644.245686	322.626481	643.261670	322.134473	S	2170.081731	1085.544503	2153.055182	1077.031229	2152.071166	1076.539221	17
6	**774.356299**	387.681788	757.329750	379.168513	756.345734	378.676505	I	2083.049703	1042.028489	2066.023154	1033.515215	2065.039138	1033.023207	16
7	871.409063	436.208170	854.382514	427.694895	853.398498	427.202887	P	***1969.965639***	985.486458	1952.939090	976.973183	1951.955074	976.481175	15
8	**970.477477**	485.742377	953.450928	477.229102	952.466912	476.737094	V	1872.912875	936.960076	1855.886326	928.446801	1854.902310	927.954793	14
9	1130.508126	565.757701	1113.481577	557.244427	1112.497561	556.752418	C	***1773.844461***	887.425868	1756.817912	878.912594	1755.833896	878.420586	13
10	1187.529590	594.268433	1170.503041	585.755158	1169.519025	585.263150	G	***1613.813812***	807.410544	1596.787263	798.897270	1595.803247	798.405262	12
11	1315.588168	658.297722	1298.561619	649.784448	1297.577603	649.292440	Q	1556.792348	778.899812	1539.765799	770.386538	1538.781783	769.894530	11
12	1430.615111	715.811194	1413.588562	707.297919	1412.604546	706.805911	D	1428.733770	714.870523	1411.707221	706.357249	1410.723205	705.865241	10
13	1869.840437	935.423857	1852.813888	926.910582	1851.829872	926.418574	Q	***1313.706827***	657.357052	1296.680278	648.843777	1295.696262	648.351769	9
14	1968.908851	984.958064	1951.882302	976.444789	1950.898286	975.952781	V	***874.481501***	437.744389	857.454952	429.231114	856.470936	428.739106	8
15	2069.956530	1035.481903	2052.929981	1026.968628	2051.945965	1026.476620	T	***775.413087***	388.210181	758.386538	379.696907	757.402522	379.204899	7
16	2169.024944	1085.016110	2151.998395	1076.502835	2151.014379	1076.010827	V	***674.365408***	337.686342	657.338859	329.173067	656.354843	328.681059	6
17	2240.062058	1120.534667	2223.035509	1112.021392	2222.051493	1111.529384	A	***575.296994***	288.152135	558.270445	279.638861	557.286429	279.146853	5
18	2371.102543	1186.054909	2354.075994	1177.541635	2353.091978	1177.049627	M	***504.259880***	252.633578	487.233331	244.120303	486.249315	243.628295	4
19	2472.150222	1236.578749	2455.123673	1228.065474	2454.139657	1227.573466	T	***373.219395***	187.113335	356.192846	178.600061	355.208830	178.108053	3
20	2569.202986	1285.105131	2552.176437	1276.591856	2551.192421	1276.099848	P	***272.171716***	136.589496	255.145167	128.076221			2
21							R	***175.118952***	88.063114	158.092403	79.549839			1

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.3	2742.307404	0.003772	RQECSIPVCGQDQVTVAMTPR
53.7	2742.307404	0.003772	RQECSIPVCGQDQVTVAMTPR
19.3	2742.307404	0.003772	RQECSIPVCGQDQVTVAMTPR

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

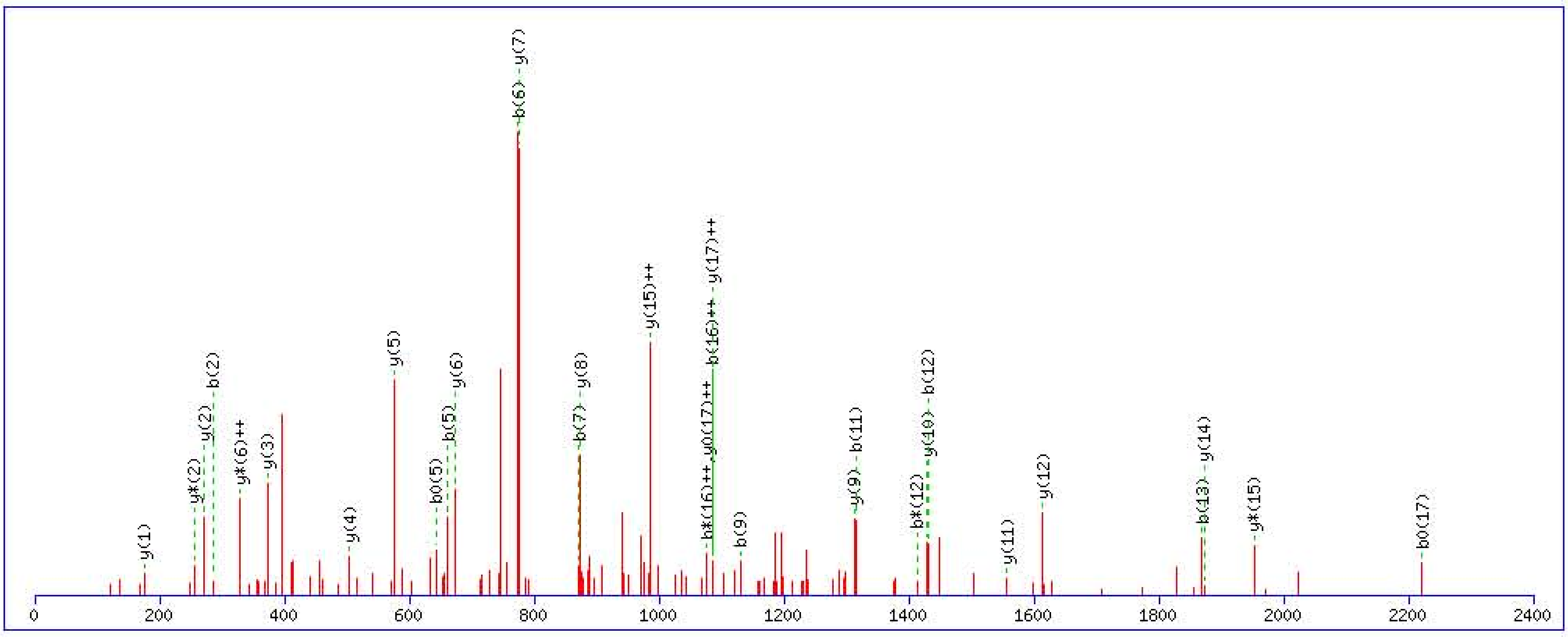
Mascot Search Results

Peptide View

MS/MS Fragmentation of **RQECSIPVCGQDQVTVAMTPR**
Found in **THRB_HUMAN**, Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2

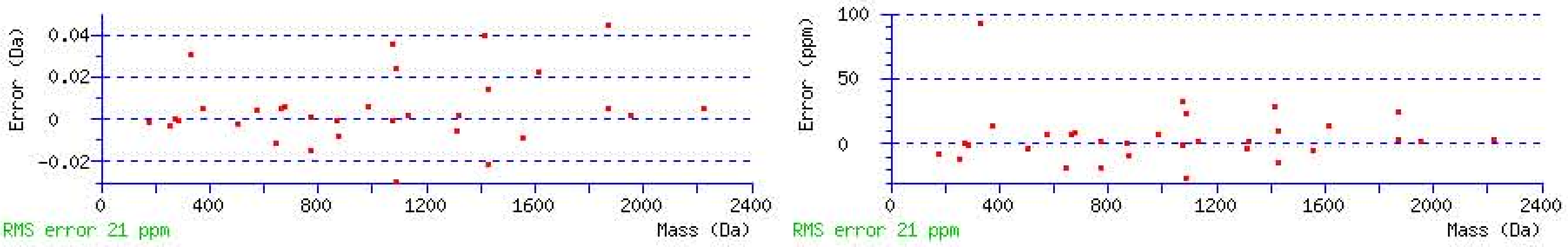
Match to Query 71079: 2742.319002 from(915.113610,3+) rtinseconds(1953) index(62801)
Title: Locus:1.1.1.2677.22 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2742.307404
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13 : Biotin:Thermo-21345 (Q)
Ions Score: 72 **Expect:** 1.6e-006
Matches : 32/232 fragment ions using 55 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	157.108387	79.057831	140.081838	70.544557			R							21
2	**285.166965**	143.087121	268.140416	134.573846			Q	2587.213551	1294.110413	2570.187002	1285.597139	2569.202986	1285.105131	20
3	414.209558	207.608417	397.183009	199.095143	396.198993	198.603135	E	2459.154973	1230.081124	2442.128424	1221.567850	2441.144408	1221.075842	19
4	574.240207	287.623742	557.213658	279.110467	556.229642	278.618459	C	2330.112380	1165.559828	2313.085831	1157.046553	2312.101815	1156.554545	18
5	**661.272235**	331.139756	644.245686	322.626481	643.261670	322.134473	S	2170.081731	1085.544503	2153.055182	1077.031229	2152.071166	1076.539221	17
6	**774.356299**	387.681788	757.329750	379.168513	756.345734	378.676505	I	2083.049703	1042.028489	2066.023154	1033.515215	2065.039138	1033.023207	16
7	**871.409063**	436.208170	854.382514	427.694895	853.398498	427.202887	P	1969.965639	985.486458	1952.939090	976.973183	1951.955074	976.481175	15
8	970.477477	485.742377	953.450928	477.229102	952.466912	476.737094	V	***1872.912875***	936.960076	1855.886326	928.446801	1854.902310	927.954793	14
9	**1130.508126**	565.757701	1113.481577	557.244427	1112.497561	556.752418	C	1773.844461	887.425868	1756.817912	878.912594	1755.833896	878.420586	13
10	1187.529590	594.268433	1170.503041	585.755158	1169.519025	585.263150	G	***1613.813812***	807.410544	1596.787263	798.897270	1595.803247	798.405262	12
11	**1315.588168**	658.297722	1298.561619	649.784448	1297.577603	649.292440	Q	***1556.792348***	778.899812	1539.765799	770.386538	1538.781783	769.894530	11
12	**1430.615111**	715.811194	1413.588562	707.297919	1412.604546	706.805911	D	***1428.733770***	714.870523	1411.707221	706.357249	1410.723205	705.865241	10
13	**1869.840437**	935.423857	1852.813888	926.910582	1851.829872	926.418574	Q	***1313.706827***	657.357052	1296.680278	648.843777	1295.696262	648.351769	9
14	1968.908851	984.958064	1951.882302	976.444789	1950.898286	975.952781	V	***874.481501***	437.744389	857.454952	429.231114	856.470936	428.739106	8
15	2069.956530	1035.481903	2052.929981	1026.968628	2051.945965	1026.476620	T	***775.413087***	388.210181	758.386538	379.696907	757.402522	379.204899	7
16	2169.024944	1085.016110	2151.998395	1076.502835	2151.014379	1076.010827	V	***674.365408***	337.686342	657.338859	329.173067	656.354843	328.681059	6
17	2240.062058	1120.534667	2223.035509	1112.021392	2222.051493	1111.529384	A	***575.296994***	288.152135	558.270445	279.638861	557.286429	279.146853	5
18	2371.102543	1186.054909	2354.075994	1177.541635	2353.091978	1177.049627	M	***504.259880***	252.633578	487.233331	244.120303	486.249315	243.628295	4
19	2472.150222	1236.578749	2455.123673	1228.065474	2454.139657	1227.573466	T	***373.219395***	187.113335	356.192846	178.600061	355.208830	178.108053	3
20	2569.202986	1285.105131	2552.176437	1276.591856	2551.192421	1276.099848	P	***272.171716***	136.589496	255.145167	128.076221			2
21							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
72.0	2742.307404	0.011598	RQECSIPVCGQDQVTVAMTPR
48.3	2742.307404	0.011598	RQECSIPVCGQDQVTVAMTPR
23.3	2742.307404	0.011598	RQECSIPVCGQDQVTVAMTPR

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

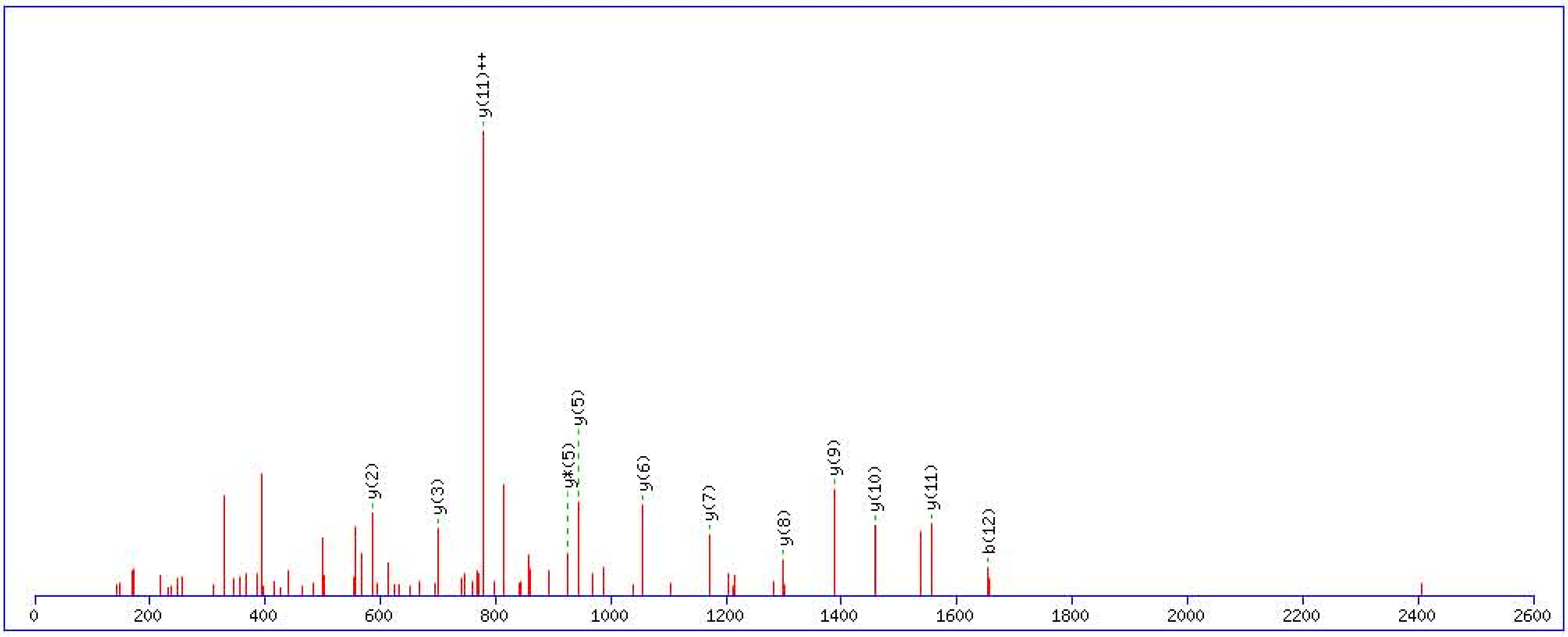
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **DMPASEDLQDLQK**
Found in **SEPP1_HUMAN**, Selenoprotein P OS=Homo sapiens GN=SEPP1 PE=1 SV=3

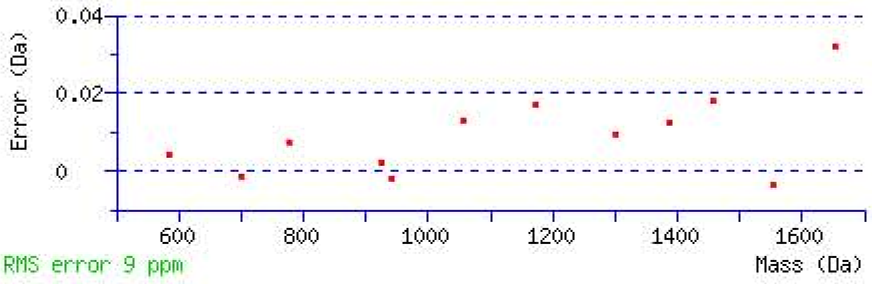
Match to Query 52119: 1799.851288 from(900.932920,2+) rtinseconds(2169) index(64230)
Title: Locus:1.1.1.2752.21 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

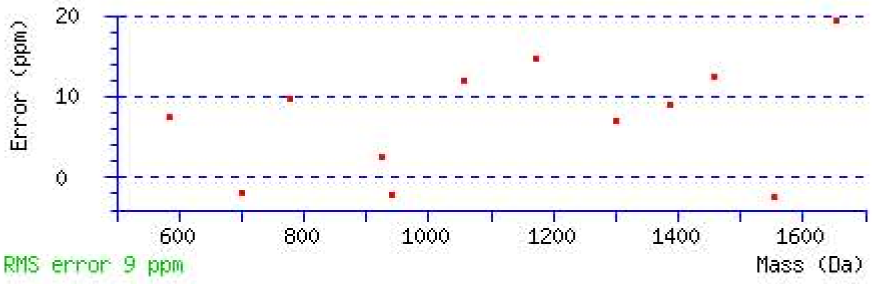
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1799.843353
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q12     : Biotin:Thermo-21345 (Q)
Ions Score: 66  Expect: 1e-006
Matches : 12/122 fragment ions using 16 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	116.034219	58.520748			98.023654	49.515465	D							13
2	247.074704	124.040990			229.064139	115.035708	M	1685.823706	843.415491	1668.797157	834.902217	1667.813141	834.410209	12
3	344.127468	172.567372			326.116903	163.562089	P	***1554.783221***	777.895249	1537.756672	769.381974	1536.772656	768.889966	11
4	415.164582	208.085929			397.154017	199.080646	A	***1457.730457***	729.368867	1440.703908	720.855592	1439.719892	720.363584	10
5	502.196610	251.601943			484.186045	242.596660	S	***1386.693343***	693.850310	1369.666794	685.337035	1368.682778	684.845027	9
6	631.239203	316.123240			613.228638	307.117957	E	***1299.661315***	650.334296	1282.634766	641.821021	1281.650750	641.329013	8
7	746.266146	373.636711			728.255581	364.631428	D	***1170.618722***	585.812999	1153.592173	577.299725	1152.608157	576.807717	7
8	859.350210	430.178743			841.339645	421.173460	L	***1055.591779***	528.299528	1038.565230	519.786253	1037.581214	519.294245	6
9	987.408788	494.208032	970.382239	485.694757	969.398223	485.202749	Q	***942.507715***	471.757496	925.481166	463.244221	924.497150	462.752213	5
10	1102.435731	551.721504	1085.409182	543.208229	1084.425166	542.716221	D	814.449137	407.728207	797.422588	399.214932	796.438572	398.722924	4
11	1215.519795	608.263535	1198.493246	599.750261	1197.509230	599.258253	L	***699.422194***	350.214735	682.395645	341.701461			3
12	1654.745121	827.876199	1637.718572	819.362924	1636.734556	818.870916	Q	***586.338130***	293.672703	569.311581	285.159429			2
13							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
65.8	1799.843353	0.007935	DMPASEDLQDLQK
38.9	1799.843353	0.007935	DMPASEDLQDLQK
1.9	1799.873230	-0.021942	QLDSKGDCQK

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

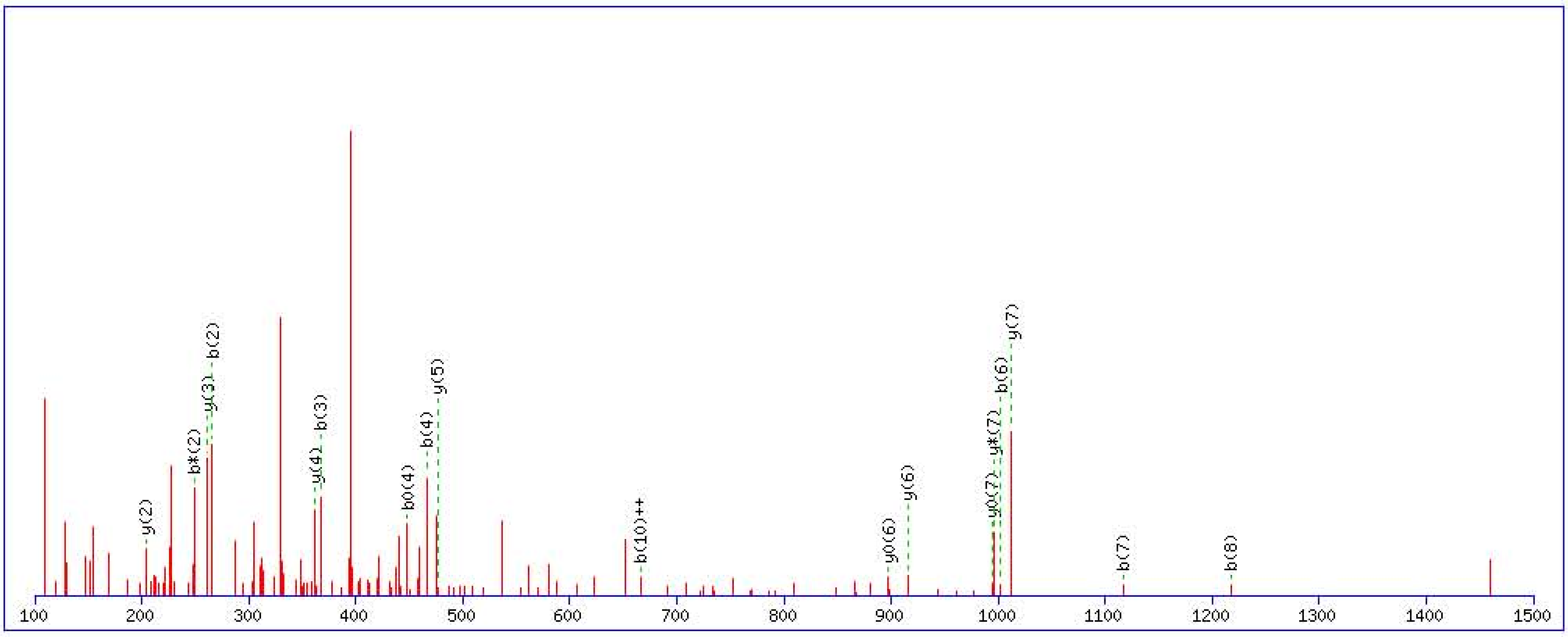
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **HQTVPQNTGGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

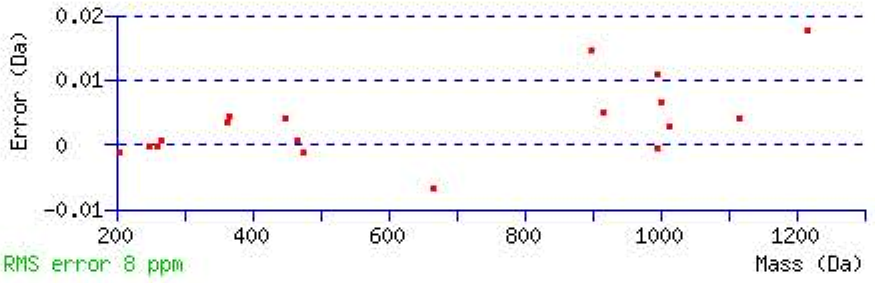
Match to Query 41955: 1476.744132 from(493.255320,3+) rtinseconds(1203) index(74677)
Title: Locus:1.1.1.2298.17 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

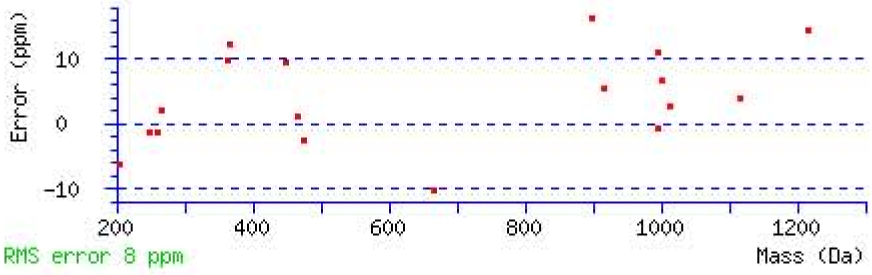
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1476.750748
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 28  Expect: 0.016
Matches : 18/108 fragment ions using 40 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	138.066188	69.536732					H							11
2	***266.124766***	133.566021	249.098217	125.052746			Q	1340.699099	670.853187	1323.672550	662.339913	1322.688534	661.847905	10
3	***367.172445***	184.089860	350.145896	175.576586	349.161880	175.084578	T	1212.640521	606.823899	1195.613972	598.310624	1194.629956	597.818616	9
4	***466.240859***	233.624068	449.214310	225.110793	448.230294	224.618785	V	1111.592842	556.300059	1094.566293	547.786784	1093.582277	547.294776	8
5	563.293623	282.150450	546.267074	273.637175	545.283058	273.145167	P	***1012.524428***	506.765852	995.497879	498.252577	994.513863	497.760569	7
6	***1002.518949***	501.763113	985.492400	493.249838	984.508384	492.757830	Q	***915.471664***	458.239470	898.445115	449.726195	897.461099	449.234187	6
7	***1116.561876***	558.784576	1099.535327	550.271302	1098.551311	549.779293	N	***476.246338***	238.626807	459.219789	230.113532	458.235773	229.621524	5
8	***1217.609555***	609.308416	1200.583006	600.795141	1199.598990	600.303133	T	***362.203411***	181.605343	345.176862	173.092069	344.192846	172.600061	4
9	1274.631019	637.819147	1257.604470	629.305873	1256.620454	628.813865	G	***261.155732***	131.081504	244.129183	122.568229			3
10	1331.652483	666.329879	1314.625934	657.816605	1313.641918	657.324597	G	***204.134268***	102.570772	187.107719	94.057497			2
11							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
28.2	1476.750748	-0.006616	HQTVPQNTGGK
8.5	1476.736115	0.008017	HQEALIGQSFYGK
1.3	1476.750748	-0.006616	HQTVPQNTGGK
1.0	1476.743317	0.000815	RNVGANGIGYQSNK

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

{MATRIX}
{SCIENCE}

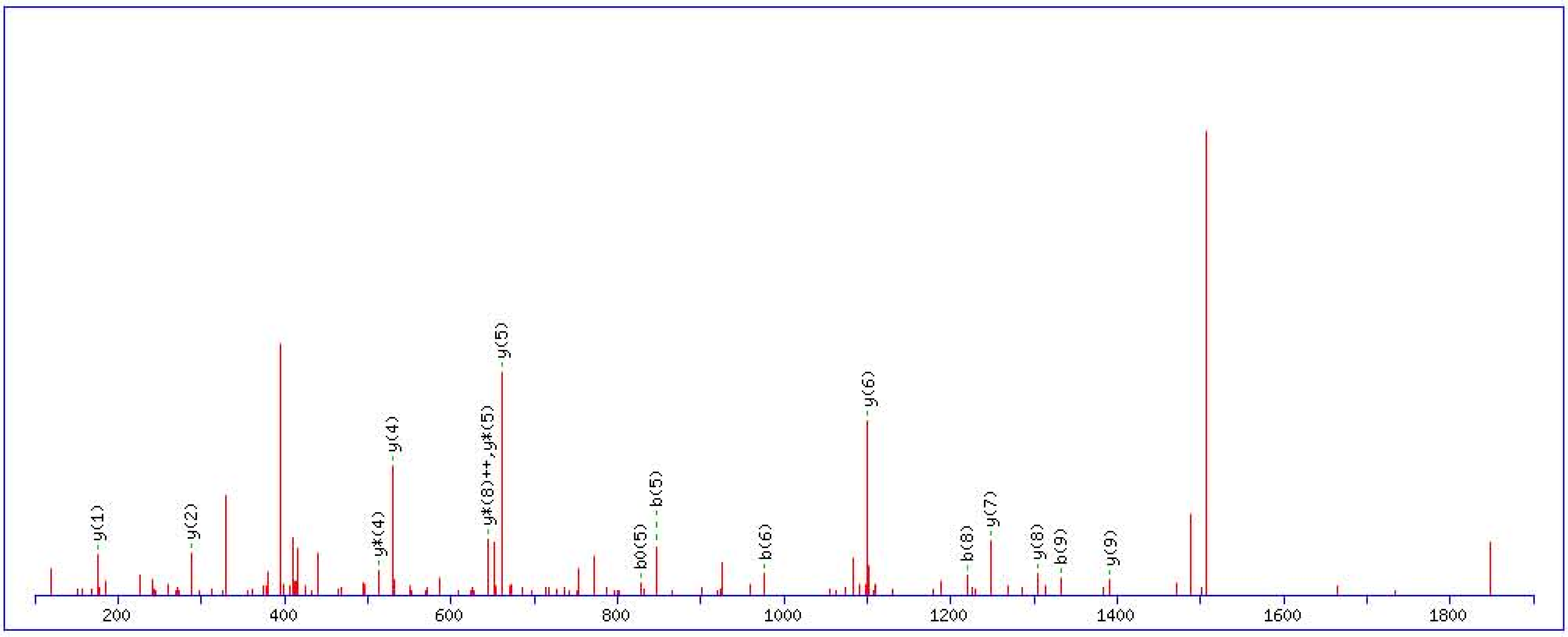
Mascot Search Results

Peptide View

MS/MS Fragmentation of **DSGFQMNQLR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

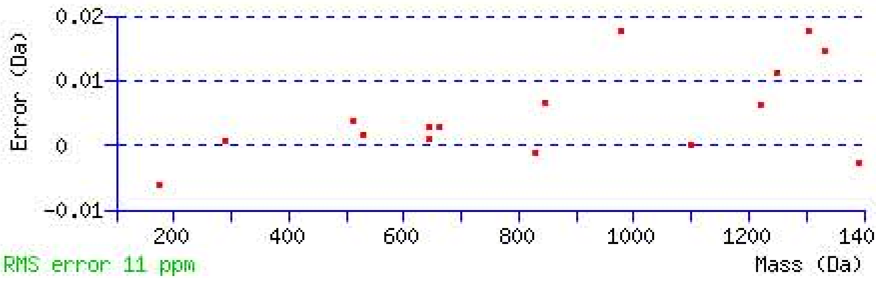
Match to Query 42764: 1505.715308 from(753.864930,2+) rtinseconds(2078) index(80802)
Title: Locus:1.1.1.2603.11 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

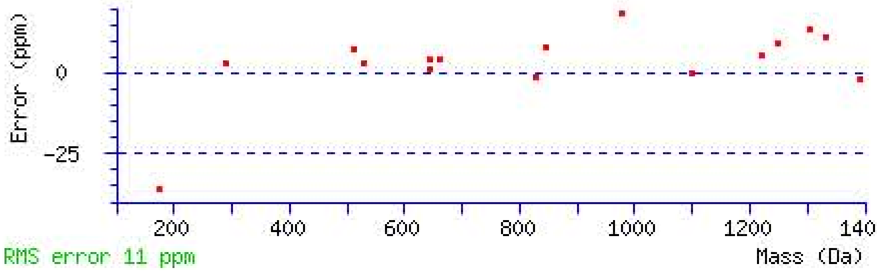
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1505.711899
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 0.0001
Matches : 16/84 fragment ions using 28 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							10
2	203.066247	102.036761			185.055682	93.031479	S	***1391.692238***	696.349757	1374.665689	687.836482	1373.681673	687.344474	9
3	260.087711	130.547493			242.077146	121.542211	G	***1304.660210***	652.833743	1287.633661	644.320469			8
4	407.156125	204.081700			389.145560	195.076418	F	***1247.638746***	624.323011	1230.612197	615.809736			7
5	**846.381451**	423.694364	829.354902	415.181089	828.370886	414.689081	Q	***1100.570332***	550.788804	1083.543783	542.275530			6
6	**977.421936**	489.214606	960.395387	480.701331	959.411371	480.209323	M	***661.345006***	331.176141	644.318457	322.662867			5
7	1091.464863	546.236069	1074.438314	537.722795	1073.454298	537.230787	N	***530.304521***	265.655899	513.277972	257.142624			4
8	**1219.523441**	610.265359	1202.496892	601.752084	1201.512876	601.260076	Q	416.261594	208.634435	399.235045	200.121160			3
9	**1332.607505**	666.807391	1315.580956	658.294116	1314.596940	657.802108	L	***288.203016***	144.605146	271.176467	136.091871			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of DSGFQMNQLR
(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	1505.711899	0.003409	DSGFQMNQLR
21.3	1505.711899	0.003409	DSGFQMNQLR
15.1	1505.703140	0.012168	DETMEEQDIKLR
6.6	1505.730530	-0.015222	QIFCQACLR
5.2	1505.704025	0.011283	MQMEIDQLR
3.9	1505.736877	-0.021569	AAMAVGGAGGSRVSSGR
3.4	1505.718384	-0.003076	AESEQEAYLR
2.8	1505.736862	-0.021554	EVMSPTGSARGRSR
0.4	1505.715271	0.000037	CELCLGIMGGKPR
0.1	1505.721802	-0.006494	GMQVSMDIPDILR

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

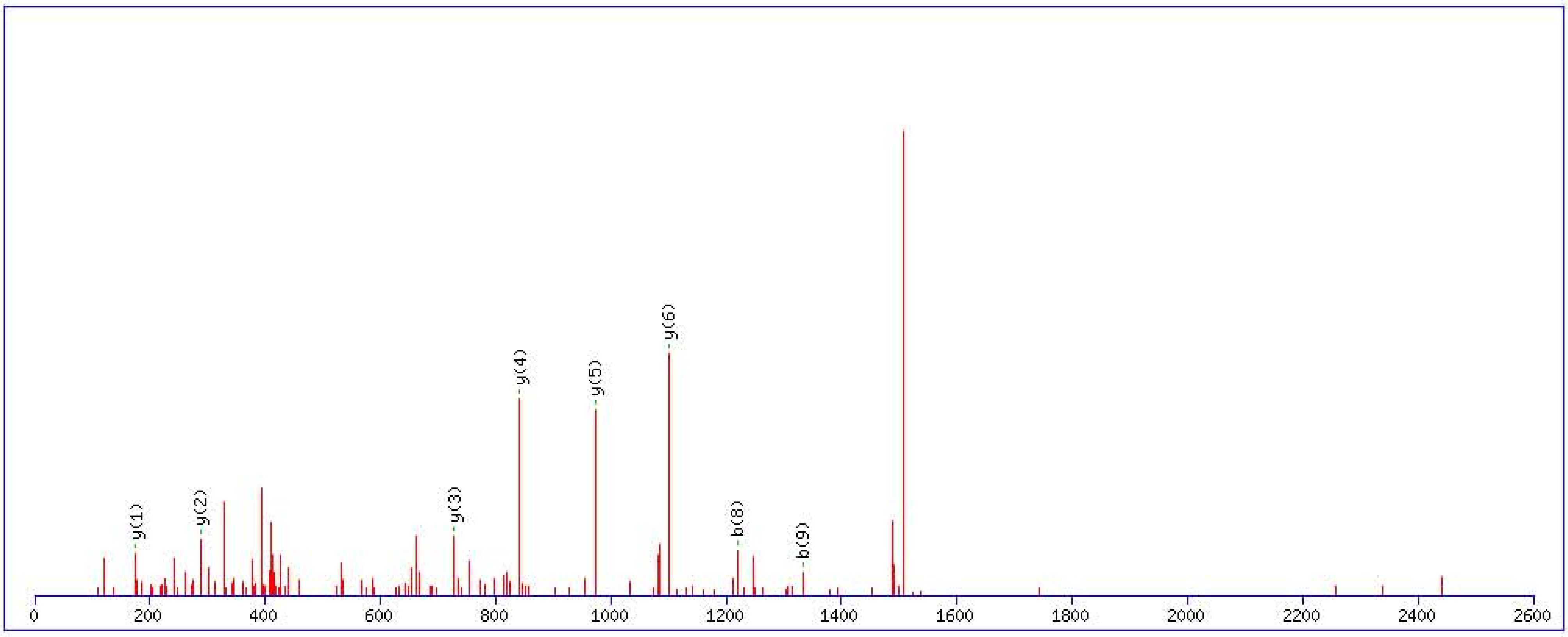
{MATRIX SCIENCE} **Mascot Search Results**

Peptide View

MS/MS Fragmentation of **DSGFQMNQLR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

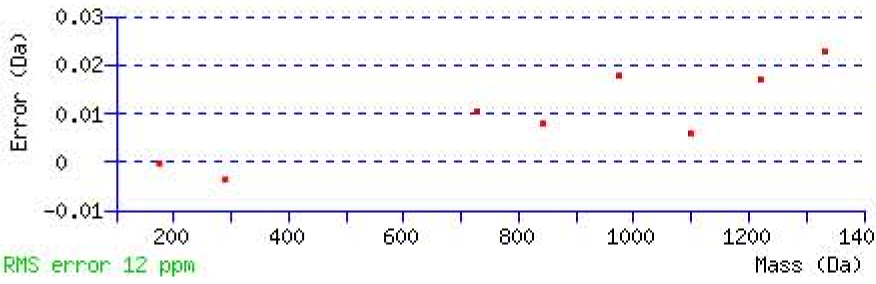
Match to Query 42767: 1505.718568 from(753.866560,2+) rtinseconds(2142) index(81222)
Title: Locus:1.1.1.2625.17 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

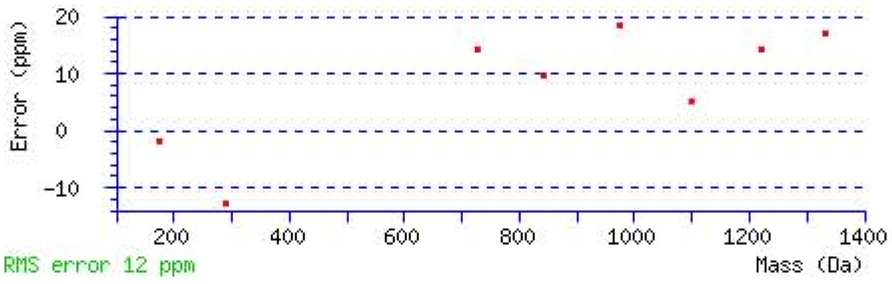
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1505.711899
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8 : Biotin:Thermo-21345 (Q)
Ions Score: 39 **Expect:** 0.00078
Matches : 8/84 fragment ions using 14 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							10
2	203.066247	102.036761			185.055682	93.031479	S	1391.692238	696.349757	1374.665689	687.836482	1373.681673	687.344474	9
3	260.087711	130.547493			242.077146	121.542211	G	1304.660210	652.833743	1287.633661	644.320469			8
4	407.156125	204.081700			389.145560	195.076418	F	1247.638746	624.323011	1230.612197	615.809736			7
5	535.214703	268.110990	518.188154	259.597715	517.204138	259.105707	Q	***1100.570332***	550.788804	1083.543783	542.275530			6
6	666.255188	333.631232	649.228639	325.117957	648.244623	324.625949	M	***972.511754***	486.759515	955.485205	478.246241			5
7	780.298115	390.652695	763.271566	382.139421	762.287550	381.647413	N	***841.471269***	421.239273	824.444720	412.725998			4
8	**1219.523441**	610.265359	1202.496892	601.752084	1201.512876	601.260076	Q	***727.428342***	364.217809	710.401793	355.704535			3
9	**1332.607505**	666.807391	1315.580956	658.294116	1314.596940	657.802108	L	***288.203016***	144.605146	271.176467	136.091871			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.9	1505.711899	0.006669	DSGFQMNQLR
11.7	1505.711899	0.006669	DSGFQMNQLR
5.6	1505.721802	-0.003234	GMQVSMDIPDILR
4.5	1505.740875	-0.022307	ECGKAFSHSSKLR
4.0	1505.704025	0.014543	MQMEIDQLR
3.9	1505.700653	0.017915	FMEDEQQLR
3.9	1505.704025	0.014543	MQMEIDQLR
3.6	1505.718384	0.000184	AESEQEAYLR
2.9	1505.703140	0.015428	DETMEEQDIKLR

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

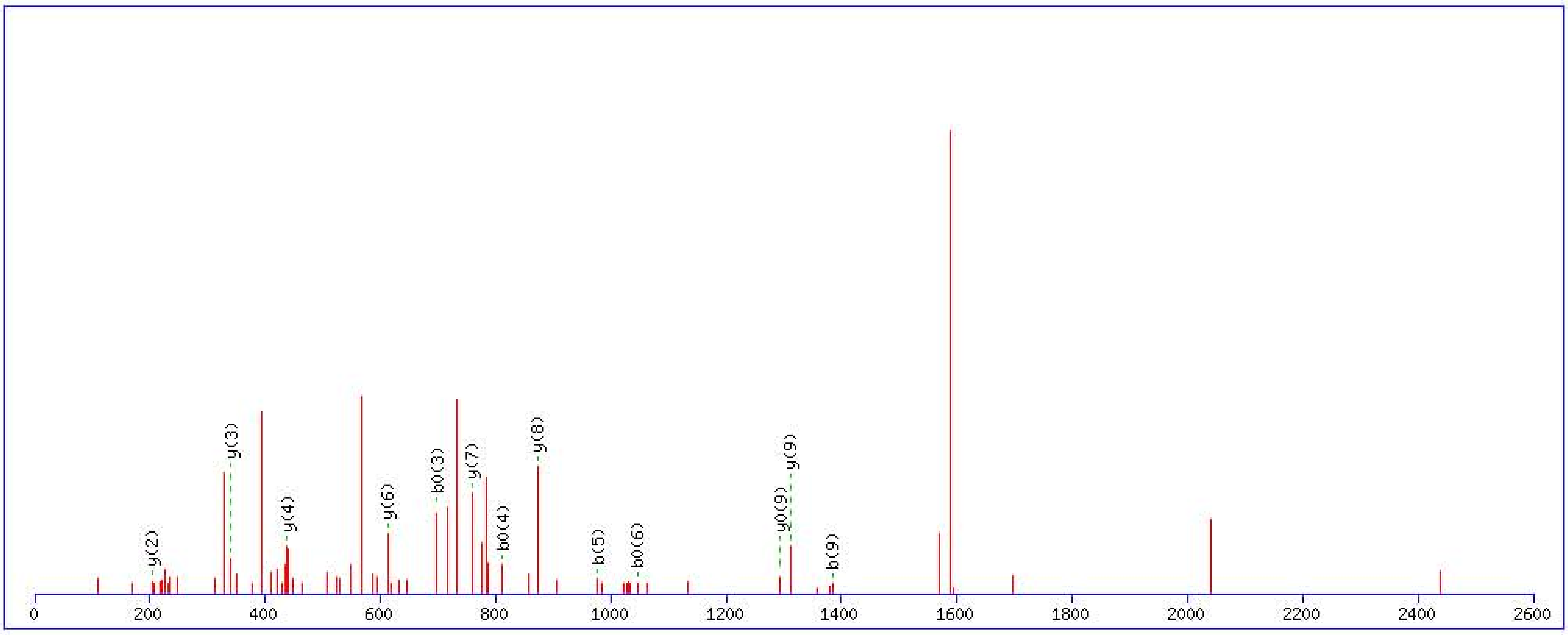
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EFQLFSSPHGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

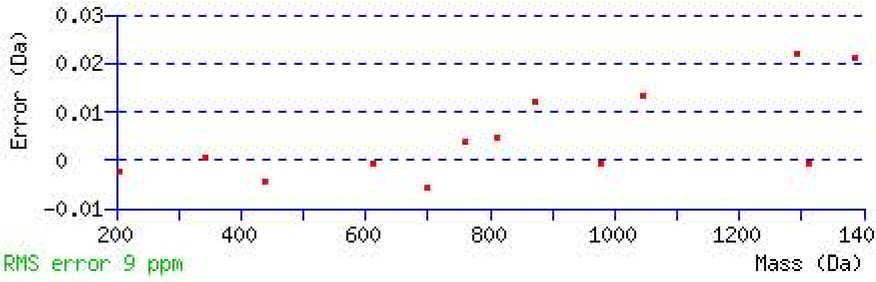
Match to Query 45395: 1586.801068 from(794.407810,2+) rtinseconds(2107) index(81006)
Title: Locus:1.1.1.2613.13 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

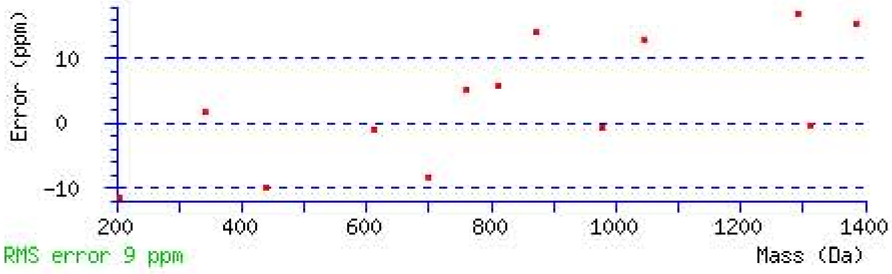
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1586.791534
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3     : Biotin:Thermo-21345 (Q)
Ions Score: 29  Expect: 0.0022
Matches : 13/108 fragment ions using 35 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	130.049869	65.528572			112.039304	56.523290	E							11
2	277.118283	139.062779			259.107718	130.057497	F	1458.756218	729.881747	1441.729669	721.368473	1440.745653	720.876465	10
3	716.343609	358.675443	699.317060	350.162168	698.333044	349.670160	Q	***1311.687804***	656.347540	1294.661255	647.834266	1293.677239	647.342258	9
4	829.427673	415.217475	812.401124	406.704200	811.417108	406.212192	L	***872.462478***	436.734877	855.435929	428.221603	854.451913	427.729595	8
5	**976.496087**	488.751682	959.469538	480.238407	958.485522	479.746399	F	***759.378414***	380.192845	742.351865	371.679571	741.367849	371.187563	7
6	1063.528115	532.267696	1046.501566	523.754421	1045.517550	523.262413	S	***612.310000***	306.658638	595.283451	298.145364	594.299435	297.653356	6
7	1150.560143	575.783710	1133.533594	567.270435	1132.549578	566.778427	S	525.277972	263.142624	508.251423	254.629350	507.267407	254.137342	5
8	1247.612907	624.310092	1230.586358	615.796817	1229.602342	615.304809	P	***438.245944***	219.626610	421.219395	211.113335			4
9	**1384.671819**	692.839548	1367.645270	684.326273	1366.661254	683.834265	H	***341.193180***	171.100228	324.166631	162.586953			3
10	1441.693283	721.350280	1424.666734	712.837005	1423.682718	712.344997	G	***204.134268***	102.570772	187.107719	94.057497			2
11							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
29.0	1586.791534	0.009534	EFQLFSSPHGK
0.6	1586.813980	-0.012912	FTQNHMLIYHKR

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

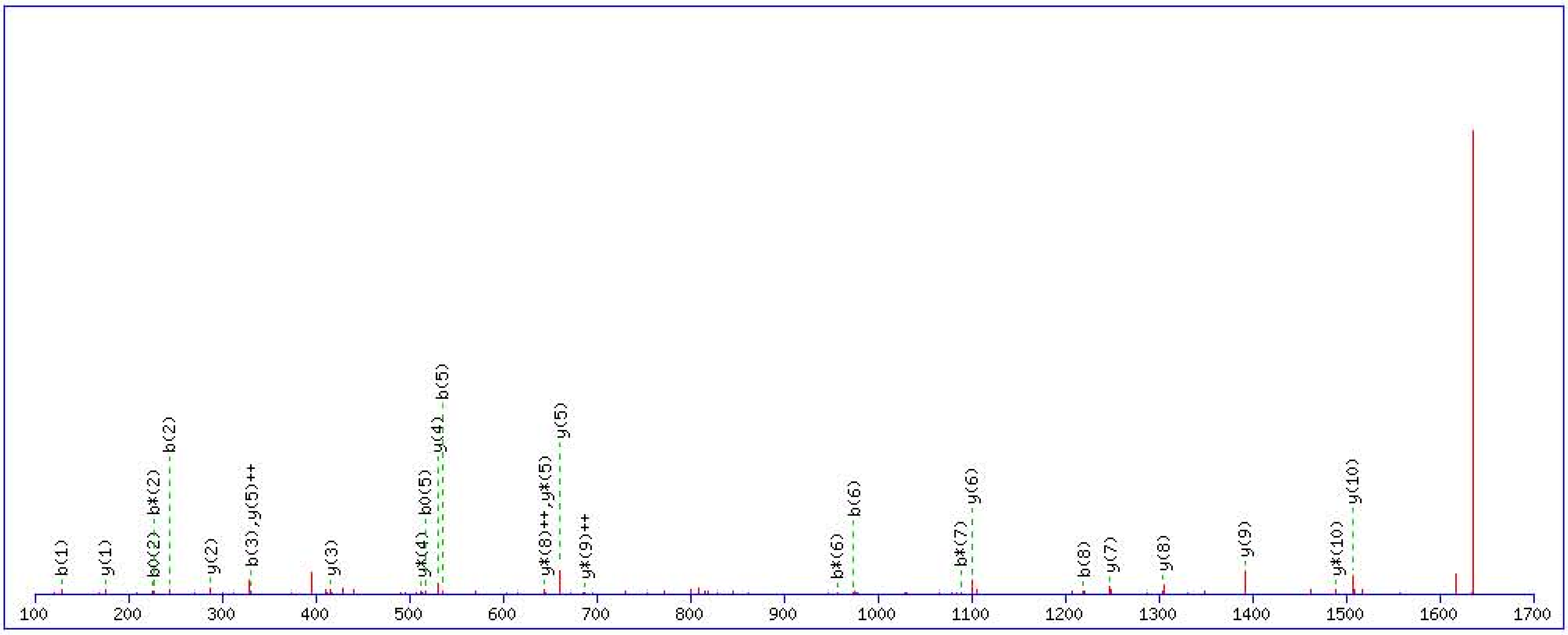
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KDSGFQMNQLR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

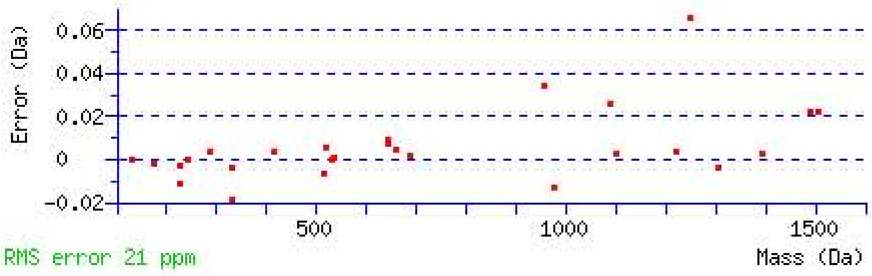
Match to Query 47839: 1633.809488 from(817.912020,2+) rtinseconds(1777) index(78760)
Title: Locus:1.1.1.2498.17 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

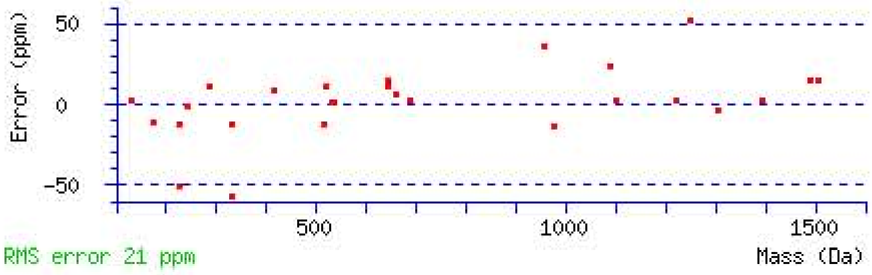
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1633.806854
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q6     : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.0028
Matches : 27/102 fragment ions using 76 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**129.102239**	65.054757	112.075690	56.541483			K							11
2	**244.129182**	122.568229	227.102633	114.054955	226.118617	113.562947	D	***1506.719181***	753.863228	1489.692632	745.349954	1488.708616	744.857946	10
3	**331.161210**	166.084243	314.134661	157.570969	313.150645	157.078961	S	***1391.692238***	696.349757	1374.665689	687.836482	1373.681673	687.344474	9
4	388.182674	194.594975	371.156125	186.081701	370.172109	185.589693	G	***1304.660210***	652.833743	1287.633661	644.320468			8
5	**535.251088**	268.129182	518.224539	259.615908	517.240523	259.123900	F	***1247.638746***	624.323011	1230.612197	615.809736			7
6	**974.476414**	487.741845	957.449865	479.228571	956.465849	478.736563	Q	***1100.570332***	550.788804	1083.543783	542.275530			6
7	1105.516899	553.262088	1088.490350	544.748813	1087.506334	544.256805	M	***661.345006***	331.176141	644.318457	322.662866			5
8	**1219.559826**	610.283551	1202.533277	601.770277	1201.549261	601.278268	N	***530.304521***	265.655899	513.277972	257.142624			4
9	1347.618404	674.312840	1330.591855	665.799566	1329.607839	665.307558	Q	***416.261594***	208.634435	399.235045	200.121160			3
10	1460.702468	730.854872	1443.675919	722.341598	1442.691903	721.849589	L	***288.203016***	144.605146	271.176467	136.091871			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
39.1	1633.806854	0.002634	KDSGFQMNQLR
11.8	1633.806854	0.002634	KDSGFQMNQLR

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

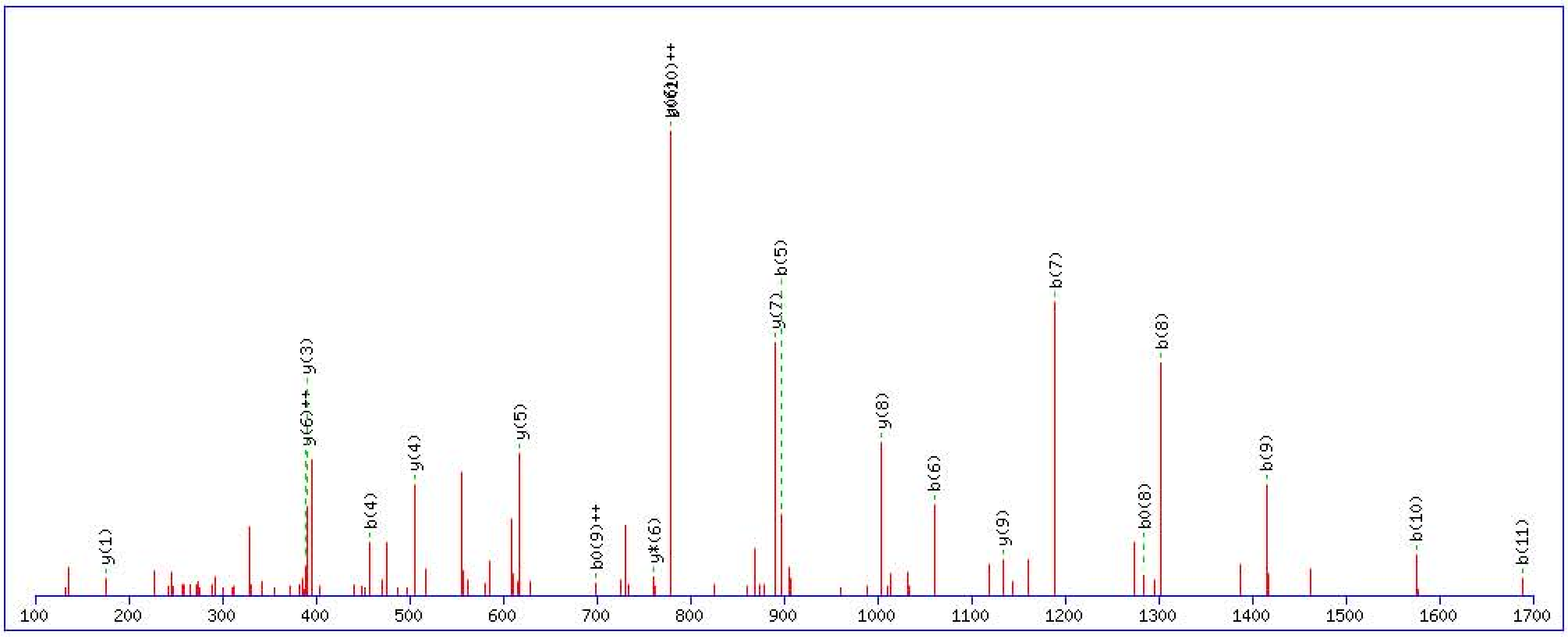
Mascot Search Results

Peptide View

MS/MS Fragmentation of **ADRDQYELLCLDNTR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

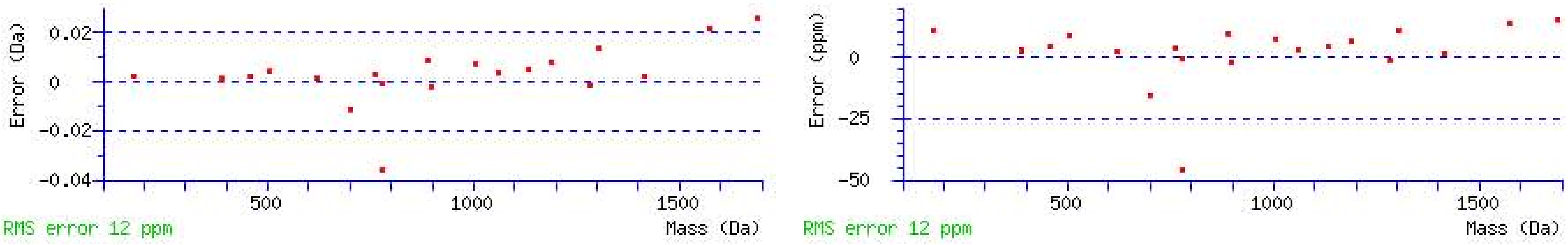
Match to Query 61451: 2192.048982 from(731.690270,3+) rtinseconds(2208) index(81702)
Title: Locus:1.1.1.2648.22 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2192.035400
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5     : Biotin:Thermo-21345 (Q)
Ions Score: 41  Expect: 0.00023
Matches : 21/160 fragment ions using 43 most intense peaks   (help)
```

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							15
2	187.071333	94.039304			169.060768	85.034022	D	2122.005587	1061.506431	2104.979038	1052.993157	2103.995022	1052.501149	14
3	343.172444	172.089860	326.145895	163.576585	325.161879	163.084577	R	2006.978644	1003.992960	1989.952095	995.479685	1988.968079	994.987677	13
4	***458.199387***	229.603332	441.172838	221.090057	440.188822	220.598049	D	1850.877533	925.942404	1833.850984	917.429130	1832.866968	916.937122	12
5	***897.424713***	449.215995	880.398164	440.702720	879.414148	440.210712	Q	1735.850590	868.428933	1718.824041	859.915658	1717.840025	859.423650	11
6	***1060.488042***	530.747659	1043.461493	522.234385	1042.477477	521.742376	Y	1296.625264	648.816270	1279.598715	640.302995	1278.614699	639.810987	10
7	***1189.530635***	595.268955	1172.504086	586.755681	1171.520070	586.263673	E	***1133.561935***	567.284605	1116.535386	558.771331	1115.551370	558.279323	9
8	***1302.614699***	651.810987	1285.588150	643.297713	1284.604134	642.805705	L	***1004.519342***	502.763309	987.492793	494.250034	986.508777	493.758026	8
9	***1415.698763***	708.353019	1398.672214	699.839745	1397.688198	699.347737	L	***891.435278***	446.221277	874.408729	437.708002	873.424713	437.215994	7
10	***1575.729412***	788.368344	1558.702863	779.855069	1557.718847	779.363061	C	***778.351214***	389.679245	761.324665	381.165971	760.340649	380.673963	6
11	***1688.813476***	844.910376	1671.786927	836.397101	1670.802911	835.905093	L	***618.320565***	309.663921	601.294016	301.150646	600.310000	300.658638	5
12	1803.840419	902.423847	1786.813870	893.910573	1785.829854	893.418565	D	***505.236501***	253.121888	488.209952	244.608614	487.225936	244.116606	4
13	1917.883346	959.445311	1900.856797	950.932036	1899.872781	950.440028	N	***390.209558***	195.608417	373.183009	187.095142	372.198993	186.603134	3
14	2018.931025	1009.969150	2001.904476	1001.455876	2000.920460	1000.963868	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
15							R	***175.118952***	88.063114	158.092403	79.549839			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.9	2192.035400	0.013582	ADRDQYELLCLDNTR
2.2	2192.021027	0.027955	AQRDVIEDCLMSLCR

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

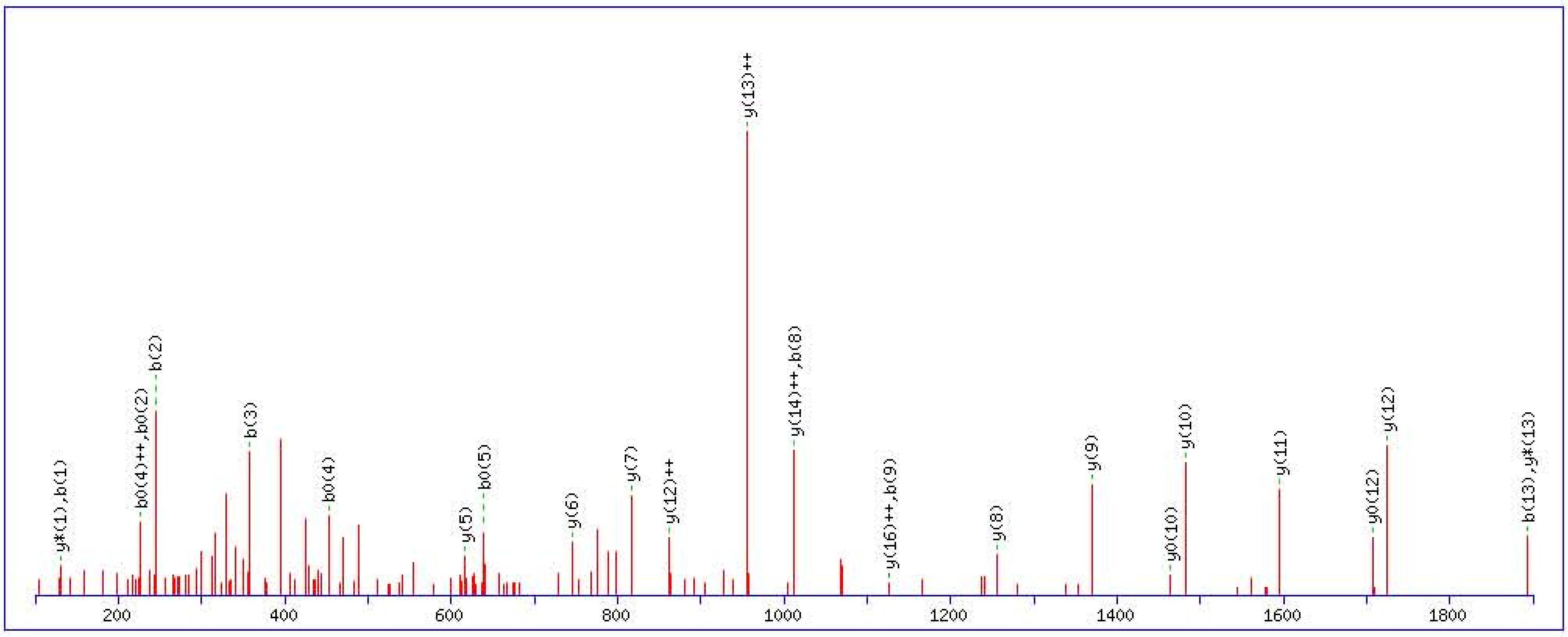
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **EDLIWELLNQAQEHFGK**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

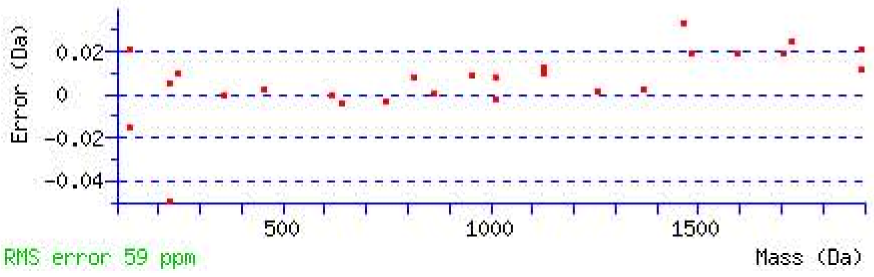
Match to Query 65379: 2380.209372 from(794.410400,3+) rtinseconds(3221) index(88365)
Title: Locus:1.1.1.2996.18 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

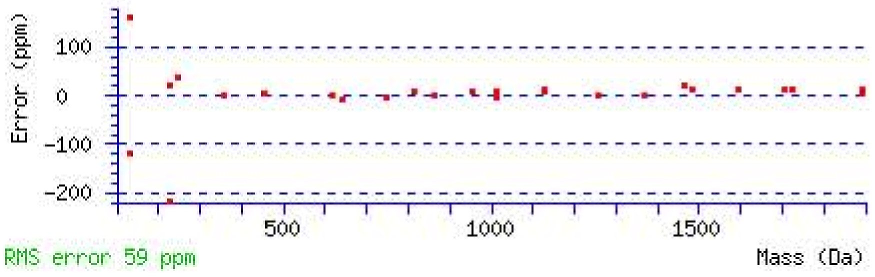
Click mouse within plot area to zoom in by factor of two about that point
Or, [Plot from] [100] to [1900] Da [Full range]
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2380.188522
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 54  Expect: 3.1e-005
Matches : 26/168 fragment ions using 33 most intense peaks   (help)
```

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	***130.049869***	65.528572			112.039304	56.523290	E							17
2	***245.076812***	123.042044			227.066247	114.036762	D	2252.153237	1126.580256	2235.126688	1118.066982	2234.142672	1117.574974	16
3	***358.160876***	179.584076			340.150311	170.578794	L	2137.126294	1069.066785	2120.099745	1060.553510	2119.115729	1060.061502	15
4	471.244940	236.126108			453.234375	227.120826	I	2024.042230	1012.524753	2007.015681	1004.011479	2006.031665	1003.519470	14
5	657.324253	329.165765			639.313688	320.160482	W	1910.958166	955.982721	1893.931617	947.469447	1892.947601	946.977438	13
6	786.366846	393.687061			768.356281	384.681779	E	***1724.878853***	862.943064	1707.852304	854.429790	1706.868288	853.937782	12
7	899.450910	450.229093			881.440345	441.223811	L	***1595.836260***	798.421768	1578.809711	789.908493	1577.825695	789.416485	11
8	***1012.534974***	506.771125			994.524409	497.765843	L	***1482.752196***	741.879736	1465.725647	733.366461	1464.741631	732.874453	10
9	***1126.577901***	563.792589	1109.551352	555.279314	1108.567336	554.787306	N	***1369.668132***	685.337704	1352.641583	676.824429	1351.657567	676.332421	9
10	1565.803227	783.405252	1548.776678	774.891977	1547.792662	774.399969	Q	***1255.625205***	628.316240	1238.598656	619.802966	1237.614640	619.310958	8
11	1636.840341	818.923809	1619.813792	810.410534	1618.829776	809.918526	A	***816.399879***	408.703577	799.373330	400.190303	798.389314	399.698295	7
12	1764.898919	882.953098	1747.872370	874.439823	1746.888354	873.947815	Q	***745.362765***	373.185020	728.336216	364.671746	727.352200	364.179738	6
13	***1893.941512***	947.474394	1876.914963	938.961120	1875.930947	938.469112	E	***617.304187***	309.155732	600.277638	300.642457	599.293622	300.150449	5
14	2031.000424	1016.003850	2013.973875	1007.490576	2012.989859	1006.998568	H	488.261594	244.634435	471.235045	236.121160			4
15	2178.068838	1089.538057	2161.042289	1081.024782	2160.058273	1080.532774	F	351.202682	176.104979	334.176133	167.591704			3
16	2235.090302	1118.048789	2218.063753	1109.535514	2217.079737	1109.043506	G	204.134268	102.570772	187.107719	94.057497			2
17							K	147.112804	74.060040	130.086255	65.546765			1





NCBI **BLAST** search of EDLIWELLNQAQEHFGK
(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	2380.188522	0.020850	EDLIWELLNQAQEHFGK
37.3	2380.188522	0.020850	EDLIWELLNQAQEHFGK
5.4	2380.199814	0.009558	GEPGLQGFPGKPGFLGEVGPPGMR
1.4	2380.212997	-0.003625	ELTLEHMETERLELAQK

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

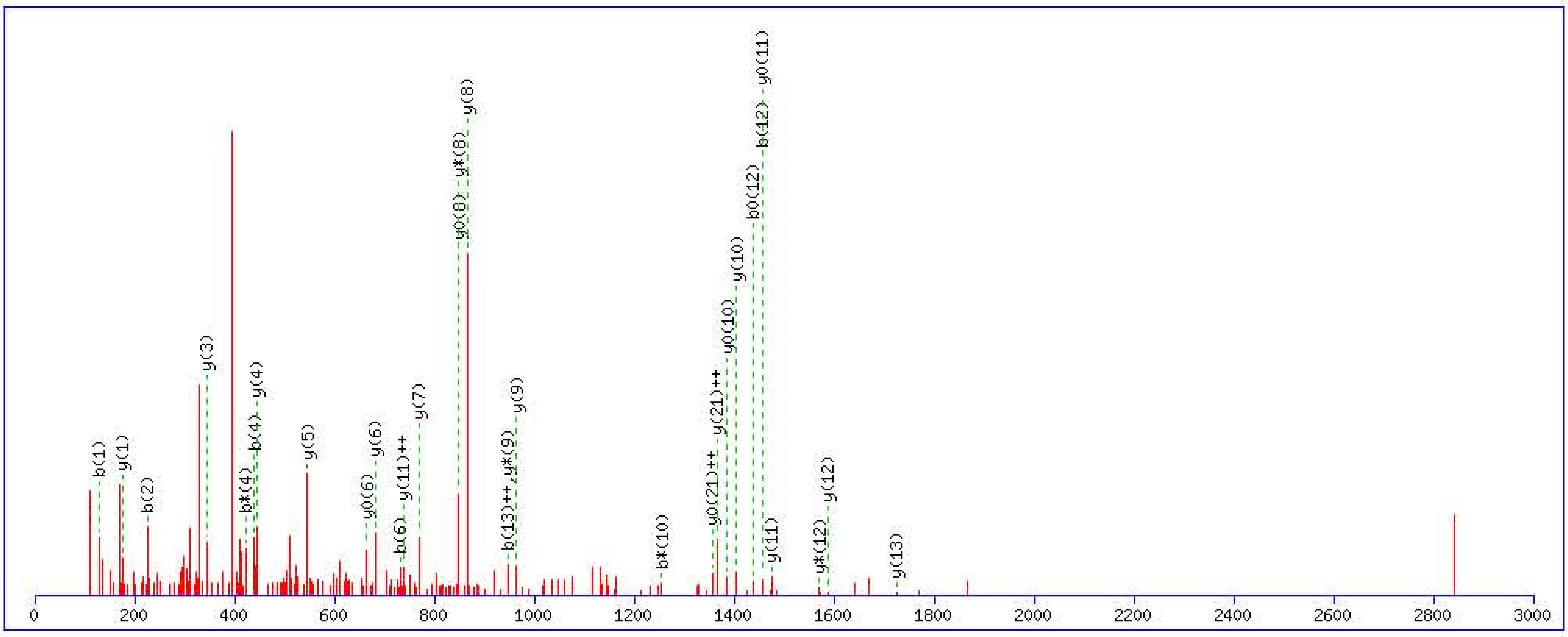
Mascot Search Results

Peptide View

MS/MS Fragmentation of **KPVDEYKDCHLAQVPSHTVVAR**
Found in **TRFE_HUMAN**, Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3

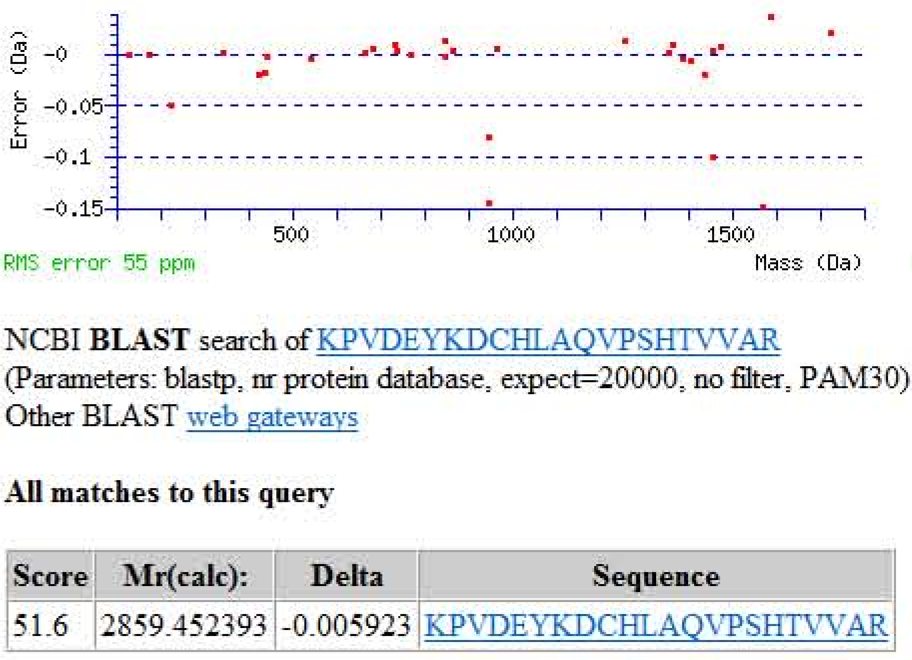
Match to Query 72786: 2859.446470 from(572.896570,5+) rtinseconds(1551) index(77284)
Title: Locus:1.1.1.2419.13 File:"2013-07-02 CLN FXIII 30 min 1st FT.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

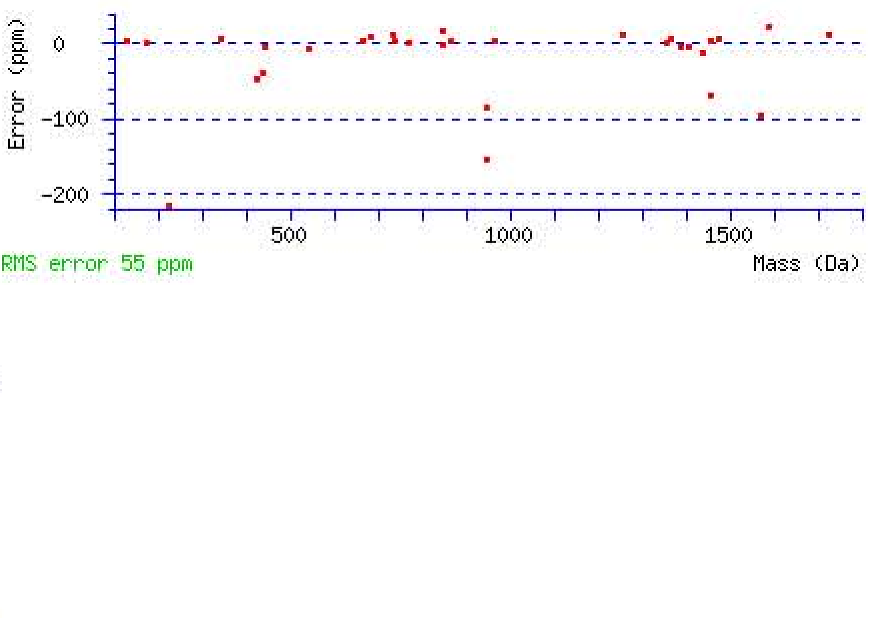
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 3000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2859.452393
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q13    : Biotin:Thermo-21345 (Q)
Ions Score: 52  Expect: 0.00021
Matches : 31/238 fragment ions using 65 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	**129.102239**	65.054757	112.075690	56.541483			K							22
2	**226.155003**	113.581139	209.128454	105.067865			P	2732.364705	1366.685990	2715.338156	1358.172716	2714.354140	1357.680708	21
3	325.223417	163.115346	308.196868	154.602072			V	2635.311941	1318.159608	2618.285392	1309.646334	2617.301376	1309.154326	20
4	**440.250360**	220.628818	423.223811	212.115544	422.239795	211.623536	D	2536.243527	1268.625401	2519.216978	1260.112127	2518.232962	1259.620119	19
5	569.292953	285.150115	552.266404	276.636840	551.282388	276.144832	E	2421.216584	1211.111930	2404.190035	1202.598655	2403.206019	1202.106647	18
6	**732.356282**	366.681779	715.329733	358.168505	714.345717	357.676497	Y	2292.173991	1146.590633	2275.147442	1138.077359	2274.163426	1137.585351	17
7	860.451245	430.729261	843.424696	422.215986	842.440680	421.723978	K	2129.110662	1065.058969	2112.084113	1056.545694	2111.100097	1056.053686	16
8	975.478188	488.242732	958.451639	479.729458	957.467623	479.237450	D	2001.015699	1001.011487	1983.989150	992.498213	1983.005134	992.006205	15
9	1135.508837	568.258057	1118.482288	559.744782	1117.498272	559.252774	C	1885.988756	943.498016	1868.962207	934.984741	1867.978191	934.492733	14
10	1272.567749	636.787513	1255.541200	628.274238	1254.557184	627.782230	H	***1725.958107***	863.482691	1708.931558	854.969417	1707.947542	854.477409	13
11	1385.651813	693.329545	1368.625264	684.816270	1367.641248	684.324262	L	***1588.899195***	794.953235	1571.872646	786.439961	1570.888630	785.947953	12
12	**1456.688927**	728.848101	1439.662378	720.334827	1438.678362	719.842819	A	***1475.815131***	738.411203	1458.788582	729.897929	1457.804566	729.405921	11
13	1895.914253	948.460765	1878.887704	939.947490	1877.903688	939.455482	Q	***1404.778017***	702.892646	1387.751468	694.379372	1386.767452	693.887364	10
14	1994.982667	997.994972	1977.956118	989.481697	1976.972102	988.989689	V	***965.552691***	483.279983	948.526142	474.766709	947.542126	474.274701	9
15	2092.035431	1046.521353	2075.008882	1038.008079	2074.024866	1037.516071	P	***866.484277***	433.745776	849.457728	425.232502	848.473712	424.740494	8
16	2179.067459	1090.037367	2162.040910	1081.524093	2161.056894	1081.032085	S	***769.431513***	385.219394	752.404964	376.706120	751.420948	376.214112	7
17	2316.126371	1158.566823	2299.099822	1150.053549	2298.115806	1149.561541	H	***682.399485***	341.703380	665.372936	333.190106	664.388920	332.698098	6
18	2417.174050	1209.090663	2400.147501	1200.577388	2399.163485	1200.085380	T	***545.340573***	273.173924	528.314024	264.660650	527.330008	264.168642	5
19	2516.242464	1258.624870	2499.215915	1250.111595	2498.231899	1249.619587	V	***444.292894***	222.650085	427.266345	214.136810			4
20	2615.310878	1308.159077	2598.284329	1299.645802	2597.300313	1299.153794	V	***345.224480***	173.115878	328.197931	164.602603			3
21	2686.347992	1343.677634	2669.321443	1335.164359	2668.337427	1334.672351	A	246.156066	123.581671	229.129517	115.068397			2
22							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.6	2859.452393	-0.005923	KPVDEYKDCHLAQVPSHTVVAR

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

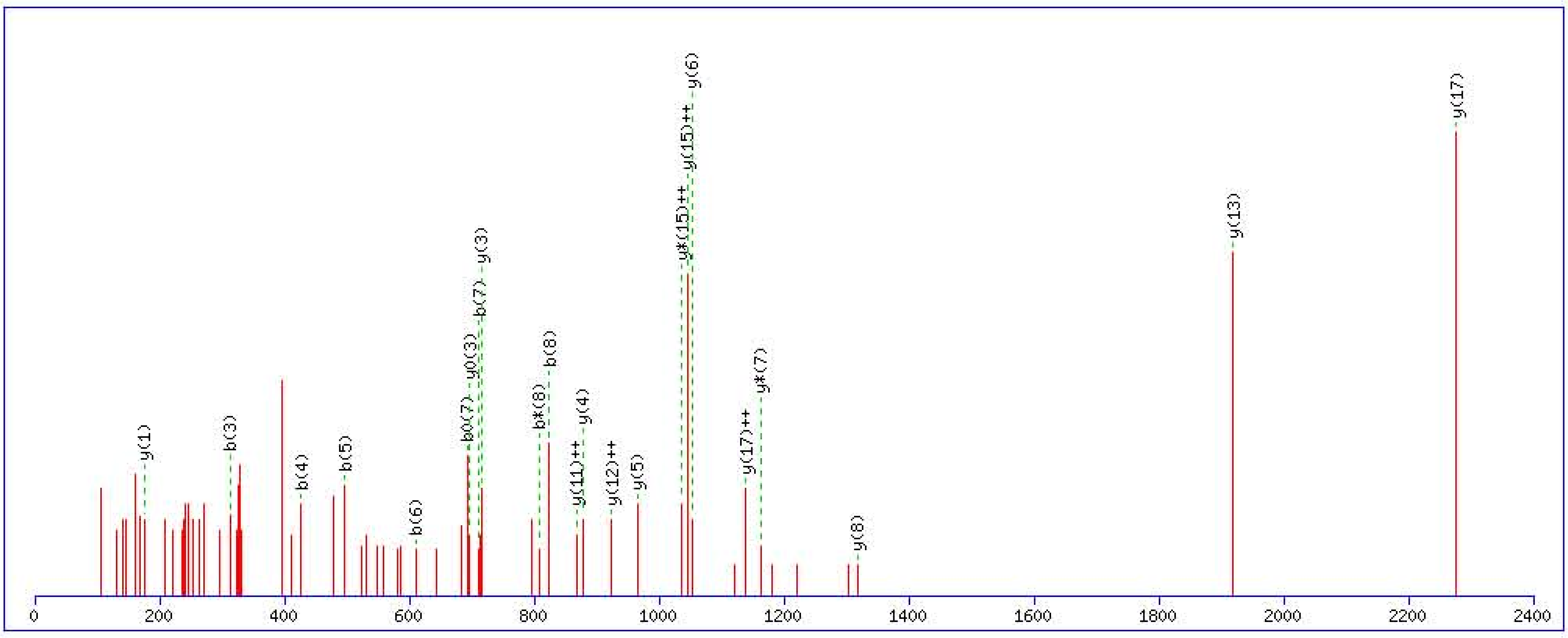
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **AKLIALTLLGMGLALFRNHQSSYQTR**
Found in **PON1_HUMAN**, Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3

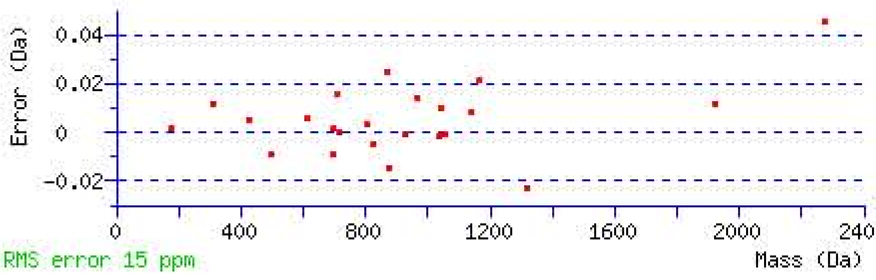
Match to Query 76278: 3212.790420 from(643.565360,5+) rtinseconds(3141) index(70240)
Title: Locus:1.1.1.3087.3 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

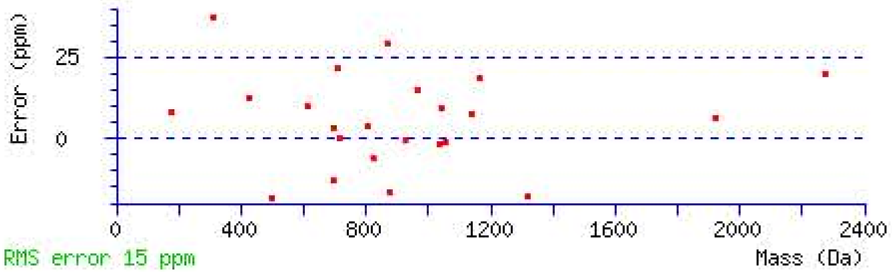
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 3212.767807
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q24 : Biotin:Thermo-21345 (Q)
Ions Score: 35 **Expect:** 0.0019
Matches : 23/284 fragment ions using 54 most intense peaks (help)

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	72.044390	36.525833					A							26
2	200.139353	100.573315	183.112804	92.060040			K	3142.738015	1571.872645	3125.711466	1563.359371	3124.727450	1562.867363	25
3	***313.223417***	157.115346	296.196868	148.602072			L	3014.643052	1507.825164	2997.616503	1499.311889	2996.632487	1498.819881	24
4	***426.307481***	213.657378	409.280932	205.144104			I	2901.558988	1451.283132	2884.532439	1442.769857	2883.548423	1442.277849	23
5	***497.344595***	249.175935	480.318046	240.662661			A	2788.474924	1394.741100	2771.448375	1386.227825	2770.464359	1385.735817	22
6	***610.428659***	305.717968	593.402110	297.204693			L	2717.437810	1359.222543	2700.411261	1350.709268	2699.427245	1350.217260	21
7	***711.476338***	356.241807	694.449789	347.728533	693.465773	347.236525	T	2604.353746	1302.680511	2587.327197	1294.167236	2586.343181	1293.675228	20
8	***824.560402***	412.783839	807.533853	404.270565	806.549837	403.778557	L	2503.306067	1252.156671	2486.279518	1243.643397	2485.295502	1243.151389	19
9	937.644466	469.325871	920.617917	460.812597	919.633901	460.320589	L	2390.222003	1195.614639	2373.195454	1187.101365	2372.211438	1186.609357	18
10	994.665930	497.836603	977.639381	489.323329	976.655365	488.831321	G	***2277.137939***	1139.072607	2260.111390	1130.559333	2259.127374	1130.067325	17
11	1125.706415	563.356846	1108.679866	554.843571	1107.695850	554.351563	M	2220.116475	1110.561875	2203.089926	1102.048601	2202.105910	1101.556593	16
12	1182.727879	591.867578	1165.701330	583.354303	1164.717314	582.862295	G	2089.075990	1045.041633	2072.049441	1036.528358	2071.065425	1036.036350	15
13	1295.811943	648.409609	1278.785394	639.896335	1277.801378	639.404327	L	2032.054526	1016.530901	2015.027977	1008.017627	2014.043961	1007.525619	14
14	1366.849057	683.928166	1349.822508	675.414892	1348.838492	674.922884	A	***1918.970462***	959.988869	1901.943913	951.475595	1900.959897	950.983587	13
15	1479.933121	740.470198	1462.906572	731.956924	1461.922556	731.464916	L	1847.933348	924.470312	1830.906799	915.957038	1829.922783	915.465030	12
16	1627.001535	814.004405	1609.974986	805.491131	1608.990970	804.999123	F	1734.849284	867.928280	1717.822735	859.415006	1716.838719	858.922998	11
17	1783.102646	892.054961	1766.076097	883.541686	1765.092081	883.049678	R	1587.780870	794.394073	1570.754321	785.880799	1569.770305	785.388791	10
18	1897.145573	949.076424	1880.119024	940.563150	1879.135008	940.071142	N	1431.679759	716.343518	1414.653210	707.830243	1413.669194	707.338235	9
19	2034.204485	1017.605880	2017.177936	1009.092606	2016.193920	1008.600598	H	***1317.636832***	659.322054	1300.610283	650.808780	1299.626267	650.316772	8
20	2162.263063	1081.635169	2145.236514	1073.121895	2144.252498	1072.629887	Q	1180.577920	590.792598	1163.551371	582.279324	1162.567355	581.787316	7
21	2249.295091	1125.151183	2232.268542	1116.637909	2231.284526	1116.145901	S	***1052.519342***	526.763309	1035.492793	518.250035	1034.508777	517.758027	6
22	2336.327119	1168.667197	2319.300570	1160.153923	2318.316554	1159.661915	S	***965.487314***	483.247295	948.460765	474.734021	947.476749	474.242013	5
23	2499.390448	1250.198862	2482.363899	1241.685587	2481.379883	1241.193579	Y	***878.455286***	439.731281	861.428737	431.218007	860.444721	430.725999	4
24	2938.615774	1469.811525	2921.589225	1461.298250	2920.605209	1460.806242	Q	***715.391957***	358.199617	698.365408	349.686342	697.381392	349.194334	3
25	3039.663453	1520.335364	3022.636904	1511.822090	3021.652888	1511.330082	T	276.166631	138.586953	259.140082	130.073679	258.156066	129.581671	2
26							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
35.2	3212.767807	0.022613	AKLIALTLLGMGLALFRNHQSSYQTR
17.0	3212.767807	0.022613	AKLIALTLLGMGLALFRNHQSSYQTR

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

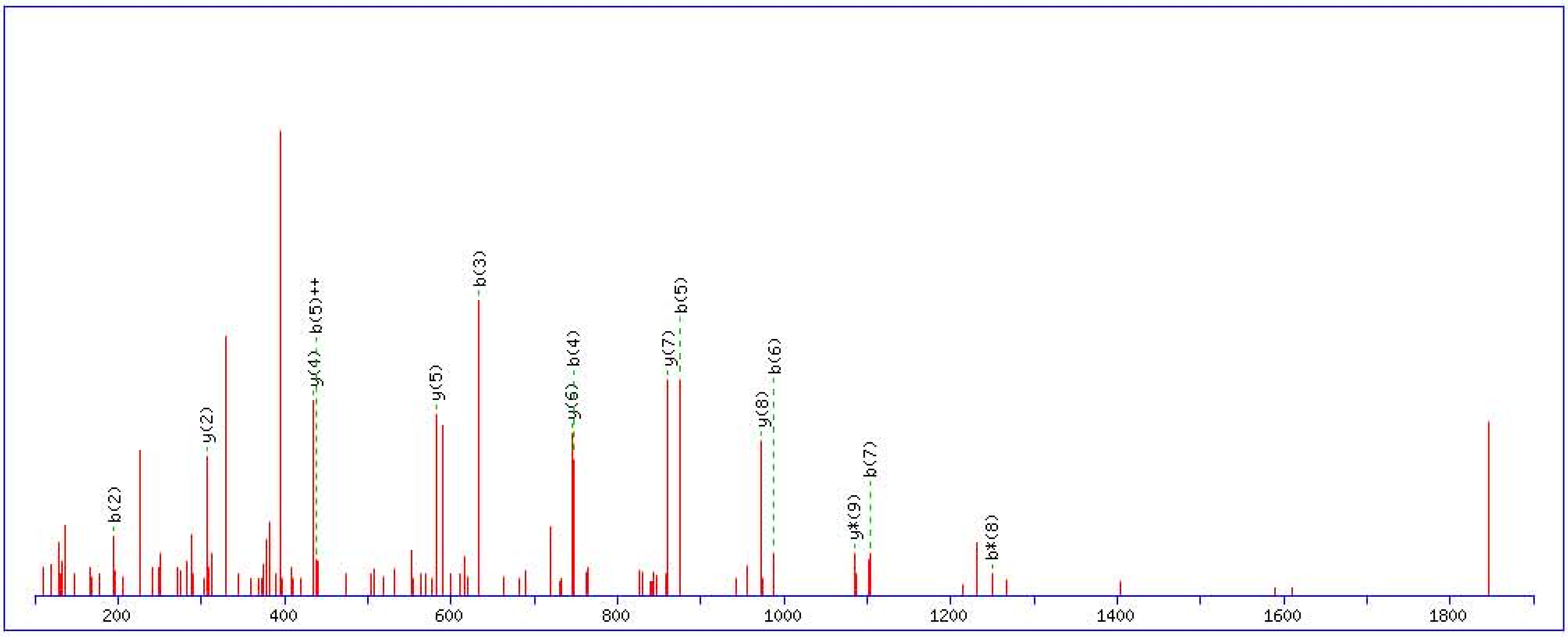
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GHQLQLDYFGACK**
Found in **SPRL1_HUMAN**, SPARC-like protein 1 OS=Homo sapiens GN=SPARCL1 PE=1 SV=2

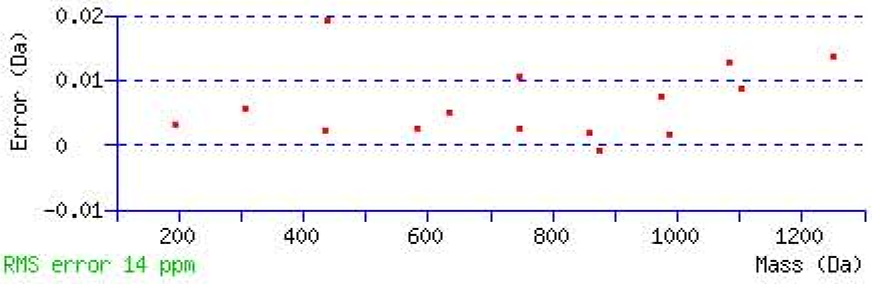
Match to Query 53232: 1846.890012 from(616.637280,3+) rtinseconds(2105) index(63749)
Title: Locus:1.1.1.2730.14 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

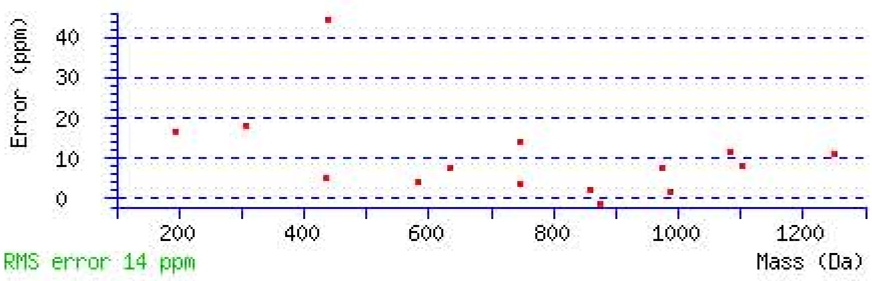
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1846.885849
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 39  Expect: 0.00024
Matches : 15/116 fragment ions using 26 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							13
2	***195.087652***	98.047464					H	1790.871661	895.939469	1773.845112	887.426194	1772.861096	886.934186	12
3	***634.312978***	317.660127	617.286429	309.146853			Q	1653.812749	827.410013	1636.786200	818.896738	1635.802184	818.404730	11
4	***747.397042***	374.202159	730.370493	365.688885			L	1214.587423	607.797350	1197.560874	599.284075	1196.576858	598.792067	10
5	***875.455620***	438.231448	858.429071	429.718174			Q	1101.503359	551.255318	1084.476810	542.742043	1083.492794	542.250035	9
6	***988.539684***	494.773480	971.513135	486.260206			L	***973.444781***	487.226029	956.418232	478.712754	955.434216	478.220746	8
7	***1103.566627***	552.286952	1086.540078	543.773677	1085.556062	543.281669	D	***860.360717***	430.683997	843.334168	422.170722	842.350152	421.678714	7
8	1266.629956	633.818616	1249.603407	625.305342	1248.619391	624.813334	Y	***745.333774***	373.170525	728.307225	364.657251			6
9	1413.698370	707.352823	1396.671821	698.839549	1395.687805	698.347541	F	***582.270445***	291.638861	565.243896	283.125586			5
10	1470.719834	735.863555	1453.693285	727.350281	1452.709269	726.858273	G	***435.202031***	218.104653	418.175482	209.591379			4
11	1541.756948	771.382112	1524.730399	762.868838	1523.746383	762.376830	A	378.180567	189.593921	361.154018	181.080647			3
12	1701.787597	851.397437	1684.761048	842.884162	1683.777032	842.392154	C	***307.143453***	154.075365	290.116904	145.562090			2
13							K	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
38.6	1846.885849	0.004163	GHQLQLDYFGACK
22.0	1846.885849	0.004163	GHQLQLDYFGACK
0.0	1846.895721	-0.005709	LQLEETMPSPYGR

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

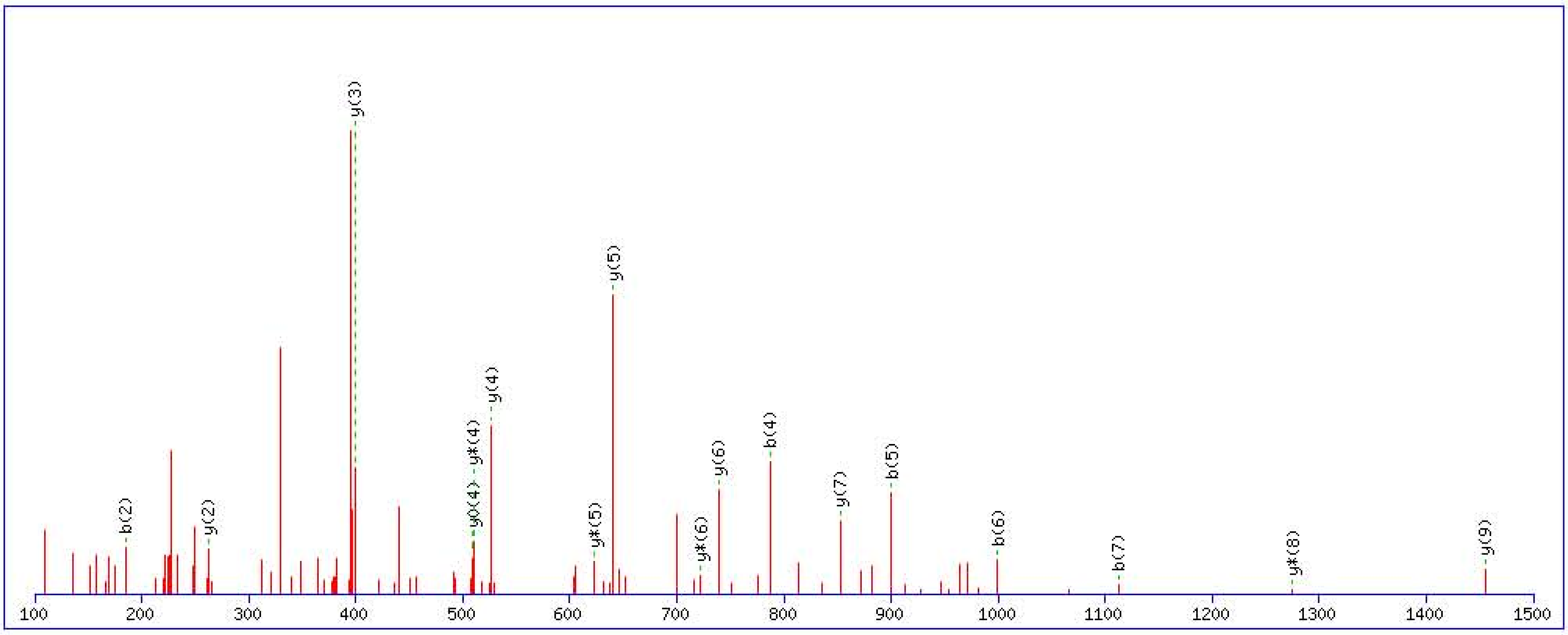
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SPYQLVLQHSR**
Found in **BGH3_HUMAN**, Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1

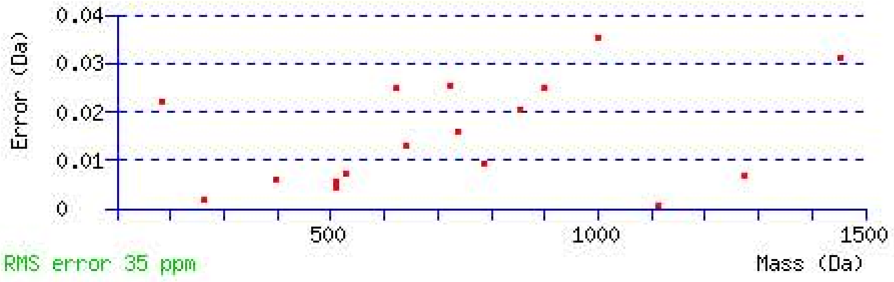
Match to Query 47994: 1637.891712 from(546.971180,3+) rtinseconds(1889) index(24437)
Title: Locus:1.1.1.2510.12 File:"2013-07-02 CLN FXIII 30 min 1st F 2.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

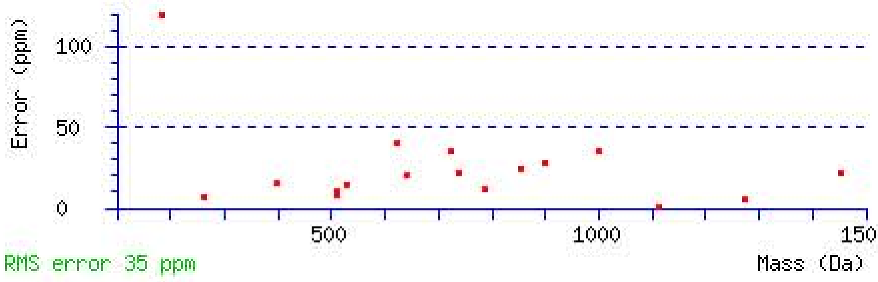
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1637.871170
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q4 : Biotin:Thermo-21345 (Q)
Ions Score: 36 **Expect:** 0.0047
Matches : 17/112 fragment ions using 31 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							11
2	**185.092068**	93.049672			167.081503	84.044389	P	1551.846431	776.426853	1534.819882	767.913579	1533.835866	767.421571	10
3	348.155397	174.581336			330.144832	165.576054	Y	***1454.793667***	727.900471	1437.767118	719.387197	1436.783102	718.895189	9
4	**787.380723**	394.194000	770.354174	385.680725	769.370158	385.188717	Q	1291.730338	646.368807	1274.703789	637.855532	1273.719773	637.363524	8
5	**900.464787**	450.736032	883.438238	442.222757	882.454222	441.730749	L	***852.505012***	426.756144	835.478463	418.242869	834.494447	417.750861	7
6	**999.533201**	500.270239	982.506652	491.756964	981.522636	491.264956	V	***739.420948***	370.214112	722.394399	361.700837	721.410383	361.208829	6
7	**1112.617265**	556.812270	1095.590716	548.298996	1094.606700	547.806988	L	***640.352534***	320.679905	623.325985	312.166630	622.341969	311.674622	5
8	1240.675843	620.841559	1223.649294	612.328285	1222.665278	611.836277	Q	***527.268470***	264.137873	510.241921	255.624598	509.257905	255.132590	4
9	1377.734755	689.371015	1360.708206	680.857741	1359.724190	680.365733	H	***399.209892***	200.108584	382.183343	191.595309	381.199327	191.103301	3
10	1464.766783	732.887029	1447.740234	724.373755	1446.756218	723.881747	S	***262.150980***	131.579128	245.124431	123.065854	244.140415	122.573846	2
11							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
36.3	1637.871170	0.020542	SPYQLVLQHSR

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

Mascot Search Results

Peptide View

MS/MS Fragmentation of **LGDDLLQCHPAVK**
Found in **PROC_HUMAN**, Vitamin K-dependent protein C OS=Homo sapiens GN=PROC PE=1 SV=1

Match to Query 51610: 1775.902722 from(592.974850,3+) rtinseconds(1935) index(62645)
Title: Locus:1.1.1.2671.16 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1775.906250
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q7      : Biotin:Thermo-21345 (Q)
Ions Score: 65  Expect: 1.9e-006
Matches : 11/110 fragment ions using 16 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	114.091340	57.549308					L							13
2	171.112804	86.060040					G	***1663.829461***	832.418369	1646.802912	823.905094	1645.818896	823.413086	12
3	286.139747	143.573512			268.129182	134.568229	D	1606.807997	803.907637	1589.781448	795.394362	1588.797432	794.902354	11
4	401.166690	201.086983			383.156125	192.081701	D	***1491.781054***	746.394165	1474.754505	737.880891	1473.770489	737.388883	10
5	514.250754	257.629015			496.240189	248.623733	L	***1376.754111***	688.880694	1359.727562	680.367419			9
6	627.334818	314.171047			609.324253	305.165765	L	***1263.670047***	632.338662	1246.643498	623.825387			8
7	1066.560144	533.783710	1049.533595	525.270436	1048.549579	524.778428	Q	***1150.585983***	575.796630	1133.559434	567.283355			7
8	1226.590793	613.799035	1209.564244	605.285760	1208.580228	604.793752	C	***711.360657***	356.183967	694.334108	347.670692			6
9	1363.649705	682.328491	1346.623156	673.815216	1345.639140	673.323208	H	***551.330008***	276.168642	534.303459	267.655368			5
10	1460.702469	730.854873	1443.675920	722.341598	1442.691904	721.849590	P	***414.271096***	207.639186	397.244547	199.125912			4
11	1531.739583	766.373430	1514.713034	757.860155	1513.729018	757.368147	A	317.218332	159.112804	300.191783	150.599530			3
12	1630.807997	815.907637	1613.781448	807.394362	1612.797432	806.902354	V	246.181218	123.594247	229.154669	115.080973			2
13							K	***147.112804***	74.060040	130.086255	65.546765			1

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.5	1775.906250	-0.003528	LGDDLLQCHPAVK
3.3	1775.879761	0.022961	VASMDSIGNLMVSPPVK
0.6	1775.927994	-0.025272	IIADIFEYTAKHMPK

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

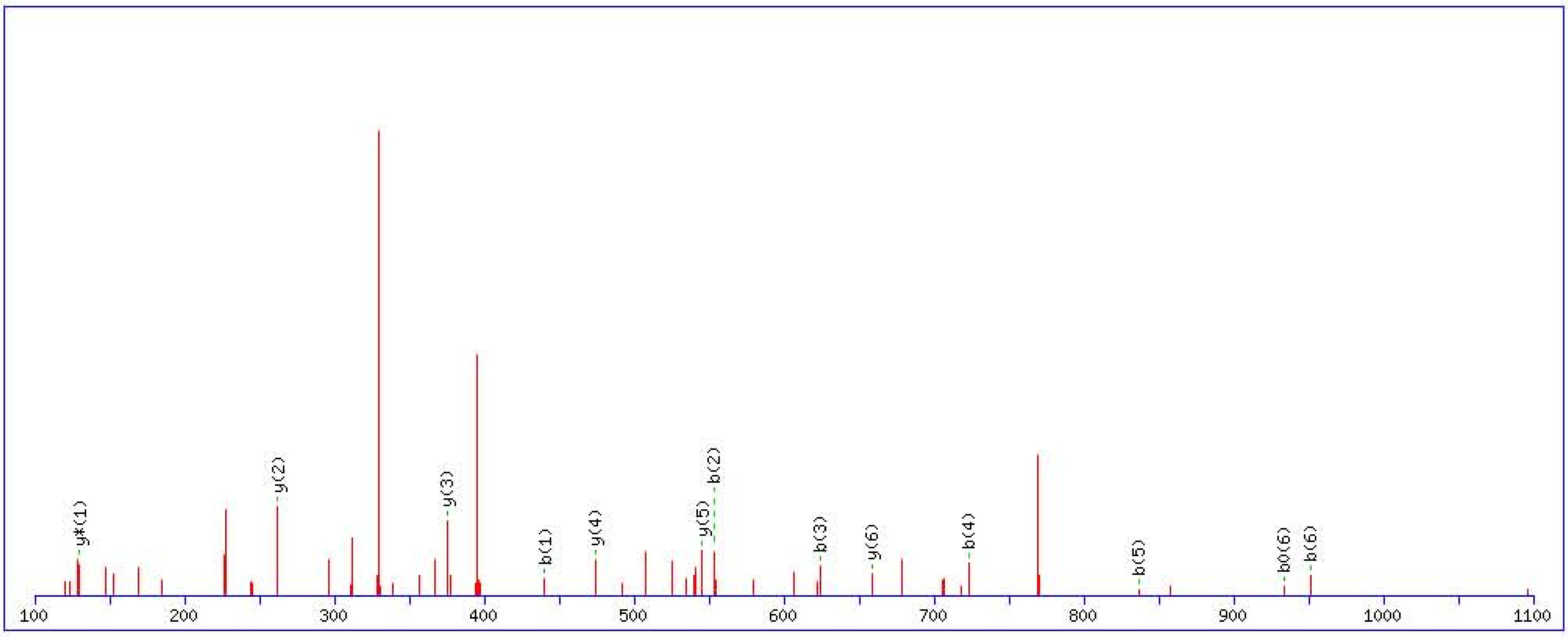
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QLAVLDK**
Found in **PROS_HUMAN**, Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1

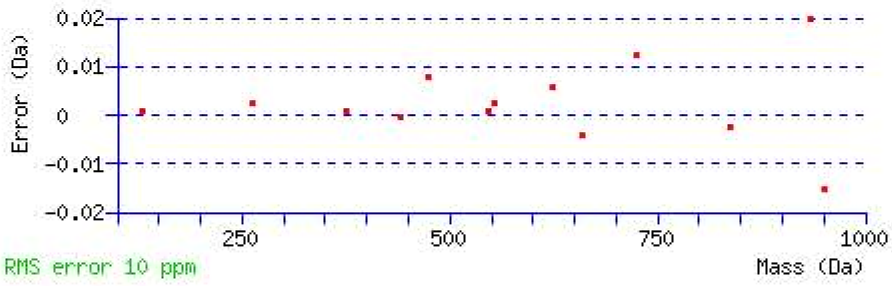
Match to Query 26123: 1096.628608 from(549.321580,2+) rtinseconds(1946) index(62739)
Title: Locus:1.1.1.2675.10 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

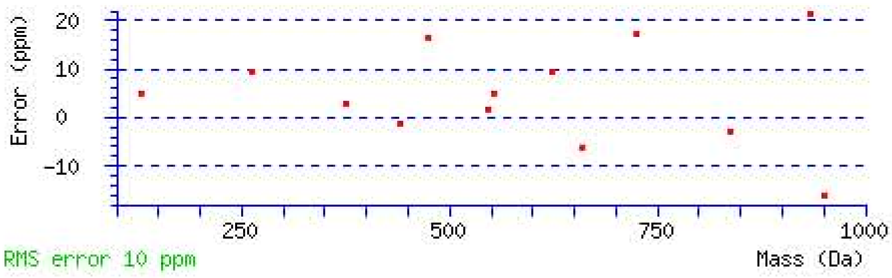
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1096.631439
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 31  Expect: 0.014
Matches : 13/60 fragment ions using 26 most intense peaks    (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	***440.232602***	220.619939	423.206053	212.106664			**Q**							7
2	***553.316666***	277.161971	536.290117	268.648697			**L**	**658.413403**	329.710340	641.386854	321.197065	640.402838	320.705057	6
3	***624.353780***	312.680528	607.327231	304.167254			**A**	**545.329339**	273.168308	528.302790	264.655033	527.318774	264.163025	5
4	***723.422194***	362.214735	706.395645	353.701461			**V**	**474.292225**	237.649750	457.265676	229.136476	456.281660	228.644468	4
5	***836.506258***	418.756767	819.479709	410.243493			**L**	**375.223811**	188.115543	358.197262	179.602269	357.213246	179.110261	3
6	***951.533201***	476.270239	934.506652	467.756964	933.522636	467.264956	**D**	**262.139747**	131.573511	245.113198	123.060237	244.129182	122.568229	2
7							**K**	147.112804	74.060040	130.086255	65.546765			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.8	1096.631439	-0.002831	QLAVLDK
15.4	1096.624054	0.004554	KPVDSVPLSR
7.3	1096.624023	0.004585	IPRENLLDK
4.2	1096.639297	-0.010689	AHVSPLFKAK
1.5	1096.631439	-0.002831	GILQLDK
1.3	1096.628052	0.000556	YQLSAIFKK
1.3	1096.631439	-0.002831	QIDVAIK
0.6	1096.642654	-0.014046	NITMHLLKK
0.1	1096.612808	0.015800	APAVTEATPLK
0.0	1096.635269	-0.006661	SSSLVIHKAR

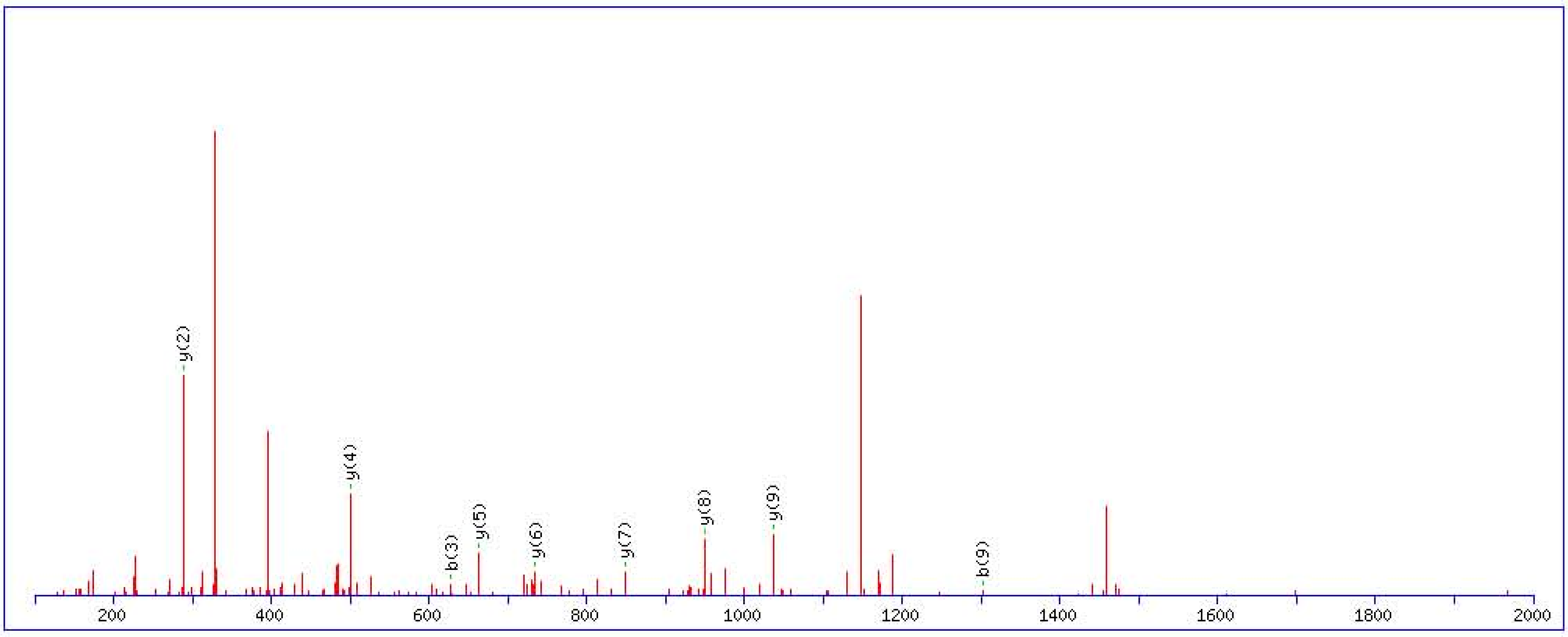
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **QSTNAYPDLR**
Found in **PROS_HUMAN**, Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1

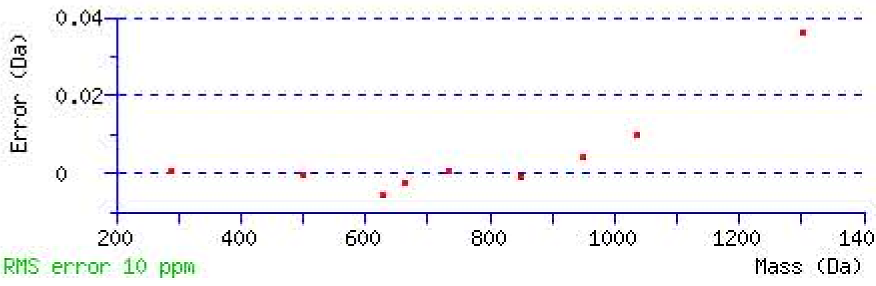
Match to Query 41871: 1474.726088 from(738.370320,2+) rtinseconds(1732) index(61237)
Title: Locus:1.1.1.2601.16 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

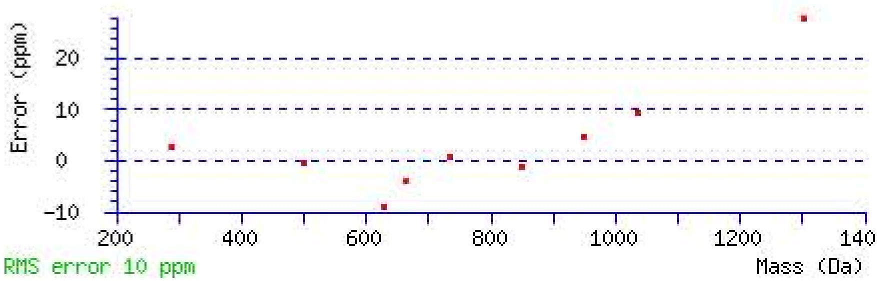
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1474.723831
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q1      : Biotin:Thermo-21345 (Q)
Ions Score: 51  Expect: 0.00016
Matches : 9/102 fragment ions using 14 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	440.232602	220.619939	423.206053	212.106664			Q							10
2	527.264630	264.135953	510.238081	255.622679	509.254065	255.130671	S	***1036.505800***	518.756538	1019.479251	510.243263	1018.495235	509.751255	9
3	**628.312309**	314.659793	611.285760	306.146518	610.301744	305.654510	T	***949.473772***	475.240524	932.447223	466.727249	931.463207	466.235241	8
4	742.355236	371.681256	725.328687	363.167982	724.344671	362.675974	N	***848.426093***	424.716684	831.399544	416.203410	830.415528	415.711402	7
5	813.392350	407.199813	796.365801	398.686538	795.381785	398.194530	A	***734.383166***	367.695221	717.356617	359.181946	716.372601	358.689938	6
6	976.455679	488.731477	959.429130	480.218203	958.445114	479.726195	Y	***663.346052***	332.176664	646.319503	323.663389	645.335487	323.171382	5
7	1073.508443	537.257860	1056.481894	528.744585	1055.497878	528.252577	P	***500.282723***	250.644999	483.256174	242.131725	482.272158	241.639717	4
8	1188.535386	594.771331	1171.508837	586.258057	1170.524821	585.766049	D	403.229959	202.118617	386.203410	193.605343	385.219394	193.113335	3
9	**1301.619450**	651.313363	1284.592901	642.800089	1283.608885	642.308080	L	***288.203016***	144.605146	271.176467	136.091871			2
10							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
51.2	1474.723831	0.002257	QSTNAYPDLR
16.7	1474.721161	0.004927	QSTHGERGHR
10.4	1474.741592	-0.015504	SSLEHGSDVYLLR
7.2	1474.744934	-0.018846	LSKEELIQNMDR
5.8	1474.746307	-0.020219	DAVQHERGPR
4.9	1474.745605	-0.019517	EPWEELFSIGLR
4.7	1474.731033	-0.004945	RGDGGKMAAAGALER
4.3	1474.727661	-0.001573	SSATLWNSPSRNR
2.8	1474.725189	0.000899	LDMNHGFVHHIR
1.7	1474.719788	0.006300	QQEELEQMRLR

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

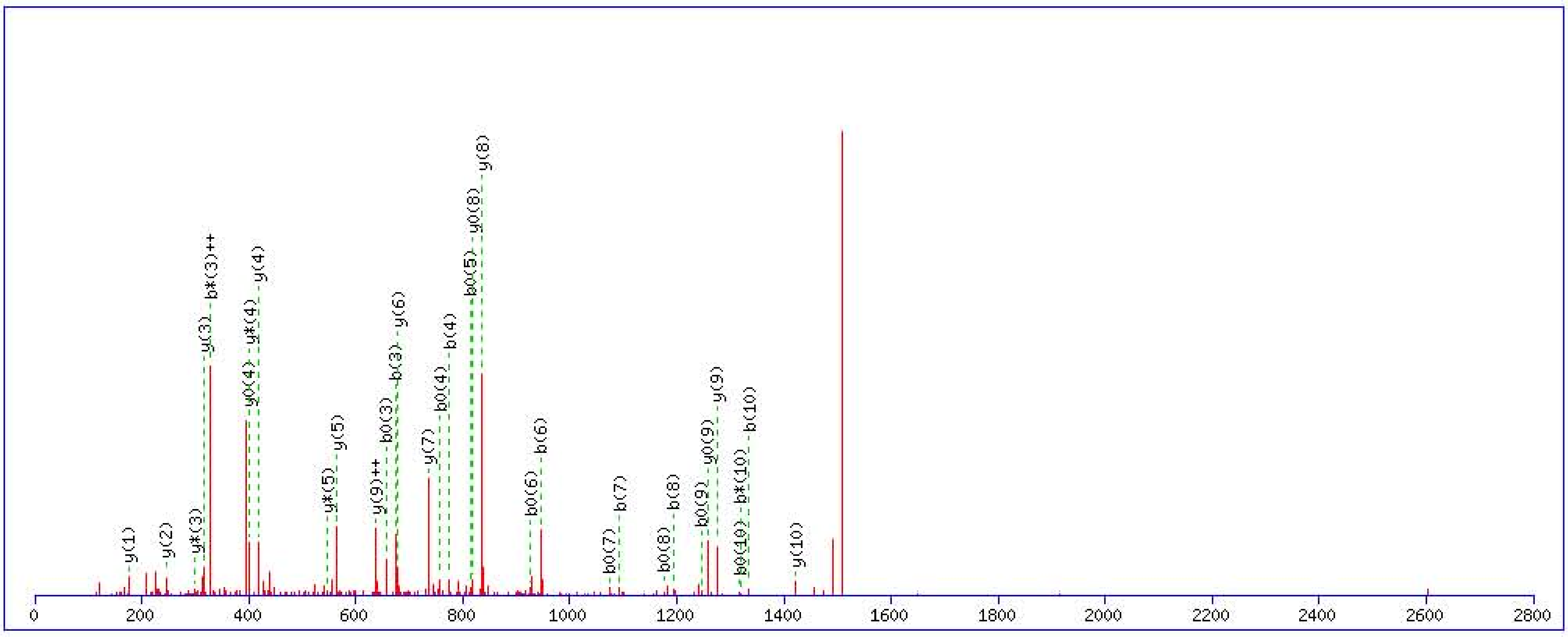
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **SFQTGLFTAAR**
Found in **PROS_HUMAN**, Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1

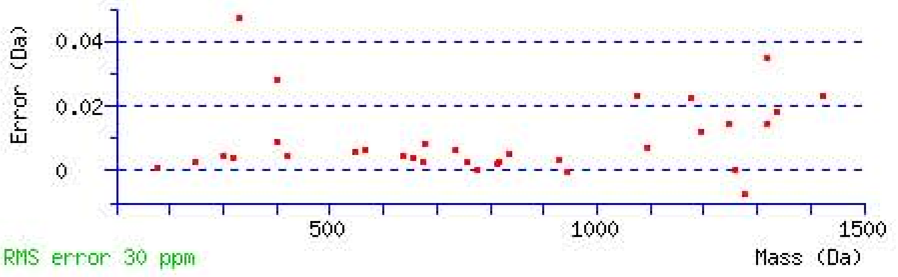
Match to Query 42922: 1508.784708 from(755.399630,2+) rtinseconds(2285) index(64947)
Title: Locus:1.1.1.2793.9 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

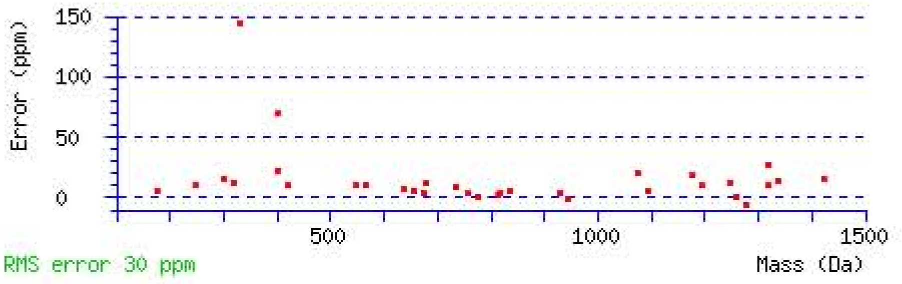
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2800 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1508.780975
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3 : Biotin:Thermo-21345 (Q)
Ions Score: 56 **Expect:** 2.7e-005
Matches : 33/110 fragment ions using 67 most intense peaks (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.039304	44.523290			70.028739	35.518008	S							11
2	235.107718	118.057497			217.097153	109.052214	F	*1422.756220*	711.881748	1405.729671	703.368474	1404.745655	702.876465	10
3	**674.333044**	337.670160	657.306495	329.156885	656.322479	328.664877	Q	*1275.687806*	638.347541	1258.661257	629.834267	1257.677241	629.342259	9
4	**775.380723**	388.194000	758.354174	379.680725	757.370158	379.188717	T	*836.462480*	418.734878	819.435931	410.221604	818.451915	409.729596	8
5	832.402187	416.704732	815.375638	408.191457	814.391622	407.699449	G	*735.414801*	368.211039	718.388252	359.697764	717.404236	359.205756	7
6	**945.486251**	473.246764	928.459702	464.733489	927.475686	464.241481	L	*678.393337*	339.700307	661.366788	331.187032	660.382772	330.695024	6
7	**1092.554665**	546.780971	1075.528116	538.267696	1074.544100	537.775688	F	*565.309273*	283.158275	548.282724	274.645000	547.298708	274.152992	5
8	**1193.602344**	597.304810	1176.575795	588.791536	1175.591779	588.299528	T	*418.240859*	209.624067	401.214310	201.110793	400.230294	200.618785	4
9	1264.639458	632.823367	1247.612909	624.310093	1246.628893	623.818085	A	*317.193180*	159.100228	300.166631	150.586953			3
10	**1335.676572**	668.341924	1318.650023	659.828650	1317.666007	659.336642	A	*246.156066*	123.581671	229.129517	115.068396			2
11							R	*175.118952*	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
56.4	1508.780975	0.003733	SFQTGLFTAAR
7.3	1508.762344	0.022364	EDFVPFTGEKKGR
6.2	1508.798721	-0.014013	SSYGVAAPVDFLRK
4.7	1508.776932	0.007776	LMGADSLQLFRSR
3.0	1508.780960	0.003748	TQPPPENLFR
1.9	1508.805939	-0.021231	SSPEHTTILRGGVR
0.8	1508.765671	0.019037	YDQALKIEMDKR
0.7	1508.762314	0.022394	EPAETLKPPEGWR
0.1	1508.765701	0.019007	TKPLSMLYVDNGR

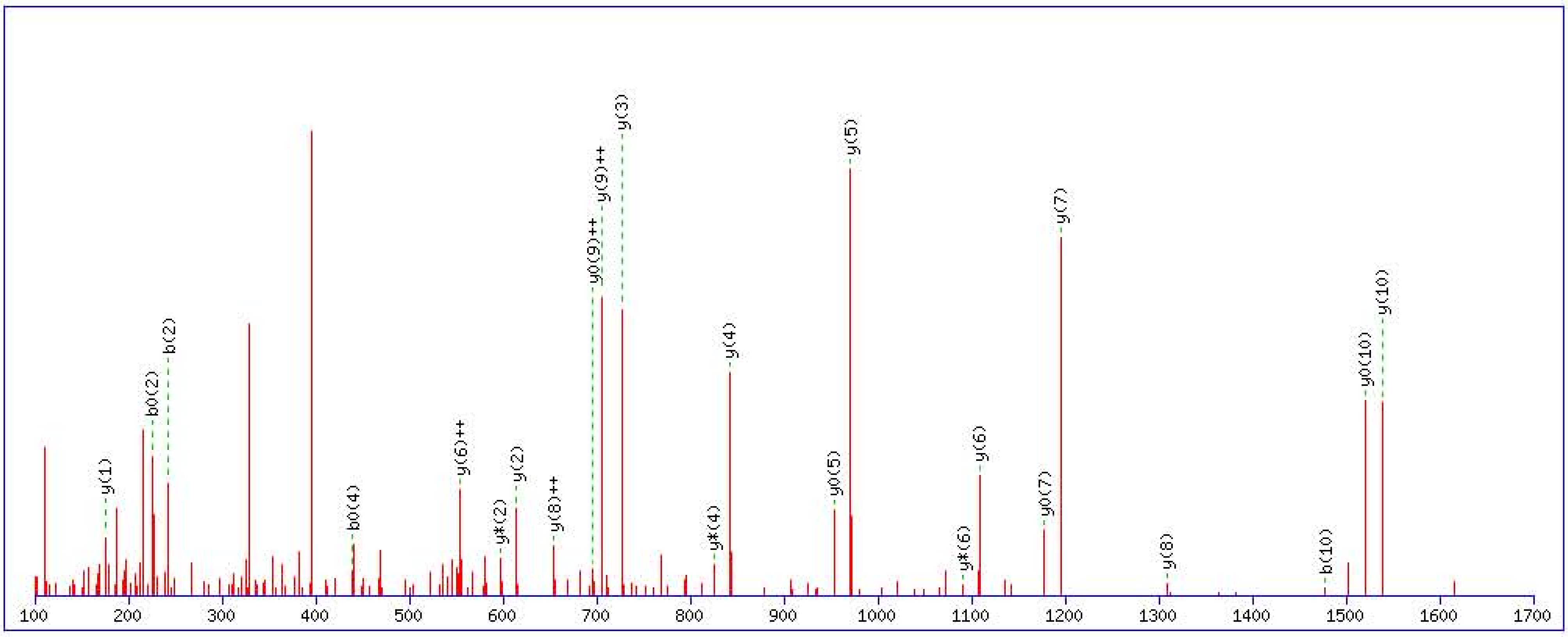
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IETISHEDLQR**
Found in **PROS_HUMAN**, Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1

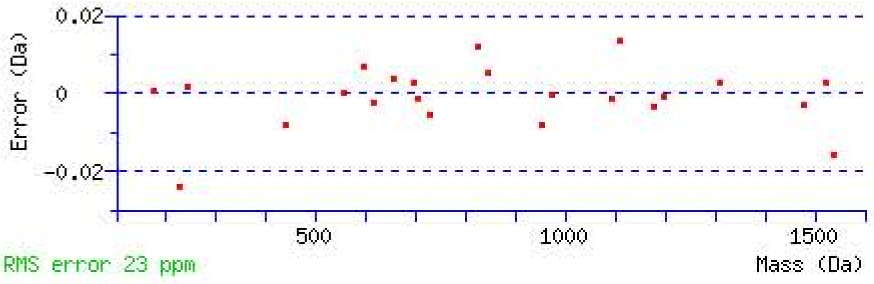
Match to Query 48396: 1650.833262 from(551.285030,3+) rtinseconds(1611) index(60348)
Title: Locus:1.1.1.2559.8 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

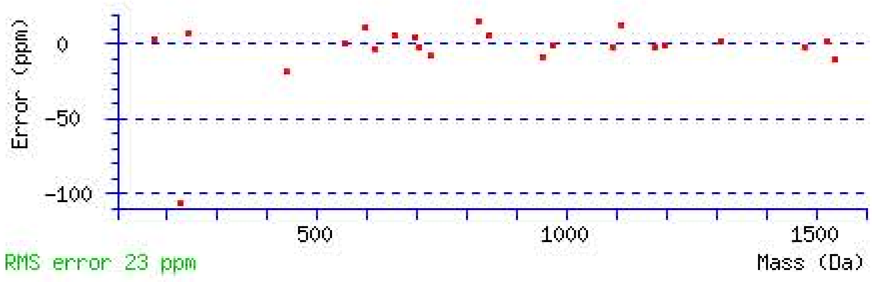
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1650.839920
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10     : Biotin:Thermo-21345 (Q)
Ions Score: 56  Expect: 5.9e-005
Matches : 23/94 fragment ions using 41 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							11
2	**243.133933**	122.070605			225.123368	113.065322	E	***1538.763154***	769.885215	1521.736605	761.371941	1520.752589	760.879933	10
3	344.181612	172.594444			326.171047	163.589162	T	1409.720561	705.363919	1392.694012	696.850644	1391.709996	696.358636	9
4	457.265676	229.136476			439.255111	220.131194	I	***1308.672882***	654.840079	1291.646333	646.326805	1290.662317	645.834797	8
5	544.297704	272.652490			526.287139	263.647208	S	***1195.588818***	598.298047	1178.562269	589.784773	1177.578253	589.292764	7
6	681.356616	341.181946			663.346051	332.176664	H	***1108.556790***	554.782033	1091.530241	546.268759	1090.546225	545.776751	6
7	810.399209	405.703243			792.388644	396.697960	E	***971.497878***	486.252577	954.471329	477.739303	953.487313	477.247295	5
8	925.426152	463.216714			907.415587	454.211432	D	***842.455285***	421.731281	825.428736	413.218006	824.444720	412.725998	4
9	1038.510216	519.758746			1020.499651	510.753463	L	***727.428342***	364.217809	710.401793	355.704535			3
10	**1477.735542**	739.371409	1460.708993	730.858135	1459.724977	730.366127	Q	***614.344278***	307.675777	597.317729	299.162503			2
11							R	***175.118952***	88.063114	158.092403	79.549839			1





NCBI **BLAST** search of IETISHEDLQR
(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	1650.839920	-0.006658	IETISHEDLQR
9.8	1650.833389	-0.000127	QQLEHIMATNR
8.0	1650.843765	-0.010503	TLQPSSQNTKAHPSR
4.2	1650.847305	-0.014043	LLFQELMSMSIAPR
3.0	1650.847305	-0.014043	LLFQELMSMSIAPR
2.6	1650.839935	-0.006673	MQLLKDVVGNDTYR
0.7	1650.822144	0.011118	QSALNTEKMYR
0.1	1650.821274	0.011988	ELSRLDKELDDYR

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

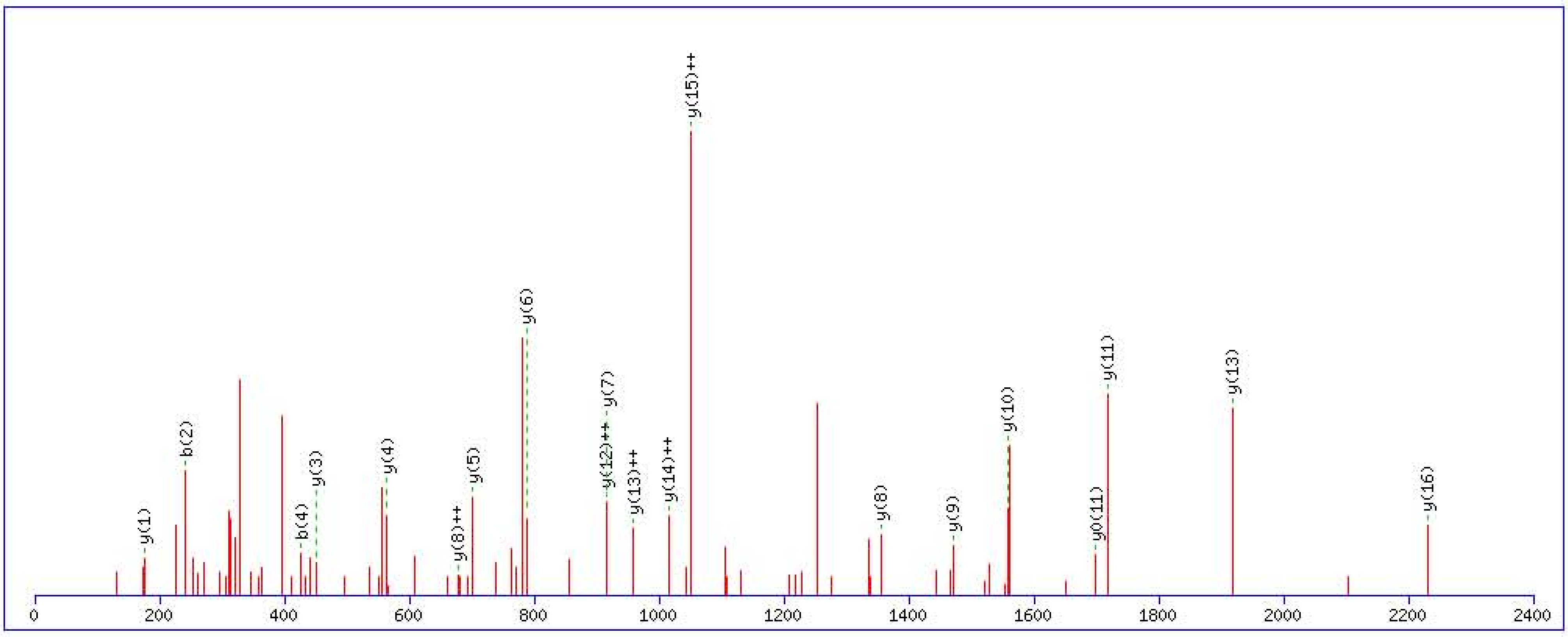
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQALSLCSDQQSHLEFR**
Found in **PROS_HUMAN**, Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1

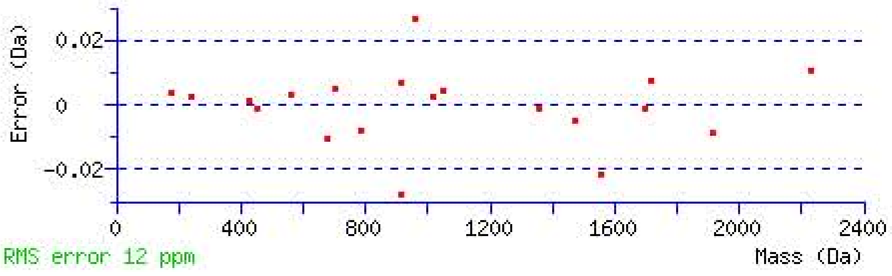
Match to Query 64932: 2342.160102 from(781.727310,3+) rtinseconds(2169) index(64226)
Title: Locus:1.1.1.2752.17 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

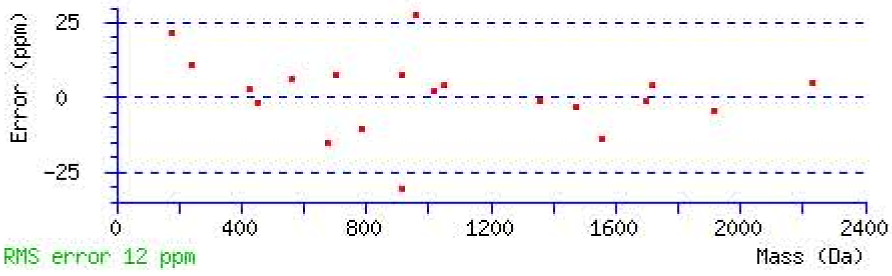
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2342.151108
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q10 : Biotin:Thermo-21345 (Q)
Ions Score: 74 **Expect:** 1.2e-006
Matches : 20/178 fragment ions using 36 most intense peaks (help)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.091340	57.549308					I							17
2	**242.149918**	121.578597	225.123369	113.065323			Q	***2230.074335***	1115.540805	2213.047786	1107.027531	2212.063770	1106.535523	16
3	313.187032	157.097154	296.160483	148.583879			A	2102.015757	1051.511516	2084.989208	1042.998242	2084.005192	1042.506234	15
4	**426.271096**	213.639186	409.244547	205.125912			L	2030.978643	1015.992959	2013.952094	1007.479685	2012.968078	1006.987677	14
5	513.303124	257.155200	496.276575	248.641926	495.292559	248.149918	S	***1917.894579***	959.450927	1900.868030	950.937653	1899.884014	950.445645	13
6	626.387188	313.697232	609.360639	305.183958	608.376623	304.691950	L	1830.862551	915.934913	1813.836002	907.421639	1812.851986	906.929631	12
7	786.417837	393.712557	769.391288	385.199282	768.407272	384.707274	C	***1717.778487***	859.392881	1700.751938	850.879607	1699.767922	850.387599	11
8	873.449865	437.228571	856.423316	428.715296	855.439300	428.223288	S	***1557.747838***	779.377557	1540.721289	770.864282	1539.737273	770.372274	10
9	988.476808	494.742042	971.450259	486.228768	970.466243	485.736760	D	***1470.715810***	735.861543	1453.689261	727.348268	1452.705245	726.856260	9
10	1427.702134	714.354705	1410.675585	705.841431	1409.691569	705.349422	Q	***1355.688867***	678.348071	1338.662318	669.834797	1337.678302	669.342789	8
11	1555.760712	778.383994	1538.734163	769.870720	1537.750147	769.378712	Q	***916.463541***	458.735408	899.436992	450.222134	898.452976	449.730126	7
12	1642.792740	821.900008	1625.766191	813.386734	1624.782175	812.894726	S	***788.404963***	394.706119	771.378414	386.192845	770.394398	385.700837	6
13	1779.851652	890.429464	1762.825103	881.916190	1761.841087	881.424182	H	***701.372935***	351.190105	684.346386	342.676831	683.362370	342.184823	5
14	1892.935716	946.971496	1875.909167	938.458222	1874.925151	937.966213	L	***564.314023***	282.660649	547.287474	274.147375	546.303458	273.655367	4
15	2021.978309	1011.492793	2004.951760	1002.979518	2003.967744	1002.487510	E	***451.229959***	226.118617	434.203410	217.605343	433.219394	217.113335	3
16	2169.046723	1085.026999	2152.020174	1076.513725	2151.036158	1076.021717	F	322.187366	161.597321	305.160817	153.084046			2
17							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
74.0	2342.151108	0.008994	IQALSLCSDQQSHLEFR
73.9	2342.151108	0.008994	IQALSLCSDQQSHLEFR
7.6	2342.151108	0.008994	IQALSLCSDQQSHLEFR

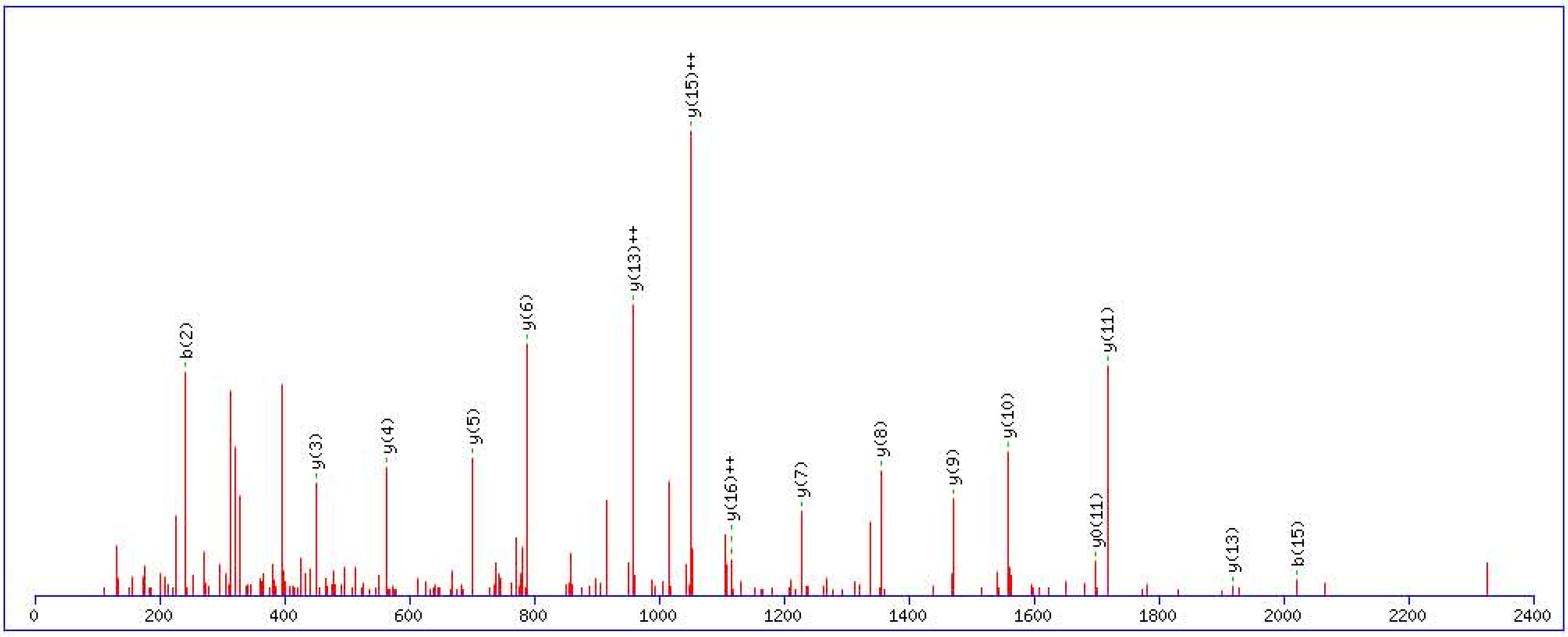
Mascot Search Results

Peptide View

MS/MS Fragmentation of **IQALSLCSDQQSHLEFR**
Found in **PROS_HUMAN**, Vitamin K-dependent protein S OS=Homo sapiens GN=PROS1 PE=1 SV=1

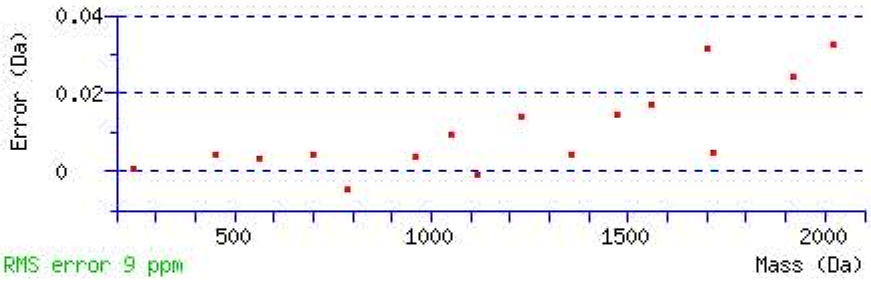
Match to Query 64933: 2342.160102 from(781.727310,3+) rtinseconds(2151) index(64080)
Title: Locus:1.1.1.2746.21 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

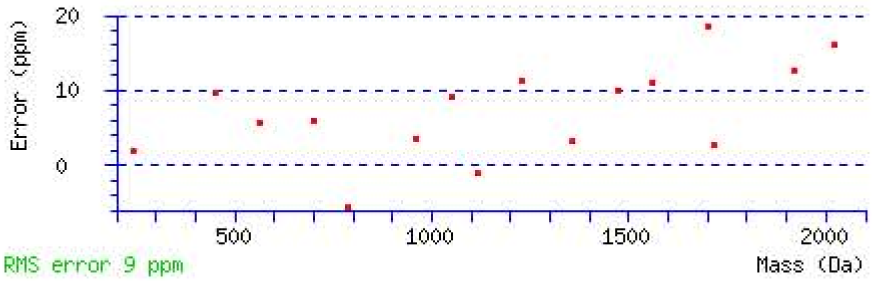
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 2400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 2342.151108
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q11     : Biotin:Thermo-21345 (Q)
Ions Score: 79  Expect: 3.6e-007
Matches : 16/178 fragment ions using 21 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.091340	57.549308					I							17
2	**242.149918**	121.578597	225.123369	113.065323			Q	2230.074335	1115.540805	2213.047786	1107.027531	2212.063770	1106.535523	16
3	313.187032	157.097154	296.160483	148.583879			A	2102.015757	1051.511516	2084.989208	1042.998242	2084.005192	1042.506234	15
4	426.271096	213.639186	409.244547	205.125912			L	2030.978643	1015.992959	2013.952094	1007.479685	2012.968078	1006.987677	14
5	513.303124	257.155200	496.276575	248.641926	495.292559	248.149918	S	***1917.894579***	959.450927	1900.868030	950.937653	1899.884014	950.445645	13
6	626.387188	313.697232	609.360639	305.183958	608.376623	304.691950	L	1830.862551	915.934913	1813.836002	907.421639	1812.851986	906.929631	12
7	786.417837	393.712557	769.391288	385.199282	768.407272	384.707274	C	***1717.778487***	859.392881	1700.751938	850.879607	1699.767922	850.387599	11
8	873.449865	437.228571	856.423316	428.715296	855.439300	428.223288	S	***1557.747838***	779.377557	1540.721289	770.864282	1539.737273	770.372274	10
9	988.476808	494.742042	971.450259	486.228768	970.466243	485.736760	D	***1470.715810***	735.861543	1453.689261	727.348268	1452.705245	726.856260	9
10	1116.535386	558.771331	1099.508837	550.258057	1098.524821	549.766049	Q	***1355.688867***	678.348071	1338.662318	669.834797	1337.678302	669.342789	8
11	1555.760712	778.383994	1538.734163	769.870720	1537.750147	769.378712	Q	***1227.630289***	614.318782	1210.603740	605.805508	1209.619724	605.313500	7
12	1642.792740	821.900008	1625.766191	813.386734	1624.782175	812.894726	S	***788.404963***	394.706119	771.378414	386.192845	770.394398	385.700837	6
13	1779.851652	890.429464	1762.825103	881.916190	1761.841087	881.424182	H	***701.372935***	351.190105	684.346386	342.676831	683.362370	342.184823	5
14	1892.935716	946.971496	1875.909167	938.458222	1874.925151	937.966213	L	***564.314023***	282.660649	547.287474	274.147375	546.303458	273.655367	4
15	**2021.978309**	1011.492793	2004.951760	1002.979518	2003.967744	1002.487510	E	***451.229959***	226.118617	434.203410	217.605343	433.219394	217.113335	3
16	2169.046723	1085.026999	2152.020174	1076.513725	2151.036158	1076.021717	F	322.187366	161.597321	305.160817	153.084046			2
17							R	175.118952	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
79.2	2342.151108	0.008994	IQALSLCSDQQSHLEFR
64.8	2342.151108	0.008994	IQALSLCSDQQSHLEFR

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

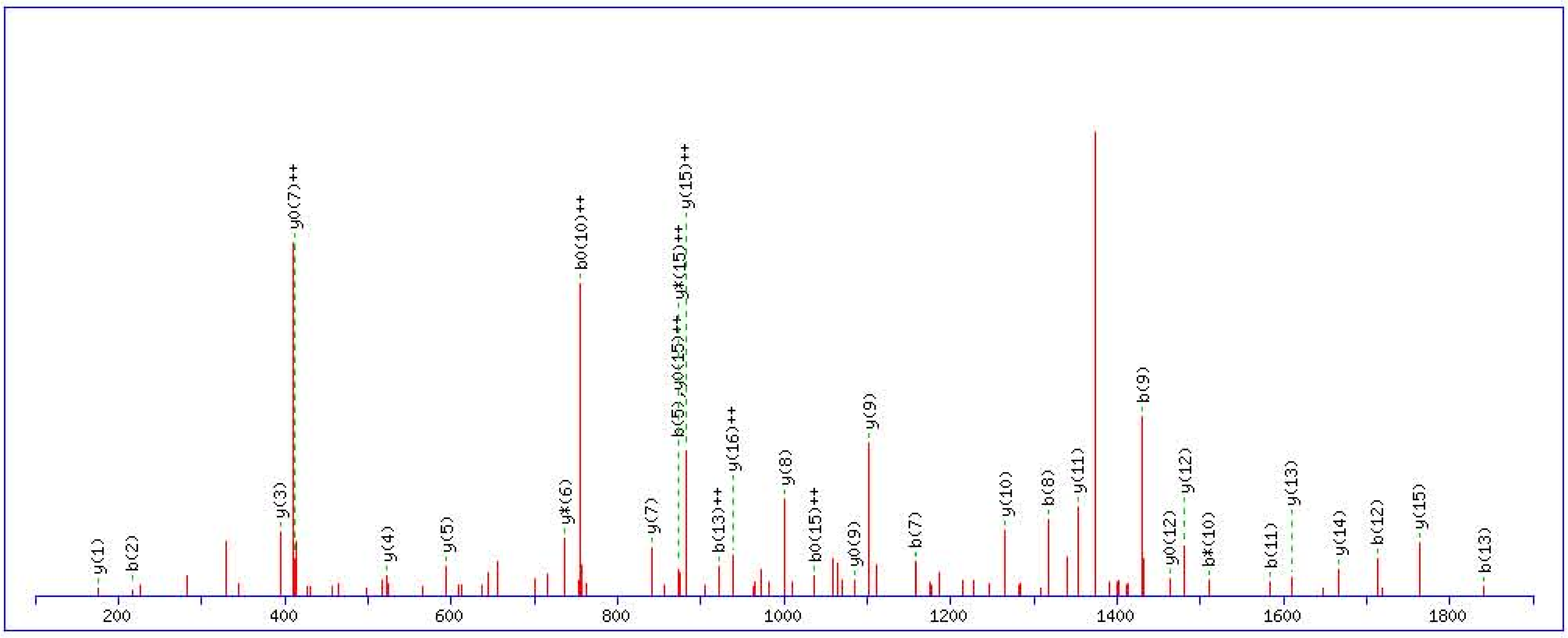
Mascot Search Results

Peptide View

MS/MS Fragmentation of **TDGCQHFCLPGQESYTCSCAQGYR**
Found in **PROZ_HUMAN**, Vitamin K-dependent protein Z OS=Homo sapiens GN=PROZ PE=1 SV=2

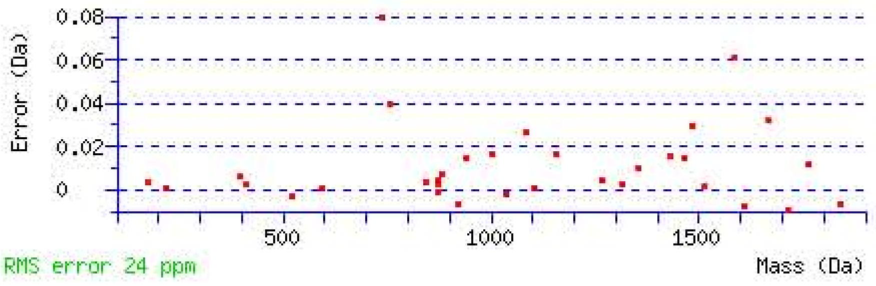
Match to Query 60152: 3192.310002 from(1065.110610,3+) rtinseconds(2031) index(63295)
Title: Locus:1.1.1.2704.18 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

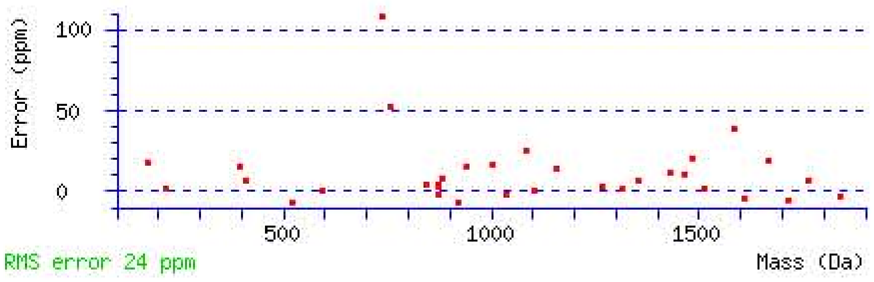
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 3192.298050
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 64  Expect: 4.1e-006
Matches : 33/256 fragment ions using 61 most intense peaks   (help)
```

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	102.054955	51.531116			84.044390	42.525833	T							24
2	***217.081898***	109.044587			199.071333	100.039304	D	3092.257619	1546.632447	3075.231070	1538.119173	3074.247054	1537.627165	23
3	274.103362	137.555319			256.092797	128.550037	G	2977.230676	1489.118976	2960.204127	1480.605701	2959.220111	1480.113693	22
4	434.134011	217.570644			416.123446	208.565361	C	2920.209212	1460.608244	2903.182663	1452.094969	2902.198647	1451.602961	21
5	***873.359337***	437.183307	856.332788	428.670032	855.348772	428.178024	Q	2760.178563	1380.592919	2743.152014	1372.079645	2742.167998	1371.587637	20
6	1010.418249	505.712763	993.391700	497.199488	992.407684	496.707480	H	2320.953237	1160.980256	2303.926688	1152.466982	2302.942672	1151.974974	19
7	***1157.486663***	579.246970	1140.460114	570.733695	1139.476098	570.241687	F	2183.894325	1092.450800	2166.867776	1083.937526	2165.883760	1083.445518	18
8	***1317.517312***	659.262294	1300.490763	650.749020	1299.506747	650.257012	C	2036.825911	1018.916594	2019.799362	1010.403319	2018.815346	1009.911311	17
9	***1430.601376***	715.804326	1413.574827	707.291052	1412.590811	706.799044	L	1876.795262	938.901269	1859.768713	930.387994	1858.784697	929.895986	16
10	1527.654140	764.330708	1510.627591	755.817434	1509.643575	755.325426	P	***1763.711198***	882.359237	1746.684649	873.845963	1745.700633	873.353954	15
11	***1584.675604***	792.841440	1567.649055	784.328166	1566.665039	783.836158	G	***1666.658434***	833.832855	1649.631885	825.319581	1648.647869	824.827572	14
12	***1712.734182***	856.870729	1695.707633	848.357455	1694.723617	847.865446	Q	***1609.636970***	805.322123	1592.610421	796.808849	1591.626405	796.316841	13
13	***1841.776775***	921.392026	1824.750226	912.878751	1823.766210	912.386743	E	***1481.578392***	741.292834	1464.551843	732.779560	1463.567827	732.287552	12
14	1928.808803	964.908040	1911.782254	956.394765	1910.798238	955.902757	S	***1352.535799***	676.771538	1335.509250	668.258263	1334.525234	667.766255	11
15	2091.872132	1046.439704	2074.845583	1037.926429	2073.861567	1037.434421	Y	***1265.503771***	633.255523	1248.477222	624.742249	1247.493206	624.250241	10
16	2192.919811	1096.963543	2175.893262	1088.450269	2174.909246	1087.958261	T	***1102.440442***	551.723859	1085.413893	543.210584	1084.429877	542.718576	9
17	2352.950460	1176.978868	2335.923911	1168.465593	2334.939895	1167.973585	C	***1001.392763***	501.200020	984.366214	492.686745	983.382198	492.194737	8
18	2439.982488	1220.494882	2422.955939	1211.981607	2421.971923	1211.489599	S	***841.362114***	421.184695	824.335565	412.671421	823.351549	412.179413	7
19	2600.013137	1300.510206	2582.986588	1291.996932	2582.002572	1291.504924	C	754.330086	377.668681	737.303537	369.155407			6
20	2671.050251	1336.028763	2654.023702	1327.515489	2653.039686	1327.023481	A	***594.299437***	297.653357	577.272888	289.140082			5
21	2799.108829	1400.058052	2782.082280	1391.544778	2781.098264	1391.052770	Q	***523.262323***	262.134800	506.235774	253.621525			4
22	2856.130293	1428.568784	2839.103744	1420.055510	2838.119728	1419.563502	G	***395.203745***	198.105510	378.177196	189.592236			3
23	3019.193622	1510.100449	3002.167073	1501.587174	3001.183057	1501.095166	Y	338.182281	169.594778	321.155732	161.081504			2
24							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
64.1	3192.298050	0.011952	TDGCQHFCLPGQESYTCSCAQGYR
27.1	3192.298050	0.011952	TDGCQHFCLPGQESYTCSCAQGYR

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

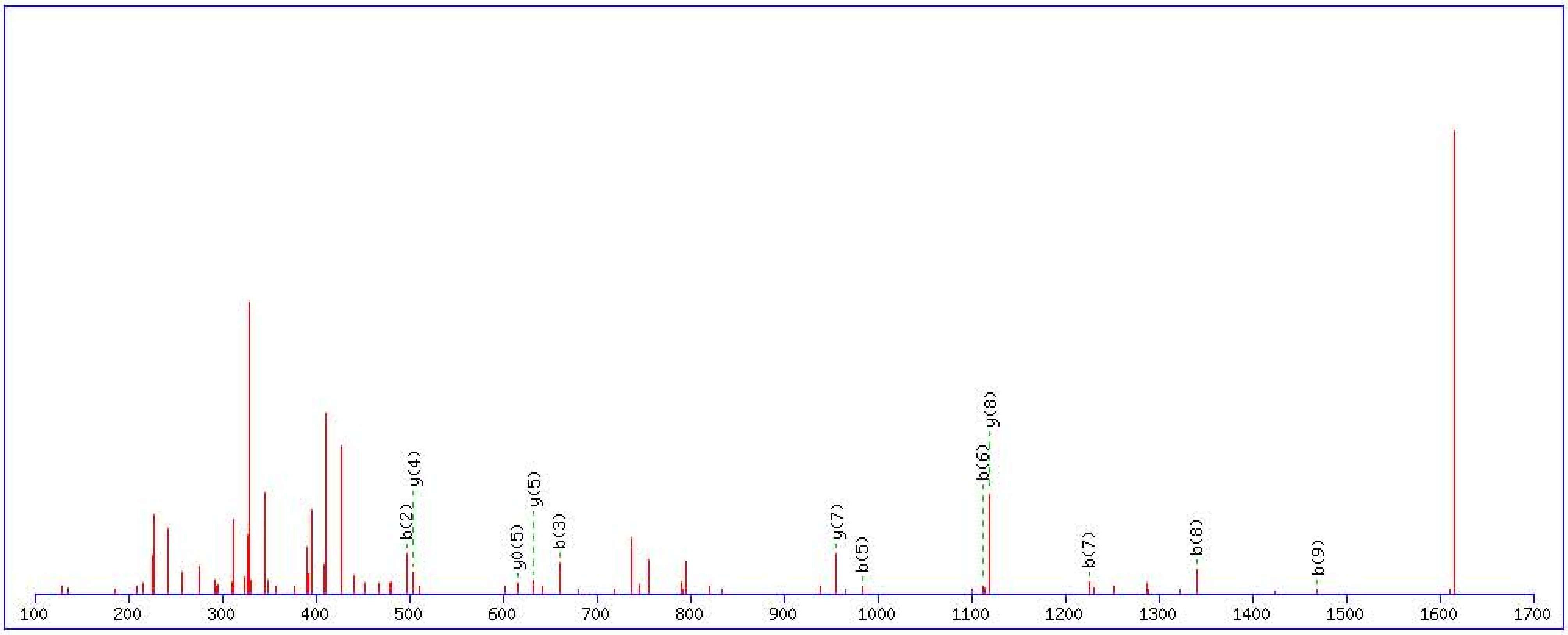
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GQYCYELDEK**
Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

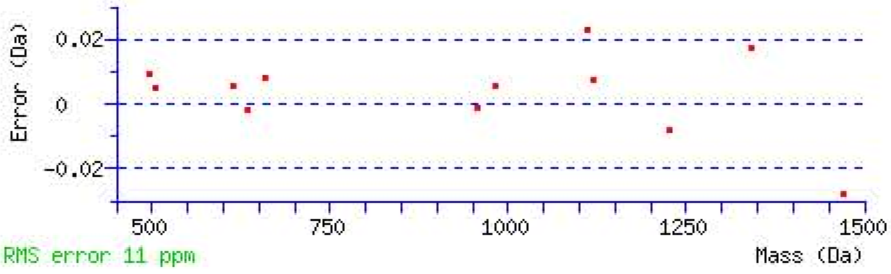
Match to Query 46570: 1614.710908 from(808.362730,2+) rtinseconds(1857) index(62021)
Title: Locus:1.1.1.2644.25 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

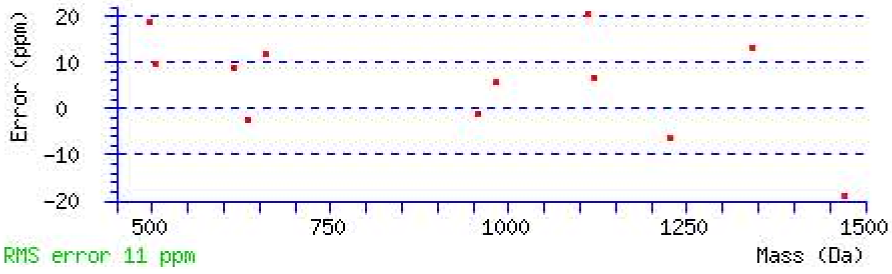
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1614.705795
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q2      : Biotin:Thermo-21345 (Q)
Ions Score: 30  Expect: 0.0039
Matches : 12/94 fragment ions using 26 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							10
2	***497.254066***	249.130671	480.227517	240.617397			Q	1558.691630	779.849453	1541.665081	771.336179	1540.681065	770.844171	9
3	***660.317395***	330.662336	643.290846	322.149061			Y	**1119.466304**	560.236790	1102.439755	551.723516	1101.455739	551.231508	8
4	820.348044	410.677660	803.321495	402.164386			C	**956.402975**	478.705126	939.376426	470.191851	938.392410	469.699843	7
5	***983.411373***	492.209325	966.384824	483.696050			Y	796.372326	398.689801	779.345777	390.176527	778.361761	389.684519	6
6	***1112.453966***	556.730621	1095.427417	548.217347	1094.443401	547.725339	E	**633.308997**	317.158137	616.282448	308.644862	615.298432	308.152854	5
7	***1225.538030***	613.272653	1208.511481	604.759379	1207.527465	604.267371	L	**504.266404**	252.636840	487.239855	244.123566	486.255839	243.631558	4
8	***1340.564973***	670.786125	1323.538424	662.272850	1322.554408	661.780842	D	391.182340	196.094808	374.155791	187.581534	373.171775	187.089526	3
9	***1469.607566***	735.307421	1452.581017	726.794147	1451.597001	726.302139	E	276.155397	138.581337	259.128848	130.068062	258.144832	129.576054	2
10							K	147.112804	74.060040	130.086255	65.546765			1



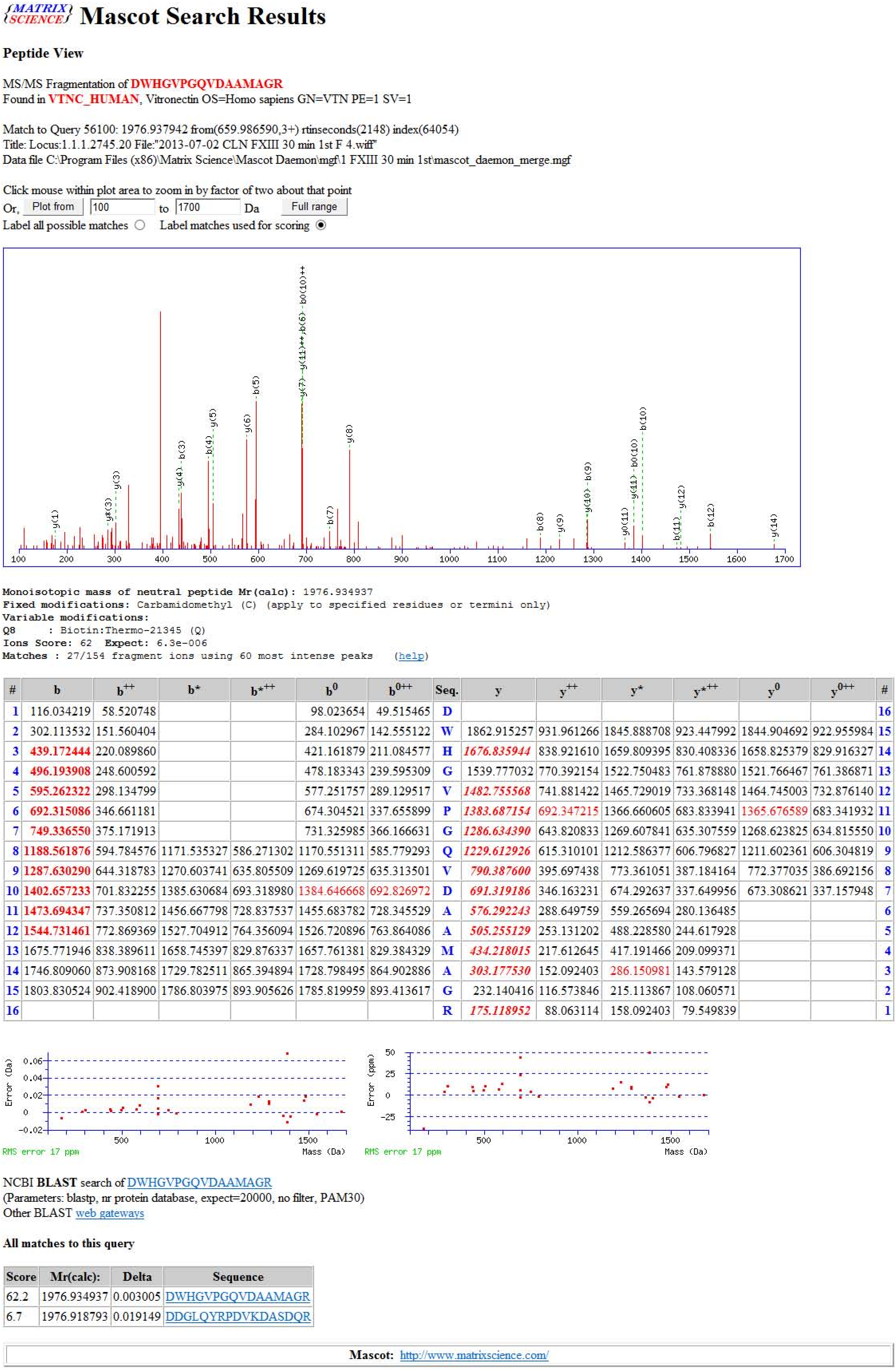


NCBI **BLAST** search of GQYCYELDEK
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST web gateways

All matches to this query

Score	Mr(calc):	Delta	Sequence
30.3	1614.705795	0.005113	GQYCYELDEK

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



Mascot Search Results

Peptide View

MS/MS Fragmentation of **DWHGVPGQVDAAMAGR**
Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

Match to Query 56100: 1976.937942 from(659.986590,3+) rtinseconds(2148) index(64054)
Title: Locus:1.1.1.2745.20 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●

```
Monoisotopic mass of neutral peptide Mr(calc): 1976.934937
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q8      : Biotin:Thermo-21345 (Q)
Ions Score: 62  Expect: 6.3e-006
Matches : 27/154 fragment ions using 60 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.034219	58.520748			98.023654	49.515465	D							16
2	302.113532	151.560404			284.102967	142.555122	W	1862.915257	931.961266	1845.888708	923.447992	1844.904692	922.955984	15
3	**439.172444**	220.089860			421.161879	211.084577	H	***1676.835944***	838.921610	1659.809395	830.408336	1658.825379	829.916327	14
4	**496.193908**	248.600592			478.183343	239.595309	G	1539.777032	770.392154	1522.750483	761.878880	1521.766467	761.386871	13
5	**595.262322**	298.134799			577.251757	289.129517	V	***1482.755568***	741.881422	1465.729019	733.368148	1464.745003	732.876140	12
6	**692.315086**	346.661181			674.304521	337.655899	P	***1383.687154***	692.347215	1366.660605	683.833941	1365.676589	683.341932	11
7	**749.336550**	375.171913			731.325985	366.166631	G	***1286.634390***	643.820833	1269.607841	635.307559	1268.623825	634.815550	10
8	**1188.561876**	594.784576	1171.535327	586.271302	1170.551311	585.779293	Q	***1229.612926***	615.310101	1212.586377	606.796827	1211.602361	606.304819	9
9	**1287.630290**	644.318783	1270.603741	635.805509	1269.619725	635.313501	V	***790.387600***	395.697438	773.361051	387.184164	772.377035	386.692156	8
10	**1402.657233**	701.832255	1385.630684	693.318980	1384.646668	692.826972	D	***691.319186***	346.163231	674.292637	337.649956	673.308621	337.157948	7
11	**1473.694347**	737.350812	1456.667798	728.837537	1455.683782	728.345529	A	***576.292243***	288.649759	559.265694	280.136485			6
12	**1544.731461**	772.869369	1527.704912	764.356094	1526.720896	763.864086	A	***505.255129***	253.131202	488.228580	244.617928			5
13	1675.771946	838.389611	1658.745397	829.876337	1657.761381	829.384329	M	***434.218015***	217.612645	417.191466	209.099371			4
14	1746.809060	873.908168	1729.782511	865.394894	1728.798495	864.902886	A	***303.177530***	152.092403	286.150981	143.579128			3
15	1803.830524	902.418900	1786.803975	893.905626	1785.819959	893.413617	G	232.140416	116.573846	215.113867	108.060571			2
16							R	***175.118952***	88.063114	158.092403	79.549839			1

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

All matches to this query

Score	Mr(calc):	Delta	Sequence
62.2	1976.934937	0.003005	DWHGVPGQVDAAMAGR
6.7	1976.918793	0.019149	DDGLQYRPDVKDASDQR

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

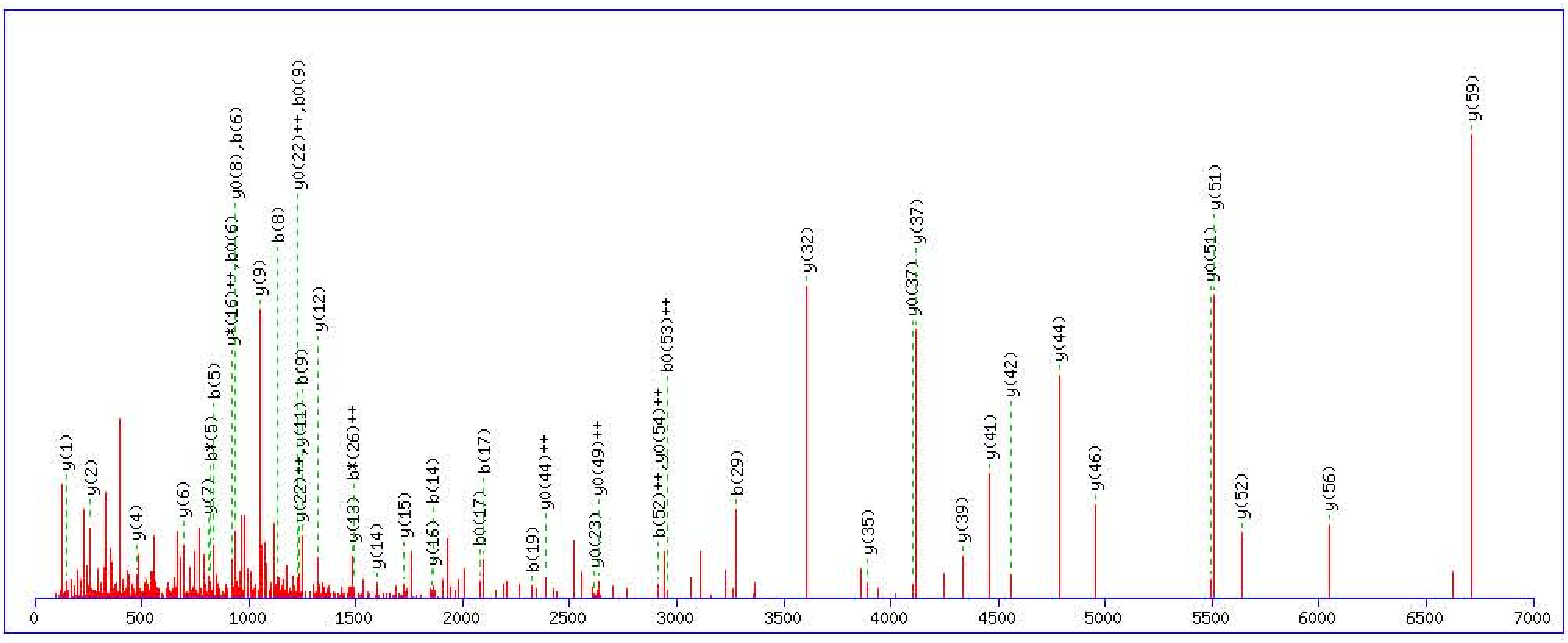
Mascot Search Results

Peptide View

MS/MS Fragmentation of **GNPEQTPVLKPEEEAPAPEVGASKPEGIDSRPETLHPGRPQPPAEEELCSGKPFDAFTDLK**
Found in **VTNC_HUMAN**, Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1

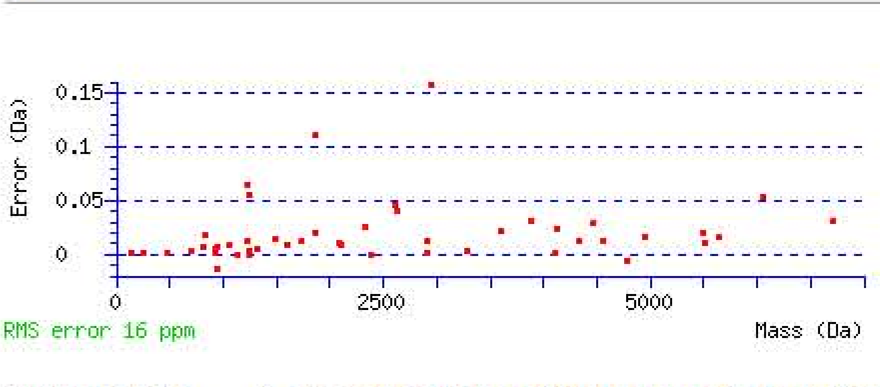
Match to Query 90933: 6883.416568 from(984.352500,7+) rtinseconds(2071) index(63551)
Title: Locus:1.1.1.2718.18 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

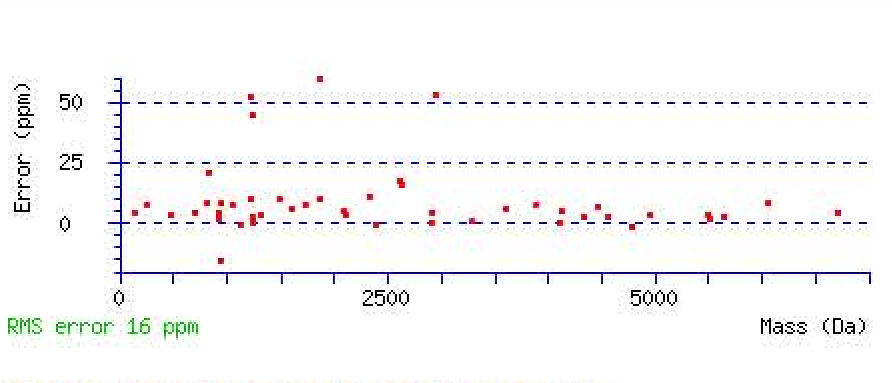
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 0 to 7000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 6883.374893
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q5      : Biotin:Thermo-21345 (Q)
Ions Score: 68  Expect: 1.7e-006
Matches : 49/708 fragment ions using 131 most intense peaks   (help)
```

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	58.028740	29.518008					G							61
2	172.071667	86.539471	155.045118	78.026197			N	6827.360757	3414.184017	6810.334208	3405.670742	6809.350192	3405.178734	60
3	269.124431	135.065854	252.097882	126.552579			P	***6713.317830***	3357.162553	6696.291281	3348.649279	6695.307265	3348.157271	59
4	398.167024	199.587150	381.140475	191.073876	380.156459	190.581868	E	6616.265066	3308.636171	6599.238517	3300.122897	6598.254501	3299.630889	58
5	**837.392350**	419.199813	820.365801	410.686539	819.381785	410.194531	Q	6487.222473	3244.114875	6470.195924	3235.601600	6469.211908	3235.109592	57
6	**938.440029**	469.723653	921.413480	461.210378	920.429464	460.718370	T	***6047.997147***	3024.502212	6030.970598	3015.988937	6029.986582	3015.496929	56
7	1035.492793	518.250035	1018.466244	509.736760	1017.482228	509.244752	P	5946.949468	2973.978372	5929.922919	2965.465098	5928.938903	2964.973090	55
8	**1134.561207**	567.784242	1117.534658	559.270967	1116.550642	558.778959	V	5849.896704	2925.451990	5832.870155	2916.938716	5831.886139	2916.446708	54
9	**1247.645271**	624.326274	1230.618722	615.812999	1229.634706	615.320991	L	5750.828290	2875.917783	5733.801741	2867.404509	5732.817725	2866.912501	53
10	1375.740234	688.373755	1358.713685	679.860481	1357.729669	679.368473	K	***5637.744226***	2819.375751	5620.717677	2810.862477	5619.733661	2810.370469	52
11	1472.792998	736.900137	1455.766449	728.386863	1454.782433	727.894855	P	***5509.649263***	2755.328270	5492.622714	2746.814995	5491.638698	2746.322987	51
12	1601.835591	801.421434	1584.809042	792.908159	1583.825026	792.416151	E	5412.596499	2706.801888	5395.569950	2698.288613	5394.585934	2697.796605	50
13	1730.878184	865.942730	1713.851635	857.429456	1712.867619	856.937448	E	5283.553906	2642.280591	5266.527357	2633.767317	5265.543341	2633.275309	49
14	**1859.920777**	930.464027	1842.894228	921.950752	1841.910212	921.458744	E	5154.511313	2577.759295	5137.484764	2569.246020	5136.500748	2568.754012	48
15	1930.957891	965.982584	1913.931342	957.469309	1912.947326	956.977301	A	5025.468720	2513.237998	5008.442171	2504.724724	5007.458155	2504.232716	47
16	2028.010655	1014.508966	2010.984106	1005.995691	2010.000090	1005.503683	P	***4954.431606***	2477.719441	4937.405057	2469.206167	4936.421041	2468.714159	46
17	**2099.047769**	1050.027523	2082.021220	1041.514248	2081.037204	1041.022240	A	4857.378842	2429.193059	4840.352293	2420.679785	4839.368277	2420.187777	45
18	2196.100533	1098.553905	2179.073984	1090.040630	2178.089968	1089.548622	P	***4786.341728***	2393.674502	4769.315179	2385.161228	4768.331163	2384.669220	44
19	**2325.143126**	1163.075201	2308.116577	1154.561927	2307.132561	1154.069919	E	4689.288964	2345.148120	4672.262415	2336.634846	4671.278399	2336.142838	43
20	2424.211540	1212.609408	2407.184991	1204.096134	2406.200975	1203.604126	V	***4560.246371***	2280.626824	4543.219822	2272.113549	4542.235806	2271.621541	42
21	2481.233004	1241.120140	2464.206455	1232.606865	2463.222439	1232.114858	G	***4461.177957***	2231.092617	4444.151408	2222.579342	4443.167392	2222.087334	41
22	2552.270118	1276.638697	2535.243569	1268.125423	2534.259553	1267.633415	A	4404.156493	2202.581885	4387.129944	2194.068610	4386.145928	2193.576602	40
23	2639.302146	1320.154711	2622.275597	1311.641437	2621.291581	1311.149429	S	***4333.119379***	2167.063328	4316.092830	2158.550053	4315.108814	2158.058045	39
24	2767.397109	1384.202193	2750.370560	1375.688918	2749.386544	1375.196910	K	4246.087351	2123.547314	4229.060802	2115.034039	4228.076786	2114.542031	38
25	2864.449873	1432.728575	2847.423324	1424.215300	2846.439308	1423.723292	P	***4117.992388***	2059.499832	4100.965839	2050.986558	4099.981823	2050.494550	37
26	2993.492466	1497.249871	2976.465917	1488.736597	2975.481901	1488.244589	E	4020.939624	2010.973450	4003.913075	2002.460176	4002.929059	2001.968168	36
27	3050.513930	1525.760603	3033.487381	1517.247329	3032.503365	1516.755321	G	***3891.897031***	1946.452154	3874.870482	1937.938879	3873.886466	1937.446871	35
28	3163.597994	1582.302635	3146.571445	1573.789361	3145.587429	1573.297353	I	3834.875567	1917.941422	3817.849018	1909.428147	3816.865002	1908.936139	34
29	**3278.624937**	1639.816107	3261.598388	1631.302832	3260.614372	1630.810824	D	3721.791503	1861.399390	3704.764954	1852.886115	3703.780938	1852.394107	33
30	3365.656965	1683.332121	3348.630416	1674.818846	3347.646400	1674.326838	S	***3606.764560***	1803.885918	3589.738011	1795.372644	3588.753995	1794.880636	32
31	3521.758076	1761.382676	3504.731527	1752.869402	3503.747511	1752.377394	R	3519.732532	1760.369904	3502.705983	1751.856630	3501.721967	1751.364622	31
32	3618.810840	1809.909058	3601.784291	1801.395784	3600.800275	1800.903776	P	3363.631421	1682.319349	3346.604872	1673.806074	3345.620856	1673.314066	30
33	3747.853433	1874.430355	3730.826884	1865.917080	3729.842868	1865.425072	E	3266.578657	1633.792967	3249.552108	1625.279692	3248.568092	1624.787684	29
34	3848.901112	1924.954194	3831.874563	1916.440920	3830.890547	1915.948912	T	3137.536064	1569.271670	3120.509515	1560.758396	3119.525499	1560.266388	28
35	3961.985176	1981.496226	3944.958627	1972.982952	3943.974611	1972.490944	L	3036.488385	1518.747831	3019.461836	1510.234556	3018.477820	1509.742548	27
36	4099.044088	2050.025682	4082.017539	2041.512408	4081.033523	2041.020400	H	2923.404321	1462.205799	2906.377772	1453.692524	2905.393756	1453.200516	26
37	4196.096852	2098.552064	4179.070303	2090.038790	4178.086287	2089.546782	P	2786.345409	1393.676343	2769.318860	1385.163068	2768.334844	1384.671060	25
38	4253.118316	2127.062796	4236.091767	2118.549522	4235.107751	2118.057514	G	2689.292645	1345.149961	2672.266096	1336.636686	2671.282080	1336.144678	24
39	4409.219427	2205.113352	4392.192878	2196.600077	4391.208862	2196.108069	R	2632.271181	1316.639229	2615.244632	1308.125954	2614.260616	1307.633946	23
40	4506.272191	2253.639734	4489.245642	2245.126459	4488.261626	2244.634451	P	2476.170070	1238.588673	2459.143521	1230.075399	2458.159505	1229.583391	22
41	4634.330769	2317.669023	4617.304220	2309.155748	4616.320204	2308.663740	Q	2379.117306	1190.062291	2362.090757	1181.549017	2361.106741	1181.057009	21
42	4731.383533	2366.195405	4714.356984	2357.682130	4713.372968	2357.190122	P	2251.058728	1126.033002	2234.032179	1117.519728	2233.048163	1117.027720	20
43	4828.436297	2414.721787	4811.409748	2406.208512	4810.425732	2405.716504	P	2154.005964	1077.506620	2136.979415	1068.993346	2135.995399	1068.501338	19
44	4899.473411	2450.240344	4882.446862	2441.727069	4881.462846	2441.235061	A	2056.953200	1028.980238	2039.926651	1020.466964	2038.942635	1019.974956	18
45	5028.516004	2514.761640	5011.489455	2506.248366	5010.505439	2505.756358	E	1985.916086	993.461681	1968.889537	984.948407	1967.905521	984.456399	17
46	5157.558597	2579.282937	5140.532048	2570.769662	5139.548032	2570.277654	E	***1856.873493***	928.940385	1839.846944	920.427110	1838.862928	919.935102	16
47	5286.601190	2643.804233	5269.574641	2635.290959	5268.590625	2634.798951	E	***1727.830900***	864.419088	1710.804351	855.905814	1709.820335	855.413806	15
48	5399.685254	2700.346265	5382.658705	2691.832991	5381.674689	2691.340983	L	***1598.788307***	799.897792	1581.761758	791.384517	1580.777742	790.892509	14
49	5559.715903	2780.361590	5542.689354	2771.848315	5541.705338	2771.356307	C	***1485.704243***	743.355760	1468.677694	734.842485	1467.693678	734.350477	13
50	5646.747931	2823.877604	5629.721382	2815.364329	5628.737366	2814.872321	S	***1325.673594***	663.340435	1308.647045	654.827161	1307.663029	654.335153	12
51	5703.769395	2852.388336	5686.742846	2843.875061	5685.758830	2843.383053	G	***1238.641566***	619.824421	1221.615017	611.311147	1220.631001	610.819139	11
52	5831.864358	2916.435817	5814.837809	2907.922543	5813.853793	2907.430535	K	1181.620102	591.313689	1164.593553	582.800415	1163.609537	582.308407	10
53	5928.917122	2964.962199	5911.890573	2956.448925	5910.906557	2955.956917	P	***1053.525139***	527.266208	1036.498590	518.752933	1035.514574	518.260925	9
54	6075.985536	3038.496406	6058.958987	3029.983132	6057.974971	3029.491124	F	956.472375	478.739826	939.445826	470.226551	938.461810	469.734543	8
55	6191.012479	3096.009878	6173.985930	3087.496603	6173.001914	3087.004595	D	***809.403961***	405.205619	792.377412	396.692344	791.393396	396.200336	7
56	6262.049593	3131.528435	6245.023044	3123.015160	6244.039028	3122.523152	A	***694.377018***	347.692147	677.350469	339.178873	676.366453	338.686865	6
57	6409.118007	3205.062642	6392.091458	3196.549367	6391.107442	3196.057359	F	623.339904	312.173590	606.313355	303.660316	605.329339	303.168308	5
58	6510.165686	3255.586481	6493.139137	3247.073207	6492.155121	3246.581199	T	***476.271490***	238.639383	459.244941	230.126109	458.260925	229.634101	4
59	6625.192629	3313.099953	6608.166080	3304.586678	6607.182064	3304.094670	D	375.223811	188.115543	358.197262	179.602269	357.213246	179.110261	3
60	6738.276693	3369.641985	6721.250144	3361.128710	6720.266128	3360.636702	L	***260.196868***	130.602072	243.170319	122.088798			2
61							K	***147.112804***	74.060040	130.086255	65.546766			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
68.5	6883.374893	0.041675	GNPEQTPVLKPEEEAPAPEVGASKPEGIDSRPETLHPGRPQPPAEEELCSGKPFDAFTDLK
3.5	6883.374893	0.041675	GNPEQTPVLKPEEEAPAPEVGASKPEGIDSRPETLHPGRPQPPAEEELCSGKPFDAFTDLK

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

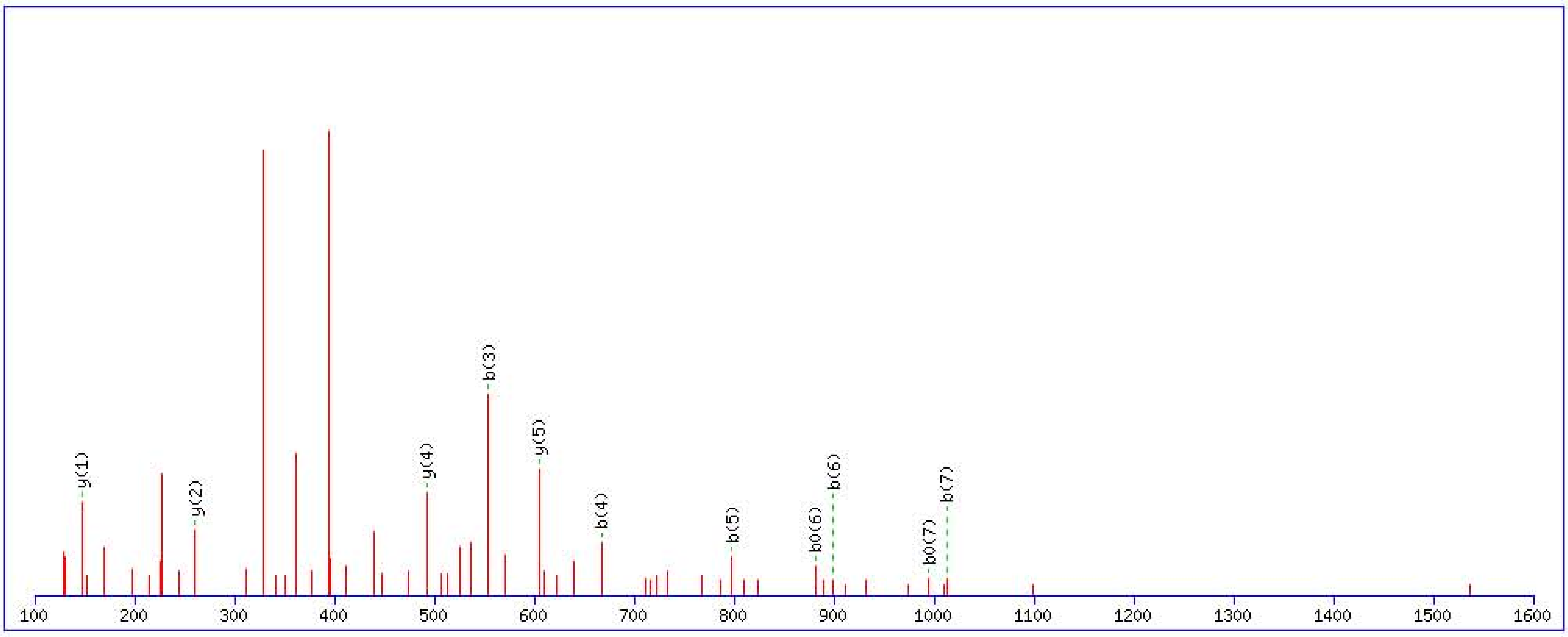
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **GGQIMTLK**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

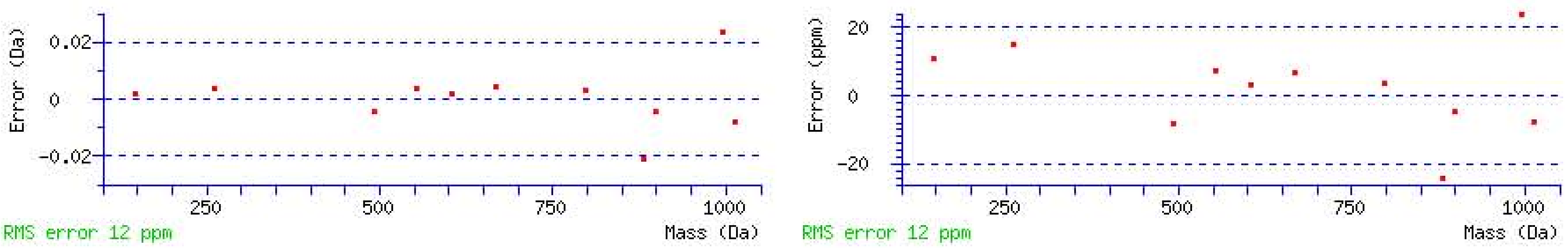
Match to Query 29910: 1157.629348 from(579.821950,2+) rtinseconds(1896) index(62320)
Title: Locus:1.1.1.2658.16 File:"2013-07-02 CLN FXIII 30 min 1st F 4.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1157.630066
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q3      : Biotin:Thermo-21345 (Q)
Ions Score: 26  Expect: 0.054
Matches : 11/66 fragment ions using 19 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.028740	29.518008					G							8
2	115.050204	58.028740					G	1101.615886	551.311581	1084.589337	542.798307	1083.605321	542.306299	7
3	***554.275530***	277.641403	537.248981	269.128129			Q	1044.594422	522.800849	1027.567873	514.287575	1026.583857	513.795567	6
4	***667.359594***	334.183435	650.333045	325.670161			I	**605.369096**	303.188186	588.342547	294.674912	587.358531	294.182904	5
5	***798.400079***	399.703678	781.373530	391.190403			M	**492.285032**	246.646154	475.258483	238.132880	474.274467	237.640872	4
6	***899.447758***	450.227517	882.421209	441.714243	881.437193	441.222235	T	361.244547	181.125912	344.217998	172.612637	343.233982	172.120629	3
7	***1012.531822***	506.769549	995.505273	498.256275	994.521257	497.764267	L	**260.196868**	130.602072	243.170319	122.088798			2
8							K	**147.112804**	74.060040	130.086255	65.546765			1



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

All matches to this query

Score	Mr(calc):	Delta	Sequence
26.3	1157.630066	-0.000718	GGQIMTLK
12.0	1157.630051	-0.000703	QLSQMLK
8.8	1157.629196	0.000152	EPQTITQLTK
7.7	1157.640411	-0.011063	AQQLLSSGNLK
7.2	1157.619293	0.010055	TNFEGPPRLK
6.9	1157.622665	0.006683	QRTDSLK
6.7	1157.630051	-0.000703	QLSQMLK
6.6	1157.630051	-0.000703	QAGAMLLK
5.6	1157.640411	-0.011063	SPGKNSSIQLK
5.5	1157.630051	-0.000703	QIKSMLQ

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

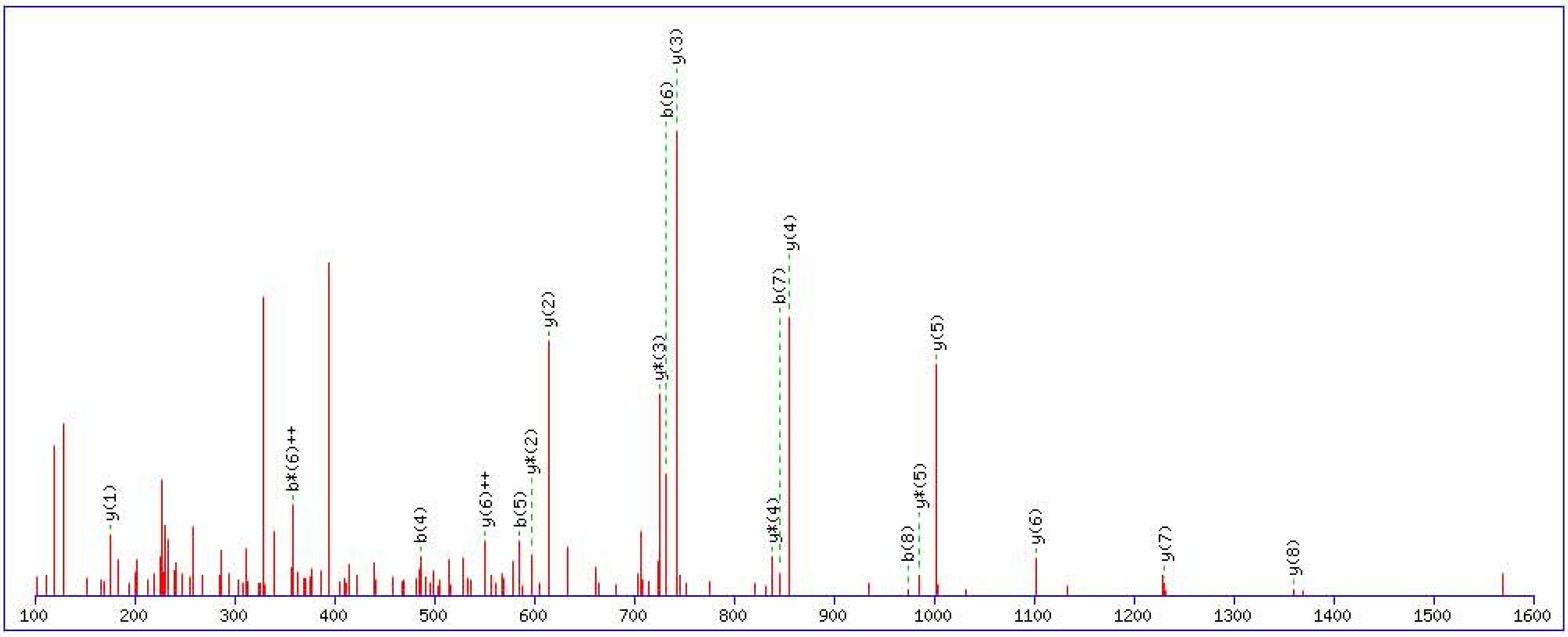
{MATRIX SCIENCE} Mascot Search Results

Peptide View

MS/MS Fragmentation of **VKEEVFIQQR**
Found in **VWF_HUMAN**, von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4

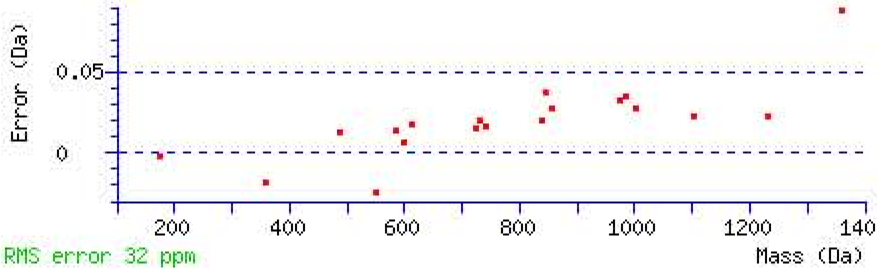
Match to Query 45382: 1585.887972 from(529.636600,3+) rtinseconds(1753) index(42147)
Title: Locus:1.1.1.2639.10 File:"2013-07-02 CLN FXIII 30 min 1st F 3.wiff"
Data file C:\Program Files (x86)\Matrix Science\Mascot Daemon\mgf\1 FXIII 30 min 1st\mascot_daemon_merge.mgf

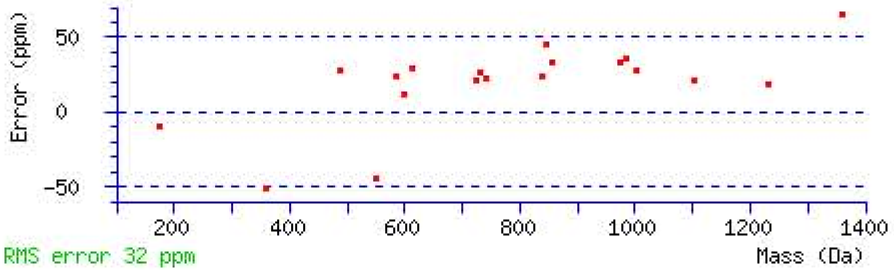
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●



```
Monoisotopic mass of neutral peptide Mr(calc): 1585.865021
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Q9      : Biotin:Thermo-21345 (Q)
Ions Score: 40  Expect: 0.00032
Matches : 19/90 fragment ions using 39 most intense peaks   (help)
```

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.075690	50.541483					V							10
2	228.170653	114.588965	211.144104	106.075690			K	1487.803897	744.405587	1470.777348	735.892312	1469.793332	735.400304	9
3	357.213246	179.110261	340.186697	170.596987	339.202681	170.104979	E	***1359.708934***	680.358105	1342.682385	671.844831	1341.698369	671.352823	8
4	**486.255839**	243.631558	469.229290	235.118283	468.245274	234.626275	E	***1230.666341***	615.836809	1213.639792	607.323534	1212.655776	606.831526	7
5	**585.324253**	293.165765	568.297704	284.652490	567.313688	284.160482	V	***1101.623748***	551.315512	1084.597199	542.802238			6
6	**732.392667**	366.699972	715.366118	358.186697	714.382102	357.694689	F	***1002.555334***	501.781305	985.528785	493.268031			5
7	**845.476731**	423.242004	828.450182	414.728729	827.466166	414.236721	I	***855.486920***	428.247098	838.460371	419.733824			4
8	**973.535309**	487.271293	956.508760	478.758018	955.524744	478.266010	Q	***742.402856***	371.705066	725.376307	363.191792			3
9	1412.760635	706.883956	1395.734086	698.370681	1394.750070	697.878673	Q	***614.344278***	307.675777	597.317729	299.162503			2
10							R	***175.118952***	88.063114	158.092403	79.549839			1





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

All matches to this query

Score	Mr(calc):	Delta	Sequence
40.3	1585.865021	0.022951	VKEEVFIQQR
27.4	1585.865021	0.022951	VKEEVFIQQR
2.9	1585.867493	0.020479	KVKELSIQIEDER
2.3	1585.886154	0.001818	QTKLGCSKVLVPEK
1.2	1585.893524	-0.005552	QDLIKSLAMLK

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